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ASPA 25th Congress Book of Abstract

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Italian Journal of Animal Science

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and Production Association

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Italian Journal of Animal Science

The *Italian Journal of Animal Science* is an international peer-reviewed open access journal publishing original scientific papers, reviews and short communications.
The journal serves as essential reading for animal scientists, technicians and all those who research animal production.
The journal encourages submissions of international relevance on the following subjects:

- Animal derived food quality and safety
- Animal genetics and breeding
- Aquaculture, poultry, companion and wild game animals
- Livestock systems, management and environment
- Non-ruminant or ruminant nutrition and feeding
- Production physiology and functional biology of farmed, companions and wild game animals.
- Animal behavior
- Animal welfare
- In vitro studies that have an application to farmed livestock

Manuscripts must address topics based on research at molecular, cellular, organ, whole animal and production system levels. Manuscripts discussing milk or meat analysis and compositions must show a direct link to either livestock production system, product quality, animal feeding/nutrition, animal genetics or breeding. Manuscripts describing laboratory animal models will be considered where the study highlights a potential benefit to farmed livestock.

Submissions discussing epidemiology, parasitology, infective diseases, food-borne diseases do not fit with the aims and scope of the journal.

Meeting reviews, book reviews and conference supplements are also published, as well as news and guidelines from the Animal Science and Production Association (ASPA). We welcome submissions from ASPA members and non-members alike.

Article publishing charge

The standard article publishing charge (APC) for this journal is US$900 / €795 / £690. Depending on your location, these charges may be subject to local taxes.
For members of the Animal Science and Production Association, the publication fee is US$450 / €400 / £345. Depending on your location, these charges may be subject to local taxes. There are no submission charges for this journal.

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Italian Journal of Animal Science

volume 24, supplement 1, 2025

ASPA 26th Congress

Turin (ITALY), June 17 –20, 2025

Guest Editors

Giustino Gaspa, Joana Maria Venda Da Graca Nery, Laura Gasco & Manuela Renna*

Table of Contents

Main Lectures XX

Oral Communications XX

Posters XX

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ASPA 26th Congress

Turin (ITALY), June 17–20, 2025

#ASPA2025

ASPA 26th Congress Book of Abstract

The 26th Congress of the Animal Science and Production Association

"Innovations in animal sciences: shaping the way for a sustainable future" is under patronage of Loghi Patrocini

Turin (ITALY),

June 17 –20, 2025

Venue

Campus SAMEV (Scuola di Agraria e medicina Veterinaria)
Largo Braccini 2, Grugliasco (TO)– ITALY

26th Congress

ASPA25

17 / 20 June 2025 | Turin, Italy

Association for Science and Animal Production

INNOVATIONS IN ANIMAL SCIENCES: SHAPING THE WAY FOR A SUSTAINABLE FUTURE

Campus SAMEV
(Scuola di Agraria e Medicina Veterinaria)
Largo Braccini 2, Grugliasco (TO) – ITALY

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The 26th Congress of the Animal Science and Production Association (ASPA) will be hosted in Grugliasco (TO) by the University of Turin. Turin hosted the first edition of the ASPA congress in 1974 and another one in 2005. The theme of the event "Innovations in Animal Sciences: Shaping the Way for a Sustainable Future," offers a unique platform for researchers, professionals, policymakers, and students from around the world to meet and address some of the most pressing challenges facing animal science today.

In an era characterized by huge technological advancements, environmental concerns, and relevant societal expectations, the role of animal science is more critical than ever. Sustainability is no longer just a goal—it is a strict requirement. The congress theme reflects a forward-looking approach, emphasizing how innovation can serve as a catalyst for change in ensuring the long-term viability and ethical integrity of animal agriculture.

A total of 539 scientific contributions have been received by the scientific committee: 350 theatre and 189 poster presentations, respectively. This great result confirms the relevant increasing trend of attendance and scientific contribution for the ASPA congress highlighted in the past editions. The scientific program will be organized into 59 thematic sessions covering 12 main topics. The program will include also 3 plenary lectures, 14 keynote speakers and a round table.

Over the course of the event, participants will explore groundbreaking research and practical applications across a wide range of topics, including precision livestock farming, animal welfare, nutrition, genetics, climate resilience, and the circular economy. These discussions are designed not only to showcase scientific progress, but also to foster interdisciplinary collaboration and inspire actionable strategies.

I wish to thank all people that have worked for the organization and the management of this event. In particular, I wish to thank prof. Paola Sacchi, president of the organizing committee, and prof. Laura Gasco, president of the scientific committee and all the components of the two committees. A special thank also to prof. Marcello Mele, Editor in Chief of the Italian Journal of Animal Science, for having contributed to the edition of the proceedings.

Nicolò Pietro Paolo Macciotta
ASPA President



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PROGRAM AT A GLANCE

Tuesday, 17th June 2025

	Campus Samev	Room VENARIA + RACCONIGI
12:00-18:00	Registration	
14.30		Opening Ceremony
14:30-14:45		Introduction to the 26th ASPA Congress **Nicolò Pietro Paolo Macciotta**, ASPA President
14:45-15:00		The 26th ASPA Congress in Torino **Paola Sacchi**, President of the ASPA 2025 Congress
15:00-15:30		"Memory is our future" **Christian Greco**, Director of Museo Egizio, Torino
15:30-16:00		"From "necessary evil" to "FeedEconomy" how livestock production has changed from the 19th century to date" **Ivo Zoccarato**, former Director of the Department of Agricultural, Forest and Food Sciences, University of Torino
16:00-16:30		"Guiding principles of AI: application in animal husbandry" **Andrea Rosati**, Secretary of EAAP - European Federation of Animal Science
16:30-16:45		Discussion
16:45-17:15		Coffee break
17:15-18:45		Round Table "The food that will come: a dialogue between science and ethics" **Giuseppe Pulina**, University of Sassari - **Alessandro Bertero**, University of Torino - **Maurizio Balistreri**, University of Tuscia Moderator: **Piero Bianucci**, science writer and journalist
18:45-20:00	Welcome cocktail (Campus SAMEV)	

Wednesday, 18th June 2025

	ROOM VENARIA	ROOM RACCONIGI	ROOM STUPINIGI
09:00-10:45	Genetics: **SUSTAINABILITY AND FUTURE PERSPECTIVES OF ANIMAL BREEDING** *Session 01*	Food Quality: **PORK AND POULTRY MEAT** *Session 02*	Alternative Proteins: **YELLOW MEALWORM REARING AND NUTRITION** *Session 03* *Invited speaker:* Karol Barragan Fonseca
10:45-11:15	Coffee Break and poster session		
11:15-13:00	Genetics: **SUSTAINABILITY AND FUTURE PERSPECTIVES OF ANIMAL BREEDING** *Session 08*	Food Quality: **EGGS AND OTHER FOODS** *Session 09*	Alternative Proteins: **YELLOW MEALWORM AND BLACK SOLDIER FLY REARING AND NUTRITION** *Session 10*
13:00-14:00	Lunch		
14:00-15:30	Genetics: **OMICS-BASED APPROACHES** *Session 15* *Invited speaker:* Augustin Blasco	Food Quality: **SHEEP MEAT** Session 16	Alternative Proteins: **INSECT REARING AND USE AS ANIMAL FEED** *Session 17*
15:30-16:00	Coffee Break and poster session		
16:00-17:30	Genetics: **GENOMIC APPLICATIONS FOR BREEDING** *Session 22*	Food Quality: **BEEF** *Session 23* *Invited speaker:* Nigel Scollan	Alternative Proteins: **INSECTS AND ALTERNATIVE PROTEINS AS ANIMAL FEEDS** *Session 24*
20.00	**Typical Dinner** (Murazzi del Po, restaurant Capodoglio)		

ROOM VALENTINO	ROOM MANDRIA	ROOM AGLIÈ	ROOM CARIGNANO
Sustainability: **FEEDING STRATEGIES** *Session 04*	Genetics: **POULTRY AND RABBIT** *Session 05*	Physiology and Reproduction: **RUMINANT PHYSIOLOGY** Session 06	Production Systems: **EFFICIENCY, HEALTH, AND SUSTAINABILITY** *Session 07* *Invited speaker:* **Emma Baxter**
Coffee Break and poster session			
Sustainability **ENTERIC EMISSIONS** *Session 11* *Invited speaker:* **Jacopo Bacenetti**	Ruminant Nutrition: **NUTRITION AND FEEDING BEHAVIOUR OF DAIRY COWS** *Session 12*	Physiology and Reproduction: **MISCELLANY** *Session 13* *Invited speaker:* **Christopher Harold Knight**	Production Systems: **CHALLENGES AND INNOVATIONS** *Session 14*
Lunch			
Sustainability: **EXTENSIVE SYSTEMS** *Session 18*	Ruminant Nutrition: **IN VITRO STUDIES AND NEW FEEDSTUFFS** *Session 19*	Welfare, Health and Behaviour: **NEW APPROACHES TO POULTRY MANAGEMENT** *Session 20*	Production Systems: **PRODUCTION STRATEGIES AND QUALITY TRAITS** *Session 21*
Coffee Break and poster session			
Sustainability: **SUSTAINABLE SUPPLY CHAINS** *Session 25*	Ruminant Nutrition: **IN VITRO METHODOLOGY AND MICROPLASTICS** *Session 26*	Welfare, Health and Behaviour: **INNOVATIONS AND PERCEPTIONS FOR SUSTAINABLE PRODUCTION** *Session 27*	Production Systems: **TRADITIONAL PRACTICES, ECONOMICS, AND WELFARE** *Session 28*
Typical Dinner (Murazzi del Po, restaurant Capodoglio)			

Thursday, 19th June 2025

	ROOM VENARIA	ROOM RACCONIGI	ROOM STUPINIGI
08:30-10:15	Genetics: **GENOMIC APPLICATIONS FOR BIODIVERSITY I** *Session 29* Vazyme	Ruminant Nutrition: **INSECTS, FATTY ACIDS AND MICROBIOTA** *Session 30* *Invited speaker:* Pablo Gutierrez Toral ferrero	Welfare, Health and Behaviour: **FROM PREVENTION TO THERAPY, UDDER HEALTH AND INNOVATIONS IN ZOOTECHNICS** *Session 31*
10:15-10:45	Coffee Break and poster session		
10:45-12:30	Genetics: **GENETIC SOLUTIONS FOR HEAT STRESS** *Session 36* *Invited speaker:* Christian Maltecca	Ruminant Nutrition: **SMALL RUMINANTS AND BY-PRODUCT USE** *Session 37*	Welfare, Health and Behaviour: **ADVANCES IN CATTLE AND BUFFALOES MANAGEMENT** *Session 38*
12:30-13:30	Lunch		
13:30-15:00	Genetics: **BREEDING FOR MASTITIS RESISTANCE** *Session 42*		Welfare, Health and Behaviour: **EXPLORING THE COW-CALF RELATIONSHIP** *Session 44* *Invited speaker:* Isabelle Veissier
15:00-15:30	Coffee Break and poster session		
15:00-19:00	**ASPA Assembly**		
20.00	**Social Dinner** (Palazzina di Caccia di Stupinigi) Transfers for Stupinigi will leave at 7.30 pm from the Campus of Grugliasco		

ROOM VALENTINO	ROOM MANDRIA	ROOM AGLIÈ	ROOM CARIGNANO
Monogastric Nutrition: **POULTRY** *Session 32* *Invited speaker:* Doug Korver SILVATEAM	Precision Farming: **COMPUTER VISION AND IMAGING TECHNOLOGIES** *Session 33*	Food Quality: **COW MILK QUALITY AND AUTHENTICATION** *Session 34*	Genetics: **GENOMIC STRATEGIES FOR FITNESS TRAITS** *Session 35* Vazyme
Coffee Break and poster session			
Monogastric Nutrition: **SWINE I** *Session 39* SILVATEAM	Precision Farming: **DATA-DRIVEN DAIRY MANAGEMENT** *Session 40* *Invited speaker:* Marco Bovo	Food Quality: **DAIRY PRODUCT QUALITY AND CHEESEMAKING PROPERTIES** *Session 41*	
Lunch			
Sustainability: **SUSTAINABLE STRATEGIES** *Session 45*	Precision Farming: **GRAZING SYSTEMS AND PASTURE MONITORING** *Session 46*	Food Quality: **SHEEP, GOAT AND BUFFALO MILK QUALITY** *Session 47*	Ruminant Nutrition: **MINOR SPECIES AND FORAGE QUALITY** *Session 43*
Coffee Break and poster session			

Social Dinner (Palazzina di Caccia di Stupinigi)
Transfers for Stupinigi will leave at 7.30 pm from the Campus of Grugliasco

Friday,
20th June 2025

	ROOM VENARIA	ROOM RACCONIGI	ROOM STUPINIGI
09:00-10:45	Genetics: **GENOMIC APPLICATIONS FOR BIODIVERSITY II** *Session 48*		Aquaculture: **MARINE SPECIES** *Session 50*
10:45-11:15	Coffee Break and poster session		
11:15-12:45	Genetics: **GENETIC STRATEGIES FOR ECONOMIC TRAITS** *Session 54*		**Aquaculture:** MISCELLANY *Session 56* *Invited speaker:* **Fabio Brambilla**
12:45-13:15	Awards and Closing Cerimony		

ROOM VALENTINO	ROOM MANDRIA	ROOM AGLIÈ	ROOM CARIGNANO
Monogastric Nutrition: **SWINE II** *Session 51*	Precision Farming: **SENSORS FOR BEHAVIOURAL MONITORING** *Session 52* MSD Animal Health	Companion Animals: **NUTRITION AND HEALTH** *Session 53* *Invited speaker:* Pier Paolo Mussa	Welfare, Health and Behaviour: **INNOVATIONS AND SUSTAINABILITY IN HORSES MANAGEMENT** *Session 49* *Invited speaker:* Ingrid Vervuert
Coffee Break and poster session			
Monogastric Nutrition: **RABBIT, POULTRY AND DONKEY** *Session 57*	Precision Farming: **INNOVATION AND SUSTAINABILITY IN LIVESTOCK** *Session 58* MSD Animal Health	Companion Animals: **GENETICS AND GENOMICS** *Session 59*	Welfare, Health and Behaviour: **BEEKEEPING, HORSES AND PIGS FARMING** *Session 55*
Awards and Closing Cerimony			

PROGRAM

Tuesday,
17th June 2025

Room Venaria + Room Racconigi

14.30	Opening Ceremony
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18.45	Welcome cocktail (Campus SAMEV)

PROGRAM

Wednesday,
18th June 2025

Room Venaria | Session 01

Genetics:
SUSTAINABILITY AND FUTURE PERSPECTIVES OF ANIMAL BREEDING

Sponsored by Fedana
Chairs: Cassandro Martino – Negro Alessio

9:00 Gomez Mayra, Landi Vincenzo, Cimmino Roberta, Rossi Dario, Zullo Gianluigi, Di Vuolo Gabriele, Neglia Gianluca, Biffani Stefano — 444
Imputation accuracy of missing genotypes in Italian Mediterranean Buffalo using 50K SNP chip

9:15 Layton Jonathan, Benzoni Lorenzo, Finocchiaro Raffaella, Van Kaam Jan-Thijs, Tiezzi Francesco, Marusi Maurizio, Cassandro Martino — 060
Genomic evaluation of methane emissions and feed efficiency in Holstein bulls

9:30 Biscarini Filippo, Cesarani Alberto, Mastrangelo Salvatore, Finocchiaro Raffaella, Van Kaam Jan-Thijs, Benzoni Lorenzo, Ciampolini Roberta, Cassandro Martino — 512
An enviromics approach to modelling GxE interactions in dairy cattle

9:45 Ferrari Valentina, Marusi Maurizio, Galluzzo Ferdinando, Cassandro Martino — 084
Calf survival in Italian Holstein: first results and services for farmers

10:00 Graziani Silvia, Cipolat-Gotet Claudio, Finocchiaro Raffaella, Tiezzi Francesco, Pieramati Camillo, Sarti Francesca Maria, Cassandro Martino — 409
Total and differential somatic cell traits in Italian Jersey Dairy Cattle Breed: preliminary results

10:15 Colombi Daniele, Bonifazi Renzo, Perini Francesco, Sbarra Fiorella, Quaglia Andrea, Calus Mario, Lasagna Emiliano — 105
Multi-breed genomic predictions for average daily gain in three Italian beef cattle breeds

10:30 Cendron Filippo, Perini Francesco, Lasagna Emiliano, Baruschello Maristella, Cassandro Martino, Penasa Mauro — 034
Genetic diversity of goose (Anser anser) and guinea fowl (Numida meleagris) local breeds using whole genome sequencing

10:45 Coffee break and Poster session

Room Racconigi | Session 02

Food Quality:
PORK AND POULTRY MEAT

Chairs: Serra Andrea – Cullere Marco

9:00 Grassi Giulia, Tavaniello Siria, Palazzo Marisa, Peng Meng, Teshale Dereje Birara, Maiorano Giuseppe — 194
Effect of the inclusion of shelled dried chestnut in the finishing diet on growth performance and meat quality of Casertana pig

9:15 Mainardi Edda, Costa Annamaria, Pallaoro Margherita, Aidos Lucia, Buoio Eleonora, Mazzola Silvia, Di Giancamillo Mauro, Modina Silvia, Di Giancamillo Alessia, Rossi Raffaella — 093
Carcass characteristics and quality parameters of Longissimus dorsi muscle of Nero di Lomellina pigs

9:30 Cappone Eleonora Erika, Fiorilla Edoardo, Gariglio Marta, Franco Riccardo, Hos Enes, Zambotto Valeria, Bianchi Chiara, Daniele Giulia Maria, Cianciabella Marta, Bongiorno Valentina, Stoppani Nadia, Soglia Dominga, Schiavone Achille — 355
Rediscovering the value of endangered Piedmontese chicken breeds through meat quality assessment

9:45 Petracci Massimiliano, Antenucci Emilia Luigia, Gagliano Mara Antonia, Bordini Martina, Mancinelli Cartoni Alice, Zampiga Marco, Soglia Francesca, Mattioli Simona, Sirri Federico — 079
Comparison of carcass and meat quality traits of fast-, medium- and slow-growing chicken genotypes fed diets with different protein-to-energy ratio

10:00 Antenucci Emilia Luigia, Mancinelli Cartoni Alice, Soglia Francesca, Gagliano Mara Antonia, Petracci Massimiliano, Dal Bosco Alessandro — 332
Effects of outdoor enrichments and dietary supplementation with n-3 PUFA and antioxidants on the meat quality traits in free range chickens

10:15 Soglia Francesca, Bordini Martina, Tavaniello Siria, Antenucci Emilia Luigia, Maiorano Giuseppe, Petracci Massimiliano — 259
Breast meat quality to classify the wooden breast defect and investigate its underlying mechanisms in fast-growing chickens

10:45 Coffee break and Poster session

Room Stupinigi | Session 03

Alternative Proteins:
YELLOW MEALWORM REARING AND NUTRITION

Sponsored by GREEN FEED CYCLES
Chairs: Athanassiou Christos – Moradei Andrea

9:00 *INVITED LECTURE*
Barragán-Fonseca Karol
Insects for Peace: transforming communities through Black Soldier Fly farming

9:30 Palumbo Bianca Federica, Deruytter David, Dalle Zotte Antonella — 251
Optimizing Tenebrio molitor reproduction: examining beetle size effect on mating preferences, and larval yield and performance

9:45 Resconi Andrea, Adamaki-Sotiraki Christina, Rigopolou Marianna, Gasco Laura, Athanassiou Christos — 055
Is age just a number? Investigating the effects of male and female age on the reproduction of Tenebrio molitor

10:00 Daluwatta Sujivi, Bellezza Oddon Sara, Candian Valentina, Loiotine Zaira, Resconi Andrea, Biasato Ilaria, Tedeschi Rosemarie, Gasco Laura — 109
Impact of different dietary protein: carbohydrates ratios and lipid inclusion levels on the growth performance, nutritional composition and AMPs gene expression of Tenebrio molitor larvae

10:15 Moradei Andrea, Spranghers Thomas, Ottoboni Matteo, Deruytter David, Pinotti Luciano — 017
Tenebrio molitor: effects of four herbs on larval composition and on their growth performance

10:30 Copelotti Emma, De Schutter Kristof, Tzompa-Sosa Daylan, Coudron Carl, Deruytter David, Mancini Simone — 032
Fully hydrogenated rapeseed oil (FHRO) enriched diet in Tenebrio molitor larvae: effects on growth performances and nutritional composition

10:45 Coffee break and Poster session

Room Valentino | Session 04

Sustainability:
FEEDING STRATEGIES

Chairs: Sandrucci Anna – Atzori Alberto

9:00 Colleluori Riccardo, Silvestrelli Simone, De Matos Vettori Julio, Cavallini Damiano, Buonaiuto Giovanni, Formigoni Andrea 489
Effects of a molasses-based liquid feed supplemented with tannins on productive performance and methane emissions in lactating dairy cows

9:15 Dell'Anno Matteo, Spedale Cristina, Frazzini Sara, Di Stefano Antonio, Baldi Antonella, Rossi Luciana, Chiofalo Vincenzo 501
Evaluation of functional characteristics of whole lemon pulp and depectinized lemon pulp for animal feeding

9:30 Spedale Cristina, Dell'Anno Matteo, Onelli Elisabetta, Moscatelli Alessandra, Puglia Marco, Pedrazzi Simone, Dell'Orto Vittorio, Chiofalo Vincenzo, Rossi Luciana 467
Functional characterization of biochar from lemon pulp by-products as innovative feed ingredients

9:45 Caratzu Maria Francesca, Lunesu Mondina Francesca, Sechi Sara, Carta Silvia, Nudda Anna, Pulina Giuseppe, Correddu Fabio 475
Carbon Footprint estimation of some European agro-industrial by-products and their effect in reducing the environmental impact of sheep and goat diets

10:00 Mantino Alberto, Finocchi Matteo, Ripamonti Alice, Silvi Alina, Casarosa Laura, Senatore Elena, Cella Fabrizio Giuseppe, Serra Andrea, Conte Giuseppe, Mele Marcello 416
Brewers' spent grains as a sustainable alternative for lactating ewes: a feeding and environmental perspective

10:15 Santoru Matteo, Muñoz-Grein Jennifer, Alvarez-Rodriguez Javier, Pinotti Luciano, Latorre Maria Angeles 190
Evaluation of Yucca schidigera extract inclusion in fattening pig nutrition: impact on performances, nitrogen use and slurry composition

10:30 Volpe Federica, Zampiga Marco, Pignata Stefano, Piscitelli Raffaela, Petracci Massimiliano, Sirri Federico 386
Comparison of the environmental impacts of chicken meat production among fast-, medium- and slow-growing genotypes fed diets with different protein-to-energy ratio

10:45 Coffee break and Poster session

Room Mandria | Session 05

Genetics:
POULTRY AND RABBIT

Chairs: Lasagna Emiliano – Mecocci Samanta

9:00 Perini Francesco, Cendron Filippo, Lasagna Emiliano, Baruchello Maristella, Cassandro Martino, Penasa Mauro — 056
Genetic characterization of two local duck breeds (Anas platyrhynchos) using whole genome sequencing

9:15 Saleh Medhat, Pierini Claudia, Landi Vincenzo, Maggiolino Aristide, Lasagna Emiliano, Mugnai Cecilia, Perini Francesco, Centoducati Gerardo, Canales Amado, Martinez Amparo, De Palo Pasquale, Ciani Elena, Bruno Silvia, Bramante Grazia, Pugliese Nicola, Circella Elena, Santos Silva Fatima, Carolino Inês, Camarda Antonio — 276
Genetic characterization and origins of the Leccese: insights into an Apulian poultry breed

9:30 Perricone Vera, Marelli Stefano, Zaniboni Luisa, Tognoli Cristina, Zeni Niko Gioacchino, Schiavone Achille, Soglia Dominga, Cerolini Silvia — 286
Phenotipic characterization and mating plan for biodiversity conservation in Modenese chicken breeders

9:45 Stoppani Nadia, Soglia Dominga, Bongiorno Valentina, Testa Pietro, Moshe David, Schiavone Achille — 350
Safeguarding local animal genetics: the conservation of the Nostrana di Morozzo chicken breed

10:00 Soglia Dominga, Stoppani Nadia, Perini Francesco, Lasagna Emiliano, Schiavone Achille, Cerolini Silvia — 353
Molecular data to safeguard genetic diversity in local chicken breed conservation

10:15 Bordini Martina, Zappaterra Martina, Petracci Massimiliano, Soglia Francesca — 258
Gene expression analysis of Collagen type III coding gene in chicken breast muscles affected by wooden breast condition

10:30 Bovo Samuele, Ribani Anisa, Bolner Matteo, Taurisano Valeria, Schiavo Giuseppina, Bertolini Francesca, Fontanesi Luca — 213
The size of the rabbit from whole genome sequencing: the dwarfism in Dwarf Lop breed is better explained as a polygenic trait

10:45 Coffee break and Poster session

Room Agliè | Session 06

Physiology and Reproduction:
RUMINANT PHYSIOLOGY

Chairs: Minuti Andrea – Kristofova Radoslava

9:00 Calanni Macchio Alfio, Iraci Fuintino Antonio, Ragona Francesca, Purrone Sissy, Trapanese Lucia, Pacelli Giovanmaria, Santinello Matteo — 167
Influence of conception time on milk yield and quality traits in primiparous Mediterranean buffalo

9:15 Benedetti Lorenzo, Piccioli-Cappelli Fiorenzo, Sfulcini Marta, Cattaneo Luca, Minuti Andrea, Trevisi Erminio — 168
Feeding dairy cows in the morning or in the evening: effects on milk production, rumen activity and feeding behavior

9:30 Niero Giovanni, Visentin Giulio, Meoni Gaia, Tenori Leonardo, Cassandro Martino, De Marchi Massimo, Penasa Mauro — 407
Impact of cow udder health status on milk metabolic pattern

9:45 Piccioli-Cappelli Fiorenzo, Mezzetti Matteo, Vercesi Alessandro, Scemama De Gialluly Sophie, Benedetti Lorenzo, Bosio Lorenzo, Greco Dante, Trevisi Erminio — 482
Effects administration of vitamin D3 delivered by liposomes to dairy cows during transition period

10:00 Lopreiato Vincenzo, Stocco Giorgia, Biffani Stefano, Liotta Luigi, Niero Giovanni, Penasa Mauro, Summer Andrea, Martinelli Nicola, Cipolat-Gotet Claudio — 551
Application of a Generalized Additive Mixed Model to evaluate the effect of season, energy status, milk yield, and milk macro-mineral content on milk fatty acids profile of Brown Swiss dairy cows

10:15 Maggiolino Aristide, Landi Vincenzo, Trevisi Erminio, Bernabucci Umberto, Lecchi Cristina, Ceciliani Fabrizio, De Palo Pasquale — 445
Hemogasanalysis patterns modifications in Holstein Friesian and Brown Swiss lactating cows coping with a natural short-term heat wave

10:30 Sfulcini Marta, Cattaneo Luca, Piccioli-Cappelli Fiorenzo, Trevisi Erminio, Minuti Andrea — 296
Early-life ruminal transfaunation using different types of in-vitro fermented inocula: effect in health and performance in dairy calves

10:45 Coffee break and Poster session

Room Carignano | Session 07

Production Systems:
EFFICIENCY, HEALTH, AND SUSTAINABILITY

Chairs: Chiofalo Biagina – Birolo Marco

9:00 Ravetto Enri Simone, Pittarello Marco, Lonati Michele, Lombardi Giampiero — 453
Can livestock site-use intensity be estimated by observation of grazing evidences in alpine pastures?

9:15 Podda Maria Giovanna, Sechi Gian Simone, Atzori Alberto Stanislao, Todde Giorgio, Cannas Antonello — 170
Optimizing dairy farm efficiency: a case study in process mapping and business process management for feeding operations

9:30 Coppa Mauro, Bellato Alessandro, Manenti Isabella, Bongioanni Luisa, Borla Laura, Donato Antonella, Mannelli Alessandro, Battaglini Luca — 499
Farm management risk factors of mastitis for mountain dairy farms in the western Alps

9:45 Ferronato Giulia, Simonetto Anna, Gilioli Gianni, Zecconi Alfonso — 306
Exploring the relationship between mastitis risk management, milk yield and global warming potential in dairy farms

10:00 Tretola Marco, Antonacci Alessandro, Silacci Paolo, Bee Giuseppe — 028
Impact of two different pen cleaning protocols on ex-vivo jejunal integrity and nutrients uptake of growing-finishing pigs fed standard or low-protein diets

10:15 *INVITED LECTURE*
Baxter Emma
How to 'End the Cage Age' for farrowing sows – updates on research, systems and best practice

10:45 Coffee break and Poster session

Room Venaria | Session 08

Genetics:
SUSTAINABILITY AND FUTURE PERSPECTIVES OF ANIMAL BREEDING

Sponsored by Fedana
Chairs: Cassandro Martino – Fumagalli Francesca

11:15 Persichilli Christian, Cassandro Martino, Senczuk Gabriele, Di Civita Marika, Bitew Mulusew Kassa, Van Kaam Jan-Thijs, Finocchiaro Raffaella, Pilla Fabio — 485
Worldwide diversity of Holstein cattle

11:30 Zanotti Andrea, Cipolat-Gotet Claudio, Summer Andrea, Sabbioni Alberto, Asti Vittoria, Tiezzi Francesco, Finocchiaro Raffaella, Van Kaam Jan-Thijs, Cassandro Martino, Layton Jonathan, Ablondi Michela — 373
The impact of inbreeding on fertility in Italian Holstein cattle

11:45 Milia Paola, Cesarani Alberto, Fabris Anna, Finocchiaro Raffaella, Marusi Maurizio, Macciotta Nicolò, Dimauro Corrado — 065
Assessing fertility: developing an index for Italian Jersey cattle

12:00 Benzoni Lorenzo, Layton Jonathan, Finocchiaro Raffaella, Marusi Maurizio, Testori Fabio, Cassandro Martino — 059
Phenotypic associations between hoof lesions and type traits in Italian Holstein population

12:15 Gomez Mayra, Cimmino Roberta, Rossi Dario, Zullo Gianluigi, Di Vuolo Gabriele, Neglia Gianluca, Biffani Stefano — 443
The role of inbreeding depression in the genetic improvement program of the Italian Mediterranean buffalo

12:30 Callegaro Simone, Tiezzi Francesco, Maltecca Christian, Fabbri Maria Chiara, Bozzi Riccardo — 129
Comprehensive analysis of inbreeding depression across growth, fertility, and survival traits in Charolais and Limousine beef cattle

12:45 Bertolini Francesca, Vegni Jacopo, Schiavo Giuseppina, Bovo Samuele, Bolner Matteo, Buttazzoni Luca, Gallo Maurizio, Fontanesi Luca — 382
Changes in allele and haplotype frequencies over the years have differentiated the genomes of Italian heavy pigs from cosmopolitan breeds

13:00 Lunch

Room Racconigi | Session 09

Food Quality:
EGGS AND OTHER FOODS

Chairs: Dal Bosco Alessandro – Di Rosa Ambra

11:15 Dalle Zotte Antonella, Singh Yazavinder, Boccato Alberto, Cullere Marco — 322
Camelina sativa: an emerging crop that can successfully be exploited in laying hen's feeding without compromising egg quality

11:30 Cullere Marco, Singh Yazavinder, Dalle Zotte Antonella, Boccato Alberto — 288
Camelina sativa: an emerging crop to enhance egg healthiness and reaching the claim "rich in omega-3 fatty acids"

11:45 Piscitelli Raffaela, Zampiga Marco, Pignata Stefano, Petracci Massimiliano, Sirri Federico — 086
Proximate composition and fatty acid profile of eggs laid by two Italian chicken breeds, their crossbreeds, and a commercial hen hybrid reared both in enriched cages and free-range system

12:00 Carta Silvia, Rubattu Roberto, Nudda Anna, Correddu Fabio — 393
Does the farming system influence the quality of the eggs in terms of chemical composition and colour parameters?

12:15 Accetta Francesca, Ben Tiba Amani, Ayoub Hai Said, Di Rosa Ambra — 317
Evaluation of geographical and botanical origin of Tunisian and Sicilian honeys using artificial senses and data fusion

12:30 Lanzoni Davide, Zanderigo Giovanni, Sundaram Tamil, Baldi Antonella, Cheli Federica, Giromini Carlotta — 039
Exploring plant-based proteins as an alternative for culture media in cellular agriculture

12:45 Pulina Giuseppe, Lunesu Mondina Francesca, Correddu Fabio, Cesarani Alberto, Nudda Anna — 574
The naturalness of food production and processing: ethical perspectives and a new metric of naturalness

13:00 Lunch

Room Stupinigi | Session 10

Alternative Proteins:
YELLOW MEALWORM AND BLACK SOLDIER FLY REARING AND NUTRITION

Sponsored by GREEN FEED CYCLES
Chairs: Rumbos Christos – Secci Giulia

11:15 Chrysanthopoulou Christina, Adamaki-Sotiraki Christina, Rumbos Christos, Athanassiou Christos — 577
Feeding Tenebrio molitor larvae with oilseed presscakes – Sustainable and nutrient-rich feeding substrates

11:30 Dell'Anno Matteo, Ferri Irene, Dametti Matilda, Spano Mattia, Mannina Luisa, Rossi Luciana — 515
Evaluation of the metabolomic profile in Tenebrio molitor reared on functional substrates

11:45 Loiotine Zaira, Bellezza Oddon Sara, Resconi Andrea, Passaro Rosa Laura, Gai Francesco, Bacenetti Jacopo, Gasco Laura, Biasato Ilaria — 072
Larval growth and bioconversion efficiency of black soldier fly (Hermetia illucens) on rice by-products: unlocking new life for agricultural waste

12:00 Nucera Daniele, Bellezza Oddon Sara, Loiotine Zaira, Passaro Rosa Laura, Piano Serenella, Biasato Ilaria, Zeppa Giuseppe, Renna Manuela, Patti Sara, Gasco Laura — 556
Stabilization of canteen waste for Hermetia illucens larvae substrate production

12:15 Passaro Rosa Laura, Bellezza Oddon Sara, Loiotine Zaira, Biasato Ilaria, Nucera Daniele, Piano Serenella, Gasco Laura — 058
Transforming canteen waste into black soldier fly larvae feed: effects on growth performance and bioconversion efficiency

12:30 Zanzot Asia, Copelotti Emma, Cacchiarelli Chiara, Trocino Angela, Mancini Simone — 161
Meat-based diets for Hermetia illucens larvae: effects on growth and proximate composition

12:45 Zafeiriadis Sofronios, Baliota Georgia, Adamaki-Sotiraki Christina, Karagiorgis Georgios, Rumbos Christos, Athanassiou Christos — 578
Sustainable management of dairy waste: exploring Hermetia illucens (L.) bioconversion potentials for efficient effluent treatment

13:00 Lunch

Room Valentino | Session 11

Sustainability: ENTERIC EMISSIONS

Chairs: Vitali Andrea – Gislon Giulia

11:15 *INVITED LECTURE*
Bacenetti Jacopo
Weaknesses, limits, biases and strengths of LCA applied to livestock systems

11:45 Braidot Matteo, Cabbia Anita, Cavallini Damiano, Spanghero Mauro, Romanzin Alberto 274
Methane emission assessment in Simmental bulls divergent for feed efficiency

12:00 Ramirez Mauricio Marco Aurelio, Toledo-Alvarado Hugo, Schiavon Stefano, Martinez-Marin Gustavo, Gallo Luigi, Nocetti Marco, Sturaro Enrico, Giannuzzi Diana, Cecchinato Alessio 087
Impact of farming systems and welfare indicators on milk infrared-predicted enteric methane emissions in Parmigiano Reggiano cheese production area

12:15 Rossi Chiara, Grossi Giampiero, Vitali Andrea, Lacetera Nicola 427
Seasonal pattern of enteric methane emissions in dairy cow

12:30 Moliso Mesfin, Ferronato Giulia, Negrini Riccardo, Ajmone Marsan Paolo, Mrode Raphael, Pinares-Patino Cesar S., Fioretti Mauro, Pascarella Lorenzo 377
Assessment of enteric methane emissions in three Italian dairy cattle breeds using DHI data

12:45 Rossi Chiara, Grossi Giampiero, Vitali Andrea, Petrocchi Jasinski Francesca, Evangelista Chiara, Basiricò Loredana, Turriziani Giovanni, Bernabucci Umberto, Lacetera Nicola 417
Effect of green forage on enteric methane emissions in Mediterranean dairy buffaloes during summer: different approaches for measurement

13:00 Lunch

Room Mandria | Session 12

Ruminant Nutrition:
NUTRITION AND FEEDING BEHAVIOUR OF DAIRY COWS

Chairs: Toral Pablo – Simoni Marica

11:15 Rocchetti Gabriele, Cattaneo Luca, Froldi Federico, Lapris Marco, Moschini Maurizio, Bani Paolo, Trevisi Erminio 049
A data fusion approach unveils the impact of 3-nitrooxypropanol on the rumen fluid and milk metabolomes of lactating Holstein dairy cows

11:30 Simoni Marica, Esposito Giulia, Paolini Annamaria, Patrissi Rosanna, Righi Federico 211
Nutritional and chemical characteristics of hay-based diets as predictors of ruminal and intestinal microbial development and function

11:45 Simoni Marica, Pitino Rosario, Boldrin Gloria, Valoppi Davide, Tedeschi Irene, Cipolat-Gotet Claudio, Righi Federico 434
Evaluation of two feeding strategies applied to robotic milking on primiparous cows

12:00 Righi Federico, Pitino Rosario, Mantovani Giorgia, Danese Tommaso, Tsiplakou Eleni, Simoni Marica 419
Comparing nitrogen supply from hay-based diets fed to dairy cows having low or high nitrogen excretion

12:15 Zambianchi Lucia, Colleluori Riccardo, Giaretta Elisa, Fusaro Isa, Spagnolo Marco, Ferrari Maria Giulia, Mammi Ludovica Maria Eugenia 549
Urinary mineral excretion in dry cows during prepartum period

12:30 Meli Giovanna, Chen Wenning, Fumo Valentina, Savoini Giovanni, Invernizzi Guido 540
Feeding behavior in heat-stressed heifers under different management practices

12:45 Amato Annalisa, Sfulcini Marta, Guenther Maverick, Larsen Grace, Guzi Savegnano Caroline, Tao Sha, Laporta Jimena 349
The impact of pre-weaning plane nutrition on mammary gland development of dairy calves

13:00 Lunch

Room Agliè | Session 13

Physiology and Reproduction: MISCELLANY

Chairs: Cerolini Silvia – Antenucci Emanuele

11:15 Lopreiato Vincenzo, Cavallo Carmelo, Floridia Viviana, Liotta Luigi, Chiofalo Vincenzo, D'Andrea Mariasilvia, Palombo Valentino — 448
Rumen epithelium transcriptome changes in response to polyphenols-enriched olive cake supplementation in finishing Limousine bulls

11:30 De Matos Luiz Gustavo, Balbi Ombretta, Salvi Gaspare, Dadi Yasmine, Martini Valeria, Agazzi Alessandro, Maggiolino Aristide, De Palo Pasquale, Lecchi Cristina — 146
Modulation of bovine immune cells by small extracellular vesicles isolated from the plasma of heat-stressed cows

11:45 Fulgione Andrea, Iovane Valentina, Gentile Antonio — 077
Prediction by molecular dynamics simulation analysis of IL-10 polymorphisms effects and association with brucellosis in Mediterranean river Buffalo

12:00 Kristofova Radoslava, Zitterl-Eglseer Karin, Capucchio Maria Teresa, Ippolito Dorotea, Gai Francesco, Firooznia Fardad, Laukova Andrea, Pogany Simonova Monika, Cikos Stefan, Spirkova Alexandra, Franc Ales, Takacsova Margareta, Placha Iveta — 145
Protective effect of thymol incorporated into gastroresistant pellets on intestinal integrity and microbiota in rabbits

12:15 Pasquariello Rolando, Di Filippo Francesca, Brevini Tiziana A.L., Gandolfi Fulvio — 019
Innovative flow cytometry-based isolation of bovine spermatids for assisted reproductive technologies

12:30 INVITED LECTURE
Knight Christopher Harold
Progress towards reasonably-precise livestock farming in the dairy sector

13:00 Lunch

Room Carignano | Session 14

Production Systems: CHALLENGES AND INNOVATIONS

Chairs: Castellini Cesare – Zappaterra Martina

11:15 D'Alessandro Angela, Di Luca Alessio, Cavaliere Gina, Martemucci Giovanni, Cimmino Fabiano, Trinchese Giovanna, Mollica Maria Pina — 045
Evaluation of physiological effects of milk from the autochthonous Capestrina goat breed using an animal model study

11:30 Perrucci Alice, Ferrari Elvira, Cavagnini Alberto, Scollo Annalisa — 018
Statistical Process Control to monitor productive items affected by PRRS virus

11:45 Ferrari Carolina, Cesarani Alberto, Gaspa Giustino, Macciotta Nicolò, Falchi Laura, Bernabucci Umberto, Negrini Riccardo — 337
Analyzing big data to evaluate heat stress tolerance in dairy cows

12:00 Menini Alessio, Marcon Caterina, Magrin Luisa, Stiletto Alice, Giampietri Elisa, Trestini Samuele, Gottardo Flaviana — 357
Innovative and participatory pathways for sustainable livestock farming and meat production: insights from the Veneto region in Italy

12:15 Di Federico Francesca, Angelucci Elisa, Davidescu Magdalena, Macchioni Lara, Salvadori Laura, Chiappalupi Sara, Sorci Guglielmo, Dal Bosco Alessandro, Bosa Luigia, Castellini Cesare, Mattioli Simona — 198
Lipid metabolism of chickens with different growth rate and kinetic activity

12:30 Birolo Marco, Pontalti Emanuele, Pirrone Fabrizio, Nalon Eleonora, Mattioli Simona, Verdiglione Rina, Dalle Zotte Antonella — 218
Effect of heat stress on growth performance and carcass traits of fast- medium- and slow-growing chicken genotypes

12:45 Franzin Alberico, Olivieri Silvia, Sciuto Simona, Provera Alessandra, Ferraris Carla, Romano Angelo, Pitti Monica, Power Karen, Leandri Rebecca, Biasibetti Elena, Pezzolato Marzia, Bozzetta Elena — 554
Exceptional mortality in an intensive "short cycle" snail farm in Northwest Italy

13:00 Lunch

Room Venaria | Session 15

Genetics:
OMICS-BASED APPROACHES

Chairs: Ajmone-Marsan Paolo – Schiavo Giuseppina

14:00 *INVITED LECTURE*
Blasco Agustín
Omics data sets are compositional: the problem and its solution

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14:30 Williams John, Colli Licia, Ren Yan, Santos Pineda Paulene, Khatkar Mehar S., Macphillamy Callum, Negrini Riccardo, Flores Ester B., Ajmone Marsan Paolo, Low Wai Yee 396
Genotyping buffalo by Targeted SNP-Capture Sequencing

14:45 Bolner Matteo, Bertolini Francesca, Bovo Samuele, Schiavo Giuseppina, Cappelloni Manolo, Gallo Maurizio, Fontanesi Luca 254
Application of metabolomics to help dissect biological factors underlying fat deposition in pigs

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15:00 Bovo Samuele, Bolner Matteo, Schiavo Giuseppina, Bertolini Francesca, Gallo Maurizio, Fontanesi Luca 244
Multi-omics dissection of lipid metabolism in Italian heavy pig breeds

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15:15 Mecocci Samanta, Cappelli Katia, Beccati Francesca, Porzio Elisabetta, Ratto Roberta, Pepe Marco, Capomaccio Stefano 303
Exercise as a modifier of the molecular clock in the athletic horse: a genome-wide study

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15:30 Coffee Break and Poster session

Room Racconigi | Session 16

Food Quality:
SHEEP MEAT

Chairs: Maggiolino Aristide – Correddu Fabio

14:00 Lopez Annalaura, Greco Margherita, Marcolli Beatrice, Moretti Vittorio Maria, Mattiello Silvana, Bellagamba Federica 234
Evaluation of the triple attitude of the alpine Ciuta sheep breed: quality assessment of milk, meat and wool

14:15 Maniaci Giuseppe, Giosuè Cristina, Ul Hassan Mahmood, Gannuscio Riccardo, Busetta Gabriele, Gaglio Raimondo, Todaro Massimo, Alabiso Marco 343
Effects of including destoned olive cake in sheep feed on meat quality and salami production

14:30 Musati Martino, Cannone Marco Sebastiano, Bertino Antonino, Mangano Fabrizio, Luciano Giuseppe, Priolo Alessandro, Mangione Guido, Foti Francesco, Scerra Manuel, Della Malva Antonella, Natalello Antonio 366
Effects of feeding bergamot by-products on performance and meat quality in lambs

14:45 Ponte Marialetizia, Pipi Marianna, Badalamenti Rosario, Bonanno Adriana, Di Grigoli Antonino 509
Effects of ensiled and dehydrated grape pomace in the ewes' diet on meat production of suckling lambs

15:00 Satta Francesca, Castangia Francesca, Pinna Aurelia, Caria Claudio, Ledda Antonello, Spezzigu Antonio, Sotgiu Francesca, Cannas Antonello 195
Enhancing meat production and quality of culled Sarda ewes

15:15 Parrini Silvia, Pugliese Carolina, Becciolini Valentina, Tocci Roberto, Sargentini Clara, Crovetti Alessandro, Sirtori Francesco, Aquilani Chiara, Bozzi Riccardo 164
Assessing quality traits of lamb meat by FT- NIRS

15:30 Coffee Break and Poster session

Room Stupinigi | Session 17

Alternative Proteins:
INSECT REARING AND USE AS ANIMAL FEED

Sponsored by GREEN FEED CYCLES
Chairs: Mancini Simone – Benini Elisa

14:00 Tognocchi Monica, Malucchi Gilda, Tinagli Sara, Canale Angelo, Perioli Riccardo, Conte Giuseppe, Mele Marcello, Serra Andrea — 437
Rearing substrate influences the chemical composition of Hermetia illucens larvae

14:15 Moradei Andrea, Ottoboni Matteo, Malabusini Serena, Jucker Costanza, Savoldelli Sara, Pinotti Luciano — 096
Enriched zinc and selenium agri-food by-products: effects on growth performance of black soldier fly

14:30 Baima Lorenzo, Merlino Valentina Maria, Bellezza Oddon Sara, Gasco Laura, Biasato Ilaria, Loiotine Zaira, Blanc Simone, Massaglia Stefano, Brun Filippo — 354
Economic and social perspectives on integrating Hermetia illucens meal in animal feed supply chain

14:45 Biasato Ilaria, Bongiorno Valentina, Loiotine Zaira, Bellezza Oddon Sara, Ribeiro Teresa, Resconi Andrea, Passaro Rosa Laura, Mendez Rondo Keidy Yasmin, Filippa Alessia, Cappone Eleonora Erika, Fiorilla Edoardo, Renna Manuela, Brugiapaglia Alberto, Schiavone Achille, Gasco Laura — 038
Live Tenebrio molitor larvae as feed ingredient for native chickens: effects on productive performance and egg quality

15:00 Copelotti Emma, Fronte Baldassare, Sangiacomo Chiara, Sogari Giovanni, Andreani Giulia, Moruzzo Roberta, Mancini Simone — 033
Black soldier fly as feed: focus on the quality of gilthead seabream (Sparus aurata L.) fillets fed with a partial fish meal replacement

15:15 Bellezza Oddon Sara, Biasato Ilaria, Loiotine Zaira, Sorrentino Federica, Caimi Christian, Rumbos Christos, Gasco Laura — 095
What about exploring new insect species? Fruit fly (Ceratitis capitata) meal as a feed ingredient in juvenile rainbow trout diets

15:30 Coffee Break and Poster session

Room Valentino | Session 18

Sustainability:
EXTENSIVE SYSTEMS

Chairs: Mele Marcello – Lunesu Mondina

14:00 Franca Antonello, Altana Giovanni, Arca Pasquale, Stanislao Atzori Alberto, Khater Stephanie, Monagheddu Arianna, Mussolino Claudio, Solinas Stefania, Vagnoni Enrico 436
A preliminary environmental characterization of Mediterranean pastoral food products based on the LCA approach

14:15 Fichter Greta, Gauly Matthias, Sabia Emilio, Zanon Thomas 016
Environmental efficiency and carbon sequestration potential of organic vs. conventional Simmental dairy farming systems in mountain regions

14:30 Sturaro Enrico, Birolo Marco, Bonavolontà Francesco, Mancinelli Cartoni Alice, Di Iacovo Francesco, Lacetera Nicola, Marconi Marco, Petracci Massimiliano, Provolo Giorgio, Verde Maria Teresa, Vitali Andrea 135
SOLSTICE: a living labs approach for assessing the overall sustainability of livestock systems through Life Cycle Assessment

14:45 Da Re Sebastiano, Raniolo Salvatore, Squartini Andrea, Sturaro Enrico, Ramanzin Maurizio 174
Impact of livestock pasture-use intensity and soil geochemical properties on microbial functional potential of nutrient cycles in Alpine pastures

15:00 Raniolo Salvatore, Da Re Sebastiano, Squartini Andrea, Sturaro Enrico, Ramanzin Maurizio 380
Grazing intensity, soil functions and greenhouse gas emissions: a case study in Alpine pastures of the Dolomites

15:15 Cavallo Carmelo, Amato Annalisa, Evola Carola, Negrini Riccardo, Tolone Marco, Liotta Luigi, Lopreiato Vincenzo 369
Temperature-humidity index breakpoints for rectal temperature and milk performance of Cinisara cows under semi-extensive dairy system

15:30 Coffee Break and Poster session

Room Mandria | Session 19

Ruminant Nutrition:
IN VITRO STUDIES AND NEW FEEDSTUFFS

Chairs: Cheli Federica – Natalello Antonio

14:00 Scicutella Federica, Bolletta Viviana, Lira De Medeiros Adja, Daghio Matteo, Foggi Giulia, Valenti Bernardo, Mannelli Federica, Mele Marcello, Viti Carlo, Pauselli Mariano, Buccioni Arianna — 238
Are in vitro experiments a suitable tool to study rumen fermentation?

14:15 Vastolo Alessandro, Montefusco Teresa, Ruggiero Alessio, Kiatti Dieu Donné, Cutrignelli Monica Isabella — 155
Effect of hazelnut and pomegranate by-products on in vitro methane reduction and ruminal fermentation in sheep

14:30 Bonizzi Serena, Colombini Stefania, Pavesi Martina, Cesari Valentina, Failla Osvaldo, Ragaglini Giorgio, Sandrucci Anna — 352
Enhancing circularity in dairy cattle farming: nutritional assessment of Morus alba leaves

14:45 Daniso Enrico, Cabbia Anita, Spanghero Mauro — 496
In vitro rumen fermentation of wheat straw after treatment with mush-room extracts (Pleurotus ostreatus and Agaricus bisporus).

15:00 Fiorbelli Erica, Moccia Davide, Rocchetti Gabriele, Atzori Alberto Stanislao, Pusceddu Antonio, Gallo Antonio — 530
Screening of Italian Mediterranean macroalgae for the potential reduction of methane emissions

15:15 Maggiolino Aristide, Caroprese Mariangela, Di Grigoli Antonino, Denora Nunzio, Lopedote Angela, Ponte Marialetizia, Marino Rosaria, Sevi Agostino, Pipi Marianna, De Palo Pasquale — 176
An innovative rumen-bypass micro-encapsulation technique for essential oils

15:30 Coffee Break and Poster session

Room Agliè | Session 20

Welfare, Health and Behaviour:
NEW APPROACHES TO POULTRY MANAGEMENT

Chairs: Tufarelli Vincenzo – Aquilani Chiara

14:00 Toth Mark, Kovacs-Weber Mária, Ancsin Zsolt, Dalle Zotte Antonella, Erdélyi Márta 371
Preliminary evaluation of mealworm frass for broiler chicken bedding

14:15 Nompleggio Lorenzo, Di Federico Francesca, Angelucci Elisa, Dal Bosco Alessandro, Castellini Cesare, Bosa Luigia, Mattioli Simona 126
Effect of kinetic activity on behaviour and productive performance of different chicken genotypes

14:30 Ciarelli Claudia, Pravato Mattia, Bordignon Francesco, Xiccato Gerolamo, Trocino Angela 461
Effect of ramps on space use of laying hens in a cage-free system

14:45 Pravato Mattia, Bordignon Francesco, Pezzuolo Andrea, Marinello Francesco, Trocino Angela, Xiccato Gerolamo 053
Relationships between environmental conditions and behaviour of laying hens in an aviary system

15:00 Lai Giorgia, Pudda Flavia, Muzzeddu Marco, Cappai Maria Grazia 552
Feeding management for nutritional welfare of griffon vultures as life-long kept vs. temporarily before release into nature

15:30 Coffee Break and Poster session

Room Carignano | Session 21

Production Systems:
PRODUCTION STRATEGIES AND QUALITY TRAITS

Chairs: Petracci Massimiliano – Perricone Vera

14:00 Molin Matteo, Bordignon Francesco, Pravato Mattia, Zuffellato Andrea, Trocino Angela, Xiccato Gerolamo — 050
Effect of group size, environmental enrichment, and temperature on growth performance and meat quality of rabbits

14:15 Peng Meng, Tavaniello Siria, Stadnicka Katarzyna, Skowron Krzysztof, Grudlewska-Buda Katarzyna, Randazzo Cinzia, Vaccalluzzo Amanda, Maiorano Giuseppe — 285
Effect of selected synbiotics injected in ovo on hatchability and chick quality

14:30 Balbo Chiara, Stocco Giorgia, Pizzamiglio Valentina, Sabellini Giulio, Valoppi Davide, Tedeschi Irene, Levante Alessia, Alinovi Marcello, Fenga Irene, Chiavaro Emma, Summer Andrea, Cipolat-Gotet Claudio — 367
The race of milk components: rising to the top during natural creaming in Parmigiano Reggiano PDO

14:45 Boldt Ariane, Sanftleben Peter, Gauly Matthias, Zanon Thomas — 015
Impact of sires' breed on calving ease, resulting fattening performance and carcass quality parameters in fattening bulls from Holstein Friesian herds in North-Eastern Germany

15:00 Cozzi Giulio, Segato Severino, Magrin Luisa — 149
Production performance and early culling rates of finishing Charolais young bulls in Italy. Results of a case study

15:15 Piscopo Nadia, Trapanese Lucia, Pierro Federica, Borzacchiello Luca, Matera Roberta, Esposito Luigi — 205
Meat quality of the Podolica cattle raised with different finishing methods in the Calabrian Apennines

15:30 Coffee Break and Poster session

Room Venaria | Session 22

Genetics:
GENOMIC APPLICATIONS FOR BREEDING

Sponsored by SINERGY
Chairs: Macciotta Nicolò – Fabbri Maria Chiara

16:00 Gomez Proto Guido, Mancin Enrico, Oian Angelica, Rulli Eugenio, Blanchet Veruska, Vevey Mario, Bernini Francesca, Strillacci Maria, Bagnato Alessandro, Sartori Cristina, Mantovani Roberto 080
Precision breeding in Valdostana cattle breed: Genomic tools applied to milk production traits

16:15 Sartori Cristina, Tuliozi Beniamino, Mancin Enrico, Rulli Eugenio, Gomez Proto Guido, Oian Angelica, Blanchet Veruska, Vevey Mario, Mantovani Roberto 550
Social dominance and other new behavioural phenotypes in Valdostana cattle: genetic parameters and relationships with selected traits

16:30 Cesarani Alberto, Rossoni Attilio, Lourenco Daniela, Gaspa Giustino 283
Genetic parameters and genome wide association study on fertility traits in Italian Brown cows

16:45 Crepaldi Paola, Bionda Arianna, Cortellari Matteo, Lopreiato Vincenzo, Rossoni Attilio, Mozafari Reza, Cesarani Alberto, Liotta Luigi, Parma Pietro 261
Robertsonian translocation 1-29: a focus on Sicilian breeds

17:00 Sardina Maria Teresa, Riggio Silvia, Carta Federica, Ben Jemaa Slim, Portolano Baldassare, Benanti Alessia, Senczuk Gabriele, Cesarani Alberto, Mastrangelo Salvatore 532
Analysis of copy number variations in the peninsular Italian sheep breeds using a high-density 600K SNP array

17:15 Letaief Neyrouz, Alhaddad Hasan, Lühken Gesine, Gaspa Giustino, Cosenza Gianfranco, Pauciullo Alfredo 104
Genetic investigation of the Lactophorin whey protein coding gene reveals novel polymorphisms in New and Old-World camelids

Room Racconigi | Session 23

Food Quality: BEEF

Chairs: Conte Giuseppe – Della Malva Antonella

16:00 *INVITED LECTURE*
Scollan Nigel David
New trends in measuring animal product quality linking sustainability and husbandry systems

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16:30 Lunesu Mondina Francesca, Carta Silvia, Rubattu Roberto, Fenu Antonio, Rassu Salvatore Pier Giacomo, Battacone Gianni, Pulina Giuseppe, Nudda Anna — 480
Animal performance, carcass traits and meat quality of Limousine, Sardo-Bruna, and their crosses

---

16:45 Valenti Bernardo, Lilli Emanuele, Bolletta Viviana, Pecorari Laura, Torquati Biancamaria, Ceccarini Federico, Calisti Silvia, Chiorri Massimo, Pauselli Mariano — 454
Animal performance and meat quality of crossbred heifers fed with phenol-rich agri-food by-products and forages

---

17:00 Gagliano Mara Antonia, Grigoletto Ilaria, Soglia Francesca, Valli Enrico, Gallina Toschi Tullia, Bendini Alessandra, Petracci Massimiliano — 257
Instrumental and sensory evaluations to assess the quality of beef meat in relation to Country of origin

---

17:15 Forte Lucrezia, Seccia Alessia, De Palo Pasquale, Calzaretti Giovanna, Incampo Giovanna, Samoilis Giorgio, Maggiolino Aristide — 230
Meat quality in veal calves fed with milk whey powder

Room Stupinigi | Session 24

Alternative Proteins:
INSECTS AND ALTERNATIVE PROTEINS AS ANIMAL FEEDS

Sponsored by GREEN FEED CYCLES
Chairs: Trocino Angela – Dell'Anno Matteo

16:00 Benini Elisa, Gordini Sabrina, Dondi Francesco, Scicchitano Daniel, Candela Marco, Gatta Pier Paolo, Bonaldo Alessio, Parma Luca 181
Bacterial Single-Cell Protein in aquafeed: implications for growth and gut health in Gilthead Sea Bream (Sparus aurata)

16:15 Cenati Clara, Pea Alessia, Perricone Vera, Petrosillo Elena, Agazzi Alessandro, Parati Katia, Savoini Giovanni 298
Dietary microalgae in broiler nutrition and their effects on performance and organ development

16:30 Correa Federico, Bordoni Alessandra, Luise Diana, Gotti Roberto, Trevisi Paolo 579
In vitro digestibility of microbial cell-derived protein sources for animal nutrition

16:45 Sportelli Federica, Vecchiato Carla Giuditta, Pinna Carlo, Montanari Irene, Delsante Costanza, Biagi Giacomo 472
Effects of insect meals on the fecal microbiota: an in vitro study on healthy and chronic enteropathic dogs

17:00 Armone Rosangela, Balouei Fatemeh, Randazzo Andrea, Nava Vincenzo, Alizzi Antonino Filippo Maria, Barbato Mario, Stefanon Bruno, Chiofalo Biagina 123
Preliminary assessment of nutrient digestibility and fecal quality in dogs fed a diet containing hydrolyzed feather meal

17:15 Spatola Gabriele, Giusti Alice, Gasperetti Laura, Nuvoloni Roberta, Dalmasso Alessandra, Chiesa Francesco, Armani Andrea 226
Insects-based products sold by e-commerce on the EU market: microbiome characterization by 16S rRNA metabarcoding

Room Valentino | Session 25

Sustainability:
SUSTAINABLE SUPPLY CHAINS

Chairs: Bava Luciana – Berton Marco

16:00 Diaz Vicuna Elena, Fiorilla Edoardo, Srikanthithasan Karthika, Zambotto Valeria, Bianchi Chiara, Capaldi Giorgio, Grillo Giorgio, Renna Manuela, Giorgino Andrea, Ozella Laura, Arneodo Valentina, Cravero Andrea, Tabasso Silvia, Forte Claudio 541

Improving livestock nutrition sustainability in a (hazel)nutshell

16:15 Latrofa Antonella, Currò Sarah, Arango Quispe Sheyla Johanna Shumyko, Guzzo Nadia, Montanari Massimo, Bailoni Lucia 559

Nutritional characterization of industrial hempseeds (Cannabis sativa L.) of different varieties

16:30 Capretti Chiara, Lanzoni Lydia, Petrocchi Francesca, Vignola Giorgio, Di Pasquale Jorgelina 431

The management of foot health as a tool to improve the sustainability of a dairy farm

16:45 Mastromonaco Giulia, Massaglia Stefano, Blanc Simone, Borra Danielle, Costamagna Chiara, Cornale Paolo, Biagini Davide, Merlino Valentina Maria 314

Measuring the importance of sustainability in animal-based product supply chains: insights from the CUB Model

17:00 Benedetti Del Rio Elena, Berton Marco, Sari Stefano, Zoratti Aloma, Corazzin Mirco, Tamburini Alberto, Gallo Luigi, Sturaro Enrico 295

Stakeholder attitude towards sustainability of dairy farming systems: a participatory process

17:15 Fatica Antonella, Tedesco Doriana, Pastorelli Grazia, Todini Luca, Fantuz Francesco, Salimei Elisabetta 099

Stakeholders' perspectives on environmental issues: preliminary results from SUNEQUMAR survey

Room Mandria | Session 26

Ruminant Nutrition:
IN VITRO METHODOLOGY AND MICROPLASTICS

Chairs: Spanghero Mauro – Mannelli Federica

16:00 Iqbal Rashid, Arango Quispe Sheyla Johanna Shumyko, Guzzo Nadia, El Hawat Rebecca, Tagliapietra Franco, Bailoni Lucia — 423
Comparative analysis of Ankomrf and gas Endeavour in vitro rumen systems: effects of headspace volume and CO2 flushing time on gas and methane production

16:15 Boldrin Gloria, Simoni Marica, Mantovani Luciana, Righi Federico — 523
In vitro comparison among commercial dietary buffers

16:30 Ghiaccio Francesca, Palmonari Alberto, Vecchiato Carla Giuditta, Federiconi Alessia, Mammi Ludovica Maria Eugenia, Silvestrelli Simone, Parazza Paola, Formigoni Andrea — 522
Evaluation of nitrate at different level of inclusion on in vitro ruminal fermentation

16:45 Abid Khalil, Kaihara Hatsumi, Barbera Salvatore, Danieli Pier Paolo, Glorio Patrucco Sara, Issaoui Rabeb, Tassone Sonia — 037
Ruminant nutrition in the age of microplastics contamination: challenges and insights

17:00 Lira De Medeiros Adja, Scicutella Federica, Mannelli Federica, Toni Elisabetta, Daghio Matteo, Viti Carlo, Del Bubba Massimo, Buccioni Arianna — 124
Effect of microplastics additives on rumen ecology: in vitro preliminary study

17:15 Kaihara Hatsumi, Issaoui Rabeb, Abid Khalil, Barbera Salvatore, Glorio Patrucco Sara, Tassone Sonia — 036
First investigation of microplastics contamination in corn silage used for dairy cow nutrition

Room Agliè | Session 27

Welfare, Health and Behaviour: INNOVATIONS AND PERCEPTIONS FOR SUSTAINABLE PRODUCTION

Chairs: Trevisi Erminio – Santinello Matteo

16:00 Mota Gutierrez Jatziri, Srikanthithasan Karthika, Blanc Simone, Forte Claudio — 021
Grab or Skip: What drives undergraduates to try animal welfare beef meat?

16:15 Celozzi Stefania, Ravelli Andrea, Corradini Anna Francesca, Battini Monica, Marescotti Maria Elena — 108
Ever been to a dairy farm? Testing the effect of virtual farm tours on consumers perceptions of livestock production

16:30 Galosi Livio, Roncarati Alessandra — 278
Protection of animals & research needs: legislative overview and future perspectives

16:45 Rambozzi Luisa, Formisano Roberta, Pasquetti Mario, Molinar Annarita, Torsiello Benedetta, Giammarino Mauro, Battaglini Luca, Sangrali Martina, Midulla Luca, Sarale Adriano, Renna Manuela — 024
Anthelmintic efficacy of pour-on Eprinomectin against gastrointestinal strongyles and relationships with milk production parameters in lactating goats

17:00 Santillo Antonella, Ciliberti Maria Giovanna, Biancardi Valentina, Mangano Fabrizio, Della Malva Antonella, Caroprese Mariangela, Marino Rosaria, Sevi Agostino, Albenzio Marzia — 132
Effect of almond and carob by products on immune competence of growing lambs

17:15 Grossi Giampiero, Vitali Andrea, Rossi Chiara, Lacetera Nicola — 340
Projections of the temperature humidity index for the Italian territory

Room Carignano | Session 28

Production Systems:
TRADITIONAL PRACTICES, ECONOMICS, AND WELFARE

Chairs: Buccioni Arianna – Zampiga Marco

16:00 Gaspa Giustino, Cesarani Alberto, Negrini Riccardo, Falchi Laura, Ferrari Carolina, Macciotta Nicolò 287
Relationship between cows' milk performances and dry period length in Italian cattle breeds

16:15 Primi Riccardo, Viola Paolo, Girotti Pedro, Spada Francesco, Ortenzi Luciano, Bernabucci Gloria, Basiricò Loredana, Ronchi Bruno 111
Study of the variation in the distribution of wild and domestic ungulates in an extensive livestock farm in Central Apennine during the seasons trough trapping rate

16:30 Lombardi Alessia, Bifulco Giovanna, Paparella Antonio, Cembalo Luigi, Neglia Gianluca, Campanile Giuseppe 208
Cost of buffalo milk: an analysis pre and post Covid

16:45 Algeri Stefano, Palladini Nicola, Tamburini Alberto, Sari Stefano, Bava Luciana 183
Management of extended lactation: effects on milk production and reproductive parameters

17:00 Iacurto Miriam, Steri Roberto, Meo Zilio David, Claps Salvatore, Quaranta Giovanni, Bosco Antonio, Cringoli Giuseppe 392
Survey on the management of cattle farms in two municipalities located in the park area of the Campania Region

17:15 Leliveld Lisette, Manfrè Claudia, Brscic Marta, Battini Monica 338
Mother-offspring management in different dairy farm animal species as guidance for the implementation of cow-calf-contact systems?

PROGRAM

Thursday,
19th June 2025

Room Venaria | Session 29

Genetics:
GENOMIC APPLICATIONS FOR BIODIVERSITY I

Sponsored by Vazyme
Chairs: Di Stasio Liliana – Barbato Mario

9:00 Benanti Alessia, Chessari Giorgio, Carta Federica, Riggio Silvia, Ben Jemaa Slim, Senczuk Gabriele, Bigi Daniele, Ciampolini Roberta, Sardina Maria Teresa, Sabbioni Alberto, Matassino Donato, Luongo Flavio, Fabbri Maria Chiara, Portolano Baldassare, Cesarani Alberto, Grande Silverio, Criscione Andrea, Mastrangelo Salvatore 220
Genomic characterisation and diversity assessment in endangered Italian sheep breeds

9:15 Pierini Claudia, Saleh Medhat, Ciani Elena, Bruno Silvia, Bramate Grazia, De Palo Pasquale, Barbato Mario, Landi Vincenzo 252
The rediscovery of a forgotten breed: the genomic characterisation of the Fasanese sheep and investigation of its Eastern European origins

9:30 Floridia Viviana, Bionda Arianna, Chiofalo Vincenzo, Cortellari Matteo, Lopreiato Vincenzo, Amato Annalisa, Virga Antonino Nazareno, Crepaldi Paola, Liotta Luigi, Barbato Mario 424
Mapping the phenotypic and genomic landscape of Montanina cattle

9:45 Albarella Sara, Barbato Mario, D'Anza Emanuele, Floridia Viviana, Cascone Ilaria, Cosenza Gianfranco, Salzano Angela, Ciotola Francesca, Peretti Vincenzo 358
A genomic perspective on the Agerolese autochthonous cattle breed

10:00 Bernini Francesca, Mancin Enrico, Sartori Cristina, Mantovani Roberto, Vevey Mario, Blanchet Veruska, Bagnato Alessandro, Strillacci Maria 335
Structural Variants shaping the aptitude of local cattle breeds

10:15 Álvarez Quiñónez Ruth Isabel, Senczuk Gabriele, Persichilli Christian, Capomaccio Stefano, Cappelli Katia, Amparo Martinez, Rivero José Luis, Vega Pla José Luis, Pilla Fabio 468
Genetic diversity and evolutionary history of Baroque horse breeds: insights from genome-wide data

10:30 Schiavo Giuseppina, Bovo Samuele, Bertolini Francesca, Bolner Matteo, Ribani Anisa, Taurisano Valeria, Dall'Olio Stefania, Manolo Cappelloni, Gallo Maurizio, Fontanesi Luca 313
Signatures of selection in Mora Romagnola, a highly inbreed autochthonous pig breed

10:45 Coffee break and Poster session

Room Racconigi | Session 30

Ruminant Nutrition:
INSECTS, FATTY ACIDS AND MICROBIOTA

Sponsored by Ferrero Mangimi
Chairs: Todaro Massimo – Scicutella Federica

8:30 Conte Giuseppe, Tognocchi Monica, Casarosa Laura, Tinagli Sara, Serra Andrea, Mele Marcello 074
A multivariate approach to investigate mutual relationship among milk fatty acids across different ruminant species

8:45 Rastello Lara, Badino Paola Constant Isabelle, Coppa Mauro, Gerbelle Mathieu, Gardini Giulia, Galli Alessandro, Trespeuch Christophe, Gasco Laura, Renna Manuela 023
Dietary black soldier fly oil reduces oxidative stress in dairy cows without affecting blood nutritional parameters

9:00 Congiu Michele, Lourenco Jeferson, Cesarani Alberto, Macciotta Nicolò, Dimauro Corrado 026
Relationship between oral microbiome and performance traits in Angus bulls

9:15 Baila Clàudia, Hervás Gonzalo, Renna Manuela, Gasco Laura, Rastello Lara, Barrio Esther, González-Merino Paloma, Bolletta Viviana, Frutos Pilar, Toral Pablo 196
Is black soldier fly oil a good alternative to replace palm distillate fatty acids in the diet of lactating sheep? Animal performance, feed efficiency and ruminal fermentation responses

9:30 Mecocci Samanta, Pietrucci Daniele, Bagatella Stefano, Castrica Marta, Acuti Gabriele, Cappelli Katia, Hassan Talal, Malik Muhammad Irfan, Curone Giulio, Arif Muhammad Adnan, Ferrulli Vincenzo, Boccardo Antonio, Grossi Silvia, Sgoifo Rossi Carlo Angelo, Trabalza Marinucci Massimo, Capucchio Maria Teresa, Forte Claudio, Pravettoni Davide 185
Gut health effects of hazelnut skin dietary supplementation in Limousine bulls

9:45 *INVITED LECTURE*
Toral Pablo
Fatty acids beyond milk nutritional quality

10:15 Coffee break and Poster session

Room Stupinigi | Session 31

Welfare, Health and Behaviour:
FROM PREVENTION TO THERAPY, UDDER HEALTH AND INNOVATIONS IN ZOOTECHNICS

Chairs: Cozzi Giulio – Celozzi Stefania

8:30 Petrera Francesca, Daminelli Paolo, Posante Antonella, Fusi Francesca, Giroletti Luca, Marino Rosanna, Abeni Fabio — 291
Evaluation of udder health status using bacteriological culture and somatic cell count after calving and at drying-off, and effects of antibiotic therapy

8:45 Bellato Alessandro, Coppa Mauro, Manenti Isabella, Bongiovanni Luisa, Borla Laura, Donato Antonella, Battaglini Luca, Mannelli Alessandro — 497
Individual risk factors for intramammary infections affecting dairy herds in Western Alps

9:00 Giannotta Gabriele, Bisutti Vittoria, Barberio Antonio, Biasio Lara, Zappaterra Martina, Vanzin Alice, Giannuzzi Diana, Cecchinato Alessio, Pegolo Sara — 385
Effect of subclinical intramammary infection on blood biochemical parameters in susceptible and resistant Holstein cattle

9:15 Rovetta Carlo, Ramirez Mauricio Marco Aurelio, El Hawat Rebecca, Bisutti Vittoria, Vanzin Alice, Giannotta Gabriele, Toscano Alessandro, Massaro Selene, Giannuzzi Diana, Gallo Luigi, Pegolo Sara, Schiavon Stefano, Tagliapietra Franco, Cecchinato Alessio — 383
Associations of body condition score and body weight changes with milk composition and fatty acids during the transition period in dairy cattle

9:30 Bisutti Vittoria, Giannuzzi Diana, Vanzin Alice, Secchi Giulia, Cecchinato Alessio, Pegolo Sara — 156
Multi-omic data integration for the identification of molecular drivers of subclinical intramammary infection in dairy cows

9:45 Andreoli Valentina, Stocco Giorgia, Zanotti Andrea, Tedeschi Irene, Valoppi Davide, Chessa Stefania, Lange-Consiglio Anna, Grolli Stefano, Cipolat-Gotet Claudio — 505
Addressing antibiotic resistance in dairy herds: the role of platelet rich plasma in mastitis treatment

10:00 Dadi Yasmine, Delosière Mylène, De Matos Luiz Gustavo, Delevaud Arnaud, Viala Didier, Salvi Gaspare, Balbi Ombretta, Penati Martina, De Palo Pasquale, Maggiolino Aristide, Bonnet Muriel, Ceciliani Fabrizio, Lecchi Cristina — 188
Proteome characterization of milk extracellular vesicles isolated from cows that experienced hyperthermia

10:15 Coffee break and Poster session

Room Valentino | Session 32

Monogastric Nutrition: POULTRY

Sponsored by Silvateam
Chairs: Trevisi Paolo – Lin Peng

8:30 *INVITED LECTURE*
Korver Doug
Impact of oxidation and inflammation on poultry health and productivity

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9:00 Srikanthithasan Karthika, Ferrocino Ilario, Raspa Federica, Nery Joana, Colombino Elena, Ippolito Dorotea, Gariglio Marta, Diaz Vicuna Elena, Fiorilla Edoardo, Mota Gutierrez Jatziri, Giorgino Andrea, Capucchio Maria Teresa, Schiavone Achille, Forte Claudio — 199
Effects of dietary commercially processed former foodstuffs on the gut ecosystem in broilers

---

9:15 Mecocci Samanta, Tang Jiayong, Acuti Gabriele, Pietrucci Daniele, Marini Daniele, Mercati Francesca, Franciosini Maria Pia, Chillemi Giovanni, Cappelli Katia, Forte Claudio, Trabalza Marinucci Massimo — 172
Dietary supplementation with hazelnut skin polyphenols affects growth performance and intestinal microbiota in broiler chickens

---

9:30 Mannelli Federica, Daghio Matteo, Scicutella Federica, Viti Carlo, Biagi Arroyo Marcinette Lucia, Galigani Ilaria, Buccioni Arianna — 202
Microbiota characterization of four autochthonous Italian chicken breeds

---

9:45 Dayan Jonathan, De Cesare Alessandra, Soglia Francesca, Zampiga Marco, Indio Valentina, Antenucci Emilia Luigia, Petracci Massimiliano, Sirri Federico — 277
Replacing vegetable oils with Hermetia illucens (Black Soldier Fly) larvae oil in broiler chicken diets: impacts on growth performance, meat quality, and caeca microbiome

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10:00 Zeni Niko Gioacchino, Perricone Vera, Schiavone Achille, Cerolini Silvia, Tognoli Cristina, Marelli Stefano, Fiamberti Federico, Zaniboni Luisa — 388
Egg-laying performance of hens fed diets containing former food products

---

10:15 Coffee break and Poster session

Room Mandria | Session 33

Precision Farming:
COMPUTER VISION AND IMAGING TECHNOLOGIES

Chairs: Chincarini Matteo – Asti Vittoria

8:30 Ozella Laura,Vitturini Davide,Grangetto Marco, Bovo Marco, Giacobini Mario — 078
Application of YOLOv8 for analyzing social dynamics in dairy cows within automated milking systems

8:45 Giannone Claudia, Lamanna Martina, Cavallini Damiano, Formigoni Andrea, Tassinari Patrizia, Bovo Marco — 046
Computer vision for monitoring the feeding behavior of dairy cows

9:00 Bordignon Francesco, Pravato Mattia, Molin Matteo, Trocino Angela, Xiccato Gerolamo, Marinello Francesco, Pezzuolo Andrea — 068
Environmental changes and hen spatial distribution in cage-free systems: a preliminary study

9:15 Urbani Rachele, Bergamasco Tommaso, Nalesso Giacomo, Menegon Francesca, Trocino Angela, Pravato Mattia, Sparesato Stefania, Manca Grazia, Di Martino Guido — 184
Development of an image analysis system at the slaughterhouse to assess laying hens' welfare on farm

9:30 Felici Martina, Behnam Armin, Bocchi Valeria, Zangoli Chiara, Mountricha Maria, Nanni Costa Leonardo, Pegolo Sara, Zappaterra Martina — 495
Evaluating infrared thermography for early detection of sub-clinical mastitis in dairy cows: the impact of Staphylococcus aureus infections on udder skin temperature

9:45 Pittarello Marco, Marengo Giacomo, Ravetto Enri Simone, Lonati Michele, Probo Massimiliano, Lombardi Giampiero — 457
Detection of livestock site-use intensity at fine-scale in mountain grazing systems using Sentinel-2 time series

10:00 Giannone Claudia, Dalla Costa Emanuela, Maccario Chiara, Atallah Elie, Bovo Marco — 048
Preliminary analyses on the identification of horse behaviors using deep learning techniques

10:15 Coffee break and Poster session

Room Agliè | Session 34

Food Quality:
COW MILK QUALITY AND AUTHENTICATION

Chairs: Musco Nadia – Niero Giovanni

8:30 Melilli Caterina, Magnani Barbara, Cecchini Maria Elena, Cupellini Flavia, Continanza Rosa Maria, Iannuzzi Giulio, Fontana Annunziata, Giaccone Daniele, Negrini Riccardo — 225
Performance of Italian Dairy Heard Information (DHI) milk laboratories assessed through three years of proficiency tests

8:45 El Hawat Rebecca, Massaro Selene, Amalfitano Nicolò, Iqbal Rashid, Bailoni Lucia, Tagliapietra Franco — 106
Terpene transfer from hemp (Cannabis sativa L.) and savory (Satureja hortensis L.) to milk of dairy cows supplemented with fresh leaves

9:00 Correddu Fabio, Carta Silvia, Nudda Anna — 479
Effect of dietary linseed on milk fatty acid profile, coagulation properties, and methane emission in local Sardo-Bruna cows

9:15 Mecocci Samanta, Rampacci Elisa, Strincardini Claudia, Costantini Claudio, Chiaradia Elisabetta, Acuti Gabriele, Verini-Supplizi Andrea, Giovagnoli Stefano, Cappelli Katia — 231
Stabilized bovine milk extracellular vesicles as anti-inflammatory and immunomodulatory agent on human macrophage-like cells

9:30 Cesarani Alberto, Senczuk Gabriele, Sardina Maria Teresa, Pilla Fabio, Dimauro Corrado, Portolano Baldassarre, Macciotta Nicolò, Mastrangelo Salvatore — 025
Comparison of machine learning algorithms to trace the geographical origin of raw milk using infrared spectra

9:45 Tedeschi Irene, Malacarne Massimo, Dall'Olio Stefania, Valoppi Davide, Andreoli Valentina, Zanotti Andrea, Stocco Giorgia, Summer Andrea, Cipolat-Gotet Claudio — 305
A comparative analysis of milk fat globule size and distribution in Holstein-Friesian and Reggiana cattle breeds

10:00 Dallavalle Giulia, Secchi Giorgia, Mancini Andrea, Vrhovsek Urska, Angeli Andrea, Aprea Eugenio, Zambanini Jessica, Endrizzi Isabella, Solovyev Pavel, Zanon Thomas, Franciosi Elena — 400
Promoting a circular bio-economy: use of wine cellar by-products as feed supplement for dairy cows and evaluation of the chemical and microbiological effects on dairy products

10:15 Coffee break and Poster session

Room Carignano | Session 35

Genetics:
GENOMIC STRATEGIES FOR FITNESS TRAITS

Sponsored by Vazyme
Chairs: Visentin Giulio – Ablondi Michela

8:30 Rulli Eugenio, Sbarra Fiorella, Quaglia Andrea, Mancin Enrico, Oian Angelica, Gomez Proto Guido, Mantovani Roberto, Sartori Cristina — 533
Genetic evaluation of climate effect on Maremmana young bulls reared in test station

8:45 Schiavo Giuseppina, Bovo Samuele, Bolner Matteo, Bertolini Francesca, Ribani Anisa, Taurisano Valeria, Dall'Olio Stefania, Maranzani Jessica, Bonacini Massimo, Fontanesi Luca — 316
Describing Reggiana cattle farms using genomic information from the breed population

9:00 Strillacci Maria, Ferrulli Vincenzo, Bernini Francesca, Pravettoni Davide, Bagnato Alessandro, Martucci Ilaria, Boccardo Antonio — 114
Genomic basis of Bovine Respiratory Disease resistance in preweaned dairy calves

9:15 Oian Angelica, Mancin Enrico, Gomez Proto Guido, Sartori Cristina, Rulli Eugenio, Mantovani Roberto — 330
GWAS analysis of fitness traits in autochthonous dual-purpose breeds

9:30 Carta Antonello, Usai Graziano, Casu Sara, Sechi Tiziana, Mulas Giuliana, Ligios Ciriaco, Salaris Sotero — 304
On the use of antibody responses as selection criteria to improve disease resistance in sheep

9:45 Riggio Silvia, Mastrangelo Salvatore, Carta Federica, Benanti Alessia, Portolano Baldassarre, Sardina Maria Teresa — 348
Prion protein gene polymorphisms in two Sicilian goat populations

10:00 Fabbri Maria Chiara, Biada Iliyass, Sirtori Francesco, Pulido-Rodríguez Lina, Bozzi Riccardo, Tiezzi Francesco — 070
Investigation of interaction between sheep and soil microbiota

10:15 Coffee break and Poster session

Room Venaria | Session 36

Genetics:
GENETIC SOLUTIONS FOR HEAT STRESS

Chairs: Negrini Riccardo – Pegolo Sara

10:45 *INVITED LECTURE*
Maltecca Christian
Elucidating the biology of heat stress in lactating sows at the intersection of genome microbiome and metabolome

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11:15 Bertolini Francesca, Bolner Matteo, Bovo Samuele, Schiavo Giuseppina, Zambonelli Paolo, Gallo Maurizio, Cappelloni Manolo, Fontanesi Luca — 384
Metabolomics identified new biomarkers to help describing feed efficiency in Italian Large White pigs

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11:30 Macciotta Nicolò, Dimauro Corrado, Correddu Fabio, Cesarani Alberto — 494
Development of a genetic index for heat stress tolerance in dairy sheep

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11:45 Usai Mario Graziano, Casu Sara, Salaris Sotero, Sechi Tiziana, Miari Sabrina, Mulas Giuliana, Carta Antonello — 270
Individual variability of tolerance to heat stress of Sarda ewes raised in the Mediterranean region

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12:00 Lecchi Cristina, Maggiolino Aristide, De Palo Pasquale, Landi Vincenzo, Salvi Gaspare, Ceciliani Fabrizio, Ryts Andreas, Cominetti Ornella, Raymond Frederic, Soussan Elodie, Bobkov Maxim — 498
Heat stress modifies the miRNA cargoes carried by small extracellular vesicles isolated from Holstein and Brown Swiss milk

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12:15 Landi Vincenzo, Pierini Claudia, Hidalgo Jorge, Bussiman Fernando, Maggiolino Aristide, Lasagna Emiliano, Sbarra Fiorella, Quaglia Andrea, De Palo Pasquale — 546
Assessing the impact of climate factors on the growth performance of Podolica bulls during pre-performance phases

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12:30 Lunch

Room Racconigi | Session 37

Ruminant Nutrition:
SMALL RUMINANTS AND BY-PRODUCT USE

Chairs: Nudda Anna – Battelli Marco

10:45 Nudda Anna, Carta Silvia, Correddu Fabio, Caratzu Maria Francesca, Cesarani Alberto, Pulina Giuseppe, Lunesu Mondina Francesca — 040
A meta-analysis on the relationship between agro-industrial byproducts supplementation and milk production traits in dairy sheep

11:00 Hassan Mahmood Ul, Gannuscio Riccardo, Maniaci Giuseppe, Alabiso Marco, Ciccarello Salvatore, Todaro Massimo — 210
Agro-industrial by-product: destoned olive cake as an alternative feed and ruminal fermentation modifier for dairy ewes

11:15 Gannuscio Riccardo, Hassan Mahmood Ul, Vastolo Alessandro, Tolone Marco, Maniaci Giuseppe, Calabrò Serena, Cutrignelli Monica Isabella, Todaro Massimo — 116
Effects of feeding prickly pear by-product silage on dairy ewes

11:30 Mangione Guido, Musati Martino, Mangano Fabrizio, Bertino Antonino, Luciano Giuseppe, Biondi Luisa, Cannone Marco Sebastiano, Lanza Massimiliano, Natalello Antonio — 365
Sesame seed meal as alternative protein source in growing lambs

11:45 Pietrucci Daniele, Mecocci Samanta, Luciano Giuseppe, Musati Martino, Priolo Alessandro, Milanesi Marco, Chillemi Giovanni, Cappelli Katia, Trabalza Marinucci Massimo, Forte Claudio, Natalello Antonio — 364
Characterization of lamb rumen and cecal microbiota in response to hazelnut skins and linseed dietary supplementation using 16S rRNA sequencing

12:00 Vasquez Mendosa Oscar Vicente, Elghandour Mona M.M.Y., Galeano Diaz Maria Johana Paola, Ortiz Heredia María Angélica, Salem Abdelfattah — 203
Effects of guanidinoacetic acid levels on growth performance and feed efficiency of finishing lambs

12:15 Porcu Maria Angela, Ledda Antonello, Correddu Fabio, Carta Silvia, Rubattu Roberto, Cannas Antonello — 463
Mitigation of the milk fat depression in ewes, caused by ryegrass herbage rich in water-soluble carbohydrate, by sodium bicarbonate: effects on milk fatty acid profile

12:30 Lunch

Room Stupinigi | Session 38

Welfare, Health and Behaviour: ADVANCES IN CATTLE AND BUFFALOES MANAGEMENT

Chairs: Bernabucci Umberto – Evangelista Chiara

10:45 Vitali Andrea, Grossi Giampiero, Rossi Chiara, Lacetera Nicola — 414
Summer dairy cows: THI-Heat_Load model for development of an alert-based cooling protocol

11:00 Ratto Roberta, Pietrucci Daniele, Renzi Francesco, Milanesi Marco, Mecocci Samanta, Bergagna Stefania, Acuti Gabriele, Guasco Cecilia, Chillemi Giovanni, Cappelli Katia — 458
Combination of PLF and omics to characterize heat stress response in Marchigiana breed

11:15 Abeni Fabio Palmiro, Negrini Riccardo, Ferla Andrea, Galli Andrea — 071
Comparative evaluation of subclinical ketosis risk in Lombardy using two methods based on DHI data

11:30 Lamanna Martina, Muca Edlira, Giannone Claudia, Bovo Marco, Romanzin Alberto, Formigoni Andrea, Cavallini Damiano — 064
Meta-Analytical study on feeding behavior and daily time budget management of dairy cows in free-stall housing using ChatGPT

11:45 Vecchio Domenico, Scali Federico, Maisano Antonio Marco, Fusi Francesca, Lorenzi Valentina, Di Vuolo Gabriele, Ambra Chiara Denise, Serrapica Maria, Cappelli Giovanna, Romeo Claudia Rosa, Bertocchi Luigi, Alborali Giovanni Loris, Santucci Giovanni, Zanella Adroaldo Josè, De La Cruz Luis Alberto, Bernardino Thiago, Stilwell George, De Carlo Esterina — 092
Antimicrobial use in buffalo farm and dynamic of correlation with animal welfare and biosecurity evaluated by ClassyFarm System

12:00 Cappelli Giovanna, Bosco Antonio, Di Vuolo Gabriele, Vecchio Domenico, Smeraldo Serena, Mancusi Andrea, Proroga Yolande, Martucciello Alessandra, Grassi Carlo, Serrapica Maria, Di Maro Orlandina, Napoletano Michele, Rinaldi Laura, De Carlo Esterina — 521
Risk factors for Toxoplasma gondii seropositivity and DNA detection in raw milk on dairy buffalo farms in Southern Italy

12:15 Santinello Matteo, Esposito Sergio, Purrone Sissy, Pierro Federica, Piscopo Federica, Ciaramella Paolo, Neglia Gianluca — 159
Blood metabolite profile in Italian Mediterranean buffalo: effect of parity, lactation stage, and calving season

12:30 Lunch

Room Valentino | Session 39

Monogastric Nutrition: SWINE I

Sponsored by Silvateam
Chairs: Cappai Maria Grazia – Braidot Matteo

10:45 Manoni Michele, Altomare Alessandra, Nonnis Simona, Mazzoleni Sharon, Tretola Marco, Bee Giuseppe, Silacci Paolo, Tedeschi Gabriella, Aldini Giancarlo, Pinotti Luciano 027
Evaluation of the impact of the dietary inclusion of salty and sugary former food products on the liver and the plasma profile of pigs through OMICS approaches

11:00 Luise Diana, Correa Federico, Rocchetti Gabriele, Errico Michela, Polimeni Barbara, Serra Andrea, Mele Marcello, Gallo Antonio, Lucini Luigi, Trevisi Paolo 462
Multi-omics characterisation of pig colostrum and association of its bioactive compounds and gut microbiota with the survival of piglets

11:15 Trevisi Paolo, Luise Diana, Palladino Giorgia, Palumbo Francesco, Scicchitano Daniel, Babbi Giulia, Castagnetti Andrea, Rampelli Simone, Candela Marco, Martelli Pier Luigi, Correa Federico 558
EU Circles Project: Multi-omics analysis reveals distinct microbial networks linked to a blend of chestnut and quebracho extract supplementation in weaned pigs under different farming conditions

11:30 Toscano Alessandro, Don Gregorio, Ramayo-Caldas Yuliaxis, Sanchez Juan Pablo, Pegolo Sara, Schiavon Stefano, Gallo Luigi, Giannuzzi Diana 246
Metataxonomic characterization of fecal microbiota of heavy pigs fed with different levels of Arthrospira platensis

11:45 Correa Federico, Luise Diana, Palumbo Francesco, Zurru Antonio, Biagi Giacomo, Trevisi Paolo 519
Effect of dietary microbial muramidase supplementation on weaned pigs' performance, health status and intestinal microbiota

12:00 Zurru Antonio, Trevisi Paolo, Laghi Luca, Palumbo Francesco, Correa Federico, Luise Diana 381
Effect of complete maize replacement by sorghum on health, welfare, performance and faecal microbiota of post-weaning piglets

12:15 Polimeni Barbara, Correa Federico, Luise Diana, Zurru Antonio, Palumbo Francesco, Trevisi Paolo 483
Postbiotic supplementation in gestating and lactating sows and its effects on piglets health and performances

12:30 Lunch

Room Mandria | Session 40

Precision Farming:
DATA-DRIVEN DAIRY MANAGEMENT

Chairs: Neglia Gianluca – Giannone Claudia

10:45 Zanchi Marco, La Porta Caterina, Forte Claudio, Zapperi Stefano, Ozella Laura — 102
Modeling dairy production under microclimatic variability in automatic milking systems using TSMixer

11:00 Pascarella Lorenzo, Fioretti Mauro, Melilli Caterina, Galli Andrea, Negrini Riccardo — 406
Effect of automatic milking system on udder health

11:15 Cavallini Damiano, Lamanna Martina, Silvestrelli Simone, Colleluori Riccardo, De Matos Vettori Julio, Buonaiuto Giovanni, Gallo Antonio, Cannas Antonello, Formigoni Andrea — 492
Substitution rate between partial mixed ration and robotic supplemental concentrate in high-producing dairy cows

11:30 Milanesi Marco, Pietrucci Daniele, Del Buono Davide, Litta Paolo, di Gangi Leonardo, Furlanello Cesare, Chillemi Giovanni — 389
New insights of climate effects on dairy production

11:45 Fumagalli Francesca, Boldini Annamaria, Gallo Antonio, Atzori Alberto Stanislao — 200
Feedback thinking in the dairy supply chain: system dynamics modelling of cheese factory

12:00 *INVITED LECTURE*
Bovo Marco
Precision Livestock Farming, from theory to practice

12:30 Lunch

Room Agliè | Session 41

Food Quality:
DAIRY PRODUCT QUALITY AND CHEESEMAKING PROPERTIES

Chairs: Stocco Giorgia – Zanon Thomas

10:45 Greco Margherita, Lopez Annalaura, Pavolini Marta, Tamburin Alberto, Bellagamba Federica, Moretti Vittorio Maria — 345
Quality of milk and cheese from cows grazing on mountain pasture from Italian Alps

11:00 Mangione Guido, Musati Martino, Caccamo Margherita, Bertino Antonino, Mangano Fabrizio, Natalello Antonio, Luciano Giuseppe, Priolo Alessandro — 543
Effect of grazing season on quality traits of cow ricotta cheese

11:15 Secchi Giorgia, Mancini Andrea, Dallavalle Giulia, Nicoli Maria Cristina, Marino Marilena, Innocente Nadia, Franciosi Elena — 399
Exploring natural additives for cheese preservation

11:30 Amalfitano Nicolò, El Hawat Rebecca, Benabid Hamida, Haddi Mohamed-Laid, Schiavon Stefano, Bittante Giovanni, Tagliapietra Franco — 446
Impact of different enzymatic coagulants and doses on the cheese-making ability of milk from different dairy species

11:45 Claps Salvatore, Perri Enzo, Benincasa Cinzia, Morone Giuseppe, Cifuni Giulia — 091
Dietary supplementation with by-products from olive oil mill wastewater processing in dairy cows affected the aromatic fingerprint in cheeses

12:00 Ferragina Alessandro, Molle Arnaud, Cipolat-Gotet Claudio, Stocco Giorgia — 474
Exploration of hyperspectral imaging for the discrimination of Parmigiano Reggiano and Grana Padano PDO cheeses and ripening time

12:15 Cozzi Giulio, Serva Lorenzo, Segato Severino, Berzaghi Paolo — 191
Evaluating Italian butter quality: a preliminary study of chemical and rheological factors across production sites

12:30 Lunch

Room Venaria + Room Racconigi | Session 42

Genetics:
BREEDING FOR MASTITIS RESISTANCE

Chairs: Capomaccio Stefano – Castiglioni Bianca

13.30 Vanzin Alice, Bisutti Vittoria, Giannuzzi Diana, Cecchinato Alessio, Gallo Luigi, Cánovas Angela, Pegolo Sara — 157
Identification of functional variants leading to alternative splicing associated with subclinical intramammary infection in dairy cattle

13.45 Ponzo Enrico, Moretti Riccardo, Masia Fernando, Vrieze Elisa, Sacchi Paola, Frizzarin Maria, Chessa Stefania — 308
Predicting mastitis Follow-Up using Time Series on Automatic Milking System data and Machine Learning Methods

14.00 D'Anza Emanuele, Barbato Mario, Floridia Viviana, Negrini Riccardo, Cascone Ilaria, Terlizzi Giuseppe Antonio, Rossetti Alberto, Cosenza Gianfranco, Ciotola Francesca, Albarella Sara, Peretti Vincenzo — 403
Genetics and bioindicators of mammary health in Agerolese cattle: an integrate analysis

14:15 Punturiero Chiara, Delle Donne Andrea, Ferrari Carlotta, Milanesi Raffaella, Carabaño Maria Jesus, Dìaz Clara, Ramon Manuel, Bagnato Alessandro, Strillacci Maria — 430
Mastitis and somatic cell count in lactating dairy cows: a resilience perspective

14:30 Pegolo Sara, Bisutti Vittoria, Vanzin Alice, Cecchinato Alessio, Giannuzzi Diana — 152
Analysis of long non-coding RNAs in dairy cows with subclinical mastitis caused by Streptococcus agalactiae and Prototheca spp

14:45 Cascone Ilaria, López-Catalina Adrian, Albarella Sara, Ciotola Francesca, Cosenza Gianfranco, Salzano Angela, Peretti Vincenzo, Gonzalez Recio Oscar — 346
Blood epigenetic patterns in mastitic buffaloes

15:00 Coffee Break and Poster session

15.00 / 19:00 ASPA Assembly

Room Carignano | Session 43

Ruminant Nutrition:
MINOR SPECIES AND FORAGE QUALITY

Chairs: Bailoni Lucia – Vastolo Alessandro

13.30 Battelli Marco, Rapetti Luca, Colombini Stefania, Galassi Gianluca, Pavesi Martina, Dai Xiaoxia, Menni Giorgio, Cesari Valentina, Crovetto Matteo — 245
Evaluation of different additives to improve soybean silage quality

13.45 Cella Fabrizio Giuseppe, Zucca Giovanni, Finocchi Matteo, Malizzi Tiziano, Ripamonti Alice, Mele Marcello, Mantino Alberto — 336
Chemical composition and nutritive value of leaves and stems of poplar clones in an innovative Mediterranean agroforestry system

14.00 Nieddu Lidia Nicoletta, Gallo Antonio, Mastroeni Carmelo, Fresu Mirko, Zara Severino, Ledda Antonello, Marzano Alessandra, Rubattu Roberto, Atzori Alberto Stanislao, Fancello Francesco — 469
Use of functional silage in the feeding of Sardinia dairy sheep

14:15 Petrocchi Jasinski Francesca, Evangelista Chiara, Basiricò Loredana, Vitali Andrea, Grossi Giampiero, Rossi Chiara, Turriziani Giovanni, Lacetera Nicola, Bernabucci Umberto — 397
Impact of green forage on milk yield and quality, digestibility, and feeding behavior in Italian Mediterranean buffaloes during the hot season

14:30 Bisello Jacopo, Currò Sarah, Guzzo Nadia, Amalfitano Nicolò, Cortese Martina, Bailoni Lucia, Tagliapietra Franco — 531
Comparison of NIR chemical predictions for alfalfa hay using portable and benchtop systems

15:00 Coffee Break and Poster session

Room Stupinigi | Session 44

Welfare, Health and Behaviour: EXPLORING THE COW-CALF RELATIONSHIP

Chairs: Brscic Marta – Cavallini Damiano

13.30 *INVITED LECTURE*
Veissier Isabelle
The evolution of the concept of animal welfare: from absence of suffering to positive welfare and beyond

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14.00 Dai Xiaoxia, Menni Giorgio, Liu Jing, Battelli Marco, Pavesi Martina, Rapetti Luca, Galassi Gianluca, Crovetto Matteo, Wenli Li, Colombini Stefania 223
Impact of endogenous ruminal lipopolysaccharides on functional activity in rumen mixed microbial communities

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14:15 Palladini Nicola, Algeri Stefano, Tamburini Alberto, Gislon Giulia, Bava Luciana 171
Welfare issues in cow-calf contact

14:30 Bocchi Valeria, Costa Angela, Visentin Giulio, Zappaterra Martina, Bolcato Marilena, Nanni Costa Leonardo, Padalino Barbara 311
Current management of calves in Italian dairy farms: preliminary overview on the welfare of calves

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14:45 Manfrè Claudia, Leliveld Lisette, Danyer Aytemiz, Brscic Marta, Battini Monica 271
Application of Qualitative Behaviour Assessment on cows before and after their separation from their calf in a cow-calf contact system

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15:00 Coffee Break and Poster session

Room Valentino | Session 45

Sustainability:
SUSTAINABLE STRATEGIES

Chairs: Mantino Alberto – Grossi Giampiero

13.30 Berton Marco, Sturaro Enrico, Bittante Giovanni, Gallo Luigi — 052
Effects of dietary concentrate level on protein feed-food and land use competition indicators

13:45 Ferronato Giulia, Tobanelli Noemi, Simonetto Anna, Gilioli Gianni — 280
The effect of feeding strategies on enteric and manure methane emissions in dairy cows: evidence from Italian farms

14.00 Benedetti Lorenzo, Bani Paolo, Froldi Federico, Bani Giovanni, Ferrero Anita, Struder Jean Pierre, Trevisi Erminio — 158
Effect of two commercial additives on pollutant emissions from dairy cow manur

14:15 Zangoli Chiara, Chrysanthopoulos Stamatis, Fernandes Elisabete A., Zappaterra Martina, Pocheville Salomé, Fangueiro David, Almeida André — 189
Ammonia and greenhouse gases emissions during storage of excreta from poultry fed with 15% Spirulina dietary inclusion

14:30 Correa Federico, Luise Diana, Palladino Giorgia, Secchi Nicola, Scicchitano Daniel, Babbi Giulia, Rampelli Simone, Candela Marco, Martelli Pier Luigi, Trevisi Paolo — 518
CIRCLES EU project: on-farm wastewater treatment with bioactivators reduces air pollution and modulate slurry microbiota in pig growing units

14:45 Dela Pierre Flavia, Fakhar Ali, Pedersen Johanna, Feilberg Anders, Dinuccio Elio, Kamp Jesper Nørlem — 442
The effect of increasing H_2SO_4 on NH_3 and NMVOC emissions from pig slurry application to permanent grass

15:00 Coffee Break and Poster session

Room Mandria | Session 46

Precision Farming:
GRAZING SYSTEMS AND PASTURE MONITORING

Chairs: Cecchinato Alessio – Matera Roberta

13.30 Aquilani Chiara, Confessore Andrea, Sirtori Francesco, Parrini Silvia, Dibari Camilla, Argenti Giovanni, De Guttry Luca, Pugliese Carolina 133
Does Virtual Fencing affect cattle behaviour and pasture utilization as compared to traditional grazing management?

13:45 Acciaro Marco, Frongia Andrea, Schneider Manuel, Giovanetti Valeria, Serra Gabriella, Cabiddu Andrea, Decandia Mauro, Pauler Caren 162
GPS as a tool to monitor grazing behavior of Sarda dairy ewes

14.00 Confessore Andrea, Aquilani Chiara, Sirtori Francesco, Rainis Simona, Pugliese Carolina 470
Virtual fencing vs. traditional grazing: impacts on dairy cows' milk yield and behavior assessed with an automatic milking system

14:15 Marchegiani Sara, Pasquini Marina, Trombetta Maria Federica, Ceccobelli Simone 098
Smart livestock grazing: GPS serving the extensive Marchigiana breeding system

14:30 Fatica Antonella, Tedesco Doriana, Todini Luca, Fantuz Francesco, Salimei Elisabetta 100
Traceability for a grazing equine system in inner areas of Centre-South Italy

15:00 Coffee Break and Poster session

Room Agliè | Session 47

Food Quality:
SHEEP, GOAT AND BUFFALO MILK QUALITY

Chairs: Valenti Bernardo – Carta Silvia

13.30 Stocco Giorgia, Biffani Stefano, Tiezzi Francesco, Valoppi Davide, Tedeschi Irene, Bozzi Riccardo, Fabbri Maria Chiara, Sirtori Francesco, Grande Silverio, Castiglioni Bianca, Cipolat-Gotet Claudio — 112
Factors affecting fat globules size of sheep milk

13:45 Valoppi Davide, Biffani Stefano, Castiglioni Bianca, Bozzi Riccardo, Fabbri Maria Chiara, Sirtori Francesco, Tiezzi Francesco, Grande Silverio, Tedeschi Irene, Cipolat-Gotet Claudio, Summer Andrea, Stocco Giorgia — 309
Effect of fat globules size on the technological properties of sheep milk

14.00 Bolletta Viviana, Pauselli Mariano, Lilli Emanuele, Veneziani Gianluca, Santillo Antonella, Bertino Antonino, Valenti Bernardo — 432
Animal performance and milk quality in grazing ewes supplemented a concentrated phenolic extract from olive-milling wastewaters

14:15 Boukrouh Soumaya, Noutfia Ali, Moula Nassim, Avril Claire, Hornick Jean-Luc, Chentouf Mouad, Cabaraux Jean-François — 570
Effects of Sulla flexuosa hay as alternative feed resource on goat's milk production and quality

14:30 Magro Silvia, Pozza Marta, Sartor Pietro, De Marchi Massimo, Niero Giovanni — 441
Feasibility of mid-infrared spectroscopy for the prediction of milk coagulation properties in the Alpine and Saanen goats breeds

14:45 Iommelli Piera, Musco Nadia, Lombardi Pietro, Sarubbi Fiorella, Tufarelli Vincenzo, Ceci Edmondo, Infascelli Federico, Tudisco Raffaella — 144
Fennel seed powder in the diet of dairy buffalo affects milk VOCs profile, antioxidant activity and SCD1 mRNA level

15:00 Coffee Break and Poster session

PROGRAM

Friday,
20th June 2025

Room Venaria + Room Racconigi | Session 48

Genetics:
GENOMIC APPLICATIONS FOR BIODIVERSITY II

Chairs: Colli Licia – Mastrangelo Salvatore

9:00 Persichilli Christian, Cesarani Alberto, Mastrangelo Salvatore, Ben Jemaa Slim, Carta Federica, Riggio Silvia, Benanti Alessia, Pilla Fabio, Senczuk Gabriele — 477
The North being cold, the South warm: genome-wide assessment of local sheep breeds in contrasting environmental conditions

9:15 Floridia Viviana, Arias Katherine Daniela, Bionda Arianna, Cortellari Matteo, Amato Annalisa, Lopreiato Vincenzo, D'alessandro Enrico, Goyache Felix, Crepaldi Paola, Liotta Luigi, Barbato Mario — 539
Uncovering the architecture of production-driven introgression in Cinisara cattle

9:30 Mancin Enrico, Oian Angelica, Gomez Proto Guido, Rulli Eugenio, Sartori Cristina, Mantovani Roberto — 293
Black boxing impacts of selection in Alpine cattle breeds

9:45 Ben Jemaa Slim, Senczuk Gabriele, Carta Federica, Riggio Silvia, Benanti Alessia, Sardina Maria Teresa, Cesarani Alberto, Mastrangelo Salvatore — 215
A genome-wide scan to identify signatures of selection in Sarda and Valle del Belice sheep breeds in relation to their geographical origin

10:00 Bionda Arianna, Manunta Aldo Luigi, Carta Antonello, Crepaldi Paola — 236
Preliminary study of the Caprera goat: an ancient feral population?

10:15 Di Civita Marika, Wiener Pamela, Friedrich Juliane, Marr Melissa, Clark Emily, Senczuk Gabriele, Pilla Fabio — 486
Exploring climate adaptation in European Merino sheep: a landscape genomics approach

10:30 Carta Federica, Chessari Giorgio, Riggio Silvia, Benanti Alessia, Sardina Maria Teresa, Carlentini Morena, Falchi Laura, Senczuk Gabriele, Criscione Andrea, Cesarani Alberto, Mastrangelo Salvatore — 243
Detection of homozygosity and heterozygosity regions in Southern Italian sheep breeds revealed by high-density SNP array

10:45 Coffee Break and Poster session

Room Carignano | Session 49

Welfare, Health and Behaviour: INNOVATIONS AND SUSTAINABILITY IN HORSES MANAGEMENT

Chairs: Padalino Barbara – Felici Martina

9:00 Mecocci Samanta, Porzio Elisabetta, Beccati Francesca, Pepe Marco, Paris Angelo, Bergagna Stefania, Chillemi Giovanni, Chiaradia Elisabetta, Cappelli Katia 118
Omic technology to monitoring resilience and adaptation to exercise and heat stress in athlete horses

9:15 Bordin Clara, Raspa Federica, Favaro Martina, Dino Giovanna, Gambino Francesca, Tazzini Antonio, Cerrato Giuseppina, Giordana Alessia, Boarino Alice, Padoan Elio, Tagliaferri Marta, Anchisi Emanuele, Valle Emanuela 525
From wastes to resources: using construction and demolition wastes to develop sustainable horse footing layers

9:30 Benedetti Beatrice, Freccero Francesca, Patroncini Francesca, Padalino Barbara 516
Towards a higher level of welfare in pasture-kept horses: development and application of a new welfare protocol

9:45 Gemma Pantaleo, Padalino Barbara 404
Animal welfare assessment of urban carriage horses in Malta

10:00 *INVITED LECTURE*
Vervuert Ingrid
Future challenges and welfare in forage feeding for sport horses

10:45 Coffee Break and Poster session

Room Stupinigi | Session 50

Aquaculture:
MARINE SPECIES

Chairs: Terova Genciana – Carbonara Claudia

9:00 Della Malva Antonella, Santillo Antonella, Caroprese Mariangela, Marino Rosaria, Francavilla Matteo, Albenzio Marzia — 224
Exploring the nutritional value of Mytilus galloprovincialis from the Gargano area (Apulia Region)

9:15 Tarricone Simona, Colonna Maria Antonietta, Ragni Marco, Trani Roberta, Giangrande Adriana, Basile Graziana, Stabili Loredana, Carbonara Claudia, Longo Caterina — 408
Flesh quality, shelf-life, and sensory properties of Sea Bream reared in a Mediterranean coastal Integrated Multi-Trophic Aquaculture (IMTA) system

9:30 Kalemi Violeta, Rimoldi Simona, Monteiro Marta, Valente Luisa, Terova Genciana — 122
Substitution of fishmeal with an insect meal blend and the effects on the intestinal microbiota of European seabass

9:45 Zarantoniello Matteo, Cattaneo Nico, Conti Federico, Cardinaletti Gloriana, Sener Idris, Ceccobelli Simone, Olivotto Ike — 031
Employing a natural microencapsulated antioxidant to mitigate dietary microplastic accumulation and oxidative stress response in juvenile European seabass (Dicentrarchus labrax)

10:00 Fanizza Cecilia, Milián-Sorribes Maria Consolación, Jover-Cerdá Miguel, Martìnez-Llorens Silvia, Trocino Angela, Tomás-Vidal Ana — 054
Estimation of protein and fat requirements for greater amberjack (Seriola dumerili) juveniles reared in RAS

10:15 Roncarati Alessandra, Quagliardi Martina, Antenucci Emanuele, Di Iorio Michele, Coccia Isabella, Santoianni Celeste, Rusco Giusy, Cariglia Michela, Pozzato Luca, Iaffaldano Nicolaia — 248
Monitoring water temperature during the growth of gilthead sea bream juveniles in sea cage aquaculture

10:30 Sicuro Benedetto, Akther Kazi Rabya, Tafuro Valentina — 082
Aquaculture in the Mediterranean region: key factors and future trends

10:45 Coffee Break and Poster session

Room Valentino | Session 51

Monogastric Nutrition: SWINE II

Chairs: Pinotti Luciano – Correa Federico

9:00 Graziosi Maria Vittoria, Luise Diana, Correa Federico, Zurru Antonio, Trevisi Paolo, Biagi Giacomo — 526
Reduction of amylose-amylopectin ratio in low-protein diets for fattening pigs: performance, health, behavioral, and environmental implications

9:15 Lin Peng, Tretola Marco, Pinotti Luciano, Bee Giuseppe, Schlegel Patrick — 360
Growth performance and nutrient balance of pigs fed low protein diets without mineral phosphate supplementation

9:30 Antonacci Alessandro, Bee Giuseppe — 187
Feeding low-protein or standard diets to growing-finishing pigs reared under environmental stressors: effects on growth and carcass composition

9:45 Tono Veronica, Toscano Alessandro, Don Gregorio, Giannuzzi Diana, Gallo Luigi, Cecchinato Alessio, Schiavon Stefano — 264
Growth performance and carcass quality of heavy pigs fed ad libitum diets with decreasing SID lysine contents

10:00 Don Gregorio, Giannuzzi Diana, Toscano Alessandro, Tono Veronica, Schiavon Stefano, Gallo Luigi — 101
Effects of a partial to total replacement of soybean meal with spirulina powder in the diets for growing pigs on fatty acid profile of loin, lard, ham trimming and liver fat

10:15 Luise Diana, Zurru Antonio, Laghi Luca, Palumbo Francesco, Correa Federico, Trevisi Paolo — 110
Increasing the energy and lysine content of sow transition diets can improve litter performance and modulate colostrum composition

10:30 Marchetti Luca, Rebucci Raffaella, Piantoni Caterina, Bontempo Valentino — 214
Effects of a combination of the active form of Vitamin D and natural triterpenes on sows health and productivity

10:45 Coffee Break and Poster session

Room Mandria | Session 52

Precision Farming:
SENSORS FOR BEHAVIOURAL MONITORING

Sponsored by MSD Animal Health
Chairs: Dalla Costa Emanuela – Antognoli Veronica

9:00 Cecchinato Alessio, Giannuzzi Diana, Rovetta Carlo, Bisutti Vittoria, Pegolo Sara, Arazi Alon, Katz Gil, Trevisi Erminio, Mele Marcello, Gallo Luigi, Tagliapietra Franco, Schiavon Stefano, Macedo Mota Lucio Flavio — 209
Leveraging 3D accelerometer data to predict heat stress in dairy cows

9:15 Cabbia Anita, Braidot Matteo, Cavallini Damiano, Spanghero Mauro, Romanzin Alberto — 273
Evaluation of feeding behaviour in growing bulls with an ear-tag accelerometer

9:30 Mondini Sara, N'cho Chris Major, Zucali Maddalena, Niu Mutian, Cossa Stefano, Sandrucci Anna — 439
Detection of on-farm indicators for early signals of lameness in dairy cows using generalized additive models

9:45 Gislon Giulia, Mondini Sara, Zucali Maddalena, Pavolini Marta, Bava Luciana, Canali Elisabetta, Sandrucci Anna — 562
Integrated sensor data for monitoring calves' condition

10:00 Pavolini Marta, Gislon Giulia, Tamburini Alberto, Bonizzi Serena, Zucali Maddalena, Moretti Vittorio Maria, Mattiello Silvana, Sandrucci Anna — 420
Use of precision livestock farming technologies on dairy cows in a mountain environment

10:15 Mattiello Silvana, Celozzi Stefania, Battini Monica, Sandrucci Anna, Ntalampiras Stavros, Presti Giorgio, Ludovico Luca A., Petrera Francesca, Abeni Fabio — 029
Monitoring the time of calving in dairy cows by means of vocalizations

10:45 Coffee Break and Poster session

Room Agliè | Session 53

Companion Animals: NUTRITION AND HEALTH

Chairs: Cutrignelli Monica – Luciano Alice

9:00 Stefanon Bruno, Sgorlon Sandy, Sandri Misa, Balouei Fatemeh 302
Variation of faecal microbiota of bitches during pregnancy and lactation on development of faecal microbiota of puppies during lactation and at weaning

9:15 Cuccaro Bianca, Albarella Sara, Ciotola Francesca, Martano Manuela, Restucci Brunella 069
Analysis of BRCA gene SNPs in dogs with mammary tumor

9:30 Ruggiero Alessio, Ferrara Maria, Vastolo Alessandro, Piccirillo Barbara, Bergero Domenico, Cutrignelli Monica Isabella 160
Functional ingredients in cats nutrition

9:45 Peripolli Chiara, Danyer Erdem, Fusi Eleonora, Siani Gerardo, Ricci Rebecca 329
Homemade diets for dogs: owners motivation and management

10:00 *INVITED LECTURE*
Mussa Pier Paolo
Evolution of pet animal nutrition in Italy: scientific, technological and professional aspects

10:45 Coffee Break and Poster session

Room Venaria + Room Racconigi | Session 54

Genetics:
GENETIC STRATEGIES FOR ECONOMIC TRAITS

Chairs: Crepaldi Paola – Cesarani Alberto

11.15 Salaris Sotero, Usai Mario Graziano, Casu Sara, Miari Sabrina, Pernisa Annalisa, Negro Alessio, Grande Silverio, Carta Antonello 294
Genetic evaluation of Sarda sheep for milk protein content based on genomic information and a female reference population

11.30 Santomassimo Chiara, Mariotti Federico, Petrini Andrea, Lasagna Emiliano, Quaglia Andrea, Sbarra Fiorella, Sarti Francesca Maria 219
Genetics and meat quality: challenges and perspectives in Vitellone Bianco dell'Appennino Centrale

11.45 Giontella Andrea, Silvestrelli Maurizio, Cucciniello Michael, Cocciolone Alessandro, Pieramati Camillo, Sarti Francesca Maria 262
Phenotypic and genetic study of hair whorls in the Maremmano horse and their correlations with the temperament index

12.00 Ablondi Michela, Asti Vittoria, Valle Emanuela, Stocco Giorgia, Bordin Clara, Moretti Riccardo, Zanotti Andrea, Sabbioni Alberto 237
Genetic parameters of horse international longitudinal show jumping results

12.15 Minozzi Giulietta, De Iorio Maria Grazia, Pagnacco Giulio 193
Selective breeding for Varroa Sensitive Hygiene (VSH) behavioral trait in honey bee (Apis mellifera) colonies: initial results of four years of selection

Room Carignano | Session 55

Welfare, Health and Behaviour: BEEKEEPING, HORSES AND PIGS FARMING

Chairs: Gottardo Flaviana – Luise Diana

11.15 Porzio Elisabetta, Busechian Sara, Mecocci Samanta, Pepe Marco, Chillemi Giovanni, Chiaradia Elisabetta, Cappelli Katia, Rueca Fabrizio, Beccati Francesca 088
The use of a fitness tracker to analyze heart rate variability in show jumping horses during standard exercise test in warm and cold environment

11.30 Bordin Clara, Zanchi Marco, Ozella Laura, Valle Emanuela 478
Strides to success: how gait and technique shape performance in show jumping

11.45 Favaro Daniele, Lazzarin Stella Bernadette, Moscon Elisa, Tonon Francesco, Contiero Barbara, Gottardo Flaviana 488
Open cage farrowing system: balancing welfare and productivity

12.00 Danieli Pier Paolo, Manganello Federico, Lazzari Filippo 506
Effectiveness of Fe (II) supplementation in Italian honey bee (Apis mellifera ligustica Spin.) under laboratory conditions

12.15 Coppola Francesca, Sagona Simona, Tafi Elena, Orlando Caterina, D'Onofrio Chiara, Boni Chiara Benedetta, Casini Lucia, Palego Lionella, Betti Laura, Giannaccini Gino, Felicioli Antonio 030
Effects of coconut oil-enriched diet administration on honey bees' survival and health

Room Stupinigi | Session 56

Aquaculture:
MISCELLANY

Chairs: Parisi Giuliana – Fanizza Cecilia

11.15 *INVITED LECTURE*
Brambilla Fabio
Sustainability and aquaculture: responsible change of diets

11.45 Rimoldi Simona, Kalemi Violeta, Betancor Mónica, Saroglia Marco, Terova Genciana 041
How nutritional programming and genotype shape the gut microbiota and influence growth of Atlantic salmon

12.00 Birolo Marco, Trabacchin Veronica, Triolone Stefano, De Bonis Marina, Uberti Giordano, Sambo Paolo, Nicoletto Carlo 222
Optimising stocking density of Largemouth bass (Micropterus salmoides) in coupled aquaponic systems

12.15 D'Agaro Edo, Gibertoni Pierpaolo, Esposito Stefano 425
New genomic tools for the conservation and management of native brown trout (Salmo trutta) in the Valle d'Aosta valley

12.30 Trabacchin Veronica, Nicoletto Carlo, Triolone Stefano, De Bonis Marina, Uberti Giordano, Sambo Paolo, Birolo Marco 450
Effects of dietary microelements supplementation on growth performance and fillet quality of Largemouth bass (Micropterus salmoides) in a coupled aquaponic system with lettuce (Lactuca sativa)

Room Valentino | Session 57

Monogastric Nutrition: RABBIT, POULTRY AND DONKEY

Chairs: Iaffaldano Nicolaia – Marchetti Luca

11.15 Xiccato Gerolamo, Bordignon Francesco, Pascual Anton, Birolo Marco, Zomeño Cristina, Trocino Angela — 057
Role of the dietary supplementation of arginine and valine: health status, digestibility, and performances of growing rabbits

11.30 Mainardi Edda, Rossi Raffaella, Ondruska Lubomir, Vizzarri Francesco — 120
Dietary supplementation with Lauraceae and Chlorellaceae in growing rabbits: effects on meat quality parameters

11.45 Bosa Luigia, Bernabucci Gloria, Di Federico Francesca, Dal Bosco Alessandro, Mattioli Simona, Mancinelli Cartoni Alice, Primi Riccardo, Girotti Pedro, Castellini Cesare — 217
Grazing behaviour and meat quality in different rabbit genotypes reared in outdoor conditions

12.00 Petrosillo Elena, Lanzoni Davide, Cenati Clara, Perricone Vera, Giromini Carlotta, Cheli Federica, Savoini Giovanni — 216
Effects of Euglena gracilis supplementation on growth performance, antioxidant status, meat quality in broiler chickens

12.15 Colonna Maria Antonietta, Carbonara Claudia, Tufarelli Vincenzo, Losacco Caterina, Tedone Luigi, Giannico Francesco, Fortunato Mariarosaria, Selvaggi Maria, Ragni Marco, Tarricone Simona — 299
Effect of zinc-enriched Camelina sativa supplementation in broiler diets on meat quality and sensory properties

12.30 Volpe Jacopo, Pittarello Marco, Nota Ginevra, Lombardi Giampiero, Lonati Michele — 459
Donkey feeding behavior in shrub- and tree-encroached pastures in Gran Paradiso National Park

Room Mandria | Session 58

Precision Farming:
INNOVATION AND SUSTAINABILITY IN LIVESTOCK

Sponsored by MSD Animal Health
Chairs: Salzano Angela – Presutti Livia

11.15 Negrini Riccardo, Barbato Mario, D'Alessandro Enrico, Liotta Luigi, Cassandro Martino, Ciardella Giorgio, Nardone Mario, Cicagna Iosef, Valentini Riccardo, Coppola Valerio, Ruggeri Federico, Melilli Caterina, Nardone Alessandro 256
InnovaRE: Research and application of innovative tools to improve resilience in ruminants

11.30 Ledda Antonello, Azzena Margherita, Domenica Giovanna, Atzori Alberto Stanislao 569
Precision livestock farming with APPàre, a digital platform for feeding and management of sheep farming in Sardinia

11.45 Steri Roberto, Iacurto Miriam, Canini Francesco, Meo Zilio David 395
Technical and practical aspects of using PLF tools in a buffalo farm: the SensorHost Software

12.00 Mastroeni Carmelo, Colombo Marco, Novara Valentina, Carboni Eliana, Gallo Antonio 440
Comparing two different weighting systems to improve whole-plant corn silage quality in the top layer of a farm bunker

12.15 Canossa Maddalena, Atzori Alberto Stanislao, Fiorbelli Erica, Gallo Antonio 178
An application of system thinking approach to study complex problems in animal nutrition: a case study of feeding behavior

12.30 Rezende Marcos, Rammauro Vittorio, Rossoni Attilio 451
Advantages of precision livestock data sharing platforms in the genomic era

Room Agliè | Session 59

Companion animals: GENETICS AND GENOMICS

Chairs: Ciotola Francesca – Marelli Stefano Paolo

11.15 Bionda Arianna, Crepaldi Paola, Liotta Luigi 228
Exploring the genomic basis of dental agenesis in Labrador Retrievers

11.30 Hernaiz Adelaida, Calvo Jorge Hugo, Cagnotti Giulia, Zaragoza Pilar, Ala Ugo, D'Angelo Antonio, García-Belenguer Sylvia, Martín-Burriel Inmaculada 312
Genomic study of idiopathic epilepsy in dogs: a natural model for human epilepsy

11.45 Boccuni Sara, Shoemake Claire, Liotta Luigi, Attard George 255
Insights into history and phenotypical traits of the maltese Hunting Dog (Kelb tal-Kaċċa ta' Malta)

12.00 Floridia Viviana, Bionda Arianna, Boccuni Sara, Shoemake Claire, Crepaldi Paola, Attard George, Liotta Luigi 221
Genetic characteristics for a breed standard definition of the Maltese Hunting Dog (Kelb tal-Kaċċa ta' Malta)

12.15 Moretti Riccardo, Viglietti Antonio, Sartore Stefano, Chessa Stefania, Sacchi Paola 333
Preliminary genomic analysis of an autochthonous dog population from the San Pietro Island

12.30 Marelli Stefano, Cannas Simona, Frattini Stefano, Polli Michele, Strillacci Maria 429
Phenotypical and Genomic analysis of Sila Sheepdog (Canis lupus familiaris)

POSTER

ALTERNATIVE PROTEINS

Tignani Maria Vittoria, Secci Giulia, Pulido-Rodríguez Lina, Parisi Giuliana 125
Evaluation of the physico-chemical stability of cricket meal and dried whole cricket during storage at room temperature

Addeo Nicola Francesco, Lanzieri Maria Rosaria, Vozzo Simone, Di Rosa Ambra, Accetta Francesca, Panettieri Valentina, Bovera Fulvia, Musco Nadia 136
Hermetia illucens as functional feed for laying hens: effect on productive performance

Palumbo Bianca Federica, Dalle Zotte Antonella, Deruytter David 253
Impact of sex ratio manipulation on reproductive output in Tenebrio molitor

Cappai Maria Grazia, Arminu Sergio, Schiavone Achille, Serra Giuseppe 545
Yellow mealworm (Tenebrio molitor) rearing on different substrates affects feed intake in captive Sardinian partridges (Alectoris barbara)

AQUACULTURE

Zarantoniello Matteo, Galdelli Alessandro, Mancini Adriano, Pasquini Marina, Fatone Francesco, Olivotto Ike 076
Reducing food losses by developing an automated hatching system prototype for early stage embryos of rainbow trout (Oncorhynchus mykiss)

Zarantoniello Matteo, Tombolini Lorenzo, Trombetta Maria Federica, Eusebi Anna Laura, Fatone Francesco, Olivotto Ike 061
Nature-based solutions for wastewater management towards a sustainable aquaculture: the CARDIMED case study

Colli Licia, Riccioni Giulia, Colussi Silvia, Fariano Lucio, Valenzano Vittorio, Bergamino Cinzia, Milanese Giulia, Gini Martina, Scala Sonia, Prearo Marino, Pastorino Paolo, Ajmone Marsan Paolo 240
The RESILTROUT project: identifying genetic markers associated to disease resistance and heat stress resilience in farmed rainbow trout (Oncorhynchus mykiss)

Antenucci Emanuele, Di Iorio Michele, Santoianni Celeste, Coccia Isabella, Galosi Livio, Cariglia Michela, Pozzato Luca, Roncarati Alessandra, Iaffaldano Nicolaia 249
Preliminary set-up of a digital system for the fish welfare improvement in cage aquaculture

Gai Francesco, Randazzo Basilio, Meola Martina, Caccamo Letteria, Carboni Stefano, Concu Danilo, Loi Barbara, Miccoli Andrea, Mirto Simone, Perdichizzi Anna, Vallainc Dario, Maricchiolo Giulia 481
Dietary effects on growth, gut health and immune response of flathead grey mullet fed black soldier fly meal

Manuguerra Simona, Arena Rosaria, Rannou Maxime, Grimaudo Federico, Curcuraci Eleonora, Santulli Andrea, Messina Concetta 573
Technology transfer for Haliotis turberculata farming in Sicily: evaluation of adaptive responses to culture conditions

COMPANION ANIMALS

Llobat Lola, Sechi Sara, Liotta Luigi, Amato Annalisa, Cavallo Carmelo, Cocco Raffaella 073
Breed-specific hematological phenotypes in dogs apparently healthy but infected by zoonotic pathogens: the case of Fonnese and Cirneco dog breeds

Armone Rosangela, Nava Vincenzo, Alizzi Antonino Filippo Maria, Randazzo Andrea, Chiofalo Biagina 128
Hydrolyzed feather meal in dog nutrition: dry food proximate composition, amino acid content, and biogenic amines

Atuahene David, Balouei Fatemeh, Stefanon Bruno, Martello Elisa, Sandri Misa, Meineri Giorgia 138
Effects of a hepatoprotective supplement on liver function, inflammation markers, and gut microbiota in overweight dogs

Accetta Francesca, Armone Rosangela, Di Rosa Ambra, Stefanon Bruno, Chiofalo Biagina 323
Hydrolyzed feather meal in dog nutrition: application of electronic senses on extruded diet

Martello Elisa, Perondi Francesca, Lonigro Nicolò, Bruni Natascia, Bigliati Mauro, Costale Annalisa, Meineri Giorgia 455
Effects of Saccharomyces cerevisiae DSM 34246 var. boulardii supplementation on nutritional status, fecal parameters, and overall well-being in healthy adult breeding cats and dogs

Persichilli Christian, Mastrangelo Salvatore, Di Civita Marika, Senczuk Gabriele, Zorzetto Chiara, Ciampolini Roberta 487
Genome-wide characterization of a local heeling dog population from Northern-Apennines

FOOD QUALITY

Brugiapaglia Alberto, Provera Riccardo, Pennisi Francesco, Mois Sara, Pezzolato Marzia, Greco Alfredo, Bozzetta Elena, Esposito Giovanna 051
Effect of High-Pressure Processing on texture of sea bream (Sparus aurata) fillets

Provera Riccardo, Brugiapaglia Alberto, Pennisi Francesco, Pezzolato Marzia, Greco Alfredo, Bozzetta Elena, Esposito Giovanna 062
High pressure processing and cryogenic treatments to kill Anisakis in fish fillet and near infrared spectroscopy to verify their application

Pulido-Rodríguez Lina, Parrini Silvia, Secci Giulia, Parisi Giuliana 117
Discriminant analysis to classify two fish species based on geographical origins and farming systems using FT-NIRS

Polidori Paolo, Vincenzetti Silvia, Pucciarelli Stefania, Polzonetti Valeria, Renzi Sofia 121
Nutritional characterization of a fermented beverage from donkey milk

Accetta Francesca, Armone Rosangela, Lanzieri Maria Rosaria, Bovera Fulvia, Di Rosa Ambra 137
Hermetia illucens as functional feed for laying hens: effect on egg quality

Dal Bosco Alessandro, Di Federico Francesca, Mattioli Simona, Bosa Luigia, Castellini Cesare 148
Alfalfa and linseed oil in rabbit diet to improve sustainability and healthiness of the meat

Mattioli Simona, Di Federico Francesca, Angelucci Elisa, Castellini Cesare, Bosa Luigia, Dal Bosco Alessandro 150
Meat quality of breast and drumstick of different ECC-approved chicken genotypes

Rebucci Raffaella, Gambazza Giuseppe, Dal Borgo Alice, Zeni Niko Gioacchino, Marchetti Luca, Lanzoni Davide, Colombini Lorenzo, Giromini Carlotta, Zaniboni Luisa 169
Impact of dietary hemp seeds in an agroecological farming system (HappyHens): functional and nutritional features of eggs from different layer breeds

Oswaldo Botia Carreño Edwin, Elghandour Mona M.M.Y., Garcia Martinez José Eduardo, Yllescas Uriel Lopez, Salem Abdelfattah 201
Effect of microencapsulated Yucca shidigera extract on milk production and composition in dairy goats

Marino Rosaria, Caroprese Mariangela, Della Malva Antonella, Santillo Antonella, Ciliberti Maria Giovanna, Sevi Agostino, Albenzio Marzia 235
Nutritional properties of Podolian meat: the impact of dietary forage to concentrate ratio

Arango Sheyla, Bailoni Lucia, Guzzo Nadia, Bianco Emanuele, Simonetti Emilio, Zerbinati Elena, Rainis Simona 267
Effect of replacing corn silage with alternative crops on milk yield and quality in Italian Simmental dairy cows

Singh Yazavinder, Mugnai Cecilia, Forte Claudio, Agradi Stella, Dalle Zotte Antonella, Blanc Simone, Costamagna Chiara, Cullere Marco 290
Sustainable rabbit production: carcass traits, physical meat quality, and shelf-life of two local breeds and a commercial hybrid

Chessari Giorgio, Tumino Serena, Cremonesi Paola, Biscarini Filippo, Avondo Marcella, Marletta Donata, Castiglioni Bianca 297
Milk microbiota composition in Girgentana goat breed

Varricchio Maria Luisa, Masucci Felicia, Scalera Grazia, Lambiase Claudia, Serrapica Francesco, De Rosa Giuseppe, Di Francia Antonio 301
Olive residues as a cost – effective feed supplement: effects on milk quality in small dairy farms

Spina Anna Antonella, Virga Antonino Nazareno, Furfaro Maria Elena, Chiofalo Vincenzo, Madeo Alessandro, Britti Domenico, Randazzo Cinzia, Bosco Georgiana, Morittu Valeria Maria 339
Inclusion of linseed and grape-derived antioxidants in the diet of Apulo-Calabrese x Goland pigs: effects on animal performance and meat quality

Ponte Marialetizia, Maggiolino Aristide, Marino Rosaria, Bonanno Adriana, Forte Lucrezia, Della Malva Antonella, De Palo Pasquale, Sevi Agostino, Di Grigoli Antonino 341
Milk production of ewes fed diets integrated with encapsulated or non-encapsulated lemon essential oil

Palumbo Maria Antonietta, Lucchini Franco, Cocconcelli Pier Sadro, Ajmone Marsan Paolo 351
In vitro production of bovine hepatocyte growth factor

Carta Silvia, Correddu Fabio, Steri Roberto, Meo Zilio David, Fenu Antonio, Rubattu Roberto, Cesarani Alberto, Pulina Giuseppe, Nudda Anna 398
Effect of grape pomace in the diet of ewes during the mid-lactation period on milk fatty acid profile and methane emissions

Niero Giovanni, Visentin Elena, Cipolat-Gotet Claudio, Stocco Giorgia, Ablondi Michela, Summer Andrea, Penasa Mauro 401
Determination of k-casein B in bovine milk through HPLC and ELISA techniques

Carta Silvia, Sanna Manuela, Murgia Marco, Nudda Anna, Mangia Nicoletta 402
Microbiological, nutritional, and sensorial characterization of bottarga di muggine produced in the east and west coast of Sardinia

Silvi Alina, Casarosa Laura, Vichi Francesca, Gasparoni Elisa, Ripamonti Alice, Tognocchi Monica, Tinagli Sara, Serra Andrea, Conte Giuseppe, Mantino Alberto, Mele Marcello 415
Effects of brewer's spent grain in dairy sheep diet on yield, nutritional quality and volatile organic compound profile of cheese

D'Ambra Katia, Trovato Roberta, Minelli Giovanna, Forte Claudio, Lo Fiego Domenico Pietro 435
Influence of pig dietary supplementation with hazelnut skin (HS) or hazelnut skin green extract (HSE) on live performance, carcass characteristics and meat quality of heavy pigs

Cavallo Carmelo, Lopreiato Vincenzo, Bosco Georgiana, Litrenta Federica, Randazzo Cinzia, Scalisi Marco, Amato Annalisa, Floridia Viviana, Liotta Luigi 452
iSafe-Graze: selection ofpProbiotic Lactic Acid Bacteria as starter cultures to enhance Conjugated Linoleic Acid content in sheep's milk cheese

Palazzo Marisa, Tavaniello Siria, Grassi Giulia, Peng Meng, Teshale Dereje Birara, Maiorano Giuseppe 460
Effect of feeding olive mill wastewater (Olea europaea L.) on meat quality of Podolian young bulls

Di Rosa Ambra, Accetta Francesca, Chiofalo Vincenzo, Furfaro Maria Elena, Virga Antonino Nazareno, Bonello Federica 490
Towards sustainable beekeeping: Warrè (people's) vs Dadant-Blatt hives. Evaluation of chemical and aromatic profile of Sicilian Acacia (Robinia pseudoacacia) Honey

Cremonesi Paola, Bonazza Francesca, Severgnini Marco, Castiglioni Bianca, Brasca Milena, Pizzi Flavia, Silvetti Tiziana, Morandi Stefano, Cipolat-Gotet Claudio, Turri Federica 514
Unveiling the unique microbiome and nutritional profile of milk from the caprine Nera di Verzasca local breed

Castiglioni Bianca, Cremonesi Paola, Ceccarani Camilla, Silvetti Tiziana, Morandi Stefano, Brasca Milena 517
Influence of cattle breeds on microbiota and quality of Valtellina Casera PDO cheese

Marino Vita Maria, Schadt Iris, La Terra Stefania, Belvedere Giovanni, Caccamo Margherita, Caggia Cinzia 524
Lysozyme and total antioxidant capacity in raw milk of Ragusano donkey: effect of lactation stage and production period

Currò Sarah, Marcolin Martina, Balzan Stefania, Fasolato Luca, Haftvani Geghani Taroyan, Chiarello Gian Luca, Costa Annamaria, Di Giancamillo Alessia, Cherif Nadia, Temraz Tarek, Radaelli Giuseppe, Fonsatti Elisa, Bortoletti Martina, Bertotto Daniela 565
Photocatalytic water remediation for sustainable fish farming: effect on rainbow trout microbial contamination and shelf-life

Fancello Francesco, Carboni Maria Rosaria, Nieddu Lidia Nicoletta, Fresu Mirko, Acciaro Marco, Piga Paola, Forte Lucrezia, Maggiolino Aristide, Atzori Alberto Stanislao 566
Effect of aging facility on chemical-physical and microbiological characterization of Limousine dry-aged meat

Al Rharad Asma, El Aayadi Soufiane, Belabbass Nouhaila, Mendes De Souza Poliana, Boukrouh Soumaya 572
Chemical composition of camel meat: a meta-analysis and meta-regression study

GENETICS

Zanon Thomas, Oian Angelica, Mantovani Roberto, Gauly Matthias 020
Veterinary treatment data from the electronic recording system for genetic selection in the Alpine Grey cattle breed

Karatosidi Despoina, Avgeris Euthimios, Michailidis Georgios 035
Investigation of genetic polymorphisms in Estrogen and Prolactin gene receptors in the autochthonous Greek black pig breed

Sbarra Fiorella, Quaglia Andrea, Bittante Giovanni, Mantovani Roberto 063
Genetics of temperament in five Italian beef cattle breeds

Sabbioni Alberto, Cerati Carlo, Sfrisi Emanuele, Benaglia Paolo 075
Environmental factors affecting the quality of boar semen for AI

Colombi Daniele, Perini Francesco, Pedota Giuseppina, Sbarra Fiorella, Quaglia Andrea, Sarti Francesca Maria, Lasagna Emiliano 107
Evaluation of genetic parameters for milk composition and technological properties in Podolica cattle breed

Parrini Silvia, Mercat Marie-José, Amaral De Jesus Andreia, Karolyi Danijel, Căndek Potokar Marjeta, Restoux Gwendal, Fabbri Maria Chiara, Crovetti Alessandro, Sirtori Francesco, Bozzi Riccardo 113
Local pig and chicken breeds: weaknesses, strengths and challenges by Italian stakeholder concept

Santillo Antonella, Caroprese Mariangela, Marino Rosaria, di Corcia Martina, Biancardi Valentina, Bruno Silvia, Martino Nicola Antonio, Monaco Davide, Temerario Letizia, Mastrorocco Antonella, Dell'Aquila Maria Elena, Lacalandra Giovanni Michele, Landi Vincenzo, Selvaggi Maria, Ciani Elena, Albenzio Marzia 130
Mapping the biodiversity in small ruminants. The LOCAL project in Apulia Region

Cosenza Gianfranco, Fulgione Andrea, Albarella Sara, Ciotola Francesca, Gallo Daniela, Pauciullo Alfredo 143
Exploring genetic variability at goat CSN2 locus using novels PCR based methods

Gabbianelli Federica, Milanesi Marco, Basiricò Loredana, Pietrucci Daniele, Macchioni Paola, Bernabucci Gloria, Arcuri Chiara, Danieli Pier Paolo, Picarone Ludovica, Bernabucci Umberto, Vitali Andrea, Lacetera Nicola, Ronchi Bruno, Chillemi Giovanni, Primi Riccardo 147
Genetic variability characterization of the "Leprino di Viterbo" rabbit breed.

Sarti Francesca Maria, Galeazzi Sara, Giovannini Samira, Cocciolone Alessandro, Grande Silverio, Sylla Lakamy 204
Phenotypic characterization of ram's reproductive system: preliminary investigation for the development of a fertility index

Di Iorio Michele, Antenucci Emanuele, Rusco Giusy, Cerolini Silvia, Iaffaldano Nicolaia 227
Phenotypic characterization of two native Italian turkey breeds: a comparative study

Arcuri Chiara, Picarone Ludovica, Pietrucci Daniele, Gabbianelli Federica, Porcai Gabriella, Cosenza Gianfranco, Gomez Mayra, Chillemi Giovanni, Milanesi Marco 229
Performance evaluation of the new SNPs array designed for Mediterranean river buffalo breed

Turri Federica, Negro Alessio, Pizzi Flavia, Grande Silverio, Biffani Stefano 233
Constitution of a semen cryobank for the conservation of the Italian small ruminant local breeds

Taurisano Valeria, Ribani Anisa, Bovo Samuele, Schiavo Giuseppina, Bertolini Francesca, Schiavitto Michele, Fontanesi Luca 239
BCO2 allele frequencies in many rabbit breeds and populations: insights from the spread of a genetic defect

Taurisano Valeria, Ribani Anisa, Utzeri Valerio Joe, Sami Dalal, Kate Johnson, Fontanesi Luca 242
Honey bee genetics from honey samples: monitoring the diffusion of Apis mellifera mitochondrial DNA lineages in Emilia Romagna over seven years

Bolner Matteo, Bovo Samuele, Schiavo Giuseppina, Bertolini Francesca, Gallo Maurizio, Fontanesi Luca 247
An initial genome-wide association study for haematological and blood clinical-biochemical parameters in Italian Duroc pigs

Ablondi Michela, Asti Vittoria, Danese Tommaso, Bordin Clara, Ozella Laura, Moretti Riccardo, Sacchi Paola, Summer Andrea, Sabbioni Alberto, Mikko Sofia, Valle Emanuela 250
CHAMP: Combining Horse Athletic Measurements with Precision Genomics

Asti Vittoria, Ablondi Michela, Moretti Riccardo, Valle Emanuela, Ozella Laura, Danese Tommaso, Sabbioni Alberto, Summer Andrea 260
Meta-analysis on early traits genetically correlated with later performance in life in horses

Asti Vittoria, Zanotti Andrea, Ablondi Michela, Malacarne Massimo, Sabbioni Alberto 263
Focus on genetic diversity within the InnoVaDiv project

Tonamo Tema Andualem, Profiti Margherita, Stocco Giorgia, Cipolat-Gotet Claudio, Summer Andrea, Chessa Stefania 265
Implementation of sheep production system through genomics and phenomics: preliminary results

Bruno Silvia, Alashqar Sara, Letaief Neyrouz, Pauciullo Alfredo, Ciani Elena, Hasan Alhadded 266
In silico functional polymorphisms analysis for milk-related genes in Camelus dromedarius species

Tarricone Simona, Colonna Maria Antonietta, De Vito Nicolò, Lacitignola Massimo, Gerardi Domenico, La Gioia Giuseppe, Campanile Domenico, Carone Maria Teresa, Cardone Giuseppe Giorgio, Ragni Marco 300
European turtle dove (Streptopelia turtur) in Apulia: preliminary estimate of the breeding population abundance

Chessari Giorgio, Reich Paula, Criscione Andrea, Mastrangelo Salvatore, Tumino Serena, Carlentini Morena, Bordonaro Salvatore, Tetens Jens, Marletta Donata 307
Heterozygosity-rich regions survey in Sicilian and worldwide horse breeds using genome-wide imputed data

Gulinelli Marta, Moretti Riccardo, Sartore Stefano, Perona Giovanni, Mimosi Antonio, Sacchi Paola, Cornale Paolo, Chessa Stefania 315
BECH. GRIS Project: genetic characterization, conservation and management of the Grigia delle Valli di Lanzo local breed

Schiavone Achille, Stoppani Nadia, Soglia Dominga, Cappone Eleonora Erika, Shirjandi Faraz, Martinez Laura, Rey Silvia, Vallecillos Antonio, Armero Eva 318
Phenotypic characterization of the Spanish Gallina Murciana chicken breed

D'Alessandro Enrico, Galeano Grazia, Giuffrè Letterio, Giosa Domenico, Tolone Marco 328
A study on diversity and pathway signals in Ragusano donkey microbiome

Capra Emanuele, Negrini Riccardo, Lazzari Barbara, Cozzi Paolo, Ajmone Marsan Paolo, Stella Alessandra, Turri Federica 331
EpiC Fun: A project investigating the epigenetic diversity and functional adaptation in local and cosmopolitan Italian cattle breed

Stoppani Nadia, Cappone Eleonora Erika, Fiorilla Edoardo, Gariglio Marta, Zambotto Valeria, Profiti Margherita, Schiavone Achille, Soglia Dominga 356
Identification of SNP markers associated with carcass trait and meat quality in Italian slow-growing chicken breeds using targeted next-generation sequencing (NGS)

Soglia Dominga, Stoppani Nadia, Maione Sandra, Schiavone Achille, Marzoni Margherita, Buccioni Arianna, Lasagna Emiliano, Castellini Cesare, Iaffaldano Nicolaia, Penasa Mauro, Cerolini Silvia 359
Genetic Polymorphism of the PAX7 Minisatellite Region in Italian Chicken Breeds

Tumino Serena, Ben Jemaa Slim, Chessari Giorgio, Mastrangelo Salvatore, Marletta Donata, Carta Federica, Cesarani Alberto, Bordonaro Salvatore, Criscione Andrea 362
Exploring signatures of selection in the indigenous Nero Siciliano pig breed

Zanotti Andrea, Ablondi Michela, Summer Andrea, Sabbioni Alberto, Asti Vittoria, Finocchiaro Raffaella, Van Kaam Jan-Thijs, Cassandro Martino, Layton Jonathan, Cipolat-Gotet Claudio 363
Does inbreeding cause a decrease in lifetime milk production?

Tumino Serena, Carlentini Morena, Chessari Giorgio, Virzì Armando, Marletta Donata, Criscione Andrea, Bordonaro Salvatore 368
Variability survey at meat production loci in Nero Siciliano pig breed

Seghrouchni Kenza, Barbato Mario, Floridia Viviana, Frattini Stefano, Liotta Luigi 374
Filling the gaps in the genomic management of Italian dog breeds

D'Alessandro Enrico, Liotta Luigi, Tolone Marco 378
Exploring head morphology and exterior traits in Nero dei Nebrodi pig

Crepaldi Paola, Negro Alessio, Bionda Arianna, Ramirez Diaz Johanna, Turri Federica, Grande Silverio, Biffani Stefano 379
Simulation of mating plans by optimal contribution selection in Camosciata delle Alpi goats

Bertolini Francesca, Munarini Filippo, Schiavo Giuseppina, Bovo Samuele, Dall'Olio Stefania, Maranzani Jessica, Bonacini Massimo, Fontanesi Luca 387
Genomic characterisation of Varzese: an iconic dual-purpose autochthonous cattle breed

Graziani Silvia, Cipolat-Gotet Claudio, Stocco Giorgia, Biffani Stefano, Valoppi Davide, Tedeschi Irene, Bozzi Riccardo, Fabbri Maria Chiara, Sirtori Francesco, Grande Silverio, Castiglioni Bianca, Tiezzi Francesco 412
Effect of breed and season on productivity, quality and dairy efficiency of two Italian dairy sheep breeds

Perini Francesco, Bordini Martina, Mancinelli Cartoni Alice, Soglia Dominga, Schiavone Achille, Cendron Filippo, Mugnai Cecilia, Mattioli Simona, Castellini Cesare, Lasagna Emiliano, Zappaterra Martina, Penasa Mauro 418
WGCNA analysis elucidates pathways involved in fatty acids biosynthesis in local chickens

Floridia Viviana, Bionda Arianna, Arias Katherine Daniela, Virga Antonino Nazareno, Crepaldi Paola, Liotta Luigi, Barbato Mario 426
Genomic insights on the history and selection trajectories of the local goat breed Comune di Sicilia

Bionda Arianna, Lopreiato Vincenzo, Liotta Luigi, Floridia Viviana, Cortellari Matteo, Crepaldi Paola, Attard George 428
Genomic characterization of the Maltese cattle breed

Lazzari Filippo, Scarpino Paolo, Danieli Pier Paolo, Cresta Eleonora, Manganello Federico 500
A study on instrumental insemination in Apis mellifera ligustica Spin. as a tool for conservation strategies of the Italian honey bee.

Danieli Pier Paolo, Di Prisco Gennaro, Manganello Federico, Ricchiuti Luciano, Terriaca Riccardo, Lazzari Filippo 502
Behavioural and productive traits of Italian honey bee (Apis mellifera ligustica Spin.) colonies: results of a survey among beekeepers in some Central Italy regions

Floridia Viviana, Dettori Maria Luisa, Pazzola Michele, Barbato Mario 544
Architecture and function of ancestral genomic components in hybrid livestock populations: the Sardo-Modicana case

Luongo Flavio, Fontana Cecilia, Pascarella Lorenzo, Fioretti Mauro, Melilli Caterina, Matassino Donato, Negrini Riccardo 547
Quality Control procedures in BNZ Biobanking: scope and outcomes

Sartore Stefano, Cannizzo Francesca Tiziana, Caracappa Santo, Moretti Riccardo, Pittarello Marco, Profiti Margherita, Sacchi Paola 575
Characterization of the Cinisara chain in northwest Sicily

Delledonne Andrea, Maltecca Christian, Tiezzi Francesco, Punturiero Chiara, Strillacci Maria Giuseppina, Bagnato Alessandro 576
How alternative models affect resilience indicators in dairy cattle

MONOGASTRIC NUTRITION

Pugliese Gianluca, Losacco Caterina, Passantino Letizia, Tarricone Simona, Schiavitto Michele, Laudadio Vito, Tufarelli Vincenzo 043
Red lentil screening by-product inclusion in rabbit diet: effects in growth traits, meat quality and gut health

Losacco Caterina, Pugliese Gianluca, Passantino Letizia, Ceci Edmondo, Giannico Francesco, Schiavitto Michele, Laudadio Vito, Tufarelli Vincenzo 044
Horehound (Marrubium vulgare L.) as a feed additive affects the productive traits, serum antioxidants, digestive enzymes, intestinal bacterial counts, and gut morphology of growing rabbits

Guerrini Alessandro, Del Zozzo Francesca, Muscatello Luisa Vera, Serra Valentina, Harper Valeria, Fiorini Lorenzo, Carlu Claire, Chabrillat Thibaut, Tedesco Doriana 066
Bioactive compounds from Silybum marianum L. and Cynara cardunculus scolymus L. improve the well-being of laying hens: preliminary data

Fiorilla Edoardo, Ferrocino Ilario, Gariglio Marta, Gai Francesco, Zambotto Valeria, Ozella Laura, Franciosa Irene, Giribaldi Marzia, Raspa Federica, Cappone Eleonora Erika, Sferra Chiara, Capucchio Maria Teresa, Schiavone Achille 119
Exploring the impact of alternative dietary proteins on growth performance, gut health and microbiota in Bianca di Saluzzo chickens

Tignani Maria Vittoria, Secci Giulia, Pulido-Rodríguez Lina, Addeo Nicola Francesco, Tucciarone Isabella, Lanzieri Maria Rosaria, Parisi Giuliana 127
Effect of cannabidiol dietary supplementation on the fatty acid profile of rabbit liver

Fatica Antonella, Pastorelli Grazia, Tedesco Doriana, Serra Valentina, Simeonidis Kalliroi, Guerrini Alessandro, Todini Luca, Fantuz Francesco, Salimei Elisabetta 142
Preliminary assessment of chemical and nutritional value, and biomass production of an area in Centre-South Italy grazed by equines

Tedesco Doriana, Guerrini Alessandro, Cambal Hera Jedd, Daulenkhan Ayaulym, Andriantsoa Ny Ivo Hasina Haniel, Marzorati Stefania 151
Larch wood waste: a functional fiber for late gestating and lactating sows

Santoru Matteo, Muñoz-Grein Jennifer, Latorre Maria Angeles, Pinotti Luciano, Rossi Luciana, Alvarez-Rodriguez Javier 192
In vitro and in vivo nutrient digestibility of a pig diet enriched with Yucca schidigera extract

Kiatti Dieu Donné, Musco Nadia, Montefusco Teresa, Ferrara Maria, Calabrò Serena 282
In vitro two-step evaluation of pineapple, cashew and mango waste for pig nutrition

Frazzini Sara, Rizzi Nicoletta, Fifi Anna Paola, Canala Benedetta, Dell'Anno Matteo, Rossi Luciana 342
Functional activity and anti-inflammatory response of Fucus vesiculosus on mouse peritoneal macrophages

Danese Tommaso, Bonaglia Adeline, Penzillo Noemi, Properzi Elisa, Simoni Marica, Valle Emanuela, Martuzzi Francesca, Righi Federico 394
The use of sieve fecal particle separator to preliminarily evaluate sry matter digestibility in horse

Trabalza Marinucci Massimo, Mecocci Samanta, D'Ambra Katia, Pietrucci Daniele, Acuti Gabriele, Minelli Giovanna, Cappelli Katia, Forte Claudio, Tabasso Silvia, Lo Fiego Domenico Pietro 447
Intestinal microbiota evaluation in finishing pigs fed hazelnut skins

Tedesco Doriana, Guerrini Alessandro, Cambal Hera Jedd, Daulenkhan Ayaulym, Andriantsoa Ny Ivo Hasina Haniel, Marzorati Stefania, La Porta Caterina 538
Effets of larch wood waste supplementation on fecal microbiota of late gestating and lactating sows

PHYSIOLOGY AND REPRODUCTION

Bornaghi Valeria, Galli Andrea, Pozzato Giulia 089
Quality control in boar semen production

Bornaghi Valeria, Galli Andrea, Paoli Laura, Vanni Roberta, Frabetti Andrea, Fornasini Daniela 094
Feasibility of using frozen semen in rabbit breeding

Matera Roberta, Calanni Macchio Alfio, Bruno Francesco, Lombardi Alessia, Aragona Francesca, Piscopo Nadia, Longobardi Valentina 179
Conception influences reproductive dynamics and lactation characteristics in primiparous Mediterranean buffalo

Zaniboni Luisa, Lopez Annalaura, Madeddu Manuela, Tognoli Cristina, Moretti Vittorio Maria, Marelli Stefano, Perricone Vera, Iaffaldano Nicolaia, Cerolini Silvia 289
Lipid profile in chicken sperm of Italian chicken breeds

Molè Concetta, Cavallo Carmelo, Torrisi Concetta, Trieste Valeria, Emmanuele Giovanni, Visalli Rosanna, Scalisi Marco, Lopreiato Vincenzo, Liotta Luigi 449
Heat stress impacts metabolism and milk quality of Ragusano donkey

Lopreiato Vincenzo, Sfulcini Marta, Cavallo Carmelo, Trevisi Erminio, Liotta Luigi, Minuti Andrea 503
Relationship between residual energy intake in Holstein calves, their performance, and milk yield during the first lactation

PRECISION FARMING

Giannuzzi Diana, Rovetta Carlo, Bisutti Vittoria, Pegolo Sara, Arazi Alon, Katz Gil, Trevisi Erminio, Mele Marcello, Gallo Luigi, Mota Lucio Flavio Macedo, Schiavon Stefano, Cecchinato Alessio 083
Variations in individual feed intake predicted by a 3D accelerometer in dairy cows

Aquilani Chiara, Confessore Andrea, Cecchini Valentina, Bovolenta Stefano, Simonetti Emilio, Pugliese Carolina 131
Virtual Fencing learning retention in dairy cows after 3 months of non-use

Scalera Grazia, Masucci Felicia, Sannino Maura, Serrapica Francesco, Di Francia Antonio, De Rosa Giuseppe 268
Adaptation and growth performance of buffalo calves in an automatic feeding system with individual pens

Malizzi Tiziano, Senatore Elena, Silvi Alina, Zucca Giovanni, Finocchi Matteo, Mantino Alberto, Turini Luca, Mele Marcello 324
Using smart collars to assess heat stress impacts on dairy cows

Cabassi Giovanni, Benedini Dario, Gambale Claudia, Monteggia Larisa, Monti Lucia, Pelizzola Valeria, Gasparini Andrea, Povolo Milena 344
Study of alpine pasture exploitation by coupling GPS trackers and activometers

Biagini Davide, Blandino Massimo, Careddu Andrea, Dinuccio Elio, Garolini Daniele, Meloni Raffaele, Pelissetti Simone, Rollè Luca, Scapino Mattia, Verna Riccardo, Lazzaroni Carla 370
Effect of fertiliser variable rate control on quality of wheat forage

Confessore Andrea, Aquilani Chiara, Bianco Emanuele, De Guttry Luca, Sirtori Francesco, Pugliese Carolina 471
Virtual Fencing and Remote Sensing: Improve the herd management of dairy cows on alpine pasture

Paolino Rosanna, Sabia Emilio, Ventura Gennaro, Vignozzi Luca, Riviezzi Amelia Maria, Claps Salvatore, Di Trana Adriana, Braghieri Ada 484
Use of remote images for natural pasture biomass prediction in sheep pre-grazing

Canali Elisabetta, Pesenti Rossi Gaia, Barbieri Sara, Azzolari Mattias, Minero Michela, Dalla Costa Emanuela 507
Use of Infrared thermography to monitor calf health and welfare

D'Alessandro Enrico, Barbato Mario, Floridia Viviana, Liotta Luigi, Lopreiato Vincenzo, Cassandro Martino, Ciardella Giorgio, Nardone Mario, Cicagna Iosef, Valentini Riccardo, Coppola Valerio, Ruggeri Federico, Melilli Caterina, Nardone Alessandro, Negrini Riccardo 529
InnovaRe: exploring innovative phenotyping for a smarter floc

Mantovani Giorgia, Simoni Marica, Danese Tommaso, Boldrin Gloria, Pitino Rosario, Righi Federico 536
Assessing the potential of portable NIR spectroscopy to evaluate the net energy content for lactation of hay forages for dairy cattle

Barbato Mario, Floridia Viviana, Liotta Luigi, D'Alessandro Enrico, Lopreiato Vincenzo, Cassandro Martino, Ciardella Giorgio, Nardone Mario, Cicagna Iosef, Valentini Riccardo, Coppola Valerio, Ruggeri Federico, Melilli Caterina, Nardone Alessandro, Negrini Riccardo 542
Exploring novel phenotypes in cattle within extensive farming systems: the InnovaRe project

Gaspa Giustino, Laura Falchi, Cesarani Alberto, Ferrari Carolina, Negrini Riccardo, Macciotta Nicolò 564
Across breeds variability of resilience indicators based on daily automatic milk system data

Ledda Antonello, Azzena Margherita Domenica Giovanna, Castangia Francesca, Cannas Antonello, Atzori Alberto Stanislao 571
APPàre, Sensors and software in decision support systems for the Sardinian dairy sheep farmers

PRODUCTION SYSTEMS

Rapetti Luca, Battelli Marco, Gambarini Giulia, Colombini Stefania, Pavesi Martina, Menni Giorgio, Dai Xiaoxia, Crovetto Matteo, Schiavon Stefano, Galassi Gianluca 085
Two different feeding systems in fattening heavy pigs: performance and nitrogen balance

Sirtori Francesco, Parrini Silvia, Aquilani Chiara, Confessore Andrea, Bozzi Riccardo, Dibari Camilla, Argenti Giovanni, De Guttry Luca, Pugliese Carolina 141
Finishing of beef cattle on pasture: effects on performance and meat quality

Tanganelli Costanza, Parrini Silvia, Moretti Maria Vittoria, De Guttry Luca, Confessore Andrea, Solinas Stefania, Sirtori Francesco, Dibari Camilla, Pugliese Carolina 327
The potential effectiveness of innovative practices in livestock and permanent pasture management: stakeholder responses

Carboni Maria Rosaria, Frongia Andrea, Salis Lorenzo, Acciaro Marco, Decandia Mauro, Sitzia Maria 376
Effects of weaning strategies on the average daily gain of Dorper-Sarda F1 lambs

Ripamonti Alice, Acciaro Marco, Decandia Mauro, Frongia Andrea, Mantino Alberto, Mele Marcello 413
Challenges and opportunities in using the n-alkane technique to determine cattle diet in agrosilvopastoral systems

Creatini Susy, Salari Federica, Roncoroni Cristina, Brajon Giovanni, Martini Mina 438
Integrating animal welfare and milk monitoring: a preliminary analysis of farm management and efficiency prediction

Sechi Gian Simone, Atzori Alberto Stanislao 557
A twenty year dairy cattle farm evolution, technical and managerial aspect

RUMINANT NUTRITION

Stefanon Bruno, Cecchini Valentina, Sgorlon Sandy, Colitti Monica 115
Variation in the faecal microbiota of deer in relation to the hunting area in the Friuli Venezia Giulia region

Oteri Marianna, Calderone Francesca, Armone Rosangela, Maio Aurora, La Malfa Tommaso, Scavo Aurelio, Scordia Danilo, Chiofalo Biagina, Gresta Fabio 139
Rhizobium inoculation in forage legumes intercropped with cereal for ruminant feeding

Menni Giorgio, Rapetti Luca, Pavesi Martina, Dai Xiaoxia, Battelli Marco, Giudice Filippo, Galassi Gianluca, Crovetto Matteo, Colombini Stefania 206
Addition of feed additives to stimulate alternative metabolic pathways through methane reduction

Catellani Alessandro, Fiorbelli Erica, Moschini Maurizio, Gallo Antonio 207
Effect of different RDP/RUP ratios on productive performances, feeding behavior, and nitrogen efficiency of high-yielding dairy cows

Bettini Stefano, Perini Francesco, Colombi Daniele, Ghilardi Marco, Trabalza Marinucci Massimo, Lasagna Emiliano 241
The effect on productive performance of a Saccharomyces cerevisiae postbiotic inclusion in the finishing diet of Chianina bullock

Scalera Grazia, Serrapica Francesco, Sannino Maura, Faugno Salvatore, Di Francia Antonio, Lambiase Claudia, De Rosa Giuseppe, Masucci Felicia 272
Sustainable feed source from ensiled peanut crop residues

Errico Michela, Catellani Alessandro, Gallo Antonio, Rocchetti Gabriele 275
High throughput UHPLC-HRMS method for the detection of purines derivatives as biomarkers of nitrogen efficiency in dairy cows

Piccirillo Barbara, Ponte Marialetizia, Pipi Marianna, Bonanno Adriana, Calabrò Serena 284
Hedysarum coronarium L.: an undiscovered forage resource for sheep feeding

Sandrini Silvia, Perricone Vera, Stranieri Angelica, Pea Alessia, Cenati Clara, Paltrinieri Saverio, Savoini Giovanni, Agazzi Alessandro 320
Influence of Enniatin B on performance and metabolic profile in dairy cow

Agazzi Alessandro, Sandrini Silvia, Perricone Vera, Cremonesi Paola, Castiglioni Bianca, Valenti Irene, Pea Alessia, Cenati Clara, Pasquali Matias 325
Fecal microbiota shifts in dairy cows consuming Enniatin B-contaminated diets

Lambiase Claudia, Calabrò Serena, Scalera Grazia, Vastolo Alessandro, Masucci Felicia, Di Francia Antonio, Serrapica Francesco 326
Feeding livestock with leftovers: exploring the potential of dry pasta residue

Petrocchi Jasinski Francesca, Evangelista Chiara, Basiricò Loredana, Meo Zilio David, Iacurto Miriam, Steri Roberto, Bernabucci Umberto 391
Effects of the Rufo® supplement on enteric methane emissions in lactating Italian Mediterranean buffaloes, measured with a laser methane detector (LMD)

Porcu Maria Angela, Ledda Antonello, Duras Bardilio, Mattu Andrea, Ruggiu Enrico, Formigoni Andrea, Cannas Antonello 464
Effect of different feeding sequences of soybean meal on lactating dairy ewes fed ryegrass rich in water-soluble carbohydrates

Fancello Francesco, Fresu Mirko, Nieddu Lidia Nicoletta, Zara Severino, Gallo Antonio, Mastroeni Carmelo, Atzori Alberto Stanislao 466
Investigation of the microbiological, physico-chemical, and fermentative quality of Baled Silage produced in Sardinia

Altomonte Iolanda, Salari Federica, Vivo Tiziana, Ceccherelli Valeria, Martini Mina 476
Fat formulation of cow milk replacers affects nutrient fecal excretions of dairy calves

Evangelista Chiara, Petrocchi Jasinski Francesca, Basiricò Loredana, Vitali Andrea, Grossi Giampiero, Rossi Chiara, Turriziani Giovanni, Lacetera Nicola, Bernabucci Umberto 491
Effect of green forage on the particle size of rations in buffaloes and its influence on sorting ability

Federiconi Alessia, Veroni Laura, Ghiaccio Francesca, Canestrari Giorgia, Indio Valentina, De Cesare Alessandra, Formigoni Andrea, Palmonari Alberto 520
Characterization of rumen-fecal microbiota in dairy cows with different productive performances

De Angelis Daria Zoe, Pompei Luigi, Giammarco Melania, Cipriani Marcella, Cortesi Francesco, Rossi Emanuela, Podaliri Michele, Iannetti Luigi, Fusaro Isa 528
Effect of different feeding regimens on fattening, carcass traits and meat quality of old Bergamasca sheep for arrosticini production: preliminary results

Primi Riccardo, Danieli Pier Paolo, Ferri Michele, Cellitti Francesca, Bottoni Irene, Napoli Francesco, Boselli Carlo, Spina Raffaello, Ronchi Bruno 537
Feeding teff (Eragrostis tef) to lactating dairy sheep: a forage option in the Mediterranean basin

Lunesu Mondina Francesca, Nudda Anna, Carta Silvia, Fenu Antonio, Rubattu Roberto, Battacone Gianni 548
Effect of starch source in finishing diets on carcass and meat quality of culling Sarda ewes

Danieli Pier Paolo, Fiore Leonardo, Lazzari Filippo, Primi Riccardo, Manganello Federico, Natoli Vincenzo, Ronchi Bruno 555
Application of Near-Infrared Spectroscopy (NIR) for the compositional assessment of teff hay

Silvestrelli Simone, Ghiaccio Francesca, Cavallini Damiano, Bongiovanni Jenny, Toni Fausto, Formigoni Andrea 560
Nutritional characterization and variability of different livestock feed used in the national feed industry

Capasso Giambattista, Rosati Leonardo, Perna Anna Maria 561
Effect of the weather pattern of two consecutive years on the floristic composition and on the quantitative-qualitative production of the forage phytomass of a summer pasture of the Southern Apennines

SUSTAINABILITY

Benzoni Lorenzo, Finocchiaro Raffaella, Layton Jonathan, Visentin Giulio, Dorigo Martina, Tiezzi Francesco, Marusi Maurizio, Bracchi Alessandro, Bonacina Greta, Zucali Maddalena, Gislon Giulia, Vitali Andrea, Rossi Chiara, Grossi Giampiero, Lacetera Nicola, Cassandro Martino 067
A holistic approach for monitoring the environmental sustainability of the Italian Holstein cattle population

Sabia Emilio, Braghieri Ada, Paolino Rosanna, Vignozzi Luca, Di Trana Adriana, Cosentino Carlo, Freschi Pierangelo, Pacelli Corrado 134
Circular animal feed: environmental impact of by-products in diet of dairy animals

Gabriele Sara, Lorenzi Valentina, Roccaro Mariana, Peli Angelo, Gallese Simone, Liberati Giorgia, Pennellini Sara, Mattacchione Federica, Bonoli Alessandra, Fusi Francesca, Bertocchi Luigi 173
Study of the relationship between animal welfare and environmental impact in Italian dairy cattle farms

Froldi Federico, Dall'Asta Margherita, Moschini Maurizio, Gallo Antonio, Rossi Filippo, Negrini Riccardo, Trevisi Erminio 180
Life cycle assessment of cow milk production: how to transfer results in different nutritional functional units

Scaglia Elena, Sergi Valeria, Giagnoni Laura, Casini David, Chiaramonti David, Ferronato Giulia, Gilioli Gianni, Caprarulo Valentina 186
Impact of in feed biochar supplementation on GHG and ammonia emissions from manure produced by Holstein calves

Di Rosa Ambra, Falqui Luciano, Perrone Giuseppe, Di Bella Daniele, Saitto Nicola, Chiofalo Vincenzo 212
Microalgae deriving from the biochemical conversion of CO2 as innovative and sustainable sources of functional additives in laying hen diets. The GREEN-EGG project

Goldaraz-Salamero Nuria, Sierra-Perez Jorge, Blanc Simone, Brun Filippo 232
Rethinking livestock feeds with hazelnut by-products: a Life Cycle thinking approach

Azzena Margherita Domenica Giovanna, Mussolino Claudio, Atzori Marco, Todde Giuseppe, Sole Stefania, Todde Giorgio, Attardi Emiliano, Carrus Mariangela, Buttu Giangavino, Atzori Alberto Stanislao 310
Analysis of sustainability and digitisation in member companies of the CAO Cooperative of Oristano

Costamagna Chiara, Blanc Simone, Agradi Stella, Mugnai Cecilia, Forte Claudio, Cullere Marco, Borra Danielle, Merlino Valentina Maria 361
The Italian rabbit sector: analysis of competitive sustainability strategies

Pompei Luigi, De Angelis Daria Zoe, Jalal Hassan, Fusaro Isa, Prasinou Paraskevi, Tavaniello Siria, Perna Anna Maria, Vignola Giorgio, Giammarco Melania 410
Inclusion of grape pomace in dairy ewes diets: effects on milk production and methane mitigation potential

Rossi Chiara, Grossi Giampiero, Vitali Andrea, Lacetera Nicola 422
Enteric methane emissions in organic Brown Swiss cows

Cavallini Damiano, Lamanna Martina, Colleluori Riccardo, Silvestrelli Simone, De Matos Vettori Julio, Buonaiuto Giovanni, Romanzin Alberto, Formigoni Andrea 493
Advancing methane detection in dairy cows during robotic milking: insights from enhanced laser and sniffer techniques

Tolone Marco, Lopreiato Vincenzo, Liotta Luigi, Chiofalo Vincenzo, Praticò Salvatore, D'Urso Provvidenza, Modica Giuseppe 511
Monitoring the greenhouse gas emissions in dairy cattle farms. The MITIgA project

Dinuccio Elio, Aimè Chiara, Angiulli Francesco Alessandro, Biagini Davide, Braghieri Alessandro, Brunoldi Matteo, Calzaferri Simone, Dela Pierre Flavia, Dondi Daniele, Finco Linda, Giannandrea Giulia, Guida Roberto, Kameswaran Nithish Kumar, Mandelli Beatrice, Montagna Paolo, Riccardi Cristina, Salvini Paola, Vai Ilaria, Vadivel Dhanalakshmi, Vitulo Paolo, Arena Maria Cristina 527
An innovative system for enteric methane recovery

Sarkar Drishti, Rossi Chiara, Grossi Giampiero, Primi Riccardo, Vitali Andrea, Lacetera Nicola 563
Dynamics of greenhouse gases in central Italian meadows: a high-resolution analysis using LI-COR gas analyzers

Pompei Luigi, Jalal Hassan, Fusaro Isa, Tavaniello Siria, Perna Anna Maria, Maiorano Giuseppe, Gramenzi Alessandro, Giammarco Melania 568
In vitro evaluation of digestibility, gas and methane production from winery by-products

WELFARE, HEALTH AND BEHAVIOUR

Maria Levrino Gustavo 022
Effects of enriched cage design on the welfare and behavior of breeding does

Massacci Francesca Romana, Cucco Lucilla, Albini Elisa, Blasi Francesca, Di Gregorio Alessandra, Orsini Serenella, Petrin Sara, Peruzzo Arianna, Paniccià Marta, Magistrali Chiara Francesca 140
Genomic analysis of Streptococcus canis and S. dysgalactiae subsp. equisimilis from different hosts in Italy 2004-2021: antimicrobial resistance and virulence profiles.

Longobardi Consiglia, Bifulco Giovanna, Pacelli Gianmaria, Ciarcia Roberto, Salzano Angela, Damiano Sara, Campanile Giuseppe 163
Effects of breeding techniques on animal welfare in rural areas

Castellani Simona, Mecocci Samanta, Bernabucci Umberto, Rampacci Elisa, Giovagnoli Stefano, Basiricò Loredana, Cappelli Katia, Lacetera Nicola 175
Effects of bovine milk extracellular vesicles on the oxidative and inflammatory status of bovine mammary and porcine intestinal epithelial cells

Rocchetti Gabriele, Errico Michela, Milanesi Marco, De Paula Nogueira Guilherme, Garcia Josè Fernando, Ajmone Marsan Paolo 177
Untargeted metabolomic analysis of heat stress response in indicine and taurine cattle

Ozella Laura, Pittarello Marco, Barzolai Clementina, Tarantola Martina 182
Effects of grazing adaptation on Italian Pezzata Rossa metabolism

Caroprese Mariangela, Marino Rosaria, De Devitiis Biagia, Pipi Marianna, Badalamenti Rosario, Maggiolino Aristide, Forte Lucrezia, Russo Ilaria, De Palo Pasquale, Di Grigoli Antonino, Prosperi Maurizio, Albenzio Marzia 279
Perspectives of Citrus essential oil as feed in sheep farming

Lorenzi Valentina, Valli Giulia, Archetti Ivonne, Tempini Michele, Gabriele Sara, Bernardo Tiziano, Sangalli Elena, Monaci Claudio, Salogni Cristian, Maisano Antonio Marco, Scali Federico, Ambra Chiara Denise, Vecchio Domenico, Bergagna Stefania, Barberio Antonio, Fusi Francesca, Bertocchi Luigi 281
Welfare conditions of replacement calves and surplus calves in dairy farms in Northern Italy

Belperio Simona, Martelli Giovanna, Nannoni Eleonora, Meneguz Marco, Sardi Luca 319
Black Soldier Fly meal and oil: effects of novel feed sources on growth traits and welfare in fattening pigs

Frongia Andrea, Acciaro Marco, Giovanetti Valeria, Serra Gabriella, Cabiddu Andrea, Sitzia Maria, Decandia Mauro 321
THI as an alert tool for decline in milk production in grazing Sarda sheep

Moretti Riccardo, Ponzo Enrico, Cuccato Matteo, Profiti Margherita, Divari Sara, Chessa Stefania, Cannizzo Francesca Tiziana, Sacchi Paola 334
MALDI-TOF mass spectrometry profiling to investigate subclinical mastitis in dairy cows

Carè Sara, Crisà Alessandra, Marchitelli Cinzia, Scatà Maria Carmela, Signorelli Federica, Calì Massimo, Meo Zilio David, Pulcini Domitilla, Capoccioni Fabrizio, Bochicchio Davide, De Matteis Giovanna 456
European partnership on animal health and welfare-EUPAHW

Greppi Martina, Raspa Federica, Cavallini Damiano, Odore Rosangela, Gnudi Giacomo, Cavallo Andrea, Bertuglia Andrea, Valle Emanuela 473
Horse welfare assessment: the parameters to consider in pain evaluation

Pesenti Rossi Gaia, Boldrin Gloria, Barbieri Sara, Dalla Costa Emanuela, Minero Michela, Canali Elisabetta 508
Effect of Pair-Housing on the reactivity of pre-weaned dairy calves

Correddu Fabio, Carta Silvia, Lunesu Mondina Francesca, Cadau Giordana, Battacone Gianni, Pulina Giuseppe, Nudda Anna 510
Effect of dietary inclusion of cocoa bean shells on behaviour indicators of animal welfare in Sardo-bruna cattle breed

Visentin Giulio, Colleluori Riccardo, Buonaiuto Giovanni, Costa Angela, Mammi Ludovica Maria Eugenia, Palmonari Alberto, Cavallini Damiano, Formigoni Andrea 553
Effect of different THI metrics on milk yield and quality attributes of Holstein cows using robot milking data

GENERAL INFORMATION

CONGRESS DATES
17th June (Tuesday) – 20th June (Friday) 2025

VENUE
University Campus of Grugliasco
largo Paolo Braccini 2, 10095 Grugliasco (Turin).

Secretariat and Registration desk times during the Congress
Tuesday 17th June 12.00 – 18.00
Wednesday 18th June 08.30 – 18.00
Thursday 19th June 08.00 – 19.00
Friday 20th June 08.30 – 13.30

REGISTRATION
The registration fee includes:

› Admission to the Scientific Sessions and the Exhibition Area

› Conference kit

› Abstract collection, available online as a supplement of the "Italian Journal of Animal Science"

› Opening Ceremony and Welcome Cocktail on Tuesday 17th June

› Typical dinner on Wednesday 18th June at Il Capodoglio Resturant (Murazzi del Po Gipo Farassino 37, 10123 Torino)

› Coffee breaks and lunches as shown in the program

› Certificate of attendance

BADGE
All participants will receive a badge, which they are requested to wear during all Congress activities to be admitted to the scientific sessions and to the social program.

LANGUAGE
The official languages of the Congress are English and Italian.
Simultaneous translation will not be provided.

MOBILE PHONES, PHOTO AND VIDEO
Participants are requested to keep their mobile phones switched off (or set to silent mode) in the session rooms. Photography and video recordings are strictly prohibited during all scientific sessions.

OPENING CEREMONY
The Opening Ceremony will take place on Tuesday 17th June 2025 at the University Campus of Grugliasco and will be followed by a Welcome Cocktail.

SOCIAL DINNER
The Social Dinner will be held on the evening of Thursday 19th June at Palazzina di Caccia di Stupinigi (TO). A transfer service by private bus will be organized, with departure at 19.30 from the University Campus of Grugliasco and return in Turin downtown, piazza Carlo Emanuele II.



4TH EDITION OF THE "ASPA YOUNG RESEARCHERS COMPETITION - BEST ORAL COMMUNICATION"

To promote and stimulate young researchers, the Animal Science and Production Association (ASPA), in collaboration with the Italian Journal of Animal Science (IJAS) and with the economic support of the Organizing Committee of the 26th ASPA Congress (2025), organizes the fourth edition of the "ASPA Young Researchers Competition - Best Oral Communication" with the aim to select the best 7 oral communications at the 26th ASPA Congress. The awarding of the best oral communications is scheduled for the 20th June at 12.45.

4TH EDITION OF THE "ASPA YOUNG RESEARCHERS COMPETITION – BEST POSTER"

To promote and stimulate young researchers, the Animal Science and Production Association (ASPA), in collaboration with the Italian Journal of Animal Science (IJAS) and with the economic support of the Organizing Committee of the 26th ASPA Congress (2025), organizes the fourth edition of the "ASPA Young Researchers Competition - Best Poster" with the aim to select the best 7 Posters at the 26th ASPA Congress. The awarding of the best posters is scheduled for the 20th June at 12.45.

TORINO AND ITS PROVINCE

The province of Turin is one of the largest provinces in Italy. It is made up of a mountainous part to the west and north along the border with France and the Aosta Valley, and a flat or hilly part in the southern and eastern areas, and it is crossed mainly by the Po River. Turin, lively and elegant, stands as a testament to both its rich history and its vibrant present. This city, immersed in greenery and gently cradled by the Po River against the backdrop of the western Alps, offers an enchanting geographical charm. As the first capital of Italy, Turin invites you to explore its layered history through its Royal Residences, palaces, and museums, as well as its parks, riverbanks, and the surrounding mountains.

The streets and squares of the city, with their long arcaded stretches and multiethnic neighborhoods, tell stories of a harmonious blend of Roman urban planning, Piedmontese baroque splendor, and modern architectural innovation. Turin is a city to be savored slowly, inviting visitors to look up and around to absorb its unique atmosphere and diverse offerings.

HOW TO REACH THE CONGRESS VENUE

› Metropolitan Trainline Service: a train every 30 minutes from Torino Porta Nuova station to Grugliasco station (10 minutes) + a 5 minutes walk

› Underground: from the city center to Fermi station + a 15 minutes walk or shuttle nr 76

› Bike sharing service: two stations near the campus

› Taxi service: call +39 011 5737 or +30 011 5730



NOTES



ASPA 26th Congress Book of Abstract

Wednesday, 18th June – Room Venaria

Session 01 – Genetics: SUSTAINABILITY AND FUTURE PERSPECTIVES OF ANIMAL BREEDING
Sponsored by Fedana

Chairs: **Cassandro Martino – Degano Lorenzo**

9:00 **Gomez Mayra, Landi Vincenzo, Cimmino Roberta, Rossi Dario, Zullo Gianluigi, Di Vuolo Gabriele, Neglia Gianluca, Biffani Stefano**
Imputation accuracy of missing genotypes in Italian Mediterranean Buffalo using 50K SNP chip..... **444**

9:15 **Layton Jonathan, Benzoni Lorenzo, Finocchiaro Raffaella, Van Kaam Jan-Tijs, Tiezzi Francesco, Marusi Maurizio, Cassandro Martino**
Genomic evaluation of methane emissions and feed efficiency in Holstein bulls..... **060**

9:30 **Biscarini Filippo, Cesarani Alberto, Mastrangelo Salvatore, Finocchiaro Raffaella, Van Kaam Jan-Thijs, Benzoni Lorenzo, Ciampolini Roberta, Cassandro Martino**
An enviromics approach to modelling GxE interactions in dairy cattle..... **512**

9:45 **Ferrari Valentina, Marusi Maurizio, Galluzzo Ferdinando, Cassandro Martino**
Calf survival in Italian Holstein: first results and services for farmers..... **084**

10:00 **Graziani Silvia, Cipolat-Gotet Claudio, Finocchiaro Raffaella, Tiezzi Francesco, Pieramati Camillo, Sarti Francesca Maria, Cassandro Martino**
Total and differential somatic cell traits in Italian Jersey Dairy Cattle Breed: preliminary results..... **409**

10:15 **Colombi Daniele, Bonifazi Renzo, Perini Francesco, Sbarra Fiorella, Quaglia Andrea, Calus Mario, Lasagna Emiliano**
Multi-breed genomic predictions for average daily gain in three Italian beef cattle breeds..... **105**

10:30 **Cendron Filippo, Perini Francesco, Lasagna Emiliano, Baruschello Maristella, Cassandro Martino, Penasa Mauro**
Genetic diversity of goose (Anser anser) and guinea fowl (Numida meleagris) local breeds using whole genome sequencing..... **034**

10:45 Coffee break and Poster session

Wednesday, 18th June – Room Racconigi

Session 02 – Food Quality: PORK AND POULTRY MEAT

Chairs: **Serra Andrea – Gariglio Marta**

9:00 **Grassi Giulia, Tavaniello Siria, Palazzo Marisa, Peng Meng, Teshale Dereje Birara, Maiorano Giuseppe**
Effect of the inclusion of shelled dried chestnut in the finishing diet on growth performance and meat quality of Casertana pig..... **194**

9:15 **Mainardi Edda, Costa Annamaria, Pallaoro Margherita, Aidos Lucia, Buoio Eleonora, Mazzola Silvia, Di Giancamillo Mauro, Modina Silvia, Di Giancamillo Alessia, Rossi Raffaella**
Carcass characteristics and quality parameters of Longissimus dorsi muscle of Nero di Lomellina pigs..... **093**

9:30 **Cappone Eleonora Erika, Fiorilla Edoardo, Gariglio Marta, Franco Riccardo, Hos Enes, Zambotto Valeria, Bianchi Chiara, Daniele Giulia Maria, Cianciabella Marta, Bongiorno Valentina, Stoppani Nadia, Soglia Dominga, Schiavone Achille**
Rediscovering the value of endangered Piedmontese chicken breeds through meat quality assessment **355**

9:45 **Petracci Massimiliano, Antenucci Emilia Luigia, Gagliano Mara Antonia, Bordini Martina, Mancinelli Cartoni Alice, Zampiga Marco, Soglia Francesca, Mattioli Simona, Sirri Federico**
Comparison of carcass and meat quality traits of fast-, medium- and slow-growing chicken genotypes fed diets with different protein-to-energy ratio **079**

10:00 **Antenucci Emilia Luigia, Mancinelli Cartoni Alice, Soglia Francesca, Gagliano Mara Antonia, Petracci Massimiliano, Dal Bosco Alessandro**
Effects of outdoor enrichments and dietary supplementation with n-3 PUFA and antioxidants on the meat quality traits in free range chickens **332**

10:15 **Soglia Francesca, Bordini Martina, Tavaniello Siria, Antenucci Emilia Luigia, Maiorano Giuseppe, Petracci Massimiliano**
Breast meat quality to classify the wooden breast defect and investigate its underlying mechanisms in fast-growing chickens **259**

10:30 //

10:45 Coffee Break and Poster session

Wednesday, 18th June – Room Stupinigi

Session 03 – Alternative Proteins: YELLOW MEALWORM REARING AND NUTRITION

Sponsored by GREEN FEED CYCLES

Chairs: **Athanassious Christos – Moradei Andrea**

9:00 INVITED LECTURE
Barragán-Fonseca Karol
Insects for Peace: Transforming Communities Through Black Soldier Fly Farming .....

9:30 **Palumbo Bianca Federica, Deruytter David, Dalle Zotte Antonella**
Optimizing Tenebrio molitor reproduction: examining beetle size effect on mating preferences, and larval yield and performance **251**

9:45 **Resconi Andrea, Adamaki-Sotiraki Christina, Rigopolou Marianna, Gasco Laura, Athanassiou Christos**
Is age just a number? Investigating the effects of male and female age on the reproduction of Tenebrio molitor **055**

10:00 **Daluwatta Sujivi, Bellezza Oddon Sara, Candian Valentina, Loiotine Zaira, Resconi Andrea, Caimi Christian, Biasato Ilaria, Tedeschi Rosemarie, Gasco Laura**
Impact of different dietary protein: carbohydrates ratios and lipid inclusion levels on the growth performance, nutritional composition and AMPs gene expression of Tenebrio molitor *larvae*..... **109**

10:15 **Moradei Andrea, Spranghers Thomas, Ottoboni Matteo, Deruytter David, Pinotti Luciano**
Tenebrio molitor: *effects of four herbs on larval composition and on their growth performance* **017**

10:30 **Copelotti Emma, De Schutter Kristof, Tzompa-Sosa Daylan, Coudron Carl, Deruytter David, Mancini Simone**
Fully hydrogenated rapeseed oil (FHRO) enriched diet in Tenebrio molitor *larvae: effects on growth performances and nutritional composition*..... **032**

10:45 Coffee Break and Poster session

Wednesday, 18th June – Room Valentino

Session 04 – Sustainability: FEEDING STRATEGIES

Chairs: **Sandrucci Anna – Atzori Alberto**

9:00 **Colleluori Riccardo, Silvestrelli Simone, De Matos Vettori Julio, Cavallini Damiano, Buonaiuto Giovanni, Formigoni Andrea**
Effects of a molasses-based liquid feed supplemented with tannins on productive performance and methane emissions in lactating dairy cows..... **489**

9:15 **Dell'Anno Matteo, Spedale Cristina, Frazzini Sara, Di Stefano Antonio, Baldi Antonella, Rossi Luciana, Chiofalo Vincenzo**
Evaluation of functional characteristics of whole lemon pulp and depectinized lemon pulp for animal feeding **501**

9:30 **Spedale Cristina, Dell'Anno Matteo, Onelli Elisabetta, Moscatelli Alessandra, Puglia Marco, Pedrazzi Simone, Dell'Orto Vittorio, Chiofalo Vincenzo, Rossi Luciana**
Functional characterization of biochar from lemon pulp by-products as innovative feed ingredients **467**

9:45 **Caratzu Maria Francesca, Lunesu Mondina Francesca, Sara Sechi, Carta Silvia, Nudda Anna, Pulina Giuseppe, Correddu Fabio**
Carbon footprint estimation of some European agro-industrial by-products and their effect in reducing the environmental impact of sheep and goat diets..... **475**

10:00 **Mantino Alberto, Finocchi Matteo, Ripamonti Alice, Silvi Alina, Casarosa Laura, Senatore Elena, Cella Fabrizio Giuseppe, Serra Andrea, Conte Giuseppe, Mele Marcello**
Brewers' spent grains as a sustainable alternative for lactating ewes: a feeding and environmental perspective..... **416**

10:15 **Santoru Matteo, Muñoz-Grein Jennifer, Alvarez-Rodriguez Javier, Pinotti Luciano, Latorre Maria Angeles**
Evaluation of Yucca schidigera extract inclusion in fattening pig nutrition: impact on performances, nitrogen use and slurry composition **190**

10:30 **Volpe Federica, Zampiga Marco, Pignata Stefano, Piscitelli Raffaela, Petracci Massimiliano, Sirri Federico**
Comparison of the environmental impacts of chicken meat production among fast-, medium- and slow-growing genotypes fed diets with different protein-to-energy ratio **386**

10:45 Coffee Break and Poster session

Wednesday, 18th June – Room Mandria

Session 05 – Genetics: POULTRY AND RABBIT

Chairs: **Lasagna Emiliano – Mecocci Samanta**

9:00 **Perini Francesco, Cendron Filippo, Lasagna Emiliano, Baruchello Maristella, Cassandro Martino, Penasa Mauro**
*Genetic characterization of two local duck breeds (*Anas platyrhynchos*) using whole genome sequencing*..... **056**

9:15 **Saleh Medhat, Pierini Claudia, Landi Vincenzo, Maggiolino Aristide, Lasagna Emiliano, Mugnai Cecilia, Perini Francesco, Centoducati Gerardo, Canales Amado, Martinez Amparo, De Palo Pasquale, Ciani Elena, Bruno Silvia, Bramante Grazia, Pugliese Nicola, Circella Elena, Santos Silva Fatima, Carolino Inês, Camarda Antonio**
Genetic characterization and origins of the leccese: insights into an Apulian poultry breed..... **276**

9:30 **Perricone Vera, Marelli Stefano, Zaniboni Luisa, Tognoli Cristina, Zeni Niko, Gioacchino, Schiavone Achille, Soglia Dominga, Cerolini Silvia**
Phenotipic characterization and mating plan for biodiversity conservation in Modenese chicken breeders..... **286**

9:45 **Stoppani Nadia, Soglia Dominga, Bongiorno Valentina, Testa Pietro, Moshe David, Schiavone Achille**
Safeguarding local animal genetics: the conservation of the Nostrana di Morozzo chicken breed..... **350**

10:00 **Soglia Dominga, Stoppani Nadia, Perini Francesco, Lasagna Emiliano, Schiavone Achille, Cerolini Silvia**
Molecular data to safeguard genetic diversity in local chicken breed conservation **353**

10:15 **Bordini Martina, Zappaterra Martina, Petracci Massimiliano, Soglia Francesca**
Gene expression analysis of collagen type III coding gene in chicken breast muscles affected by wooden breast condition **258**

10:30 **Bovo Samuele, Ribani Anisa, Bolner Matteo, Taurisano Valeria, Schiavo Giuseppina, Bertolini Francesca, Fontanesi Luca**
The size of the rabbit from whole genome sequencing: the dwarfism in Dwarf Lop breed is better explained as a polygenic trait..... **213**

10:45 Coffee Break and Poster session

Wednesday, 18th June – Room Agliè

Session 06 – Physiology and Reproduction: RUMINANT PHYSIOLOGY

Chairs: **Minuti Andrea – Radoslava Kristofova**

9:00 **Calanni Macchio Alfio, Iraci Fuintino Antonio, Ragona Francesca, Purrone Sissy, Trapanese Lucia, Pacelli Giovanmaria, Santinello Matteo**
Influence of conception time on milk yield and quality traits in primiparous Mediterranean buffalo..... **167**

9:15 **Benedetti Lorenzo, Piccioli-Cappelli Fiorenzo, Sfulcini Marta, Cattaneo Luca, Minuti Andrea, Trevisi Erminio**
Feeding dairy cows in the morning or in the evening: effects on milk production, rumen activity and feeding behavior..... **168**

9:30 **Niero Giovanni, Visentin Giulio, Meoni Gaia, Leonardo Tenori, Cassandro Martino, De Marchi Massimo, Penasa Mauro**
Impact of cow udder health status on milk metabolic pattern..... **407**

9:45 **Piccioli-Cappelli Fiorenzo, Mezzetti Matteo, Vercesi Alessandro, Scemama De Gialluly Sophie, Benedetti Lorenzo, Bosio Lorenzo, Greco Dante, Trevisi Erminio**
Effects administration of vitamin D3 delivered by liposomes to dairy cows during transition period..... **482**

10:00 **Lopreiato Vincenzo, Stocco Giorgia, Biffani Stefano, Liotta Luigi, Niero Giovanni, Penasa Mauro, Summer Andrea, Martinelli Nicola, Cipolat-Gotet Claudio**
Application of a generalized additive mixed model to evaluate the effect of season, energy status, milk yield, and milk macro-mineral content on milk fatty acids profile of Brown Swiss dairy cows..... **551**

10:15 **Maggiolino Aristide, Landi Vincenzo, Trevisi Erminio, Bernabucci Umberto, Lecchi Cristina, Ceciliani Fabrizio, De Palo Pasquale**
Hemogasanalysis patterns modifications in Holstein Friesian and Brown Swiss lactating cows coping with a natural short-term heat wave..... **445**

10:30 **Sfulcini Marta, Cattaneo Luca, Piccioli-Cappelli Fiorenzo, Trevisi Erminio, Minuti Andrea**
Early-life ruminal transfaunation using different types of in-vitro fermented inocula: effect in health and performance in dairy calves..... **296**

10:45 Coffee Break and Poster session

Wednesday, 18th June – Room Carignano

Session 07 – Production Systems: EFFICIENCY, HEALTH, AND SUSTAINABILITY

Chairs: **Chiofalo Biagina – Birolo Marco**

9:00 **Ravetto Enri Simone, Pittarello Marco, Lonati Michele, Lombardi Giampiero**
Can livestock site-use intensity be estimated by observation of grazing evidences in alpine pastures?.... **453**

9:15 **Podda Maria Giovanna, Sechi Gian Simone, Todde Giorgio, Cannas Antonello, Atzori Alberto Stanislao**
Optimizing dairy farm efficiency: a case study in process mapping and business process management for feeding operations..... **170**

9:30 **Coppa Mauro, Bellato Alessandro, Manenti Isabella, Bongioanni Luisa, Borla Laura, Donato Antonella, Mannelli Alessandro, Battaglini Luca**
Farm management risk factors of mastitis for mountain dairy farms in the western Alps..... **499**

9:45 **Ferronato Giulia, Anna Simonetto, Gilioli Gianni, Zecconi Alfonso**
Exploring the relationship between mastitis risk management, milk yield and global warming potential in dairy farms..... **306**

10:00 **Tretola Marco, Antonacci Alessandro, Silacci Paolo, Bee Giuseppe**
Impact of two different pen cleaning protocols on ex-vivo jejunal integrity and nutrients uptake of growing-finishing pigs fed standard or low-protein diets..... **028**

10:15 INVITED LECTURE
Baxter Emma
How to 'End the Cage Age' for farrowing sows – updates on research, systems and best practice.....

10:45 Coffee Break and Poster session

Wednesday, 18th June – Room Venaria

Session 08 – Genetics: SUSTAINABILITY AND FUTURE PERSPECTIVES OF ANIMAL BREEDING

Sponsored by Fedana

Chairs: **Cassandro Martino – Fumagalli Francesca**

11:15 **Persichilli Christian, Cassandro Martino, Senczuk Gabriele, Di Civita Marika, Bitew Mulusew Kassa, Van Kaam Jan-Thijs, Finocchiaro Raffaella, Pilla Fabio**
Worldwide diversity of Holstein cattle **485**

11:30 **Zanotti Andrea, Cipolat-Gotet Claudio, Summer Andrea, Sabbioni Alberto, Asti Vittoria, Tiezzi Francesco, Finocchiaro Raffaella, Van Kaam Jan-Tijs, Cassandro Martino, Layton Jonathan, Ablondi Michela**
The impact of inbreeding on fertility in Italian Holstein cattle **373**

11:45 **Milia Paola, Cesarani Alberto, Fabris Anna, Finocchiaro Raffaella, Marusi Maurizio, Macciotta Nicolò, Dimauro Corrado**
Assessing fertility: developing an index for Italian Jersey cattle **065**

12:00 **Benzoni Lorenzo, Layton Jonathan, Finocchiaro Raffaella, Marusi Maurizio, Testori Fabio, Cassandro Martino**
Phenotypic associations between hoof lesions and type traits in Italian Holstein population..... **059**

12:15 **Gomez Mayra, Cimmino Roberta, Rossi Dario, Zullo Gianluigi, Di Vuolo Gabriele, Neglia Gianluca, Biffani Stefano**
The Role of Inbreeding Depression in the Genetic Improvement Program of the Italian Mediterranean Buffalo..... **443**

12:30 **Callegaro Simone, Tiezzi Francesco, Maltecca Christian, Fabbri Maria Chiara, Bozzi Riccardo**
Comprehensive analysis of inbreeding depression across growth, fertility, and survival traits in Charolais and Limousine beef cattle..... **129**

12:45 **Bertolini Francesca, Vegni Jacopo, Schiavo Giuseppina, Bovo Samuele, Bolner Matteo, Buttazzoni Luca, Gallo Maurizio, Fontanesi Luca**
Changes in allele and haplotype frequencies over the years have differentiated the genomes of Italian heavy pigs from cosmopolitan breeds..... **382**

13:00 Lunch

Wednesday, 18th June – Room Racconigi

Session 09 – Food Quality: EGGS AND OTHER FOODS

Chairs: **Dal Bosco Alessandro – Di Rosa Ambra**

11:15 **Dalle Zotte Antonella, Singh Yazavinder, Boccato Alberto, Cullere Marco**
Camelina sativa: an emerging crop that can successfully be exploited in laying hen's feeding without compromising egg quality..... **322**

11:30 **Cullere Marco, Singh Yazavinder, Dalle Zotte Antonella, Boccato Alberto**
Camelina sativa: an emerging crop to enhance egg healthiness and reaching the claim "rich in omega-3 fatty acids"..... **288**

11:45 **Piscitelli Raffaela, Zampiga Marco, Pignata Stefano, Petracci Massimiliano, Sirri Federico**
Proximate composition and fatty acid profile of eggs laid by two Italian chicken breeds, their crossbreeds, and a commercial hen hybrid reared both in enriched cages and free-range system **086**

12:00 **Carta Silvia, Rubattu Roberto, Nudda Anna, Correddu Fabio**
Does the farming system influence the quality of the eggs in terms of chemical composition and colour parameters? **393**

12:15 **Accetta Francesca, Ben Tiba Amani, Ayoub Hai Said, Di Rosa Ambra**
Evaluation of geographical and botanical origin of Tunisian and Sicilian honeys using artificial senses and data fusion..... **317**

12:30 **Lanzoni Davide, Zanderigo Giovanni, Petrosillo Elena, Sundaram Tamil, Baldi Antonella, Cheli Federica, Giromini Carlotta**
Exploring plant-based proteins as an alternative for culture media in cellular agriculture **039**

12:45 **Pulina Giuseppe, Lunesu Mondina Francesca, Correddu Fabio, Cesarani Alberto, Nudda Anna**
The naturalness of food production and processing: ethical perspectives and a new metric of naturalness **574**

13:00 Lunch

Wednesday, 18th June – Room Stupinigi

Session 10 – Alternative Proteins: YELLOW MEALWORM AND BLACK SOLDIER FLY REARING AND NUTRITION
Sponsored by GREEN FEED CYCLES

Chairs: **Rumbos Christos – Secci Giulia**

11:15 **Chrysanthopoulou Christina, Adamaki-Sotiraki Christina, Rumbos Christos I., Athanassiou Christos**
Feeding Tenebrio molitor larvae with oilseed presscakes – Sustainable and nutrient-rich feeding substrates..... **577**

11:30 **Dell'Anno Matteo, Ferri Irene, Dametti Matilda, Spano Mattia, Mannina Luisa, Rossi Luciana**
Evaluation of the metabolomic profile in Tenebrio molitor reared on functional substrates **515**

11:45 **Loiotine Zaira, Bellezza Oddon Sara, Resconi Andrea, Passaro Rosa Laura, Gai Francesco, Bacenetti Jacopo, Gasco Laura, Biasato Ilaria**
Larval growth and bioconversion efficiency of black soldier fly (Hermetia illucens) on rice by-products: unlocking new life for agricultural waste **072**

12:00 **Nucera Daniele, Bellezza Oddon Sara, Loiotine Zaira, Passaro Rosa Laura, Piano Serenella, Biasato Ilaria, Zeppa Giuseppe, Renna Manuela, Patti Sara, Gasco Laura**
Stabilization of canteen waste for Hermetia illucens larvae substrate production..... **556**

12:15 **Passaro Rosa Laura, Bellezza Oddon Sara, Loiotine Zaira, Biasato Ilaria, Sorayani Bafqi Reyhane, Nucera Daniele, Piano Serenella, Gasco Laura**
Transforming canteen waste into black soldier fly larvae feed: effects on growth performance and bioconversion efficiency..... **058**

12:30 **Zanzot Asia, Copelotti Emma, Cacchiarelli Chiara, Trocino Angela, Mancini Simone**
Meat-based diets for Hermetia illucens larvae: effects on growth and proximate composition **161**

12:45 **Zafeiriadis Sofronios, Baliota Georgia, Adamaki-Sotiraki Christina, Karagiorgis Georgios, Rumbos Christos, Athanassiou Christos**
Sustainable management of dairy waste: exploring Hermetia illucens (L.) bioconversion potentials for efficient effluent treatment..... **578**

13:00 Lunch

Wednesday, 18th June – Room Valentino

Session 11 – Sustainability: ENTERIC EMISSIONS

Chairs: **Vitali Andrea – Gislon Giulia**

11:15 INVITED LECTURE
Bacenetti Jacopo
Weaknesses, limits, biases and strengths of LCA applied to livestock systems .....

11:45 **Braidot Matteo, Cabbia Anita, Cavallini Damiano, Spanghero Mauro, Romanzin Alberto**
Methane emission assessment in Simmental bulls divergent for feed efficiency..... **274**

12:00 **Ramirez Mauricio Marco Aurelio, Toledo-Alvarado Hugo, Schiavon Stefano, Martinez-Marin Gustavo, Gallo Luigi, Nocetti Marco, Sturaro Enrico, Giannuzzi Diana, Cecchinato Alessio**
Impact of farming systems and welfare indicators on milk infrared-predicted enteric methane emissions in Parmigiano Reggiano cheese production area **087**

12:15 **Rossi Chiara, Grossi Giampiero, Vitali Andrea, Lacetera Nicola**
Seasonal pattern of enteric methane emissions in dairy cow **427**

12:30 **Moliso Mesfin Mekonnen, Ferronato Giulia, Pinares-Patino Cesar, Mrode Raphael, Fioretti Mauro, Melilli Caterina, Pascarella Lorenzo, Ajmone Marsan Paolo, Negrini Riccardo**
Assessment of enteric methane emissions in three Italian dairy cattle breeds using DHI data **377**

12:45 **Rossi Chiara, Grossi Giampiero, Vitali Andrea, Petrocchi Jasinski Francesca, Evangelista Chiara, Basiricò Loredana, Turriziani Giovanni, Bernabucci Umberto, Lacetera Nicola**
Effect of green forage on enteric methane emissions in Mediterranean dairy buffaloes during summer: different approaches for measurement **417**

13:00 Lunch

Wednesday, 18th June – Room Mandria

Session 12 – Ruminant Nutrition: NUTRITION AND FEEDING BEHAVIOUR OF DAIRY COWS

Chairs: **Toral Pablo – Simoni Marica**

11:15 **Rocchetti Gabriele, Cattaneo Luca, Froldi Federico, Lapris Marco, Moschini Maurizio, Bani Paolo, Trevisi Erminio**
A data fusion approach unveils the impact of 3–nitrooxypropanol on the rumen fluid and milk metabolomes of lactating Holstein dairy cows..... **049**

11:30 **Simoni Marica, Esposito Giulia, Paolino Annamaria, Patrissi Rosanna, Righi Federico**
Nutritional and chemical characteristics of hay-based diets as predictors of ruminal and intestinal microbial development and function **211**

11:45 **Simoni Marica, Pitino Rosario, Boldrin Gloria, Valoppi Davide, Tedeschi Irene, Cipolat-Gotet Claudio, Righi Federico**
Evaluation of two feeding strategies applied to robotic milking on primiparous cows **434**

12:00 **Righi Federico, Pitino Rosario, Mantovani Giorgia, Danese Tommaso, Tsiplakou Eleni, Simoni Marica**
Comparing nitrogen supply from hay-based diets fed to dairy cows having low or high nitrogen excretion..... **419**

12:15 **Zambianchi Lucia, Colleluori Riccardo, Giaretta Elisa, Fusaro Isa, Spagnolo Marco, Ferrari Maria Giulia, Mammi Ludovica Maria Eugenia**
Urinary mineral excretion in dry cows during prepartum period..... **549**

12:30 **Meli Giovanna, Chen Wenning, Fumo Valentina, Savoini Giovanni, Invernizzi Guido**
Feeding behavior in heat-stressed heifers under different management practices **540**

12:45 **Amato Annalisa, Sfulcini Marta, Guenther Maverick, Larsen Grace, Guzi Savegnano Caroline, Tao Sha, Laporta Jimena**
The impact of pre-weaning plane nutrition on mammary gland development of dairy calves..... **349**

13:00 Lunch

Wednesday, 18th June – Room Agliè

Session 13 – Physiology and Reproduction: MISCELLANY

Chairs: **Cerolini Silvia – Antenucci Emanuele**

11:15 **Lopreiato Vincenzo, Cavallo Carmelo, Floridia Viviana, Liotta Luigi, Chiofalo Vincenzo, D'Andrea Mariasilvia, Palombo Valentino**
Rumen epithelium transcriptome changes in response to polyphenols-enriched olive cake supplementation in finishing Limousine bulls **448**

11:30 **De Matos Luiz Gustavo, Balbi Ombretta, Salvi Gaspare, Dadi Yasmine, Ceciliani Fabrizio, Martini Valeria, Agazzi Alessandro, Maggiolino Aristide, De Paolo Pasquale, Lecchi Cristina**
Modulation of bovine immune cells by Small Extracellular Vesicles solated from the plasma of heat-stressed Cows..... **146**

11:45 **Fulgione Andrea, Iovane Valentina, Gentile Antonio**
Prediction by molecular dynamics simulation analysis of IL-10 polymorphisms effects and association with brucellosis in Mediterranean river Buffalo **077**

12:00 **Kristofova Radoslava, Zitterl-Eglseer Karin, Capucchio Maria Teresa, Ippolito Dorotea, Gai Francesco, Firooznia Fardad, Laukova Andrea, Pogany Simonova Monika, Cikos Stefan, Spirkova Alexandra, Franc Ales, Takacsova Margareta, Placha Iveta**
Protective effect of thymol incorporated into gastroresistant pellets on intestinal integrity and microbiota in rabbits **145**

12:15 **Pasquariello Rolando, Di Filippo Francesca, Brevini Tiziana A.L., Gandolfi Fulvio**
Innovative flow cytometry-based isolation of bovine spermatids for assisted reproductive technologies..... **019**

12:30 INVITED LECTURE
Knight Christopher Harold
Progress towards reasonably-precise livestock farming in the dairy sector

13:00 Lunch

Wednesday, 18th June – Room Carignano

Session 14 – Production Systems: CHALLENGES AND INNOVATIONS

Chairs: **Castellini Cesare – Zappaterra Martina**

11:15 **D'alessandro Angela, Di Luca Alessio, Cavaliere Gina, Martemucci Giovanni, Cimmino Fabiano, Trinchese Giovanna, Mollica Maria Pina**
Evaluation of physiological effects of milk from the autochthonous Capestrina goat breed using an animal model study **045**

11:30 **Perrucci Alice, Ferrari Elvira, Cavagnini Alberto, Scollo Annalisa**
Statistical process control to monitor productive items affected by PRRS virus **018**

11:45 **Ferrari Carolina, Cesarani Alberto, Gaspa Giustino, Macciotta Nicolò, Falchi Laura, Bernabucci Umberto, Negrini Riccardo**
Analyzing big data to evaluate heat stress tolerance in dairy cows..... **337**

12:00 **Menini Alessio, Marcon Caterina, Magrin Luisa, Stiletto Alice, Giampietri Elisa, Trestini Samuele, Gottardo Flaviana**
Innovative and participatory pathways for sustainable livestock farming and meat production: insights from the Veneto region in Italy **357**

12:15 **Di Federico Francesca, Angelucci Elisa, Davidescu Magdalena, Macchioni Lara, Salvadori Laura, Chiappalupi Sara, Sorci Guglielmo, Dal Bosco Alessandro, Bosa Luigia, Castellini Cesare, Mattioli Simona**
Lipid metabolism of chickens with different growth rate and kinetic activity..... **198**

12:30 **Birolo Marco, Pontalti Emanuele, Pirrone Fabrizio, Nalon Eleonora, Mattioli Simona, Verdiglione Rina, Dalle Zotte Antonella**
Effect of heat stress on growth performance and carcass traits of fast- medium- and slow-growing chicken genotypes **218**

12:45 **Franzin Alberico, Olivieri Silvia, Sciuto Simona, Provera Alessandra, Ferraris Carla, Romano Angelo, Pitti Monica, Power Karen, Leandri Rebecca, Biasibetti Elena, Pezzolato Marzia, Bozzetta Elena**
Exceptional mortality in an intensive "short cycle" snail farm in Northwest Italy..... **554**

13:00 Lunch

Wednesday, 18th June – Room Venaria

Session 15 – Genetics: OMICS-BASED APPROACHES

Chairs: **Ajmone-Marsan Paolo – Schiavo Giuseppina**

14:00 INVITED LECTURE
Blasco Agustín
Omics data sets are compositional: the problem and its solution

14:30 **Williams John, Colli Licia, Ren Yan, Santos Pinder Paulene, Khatkar Mehar, Macphillamy Callum, Negrini Riccardo, Flores Ester, Ajmone Marsan Paolo, Low Wai Yee**
Genotyping Buffalo by Targeted SNP-Capture Sequencing **396**

14:45 **Bolner Matteo, Bertolini Francesca, Bovo Samuele, Schiavo Giuseppina, Cappelloni Manolo, Gallo Maurizio, Fontanesi Luca**
Application of metabolomics to help dissect biological factors underlying fat deposition in pigs **254**

15:00 **Bovo Samuele, Bolner Matteo, Schiavo Giuseppina, Bertolini Francesca, Gallo Maurizio, Fontanesi Luca**
Multi-omics dissection of lipid metabolism in Italian heavy pig breeds **244**

15:15 **Mecocci Samanta, Cappelli Katia, Beccati Francesca, Porzio Elisabetta, Ratto Roberta, Pepe Marco, Capomaccio Stefano**
Exercise as a modifier of the molecular clock in the athletic horse: a genome-wide study **303**

15:30 Coffee Break and Poster session

Wednesday, 18th June – Room Racconigi

Session 16 – Food Quality: SHEEP MEAT

Chairs: **Maggiolino Aristide – Correddu Fabio**

14:00 **Lopez Annalaura, Greco Margherita, Marcolli Beatrice, Moretti Vittorio Maria, Mattiello Silvana, Bellagamba Federica**
Evaluation of the triple attitude of the alpine Ciuta sheep breed: quality assessment of milk, meat and wool **234**

14:15 **Maniaci Giuseppe, Giosuè Cristina, Ul Hassan Mahmood, Gannuscio Riccardo, Busetta Gabriele, Gaglio Raimondo, Todaro Massimo, Alabiso Marco**
Effects of including destoned olive cake in sheep feed on meat quality and salami production **343**

14:30 **Musati Martino, Cannone Marco Sebastiano, Bertino Antonino, Mangano Fabrizio, Luciano Giuseppe, Priolo Alessandro, Mangione Guido, Foti Francesco, Scerra Manuel, Della Malva Antonella, Natalello Antonio**
Effects of feeding bergamot by-products on performance and meat quality in lambs **366**

14:45 **Ponte Marialetizia, Pipi Marianna, Badalamenti Rosario, Bonanno Adriana, Di Grigoli Antonino**
Effects of ensiled and dehydrated grape pomace in the ewes' diet on meat production of suckling lambs **509**

15:00 **Satta Francesca, Castangia Francesca, Pinna Aurelia, Caria Claudio, Ledda Antonello, Spezzigu Antonio, Sotgiu Francesca, Cannas Antonello**
Enhancing meat production and quality of culled Sarda ewes **195**

15:15 **Parrini Silvia, Pugliese Carolina, Becciolini Valentina, Tocci Roberto, Sargentini Clara, Crovetti Alessandro, Sirtori Francesco, Aquilani Chiara, Bozzi Riccardo**
Assessing quality traits of lamb meat by FT- NIRS **164**

15:30 Coffee Break and Poster session

Wednesday, 18th June – Room Stupinigi

Session 17 – Alternative Proteins: INSECT REARING AND USE AS ANIMAL FEED
Sponsored by GREEN FEED CYCLES

Chairs: **Mancini Simone – Benini Elisa**

14:00 **Tognocchi Monica, Malucchi Gilda, Tinagli Sara, Canale Angelo, Perioli Riccardo, Conte Giuseppe, Mele Marcello, Serra Andrea**
Rearing substrate influences the chemical composition of Hermetia Illucens larvae **437**

14:15 **Moradei Andrea, Ottoboni Matteo, Malabusini Serena, Jucker Costanza, Savoldelli Sara, Luciano Alice, Pinotti Luciano**
Enriched zinc and selenium agri-food by-products: effects on growth performance of black soldier fly **096**

14:30 **Baima Lorenzo, Merlino Valentina Maria, Bellezza Oddon Sara, Gasco Laura, Biasato Ilaria, Loiotine Zaira, Blanc Simone, Massaglia Stefano, Brun Filippo**
Economic and social perspectives on integrating Hermetia illucens *meal in animal feed supply chains*..... **354**

14:45 **Biasato Ilaria, Bongiorno Valentina, Loiotine Zaira, Bellezza Oddon Sara, Ribeiro Teresa, Resconi Andrea, Passaro Rosa Laura, Mendez Rondo Keidy Yasmin, Filippa Alessia, Cappone Eleonora Erika, Fiorilla Edoardo, Renna Manuela, Brugiapaglia Alberto, Schiavone Achille, Gasco Laura**
Live Tenebrio molitor larvae as feed ingredient for native chickens: effects on productive performance and egg quality **038**

15:00 **Copelotti Emma, Fronte Baldassare, Sangiacomo Chiara, Sogari Giovanni, Andreani Giulia, Moruzzo Roberta, Mancini Simone**
Black soldier fly as feed: focus on the quality of gilthead seabream (Sparus aurata L.) fillets fed with a partial fish meal replacement **033**

15:15 **Bellezza Oddon Sara, Biasato Ilaria, Loiotine Zaira, Sorrentino Federica, Caimi Christian, Rumbos Christos, Gasco Laura**
What about exploring new insect species? Fruit fly (Ceratitis capitata) meal as a feed ingredient in juvenile rainbow trout diets..... **095**

15:30 Coffee Break and Poster session

Wednesday, 18th June – Room Valentino

Session 18 – Sustainability: EXTENSIVE SYSTEMS

Chairs: **Mele Marcello – Lunesu Mondina**

14:00 **Franca Antonello, Altana Giovanni, Arca Pasquale, Atzori Alberto, Stanislao, Khater Stephanie, Monagheddu Arianna, Mussolino Claudio, Solinas Stefania, Vagnoni Enrico**
A preliminary environmental characterization of Mediterranean pastoral food products based on the LCA Approach..... **436**

14:15 **Fichter Greta, Gauly Matthias, Sabia Emilio, Zanon Thomas**
Environmental efficiency and carbon sequestration potential of organic vs. conventional Simmental dairy farming systems in mountain regions..... **016**

14:30 **Sturaro Enrico, Birolo Marco, Bonavolontà Francesco, Mancinelli Cartoni Alice, Di Iacovo Francesco, Lacetera Nicola, Marconi Marco, Petracci Massimiliano, Provolo Giorgio, Verde Maria Teresa, Vitali Andrea**
SOLSTICE: a living labs approach for assessing the overall sustainability of livestock systems through Life Cycle Assessment..... **135**

14:45 **Da Re Sebastiano, Raniolo Salvatore, Squartini Andrea, Sturaro Enrico, Ramanzin Maurizio**
Impact of livestock pasture-use intensity and soil geochemical properties on microbial functional potential of nutrient cycles in Alpine pastures..... **174**

15:00 **Raniolo Salvatore, Da Re Sebastiano, Squartini Andrea, Sturaro Enrico, Ramanzin Maurizio**
Grazing intensity, soil functions and greenhouse gas emissions: a case study in Alpine pastures of the Dolomites **380**

15:15 **Cavallo Carmelo, Amato Annalisa, Evola Carola, Negrini Riccardo, Tolone Marco, Liotta Luigi, Lopreiato Vincenzo**
Temperature-humidity index breakpoints for rectal temperature and milk performance of Cinisara cows under semi-extensive dairy system..... **369**

15:30 Coffee Break and Poster session

Wednesday, 18th June – Room Mandria

Session 19 – Ruminant Nutrition: IN VITRO STUDIES AND NEW FEEDSTUFFS

Chairs: **Cheli Federica – Natalello Antonio**

14:00 **Scicutella Federica, Bolletta Viviana, Lira De Medeiros Adja, Daghio Matteo, Foggi Giulia, Valenti Bernardo, Mannelli Federica, Mele Marcello, Viti Carlo, Pauselli Mariano, Buccioni Arianna**
Are in vitro experiments a suitable tool to study rumen fermentation? **238**

14:15 **Vastolo Alessandro, Montefusco Teresa, Ruggiero Alessio, Kiatti Dieu Donné, Cutrignelli Monica Isabella** .....
Effect of hazelnut and pomegranate by-products on in vitro methane reduction and ruminal fermentation in sheep..... **155**

14:30 **Bonizzi Serena, Colombini Stefania, Pavesi Martina, Cesari Valentina, Failla Osvaldo, Ragaglini Giorgio, Sandrucci Anna**
Enhancing circularity in dairy cattle farming: nutritional assessment of Morus alba leaves **352**

14:45 **Daniso Enrico, Cabbia Anita, Spanghero Mauro**
In vitro rumen fermentation of wheat straw after treatment with mush-room extracts (Pleurotus ostreatus and Agaricus bisporus). **496**

15:00 **Fiorbelli Erica, Moccia Davide, Rocchetti Gabriele, Atzori Alberto Stanislao, Pusceddu Antonio, Gallo Antonio**
Screening of Italian Mediterranean macroalgae for the potential reduction of methane emissions **530**

15:15 **Maggiolino Aristide, Caroprese Mariangela, Di Grigoli Antonino, Denora Nunzio, Lopedote Angela, Ponte Marialetizia, Marino Rosaria, Sevi Agostino, Pipi Marianna, De Palo Pasquale**
An innovative rumen-bypass micro-encapsulation technique for essential oils **176**

15:30 Coffee Break and Poster session

Wednesday, 18th June – Room Agliè

Session 20 – Welfare, Health and Behaviour: NEW APPROACHES TO POULTRY MANAGEMENT

Chairs: **Tufarelli Vincenzo – Aquilani Chiara**

14:00 **Toth Mark, Kovacs-Weber Mária, Ancsin Zsolt, Dalle Zotte Antonella, Erdélyi Márta**
Preliminary evaluation of mealworm frass for broiler chicken bedding **371**

14:15 **Nompleggio Lorenzo, Di Federico Francesca, Angelucci Elisa, Dal Bosco Alessandro, Castellini Cesare, Bosa Luigia, Mattioli Simona**
Effect of kinetic activity on behaviour and productive performance of different chicken genotypes..... **126**

14:30 **Ciarelli Claudia, Pravato Mattia, Bordignon Francesco, Xiccato Gerolamo, Trocino Angela**
Effect of ramps on space use of laying hens in a cage-free system..... **461**

14:45 **Pravato Mattia, Bordignon Francesco, Pezzuolo Andrea, Marinello Francesco, Trocino Angela, Xiccato Gerolamo**
Relationships between environmental conditions and behaviour of laying hens in an aviary system..... **053**

15:00 **Lai Giorgia, Pudda Flavia, Muzzeddu Marco, Cappai Maria Grazia**
Feeding management for nutritional welfare of griffon vultures as life-long kept vs. temporarily before release into nature..... **552**

15:15 //

15:30 Coffee Break and Poster session

Wednesday, 18th June – Room Carignano

Session 21 – Production Systems: PRODUCTION STRATEGIES AND QUALITY TRAITS

Chairs: **Petracci Massimiliano – Perricone Vera**

14:00 **Molin Matteo, Bordignon Francesco, Pravato Mattia, Zuffellato Andrea, Trocino Angela, Xiccato Gerolamo**
Effect of group size, environmental enrichment, and temperature on growth performance and meat quality of rabbits..... **050**

14:15 **Peng Meng, Tavaniello Siria, Stadnicka Katarzyna, Skowron Krzysztof, Grudlewska-Buda Katarzyna, Randazzo Cinzia, Vaccalluzzo Amanda, Maiorano Giuseppe**
Effect of selected synbiotics injected in ovo on hatchability and chick quality..... **285**

14:30 **Balbo Chiara, Stocco Giorgia, Pizzamiglio Valentina, Sabellini Giulio, Valoppi Davide, Tedeschi Irene, Levante Alessia, Alinovi Marcello, Fenga Irene, Chiavaro Emma, Summer Andrea, Cipolat-Gotet Claudio**
The race of milk components: rising to the top during natural creaming in Parmigiano Reggiano PDO. **367**

14:45 **Boldt Ariane, Gauly Matthias, Sanftleben Peter, Zanon Thomas**
Impact of sires' breed on calving ease, resulting fattening performance and carcass quality parameters in fattening bulls from Holstein Friesian herds in North-Eastern Germany **015**

15:00 **Cozzi Giulio, Segato Severino, Cozzi Giulio, Magrin Luisa**
Production performance and early culling rates of finishing Charolais young bulls in Italy. Results of a case study..... **149**

15:15 **Piscopo Nadia, Trapanese Lucia, Pierro Federica, Borzacchiello Luca, Matera Roberta, Esposito Luigi**
Meat quality of the Podolica cattle raised with different finishing methods in the Calabrian Apennines..... **205**

15:30 Coffee Break and Poster session

Wednesday, 18th June – Room Venaria

Session 22 – Genetics: GENOMIC APPLICATIONS FOR BREEDING
Sponsored by SINERGY

Chairs: **Macciotta Nicolò – Fabbri Mariachiara**

16:00 **Gomez Proto Guido, Mancin Enrico, Oian Angelica, Rulli Eugenio, Blanchet Veruska, Vevey Mario, Bernini Francesca, Strillacci Maria, Bagnato Alessandro, Sartori Cristina, Mantovani Roberto**
Precision breeding in Valdostana cattle breed: Genomic tools applied to milk production traits **080**

16:15 **Sartori Cristina, Tuliozi Beniamino, Mancin Enrico, Rulli Eugenio, Gomez Proto Guido, Oian Angelica, Veruska Blanchet, Vevey Mario, Mantovani Roberto**
Social dominance and other new behavioural phenotypes in Valdostana cattle: genetic parameters and relationships with selected traits..... **550**

16:30 **Cesarani Alberto, Rossoni Attilio, Lourenco Daniela, Gaspa Giustino**
Genetic parameters and genome wide association study on fertility traits in Italian Brown cows..... **283**

16:45 **Crepaldi Paola, Bionda Arianna, Cortellari Matteo, Lopreiato Vincenzo, Rossoni Attilio, Mozafari Reza, Cesarani Alberto, Liotta Luigi, Parma Pietro**
Robertsonian translocation 1–29: a focus on Sicilian breeds..... **261**

17:00 **Sardina Maria Teresa, Riggio Silvia, Carta Federica, Ben Jemaa Slim, Portolano Baldassare, Benanti Alessia, Senczuk Gabriele, Cesarani Alberto, Mastrangelo Salvatore**
Analysis of copy number variations in the peninsular Italian sheep breeds using a high-density 600K SNP array..... **532**

17:15 **Letaief Neyrouz, Alhaddad Hasan, Lühken Gesine, Gaspa Giustino, Gianfranco Cosenza, Pauciullo Alfredo**
Genetic investigation of the Lactophorin whey protein coding gene reveals novel polymorphisms in New and Old-World camelids..... **104**

Wednesday, 18th June – Room Racconigi

Session 23 – Food Quality: BEEF

Chairs: **Conte Giuseppe – Della Malva Antonella**

16:00 INVITED LECTURE
Scollan Nigel David, Perkins Lynda, Hocquette Jean-Francois, Berri Celcile, Martin Bruno
New trends in measuring animal product quality linking sustainability and husbandry systems.....

16:30 **Lunesu Mondina Francesca, Carta Silvia, Rubattu Roberto, Fenu Antonio, Rassu Salvatore Pier Giacomo, Battacone Gianni, Pulina Giuseppe, Nudda Anna**
Animal performance, carcass traits and meat quality of Limousine, Sardo-Bruna, and their crosses..... **480**

16:45 **Valenti Bernardo, Lilli Emanuele, Bolletta Viviana, Pecorari Laura, Torquati Biancamaria, Ceccarini Federico, Calisti Silvia, Chiorri Massimo, Pauselli Mariano**
Animal performance and meat quality of crossbred heifers fed with phenol-rich agri-food by-products and forages..... **454**

17:00 **Gagliano Mara Antonia, Grigoletto Ilaria, Soglia Francesca, Valli Enrico, Gallina Toschi Tullia, Bendini Alessandra, Petracci Massimiliano**
Instrumental and sensory evaluations to assess the quality of beef meat in relation to Country of origin..... **257**

17:15 **Forte Lucrezia, Seccia Alessia, De P`alo Pasquale, Calzaretti Giovanna, Incampo Giovanna, Samoilis Giorgio, Maggiolino Aristide**
Meat quality in veal calves fed with milk whey powder..... **230**

Wednesday, 18th June – Room Stupinigi

Session 24 – Alternative Proteins: INSECTS AND ALTERNATIVE PROTEINS AS ANIMAL FEEDS
Sponsored by GREEN FEED CYCLES

Chairs: **Trocino Angela – Dell'Anno Matteo**

16:00 **Benini Elisa, Gordini Sabrina, Dondi Francesco, Scicchitano Daniel, Candela Marco, Gatta Pier Paolo, Bonaldo Alessio, Parma Luca**
Bacterial single-cell protein in aquafeed: implications for growth and gut health in gilthead sea bream (Sparus aurata)..... **181**

16:15 **Cenati Clara, Pea Alessia, Perricone Vera, Petrosillo Elena, Agazzi Alessandro, Parati Katia, Savoini Giovanni**
Dietary microalgae in broiler nutrition and their effects on performance and organ development..... **298**

16:30 **Correa Federico, Bordoni Alessandra, Luise Diana, Gotti Roberto, Trevisi Paolo**
In vitro digestibility of microbial cell-derived protein sources for animal nutrition..... **579**

16:45 **Sportelli Federica, Pinna Carlo, Montanari Irene, Delsante Costanza, Vecchiato Carla Giuditta, Biagi Giacomo**
Effects of insect meals on the fecal microbiota: an in vitro study on healthy and chronic enteropathic dogs..... **472**

17:00 **Armone Rosangela, Balouei Fatemeh, Randazzo Andrea, Nava Vincenzo, Alizzi Antonino Filippo Maria, Barbato Mario, Stefanon Bruno, Chiofalo Biagina**
Preliminary assessment of nutrient digestibility and fecal quality in dogs fed a diet containing hydrolyzed feather meal..... **123**

17:15 **Spatola Gabriele, Giusti Alice, Gasperetti Laura, Nuvoloni Roberta, Dalmasso Alessandra, Chiesa Francesco, Armani Andrea**
Insects-based products sold by e-commerce on the EU market: microbiome characterization by 16S rRNA metabarcoding..... **226**

Wednesday, 18th June – Room Valentino

Session 25 – Sustainability: SUSTAINABLE SUPPLY CHAINS

Chairs: **Bava Luciana – Berton Marco**

16:00 **Diaz Vicuna Elena, Fiorilla Edoardo, Srikanthithasan Karthika, Zambotto Valeria, Bianchi Chiara, Capaldi Giorgio, Grillo Giorgio, Renna Manuela, Giorgino Andrea, Ozella Laura, Arneodo Valentina, Cravero Andrea, Tabasso Silvia, Forte Claudio**
Improving livestock nutrition sustainability in a (hazel)nutshell **541**

16:15 **Latrofa Antonella, Currò Sarah, Arango Sheyla, Guzzo Nadia, Montanari Massimo, Bailoni Lucia**
*Nutritional characterization of industrial hempseeds (*Cannabis sativa L.*) of different varieties*..... **559**

16:30 **Capretti Chiara, Lanzoni Lydia, Petrocchi Francesca, Vignola Giorgio, Di Pasquale Jorgelina**
The management of foot health as a tool to improve the sustainability of a dairy farm **431**

16:45 **Mastromonaco Giulia, Massaglia Stefano, Blanc Simone, Borra Danielle, Costamagna Chiara, Cornale Paolo, Biagini Davide, Merlino Valentina Maria**
Measuring the importance of sustainability in animal-based product supply chains: insights from the CUB Model **314**

17:00 **Benedetti Del Rio Elena, Berton Marco, Sari Stefano, Zoratti Aloma, Corazzin Mirco, Tamburini Alberto, Gallo Luigi, Sturaro Enrico**
Stakeholder attitude towards sustainability of dairy farming systems: a participatory process **295**

17:15 **Fatica Antonella, Tedesco Doriana, Pastorelli Grazia, Todini Luca, Fantuz Francesco, Salimei Elisabetta**
Stakeholders' perspectives on environmental issues: preliminary results from SUNEQUMAR survey..... **099**

Wednesday, 18th June – Room Mandria

Session 26 – Ruminant Nutrition: IN VITRO METHODOLOGY AND MICROPLASTICS

Chairs: **Spanghero Mauro – Mannelli Federica**

16:00 **Iqbal Rashid, Arango Sheyla, Guzzo Nadia, El Hawat Rebecca, Tagliapietra Franco, Bailoni Lucia**
Comparative analysis of AnkomRF and gas Endeavour in vitro rumen systems: effects of headspace volume and CO2 flushing time on gas and methane production **423**

16:15 **Boldrin Gloria, Simoni Marica, Mantovani Luciana, Righi Federico**
In vitro comparison among commercial dietary buffers..... **523**

16:30 **Ghiaccio Francesca, Palmonari Alberto, Vecchiato Carla Giuditta, Federiconi Alessia, Mammi Ludovica Maria Eugenia, Silvestrelli Simone, Parazza Paola, Formigoni Andrea**
Evaluation of nitrate at different level of inclusion on in vitro ruminal fermentation **522**

16:45 **Abid Khalil, Kaihara Hatsumi, Barbera Salvatore, Danieli Pier Paolo, Glorio Patrucco Sara, Issaoui Rabeb, Tassone Sonia**
Ruminant nutrition in the age of microplastics contamination: challenges and insights..... **037**

17:00 **Lira De Medeiros Adja, Scicutella Federica, Mannelli Federica, Toni Elisabetta, Daghio Matteo, Viti Carlo, Del Bubba Massimo, Buccioni Arianna**
Effect of microplastics additives on rumen ecology: in vitro preliminary study..... **124**

17:15 **Kaihara Hatsumi, Issaoui Rabeb, Abid Khalil, Barbera Salvatore, Glorio Patrucco Sara, Tassone Sonia**
First investigation of microplastics contamination in corn silage used for dairy cow nutrition **036**

Wednesday, 18th June – Room Agliè

Session 27 – Welfare, Health and Behaviour: INNOVATIONS AND PERCEPTIONS FOR SUSTAINABLE PRODUCTION

Chairs: **Trevisi Erminio – Santinello Matteo**

16:00 **Mota Gutierrez Jatziri, Srikanthithasan Karthika, Blanc Simone, Forte Claudio**
Grab or Skip: What drives undergraduates to try animal welfare beef meat?..... **021**

16:15 **Celozzi Stefania, Ravelli Andrea, Corradini Anna Francesca, Battini Monica, Marescotti Maria Elena**
Ever been to a dairy farm? Testing the effect of virtual farm tours on consumers perceptions of livestock production **108**

16:30 **Galosi Livio, Roncarati Alessandra**
Protection of animals & research needs: legislative overview and future perspectives **278**

16:45 **Rambozzi Luisa, Formisano Roberta, Pasquetti Mario, Molinar Annarita, Torsiello Benedetta, Giammarino Mauro, Battaglini Luca, Sangrali Martina, Midulla Luca, Sarale Adriano, Renna Manuela**
Anthelmintic efficacy of pour-on Eprinomectin against gastrointestinal strongyles and relationships with milk production parameters in lactating goats **024**

17:00 **Santillo Antonella, Ciliberti Maria Giovanna, Biancardi Valentina, Mangano Fabrizio, Della Malva Antonella, Caroprese Mariangela, Marino Rosaria, Sevi Agostino, Albenzio Marzia**
Effect of almond and carob by products on immune competence of growing lambs **132**

17:15 **Grossi Giampiero, Vitali Andrea, Rossi Chiara, Lacetera Nicola**
Projections of the temperature humidity index for the Italian territory **340**

Wednesday, 18th June – Room Carignano

Session 28 – Production Systems: TRADITIONAL PRACTICES, ECONOMICS, AND WELFARE

Chairs: **Buccioni Arianna – Zampiga Marco**

16:00 **Gaspa Giustino, Cesarani Alberto, Negrini Riccardo, Laura Falchi, Ferrari Carolina, Macciotta Nicolò**
Relationship between cows' milk performances and dry period length in Italian cattle breeds **287**

16:15 **Primi Riccardo, Viola Paolo, Girotti Pedro, Spada Francesco, Ortenzi Luciano, Bernabucci Gloria, Basiricò Loredana, Ronchi Bruno**
Study of the variation in the distribution of wild and domestic ungulates in an extensive livestock farm in Central Apennine during the seasons trough trapping rate **111**

16:30 **Lombardi Alessia, Bifulco Giovanna, Paparella Antonio, Cembalo Luigi, Neglia Gianluca, Campanile Giuseppe**
Cost of buffalo milk: an analysis pre and post Covid **208**

16:45 **Algeri Stefano, Palladini Nicola, Tamburini Alberto, Sari Stefano, Bava Luciana**
Management of extended lactation: effects on milk production and reproductive parameters **183**

17:00 **Iacurto Miriam, Steri Roberto, Meo Zilio David, Claps Salvatore, Giovanni Quaranta, Antonio Bosco, Giuseppe Cringoli**
Survey on the management of cattle farms in two municipalities located in the park area of the Campania Region **392**

17:15 **Leliveld Lisette, Manfrè Claudia, Brscic Marta, Battini Monica**
Mother-offspring management in different dairy farm animal species as guidance for the implementation of cow-calf-contact systems? **338**

Thursday, 19th June – Room Venaria

Session 29 – Genetics: GENOMIC APPLICATIONS FOR BIODIVERSITY I

Chairs: **Di Stasio Liliana – Barbato Mario**

8:30 **Benanti Alessia, Chessari Giorgio, Carta Federica, Riggio Silvia, Ben Jemaa Slim, Senczuk Gabriele, Bigi Daniele, Ciampolini Roberta, Sardina Maria Teresa, Sabbioni Alberto, Matassino Donato, Luongo Flavio, Fabbri Maria Chiara, Portolano Baldassare, Cesarani Alberto, Grande Silverio, Criscione Andrea, Mastrangelo Salvatore**
Genomic characterisation and diversity assessment in endangered Italian sheep breeds **220**

8:45 **Pierini Claudia, Saleh Medhat, Ciani Elena, Bruno Silvia, Bramate Grazia, De Palo Pasquale, Barbato Mario, Landi Vincenzo**
The rediscovery of a forgotten breed: the genomic characterisation of the Fasanese sheep and investigation of its Eastern European origins **252**

9:00 **Floridia Viviana, Bionda Arianna, Chiofalo Vincenzo, Cortellari Matteo, Lopreiato Vincenzo, Amato Annalisa, Virga Antonino Nazareno, Crepaldi Paola, Liotta Luigi, Barbato Mario**
Mapping the phenotypic and genomic landscape of Montanina cattle **424**

9:15 **Albarella Sara, Barbato Mario, D'Anza Emanuele, Floridia Viviana, Cascone Ilaria, Gianfranco Cosenza, Salzano Angela, Ciotola Francesca, Peretti Vincenzo**
A genomic perspective on the Agerolese autochthonous cattle breed **358**

9:30 **Bernini Francesca, Mancin Enrico, Sartori Cristina, Mantovani Roberto, Vevey Mario, Blanchet Veruska, Bagnato Alessandro, Strillacci Maria**
Structural Variants shaping the aptitude of local cattle breeds **335**

9:45 **Álvarez Quiñónez Ruth Isabel, Senczuk Gabriele, Persichilli Christian, Capomaccio Stefano, Cappelli Katia, Amparo Martinez, Rivero José Luis, Vega Pla José Luis, Pilla Fabio**
Genetic diversity and evolutionary history of Baroque horse breeds: insights from genome-wide data ... **468**

10:00 **Schiavo Giuseppina, Bovo Samuele, Bertolini Francesca, Bolner Matteo, Ribani Anisa, Taurisano Valeria, Dall'Olio Stefania, Cappelloni Manolo, Gallo Maurizio, Fontanesi Luca**
Signatures of selection in Mora Romagnola, a highly inbreed autochthonous pig breed **313**

10:45 Coffee Break and Poster session

Thursday, 19th June – Room Racconigi

Session 30 – Ruminant Nutrition: INSECTS, FATTY ACIDS AND MICROBIOTA
Sponsored by Ferrero Mangimi

Chairs: **Todaro Massimo – Scicutella Federica**

8:30 **Conte Giuseppe, Tognocchi Monica, Casarosa Laura, Tinagli Sara, Serra Andrea, Mele Marcello**
A multivariate approach to investigate mutual relationship among milk fatty acids across different ruminant species **074**

8:45 **Rastello Lara, Badino Paola, Constant Isabelle, Coppa Mauro, Gerbelle Mathieu, Gardini Giulia, Galli Alessandro, Trespeuch Christophe, Gasco Laura, Renna Manuela**
Dietary black soldier fly oil reduces oxidative stress in dairy cows without affecting blood nutritional parameters **023**

9:00 **Congiu Michele, Lourenco Jeferson, Cesarani Alberto, Macciotta Nicolò, Dimauro Corrado**
Relationship between oral microbiome and performance traits in Angus bulls **026**

9:15 **Baila Clàudia, Hervás Gonzalo, Renna Manuela, Gasco Laura, Rastello Lara, Barrio Esther, González-Merino Paloma, Bolletta Viviana, Trespeuch Chrisophe, Frutos Pilar, Toral Pablo**
Is black soldier fly oil a good alternative to replace palm distillate fatty acids in the diet of lactating sheep? Animal performance, feed efficiency and ruminal fermentation responses **196**

9:30 **Mecocci Samanta, Pietrucci Daniele, Bagatella Stefano, Castrica Marta, Acuti Gabriele, Cappelli Katia, Hassan Talal, Malik Muhammad Irfan, Curone Giulio, Arif Muhammad Adnan, Ferrulli Vincenzo, Boccardo Antonio, Grossi Silvia, Sgoifo Rossi Carlo Angelo, Trabalza Marinucci Massimo, Capucchio Maria Teresa, Forte Claudio, Pravettoni Davide**
Gut health effects of hazelnut skin dietary supplementation in Limousine bulls **185**

9:45 INVITED LECTURE
Toral Pablo, Frutaos Pilar, Barrio Esther, Baila Clàudia, Hervás Gonzalo
Fatty acids beyond milk nutritional quality
10:15 Coffee Break and Poster session

Thursday, 19th June – Room Stupinigi

Session 31 – Welfare, Health and Behaviour: FROM PREVENTION TO THERAPY, UDDER HEALTH AND INNOVATIONS IN ZOOTECHNICS

Chairs: **Cozzi Giulio – Celozzi Stefania**

8:30 **Petrera Francesca, Daminelli Paolo, Posante Antonella, Fusi Francesca, Giroletti Luca, Marino Rosanna, Abeni Fabio**
Evaluation of udder health status using bacteriological culture and somatic cell count after calving and at drying-off, and effects of antibiotic therapy **291**

8:45 **Bellato Alessandro, Coppa Mauro, Manenti Isabella, Bongiovanni Luisa, Borla Laura, Donato Antonella, Battaglini Luca, Mannelli Alessandro**
Individual risk factors for intramammary infections affecting dairy herds in Western Alps..... **497**

9:00 **Giannotta Gabriele, Bisutti Vittoria, Barberio Antonio, Biasio Lara, Zappaterra Martina, Vanzin Alice, Giannuzzi Diana, Cecchinato Alessio, Pegolo Sara**
Effect of subclinical intramammary infection on blood biochemical parameters in susceptible and resistant Holstein cattle..... **385**

9:15 **Rovetta Carlo, Ramirez Mauricio Marco Aurelio, El Hawat Rebecca, Bisutti Vittoria, Vanzin Alice, Giannotta Gabriele, Toscano Alessandro, Massaro Selene, Giannuzzi Diana, Gallo Luigi, Pegolo Sara, Schiavon Stefano, Tagliapietra Franco, Cecchinato Alessio**
Associations of body condition score and body weight changes with milk composition and fatty acids during the transition period in dairy cattle..... **383**

9:30 **Bisutti Vittoria**
, Giannuzzi Diana, Vanzin Alice, Secchi Giulia, Cecchinato Alessio, Pegolo Sara
Multi-omic data integration for the identification of molecular drivers of subclinical intramammary infection in dairy cows..... **156**

9:45 **Andreoli Valentina, Stocco Giorgia, Zanotti Andrea, Tedeschi Irene, Valoppi Davide, Chessa Stefania, Lange-Consiglio Anna, Grolli Stefano, Cipolat-Gotet Claudio**
Addressing antibiotic resistance in dairy herds: the role of platelet rich plasma in mastitis treatment..... **505**

10:00 **Dadi Yasmine, Delosière Mylène, De Matos Luiz Gustavo, Delevaud Arnaud, Viala Didier, Salvi Gaspare, Balbi Ombretta, Penati Martina, De Palo Pasquale, Maggiolino Aristide, Bonnet Muriel, Ceciliani Fabrizio, Lecchi Cristina**
Proteome characterization of milk extracellular vesicles isolated from cows that experienced hyperthermia..... **188**

10:15 Coffee Break and Poster session

Thursday, 19th June – Room Valentino

Session 32 – Monogastric Nutrition: POULTRY
Sponsored by Silvateam

Chairs: **Trevisi Paolo – Lin Peng**

8:30 INVITED LECTURE
Korver Doug
Impact of oxidation and inflammation on poultry health and productivity .....

9:00 **Srikanthithasan Karthika, Ferrocino Ilario, Raspa Federica, Nery Joana, Colombino Elena, Ippolito Dorotea, Gariglio Marta, Diaz Vicuna Elena, Fiorilla Edoardo, Mota Gutierrez Jatziri, Giorgino Andrea, Capucchio Maria Teresa, Schiavone Achille, Forte Claudio**
Effects of dietary commercially processed former foodstuffs on the gut ecosystem in broilers **199**

9:15 **Mecocci Samanta, Tang Jiayong, Acuti Gabriele, Pietrucci Daniele, Marini Daniele, Mercati Francesca, Franciosini Maria Pia, Stefanetti Valentina, Chillemi Giovanni, Tabasso Silvia, Cappelli Katia, Forte Claudio, Trabalza Marinucci Massimo**
Dietary supplementation with hazelnut skin polyphenols affects growth performance and intestinal microbiota in broiler chickens **172**

9:30 **Mannelli Federica, Daghio Matteo, Scicutella Federica, Viti Carlo, Biagi Arroyo Marcinette Lucia, Galigani Ilaria, Buccioni Arianna**
Microbiota characterization of four autochthonous Italian chicken breeds **202**

9:45 **Dayan Jonathan, De Cesare Alessandra, Soglia Francesca, Zampiga Marco, Indio Valentina, Antenucci Emilia Luigia, Petracci Massimiliano, Sirri Federico**
Replacing vegetable oils with Hermetia Illucens *(Black Soldier Fly) larvae oil in broiler chicken diets: impacts on growth performance, meat quality, and caeca microbiome* **277**

10:00 **Zeni Niko Gioacchino, Perricone Vera, Schiavone Achille, Cerolini Silvia, Tognoli Cristina, Marelli Stefano, Fiamberti Federico, Zaniboni Luisa**
Egg-laying performance of hens fed diets containing former food products **388**

10:15 Coffee Break and Poster session

Thursday, 19th June – Room Mandria

Session 33 – Precision Farming: COMPUTER VISION AND IMAGING TECHNOLOGIES

Chairs: **Chincarini Matteo – Asti Vittoria**

8:30 **Ozella Laura, Vitturini Davide, Grangetto Marco, Bovo Marco, Giacobini Mario**
Application of YOLOv8 for analyzing social dynamics in dairy cows within automated milking systems..... **078**

8:45 **Giannone Claudia, Lamanna Martina, Cavallini Damiano, Formigoni Andrea, Tassinari Patrizia, Bovo Marco**
Computer vision for monitoring the feeding behavior of dairy cows..... **046**

9:00 **Bordignon Francesco, Pravato Mattia, Molin Matteo, Trocino Angela, Xiccato Gerolamo, Marinello Francesco, Pezzuollo Andrea**
Environmental changes and hen spatial distribution in cage-free systems: a preliminary study..... **068**

9:15 **Urbani Rachele, Bergamasco Tommaso, Nalesso Giacomo, Menegon Francesca, Trocino Angela, Pravato Mattia, Sparesato Stefania, Manca Grazia, Di Martino Guido**
Development of an image analysis system at the slaughterhouse to assess laying hens' welfare on farm **184**

9:30 **Felici Martina, Behnam Armin, Bocchi Valeria, Zangoli Chiara, Mountricha Maria, Nanni Costa Leonardo, Pegolo Sara, Zappaterra Martina**
Evaluating infrared thermography for early detection of sub-clinical mastitis in dairy cows: the impact of Staphylococcus aureus *infections on udder skin temperature* **495**

9:45 **Pittarello Marco, Marengo Giacomo, Ravetto Enri Simone, Lonati Michele, Probo Massimiliano, Lombardi Giampiero**
Detection of livestock site-use intensity at fine-scale in mountain grazing systems using Sentinel-2 time series..... **457**

10:00 **Giannone Claudia, Dalla Costa Emanuela, Maccario Chiara, Atallah Elie, Bovo Marco**
Preliminary analyses on the identification of horse behaviors using deep learning techniques..... **048**

10:15 Coffee Break and Poster session

Thursday, 19th June – Room Agliè

Session 34 – Food Quality: COW MILK QUALITY AND AUTHENTICATION

Chairs: **Musco Nadia – Niero Giovanni**

8:30 **Melilli Caterina, Magnani Barbara, Cecchini Maria Elena, Cupellini Flavia, Continanza Rosa Maria, Iannuzzi Giulio, Fontana Annunziata, Giaccone Daniele, Negrini Riccardo**
Performance of Italian Dairy Heard Information (DHI) milk laboratories assessed through three years of proficiency tests..... **225**

8:45 **El Hawat Rebecca, Massaro Selene, Amalfitano Nicolò, Iqbal Rashid, Bailoni Lucia, Tagliapietra Franco**
*Terpene transfer from Hemp (*Cannabis sativa L.*) and Savory (*Satureja hortensis L.*) to milk of dairy cows supplemented with fresh leaves* **106**

9:00 **Correddu Fabio, Carta Silvia, Nudda Anna**
Effect of dietary linseed on milk fatty acid profile, coagulation properties, and methane emission in local Sardo-Bruna cows **479**

9:15 **Mecocci Samanta, Rampacci Elisa, Strincardini Claudia, Costantini Claudio, Chiaradia Elisabetta, Acuti Gabriele, Verini-Supplizi Andrea, Giovagnoli Stefano, Cappelli Katia**
Stabilized bovine milk extracellular vesicles as anti-inflammatory and immunomodulatory agent on human macrophage-like cells **231**

9:30 **Cesarani Alberto, Senczuk Gabriele, Sardina Maria Teresa, Pilla Fabio, Dimauro Corrado, Portolano Baldassarre, Macciotta Nicolò, Mastrangelo Salvatore**
Comparison of machine learning algorithms to trace the geographical origin of raw milk using infrared spectra **025**

9:45 **Tedeschi Irene, Malacarne Massimo, Dall'Olio Stefania, Valoppi Davide, Andreoli Valentina, Zanotti Andrea, Stocco Giorgia, Summer Andrea, Cipolat-Gotet Claudio**
A comparative analysis of milk fat globule size and distribution in Holstein-Friesian and Reggiana cattle breeds **305**

10:00 **Dallavalle Giulia, Secchi Giorgia, Mancini Andrea, Vrhovsek Urska, Angeli Andrea, Aprea Eugenio, Zambanini Jessica, Endrizzi Isabella, Solovyev Pavel, Zanon Thomas, Franciosi Elena**
Promoting a circular bio-economy: use of wine cellar by-products as feed supplement for dairy cows and evaluation of the chemical and microbiological effects on dairy products **400**

10:15 Coffee Break and Poster session

Thursday, 19th June – Room Carignano

Session 35 – Genetics: GENOMIC STRATEGIES FOR FITNESS TRAIT
Sponsored by Vazyme

Chairs: **Visentin Giulio – Ablondi Michela**

8:30 **Rulli Eugenio, Sbarra Fiorella, Quaglia Andrea, Mancin Enrico, Oian Angelica, Gomez Proto Guido, Mantovani Roberto, Sartori Cristina**
Genetic evaluation of climate effect on Maremmana young bulls reared in test station **533**

8:45 **Giuseppina Schiavo, Bovo Samuele, Bolner Matteo, Bertolini Francesca, Ribani Anisa, Taurisano Valeria, Dall'Olio Stefania, Maranzani Jessica, Bonacini Massimo Fontanesi Luca**
Describing Reggiana cattle farms using genomic information from the breed population **316**

9:00 **Maria Strillacci, Ferrulli Vincenzo, Bernini Francesca, Pravettoni Davide, Bagnato Alessandro, Martucci Ilaria, Boccardo Antonio**
Genomic basis of Bovine Respiratory Disease resistance in preweaned dairy calves **114**

9:15 **Oian Angelica, Mancin Enrico, Gomez Proto Guido, Sartori Cristina, Rulli Eugenio, Mantovani Roberto**
GWAS analysis of fitness traits in autochthonous dual-purpose breeds **330**

9:30 **Carta Antonello, Usai Graziano, Casu Sara, Sechi Tiziana, Mulas Giuliana, Ligios Ciriaco, Salaris Sotero**
On the use of antibody responses as selection criteria to improve disease resistance in sheep **304**

9:45 **Riggio Silvia, Mastrangelo Salvatore, Carta Federica, Benanti Alessia, Portolano Baldassarre, Sardina Maria Teresa**
Prion protein gene polymorphisms in two Sicilian goat populations **348**

10:00 **Fabbri Maria Chiara, Biada Iliyass, Sirtori Francesco, Pulido-Rodríguez Lina, Bozzi Riccardo, Tiezzi Francesco**
Investigation of interaction between sheep and soil microbiota **070**

10:15 Coffee Break and Poster session

Thursday, 19th June – Room Venaria

Session 36 – Genetics: GENETIC SOLUTIONS FOR HEAT STRESS

Chairs: **Negrini Riccardo – Pegolo Sara**

10:45 INVITED LECTURE
Maltecca Christian, Gini Chiara, Johnson Jay, Brito Luiz, Harrod Mary Kate, Van Vliet Stephan, Tiezzi France co
Elucidating the biology of heat stress in lactating sows at the intersection of genome microbiome and metabolome

11:15 **Bertolini Francesca, Bolner Matteo, Bovo Samuele, Schiavo Giuseppina, Zambonelli Paolo, Gallo Maurizio, Cappelloni Manolo, Fontanesi Luca**
Metabolomics identified new biomarkers to help describing feed efficiency in Italian Large White pigs . **384**

11:30 **Macciotta Nicolò, Dimauro Corrado, Correddu Fabio, Cesarani Alberto**
Development of a genetic index for heat stress tolerance in dairy sheep **494**

11:45 **Usai Mario Graziano, Casu Sara, Salaris Sotero, Sechi Tiziana, Miari Sabrina, Mulas Giuliana, Carta Antonello**
Individual variability of tolerance to heat stress of Sarda ewes raised in the Mediterranean region **270**

12:00 **Lecchi Cristina, Maggiolino Aristide, De Palo Pasquale, Landi Vincenzo, Salvi Gaspare, Ceciliani Fabrizio, Ryts Andreas, Cominetti Ornella, Raymond Frederic, Soussan Elodie, Bobkov Maxim**
Heat stress modifies the miRNA cargoes carried by small extracellular vesicles isolated from Holstein and Brown Swiss milk **498**

12:15 **Landi Vincenzo, Pierini Claudia, Hidalgo Jorge, Bussiman Fernando, Maggiolino Aristide, Lasagna Emiliano, De Palo Pasquale, Quaglia Andrea, Sbarra Fiorella**
Assessing the impact of climate factors on the growth performance of Podolica bulls during pre-performance phases **546**

12:30 Lunch

Thursday, 19th June – Room Racconigi

Session 37 – Ruminant Nutrition: SMALL RUMINANTS AND BY-PRODUCT USE
Sponsored by Ferrero Mangimi

Chairs: **Nudda Anna – Battelli Marco**

10:45 **Nudda Anna, Carta Silvia, Correddu Fabio, Caratzu Maria Francesca, Cesarani Alberto, Pulina Giuseppe, Lunesu Mondina Francesca**
A meta-analysis on the relationship between agro-industrial byproducts supplementation and milk production traits in dairy sheep **040**

11:00 **Hassan Mahmood Ul, Gannuscio Riccardo, Maniaci Giuseppe, Alabiso Marco, Ciccarello Salvatore, Todaro Massimo**
Agro-industrial by-product: destoned olive cake as an alternative feed and ruminal fermentation modifier for dairy ewes **210**

11:15 **Gannuscio Riccardo, Hassan Mahmood Ul, Vastolo Alessandro, Tolone Marco, Maniaci Giuseppe, Calabrò Serena, Cutrignelli Monica Isabella, Todaro Massimo**
Effects of feeding prickly pear by-product silage on dairy ewes **116**

11:30 **Mangione Guido, Musati Martino, Mangano Fabrizio, Bertino Antonino, Luciano Giuseppe, Biondi Luisa, Cannone Marco Sebastiano, Lanza Massimiliano, Natalello Antonio**
Sesame seed meal as alternative protein source in growing lambs **365**

11:45 **Pietrucci Daniele, Mecocci Samanta, Luciano Giuseppe, Musati Martino, Priolo Alessandro, Milanesi Marco, Chillemi Giovanni, Cappelli Katia, Trabalza Marinucci Massimo, Forte Claudio, Natalello Antonio**
Characterization of lamb rumen and cecal microbiota in response to hazelnut skins and linseed dietary supplementation using 16S rRNA sequencing **364**

12:00 **Vazquez Mendoza Oscar Vincente, Elghandour Mona, Galeano Diaz Maria Johana Paola, Ortiz Heredia María Angélica, Salem Abdelfattah**
Effects of guanidinoacetic acid levels on growth performance of finishing lambs **203**

12:15 **Porcu Maria Angela, Ledda Antonello, Correddu Fabio, Carta Silvia, Rubattu Roberto, Cannas Antonello**
Mitigation of the milk fat depression in ewes, caused by ryegrass herbage rich in water-soluble carbohydrate, by sodium bicarbonate: effects on milk fatty acid profile **463**

12:30 Lunch

Thursday, 19th June – Room Stupinigi

Session 38 – Welfare, Health and Behaviour: ADVANCES IN CATTLE AND BUFFALOES MANAGEMENT

Chairs: **Bernabucci Umberto – Evangelista Chiara**

10:45 **Vitali Andrea, Grossi Giampiero, Rossi Chiara, Lacetera Nicola**
Summer dairy cows: THI-Heat_Load model for development of an alert-based cooling protocol **414**

11:00 **Ratto Roberta, Pietrucci Daniele, Renzi Francesco, Milanesi Marco, Mecocci Samanta, Bergagna Stefania, Acuti Gabriele, Guasco Cecilia, Chillemi Giovanni, Katia Cappelli**
Combination of PLF and omics to characterize heat stress response in Marchigiana breed **458**

11:15 **Abeni Fabio Palmiro, Negrini Riccardo, Ferla Andrea, Galli Andrea**
Comparative evaluation of subclinical ketosis risk in Lombardy using two methods based on DHI data **071**

11:30 **Lamanna Martina, Muca Edlira, Giannone Claudia, Bovo Marco, Romanzin Alberto, Formigoni Andrea, Cavallini Damiano**
Meta-Analytical study on feeding behavior and daily time budget management of dairy cows in free-stall housing using ChatGPT **064**

11:45 **Vecchio Domenico, Scali Federico, Maisano Antonio Marco, Fusi Francesca, Lorenzi Valentina, Di Vuolo Gabriele, Ambra Chiara Denise, Serrapica Maria, Cappelli Giovanna, Romeo Claudia Rosa, Bertocchi Luigi, Alborali Giovanni Loris, Santucci Giovanni, Zanella Adroaldo Josè, De La Cruz Luis Alberto, Bernardino Thiago, Stilwell George, De Carlo Esterina**
Antimicrobial use in buffalo farm and dynamic of correlation with animal welfare and biosecurity evaluated by ClassyFarm System **092**

12:00 **Cappelli Giovanna, Bosco Antonio, Di Vuolo Gabriele, Vecchio Domenico, Smeraldo Serena, Mancusi Andrea, Proroga Yolande, Martucciello Alessandra, Grassi Carlo, Serrapica Maria, Di Maro Orlandina, Napoletano Michele, Rinaldi Laura, De Carlo Esterina**
Risk factors for Toxoplasma gondii *seropositivity and DNA detection in raw milk on dairy buffalo farms in Southern Italy* **521**

12:15 **Santinello Matteo, Esposito Sergio, Purrone Sissy, Pierro Federica, Piscopo Federica, Ciaramella Paolo, Neglia Gianluca**
Blood metabolite profile in Italian Mediterranean buffalo: effect of parity, lactation stage, and calving season. **159**

12:30 Lunch

Thursday, 19th June – Room Valentino

Session 39 – Monogastric Nutrition: SWINE I
Sponsored by Silvateam

Chairs: **Cappai Maria Grazia – Braidot Matteo**

10:45 **Manoni Michele, Altomare Alessandra, Nonnis Simona, Mazzoleni Sharon, Tretola Marco, Bee Giuseppe, Silacci Paolo, Tedeschi Gabriella, Aldini Giancarlo, Pinotti Luciano**
Evaluation of the impact of the dietary inclusion of salty and sugary former food products on the liver and the plasma profile of pigs through OMICS approaches **027**

11:00 **Luise Diana, Correa Federico, Rocchetti Gabriele, Errico Michela, Polimeni Barbara, Serra Andrea, Mele Marcello, Gallo Antonio, Lucini Luigi, Trevisi Paolo**
Multi-omics characterisation of pig colostrum and association of its bioactive compounds and gut microbiota with the survival of piglets **462**

11:15 **Trevisi Paolo, Luise Diana, Palladino Giorgia, Palumbo Francesco, Scicchitano Daniel, Babbi Giulia, Castagnetti Andrea, Rampelli Simone, Candela Marco, Martelli Pier Luigi, Correa Federico**
EU Circles Project: Multi-omics analysis reveals distinct microbial networks linked to a blend of chestnut and quebracho extract supplementation in weaned pigs under different farming conditions **558**

11:30 **Toscano Alessandro, Don Gregorio, Ramayo-Caldas Yuliaxis, Sanchez Juan Pablo, Pegolo Sara, Schiavon Stefano, Gallo Luigi, Giannuzzi Diana**
Metataxonomic characterization of fecal microbiota of heavy pigs fed with different levels of Arthrospira platensis..... **246**

11:45 **Correa Federico, Luise Diana, Palumbo Francesco, Zurru Antonio, Biagi Giacomo, Trevisi Paolo**
Effect of dietary microbial muramidase supplementation on weaned pigs' performance, health status and intestinal microbiota **519**

12:00 **Zurru Antonio, Trevisi Paolo, Laghi Luca, Palumbo Francesco, Correa Federico, Luise Diana**
Effect of complete maize replacement by sorghum on health, welfare, performance and faecal microbiota of post-weaning piglets **381**

12:15 **Polimeni Barbara, Correa Federico, Luise Diana, Zurru Antonio, Palumbo Francesco, Trevisi Paolo**
Postbiotic supplementation in gestating and lactating sows and its effects on piglets health and performances **483**

12:30 Lunch

Thursday, 19th June – Room Mandria

Session 40 – Precision Farming: DATA-DRIVEN DAIRY MANAGEMENT

Chairs: **Neglia Gianluca – Giannone Claudia**

10:45 **Zanchi Marco, La Porta Caterina, Forte Claudio, Zapperi Stefano, Ozella Laura**
Modeling dairy production under microclimatic variability in automatic milking systems using TSMixer..... **102**

11:00 **Pascarella Lorenzo, Fioretti Mauro, Melilli Caterina, Galli Andrea, Negrini Riccardo**
Effect of automatic milking system on udder health..... **406**

11:15 **Cavallini Damiano, Lamanna Martina, Silvestrelli Simone, Colleluori Riccardo, De Matos Vettori Julio, Buonaiuto Giovanni, Gallo Antonio, Cannas Antonello, Formigoni Andrea**
Substitution rate between partial mixed ration and robotic supplemental concentrate in high-producing dairy cows..... **492**

11:30 **Milanesi Marco, Pietrucci Daniele, Del Buono Davide, Litta Paolo, Di Gangi Leonardo, Furlanello Cesare, Chillemi Giovanni**
New insights of climate effects on dairy production **389**

11:45 **Fumagalli Francesca, Boldini Annamaria, Gallo Antonio, Atzori Alberto Stanislao**
Feedback thinking in the dairy supply chain: system dynamics modelling of cheese factory..... **200**

12:00 INVITED LECTURE
Bovo Marco
Precision Livestock Farming, from theory to practice

12:30 Lunch

Thursday, 19th June – Room Agliè

Session 41 – Food Quality: DAIRY PRODUCT QUALITY AND CHEESEMAKING PROPERTIES

Chairs: **Stocco Giorgia – Zanon Thomas**

10:45 **Greco Margherita, Lopez Annalaura, Pavolini Marta, Tamburin Alberto, Bellagamba Federica, Moretti Vittorio Maria**
Quality of milk and cheese from cows grazing on mountain pasture from Italian Alps **345**

11:00 **Mangione Guido, Musati Martino, Caccamo Margherita, Bertino Antonino, Mangano Fabrizio, Natalello Antonio, Luciano Giuseppe, Priolo Alessandro**
Effect of grazing season on quality traits of cow ricotta cheese **543**

11:15 **Secchi Giorgia, Mancini Andrea, Dallavalle Giulia, Nicoli Maria Cristina, Marino Marilena, Innocente Nadia, Franciosi Elena**
Exploring natural additives for cheese preservation **399**

11:30 **Amalfitano Nicolò, El Hawat Rebecca, Benabid Hamida, Haddi Mohamed-Laid, Schiavon Stefano, Bittante Giovanni, Tagliapietra Franco**
Impact of different enzymatic coagulants and doses on the cheese-making ability of milk from different dairy species **446**

11:45 **Claps Salvatore, Perri Enzo, Benincasa Cinzia, Morone Giuseppe, Cifuni Giulia, Cifuni Giulia**
Dietary supplementation with by-products from olive oil mill wastewater processing in dairy cows affected the aromatic fingerprint in cheeses **091**

12:00 **Ferragina Alessandro, Molle Arnaud, Cipolat-Gotet Claudio, Stocco Giorgia**
Exploration of hyperspectral imaging for the discrimination of Parmigiano Reggiano and Grana Padano PDO cheeses and ripening time **474**

12:15 **Cozzi Giulio, Serva Lorenzo, Segato Severino, Berzaghi Paolo**
Evaluating Italian butter quality: A preliminary study of chemical and rheological factors across production sites **191**

12:30 Lunch

Thursday, 19th June – Room Venaria

Session 42 – Genetics: BREEDING FOR MASTITIS RESISTANCE

Chairs: **Capomaccio Stefano – Castiglioni Bianca**

13:30 **Vanzin Alice, Bisutti Vittoria, Giannuzzi Diana, Cecchinato Alessio, Gallo Luigi, Cánovas Angela, Pegolo Sara**
Identification of functional variants leading to alternative splicing associated with subclinical intramammary infection in dairy cattle **157**

13:45 **Ponzo Enrico, Moretti Riccardo, Masia Fernando, Vrieze Elisa, Sacchi Paola, Frizzarin Maria, Chessa Stefania**
Predicting mastitis follow-up using time series on automatic milking system data and machine learning methods **308**

14:00 **D'Anza Emanuele, Barbato Mario, Floridia Viviana, Negrini Riccardo, Cascone Ilaria, Terlizzi iuseppe Antonio, Ciotola Francesca, Albarella Sara, Peretti Vincenzo**
Genetics and bioindicators of mammary health in Agerolese cattle: an integrate analysis **403**

14:15 **Punturiero Chiara, Delle Donne Andrea, Ferrari Carlotta, Milanesi Raffaella, Carabano Maria Jesus, Diaz Clara, Ramon Manuel, Bagnato Alessandro, Strillacci Maria**
mastitis and somatic cell count in lactating dairy cows: a resilience perspective **430**

14:30 **Pegolo Sara, Bisutti Vittoria, Vanzin Alice, Cecchinato Alessio, Giannuzzi Diana**
Analysis of long non-coding RNAs in dairy cows with subclinical mastitis caused by Streptococcus agalactiae *and* Prototheca spp- **152**

14:45 **Cascone Ilaria, López-Catalina Adrian, Albarella Sara, Ciotola Francesca, Cosenza Gianfranco, Salzano Angela, Gonzalez Recio Oscar**
Blood epigenetic patterns in mastitic buffaloes **346**

15:00 Coffee Break and Poster session

Thursday, 19th June – Room Racconigi

Session 43 – Ruminant Nutrition: MINOR SPECIES AND FORAGE QUALITY

Chairs: **Bailoni Lucia – Vastolo Alessandro**

13:30 **Battelli Marco, Rapetti Luca, Colombini Stefania, Galassi Gianluca, Pavesi Martina, Dai Xiaoxia, Menni Giorgio, Cesari Valentina, Crovetto Matteo**
Evaluation of different additives to improve soybean silage quality **245**

13:45 **Cella Fabrizio Giuseppe, Zucca Giovanni, Finocchi Matteo, Malizzi Tiziano, Ripamonti Alice, Mele Marcello, Mantino Alberto**
Chemical composition and nutritive value of leaves and stems of poplar clones in an innovative Mediterranean agroforestry system **336**

14:00 **Nieddu Lidia Nicoletta, Gallo Antonio, Mastroeni Carmelo, Fresu Mirko, Zara Severino, Ledda Antonello, Marzano Alessandra, Rubattu Roberto, Atzori Alberto Stanislao, Fancello Francesco**
Use of functional silage in the feeding of Sardinia dairy sheep **469**

14:15 **Petrocchi Jasinski Francesca, Evangelista Chiara, Basiricò Loredana, Vitali Andrea, Grossi Giampiero, Rossi Chiara, Turriziani Giovanni, Lacetera Nicola, Bernabucci Umberto**
Impact of green forage on milk yield and quality, digestibility, and feeding behavior in Italian Mediterranean buffaloes during the hot season **397**

14:30 **Bisello Jacopo, Currò Sarah, Guzzo Nadia, Amalfitano Nicolò, Cortese Martina, Bailoni Lucia, Tagliapietra Franco**
Comparison of NIR chemical predictions for alfalfa hay using portable and benchtop systems **531**

15:00 Coffee Break and Poster session

Thursday, 19th June – Room Stupinigi

Session 44 – Welfare, Health and Behaviour: EXPLORING THE COW-CALF RELATIONSHIP

Chairs: **Brscic Marta – Cavallini Damiano**

13:30 INVITED LECTURE
Veissier Isabelle, Terlouw Claudia, Botreau Raphaëlle, Deiss Véronique, Cowie Sarah
The evolution of the concept of animal welfare: from absence of suffering to positive welfare and beyond ...

14:00 **Dai Xiaoxia, Menni Giorgio, Liu Jing, Battelli Marco, Pavesi Martina, Rapetti Luca, Galassi Gianluca, Crovetto Matteo, Wenli Li, Colombini Stefania**
Impact of endogenous ruminal lipopolysaccharides on functional activity in rumen mixed microbial communities **223**

14:15 **Palladini Nicola, Algeri Stefano, Tamburini Alberto, Gislon Giulia, Bava Luciana**
Welfare issues in cow-calf contact **171**

14:30 **Bocchi Valeria, Costa Angela, Visentin Giulio, Zappaterra Martina, Bolcato Marilena, Nanni Costa Leonardo, Padalino Barbara**
Current management of calves in Italian dairy farms: preliminary overview on the welfare of calves ... **311**

14:45 **Manfrè Claudia, Leliveld Lisette, Danyer Aytemiz, Brscic Marta, Battini Monica**
Application of Qualitative Behaviour Assessment on cows before and after their separation from their calf in a cow-calf contact system **271**

15:00 Coffee Break and Poster session

Thursday, 19th June – Room Valentino

Session 45 – Sustainability: SUSTAINABLE STRATEGIES

Chairs: **Mantino Alberto – Grossi Giampiero**

13:30 **Berton Marco, Sturaro Enrico, Bittante Giovanni, Gallo Luigi**
Effects of dietary concentrate level on protein feed-food and land use competition indicators **052**

13:45 **Ferronato Giulia, Tobanelli Noemi, Simonetto Anna, Gilioli Gianni**
The effect of feeding strategies on enteric and manure methane emissions in dairy cows: evidence from Italian farms **280**

14:00 **Benedetti Lorenzo, Bani Paolo, Froldi Federico, Bani Giovanni, Ferrero Anita, Struder Jean Pierre, Trevisi Erminio**
Effect of two commercial additives on pollutant emissions from dairy cow manure **158**

14:15 **Zangoli Chiara, Chrysanthopoulos Stamatis, Fernandes Elisabete, Zappaterra Martina, Pocheville Salomé, Fangueiro David, Almeida André**
Ammonia and greenhouse gases emissions during storage of excreta from poultry fed with 15% Spirulina dietary inclusion **189**

14:30 **Correa Federico, Luise Diana, Palladino Giorgia, Secchi Nicola, Scicchitano Daniel, Babbi Giulia, Rampelli Simone, Candela Marco, Martelli Pier Luigi, Trevisi Paolo**
CIRCLES EU Project: On-farm wastewater treatment with bioactivators reduces air pollution and modulate slurry microbiota in pig growing units **518**

14:45 **Dela Pierre Flavia, Fakhar Ali, Pedersen Johanna, Feilberg Anders, Dinuccio Elio, Kamp Jesper Nørlem**
The effect of increasing H_2SO_4 on NH_3 and NMVOC emissions from pig slurry application to permanent grass **442**

15:00 Coffee Break and Poster session

Thursday, 19th June – Room Mandria

Session 46 – Precision Farming: GRAZING SYSTEMS AND PASTURE MONITORING

Chairs: **Cecchinato Alessio – Matera Roberta**

13:30 **Aquilani Chiara, Confessore Andrea, Sirtori Francesco, Parrini Silvia, Dibari Camilla, Argenti Giovanni, De Guttry Luca, Pugliese Carolina**
Does Virtual Fencing affect cattle behaviour and pasture utilization as compared to traditional grazing management? **133**

13:45 **Acciaro Marco, Frongia Andrea, Schneider Manuel, Giovanetti Valeria, Serra Gabriella, Cabiddu Andrea, Decandia Mauro, Pauler Caren**
GPS as a tool to monitor grazing behavior of Sarda dairy ewes. **162**

14:00 **Confessore Andrea, Aquilani Chiara, Sirtori Francesco, Rainis Simona, Pugliese Carolina**
Virtual fencing vs. traditional grazing: impacts on dairy cows' milk yield and behavior assessed with an automatic milking system **470**

14:15 **Marchegiani Sara, Pasquini Marina, Trombetta Maria Federica, Ceccobelli Simone**
Smart livestock grazing: GPS serving the extensive Marchigiana breeding system **098**

14:30 **Fatica Antonella, Tedesco Doriana, Todini Luca, Fantuz Francesco, Salimei Elisabetta**
Traceability for a grazing equine system in inner areas of Centre-South Italy **100**

15:00 Coffee Break and Poster session

Thursday, 19th June – Room Agliè

Session 47 – Food Quality: SHEEP, GOAT AND BUFFALO MILK QUALITY

Chairs: **Valenti Bernardo – Carta Silvia**

13:30 **Stocco Giorgia, Biffani Stefano, Tiezzi Francesco, Valoppi Davide, Tedeschi Irene, Bozzi Riccardo, Fabbri Maria Chiara, Sirtori Francesco, Grande Silverio, Castiglioni Bianca, Cipolat-Gotet Claudio**
Factors affecting fat globules size of sheep milk **112**

13:45 **Valoppi Davide, Biffani Stefano, Castiglioni Bianca, Bozzi Riccardo, Fabbri Maria Chiara, Sirtori Francesco, Tiezzi Francesco, Grande Silverio, Tedeschi Irene, Cipolat-Gotet Claudio, Summer Andrea, Stocco Giorgia**
Effect of fat globules size on the technological properties of sheep milk **309**

14:00 **Bolletta Viviana, Pauselli Mariano, Lilli Emanuele, Veneziani Gianluca, Santillo Antonella, Bertino Antonino, Valenti Bernardo**
Animal performance and milk quality in grazing ewes supplemented a concentrated phenolic extract from olive-milling wastewaters **432**

14:15 **Boukrouh Soumaya, Noutfia Ali, Moula Nassim, Avril Claire, Hornick Jean-Luc, Chentouf Mouad, Cabaraux Jean-François**
Effects of Sulla Flexuosa *hay as alternative feed resource on goat's milk production and quality* **570**

14:30 **Magro Silvia, Pozza Marta, Sartor Pietro, De Marchi Massimo, Niero Giovanni**
Feasibility of mid-infrared spectroscopy for the prediction of milk coagulation properties in the Alpine and Saanen goats breeds **441**

14:45 **Iommelli Piera, Musco Nadia, Lombardi Pietro, Sarubbi Fiorella, Tufarelli Vincenzo, Ceci Edmondo, Infascelli Federico, Tudisco Raffaella**
Fennel seed powder in the diet of dairy buffalo affects milk VOCs profile, antioxidant activity and SCD1 mRNA level **144**

15:00 Coffee Break and Poster session

Friday, 20th June – Room Venaria

Session 48 – Genetics: GENOMIC APPLICATIONS FOR BIODIVERSITY II

Chairs: **Colli Licia – Mastrangelo Salvatore**

9:00 **Persichilli Christian, Cesarani Alberto, Mastrangelo Salvatore, Ben Jemaa Slim, Carta Federica, Riggio Silvia, Benanti Alessia, Pilla Fabio, Senczuk Gabriele**
The North being cold, the South warm: genome-wide assessment of local sheep breeds in contrasting environmental conditions **477**

9:15 **Floridia Viviana, Arias Katherine Daniela, Bionda Arianna, Cortellari Matteo, Amato Annalisa, Lopreiato Vincenzo, D'alessandro Enrico, Goyache Felix, Crepaldi Paola, Liotta Luigi, Barbato Mario**
Uncovering the architecture of production-driven introgression in Cinisara cattle **539**

9:30 **Mancin Enrico, Oian Angelica, Gomez Proto Guido, Rulli Eugenio, Sartori Cristina, Mantovani Roberto**
Black boxing impacts of selection in alpine cattle breeds **293**

9:45 **Ben Jemaa Slim, Senczuk Gabriele, Carta Federica, Riggio Silvia, Benanti Alessia, Sardina Maria Teresa, Cesarani Alberto, Mastrangelo Salvatore**
A genome-wide scan to identify signatures of selection in Sarda and Valle del Belice sheep breeds in relation to their geographical origin **215**

10:00 **Bionda Arianna, Manunta Aldo Luigi, Carta Antonello, Crepaldi Paola**
Preliminary study of the Caprera goat: an ancient feral population? **236**

10:15 **Di Civita Marika, Wiener Pamela, Friedrich Juliane, Marr Melissa, Clark Emily, Senczuk Gabriele, Pilla Fabio**
Exploring climate adaptation in European Merino sheep: a landscape genomics approach **486**

10:30 **Carta Federica, Chessari Giorgio, Riggio Silvia, Benanti Alessia, Sardina Maria Teresa, Carlentini Morena, Falchi Laura, Senczuk Gabriele, Criscione Andrea, Cesarani Alberto, Mastrangelo Salvatore**
Detection of homozygosity and heterozygosity regions in Southern Italian sheep breeds revealed by high-density SNP array **243**

10:45 Coffee Break and Poster session

Friday, 20th June – Room Racconigi

Session 49 – Welfare, Health and Behaviour: INNOVATIONS AND SUSTAINABILITY IN HORSES MANAGEMENT

Chairs: **Padalino Barbara – Felici Martina**

9:00 **Mecocci Samanta, Porzio Elisabetta, Beccati Francesca, Pepe Marco, Paris Angelo, Bergagna Stefania, Chillemi Giovanni, Chiaradia Elisabetta, Cappelli Katia**
Omic technology to monitoring resilience and adaptation to exercise and heat stress in athlete horses **118**

9:15 **Bordin Clara, Raspa Federica, Favaro Martina, Dino Giovanna, Gambino Francesca, Tazzini Antonio, Cerrato Giuseppina, Giordana Alessia, Boarino Alice, Padoan Elio, Tagliaferri Marta, Anchisi Emanuele, Valle Emanuela**
From wastes to resources: using construction and demolition wastes to develop sustainable horse footing layers..... **525**

9:30 **Benedetti Beatrice, Freccero Francesca, Patroncini Francesca, Padalino Barbara**
Towards a higher level of welfare in pasture-kept horses: development and application of a new welfare protocol..... **516**

9:45 **Gemma Pantaleo, Padalino Barbara**
Animal welfare assessment of urban carriage horses in Malta..... **404**

10:00 INVITED LECTURE
VERVUERT Ingrid
Future challenges and welfare in forage feeding for sport horses

10:30 //

10:45 Coffee Break and Poster session

Friday, 20th June – Room Stupinigi

Session 50 – Aquaculture: MARINE SPECIES

Chairs: **Terova Genciana – Carabonara Claudia**

9:00 **Della Malva Antonella, Santillo Antonella, Caroprese Mariangela, Marino Rosaria, Francavilla Matteo, Albenzio Marzia**
Exploring the nutritional value of Mytilus Galloprovincialis from the Gargano area (Apulia Region)... **224**

9:15 **Tarricone Simona, Colonna Maria Antonietta, Ragni Marco, Trani Roberta, Giangrande Adriana, Basile Graziana, Stabili Loredana, Carbonara Claudia, Longo Caterina**
Flesh quality, shelf-life, and sensory properties of Sea Bream reared in a Mediterranean coastal Integrated Multi-Trophic Aquaculture (IMTA) system..... **408**

9:30 **Kalemi Violeta, Rimoldi Simona, Monteiro Marta, Valente Luisa, Terova Genciana**
Substitution of fishmeal with an insect meal blend and the effects on the intestinal microbiota of European seabass..... **122**

9:45 **Zarantoniello Matteo, Cattaneo Nico, Conti Federico, Cardinaletti Gloriana, Sener Idris, Ceccobelli Simone, Olivotto Ike**
Employing a natural microencapsulated antioxidant to mitigate dietary microplastic accumulation and oxidative stress response in juvenile European seabass (Dicentrarchus labrax)..... **031**

10:00 **Fanizza Cecilia, Milián-Sorribes Maria Consolación, Jover-Cerdá Miguel, Martìnez-Llorens Silvia, Trocino Angela, Tomás-Vidal Ana**
Estimation of protein and fat requirements for greater amberjack (Seriola dumerili) juveniles reared in RAS..... **054**

10:15 **Roncarati Alessandra, Quagliardi Martina, Antenucci Emanuele, Di Iorio Michele, Coccia Isabella, Santoianni Celeste, Rusco Giusy, Cariglia Michela, Pozzato Luca, Iaffaldano Nicolaia**
Monitoring water temperature during the growth of gilthead sea bream juveniles in sea cage aquaculture..... **248**

10:30 **Sicuro Benedetto, Akther Kazi Rabya, Tafuro Valentina**
Aquaculture in the Mediterranean region: key factors and future trends **082**

10:45 Coffee Break and Poster session

Friday, 20th June – Room Valentino

Session 51 – Monogastric Nutrition: SWINE II

Chairs: **Pinotti Luciano – Correa Federico**

9:00 **Graziosi Maria Vittoria, Luise Diana, Correa Federico, Zurru Antonio, Trevisi Paolo, Biagi Giacomo**
Reduction of amylose-amylopectin ratio in low-protein diets for fattening pigs: performance, health, behavioral, and environmental implications **526**

9:15 **Lin Peng, Tretola Marco, Pinotti Luciano, Bee Giuseppe, Schlegel Patrick**
Growth performance and nutrient balance of pigs fed low protein diets without mineral phosphate supplementation **360**

9:30 **Antonacci Alessandro, Bee Giuseppe**
Feeding low-protein or standard diets to growing-finishing pigs reared under environmental stressors: effects on growth and carcass composition **187**

9:45 **Tono Veronica, Toscano Alessandro, Don Gregorio, Giannuzzi Diana, Gallo Luigi, Cecchinato Alessio, Schiavon Stefano**
Growth performance and carcass quality of heavy pigs fed ad libitum *diets with decreasing SID lysine contents* **264**

10:00 **Don Gregorio, Giannuzzi Diana, Toscano Alessandro, Tono Veronica, Schiavon Stefano, Gallo Luigi**
Effects of a partial to total replacement of soybean meal with spirulina powder in the diets for growing pigs on fatty acid profile of loin, lard, ham trimming and liver fat **101**

10:15 **Luise Diana, Zurru Antonio, Laghi Luca, Palumbo Francesco, Correa Federico, Trevisi Paolo**
Increasing the energy and lysine content of sow transition diets can improve litter performance and modulate colostrum composition **110**

10:30 **Marchetti Luca, Rebucci Raffaella, Piantoni Caterina, Bontempo Valentino**
Effects of a combination of the active form of Vitamin D and natural triterpenes on sows health and productivity **214**

10:45 Coffee Break and Poster session

Friday, 20th June – Room Mandria

Session 52 – Precision Farming: SENSORS FOR BEHAVIOURAL MONITORING

Chairs: **Dalla Costa Emanuela – Antognoli Veronica**

9:00 **Cecchinato Alessio, Giannuzzi Diana, Rovetta Carlo, Bisutti Vittoria, Pegolo Sara, Arazi Alon, Katz Gil, Trevisi Erminio, Mele Marcello, Gallo Luigi, Tagliapietra Franco, Schiavon Stefano, Macedo Mota Lucio Flavio**
Leveraging 3D accelerometer data to predict heat stress in dairy cows..... **209**

9:15 **Cabbia Anita, Braidot Matteo, Cavallini Damiano, Spanghero Mauro, Romanzin Alberto**
Evaluation of feeding behaviour in growing bulls with an ear-tag accelerometer..... **273**

9:30 **Mondini Sara, N'cho Chris Major, Zucali Maddalena, Niu Mutian, Cossa Stefano, Sandrucci Anna**
Detection of on-farm indicators for early signals of lameness in dairy cows using generalized additive models..... **439**

9:45 **Gislon Giulia, Mondini Sara, Zucali Maddalena, Pavolini Marta, Bava Luciana, Canali Elisabetta, Sandrucci Anna**
Integrated sensor data for monitoring calves' condition..... **562**

10:00 **Pavolini Marta, Gislon Giulia, Tamburini Alberto, Bonizzi Serena, Zucali Maddalena, Moretti Vittorio Maria, Mattiello Silvana, Sandrucci Anna**
Use of precision livestock farming technologies on dairy cows in a mountain environment..... **420**

10:15 **Mattiello Silvana, Celozzi Stefania, Battini Monica, Sandrucci Anna, Ntalampiras Stavros, Presti Giorgio, Ludovico Luca A., Petrera Francesca, Abeni Fabio**
Monitoring the time of calving in dairy cows by means of vocalizations **029**

10:45 Coffee Break and Poster session

Friday, 20th June – Room Agliè

Session 53 – Companion Animals: NUTRITION AND HEALTH

Chairs: **Cutrignelli Monica – Luciano Alice**

9:00 **Stefanon Bruno, Sgorlon Sandy, Sandri Misa, Balouei Fatemeh**
Variation of faecal microbiota of bitches during pregnancy and lactation on development of faecal microbiota of puppies during lactation and at weaning **302**

9:15 **Cuccaro Bianca, Albarella Sara, Ciotola Francesca, Martano Manuela, Restucci Brunella**
Analysis of BRCA gene SNPs in dogs with mammary tumor **069**

9:30 **Ruggiero Alessio, Ferrara Maria, Vastolo Alessandro, Piccirillo Barbara, Bergero Domenico, Cutrignelli Monica Isabella**
Functional ingredients in cats' nutrition **160**

9:45 **Peripolli Chiara, Danyer Erdem, Fusi Eleonora, Siani Gerardo, Ricci Rebecca**
Homemade diets for dogs: owner's motivation and management **329**

10:00 INVITED LECTURE
Mussa Pier Paolo
Evolution of pet animal nutrition in Italy: scientific, technological and professional aspects .....

10:45 Coffee Break and Poster session

Friday, 20th June – Room Venaria

Session 54 – Genetics: GENETIC STRATEGIES FOR ECONOMIC TRAITS

Chairs: **Crepaldi Paola – Cesarani Alberto**

11:15 **Salaris Sotero, Usai Mario Graziano, Casu Sara, Miari Sabrina, Pernisa Annalisa, Negro Alessio, Grande Silverio, Carta Antonello**
Genetic evaluation of Sarda sheep for milk protein content based on genomic information and a female reference population **294**

11:30 **Santomassimo Chiara, Mariotti Federico, Petrini Andrea, Lasagna Emiliano, Quaglia Andrea, Sbarra Fiorella, Sarti Francesca Maria**
Genetics and meat quality: challenges and perspectives in Vitellone Bianco dell'Appennino centrale ... **219**

11:45 **Giontella Andrea, Silvestrelli Maurizio, Cucciniello Michael, Cocciolone Alessandro, Pieramati Camillo, Sarti Francesca Maria**
Phenotypic and genetic study of hair whorls in the Maremmano horse and their correlations with the temperament index **262**

12:00 **Ablondi Michela, Asti Vittoria, Valle Emanuela, Stocco Giorgia, Bordin Clara, Moretti Riccardo, Zanotti Andrea, Sabbioni Alberto**
Genetic parameters of horse international longitudinal show jumping results **237**

12:15 **Minozzi Giulietta, De Iorio Maria Grazia, Pagnacco Giulio**
Selective breeding for Varroa Sensitive Hygiene (VSH) behavioral trait in honey bee (Apis mellifera) colonies: initial results of four years of selection **193**

Friday, 20th June – Room Carignano

Session 55 – Welfare, Health and Behaviour: BEEKEEPING, HORSES AND PIGS FARMING

Chairs: **Gottardo Flaviana – Luise Diana**

11:15 **Porzio Elisabetta, Busechian Sara, Mecocci Samanta, Pepe Marco, Chillemi Giovanni, Chiaradia Elisabetta, Cappelli Katia, Rueca Fabrizio, Beccati Francesca**
The use of a fitness tracker to analyze heart rate variability in show jumping horses during standard exercise test in warm and cold environment **088**

11:30 **Bordin Clara, Zanchi Marco, Ozella Laura, Valle Emanuela**
Strides to success: How gait and technique shape performance in show jumping **478**

11:45 **Favaro Daniele, Lazzarin Stella Bernadette, Moscon Elisa, Tonon Francesco, Contiero Barbara, Gottardo Flaviana**
Open cage farrowing system: balancing welfare and productivity **488**

12:00 **Danieli Pier Paolo, Manganello Federico, Lazzari Filippo**
Effectiveness of Fe (II) supplementation in Italian honey bee (Apis mellifera ligustica Spin.) under laboratory conditions..... **506**

12:15 **Coppola Francesca, Sagona Simona, Tafi Elena, Orlando Caterina, D'Onofrio Chiara, Boni Chiara Benedetta, Casini Lucia, Palego Lionella, Betti Laura, Giannaccini Gino, Felicioli Antonio**
Effects of coconut oil-enriched diet administration on honey bees' survival and health **030**

Friday, 20th June – Room Stupinigi

Session 56 – Aquaculture: MISCELLANY

Chairs: **Parisi Giuliana – Fanizza Cecilia**

11:15 INVITED LECTURE
Brambilla Fabio
Sustainability and aquaculture: responsible change of diets.....

11:45 **Rimoldi Simona, Kalemi Violeta, Betancor Mónica, Saroglia Marco, Terova Genciana**
How nutritional programming and genotype shape the gut microbiota and influence growth of Atlantic salmon..... **041**

12:00 **Birolo Marco, Trabacchin Veronica, Triolone Stefano, De Bonis Marina, Uberti Giordano, Sambo Paolo, Nicoletto Carlo**
Optimising stocking density of Largemouth bass (Micropterus salmoides) in coupled aquaponic systems **222**

12:15 **D'Agaro Edo, Gibertoni Pierpaolo, Esposito Stefano**
New genomic tools for the conservation and management of native brown trout (Salmo trutta) in the Valle d'Aosta region **425**

12:30 **Trabacchin Veronica, Nicoletto Carlo, Triolone Stefano, De Bonis Marina, Uberti Giordano, Sambo Paolo, Birolo Marco**
*Effects of dietary microelements supplementation on growth performance and fillet quality of Largemouth bass (*Micropterus salmoides*) in a coupled aquaponic system with lettuce (Lactuca sativa)*..... **450**

Friday, 20th June – Room Valentino

Session 57 – Monogastric Nutrition: RABBIT, POULTRY AND DONKEY

Chairs: **Nicolaia Iaffaldano – Marchetti Luca**

11:15 **Xiccato Gerolamo, Bordignon Francesco, Pascual Anton, Birolo Marco, Zomeño Cristina, Trocino Angela**
Role of the dietary supplementation of arginine and valine: health status, digestibility, and performances of growing rabbits **057**

11:30 **Mainardi Edda, Rossi Raffaella, Ondruska Lubomir, Vizzarri Francesco**
Dietary supplementation with Lauraceae and Chlorellaceae in growing rabbits: effects on meat quality parameters **120**

11:45 **Bosa Luigia, Bernabucci Gloria, Di Federico Francesca, Dal Bosco Alessandro, Mattioli Simona, Mancinelli Cartoni Alice, Primi Riccardo, Girotti Pedro, Castellini Cesare**
Grazing behaviour and meat quality in different rabbit genotypes reared in outdoor conditions **217**

12:00 **Petrosillo Elena, Lanzoni Davide, Cenati Clara, Perricone Vera, Giromini Carlotta, Cheli Federica, Savoini Giovanni**
Effects of euglena gracilis supplementation on growth performance, antioxidant status, meat quality in broiler chickens **216**

12:15 **Colonna Maria Antonietta, Carbonara Claudia, Tufarelli Vincenzo, Losacco Caterina, Tedone Luigi, Giannico Francesco, Fortunato Mariarosaria, Selvaggi Maria, Ragni Marco, Tarricone Simona**
Effect of zinc-enriched Camelina sativa supplementation in broiler diets on meat quality and sensory properties **299**

12:30 **Volpe Jacopo, Pittarello Marco, Nota Ginevra, Lombardi Giampiero, Lonati Michele**
Donkey feeding behavior in shrub- and tree-encroached pastures in Gran Paradiso National Park **459**

Friday, 20th June – Room Mandria

Session 58 – Precision Farming: INNOVATION AND SUSTAINABILITY IN LIVESTOCK

Sponsored by MSD Animal Health

Chairs: **Salzano Angela – Presutti Livia**

11:15 **Negrini Riccardo, Barbato Mario, D'Alessandro Enrico, Liotta Luigi, Cassandro Martino, Ciardella Giorgio, Nardone Mario, Cicagna Iosef, Valentini Riccardo, Coppola Valerio, Ruggeri Federico, Melilli Caterina, Nardone Alessandro**
InnovaRE: Research and application of innovative tools to improve resilience in ruminants..... **256**

11:30 **Canossa Maddalena, Atzori Alberto Stanislao, Fiorbelli Erica, Gallo Antonio**
An application of system thinking approach to study complex problems in animal nutrition: a Case study of feeding behavior **178**

11:45 **Steri Roberto, Iacurto Miriam, Canini Francesco, Meo Zilio David**
Technical and practical aspects of using PLF tools in a buffalo farm: the SensorHost Software..... **395**

12:00 **Mastroeni Carmelo, Colombo Marco, Novara Valentina, Carboni Eliana, Gallo Antonio**
Comparing two different weighting systems to improve whole-plant corn silage quality in the top layer of a farm bunker..... **440**

12:15 **Ledda Antonello, Azzena Margherita Domenica Giovanna, Atzori Alberto Stanislao**
Precision livestock farming with APPàre, a digital platform for feeding and management of sheep farming in Sardinia..... **569**

12:30 **Rezende Marcos, Vittorio Rammauro, Attilio Rossoni**
Advantages of precision livestock data sharing platforms in the genomic era **451**

Friday, 20th June – Room Agliè

Session 59 – Companion animals: GENETICS AND GENOMICS

Chairs: **Ciotola Francesca – Marelli Stefano Paolo**

11:15 **Bionda Arianna, Crepaldi Paola, Liotta Luigi**
Exploring the genomic basis of dental agenesis in Labrador Retrievers..... **228**

11:30 **Hernaiz Adelaida, Calvo Jorge Hugo, Cagnotti Giulia, Zaragoza Pilar, Ala Ugo, D'Angelo Antonio, García-Belenguer Sylvia, Martín-Burriel Inmaculada**
Genomic study of idiopathic epilepsy in dogs: a natural model for human epilepsy..... **312**

11:45 **Boccuni Sara, Shoemake Claire, Liotta Luigi, Attard George**
Insights into history and phenotypical traits of the Maltese Hunting Dog (Kelb tal-Kaċċa ta' Malta)..... **255**
12:00 **Floridia Viviana, Bionda Arianna, Boccuni Sara, Shoemake Claire, Crepaldi Paola, Attard George, Liotta Luigi**
Genetic characteristics for a breed standard definition of the Maltese Hunting Dog (Kelb tal-Kaċċa ta' Malta)....**221**
12:15 **Moretti Riccardo, Viglietti Antonio, Sartore Stefano, Chessa Stefania, Sacchi Paola**
Preliminary genomic analysis of an autochthonous dog population from the San Pietro Island..... **333**
12:30 **Marelli Stefano, Cannas Simona, Frattini Stefano, Polli Michele, Strillacci Maria Giuseppina**
Phenotypical and genomic analysis of Sila Sheepdog (Canis lupus familiaris)..... **429**

ASPA 26th Congress Book of Abstract

POSTER

ALTERNATIVE PROTEINS

Tignani Maria Vittoria, Secci Giulia, Pulido-Rodríguez Lina, Parisi Giuliana
Evaluation of the physico-chemical stability of cricket meal and dried whole cricket during storage at room temperature..... **125**
Addeo Nicola Francesco, Lanzieri Maria Rosaria, Vozzo Simone, Di Rosa Ambra, Accetta Francesca, Panettieri Valentina, Bovera Fulvia, Musco Nadia
Hermetia illucens as functional feed for laying hens: effect on productive performance **136**
Palumbo Bianca Federica, Dalle Zotte Antonella, Deruytter David
Impact of sex ratio manipulation on reproductive output in Tenebrio molitor **253**
Cappai Maria Grazia, Arminu Sergio, Pudda Flavia, Schiavone Achille, Serra Giuseppe
Yellow mealworm (Tenebrio molitor) rearing on different substrates affects feed intake in captive sardinian partridges (Alectoris barbara barbara)..... **545**

AQUACULTURE

Zarantoniello Matteo, Galdelli Alessandro, Mancini Adriano, Pasquini Marina, Fatone Francesco, Olivotto Ike
Reducing food losses by developing an automated hatching system prototype for early stage embryos of rainbow trout (Oncorhynchus mykiss)..... **061**
Zarantoniello Matteo, Tombolini Lorenzo, Trombetta Maria Federica, Eusebi Anna Laura, Fatone Francesco, Olivotto Ike
Nature-based solutions for wastewater management towards a sustainable aquaculture: the CARDIMED case study.. **076**
Colli Licia, Riccioni Giulia, Colussi Silvia, Fariano Lucio, Valenzano Vittorio, Bergamino Cinzia, Milanese Giulia, Gini Martina, Scala Sonia, Prearo Marino, Pastorino Paolo, Ajmone Marsan Paolo
The RESILTROUT project: identifying genetic markers associated to disease resistance and heat stress resilience in farmed rainbow trout (Oncorhynchus mykiss) **240**
Antenucci Emanuele, Di Iorio Michele, Santoianni Celeste, Coccia Isabella, Galosi Livio, Cariglia Michela, Pozzato Luca, Roncarati Alessandra Iaffaldano Nicolaia
Preliminary set-up of a digital system for the fish welfare improvement in cage aquaculture..... **249**
Gai Francesco, Randazzo Basilio, Meola Martina, Caccamo Letteria, Carboni Stefano, Concu Danilo, Loi Barbara, Miccoli Andrea, Mirto Simone, Perdichizzi Anna, Vallainc Dario, Maricchiolo Giulia
Dietary effects on growth, gut health and immune response of flathead grey mullet fed black soldier fly meal..... **481**
Manuguerra Simona, Arena Rosaria, Rannou Maxime, Grimaudo Federico, Curcuraci Eleonora, Santulli Andrea, Messina Concetta
Technology transfer for Haliotis turberculata farming in Sicily: evaluation of adaptive responses to culture conditions..... **573**

COMPANION ANIMALS

Llobat Lola, Sechi Sara, Liotta Luigi, Amato Annalisa, Cavallo Carmelo, Cocco Raffaella
Breed-specific hematological phenotypes in dogs apparently healthy but infected by zoonotic pathogens: the case of Fonnese and Cirneco dog breeds..... **073**
Armone Rosangela, Nava Vincenzo, Alizzi Antonino Filippo Maria, Randazzo Andrea, Chiofalo Biagina
Hydrolyzed feather meal in dog nutrition: dry food proximate composition, amino acid content, and biogenic amines..... **128**

Balouei Fatemeh, Stefanon Bruno, Martello Elisa, Atuahene David, Sandri Misa, Meineri Giorgia
Effects of a hepatoprotective supplement on liver function, inflammation markers, and gut microbiota in overweight dogs **138**
Accetta Francesca, Armone Rosangela, Di Rosa Ambra, Stefanon Bruno, Chiofalo Biagina
Hydrolyzed Feather Meal in dog nutrition: application of electronic senses on extruded diet **323**
Martello Elisa, Perondi Francesca, Lonigro Nicolò, Bruni Natascia, Bigliati Mauro, Costale Annalisa, Meineri Giorgia
Effects of Saccharomyces cerevisiae DSM 34246 var. boulardii supplementation on nutritional status, fecal parameters, and overall well-being in healthy adult breeding cats and dogs **455**
Persichilli Christian, Mastrangelo Salvatore, Di Civita Marika, Senczuk Gabriele, Zorzetto Chiara, Ciampolini Roberta
Genome-wide characterization of a local heeling dog population from Northern-Apennines **487**

FOOD QUALITY

Brugiapaglia Alberto, Provera Riccardo, Pennisi Francesco, Mois Sara, Pezzolato Marzia, Greco Alfredo, Bozzetta Elena, Esposito Giovanna
Effect of High-Pressure Processing on texture of gilthead sea bream (Sparus aurata) fillets **051**
Provera Riccardo, Brugiapaglia Alberto, Pennisi Francesco, Pezzolato Marzia, Greco Alfredo, Bozzetta Elena, Esposito Giovanna
High pressure processing and cryogenic treatments to kill Ani-sakis in fish fillet and near infrared spectroscopy to verify their application **062**
Pulido-Rodríguez Lina, Parrini Silvia, Secci Giulia, Parisi Giuliana
Discriminant analysis to classify two fish species based on geographical origins and farming systems using FT-NIRS **117**
Vincenzetti Silvia, Pucciarelli Stefania, Polzonetti Valeria, Renzi Sofia, Malandrino Laura, Vici Giorgia, Coman Maria Magdalena, Polidori Paolo
Nutritional characterization of a fermented beverage from donkey milk **121**
Accetta Francesca, Armone Rosangela, Lanzieri Mariarosaria, Bovera Fulvia, Di Rosa Ambra
Hermetia illucens as functional feed for laying hens: effect on egg quality **137**
Dal Bosco Alessandro, Mattioli Simona, Bosa Luigia, Di Federico Francesca, Castellini Cesare
Alfalfa and linseed oil in rabbit diet to improve sustainability and healthiness of the meat **148**
Mattioli Simona, Di Federico Francesca, Angelucci Elisa, Castellini Cesare, Bosa Luigia, Dal Bosco Alessandro
Meat quality of breast and drumstick of different ECC-approved chicken genotypes **150**
Rebucci Raffaella, Gambazza Giuseppe, Dal Borgo Alice, Zeni Niko Gioacchino, Marchetti Luca, Lanzoni Davide, Colombini Lorenzo, Giromini Carlotta, Zaniboni Luisa
Impact of dietary hemp seeds in an agroecological farming system (HappyHens): functional and nutritional features of eggs from different layer breeds **169**
Oswaldo Botia Carreño Edwin, Elghandour Mona M.M.Y., Garcia Martinez José Eduardo, Yllescas Uriel Lopez, Salem Abdelfattah
Effect of microencapsulated Yucca shidigera extract on milk production and composition in dairy goats **201**
Marino Rosaria, Caroprese Mariangela, Della Malva Antonella, Santillo Antonella, Ciliberti Maria Giovanna, Sevi Agostino, Albenzio Marzia
Nutritional properties of Podolian meat: the impact of dietary forage to concentrate ratio **235**
Arango Sheyla, Guzzo Nadia, Bianco Emanuele, Simonetti Emilio, Zerbinati Elena, Rainis Simona, Bailoni Lucia
Effect of replacing corn silage with alternative crops on milk yield and quality in Italian Simmental dairy cows **267**
Singh Yazavinder, Mugnai Cecilia, Forte Claudio, Agradi Stella, Dalle Zotte Antonella, Blanc Simone, Costamagna Chiara, Cullere Marco
Sustainable rabbit production: carcass traits, physical meat quality, and shelf-life of three local breeds **290**
Chessari Giorgio, Tumino Serena, Cremonesi Paola, Biscarini Filippo, Avondo Marcella, Marletta Donata, Castiglioni Bianca
Milk microbiota composition in Girgentana goat breed **297**
Varricchio Maria Luisa, Masucci Felicia, Scalera Grazia, Lambiase Claudia, Serrapica Francesco, De Rosa Giuseppe, Di Francia Antonio
Olive residues as a cost – effective feed supplement: effects on milk quality in small dairy farms **301**
Spina Anna Antonella, Virga Antonino Nazareno, Furfaro Maria Elena, Chiofalo Vincenzo, Madeo Alessandro, Britti Domenico, Randazzo Cinzia, Bosco Georgiana, Morittu Valeria Maria
Inclusion of linseed and grape-derived antioxidants in the diet of Apulo-Calabrese x Goland pigs: effects on animal performance and meat quality **339**
Ponte Marialetizia, Maggiolino Aristide, Marino Rosaria, Bonanno Adriana, Forte Lucrezia, Della Malva Antonella, De Palo Pasquale, Sevi Agostino, Di Grigoli Antonino
Milk production of ewes fed diets integrated with encapsulated or non-encapsulated lemon essential oil **341**

Palumbo Maria Antonietta, Lucchini Franco, Cocconcelli Pier Sadro, Ajmone Marsan Paolo
In vitro production of bovine hepatocyte growth factor **351**
Carta Silvia, Correddu Fabio, Steri Roberto, Meo Zilio David, Fenu Antonio, Rubattu Roberto, Cesarani Alberto, Pulina Giuseppe, Nudda Anna
Effect of grape pomace in the diet of ewes during the mid-lactation period on milk fatty acid profile and methane emissions **398**
Niero Giovanni, Visentin Elena, Cipolat-Gotet Claudio, Stocco Giorgia, Ablondi Michela, Summer Andrea, Penasa Mauro
Determination of κ-casein B in bovine milk through HPLC and ELISA techniques **401**
Carta Silvia, Chessa Margherita, Sanna Manuela, Murgia Marco, Nudda Anna, Mangia Nicoletta
Microbiological, nutritional, and sensorial characterization of bottarga of Mugil cephalus produced in the east and west coast of Sardinia **402**
Silvi Alina, Casarosa Laura, Vichi Francesca, Gasparoni Elisa, Ripamonti Alice, Tognocchi Monica, Tinagli Sara, Serra Andrea, Conte Giuseppe, Mantino Alberto, Mele Marcello
Effects of brewer's spent grain in dairy sheep diet on yield, nutritional quality and volatile organic compound profile of cheese **415**
D'Ambra Katia, Trovato Roberta, Minelli Giovanna, Forte Claudio, Lo Fiego Domenico Pietro
Influence of pig dietary supplementation with hazelnut skin (HS) or hazelnut skin green extract (HSE) on live performance, carcass characteristics and meat quality of heavy pigs **435**
Cavallo Carmelo, Lopreiato Vincenzo, Bosco Georgiana, Litrenta Federica, Randazzo Cinzia, Scalisi Marco, Amato Annalisa, Floridia Viviana, Liotta Luigi
iSafe-Graze: selection of probiotic Lactic Acid Bacteria as starter cul-tures to enhance Conjugated Linoleic Acid content in sheep's milk cheese **452**
Palazzo Marisa, Tavaniello Siria, Grassi Giulia, Peng Meng, Teshale Dereje Birara, Maiorano Giuseppe
Effect of feeding olive mill wastewater (Olea europaea L.) on meat quality of Podolian young bulls **460**
Di Rosa Ambra, Accetta Francesca, Chiofalo Vincenzo, Furfaro Maria Elena, Virga Antonino Nazareno, Bonello Federica
Towards sustainable beekeeping: Warrè (people's) vs Dadant-Blatt hives. Evaluation of chemical and aromatic profile of Sicilian Acacia (Robinia pseudoacacia) Honey **490**
Cremonesi Paola, Bonazza Francesca, Severgnini Marco, Castiglioni Bianca, Brasca Milena, Pizzi Flavia, Silvetti Tiziana, Morandi Stefano, Cipolat-Gotet Claudio, Turri Federica
Unveiling the unique microbiome and nutritional profile of milk from the caprine Nera di Verzasca local breed **514**
Cremonesi Paola, Ceccarani Camilla, Silvetti Tiziana, Morandi Stefano, Bonazza Francesca, Brasca Milena Castiglioni Bianca
Influence of cattle breeds on microbiota and quality of Valtellina Casera PDO cheese **517**
Marino Vita Maria, Schadt Iris, La Terra Stefania, Belvedere Giovanni, Caccamo Margherita, Caggia Cinzia
Lysozyme and total antioxidant capacity in raw milk of Ragusano donkey: effect of lactation stage and production period **524**
Currò Sarah, Marcolin Martina, Balzan Stefania, Fasolato Luca, Haftvani Geghani Taroyan, Chiarello Gian Luca, Costa Annamaria, Di Giancamillo Alessia, Cherif Nadia, Temraz Tarek, Radaelli Giuseppe, Fonsatti Elisa, Bortoletti Martina, Bertotto Daniela
Photocatalytic water remediation for sustainable fish farming: effect on rainbow trout microbial contamination and shelf-life **565**
Fancello Francesco, Carboni Maria Rosaria, Nieddu Lidia Nicoletta, Fresu Mirko, Acciaro Marco, Piga Paola, Forte Lucrezia, Maggiolino Aristide, Atzori Alberto Stanislao
Effect of aging facility on chemical-physical and microbiological characterization of Limousine dry-aged meat **566**
Al Rharad Asma, El Aayadi Soufiane, Belabbass Nouhaila, Mendes De Souza Poliana, Boukrouh Soumaya
Chemical composition of camel meat: a meta-analysis and meta-regression study **572**

GENETICS

Zanon Thomas, Oian Angelica, Mantovani Roberto, Gauly Matthias
Veterinary treatment data from the electronic recording system for genetic selection in the Alpine Grey cattle breed **020**
Karatosidi Despoina, Avgeris Euthimios, Michailidis Georgios
Investigation of genetic polymorphisms in Estrogen and Prolactin gene receptors in the autochthonous Greek black pig breed **035**
Sbarra Fiorella, Quaglia Andrea, Bittante Giovanni, Mantovani Roberto
Genetics of temperament in five Italian beef cattle breeds **063**
Sabbioni Alberto, Cerati Carlo, Sfrisi Emanuele, Benaglia Paolo
Environmental factors affecting the quality of boar semen for AI **075**

Colombi Daniele, Perini Francesco, Pedota Giuseppina, Sbarra Fiorella, Quaglia Andrea, Sarti Francesca Maria, Lasagna Emiliano
Evaluation of genetic parameters for milk composition and technological properties in Podolica cattle breed **107**
Parrini Silvia, Mercat Marie-José, Amaral De Jesus Andreia, Karolyi Danijel, Cändek Potokar Marjeta, Restoux Gwendal, Fabbri Maria Chiara, Crovetti Alessandro, Sirtori Francesco, Bozzi Riccardo
Local pig and chicken breeds: weaknesses, strengths and challenges by Italian stakeholder concept **113**
Santillo Antonella, Caroprese Mariangela, Marino Rosaria, Di Corcia Martina, Bruno Silvia, Martino Nicola, Monaco Davide, Dell'aquila Maria Elena, Landi Vincenzo, Selvaggi Maria, Temerario Letizia, Mastrorocco Antonella, Lacalandra Giovanni Michele, Ciani Elena, Albenzio Marzia
Mapping the biodiversity in small ruminants. The LOCAL project in Apulia Region **130**
Cosenza Gianfranco, Fulgione Andrea, Albarella Sara, Ciotola Francesca, Gallo Daniela, Pauciullo Alfredo
Exploring genetic variability at goat CSN2 locus using novels PCR based methods **143**
Gabbianelli Federica, Milanesi Marco, Basiricò Loredana, Pietrucci Daniele, Macchioni Paola, Bernabucci Gloria, Arcuri Chiara, Danieli Pier Paolo, Picarone Ludovica, Bernabucci Umberto, Vitali Andrea, Lacetera Nicola, Ronchi Bruno, Giovanni Chillemi, Primi Riccardo
Genetic variability characterization of the "Leprino di Viterbo" rabbit breed. **147**
Sarti Francesca Maria, Galeazzi Sara, Giovannini Samira, Cocciolone Alessandro, Grande Silverio, Sylla Lakamy
Phenotypic characterization of ram's reproductive system: preliminary investigation for the development of a fertility index **204**
Di Iorio Michele, Antenucci Emanuele, Rusco Giusy, Cerolini Silvia, Iaffaldano Nicolaia
Phenotypic characterization of two native Italian turkey breeds: a comparative study **227**
Arcuri Chiara, Picarone Ludovica, Pietrucci Daniele, Gabbianelli Federica, Porcai Gabriella, Milanesi Marco, Cosenza Gianfranco, Gomez Carpio Mayra, Chillemi Giovanni
Performance evaluation of the new SNPs array designed for Mediterranean river buffalo breed **229**
Turri Federica, Negro Alessio, Pizzi Flavia, Grande Silverio, Biffani Stefano
Constitution of a semen cryobank for the conservation of the Italian small ruminant local breeds **233**
Taurisano Valeria, Ribani Anisa, Bovo Samuele, Schiavo Giuseppina, Bertolini Francesca, Schiavitto Michele, Fontanesi Luca
BCO2 allele frequencies in many rabbit breeds and populations: insights from the spread of a genetic defect **239**
Taurisano Valeria, Ribani Anisa, Utzeri Valerio Joe, Sami Dalal, Nelson Johnson Kate Elise, Fontanesi Luca
Honey bee genetics from honey samples: monitoring the diffusion of Apis mellifera mitochondrial DNA lineages in Emilia Romagna over seven years **242**
Bolner Matteo, Bovo Samuele, Schiavo Giuseppina, Bertolini Francesca, Gallo Maurizio, Fontanesi Luca
An initial genome-wide association study for haematological and blood clinical-biochemical parameters in Italian Duroc pigs **247**
Ablondi Michela, Asti Vittoria, Danese Tommaso, Bordin Clara, Ozella Laura, Moretti Riccardo, Sacchi Paola, Summer Andrea, Sabbioni Alberto, Mikko Sofia, Valle Emanuela
CHAMP: Combining Horse Athletic Measurements with Precision Genomics **250**
Asti Vittoria, Ablondi Michela, Moretti Riccardo, Valle Emanuela, Ozella Laura, Danese Tommaso, Sabbioni Alberto, Summer Andrea
Meta-analysis on early traits genetically correlated with later performance in life in horses **260**
Asti Vittoria, Zanotti Andrea, Ablondi Michela, Malacarne Massimo, Sabbioni Alberto
Focus on genetic diversity within the InnoVaDiv project **263**
Tonamo Tema Andualem, Profiti Margherita, Stocco Giorgia, Cipolat-Gotet Claudio, Summer Andrea, Chessa Stefania
Implementation of sheep production system through genomics and phenomics: preliminary results **265**
Bruno Silvia, Alashqar Sara, Letaief Neyrouz, Pauciullo Alfredo, Ciani Elena, Hasan Alhadded
In silico functional polymorphisms analysis for milk-related genes in Camelus dromedarius species **266**
Tarricone Simona, Colonna Maria Antonietta, De Vito Nicolò, Lacitignola Massimo, Gerardi Domenico, La Gioia Giuseppe, Campanile Domenico, Carone Maria Teresa, Cardone Giuseppe Giorgio, Ragni Marco
European turtle dove (Streptopelia turtur) in Apulia: preliminary estimate of the breeding population abundance **300**
Chessari Giorgio, Reich Paula, Criscione Andrea, Mastrangelo Salvatore, Tumino Serena, Carlentini Morena, Bordonaro Salvatore, Tetens Jens, Marletta Donata
Heterozygosity-rich regions survey in Sicilian and worldwide horse breeds using genome-wide imputed data **307**
Gulinelli Marta, Moretti Riccardo, Sartore Stefano, Perona Giovanni, Mimosi Antonio, Sacchi Paola, Cornale Paolo, Chessa Stefania
BECH. GRIS Project: genetic characterization, conservation and management of the Grigia delle Valli di Lanzo local breed **315**
Schiavone Achille, Stoppani Nadia, Soglia Dominga, Cappone Eleonora Erika, Shirjandi Faraz, Laura Martinez, Silvia Rey, Antonio Vallecillos, Eva Armero
Phenotypic and genetic characterization of the Spanish Gallina Murciana chicken breed **318**

D'Alessandro Enrico, Galeano Grazia, Giuffrè Letterio, Giosa Domenico, Tolone Marco
A study on diversity and pathway signals in Ragusano donkey microbiome **328**
Capra Emanuele, Negrini Riccardo, Lazzari Barbara, Cozzi Paolo, Ajmone Marsan Paolo, Stella Alessandra, Turri Federica
EpiC Fun: A project investigating the epigenetic diversity and functional adaptation in local and cosmopolitan Italian cattle breed **331**
Stoppani Nadia, Cappone Eleonora Erika, Fiorilla Edoardo, Gariglio Marta, Zambotto Valeria, Profiti Margherita, Schiavone Achille, Soglia Dominga
Identification of SNP markers associated with carcass trait and meat quality in Italian slow-growing chicken breeds using targeted next-generation sequencing (NGS) **356**
Soglia Dominga, Stoppani Nadia, Maione Sandra, Schiavone Achille, Marzoni Margherita, Buccioni Arianna, Lasagna Emiliano, Castellini Cesare, Iaffaldano Nicolaia, Penasa Mauro, Cerolini Silvia
Genetic polymorphism of the PAX7 minisatellite region in Italian chicken breeds **359**
Tumino Serena, Ben Jemaa Slim, Chessari Giorgio, Mastrangelo Salvatore, Marletta Donata, Carta Federica, Cesarani Alberto, Bordonaro Salvatore, Criscione Andrea
Exploring signatures of selection in the indigenous Nero Siciliano pig breed **362**
Zanotti Andrea, Ablondi Michela, Summer Andrea, Sabbioni Alberto, Asti Vittoria, Finocchiaro Raffaella, Van Kaam Jan-Tijs, Cassandro Martino, Layton Jonathan, Cipolat-Gotet Claudio
Does inbreeding cause a decrease in lifetime milk production? **363**
Tumino Serena, Carlentini Morena, Chessari Giorgio, Virzì Armando, Marletta Donata, Criscione Andrea, Bordonaro Salvatore
Variability survey at meat production loci in Nero Siciliano pig breed **368**
Seghrouchni Kenza, Barbato Mario, Floridia Viviana, Frattini Stefano, Liotta Luigi, Seghrouchni Kenza
Filling the gaps in the genomic management of italian dog breeds **374**
D'Alessandro Enrico, Liotta Luigi, Tolone Marco
Exploring head morphology and exterior traits in Nero dei Nebrodi pig **378**
Crepaldi Paola, Negro Alessio, Bionda Arianna, Ramirez Diaz Johanna, Turri Federica, Grande Silverio, Biffani Stefano
Simulation of mating plans by optimal contribution selection in Camosciata delle Alpi goats **379**
Bertolini Francesca, Munarini Filippo, Schiavo Giuseppina, Bovo Samuele, Dall'Olio Stefania, Jessica Maranzani, Massimo Bonacini, Fontanesi Luca
Genomic characterisation of Varzese: an iconic dual-purpose autochthonous cattle breed **387**
Graziani Silvia, Cipolat-Gotet Claudio, Stocco Giorgia, Biffani Stefano, Valoppi Davide, Tedeschi Irene, Bozzi Riccardo, Fabbri Maria Chiara, Sirtori Francesco, Grande Silverio, Castiglioni Bianca, Tiezzi Mazzoni Della Stella Maestri Francesco
Effect of breed and season on productivity, quality and dairy efficiency of two Italian dairy sheep breeds **412**
Perini Francesco, Bordini Martina, Mancinelli Cartoni Alice, Soglia Dominga, Schiavone Achille, Cendron Filippo, Mugnai Cecilia, Mattioli Simona, Castellini Cesare, Lasagna Emiliano, Zappaterra Martina, Penasa Mauro
WGCNA analysis elucidates pathways involved in fatty acids biosynthesis in local chickens **418**
Floridia Viviana, Bionda Arianna, Arias Katherine Daniela, Virga Antonino Nazareno, Crepaldi Paola, Liotta Luigi, Barbato Mario
Genomic insights on the history and selection trajectories of the local goat breed Comune di Sicilia **426**
Bionda Arianna, Lopreiato Vincenzo, Liotta Luigi, Floridia Viviana, Cortellari Matteo, Crepaldi Paola, Attard George, Floridia Viviana
Genomic characterization of the Maltese cattle breed **428**
Lazzari Filippo, Scarpino Paolo, Danieli Pier Paolo, Cresta Eleonora, Manganello Federico
A study on instrumental insemination in Apis mellifera ligustica Spin. as a tool for conservation strategies of the Italian honey bee. **500**
Danieli Pier Paolo, Di Prisco Gennaro, Manganello Federico, Ricchiuti Luciano, Terriaca Riccardo, Lazzari Filippo
Behavioural and productive traits of Italian honey bee (Apis mellifera ligustica Spin.) colonies: results of a survey among beekeepers in some Central Italy regions **502**
Floridia Viviana, Dettori Maria Luisa, Pazzola Michele, Barbato Mario
Architecture and function of ancestral genomic components in hybrid livestock populations: the Sardo-Modicana case **544**
Luongo Flavio, Fontana Cecilia, Pascarella Lorenzo, Fioretti Mauro, Melilli Caterina, Matassino Donato, Negrini Riccardo
Quality Control procedures in BNZ Biobanking: scope and outcomes **547**
Sartore Stefano, Cannizzo Francesca Tiziana, Caracappa Santo, Moretti Riccardo, Pittarello Marco, Profiti Margherita, Sacchi Paola
Characterization of the Cinisara chain in northwest Sicily **575**
Delledonne Andrea, Maltecca Christian, Tiezzi Francesco, Punturiero Chiara, Strillacci Maria Giuseppina, Bagnato Alessandro
How alternative models affect resilience indicators in dairy cattle **576**

MONOGASTRIC NUTRITION

Pugliese Gianluca, Losacco Caterina, Passantino Letizia, Tarricone Simona Tarricone, Schiavitto Michele, Laudadio Vito, Tufarelli Vincenzo
Red lentil screening by-product inclusion in rabbit diet: effects in growth traits, meat quality and gut health **043**
Losacco Caterina, Pugliese Gianluca, Passantino Letizia, Ceci Edmondo, Giannico Francesco, Schiavitto Michele, Laudadio Vito, Tufarelli Vincenzo
Horehound (Marrubium vulgare L.) as a feed additive affects the productive traits, serum antioxidants, digestive enzymes, intestinal bacterial counts, and gut morphology of growing rabbits **044**
Guerrini Alessandro, Del Zozzo Francesca, Muscatello Luisa Vera, Serra Valentina, Harper Valeria, Fiorini Lorenzo, Carlu Claire, Chabrillat Thibaut, Tedesco Doriana
Bioactive compounds from Silybum marianum L. and Cynara cardunculus scolymus L. improve the well-being of laying hens: preliminary data **066**
Fiorilla Edoardo, Ferrocino Ilario, Gariglio Marta, Gai Francesco, Zambotto Valeria, Ozella Laura, Franciosa Irene, Giribaldi Marzia, Raspa Federica, Cappone Eleonora Erika, Sferra Chiara, Capucchio Maria Teresa, Achille Schiavone
Exploring the impact of alternative dietary proteins on growth performance, gut health and microbiota in Bianca di Saluzzo chickens **119**
Tignani Maria Vittoria, Secci Giulia, Pulido-Rodríguez Lina Fernanda, Addeo Nicola Francesco, Tucciarone Isabella, Lanzieri Maria Rosaria, Parisi Giuliana
Effect of cannabidiol dietary supplementation on the fatty acid profile of rabbit liver **127**
Fatica Antonella, Pastorelli Grazia, Tedesco Doriana, Serra Valentina, Simeonidis Kalliroi, Guerrini Alessandro, Todini Luca, Fantuz Francesco, Salimei Elisabetta
Preliminary assessment of chemical and nutritional value, and biomass production of an area in Centre-South Italy grazed by equines **142**
Tedesco Doriana, Guerrini Alessandro, Cambal Hera Jedd, Daulenkhan Ayaulym, Andriantsoa Ny Ivo Hasina Haniel, Marzorati Stefania
Larch wood waste: a functional fiber for late gestating and lactating sows **151**
Santoru Matteo, Muñoz-Grein Jennifer, Latorre Maria Angeles, Pinotti Luciano, Rossi Luciana, Alvarez-Rodriguez Javier
In vitro and in vivo nutrient digestibility of a pig diet enriched with Yucca schidigera extract **192**
Kiatti Dieu Donné, Musco Nadia, Montefusco Teresa, Ferrara Maria, Calabrò Serena
In vitro two-step evaluation of pineapple, cashew and mango waste for pig nutrition **282**
Frazzini Sara, Rizzi Nicoletta, Fifi Anna Paola, Canala Benedetta, Dell'Anno Matteo, Rossi Luciana
Functional activity and anti-inflammatory response of Fucus vesiculosus on mouse peritoneal macrophages **342**
Danese Tommaso, Bonaglia Adeline, Penzillo Noemi, Properzi Elisa, Simoni Marica, Valle Emanuela, Martuzzi Francesca, Righi Federico
The use of sieve fecal particle separator to preliminarily evaluate dry matter digestibility in horse **394**
Trabalza Marinucci Massimo, Mecocci Samanta, D'ambra Katia, Pietrucci Daniele, Acuti Gabriele, Minelli Giovanna, Cappelli Katia, Forte Claudio, Tabasso Silvia, Lo Fiego Domenico Pietro
Intestinal microbiota evaluation in finishing pigs fed hazelnut skins **447**
Tedesco Doriana, Guerrini Alessandro, Cambal Hera Jedd, Daulenkhan Ayaulym, Andriantsoa Ny Ivo Hasina Haniel, Marzorati Stefania, La Porta Caterina
Effets of larch wood waste supplementation on fecal microbiota of late gestating and lactating sows **538**

PHYSIOLOGY AND REPRODUCTION

Bornaghi Valeria, Galli Andrea, Pozzato Giulia
Quality control in boar semen production **089**
Bornaghi Valeria, Galli Andrea, Paoli Laura, Vanni Roberta, Frabetti Andrea, Fornasini Daniela
Feasibility of using frozen semen in rabbit breeding **094**
Matera Roberta, Calanni Macchio Alfio, Bruno Francesco, Lombardi Alessia, Aragona Francesca, Piscopo Nadia, Longobardi Valentina
Conception influences reproductive dynamics and lactation characteristics in primiparous Mediterranean buffalo **179**
Zaniboni Luisa, Lopez Annalaura, Madeddu Manuela, Tognoli Cristina, Moretti Vittorio Maria, Marelli Stefano Paolo, Perricone Vera, Iaffaldano Nicolaia, Cerolini Silvia
Lipid profile in chicken sperm of Italian chicken breeds **289**

Molè Concetta, Cavallo Carmelo, Torrisi Concetta, Trieste Valeria, Emmanuele Giovanni, Visalli Rosanna, Scalisi Marco I, Lopreiato Vincenzo, Liotta Luigi
Heat stress impacts metabolism and milk quality of Ragusano donkey **449**
Lopreiato Vincenzo, Sfulcini Marta, Cavallo Carmelo, Trevisi Erminio, Liotta Luigi, Minuti Andrea
Relationship between residual energy intake in Holstein calves, their performance, and milk yield during the first lactation **503**

PRECISION FARMING

Giannuzzi Diana, Rovetta Carlo, Bisutti Vittoria, Pegolo Sara, Arazi Alon, Katz Gil, Trevisi Erminio, Mele Marcello, Gallo Luigi, Mota Lucio Flavio Macedo, Schiavon Stefano, Cecchinato Alessio
Variations in individual feed intake predicted by a 3D accelerometer in dairy cows **083**
Aquilani Chiara, Confessore Andrea, Cecchini Valentina, Bovolenta Stefano, Simonetti Emilio, Pugliese Carolina
Virtual Fencing learning retention in dairy cows after 3 months of non-use **131**
Scalera Grazia, Masucci Felicia, Sannino Maura, Serrapica Francesco, Di Francia Antonio, De Rosa Giuseppe
Adaptation and growth performance of buffalo calves in an automatic feeding system with individual pens **268**
Malizzi Tiziano, Senatore Elena, Silvi Alina, Zucca Giovanni, Finocchi Matteo, Mantino Alberto, Turini Luca, Mele Marcello
Using smart collars to assess heat stress impacts on dairy cows **324**
Cabassi Giovanni, Benedini Dario, Gambale Claudia, Monteggia Larisa, Monti Lucia, Pelizzola Valeria, Gasparini Andrea, Povolo Milena
Study of alpine pasture exploitation by coupling GPS trackers and accelerometers **344**
Biagini Davide, Blandino Massimo, Careddu Andrea, Dinuccio Elio, Garolini Daniele, Meloni Raffaele, Pelissetti Simone, Rollè Luca, Scapino Mattia, Verna Riccardo, Lazzaroni Carla
Effect of fertiliser variable rate control on quality of wheat forage **370**
Confessore Andrea, Aquilani Chiara, Bianco Emanuele, De Guttry Luca, Sirtori Francesco, Pugliese Carolina
Virtual Fencing and Remote Sensing: improve the herd management of dairy cows on alpine pasture **471**
Paolino Rosanna, Sabia Emilio, Ventura Gennaro, Vignozzi Luca, Riviezzi Amelia Maria, Claps Salvatore, Di Trana Adriana, Braghieri Ada
Use of remote images for natural pasture biomass prediction in sheep pre-grazing **484**
Canali Elisabetta, Pesenti Rossi Gaia, Barbieri Sara, Azzolari Mattias, Minero Michela, Dalla Costa Emanuela
Use of Infrared thermography to monitor calf health and welfare **507**
D'Alessandro Enrico, Barbato Mario, Floridia Viviana, Liotta Luigi, Lopreiato Vincenzo, Cassandro Martino, Ciardella Giorgio, Nardone Mario, Cicagna Iosef, Valentini Riccardo, Coppola Valerio, Ruggeri Federico, Melilli Caterina, Nardone Alessandro, Negrini Riccardo
InnovaRe: exploring innovative phenotyping for a smarter flock **529**
Mantovani Giorgia, Simoni Marica, Danese Tommaso, Boldrin Gloria, Pitino Rosario, Righi Federico
Assessing the potential of portable NIR spectroscopy to evaluate the net energy content for lactation of hay forages for dairy cattle **536**
Barbato Mario, Floridia Viviana, Liotta Luigi, D'Alessandro Enrico, Lopreiato Vincenzo, Cassandro Martino, Ciardella Giorgio, Nardone Mario, Cicagna Iosef, Valentini Riccardo, Coppola Valerio, Ruggeri Federico, Melilli Caterina, Nardone Alessandro, Negrini Riccardo
Exploring novel phenotypes in cattle within extensive farming systems: the InnovaRe project **542**
Gaspa Giustino, Laura Falchi, Cesarani Alberto, Ferrari Carolina, Negrini Riccardo, Macciotta Nicolò
Across breeds variability of resilience indicators based on daily automatic milking system data **564**
Ledda Antonello, Azzena Margherita Domenica Giovanna, Contena Manuela, Castangia Francesca, Cannas Antonello, Atzori Alberto Stanislao
APPàre, sensors and software in decision support systems for the Sardinian dairy sheep farmers **571**

PRODUCTION SYSTEMS

Rapetti Luca, Battelli Marco, Gambarini Giulia, Colombini Stefania, Pavesi Martina, Menni Giorgio, Dai Xiaoxia, Crovetto Matteo, Schiavon Stefano, Galassi Gianluca
Two different feeding systems in fattening heavy pigs: performance and nitrogen balance **085**
Sirtori Francesco, Parrini Silvia, Aquilani Chiara, Confessore Andrea, Bozzi Riccardo, Dibari Camilla, Argenti Giovanni, De Guttry Luca, Pugliese Carolina
Finishing of beef cattle on pasture: effects on performance and meat quality **141**
Tanganelli Costanza, Parrini Silvia, Moretti Maria Vittoria, De Guttry Luca, Confessore Andrea, Solinas Stefania, Sirtori Francesco, Dibari Camilla, Pugliese Carolina
The potential effectiveness of innovative practices in livestock and permanent pasture management: stakeholder responses. **327**
Carboni Maria Rosaria, Frongia Andrea, Salis Lorenzo, Acciaro Marco, Decandia Mauro, Sitzia Maria
Effects of weaning strategies on the average daily gain of Dorper-Sarda F1 lambs **376**
Ripamonti Alice, Acciaro Marco, Decandia Mauro, Frongia Andrea, Mantino Alberto, Mele Marcello
Challenges and opportunities in using the n-alkane technique to determine cattle diet in agrosilvopastoral systems **413**
Creatini Susy, Salari Federica, Roncoroni Cristina, Brajon Giovanni, Martini Mina *Integrating animal welfare and milk monitoring: a preliminary analysis of farm management and efficiency prediction* **438**
Sechi Gian Simone, Atzori Alberto Stanislao
A twenty-year dairy cattle farm evolution, technical and managerial aspect **557**

RUMINANT NUTRITION

Stefanon Bruno, Cecchini Valentina, Sgorlon Sandy, Colitti Monica
Variation in the faecal microbiota of deer in relation to the hunting area in the Friuli Venezia Giulia region **115**
Oteri Marianna, Calderone Francesca, Armone Rosangela, Maio Aurora, La Malfa Tommaso, Scavo Aurelio, Scordia Danilo, Chiofalo Biagina, Gresta Fabio
Rhizobium inoculation in forage legumes intercropped with cereal for ruminant feeding **139**
Menni Giorgio, Rapetti Luca, Pavesi Martina, Dai Xiaoxia, Battelli Marco, Giudice Filippo, Galassi Gianluca, Crovetto Matteo, Colombini Stefania
Addition of feed additives to stimulate alternative metabolic pathways through methane reduction **206**
Catellani Alessandro, Fiorbelli Erica, Moschini Maurizio, Gallo Antonio
Effect of different RDP/RUP ratios on productive performances, feeding behavior, and nitrogen efficiency of high-yielding dairy cows **207**
Bettini Stefano, Perini Francesco, Colombi Daniele, Ghilardi Marco, Trabalza Marinucci Massimo, Lasagna Emiliano
The effect on productive performance of a Saccharomyces cerevisiae postbiotic inclusion in the finishing diet of Chianina bullock **241**
Scalera Grazia, Serrapica Francesco, Sannino Maura, Faugno Salvatore, Di Francia Antonio, Lambiase Claudia, De Rosa Giuseppe, Masucci Felicia
Sustainable feed source from ensiled peanut crop residues **272**
Errico Michela, Catellani Alessandro, Gallo Antonio, Rocchetti Gabriele
High throughput UHPLC-HRMS method for the detection of purines derivatives as biomarkers of nitrogen efficiency in dairy cows **275**
Piccirillo Barbara, Ponte Marialetizia, Pipi Marianna, Bonanno Adriana, Calabrò Serena
Hedysarum coronarium L.: an undiscovered forage resource for sheep feeding **284**
Sandrini Silvia, Perricone Vera, Stranieri Angelica, Pea Alessia, Cenati Clara, Paltrinieri Saverio, Savoini Giovanni, Agazzi Alessandro
Influence of Enniatin B on performance and metabolic profile in dairy cow **320**
Agazzi Alessandro, Sandrini Silvia, Perricone Vera, Cremonesi Paola, Castiglioni Bianca, Valenti Irene, Pea Alessia, Cenati Clara, Pasquali Matias
Fecal microbiota shifts in dairy cows consuming Enniatin B-contaminated diets **325**
Lambiase Claudia, Calabrò Serena, Scalera Grazia, Vastolo Alessandro, Masucci Felicia, Di Francia Antonio, Serrapica Francesco
Feeding livestock with leftovers: exploring the potential of dry pasta residue **326**

Petrocchi Jasinski Francesca, Evangelista Chiara, Basiricò Loredana, Meo Zilio David, Iacurto Miriam, Steri Roberto, Bernabucci Umberto
Effects of the Rufo® supplement on enteric methane emissions in lactating Italian Mediterranean buffaloes, measured with a laser methane detector (LMD) **391**
Spina Anna Antonella, Grande Raffaella, Perri Alessia, Granato Martina, Britti Domenico, Morittu Valeria Maria
Total mixed ration in calf weaning: long-term effects on heifer performance..... **421**
Porcu Maria Angela, Ledda Antonello, Duras Bardilio, Mattu Andrea, Ruggiu Enrico, Formigoni Andrea, Cannas Antonello
Effect of different feeding sequences of soybean meal on lactating dairy ewes fed ryegrass rich in water-soluble carbohydrates **464**
Fancello Francesco, Fresu Mirko, Nieddu Lidia Nicoletta, Zara Severino, Gallo Antonio, Mastroeni Carmelo, Atzori Alberto Stanislao
Investigation of the microbiological, physico-chemical, and fermentative quality of baled silage produced in Sardinia **466**
Altomonte Iolanda, Salari Federica, Vivo Tiziana, Ceccherelli Valeria, Minieri Sara, Martini Mina
Fat formulation of cow milk replacers affects nutrient fecal excretions of dairy calves..... **476**
Evangelista Chiara, Petrocchi Jasinski Francesca, Basiricò Loredana, Vitali Andrea, Grossi Giampiero, Rossi Chiara, Turriziani Giovanni, Lacetera Nicola, Bernabucci Umberto
Effect of green forage on the particle size of rations in buffaloes and its influence on sorting ability..... **491**
Federiconi Alessia, Veroni Laura, Ghiaccio Francesca, Canestrari Giorgia, Indio Valentina, De Cesare Alessandra, Formigoni Andrea, Palmonari Alberto
Characterization of rumen-fecal microbiota in dairy cows with different productive performances..... **520**
De Angelis Daria Zoe, Pompei Luigi, Giammarco Melania, Prasinou Paraskevi, Cipriani Marcella, Cortesi Francesco, Rossi Emanuela, Podaliri Michele, Iannetti Luigi, Fusaro Isa
Effect of different feeding regimens on fattening, carcass traits and meat quality of old bergamasca sheep for arrosticini production: preliminary results..... **528**
Primi Riccardo, Danieli Pier Paolo, Ferri Michele, Cellitti Francesca, Bottoni Irene, Napoli Francesco, Boselli Carlo, Spina Raffaello, Ronchi Bruno
Feeding teff (Eragrostis tef) to lactating dairy sheep: a forage option in the Mediterranean basin..... **537**
Lunesu Mondina Francesca, Nudda Anna, Carta Silvia, Fenu Antonio, Rubattu Roberto, Battacone Gianni
Effect of starch source in finishing diets on carcass and meat quality of culling Sarda ewes..... **548**
Danieli Pier Paolo, Fiore Leonardo, Lazzari Filippo, Primi Riccardo, Manganello Federico, Natoli Vincenzo, Ronchi Bruno
Application of Near-Infrared Spectroscopy (NIR) for the compositional assessment of teff hay..... **555**
Silvestrelli Simone, Ghiaccio Francesca, Cavallini Damiano, Bongiovanni Jenny, Toni Fausto, Formigoni Andrea
Nutritional characterization and variability of different livestock feed used in the national feed industry..... **560**
Capasso Giambattista, Rosati Leonardo, Perna Anna Maria
Effect of the weather pattern of two consecutive years on the floristic composition and on the quantitative-qualitative production of the forage phytomass of a summer pasture of the Southern Apennines..... **561**

SUSTAINABILITY

Finocchiaro Raffaella, Benzoni Lorenzo, Layton Jonathan, Visentin Giulio, Dorigo Martina, Tiezzi Mazzoni Della Stella Maestri Francesco, Marusi Maurizio, Bracchi Alessandro, Bonacina Greta, Zucali Maddalena, Gislon Giulia, Vitali Andrea, Rossi Chiara, Grossi Giampiero, Lacetera Nicola, Cassandro Martino
A holistic approach for monitoring the environmental sustainability of the Italian Holstein cattle population **067**
Sabia Emilio, Braghieri Ada, Paolino Rosanna, Vignozzi Luca, Di Trana Adriana, Cosentino Carlo, Freschi Pierangelo, Pacelli Corrado
Circular animal feed: environmental impact of by-products in diet of dairy animals..... **134**
Gabriele Sara, Lorenzi Valentina, Roccaro Mariana, Peli Angelo, Gallese Simone, Liberati Giorgia, Pennellini Sara, Mattacchione Federica, Bonoli Alessandra, Fusi Francesca, Bertocchi Luigi
Study of the relationship between animal welfare and environmental im-pact in Italian dairy cattle farms..... **173**
Froldi Federico, Dall'Asta Margherita, Moschini Maurizio, Gallo Antonio, Rossi Filippo, Negrini Riccardo, Trevisi Erminio
Life cycle assessment of cow milk production: how to transfer results in different nutritional functional units..... **180**
Scaglia Elena, Sergi Valeria, Giagnoni Laura, Casini David, Chiaramonti David, Giulia Ferronato, Gilioli Gianni, Caprarulo Valentina
Impact of in feed biochar supplementation on GHG and ammonia emissions from manure produced by Holstein calves..... **186**

Di Rosa Ambra, Falqui Luciano, Perrone Giuseppe, Di Bella Daniele, Saitto Nicola, Chiofalo Vincenzo
Microalgae deriving from the biochemical conversion of CO2 as innovative and sustainable sources of functional additives in laying hen diets. The GREEN-EGG project **212**
Goldaraz-Salamero Nuria, Sierra-Perez Jorge, Blanc Simone, Brun Filippo
Rethinking livestock feeds with hazelnut by-products: a Llife Cycle Thinking approach **232**
Azzena Margherita Domenica Giovanna, Mussolino Claudio, Atzori Marco, Todde Giuseppe, Sole Stefania, Todde Giorgio, Attardi Emiliano, Carrus Mariangela, Buttu Giangavino, Atzori Alberto Stanislao
Analysis of sustainability and digitisation in member companies of the CAO Cooperative of Oristano **310**
Costamagna Chiara, Blanc Simone, Agradi Stella, Mugnai Cecilia, Forte Claudio, Cullere Marco, Borra Danielle, Merlino Valentina Maria
The Italian rabbit sector: analysis of competitive sustainability strategies **361**
Pompei Luigi, De Angelis Daria Zoe, Jalal Hassan, Fusaro Isa, Prasinou Paraskevi, Tavaniello Siria, Perna Anna Maria, Vignola Giorgio, Giammarco Melania
Inclusion of grape pomace in dairy ewes diets: effects on milk production and methane mitigation potential **410**
Rossi Chiara, Grossi Giampiero, Vitali Andrea, Lacetera Nicola
Enteric methane emissions in organic Brown Swiss cows **422**
Cavallini Damiano, Lamanna Martina, Colleluori Riccardo, Silvestrelli Simone, De Matos Vettori Julio, Buonaiuto Giovanni, Romanzin Alberto, Formigoni Andrea
Advancing methane detection in dairy cows during robotic milking: insights from enhanced laser and sniffer techniques **493**
Tolone Marco, Lopreiato Vincenzo, Liotta Luigi, Chiofalo Vincenzo, Praticò Salvatore, D'urso Provvidenza, Modica Giuseppe
Monitoring the greenhouse gas emissions in dairy cattle farms. The MITIgA project **511**
Dinuccio Elio, Aimè Chiara, Angiulli Francesco Alessandro, Biagini Davide, Braghieri Alessandro, Brunoldi Matteo, Calzaferri Simone, Dela Pierre Flavia, Dondi Daniele, Finco Linda, Giannandrea Giulia, Guida Roberto, Kameswaran Nithish Kumar, Mandelli Beatrice, Montagna Paolo, Riccardi Cristina, Salvini Paola, Vai Ilaria, Vadivel Dhanalakshmi, Vitulo Paolo, Arena Maria Cristina
An innovative system for enteric methane recovery **527**
Sarkar Drishti, Rossi Chiara, Grossi Giampiero, Primi Riccardo, Vitali Andrea, Lacetera Nicola
Dynamics of greenhouse gases in central Italian meadows: a high-resolution analysis using LI-COR gas analyzers **563**
Pompei Luigi, Jalal Hassan, Fusaro Isa, Tavaniello Siria, Perna Anna Maria, Maiorano Giuseppe, Alessandro Gramenzi, Giammarco Melania
In vitro evaluation of digestibility, gas and methane production from winery by-products **568**

WELFARE, HEALTH AND BEHAVIOUR

Maria Levrino Gustavo
Effects of enriched cage design on the welfare and behavior of breeding does **022**
Massacci Francesca Romana, Cucco Lucilla, Albini Elisa, Blasi Francesca, Di Gregorio Alessandra, Orsini Serenella, Petrin Sara, Peruzzo Arianna, Paniccià Marta, Magistrali Chiara Francesca
Genomic analysis of Streptococcus canis and S. dysgalactiae subsp. equisimilis from different hosts in Italy 2004–2021: antimicrobial resistance and virulence profiles. **140**
Longobardi Consiglia, Bifulco Giovanna, Pacelli Gianmaria, Ciarcia Roberto, Salzano Angela, Damiano Sara, Campanile Giuseppe
Effects of breeding techniques on animal welfare in rural areas **163**
Castellani Simona, Mecocci Samanta, Bernabucci Umberto, Rampacci Elisa, Giovagnoli Stefano, Basiricò Loredana, Cappelli Katia, Lacetera Nicola
Effects of bovine milk extracellular vesicles on the oxidative and inflammatory status of bovine mammary and porcine intestinal epithelial cells **175**
Rocchetti Gabriele, Errico Michela, Milanesi Marco, De Paula Nogueira Guilherme, Garcia Josè Fernando, Ajmone Marsan Paolo
Untargeted metabolomic analysis of heat stress response in indicine and taurine cattle **177**
Ozella Laura, Pittarello Marco, Barzolai Clementina, Tarantola Martina
Effects of grazing adaptation on Italian Pezzata Rossa metabolism **182**
Caroprese Mariangela, Marino Rosaria, De Devitiis Biagia, Pipi Marianna, Badalamenti Rosario, Maggiolino Aristide, Forte Lucrezia, Russo Ilaria, De Palo Pasquale, Di Grigoli Antonino, Prosperi Maurizio, Albenzio Marzia
Perspectives of Citrus essential oil as feed in sheep farming **279**

Lorenzi Valentina, Valli Giulia, Archetti Ivonne, Tempini Michele, Gabriele Sara, Bernardo Tiziano, Sangalli Elena, Monaci Claudio, Salogni Cristian, Maisano Antonio Marco, Scali Federico, Ambra Chiara Denise, Vecchio Domenico, Stefania Bergagna, Barberio Antonio, Fusi Francesca, Bertocchi Luigi
Welfare conditions of replacement calves and surplus calves in dairy farms in Northern Italy **281**
Belperio Simona, Martelli Giovanna, Nannoni Eleonora, Meneguz Marco, Sardi Luca
Black soldier fly meal and oil: effects of novel feed sources on growth traits and welfare in fattening pigs **319**
Frongia Andrea, Acciaro Marco, Giovanetti Valeria, Serra Gabriella, Cabiddu Andrea, Sitzia Maria, Decandia Mauro
THI as an alert tool for decline in milk production in grazing Sarda sheep **321**
Moretti Riccardo, Ponzo Enrico, Cuccato Matteo, Profiti Margherita, Divari Sara, Chessa Stefania, Cannizzo Francesca Tiziana, Sacchi Paola
MALDI-TOF mass spectrometry profiling to investigate subclinical mastitis in dairy cows **334**
Carè Sara, Crisà Alessandra, Marchitelli Cinzia, Scatà Maria Carmela, Signorelli Federica, Calì Massimo, Meo Zilio David, Pulcini Domitilla, Capoccioni Fabrizio, Bochicchio Davide, De Matteis Giovanna
European partnership on animal health and welfare-EUPAHW **456**
Greppi Martina, Raspa Federica, Cavallini Damiano, Odore Rosangela, Gnudi Giacomo, Cavallo Andrea, Bertuglia Andrea, Valle Emanuela
Horse welfare assessment: the parameters to consider in pain evaluation **473**
Pesenti Rossi Gaia, Boldrin Gloria, Barbieri Sara, Dalla Costa Emanuela, Minero Michela, Canali Elisabetta
Effect of Pair-Housing on the reactivity of pre-weaned dairy calves **508**
Correddu Fabio, Carta Silvia, Lunesu Mondina Francesca, Cadau Giordana, Battacone Gianni, Pulina Giuseppe, Nudda Anna
Effect of dietary inclusion of cocoa bean shells on behaviour indicators of animal welfare in Sardo-bruna cattle breed **510**
Visentin Giulio, Colleluori Riccardo, Buonaiuto Giovanni, Costa Angela, Mammi Ludovica Maria Eugenia, Palmonari Alberto, Cavallini Damiano, Formigoni Andrea
Effect of different THI metrics on milk yield and quality attributes of Holstein cows using robot milking data **553**

INVITED SPEAKERS

P1

From "necessary evil" to "FeedEconomy" how livestock production has changed from the 19th century to date

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The relationship between man and animal in order to obtain a mutual benefit is relatively recent in the history of humanity. The first attempts of livestock production are approximately collocated about 11,000 years ago (after the last glacial period) with sheep domestication. In this contest animal husbandry (zootechnics) can appear as newborn science. The word zootechnics have been introduced around 1835–1845 by the French agronomist, and head of the *Institute National d'Agronomie* of Versailles, Adrien De Gasparin (1783–1862). He proposed the first chair of animal husbandry, which was given to Eugène Baudement (1816–1863) who can be considered the founder of the modern zootechnics. Before then, such teaching has been referred to as pastoralism or animal hygiene. These were the first steps of a new science that defined its subject domain in the field of interaction between anatomy, physiology and economics in such a way that the farmer would be able to obtain maximum production from the *animal machine*. In less than two hundred years the new science has made great strides. However, in Italy, at the time, livestock was not kept in high regard. This observation allowed Camillo Cavour (1810–1861), who considered livestock the most essential branch of the rural economy, to state that cows in our country presented a singular problem: production was far from being proportionate to the expenses that they involved. As pointed out, Cavour's epoch was the one in which livestock was considered '*un male necessario*' (a necessary evil) in fact agricultural production depended largely on manure, which remained the key fertilizer. The availability of manure was closely linked to the amount of livestock on the farm, so it was necessary to have an adequate amount of forage, which was obtained from extensive grassland or by resorting to external purchase. The period between the second half of the 19th century and the first half of the 20th century can be considered as the one in which animal husbandry was established as an academic discipline. In these hundred years, numerous treatises on animal husbandry were published. Particularly in France and Germany, such as those by Sanson, Cornevin, Dechambre and Settegast to name a few, many of which were also translated into Italian by teachers from our schools. In Italy too, there are renowned zootechnical veterinarians who have written various treatises, including Baldassarre, Mascheroni, Marchi, Faelli, Chiari and Fogliata. After the First World War, agronomists also began to take an interest in zootechnics, and there was a lengthy debate as to whether zootechnics was a veterinary or an agronomic competence. Around 1930, artificial insemination received a great boost, along with the fight against bovine sterility, and thanks to the work of Prof. Bonadonna, veterinarian and teacher in Agricultural Faculty of Milano, a pioneer in this field, it became common practice on our farms after the war. Finally, after the Second World War, 'scientific animal husbandry' flourished, whose basis would no longer be purely experiential but would also be based on a solid scientific method. The development of research also resulted in greater specialisation of the areas of interest and with it an explosion of disciplinary areas that were formerly included in general and special zootechnics. Research in animal nutrition and feeding, feed technology, animal genetics, genetic improvement and zootechnical hygiene became more and more necessary and requested training courses. In the same moment pig, cattle, sheep and goat breeding emerged from special zootechnics. Avian and rabbit, once confined to 'minor breeding' are now scientific branches of animal production. Disciplines such as fish production, that were once the almost exclusive prerogative of zoologists, are born. Around the 1970s-80s, the university was able to adapt its curricula to these changes. Since then, animal husbandry has evolved steadily, and with the advent of the Anthropocene like other knowledge, development has become exponential, enabling production achievements, in all sectors unimaginable until a few years ago. Today the complex world of animal production is worth about 17 million euros, more than 30 percent of the agricultural production, and the concept of 'FeedEconomy' has been recently introduced, by which we measure the value connected with the entire 'livestock supply chain' (including petfood production), which at the national level has reached 150 million euros. Nevertheless, in a urbanised and post-industrial Society that prioritises service aspects over productive ones, the animal husbandry will have to be able to meet the future challenges on the horizon. These include the environmental sustainability of intensive livestock and animal welfare, food safety and, more recently, the problems posed by the spread of novel foods and cultivated meat not forgetting the importance of safeguarding equitable farm income of livestock production.

P2

Guiding principles of AI: application in animal husbandry

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It is imperative to comprehend the transformative impact of Artificial Intelligence (AI) on society, and, more specifically, its applications within livestock farming. Two contrasting perspectives can be identified: one that perceives the rise of AI as potentially

disconcerting, and another that regards it as a pathway to an improved future. Regardless of these divergent viewpoints, it is contended that AI will fundamentally reshape both professional and personal domains. In doing so, it represents an evolutionary advancement from the scientific breakthroughs that characterised the industrial era, while simultaneously introducing a novel form of intelligence that exceeds conventional human capabilities. Initially, attention must be directed towards the progression from advanced data analysis to deep learning in livestock farming. Currently, AI applications in this sector primarily involve the processing of data acquired from multiple sensors, which is then integrated into statistical models to yield actionable insights. However, it is critical to emphasise that deep learning—an advanced methodology that employs neural networks with numerous hidden layers—is anticipated to assume an increasingly significant role. Unlike traditional neural networks, which typically consist of an input layer, one or two hidden layers, and an output layer, deep learning architectures may encompass tens or even hundreds of layers, thereby facilitating the capture of more complex patterns and subtle nuances in the data. A review of AI's application in livestock farming reveals that the rapid pace of technological advancement means that contemporary cutting-edge systems may quickly become outdated. This dynamic necessitates continual updates and the involvement of specialised professionals. Modern farms are progressively integrating the Internet of Things to collect data from both internal and external sources, thereby empowering AI systems to make informed decisions regarding a range of issues—from selecting replacement animals and optimising feeding regimes to managing sales and purchases. The efficacy of these systems is contingent upon the quality of the data collected; robust, diverse datasets are essential for effective training of AI models, although such datasets remain relatively scarce. Notwithstanding these challenges, AI presents substantial opportunities to enhance operational efficiency, promote animal welfare, and augment productivity throughout the entire supply chain. AI has the potential to ameliorate management inefficiencies that lead to the wastage of resources by utilising real-time data to automatically adjust operational practices. For instance, by customising feeding protocols to the individual requirements of each animal, AI can reduce waste while enhancing overall efficiency. Moreover, through the monitoring of environmental parameters, such as land use, greenhouse gas emissions, and energy consumption, AI can contribute to reducing the environmental footprint of farming operations and bolster resilience against climatic stress. The capacity for early detection of health issues through continuous monitoring further underscores the transformative potential of AI in livestock management. Several prospective developments in AI-assisted livestock farming are envisaged. These include fully automated farm management systems that coordinate logistics, staff administration, and maintenance; advanced predictive analytics designed to preempt health and behavioural issues in animals; and personalised feed management systems tailored to the unique requirements of each animal. Furthermore, there exists the potential for refined genetic selection techniques that may accelerate livestock improvement. Nevertheless, these promising innovations are tempered by challenges such as data security concerns, issues regarding sensor reliability, the necessity for specialised skills, ethical implications, and substantial implementation costs. A substantial aspect of the discussion contrasts human decision-making with the computational capabilities of AI. Traditional farm management is predicated on human experience, intuition, and abstract reasoning, qualities that enable farmers to navigate complex and interrelated factors. In contrast, AI utilises exhaustive computational analyses to process vast quantities of data, generating extensive decision trees to identify the most advantageous outcomes. This divergence raises the possibility that AI's capacity for long-term prediction may eventually surpass human intuition, potentially relegating farmers to supervisory roles rather than active decision-makers.

Although AI may ostensibly simplify certain tasks, its effective integration necessitates continuous learning and the acquisition of new skills. It is anticipated that specialised roles will emerge to serve as intermediaries between sophisticated AI technologies and day-to-day farm operations, thereby reshaping traditional work practices within the livestock sector. Broader societal issues—such as global disparities in AI adoption—warrant consideration. Disparities in economic, technological, and infrastructural capacities suggest that advanced nations with greater resources will be better positioned to harness AI, whereas less developed regions may encounter difficulties in keeping pace. Furthermore, energy availability is identified as a critical factor, reminiscent of past industrial revolutions in which resource abundance determined the pace of technological progress. AI governance also constitutes a key concern. At present, a limited number of multinational corporations—primarily based in the United States and China—dominate AI development and control extensive data storage infrastructures. This concentration of power raises significant issues regarding data privacy, geopolitical vulnerabilities, and the potential for market monopolisation. As reliance on AI within the farming sector increases, the establishment of stringent regulatory frameworks to protect confidential information becomes increasingly imperative.

Finally, the delicate balance between trust and scepticism in the age of AI must be considered. The opaque nature of AI's decision-making processes compels users either to trust its outcomes implicitly or to risk interfering with its performance. Drawing an analogy with the fictional AI HAL 9000, this discussion cautions against the potential hazards of uncritical reliance on AI and questions whether humans will be able to maintain effective control over decision-making processes in the future.

Although AI promises considerable benefits for livestock farming—ranging from improved efficiency and sustainability to enhanced animal welfare—it concurrently presents substantial challenges. As the computational power of AI continues to expand, there is a risk that human intuition and decision-making may gradually be supplanted, ultimately resulting in a future in which machines dominate operational processes. Addressing these challenges will necessitate careful attention to data quality,

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robust security measures, ethical considerations, and the development of comprehensive regulatory frameworks, thereby ensuring that the benefits of AI are fully realised without compromising essential human oversight.

I1

Insects for peace: transforming communities through black soldier fly farming

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Small-scale Black Soldier Fly (BSF) farming systems are becoming known as innovative and sustainable solutions for improving food security, managing organic waste, and strengthening livelihoods in rural and post-conflict regions of the Global South. This presentation explores the multiple sustainability benefits of BSF farming when implemented at the local level, focusing on its contributions to social inclusion, economic resilience, and environmental recovery. While the *Insects for Peace* initiative in Colombia serves as a central case study, the broader analysis draws from diverse experiences to highlight the transformative potential of decentralised BSF production systems.

Through the bioconversion of food scraps, crop residues, and animal manure into protein-rich larvae and nutrient-dense frass, small-scale BSF systems close nutrient loops and improve agroecological performance. These systems offer a low-cost, high-impact alternative to imported feed and synthetic fertilizers, empowering farmers to reduce input costs and increase productivity using locally available resources.

Socially, smallholder BSF farming fosters empowerment through capacity building, collaboration, and local innovation. In Colombia, the *Insects for Peace* initiative engages families in post-conflict territories to produce BSF larvae for feeding poultry and fish, while applying frass as fertilizer for crops. The model strengthens food sovereignty, reduces community vulnerability, and promotes reconciliation through shared agroecological practices. In Kenya, similar initiatives have shown that small-scale BSF systems can be adopted rapidly with minimal infrastructure, creating opportunities particularly for women and youth to take on leadership in circular farming.

Economically, BSF farming allows farmers to diversify income by selling larvae, frass, or value-added insect-based products. The use of local waste materials not only lowers production costs but also creates new markets around sustainable feed and fertilizers. In both Colombia and Kenya, these practices have led to increased farm efficiency, new entrepreneurship, and the emergence of micro-economies rooted in sustainability. From an environmental perspective, BSF farming helps mitigate the negative impacts of waste by transforming it into valuable outputs. This process reduces methane emissions, decreases pollution, and restores soil health. The use of frass enhances soil microbial life, structure, and moisture retention, directly supporting climate-resilient agriculture. BSF systems also reduce pressure on ecosystems by offering alternatives to fishmeal and soymeal, two major drivers of deforestation and overfishing.

Despite these benefits, small-scale BSF farming faces challenges related to regulatory gaps, market integration, and cultural acceptance. Clearer guidelines, inclusive policy frameworks, and awareness-raising initiatives are needed to unlock its full potential. Building alliances among governments, researchers, and communities can support its integration into formal agri-food strategies. Within the Global South, BSF farming offers a compelling entry point for transitioning towards circular, resilient agricultural systems. Its adaptability, simplicity, and synergy with existing farming practices make it particularly suited for rural and peri-urban contexts facing resource constraints. The *Insects for Peace* initiative exemplify how BSF can serve not only as a livelihood tool but also as a platform for rebuilding trust, cooperation, and ecological balance in post-conflict areas. Ultimately, while this presentation centres on BSF farming, it contributes to a broader call to recognise the value of insects in building sustainable and regenerative agri-food systems. Insect farming is not limited to feed or food, it has the potential to support ecosystem services, restore degraded landscapes, strengthen circular economies, and promote new social relations around sustainability. By optimising the socioecological roles of insects, we can unlock innovative pathways toward agri-food systems that are more inclusive, equitable, and ecologically grounded.

I2

How to 'End the Cage Age' for farrowing sows – updates on research, systems and best practice

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The European Citizens' Initiative (ECI) to 'End the Cage Age' has galvanised the debate about the future of confinement systems, including the farrowing crate for expectant and lactating sows. In 2021, it led to the European Commission stating that 'by the end of 2023, a legislative proposal to phase out, and finally prohibit all cage systems would be in place', possibly as soon as 2027. This would follow an appropriate transition period, after a robust scientific impact assessment as part of their evaluation (or 'fitness check') on current animal welfare regulations (Council Directive 98/58/EC). Although the debate continues, it is clear

that permanent crating of farrowing and lactating sows is not sustainable. Legislation already restricts farrowing crate use in Sweden (since 1987), Switzerland (since 1997 with a 10 year transition period) and Norway (since 2000), while New Zealand, Austria and Germany have announced phasing out of farrowing crates by 2025, 2033 and 2036 respectively. Several other countries in Europe have made pledges to reduce use of confinement systems, including preventing any new crates from being built (e.g. Denmark from 2023, Finland from 2024, France from 2025) and may set national regulations to restrict use. There are also several market initiatives as well as national subsidies offering incentives to encourage uptake of high welfare systems. However, many EU members may wait to see what the EC propose following their initial response to the ECI. Whilst many producers have accepted changes are needed, they are concerned about making costly mistakes when installing a system. Decision makers need clear guidance on optimum systems, management and costs.

Lack of clarity stalls progress and perpetuates use of systems with known welfare consequences, particularly for the sow, as close confinement prevents full expression of highly motivated nest-building behaviors, disrupting hormonal modulation of farrowing and increasing stress. The physical restriction has been further exacerbated as modern hyperprolific sows and their litters are much larger than many crates were designed to accommodate. Reducing confinement has positive impacts for sows but also piglets, with improvements in maternal behaviour, colostrum quality, udder access and weight gain. To fully realise these benefits, it is important to optimise the '3 Ps' of pens, people and pigs. Whilst much research has been conducted on optimal pen design of alternatives, less attention has been given to optimising pig selection and developing best practice approaches to support staff. These areas should be targeted with an effort to combine fundamental research with knowledge that can be gained from early adopters becoming more experienced with reduced confinement systems. Despite the extensive research into different systems there remains a lack of clarity on what works and what will be compliant in the future. There is also a lack of knowledge about the potential for long-term benefits of higher welfare systems for the pigs (e.g. sow longevity, piglet growth and health status) and how those translate into benefits for other stakeholders, including how this might impact on sustainability and food security goals.

Transitioning from conventional farrowing crates to any alternative involves making a number of important decisions. Many of these decisions will involve trade-offs between the needs of the sow, her piglets, the farmer and other stakeholders (e.g. consumers) and various competing externalities (e.g. environmental targets). The decision making process is multi-layered. If a farmer chooses to transition from farrowing crates to an alternative system they will first decide should I retrofit an existing building or new build? The latter is likely to be the optimum choice, as space per sow place (square meters) should increase given the mismatch between conventional crates and the minimal spatial footprint they occupy and the size of modern hyperprolific sows and litters. In contrast to a farrowing crate which is designed for the sow not to be able to turn around, pens for free farrowing and for temporary crating must allow space for the sows to turn-around. The area needed depends on sow dimensions and how they dynamically move. Retrofitting a barn will require reducing the herd size to facilitate these basic requirements and is unlikely to be a long-term cost effective strategy.

There are then specific decisions about the type of system and the fixtures and fittings within it that can impact on animal welfare, performance, as well as management routines and overall efficiency. Deciding on that minimum space is undoubtedly important but quality of space is equally important including details of design that can promote good maternal behaviors, good hygiene and facilitate efficient and safe working routines. This presentation has attempted to synthesise the latest evidence base with important practical insights from early-adopters of non-crate systems that will help farmers, industry stakeholders and policy makers navigate the transition process from crates to 'free' farrowing and inform the key decisions and choices required.

I3
Weaknesses, limits, biases and strengths of LCA applied to livestock systems

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Over the years, the request for consistent and widely accepted methods to quantify the environmental impact of the different production processes has grown. Several methods, tools and approaches were developed; among these, the Life Cycle Assessment (LCA) is the most adopted. The LCA approach allows a holistic assessment of the potential environmental impact of products, processes and services. Defined by two specific ISO standards (14040 and 14044) as well as by specific guidelines (e.g. Product Category Rules and Product Environmental Footprint category Rules), LCA is increasingly applied also to the agricultural sector, despite this method was originally developed for industrial processes where the quantification of the inputs and outputs characterising the production processes is more straightforward. This poses additional challenges considering that in agricultural processes a detailed mapping of the consumed production factors as well as of the pollutant emissions into the environment could be problematic, in particular for small farms and small producers.

Among the different agricultural production chains, the livestock ones are the most investigated with LCA. This is mainly related to the higher environmental impact of animal products with respect to vegetable ones. Despite this wide application to different livestock products (dairy, pig, poultry, small ruminants, aquaculture, insects, heliciculture) as well as to different rearing systems (e.g.

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conventional vs organic, intensive vs extensive), the LCA application to the livestock sector presents several weaknesses and limits. Some of these are intrinsically related to the LCA approach but some others are specifically related to the livestock sector.
About the weaknesses and limits intrinsically related to the LCA approach the following aspects should be considered:

- having been originally developed to evaluate the environmental performances of industrial processes, LCA is well designed and can be easily adopted to assess production systems characterised by a clear relationship between the consumption of production factors and productivity. This only rarely applies to agricultural production and, in particular, to livestock production.
- LCA relies heavily on the availability of quality data across the entire life cycle. Incomplete, outdated, or poorly representative and/or localised data can lead to inaccurate results. The availability of representative data is not only a time and money demanding activity but sometimes it can turn out to be the immovable obstacle that prevents the execution of the study. LCA is based on data and consequently, in case of lack of data some peculiar aspects cannot be evaluated. This lack can refer to inventory data (e.g. variation of enteric methane emissions due to changes in the diet) or to characterisation factors (e.g. for antibiotics) but in any case it can be solved only with additional research efforts.
- Environmental impacts can vary significantly over time and across different geographical locations. LCA often struggles to capture adequately the temporal and spatial variability. Besides this, historical data may not accurately reflect current practices or technological advancements, potentially leading to outdated conclusions.

Regarding the LCA application to the livestock systems the main weaknesses and limits are:

- Livestock systems often serve multiple functions beyond food production, including nutrient cycling, maintenance of soil fertility, and social and cultural roles. Evaluating all these functions is crucial for a comprehensive assessment. Nevertheless, solving multifunctionality can require additional data and could introduce subjectivity and arbitrariness while reducing the comparability of the achieved results.
- Some environmental impacts related to livestock activities are only roughly evaluated. For example, even if the impact of livestock systems on land use change, habitat loss, and biodiversity is significant, their assessment is still an unsolved issue in LCA. Other environmental effects related to livestock such as olfactory nuisance are not directly assessed and the odor impact can only partially be appreciated because some of the responsible substances also affect other environmental effects (e.g. NMVOC).
- Ecosystem services and animal welfare are not directly considered in LCA, they can be appreciated only if they directly affect the productive performance of the system. Otherwise, their appreciation is related to the adoption of additional tools and assessment methodologies.
- Despite the huge and continuous efforts of the LCA community, most of the LCA studies focused on livestock systems select mass-based functional units and, in this way, can only sparely evaluate the quality of the produced food.

Despite the above-mentioned limitations, the LCA represents a powerful and irreplaceable approach to evaluating the environmental sustainability of the livestock sector. In fact, this approach presents also several strengths, among which the most interesting is that with the same dataset it allows the quantification of different environmental effects and the identification of trade-off among them.
Furthermore, in all the agricultural sectors and, consequently, also in the livestock one, the adoption of innovative practices and technologies (e.g. precision feeding, manure management systems) can greatly affect environmental performance. In particular when the LCA application refers to the assessment of technical solutions, the study outcomes can be a reliable and valuable starting point for science-based choices that bring towards the realisation of sustainable rearing systems. In this context, the aim of this contribution is to present concrete examples of the application of LCA to various technological mitigation strategies adopted in livestock systems. These case studies are intended to highlight not only the methodological challenges and limitations encountered during the environmental assessment, but also the strengths and added value that LCA can provide in this specific context. The analysis will explore how LCA has been employed to evaluate the environmental benefits of a range of innovative solutions—such as emission reduction systems during animal rearing and manure management, precision feeding and milking techniques, and novel approaches to the design and operation of livestock facilities. By critically discussing these examples, the contribution seeks to demonstrate the potential of LCA as a robust tool to guide the development of more sustainable livestock systems. Ultimately, it underscores the relevance of LCA-based evidence in supporting informed decision-making by both practitioners and policymakers, fostering continuous improvement in the sector's environmental performance.

I4

Progress towards reasonably-precise livestock farming in the dairy sector

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It is considerably more than a decade since Daniel Berckmans coined the phrase Precision Livestock Farming (PLF) to

encapsulate the use of sensors and smart technology to assist livestock management. His concept envisaged that uniform management resulted in the majority of animals operating suboptimally, but PLF would be able to 'tweak' management on an individual basis to address that. Time has moved on. Have we achieved the goal of personalised and optimised precision management? Sensors are now in widespread use not only for reproductive management but also for health and welfare improvement. Feeding is more sophisticted than it was. But to phrase the question a different way, is there still considerable variability between animals, with some operating more efficiently than others? I would contend that there undoubtedly is! Indeed I would go further and say that the goal of precision was at best overstated and at worst counterproductive, because it was (and is) unachievable. My preferred vision is of 'CALM' farming, that is to say Computing Assisted Livestock Management, by which I mean the use of the same sensors and technologies to identify the individual cow(s) that are in most need of focused husbandry and provide the information about them that will allow the stockman or veterinarian to make the appropriate management decision. Rather than 'precision' this might be thought of as 'very best guess' and, importantly, the outcome is generated by a skilled individual, not by what has come to be known as Artificial Intelligence, AI. Furthermore, the route it takes to improved productivity/profitabilty is through imnproved health/wellbeing, so both farmer and animal benefit. In my view, we have come a long way towards that goal, and in a research sense most of the required capabilities are in place. Sensors are available to monitor many aspects of animal behaviour and performance, including numerous health and wellbeing related traits such as drinking, eating, ruminating and more. The factors that limit more widespread adoption of PLF/CALM are primarily at the commercial level rather than technological: to achieve a holistic approach one would need to combine data from several manufacturers, and for obvious reasons that is an exercise fraught with difficulty. Meanwhile, back at the research level the technologists are moving from 'jewellery' (ie small sensors worn by individual animals) to 'ambient sensing', primarily barn-level video analytics that dissect the individual from the group, discriminating between those behaving 'normally' and those not. The presumption is that such systems will be cheaper to implement since one requires only one or a few video cameras per barn versus at least one sensor per animal. This may be false economy: a basic accelerometer (the technology at the heart of many sensors) costs cents rather than euros to produce, and most of the cost of sensor technologies is associated with the software development and data crunching elements (which are most probably greater in ambient sensing) rather than the hardware. Whatever the tool, adoption requires a business decision by the farmer, and in this regard there is a problem. Farmers have invested in reproductive management sensors not because they are convinced by the economic *cost* of culling barren cows (culling is often associated with necessary genetic progress) but because they have been indoctrinated into believing in the economic *value* of a short calving interval. Whether that is right or wrong, they have invested. For health, the reverse scenario applies. Consider mastitis. From the farmers perspective, the *cost* is temporary lost milk and inconvenience, whereas the *value* of good health is an unknown. PLF/CALM developed reasonably quickly, but could have done so much more rapidly if animal scientists and computer/electronic engineers had learned to speak each other's language sooner. Having said that we have made good progress towards *reasonably precise* management, my hope is that we shall soon also learn to speak the same langauge as economists, so that as a tripartite we can get it over the line.

15

Omics data are compositional. The problem and its solution

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Compositional data (e.g. metagenomic data) come from non-negative variables expressed as proportions that add up to 1. In compositional data, when a subset of variables is extracted and re-expressed as proportions that add up to 1, the relationships between the variables change, the correlations between them are no longer the same as in the full database; we say that there is no sub-compositional coherence. To avoid the aforementioned problems, compositional data is analysed as ratios, which do not present these problems. The logarithm of the ratio is used so that the data are on the real line, avoiding percentages, and the distributions are also more symmetrical. With p compositional variables, the 'full space' is defined by all the possible $p(p–1)/2$ log-ratios, but as in metagenomics there is an enormous number of variables, subsets of fewer dimensions trying to represent the full space are used. The simplest and least recommended, which is the one we will use, is the additive log-ratio (ALR), where the variables x_i are represented with respect to a reference variable: $\log(x_i/x_{REF})$. Another alternative (CLR) is to use the geometric mean G of the variables within each sample as a reference $\log(x_i/G)$, thus centring the $\log(x_i)$, and another alternative (ILR) is to use geometric means of subsets of variables $\log(G_i/G_k)$, called 'balances'. These alternatives use $p–1$ or p log-ratios, much less than the $p(p–1)/2$ log-ratios of the full space. The CLR is isometric to the 'full space', it preserves the distances between variables, but it has no subcompositional coherence because each subset of variables has a different G. The ILR is isometric and has subcompositional coherence, but the balances are very difficult to interpret. The ALR has some advantages. If we choose an x_{REF} having very little variability between individuals in the sample, comparing two $\log(x_i/x_{REF})$ is almost like comparing two $\log(x_i)$, something easier to interpret. The geometric mean G of the CLR is much more variable between individuals and that is

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why the CLR is not as easy to interpret. However, the ALR is not recommended because it is not isometric with respect to the 'full space' of all the possible $p(p-1)/2$ log-ratios and the result depends on the x_{REF} selected. However, if we project the reduced space of the ALR created with an x_{REF} having very little variability onto the 'full space', using Procrustes analysis, we can find that the correlation of the coordinates of the individuals in both spaces is close to 1, therefore the two spaces have a similar geometry, and ALR is approximately isometric. In metagenomics, we find microorganisms with similar abundances in all individuals, and there are so many microorganisms that we are likely to find one that varies little between individuals and that simultaneously gives rise to a high Procrustes correlation between the coordinates of individuals in ALR and the full space. This is exactly what we have done; we have taken several metagenomic databases from different sources and for all of them we have found several possible variables that are candidates for reference variables, which allow us to work in a space that has subcompositional coherence and is approximately isometric, but with variables that are much easier to interpret. Once we have carried out the analysis with ALR, we face a new problem: metagenomic data usually has a large number of zeros. This may be due to a sequencing error, but more often than not it is because there are no such microorganisms in a particular individual, or in so low abundance that they cannot be detected. In any case, we cannot work with log ratios when there are zeros or with quotients when there are zeros in the denominator. By trying to solve the problem of compositional data we have created a new problem. Fortunately, we can prove that subcompositions expressed in proportions, are not that incoherent when the number of parts of the subcomposition is very large, as it happens in –omics data, and therefore we do not need ratios or log-ratios. We can analyse the proportions in their current form, including all the zeroes.

The problem of subcompositional coherence arises with -omics data, for example in metagenomics, where the number of microorganisms quantified in a sample can vary depending on the quality of the reference databases used to process the DNA. These databases are in continuous expansion as new microbial species are discovered. What we have done is to take a full file F with abundance data for many microorganisms and generate another reduced file R containing only 1/3 of the microorganisms from the previous one in the same individuals, taken them at random but weighing their abundance in the original file. With this we intend to simulate a realistic situation, in which a researcher starts his work with a file like R, but due to the improvement of the reference data bases, she introduces new bacteria until she arrives at the much larger file F. If we calculate the Pearson correlations between the variables in the F and R files, and the coefficient of concordance between variables, both are close to 1, indicating that the relative proportions of the variables are barely affected and we have approximate subcompositional coherence. Furthermore, projecting the R file onto the F file with a Procrustes analysis, the Procrustes correlations between the coordinates of the points are close to unity, and the Euclidean distances between variables in the F and R files are also preserved. Finally, a number of common analyses on the microbiome, such as Alpha diversity, PLS, PCA, Random Forest, Alpha diversity or M-BLUP give the same results in the F and R files.

These conclusions only apply to omics data, where a large number of variables are handled, so the problem of compositionality is diluted. It does not apply to other cases, such as fatty acid analysis or the relative composition of samples with few components. Some technicalities remain, such as the problem of having highly asymmetric variables (abundances), but this may be of little relevance when comparing means if sufficient data are available (the distribution of the mean is normal even if the original data are not), or it can be solved by other transformations that allow working with zeros.

I6

Advances and trends in measuring animal product quality linking sustainability and husbandry systems

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The global demand for food of animal origin is projected to rise by 20–30% within the next decade, primarily driven by population growth and changing dietary preferences. This will likely result in the intensification of livestock production systems worldwide. However, the expansion of animal agriculture raises major concerns. These include environmental impacts such as greenhouse gas emissions, eutrophication, and excessive resource use; ethical issues concerning animal welfare in production, transport, and slaughter; and public health risks linked to nutritional meat quality and chronic disease incidence. In response, institutions like the FAO and WHO advocate for rebalancing protein intake between plant and animal sources (targeting a 50:50 split), whereas current Western diets in Europe derive about 65–70% of protein from animal sources.

European consumption of animal products has plateaued or declined, except for poultry. This shift coincides with the European Green Deal's 'Farm to Fork' strategy, which promotes more plant-based diets and aims to reduce red and processed meat intake. Simultaneously, there is a rising consumer demand for ethically produced, environmentally responsible, and higher-quality animal products. Livestock production systems vary widely in their environmental footprints, welfare standards, and

product quality, which influence consumer perception, health outcomes, and market value. Consequently, the livestock sector is under increasing pressure to transition towards more sustainable and welfare-friendly practices, including the growth of organic farming (with a goal of 25% of EU farmland under organic management by 2030), reduced use of confinement and synthetic inputs, and increased reliance on outdoor access, biodiversity, and natural processes.

Despite current trends, robust scientific evidence remains lacking on the sustainability and intrinsic quality of animal products across different husbandry systems. There is a clear need to better assess and communicate the safety, nutritional value, sensory qualities, and ethical attributes of animal-sourced foods to support consumer choice, reduce food fraud, and inform policy. The INTAQT (INTegrity of food of Animal origin through a Quality Transition) project explores how livestock husbandry practices influence the intrinsic quality of animal products through a comprehensive, multi-criteria, science-based assessment. The project embraces the concept of 'One Quality' which integrates product quality with sustainability and ethical considerations.

INTAQT investigates beef, chicken, and dairy products from a broad spectrum of European husbandry systems, ranging from extensive (e.g. pasture-based) to intensive models. It adopts a participatory, multi-actor approach involving stakeholders from across the agri-food chain—including farmers, advisors, breeders, processors, retailers, scientists, certification bodies, and consumers. The project pursues four main objectives (1) develop models that quantify the impact of husbandry systems on key product quality traits (safety, nutrition, sensory attributes). (2) Co-create rapid, cost-effective analytical tools to predict intrinsic product quality and authenticate husbandry systems and animal genotypes. (3) Co-develop multi-criteria scoring systems to evaluate and compare product quality traits. (4) Promote and validate husbandry practices that consistently deliver high-quality, safe, healthy, and appealing animal-sourced foods aligned with both consumer expectations and sustainability goals. In addressing these aims, INTAQT contributes to the transformation of European livestock production toward systems that are productive, sustainable, ethical, and in line with modern societal values. This paper will focus on output from the INTAQT project. Specifically, the role of rapid technology in livestock systems in addition to how emerging tools and methods can help measure and improve sustainability will be explored.

INTAQT is investigating cutting edge, rapid technology to assess meat quality (beef and chicken) and differentiate parameters such as production system, lipids, sensory quality and Meat Standards Australia (MSA) assessment. Rapid Evaporative Ionisation Mass Spectrometry (REIMS) is a very sensitive, ambient technique that requires minimal sample preparation. REIMS produces a chemical fingerprint if ionised compounds within a sample which is analysed in real time. The output from REIMS can be used to develop chemometric models by utilising calibration and cross-validation datasets to predict various production parameters. The use of REIMS to assess and discriminate the quality of meat products is a rapidly growing sub field in 'omics' technology. Beef samples ($n = 518$), from five countries (France, Spain, Switzerland, Italy and the United Kingdom) and spanning across a gradient of five production systems have been analysed using REIMS and chemometric models have been developed from the output.

Another dimension of the INTAQT project is advancing the ability to measure the sustainability of livestock production systems. Sustainability in livestock production systems involves balancing the three interconnected pillars: environmental (GHG emissions, land and water use and biodiversity), economic, and social (public health, food security). Livestock systems are complex and vary widely in their impact across these dimensions, which is why robust, science-based assessment tools for measurement are essential. The INTAQT project advances sustainability measurement by integrating these pillars into its evaluations. One way in which sustainability is being assessed is through the measurement of Nutritional Life Cycle Assessment (nLCA). Synthesising data from farm, pre- and post-slaughter and meat quality, nLCA integrates the nutritional value of food products with environmental impact, assessing sustainability through both health outcomes and resource use. Unlike traditional Life Cycle Assessment (LCA), which typically uses mass based functional units to express carbon footprint (e.g. kg C02e/kg of liveweight/deadweight), nLCA focuses on nutritional functional units to express nutritional density, such as omega-3 PUFA, protein content, protein quality (e.g. Digestible Indispensable Amino Acid Scores) and Nutrient Density Scores (NDS) per unit of product. This allows for a more holistic approach to evaluating sustainability in food production.

As global demand for animal-sourced foods rises, addressing the environmental, social, and economic challenges of livestock production is of increasing importance. The INTAQT project advances how we assess and improve these systems through rapid technologies like REIMS and holistic sustainability measurement tools such as nLCA. These innovations support the shift toward transparent, sustainable, and ethically aligned food systems, helping consumers, producers, and policymakers make more informed decisions.

17

Fatty acids beyond milk nutritional quality

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In recent decades, milk fatty acids have received a great deal of research attention due to their key role determining the

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nutritional quality of milk fat. The search for healthier animal-derived foods (i.e. richer in potentially health-promoting compounds for human consumers) has been one of the main drivers for the improvement of our knowledge on the fatty acid composition of the milk and of the digestive content (ruminal, omasal and duodenal) of dairy ruminants. However, although it is now recognised that there is a direct link between milk fat consumption and human health (mainly in relation to the presence of bioactive compounds), fatty acids are of great interest for animal scientists beyond the quality of final products. Firstly, fatty acids play a fundamental role as energy sources for the lactating (and non-lactating) ruminant. Secondly, some fatty acids are known to have biological effects not only on human consumers but also on the host animal (e.g. conjugated linoleic acids). Third, some milk fatty acids serve as biomarkers with application in research (e.g. to advance our knowledge of the ruminal environment and body metabolism) and in the dairy sector (e.g. as indicators of traits of interest in breeding programs).

For this invited talk we will combine results from both the literature and from our research projects to summarise the state-of-the-art about the relationship between the fatty acid composition of milk and digesta and certain productive traits or metabolic characteristics of dairy ruminants and their ruminal microbiota. An example is the relationship between fatty acids and feed efficiency. The latter is a complex phenotype with physiological mechanisms that have yet to be unraveled, but data suggest that milk and digesta fatty acids might be proxies for discriminating the most efficient animals. In this regard, some studies in sheep and cattle suggest that a greater extent of ruminal biohydrogenation could be related to a higher efficiency of feed utilisation, probably due to the role of biohydrogenation as a detoxification mechanism for microbiota. Nevertheless, further research would be needed to validate this link between biohydrogenation and feed efficiency under different conditions (e.g. basal diet, moment of lactation, etc.), which might contribute to explain the inconsistent results found in other studies. In addition, greater biohydrogenation extent would decrease the rumen outflow of unsaturated fatty acids and detrimentally affect their content in milk, leading to a contradiction between recommendations to improve feed efficiency and milk fat quality. To face the challenge posed by this contradiction, the knowledge gained over the last decades about biohydrogenation-induced milk fat depression might be useful. This syndrome may indeed be considered a valuable model to understand feed (in)efficiency and the relationship between this condition and milk fatty acid composition. Furthermore, it should be noted that ruminal biohydrogenation represents a rich source of fatty acids with potential implications for animal performance or health that are still poorly characterised (e.g. hydroxy- and oxo-fatty acids, conjugated linolenic acids, or minor *trans* fatty acids). Unfortunately, the advances in chromatographic techniques for the separation of fatty acids have not always been accompanied by the publication of more detailed lipid profiles because the attention is often focused on fatty acids with confirmed activity, excluding other fatty acids with unknown or unclear effects at the time. Further research would be needed to improve our knowledge of the biological effects of certain fatty acids present in milk fat, but uncommon in other foods, or commercially unavailable in pure form.

Among the most characteristic lipids in ruminant milk fat are the odd- and branched-chain fatty acids. These fatty acids are largely derived from cell membranes of bacteria leaving the rumen and have therefore been examined as non-invasive markers of the rumen bacterial community and, by extension, of rumen function. This has encouraged research to characterise milk odd- and branched-chain fatty acids responses to changes in diet composition, their use as predictors of rumen microbial protein synthesis, or the relationship between their content in milk and physiological factors of the host animal (e.g. lactation stage and parity), among others. Furthermore, the use of milk fatty acids as biomarkers of ruminal methane emissions has also gained interest in the last years. A review of the literature about this topic suggests that prediction models could be highly dependent on the level of detail of milk fatty acid analysis. Most studies only identify major milk fatty acids, without no evident scientific basis to exclude other compounds. In fact, in publications where detailed lipid characterisation was conducted, equations usually contain minor biohydrogenation metabolites (e.g. *cis*-13 18:1, *cis*-15 18:1 or *trans*-11 *cis*-15 18:2), which highlights the relevance of avoiding oversimplified milk fatty acid profiles in scientific publications. Even if not all fatty acids seem of interest for the objective of a specific study, reporting lipid profiles that are as complete as possible contributes to improve the overall quality of the fatty acid-related literature, making it more adequate for future meta-analysis, modeling and retrospective studies. Finally, regarding the relationship between fatty acids and resilience, it is worth mentioning that to date there are still few studies available. In addition, published results are not always promising. In our research team we have investigated the resilience of dairy sheep to nutritional challenges, specifically feed restriction. These types of challenges are expected to increase in frequency and severity in the coming years (due to climate change and feed supply crises), but although we have observed that they induce very dynamic responses in fatty acid composition (and in other lipid biomarkers of the rumen microbiota, such as dimethylacetals), it is unclear to what extent they may be indicative of individual differences in animal resilience.

Overall, the relevance of milk fatty acids in animal science goes beyond their role in determining the nutritional quality of milk. In some cases, however, their usefulness is not yet clear, as research is still at a preliminary stage. Targeted research on these issues could certainly help to advance our knowledge faster. In addition, a greater methodological effort to report more detailed fatty acid profiles (including compounds that a priori are not necessary for the specific purpose of a given study) would also be beneficial to provide information that can be useful in the future (e. g., for develope or validate prediction models).

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18

Impact of oxidation and inflammation on poultry health and productivity

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Oxidation can damage the nutrient quality of poultry diets, impiar the productivity of the birds, and decrease the nutritional, health and organoleptic qualities of poultry products. Biological oxidation as it relates to animal feeding and nutrition refers to the damage associated with the generation of free radicals—unpaired electrons that are reactive to other molecules. Lipid peroxidation typically occurs when a carbon-carbon double bond in a fatty acid degrades to generate a free radical, thus damaging the fatty acid. The free radical molecule is highly unstable, and the damaged fatty acid containing the unpaired electron seeks to obtain an electron from another molecule. The radical then reacts with a second molecule, leaving a damaged original molecule, and a new, also unstable radical molecule, which in turn seeks to react with an additional molecule. In this way, a chain reaction of oxidative damage occurs, until the unpaired electron reacts with an antioxidant, a molecule capable of donating an electron or absorbing the unpaired electron while itself remaining stable.

Dietary fats and oils are susceptible to oxidation. The highly unsaturated nature of the fatty acids in some oils such as corn oil, soybean oil, canola oil, sunflower oil and fish oil make them particularly susceptible to oxidation. The high number of C-C double bonds in the fatty acid chains of highly unsaturated oils are prone to the development and propagation of free radicals. In feeds, free radicals generated primarily from lipid oxidation can participate in chain reactions that damage other lipid molecules, as well as proteins and vitamins, thus reducing the nutritive quality of the feed. In the body, free radicals can arise as a byproduct of normal energy metabolism and immune cell activity, as well as from consumption of oxidatively damaged lipids. Lipid membranes are particularly susceptible to oxidative damage, as are other biological molecules such as DNA, proteins and vitamins. Additionally, the free radicals and damaged nutrients can be absorbed from the feed and have deleterious effects on the productivity and health of the animal, and on the quality of the products. In the body, antioxidant molecules help to mitigate the negative effects of oxidation, and optimal health requires a balance of antioxidant function and free radical generation. Proper antioxidant protection is necessary to limit the damage caused by pro-oxidant molecules in the body. Therefore, it is critical to minimise oxidative stresses induced by the feed, and provide antioxidant protection to the tissues of the animal. Heat stress increases the generation of free radicals and increases the demand for antioxidant nutrients. Heat stress causes alterations in intestinal barrier function, leading to increased bacterial translocation and inflammation. The inflammatory immune response involves the generation of pro-oxidant molecules used by innate immune cells to kill invading pathogens. Increased oxidation in muscles increases the incidence of myopathies such as woody breast and white striping defects, which reduces meat quality. Incorporation of high levels of polyunsaturated fatty acids, as well as oxidatively damaged fatty acids into adipose and muscle tissues can decrease shelf life and increase the occurrence of off-flavours in poultry meat and eggs. Generally, the antioxidants that are most effective for preventing in-feed oxidation are different than those most effective at preventing in the vivo oxidation that reduces productivity and product quality. In-feed antioxidants tend to be based on compounds having one or more phenol groups. Examples of synthetic in-feed antioxidants include ethoxyquin, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), tertiary butylhydroquinone (TBHQ) and propyl gallate (PG). Natural antioxidants are also usually based on a phenol group and include, but are not limited to, tannins, phenolic acids, chlorogenic acids, flavonoids, lignans and stilbenes. Some nutrients contribute to antioxidant function within the body of the animal through their roles in antioxidant enzymes and systems, such as copper, zinc, manganese, selenium, vitamin A, vitamin E and vitamin C. These antioxidant nutrients are usually ineffective at preventing in-feed oxidation, and may in fact have pro-oxidant activity in the feed. Generally, the antioxidant nutrients are most effective in vivo, whereas the phenolic-based natural and synthetic antioxidants are more effective in feed. However, although the antioxidants with protective effects in feed, may also be active in the digestive tract and in addition may have carry-over effects to the animal itself. Vitamin E is a potent phenol-based in vivo antioxidant, that is sometimes used to stabilise feed, although it is much less effective than the synthetic antioxidants. There is some redundancy of antioxidant function, in that in some cases, low intake of an antioxidant nutrient can be compensated by increased intake of another antioxidant nutrient.

Oxidation is a major concern for the poultry industry. Effective control of oxidation can increase poultry performance, health, and the wholesomeness and healthfulness of poultry products. Effective control of oxidation involves a knowledge of the susceptibility of feed ingredients to oxidation, and strategic selection of products to mitigate both in-feed and *in vivo* oxidation. It is critical to recognise that the products that are most effective in preventing oxidative damage to the feed and those effective in preventing oxidative damage in the body of the bird and in poultry products will likely be different. Therefore, an integrated approach to control oxidation before and after the feed is consumed.

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19

Elucidating the biology of heat stress in lactating sows at the intersection of genome microbiome and metabolome

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Heat stress presents a substantial economic challenge for the agricultural sector, particularly in livestock production. As production demands escalate, pigs—especially lactating sows—become increasingly susceptible to heat-related stress. This vulnerability is largely due to elevated metabolic heat loads from growth demands, larger litter sizes, and lactation. Notably, the observed individual variability in heat stress responses suggests that genetic background may play a critical role in determining how sows cope with these challenges. Body temperature, changes in behavior related to feed and water intake, the amount of time spent lying or standing, and other coping mechanisms such as panting are typically used as phenotypic indicators of heat stress. Biochemical biomarkers such as cytokines or heat stress proteins in plasma can also be used to identify stress conditions. In several species, research has highlighted how heat stress induces changes in gut microbial communities related to structural composition, metabolic function, and metabolites. The overarching goal of our research is to understand how pigs' hologenome regulates and responds to heat stress, both to select for more tolerant individuals and to identify potential biomarkers for selection and management.

In this study, we investigated the relationship between genetic background and the gut microbiome's response to heat stress in lactating sows. We performed metagenomic, metatranscriptomic, and metametabolomic analyses of the gastrointestinal tract of 25 multiparous lactating sows, genetically divergent for heat tolerance, and divided into two groups: heat-tolerant (HT, $n = 13$) and heat-susceptible (HS, $n = 12$). The sows were housed in farrowing crates within environmental chambers and exposed to cyclic heat waves. Sampling occurred at three time points: (T1) trial beginning, (T2) mid-trial, and (T3) end of trial. Bioinformatics and quality control (QC) were performed using ATLAS HUMANN 3.0 for metagenome analysis and XCMS for metatranscriptome and metametabolome analysis. Our analysis identified 835 metagenome-assembled genomes (MAGs) and 7,383,614 genes linked to 399 KEGG-annotated modules. Alpha diversity values for HT and HS sows were as follows: 4.93 (HT) and 4.97 (HS) at T1, 5.17 (HT) and 4.95 (HS) at T2, and 5.35 (HT) and 5.04 (HS) at T3. PERMANOVA analysis revealed a significant effect of time × genetic background ($p < 0.01$). Principal coordinates analysis (PCoA) on beta diversity and canonical correspondence analysis (CCA) separated groups according to time and genetic background. Differential abundance analysis revealed significant changes in 217 MAGs from T1 to T3, with 67 MAGs showing significant contrasts between sampling stages and genetic backgrounds: 14 at T1, 7 at T2, and 46 at T3. Significant MAGs belonged to the genera Bacillota, Bacteroidota, Spirochetota, Campylobacteriota, and Verrucomicrobiota. Notably, significant MAGs that were over-represented in HT individuals were associated with short-chain fatty acid (SCFA) production. These compounds are known to have anti-inflammatory effects, improve gut barrier function, and serve as stress buffers. Conversely, HS individuals were enriched in MAGs responsible for immune modulation (pro-inflammatory). Additional MAGs were associated with gut permeability. When considering genes and metabolic pathways, HT pigs showed higher metabolic capacity for cysteine and lysine biosynthesis, pathways related to antioxidant capabilities, and heat shock protein synthesis. Among the 9,942 detected metabolites, 143 showed significant differences, with 105 metabolites upregulated and 38 downregulated in HT pigs. Key findings include elevated levels of nitenpyram, all-trans decaprenyl diphosphate, Asp–Asp, and N-pentadecanoyl-L-homoserine lactone in HT pigs, indicating changes in energy metabolism, protein turnover, and gut microbiome dynamics. Principal component analysis (PCA) and orthogonal partial least squares discriminant analysis (OPLS-DA) revealed distinct clustering between HT and HS groups, with heat stress driving significant metabolic divergence. Hierarchical clustering across time points demonstrated sustained gut microbiome and metabolomic shifts in HT pigs and adaptive metabolic responses (e.g. alpha,alpha'-Trehalose 6-palmitate). Pathway analysis identified upregulated processes in HT pigs, including glycerophospholipid metabolism, fatty acid elongation, and linoleic acid metabolism, while pathways such as sphingolipid metabolism and insulin resistance were downregulated. Heat stress influenced lipid remodeling, emphasising glycerophospholipid metabolism as a critical adaptive mechanism for maintaining membrane stability. These findings underscore the potential influence of genetic background on microbiome responses to heat stress, highlighting pathways for future research aimed at improving heat tolerance in pigs. This work is supported by the foundational and applied science program, project awards 2020-67015-315375, 2022-67015-30319 and 2023-67015-39563 from the U.S. Department of Agriculture's National Institute of Food and Agriculture.

I10

Precision Livestock Farming: from theory to practice

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Precision Livestock Farming (PLF) is a rapidly emerging interdisciplinary field that integrates animal science, data analytics, engineering, and information technology to optimise livestock management through real-time monitoring and automated decision-making. Initially conceptualised in the early 2000s as an extension of Precision Agriculture, PLF aimed to enhance productivity, animal health, and welfare while minimising environmental impact and reducing labor costs. Over the last two decades, the theory of PLF has evolved significantly, and its transition to practical applications is gaining momentum globally. However, the journey from theory to practice remains complex, necessitating a deeper understanding of technological, biological, socio-economic, and ethical dimensions.

At the core of PLF are sensor technologies and data-driven tools designed to capture and analyze behavioral, physiological, and environmental parameters of livestock in real-time. Wearable sensors, video imaging systems, RFID tags, accelerometers, thermal cameras, and IoT-enabled devices allow continuous and non-invasive monitoring of individual animals. Data collected through these means is processed using advanced algorithms, artificial intelligence (AI), and machine learning (ML) to detect anomalies, predict disease outbreaks, optimise feeding regimens, manage reproduction, and support welfare assessments.

From a theoretical standpoint, PLF is grounded in the concept of the '4Rs'—providing the right treatment, to the right animal, at the right time, and in the right way. This principle has informed the development of dynamic models for precision feeding, automated milking systems, early disease detection (e.g. mastitis, lameness), and behavior-based welfare assessment tools. The integration of digital twins—virtual representations of physical livestock—further enhances predictive capabilities, allowing farmers to simulate various management scenarios and assess their impact before implementation.

Despite the promising theoretical frameworks, the practical implementation of PLF faces several barriers. These include high initial investment costs, limited digital infrastructure in rural areas, data ownership and interoperability challenges, and resistance to change among traditional farmers. Moreover, the reliability and accuracy of some sensor systems in field conditions vary significantly, affecting trust and adoption rates. Ethical concerns related to animal surveillance, data privacy, and potential job displacement due to automation also warrant critical reflection.

In practice, the adoption of PLF is uneven across livestock sectors and geographies. The dairy industry has been a frontrunner, particularly in high-income countries, with widespread use of automatic milking systems (AMS), estrus detection sensors, and health monitoring collars. In contrast, the pig and poultry sectors have seen slower uptake, although innovations like environmental control systems, camera-based weight estimation, and sound-based respiratory health monitoring are gaining traction. Recent efforts to apply PLF in extensive systems, such as pasture-based beef and sheep production, are also expanding, supported by GPS tracking and satellite-based monitoring tools.

One of the key success factors in translating PLF theory into practice is stakeholder collaboration. Multi-actor innovation platforms, involving farmers, researchers, technology providers, veterinarians, and policymakers, are instrumental in co-designing user-friendly and cost-effective solutions. Additionally, education and training programs tailored to different user groups can bridge knowledge gaps and foster digital literacy in the livestock sector.

From a research perspective, PLF offers immense potential to generate new insights into animal behavior, welfare, and physiology. It enables longitudinal studies at individual animal levels, contributing to precision phenotyping and genomics. Furthermore, real-time data analytics supports proactive management strategies, shifting the paradigm from reactive to preventive livestock farming.

Looking ahead, the convergence of PLF with other technologies such as blockchain, 5G connectivity, robotics, and edge computing is poised to transform livestock systems into smart, sustainable, and resilient enterprises. Policymakers and funding agencies are increasingly recognising the role of PLF in achieving food security, climate goals, and animal welfare standards, thus encouraging further investment and regulatory frameworks.

In conclusion, Precision Livestock Farming is not merely a technological advancement but a paradigm shift in how livestock are managed, monitored, and understood. While theoretical foundations are well-established, scaling PLF from pilot projects to mainstream agricultural practice requires integrated strategies that address technical, economic, social, and ethical challenges. By fostering collaboration across disciplines and sectors, and by focusing on farmer-centric innovations, PLF can fulfill its promise of transforming livestock farming into a more sustainable, efficient, and humane system.

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I11

The evolution of the concept of animal welfare: from absence of suffering to positive welfare and beyond

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The first animal welfare laws, dating from the 19 th century, focused on the need to ban cruelty against animals. During the second half of 20 th century, the absence of suffering was the main driver for animal welfare (see for instance the Brambell report). Measures were taken at European level (by the Council of Europe and the European Union) to prevent animal suffering. For instance, small individual crates were banned for calves and stunning was made compulsory at slaughter. Again, the five freedoms insist on the negative aspects that must be avoided: they state that animals must be fed in a way to avoid hunger, that injuries, diseases or distress must be avoided, and that animals must be able to express certain behaviours. At that time, some authors indicated that welfare is more complex than absence of cruelty and suffering, and that the motivations of animals must be taken into account. More recently, it was argued that animals can also enjoy positive experiences, such as comfort, pleasure, and joy. The concept of positive animal welfare has been recently proposed to capture a state where positive experiences predominate. But is the valence of the environment –the fact that positive stimuli (e.g. good food, comfortable lying area) predominate over negative ones (e.g. painful stimuli, removal of preferred partners)—enough to determine welfare? We argue that valence but also complexity of the environment and the possibility to act purposefully play also a role in determining welfare. Animals display signs of boredom when maintained in unchanging environments, even if they fulfill their basic needs. By contrast, they express and develop agency in environments offering possibilities to act efficiently. While valence of the environment is essential to ensure good welfare, it may be insufficient if the environment does not offer complexity and possibility to act. For the latter two notions, however, there might be optimal values, depending on the animal's capacities and motivation to process complex information and to act on its environment. We will revisit the literature on animal welfare and mental states along these lines to propose a new approach to animal welfare.

I12

Future challenges and welfare in forage feeding for sport horses

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Due to its nutritional characteristics, the horse is adapted to the continuous intake of small amounts of forage. During 24-hour pasturing or hay feeding *ad libitum*, horses show numerous feeding periods (10–15) within a day, and periods without feed intake do not last longer than 3–4 h. To cover the specific need to chew and to ensure physiological conditions in the gastrointestinal tract, a minimum amount of forage of 1.5–2 kg dry matter (DM) per 100 kg body weight (BW) per day is recommended in performance horses. However, due to dryness with high ambient temperatures or numerous rainfalls already at the beginning of the main vegetation period in spring, a shortage of forage is an increasing issue of concern in horse nutrition. In consequence climatic changes demand forage alternatives for sport horses.
Reduce nutrient losses by harvesting! Forage production relies directly on weather conditions, being particularly vulnerable to periods of drought or rainfalls, with considerable impacts on production i.e. on the length of the growing period, productivity and quality of forage and pasture. To overcome the main negative impacts of climate changes, it is necessary to identify and evaluate adaptation measures, namely the selection of varieties and cultivars that are better adapted for the future.
All tools that are suitable to harvest forage without significant nutrient losses (i.e. early first cut in the beginning of blossom, cutting length >6 cm) and without further contamination (e.g. soil) should be considered on the field. In order to reduce high nutrient losses during meadow hay production, i.e. the so-called crumb losses during soil drying by turning and swathing on the field, artificial drying processes are an interesting option in which investments should be made in the future. For meadow hay, under-roof drying with cool or warm air is recommended. The cuttings are first pre-dried to a residual moisture content of 30 % on the field. In the following, the drying process to a residual moisture content of 10–14 % should be done by under-roof drying. For the post-drying process waste heat from biogas may provide the necessary heat supply of 5–10 °C > ambient temperature. In this way, the nutrient losses can be significantly reduced.

Consider feed hygiene! By drying the meadow hay ≥86 % DM, the so-called storage stability is achieved. This means that losses due to microbial spoilage i.e. by bacteria, fungi and yeasts can be prevented during storage as the growth of microorganisms is suppressed by the withdrawal of water.
In addition to sufficient drying, the storage of feedstuffs also needs special attention. Contamination of forage by dirt, rodents and storage pests can lead to spoilage during storage. Clean storage areas protected from moisture and rodents protect the dried forage from spoilage.
Avoid luxury consumption. The daily forage intake in sport horses should be adjusted to a daily intake of 1.5–2 kg DM per 100 kg BW. It should be avoided that forage are mixed with the litter and thus removed unused when mucking out. Innovative feeding techniques, i.e. time-controlled access to forage enable a high meal frequency despite restrictive allocation of forage. If such feeding techniques are not available, the meadow hay or haylage can be offered in a hay net. A hay net should also be stretched over hayracks on paddocks or pastures in order to minimise both the luxury consumption and the forage losses in front of the rack.
Hay steaming or soaking? The premise is to produce meadow hay with a low microbial contamination. Hay steaming can significantly reduce contamination with bacteria, fungi and yeasts, so the use of hay steamers should also be taken into account. However, it should be noted that nutrients such as sugars are lost through steaming. Additionally, data about hay steaming showed that protein availability, especially lysine, is reduced by heat reactions, i.e. the reaction of lysine with sugars. The availability of sufficient amount of protein is extremely important in sport horses as protein is used as an energetic substance during exercise and sufficient protein is necessary for protein synthesis after a strenuous workload.
Soaking meadow hay for 30 minutes, whereby the hay must be completely soaked in water, also leads to a significant reduction in bacteria, moulds and yeasts. However, nutrient losses (sugars, proteins and minerals) must also be taken into account during hay soaking.
Alfalfa, the 'queen' of forage plants. Alfalfa (*Medicago sativa*) is a deep-rooted, drought-tolerant legume that will gain importance in sport horse nutrition with increasing climate changes.
Alfalfa is characterised by high protein, calcium and magnesium contents. However, harvesting of alfalfa is difficult, as the structure as well as the nutrient contents of the plant create unfavourable conditions for forage preservation. On the one hand, soil drying leads to high losses of the valuable leaf mass, on the other hand, air drying is energetically expensive. The highly buffering nutrient content and the difficult-to-compact structure of alfalfa also result in unfavourable ensiling properties which requires special attention to the ensiling process. In future, more attention should be drawn on harvesting methods and feeding techniques to achieve optimal conditions using alfalfa hay or alfalfa silage as a forage source in equine nutrition.

I13

Evolution of pet animal nutrition in Italy: scientific, technological and professional aspects

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The last century has been characterised by enormous changes that have no parallel in the history of humanity. The human population has gone from 1 billion to 7 billion thanks to important scientific and technological discoveries and their applications. Dogs and cats, initially often provided a contribution to research and subsequently they benefited from the acquired scientific knowledge and its practical application.
The first studies on dog nutrition date back to 1700: Francois Magendie (1783–1855) identified the role of nitrogen in dogs; Max Josef Pettenkofer (1818–1901) published one of the first works on dog nutrition in 1864. Later, Casimir Funk (1884–1967) introduced the term 'vitamins' in 1912 and in 1932 Max Kleiber (1893–1976) identified the first equation for determining energy requirements as a function of weight: MR = aM^0.75. In the 1930s dogs and cats were used for the minerals and vitamins study and in 1943 C. Mc Kay in the preface of his book 'Nutrition of the dog' underlines the fact that 'regarding the nutrition of these animals, from a scientific point of view, there is a level of misinformation probably higher than that regarding other species, with the result that many animals age and die prematurely'. Since the second half of the last century, many gaps have been filled by works such as those of the National Research Council (publications of 1974, 1985, 2006), books such as 'Small animal clinical nutrition' (1983, 1984, 1987, 2000, 2007), AAFCO publications. In Europe, FEDIAF has been updating the nutritional requirements of dogs, cats and, lately, pet rabbits since 2008. In Italy, the most recent book 'Nutrizione e alimentazione del cane e del gatto' is dated 2021 and published by Edagricole. Towards the end of the last century, courses on pet nutrition were introduced in Italian Faculties of Veterinary Medicine and dedicated scientific societies were founded: SCIVAC, AIVPA, SIANA in Italy and ESVCN in Europe. Alongside animals specific studies, others, relating to food processing technologies, have emerged and have allowed the birth of specialised industries. The most striking examples concern the manufacture of wet foods through large-scale sterilisation and that of dry foods through extrusion. Both have the purpose of preserving perishable products over time; extrusion has also

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the purpose of making them more digestible and chewable. The two technologies share the use of temperature, but with different times and quantities: sterilization uses longer times, extrusion very short times and, sometimes, higher temperatures. Many studies have investigated their effect on the elimination of pathogenic organisms and anti-nutritional factors, as well as the impact on the persistence of vitamins, with more than satisfactory, but often unknown, results. Little by little, thanks to new scientific and technological discoveries, and the evolution of our society, pre-packaged foods have gained new admirers with consequent increases in market shares, which went from 254 million euros in 1985 to 1000 million in the early 2000s and, in 2022, to 2,419 million foods for dogs and cats plus 12 million for other animals (birds, fish, small rodents...). There are 12 million Italian families interested in shopping (46.9% of the total). The number of pets in the family has also risen, reaching a total of 64.8 million, distributed as follows: dogs 8.7 million, cats 10.1, small mammals 1.8, reptiles 1.4, birds 12.9 fish 29.9. More than the number, the care for these animals, which have become true members of the family, has increased. This complex of phenomena had a strong impact on the veterinary professional who, in the meantime, had an increment in the number of graduates.
Between 1880 and 1980 the number of members of the professional order had grown from 1972 to 6300, but with a substantially stable relationship with the Italian population (1:10,000). Since then there has been an exponential increase in the number of members to 35,350 with a ratio of 6:10,000 and a progressive increase in women (37.4% in 2008 and 49.17% in 2024). Pets have contributed to limiting the crisis in professional practice and increasing the activity in nutritional counselling. The recruitment of veterinarians by the feed industry has contributed substantially to the spread of scientific knowledge about nutrition, playing a fundamental role in the prevention and treatment of many diseases. These are often the work of veterinarians working in the feed and supplement industry and find their way into many areas: Research and Development, Registration and Regulation, Marketing, 'Technical' Service, Promotion/Information, Sales. Compared to the past, much has been lost at the professional level, but much has also been gained.

I14

Sustainability and aquaculture: responsible change of diet

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In recent years, sustainability has become a key concept in the aquaculture sector, reflecting the growing global awareness of the need to protect natural resources while meeting the rising demand for aquatic food products. Among the various aspects of aquaculture being re-evaluated through a sustainability lens, fish nutrition and feed formulation stand out as critical areas of innovation and transformation. Traditionally, fish feed formulations have relied heavily on fishmeal and fish oil, both of which are derived from wild-caught fish. These ingredients are valued for their high-quality protein content and essential fatty acids, particularly omega-3s like EPA (eicosapentaenoic acid) and DHA (docosahexaenoic acid), which are vital for the growth and health of farmed fish. However, the overreliance on these marine-based resources has raised serious environmental and ethical concerns, such as overfishing, biodiversity loss, and pressure on marine ecosystems. Due to these concerns, and in response to the growing demand for certified sustainable aquaculture, the industry has been steadily reducing the inclusion of fishmeal and fish oil in feed formulations. Instead, the sector is increasingly turning to alternative sources of protein and lipids that are more environmentally friendly and economically viable. A notable development in this transition is the shift in the source of fishmeal and fish oil. Rather than using whole wild fish, many feed producers now rely on by-products from fish processing, such as heads and trimmings, to produce these ingredients. This approach not only reduces waste but also helps to relieve fishing pressure on wild stocks. However, this change also leads to variability in the nutritional composition of fishmeal and fish oil, which must be carefully evaluated to maintain feed quality and meet the nutritional requirements of farmed species. In parallel, a wide range of novel and alternative protein sources is being introduced into aquaculture feeds. These include:

- Animal by-products, such as poultry meal, poultry blood meal, hemoglobin powder, and hydrolyzed feather meal. These ingredients are derived from slaughterhouse waste and offer high protein content with a relatively low environmental impact, especially when produced under strict sanitary and quality standards.
- Single Cell Proteins (SCP), which are produced from microorganisms like bacteria, yeast, or fungi. These proteins can be cultivated on various substrates, including agricultural waste or industrial gases (e.g. methane), making them highly sustainable. SCPs offer excellent nutritional profiles and are free from many of the environmental and ethical issues associated with animal- or fish-derived ingredients.
- Insect meal, especially from species like the black soldier fly (*Hermetia illucens*), is gaining attention as a promising alternative. Insects are natural components of many fish diets in the wild, and insect farming can be done using organic waste streams, making it a circular and efficient process. Insect protein is rich in essential amino acids, fats, and micronutrients, and it has a low carbon footprint.

As feed formulation evolves, lipid sources are also undergoing significant changes. One of the most promising innovations is

the use of algal oil. Produced from marine microalgae, algal oil is a plant-based source of long-chain omega-3 fatty acids, including EPA and DHA. It represents a sustainable and scalable alternative to fish oil and can be used to maintain the nutritional quality of farmed fish for human consumption. However, the adoption of these innovative raw materials is not without challenges. Beyond nutritional adequacy, it is essential to ensure that these ingredients are homogeneous, traceable, safe, and available in sufficient quantities to meet the growing global demand. Feed manufacturers and aquaculture producers must also consider factors such as digestibility, palatability, processing requirements, and potential impacts on fish health and product quality. Another crucial aspect is the regulatory framework and consumer acceptance. The use of novel ingredients, particularly those derived from insects, animal by-products, or microbial sources, may face regulatory restrictions in some regions or hesitancy from consumers. Therefore, transparency, proper labeling, and education are essential to facilitate broader adoption. In conclusion, the future of sustainable aquaculture will increasingly depend on the innovation and diversification of feed ingredients. Moving away from finite marine resources and embracing a wide range of alternative proteins and lipids—such as fish processing by-products, animal-derived proteins, single-cell proteins, insect meal, and algal oil—offers a viable path forward. These alternatives not only support environmental sustainability but also contribute to the economic resilience and nutritional efficiency of aquaculture systems. By investing in research, improving feed formulations, and scaling sustainable raw material production, the aquaculture industry can continue to grow responsibly, providing healthy and nutritious seafood to a growing global population without compromising the health of our oceans.

O444

Imputation accuracy of missing genotypes in Italian mediterranean buffalo using 50K SNP chip

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Genotype imputation is a widely used practice in modern genomic research, enhancing the precision of both genomic selection and genome-wide association studies. This study evaluates the effectiveness of genotype imputation in the Italian Mediterranean Buffalo (IMB) using the Beagle v. 5.5 software. The dataset comprised 3,120 individuals and 52,917 SNPs. A series of simulations were conducted by introducing missing data at both the SNP and individual levels. To assess the impact of missing data, 5%, 10%, 20%, and 30% of animals were randomly selected, and within each group, 5%, 10%, 20%, and 30% of SNPs were systematically removed. For each percentage of missing data, 20 replicates were performed. The accuracy of the imputation was evaluated by comparing imputed genotypes with the original dataset using metrics such as imputation accuracy and the *--genome* command in PLINK v. 1.9. The analysis focused on three key metrics: the proportion of loci with completely different genotypes (Z0), loci with one shared allele (Z1), and loci with two identical alleles (Z2). For identical samples, Z0 is expected to be 0, and Z2 should equal 1. Beagle demonstrated exceptional performance across different levels of missing data, achieving an imputation accuracy exceeding 95%. This was corroborated by a Z2 value of 99.82%. Z1 indicates that 0.18% of the individuals shared an allele, therefore, out of a total of 52,917 SNPs, the discrepancy was 0.12%. In conclusion, this study confirms the feasibility and reliability of Beagle for genotype imputation in the IMB population. These findings underscore its potential to refine genotype panels and enhance the accuracy of genomic selection in livestock populations.

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O060

Genomic evaluation of methane emissions and feed efficiency in Holstein bulls

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Climate change poses a critical global challenge, with the livestock sector contributing significantly to greenhouse gas (GHG) emissions, particularly methane (CH_4) and carbon dioxide (CO_2). Dairy cattle, as a major source of enteric methane, play a pivotal

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role in the environmental footprint of agriculture. A potential method to reduce CH_4 emissions in dairy cattle is through genetic selection. Building on previous research indicating that breeding and selection in dairy bulls can influence the phenotypic expression of traits in their progeny, this study evaluated CH_4 and CO_2 emissions and feed intake in 194 growing Holstein bulls, addressing a gap in research that has primarily focused on cows. Between March 2018 and November 2024, a Greenfeed system collected a total of 3,578 valid CH_4 and CO_2 records. Feed intake was recorded using five Roughage Intake Control (RIC) systems, capturing 8,307 feed intake records from 258 bulls. Additionally, 2,748 live weight records were collected from 586 bulls in the same time span. Genotypic data was obtained on various medium density chips and then imputed to 70K SNP markers following quality control. Genetic analyses were conducted using a ssGBLUP mixed model, with variance components and genetic parameters estimated with the BLUPf90 software platform. Heritability for CH_4, feed intake, and live weight was 0.30, 0.31, and 0.43, respectively. A third measure, 'feed saved while growing', was obtained by correcting the GEBV for feed intake with live weight. The moderate heritability shown by methane and the growing traits indicates that genetic progress through selection is a viable means to reduce the environmental impact of dairy cattle.

O512

An enviromics approach to modelling GxE interactions in dairy cattle

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Genotype-by-environment (GxE) interactions are sometimes of sizeable magnitude and can consequently affect significantly the accuracy of genetic and phenotypic predictions. This is especially relevant under climate change and for dairy cattle, given the worldwide range of breeding populations. Several methods have been proposed to account for GxE interactions in genetic models, from multiple-trait models to reaction-norms. In this work, we propose to use the enviromics approach, which is based on the measuring of environmental covariables (envirotyping) that provide an environmental relatedness matrix: together with the kinship matrix, this approach can better capture the covariance between records and GxE interactions compared to the modelling of environments as all-encompassing black boxes. As a first preliminary step, we estimated the size of GxE interactions in Holstein-Friesian dairy cattle. We took the average milk production records of the daughters of 611 sires from three territories in Northern Italy, in the year 2021: Cremona, Mantova and Cuneo. The kinship matrix was estimated from pedigree records. Days in milk, the average age of cows, the month and day of milk recording and the number of days from the latest insemination were used as systematic effects. A linear mixed model that treated milk from each environment as a separate trait was fitted to the data. The MCMC method implemented in the BGLR R package was used to solve the model. Heritability estimates ranged from 0.43 to 0.49, while genetic correlations ranged from 0.367 to 0.414. These results indicate the presence of significant GxE interactions that should be accounted for in genetic models. The collating of environmental descriptors is currently in progress and, when completed, it will allow us to construct the environmental covariance matrix. This enviromics approach will be benchmarked against traditional strategies for the modelling of GxE interactions in terms of (i) the estimation of breeding values and their ranking across environments, and (ii) the accuracy of phenotypic predictions across environments.

O084

Calf survival in Italian Holstein: first results and services for farmers

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Until now, little is known about calf survival during the rearing period. In Italy, over 20% of female calves do not reach first calving (ANAFIBJ database, 2024). Reducing calf mortality is crucial for ensuring economic stability and enhancing animal welfare on

commercial dairy farms. The death of calves and young stock during the rearing period leads to revenue losses, fewer replacement heifers, increased veterinary expenses, and a decline in animal welfare. The aim of this preliminary study was to investigate environmental factors affecting calf mortality as a first step towards including calf survival in genetic evaluations of the Italian Holstein population. First, we analysed data stored in the national database which includes information of 5,220,084 cows born between 2010 and 2024. From these we selected data on 1,040,678 females with a recorded death date exceeding 48 hours (to exclude stillborn calves) and no calving date. Animals with a death date exceeding 36 months and without calving date were removed ($n = 109,175$). Using the available data on birth and death dates, it was possible to calculate the age at death, expressed in days. This allowed us to identify the age ranges in which calf mortality is most frequent (2–90 days, 90 days-12 months, 12–24 months, and 24–36 months). This analysis was conducted both at national and at farm level. At the national level, the analysis revealed that the most critical period is the age range between 2 and 90 days, with losses reaching 10% in 2023. However, at the farm level, the values varied significantly, primarily due to differences in management practices. Hence, we wanted to develop a farmer-oriented service to be integrated into ANAFIBJ *HerdUp* platform. This service will provide actionable insights and management tools to improve calf care and survival rates at farm level. Moreover, our aim is to establish a genetic evaluation for calf survival, enabling farmers to include survival as a selection criterion in their breeding programs. This preliminary study highlights the critical need to address calf mortality during the rearing period and serve as a foundation for further research and practical applications at farm level. Further investigations are required in order to set up a genetic and genomic evaluation for calf survival.

O409

Total and differential somatic cell traits in Italian Jersey dairy cattle breed: preliminary results

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Mastitis is currently one of the most impacting issues on the profitability and the sustainability of dairy farming. Somatic cell count (SCC) has been used for years as an indicator of udder health to support mastitis monitoring in dairy cows. However, despite its wide use on assessing milk quality, SCC does not allow to distinguish specifically the different cell populations involved in the inflammatory process of the udder. For this reason, differential somatic cell count (DSCC) has been introduced as a new trait which can be recorded routinely in dairy herds, just like SCC. Since DSCC represents the percentage of polymorphonuclear neutrophils (PMN) combined with lymphocytes on the total of somatic cells, it allows alongside SCC a faster and more accurate distinction between cows with healthy udders and those affected by either acute or chronic inflammation. So far, DSCC has been analyzed in a limited number of studies, mostly conducted in the Holstein breed. Therefore, the aim of this study was to investigate the variability of DSCC and SCC traits in Italian Jersey dairy cattle breed to provide a foundation for future studies. Data were collected from a population of 5,941 Jersey cows registered in the ANAFIBJ herdbook and reared in 484 Italian herds during a period spanning from 2015 to 2023. A linear model was tested to explain the variability of DSCC and SCC according to parity. The results show an increasing trend in SCC and DSCC as parity rises, aligning with the higher risk of infection associated with increased parity. Older cows are generally more vulnerable to inflammation or infection due to a decline in immune function and heightened metabolic stresses. Moreover, ROC curves were produced to determine the best cut-off values of DSCC for assessing the status of udder health when combined with SCC (below and above 200,000 cells/mL). Thus, for each interaction between parity and month of lactation an optimal cut-off value of DSCC was determined. One of the best ROC curves was estimated for the interaction between parity 2 and month of lactation 1: this showed an optimal cut-off value of 65.85% DSCC and an AUC of 0.847 (978 healthy and 314 sick animals). ROC curves proved to be a valuable tool for enhancing herd management. A robust predictive model based on differential cell count helps to avoid unnecessary treatments. This could be further supported by comparing the DSCC cut-off values derived from the ROC curves with those obtained using mastitis diagnosis as the gold standard.

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O105

Multi-breed genomic predictions for average daily gain in three Italian beef cattle breeds

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Marchigiana, Chianina, and Romagnola are three Italian autochthonous beef cattle breeds that have been historically selected for meat production. Recent advancements suggest that using genomic data and multi-breed models to combine information from different populations may help to increase the accuracy of genomic predictions, particularly when the available data per breed is limited. This study aimed to evaluate and compare the accuracy of genomic predictions for average daily gain (ADG) in the three Italian breeds, evaluating if multi-breed models could increase the predictability. Different scenarios were validated using a dataset including phenotypes recorded on 5,303 young bulls of the three breeds during performance test, along with their pedigree containing 23,793 individuals, 4,593 of them being genotyped. The implemented scenarios were: pedigree Best Linear Unbiased Prediction (pBLUP) and single-step Genomic BLUP (ssGBLUP) single-trait single-breed evaluations; pBLUP and ssGBLUP single-trait multi-breed evaluations where ADG was considered as the same trait across all breeds, and ssGBLUP multi-trait multi-breed evaluations where ADG was considered as a different correlated trait across breeds. In addition, single- and multi-breed ssGBLUP evaluations were implemented including weight at one year of age and muscularity as correlated traits to ADG in a multi-trait approach. Results highlighted that the inclusion of genomic data improved the accuracy of prediction models (0.29–0.37 versus 0.27–0.30). Moreover, single-trait multi-breed scenarios, where ADG was considered as the same trait, resulted the best performing in term of accuracy compared to any other model for those breeds with lower heritabilities for ADG (Marchigiana and Chianina, accuracy respectively of 0.35 and 0.33), confirming the importance of multi-breed models in leveraging data from populations with higher heritabilities. Lastly, adding two correlated traits next to ADG in the single- and multi-breed ssGBLUP yielded higher accuracies (0.39–0.42) compared to the single-trait models, apart from Chianina breed where genetic correlation between such traits were not observed. The observed increases in accuracy when using multi-trait multi-breed models suggest that such models could be useful when selecting for novel traits with few records or low heritabilities, and for the genetic improvement of local populations where limited availability of data could challenge the genetic selection.

O034

Genetic diversity of goose (*Anser anser*) and guinea fowl (*Numida meleagris*) local breeds using whole genome sequencing

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The conservation of genetic diversity in local poultry breeds is essential for maintaining unique genetic resources and ensuring their adaptability to future agricultural and environmental challenges. Local breeds like the Oca Padovana (OPD) and the Faraona Camosciata (FAC) represent valuable genetic reservoirs that contribute to biodiversity and cultural heritage. This study aimed to evaluate the genetic variability of OPD and FAC to assess their conservation status. For both breeds 50 animals were sampled: 16 males and 34 females for the OPD, and 26 males and 24 females for the FAC. Blood samples (2 mL per individual) were collected to extract DNA, followed by whole-genome sequencing. The sequencing data were subjected to SNP calling analysis, resulting in the identification of more than 200,000 SNP molecular markers for each breed. These markers were used to estimate genetic variability indices such as minor allele frequency, expected heterozygosity (H_E), observed heterozygosity (H_O), and inbreeding coefficients based on homozygosity (F_{HOM}) and runs of homozygosity (F_{ROH}). To further assess the variability within OPD and FAC, genetic structure analyses were performed using Admixture, multidimensional scaling, and identification of runs of homozygosity. Low levels of H_E and H_O were observed in both breeds (OPD: $H_E = 0.129 \pm 0.071$ and $H_O = 0.143 \pm 0.149$; FAC: $H_E = 0.219 \pm 0.145$ and $H_O = 0.221 \pm 0.280$), coupled with high inbreeding coefficients due to an excess of homozygosity (OPD: $F_{HOM} = 0.473 \pm 0.174$ and $F_{ROH} = 0.451 \pm 0.376$; FAC: $F_{HOM} = 0.528 \pm 0.098$ and $F_{ROH} = 0.536 \pm 0.138$). Genetic structure analyses revealed low variability within the OPD and highlighted

the presence of two distinct subpopulations within the FAC. These findings were corroborated by genetic background analyses. The runs of homozygosity identification enabled the characterisation of specific genomic regions with high homozygosity, including genes of potential significance. The present study provided the genetic characterisation of the OPD and FAC local breeds, contributing valuable starting information for optimising conservation plans for the two breeds.

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O194

Effect of the inclusion of shelled dried chestnut in the finishing diet on growth performance and meat quality of Casertana pig

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Chestnut by-products can be used to integrated the diet of local pigs while keeping production costs reasonable and improving the quality of meat and meat products. This study aimed to assess the effect of the inclusion of chestnut flour (*Castanea sativa* Mill.) in the finishing diet of Casertana pigs on growth performance, carcass characteristics and meat quality. Twenty-four barrows 15 months old were randomly assigned to two dietary treatments: 12 pigs of an average live weight of 148.2 ± 18.8 kg fed a diet based on farm feed (composed of cereals and legumes) (Control, CT); 12 pigs of an average live weight of 156.8 ± 20.4 kg fed a diet supplemented with 10% shelled dried chestnut flour (CH). The finishing trial lasted 48 days, preceded by a 2-week adaptation period. The animals were divided into eight pens (3 pigs/pen) and housed in a straw-based indoor system. All pigs had ad libitum access to feed and water. Individual average daily gain (ADG) and feed efficiency of each group were calculated. At slaughter, the carcasses were weighed and the yield was determined. The backfat thickness was measured. *Semimembranous* muscle samples from each carcass were removed and vacuum-packed and stored at -20 °C until chemical analysis. Data were processed by one-way ANOVA. Pigs from CH group were heavier than CT pigs ($p < 0.05$) and showed a higher ADG (+ 94 g; $p < 0.01$), probably related to the greater palatability of the diet provided to CH pigs. CH pigs had a lower feed efficiency ($p < 0.05$) and carcass yield ($p = 0.082$). Furthermore, a slightly higher backfat thickness was recorded in the CH group (4.67%; $p = 0.073$). The use of chestnuts in the finishing diet increased ($p < 0.05$) the pH value and reduced ($p < 0.05$) the water holding capacity and color coordinates (L* and b*) of meat; as well as reduced the dry matter and total lipid ($p < 0.05$). Protein, ash and cholesterol were not affected by the treatment ($p > 0.05$). The total saturated fatty acids content, atherogenic and thrombogenic indices were slightly lower in CH group compared to CT one. Meat from CH pigs had a higher flavonoid and lower vitamin E contents compared to CT ($p < 0.05$). In conclusion, the use of shelled dried chestnuts in the finishing diet influenced in vivo and post mortem performance of Casertana pigs and slightly influenced meat quality. Considering its exploratory nature, this study needs further investigation, such as the treatment time and/or level of chestnut inclusion in the diet.

O093

Carcass characteristics and quality parameters of *Longissimus dorsi* muscle of Nero di Lomellina pigs

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The lack of information on the Italian autochthonous pig, and the importance of preserving biodiversity, encourages research to deepen knowledge about these breeds. In 2020, the Nero di Lomellina (NL) pig was recognised by the National Pig Breeders Association (ANAS) as a reconstructed Italian pig breed. In literature there are few available data on NL carcass characteristics and meat quality parameters A total of 28 pig, half NL and half commercial hybrid pig (CH) reared in the same condition, was selected and slaughter at about 170 kg of LW (Ethic Committee of the University of Milan n° 89/2021). Carcass parameters were evaluated and the left *Longissimus lumborum (LL)* muscle was excised from each carcass and transported to the lab for the determination of the physical and chemical parameters. No differences between two breeds were observed in carcass characteristics ($p > 0.05$). The pH_{24}, cooking losses and shear force of LL muscle, revealed no differences between breeds ($p > 0.05$). Drip losses resulted lower in NL muscle than in those from CH breed ($p < 0.05$). The LL muscle colour indexes measured at 1, 4 and 8 days of refrigerated storage at 4 °C showed a higher L* value in CH than in NL breed ($p < 0.05$). The colour parameters showed a significant decrease over time ($p < 0.05$). Chemical composition of LL muscle showed that ether extract resulted higher in NL ($p < 0.05$) compared to commercial breed. Overall, these data showed that the NL carcass characteristics was comparable with those of commercial pig. The present results suggest that the

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lower drip losses and the higher intramuscular fat content of LL muscle from NL pig may positively influence meat sensory parameters such as tenderness and juiciness. Further studies are needed in order to better evaluate the sensory profile, fatty acid composition and oxidative stability of LL muscle from NL pig.

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O355

Rediscovering the value of endangered Piedmontese chicken breeds through meat quality assessment

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In Piedmont (Northwest Italy), three poultry breeds are recognised: Bianca di Saluzzo (BS), Bionda Piemontese (BP) and Millefiori Piemontese (MP). To characterise these breeds, at 29 d of age (T0), 344 chicks were divided by breed and sex. Every 14 days, individual live weight (LW), pen-level average daily feed intake (ADFI) and feed conversion ratio (FCR) were assessed. At 182 d (T12), all males LW was recorded, and 15 males/breed were slaughtered for meat quality analysis, including the assessment of colour (CIELAB; L* = lightness, a* = redness, b* = yellowness), pH after 24h refrigeration and chemical composition. Breasts (*Pectoralis major*) were also boiled sous-vide to evaluate the cooking losses and colour changes. Commercial breasts were purchased from the market for comparison, considering fast-growing broilers (BR) and medium-growing Naked Neck (NN) chickens. Growth performance data were analysed by generalised linear mixed model and data for meat quality by one-way ANOVA and Tukey's post-hoc test ($p < 0.05$). At T0, no differences were observed in male LW, while at T12 the heaviest breed resulted MP (3225 g), followed by BP (3034 g) and BS (2912 g; $p < 0.001$). BP males showed the highest ADFI compared to MP and BS (99.4 g, 98.6 g and 87.8 g, respectively; $p < 0.001$). FCR showed no significant differences. Regarding meat quality, the highest pH value was recorded in BR (6.01), while the lowest in MP (5.63; $p = 0.029$). BR also had the lightest raw meat (L*=58.3), while MP, BP and BS were darker ($p < 0.001$). BR had higher a* values (2.70) compared to MP (–0.01; $p = 0.002$). MP, BP and BS showed higher b* values than BR and NN (12.8, 12.4, 10.4, 4.70 and 4.73; $p < 0.001$). After cooking, NN breasts were lighter (L*=83.53; $p < 0.001$), while BS and BP showed the highest redness (a*=3.16 and 3.12; $p < 0.001$). MP, BS and BP exhibited the most intense yellowness (b* = 16.75, 16.24 and 15.68; $p < 0.001$). Cooking losses were higher in BR (23.9%) than NN (17.9%), MP (13.9%), BS (13.5%) and BP (12.8%; $p < 0.001$). BS, MP and BP had higher crude protein values (25.0%) than NN (23,6%) and BR (22,9%; $p < 0.001$). Crude fat was highest in BR (1.48%; $p < 0.001$), while BP had the highest dry matter content (95.9%; $p < 0.001$). Ash content was highest in BP (1,42%; $p < 0.001$). These findings suggest significant differences between commercial hybrids and native breeds, emphasising the need to value the latter to preserve biodiversity and develop niche markets for local and authentic products.

O79

Comparison of carcass and meat quality traits of fast-, medium – and slow-growing chicken genotypes fed diets with different protein-to-energy ratio

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This study was conducted as part of a comprehensive project focused on the evaluation of novel slow-growing chicken genotypes as one of the several policies of the Better Chicken Commitment (BCC) that many companies have recently signed up. The main scope of this trial was to evaluate carcass cut yields and meat quality traits in chickens belonging to three genotypes differing in growth rate and fed either a control or low-protein diet. For this aim, a total of 1,800 one-d-old male chickens belonging to fast- (FG, Ross 308), medium- (MG, Ranger Gold) and slow-growing (SG, Gray Kabir Naked Neck) genotypes were housed in an environmentally controlled poultry facility and randomly allotted in 36 concrete floor pens (6 m^2; 50 birds/pen), in compliance with BCC requirements. The birds received, throughout the trial, a multi-phase basal diet with two lysine-to-metabolizable energy ratios (CON: commercial standard; LOW: –10% lysine but the same metabolizable energy compared to CON). All birds were slaughtered in a commercial abattoir at the same body weight (~2.8 kg), which was reached at different ages (FG = 34d,

MG = 50d, SG = 77d). Fifteen carcasses per group were randomly selected and used to assess cut yields (breast, thighs, drumsticks, wings and back) and quality traits of breast meat (pHu, colour, cooking losses, shear force, TBARS and carbonyls). A two-way ANOVA was performed including genotype (FG, MG and SG), diet (CON and LOW) and their interaction in the model. As expected, total yield of high-value cuts (breast, legs and wings) was impaired in both SG and MG carcasses when compared with FG group (74.3 and 76.2 *vs*. 79.4%, $p < 0.001$) basically as a consequence of dramatic decrease of breast percentage (29.9 *vs.* 35.9 *vs.* 39.6%, $p < 0.001$). As for the dietary treatment, only FG and MG birds exhibited lower ($p < 0.001$) percentage of breast meat when fed LOW diet, while SG chickens were unaffected. Likewise, meat quality traits strongly differed among genotypes. Breast meat from both MG and SG strains exhibited lower pHu, darker and yellower colour, higher cooking losses and shear force. In addition, SG evidenced higher TBARS values when compared with both MG and FG (0.86 *vs.* 0.50 and 0.50 mg/kg, $p < 0.001$). Overall, the dietary treatment did not affect meat quality traits. These findings evidenced that the adoption of slow-growing genotypes strongly affects the profitability at slaughter and allows producers to obtain meat with peculiar quality properties (i.e. appearance, texture, etc.).

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O332

Effects of outdoor enrichments and dietary supplementation with n-3 PUFA and antioxidants on the meat quality traits in free range chickens

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This study aimed to evaluate the effects of outdoor enrichments and dietary supplementation with n-3 PUFA and antioxidants on quality and oxidative status of thigh meat belonging to free-range chickens. More in detail, 4 farms were considered: 2 having an outdoor area without pasture (U) and 2 equipped with an enriched (E) outdoor space with grass and trees. Birds (Hubbard RedJA57, males) belonging to each farm were fed either a control (C) or a supplemented diet with n-3 PUFA and antioxidants (S, 5% linseed, vitamin E, and selenium) and slaughtered at 56d of age. Thighs were collected to evaluate the main meat quality traits (pHu and colour) ($n = 120$; 15/group) and oxidative status (TBARS, carbonyls, and free thiol groups) ($n = 64$; 8/group). Analyses were performed at 0, 3, and 7 d of refrigerated storage (4 °C) with the aim of assessing potential differences in the oxidative stability of thigh meat ascribable to the considered effects. Data were analysed by two-way ANOVA including the outdoor enrichments and diet as well as their interaction in the model. When significant, means were separated by Tukey-HSD test ($p < 0.05$). A significant effect of the outdoor enrichment was found for the main quality parameters at the beginning of storage as higher pHu along with lower lightness were observed in E in respect to U (6.11 vs. 5.92; $p < 0.001$ and 53.6 vs. 54.8; $p < 0.001$, respectively). On the other hand, the dietary enrichment with n-3 PUFA and antioxidants exerted only marginal effects. As for the analyses performed during refrigerated storage, overall, supplementation with antioxidants in chicken fed a n-3 PUFA diet was not able prevent the development of oxidative reactions affecting the lipid and the protein fractions when the outdoor space was enriched. In fact, despite the storage time considered, the highest TBARS and carbonylation levels were measured in 'ExS' and 'ExC' groups, respectively. It is worth noting that enriched diet promoted the occurrence of oxidative modifications affecting the proteins in U, as depicted by the significantly lower ($p < 0.05$) free thiol groups content detected in 'UxS' group at all storage times. Overall, these findings evidenced that when dietary supplementation with n-3 PUFA is adopted as a strategy to improve the nutritional profile of chicken meat even if antioxidants are also added, their inclusion should be carefully implemented considering the rearing system adopted.

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0259

Breast meat quality to classify the wooden breast defect and investigate its underlying mechanisms in fast-growing chickens

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The present study falls within the research activities to be implemented in the PRIN 2022 PACHOL4 project, which aims at

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broadening the knowledge on the molecular basis of Wooden Breast (WB) defect. This condition commonly affects the *Pectoralis major* muscles (PMs) of the fast-growing meat-type chickens impairing the quality of the forthcoming meat and resulting in high downgrading rates and economic losses at processing. An accurate classification of PMs is essential to investigate the factors likely involved in the onset of this abnormality and avoid misleading results. For this purpose, a total of 180 PMs belonging to three homogenous flocks (Ross 308 males 45-d old, 3.2 kg of live weight; ADWG >85g; $n = 60$/flock) were collected in a commercial abattoir 3 h post-mortem and classified according to their macroscopic features as normal (NORM, $n = 30$/flock) and abnormal (ABN, severe WB; $n = 30$/flock). Quality traits (pHu and color) and technological properties (drip and cooking losses, and shear force) were measured to characterise the samples and select those to be considered for further analyses at protein level. The effect of WB on the quality traits of chicken PMs ($n = 180$; 30 PMs/group/flock) was tested by Student t-test using STATISTICA 10 (StatSoft). Then, Principal Component Analysis (PCA) and Hierarchical Cluster Analysis (HCA) were performed in R environment (v.4.3.2) using meat quality data to validate the classification performed at sampling. As expected, most of the selected parameters were affected by the occurrence of WB. PCA allowed identifying pHu, lightness, cooking loss, and shearing force as potentially useful parameters for sample classification and HCA showed sample clustering partially resembling the macroscopic evaluation implemented at the processing plant, thereby mostly validating the initial PM classification. That allowed us to properly select a total of 30 PMs ($n = 15$/group) to be considered for extracting the proteins and perform western blot analyses (currently in progress) to quantify the expression of collagen type 4 (with special reference to the alpha 1 chain), a network-forming collagen which has been recently hypothesised to play a role in the onset of this defect. The outcomes of the present study could likely provide novel insights on the mechanisms underlying the onset and progression of growth-related defects in fast-growing broilers.

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O251

Optimizing *Tenebrio molitor* reproduction: examining beetle size effect on mating preferences, and larval yield and performance

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This study investigated the impact of beetle size on mating preferences (Experiment 1), and larval production, average weight, and average daily gain (ADG) of *Tenebrio molitor* larvae (Experiment 2). In Experiment 1, 14-day-old beetles were divided into two experimental groups, each with 18 replicates. Group 1 featured a small male as a primary chooser, while group 2 featured a large male. Each male was presented with two potential mates: one small female and one large female. Mate selection preferences were evaluated by observing male choices between small and large females during the first approach, the first mating, and the second mating. In Experiment 2, beetles were divided into three experimental groups, each with 6 replicates and one reserve. Each group included 20 beetles (10 males and 10 females) of specific weight ranges: Group 1 (80–100 mg), Group 2 (101–120 mg), and Group 3 (121–140 mg). Beetles were reared for 4 weeks (four oviposition cycles), and at each cycle, the number of larvae was counted when they reached 3 weeks of age. Average larval weights were recorded at 3 and 8 weeks of age, and ADG was calculated. Mating preferences was analyzed using a two-proportion z-test, while data from Experiment 2 were evaluated via one-way ANOVA using SAS's GLM procedure with the experimental group as a fixed effect. Results showed that small males significantly preferred large females during the first approach, and large males mated more frequently with large females during the first mating. Small males also preferred large females during the second mating. In Experiment 2, beetle size did not significantly affect the number of larvae produced per crate. However, larvae from groups 2 and 3 exhibited significantly higher weights at 3 weeks of age, and group 3 larvae were the heaviest at 8 weeks of age, with the highest ADG. This study highlights that males preferentially mate with larger females and that selecting for larger beetles can improve larval yield, especially in terms of average individual weight.

O055

Is age just a number? Investigating the effects of male and female age on the reproduction of Tenebrio molitor

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Tenebrio molitor (TM) is among the most widely reared insects in the world for food and feed purposes. In this insect species, the academic sector has mostly addressed topics related to larval stage, from the use of the larvae in food and feed, to the larvae's capacity to

consume agro-industrial by-products. However, adult breeding strategies are a necessary tool for any rearing facility. This study investigates the effect of adult age on their fecundity and fertility. A total of 960 pupae were collected, sexed and divided in 4 age categories (1–4 weeks old [WO]). Sixteen treatments were created, each composed of 5 males (M) and 5 females (F) belonging to a specific age category. Adults were placed in plastic vials containing 60 g of white flour which served as oviposition substrate, while agar was provided 3 times per week as moisture source. Per treatment, 6 replicates were performed. Egg production and hatchability were recorded every 7 days for a 4-week period. Based on the statistical analysis conducted using SPSS software ($p < 0.05$), it was observed that pairs involving younger females produced significantly higher number of eggs compared to pairs with older females. This outcome was consistent regardless of the age of the males. In particular the pairs with 1 WO females produce more eggs than the pairs with 4 WO females ($p < 0.05$). Similar to egg production, hatching was influenced by the age of the females rather than male age. However, the number of hatching larvae showed an opposite trend: a higher number of larvae was produced by older females. Particularly, the pairs with 3 WO females produced more larvae than pairs with 1 WO females ($p < 0.01$). The results of the experiment suggest that female age is the main driver of fertility, and females reach their peak of fertility 3 weeks after metamorphosis. These findings can support breeding strategies of TM rearing facilities.

O109

Impact of different dietary protein: carbohydrates ratios and lipid inclusion levels on the growth performance, nutritional composition and AMPs gene expression of *Tenebrio molitor* larvae

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The use of insects as food has become an exponential interest all over the world. Insects are highly nutritious (high in proteins, lipids, essential amino acids, minerals and vitamins) and produce valuable antimicrobial peptides (AMPs). In unison, insects can convert low- and high-quality organic materials (food industry side streams and agricultural by-products), into high-quality insect biomass. The yellow mealworm [*Tenebrio molitor* (TM)] is one of the four species that received the EU approval as Novel Food. It is therefore curious to investigate how to improve its composition by modulating the rearing substrate. Four different diets (D) were formulated to have two different protein: carbohydrate ratios and lipid levels (D1 = 1:3 and 7.5%, D2 = 1:3 and 9.5%, D3 = 1:2 and 7.5% and D4 = 1:2 and 9.5%) by using cheap agricultural and bakery by-products. Wheat bran was used as the control diet. Four-week-old TM larvae [L] were fed on the diets (10000 L/replicate, 5 replicates/D) under 28°C temperature and 60% relative humidity. At least100 L/replicate were randomly sampled for performance analyses until the percentage difference between two weeks-weight measurement was less than 50%. Ten L/replicate were sampled for AMP analyses at the end of the growing period. The expression level of genes encoding for two AMPs (Coleoptericin-1 and Cecropin-2) were evaluated. Data was analyzed by means of one-way ANOVA (IBM SPSS Statistics V20.0.0, p value <0.05). Gene expression data were subjected to a logarithmic (log10) transformation for normality before the statistical analysis. Average final weight (FW) and protein biomass (PB) of larvae was higher and Feed conversion ratio (FCR) was lower in D3 and D4 ($p > 0.05$) with 10 weeks of development, compared to D1 and D2 ($p < 0.001$) which were statistically different from each other ($p < 0.001$) and ended their development in 9 weeks. D4 had the best of 96mg AW, 104.04g PB and 3.01FCR. The highest survival rate (SR) and larval crude protein (CP) were in D1 ($p < 0.05$) and no statistical difference between D3 and D4 ($p > 0.05$). D4 had 91.68% SR and 37.57 CP. The lowest ether-extract was in D4 (33.03) ($p > 0.05$) and no significant difference with D3 and D1 ($p > 0.01$). D2 was statistically different from all others. D4 had the highest expression levels of genes encoding for AMPs (fold change = Colepotericin-1: 6.62; Cecropin-2: 8.92). Whole, TM larvae fed on D4 exhibited maximum performances as well as highest expression levels of selected genes.

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O017

Tenebrio molitor: effects of four herbs on larval composition and on their growth performance

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Mealworms (MWs) can grow on bakery waste and upgrade them into high-quality biomass to produce animal feed. The dough products are sometimes prepared with small quantities of herbs that can have a negative effect on MWs growing performances. This trial investigated the effects of including four different herbs in the MWs substrate: basil, oregano, rosemary and thyme, in two concentrations, 0.125% and 2% on a dry matter basis. All treatments were performed in duplicate. Ten thousand 4-week-old larvae were placed on 2.1 kg of substrates and reared for five weeks under dark conditions at 27 °C with 60% relative humidity. The data, which included growth performance, harvested prepupal biomass (wet weight), moisture content, and nutritional profile, were analyzed using a one-way ANOVA. *P*-values below 0.05 were considered statistically significant. Samples were taken by each tray during the trial to record growth performance parameters and resulted in no differences between groups ($p > 0.05$). The collection of the insects was initiated upon the appearance of the first pupae (nine-week-old larvae). The chemical composition, the total polyphenolic content (TPC) and the antioxidant activity of the resulting larvae were analyzed. The dry matter content showed no differences among groups ($p > 0.05$). The protein content was hindered by a greater herb inclusion ($p = 0.002$) and the fat level was slightly reduced by the inclusion of oregano ($p = 0.024$). The larval TPC has been worsened by the highest herb inclusion ($p < 0.001$) and a negative Spearman correlation (–0.463) was observed between the substrate's TPC and the MWs' TPC. Conversely, the incorporation of herbs led to an augmentation in larval antioxidant activity, as evidenced by measurements of ABTS ($p < 0.001$) and FRAP ($p < 0.001$). The inclusion of herbs did not modify larval growth performance; however, a higher inclusion level of the tested herbs resulted in modifications to larval chemical composition, with a concomitant detriment to larval TPC and an improvement in antioxidant activity. Further researches are needed to understand the observed effects.

O032

Fully hydrogenated rapeseed oil (FHRO) enriched diet in *Tenebrio molitor* larvae: effects on growth performances and nutritional composition

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The nutritional composition of insects might be closely related to their diet, and there has been growing interest in investigating this aspect, because of their versatility and capacity to use a wide range of side streams and by-products. Specifically, the nutritional profile of *Tenebrio molitor* larvae (mealworm) is characterised by a good amount of fatty acids (FA), mostly mono and polyunsaturated fatty acids (MUFA and PUFA). This study aimed to investigate the effect of dietary saturated fatty acids (SFA) on the fatty acid profile of mealworms. Six substrates were formulated by mixing different ratios of wheat bran (used as control, CTRL) and fully hydrogenated rapeseed oil (FHRO), rich in stearic acid (C18:0.91%) in the following ratios: 50:1, 25:1, 15:1, 10:1, 7:1, and 5:1. Larvae near to the last instar were fed for two weeks with the substrates. Larvae were sampled at T0-T7-T11-T14 and subjected to a 24-hour fasting. Rearing performances of mealworms along with proximate and fatty acids were analysed. Results showed that CTRL larvae's final average weight (157.11 mg) and growth rate at T14 (5.28 mg/day) were lower than those fed with the intermediate FHRO inclusion diets (respectively 162.51 mg and 5.67 mg/day). The mortality rate increased with higher concentrations of FHRO and over the trial period reaching 14%. Increasing FHRO caused a significant increase in the total lipids (up to 34.34 on a dry matter basis) and decreased crude protein content. Furthermore, the levels of PUFA decreased, while C18:0 and SFA increased significantly reaching 9.20 g/100g of total FA values in larvae fed the highest quantity of FHRO. These results suggest that due to the plasticity of the nutritional composition of mealworms, a careful selection of substrates should be made to obtain specific feed and food products.

O489

Effects of a molasses-based liquid feed supplemented with tannins on productive performance and methane emissions in lactating dairy cows

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The inclusion of molasses-based liquid feeds (LF) in total mixed rations (TMR) has the potential to enhance dry matter intake as well as milk yield and its components. Sugars in these feeds promote mostly the growth of cellulolytic bacteria, which may influence ruminal methane production. Additionally, LF could be a carrier for compounds such as tannins, known for their ability to mitigate methane emissions. Moreover, their feeding is feasible in automatic milking systems (AMS), offering a potential approach to precision feeding and methane mitigation. This study aimed to evaluate the effects of a molasses-based LF supplemented with tannins, delivered via AMS, on the productive performance and methane emissions of dairy cows. Twenty multiparous lactating Holstein cows (229 ± 66 days in milk) were monitored over a 10-week trial conducted at the experimental-teaching dairy farm of the University of Bologna. The cows were housed in a free-stall barn equipped with a free-flow AMS. The control group (CTR, $n = 10$) received a partial mixed ration (PMR) and AMS pelleted concentrate; additionally, the treatment group (TRT, $n = 10$) received in the AMS 473 g/cow/day as fed of the molasses-based LF supplemented with tannins (71 g dry matter/cow/day). Milk yield and composition were recorded individually, while rumination time and reticular temperature were measured using a rumination monitoring system and reticular boluses, respectively. Fecal samples were collected weekly and analysed for composition. Methane emissions were measured using sniffer techniques (Moologger, Tecnosens, Italy) during automatic milking. From the second week of the trial, the TRT group showed a higher number of AMS visits (3.28 vs. 2.63/cow/day) and milkings (2.95 vs. 2.49/cow/day). Rumination time, reticular temperature, fecal composition, individual methane production and intensity were not significantly affected by the supplementation of molasses-based LF with tannins. Milk yield and energy corrected milk were higher in the TRT group (36.8 vs. 34.8 kg/day and 41.2 vs. 39.1 kg/day, respectively), while protein, fat, and lactose contents were not different between groups. These preliminary findings suggest that LF delivered via AMS could promote higher number of visits on the AMS and higher milk yield. Obtaining these benefits on late lactation cows could make LF a valuable tool in enhancing cows productivity and the number of visits in barns equipped with AMS.

O501

Evaluation of functional characteristics of whole lemon pulp and depectinized lemon pulp for animal feeding

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The increasing interest for the reutilisation of agro-industrial by-products in animal nutrition is a valuable strategy to minimise waste and modulate the quality of diet, animal health and performance. Several agricultural by-products contain biologically active constituents with high nutritional and nutraceutical value, such as antioxidant compounds and antimicrobial molecules. This study investigated the chemical composition, antioxidant, antimicrobial and prebiotic activity of whole lemon pulp (WLP) and depectinised lemon pulp (DLP) as a circular by-product for animal nutrition. WLP and DLP dried samples ($n = 2$) were analyzed for dry matter content (DM), crude protein (CP), ether extract (EE), neutral detergent fiber (NDF) and ash content by using the standard procedures from the Association of Official Analytical Chemists. The antioxidant capacity analysis was carried out after extraction by using three different solvents (acetone 70% (v/v), methanol 50%, v/v; and deionised water) by the 2,2′-Azino-bis(3-ethylbenzothiazoline-6-sulfonic acid) (ABTS) radical cation decolourisation assay. O138 *Escherichia coli* inhibitory activity was assessed for each extract trough the microdilution method at different concentrations (25% v/v, 12.5% v/v, 6.25% v/v). Bacterial growth was measured spectrophotometrically at 620 nm over 6 hours at 60 min intervals. The growth of *L. plantarum* and *L. reuteri,* incubated at 35 °C, was determined via measurement by measuring the optical density of each culture at 620 nm at specific intervals spectrophotometrically. Each test was conducted in technical triplicate and biological triplicate. The results of bromatological composition showed higher content of NDF (61.53) and EE (4.77%) in DLP compared to WLP on a dry matter basis (27.44% and 1.67, respectively). Both of WLP and DLP showed antioxidant activity, particularly in acetone and methanol extracts, which demonstrated higher antioxidant ability compared to the water extracts ($p < 0.0001$). WLP showed higher inhibitory effects against verocytotoxic *E. coli* growth compared to DLP, probably due to the retention of functional compounds that may be partially lost during the depectinisation process. The addition of WLP and DLP extracts did not interfere with the normal growth dynamics of the probiotics during binary fission. Despite the lower antioxidant and O138 *E. coli* inhibitory activity of DLP compared to WLP, it represents the final residue of lemon processing. Its residual antibacterial activity combined with its cost-effective opportunity, makes DLP an ideal candidate for revalorisation in animal nutrition.

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O467

Functional characterization of biochar from lemon pulp by-products as innovative feed ingredients

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The growing concern for the climate change has led to increased attention to agriculture and livestock. Sustainable strategies have been developed to increase the sustainability and circular economy in this sector, however innovative and valuable solutions are still necessary for the enhancement of resource efficiency. Biochar is a recalcitrant carbon-based material obtained by pyrolysis or gasification process. This material has gained significant attention due to its potential environmental benefits, such as CO_2 capture, promoting circular economy with the possibility to use it as feed ingredient. The properties of biochar depend on its physical characteristics, which are influenced by the biomass used during the production process. This study investigated the chemical composition, morphological characteristics and antioxidant activity of biochar obtained by pyrolysis of whole lemon pulp (WLP) and depectinised lemon pulp (DLP) as innovative feed ingredients. WLP and DLP dried biomasses were pyrolysed using an auger pyrolyzer at 600 °C of inlet temperature for a residence time of 60 minutes (average temperature: 410 °C). The resulting biochar samples were analysed for bromatological composition using the standard procedures from the Association of Official Analytical Chemists. Morphological characterisation was performed through scanning electron microscopy. Antioxidant analysis was carried out after extraction using water as solvent through the ABTS radical cation decolourisation assay. The biochar yield was 30% for both WLP and DLP, based on the starting biomass (w/w). The results of the bromatological composition showed a similar nitrogen content in DLP biochar and the WLP biochar (2.38% and 2.10%, respectively, on a dry matter basis), and DLP biochar revealed a lower ash content compared to the WLP biochar (1.93% and 5.27% respectively, on a dry matter basis). Morphological analysis showed nanoporous structures possibly ascribable to the vessels or fibres of xylem in DLP. Functional characterisation and antioxidant capacity revealed a higher ability of WLP compared to DLP biochar ($p < 0.05$). This study highlights the potential of biochar derived from whole lemon pulp and depectinised lemon pulp as innovative and sustainable feed ingredients. Furthermore, the results underline the importance of biomass selection in biochar characteristics, paving the way for its supplementation into sustainable animal nutrition.

O475

Carbon Footprint estimation of some European agro-industrial by-products and their effect in reducing the environmental impact of sheep and goat diets

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The use of some agro-industrial by-products in small ruminants' diet has been long investigated, especially in terms of their effects on animal performances and derived products quality. However, little information is present in literature concerning the environmental impact of agro-industrial by-products and the effect of their inclusion on the carbon footprint (CFP) of small ruminants' diets. The aims of this work were (i) to estimate the European annual production of the by-products deriving from winery, olive oil, tomato, and beer industry processing; (ii) to estimate the carbon footprint of the considered dried by-products; and (iii) to evaluate potential reductions in the environmental footprint of small ruminant diets through their inclusion. A literature search was conducted to primarily assess the annual production of grape, olive, tomato pomace, and brewers' grains in Europe. The CFP of each by-product was estimated following a Life Cycle Assessment approach, taking into account the drying process and by using 1 kg of dried by-product as a functional unit. Four diets reporting the typical proportions of components used in sheep and goats were considered to estimate the reduction in CFP associated with the use of each by-product, calculated as the difference between the CFP of the treatment diet (which includes the by-product) and the corresponding control diet (without by-product inclusion). Annual productions resulted in 1290; 1790; 95 and 2092 kt of dry matter for grape, olive, tomato pomace, and brewers' grains, respectively. The estimated CFP was equal to 0.26; 0.22; 0.31; and 0.21 kg of CO_2 equivalents per kg of dried by-product for grape, olive, tomato pomace, and brewers' grains, respectively. The inclusion of the grape pomace in replacement of sugar beet pulp lowered the CFP of the control diet by –4.5%. A reduction of –25.0% of the diet CFP was obtained by using olive pomace in replacement

of sugar beet pulp; while the inclusion of tomato pomace allowed to reduce the CFP of the control diet by –34.7%. Finally, a reduction of –28.0% of the CFP of the diet was achieved when brewers' spent yeast replaced soybean meal. In conclusion, the reuse of agro-industrial by-products in animal feeding can effectively represent a valuable alternative to conventional feedstuffs, lowering the overall environmental footprint of small ruminants' diets.

O416

Brewers' spent grains as a sustainable alternative for lactating ewes: a feeding and environmental perspective

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In Mediterranean regions, dairy sheep farming plays a key role in rural economies. These systems often rely on grazing but concentrate feed supplementation is needed when pasture is absent or poorly available. Incorporating local agro-industrial by-products into ruminant diets instead of purchased feeds based on cereal grains and soybean could reduce the environmental impact of milk and feed/food competition without compromising animal performance. The aim of the present on-farm trial was to assess the effect of replacing commercial concentrate feeds with dried brewers' spent grain on ewe milk production and quality, as well as its environmental impact. The feeding trial was carried out in a dairy sheep farm located in southern Tuscany (Italy). The brewers' spent grains were collected directly from a local microbrewery and then dried on-farm using an electric dryer. Two homogeneous groups each consisting of 12 lactating ewes was formed: conventional feeding (CON) and dried brewers' spent grain feeding (DBG). The CON group was supplemented with 600 g ewe^{-1} d^{-1} of a commercial concentrate, 100 g ewe^{-1} d^{-1} of oat grains, and 1000 g ewe^{-1} d^{-1} of alfalfa hay. The DBG group was supplemented with 500 g ewe^{-1} d^{-1} of brewers' spent grain, 100 g ewe^{-1} d^{-1} of oat grains, and 1000 g ewe^{-1} d^{-1} of alfalfa hay. Additionally, both groups received 900 g ewe^{-1} d^{-1} of oat-clover hay overnight. Individual milk production was measured and sampled twice a day at the following time points: start date, end of the adaptation period, (two weeks), first week of experiment; and second week of experiment. Furthermore, the carbon footprint analysis associated with the feeds' production process and enteric emissions was carried out. The results of the statistical analysis showed no significant differences between the feeding treatments across all analyzed parameters: milk yield, FPCM yield, as well as fat, protein, lactose, and urea content. Instead, the environmental impact of the two experimental diets differed, with values of 4.93 and 1.35 kg CO_2eq for the CON and DBG daily diets, respectively. Similarly, emissions per kg of FPCM were 4.97 and 1.98 kg CO_2eq for CON and DBG. The trial demonstrated that the use of local brewers' spent grains proved to be an excellent substitute for concentrate feeds, ensuring a significant reduction in emissions associated with sheep milk production. Further studies are needed to demonstrate the scalability of the project at the territorial level.

O190

Evaluation of *Yucca schidigera* extract inclusion in fattening pig nutrition: impact on performances, nitrogen use and slurry composition

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This study aimed to evaluate the effects of a Yucca schidigera extract (YSE, 10.8% saponin richness) on the performances, nitrogen balance and environmental impact of fattening lean pigs.
For it, a total of 40 Pietrain × (Landrace × Large White) pigs, with 76.1 ± 5.2 kg of mean body weight (BW), 50% boars and 50% gilts, were involved in a trial that lasted 42 days. The parameters evaluated were: growth performances, farm nitrogen (N) mass balances, fecal and slurry composition and carcass and meat quality. Animals were allocated in 20 pens (two pigs each one). There were four treatments in a factorial design 2 × 2, with two sexes (boars and gilts) and two diets (0 and 300 mg/kg of YSE). The dietary treatment did not influence the average daily gain (ADG), average daily feed intake (ADFI) and feed conversion ratio (FCR) and neither affected the characteristics of carcass (yield, lean content, backfat thickness) or meat (color and marbling, chemical composition and texture). Also, the administration of YSE produced no impact on the estimated N excretion, fecal ammonia (NH3-N) content or total volatile fatty acid (VFA) content and VFA profile of the feces. Nevertheless, even not statistically significant, it is worth to note that the YSE inclusion in pigs' diet carried out a reduction in the total N (–21.5%) and in the NH3-N (–27.8%) content in the slurry. In relation to sex, the differences were that

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gilts tended to grow slower (0.96 vs 1.02 ± 0.03 kg/d; $p < 0.10$) and showed paler meat (49.1 vs 50.1 ± 0.47; $p < 0.05$) (lower lightness) with higher protein content than boars (23.7 vs 23.1 ± 0.12%; $p < 0.05$). Also, boars demonstrated better capacity to retain N (22.4 vs 25.0 ± 0.59 g/d; $p < 0.05$), but a lower fecal consistency (31.2 vs 28.9 ± 0.64; $p < 0.01$) and a slightly higher total VFA (304 vs 308 ± 14.4 µmol/g DM) and butyric acid concentration (9.78 vs 10.69 ± 0.41%) in the feces ($p < 0.10$) than gilts. In conclusion, YSE can be included in pigs' diet during the finishing period, regardless of sex, without affecting their performances, with promising results on the environmental impact.

O386

Comparison of the environmental impacts of chicken meat production among fast-, medium- and slow-growing genotypes fed diets with different protein-to-energy ratio

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In next few years, the European chicken meat production could change remarkably due to the adoption of the Better Chicken Commitment (BCC) requirements. This study aimed to assess the environmental implications of using some BCC-approved genotypes when fed different dietary regimens. A total of 1,800 one-d-old male chicks of three genotypes ($n = 600$/genotype), i.e. fast- (FG), medium- (MG) and slow-growing (SG) exhibiting an average growth rate of >70, 40–50 and 30–40 g/d, respectively, were fed 3-phase basal diet (starter, grower, finisher) with two crude protein (CP)-to-energy ratios, i.e. conventional (CON; 22.5, 20.5, 18.5%) and 10% lower CP content (LOW; 20.3, 18.3, 16.5%). FG, MG and SG were slaughtered at 34, 50 and 77 days, respectively, at a similar range of commercial weight for medium-size broilers. Life Cycle Assessment (LCA) was conducted from cradle-to-abattoir and the functional unit was 1 kg of eviscerated carcass. Primary data on growth performances and slaughtering yields were collected, and N excretion was calculated as the difference between N input (i.e. N from feed and day-old chick) and N retained in the body at slaughter age. Power energy consumption was based on literature sources, while manure CH_4, N_2O and NH_3 emissions were calculated according to FAO LEAP guidelines. Data were modelled on OpenLCA 2.0.2 and the considered impact categories were global warming (GWP, kg CO_2 eq), calculated through the ReCiPe 2016 midpoint (H) method, acidification (AP, kg SO_2 eq) and eutrophication potentials (EP, kg PO_4^{3-} eq), obtained according to the CML-IA baseline method. The effects of genotype under the same feeding program and diet in each genotype were investigated. For both feeding programs, the FG contributed less to all environmental indicators, while the SG was identified as the most impactful, having a GWP 2.5 times higher than FG and presenting a substantial increase of both AP (+80/85%) and EP (+80/95%). The MG showed intermediate impact values, with an increase of GWP (+40%), AP and EP (+25/30%) compared to FG. When the effect of diet was considered, minor differences were observed for all the impact categories. In example, it was estimated that GWP can be slightly reduced by adopting LOW program in MG (–0.2%) and SG (–2.4%) compared to CON. In conclusion, chicken meat production with MG and SG genotypes had negative effects on the selected impact categories, whereas the adoption of feeding programs matching their nutritional requirements could enhance sustainability traits.
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O056

Genetic characterization of two local duck breeds (*Anas platyrhynchos*) using whole genome sequencing

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The future environmental and ecological challenges are leading to preserving the genetic biodiversity and ensuring adaptability of indigenous poultry breeds. The aim of the present study was to characterise the genetic diversity and evaluates the conservation status of two Italian local duck breeds at risk of extinction: the Germanata Veneta (GER) and the Mignon (MIG). For each breed, 50 animals were sampled, consisting of 13 males and 37 females for GER, and 9 males and 41 females for MIG. The DNA obtained from blood samples was genotyped using whole-genome sequencing, and SNPs were identified through SNP calling analysis. More than 200,000 SNPs were identified for each breed and they were used to estimate genetic diversity indices, including minor allele frequency (MAF), expected heterozygosity (H_E), observed heterozygosity (H_O), inbreeding coefficient based on homozygosity (F_{HOM}), and inbreeding coefficient based on runs of homozygosity (F_{ROH}). Low levels of genetic variability were observed in both breeds (GER: MAF = 0.193 ± 0.127,

$H_E = 0.269 \pm 0.148$, $H_O = 0.272 \pm 0.260$; MIG: MAF = 0.190 ± 0.132, $H_E = 0.238 \pm 0.147$, $H_O = 0.245 \pm 0.172$), with high levels of inbreeding (GER: $F_{HOM} = 0.305 \pm 0.184$, $F_{ROH} = 0.372 \pm 0.222$; MIG: $F_{HOM} = 0.369 \pm 0.163$, $F_{ROH} = 0.313 \pm 0.126$). Genetic structure analyses revealed distinct patterns of variability, with appreciable heterogeneity in GER, while MIG exhibited a clear substructure, as further supported by phylogenetic analysis and Admixture results. The genomic regions associated with selection pressure were identified through ROH analysis. Significant ROH were observed on chromosomes 1, 2, 10, and 11 for the GER breed, and on chromosome 19 for the MIG breed. These findings elucidate the genetic diversity of GER and MIG duck breeds, providing insights into their genomic variability and the potential adaptive processes influenced by selection pressures. Furthermore, this research generates actionable data to inform breeding and conservation programs aimed at mitigating the risk of extinction.

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O276

Genetic characterization and origins of the Leccese: insights into an Apulian Poultry Breed

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The Leccese chicken breed (LEC) is a Mediterranean type of hen, indigenous of the province of Lecce. In 1930 some individuals were retrieved and brought to the 'Presta Columella' agronomic institute. Here the Provincial Chicken Coop of Lecce was established, with the aim of improving productivity, and supply breeders and eggs to local farmers. In the post-war period, local chicken was replaced by industrial breeds. The historical records about LEC have been lost and the present-day ownership is limited to a few small-scale breeders. The aim of this study is to provide a comprehensive reconstruction of the historical development of the breed, integrating bibliographic research and high-density genome analysis. A total number of 83 individuals were genotyped through Axiom 600k Chicken Genotyping Array. In addition, samples of some Apulian populations not directly attributable to the LEC, the Atriana breed (Abruzzo) and some Spanish and Portuguese breeds were added. Breeds from other European countries and some industrial genotypes data were also added from the SYNBREED project database. The results showed an inbreeding coefficient of –0.087. This level of heterozygosity, that exceeds the expectations of the Hardy-Weinberg equilibrium, indicates an effective reproductive management and the absence of recent inbreeding. The analysis of runs of homozygosity (ROH) revealed an average segment length of 112.4 kb per individual, with a mean of 18 segments. Most ROH segments were less than 500 kb, indicating that deep inbreeding events are limited. The distribution of ROH demonstrates the presence of genome regions with shared segments, suggesting potential selection signals. The PCA analysis highlighted a clear separation of the LEC breed from the other populations. Significantly distant from the cosmopolitan commercial breeds and with an intermediate position with the local Portuguese breeds. These results confirm that LEC poultry breed presents a distinct genetic structure and a unique gene pool, which is compatible with selection for local adaptations. On a global scale, PCA and genetic distances analysis show a closeness with Andalusian breeds, that may be linked to the era of Spanish domination. Closeness is also observed with Finnish and German breeds. This phenomenon may be explained with the notable mobility of the poultry germplasm tied with ornamental breeding activities, but also the existence of common genetic lines in the foundation of some breeds.

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O286

Phenotypic characterization and mating plan for biodiversity conservation in Modenese chicken breeders

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Preserving local chicken breeds is essential as global poultry demand rises. While commercial hybrids dominate, native breeds are declining, reducing genetic diversity. Though less productive, local breeds offer cultural, socioeconomic, and environmental value, adapting well to local climates. Recognising their importance beyond economics, conserving endangered breeds supports biodiversity, sustainable farming, and future food security. The aim of the present research is to describe the Modenese chicken breed, renowned for its distinctive physical characteristics and adaptability, from a genetic and phenotypic point of view. In the conservation center of the University of Milan, Lodi, a total of 9 roosters (R) and 14 hens (H) of the Modenese breed were housed. The birds were reared in floor pens, provided with a 14L:10D photoperiod, and fed *ad libitum*, with water supplied via nipple drinkers. Breeding families (F1: 1R + 4H; F2: 1R + 3H; F3: 1R + 6H) were established based on the results of molecular DNA analysis (24 microsatellite markers; AVIANDIV-FAO) aimed at reducing inbreeding levels and maximising the flock's genetic variability. Breeding performance was recorded from March to June. A phenotypic characterisation of morphological and reproductive traits was carried out. Birds were measured and weighed according to FAO body measurements protocol. Reproductive data focused on oviposition, fertility and hatchability. The average live weight was 2.53 kg in roosters and 2.25 kg in hens, the average egg weight was 54.2 g. The highest egg production was recorded in March and April. Fertility was 88.71%, while hatchability on total eggs set and on fertile eggs were 71.51% and 80.61%, respectively. For genetic characterisation, DNA extracted from feathers was genotyped using 26 microsatellite markers. Total number (Na), and effective number (Ne) of alleles, observed (Ho) and expected (He) heterozygosity, and F (Wright's inbreeding coefficient) indexes were calculated. A total of 76 alleles were identified and 3 loci were not polymorphic. The average Na was 2.7, and Ne was 2.0. Observed and expected heterozygosity were 0.41 and 0.43 respectively, with F = 0.03. The results support the importance of objective characterisation in traditional Italian breeds from both genetic and phenotypic perspectives to gather effective data for defining conservation strategies and breeding plans aimed at improving genetic variability and productivity in unique populations.

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O350

Safeguarding local animal genetics: the conservation of the Nostrana di Morozzo chicken breed

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This study explores the distinctive phenotypic and genotypic characteristics of Nostrana di Morozzo (NM) chicken breed, highlighting its importance for the safeguarding and conservation of local genetic resources. Originating from the Morozzo (CN) area in the Piedmont region of northwestern Italy, NM is one of the traditional Piedmontese chicken breeds together with Bionda Piemontese, Bianca di Saluzzo and Millefiori Piemontese. The study involved 40 chickens from 20 farms (2 chickens/farm) within the Morozzo area. Data collection focused on key phenotypic traits including live weight, plumage coloration, egg production, fertility, and hatchability rates. The findings demonstrated that NM is characterised by an aggressive temperament, particularly in roosters, reminiscent of wild-type chickens, and a marked sexual dimorphism. Hens exhibited a lighter body weight, ranging from 1.9 to 2.2 kg, with an annual egg production of 180–200 per hen. Roosters have a variable weight between 2.4 and 2.7 kg. Plumage coloration also differed significantly: roosters displayed red to dark blond plumage with blue-black tails and chests, while hens had brown-red or 'wild' coloring. Depending on the farm, fertility rates varied from 73% to 95% with one male for 15 females. Hatchability rates were notably high, reaching 90%. Phenotypically, the breed stands out as a dual-purpose chicken that is comparatively lighter than other Piedmontese breeds. On the genotypic level, a panel of 26 microsatellite markers was used to characterise the breed. The genetic distance analysis revealed a clear separation of the NM from other

Piedmontese breeds, with a high significant *p*-value (<0.001). Similar patterns of genetic distinctiveness were observed in a broader context, where comparisons with other Italian local chicken breeds also confirmed genetic diversity and uniqueness of the NM. In conclusion, both phenotypic and genotypic analyses confirm the distinctiveness of the Nostrana di Morozzo breed, underlining its unique identity and value among Piedmontese chicken breeds. These findings support the importance of its conservation as a vital local genetic resource.

O353

Molecular data to safeguard genetic diversity in local chicken breed conservation

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Local chicken breeds, irrespective of their current population size, are likely to provide an important reservoir of genetic diversity. Effective genetic management is crucial for their survival and long-term viability. The implementation of strategies to monitor and preserve genetic variability is essential for safeguarding the evolutionary potential and adaptive resilience of these populations to changing environmental conditions. The aim of this study was to illustrate how microsatellite genetic data can be an excellent tool for preserving genetic variability in small local chicken breeds. Under the TUBAVI project, chicken breeders from 17 breeds were characterised by microsatellite markers. For each animal the heterozygosity index (H) and the parentage index (P) were calculated. The H index is the number of observed heterozygous loci/number of loci analysed. Index P is the proportion of shared alleles between breeding animals. These two indices were combined into a conservation index (C) calculated as the difference between H and P. The index ranges from 1 (H = 1 and $p = 0$) to –1 (H = 0 and $p = 1$). Monitoring both heterozygosity and parentage in the offspring allowed to evaluate the results of the mating plans carried out. As a model, in the present study reports data from seven generations of the Bionda Piemontese breed under a conservation plan: 660 breeders were genotyped with 14 microsatellite markers. The number of alleles/locus (Na), the effective number of alleles (Nea), H, C, and P for each generation were calculated. The results showed a loss of genetic variability of 4%, 2%, and 1% for Na, Nea, and H respectively while P increase by2% on average in each generation. The conservation index decreased from 0.28 to 0.15 across generations. These results showed as the microsatellite markers in small populations are a valid tool to contain inbreeding and to monitor the genetic variability. Furthermore, the results of this study emphasize the importance of long-term monitoring and proactive management in conservation programs. The TUBAVI project serves as a model for the application of molecular tools in conservation programs, demonstrating their potential to safeguard the genetic resources of local breeds for future generations.

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O258

Gene expression analysis of Collagen type III coding gene in chicken breast muscles affected by wooden breast condition

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Fibrillar collagen proteins composing the extracellular matrix (ECM) of chicken skeletal muscles exert pivotal roles in providing functional and structural support for muscle fibers. Among them, collagen type III is known to be predominantly expressed during the embryonic stage of muscle development, as well as in cellular response to muscle injury and inflammation. In the past few years, alterations in the ECM composition, especially referring to the collagen components, have been associated with the occurrence and progression of wooden breast (WB), a quality defect affecting the Pectoralis major muscle (PM) of broilers selected for rapid growth-rate and high breast-yield. The present study was aimed at assessing the level of expression of the Collagen type III alpha 1 chain (COL3A1) gene, encoding the homonymous protein, in PMs affected (WB) and not affected (NORM) by the WB defect, to address its potential involvement in the occurrence of this condition. To this purpose, ten PMs ($n = 5$/group) from fast-growing broilers (45d-old; 3.0 kg of live weight) were collected 3h post-mortem and stored at –80 °C until the PMs were used to perform Quantitative Real-Time PCR of COL3A1 mRNA using GAPDH as normalising gene. After testing the normality of data distribution

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by means of the Shapiro-Wilk test, differences between groups were assessed by using the non-parametric Mann-Whitney U test. Statistical analyses were performed in R environment (v.4.3.2). As the outcome of the study, COL3A1 normalised gene expression was significantly higher in WB compared to NORM samples ($p < 0.05$), which is in line with the abnormal collagen accumulation characterising WB-affected breasts. Also, since collagen type III expression increases when muscular stress and injury occur, its higher expression at the gene level in WB samples might be considered directly related to the fibrosis condition occurring as a response to the injury status in myopathic muscles. Since collagen expression varies with age and this type of collagen is predominantly expressed during early muscle development, it is also possible that an abnormal regulation of its expression may be associated with a status of embryonic-like tissue in WB samples. Further analyses are warranted to elucidate whether its higher expression is directly related to the onset of this condition or a result of the fibrotic process characterising this defect.

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O213

The size of the rabbit from whole genome sequencing: the dwarfism in Dwarf Lop breed is better explained as a polygenic trait

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The domestication of the European rabbit (*Oryctolagus cuniculus*) has led to the development of a wide variety of breeds mainly distinguished by a few external traits, such as coat colour and body size. Rabbit breeds are categorised into four major classes based on body size: dwarf, small, medium, and large, with adult body weight ranging from less than 1.0 to more than 3.0 kg. Classical genetic studies and subsequent genomic analyses have shown that body size in rabbit has a polygenic basis, with a major gene determining a type of dwarfism caused by a semi-lethal 12.1 kb deletion in the *HMGA2* gene, primarily found in the Netherland Dwarf breed. In this study, our goal was to genetically dissect the dwarfism in another rabbit dwarf breed, the Dwarf Lop. Using a DNA-pool sequencing approach, we obtained whole genome sequencing data from 25 Dwarf Lop rabbits, which was then compared to whole genome sequencing data obtained using the same approach from six non-dwarf rabbit breeds. Reads were aligned to the rabbit reference genome and single nucleotide with dwarfism in Dwarf Lop rabbits, pairwise F_{ST} analyses were used to compare Dwarf Lop with all other breeds This analysis identified several candidate regions on rabbit chromosomes (OCU) 2, OCU3, OCU7, OCU8, OCU12 OCU14, OCU16, OCU17 and OCU18. These regions contain genes that have already been associated with body size in other species. The most differentiated region was on OCU2, in the position of the *LCORL* and *NCAPG* genes, which are well known to affect stature in mammals. The results suggest that the small body size in Dwarf Lop is polygenic with a few major genes. Additionally, the *HMGA2* 12.1 kb allele is not a major factor influencing the small size in this other dwarf breed.

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O167

Influence of conception time on milk yield and quality traits in primiparous Mediterranean buffalo

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The age at first calving (AFC) is a crucial parameter in dairy herd management, impacting genetic progress, feeding costs, and overall profitability. With the rising demand for buffalo milk products and improvements in management practices, Italy has made significant advancements in reducing AFC. This study investigates the influence of AFC on the productive traits of primiparous buffaloes, using 362,703 test-day records from 50,661 Italian Mediterranean buffaloes across 115 herds collected between 2013 and 2023. Productive traits included milk yield (kg/day), energy-corrected milk (ECM; kg/day), and fat and protein content (%), while somatic cell score (SCS) was calculated as a linear transformation of somatic cell count (SCC). A repeated mixed linear model was applied to assess the effects of days in milk, calving year, season, and their interactions on productive traits. Results show a significant reduction in AFC, from 36 to 35 months, between 2013 and 2023. Buffaloes calving at ≥42 months produced +0.52 kg/day more milk and +0.90 kg/day more ECM, with a slightly higher fat content (+0.04%) compared to those calving at ≤32 months. Whereas somatic cell scores were lowest in buffaloes with an AFC between 32 and 35 months ($p < 0.05$), with higher SCS observed

in both earlier and later calving groups. Buffaloes that calved during winter and spring produced significantly more milk and ECM and lower SCS than those calving in summer or autumn, while the highest fat and protein contents were recorded in autumn. Buffaloes calving between 34 and 37 months achieved a favorable balance of milk yield, fat content, and reproductive efficiency across all seasons. This trend was consistent throughout lactation, with buffaloes calving at older AFC producing higher milk, ECM, and fat content at peak compared to those calving at younger AFC. This study highlights the potential to promote early maturing heifers to improve sustainability and animal welfare while reducing costs. However, optimising heifer management from weaning to the pre-pubertal phase requires further investigation.

O168

Feeding dairy cows in the morning or in the evening: effects on milk production, rumen activity and feeding behavior

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Matching the nutrient demand of the mammary gland with the nutrients available from feed intake and rumen fermentation could enhance milk production. Nighttime feeding has been suggested as a method to boost efficiency in dairy cows. In this study, we evaluated the impact of this approach on milk production, metabolic profile, and various behavioral traits under thermoneutral conditions. During winter, 40 lactating multiparous Holstein cows (parity = 2.8 ± 0.9, body weight = 638 ± 46.0 kg, milk yield = 40.6 ± 6.1 kg/d, days in milk = 127 ± 54.5 d; mean ± SD) were enrolled in a 2 × 2 cross-over design with 14-d periods and were either *ad libitum* fed in morning (0800 h; DF) or in the evening (2000 h; EF). Milk production, dry matter and water intakes, rumination and lying times, and rumen temperature were automatically recorded throughout the day, and feeding behavior was characterised. Blood samples were collected at the end of the periods at 0800 and 2000 h to determine metabolic profile. Data were analyzed with repeated measures mixed models (proc GLIMMIX of SAS). Average daily temperature humidity index was always below 50. Milk yield was greater in EF than in DF (39.8 vs 37.9 ± 0.99 kg/d, $p < 0.01$), because of the lower yield recorded in DF in the afternoon milking ($p < 0.01$). However, fat content was greater in DF, resulting in similar fat yields. DMI and eating time were not different between groups (27.4 vs 27.6 ± 0.45 kg/d, $p = 0.55$; 184 vs 188.9 ± 6.6 min/d, $p = 0.23$), but EF had more and smaller meals ($p < 0.01$). Particularly, DF cows ate more in the morning but less in the overnight period ($p < 0.01$). DF cows were more active during the daytime and the opposite was true overnight, with the major difference observed between 0800 and 1000 h. Plasma glucose was greater in DF at 0800 but lower at 2000 ($P \leq 0.01$), whereas beta hydroxybutyrate had the opposite pattern ($p < 0.01$). Urea was greater in EF at 2000 ($p < 0.01$). In the present study, in thermoneutral conditions, feeding cows at night increased milk and fat yields compared with morning feeding. This change also impact feeding behavior, with a partial shifting of the main activities, and blood markers of energy metabolism.

O407

Impact of cow udder health status on milk metabolic pattern

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Udder health of dairy cows is a major concern in the field of milk production. The characterisation of biological markers associated with subclinical and clinical mastitis is a strategy to screen for udder health status in dairy cattle, to identify animals resistant to udder inflammation, and to develop decision supporting tools aimed at reducing the use of antibiotics. In this context, proton nuclear magnetic resonance (^{1}H NMR) spectroscopy can be potentially used to characterise milk metabolic markers. Therefore, this study aimed to assess the ability of ^{1}H NMR spectroscopy to distinguish milk produced by cows with different udder health status based on the milk metabolic profile. A total of 420 individual milk samples were repeatedly collected on 62 cows on a single farm (264 samples from 39 Simmental, 135 samples from 20 crossbreed, and 21 samples from 3 Holstein cows). Milks were analyzed through ^{1}H NMR spectroscopy to detect and quantify the metabolites. The same samples were analyzed for somatic cell count (SCC, cells/μL) and differential somatic cell count (DSCC, %). As regards udder health status, cows were defined as 'healthy' if SCC ≤200 cells/μL and DSCC ≤66.3%, and 'non-healthy' in all

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other cases. A discriminant analysis was performed to assess the possibility to distinguish milk produced from healthy and non-healthy cows based on ^{1}H NMR spectra. Sources of variation of the relative abundance of each metabolite were investigated through a mixed linear model that included the fixed effects of stage of lactation, parity, breed, and udder health status, and the random effect of cow nested within breed. Healthy and non-healthy cows were correctly identified in 83.3% and 82.0% of the cases, respectively. The mixed model analysis highlighted that out of the 35 identified metabolites, milk from healthy cows had a lower content of 5 compounds (with O-acetyl carnitine as the most depressed metabolite) and greater content of 6 compounds (with mannose as the most elevated metabolites) compared to milk from non-healthy cows. Results suggest that milk ^{1}H NMR spectra are useful to identify milk candidate biomarkers to discriminate healthy and non-healthy cows.

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O482

Effects of administration of vitamin D3 delivered by liposomes to dairy cows during transition period

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In high-yielding dairy cows, during the transition period (TP) the metabolism undergoes drastic changes, often inducing a poor calcium homeostasis after calving. A key metabolite for Ca absorption from gut and its mobilisation from skeletal bones is vitamin D3 (vD3), which also helps the organism to counteract negative aspects on Ca metabolism due to inflammation. The liver is involved in the conversion of vD3 over its active form, but the liver functions are often impaired in dairy cows during TP. Nano-liposome has been proposed as a potential carrier for vD3 for ruminants, even supported by results documenting its resistance against rumen fermentation *in vitro* and a good absorption in the human gut. Thus, 26 Holstein dairy cows were divided in 2 homogeneous groups and fed 40000 UI/d vD3 delivered either as a spray-dried traditional supplement (CTR) or by nano-liposome (D3LP – Lipobox® Farmer S.p.A.) starting from -21 days before calving till to 28 days after calving. The cows were checked for performance and plasma inflammo-metabolic profile. Compared to CTR, D3LP cows had lower rectal temperature at 3 days from calving (DFC) ($p = 0.06$), a tendency toward higher dry matter intake (22.8 vs 21.0, kg/d, $p = 0.09$) and milk yield (42.3 vs 39.3 kg/d, $p = 0.08$) between calving and 28 DFC, while no differences were observed for body weight, body condition score, rumination time and average milk content of fat, protein, casein, lactose, somatic cells and urea. Compared to CTR, D3LP cows had lower level of plasma haptoglobin at 3 DFC (0.34 vs 0.65 g/L, $p = 0.02$) and higher level of plasma zinc at 1 DFC (7.08 vs 4.67 µmol/L, $p = 0.03$), even suggesting a mitigated inflammatory condition after calving, while no differences appeared on the plasma concentration of the other analytes assessed. The first day after calving D3LP cows had higher plasma calcium (2.06 vs 1.84 mmol/L, $p = 0.02$), and lower inorganic phosphorus concentration (1.07 vs 1.56 mmol/L, $p < 0.01$), likely reflecting a greater gut absorption and a lowered bone mobilisation of Ca in D3LP cows, as partly justified by the lower levels of alkaline phosphatase always observed in D3LP cows. These results support the effectiveness of vitamin D3 delivered by liposome as an effective measure to lower the risk of hypocalcemia and the inflammation severity in dairy cows during the TP, which makes them more resilient in this critical phase promoting better performance and lower metabolic distress.

O551

Application of a generalized additive mixed model to evaluate the effect of season, energy status, milk yield, and milk macro-mineral content on milk fatty acids profile of Brown Swiss dairy cows

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Fatty acids (FAs) in milk help understanding the metabolic processes of dairy cows but also determining its nutritional value, with

variations influenced by factors like energy status, diet, and physiological conditions. Hence, this study aimed to investigate the pattern of milk FAs of 1,060 milk samples from Brown Swiss cows (54 farms, North Italy). Dairy cows were sampled once during the evening milking (20 cows/herd). A Generalised Additive Mixed Model (GAMM) was used to evaluate how the energy status of the cows (based on milk BHB and urea), Temperature Humidity Index (THI), milk yield (MY), milk macro-mineral profile (K, Na, and Cl), and days in milk (DIM) can influence the FAs profile. This approach combines both linear and non-linear relationships between predictors and outcomes, accounting for fixed effects (parametric terms) and non-linear effects (smooth terms) to better capture the data complexity. All milk samples were analyzed for composition using a Fourier-Transform Infrared spectrophotometer, and for minerals via wavelength dispersive x-ray fluorescence. The GAMM model included the effect of herd size, feeding management, altitude, resting area types, and milking management and parity as parametric terms, and the effect of fat*BHB, urea, Na, K, Cl, DIM, THI, and MY as smooth terms. The dependent variables tested were the FAs categorized as de-novo, mixed, pre-formed, trans, UFA, MUFA, PUFA, C16, C18, and C18:1 (g/100g of FAs). All the factors included in the model influenced the FAs ($p < 0.05$). Interestingly, the smooth effect of THI was achieved only on C18 and C18:1, whereas MY only affected de-novo, mixed, pre-formed, C16, C18, and PUFA. Considering the effect of energy status of cows, de-novo and pre-formed FAs increased with decreasing values of BHB and decreasing values of urea. Similar trend was found for the mixed FAs. MUFA (positively associated with urea) increased with the increase of BHB and the decrease of fat. Noteworthy, C18 decreased with decreasing values of BHB and increased markedly when THI exceeded 50. De-novo, pre-formed, and PUFA increased at increasing levels of Na and K, whereas C18, C18:1, UFA, and MUFA decreased at increasing levels of K. This study emphasizes the critical role of managing heat stress, energy balance, and adequate mineral supplementation in optimising milk fatty acid composition. Implementing these strategies can enhance milk quality and nutritional value, leading to improved dairy product outcomes.

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O445

Hemogasanalysis patterns modifications in Holstein Friesian and Brown Swiss lactating cows coping with a natural short-term heat wave

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The aim of the study was to assess the different adaptative hemogasanalysis patterns responses in Brown Swiss (BS) and Holstein Friesian (HF) lactating cows to a natural summer 4-days heat wave. Forty multiparous BS ($n = 20$) and HF ($n = 20$) dairy cows were involved, balanced for Days in Milk (DIM), Energy Corrected Milk (ECM) Yield and Body Condition Score (BCS). The barn was provided with sprinklers and fans that were switched off for 4 consecutive days during the occurrence of a natural heat wave. Before the switching off of the cooling system the THI conditions were under the threshold provided for both the breeds. Respiration rate (RR) was recorded at 4 AM, 3 PM and 8 PM each day. At the same time points, blood samples were collected by the jugular vein for the determination of lactate, blood pH, partial pressure of Oxygen (pO_2), partial pressure of carbon dioxide (pCO_2) hydrogen ion activity in blood (pH), base excess in extracellular fluid (BE), bicarbonate level (HCO_3^-), average Oxygen saturation (total carbon dioxide (TCO_2), using an Abbott – i-STAT portable Analyser. Hematocrit was also assessed using capillary tubes. Vaginal temperature (VT) was recorded continuously (bottom-type temperature logger iButton Temperature Loggers, model DS1922L). THI and vaginal temperatures confirmed that cows before the switching off of the cooling system were not experiencing heat stress and they started to cope with it during the four days of the natural heat wave. Moreover RR, consistently with the current knowledge, showed a high correlation with VT. All the hemogasanalysis patterns showed to be affected by the environmental temperature in both the breeds, although in BS these modifications were less wide than in HF. All the investigated patterns showed to be affected by the environmental climate conditions and by the vaginal temperature. As hypothesised, BS and HF cows recorded different hemogasanalysis patterns trends, mainly in the early adaptation period during the heatwave, confirming the different adaptive response of these two breeds in acclimatisation to warm environmental conditions. Also correlation between hemogasanalysis patterns and THI, RR and vaginal temperature confirmed that these parameters are strongly affected by animals' thermal comfort conditions. This study contributes to highlight that BS and HF cope with acclimatation challenges activating different physiological responses, as well as hemogasanalysis is a feasible way for deepening knowledge on the overall modifications in blood biochemistry and acid-base balance.

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O296

Early-life ruminal transfaunation using different types of in-vitro fermented inocula: effect in health and performance in dairy calves

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This study evaluated the effect of in-vitro fermented inocula on growth performance and metabolism in Holstein calves from 0 to 70 d of age. After receiving 3 L of colostrum, 30 calves were allocated to 3 groups ($n = 10$): control (CTR; no inoculum), high fermentability (HI; in-vitro rumen inoculum with substrate of corn and barley), and low fermentability (LO; in-vitro rumen inoculum with substrate of alfalfa and beet pulp). For fermentation, 0.5 g of ground substrate was mixed with 31.4 mL of buffer and 15.7 mL of rumen, and incubated at 37 °C for 24 hours. Then, 2.5 mL of glycerol was added to protect cells during freezing, and samples were stored at -80 °C. Calves received 15 mL of inoculum from 3 to 7 d and 50 mL from 8 to 28 d, mixed with ground feed to prevent esophageal groove closure. Calves were housed in individual hutches, fed milk replacer until weaning (60 d), and ad libitum starter (5–60 d), then ad libitum concentrate after weaning. Feed intake was recorded daily from 0 to 60 d. Body weight (BW) was recorded, and blood samples were collected throughout the study to assess metabolic profiles and volatile fatty acids concentrations (VFAs). Rumen fluid was sampled at 60 and 70 d. Data were analyzed using repeated measures (PROC GLIMMIX, SAS). The starter intake from 50 to 59 d was higher in CTR group ($p = 0.02$). BW and average daily gain did not differ among groups. At 28d, CTR calves had lower cholesterol ($p = 0.06$), protein ($p = 0.07$), and albumin ($p = 0.03$) than HI and LO. CTR calves tended to have lower phosphorus (3.06 vs 3.24 vs 3.24 ± 0.15 mmol/L in CTR, HI, and LO, respectively; $p = 0.10$) and β-hydroxybutyrate (0.11 vs 0.12 vs 0.14 ± 0.03 mmol/L in CTR, HI, and LO, respectively; $p = 0.08$). Paraoxonase was lower in HI group (58.7 vs 56.5 vs 65.0 ± 5.7 U/mL in CTR, HI, and LO, respectively; $p = 0.10$). Total plasma VFAs were lower in CTR (250.5 vs 260.9 vs 295.5 ± 34.4 µmol/L in CTR, HI, and LO, respectively; $p = 0.10$), and butyrate trends differed among groups (TIME × TRT; $p = 0.06$). Rumen proportion of isobutyric acid tended to be higher in CTR group (CTR vs HI: $p = 0.08$; CTR vs LO: $p = 0.06$), and isovalerate proportions changed over time (TIME × TRT; $p = 0.10$). Despite some differences observed in metabolic parameters and rumen fermentation profiles, the supplementation of in-vitro fermented inocula did not result in significant effects on performance or metabolism in calves during the pre- and post-weaning. Research supported by 'Romeo ed Enrica Invernizzi foundation', Milan, Italy, and by the Doctoral School on the Agro-Food System (Agrisystem) of the Università Cattolica del Sacro Cuore (Italy).

O453

Can livestock site-use intensity be estimated by observation of grazing evidences in alpine pastures?

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The vegetation of Alpine summer pastures is an essential source of high-quality feed for livestock in mountain farming systems. Livestock grazing—through defoliation, trampling, and excreta deposition—directly impacts plant species composition by removing biomass, compacting the soil, and altering nutrient availability. The effects on grassland vegetation can significantly vary across pastures due to the uneven distribution and site-use intensity of grazing animals, a variability which increases with the heterogeneity of environmental conditions. Understanding site-use intensity is crucial for implementing appropriate management strategies to preserve optimal vegetation composition. However, reliable animal distribution data are often difficult to obtain. Direct methods such as visual monitoring or GPS collars, are generally costly and labor-intensive, while indirect proxies, such as spatial modeling through distribution probability maps, may not account for all relevant variables. In a summer pasture in NW Italian Alps (Gran Paradiso National Park, 1800–2400 m a.s.l.) grazed by 100 Pustertaler-Barà (87 LU), we equipped 10 focal animals with GPS collars to monitor livestock distribution over an 83-ha area during the 75-day grazing season. Once grazing ended, grazing evidences (defoliation, trampling, dung deposition) were visually assessed on 715 ground control points regularly spaced across the pasture, using a five grade scale (1 = absence, 5 = extreme). Then we tested which of these evidences best captured site-use intensity as measured by GPS fixes in 5-m buffers around each control point. All three indices proficiently detected the variations recorded in site-use intensity across the pasture. Defoliation provided the most promising results, outlining significant differences along the scale, except for extreme intensities. Dung deposition index also

performed well, despite high precipitation in the valley might have fostered feces degradation. Trampling index was less reliable, being ineffective in differentiating among moderate, high, or extreme intensities. These findings highlight the potential of easy-to-record grazing evidences (particularly, defoliation and dung deposition) as practical tools for assessing grazing site-use intensity in extensive Alpine pastures. This approach can support effective pasture management strategies, preventing vegetation degradation and ensuring long-term sustainability of mountain farming systems.
Research supported by Gran Paradiso National Park.

O170

Optimizing dairy farm efficiency: a case study in process mapping and business process management for feeding operations

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This study adopts a process mapping approach with Key Performance Indicators (KPIs), widely used in several sectors such as manufacturing, logistics and healthcare but rarely applied in the dairy sector. The study was conducted on a dairy farm in Arborea, Italy, with 227 lactating cows. Process analysis tools, such as flowcharts and SIPOC diagrams, were used to model the current 'As-Is' feeding process, focusing on Total Mixed Ration (TMR) preparation. The analysis identified three key sub-processes: warehouse management, TMR preparation, feed distribution and animal response. A KPI framework was developed to assess performance across technical (e.g. premix and TMR homogeneity, deviation between actual and calculated rations), operational (e.g. preparation and mixing time), mechanical (e.g. equipment and wear), and animal response (e.g. feed efficiency, metabolic health, and daily yield). Results revealed a total TMR preparation time of 1 hour and 23 minutes, with the following breakdown: 13 min for loading (16% of the total time); 26 min (31%) spent on transfer operations, influenced by the farm layout and equipment arrangement; 9 min for mixing, representing 11% of the total time; 9 min for unloading, also 11% of the total; 26 min (31%) lost to unforeseen disruptions (water shortages, supplement depletion, etc). Eliminating disruptions could reduce preparation time to 57 minutes per day or 15 sec per cow. Process mapping highlighted inefficiencies and critical improvement areas, including inventory management, facility layout, and operational procedures, providing the foundation for an optimised 'To-Be' process. It allows enhancing dairy operations by maximising efficiency, with focus on rumen health, and boosting milk production. Additional improvements include reducing TMR mixer wagon preparation time, minimising feed waste, and ensuring precision and consistency in diet distribution, for efficiency and cost minimisation. The process benchmarked against industry standards and monitored with the KPI framework allows evaluating improvements in operational and economic performance and performing cost analysis. The study is part of the PhD course in Sustainable Development and Climate Change and is integrated into the 'Dairy Chain project' (PSR Sardegna 16.1- FEASR).

O499

Farm management risk factors of mastitis for mountain dairy farms in the western Alps

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Assistance and veterinary services for dairy farms are scarce in mountain internal areas, because of logistic limitations, inducing a high incidence of diseases on dairy herds, like mastitis. Here, prevention is a key strategy to improve herd's health and farm efficiency. This study aimed to identify the risk factors of mastitis at a farm management level for mountain dairy herds in the western Italian Alps. Eight dairy farms of Lanzo's Valleys were selected; 6 of them were transhumant herds. Each farm was visited 3 times: once in spring, twice in summer, 3 to 5 days after transhumance and approximately 1 month later. At each visit, milk samples from individual cow were collected for milk composition, somatic cell count (SCC) and microbiological analysis, focusing on pathogens responsible for mastitis. Simultaneously, on-farm surveys were carried out to collect data on animal characteristics, production, feeding at farm and on pasture, management practices, available infrastructure, workforce, etc. Data from individual animals were averaged at a herd level. A correlation matrix was run on microbiological and farm characteristics and management data. As expected, SCC and contagious pathogens (CnP) were positively correlated ($p < 0.01$). Both SCC and CnP were positively related to average herd lactation rank ($p < 0.05$), and negatively with barn oldness ($p < 0.01$). High SCC and CnP were associated to several variables indicating a highly extensive

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farm management: a long grazing time per day ($p < 0.05$); high altitude of grazed plots ($p < 0.01$); low annual stocking rate ($p < 0.01$), high pasture and low conserved forages and concentrate proportions in cow diet ($p < 0.05$). High CnP was also associated to large upland pasture surface ($p < 0.05$). High SCC was associated to low milk yield/cow × year, low milk yield/ workforce unit, high proportion of hay in winter diet and the time spent by walking during transhumance ($p < 0.05$). In conclusion, mountain grazing systems with a high degree of extensification (large surface, high altitude, low stocking rate, low milk yield, long cow lifespan, etc.) showed a higher mastitis risk.

O306

Exploring the relationship between mastitis risk management, milk yield and global warming potential in dairy farms

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Mastitis represents a significant challenge for the dairy industry, causing reduced milk yield, economic losses, and increased environmental impact. This study presents a predictive model to assess the risk of mastitis according to farm structures and management, and its impact on milk production and Global Warming Potential (GWP). The model incorporates factors such as bedding materials, hygiene practices, milking systems, and herd health monitoring. It has been tailored to an Italian production environment, considering Holstein cows reared in free stall housing. The impact of mastitis on the GWP of milk production has been assessed using the Life Cycle Assessment method with a 'cradle to farm gate' approach. A simulation study has been performed considering 27,456 scenarios with a milking parlor (MP) and 1,152 scenarios with the automatic milking system (AMS). In MP scenarios, the average milk production was 29.99 ± 1.96 kg, reflecting a 13% decrease compared to the baseline (optimal situation without any mastitis). Factors such as overcrowding, health surveillance, cleanliness of resting areas, and post-dipping practices were identified as key influences on production. Overcrowding led to an average 16.26% reduction in milk yield, while continuous health surveillance reduced milk loss by 10%. Bedding material also played a relevant role, with sand and straw related to smaller reductions in production. GWP in MP scenarios ranged from 1.37 to 1.78 kg CO_2eq/kg FPCM. The optimal performance in MP scenarios occurred with effective health management, continuous surveillance, sand bedding, and proper pre- and post-dipping routines, achieving 34.16 kg FPCM and 1.07 kg CO_2eq/kg FPCM in deep litter systems. In AMS scenarios, the average FPCM production was 34.75 ± 4.26 kg, with an average GWP of 1.43 ± 0.26 kg CO_2eq/kg FPCM. Continuous health monitoring and cleanliness of resting areas had a significant impact on milk yield, as well as the AMS type influenced performance. The optimal performance in AMS scenarios was observed with no overcrowding, sand bedding, cleanliness, and health group separation, yielding 43.12 kg FPCM and 0.93 kg CO_2eq/kg FPCM in deep litter systems. The model provides a framework for optimising dairy farm practices, highlighting the critical role of health monitoring, hygiene, and bedding selection in achieving sustainable milk production.

O028

Impact of two different pen cleaning protocols on ex-vivo jejunal integrity and nutrients uptake of growing-finishing pigs fed standard or low-protein diets

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This study evaluated the effects of a strict pen cleaning protocol (SCP) versus a non-strict pen cleaning protocol (NSCP) on pigs fed either a low-protein (LP) or standard (ST) diet. The focus was on measuring the active uptake of selected amino acids (L-glutamate, L-arginine, L-methionine) and glucose, as well as assessing intestinal epithelial integrity through trans-epithelial electrical resistance (TEER). A total of 21 Swiss Large White female pigs, with an initial body weight of approximately 20 kg and a final body weight of 107 kg, were used. Pigs were assigned by body weight and litter to one of four treatment groups: SCP-LP, SCP-ST, NSCP-LP, or NSCP-ST. Diets were provided ad libitum, with the ST diet containing 16.37% crude protein (CP) in the grower phase and 12.47% CP in the finisher phase. The LP diet reduced CP and essential amino acid (EAA) content (lysine, methionine, threonine, tryptophan, and valine) by approximately 20%. All diets were isocaloric and formulated according to Swiss pig feeding recommendations for average body weights of 40 and 80 kg during the grower and finisher phases, respectively. Jejunal segments were collected at slaughter and mounted in Ussing chambers to evaluate nutrient uptake and epithelial integrity. Statistical analysis was conducted using one-way ANOVA (R

version 4.3.3; 'aov' package), with cleaning protocol, protein level, and their interaction included as fixed effects. The active uptake of amino acids and D-glucose was not significantly affected by the cleaning protocol, dietary protein level, or their interaction. However, regardless of protein content, NSCP significantly increased TEER values (+28.9%, $p = 0.031$) compared to SCP, indicating improved intestinal epithelial integrity. These findings suggest that strict pen cleaning protocols may slightly reduce intestinal epithelial integrity. However, it is unclear whether this reduction has any significant impact on pig gut health. Further analyses are warranted to better characterise these effects and their potential implications for animal well-being and performance.

O485

Worldwide diversity of Holstein cattle

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Holstein-Friesian is the most reared dairy cattle breed on a global scale. Previous studies have inspected its genetic diversity, coming to the conclusion that slightly different breeding schemes had an impact on the structure of the Italian Holstein population. The aim of this study is to assess if the genomewide structure of Holstein populations can diverge at a global level. For this purpose, with the official support of World Holstein Friesian Federation (WHFF), we retrieved 250 genotypes per population from recognised Holstein Herd Book organisations across 19 countries (Belgium, Canada, Colombia, Czech Republic, Denmark, Finland, France, Germany, Hungary, Italy, Latvia, the Netherlands, New Zealand, Poland, Portugal, Spain, Swiss Confederation, Sweden and United Kingdom). We also retrieved genotypes from other countries from public databases. All of the genotypes came from cows and were produced with at least medium density to high density beadchips. We retrieved production data for each animal, and the breeding goals of each organisation in order to assess the representativeness of the sampled animals within their respective countries and to understand any differences among the populations. We calculated genetic diversity indices (Ne, He, Ho, FROH). Then, we inspected the genetic structure of the studied populations through an ADMIXTURE analysis, and an MDS. Our results show slightly different values for all the genetic diversity indices, which indicates differing management strategies of inbreeding and genetic drift. The results of the ADMIXTURE and MDS analyses provide consistent outputs, highlighting the divergence of the studied populations at various levels. This study suggests that despite significant genetic exchange, divergent breeding strategies can result in the diversification of genetic structure within the same breed, contributing to the observed diversity. Future objectives of the study are to obtain genotypes from more countries to comprehensively map the genetic variability of Holstein cattle. In the longer term, we aim to analyse this diversity and to identify genomic characteristics of each national population. This may be useful for the traceability of the products and for a transnational management of the Holstein genetic diversity.

O373

The impact of inbreeding on fertility in Italian Holstein cattle

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Genomic selection in cattle has achieved remarkable results across various traits. Recent estimates in Holstein cattle indicate an increase in genetic progress of 50% to 100% for yield traits and 200% to 300% for fitness traits, driven by genomic selection. While the negative effects of inbreeding on productive traits are well-documented, its impact on fertility is more challenging due to the complexity of the related traits. The objective of this study was to estimate with an animal model, the effect of inbreeding on reproductive traits in Italian Holstein cattle. The heifers' dataset included 37,314 individuals with fertility records including age at first insemination (AFI), first service to conception (IFL) and conception rate (CR). The cows' dataset included 29,056 individuals with fertility traits records including days at first service (DTFS), IFL and CR. The inbreeding coefficient for each individual was calculated using two methods: pedigree-based coefficients (FPED) and genomic data, which assessed runs of homozygosity (FROH). The FPED, defined as the probability of two identical alleles by descent, was computed with the OptiSel R package. The ROH segments

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were identified using DetectRUNS package in R with a minimum of 15 SNPs per run, a length of at least 1 Mb, a maximum distance of 500 kb between SNPs, a density of at least 1 SNP per 100 kb, and allowance for one missing and one heterozygous SNP per run. The FROH was calculated as the proportion of the genome covered by ROH. The effect of inbreeding was quantified by regressing phenotypes on FPED and FROH implementing an animal model in ASReml-R correcting for herd, year and parity (only for cows). In the heifers' database, an average inbreeding coefficient of 7.96% ± 2.03 based on FPED and of 17% ± 3.0 based on FROH was found. Similarly, in the cows' database an average inbreeding coefficient of 7.98% ± 2.00 based on FPED and of 17% ± 3.0 based on FROH. Preliminary results based on a subset of 11,935 heifers and 20,067 cows showed that an increase of 1% in FROH was linked with an increase in IFL of 0.32 days ($p < 0.05$) for heifers and of 0.45 days ($p < 0.05$) for cows, whereas FPED was not significant in the model. Moreover, the analysis of AFI revealed a significant effect on FROH in heifers, with an increase of 0.01 days ($p < 0.05$) for each 1% increase in inbreeding. Further analyses are ongoing to evaluate the effect of inbreeding based on the full dataset.

O065

Assessing fertility: developing an index for italian Jersey cattle

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Selection for milk production traits has led to a decline in dairy cattle fertility due to unfavorable genetic correlations. However, fertility remains crucial in dairy farming for maintaining regular productive cycles, ensuring continuous milk supply, and reducing costs tied to non-productive cows. The aim of this study was to estimate genetic parameters for fertility and production traits in Italian Jersey cattle. Conception rate (CR) and interval between first and last insemination (IFL) were used as fertility indicators, while the included production traits were milk, protein, and fat yield (MY, PY, and FY, respectively). Two datasets, one for primiparous and one for multiparous cows (parities from 2 to 4) were considered. The datasets comprised 27,999 records from 480 herds for primiparous and 30,783 records from 737 herds for multiparous. Heritability estimates for production traits were obtained using single-trait repeatability models. Additionally, a multiple-trait analysis including fertility and production traits was performed to estimate genetic correlations among these traits within each dataset. For the primiparous, the models included year-month of calving as fixed effect and herd, animal, and residual as random effects. For the multiparous, parity and permanent environmental were also added in the models as fixed and random effects, respectively. Heritability estimates for CR and IFL in the single-trait model for both datasets were low, 0.03 and 0.04, respectively. Strong favorable correlations were found between CR and IFL (–0.94 ± 0.02 and –0.98 ± 0.01 for primiparous and multiparous, respectively). In primiparous, low favorable genetic correlations were observed among fertility traits and PY and MY. In the multiparous dataset, low favorable genetic correlations were instead found among fertility traits and PY and FY. Despite low heritability estimates, findings suggest that incorporating fertility traits into breeding programs, for Italian Jersey cattle, could support balanced herd management and sustainability.

O059

Phenotypic association between hoof lesions and type traits in italian Holstein population

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Hoof lesions are a leading cause of unwanted culling in the dairy industry, contributing to lameness, production losses, and in severe cases, mortality. While over 51,000 hoof trimming records have been collected from June 2023 to January 2025 in Italian dairy herds on Italian Holstein dairy cows, there is not yet enough data for a hoof health trait. However, historical classification traits may provide a proxy trait until a sufficient lesion dataset can be established. This study examines the relationship between hoof lesion data and three type traits in first parity Italian dairy cows. Specifically, it focuses on locomotion score, overall feet and legs score, and total point score. After filtering to a single parity and merging with corresponding classification records, 6,304 binary lesion records remained from 126 herds. Preliminary analyses revealed a small but significant association between lesion presence and specific type traits. Locomotion scores showed a weak negative correlation with lesion presence (corr = –0.1004, $p < 0.05$) and an effect size of 0.211. Similar trends were observed for the correlation between lesion presence and feet and leg scores (corr = –0.1148, $p < 0.05$), with an effect size of 0.240. However, total type scores showed no significant differences

between cows with and without lesions. These findings suggest that while classified traits can indicate a higher tendency to develop lesions, there is insufficient evidence to effectively select against hoof lesions using classification traits. Further research using genotypic analyses is required to determine the genetic correlations between lesions and type traits. Identification of these genetic relationships will provide a more accurate assessment of the potential for indirect selection on hoof health via classification traits.

O443

The role of inbreeding depression in the genetic improvement program of the italian Mediterranean Buffalo

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Inbreeding depression (ID) refers to a reduction in productive performance or overall fitness caused by mating between closely related individuals. This phenomenon can occur in all species, mainly if undergoing genetic improvement programs. Examples from dairy cattle breeding show that ID is a major problem and appropriate actions should be taken to monitor and control it. In the Italian Mediterranean Buffalo (IMB) the effects of ID are not well documented and the objective of this study was to fill the gap and to estimate ID in productive traits of IMB. Results from the official genetic evaluation were used. Only buffalo cows with at least one lactation record, complete genealogy and inbreeding coefficient greater than zero were used. The final dataset included a total of 3,614 animals. The traits considered in this study were milk kg, fat and protein (% and kg), and cheese yield (kg). The approach used to estimate ID was to regress residuals from the official genetic evaluation, i.e. the differences between the observed values and the values predicted by the official model which do not consider inbreeding, on the individual inbreeding coefficient. The results showed that inbreeding negatively impacts the productive performance of buffaloes. All traits, except fat percentage and cheese yield, were adversely affected by inbreeding. For instance, a 1% increase in inbreeding was associated with a reduction of approximately 10 kg of milk per 270 d lactation ($p < 0.05$). In conclusion, these findings stress the importance of avoiding inbreeding to sustain long-term productivity and also show that in spite of the lower production level than dairy cattle, also dairy buffalo is at risk. Implementing additional mating strategies to control inbreeding and mitigate the loss of genetic diversity is essential to ensuring the success and sustainability of breeding programs for the IMB.

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O129

Comprehensive analysis of inbreeding depression across growth, fertility, and survival traits in Charolais and Limousine beef cattle

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The National Herd Book count approximately 23,000 Charolais and 92,000 Limousine cattle in Italy, underscoring their importance to the national beef industry. Monitoring genetic diversity in these populations is essential to mitigate the adverse effects of inbreeding, which can reduce fitness and key economic traits such as fertility and growth. Traditionally, inbreeding has been assessed using pedigree-based coefficients, but genomic tools now provide greater precision by incorporating genetic markers. These advancements enable more accurate identification of at-risk animals and assessment of inbreeding depression, even in populations with incomplete pedigrees. However, the rapid genetic gain facilitated by genomic evaluations raises concerns about the accumulation of inbreeding and its impact on genetic diversity. This study aimed to evaluate the effects of inbreeding and inbreeding depression on growth, fertility, and longevity in Charolais and Limousine cattle. The analysis included phenotypic comparisons between animals with higher and lower levels of inbreeding. Four growth traits (birth weight [BW], weaning weight [WW], yearling weight [YW], and average daily gain [ADG]), two fertility traits (age at first calving [AFC] and first calving interval [FCI]), and stayability (STAY; second to fourth calving) as a measure of longevity were analysed. Inbreeding coefficients were calculated using three approaches: pedigree-based (F_{PED}), genomic relationship matrix-based (F_{GRM}), and runs of homozygosity (F_{ROH}). For genomic analyses, animals were

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genotyped with a panel of 28,299 SNPs (GeneSeek GGP Bovine LD v3; Illumina Inc.). Increased inbreeding, based on either pedigree or genomic measures, was associated with reductions in BW, WW, YW, and ADG in both breeds. For F_{PED} production drops by 1.20 g, 0.25 kg, 0.19 kg, and 0.02 kg per 1% increase in inbreeding for ADG, WW, YW, and BW, respectively. Fertility traits were largely unaffected, except for AFC in Limousine cattle, where higher inbreeding was linked to an increase in AFC. Longevity was significantly impacted, with higher inbreeding negatively affecting animals' ability to remain productive over multiple parities. These findings highlight the detrimental effects of inbreeding on economically important traits in Charolais and Limousine cattle. Effective breeding strategies are crucial to mitigate inbreeding, preserve genetic diversity, and ensure long-term productivity and resilience in these populations.

O382

Changes in allele and haplotype frequencies over the years have differentiated the genomes of Italian heavy pigs from cosmopolitan breeds

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Genetic selection improves a livestock population, leading to modified allele frequencies compared to a base population. Therefore, monitoring and understanding how a population genome has been shaped by artificial directional selection is important to gain insights into the long-term effects of a breeding program. Italian heavy pig breeds (Italian Duroc, Italian Landrace and Italian Large White) have originated from the corresponding cosmopolitan breeds until tailored breeding programs designed for the needs of the Italian dry-cured ham value chain were implemented in September 1990. In this study, we monitored how the genomes of these three Italian heavy pig breeds have been shaped over the years. We genotyped approximately 13,000 pigs from these three breeds, born over three decades (from 1990 to 2021), using a 70k single nucleotide polymorphism (SNP) array. A total of 21,918 SNPs were retained after quality control with PLINK. SNPs were phased with SHAPEIT2 and haplotypes were identified with *GHap*. Over time changes in allele and haplotype frequencies were evaluated using logistic regression and delta models, implemented in the R package glm. Whole-genome resequencing datasets from 125 Duroc, Landrace and Large White pigs of other populations were obtained from the European Nucleotide Archive. From these datasets, *samtools* was used to retrieve the same SNPs used in the Italian breeds. Global Fixation index (F_{ST}) pairwise values were calculated using PLINK and population stratification analysis was conducted using the ADMIXTURE software to compare the Italian breeds with the other populations. From these analyses, the genomic profiles of the Italian breeds clearly differentiated compared to the corresponding cosmopolitan counterparts. The results demonstrated that the combination of artificial directional selection driven by specific breeding objectives and the possible effect of genetic drift have substantially modified the genomic structure of Italian heavy pig breeds.

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O322

Camelina sativa: an emerging crop that can successfully be exploited in laying hen's feeding without compromising egg quality

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The project exploited the oil and cake obtained from *Camelina sativa*, an oilseed crop that is gaining attention thanks to its nutritional profile and sustainability potential, as innovative feed ingredients for laying hens. The primary target was to test if eggs obtained from hens fed with *Camelina sativa* products could reach the claim 'rich in omega-3 fatty acids' (companion paper). However, also other quality features are of utmost importance to ensure egg marketability, including physical traits, nutritional composition and storage stability. The experiment involved $n = 100$ White Livorno hens (same age) which were distributed into two dietary groups ($n = 2$ replicated outdoor pens each). Control hens were fed a commercial diet, while CAM hens received a diet where 5% *Camelina sativa* cake and 1% oil replaced some conventional ingredients (2% soybean oil, 1% sunflower meal, 1%

soybean meal, and 2% corn) of the Control diet. $N = 12$ eggs/treatment were sampled at days 1 and 28 to assess proximate composition. Further $n = 12$ eggs/treatment (day 28) were dedicated to a retail display trial (28 days, room temperature). All the remaining eggs collected from both groups at day 28 were dedicated to physical analyses. Eggs were analyzed at the LabCNX Laboratory (University of Padova). Data were analyzed by a one-way ANOVA with diet as fixed effect. Oxidation results were subjected to a two-way ANOVA where diet and time were considered as fixed effects as well as the interaction. Results showed that CAM diet did not affect the proximate composition of hens' eggs. Instead, CAM eggs highlighted a higher fracture toughness than Control ones (4.61 *vs* 4.10 kg for CAM and Control eggs, respectively; $p < 0.01$). Both values, however, were technically satisfactory. CAM and Control eggs showed a low oxidation degree along storage, but at day 28 CAM eggs displayed higher values than Control ones (0.83 *vs* 0.75 mg MDA/kg egg, respectively; $p < 0.05$). In addition, the oxidative status of Control eggs did not change during storage, whereas CAM eggs displayed higher values at day 28 than day 0 ($p < 0.001$). Also, the interaction diet*day was significant and depicted that CAM eggs at day 28 of storage displayed a higher oxidation than both CAM and Control eggs at day 0, while Control eggs at day 28 were intermediate ($p < 0.01$). Despite the above-mentioned differences in CAM *vs* Control eggs, overall results indicated that *Camelina sativa* can provide interesting ingredients to be incorporated into laying hens' diet as partial replacement to conventional feedstuffs.

The present work was funded within the call 'Bando per il finanziamento di progetti di valorizzazione dei brevetti (Brevetti+) – Piano Nazionale di Ripresa e Resilienza – NextGeneration EU, Ministero dello Sviluppo Economico (rif. 102021000019961, prot. BRE0001475)'.

O288

Camelina sativa: an emerging crop to enhance egg healthiness and reaching the claim 'rich in omega-3 fatty acids'

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The present project aimed at developing and testing a diet for laying hens in order to obtain eggs reaching the nutritional claim 'rich in omega-3' fatty acids (FA), exploiting a resilient and sustainable feedstuff with an interesting nutritional profile and remarkable linolenic acid (ALA: C18:3 *n*-3) content: *Camelina sativa*. To this purpose, a total of $n = 100$ White Livorno hens of the same age were randomly allocated into two dietary treatments ($n = 2$ replicated outdoor pens/treatment): a group was fed with a commercial diet for laying hens (Control), and another group received a diet where *Camelina sativa* cake (5%) and oil (1%) were incorporated in substitution of conventional ingredients (CAM). Diets were isonitrogen and isoenergy and were fed *ad libitum* throughout the trial. Once a week, and for 28 days, $n = 12$ eggs/treatment ($n = 6$/replicate) were sampled and dedicated to the FA analysis and the subsequent FA content calculations (LabCNX Laboratory; University of Padova). Data were analyzed by a one-way ANOVA with diet as fixed effect. Least square means were obtained, and post-hoc pairwise comparison was carried out applying the Bonferroni correction. The significance was considered at 5% confidence level. As expected, at the beginning of the experiment eggs collected from the two groups displayed similar FA profiles, showing a 1.56% *n*-3 (119 mg/100 g egg) of which ALA was 0.96% (73.5 mg/100 g egg). Week after week, eggs of the CAM group displayed an increase of total *n*-3 (both proportion and amount) compared to the Control group. This was attributable to the ALA as well as to the eicosapentaenoic (EPA: C20:5 *n*-3) and docosahexaenoic (DHA: C22:6 *n*-3) FA. These two FA are endogenously synthesised by desaturation and elongation metabolic pathways starting from their precursor (ALA). At day 28, CAM eggs showed a 4.07% *n*-3 (313 mg/100 g egg), a 2.90% ALA (227 mg/100 g egg) and 1.05% EPA + DHA (81 mg/100 g egg), which were remarkably enhanced compared to the Control eggs ($p < 0.001$). According to the Regulation (EU) N. 1924/2006 and subsequent modifications, the nutritional claim 'rich in omega-3 FA' can be used when reaching 600 mg ALA/100 g and 100 kcal product, or 80 mg EPA + DHA/100 g and 100 kcal product. Therefore, the incorporation of *Camelina sativa* into the diet for laying hens allowed to remarkably enhance eggs' healthiness, enriching their omega-3 FA content up to reaching the nutritional claim 'rich in omega-3 FA' in 28 days.

The present work was funded within the call 'Bando per il finanziamento di progetti di valorizzazione dei brevetti (Brevetti+) – Piano Nazionale di Ripresa e Resilienza – NextGeneration EU, Ministero dello Sviluppo Economico (rif. 102021000019961, prot. BRE0001475)'.

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O086

Proximate composition and fatty acid profile of eggs laid by two Italian chicken breeds, their crossbreeds, and a commercial hen hybrid reared both in enriched cages and free-range system

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The growing focus on sustainability and animal welfare has boosted interest in local chicken breeds, valued for their resilience, adaptability, and contribution to biodiversity. These breeds, well-suited to alternative rearing systems, also offer great potential for valorisation of cultural animal foods. This study was aimed to analyze the proximate composition and fatty acid (FA) profile of egg yolk from two Italian breeds, Bionda Piemontese (BP) and Robusta Maculata (RM), their crossbreeds with the Sassò strain (BPxS and RMxS), and a commercial hybrid, Lohmann Brown (LB), reared both in enriched cages and free-range pens (3 replicates of 10 birds/genotype/system; 300 hens total). All bird was fed the same commercial diet from 25 to 66 weeks of age. Eggs ($n = 100$/group/sampling point) were collected three times at 32, 47, and 66 weeks, and yolks ($n = 6$ pools/group) were analyzed for moisture, crude protein, lipid, ash, and FA composition. FA were analyzed using a Carlo Erba HRCG 6150 gas chromatograph equipped with a FID detector. Data were analyzed using two-way ANOVA to evaluate the effects of genotype, rearing system and their interaction. The results showed that the genotype but not the rearing system significantly influenced yolk proximate composition. RMxS and LB presented higher moisture content than BP and BPxS (48.8 and 48.7 vs. 47.5 and 47.4%, respectively; $p < 0.001$). Protein content peaked in BPxS, while RM exhibited the lowest value (17.2 vs. 16.5%, respectively; $p < 0.05$). Ash content was greater in LB, BP and RM than in RMxS raised in free-range (2.43, 2.45 and 2.37 vs. 1.69%, respectively; $p < 0.05$). Genotype also affected total FA profile. BP yolks contained the highest amount of total saturated FA, while RM ones showed the lowest value (35.5 and 33.8%, respectively; $p < 0.05$). Total monounsaturated FA were more abundant in LB and RMxS yolks compared to RM ones (39.9 and 39.9 vs. 37.6%, respectively; $p < 0.01$). Both the genotype and the rearing system significantly influenced total polyunsaturated FA (PUFA) content. Indeed, while RM eggs displayed the highest PUFA content among all genotypes (28.5%; $p < 0.01$), free-range eggs exhibited higher yolk PUFA levels compared to cage ones (27.1 vs. 26.1%, respectively; $p < 0.01$). This study highlights the impact of genotype and rearing system on egg yolk composition and FA profile, providing information that might be useful to enhance the valorisation of local chicken breeds and exploitation of derived foods.
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O393

Does the farming system influence the quality of the eggs in terms of chemical composition and colour parameters?

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The growing attention of the consumers on animal welfare pushed the poultry livestock sector to replace the conventional battery cage system for laying hens with alternative rearing systems. Due to the close relation between the animal welfare and quality of the products, the farming system of the laying hens could influence the chemical composition and the physical characteristics of the eggs. The aim of this study was to compare the physical and chemical parameters of market eggs coming from different rearing system. Sixty brown and white shelled eggs from five different breeding systems have been analysed. The breeding systems considered in the study were: cage (CA), ground farm (GR), outdoor (OUT), free range (FREE), and organic (ORG). Within each breeding system 4 farms were selected from which 3 eggs were randomly analysed. The physical (weight of yolk, albumen and shell, and colour parameters of the yolk) and chemical parameters (dry matter, fat and protein content of the yolk) were measured. Data were analysed with a general mixed model in which the breeding system was considered as fixed effect and the farm as random. The eggs from FREE and ORG had lower total weight (62.26 ± 5.38 g and 62.29 ± 3.8 g, respectively, mean ± SD) compared to the eggs from CA (69.31 ± 4.0 g). The weight of the lyophilised yolk was higher in eggs from ORG and CA (9.06 ± 0.68 g and 8.97 ± 0.53 g) compared to that come from OUT (7.82 ± 0.93 g). However, no difference was found on the proportion of yolk, albumen and shell among different breeding systems. A strong difference was found for redness parameter that was lower in ORG compared to CA (3.91 ± 3.13 and 11.18 ± 5.54). The overall mean of protein and fat concentration was equal to 16.15 ± 0.39 % and 26.67 ± 0.91 %. No difference was found for protein content among the different breeding system, while eggs from CA and FREE had higher fat concentration compared to GR ($p < 0.05$). In conclusion, eggs from CA were heavier and had larger yolk compared to outdoor. Moreover, the eggs from CA had higher redness parameter compared to the ORG that might be due to colouring agents supplemented to the cage hen diet that are not allowed in the organic farms. As regard the quality of the

eggs in terms of fat, the eggs from cage and those of the free range are the most similar.

O317

Evaluation of geographical and botanical origin of Tunisian and Sicilian honeys using artificial senses and data fusion

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It is widely accepted that the nutritional and medicinal properties of honey are closely related to the botanical origin of the plants at the base of honey production. However, when discussing the nutritional and medicinal benefits of honey, it is essential to consider the importance of the geographical origin and its link to the honey composition. In other words, the geographical and floral origins are interconnected, contributing to the unique 'fingerprint' of each honey. Therefore, the main aim of this study was to assess the geographical and botanical origins of honeys from Tunisia and Italy using a sensory instrumental platform. Specifically, an E-Eye, an E-nose and an E-Tongue (Alpha MOS, Toulouse, France) were used for analysis. Thirty unifloral honey samples were analyzed, including 12 Tunisian honeys: 6 Orange (TOM) (*Citrus sinensis-Rutaceae*) and 6 Eucalyptus (TEM) (*Eucalyptus-Myrtaceae*) from the Monastir province, as well as 18 Italian samples from Sicily: 6 Orange (IOM) (*Citrus sinensis-Rutaceae*) and 6 Eucalyptus (IEM) (*Eucalyptus-Myrtaceae*) from Messina province and 6 Orange (IOC) (*Citrus sinensis-Rutaceae*) from Catania province. Additionally, the following physicochemical parameters were measured: % Brix, °Bé, water content, pH, acidity, temperature, conductivity, and dissolved solids. All results were individually evaluated and the discrimination index (DI) was calculated. These data were then subjected to data fusion and PCA analysis for a comprehensive evaluation. The results from the individual electronic instrument highlighted the relationship between botanical and geographical origin, especially with regard to volatile profile. Specifically, the E-Eye and the E-Tongue showed a very high DI (98) among all sample groups, accurately distinguishing both the botanical and geographical origin of the analyzed honeys, while the E-Nose demonstrated a greater ability to differentiate between Italian and Tunisian honeys, with some overlap between the volatile profiles of Tunisian orange (TO) and eucalyptus (TE) honeys. The results from the data fusion, which produced a DI of 92, emphasised the capacity of the artificial senses to distinguish both the botanical and geographical origin of honey, confirming their value as useful tools for honey authentication.

O039

Exploring plant-based proteins as an alternative for culture media in cellular agriculture

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The food sector is currently one of the most debated fields, particularly regarding its sustainability. While the livestock industry has actively worked to mitigate its environmental impact, scientific innovation must contribute further to address this challenge. In this context, cultured meat emerges as a revolutionary option, with the potential to overcome many ethical and environmental issues associated with conventional meat production. However, the development of this innovative product faces significant challenges, chief among them being the formulation of culture media that are free of animal-derived components, economically sustainable, and compatible with cellular requirements. For this reason, the aim of this work was to evaluate protein extracts derived from hempseeds (HSs) as constituents of the culture medium for murine C2C12 muscle cells. Specifically, following alkaline extraction and isoelectric precipitation, protein isolates from HSs were tested at various concentrations (1:2 dilutions) on C2C12 cells. The results demonstrated that all concentrations, except for the initial stock solution, effectively supported cell growth and proliferation for up to 48 h, as assessed using the Alamar Blue colorimetric assay. Among all the tested concentrations, 0.6 mg/mL was selected for further analysis and incorporated as a component of an edible bioink used for 3D bioprinting. The experiments showed that 0.6 mg/mL of HS protein extract was capable of sustaining cell viability in 3D structures for up to 7 days, as confirmed by the Live/Dead assay and confocal microscopy analysis. These findings indicate that HSs, characterised by high nutritional profile (94.6 ± 0.12% of DM; 23.1 ± 0.57% of crude protein; 27.9 ± 0.75 of lipids), hold great potential as a sustainable, accessible, and alternative protein source for the formulation of culture media in the context of cellular agriculture. Further research is required to explore other plant-based matrices or

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food industry co-products that could reduce costs and optimise cell growth parameters. The integration of natural-origin ingredients with advanced technologies such as bioprinting could pave the way for novel approaches to cultivated meat production, bringing this solution closer to commercial reality and aligning it with the principles of a circular economy.

O574

The naturalness of food production and processing: ethical perspectives and a new metric of naturalness

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The work examines the idea of naturalness in food production and processing from an ethical standpoint, highlighting that consumer demand for 'natural' products is closely linked to perceptions of health, trust, and cultural values. Drawing on insights from existing literature, the study explores different dimensions of naturalness—historical, property-based, and relational—each offering unique perspectives on what makes food 'natural'. The work introduces the Naturalness Evaluation Score (NES), a metric developed to assess the level of naturalness in food products. The NES is based on five core sub-indicators: source authenticity, technological intervention, processing, environmental impact, and transparency. Each sub-indicator contributes to an overall score, which categorises food products on a spectrum from highly natural to highly synthetic. By using this index, the study seeks to provide an objective tool to help consumers make informed decisions, support policymakers in regulating naturalness claims, and promote fairness and clarity in labeling practices. The first evaluation of the NES was carried out through the administration of questionnaires on agrifood operators' opinion leaders. Most of the respondents positively assessed the NES tool, although they suggested the need for better communication of the results and greater involvement of consumers. In general, the findings indicate that the NES is considered a promising indicator, but its implementation could be enhanced with focused efforts on communication and consumer involvement. Additionally, a more thorough exploration of how the reliability of statistical models is perceived could contribute to a better understanding and greater acceptance.

O577

Feeding *Tenebrio molitor* larvae with oilseed presscakes – Sustainable and nutrient-rich feeding substrates

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Over the past decade, insects have increasingly been recognised as a viable alternative protein source. More specifically, insect farming has gained attention for its sustainability, particularly due to insects' capacity to thrive on agricultural byproducts that would otherwise be discarded or sold at minimal value. This aligns with the principles of the circular economy by repurposing waste into valuable resources. In this context, recent research has explored the use of various agricultural byproducts as insect feed. However, the potential of byproducts derived from oilseed production—rich in protein, lipids, and energy—remains largely underexamined. Oilseed presscakes, a secondary product of oil extraction, present a promising nutrient source for insect rearing while at the same time contribute to the creation of nutrient cycles in the food system. This study evaluates the effectiveness of oilseed presscakes as single feeding substrates as well as ingredients in complex diets for the larvae of *Tenebrio molitor* (yellow mealworm). The presscakes utilised in this research were derived from the processing of pumpkin, sunflower, hemp, linseed, thistle, walnut, almond, and sesame seeds. For both bioassays, 50 early-instar larvae were introduced into vials (7.5 cm in diameter) containing each type of presscake or diet as a feed source, with agar (20 g/L) provided to maintain moisture levels. The study assessed larval survival and weight progression until pupation, while also determining the feed conversion ratio (FCR) and total development time. The findings highlight the potential of oilseed presscakes as effective feeding substrates for *T. molitor*. Indicatively, larvae of *T. molitor* grew well on sesame, almond, sunflower, and walnut press cakes. Diets consisted of sunflower and cannabis press cake, as well as of pumpkin and either cannabis, thistle, or line press cake also supported larval growth. Based on the above, this research reinforces the role of insect farming in

sustainable food systems by integrating agricultural byproducts into a circular economy framework.

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O515

Evaluation of the metabolomic profile in *Tenebrio molitor* reared on functional substrates

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The growing demand for sustainable food and feed emphasises edible insects as a viable alternative. *Tenebrio molitor* larvae offer a sustainable option able to efficiently convert low-value by-products into protein-rich biomass. Their minimal rearing requirements and potential for bioactive compound enrichment further enhance their value as functional ingredients. This study investigated the metabolomic profile of 7-week-old *T. molitor* larvae reared on innovative growth substrates ($n = 8$ trays/group, 100 g larvae/tray) over a 14-day feeding period with fresh substrate provided weekly. The experimental groups included a control group (CTRL) fed wheat bran, and two treatment groups: TRT1, supplemented with 12.5% w/w chestnut shell, and TRT2, supplemented with 25% w/w chestnut shell. Subsequently, larvae were processed into insect meals for characterising their nutritional profiles. Chemical analyses were conducted according to the standardised procedures for evaluating the content of dry matter, crude protein, ether extract, and ashes. Nuclear Magnetic Resonance (NMR) spectroscopy was employed to assess the metabolomic profile, identifying free amino acids, organic acids, sugars, nitrogen bases, and fatty acids. Results indicated a significant increase in crude protein in TRT1 compared to CTRL and TRT2 ($p = 0.0391$). Asparagine, which has been associated with allergenic glycoproteins, was detected only in the CTRL group and not in TRT1 and TRT2. Pyroglutamate, known for its antimicrobial properties in the literature, exhibited the opposite trend. Significant differences were observed for arginine, glutamine, and histidine content, which was higher in the CTRL group compared to treatment groups ($p < 0.0001$). Metabolite profiles of TRT1 and TRT2 were similar but clearly distinct from CTRL. Notably, larvae enriched with chestnut shells revealed presence of uracil, uridine, and glucose, while fumarate was absent. These compounds are associated with energy metabolism and negatively correlate with ATP concentration. Enrichment analysis displayed enhanced glyoxylate and dicarboxylate metabolism in TRT1 and TRT2 compared to CTRL. NMR spectroscopy was efficient in linking insect metabolism to growth substrates. This study underscores the potential of chestnut shells as a cost-effective substrate, enhancing the nutritional and functional properties of insect meals, and supports the use of NMR spectroscopy for detailed metabolic profiling in insect farming.

O072

Larval growth and bioconversion efficiency of black soldier fly (*Hermetia illucens*) on rice by-products: unlocking new life for agricultural waste

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Rice is one of the major cereal crops worldwide, and its processing generates several by-products that can be valorised by the black soldier fly. In this study, different rice by-products (RBP) were tested: rice husk, rice chaff, immature rice, and two types of broken rice, from white and parboiled variants. The RBP were included in analogous relative proportions in 4 iso-nitrogenous, -lipidic and -energetic diets (C, 0% rice; CR1, 11.5% white RBP; CR2, 13.5% combined white and parboiled RBP; CR3: 15% parboiled RBP). Each diet had 5 replicate trays with 14286 larvae each and 0.7 g diet/larva. The Gainesville diet served as control. Starting from six-day-old larvae, and every two days, average larval weights, pH, temperature (T-°C), and height (H-cm) of the substrates were recorded. The trial ended when the percentage difference in larval growth between two consecutive samplings was ≤50%. Larvae were inactivated at -80 °C, freeze-dried, and analyzed for dry matter (DM), crude protein (CP), ether extract (EE), chitin, ash content (%) and gross energy (GE, MJ/kg). Data were analyzed using IBM SPSS Statistics software (V20.0.0; $p \leq 0.05$). The statistical analyses included GLMM models (larval weights, T, pH, H) and One-way ANOVA (survival rate [SR], growth rate [GR], specific growth rate [SGR], bioconversion efficiency corrected for residue [BER], reduction rate [RR], waste reduction index [WRI], and larval chemical analyses). The CR1 showed the best average larval weight (155mg,), GR

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(0.02g/day), and bioconversion (DM%) (BER, 40.7%; RR, 55.6%; WRI, 8.00 – $p < 0.001$). In contrast, C displayed the lowest larval weight (76mg), GR (0.01g/day), WRI (5.2) among the treatments ($p < 0.001$) with similar BER and RR when compared to CR2 and CR3 ($p > 0.05$). However, C showed the highest substrate T (32 °C), pH (5.6), and H (8cm) in comparison with the other treatments ($p < 0.001$). Regarding larval chemical composition, C exhibited the highest CP and ash contents, along with the lowest DM and GE, among treatments ($p < 0.001$), while EE and chitin were comparable to CR3 or CR1 and CR3 treatments, respectively ($p > 0.05$). The CR1 showed the lowest CP ($p < 0.001$), similar DM, EE and ash when compared to the CR2 treatment ($p > 0.05$). Furthermore, GE was similar across RBP diets (CR2-CR3, $p > 0.05$), and chitin was unaffected by diet ($p > 0.05$). In conclusion, the use of 11.5% white rice by-products appears to be the most promising for achieving high larval biomass with efficient bioconversion.

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O556

Stabilization of canteen waste for *Hermetia illucens* larvae substrate production

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Hermetia illucens (HI) shows promise in converting organic waste into valuable by-products. This study aimed to collect and stabilise canteen food waste, evaluating its quality and safety for potential HI rearing. After collection, the waste was homogenised and treated with heat and acidification to determine the most effective method for achieving microbiological stability and safety over 120 days. Heat treatments included pasteurisation (80 °C for 20, 30, and 45 min) and sterilisation (121 °C for 20 and 60 min). Acidification treatments involved adding vinegar to lower the pH below 4.2 or adding 1g per kg of sorbic and benzoic acid. Post-treatment, samples were stored at room temperature, and microbiological analyses were performed every two weeks. Parameters assessed included pH, water activity, and counts of *Salmonella*, *Listeria monocytogenes*, total bacteria, yeasts and molds, lactic acid bacteria, *Enterobacteriaceae*, coliforms, staphylococci, and spore-forming bacteria. Data were analyzed using One-Way ANOVA ($p < 0.05$). Sterilised samples showed no detectable microbiological contamination or pathogens. The 45-minute pasteurisation resulted in a lower bacterial load compared to other pasteurisation times ($p < 0.05$), with lactic acid bacteria predominating. Shorter pasteurisation times (20 and 30 minutes) exhibited higher levels of aerobic and anaerobic spore-forming bacteria. Although *Bacillus cereus*, *Clostridium perfringens*, and *Clostridium botulinum* were not found, the high spore levels in these samples would make them unsuitable for insect breeding facilities, as spores can survive for extended periods. Acetic acid treatment, which reduced pH to 3.5–4.0 within 15 days, effectively reduced microbial loads, controlling pathogenic species and potential toxin producers. This method proved both economically and environmentally sustainable, utilising wine vinegar from discarded wine, and was selected for further seasonal testing. After 60 days in the second round of storage, acidified samples showed no pathogens, fecal contaminants, or staphylococci, although spore-forming bacteria remained at low levels (<3 log UFC/g). Acetic acid also neutralised *Listeria monocytogenes*. These findings emphasise the need for effective risk management and proper hygiene practices. They could also form the basis for a sustainable protocol for stabilising food waste from company canteens, supporting also EU legislative processes.

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O058

Transforming canteen waste into black soldier fly larvae feed: effects on growth performance and bioconversion efficiency

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The black soldier fly (BSF) larvae have a remarkable ability to bioconvert unused nutrients from organic waste into proteins, lipids, and chitin. This study aims to evaluate canteen waste as a rearing substrate for BSF larvae, leveraging their bioconversion capacity and identifying the optimal waste-based diet for growth performance and bioconversion efficiency. Since canteen waste is not yet approved for feed application, the project aims to valorise BSF larvae for technological applications. Canteen waste included discarded pasta, rice, meat, bread, vegetables, and fruit scraps. To ensure safety, it was stabilised with acetic acid, chosen based on microbiological, economic, and environmental considerations. Stabilisation aimed to standardise nutritional composition throughout the year despite variability. After stabilisation, the treated waste was incorporated into a core diet (Gainesville

diet; GA) at increasing inclusion levels: 0%, 10%, 20%, 40%, 60%, 80%, and 100%, labelled GA, W10, W20, W40, W60, W80, and W100, respectively. Each diet was inoculated with 12.500 5-day-old larvae (0.8 g/larva, 5 replicates per diet) and reared under controlled conditions (28 °C, 60% RH, 0:24 L:D). Larvae were sampled every two days until growth rates dropped below 50% between two consecutive samplings. Final larval weight, total biomass, and frass were measured, while survival rate and bioconversion parameters calculated: Bioconversion Efficiency Corrected for Residue (BER), Reduction Rate (RR), and Waste Reduction Index (WRI). Statistical analysis was performed using One-Way ANOVA ($p \leq 0.05$). Results showed high mortality in W100, preventing trial completion. Development time varied, with peak larval weight at 12 days for GA, 14 days for W10 and W20, 16 days for W40, 20 days for W60, and 28 days for W80. W40 larvae had the highest weight ($p < 0.001$) and BER ($p < 0.001$), outperforming all other groups. The GA diet had the highest WRI ($p < 0.001$), indicating faster growth, while W60 and W80 had the highest RR ($p < 0.001$), likely due to higher moisture content causing evaporation. In conclusion, W40 was the most effective substrate. These findings confirm that canteen waste, when properly combined with a core diet, can support BSF larvae rearing, offering a sustainable waste management solution while contributing to the circular economy. Moreover, canteen waste stabilisation and mixing with a core diet could reduce the impact of nutrient variability on larval growth and bioconversion.

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O161

Meat-based diets for *Hermetia illucens* larvae: effects on growth and proximate composition

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Edible insects are an innovative food and feed resource that is rapidly gaining interest worldwide, as they represent a valid solution to current sustainability issues and food security. Among the species used, black soldier fly (BSF, *Hermetia illucens*) is one of the most reared species for feed purposes, due to its ability to bio-convert a wide variety of substrates (high in proteins and lipids). Farmed insects for feed and food purposes are considered in the European Union fully-fledged farm animals (Reg. EU 1069/2009) and, as such, rearing substrates must be composed of the authorised ingredients (Reg. EU 68/2013), which does not include any feed component containing meat or fish (Reg. (EC) 999/2001). This study explored the effects of meat-based diets on growth performances and proximate composition of BSF larvae. Three rearing substrates were formulated (three replicates/diet); one made by 100% plant ingredients (C) and two containing a mixture (1:1:1) of pork, chicken and turkey meat in raw (R) and processed (P) forms (75% plant ingredients +25% raw or processed meat). For each crate, 1000 nine-year-old larvae were employed, feed was administered once. Larvae were sieved at the appearance of the first prepupae. Better growth performances were reported in meat-fed larvae, which resulted in higher growth rates (5.42 mg/d, 5.30 mg/d, 3.86 mg/d for R, P and C larvae respectively; p value 0.013) and consequently shorter development time (20, 21 and 22 days for R, P and C larvae respectively). Likewise, FCR values (5.13, 5.36, 6.60 for R, P, and C larvae, respectively; p value 0.009) highlighted the better performances of the meat-fed larvae. Unexpectedly, larvae did not show significant differences in protein content, whereas larvae fat contents followed the diets characteristics, with higher amounts of fats on DM respectively in larvae fed R, P and C (17.24%, 14.27%, 8.72%; p value <0.001). No changes were highlighted for DM and ashes. These results proved the suitability of meat-based substrates in BSF larvae rearing, confirming the potentiality of BSF to play a key role in a circular economy system, increasing food-chain productions and reducing waste material. The authorisation of meat-based substrates for insects rearing would represent a huge step forward in terms of sustainability, giving a second life to wastes and by-products containing meat. Future studies will focus on potential risks related to the use of meat-fed larvae as feed and food.

O578

Sustainable management of dairy waste: exploring *Hermetia illucens* (L.) bioconversion potentials for efficient effluent treatment

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Current dairy waste management focuses on reducing organic material to mitigate pollution, odors, and pathogens rather than

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adopting sustainable solutions. This study explores black soldier fly larvae (BSFL) (*Hermetia illucens*) as a biological agent for processing eight dairy waste effluents, including expired dairy products and lactose byproducts. Rearing substrates combined these wastes with wheat bran, while water-soaked tea leaves were also tested. Control diets included wheat bran with water and poultry feed with water. BSFL growth and survival were monitored every three days until 5% reached the prepupal stage. All dairy waste substrates supported high BSFL survival (>90%) and rapid development (10–13 days), with yogurt-based diets yielding the highest larval weight, frass production, and superior feed conversion efficiency. Proximate analysis showed that all diets, except for tea leaves, produced high-quality larvae with 30–40% dry matter, >30% protein, and >20% fat. These results highlight BSFL's potential to upcycle dairy waste into valuable biomass, supporting biorefinery applications such as animal feed, lipid extraction, and chitin-based bioplastics.

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O274

Methane emission assessment in Simmental bulls divergent for feed efficiency

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Methane generated from the livestock sector represents a relevant environmental issue as well as a significant energy loss for the animals. Feed efficiency is a widely investigated trait that could be a useful tool to reach sustainable animal production. Selecting animals with high feed efficiency represents a possible cumulative and permanent way to reduce environmental impact. The present study aims to evaluate the methane production of growing bulls divergent in feed efficiency using a laser methane detector (LMD). This instrument represents a cheap and easy alternative to gold standard methods when methane is assessed *in vivo*. In our trial, 128 Italian Simmental bulls were monitored for 3 days, and for each subject, the methane production was measured for 5 minutes twice a day using LaserMethane Smart (CrowCon instruments). Analysing the collected profile, respiratory peaks, eructation peaks, and their intensity were identified for each animal. Animals were divided into high and low feed efficiency groups based on their residual feed intake, and the main traits of methane production were compared. Overall, a comparable number of total peaks (respiratory + eructation) with similar average concentration (47.91 ppm/m) characterised the two groups. Furthermore, the eructation events did not differ in total number (17.37 peaks on average) or intensity (144.3 ppm/m), leading to an estimated daily methane production of 250.4 g CH_4/day with no significant difference between the two groups. The results achieved suggest that enteric methane production does not differ between growing bulls divergent for feed efficiency. Research supported by PRIN2022 M4C2 Inv.1.1 'Improvement of assessment at individual level of feed efficiency and methane emissions: From research to cattle breeding' 2022KSFEKE. Funded by the European Union – NextGeneration EU.

O087

Impact of farming systems and welfare indicators on milk infrared-predicted enteric methane emissions in Parmigiano Reggiano cheese production area

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Reducing enteric methane emissions (EME) is an important goal for the dairy industry due to its contribution to global climate change. Certified food chains, such as Parmigiano Reggiano (PR) cheese, are particularly interested in monitoring their environmental impact. However, measuring EME production is complex and expensive. A cost-effective, rapid method applicable at the population level is calculating EME characteristics by predicting fatty acids (FA) using milk Fourier Transform Infrared (FTIR) spectroscopy. This study assessed the variation of EME-derived traits according to dairy farming systems and farm global animal welfare (AW) in the PR production area. This study merged milk test- day records, FTIR spectra and farm AW assessment information into a final data set containing 1,277,747 records corresponding to 176,663 cows and 940 multi-breed dairy farms. Dairy systems were identified using a clustering approach. The EME traits included: CH_4 yield per kilogram of DMI (dry matter intake, CH_4/DMI), CH_4 intensity of milk (CH4/CM), daily CH_4 production per cow (dCH_4), CH_4 intensity of fresh cheese (CH_4/CY_{CURD}) and CH_4 intensity of cheese solids (CH_4/CY_{SOLIDS}). The EME traits

were calculated from milk FAs predicted from milk FTIR spectra. The global-farm AW parameters included in the model were: management (MGT), structure and equipment (SAE) and animal-based measures (ABM). These parameters were divided into classes based on the score (0–100%): low (≤25th), medium (>25th to ≤75th) and high (>75th). The linear mixed model included as fixed effects days in milk (DIM), month, year, parity, breed, dairy system, and the interactions of breed with DIM, dairy system, and parity. Random effects were animal nested within breed, and herd nested in the interaction between the dairy system, MGT, SAE and ABM. The dairy system and its interaction with breed effects were significant for all traits ($p < 0.05$). Regarding AW parameters, MGT was significant for CH_4/DMI and dCH_4, while ABM was significant for dCH_4. The AW effect on EME varied in direction depending on the trait. Regarding the dairy system, the modern dairy system using total mixed rations had higher daily EME per cow but lower EME when adjusted for production traits compared to the other systems. These findings emphasize the necessity of integrating multiple factors for a comprehensive evaluation and monitoring of the environmental impact of dairy production.

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O427

Seasonal pattern of enteric methane emissions in dairy cow

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The influence of season on greenhouse gas (GHG) emissions from livestock buildings is not clear, and very little is known about the existence of a seasonal pattern of enteric methane emission in dairy cows. Therefore, the objective of this study was to compare the emissions of CH_4 and CO_2 in dairy cows during winter and summer seasons. The trial was carried out on a commercial dairy farm, where an average of 64 lactating Holstein Friesian cows was monitored for one month during winter and summer. Cows fed a total mixed ration that did not vary among the two seasons. CH_4 and CO_2 emissions were determined using the Sniffer system (Tecnosens, IT) that allows to continuous measurement of the gas concentrations recording data at 1-second intervals. The Sniffer was installed in the automatic milking system (AMS) with the sampling tube reaching the AMS feeder to catch the exhaled breath while the cows were milked. Daily CH_4 and CO_2 concentrations for each animal were calculated by matching the sniffer and the AMS dataset and defining the emissive levels per cow visit. Raw data of emissions were cleaned by using standardising criteria that were applied to the winter and summer dataset including the removal of the outlier and negative data, and the background gas correction. The average milk production during summer was approximately 5% lower compared to the winter period. Analogously, also the emissions of CH_4 and CO_2 were lower during summer. Average daily emissions of CH_4 and CO_2 per animal were respectively 538.8 ± 136.5 ppm and 6766.7 ± 1519.5 ppm in winter, and 269.4 ± 85.1 ppm and 3415.2 ± 910.4 ppm in summer. However, the CH_4-to-CO_2 ratio calculated from the average concentrations per season was 0.08 for both periods. Further studies and information are necessary to confirm the trend described in winter and summer and additional trials need to include the measurement of CH_4 and CO_2 emissions during spring and autumn to provide a complete overview of the potential seasonal influence on the enteric emissions.

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O377

Assessment of enteric methane emissions in three Italian dairy cattle breeds using Dairy Herd Improvement (DHI) data

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In recent years, the dairy sector environmental impact, particularly methane (CH_4) emissions, has drawn significant attention due to its role in global warming. Establishing context-specific emission factors baselines is essential for accurate inventories, evaluating mitigation strategies tailored to regional conditions. Our study evaluated the IPCC Tier 2 approach for estimating CH_4 emissions, comparing results based on default values and

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diet-specific data across three dairy cattle breeds in Italy. Data were collected from 138 farms housing Holstein, Red Pied, and Brown Swiss breeds, encompassing 8,172 lactating cows, 7,163 heifers, and 1,172 dry cows. Longitudinal DHI data included information on milk yield, fat and protein content (FPCM), and herd composition. Dietary data encompassed detailed daily ration composition and feed quantities for each animal category. Enteric CH_4 production (MeP), yield (MeY), and intensity (MeI) were estimated for three dairy cattle categories across three breeds using two methods: (i) the IPCC Tier 2 (2021) approach with default values for diet digestibility (DE), NDF and daily Gross Energy Intake (GEI) estimated via an energy model, and (ii) the IPCC Tier 2 (2021) approach incorporating specific diet data for DE, NDF, and GEI. Subsequently, CH_4 farm intensity (kg CH_4 per herd/kg FPCM) was evaluated. Mean differences were assessed with Kruskal-Wallis test. The study revealed significant differences ($p < 0.05$) in emissions among the breeds. Holstein cattle exhibited the highest MeP (443.5 ± 55.6 kg CH_4/d) emissions but the lowest MeI (13.9 ± 3.8 kg CH_4/kg FPCM), whereas the Red Pied showed the lowest MeP (411.0 ± 65.3 kg CH_4/d) emissions but the highest MeI (19.5 ± 6.3 kg CH_4/kg FPCM). A similar trend was observed in CH_4 farm intensity (CH_4herd/kg FPCM; 21.2 ± 6.0 in Holstein and 30.0 ± 9.9 in Red Pied). The estimation method significantly influenced CH_4 emission estimates. In Holstein cattle, lactating cows demonstrated higher MeI, while dry cows had higher MeP, and heifers exhibited higher MeP and MeY. Additionally, farm intensity was higher in this breed. For Red Pied cattle, higher emissions (MeP, MeY) were observed in lactating cows and heifers; and MeP only in dry cows, also displaying increased farm MeI. The findings of this study have the potential to facilitate a more accurate quantification and monitoring of enteric CH_4 emissions at the farm level in the Italian scenario.

O417

Effect of green forage on enteric methane emissions in Mediterranean dairy buffaloes during summer: different approaches for measurement

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In ruminant species, diet plays a pivotal role in modulating fermentative processes and, consequently, shaping enteric methane (CH_4) emissions. Accurate assessment of the impact of diet on CH_4 production requires robust measurement techniques, which have been adopted only to a very limited extent in dairy buffaloes. This study was aimed at investigating the effect of green forage inclusion in the total mixed ration (TMR) of lactating buffaloes on CH_4 and CO_2 emissions. The trial was carried out during summer (July-August 2024) by using two different CH_4 and CO_2 detection approaches: A Sniffer system (Tecnosens, IT), and a Green-Feed unit (C-Lock Inc., US). A first group of 33 buffaloes were milked by an automatic milking system (AMS) where a Sniffer was installed by placing the air inlets in the feed bin. The Green-Feed unit was used for a group of 25 ear-tagged buffaloes, which were milked through a conventional milking system. Training of this group of animals to make them voluntarily approaching the Green-Feed lasted four weeks, and at the end of trial 10 buffaloes had visited the instrument providing experimental data. In July, both groups were fed the standard TMR diet for three weeks. Over the next six weeks, experimental animals were fed the test diet, which included 5 kg/head/day of *Sorghum bicolor* as green forage in the TMR. The two diets were formulated to be iso-proteic and iso-energetic. The TMR was distributed two times per day using a towed mixer wagon to ensure consistent mixing and uniformity. Daily dry matter intake (DMI) was calculated as the difference between the total TMR provided and the 24-hour feed refusals. Values of ambient temperature and relative humidity, were recorded continuously using a datalogger and were used for calculation of the temperature humidity index (THI). Values of THI did not vary during the nine weeks of the trial, and the DMI did not differ between buffaloes fed standard or test diet. Finally, regardless the detection approach utilised, no significant differences for CH_4 and CO_2 emissions were found between animals fed the two diets. In conclusion, results from this preliminary study indicated that the addition of green forage to buffaloes' diet would not affect CH_4 and CO_2 emissions. To strengthen and expand results reported herein, further trials involving a higher number of animals and considering potential seasonal effects are being carried out.

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O049

A data fusion approach unveils the impact of 3-nitrooxypropanol on the rumen fluid and milk metabolomes of lactating Holstein dairy cows

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This study utilised an integrated approach, combining rumen and milk metabolomic profiling, to investigate the biochemical effects of 3-nitrooxypropanol (3-NOP), an effective and safe methanogenesis inhibitor with benefits on dairy environmental sustainability. A controlled feeding trial was conducted with dairy cows fed a diet supplemented with 60 mg/kg dry matter (DM) of 3-NOP in two experimental periods (i.e. winter and summer feeding phases). Rumen fluid and milk samples were collected and analysed using ultra-high-performance liquid chromatography coupled with high-resolution mass spectrometry (UHPLC-HRMS). Metabolite profiles from the treated ($n = 28$) and control ($n = 28$) groups were compared to assess the impact of 3-NOP on rumen fermentation and milk composition. Statistical analyses revealed that the treatment (3-NOP) and experimental period significantly influenced rumen metabolites, whereas no significant differences were observed in the milk metabolome due to 3-NOP supplementation. Untargeted metabolomic analysis, supported by supervised and unsupervised multivariate statistics, identified significant alterations in rumen metabolites. Key findings included a reduction in methanogenesis-related compounds (e.g. methyl-coenzyme M and coenzyme B) and shifts in metabolic pathways associated with nitrogen and nucleic acid metabolism, indicative of changes in microbial fermentation and protein synthesis. As far as the milk metabolome is concerned, the changes in some discriminant metabolites (i.e. glycerophospholipids, small peptides, and nucleic acids) reflect modified rumen fermentations and overall suggest that 3-NOP does not significantly affect the metabolic status of dairy cows.

O211

Nutritional and chemical characteristics of hay-based diets as predictors of ruminal and intestinal microbial development and function

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Although gastrointestinal symbiotic microbial population is known to adapt to different diet characteristics, little is known on the dynamics of microbial populations and their functionality in the rumen and intestine of cows fed hay-based diets. The objective of the study was to investigate a possible relation between the dairy cows' diets nutritional and chemical characteristics, and microbial protein synthesis in rumen fluid and large intestine. Rumen fluid and fecal samples were collected, via stomach tube and from the rectum respectively, from 30 pluriparous cows fed hay-based diets, blocked by parity, milk yield and days in milk (DIM). Microbial protein yield, enzyme activities (cellulase, emicellulase and amilase) and pH were determined in rumen fluid and feces. The volatile fatty acids (VFA) were quantified in the rumen fluid. Samples of diets were collected and analyzed for dry matter (DM), Ash, crude protein (CP), ether extract (EE), neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), Starch, potentially digestible NDF (pdNDF), undigestible NDF (uNDF) and Amino acid profile. Based on the diet characteristics, data were analyzed dividing the animals alternatively in the following groups: low(L), medium (M) and high (H) forage/concentrate ratio (FC), CP content and NDF/starch ratio. Differences between microbial protein load (MPl), enzymatic activity and pH in rumen fluid and feces, and AGV in rumen fluid were analyzed by GLM procedure; a stepwise regression was applied to determine the variables which best predicted variation in rumen and fecal parameters. In L-CP cows, rumen AGV and fecal amylase, cellulase, and microbial biomass were significantly lower than in the other groups ($p < 0.05$). In the L-NDF/starch group the ruminal CP (as % of microbial mass), the entodynomorph and the total protozoal count were significantly higher than in the others (5.57 ± 0.42 vs 3.67 ± 0.42; 197.70 ± 51.4 vs 313.76 ± 51.4; 209.85 ± 52.98 vs 331.82 ± 52.98; $p < 0.05$). Amylase was also higher in the feces of the L-NDF/starch group (116.60 ± 0.12 vs 200 ± 0.12; $p < 0.05$). The ruminal butyric acid was significantly

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lower in the H-FC group (104.21 ± 37.43; 146.04 ± 37.43; 232.36 ± 37.43; $p < 0.05$) compared to the others. The stepwise regression analysis showed that the FC and the PG levels explain the propionic and lactic AGV, the rumen cellulase and, in the feces, the CP in the microbial mass and amylase (R2 > 0.90). The results suggest that a better understanding on the role of FC and CP in affecting the microbial mass in the digestive system may be key in regulating these populations to improve animal performance.

O434

Evaluation of two feeding strategies applied to robotic milking in primiparous cows

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The success of robotic milking systems (RMS) relies heavily on the ability to stimulate cows to voluntarily access the robot through a feedstuff lure. The latter is usually exploited also to customise the supply of nutrients to the dairy cows based on their specific requirements. This is particularly relevant for primiparous cows, whose growth requirements can limit productivity. We hypothesised that a high-energy feedstuff supplied at low doses may increase milking frequency (MF), while improving partial mixed ration intake (PMRI) and milk yield in primiparous cows. A commercial dairy herd, housing an average of 80 primiparous Holstein cows (643 kg BW, 175 DIM), located in northern Italy and equipped with 2 RMS (GEA DairyRobot R 9500, GEA Bönen, Germany), was involved in a double-reversal design. Two feeding strategies (FS) were tested: high doses of low-energy feedstuff (HDLE; %DM: NDF 31, starch, CP 19) and low doses of high-energy feedstuff (LDHE; %DM: NDF 18, starch 34, CP 21), supplied in the RMS at an average amount of 3.5 and 2.5 kg/cow/day, respectively. The trial was divided into 4 periods of 30 days (HDLE-LDHE-HDLE-LDHE), with 23 days of adaptation followed by 2 samplings performed at an interval of 7 days. Daily PMRI was measured at the herd level during each sampling. Feedstuff consumption, MF, n. of visits, n. of failures and daily milk yield were recorded individually twice, while individual feeding, ruminating and inactivity times were recorded daily, during the 7 days interval of each experimental period. Milk samples were collected individually on sampling days and analysed using MIRS to assess milk quality. Data were analysed through ANOVA using SPSS software (IBM SPSS Statistics for Windows, Version 28.0; IBM Corp., Armonk, NY). Despite different feedstuff consumption levels (3.37 vs 2.79 for HDLE and LDHE, respectively), no variations were observed in PMRI, DMI, daily milk yield and quality between the 2 FS considered. Although not significantly, the application of the LDHE strategy increased MF (3.4 vs 3.24 for LDHE and HDLE, respectively) and decreased the n. of failures (1.12 vs 1.94 for LDHE and HDLE, respectively). Higher feeding and rumination times, along with lower inactivity times were recorded under the LDHE strategy (258 vs 233 min, 38 vs 34 %, 645 vs 698 min for LDHE vs HDLE respectively, $p < 0.05$). The LDHE FS can promote a more homogeneous daily diet intake improving the rumen activity of primiparous cows.

O419

Comparing nitrogen supply from hay-based diets fed to dairy cows having low or high nitrogen excretion

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This study aims to characterise the nitrogen (N) supply from hay-based diets fed to lactating dairy cows (LC) having low or high N excretion (lNEx or hNEx). Twenty herds (184 ± 89 cows; 178 ± 19 DIM; 678 ± 33 BW) were enrolled in the study. Feed intake and diet formula were recorded by farm during 2 consecutive days. Dietary ingredients and the TMR offered and refused were sampled, chemically analyzed, and feeds analysis were inputted in the CNCPS model to estimate N fractions. Fecal and urine samples were collected 4 and 2 times respectively, from 10% of the LC. Milk yield was recorded, and 2 bulk milk samples were collected at 12h intervals. The BW was measured on 20% of the LC. The urinary creatinine content was determined through the Jaffe colorimetric method and used to calculate urinary output. The dietary and fecal uNDF was measured through 240 h in vitro fermentation and used to estimate fecal output. The N content of diets, orts, faeces, urine and milk was determined by Dumas method and used to calculate N intake (NI), fecal (FN) and urinary (UN) N excretions (NEx). Milk Urea Nitrogen (MUN) was determined by Milkoscan and summed to FN and UN for NEx calculation. The dietary aminoacid (AA) content was estimated using the internal standard method (Trp), and an external calibration curve (all other AA) after analysis of the samples through RP-UPLC/ESI-MS in the SIR scan mode. The herd were categorised as low, intermediate, or high NI (<600, 601 to 650 and >650 g/d respectively) and, within each intake category, as lNEx or hNEx (respectively the lower and higher 50% of the data). Differences in N nutrients supply were assessed through Student's T test setting the statistical threshold at $p < 0.10$. The diets administered to lNEx (μ= 439.29 ± 63.89 g/d) and hNEx

(μ= 549.15 ± 61.65 g/d) were similar for CP content (16.70 ± 1.12 and 16.3 ± 0.94% respectively) and no differences were found in the proportion of the N fractions. The diets fed to the lNEx herds had higher content of Met (0.26 ± 0.03 vs 0.24 ± 0.02% DM; $p = 0.040$) and Ser (0.66 ± 0.07 vs 0.61 ± 0.04% DM; $p = 0.034$), and a trend for a higher content of Ala (0.0.67 ± 0.04 vs 0.64 ± 0.05% DM; $p = 0.058$), Thr (0.57 ± 0.06 vs 0.54 ± 0.03% DM; $p = 0.090$), and total AA (12.08 ± 0.87 vs 11.40 ± 1.01% DM; $p = 0.061$). The NEx from LC fed hay-based diets seems to be reduced by the administration of higher amount of AA, particularly Met and Ser, but is not affected by the N fractions addressing also the role of dietary energy, management and genetic in modulating NEx.

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O549

Urinary mineral excretion in dry cows during prepartum period

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The control of mineral supplementation during the prepartum period is considered essential to prevent clinical and subclinical hypocalcemia and other mineral disturbances after calving. Moreover, an inefficient management of mineral resources can increase production costs and contribute to nutrient accumulation in agricultural soils, with potential negative impacts on the ecosystem. This study aimed to evaluate urinary mineral excretion patterns in prepartum dairy cows, during the critical summer period, on field conditions. Between July and October urine samples were collected monthly from 172 dry Holstein cows in 4 different farms (A, B, C, D), on average 20 ± 3 days before the expected calving date. Urine pH and chemistry analysis including Cl, K, Na, Mg, Ca, and P were investigated. The concentration of urinary minerals was normalised to urinary creatinine one. Dry cows were fed with TMR supplemented with anionic salts to prevent the risk of milk fever, based on the farm nutritionist recommendations. Diets' composition and mineral content were analyzed using NIRS and X-Ray Fluorescence Spectrometer (XRF). Feed and urine data were statistically analysed by mixed model having farm as a fixed effect and cow as random (JMP Pro v.18). Diets differed for levels of Cl, Na, Mg, S and Ca. Farm A had the highest dietary levels of Cl, Na and Mg and the lowest level of Ca, compared to the other farms, while S content was significantly higher in farm B. Farm A resulted to have the lowest average dietary cation-anion difference (DCAD), (–209.54 mEq/Kg DM), while average DCAD values observed in the other farms were positive (+122.27 mEq/Kg DM). As expected, urinary pH and mineral excretion were significantly affected by the dietary DCAD. Urine pH was lower in animals housed in farm A compared to the others (6.42 vs 7.33), and farm A exhibited higher urinary excretion of Na, Mg, Cl and Ca, suggesting an effective dietary-induced calcium mobilisation and Mg absorption. The study highlights the high variability of mineral supplementation among farms, despite the accepted recommendations for dry cows. Moreover, these results underline the importance of monitoring urinary mineral excretion in the prepartum period to improve calcium status and to optimise dietary supplementation. An integrated approach that considers seasonal metabolic needs, feeding procedures, and environmental impact is essential for precision nutrition in dairy farming.

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O540

Feeding behavior in heat-stressed heifers under different management practices

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This study aimed to evaluate the effects of different housing management strategies on the feeding behavior of Italian Holstein heifers during the summer in Northern Italy. Specifically, it assessed the impact of twice-daily feeding and the use of micro-cooling strategies. The 42-day trial was conducted during summer and involved 36 heifers (average age: 13.7 months), randomly assigned to three experimental groups ($n = 12$): (F) with water-cooled mattresses and a micro-cooling system at the level of feeders and waterers fed once a day at 12 pm; (N) feed twice a day at 6 am and 11 pm; (C) fed once a day at 12 pm without microstructural intervention. Environmental temperature and relative humidity were continuously monitored, and the temperature-humidity index (THI) was calculated. Feed intake (FI), dry matter intake (DMI), and water intake (WI) were measured daily, as well as the number of feeding and water visits and the time spent eating and drinking. Data were analyzed using the proc GLIMMIX of SAS and significance was assigned at $P \leq 0.05$. The results indicated that

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the different management strategies significantly affected DMI, FI and feeding behavior. No significant differences were observed in the time spent at feeding stations or the number of feeding events between groups. However, within three hours post-feeding, heifers in groups F and C (fed once daily; C: 5.64 ± 0.30; F: 5.30 ± 0.30 kg) exhibited significantly higher feed intake compared to group N (fed twice daily; morning: 3.51 ± 0.18; evening: 3.30 ± 0.18 kg; $p < 0.05$). Additionally, groups F and C showed higher feed intake during the eight hours following the single administration, whereas group N, had a more stable feeding pattern, characterised by reduced daytime feed intake and increased nocturnal activity. No significant differences were observed in WI among the groups, however when THI exceeded 75 animals in groups C and N spent significantly more time at the watering station compared to group F. In conclusion, micro-cooling systems and feeding schedules significantly influenced feeding and drinking behavior of Italian Holstein heifers during summer.

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O349

The impact of pre-weaning plan of nutrition on mammary gland development of dairy calves

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An adequate plan of nutrition for calves during the pre-weaning stage plays a crucial role in their growth and development, with long-term effects on lifetime productivity. In this context, an increased plane of nutrition impacts not only body weight (BW) and body growth, but also organ growth and development including the mammary gland (MG). The aim of our study was to evaluate differences in MG development in calves fed an enhanced or conventional plane of nutrition during the pre-weaning phase. Sixty-four Holstein heifer calves were assigned to two treatments at 2d of life ($n = 32$/trt): enhanced (ENH; 9 L/d) milk replacer (MR; Land O Lakes Cow's Match Cold Front) or conventional (CON; 3.99 L/d) MR, from birth until weaning (56 d). Calves were individually housed with ad libitum access to starter at 3d (Purina Ampli-Calf 22). The MG measurements (teat length, distance between teats, and ultrasonography) were taken at 28, 42 and 56d. Distance measurements were taken using digital calipers and mammary ultrasounds (Mindray Z60, Shenzhen, China) were performed using a convex probe to visualise MG size. Twenty-four calves ($n = 12$/trt) were euthanised at 61.92 ± 0.17d, where the MG parenchyma (mPAR) was dissected away from the fat pad (mFP) and weighed. Data were analyzed with PROC MIXED of SAS. Results show that the ENH group have longer front teats (10.64 *vs.* 9.91 ± 0.22 mm; $p < 0.05$) and longer rear teats (9.17 *vs.* 8.51 ± 0.19 mm; $p < 0.0001$) compared to CON group. Similarly, the estimated MG area was larger in ENH compared to CON calves (619.46 *vs.* 529.39 ± 15.14 mm^2, respectively; $p < 0.0001$). Additionally, ENH calves showed higher mFP weight (180.23 *vs.* 78.71 ± 12.26 g; $p < 0.0001$) and mPAR weight (6.51 *vs* 2.50 ± 0.79 g; Trt: $p < 0.05$) compared to CON calves (weights expressed as absolute values, not adjusted for BW). Furthermore, the mFP area measured with ultrasound was significantly larger in ENH calves (1,214.25 *vs*. 711.63 ± 97.75 mm^2; $p < 0.001$) as well as the mPAR area (936.32 *vs*. 639.04 ± 92.18 mm^2; $p < 0.05$), compared to the CON calves.

These findings highlight that an enhanced plan of nutrition in calves during the pre-weaning phase significantly enhances MG development, as evidenced by increased teat length, MG area, and weights of both mammary parenchyma and fat pad. Providing enhanced nutritional strategies during early life plays a crucial role in promoting MG development, with potential benefits for future lactation performance in dairy cattle.

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O448

Rumen epithelium transcriptome changes in response to polyphenols-enriched olive cake supplementation in finishing Limousine bulls

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Integrating olive cake (OC) into animal diets represents an established strategy to promote circular economy principles while potentially enhancing the quality of animal-derived products. However, whether OC can improve animal health and influence ruminal response remains uncertain. This study aimed to assess the impact of polyphenol-enriched olive cake (EOC) supplementation on the rumen epithelium transcriptome of finishing Limousine bulls. Thirty bulls, averaging 303.77 ± 42.84 days of age and 446.50 ± 18.11 kg body weight (mean ± SD), were enrolled in the study for an 80-day feeding trial. The animals were randomly assigned to two groups: the treatment group, which received a concentrate diet with 13% EOC inclusion, and the control group, which was fed a standard concentrate diet without EOC inclusion. At slaughter, ruminal papillae were harvested from the ventral sac of the rumen for the RNA sequencing analysis. Total RNA was extracted, sequenced using the Illumina platform, and mapped to the *Bos taurus* genome assembly (ARS-UCD2.0). Statistical analysis was performed using the edgeR package, considering treatment as fixed effect. A correction for multiple testing was applied, and differentially expressed genes (DEGs) were considered significant at FDR ≤0.05. Functional pathway analysis and gene network analysis were conducted using DIA and PANEV software, respectively, to identify the most affected pathways and elucidate the roles and relationships among key genes and pathways of interest. A total of 531 statistically significant DEG (387 upregulated and 144 downregulated) were identified in response to EOC supplementation. KEGG functional analysis revealed that these DEGs were primarily involved in lipid metabolism, the digestive system, glycan biosynthesis and carbohydrate metabolism. More in details, the DEG list included genes associated with protein processing in endoplasmic reticulum, glycerophospholipid metabolism, ether lipid metabolism, alpha-linolenic and linolenic acid metabolism, mineral absorption, and mucin type o-glycan biosynthesis pathways. Notably, the top-upregulated genes were *ATP12A*, *KLK9*, *CPHL1*, *LOC781146*, and *KRT86*, while the top-downregulated genes included *DES*, *ACTG2*, *CNN1*, *SYNM* and *LOC100298890*. In summary, preliminary analysis suggests that EOC supplementation modulates key metabolic processes in the rumen epithelium of Limousine bulls, particularly affecting lipid and carbohydrate metabolism as well as digestive functions.

O146

Modulation of bovine immune cells by small extracellular vesicles isolated from the plasma of heat-stressed cows

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Warm weather has recently emerged as a global environmental concern. From the perspective of animal welfare, hyperthermia negatively impacts critical functions of immune cells. Small extracellular vesicles (sEVs), which play a role in cell-to-cell communication, can influence immune responses by delivering their cargo to target cells, a process affected by external stressors. This study aimed to investigate the immunomodulatory effects of plasma-derived sEVs from cows under two different conditions: thermal comfort (TC, THI <68) and a natural four-day heatwave (hyperthermia, HS, THImax = 84, THImin = 69). The sEVs were isolated from the plasma of three healthy Holstein cows in both TC and HS conditions. Immune cells, including monocytes (CD14+) and polymorphonuclear leukocytes (PMNs), were purified from the blood of six clinically healthy Holstein cows during TC conditions. Monocytes were isolated using Magnetic Activated Cell Sorting, and PMNs were obtained through a Percoll gradient isolation. These cells were then co-cultured with sEVs from both conditions. For this study. To assess the effects of sEVs, immune cells were exposed to increasing concentrations of EV proteins (1, 5, 25, 125, and 625 µg/mL). Statistical analysis was performed using SAS® software (SAS Institute Inc., Cary, NC, USA). Results revealed that no significant differences were observed between the doses of sEV proteins tested for PMN viability in either Holstein or Brown-Swiss cows. Therefore, we proceeded with a concentration of 5 µg/mL for further experiments. Regarding PMN chemotaxis, a reduction was observed in both breeds, with a 22% decrease in Holstein cows and a 10.31% decrease in Brown-Swiss cows. Furthermore, for PMNs from Holstein cows, there was a significant decrease in phagocytosis of E. coli and S. aureus, as well as a decrease in ROS production. In contrast, no significant differences were found in Brown-Swiss cows. Additionally, CD14+ co-cultured with HS sEVs exhibited significantly reduced chemotaxis and phagocytosis compared to those co-cultured with TC sEVs. In conclusion, sEVs released during heatwave conditions impaired immune cell phagocytic function, potentially increasing the susceptibility of cows to infections.

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O077

Prediction by molecular dynamics simulation analysis of IL-10 polymorphisms effects and association with brucellosis in Mediterranean river Buffalo

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Interleukin-10 (IL-10) is one of the key anti-inflammatory cytokines produced during infections to suppress inflammation and limit the tissue and host damage. However, some Gram-negative bacteria, like *Brucella abortus* (*B. abortus*), use IL-10 to neutralise the host defensive mechanisms thus surviving within the host cells. The presence of single nucleotide polymorphisms (SNPs) in *IL-10* could alter the structure of the encoded protein and its interaction with the proper receptor IL-10R, thus possibly compromising the inflammatory response pathways. Brucellosis, caused by *B. abortus*, represents a serious economic problem for the livestock industry; it induces late term abortion, decreased milk production and animal culling. Despite the implementation of control and eradication plans over the years, buffalo brucellosis remains a problem in some southern regions of Italy such as Campania and Sicilia. The Molecular Dynamics Simulations (MDS) analysis can be considered an efficient tool for investigating any conformational and structural changes in the native protein structure caused by the presence of SNPs. This analysis includes the use of computational prediction tools such as GROMACS and PyMol for investigating the structural and functional effects of SNPs on protein by quantifying the following parameters: Root Mean Square Deviation (RMSD), Root Mean Square Fluctuation (RMSF), Radius of Gyration (RoG) and H-bonds numbers. This research explores whether an IL-10 SNP could compromise the protein functionality thus influencing the susceptibility of the Italian Mediterranean river buffaloes to brucellosis. A total of 192 buffaloes from the province of Caserta, grouped in positive and negative to *B. abortus*, were enrolled for the study. Results from the IL-10 sequencing and MDS analysis evidenced that the substitution of Threonine at position 175 with Methionine within the IL-10 protein (i.e. T175M), affects the IL-10/IL-10R interaction. Finally, the Odds Ratio (OR) was adopted for analyzing the genotyping results and thus evaluating a possible association between genotype and brucellosis. This analysis evidenced the association of the T allele (codifying for Methionine) with resistance to brucellosis (OR = 0.45; p-value = 0.015), thus supporting the MDS results.The MDS analysis could represent a valid approach to better understand how variations in protein structure, caused by SNPs, influence disease susceptibility, such as brucellosis, and could aid in developing treatment or genetic selection strategies.

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O145

Protective effect of thymol incorporated into gastroresistant pellets on intestinal integrity and microbiota in rabbits

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Thymol represents a major compound of *Thymus vulgaris* widely used as a medicinal plant to control the development of antimicrobial resistance. To ensure its release in the site of the small intestine with the highest absorption, we incorporated pellets containing thymol coated with enterosolvent, gastroresistant film into the rabbit diet. After weaning at 35 days of age, 48 rabbits of both sexes were allocated to control (C) and experimental groups (TA, thymol addition 250 mg/kg feed for 21 days and then withdrawn for 7 days, TW) of 24 animals with six replicates in each (one replicate consisting of two cages, one cage/two animals). Six rabbits in each group (equal male-to-female ratio per treatment) were slaughtered at 56 (C and TA) or 63 (C and TW) days of age. The level of thymol in plasma, duodenal (DW) and jejunal wall (JW), caecum, and colon content were analysed by means of solid-phase microextraction and GC/MS. The effect of thymol on intestinal wall integrity was evaluated by histomorphometry parameters and gene expression of tight junction proteins, and microbiota of the large intestine was also investigated. Differences between diets with and without thymol addition were analysed by two-way analysis of variance (ANOVA) and three main objectives were examined: the effect of time, the effect of thymol, and the interaction between time and thymol addition. The concentration of thymol during TA in the digestive tract was relatively balanced and the correlation between the DW and plasma indicated thymol effective absorption

(r_s=0.933, $p < 0.001$); after TW the concentration was in the caecum lower than in DW and JW ($p < 0.05$). Thymol showed a tendency to positively influence the villus height to crypt depth (Cd) ratio in the duodenum (Cd, $p < 0.01$), only junctional adhesion molecule JAM3 in jejunum decreased during TA ($p < 0.05$). The inhibitory effect during TA on coagulase-negative ($p < 0.0001$) and during both periods on coagulase-positive staphylococci ($p < 0.05$) in caecum was found probably as a consequence of caecotrophy. In conclusion, thymol in gastro-resistant form ensured its release at the site of greatest absorption in the duodenum and jejunum, and prevented its degradation due to adverse conditions in the stomach; did not weaken the structure of the intestinal wall, on the contrary, it showed a tendency to positively influence the villus height to crypt depth ratio and consequently to prevent the proliferation of pathogenic bacteria.

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O019

Innovative flow cytometry-based isolation of bovine spermatids for assisted reproductive technologies

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The green revolution has introduced significant challenges in animal breeding, demanding innovative strategies to balance the increasing global need for food with improvements in animal welfare, disease resistance, and adaptability to climate change. A critical approach to enhance cattle breeding efficiency involves shortening the generation interval, combining genomic selection with advanced assisted reproductive techniques (ARTs). Among ARTs, *in vitro* gametogenesis and the use of spermatids for intracytoplasmic injection represent a promising emerging frontier. However, their success depends on the precise isolation and handling of these immature gametes. This work aimed to develop a robust flow cytometry-based procedure for isolating stage-specific bovine spermatids from bull testis, using fluorescence-activated cell sorting (FACS). To this end, testicular parenchyma was digested using DMEM/F12 medium containing Pronase. Thereafter, the cell suspension was fixed using 70% ethanol solution and stained using syto 16. Cell sorting was carried out using BD FacsMelody. Data were analyzed using FlowJo software. Immediately after sorting, nuclei of isolated cells were visualised using Eclipse TE200 microscope. The results indicate that we successfully separated two distinct populations of spermatids based on their apparent DNA content (SYTO16 staining), size and granularity. Epifluorescence microcopy confirmed clear morphological distinctions of the nuclei of the isolated spermatid populations. Specifically, spermatids collected from steps 1–9 appeared as a homogeneous population of round spermatids, identifiable by a spherical nucleus with visible nucleoli. Spermatids from steps 15–16 comprised a heterogeneous population of elongating and elongated cells, with smaller or polarized nuclei, typical of later stages of spermiogenesis in mammals, while intermediate stages (steps 10–14) showed lower separation efficiency. Our results provide a promising approach for isolating pure spermatid stages from bull testis, paving the way for functional and molecular analyses not only to study spermatogenesis *in vitro* but also to understand how to improve spermatid competence for successful fertilisation and embryo development. Overall, this work supports efforts to enhance genetic gain and promote sustainability in cattle breeding programs.

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O045

Evaluation of physiological effects of milk from the autochthonous Capestrina goat breed using an animal model study

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European, national, and regional policies emphasise the importance of preserving autochthonous livestock breeds to maintain biodiversity, promote sustainability in animal production systems, and support the economy of marginal areas. The autochthonous Capestrina goat breed is of limited size and is at risk of abandonment by breeders who prefer more productive, cosmopolitan breeds, such as Saanen, a high-milk-producing dairy goat. Using an 'animal model' approach, the study was designed to evaluate the potential anti-inflammatory and antioxidant effects of goat milk from the Capestrina breed (CAP) compared to the Saanen breed (SAAN), focusing on hepatic mitochondrial function. C57Bl/6 mice were divided into three experimental groups (N.7):

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a control group (CTR) fed a standard diet, and two groups that received isoeneregetic diet with daily doses of raw milk from either CAP or SAAN goats as supplement. The study, lasted 15 days, assessed feed intake, body weight, inflammatory markers, antioxidant enzyme activity, metabolic hormone levels, and hepatic mitochondrial function. Results showed that the mice of the three groups eat the same amount of food, and no significant difference ($p > 0.05$) was found for the body weight. Overall, both groups receiving CAP and SAAN milk showed improvement in the physiological parameters of the animals. However, compared to the CTR, CAP group displayed markedly ($p < 0.05$) lower levels of the main inflammatory markers in serum and in the liver, favorable regulation of leptin and adiponectin levels, two key hormones in hunger-satiety regulatory processes, and an improvement in antioxidant and detoxifying defenses. These benefits are associated with the improvement in hepatic mitochondrial function in the groups receiving goat milk, as indicated by the increased rate ($p < 0.05$) of oxygen consumption using both succinate and palmitoyl-carnitine as substrates. In conclusion, both CAP and SAAN milk displayed anti-inflammatory and antioxidant properties compared to the CTR; however, CAP milk showed more marked bio-functional effects attributable to the modulation of hepatic mitochondrial function leading to beneficial effects on liver function and systemic metabolism. These findings highlight the potential effects of CAP milk as a functional food to support metabolic health, opening the way to further research on its role in managing inflammation-related metabolic disorders, and for the productive valorisation of the breed.

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O018

Statistical process control to monitor productive items affected by PRRS virus

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The idea of a next-generation farm (NGF), an innovative facility that employs modern technologies to enhance welfare and biosecurity, such as air filtration systems, might be the answer to the unavoidable sustainable transition of the pig industry. The objective was to outline and contrast the productive dynamics of a NGF and a conventional farm during a cohort-study, while both facing a Porcine Reproductive and Respiratory Syndrome (PRRS) outbreak over a 20-month observation time frame. The NGF and traditional farms chosen were two farrowing locations; initially, the conventional farm was categorised as a positive stable with a vaccinated herd (category II-vx), while the NGF was negative. During the third trimester of observation, both scenarios experienced a PRRS outbreak with a field Type 1 (European genotype) strain, which was classified as heterologous to the field type in the conventional farm according to sequencing in ORF7. In both systems, a routine PRRS monitoring program was carried out through RT-PCR testing of processing fluids for every 3-week batch and blood samples from weaning-age piglets, collected batch-wise only in the conventional farm. These two farms shared the same feed, genetics, size, management, owner, and location, but had entirely different facilities. For every farm, two productive items were examined using the Statistical Process Control (SPC) method. The time-to-stability (TTS) was 91 weeks for the traditional farm as opposed to 49 for the NGF. Prior to the PRRS outbreak, the non-productive days per sow stood at 7.1 in the conventional farm compared to 5.6 in the NGF, while the fertility rate was 93.5% against 92.5%. In the SPC chart for non-productive days, three over four (75%) out-of-control (OC) signals were identified during the shorter TTS in the NGF, whereas in the traditional farm OC signals were twice as numerous. A comparable situation was noted in the SPC charts for fertility rates. The traditional farm SPC charts showed a higher frequency of 'alarms' throughout the entire observation period, even after the negative results to PTRSV laboratory analysis, indicating the health status instability of the herd. This does not happen in the NGF charts, where the data points of both productive items were quickly back to statistical control. The innovative facility of the NGF allowed a rapid return to PRRSV negativity status and subsequent maintenance, compared to the conventional farm, as also verified by TTS.

O337

Analyzing big data to evaluate heat stress tolerance in dairy cows

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Heat stress (HS) poses a significant challenge to the productivity, health, and welfare of dairy cows due to their elevated metabolic heat production. HS adverse effects result in significant economic losses for the dairy industry and implications for global food security. The effects of climate change are expected to further exacerbate these challenges, highlighting the need for effective and sustainable mitigation strategies. Identifying and monitoring lactating cows with superior adaptation to heat stress is a promising approach. In this study, we leverage temperature-humidity index (THI) data and longitudinal dairy herd improvement (DHI) records from 2021 to 2024 to evaluate the impact of critical THI thresholds on the performance of 107250 dairy cows across 711 farms in Italy. Our goal is to identify highly resistent animals to HS and investigate routine dairy farm analyses that may serve as indicators of resilience to HS. The dataset includes longitudinal DHI records, temperature and humidity measurements inside the barn recorded every 15 minutes, as well as external temperature and humidity data. Particular attention is given to heat stress during summer months (June to September), while cooler periods (November to February) serve as controls. For cows with complete records on milk production, DHI parameters, breed, calving date, and parity, milk yield throughout the study period was modeled using Wood's lactation prediction curve. The mean (±SD) milk yield was computed and stratified by parity (primiparous, second-parity, and multiparous), aggregated at both the farm level and across all participating farms to assess the best responder animals. The final dataset included 2640134 lactation curves for primiparous cows, 2207231 for second-parity cows, and 2939325 for multiparous cows (parity 3+). After identifying the best responder cows to HS, the results highlighted 8237 primiparous, 7783 second-parity, and 10061 multiparous cows that maintained their milk production at least one SD above the farm's mean under HS conditions. Following this, we are investigating potential indicators of HS resilience using routine dairy farm analyses, applying statistical analyses in the R environment. This approach allows for a detailed assessment of environmental factors affecting milk production dynamics, with significant implications for managing heat stress and identifying resilient animals.

O357

Innovative and participatory pathways for sustainable livestock farming and meat production: insights from the Veneto region in Italy

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The livestock sector faces pressing challenges in addressing environmental sustainability, animal welfare, and production efficiency. The EU's Farm to Fork strategy aligns with these concerns, underscoring the need for sustainable production systems. These challenges have sparked ethical and political debates, compelling stakeholders to balance conflicting demands. Although progress has been made in understanding these issues, the existing literature lacks a comprehensive analysis, highlighting the need for participatory and collaborative approaches. This research aims to address this gap by exploring actions and strategies to improve sustainability in beef farming, engaging farmers, farmers' organisations, supply chain associations, and advisors to evaluate the potential for large-scale adoption of the Sustainable Farming standard, through a qualitative and participatory approach. In 2024, four different focus groups, involving 41 beef farmers, were conducted across the main beef-producing provinces of Veneto, the leading Italian region for beef production from specialised farms. In addition, a participatory workshop was organised at a benchmark livestock farm, involving 73 participants, including representatives from the regional livestock sector, institutions, and civil society. The workshop included a farm experience and discussion sessions supported by Wooclap software, along with questionnaires designed to gather data on participants' perceptions of the farm experience. The findings from the focus groups highlighted widespread interest in innovative practices such as conservation agriculture, renewable energy, and improved housing conditions. However, the adoption of the Sustainable Farming standard was recognised as both a promising opportunity to promote sustainable beef production and a challenging endeavor due to implementation costs, bureaucracy, and low consumer awareness. Findings underscore the importance of effective communication and coordinated actions. Similarly, the workshop results reveal a strong appreciation for sustainable practices, animal welfare, and innovative technologies, emphasising their importance for the sector's competitiveness. The event also established a replicable model for fostering dialogue, co-designing strategies, and strengthening ties among stakeholders. It highlighted the importance of participatory approaches and collaboration to develop sustainable strategies and bridge the gap between producers and consumers.

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O198

Lipid metabolism of chickens with different growth rate and kinetic activity

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Slow-growing chickens (SG) are becoming interesting in the EU scenario for alternative production (i.e. free-range, organic), and by 2026, they will be used in the conventional system as demanded by the European Chicken Commitment (ECC). Many studies showed that SG genotypes are characterised by greater kinetic activity compared to fast-growing (FG) ones; however, little information is available on the impact of this activity on metabolic traits and productive performance.

To answer that, two ECC chicken genotypes, presenting intermediate (MG, 40–50 g/d; Ranger Gold) and slow (SG, 30–40 g/d, Kabir) growing rhythm, have been reared indoor and compared to FG ones (>65 g/d; Ross 308). A total of 300 chickens divided into 2 experimental groups (25 birds/replicates/genotypes) were housed in indoor pens and subjected to the following treatments: control (C, no stimulated exercise) and moderate exercise (EXC, stimulated locomotor activity starting from 15 d of age, 1 h/day at 4 km/h on average). The animals were fed with the same commercial diet (starter: day 1–15; grower: day 16–31; finisher: from 32 until slaughtering). Two chickens/replicates/genotypes ($n = 8$) were slaughtered at commercial ages (45, 56, 81d) and thigh muscles were excised and sampled in ice for the β-oxidation assay or formalin-fixed paraffin-embedded for histological evaluation. The kinetic activity affected the β-oxidation that was higher in SG muscles at all ages and in those of MG birds starting at 56 days of age, whereas no effect was observed in FG birds. However, no differences in lipid metabolism were recorded in the C group between genotypes. The histological analysis showed damaged (mainly necrotic) myofibers in the glycolytic muscles of FG chickens C group at 81 days, which appeared ameliorated with exercise. Lipid infiltration characterised oxidative muscles of both SG groups at 81 days. Concluding, the FG chickens showed muscle damage reminiscent of dystrophies, especially in the last rearing period, and exercise ameliorated the overall morphology. The SG chickens showed more active lipid metabolism in the thigh than the other genotypes, but the anomalous fat infiltration in these animals should be further investigated.

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O218

Effect of heat stress on growth performance and carcass traits of fast- medium- and slow-growing chicken genotypes

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Heat stress is a major challenge in broiler farming, leading to reduced growth rates and economic losses, particularly in high-performing conventional genotypes, which are also susceptible to health and welfare issues, as well as meat quality defects, even under optimal rearing conditions. This study evaluated the effect of heat stress on growth performance and carcass traits of fast-growing (FG, Ross 308), medium-growing (MG, Ranger Gold), and slow-growing (SG, Naked Neck Kabir) chickens reared under thermoneutral conditions (22.8 ± 2.8 °C) or exposed to high temperatures (27.2 ± 2.8 °C) until slaughter (40 days for FG, 55 days for MG, and 75 days for SG). A total of 720 one-day-old male chicks were housed in 36 pens according to a bi-factorial design (3 genotypes ×2 environmental temperatures) and weekly monitored for live weight, while mortality and feed intake were recorded daily. Data were analysed by ANOVA using SAS software, with genotype and temperature included as fixed effects in the model. During the trial, 12 chickens died, resulting in an average mortality rate of 1.7%, with no significant differences observed among groups. FG chickens exhibited higher daily weight gain and feed intake than MG and SG, along with a more efficient feed conversion ratio ($p < 0.001$). Elevated ambient temperature significantly reduced final body weight (–10%), daily weight gain (–11%), and feed intake (–9%) compared to thermoneutral conditions ($p < 0.001$), with no impact on feed conversion ratio across genotypes. FG and MG genotypes were more adversely affected by heat stress than SG, as shown by a significant

genotype × temperature interaction. Regarding slaughter traits, MG exhibited the highest cold carcass weight and dressing percentage ($p < 0.001$). FG showed greater breast yield and a larger Pectoralis major muscle proportion (+5% and +23% compared to MG and SG, respectively; $p < 0.001$), while SG achieved the highest yields for wings, thighs, and drumsticks ($p < 0.001$). Elevated temperatures also reduced cold carcass weight ($p < 0.001$). Breast muscle abnormalities, particularly wooden breast, were observed only in FG chickens and increased under heat stress conditions ($p < 0.05$). In conclusion, elevated temperatures significantly affect growth performance, and carcass traits in broilers. Slower-growing genotypes, like Naked Neck Kabir, exhibited better adaptability to heat stress but may grow too slowly (37.1 g/d on average) for conventional farming systems.

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O554

Exceptional mortality in an intensive 'short cycle' snail farm in Northwest Italy

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Land snail farming, i.e heliciculture, is quite widespread among several Italian regions, mainly for food and cosmetics purposes. Recently, a number of farms have tested a new intensive outdoor breeding practice called 'short cycle', which starts with the introduction of baby (few weeks old) *Cornu aspersum* snails in Spring, ending with their harvest four to six months later. In mid-August 2024, an exceptional mortality event occurred in a 'short cycle' snail farm located in Cherasco (Piedmont, Northwest Italy), where >80% of the individuals were found dead. Twelve 45x3 m pens were involved in the event. On June 7th, baby *C. aspersum* snails were placed in the pens previously planted with cabbage and chard. As outlined by the farmer, the snails died after several days characterised by elevated temperatures and humidity, and two storms were also reported during those days. In addition, in the same period the irrigation system was mistakenly activated during daylight hours. Three weeks later, samples of dead, dying and living snails, for a total of 67 individuals, were collected and subjected to diagnostic examinations. Necropsies and histopathological analyses were performed. Microbiological analyses were conducted on a pool of ten living snails. In addition, snail samples (dead, dying, and living ones) were tested for Herpesviridae by End Point PCR. Most dead individuals were already in advanced autolysis, and many of them were found mouldy. No gross lesions were observed on living animals. Histopathological exams in several cases revealed inflammatory processes in the lungs, and few additional signs of inflammation in other tissues. Snail samples were also tested negative for Herpesviridae family. *Pseudomonas graminis* and *Aeromonas hydrophila* were identified using mass spectrometry. The overall findings from field observations and histological results suggest that snails were aestivating when the outbreak occurred. It is possible to argue that snails died afterwards inflammatory phenomena, as observed in histopathological surveys. *A. hydrophila* is considered an opportunistic pathogen of different animal groups, but no matching symptoms were observed on our samples. In sum, the anamnesis and laboratory results are still not sufficient to make a conclusive diagnosis, and further analyses are thus required. It may be stated that stressful environmental conditions coupled with incorrect management practices could have played a role in this mass mortality event.

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O396

Genotyping buffalo by targeted SNP-capture sequencing

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Single Nucleotide Polymorphisms (SNP) are now widely used in research, in animal breeding and for the preservation of biodiversity. Genotyping the large numbers of SNP needed for these applications has been achieved using pre-defined arrays. However, the arrays are inflexible, are unable to detect new variation and are relatively expensive. As sequencing costs decrease genotyping by sequencing (GBS) is becoming an option. Region

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targeted GBS focused on SNP distributed across the genome reduces the complexity of the data, facilitates high-throughput genotyping by multiplexing and reduces the cost per genotype. A further advantage of SNP-capture GBS is that it provides flexibility. A core set of capture probes can be designed for a species, then additional capture probes can be readily added to customise the assay for specific sub-species, populations or breeds. We developed and tested a core SNP-Capture probe set which is optimised for both river and swamp type buffalo. The set was selected using data from the 1000 Buffalo Genomes Project to identify SNP with high polymorphic information content (PIC) in both buffalo types. The starting point was the 90K Axiom Buffalo SNP array, which was pruned to remove poor quality SNP and SNP with low PIC in either buffalo type. SNP with high PIC were then added to achieve uniform coverage across the genome using the reference river and swamp buffalo genome sequences. The final core set comprises 54K 120bp capture probes covering the autosomes and the X chromosome plus 129 mitochondrial and Y chromosome probes. To facilitate comparison with existing data 15,672 high quality SNP from the Axiom array are included in the core set. We tested Capture GBS using this core SNP set in both river and swamp type buffalo. Samples from 48 buffalo per type were selected that included both males and females which had been genotyped with the Axiom array. A 98% concordance between genotypes obtained from the Axiom array and the targeted SNP-Capture GBS was observed. In addition, we examined the depth of sequence coverage necessary to obtain reliable genotypes, without the need for imputation. Multiplexing was assessed, from 8 samples per reaction giving 30X coverage per sample to 48 samples per reaction giving 5X coverage.
Targeted SNP-Capture GBS provides the ability to develop and optimise genotyping panels for new species, and to customise the SNP set at will, which is not possible for array-based genotyping.

O254

Application of metabolomics to help dissect biological factors underlying fat deposition in pigs

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Adequate fat deposition in the legs is essential for high-quality dry-cured ham production, as fat plays a critical role in flavor development, texture, and the curing process of dry-cured ham. For the Italian Large White breed, this is indirectly assessed by measuring traits like backfat thickness (BFT), to ensure pigs have sufficient subcutaneous fat, lean cut (LC), used to estimate fat-to-lean ratios and ham weight (HW), as heavier hams typically come from pigs with higher fat deposition. Recent advancements in omics technologies suggest that plasma untargeted metabolomics can be a promising source of biomarkers to improve accuracy in evaluation and selection. In this study, we used untargeted metabolomics to characterise the plasma of more than 700 Italian Large White pigs, categorised based on their breeding values for BFT, LC and HW traits. The pigs were grouped into three distinct pools based on the trait of interest: one for BFT, one for LC, and one for HW. Each pool consisted of animals with extreme and divergent breeding values (i.e. high and low) for their respective traits. Discriminant metabolites of high vs low within pools were identified using the machine learning Boruta algorithm. Among the 722 metabolites profiled, 23 were discriminant for the BFT pool, 23 for the LC pool and 26 for the HW pool, with approximately 20% of metabolites shared by two or more pools. These discriminant metabolites mainly belong to lipid-related pathways such as glycosyl ceramides and mevalonate metabolism and have a heritability that, for two lipids, was higher than 0.5. The findings underscore the biological uniqueness of the three traits considered and the potential of metabolomics to uncover novel biochemical markers relevant to fat deposition. These metabolites may represent promising candidates to enhance the accuracy of selection and evaluation processes in breeding programs aimed at optimising fat deposition for high-quality dry-cured ham production.
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O244

Multi-omics dissection of lipid metabolism in Italian heavy pig breeds

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Metabolomics can provide a comprehensive overview of circulating metabolites in animals, considered as endophenotypes or molecular phenotypes. These molecules are the products of various metabolic pathways controlled, modified or catalysed by a wide range of enzymes, regulators and other protein products. Metabolites can be used to dissect more complex phenotypes that have direct or indirect economic value in animal breeding. The lipid fraction of the animal

metabolome can help describe the lipidome, providing new insights into the genetic and physiological mechanisms underlying fat related traits. Fat deposition and composition traits are particularly important in the Italian heavy pig production sector, due to their impact on carcass, meat quality and production traits. In this study, we combined genomic and lipidomic information from approximately 700 Italian Large White (ILW) and 300 Italian Duroc (IDU) pigs to analyse genetic factors affecting the pig plasma lipidome. These pigs were genotyped with a 60,000 single nucleotide polymorphism (SNP) panel and their lipid profiles, consisting of ~300 lipids and derived metabolites were analysed. Lipidomic profiles were initially compared between the two breeds using multivariate approaches. A total of 30 sphingolipids were found to be differentially abundant in the plasma of pigs from these two breeds. Additionally, genome wide association studies identified significant SNPs for 78 and 54 molecules in ILW and IDU pigs, respectively. The same QTL identified in both breeds had opposite allele frequencies, suggesting that lipid related metabolism is controlled by different genetic mechanisms in these breeds.

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O303

Exercise as a modifier of the molecular clock in the athletic horse: a genome-wide study

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The methylome and its fluctuations are emerging as fine-tuning mechanisms for many biological phenomena. The analyses of these variations so-called 'molecular clocks' may indicate the true biological age of an organism; molecular clocks are largely influenced by the environment.

The aim of this 'proof of concept' is to investigate the genome-wide methylation status in elite athletic horses to verify if physical exercise can improve or worsen biological age. To do so, we used an innovative tool: Illumina Horvath mammalian methylation chip (HorvathMammalMethylChip40) which allows monitoring the CpG methylation of over 37,000 conserved mammalian loci to assess whether exercise can accelerate or decelerate the molecular clock. The success of the technology with the equine species is already demonstrated by the previous use by the group of Finno and collaborators. The subjects recruited in the study were elite athlete horses participating into two equestrian disciplines: 20 gallop-race Thoroughbred (from 3 to 5 years old) and 20 show jumping Italian saddle (from 8 to 12 years old). The horses were subjected to the same training program according to the specific discipline. DNA was extracted from blood samples (buffy coat) collected via venipuncture into EDTA tubes and processed by the service connected to the Clock Foundation (https://clockfoundation.org/). We compared data from our samples to the molecular clock baseline identified by retrieving the data produced in the study by Horvath et al. (2022), based on key methylation loci from 42 blood samples (buffy coat) of 24 different breeds. The analyses are ongoing and are confirming that exercise and the molecular clock are interconnected revealing a shift of methylated positions correlating with age. This approach will also open the possibility of comparative analyses with humans and other species where athletic performance is a desired and pursued trait.

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O234

Evaluation of the triple attitude of the alpine Ciuta sheep breed: quality assessment of milk, meat and wool

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Local breeds and traditional farming systems play a key role in preserving rural biodiversity, especially in mountain areas. The survival of a breed depends on its ability to meet market demands for derived products and to exploit their inner quality. The Val3Ciuta project aims to characterise and promote the products derived from the Ciuta sheep—meat, milk, and wool—recovering the potential triple purpose of this native breed from the alpine area of Lombardy, Italy. Through chemical analyses, the nutritional properties and specific chemical markers of meat and milk were identified and linked to a traditional farming system based on grazing practices, use of local forages and natural reproductive cycles. Fresh ($N = 60$) and cured ($N = 26$) meat samples were collected during spring and winter seasons of 2023–2024. Ciuta sheep chops were identified as lean meat (<5% fat), regardless of

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commercial category (light or heavy lambs, ewes, ram). Traditional dry-cured products, *violino* and *bresaola,* comprised 45% protein and 4–5% fat, of which 45–50% was unsaturated. Milk quali-quantitative parameters were measured in an 11-week trial ($N = 110$). On average, 336g of milk were collected per ewe during a single daily milking, with top producers yielding up to 698g, with part of milk still suckled by lambs. Ewes were also assessed for their milking attitude. Discomfort behaviors at milking decreased over the trial (from 1.9 to 1.3 movements/min), with individual differences, indicating promising potential for selection in milk production among ewes. Milk comprised 4.8% lactose, 5.8% protein, and 4.6% fat, with an excellent n-6/n-3 ratio (1.4) and beneficial fatty acids content (2.9% BCFAs, 1.3% CLAs). Somatic cell counts were below the threshold suggested for healthy sheep mammary glands and high milk quality (<250,000cells/mL). Wool quality was assessed; contributing to its valorisation and to the development of a local supply chain for the future, considering that wool is still considered a by-product to discard. Each sheep yielded about 1.5kg of wool per shearing, with a yield on greasy wool of 75% in line with non-Merino small breeds. The average fiber diameter of 30.0µm (61.8% comfort factor) highlighted a rather coarse wool but usable for textile purposes. These outcomes promote an added value for the Ciuta sheep, providing farmers with original knowledge, stimulating interest from agricultural entrepreneurs, and supporting biodiversity conservation in the alpine area.

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O343

Effects of including destoned olive cake in sheep feed on meat quality and salami production

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The residual cake produced during olive oil extraction is rich in oil and can be used in animal feed due to its high content of fatty acids and bioactive compounds, which may influence meat quality. This study examined the effect of incorporating destoned olive cake (OC) into sheep feed on meat and salami production. A total of 124 ewes (homogeneous for parity and milk yield) were randomly assigned to control (CTR) and experimental (EXP) groups. All ewes grazed pasture, with CTR ewes receiving 0.5 kg/d/ewe of commercial concentrate, while EXP ewes were given the same concentrate supplemented with 17% OC on a fresh matter basis. After a 16-week trial, 10 ewes (5 from each group) were slaughtered (BW 46.9 ± 6.9 kg and 59.4 ± 5.2 kg, respectively), and the meat from their carcasses was used to produce salami. The meat from each group was minced and divided into three portions to prepare the following mixtures: 100% sheep meat (SM), 90% SM +10% heifer meat (HM), and 90% SM +10% pork lard (PL). All mixtures were seasoned, stuffed into natural casings, and aged for 32 days in a controlled chamber (11–20 °C temperature, 62–88% humidity). The chemical composition, fatty acid profile, microbiological aspects, and sensory properties of the salami were evaluated. Salami made from SM had lower L* values and higher a*, b*, and Chroma values compared to HM and PL. EXP salami showed lower weight loss than CTR (40.9% vs. 45.5%), with SM and HM mixtures having higher weight loss than PL. EXP salami had lower water (38.7% vs. 44.3%) and protein content (25.8% vs. 28.6%), but higher fat content (29.6% vs. 20.6%). Within each group, water content increased from SM to HM to PL. The inclusion of OC in the diet increased polyphenol content and monounsaturated fatty acids, primarily oleic acid, while reducing saturated fatty acids in SM. No significant effect on lipid oxidation was observed in the salami. Lactic acid bacteria and coagulase-negative staphylococci reached ~8.0 log CFU/g in both groups' salami, with no pathogenic bacteria found. In sensory analysis, EXP salami had a more pronounced olfactory impact, with vegetal and herbal notes, and hints of undergrowth and oxidative characteristics from the OC in the diet.In conclusion, OC is a valuable feed supplement for ewes, including those at the end of their productive life. Although OC influenced product quality at varying levels, further studies are needed to investigate different inclusion levels to optimise its health benefits.

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O366

Effects of feeding bergamot by-products on performance and meat quality in lambs

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In recent decades, the demand for meat has increased steadily, representing a challenge for the future. In this scenario, the use of local agro-industrial by-products as replacer of conventional feedstuff may be a strategy to reduce environmental impact of livestock sector, mitigate emission for feed transportation, and limiting feeding cost, following a circular economy approach. In light of above, this study aimed to evaluate the effects of dietary inclusion of various bergamot by-products, cultivated in Mediterranean region, on growth performance and meat quality of lambs. Thirty 40-days old male lambs (15.0 ± 1.79 kg initial body weight) were selected and assigned to three experimental groups. The 1st group were fed with a conventional (CON) diet, formulated as follow: maize (43%), hay (30%), soybean meal (22%), molasses (3%), and vitamin-mineral (2%). The 2nd one (BER) received the CON diet with 10% of dried bergamot pulp. The 3rd group (FIB) received CON diet with 10% of the residual of dried bergamot pulp after phenolic extraction. The bergamot by-products partially replaced the maize counterpart. On day 50 on feeding trial, lambs were weighed and sacrificed in local abattoir. Carcasses were weighed 24 h after slaughter and *Longissimus thoracis et lumborum* muscles were collected for subsequent analyses. The daily intake of experimental diets was not affected by treatment (850, 906, and 892 g FM/day for CON, BER, and FIB respectively). Similar feed intake also corresponded to similar growth performances among experimental groups, indeed final body weight, hot and cold carcass weight, and average daily gain did not show significant differences. Also, pH of rumen and abomasum were not influenced by dietary treatment. Concerning meat quality analyses, water holding capacity, drip loss (48 and 96 h), and cooking loss were assessed, but none of them showed significant differences. The meat colour was evaluated during a shelf-life trial over 7 days but was comparable between dietary treatment. Bergamot by-products may be implemented in lamb diet without affecting growth performance. However, we hypothesised that bioactive compounds present in bergamot may affect metabolism of lambs modifying some traits of meat quality. Further analyses are ongoing to clarify this hypothesis.

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O509

Effects of ensiled and dehydrated grape pomace in the ewes' diet on meat production of suckling lambs

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The use of agri-food by-products, as grape pomace (GP), in animal nutrition has been recently proposed as a sustainable strategy aligned with principles of the circular economy. Specifically, the polyphenols content of GP aroused growing interest due to its positive effects on performance of livestock animals; indeed, GP showed to improve animals oxidative status, growth rate and meat quality. Being Italy the world's leading wine producer, a large amount of GP is obtained; this, however, is typically available for few months per year, due to its high water content which limits its shelf life. For this reason, it would be useful to validate conservation methods able to preserve the nutritional properties of GP, such as ensiling, other than the more expensive dehydration. The experiment aimed to evaluate the effects of feeding polyphenol-rich GP, stabilised by ensiling (GPE) or dehydration (GPD), on productive performance of transition ewes and their suckling lambs. Twenty four ewes in the final stage of pregnancy were divided into 3 homogeneous groups for parity, stage of pregnancy, weight and milk yield of the previous lactation, and treated with different diets: one group received a control diet (C), consisting of hay *ad libitum* and an amount of concentrate feed adjusted according to ewes' physiological phase, while the other two groups received the same diet integrated with GPE (1.2 kg/day per head) or GPD (0.6 kg/day per head). The experimental period lasted about 10 weeks, from 4 weeks before lambing to the slaughter of suckling lambs. Lambs suckled colostrum and milk as their only feed until slaughter. The somatic cell count was the only milk parameter that differed among groups ($p < 0.05$), resulting higher in ewes of group C than in those of groups fed GP. As expected, the sex of lambs influenced the carcass composition, with female carcasses being fattier. The most interesting effect of diet was observed in the polyphenols content ($p < 0.05$) of meat of suckling lambs, which was higher in the GPE group compared to the C group. A similar increase was found for the antioxidant capacity of meat, assessed by TEAC assay, although the difference did not reach statistical significance. Ultimately, the experiment showed promising results, as the GP-based diets did not influence negatively milk production and lamb growth, while suggesting that the antioxidant properties of a polyphenol-rich diet to nursing ewes may be transferred to the meat of suckling lambs.

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O195

Enhancing meat production and quality of culled sarda ewes

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The INCOVI project (funded by the PSR SARDEGNA 2014/2022, fondo FEASR misura 16.1) aims to identify innovative strategies to enhance the value of Sardinian end-of-career ewes by optimising feeding and meat processing techniques. It has three main objectives: (1) improving the fattening condition of the culled sheep and their homogeneity; (2) increasing meat marketability by lightening meat colour by using straw as fiber source and supplementing vitamin E; (3) improving the shelf-life of the derived products. In this report, only the first two goals are reconsidered. A trial was conducted on 77ewes, divided into three groups. One group was made of ewes in good BCS (group F + E,27 ewes; BCS minimum 2.75: mean 3.33; st.dev. ± 0.33), which received a maintenance diet supplemented with high doses of vitamin E (0.6 g/ewe for day). Two groups were made by lean ewes, which received the same fattening diet: one group including high doses of vitamin E (group L + E; 25 ewes; BCS maximum 2.50:mean 2.41 ± 0.25), the other without vitamin E supplementation (group L; 25 ewes; BCS maximum 2.50: mean 2.40 ± 0.28). The ewes were monitored weekly for 28days for live weight and body condition score (BCS). Depth and fat thickness at Longissimus thoracis (T12-T13) et lumborum (L3-L4) were assessed three times (week 0, 2 and 4) by ultrasound measurements.. The BCS variations during the trial were significantly higher in the group L + E compared to the other groups (L + E= +0.25; F= +0.03; L=-0.07; $p < 0.05$). The variation in the live body weight (kg) was significantly higher in the group L + E compared to the other groups (L + E= +0.50; F=-2.31; L= +0.38; $p < 0.05$). Group L + E showed the fastest and most uniform fattening, suggesting that vitamin E improved body reserve recovery. The use of ultrasound scans of fat and muscle performed during the study showed a significantly greater fattening in the lean groups (L + E and L) compared to the F + E group, both in the thickness (mm) of lumbar fat (F= +0.19; L + E= +1.29; L= +1.10; $p < 0.05$) and thoracic fat (F = +0.55; L + E = +1.27; L = +1.35; $p < 0.05$). These results, obtained through ultrasound fat measurements, provided a clearer understanding of the animals' body reserve variation compared to the use of BCS and live weight.

These preliminary findings, which will be completed by meat quality evaluation, indicate that it is possible to improve meat production with culled ewes within a short period of fattening and indicate an important role of vitamin E in body reserve replenishment.

O164

Assessing quality traits of lamb meat by FT-NIRS

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Near-infrared spectroscopy is used for quality control in the agri-food industry. It could assess the quality of less common products, such as ovine meat, particularly high-value local lamb. This study aimed to evaluate the feasibility of near-infrared reflectance spectroscopy (NIRS) for predicting the fatty acid composition and physical quality traits of lamb meat. A total of 160 intact non-ground fresh meat samples from Massese and crossbreed lambs were considered. Meat samples were referred to animals raised in extensive and indoor regimes in Tuscany and to different muscles (*Longissimus dorsi, Triceps brachii and Semimembranosus)*. Samples were analyzed using traditional techniques for fatty acid composition, color parameters, water holding capacity, and texture profile. For each sample, three slices of equal thickness were acquired by Antaris II FT-NIRS (Thermo Fisher Scientific) instrument, in absorbance mode. Each spectral measurement was obtained from 32 scans performed at a resolution of 4 cm^{-1} over the range of 4000–9999 cm^{-1}. A principal component analysis of original spectra was applied to identify outliers based on the high residual values and high Hotelling's T2 statistic values. Afterwards, when necessary, mathematical pre-treatments (derivate or multiplicative scatter correction) were applied to raw spectral data. Chemometrics between traditional analysis and spectral data were carried out using partial least squares regression (PLS), including calibration and cross-validation models. The best results were evaluated regarding coefficient of determination in calibration (R^2), cross-validation (R^2cv), and root mean square error in calibration and cross-validation. Results achieved R^2 higher than 0.8 for the several FA groups of fatty acids SFA, MUFA and PUFA, even if the model lost accuracy and precision in cross-validation. For physical traits, R^2 ranged from 0.73 for lightness to 0.56 for redness and yellowness, achieving lower results for WHC and pH (~0.56). In contrast, the higher coefficient of determination for physical traits was achieved for the texture parameter (~0.8). A lack of

accuracy is highlighted in cross-validation, with RMSE showing relatively high values and models characterised by lower precision. These results show the potential of NIRS as a rapid and convenient tool to predict the main FA in lamb meat, even if external validation is necessary.

O437

Rearing substrate influences the chemical composition of *Hermetia illucens* larvae

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The insect meal is considered as an excellent opportunity for the replacement of part of the protein in animals' diet. One of the most widely used insect meals is that from *Hermetia Illucens* (HI). The chemical composition of HI larvae may vary depending on the growing medium. Insect meal, normally obtained after degreasing the larvae, still has a good amount of fat which is certainly the component most influenced by the rearing substrate. In this research we aimed at evaluating the effect of four rearing substrates respectively based on leftovers from bread (B), vegetables (V), eggs (E) and fish (F) on the gross and fatty acid composition of HI larvae. The results showed that rearing substrate did not affect the protein content (about 35% for each group), whereas total lipids did: 24% for B and F, 18% for E and 9% for V. The greatest effects were observed for the fatty acid composition. As it is well known, the main fatty acid in fat of HI larvae is lauric acid (C12:0); in F and E treatments the percentage of myristic acid was about 50% lower than in B treatment, respectively 28%, 23% and 55% of the total fatty acids or 995 mg, 1630 mg, and 3167 mg per 100 g of fresh weight (FW) of the larvae. The rearing substrate affected also the amount of long-chain omega 3. The content of EPA and DHA in fat from group V and B was negligible, while in fat from E and F was 2% and 4% of total FA, respectively. This resulted in a markedly different n6-n3 ratio: 15 in P, 5 in V, 3 in E and 0.4 in F. In absolute quantities, the F larvae contained 365 mg/100g of FW of EPA + DHA. Considering that 100 g of FW of larvae F provide less than 420 Kcal, the amount of EPA + DHA allows to obtain the CLAIM rich in omega 3. The content of CLA in fat of HI was significantly affected by rearing substrate: 0.5%, 1.6%, 4.8% and 7.58% for F, B, E, V treatments, respectively. In absolute terms (mg/100 g of FW) the E rearing substrate allowed to obtain the highest CLA content (203 mg) while fat from V, B and E contained 116, 93 and 27 mg/100 g of FW, respectively. In conclusion, fatty acid composition of HI larvae can be conveniently modulated by changing the rearing substrate composition, in order to improve the nutritional quality of the lipid. Thus, HI meal can be used in animal feeding not only as alternative dietary protein source, but also to dietary source of selected fatty acid in order to improve the nutritional quality of lipids of the animal products.

O096

Enriched zinc and selenium agri-food by-products: effects on growth performance of black soldier fly

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Selenium (Se) is an essential element for both animals and humans. It is involved in the functioning of several enzyme systems and various biochemical reactions, particularly those that protect cells from damage. Zinc (Zn), meanwhile, improves immune function by enhancing the immune response, making animals more resistant to infections and diseases. Black soldier fly (BSFL) larvae are recognised for their capacity to bioaccumulate microelements and can be reared on a wide range of substrates. Furthermore, the incorporation of Se and/or Zn has the potential to result in the production of an enriched insect meal. This study investigated the effects of incorporating Zn and/or Se into the rearing substrate of black soldier fly larvae (BSFL). Five different substrates were evaluated: (I) a control diet based on plant ingredients (Gainesville diet, CTR); (II) a substrate derived from okara and potato waste (OkPa); (III) OkPa-Zn, supplemented with 150 mg/kg of Zn; (IV) OkPa-Se, containing 0.3 mg/kg of Se; and (V) OkPa-Zn + Se, enriched with both 150 mg/kg of Zn and 0.3 mg/kg of Se. The larvae were reared in darkness at 26 °C with 60% relative humidity, and their growth performance was assessed. For each diet, 500 larvae were used, with five replicates per treatment. The mean weight of individual larvae was not significantly affected by the type of substrate ($p > 0.05$). However, by the end of the trial, the CTR group exhibited a significantly higher total biomass ($p < 0.05$). Survival rates remained consistent across all treatments ($p > 0.05$). These findings suggest that okara and potato-based substrates, with and without Zn and Se supplementation, are suitable for BSFL rearing. Further research is

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recommended to explore the larval composition, trace mineral assimilation, and reproductive outcomes in black soldier fly.

O354

Economic and social perspectives on integrating *Hermetia illucens* meal in animal feed supply chains

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Proteins are a key component for the farmed animals. Soybean is currently the most used protein source but faces scrutiny due to environmental and social concerns (deforestation, water use and feed-food competition). Additionally, soybean production in Italy and Europe fails to meet the livestock sector's demands. Given the importance of pigs, poultry, and fish supply chains, finding alternative protein sources is critical. Insect meals emerge as viable alternatives due to their nutrient content. Several studies have highlighted the nutritional benefits of Hermetia illucens (BSF). However, the insect food supply chain in Italy remains underdeveloped, necessitating an assessment of its economic and social impact for broader application in livestock farming. This study evaluates the economic feasibility of producing and using BSF meal, exploring its potential in various animal supply chains. A first experimental design involved a cost analysis model comparing traditional and BSF feeding systems in a pig farm. Econometric models and Direct Costing Assessment were used. Fishmeal and soybean, identified as primary foods, were replaced with BSF at inclusion levels of 3–9%, and a control diet without BSF was maintained. The key issues in assessing the convenience of different rations are environmental and economic sustainability. Preliminary data show significant impacts when replacing fishmeal with BSF. Nutritionally, BSF lacks essential amino acids, necessitating their supplementation in piglet diets, thus raising costs. Additionally, BSF is currently three times the price of fishmeal and ten times that of soy meal, heavily influencing the overall ration cost. However, large-scale markets could benefit from the environmental and social advantages of a circular, local production system. These benefits, combined with positive animal health impacts, could drive the adoption of insect-based proteins in animal feed. Despite current high costs and nutritional challenges, insect meal shows promise as a sustainable protein source for animal feed. With further development and scaling, it could support a more environmentally friendly and socially beneficial livestock industry.

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O038

Live *Tenebrio molitor* larvae as feed ingredient for native chickens: effects on productive performance and egg quality

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The use of live insect larvae has already been identified as a promising environmental enrichment for native chickens, but very little information is available about their use as feed ingredient. Therefore, this study aimed to investigate the effects of live *Tenebrio molitor* (TM) larvae on productive performance and egg quality of Bionda Piemontese native hens. A total of 198 40-week-old Bionda Piemontese birds were randomly allotted to 3 isonitrogenous and isoenergetic diets (6 pens/diet, 11 birds/pen [1 cockerel and 10 hens]): C (control, consisting of a core feed [90%] and a feed mix [10%, mimicking the larval nutritional profile]), TM5 and TM10 (containing 5% and 10% of live TM larvae calculated in dry matter [DM] on the daily feed intake [DFI] of the birds as partial or complete replacement of the feed mix, respectively). Bird productive performance (live weight [LW], DFI, laying rate [LR], egg mass [EM], and feed conversion ratio [FCR]) and egg physico-chemical quality (10 eggs/replicate) were evaluated at the beginning (T0), middle (T1 [42 days]) and end (T2 [84 days]) of the trial. Data were analyzed by IBM SPSS software (GLMM with T0 as covariate, $p \leq 0.05$). Dietary live TM larvae inclusion did not influence LW, EM and FCR ($p > 0.05$), while TM5-fed hens displayed lower LR than C at T1 ($p < 0.05$). The TM groups were characterised by lower DFI (considering mash feed only) when compared to C ($p < 0.001$), whereas increasing DFI (considering mash feed and larvae DM intake) was identified in birds fed TM diets than C ($p < 0.001$). Dietary live TM larvae inclusion did not influence egg weight, length, width and shape index ($p > 0.05$). Shells from TM-fed hens showed lower lightness and higher yellowness and chroma than C ($p < 0.05$), with the TM5 groups being also characterised by lower hue when

compared to C ($p < 0.01$). Albumen ratio and Haugh unit decreased in hens fed TM diets ($p < 0.05$), whereas yolk ratio tended to increase ($p = 0.087$). Dietary live TM larvae inclusion did not influence shell ratio ($p > 0.05$), but surface and index were higher in TM10 group than C ($p < 0.01$). Lastly, whole eggs from TM10-fed hens displayed lower DM and gross energy contents when compared to C ($p < 0.05$), tending to be characterised by reduced crude protein as well ($p = 0.052$). In conclusion, the use of live TM larvae as feed ingredient for native chickens may impair bird productive performance and egg nutritional profile, but lead to the production of darker eggs with more resistant shell.

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O033

Black soldier fly as feed: focus on the quality of gilthead seabream (*Sparus aurata* L.) fillets fed with a partial fish meal replacement

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The aquaculture sector has experienced significant development in recent years. Similar to other agri-food sectors, aquaculture has a considerable environmental impact, largely due to the use of feed ingredients like fishmeal and fish oil which are no longer sustainable. This project explored the potential of using *Hermetia illucens* (black soldier fly) larvae meal (BSFLM) as a sustainable alternative to fishmeal in gilthead seabream diets, focusing on its impact on product quality, nutritional profile, and sensory evaluation. The trial was designed as a finishing period up to the commercial size (350–400g). The fish were reared in six tanks and fed a conventional diet (control) and an experimental diet with partial substitution of the fishmeal (10%) with partially defatted BSFLM (3 replicates per diet). The fish were weighed at the beginning and end of the trial to assess the effects of the two distinct diets on growth performance and conversion ratio. Subsequently, fish fillets were sampled and analysed to determine their physio-chemical, nutritional and quality characteristics. Fillets were analysed to determine the dry matter, crude protein, ether extract and ashes, pH and colour. A panel of food experts was involved in a duo-trio test on raw and cooked fillets. Results showed no significant differences in growth performances, quality and proximate analyses. However, when the panellists were involved, assessors correctly identified the raw samples in the duo-trio test and found differences in colour, texture, flaking, and odour intensity. On the other hand, only about 50% of the assessors correctly identified the cooked samples in the duo-trio test. These results suggest that BSFLM is an alternative feed ingredient source in aquaculture that could affect the sensory properties of raw fillets without altering the nutritional composition.

Research supported by the Next Generation EU call from the Italian Ministry of University and Research (MUR) PRIN 2022 PNRR (Progetti di Rilevante Interesse Nazionale 2022 Piano Nazionale di Ripresa e Resilienza) grant.

O095

What about exploring new insect species? Fruit fly (*Ceratitis capitata*) meal as a feed ingredient in juvenile rainbow trout diets

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Insects represent the largest class within the animal kingdom, yet only eight species are currently authorised for use in feed. Among the vast diversity of insect species, it is highly probable that many others possess potential for application in feeding livestock and aquaculture species. Therefore, the aim of the present study was to evaluate the suitability of an unauthorised insect meal derived from the fruit fly (FF) *Ceratitis capitata* as feed ingredient for juvenile rainbow trout.

Different inclusion levels of FF were evaluated in iso-energetic, -nitrogenous, and -lipidic diets, specifically 4% (FF4), 8% (FF8), and 12% (FF12), alongside a control diet (C). A total of 800 fish (15.5 ± 1.1 g) were allocated into 20 tanks, with 5 replicates per treatment (40 fish/tank). The water temperature was 15 °C ± 1 °C, with a dissolved oxygen level of 8 mg/L. The fish were fed daily (7 days per week) at a rate equivalent to 2.7% of the total biomass weight, with feeding adjustments being made biweekly based on the recorded biomass of each replicate. The trial ended when the fish achieved a threefold increase in body weight. At the beginning of the trial, 50 fish (10 pools, 5 fish/pool) were euthanised by overanesthesia for baseline measurements of whole-body composition (WBC). Similarly, after 46 days of feeding, an equivalent number of fish per dietary treatment (10 pools, 5 fish/pool) was sampled to assess WBC. In both cases, samples were stored at –20 °C and freeze-dried for chemical analyses evaluation, such as dry matter, ash, crude protein, and ether extract. To assess growth

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performance, the feed conversion ratio, weight gain, specific growth rate, and protein efficiency ratio were calculated. Additionally, the survival rate, Fulton condition factor, hepatosomatic viscerosomatic indexes were measured to evaluate the health status of the fish. Data were analyzed by One-Way ANOVA ($p < 0.05$). No significant differences in growth performance, WBC or health status variables were observed among the dietary treatments ($p < 0.05$). These findings indicate that the inclusion of this novel insect-derived protein source in the diets of juvenile rainbow trout does not negatively impact their growth or overall physiological condition. This suggests that FF protein meal could serve as a viable and sustainable alternative to traditional protein sources in aquaculture diets, offering potential benefits for resource management without compromising animal health or development.

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O436

A preliminary environmental characterization of mediterranean pastoral food products based on the LCA approach

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Mediterranean pastoral systems are facing significant challenges due to climate change, which is impacting pasture productivity, water availability, and increasing risks of overgrazing and biodi-versity loss. Addressing these issues requires environmental impact assessment to develop mitigation strategies and promote sustainability, enhancing resource efficiency, resilience, and high-quality products valorisation. Within the framework of the PASTINNOVA project (https://past-innova.eu/), a Life Cycle Assessment (LCA) study was conducted to characterise the environmen-tal profile of key Mediterranean pastoral products. Case studies included: (i) sheep milk from Cy-prus, Croatia, Corsica (France), Greece, and Sardinia (Italy); (ii) goat milk from Corsica (France)and Morocco); (iii) lamb meat from Spain and Marche (Italy). Each case study included six farms (excluding France with 3). The LCA study was carried out by adopting a 'from-cradle-to-farm-gate' system boundaries with mass-based and area-based functional units (FUs): (i) 1 kg of fat and protein corrected milk (1 kg FPCM) for milk or 1 kg of live weight (1 kg LW) for meat, and ii) 1hectare of Utilised Agricultural Area (1 ha UAA). Allocation impacts for milk and meat were per-formed using biophysical (energy content) criteria. Emission intensity was estimated using 173essential farm inputs and expressed as kg of CO_{2eq} per FU. A simplified LCA spreadsheet wasused to perform carbon footprint (CF) calculations using an IPCC (2019) Tier 2 approach. The preliminary results suggested that the emission intensity was as follow: sheep milk: 1.42–5.18 kgCO_{2eq} kg FPCM^{-1}; 244–7484 kg CO_{2eq} ha^{-1} UAA. For goat milk: 0.98–2.28 kg CO_{2eq} kg FPCM^{-1}; 219–1,363 kg CO_{2eq} ha^{-1} UAA. Lamb meat: 6.19–18.85 kg CO_{2eq} g LW^{-1}; 28–5566 kg CO_{2eq} ha^{-1} UAA. Dual-aptitude systems: 2.30–5.50 kg CO_{2eq} kg FPCM^{-1}, 9.40–27.20 kg CO_{2eq} kg LW^{-1}; 433 and 2,167 kg CO_{2eq} ha^{-1} UAA. Enteric CH_4 emissions remained the largest contributor (65–82% of total emissions). These findings highlight regional variability driven by local practices, climate, and land management. Final results, currently in progress, aim to inform strategies for reducing emissions, maintaining ecological balance, and preserving the value of pastoral products. Sustainable practices can enhance resilience and viability, reflecting the socio-geographical complexity of the Mediterranean pastoral systems.

O16

Environmental efficiency and carbon sequestration potential of organic *vs*. conventional Simmental dairy farming systems in mountain regions

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The Sixth Assessment Report of the Intergovernmental Panel on Climate Change stated that human activities caused global warming, mainly through emissions of greenhouse gases (GHGs); livestock supply chains contribute 14.5% of global anthropogenic GHG emissions. This study aims to provide a comprehensive comparison between conventionally and organically managed mountain dairy farms, specifically focusing on dual-purpose Simmental cattle. The study included 30 dairy Simmental Alpine farms located in the Autonomous Province of Bolzano, Italy. Half farms ($n = 15$) were Conventional Dairy Cattle (CON) and half ($n = 15$) Organic Dairy Cattle (ORG). Through the LCA approach using the commercial software openLCA 2.0.1 with the Agribalyse v. 3.0.1 database, six impact categories was investigated: Global Warming Potential (GWP_{100}), Marine Eutrophication (ME), Terrestrial Acidification (TA), Land Use (LU), and Water Use (WU) were quantified. Tow functional units (FU) was used one kg of Energy Corrected Milk

(ECM) and one m^2 of on-farm agricultural area. In addition, individual farm's efficiency to provide human edible food was assessed via calculating milk yield deriving from roughage and net protein provision, based on the amount of human edible protein in the animal diet *vs*. the amount of human edible protein inside the milk. The data were analyzed by general lineal models, differences were considered significant at $p < 0.05$. Further, carbon sequestration by permanent grassland was calculated for each farm following the equation suggested by Petersen et al. (2013). Results showed no significant differences was found in term of GWP_{100} between groups for both FUs, (1.14 ± 0.18 *vs* 1.31 ± 0.23 kg CO_2.e per kg ECM and 1.24 ± 0.58 *vs* 0.99 ± 0.25 kg CO_2.e per m^2, CON *vs* ORG respectively), while in terms of ME the CON system shows a significantly greater impact than ORG, conversely in terms of LU the ORG system is significantly less efficient than CON for both FUs. In the case of net food production, the conventional farms showed an overall higher efficiency, mainly due to maize silage input. No significant difference was found in the C sequestration from permanent grassland between the two groups. Enhancing sustainability in these systems requires considering not only emissions but also their role in converting non-edible feed into food, maintaining low local environmental impact, preserving grasslands, and supporting ecosystem services.

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O135

SOLSTICE: a living labs approach for assessing the overall sustainability of livestock systems through Life Cycle Assessment

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This research aims to establish a network of living labs to support the transition towards efficient and sustainable livestock farming systems at national level. The Agritech Hub is an Italian Center for Technology in Agriculture, organised in 9 spokes: in the frame of Spoke 5—Sustainable productivity and mitigation of environmental impact in livestock systems—a network of Living Labs (LL), known as SOLSTICE, has been established, covering a range of farming systems in different regions of Italy. The SOLSTICE initiative encompasses a diverse range of farmed animal species and categories, including dairy and meat cattle, buffaloes, goats and sheep, as well as pigs, rabbits, and poultry. Currently involving 31 stakeholders (farmers, associations, industries, policy makers, advisory services) and 6 universities (Padua, Bologna, Milan, Naples, Pisa, Tuscia), SOLSTICE activities focus on defining and transferring innovative management practices (feeding strategies, farm management, and manure management), along with implementing new technologies and monitoring systems in field conditions. The overarching objectives are to reduce greenhouse gas emissions (GHGe), improve animal health and welfare, and enhance overall farm efficiency. The challenge, but also the strength, of SOLSTICE is to apply the same systematic approach to completely different supply chains, encompassing both intensive and alternative livestock farming systems in highly productive as well as in marginal areas of Italy. The results obtained in the different living labs will be presented, with a particular focus on the innovations tested in each sector and on the strategies developed to guarantee sustainability to the outcomes after the end of the project. A flagship solution of the project is a simplified software application designed to assess the environmental performance of farms through Life Cycle Assessment, based on an intuitive and simple interface, designed to support the decision making at farm and system level.

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O174

Impact of livestock pasture-use intensity and soil geochemical properties on microbial functional potential of nutrient cycles in alpine pastures

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Alpine pastures deliver provisioning (forage) and non-provisioning ecosystem services, including the regulation of N cycle. We report here the results of two studies conducted in three summer farms in the Italian eastern Alps during the summers of 2020 and 2023 to investigate the effects of pasture-use intensity by dairy cows on soil geochemical properties, microbial communities and N cycle. We monitored livestock pasture-use intensity with GPS tracking and categorised it into three levels (Low, Medium, and High) in 2020 and two levels (Low and High) in 2023, based on the 2020 results. We assessed geochemical properties (pH, total C, organic C, total N, and C/N ratio) with chemical analyses and used real-time PCR to measure the total microbial abundance (16S gene) and the potentials of nitrogen fixation (*nifH* gene), nitrification (*amoA* genes of archaea and bacteria), intermediate denitrification (*nirK* gene) and final denitrification (*nosZ* gene) before, during and after the grazing season. Geochemical properties differed between summer farms, reflecting permanent soil features. Pasture-use intensity did not influence pH, while total C, organic C, total N, and C/N ratio were higher at the Low than at the other intensity classes. Higher pasture-use intensities increased the total microbial abundance and the various steps of the N cycle, except for terminal denitrification that was not affected. This result might suggest a possible mismatch, at high pasture-use intensities, between the intermediate and terminal steps of nitrification that might lead to N_2O volatilisation and should be further investigated. The effects of pasture-use intensity on soil geochemical properties and microbial genes were consistent across years, apart from few differences in statistical significance. The abundances of the genes related to general microbial populations, nitrogen fixation and denitrification increased from the beginning to the end of the summer in 2020. These results were only partially confirmed in 2023, possibly because of climatic trends, warranting further investigation. These studies indicate that pasture-use intensity may influence soil microbial communities and N cycle both directly, likely through nutrients deposition, and indirectly through changes in the soil geochemistry. They also provide gene-based proxies for future studies addressing the interface between grazing management, soil microbial communities and nitrogen dynamics in alpine pastures.

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0380

Grazing intensity, soil functions and greenhouse gas emissions: a case study in Alpine pastures of the Dolomites

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Alpine grasslands are crucial ecosystems for mountain livestock farming and provide a variety of non-provisioning ecosystem services. Among these services, soil microbial biodiversity and regulation of greenhouse gases fluxes can be influenced by grazing management. This study aimed to explore the relations among pasture-use intensity, the taxonomic and functional profiles of soil bacterial and fungal communities, and greenhouse gases emissions (nitrous oxide and methane) in a historical alpine pasture grazed by dairy cattle in the Dolomites, northeastern Italian Alps. Pasture-use intensity was assessed with GPS tracking to distinguish between intensively and extensively used areas. Within these areas, soil DNA and greenhouse gas emissions were sampled at three sampling times: pre-grazing, during grazing, and post-grazing. Soil bacterial and fungal taxonomic compositions and functions were inferred from DNA sequencing using the FAPROTAX and FUNGuild libraries. Soil greenhouse gases emissions were estimated using a portable FTIR gas analyzer (GASMET GT5000). These variables were analyzed as function of pasture-use intensity and sampling time. The soil bacterial and fungal taxonomic and functional profiles varied significantly with pasture-use intensity but remained stable across sampling times. Soil emissions of nitrous oxide were lower and more variable than those of methane (nitrous oxide: $5.82 \times 10^{-4} \pm 7.61 \times 10^{-4}$ mg m^{-2} h^{-1}; methane: $1.63 \times 10^{-3} \pm 1.28 \times 10^{-3}$ mg m^{-2} h^{-1}) and did not vary with pasture-use intensity and sampling time. No correlations were observed between greenhouse gases emissions and bacterial or fungal communities at either the taxonomic or the functional levels. These findings suggest that pasture-use intensity can influence microbial communities without remarkable effect, detectable with FTIR, on greenhouse gases emissions. Future research including in the methodological framework also the assessment of the soil nitrogen and carbon cycles, is needed to better understand the variability of greenhouse gas emissions in pasture

ecosystems. However, results highlight the potential of this multidisciplinary approach to provide new insights into the influence of grazing on the complex ecosystem functions in alpine pastures in order to support their sustainable management.

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O369

Temperature-humidity index breakpoints for rectal temperature and milk performance of Cinisara cows under semi-extensive dairy system

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The cows' ability to thermoregulate is part of the adaptive capacity of some local breeds, such as the Cinisara cow. However, the ability to thermoregulate during heat stress depends on several factors, including the physiological state. This study aimed to establish the Temperature Humidity Index (THI) breakpoints of dry and lactating Cinisara cows during the hot season. The study was carried out between June and September 2024 in a commercial dairy farm located in Cinisi (Sicily, Italy). A total of 53 dry (DC) and lactating (LC) Cinisara cows were enrolled. All cows were raised in a semi-extensive dairy system, grazing most of the time. Ambient temperature and humidity were recorded to calculate the THI every 15 min by 3 probes. The rectal temperature (RT) was monthly recorded after the morning (0700h) and evening milking (1700h). Milk Yield (MY) was recorded, and milk samples were monthly collected during the study period. Data were analyzed with the PROC GLIMMIX, REG, and NLIN of SAS. DC group had a higher RT than LC (38.63 vs. 38.51 ± 0.12 °C; $p < 0.05$), especially in August (+0.17 °C) and September (+0.23 °C) when daily mean THI was 77 and 75, respectively. Regarding THI breakpoints for RT, LC group had a THI breakpoint of 78.16 ($R = 0.85$; $p < 0.05$), with the RT increasing by 0.04 °C for every unit increase in THI below the threshold, and by 0.14 °C for every unit increase in THI above the threshold. No significant and abrupt changes in RT was observed in DC group ($R = 0.89$; $p < 0.05$), whit the RT increasing by 0.08 °C for every unit increase in THI in the THI range of 67 and 81. The MY recorded throughout the study period was 20.11, 17.53, 13.43, and 18.29 kg/d at mean THI of 73, 77, 78, and 75, respectively. There was a strong relationship between MY and THI ($R = 0.76$; $p < 0.01$), with the MY decreasing by -1.14 kg/d for every unit increase in the THI range of 73 and 78. Milk Fat, protein, and lactose content reached the lowest values at the highest mean THI and the decline was linear according to the THI. Milk urea content was lowest at THI of 78, meaning that, when cows are grazing-based, the urea metabolism is markedly driven from the pasture availability and intake than muscle catabolism. In conclusion, for the first time it was established the THI breakpoints for RT of Cinisara cows, pointing out that this breed have a better thermoregulation under heat seasons than other breeds, considering that Cinisara has a low-management level without cooling system.

O238

Are *in vitro* experiments a suitable tool to study rumen fermentation?

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In the last century, *in vitro* experiments became widely used to study rumen ecology because they are inexpensive and less time-consuming compared to the *in vivo*, characterised by the possibility of having many replicates, and friendly for animal welfare. However, limitations have been observed as *in vitro* experiments cannot completely replicate the morphology and physiology of living animals. Continuous research has improved the *in vitro* systems to fill the gap, highlighting that the choice of a model fitting with the scope of the experiment is fundamental. The crucial points of in-batch experiments are organic matter recycling, fermented feed, the ratio of *inoculum* and feeds, and feed transit. Instead, in the *in vivo* experiments the sampling procedure of rumen liquor mainly affects the fatty acid profile due to possible changes in the ratio among microbial communities as they are differently distributed on solid feed particles, liquid phase, or

rumen wall. This trial compared the fatty acid profile of rumen liquor, as biomarkers of rumen microbial metabolism, after an in-batch experiment with that from an *in vivo* experiment, where dairy ewes were fed the same two diets fermented *in vitro* using ovine rumen liquor as *inoculum*. The two diets, isoenergetic and isoproteic, consisted of a commercial diet and a diet containing olive leaves as an unconventional ingredient. Each diet was fermented with six replicates in the *in vitro* fermentation lasting 24 h and *in vivo*. The rumen liquor of the *in vivo* trial was sampled after 1 month of feeding. The fatty acid profiles (individual fatty acid/total of fatty acids) from the *in vitro* experiment were notably similar to those evaluated *in vivo*. Only minor changes were found in the fatty acid concentrations between rumen liquors, but the trend was the same for several fatty acids. Few fatty acids changed their concentration comparing groups (*in vivo* and *in vitro*) per treatment. The C10:1 concentration differed among groups, being higher in the *in vitro* treated group than the *in vivo* treated one. The C17:0 iso, C18:0 iso, and C22:6 n3 concentrations were higher *in vitro* control group than in the *in vivo* control group. Our results showed that *in vitro* experiments can be useful for studying fatty acid metabolism as a marker of rumen ecology.

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O155

Effect of hazelnut and pomegranate by-products on *in vitro* methane reduction and ruminal fermentation in sheep

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Incorporating agro-industrial by-products in animal diets is a key opportunity to transition towards a sustainable livestock system, reducing the financial demands of their disposal. Hazelnuts and pomegranate are among the main products used in the Italian food industry due to their nutritional characteristics. The by-products of industrial processing (skin and peel, respectively) could be ideal for inclusion in ruminant diets thanks to their chemical composition, which includes bioactive compounds (e.g. tannins) that can affect ruminal fermentation. To investigate the possible inclusion of hazelnut (HZ) and pomegranate (PG) by-products in a sheep diet, experimental isoprotein (20% as feed) concentrates were formulated with two levels (High and Low) of by-products and included into diets. *In vitro* study was conducted using a 2x6 factorial model: 2 forage/concentrate ratio (F/C 60/40 and 90/10) and 6 levels (Control, CTR H-L; HZ H-L; PG H-L). Sixty bottles were incubated at 39 °C under anaerobic condition using *in vitro* gas production technique with sheep rumen liquor as *inoculum*. Twenty-four were stopped at 24 hours for methane analysis and 36 end the fermentation at 120 hours for fermentation kinetics assessment. At both timepoint, organic matter degradability (OMD) was estimated, and volatile fatty acid (VFA) were determined. Two-way ANOVA were used to observe the effect of F/C and diet factors, while polynomial contrasts were applied to observe the dose effect. At 120h of incubation the inclusion of HZ and PG reduce the OMD compared to CTR, with significance depending on the F/C and dose. Nevertheless, PG diets (at both F/C ratio) showed the highest production of VFA, acetate, and propionate, suggesting an improvement of fermentation efficiency. After 24 hours of incubation, the inclusion of by-products in diets 90/10 ratio did not affect OMD parameter. All experimental diets (90/10) showed lower values of methane production (CH_4, ml/OMD) than CTR, indicating a positive effect of the by-products on emission reduction. The diets with HZ and PG (90/10) showed higher VFA and acetate production. In conclusion, the incorporation of hazelnut and pomegranate by-products into sheep diets demonstrates dual benefits: improving fermentation profiles and reducing methane emissions. The findings suggest that these by-products, particularly in 90/10 forage-concentrate ratio, could use in sheep diet particularly for extensive ruminant systems.

Research supported by Progetto PRIN 2022 PNRR 'UseFul3' (Upcycling of agro-induStrial by-products to improvE Food chain sUstainability, reduce polLution, and increase animaL heaLth and productivity) – CUP: E53D23014940001

O352

Enhancing circularity in dairy cattle farming: nutritional assessment of *Morus alba* leaves

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There is a growing need to promote the efficient use of resources to enhance the efficiency of livestock sector and reduce the environmental impact associated with production. To achieve these goals, it is important to evaluate alternative forage systems capable of fostering resource circularity. Previous studies highlighted the notable nutritional value of *Morus* species leaves. This study aimed to evaluate three cultivars of *Morus alba* L. (white mulberry) as a complementary feed for ruminants. The leaves of Ichinose, Florio and Kokuso, were manually harvested at three different times during 2024, in May, July and September. Bromatological and *in vitro* digestibility analyses using ruminal fluid were carried out. Net Energy for Lactation (NE_L) and Organic Matter Digestibility (OMD) were calculated. Preliminary data were analysed with the SAS® statistical software using MIXED model.

Dry matter increased over the season, with the lowest value recorded at the second harvest of Florio (26.6%). A similar trend was observed for ash content, with the highest value noted in the third harvest of Ichinose (14.8%). However, on average, this cultivar exhibited the lowest ash values (12.0%). Neutral Detergent Fibre reached its highest value in Florio (51.2%), while Acid Detergent Fibre increased over time ($p < 0.05$), with the highest values across all cultivars in the third harvest (28.3%). Crude Protein showed an opposite trend, decreasing significantly ($p < 0.001$) over time from 16.2% to 14.4%, with the highest values recorded in Florio (15.9%). Ether extract content was highest in Kokuso (2.14%) and, on average, increased at the final harvest (2.39%). Soluble sugars were higher during the first (9.67%) and third harvests (8.75%), but without a significant species effect, present ($p < 0.001$) for all other parameters examined. On average, OMD (% of DM) was 70.0%, with significant differences across harvests ($p < 0.001$), showing higher values at the first harvest (79.4%). The average NE_L (MJ/kg of DM) was 5.77, with significant variations related to the harvest period, decreasing throughout the season from 6.37 to 5.36. The results are encouraging: these cultivars demonstrate excellent nutritional potential. Quality varies throughout the season, but the decline is less pronounced compared to herbaceous species, allowing their use, either directly or indirectly, throughout the vegetative period. This offers the opportunity to enhance circularity and improve farm self-sufficiency.

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O496

In vitro rumen fermentation of wheat straw after treatment with mushroom extracts (*Pleurotus ostreatus* and *Agaricus bisporus*)

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Mushrooms get nutrients from the soil fibrous substrates by producing enzymes via the radical apparatus to attack lignin and cellulose (mainly Laccases and Mn peroxidases). In fungi cultivation, the spent mushroom substrate (SMS) is a mix of plant materials (e.g. straw, cereals, hays, etc.) on which the mushrooms grow (3–5 kg of SMS/kg of mushrooms). A further by product is the basal bodies of the mushrooms (MBB), which are tissue portions in Contact with the substrate and discharged immediately after harvesting (around 10% of commercial products). Both these by products are promising sources of lignolytic enzymes. The current lab-scale project aims to evaluate the improvement of fibre digestibility of wheat straw after treatment with enzymatic extracts from SMS and MBB of *Pleurotus ostreatus* (PO) and *Agaricus bisporus* (AB), using two extraction solvents. The SMS and MBB of PO and AB were provided in two separate amounts at the end of two cultivation cycles. Liquid extracts were prepared by mixing 500 g of fresh material with 1000 mL of deionised water or 0.2 M acetate buffer (pH 5.4) and filtering the mixture. All extracts had an acidic environment (pH 5.2–6.0), being more pronounced for the acetate solvents ($p < 0.01$). In enzymatic analysis, AB extracts had higher Laccase activity than PO extracts (155 vs 29 units/mL, $p < 0.01$). On the contrary, Mn peroxidases showed a significant interaction ($p < 0.01$) between mushroom and solvent, being PO-MBB extracts (37.0 units/mL) higher ($p < 0.01$) than PO-SMS, AB-MBB and SMS (27.5, 18.0 and 26.1 units/mL, respectively). Furthermore, the utilisation of the acetic buffer solvent improved the Mn peroxidase activity (32.2 vs 22.4 units/mL, $p < 0.05$). Milled wheat straw was immersed in extracts for 48 h at 25 °C, dried (60 °C) and then inserted in filter bags (Ankom F57, three replicates per run) to determine rumen NDF degradability (NDFD), using an Ankom Daisy II Incubator, and in 100 mL glass syringes for gas production tests. Wheat straw incubated in SMS extracts and in MBB acetic solvent extracts showed significantly higher NDFD ($p < 0.05$) than untreated straw for both mushrooms. Wheat straw incubated in extracts with acetic solvent produced more gas ($p < 0.05$) than untreated straw for both mushrooms, whereas SMS extracts from AB had a lower in vitro gas production ($p < 0.05$). In conclusion, mushroom extracts from commercial by products, primarily those from SMS of *Pleurotus*, increase rumen in vitro fermentability of wheat straw.

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O530

Screening of Italian Mediterranean macroalgae for the potential reduction of methane emissions

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The large interest of public and scientific sectors in the reduction of greenhouse gas (GHG) emissions, specifically in methane (CH_4) enteric emissions, provides an opportunity for the Italian nation to test bio compounds and feed additives. From the perspective of economic circularity and the potential use of seaweed as a feed additive in animal rations the current case study aims to investigate 30 species of macroalgae (MAs), collected along the coast of the Sardinian region (Italy) in central western Mediterranean Sea, for their potential capacity to reduce CH_4 under *in vitro* rumen fermentation technique. The experimental design included treatments (TRT) where each MA was individually added at 2% dry matter (DM) to a total mixed ration (TMR) and compared to a control (TMR without MAs) and a 'gold standard' (the red alga *Asparagopsis taxiformis*). The rumen fluid was collected from two canulated Holstein dry cows fed at maintenance level and farmed at the CERZOO San Bonico, Piacenza, Italy and incubated in 100 mL glass bottles containing ~220 g of TMR, rumen fluid, and a buffer solution. Pressure in the headspace was measured using manometers, and 2.5 mL of gas was analyzed via gas chromatography (Agilent 7820A, Agilent Technologies) at 2, 5, 9, 24, 48, and 72 h. For each TRT, 2 analytical replicates per hour, and 2 experimental runs ($31 \times 2 \times 6 \times 2 = 744$ samples) were analyzed. On average, total gas production was 195.0 ± 6.40 mL/g of organic matter (OM), with mean production of CH_4, hydrogen (H_2) and carbon dioxide (CO_2) values of 13.01 ± 0.30, 0.12 ± 0.004, and 100.05 ± 2.20 mL, respectively. Among MAs, the green algea *Halimeda tuna, Codium decorticatum, Flabellia petiolata,* and the red alga *Phyllophora crispa* showed statistically different gas production: –30.98, –29.43, –29.91, –28.25 mL/g OM respectively, and CH_4 production of –1.71, –1.58, —1.61, –1.54 ml, respectively compared to the control. The brown species *Cystoseira compressa* showed a significant reduction of CH_4 production –1.53 mL, while the red algae *Corallina elongata* and *Gracilaria gracilis* showed a significant increase of H_2 production, respectively of +0.018 and +0.017 compared to the control. These preliminary findings indicate the potential of macroalgae to mitigate ruminal CH_4 emissions; however, further research is needed to link these effects to specific bioactive compounds.

O176

An innovative rumen-bypass micro-encapsulation technique for essential oils

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The aim of this trial was to provide novel technologies for the production of rumen by-pass essential oils to be released in the abomasum. For this purpose, 99.98% of pure limonene (Lim) was microencapsulated. Microparticles were produced using the prilling/vibration technique. An emulsion with Lim oil and alginate was combined with Eudragit EPO 30% (w/w) or Edraguard® 30% (w/w) for the production of the 3 experimental formulations (F). *In vitro* Digestion (IVD) trial for each F was performed on rumen fluid into quadruplicate. IVD was conducted for 6, 12, 18 and 24h using the Daisy II incubator system. In each jar, 14 bags were introduced, each containing 0.5 g of microcapsules. The content of the bag was weighed to calculate the disappearance (w/w), and rumen fluid was sampled for Lim quantification. The concentration of Lim was carried out using SPME/GC-MS. The F1 and F2 had a disappearance of over 50% after 6h of digestion ($p < 0.01$), increasing to more than 80% and 70%, respectively after 24h ($p < 0.01$), while, in F3 no significant disappearance ($p > 0.05$) was observed, ranging between 0.5% (6h) and 1.3% (24h). Lim content ranged from 1472 µg/L at 6h to 1959 µg/L at 24h for F1, from 1021 µg/L at 6h to 1488 µg/L at 24h for F2, and from 2 µg/L at 6h to 9 µg/L at 24h for F3, respectively. Two out of the three formulations (F1 and F2) showed low resistance in the rumen environment. In contrast, the use of Endraguard® in core-shell exhibited a very high resistance up to 24 hours, laying the groundwork for future research on the microencapsulation of substances characterised by rumen-bypass.

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O371

Preliminary evaluation of mealworm frass for broiler chicken bedding

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Sustainable poultry farming is essential for conserving nature resources, reducing environmental impact of production, and enhancing welfare. In this context alternative protein sources like insect meals in poultry diets have good potential. However, insect protein production generates substantial by-products, notably insect excrement, or frass. At present, frass is utilised as organic fertilizer in crop production supporting sustainability. In addition, due to its high absorbing capacity, it might be suitable bedding material in poultry management, and having sand-like texture, it can provide optimum environment for natural behavior (dust bathing), and thus it may improve animal welfare.

The experiment involved Ross 308 broiler chickens, which were distributed into three groups (2 replicated pens each) and farmed between 21 and 42 days of age. In the Control group (C) wood shavings were used as bedding material, whereas in the other two groups mealworm (*Tenebrio molitor*) frass was included at 50% (F50) and 75% (F75) inclusion levels. All other rearing conditions were identical across the three experimental groups. Production parameters, footpad dermatitis (FPD) and hock burn (HB) incidences, and litter quality (moisture content and microbial load) was analyzed. Data were analyzed by a one-way ANOVA with bedding material as fixed effect. Results showed no significant differences in live performance across the three groups. Incidence of FPD was numerically lower in the F50 group (5%), than in the (C (18%) and F75 groups (18%), while hock burn appearance decreased significantly ($p < 0.05$) in F75 (50%) group compared to C group (77%). Microbial load, specifically Mesophilic bacteria, Enterobacteriaceae, and E. coli counts was numerically reduced in the F50 group, compared to C group. No pathogenic microorganisms were detected. This effect was less pronounced in the F75 group.

Results showed that the inclusion of frass as a bedding material does not appear to compromise the live performance of broiler chickens. Preliminary findings also suggest potential improvement in animal welfare indicators (FPD, HB). However, further research is needed to validate these findings with larger flocks. This research was supported by the University of Padova (Italy) funds (2023-prot. BIRD234733/23), and by INEF (Insect Novel Ecologic Food) insect farm (Piombino Dese, Treviso, Italy).

O126

Effect of kinetic activity on behaviour and productive performance of different chicken genotypes

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Citizens and EU regulating agencies are increasingly aware of animal welfare and product quality issues, which has led from one hand to the request for more stringent policy standards on broiler chicken welfare, and on the other hand to an increasing demand for poultry meat from less-intensive farming systems. In this context, an initiative directed by the European Chicken Commitment (ECC) is driving the market toward the use of slow-growing chicken genotypes also in conventional systems, to improve animal welfare, sustainability, and food safety in the poultry meat chain. The present investigation aimed to test two ECC-approved chicken genotypes presenting slow (SG: 30–40 g/d, Kabir) and medium-growth rate (MG, 40–50 g/d; Ranger Gold) compared to fast-growing one (FG >65 g/d, Ross 308) in terms of behaviour and productive performance. A total of 360 chickens were divided into 2 experimental groups (15 birds/replicates/genotypes), housed in indoor pens and subjected to the following treatments: control (C, no stimulated exercise) and moderate exercise (EXC, stimulated locomotor activity starting from 15 d of age, 1 h per day at 4 km/h on average). The animals fed the same commercial diets (starter: 1 to 20d; finisher: 21 until slaughtering) and the daily feed intake (DFI), and daily weight gain (DWG) were registered and feed conversion ratio (FCR) calculated. The behaviour observation was recorded daily using a computerised system (Noldus Technology, Wageningen, The Netherlands) consisting of two different software programs: Media Recorder, to record the videos with the use of cameras and Observer XT, to analyse the videos. Each video was scanned four times, every 15 min for 10 s. The DWG found was in the range of what reported for the MG and SG genotypes, while it was lower for the FG genotype (55 g/d/bird). Results showed a better FCR in FG (2.1) and MG (2.5) genotypes while was higher in SG genotype (3.41), but DFI in EXC groups of FG and M groups increased compared to C groups, while it was unchanged in SG groups. Positive behaviour (comfort) was registered in SG groups, more

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active behaviour (run, walking, interaction) was exhibited and no differences in productive performance were observed due to the induced movement. Concluding, SG demonstrated a very good response to the exercise and no stress behaviour was registered, MG showed an intermediate trend between the other two genotypes, while FG showed stressed behaviour and an increased DFI.
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O461

Effect of ramps on space use of laying hens in a cage-free system

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The effect of the presence of ramps in a three-tiers aviary system was evaluated on space use, as for animal distribution and egg laying position, and animal welfare, as for the occurrence of foot pad and keel bone lesions. To this purpose, 1800 Hyline Brown laying hens were housed in 8 modules (each with 225 hens), half with two ramps (one between the ground and the first tier; one between the second and the third tiers) and half without, and controlled from 18 to 47 weeks of age. Data were submitted to analysis of variance using a model with the main effects of the presence of ramps and the weeks of age (when relevant) and the PROC MIXED or GLIMMIX of SAS, depending on the data distribution; the module was used as a random effect. As for animal distribution measured once a week by direct observation around 11 a.m., the presence of ramps significantly decreased the number of hens on the first tier (28.1% to 22.3% of observed hens), the third tier (11.3% vs 8.71%), and the perches of the first tier (3.01% vs 2.85%), while increasing the number of animals observed on the ground and the second tier (4.92% to 5.11%) ($p < 0.001$), this latter where nests were located. Accordingly, in modules with ramps, more eggs were laid in the nests (97.8% vs. 97.1% of total eggs) and less eggs were found on the wire nets of the third tiers (0.33 vs. 1.16%) ($p < 0.001$). As regards foot pad and keel bone lesions, on average of all observations, no significant effect of the presence of ramps was recorded on their occurrence which significantly increased with age (foot pad lesions from 0% to 31.5% and keel bone lesions from 1.75% to 24.5% from 21 to 47 weeks of age). Nevertheless, when foot pad lesions firstly appeared (i.e. week 30) due to a degradation of litter quality because of unsuitable management of ventilation inside the barn, their occurrence was lower in hens kept in modules with ramps compared to those without ramps (19.3% vs. 28.9%; $p < 0.01$). In conclusions, the presence of ramps facilitated the displacements of hens between the third and the second tiers of the aviary which increased the use of nests for laying; additionally, the displacements between the first tier and the ground were facilitated which potentially could increase opportunities for comfort behaviours, such as dust bathing in the litter, on one side, and the possibility of moving away from the litter when conditions are not optimal, on the other side.PNRR I.3.3 innovativi (CUP: C96E23000010005) funded the PhD grant of Mattia Pravato.

O053

Relationships between environmental conditions and behaviour of laying hens in an aviary system

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The study explored the relationships between environmental conditions and behaviour of laying hens of two genotypes (225 brown- and 225 white-feathered) kept in two pens of a multi-tier aviary system. During the month of January 2024, for 3 weeks (hens from 31 to 33 weeks of age), environmental conditions as for temperature, humidity, CO_2, NH_3, decibel, lux, and particulate matter (PM_1, $PM_{2.5}$, PM_4, PM_{10}), were recorded using a multi-sensor placed at the animal level across the various tiers of the aviary: litter level (10 cm above the ground), between first-second tier (180 cm), and third tier (270 cm). Hen behaviour was assessed through the analysis of daily video recordings for 3 days. Correlations between environmental data and the number of animals showing behaviours at different hours and for all available recordings were calculated using PROC CORR of SAS. As for behaviours at the litter level, pecking and scratching were correlated with relative humidity, NH_3, and lux ($r = +0.15$; $p < 0.001$), whereas dust bathing was correlated with air particulate ($PM_{2.5}$, PM_4, and PM_{10}) and temperature ($r = +0.26$ and $r = +0.21$, respectively; $p < 0.001$). On the first tier of the aviary, scratching and pecking were positively correlated with humidity, NH_3, lux, PM_{10} ($r = +0.30$; $p < 0.001$), whereas preening was significantly correlated with NH_3, lux, decibel, and particulate matter ($r = +0.23$; $p < 0.001$). Resting on perches was negatively correlated with NH_3 and decibel ($r = -0.32$; $p < 0.001$). On the second tier, resting on perches was negatively correlated with decibel, CO_2, lux, and

particulate matter ($r = -0.26$; $p = 0.001$), whereas scratching and pecking were negatively correlated with temperature ($r = -0.21$; $p < 0.001$), and positively with CO_2 and decibel ($r = +0.18$; $p < 0.001$). On the third tier, pecking and scratching were correlated with light, humidity, NH_3, and PM_{10} ($r = +0.30$; $p < 0.001$). Resting on perches was moderately and negatively correlated with decibel, CO_2, temperature, and particulate matter ($r = -0.55$; $p < 0.001$) while resting and pecking showed weak correlations with NH_3, lux, decibel, PM_1 ($+0.14 < r > +0.21$). In conclusions, over a short period of time (3 weeks) and under the controlled indoor conditions of the farm, behaviours of hens were significantly correlated with environmental variables, although the degree of the correlations was weak or moderate. In perspective, data collected over longer periods and in different seasons should be considered for a comprehensive evaluation.

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O552

Feeding management for nutritional welfare of griffon vultures as life-long kept *vs*. temporarily housed before release into nature. A comparison with wild specimens feeding behavior

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This study aimed to evaluate the nutritional status and feeding behavior of Griffon vultures (*Gyps fulvus*) in response to feeding practices at a wildlife rescue center in Sardinia, considering different management purposes. Observations focused on vultures kept for life-long captivity *vs*. those temporarily housed for rehabilitation and subsequent release into the wild, comparatively to wild specimens. The nutritional assessment spanned three months and included 32 individuals. Each bird was individually weighed at the beginning and end of the observation period, and its Body Condition Score (BCS) was recorded using a 5-point scale. Daily feed intake, as a percentage of dry matter (DM) relative to body weight, and feeding behavior were monitored to assess responses to feeding practices. In captivity, vultures demonstrated no evidence of hierarchical access to feed (carcasses), with all individuals approaching feeding sites simultaneously and without dominance-related conflicts. However, daily intake as percentage of BW varied based on the group size, with larger groups consuming proportionally less per individual (8 individuals: 5.6% *vs*. 6 inviduals: 9.4%). Ideal body weight for release into the wild was determined to be between 7.8 and 8.1 kg, corresponding to a BCS of 3/5 in our scale. To gain insights into the behavior of rehabilitated vultures in their natural environment, observations extended beyond the rescue center, with camera traps placed at feeding sites in the wild. No hierarchical approach was observed in the nature, confirming behavioral data on captive birds. This study presents the first implementation of body condition and body weight intervals for *Gyps fulvus*. These findings offer a foundation for assessing the readiness of rehabilitated vultures for release and ensuring optimal management practices in captivity. Understanding the interplay between feeding behavior, nutritional status, and group dynamics of birds in response to captive conditions *vs.* natural settings is essential for improving nutritional welfare and management strategies of vultures.

O050

Effect of group size, environmental enrichment, and temperature on growth performance and meat quality of rabbits

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The present study aimed at evaluating how group size, environmental enrichment and room temperature can affect performance, carcass yield, and meat quality of growing rabbits. To this purpose, 512 rabbits (854 ± 124 g live weight; 33 days of age; mixed sex) were housed in elevated pens in two rooms maintained at different thermal conditions until slaughtering (71 d). The rabbits were randomly divided into eight experimental groups according to a three-factorial arrangement with 2 group sizes (8 vs. 32 rabbits per pen), 2 environmental conditions (18–20 °C vs. 25–26 °C), and provision or not of environmental enrichment (wooden sticks). During the trial, the rabbits were

fed *ad libitum*. At 71 days of age, all animals were slaughtered in a commercial slaughterhouse and 128 carcasses were randomly selected to evaluate carcass traits, muscle pH and colour indices. Overall, the rate of dead and excluded animals (live weight <2.2 kg) was 16.6% without differences among treatments. Group size and environmental enrichment did not influence daily growth rate (44.9 g/d on average) and feed intake (139 g/d on average) during the trial. However, rabbits housed in groups of 8 per pen showed a higher final live weight compared with rabbits in groups of 32 per pen (2541 g *vs*. 2494 g; $p < 0.05$). Rabbits housed at higher temperature showed a lower feed intake (131 g/d *vs*. 146 g/d; $p < 0.01$), daily weight gain (43.5 *vs*. 46.3 g/d; $p < 0.01$), and final live weight (2475 *vs*. 2560 g; $p < 0.001$), compared with those reared at neutro-thermal conditions, whereas feed conversion ratio did not differ (3.09 on average). Dressing out percentage changed only according to room temperature, i.e. it was higher (+2%; $p < 0.01$) in rabbits submitted to the thermal stress. Meat quality was affected only by group size, where rabbits kept in groups of 32 showed a lower muscle-to-bone ratio (–7%; $p < 0.05$) and higher L* index of *longissimus lumborum* and *biceps femoris* (+2% and +3%, respectively; $p < 0.05$) compared to rabbits kept in groups of 8. In conclusion, at high environmental temperature (25–26 °C), growth performances impaired as for final live weight, whereas slaughter dressing percentage increased. On the other hand, group size and environmental enrichment played a minor role on rabbit growth performance and meat quality.

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O285

Effect of selected synbiotics injected *in ovo* on hatchability and chick quality

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In modern broiler chickens, embryonic development constitutes a significant portion of their productive lifespan and can also affect overall growth and performance. Probiotics and prebiotics are promising candidates for early-life programming. As the earliest method to stimulate the intestinal environment, they could offer a viable strategy to eliminate all non-prudent use of antibiotics. A small-scale preliminary experiment was conducted to test an in-vitro selected combination of prebiotics and probiotics for in ovo injection. At the 12th day of incubation, after candling, 240 fertilised embryos were divided into four groups: A, injected with 0.2 ml physiological saline; B, injected with 0.2 mL of physiological saline containing 1% non-vegetable protein hydrolysate (extract A) and 1×10^4 CFU *Lactobacillus rhamnosus* H25 (H25); C, injected with 0.2 mL of physiological saline containing 2% extract A and 1×10^4 CFU H25; D, injected with 0.2 mL of physiological saline containing 0.5% extract A and 0.5% liquid seaweed extract (Extract B) with 1×10^4 CFU H25. The hatchability was calculated and hatched chicks were assessed for quality using the Pasgar score; morphometric measurements including hatchling weight and length were also recorded. Data were analyzed by one-way ANOVA. The hatchability was above 95% among the four groups, and no significant effects were observed with synbiotic treatments. No significant differences were observed in chick weight (46.78 ± 3.38 g to 47.34 ± 3.19 g). The Pasgar score, assessed on a 10-point scale, was similar ($p > 0.05$) among the four groups, ranging from 9.36 ± 0.70 to 9.53 ± 0.54. Specifically, the abdomen was soft in all tested chicks; chick quality like poor activity and deformities of the beak, were random occurrences; while a higher occurrence was found for the incidences of red hock joint, but similar among groups ($p = 0.694$). The incidence of abnormalities in the navel condition did not differ among the groups ($p = 0.138$). The chick body length in groups C and D was higher ($p < 0.05$) than the C and B groups. Overall, this study demonstrates that *in ovo* injection of different synbiotic combinations has no negative effect on hatchability and hatchling quality. Further research is needed to study the effect on post-hatch growth and gut microbiota modulation.

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O367

The race of milk components: rising to the top during natural creaming in Parmigiano Reggiano PDO

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Natural creaming is a fundamental step in the production process of traditional Italian hard cheeses from raw milk such as Parmigiano Reggiano (PR) Protected Designation of Origin (PDO). This study aims to validate a lab-scale system designed to investigate the separation dynamics of milk components under different natural creaming methods. A total of 20 milk batches were monitored during creaming in 4 dairies producing PR PDO. The monitored natural creaming methods included the static, using the traditional vat system and the dynamic, using circular creaming tank. These conditions were simulated at the MilCA laboratory of the University of Parma using glass cylinders (height: 45 cm; internal diameter: 20 cm; volume: 13 l) at 20 °C. Both at the dairies and laboratory, 5 fractions of skimmed milk + cream and 4 fractions + cream were collected for the static and dynamic natural creaming methods, respectively. The implementation of the experimental design produced a total of 390 observations. For each observation, composition, pH, fatty acids, minerals, somatic cell count, bacteria, density, color, viscosity and fat globule size were determined. Least square means (ANOVA) and correlations were evaluated to compare field with laboratory conditions on all the milk quality traits, while Levene's test was applied to assess the heteroscedasticity of variances. Additionally, the repeatability of the laboratory method was determined. The results highlighted differences in the gravity separation of milk quality traits between the two natural creaming methods (static vs. dynamic). The laboratory method was found to be highly accurate in simulating field conditions, with correlation values for each individual trait exceeding 70%, and the Levene's test was not significant. The validation of a laboratory method to simulate natural creaming opens new scenarios for studying the gravity separation of milk components under different conditions. Moreover, it offers a technique that can be routinely implemented, serving as a valuable monitoring tool for the production of cheeses from milk standardised for fat content.

O015

Impact of sires' breed on calving ease, resulting fattening performance and carcass quality parameters in fattening bulls from Holstein Friesian herds in North-Eastern Germany

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Historically, cattle were bred for various purposes, including milk and meat production as well as labour. As breeding has become increasingly specialised over the last decades, modern dairy breeds have mainly been focusing on milk production, producing bull and surplus female calves with low economic value. To address this dilemma, the present study, conducted in Holstein Friesian test herds in North-Eastern Germany, evaluates how crossbreeding with beef bulls and pure breeding affects calving ease and subsequent fattening performance, and carcass quality. For the study pedigree information, calving information as well as fattening performance and carcass quality parameters of 5,217 fattening bulls were considered. Results showed that crossbred calves had higher birth weights and better carcass conformation ratings than purebred dairy calves, reflecting beef breeds' superior muscle development. However, crossbreeding also increased the frequency of difficult births (dystocia), which was shown to have a negative effect on the fattening performance of affected animals. The effect of parity was not relevant for fattening and carcass quality parameters but highlighted the present breeding practice of using beef sires in multiparous cows rather than in primiparous ones. Seasonal variations were also observed, with spring and summer-born bulls exhibiting faster weight gain, likely due to better forage availability and warmer temperatures. To sum up, the study underscores the need for careful management, such as sire selection and targeted mating, to balance the benefits of crossbreeding while minimising the risk of dystocia and subsequent poor fattening performance. Additionally, it emphasises sustainability in feed practices, advocating for roughage-based diets to decrease food-feed competition, which enhances the environmental sustainability of beef production.

O149

Production performance and early culling rates of finishing Charolais young bulls in Italy. Results of a case study

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The trade balance of the beef sector in Italy is negative and second only to that of the fish sector. In 2023, the self-supply rate of beef has further declined to around 40%. This huge deficit in domestic production is compensated for by importing fresh and frozen meat from animals bred and slaughtered abroad and young live cattle that complete their fattening cycle in our country. Approximately 85% of imported live cattle reaching our fattening units a single origin: France, reflecting a strong integration between the two countries' beef supply chains that has been very consolidated in recent decades. Charolais and Limousine are the main imported

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breeds and are selected for their excellent growth performance and muscular development. This study aimed at analyzing the current fattening performance of Charolais cattle in Italy by monitoring a large number of batches of young bulls in a beef farm located in the province of Padua. During the three-year period 2021–2023, 106 batches of Charolais young bulls (3742 heads) imported from France were monitored. The data retrieved by the farm recording system considered arrival and final live weights of the animals, and the days of fattening to calculate the average daily gain. Healthy bulls that regularly completed their fattening had a daily gain of 1.61 ± 0.20 kg/d (mean ± standard deviation) with a final weight of 741 ± 42 kg. These data were compared with the performance of young bulls belonging to the same genetic type reported in published studies conducted in Italy over the last two decades. A special focus was addressed to the animals that did not complete their regular fattening cycle in order to identify time and reasons for their early culling. The average value of injured animals was 2.86% as the sum of bulls that died (1.20%) and animals that were emergency slaughtered because of lameness events (1.20%) or further health problems (0.45%). These results allowed to recognise the strengths and weaknesses points of the current fattening system of Charolais young bulls in Italy, identifying crucial issues such as the adaptation and the management of the animals after the arrival from France. The analysis of the culling events provided important insights for the improvement of the management strategies of the production process along the entire supply chain starting from the country of origin of the animals with positive potential effects on sustainability and animal welfare issues.

O205

Meat quality of the Podolica cattle raised with different finishing methods in the Calabrian Apennines

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The climate changes that are characterising the 21st century affect the environments and natural trophic resources. In the Mediterranean Biogeographic Region, the Podolian cattle plays an important role, in terms of environmental sustainability, ecosystem services and maintenance of biodiversity, due to its high resistance and adaptability to extreme conditions with little vegetation. Although they can optimise poor quality pastures, to obtain a milk production sufficient for raising calves, and for the albeit limited production of cheese, the integration of energy and proteins in the diet is a common practice also for meat production. The modern market requires lean and slightly marbled meat, characteristics possessed by the Podolian obtained through finishing techniques. Podolians are usually raised in extensive conditions and subsequently finished indoors with cereal supplementation. The finishing system is one of the main factors that influence the quality of the meat. Some authors have shown that the grazing system can determine greater tenderness in the meat, due to differences in the final pH or in the pH of the carcass and the drop in post-mortem temperature, compared to the meat obtained from cattle raised on concentrate feed. The aim of this study was to investigate the effects of different finishing systems on the quality of three muscles (Longissimus thoracis et lumborum, Biceps femoris and Semitendinosus) of Podolica cattle raised in the Calabrian Apennines. Thirty calves were divided into 2 groups: 15 were finished in grazing conditions typical of the Calabrian Apennines (Hedysarium coronarium pasture) while 15 cattle were finished indoors using rations composed of grass hay, olive pruning, durum or weak wheat straw, concentrates. The finishing period lasted 120 days. For meat quality, the comparison was made in relation to color, shear force, texture profile analysis and fatty acid profile. In addition, the taste panel evaluation was performed only on the Longissimus thoracis et lumborum muscle. Instrumental analyses shows that meat of pasture group is less red, lighter and less tender (p 0.05), and contain a lower percentage of separable fat ($p < 0.01$). In conclusion, our work allows us to state that through the best breeding conditions it is possible to guarantee animal welfare and environmental protection as well as to obtain high quality meat. These results can be achieved through the choice of finishing times and methods.

O080

Precision breeding in Valdostana cattle: genomic tools applied to milk, protein, and fat traits

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Genomic information has become an essential tool in livestock breeding, offering the potential to enhance the accuracy of breeding value predictions, particularly in populations with complex breeding structures. In the Valdostana cattle breed, subdivided

into Valdostana Pezzata Nera (VPN) and Valdostana Pezzata Rossa (VPR), genomic data serves as a powerful resource to address challenges associated with smaller population sizes and limited pedigree depth. This study aimed to evaluate the genetic and genomic breeding values (EBV and GEBV) for milk yield, protein content, and fat content across these two dual-purpose breeds. A total of 10,578 animals were genotyped using an 80K SNP array, including 4,199 VPN and 6,388 VPR. Phenotypic records comprised 402,608 production records for milk yield (kg), protein percentage, and fat percentage, collected over multiple lactation periods. The EBV estimation was conducted using an animal model based on a test-day approach routinely used in breed evaluations. For GEBV analysis, the same model was extended to incorporate genomic information through a single-step GBLUP (ssGBLUP) approach. The comparison between EBV and GEBV revealed high correlations across traits and methods, with values ranging from 0.94 to 0.99. The ratio of GEBV to EBV animal accuracy varied by trait and breed, with values spanning from 0.68 to 0.78. Notably, milk yield in VPN showed the highest ratio, while fat content in VPR exhibited the lowest. When both populations were analyzed together, EBV and GEBV correlations varied significantly across traits, ranging from 0.96 for milk yield to 0.98 for protein content, reflecting strong agreement for protein and milk fat. GEBV/EBV ratios were highest for protein content (0.74) and milk yield (0.69), whereas fat content displayed a much lower ratio (0.56). These results demonstrate that the inclusion of genomic information enhances the precision of breeding value predictions while highlighting trait-specific challenges. This underscores the importance of tailored genomic evaluations in genetic improvement programs for dual-purpose cattle breeds.
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O550

Social dominance and other new behavioural phenotypes in Valdostana cattle: genetic parameters and relationships with selected traits

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The term 'Valdostana' refers to two local breeds of cattle from the north-western Alps: the Aosta Red Pied (PR) and the Aosta Black Pied-Chestnut (CN). Both breeds are the only producers of PDO Fontina cheese and other local cheeses. In addition to the dual purpose of milk and meat, the CN has the aptitude for fighting, which is expressed in the *Batailles de Reines*, traditional competitions in which pairs of cows engage in bloodless and ritual fights, transposing the spontaneous encounters for social dominance that take place during the mountain pasture. Summer grazing is a common practice involving cows of both breeds and represents an important ecosystem service. Thanks to the recent National Project 'Dualbreeding', new phenotypes have been started to be recorded in both Valdostana breeds, also including behavioural traits linked to the typical features of the breeds: the social dominance in herd (DOM), the aggressiveness (AGG) and the aptitude to pasture (PAS), in addition to the mungibility (MUN) and the general desirability (DES) of a subject. All these traits are linearly scored by expert technicians once in cow's life, at around 3 years of age. The present work aimed to estimate the variance components for these traits and their genetic correlations with traits of current selection interest: milk yield, morphology (muscularity, udder) and fighting ability. A 5-years dataset of 8090 single-cow's records and 39882 individuals in pedigree was considered for PR, and 3733 records for 24114 individuals in pedigree for CN. Average-breed heritability values (h^2) were 0.22 (DOM), 0.06 (AGG), 0.05 (PAS), 0.07 (MUN), and 0.18 (DES). In both breeds, DOM has a negative correlation (r) with milk yield (avg $r = -0.21$), udder (avg $r = -0.72$), and a positive r with fighting ability ($r = 0.37$) and muscularity ($r = 0.76$). Positively correlated with DOM in PR, but not in CN, AGG is not correlated with milk yield as well as with fighting ability. PAS was positively correlated with milk in PR ($r = 0.39$), whereas no significant r was found in CN. Mungibility was significantly correlated with milk in both breeds (avg $r = 0.65$). Interestingly DES reflects the main interests of the breeders: it has positive r with DOM and fighting ability in CN (avg $r = 0.47$) and not in PR, and opposite r with milk in PR and CN (0.41 and 0.30. resp.). Results well depict the peculiar attitudes of Valdostana breeds, offering new insights for the breeding management of the populations.
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O283

Genetic parameters and genome wide association study on fertility traits in Italian Brown cows

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Fertility is essential for securing the economic and environmental sustainability of dairy farms. The genetic background of cow's fertility was investigated using single nucleotide polymorphism (SNP) and field data provided by ANARB. The goals of this work were to estimate the genetic parameters and to study the associations between SNP genotypes and 4 fertility traits: caving to insemination (C_INS), first insemination to conception (INS_Co), calving interval (CI) and number of inseminations (nINS). Fertility was scored on 540,292 cows born between 1994 and 2023. The number of phenotypic records varied among traits: 744,769 (C_INS), 562,384 (INS_Co), 1,001,022 (CI) and 744,769 (nINS). Genotypes at 29,243 SNP loci were available on 31,176 cows (ARS-UCD 1.2). Fertility data (y) were analyzed using both single-trait and 4-traits repeatability animal models: $y = Xb + Zu + Wp + e$ including the fixed effects (b) of herd-year combination, calving season, parity, the random animal effect $u \sim N(0, A\sigma^2_A)$, the permanent environmental effect $p \sim N(0, I\sigma^2_{PE})$ and the residual $e \sim N(0, I\sigma^2_E)$, where: A, I, σ^2_A, σ^2_{PE} and σ^2_E were the numerator relationship matrix, the identity matrix and the variance components, respectively. Three generations from phenotypic records were traced back in the pedigree. Variance components were obtained through Gibbs sampling approach (GIBBSF90+ with 300,000 rounds, thin-interval 5, burn-in 10,000 samples). The GWAS analysis was conducted with the same model replacing A with H that combines pedigree and genomic relationship matrix; *p*-values of SNP effects were derived from POSTGSF90 software. The Bonferroni adjusted $p < 0.05$ was used to assess SNP effects' significance. For the single-trait analysis, C_INS showed the highest heritability (0.07 ± 0.002), followed by CI (0.05 ± 0.001), INS_Co and nINS (0.02 ± 0.002). The 4-trait analysis delivered smaller heritability for C_INS (0.04 ± 0.002) but higher estimates for CI (0.11 ± 0.002), INS_Co (0.13 ± 0.002) and nINS (0.04 ± 0.001). The repeatability ranges from 0.05 to 0.13 for both analyses. Genetic correlations were moderate to high (from 0.502 CI-C_INS to 0.928 C_INS-nINS) except for C_INS-INS_Co (0.022). Three SNPs overcome the significant threshold: BTA-48456-no-rs (BTA2:96.49 Mb), Hapmap31788-BTA-149223 (BTA6:10.72 Mb) for nINS and Hapmap31788-BTA-149223 for CI (BTA4:45.87 Mb). Despite its low heritability, these results suggest that the inclusion of fertility as a breeding goal is feasible.

O261

Robertsonian translocation 1–29: a focus on Sicilian breeds

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Robertsonian translocation 1;29 (rob(1;29)) is the most widespread chromosomal aberration in meat cattle, known to cause fertility impairment in heterozygous carriers. While karyological screening programs exist for some breeds, SNP data analysis has proven to be a faster and more cost-effective method to identify carriers. We analysed SNP data from 1,938 individuals across 11 Italian cattle breeds, routinely collected by breeders' associations. Principal component and haplotype analyses on the first 6Mb of BTA29 allowed us to screen for rob(1;29), and partitioning methods to identify the smallest subset of SNPs that could reliably detect carriers. The frequency of rob(1;29) carriers in 5 beef breeds of Podolian origin aligned with previous reports, while no carriers were identified in Piedmontese or Pezzata Rossa Italiana breeds. 2% of Modicana and Bruna Italiana, and 1% of Pezzata Rossa d'Oropa were carriers. A striking 40% of Cinisara individuals carried rob(1;29), with 4% being homozygous. Genomic inbreeding (F_{ROH}) analysis revealed that the Cinisara breed exhibited relatively low values, implying that its high frequency of rob(1;29) cannot be justified by high levels of inbreeding. One to three SNPs from this region were sufficient to distinguish between carriers and wild-type individuals. While no hotspots of high linkage disequilibrium (LD) were observed between BTA1 and BTA29 in heterozygous rob(1;29) individuals, the average LD was significantly higher in carriers compared to wild-type individuals. Pedigree analyses were performed in Modicana and Cinisara breeds to identify potential fertility-related issues associated with rob(1;29), not

previously reported by breeders. After data cleaning, no differences were observed in the number of offspring, inter-calving intervals, or in longevity between carriers and wild-type individuals. Nevertheless, the data currently collected may not be reliable or comprehensive enough to allow a thorough and satisfactory evaluation of this issue. Our findings confirm the feasibility of using a small SNP set for rob(1;29) carrier detection, advocating its inclusion in routine genotyping panels. Particularly for breeds with a high prevalence of the translocation, like the Cinisara, systematic data collection, genotyping, and fertility monitoring programs are crucial to effectively study and manage rob(1;29).

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O532

Analysis of copy number variations in the peninsular Italian sheep breeds using a high-density 600K SNP array

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CNVs are DNA segments ranging in size from 1 kilobase (kb) to several megabases (Mb) in which duplication, deletion, and translocation have occurred. They are an important source of genomic structural variation. CNVs are considered as a primary contributor to phenotypic variation in several species, including livestock although some of them are neutral. They act through multiple mechanisms, such as altering gene dosage or disrupting regulatory elements. The aim of this study was to detect CNVs in four peninsular Italian sheep breeds (Valle del Belice, Sarda, Noticiana and Barbaresca). The Valle del Belice and Sarda are important dairy breeds, the Barbaresca is a dual-purpose breed and the Noticiana is an ancient breed, reared in Sicily, used but not selected for milk production. The Illumina Ovine Infinium HD (600K) BeadChip and PennCNV software were used to identify CNVs and CNV regions (CNVRs) within the genome of 354 animals. We identified 10,233 CNVs, which were merged into 1,750 CNVRs, ranging from 1 kb to 1 Mb in length, representing approximately 2.9% of the whole ovine genome (Oar_v4.0). Out of all detected CNVRs, 52, 58, 76, and 47 CNVRs presented frequency above 10% in Valle del Belice, Sarda, Noticiana and Barbaresca, respectively. Gene ontology and pathway enrichment analysis were performed to identify candidate genes associated with important economic traits. For all four breeds, results showed the presence of several functional genes related to adaptation, innate immune response, olfactory and gustatory receptors, milk production and reproduction such as ABCC4, DQA, OLA-I, FILIP1, SENP6, TRIM and OR genes. The implementation of CNVs existing maps based on the Illumina Ovine SNP600K BeadChip array with our information will be useful for future investigation of structural variations underling traits of interest in sheep. Further analyses will be conducted to evaluate the effects of these CNVRs on phenotypic and production traits in peninsular Italian breeds.

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O104

Genetic investigation of the Lactophorin whey protein coding gene reveals novel polymorphisms in New and Old-World camelids

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Despite their lower proportion compared to caseins, whey proteins play a significant role in the food industry. One of the most abundant whey proteins in camel milk is Lactophorin, a hormone-regulated mucin produced in the mammary gland and a key component of the milk fat globule membrane. This protein also contributes to the immune response, helping to prevent infections. In this context, the entire Lactophorin coding gene, along with its regulatory regions, has been sequenced for dromedary, bactrian, llama and alpaca for a total of ~3,100 bp. The gene structure was found to be conserved among the four camelid

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species, with slight differences in size (2,263 bp in dromedary and bactrian camels, and 2,192 in llama and alpaca). The analysis of promoter sequences (662 bp) revealed a total of 179 common transcription factor binding sites (TFBS), including factors related to milk and protein expression. Intraspecies sequence comparison demonstrated that New World Camelids (NWC) have greater genetic diversity, with 32 and 40 polymorphic sites identified in alpacas and llamas, respectively, compared to 23 in dromedary and bactrian camels. In interspecies comparison, a total of 153 variations were identified. Among the identified SNPs, two mutations (g.163 A > G and g.563 C > T) were located in the promoter region. The first SNP, shared by llamas and alpacas, created a TFBS for EMBP-1, while the second SNP, found in dromedaries, resulted in the loss of a TFBS for NF-Kappa B, potentially affecting the immune response. In the exonic regions, four nonsynonymous SNPs were identified: g.2324 G > A, g.2419 C > G, g.2421 G > A and g.2823 C > T. Notably, the first mutation, responsible for the amino acid replacement p.42Glu > Ser, was found to be deleterious, potentially affecting the functional properties of the protein *in silico*. The latter mutation (p.130Ser > Pro) altered the secondary structure of the protein, strongly favoring a coil structure. An allele-specific PCR (AS-PCR) was developed and used to genotype g.2324 G > A in the NWC. In the analysed population, the frequency of the G allele (Glu) was 0.83. Interspersed elements were also investigated, showing a proportion of 17.76% in dromedaries, 16.57% in bactrian camels, and 14.58% in NWC. This study underscores the evolutionary conservation of Lactophorin coding gene and highlights its potential as a candidate gene for further research exploring associations with dairy traits and immune response regulation.

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O480

Animal performance, carcass traits and meat quality of Limousine, Sardo-Bruna, and their crosses

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The aim of this study was to compare animal performance, carcass traits and meat quality of Sardo-Bruna breed with specialised meat purebred or obtained by crossbreeding. Ten Sardo-Bruna (SB; 5 males, 5 females), 10 Limousine (L; 5 males, 5 females) and 10 Limousine × Sardo-Bruna crossbreed (LxSB; 5 males, 5 females) were compared simultaneously from 12 to 20 ± 1 (mean ± SEM) months old. During the trial, body weight (BW) was recorded once a month for estimating the average daily gain (ADG). At slaughter, carcass measurements, pH and color traits were recorded from the left side of the carcass. Proximate composition, fatty acid (FA) profile, cooking and drip losses were evaluated using the *Longissimus thoracis et lumborum* muscle. The slaughter BW did not differ among genetic types (L:623, LxSB:634, SB:588 kg; $p = 0.16$). However, the L and L×SB genetic types showed higher cold carcass yield compared to SB group (L: 61.6, L×SB: 62.7, SB: 57.9 %, $p < 0.001$). Females had lower ADG ($p = 0.0004$), slaughter weight ($p < 0.0001$), hot and cold carcass weights ($p < 0.0001$), hot and cold carcass yields ($p = 0.03$, and 0.04; respectively), and cooking losses than males ($p = 0.013$). Males group showed a lower intramuscular fat content ($p < 0.0001$) and rib fat thickness ($p = 0.004$) compared to females. No relevant differences among genetic types and between sexes were observed for meat and fat colors and pH. Concerning the FA profile, SB genetic type evidenced a higher oleic acid content (SB: 37.12, L×SB: 34.47, L:31.31 %, $p = 0.001$) and a better nutritional index ($p = 0.049$) than other genetic types while males had a higher PUFA content than females (9.82 *vs.* 5.81 ± 0.473; %; $p < 0.0001$). In conclusion, the results of this study showed that crossbreeding local Sardo-Bruna cattle breed with specialised beef breed such as Limousine could be a valid strategy to enhance carcase yield without effects on meat quality.

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O454

Animal performance and meat quality of crossbred heifers fed with phenol-rich agri-food by-products and forages

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The dairy industry produces crossbreed heifers that are a secondary output and have lower carcass value than specialised meat breeds. Exploiting alternative, low-cost, and bioactive-rich feeds with low competition with human food could be a viable strategy to improve meat quality, market appeal and sustainability of the supply chain. This study investigated the effect of a total mixed ration (TMR) based on non-human-edible, phenol-rich feed ingredients on Holstein × Belgian White-Blue crossbreed heifers performance and meat quality traits. Two groups of 11 animals, balanced for weight and age, were fed for 251 days with a commercial (CTR) or experimental (NHE) TMR. The CTR diet consisted of a concentrate (85%) composed mainly by cereals and straw (15%). The NHE diet consisted of a concentrate (62%) composed mainly by co-products (20%

hazelnut skins, 17% dried sugar beet pulp, 20% Spelta grains by-products), 30% of horse bean and 38% hay (19% sainfoin, 13% mixed, and 6% alfalfa). Animal performance, SEUROP classification, human edible feed efficiency (HEFE), and meat quality traits (fatty acid composition and lipid oxidation, colour, and myoglobin evolution over 7-day refrigerated storage) were evaluated. A blind and informed sensory analysis was conducted with trained panelists. The human-edible ingredients accounted for 44% and 21% of the CTR and NHE diets, respectively. The HEFE was lower for NHE group ($p \leq 0.05$). Average daily gain, carcass weight, SEUROP classification, and dressing percentage were similar between groups. NHE meat showed more C18:3 ω-3, C18:3 ω-6, and *trans* 6 ÷ 9 C18:1 isomers, but lower PUFA ω-6/ω-3 ratio, ($p \leq 0.05$). The *trans*10/*trans*11 C18:1 ratio decreased by 63% for NHE meat ($p = 0.03$). Meat lipid oxidation and myoglobin isoforms over refrigerated storage were not affected by the diet ($p > 0.05$). The NHE meat showed stable chroma and yellow index over 7-day storage, whereas the same parameters deteriorated after 7 and 3 days, respectively, in the CTR group ($p \leq 0.05$). Sensory evaluation indicated a trend toward improved tenderness for NHE meat after informed tasting ($p = 0.06$). In conclusion, feeding phenol-rich by-products and hay to crossbreed heifers was not detrimental for animal performance. The NHE diet enhanced meat fatty acid composition and colour stability without compromising sensory parameters, potentially improving its market appeal. However, the HEFE was lower for the NHE group, requiring further assessments of overall sustainability.

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O257

Instrumental and sensory evaluations to assess the quality of beef meat in relation to country of origin

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This study aimed to characterise beef meat from different European countries implementing different farming and feeding systems. Quality attributes were evaluated using both sensory and instrumental methods on a total of 184 meat samples (*Longissimus thoracis et lumborum* – LTL, 9th rib, weighing approximately 200 grams) which were collected from 5 Countries: IT ($n = 28$; indoor system with high feed input, from Italy), ES ($n = 18$; indoor system with high input feed, from Spain), CH ($n = 71$; indoor system with medium input feed or grass-based system with low input feed, from Switzerland), UK ($n = 31$; grass-based system with high input feed, from the United Kingdom), and FR ($n = 36$; indoor system with medium input feed or grass-based system with high input feed, from France). Samples were used for assessing color (L*a*b*; $n = 5$ replicates/sample), shear force on both raw and cooked samples (Warner Bratzler shear test; $n = 5$ replicates/sample) and lipid oxidation (TBARS). As for sensory evaluation, 72 beef samples were then selected for the consumer test (120 assessors). Each taster evaluated seven samples, assessing tenderness and juiciness intensity on verbal scales, along with olfactory, gustatory, and overall liking. The evaluation concluded with a brief section gathering sociodemographic and personal data. Instrumental data were analyzed using One-way ANOVA by testing the effect of Country of origin. When significant, means were separated by Tukey-HSD test ($p < 0.05$). Statistical analyses of the results collected from sensory tests is currently ongoing. As for color, significant differences were observed for lightness ($p < 0.001$) and redness ($p = 0.022$). Indeed, samples from CH (L*=39.6) and ES (L*=38.5) were lighter if compared with other groups. In addition, samples belonging to UK showed the highest ($p < 0.05$) redness. As for shear force, the samples from UK exhibited higher tenderness ($p < 0.001$) both raw and after cooking. With regard to lipid oxidation, CH samples showed the highest ($p < 0.001$) TBARS. Overall, the abovementioned differences may be explained considering that the farming system adopted in each Country may have resulted in peculiarities in the quality traits of the forthcoming meat. In addition, to provide a more comprehensive characterisation of the meat, these results will be combined with those of the sensory evaluation.

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O230

Meat quality in veal calves fed with milk whey powder

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In the context of promoting sustainability and reducing waste from the human food industry, milk whey, a nutrient-rich by-product of cheese production, represents a promising alternative in animal nutrition. Rich in lactose, proteins, and minerals, whey has demonstrated its potential as a cost-effective and environmentally friendly feed ingredient for livestock, contributing to the circular economy in livestock production. This study aims to evaluate the replacement of conventional milk replacer with milk whey powder in the diets of veal calves, exploring its impact on meat quality during dry aging. The trial involved 36 male Belgian Blue × Holstein calves randomly divided into two experimental groups. The control group (C) was fed a commercial milk replacer, while the treated group (W) received whey powder for a period of 200 days. At the end of the feeding trial, the animals were slaughtered at a live weight of 234.2 kg ± 1.6 and the left loin was collected from each carcass. The loins were subjected to a 42-day dry-aging period in a dynamic dry aging cabinet. At the start of aging and at weekly intervals (D0, D7, D14, D21, D28, D35), a steak approximately 30 mm thick was sampled from each loin for the analysis. Physico-chemical, colorimetric, oxidative, and textural parameters were evaluated, along with the volatile compound profile and weight loss measurements throughout the dry aging period. Preliminary data were tested for normal distribution and variance homogeneity using the Shapiro-Wilk test. Subsequently, data were analyzed using analysis of variance (ANOVA) via the General Linear Model (GLM) procedure in SAS (2018), considering the experimental group and aging time as independent variables. A Tukey test for repeated measures was performed to assess differences between means over the aging period. The experimental group had no significant effect on any of the analyzed parameters. However, aging time significantly affected some patterns. Lightness increased from D0 to D14 in both experimental groups ($p < 0.05$). Thiobarbituric acid reactive substances (TBARS) levels increased from D0 to D28 in C group ($p < 0.05$). Based on these preliminary results the use of milk whey powder in the diets of veal calves did not affect the qualitative parameters of meat during dry aging. Therefore, it can represent a viable and sustainable alternative to conventional milk replacers.

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O181

Bacterial single-cell protein in aquafeed: implications for growth and gut health in gilthead Sea Bream (*Sparus aurata*)

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Bacteria single cell protein (SCP) is a promising source as protein for aquafeed due to the high protein content and their ability to modulate their composition according to different production setting as well as the high growth rate and their ability to growth on different agro-industrial by-products thus leading to low environmental footprint and affordable production costs. Their use as raw feed material has been examined in several farmed species, however, research on Mediterranean fish species is still scarce. To investigate the effects of dietary SCP, a study was conducted to assess growth performances, i.e. specific growth rate (SGR), feed intake (FI), feed conversion ratio (FCR), protein efficiency rate (PER), protein efficiency, protein apparent digestibility (AD), plasma biochemistry, gut histology, and gut microbiota response of gilthead sea bream (*Sparus aurata*) fed diets containing increasing levels of SCP, compared to a control diet without SCP. Three isoproteic, isolipidic and isoenergetic extruded diets (44% protein, 19% lipid, 22.42 MJ/kg) were formulated with different bacterial SCP (derived from *Corinebacterium glutamicum*) level (10% SCP, SCP10; 15% SCP SCP15; 20% SCP SCP20) to replace plant protein ingredients, while a control diet (CTRL) was formulated without SCP. The growth trial was performed at the Laboratory of Aquaculture of the University of Bologna (Cesenatico, Italy) where 45 fish (initial body weight of 75 g) per tank were randomly distributed in twelve 500 L tanks. Each diet was administered to triplicate tanks over 108 days. Individual fish weights were recorded at the beginning and end of the trial. Carcass composition was analyzed from pooled ($n = 5$ *per tank*) samples at both time points. Blood samples ($n = 5$ *per tank*) were collected, centrifuged, and stored at −80 °C for analysis. Histological evaluation was performed on the intestines of selected fish ($n = 3$ *per tank*). Digesta from the distal intestine was sampled and stored for microbiota analysis ($n = 5$ *per tank*). Additionally, AD for dry matter and protein were assessed using yttrium oxide. Results showed that, at the end of the trial, there were no significant differences on SGR, FI, FCR, PER and AD. Most of plasma analytes were found to be equal for all treatments, except for those related to nucleic acids molecules degradation such as phosphorus and urea which were higher in SCP10 and SCP20 compared to CTRL (respectively, $p = 0.0025$ and $p = 0.0006$). No morphological alterations were found in the intestines of any of the fish analysed. Variations in the gut microbiota (GM) structure were observed where SCP positively influenced GM internal diversity ($p < 0.01$), which increased with higher levels of dietary SCP inclusion. Furthermore, SCP inclusion increased the abundance of *Bacillus spp*., a taxa that can potentially enhance nutrition, support the immune system, and improve disease resistance. In conclusion, incorporating up to 20% SCP in the diet of gilthead sea bream is a viable strategy, showing no negative effects on growth, feed efficiency, or health parameters. Moreover, it promoted a beneficial shift in gut

microbiota composition, favoring bacteria associated with improved digestion and immune function in fish.

O298

Dietary microalgae in broiler nutrition and their effects on performance and organ development

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Microalgae are unicellular, photosynthetic organisms that convert inorganic nutrients into biomass, including proteins, carbohydrates, lipids, and beneficial compounds such as polyphenols and carotenoids. As feed additives, they offer a promising alternative for animal production, promoting gut health through their antibacterial, anti-inflammatory, and antioxidant properties. Euglena gracilis (EG), in particular, is known for its intracellular β-glucan (paramylon) granules, making it an excellent candidate for enhancing poultry health and performance. This study aimed to assess the effects of EG on growth performance and relative organ index. A total of 240 male 1-day-old broiler chickens (ROSS308) were divided into two homogeneous groups, receiving either the basal diet (CTR) or the basal diet supplemented with 190 mg/kg feed of EG (TRT). Each group was composed of 120 chickens, distributed across 12 replicates (10 birds/replicate). Initial body weight was determined at the beginning of the trial and growth performance were evaluated at days 11, 20, and 40. On each of these days, one animal per replicate was sacrificed. Liver, spleen, and Bursa Fabricius were collected to determine Relative Organ Index. Data were analysed using one-way ANOVA (GraphPad Prism), with statistical significance set at $p < 0.05$. EG was produced at the Istituto Sperimentale Italiano Lazzaro Spallanzani (Rivolta d'Adda, CR), with the following chemical composition: DM 94.24%, CP 56.46%, CF 1.24%, EE 4.42%, and ash 11.89%. No significant differences were found in body weight (BW), average daily gain (ADG), average daily feed intake (ADFI), or feed conversion ratio (FCR) at any timepoint ($p > 0.05$). Similarly, there were no significant differences in relative organ index between the two groups ($p > 0.05$). Overall, the inclusion of EG in poultry diets under optimal environmental conditions did not show significant benefits in performance. However, further investigation under more challenging conditions may provide valuable insights into its potential to support animal health.This study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

O579

In vitro digestibility of microbial cell-derived protein sources for animal nutrition

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The search for sustainable alternatives to conventional protein sources in animal feed has increasingly focused on microbial biomass, which offers high protein content and environmental advantages. This study evaluated the in vitro digestibility of two microbial protein matrices—one containing 77.3% protein (MYCO-75) and another with 73.8% protein (NT-70)—in comparison with a standard fishmeal (72%) (Control). To standardise the digestion process, protein powders were solubilised in water at a 1:4 w/v ratio. Each sample was digested in duplicate using a two-step enzymatic protocol simulating gastric and intestinal phases. Post-digestion, samples were centrifuged, filtered (0.22 µm), and analyzed. The OPA assay was used to quantify soluble proteins in both digested and undigested fractions. Additionally, complete hydrolysis with HCl 6N at 110 °C for 24 h was performed to determine the total amino acid pool, enabling calculation of the degree of hydrolysis (DH%). For free amino acid analysis, samples underwent derivatisation with FMOC-Cl, followed by HPLC with diode array and fluorescence detection. The degree of hydrolysis was significantly higher in MYCO-75 compared to both NT-70 and the control, suggesting a more effective breakdown of the protein matrix into smaller peptides. NT-70, while showing a DH% similar to fishmeal, led to the significantly greater release of several key amino acids, including threonine ($p = 0.001$), glycine ($p = 0.004$), valine ($p = 0.01$), isoleucine ($p = 0.02$), and aspartic acid ($p = 0.01$). While, MYCO-75, showed a notably higher release of glutamic acid ($p = 0.04$), aligning with its amino acid profile. Importantly, considering the total hydrolysis and free amino acid results, MYCO-75 was associated with a greater release of peptides and potentially bioactive protein

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fragments, rather than a simple increase in free amino acids. Further studies—including *in vitro* colonic fermentation and *in vivo* trials—are needed in order to confirm these preliminary findings.

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O472

Effects of insect meals on the fecal microbiota: an in vitro study on healthy and chronic enteropathic dogs

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Use of insects in dog nutrition is gaining popularity as they may represent a promising protein source in petfood. This *in vitro* study (7 treatments, 5 flasks each) was set up as follows: an indigested residue (10g/l) of a chicken-based dry petfood (CTRL); CTRL added to 4 different insect species, 2x *H. illucens* (HI1-HI2); 2x *T. molitor* (TM1-TM2); *A. domesticus* (AD); *Z. morio* (ZM). Each insect was added to CTRL at 30% inclusion level, with the amount established according to the insect's total digestibility coefficient. All the treatments contained a canine fecal suspension from either healthy dogs (HD) or dog with chronic enteropathy (CE), diluted with an enrichment broth. Flasks were incubated in an anaerobic chamber at 39 °C for 24h. Aliquots of inocula were collected at 6 and 24h for chemical and microbial analyses by qPCR. Differences among insects and between HD and CE were analyzed using mixed-models with *posthoc* and Mann-Whitney or unpaired *T*-Test for parametric or not data, respectively. Significance was set at $p < 0.05$. Fecal microbiota and, to a minor extent pH, NH_3, and volatile fatty acids (VFA), differed between HD and CE at 6h and 24h. Contrary to what literature reports, HD microbiota appears to be more modulable since bacteria were affected by insects more in HD than in CE. Among insects, HI2 produced the most significant effects in HD. At 6h, total bacteria were decreased by all treatments in both HD and CE. In the HD inoculum, the comparison among insect and CTRL at 6h showed that butyrate increased in HI1(+16%), HI2 (+11%), TM1(+11%) and ZM (+14%); isobutyrate increased in AD (+24%); isovalerate increased in HI1(+18%) and AD (+12%) and decreased in TM1(–26%). At 24h NH_3 decreased in ZM (–37%), despite higher protein content compared to CTRL. In the CE inoculum, the comparison among insect and CTRL at 6h showed that acetate decreased in HI2(–24%); butyrate increased in TM1(+40%) and ZM (+34%); isobutyrate decreased in TM1(–66%) and ZM (–58%). Isovalerate decreased, at 6h and 24h respectively, in TM1(–69%; -35%) and ZM (–63%; -28%), while it increased in HI1(+14%), HI2(+11%) and AD (+16%) at 24h. Total VFA decreased at 24h in TM1(–19%). Contrary to the expectation, NH_3 did not increase with the addition of insect protein to CTRL, and rather the amount of some isoacids decreased with certain insects. This study showed that, among insects, *H. illucens* induced the most significant changes in the fecal microbiota, with more relevant effects in HD compared to CE.

O123

Preliminary assessment of nutrient digestibility and fecal quality in dogs fed a diet containing hydrolyzed feather meal

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There is increasing interest in alternative protein sources to enhance the sustainability of agri-food systems. The aim of this study was to preliminarily assess the adaptability of healthy dogs to the inclusion of hydrolyzed feather meal in their diet, through the evaluation of nutrient digestibility and fecal quality. Two extruded isoenergetic, isonitrogenous, and isolipidic commercial diets, formulated to meet the nutritional requirements of adult dogs, were prepared: one containing poultry meal (control diet; CTR) as the source of animal-origin proteins (160 g/kg of feed) and the other one containing 90 g/kg of poultry meal and 70 g/kg of hydrolyzed feather meal (treatment diet; TRT). Diets were fed to eight dogs (four adult female and four adult male English Setters) for 45 days. Fecal consistency score (FCS) was assessed on days 0, 3, 7, 15, and 45 (1 = dry feces, 5 = liquid feces), and fecal samples were collected to assess their chemical composition using official methods. Apparent total tract digestibility was also calculated. Significant differences in the fecal nutrients and nutrient digestibility between the TRT and CTR groups were assessed using a generalised linear mixed model. Each focal analytical parameter served as response variable, with Diet (PM or HFM), Time and their interaction as fixed effects, and the experimental phase as random variable. Significance was assumed at $\alpha = 0.05$. Throughout the study, FCS remained

optimal, ranging from 2.2 to 2.5. The assessment of digestibility during the sampling period showed that the treatment diet moderately improved crude protein (CP) and fat digestibility, while significantly enhancing dry matter (DM), starch, and organic matter (OM) ($p < 0.05$). At specific time points, namely Day 3 and 7, the treated group recorded significantly higher digestibility values for DM (Day 3: 87.70% vs. 84.40%; Day 7: 88.60% vs. 85.70%), starch (Day 3: 96.20% vs. 95.00%; Day 7: 96.70% vs. 95.30%), and OM (Day 3: 90.40% vs. 88.40%; Day 7: 91.10% vs. 88.90%) ($p < 0.05$). The interaction between diet and time did not have a significant effect on nutrient digestibility. These findings support further exploration of this sustainable protein source in dogs' nutrition.Research supported by the Project 'BIO = C=O', PON-MISE I&C 2014–2020 FESR, codex N. F/200078/03/X45.

O226

Insect-based products sold by e-commerce on the EU market: microbiome characterization by *16S* rRNA metabarcoding

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Insect based products (IBPs) are Novel Foods recently introduced in the European Union market. The microbiological profile of these products is still poorly investigated, presenting new challenges in terms of food safety. Next Generation Sequencing technologies, particularly *16S* rRNA metabarcoding, allows the characterisation of the microbiome of foodstuffs.
In this study, the microbiome of 40 processed IBPs sold online in the EU were characterised by metabarcoding. The V3 andV4 regions of the *16S* rRNA gene was sequenced by Illumina technology. Then, microbial diversity indices and microbial composition were computed. IBPs were grouped according to species (*Tenebrio molitor*, *Locusta migratoria*, *Acheta domesticus* and *Alphitobius diaperinus*) food category (e.g. powder, bakery products, pasta etc), ingredient pattern (IG), established according to the presence and quantity of specific ingredients other than insects, and e-commerce platform of origin (e-CO) for statistical analysis. Bacillota (53.1%) and Pseudomonadota (37%) were found to be the most abundant phyla and *Aeromonadaceae* (18.2%) and *Bacillaceae* (12.4%) were found to be the most abundant families. Among genera, *Aeromonas*, *Bacillus*, *Clostridium*, *Staphylococcus* and lactic acid bacteria (LAB) genera were those of major interest for their implication on food safety. Notably, *Aeromonas* spp. were detected in processed IBPs for the first time, highlighting the need for further risk assessments. Powdered and ready-to-eat IBPs appeared particularly susceptible to contamination. Despite the limits of the applied method in depicting the viability of microorganisms, our study could support the risk evaluation of IBPs by providing their microbial characterisation. A combined approach with traditional cultural methods should be considered for ensuring IBPs safety and traceability, allowing the sector development.
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O541

Improving livestock nutrition sustainability in a (hazel)nutshell

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Livestock feed production and agro-industrial by-products play major roles in the environmental impact of the global food chain, actively contributing to its total greenhouse gases emissions. For a greater sustainability, the inclusion of agro-industrial by-products in animal feed is a solution currently being explored. Hazelnut skins (HS), by-product of the roasting process, represent not only the industry's exclusive waste in the post-harvesting phase, but also a promising, low-cost source of bioactive compounds, valuable dietary fibres, polyunsaturated fatty acids and phenols. The present study aims to evaluate the effects of HS inclusion in beef cattle diet, representing the first research of its kind in literature. A total of 80 Piedmontese beef bulls (age 7–9 months; average weight 282 ± 65 kg) were divided into two dietary groups (control – CTR, test – T; 4 replicates/group), and subjected to a feeding trial composed of a fattening (5 months) and a finishing phase (2 months). The experimental diets of each phase were iso-energetic and iso-nitrogenous, consisting of straw/hay and standard concentrate feed. In the T feed, an 8% HS inclusion partially replaced corn and barley (T fattening) and only corn (T finishing). Total Phenolic Content (TPC) and lipid peroxidation

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of all experimental feeds (CTR and T, fattening and finishing) were evaluated using the Folin-Ciocalteu and TBARS assays, respectively. Animals' individual weight was recorded before allocation (T0), at diet shift (fattening to finishing) (T1), and on slaughter day (T2) and feed intake (FI) was measured at replicate level by-weekly. Recorded data were used to calculate average daily gain (ADG) and individual feed/straw/hay intake (iFI/iSI/iHI). Differences across treatments and replicates were evaluated with two-sample *t*-test and One-way ANOVA, respectively (RStudio software, libraries 'stats' & 'car'). TPC content was higher ($p < 0.05$) in T feed (both phases), while TBARS results showed no differences. The ADG presented uniform results (C= 1.223 kg; T= 1.188 kg; $p > 0.05$), on the contrary of the finishing iFI (C = 10.26 kg; T = 12.22 kg; $p < 0.001$) and iSI (C = 0.82 kg; T = 0.62 kg; $p < 0.001$). Our findings, characterised by an overall absence of negative impacts and economically favorable changes in the iFI and iSI, support the HS' economic and nutritional re-evaluation through the inclusion in farm animals' feed, and answer the public's growing request for a more sustainable food supply chain.

O559

Nutritional characterization of industrial hempseeds (*Cannabis sativa* L.) of different varieties

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Hemp (*Cannabis sativa* L.) is a resilient and promising alternative to traditional crops due to its greater environmental sustainability and versatility in agriculture, textiles, construction, human and animal nutrition. This study aims to characterise five industrial hempseed varieties and their cakes to: (i) evaluate chemical composition and oil yield through cold-pressing; and (ii) collect spectral for the development of spectral libraries through Near InfraRed technology. Five hempseed samples were provided by the Research Centre for Cereal and Industrial Crops (CREA) in Rovigo (Italy). According to EU legislation, the varieties were certified to contain less than 0.3% Δ9-tetrahydrocannabinol. The varieties included two monoecious (Carmaleonte and Codimono), and three dioecious (Carmagnola, Fibranova and Eletta Campana) types. Ten samples of seeds and cakes were analyzed for chemical composition (AOAC 1996), fatty acid (FA) profile (GC, Agilent Technologies), and mineral content (ICP-OES, Spectro Analytical Instruments GmbH). NIR spectral data were collected using benchtop (FoodScan, FOSS; 850–1080 nm) and handheld (PoliSpec NIR, ITPhotonics, 900–1680 nm) devices. The contents of crude protein (CP), lipids and neutral detergent fiber (NDF) in hempseed varieties were 25.2, 32.3, 35.9 % on dry matter (DM) resp. NDF showed higher variation coefficients (9.5%) compared to CP (3.2%) and lipids (3.8%). The oil yield from the seeds varied from 17.6% (Carmagnola and Eletta Campana) to 20.0% (Codimono). As expected, lipid content decrease in cake samples to 19,9% DM, while CP and NDF increased to 29.9 and 42.8% DM resp. Fatty acid profiles were consistent across hempseed, cake and oil samples, with average percentage of 11.8, 16.5, 71.8, 55.9, 15.9 % of total FA for SFA, MUFA, PUFA, n6, n3 resp. The Carmaleonte variety showed the highest MUFA content (20.2% of total FA) and lowest PUFA content (67.7% of total FA) with the highest n6/n3 ratio (4.57) compared to others varieties (3.58). Potassium, magnesium, and calcium were the most abundant minerals in hempseeds (6775, 3883, 1390 mg/kg DM; resp.), with concentration increasing by an average of 19% in cake samples. These preliminary results show the interesting nutritional characteristics of hempseed and its oil-extraction by-products (cake). The high levels of PUFA, particularly n3 fatty acids in seed, cake and oil samples highlight its promising health perspective, both for animal and human nutrition.

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O431

The management of foot health as a tool to improve the sustainability of a dairy farm

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Lameness is one of the most important diseases in dairy farms, with a prevalence ranging from 20% to 25% in European herds. About 90% of lameness cases are associated with several foot lesions such as digital dermatitis, interdigital phlegmon, and sole ulcers. It was widely demonstrated the foot lesions not only compromise animal welfare but also reduces milk yield, reproductive performance, and overall herd longevity. Several studies estimated the economic impact of foot lesions, but their environmental impact has received little attention so far. The study was

conducted on a commercial dairy farm with 320 milking cows, located in northern Italy, where a foot health management protocol was implemented. The protocol included a weekly routine of hoof trimming, daily inspection of foot conditions, and the implementation of data collection with a specific recording system. Additionally, nutritional adjustments, particularly in mineral supplementation (zinc) and biotin, were introduced to promote hoof health. Data collection included lameness and disease recording and milk production records. The aim of the study was to evaluate the effects of the foot health management protocol on foot lesions, herd performance, and environmental outcomes. Data collected before and after the protocol implementation were analyzed over a two-year period. The results showed that the occurrence of severe foot diseases decreased significantly; particularly there were significant differences ($p < 0.05$) in the percentages of sole ulcers and abscesses before and after the implementation. The incidence of laminitis detected also had a significant difference between the years showing the benefits of an earlier detection and intervention. The percentage of healthy animals increased significantly overall the two years of analysis ($p < 0.05$) and showed a large effect; over 80% of heifers were identified as healthy at their first evaluation. Herd milk production data showed a significant average increase ($p < 0.05$). These findings are consistent with previous research indicating that proper foot health management is essential for improving both economic and sustainability outcomes in dairy farming. Effective protocols not only mitigate the economic loss associated with foot disease but also contribute to reducing the environmental footprint of dairy farming.

O314

Measuring the importance of sustainability in animal-based product supply chains: insights from the CUB Model

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Ensuring sustainability across all aspects of the food system has emerged as a significant challenge, particularly for animal-based products. This sector requires strategies to minimise environmental impacts, improve animal welfare and adopt responsible production practices. As consumers play a key role in the transition to a sustainable food system, understanding their perception of sustainability in different supply chains is essential. This is particularly relevant for animal-based products, which face competition from plant-based alternatives and increased consumer awareness of the environmental and ethical concerns. In this context, this research aimed to evaluate the importance and the perception of sustainability aspects in different animal-based supply chains. An online survey was conducted with 1000 Italian respondents, responsible of purchasing. This study assessed the importance consumers place on sustainability features and their interest in guaranteed sustainable animal products. The importance of sustainability was analyzed in relation to socio-demographic characteristics (e.g. age and gender) and the specific supply chains (cheese, meat and cold cuts). Consumers rated their interest in sustainability for each supply chain using a 10-point Likert scale. Responses were analyzed using the Combination of a discrete Uniform and a shifted Binomial distribution (CUB) to assessed the level of preferences and uncertainty in evaluations. Participants also identified the three most important sustainability attributes from a list of 12 for each supply chain. Finally, using a 5-point Likert scale, they rated how their consumption of cheese, meat and cold cuts might change due to climate chance and environmental concerns. These responses were compared using the Correlation Analysis (CA). The results showed that Italian consumers value sustainability in all three supply chains, with the highest importance attributed to the meat one, which rated a higher level of 'liking' ($1 - \xi = 0.77$) and lower response uncertainty ($1 - \pi = 0.38$) compared to others. Furthermore, the importance attached to sustainability is significantly influenced by socio-demographic characteristics such as age and gender. The correlation between expected changes in consumption and the sustainability attributes considered important revealed significant links between the importance attached to sustainability aspects and the willingness of consumers to change their consumption behavior.

O295

Stakeholder attitude towards sustainability of dairy farming systems: a participatory process

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Globally, dairy farming systems are important contributors to the environmental impact of livestock farming. In Italy, the dairy sector represents one third of the economic value of national livestock sector. However, its sustainability level must be addressed

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in order to match consumers' concerns and expectations on its interaction with the surrounding ecosystem. The aim of this study, as part of a wider project (PRIN 2022), was to address the perception of different stakeholders about the sustainability of dairy farming systems in Northern Italy. To this aim, we asked stakeholders' opinions (farmers, retailers, technical assistants, veterinarians, policy makers and teachers at agricultural institutes) through an online survey sent to a representative sample of the supply chain, collecting 73 surveys. The survey was composed in order to collect data on the perception of the stakeholders on the relation between livestock farming and sustainability, the aspects that can be improved in dairy systems, the main problems they are facing, the indicators used to assess dairy farms' sustainability and, finally, the identification of which type of stakeholders the interviewee represented. In the second step, 3 focus groups were organised in the 3 study areas involved (Veneto, Lombardia, Friuli Venezia Giulia), each of which consisted of a maximum of 10 participants, for a qualitative evaluation of the previously obtained results. The results highlighted that the 3 main strategies to implement in order to increase dairy sector's sustainability were the following: enhancing manure management, increase animal welfare and increase productive efficiency. On the other hand, the 3 main problems highlighted by the participants concerned the excessive costs, the lack of technical support to apply new management strategies, and the need for motivation. Moreover, results showed the importance of having various types of stakeholders' point of view to obtain a general understanding of sustainability at landscape level. This way, data on the stakeholders' perception revealed important information to proceed with the investigation and test of useful indicators to assess the level of sustainability of dairy farming systems.

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O099

Stakeholders' perspectives on environmental issues: preliminary results from SUNEQUMAR survey

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An online survey was conducted by the means of a questionnaire to detect the perceptions of environmental impacts, and to identify the main farming activities and management difficulties focused on marginal areas of Centre-South Italy. The demographic profile of the interviewees ($n = 100$) is as follows: 69.8% ranging 18–25 yrs old, 27.1% are within 26–60 yrs old, more than half are female (55.2%), and almost all of them are Italian (99.0%), distributed in North (3.1%), Centre (82.3%) and South (13.5%). Regarding the feeding habits, 93.8% of the interviewees declares to be omnivorous, a smaller percentage vegetarian (3.1%) and vegan (2.1%). Animal rights activists and environmentalists account for 5.2% and 26% of the surveyed population, respectively. Stakeholders interviewed included farmers, breeders, agronomists and technical advisors, students, and researchers. About 74% of interviewees believe to be informed on environmental issues mainly by internet and social networks (61.5%), but the role played by protected areas is little known in 52.1% of surveyed cases. The natural environments are considered not sufficiently protected by 69.8% of interviewees. As far as the perception of the effects of climate changes is concerned, reduced availability of water (40.6%), increase in rainfall intensity (29.2%), melting glaciers (27.1%) are the main concerns. Industry (34.4%), infrastructure (28.1%) and the expansion of urban areas (27.1%) are perceived as main risk for environment conservation, while agriculture (17.7%) is considered to have a comparatively minor effect. The main environmental threats to natural ecosystems are considered pollution from urban sewage (43.8%), littering (43.8%), invasive wildlife (28.1%) but also inadequate pasture management (19.8%). Twenty-four percent of the interviewees consider to be ineffective the environmental policies implemented by Institutions. Finally, among the surveyed farmers ($n = 10$), 90% raises dairy cattle from Holstein, Jersey and Pezzata Rossa breeds in semi-intensive or semi-extensive systems, mainly located in rural areas of Centre-South Italy. The average size of the farm is 90 heads. The main concern reported by farmers is associated with damages to crops by wildlife (40%).

The survey has been approved by the Bioethics Committee of the University of Molise. The research was supported by project PRIN 20224L4WSR, funded by Next Generation EU (CUP: H53D23005120).

O423

A comparative analysis of ankomRF and gas endeavour *in vitro* rumen systems: effects of headspace volume and CO_2 flushing time on gas and methane production

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This study examined the effects of different experimental conditions (CO_2 flushing time and bottle headspace volume) on total gas production (GP) and methane kinetics using two commercial *in vitro* fermentation systems: the 'AnkomRF GP system' and the 'Gas Endeavour system'. *In vitro* incubations were conducted by mixing rumen fluid from 3 lactating cows with Menke buffer at a 1:2 ratio, using a lactating total mixed ration as fermentation substrate (1.000 ± 0.002 g DM/150 mL medium). Incubations lasted 24 hours. GP kinetics were measured with both systems, while methane production was measured via gas chromatography at the end of incubation. Moreover, kinetic of methene production was measured with Gas Endeavour system. The experimental design compared the 2 systems (AnkomRF vs. Gas Endeavour), 2 bottle headspace volumes (low: 70 mL; high: 170 mL), and 3 CO_2 flushing times (60, 30, and 10 minutes). Each experimental treatment was conducted in duplicate across three consecutive incubation runs, with 3 blanks per run (for a total of 90 *in vitro* rumen simulations). Statistical analysis showed significant differences in total GP between the systems, with AnkomRF producing 7.8% more gas than Gas Endeavour (214 ± 28 vs. 198 ± 29 mL/g DM; $p < 0.01$). Shortening CO_2 flushing time from the conventional 60 minutes to 30 and 10 minutes reduced GP and increased variability (203 ± 25.9, 200 ± 31.9, and 174 ± 33.0 mL/g DM.; $p < 0.05$, resp.). Reducing bottle headspace volume increased GP with the Gas Endeavour system (+19.4%; $p < 0.01$) but slightly reduced GP with AnkomRF (–9.7%; $p < 0.10$). Methane production after 24 h was 9.6% higher in AnkomRF compared to Gas Endeavour (38.4 ± 10.1 vs. 34.7 ± 9.0 mL/g DM; $p < 0.01$). Reducing CO_2 flushing time from 60 to 10 minutes decreased methane production by 12% ($p < 0.05$), whereas 30 minutes had a negligible effect. Reducing headspace volume increased methane production with both systems ($p < 0.01$). In conclusion, the observed differences in gas and methane measurements can be attributed to the distinct detection mechanisms of the two systems and their interaction with bottle headspace volume. These findings emphasise the critical role of equipment, system settings, and CO_2 flushing time in accurately evaluating gas and methane production. Information on substrate degradability and volatile fatty acids production will provide a more comprehensive understanding of how laboratory operating conditions influence experimental results.

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O523

In vitro comparison among commercial dietary buffers

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Dietary buffers play a crucial role in mitigating rumen and possibly intestinal acidity, thus improving microbial and enzymatic activity, particularly when high concentrate diets are fed to dairy cattle. Neutralising capacity (NC) evaluation is a reliable method to test the potential efficacy as buffering agents. The trial aimed to compare the NC of 6 commercial dietary buffers (DB1-6) and sodium bicarbonate (SB) under different conditions. The DB were analysed using powder X-ray diffraction to determine the total calcium carbonate content and the proportion of the 3 main calcium structures, viz. calcite, aragonite and Mg-calcite. The NC was evaluated in triplicate by titration with 0.5 N acetic acid (weak acid – WA) of 200 mg of DB and SB in water solution to reach pH 6, 5 and 4. A further test was performed by dissolving SB and DB in rumen fluids (RF) at the commercially suggested doses (160 and 80 g/cow/d respectively; additionally, DB5 was tested at 60 g/cow/d, and at 80 g/cow/d but diluted at a 1:1 ratio with SB), assuming a total RF content of 180 L. The latter test was replicated with 3 RF (initial pH: 6.61, 6.82, and 6.46); the RF-DB solutions (RFB) were titrated with 0.1 M HCl (strong acid – SA). WA and SA volumes required to reach each pH were compared among products. Data were analysed using a multivariate GLM using SPSS software v.29 (IBM SPSS Statistics for Windows; IBM Corp., Armonk, NY). The LSD post-hoc test was applied for pairwise comparisons. The DB different mainly for the calcite content, which was <5 wt% in DB5; 5–15 wt% in DB1, DB4 and DB6; 15–25 wt% in DB3; and >75% in DB2. Only DB4 and DB5 have more than 15 wt% of aragonite. The highest NC at pH 6 with WA was achieved by DB6, followed by SB and DB3 (4.2, 3.7 and 3.2 mL of WA respectively; $p < 0.001$). The DB3 shows the highest NC also at pH 5

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(8.5 mL of WA; $p < 0.001$), while DB1, DB2 and DB3 required higher WA volume than the other DB (> 34.4 vs <28.9 mL of WA; $p < 0.001$) at pH 4. The WA volume required to reach pH 4 seems to be related to the DB calcite content. Despite the tested doses, no differences were detected in the initial pH of the RFB (except for SB) and in the HCl volume necessary to reach pH 6. The highest NC in RF to reach pH 5 and 4 were obtained by SB and DB2 (54.3 and 55.3, $p = 0.036$; 100.2 and 105.8, $p = 0.019$; respectively). The results suggest that the mineral structure of the DB influences their solubility and, consequently, their NC over time.

O522

Evaluation of nitrate at different level of inclusion on in vitro ruminal fermentation

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The use of nitrate (NO_3^-) as a feed additive for ruminants has gained significant attention due to its ability to mitigate methane (CH_4) emissions, one of the major greenhouse gases produced during ruminal fermentation, and to potentially provide nitrogen for microbial protein synthesis. NO_3^- acts as an alternative electron acceptor, diverting H_2 from methanogenesis to more thermodynamically favorable pathways, leading to the reduction of NO_3^- to nitrite and then to ammonia. However, the potential for NO_3^- accumulation poses a risk of toxicity, necessitating careful evaluation of NO_3^- inclusion levels. This study investigated the effects of 3 inclusion levels of calcium NO_3^- (200 mg/L NitL, 500 mg/L NitM, and 1000 mg/L NitH) compared to a control (CTR) on *in vitro* ruminal fermentation. Key parameters assessed involved CH_4 production, total gas (GT) production, dry matter digestibility (DMD), volatile fatty acid (VFA) profiles, and NH_3 concentrations. A total mixed ration substrate was fermented with rumen fluid collected from dairy cows, and fermentation was monitored for 24 hours. The trial included 6 different runs, each with 3 treatments and a CTR, tested in triplicate per run. Results revealed a significant dose-dependent reduction: NitH reduced CH_4 by 53.7% and GT by 34.89% at 24 h compared to the CTR ($p < 0.05$). NitM also significantly reduced CH_4 production by up to 48.1% but had less pronounced effects on GT. These findings demonstrate the potential of NO_3^- to substantially mitigate CH_4 emissions in a dose-dependent manner. DMD decreased significantly ($p < 0.05$), with reductions of 18.16% and 21.45% observed for NitM and NitH compared to the CTR (CTR: 51.66 ± 0.21%DM; NitM: 42.28 ± 4.08%DM; NitH: 40.58 ± 2.82%DM), suggesting a potential trade-off between CH_4 mitigation and feed digestibility. VFA analysis showed a shift in fermentation pathways, with an increased proportion of acetate ($p < 0.001$), and a reduced proportion of propionate ($p < 0.05$) and butyrate ($p < 0.001$). The acetate-to-propionate ratio increased significantly, indicating a shift toward acetate-dominant fermentation (from 1.81 in CTR to 2.11 in NitH; $p < 0.001$). NH_3 concentrations were significantly higher in nitrate treatments, reflecting enhanced deamination activity and the utilisation of nitrate as an NPN source.Research supported by Agritech National Research Center and received funding from the European Union Next-Generation EU PNRR – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022).

O037

Ruminant nutrition in the age of microplastics contamination: challenges and insights

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The widespread presence of microplastics (MPs, plastic fragments ranging from 1 µm to 5 mm), in agricultural systems is raising significant concerns regarding their interactions with the ruminant digestive system. Within this system MPs can enter through contaminated feed and water or may be generated by the fragmentation of ingested plastics. In the rumen, MPs disrupt ruminal fermentation by altering microbial diversity, notably reducing the abundance of cellulose-degrading bacteria. This microbial imbalance could increases rumen acidity, impairs fiber and protein degradation, and reduces the synthesis of volatile fatty acids and ammonia nitrogen, all of which are crucial for energy production and microbial protein synthesis. Moreover, MPs could act as vectors for heavy metals, which are released during rumen degradation and rumination, intensifying oxidative stress, impairing enzymatic activity, and disrupting metabolic homeostasis. In the intestine, MPs could reduce the activity of protein-digesting enzymes and cause physical damage to the intestinal epithelium, particularly in the jejunum. While the most MPs are excreted in feces, a small fraction translocate into the bloodstream and excreted via urine and milk, raising food safety concerns. However, the ruminant digestive system can influence the fate of MPs. Rumen microbiota, such as *Pseudomonas* spp. and

Acinetobacter spp., can enzymatically degrade polyethylene terephthalate MPs into shorter-chain molecules, which effects are not studied yet. This degradation process appears more effective than bacterial activity alone, suggesting a synergistic interaction among diverse ruminal microbial populations. This complex bidirectional interplay, where MPs not only alter digestive functions but are also biodegraded by the ruminant digestive system, underscores the need to determine the metabolic and physiological consequences of these degradation by-products and to develop integrated strategies preventing MPs contamination ruminants' digestive system, promoting the sustainability of ruminant breeding and safe food systems.

O124

Effect of microplastics additives on rumen ecology: *in vitro* preliminary study

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Global plastic production reached 390.7 million tons in 2021, with projections of doubling in 20 years. Its durability and widespread use have led to significant environmental accumulation. When plastics degrade, they form microplastics (MPs)—particles smaller than 5 mm—that persist in ecosystems and are absorbed by plants or ingested by animals, and humans. Therefore, MPs in the rumen can be an indirect route for milk contamination. Understanding how MPs behave and accumulate in the rumen is essential to assess the potential transfer of these contaminants into milk and subsequently into the food chain. Furthermore, additives in MP have been linked to various health problems, including metabolic disorders, cancer, and endocrine disruption, due to their ability to migrate through the lymphatic system or trigger inflammatory processes. This study investigated how MP chemical additives, such as bisphenols (BIS) and phthalates (PHT), affect rumen fermentation in an *in vitro* experiment, focusing on microbial community changes and using the fatty acids (FA) as biomarkers. An *in vitro* trial was designed according to Tillie and Terry methods using ovine rumen liquor inoculating anaerobically with 12 treatments: a control without additives (CON), 5 bisphenols (BIS), or 6 phthalates (PHT) added to CON at 0.6225 mg/ml. Fatty acids were analyzed by gas chromatography, and 16S rRNA gene sequencing was used to assess microbial communities. Results showed that BIS and PHT altered the FA profiles differently. Bisphenols reduced saturated FA (e.g. bisphenol A: 43.0 g/100 g $_{FA}$ *vs.* CON: 68.0 g/100 g $_{FA}$) and increased monounsaturated FA, unlike phthalates. Bisphenols also affected biohydrogenation intermediates (e.g. C18:1c9, C18:3c9c12c15), branched-chain FA (e.g. C15 ante), and long-chain FA (e.g. C20:1). Phthalates showed a milder impact on FA metabolism. The α-diversity detected in the microbial community differs on Simpson, Shannon, and Richness indexes. Also, the structure of the microbial communities in the treatments differs. These findings reveal the distinct metabolic effects of bisphenols and phthalates.

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O036

First investigation of microplastics contamination in corn silage used for dairy cow nutrition

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Microplastics (MPs), plastic debris from 1 µm to 5 mm derived mainly from weathering degradation of discarded plastic items, have been detected in the bodies and various derived products of ruminants, including blood, feces, milk, and meat. This contamination in livestock can raise concerns for both animals and human health. I*n vitro* studies have reported that MPs can cause tissue inflammation and release the toxic elements retained within them. The intensive usage of plastics in farms to store feeds is widely observed and this could be a potential contamination source in feeds. Notably, corn silage—a dietary staple for dairy cows—is stored for several months under plastic covers during the fermentation process, which may expose it to MPs contamination. This study aimed to investigate, for the first time, MPs contamination in corn silage from three dairy farms situated in northwestern Italy, utilising an extraction method specifically optimised for this complex matrix. Corn silage samples ($n = 3$) were collected, dried at 60 °C overnight, and ground 4 mm. MPs extraction process involved KOH digestion, Fenton reactions, and MPs recovery with each reaction separated by filtration with a 30 µm sieve and then collected MPs were quantified by a stereomicroscope. The analysis was conducted in triplicate with an environmental blank, avoiding the use of plastic materials. The results demonstrated a widespread of MPs in corn silage across all the farms. Statistical analysis revealed significant differences in MPs contamination levels among the

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farms, with the highest concentration detected at 47.0 ± 2.65 items/g dry matter (DM) and the lowest at 34.0 ± 6.56 and 32.7 ± 3.79 items/g DM, indicating potential variability in contamination sources or management practices. This study demonstrated, for the first time, the presence of MPs in corn silage, highlighting significant differences among farms. Future studies are needed to validate this finding by increasing the number of analytical samples and to identify the sources of MPs in feeds with the final goal of producing corn silage with decreased MPs levels.

O021

Grab or Skip: what drives undergraduates to try animal welfare beef meat?

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Certificated animal welfare (AW) meat is debatably perceived as a more ethical and environmentally sustainable alternative to conventional farmed meat, but several barriers exist to its acceptance in the market. The attitudes of youth have not been reported to date even though this specific consumer segment has more flexible dietary habits and is more concerned about AW and environmental issues. Thus, youth represent a demographic that may be more accepting of AW meat and for whom the pro-environmental consequences of early adoption may be realised across an entire lifetime. This study makes some important contributions on matters relevant to the EU market of animal welfare beef meat by exploring the awareness of consumers regarding this product. Thus, in this study of college-aged Italians, we examined the predictor factors, such as gender, age, level of animal welfare familiarity, subjective knowledge and level of ethically minded consumer behavior (EMCB) influence youth on intention to try AW beef. The data were collected between October-December 2024 through an online questionnaire consisting of a total of 21 questions which include a 10-item EMBC scale, using five-point Likert scale. A convenience sample of 356 Italian college-aged participants (women = 218 and men = 102) completed the questionnaire. Subjects older than 30 years old, those who did not give consent to use their data, and individuals with missing information ($n = 24$) were excluded from the analysis. Cumulative Link Mixed Models show that gender, familiarity, EMBC score, and age predict the willingness to try AW beef. The findings indicate that a high EMBC score and being women increased the willingness to try AW beef, while the older age groups and those less familiar with AW beef decreased this likelihood. Subjective knowledge level had no effect. These findings provide timely and actionable information for AWM producers and marketers and policymakers and help improve understanding of how familiarity and ethical mind shape peoples' food behavior and psychological traits in sustainable meat choices.

O108

Ever been to a dairy farm? Testing the effect of virtual farm tours on consumers' perceptions of livestock production

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Public trust in animal production in Europe has declined in recent years, with consumers increasingly concerned about animal welfare and viewing intensive dairy farming negatively, as extensively reported in scientific literature. In the frame of the AWare project, which aims to explore ways of making information about livestock production more transparent to consumers, this study investigates the impact of 360° immersive videos taken on a dairy cattle farm on consumer perceptions of farming practices. A convenience sample was recruited through a survey implemented on the *Qualtrics* online survey platform. Only respondents who had consumed or purchased milk in the two months prior to the interview and older than 18 years old were selected ($n = 62$). The online questionnaire comprised several sections. The first section presented three 360° immersive videos depicting key moments in the daily routine of a dairy cow (feeding, resting and milking) were presented to participants. Participants could choose whether or not to watch the videos. Following the videos, respondents answered a series of close-ended questions related to their perception and feelings about the immersive video content, their knowledge and familiarity with dairy farming practices, their purchase behavior and consumption habits regarding milk, and socio demographic characteristics. The majority of the respondents (88%) choose to engage with the interactive videos, while 12% opted out of the immersive experience. Among those who chose not to watch the video, 75% expressed trust in farmers, believing that they knew best how to raise animals, while 25% indicated that they were concerned about seeing images that might make them feel guilty about consuming dairy products. The interviewed sample demonstrated a high level of knowledge and familiarity regarding dairy farming practices. However, 9% of

respondents reported having gained comprehensive new knowledge from the 360° experience. Although preliminary, the findings suggest that immersive technology effectively enhances consumer understanding of dairy farming practices, especially for those with limited prior knowledge. This could have important implications for improving transparency in the livestock production sector and addressing consumer concerns about animal welfare.
Research supported by Piano di Sostegno alla Ricerca (PSR) 2023 – 'My First SEED Grant', University of Milan

O278

Protection of animals & research needs: legislative overview and future perspectives

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Italy has a long history of protecting animals used for scientific purposes, as the first Italian law ruling the protection of animals used for research and testing dates back to 1913, when the country was under the Vittorio Emanuele III's Kingdom. Nowadays, animal testing is regulated by Legislative Decree 26/2014, based on the Directive 2010/63/UE of the European Parliament. Seven years after the law come into force, the Ministerial Decree of 5 August 2021 was published, establishing very specific training modules that the operator have to obtain to work in the field of animal testing. Like every beginning, the application of this Decree caused several troubles for the Research Institutions and for the researchers themselves. After some months, the Directorial Decree of 18 March 2022, has clarified many aspects of training and has in fact allowed the institutions to establish training courses adequate to comply with the legislation. Currently, there are several theoretical modules available online and recognised by the Ministry of Health, especially to train personnel to work with laboratory rodents, but also with species of zootechnical interest. As for the practical modules, they are often accessible only to the internal staff of the organising institution, it is therefore necessary to check all the training opportunities available in the country. Having the need to comply with these regulations, the researcher who manages species of zootechnical interest is faced with two options: limit his research to observational studies and the collection of non-invasive samples or work in an authorised animal facility and have adequate training. The aim of this presentation is to illustrate the current regulatory framework, to offer ideas to improve the activity of researchers working with zootechnical animals, such as the use of non-invasive diagnostic methods and the increase in the number of species authorised in each facility according to D.lgs. 26/2014.

O024

Anthelmintic efficacy of pour-on Eprinomectin against gastrointestinal strongyles and relationships with milk production parameters in lactating goats

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The aims of this study were (i) to evaluate the efficacy of pour-on eprinomectin (EPM) in lactating goats naturally infested with gastrointestinal strongyles, and (ii) to assess the related effects on their milk quanti-qualitative performance. Forty-two multiparous Camosciata delle Alpi goats reared in two semi-extensive farms (F1, $n = 20$; F2, $n = 22$) were included in the trial. In both farms, the goats were divided into two groups, which were balanced based on their infestation from gastrointestinal strongyles (number of eggs per gram of faeces, EPG), milk yield and gross composition. In each farm, the goats were then randomly assigned to a control (CTRL) or a treated (EPM) group. The EPM goats were treated with Eprinex® Multi Pour-On 5 mg/mL at the dosage of 1 mg/kg body weight (BW), while the CTRL goats did not receive any antiparasitic treatment. Starting on the day of drug treatment, and then once a week for the following 28 days, milk yield was recorded, and faeces and milk samples were collected individually. Faeces were subjected to copromicroscopic analysis, while milk samples were analysed for fat, protein, and lactose contents. Data were subjected to two-way ANCOVA using R software; the model included the effects of treatment, time (as a repeated measure), their interaction, and initial values as a covariate. Lower EPG values were found in EPM than CTRL goats in F1 (3316 *vs* 5485; $p < 0.001$), while no differences were found between groups in F2 (2864 *vs* 2986; $p = 0.637$). Coprocultures allowed to identify L3 larvae belonging to the genera *Haemonchus*, *Teladorsagia* and *Trichostrongylus*. In both farms, the treatment determined a reduction of *Teladorsagia* and *Trichostrongylus* larvae ($p < 0.001$). However, EPM goats showed significantly higher percentages of *Haemonchus* larvae when compared to CTRL ones (F1: 98.4% *vs* 92.3%; F2: 97.6% *vs* 92.5%; $p < 0.001$). In both farms, the treatment did not significantly affect milk yield and composition (fat, protein

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and lactose contents and yields). An exception was observed for milk lactose and protein contents, which were approximately 1 g/kg lower in EPM goats compared to CTRL goats in F1 and F2, respectively ($p < 0.001$). The obtained results suggest that pour-on EPM at the recommended dosage of 1 mg/kg BW is not effective in reducing *Haemoncus* in multiparous lactating goats. Further studies should identify the dosage able to reduce the parasite load, to avoid impairments of the short-term productive performance of dairy goats.

O132

Effect of almond and carob by products on immune competence of growing lambs

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Livestock sector exerts enormous pressure on the environment, especially the impact of feed production includes not only land and water use, fertilizers, pesticides, agricultural operations etc, but also the use of human-edible feed crops which threatens world food security. REFRESH project aims to reshape animal feeding system by using agro-industrial by-products (AIBP) as feed. AIBP are indeed inedible for humans but widely accepted as animal feeds, particularly for ruminants, and some of them contain bioactive compounds, such as polyphenols, vitamins, and flavonoids, which can improve animal welfare and product quality. The present work aims at evaluating the effect of almond (AL) and carob (CA) by-products on cytokine profile and Immunoglobulig-(Ig)G of growing lambs. Fifty finishing lambs were divided into 5 experimental groups and fed with a conventional diet (CON), and with a conventional diet partially replaced with AL at 14% (AL14) and 28% (AL28) on DM, and with CA at 25% (CA25) and 50% (CA50) on DM, for 60 days. Peripheral blood was collected at 0, 30, and 60 days and cytokine profile in terms of Inteleukin (IL)-6, IL-10, Interferon (IFN)-γ, and IL-β and IgG was performed on the plasma by ELISA. Data were analysed with a mixed model ANOVA using the feeding strategy as a fixed effect for cytokine secretion; in addition, the time of the experiment was tested as a fixed effect for IgG secretion. On average, IFN- γ secretion was significantly influenced by the feeding strategy ($p = 0.04$), showing a lower value in CA50 compared to AL-supplementation at both doses tested. The IL-6 value increased ($p < 0.001$) in the AL14, CA25 and CA50 groups compared to CON. IL-1 β was influenced by the dietary strategy ($p = 0.078$) and decreased in the AL28 group compared to CA25. IL-10 secretion was higher ($p < 0.001$) in the AL28, CA25 and CA50 groups compared to the CON group. Humoral immunity as measured by total IgG was significantly influenced by both the feeding strategy ($p = 0.0018$) and the time of the experiment ($p < 0.001$). On average, a lower level in the AL14 group compared to the AL28 group and CA supplementation. Furthermore, total IgG decreased across the time of the experiment, showing the lowest value after 60 days. The present results demonstrated that in growing lambs a partial replacement of feed with AIBP is able to modulate their immune competence with an overall increase in cytokines with pro- and anti-inflammatory roles.

Research supported by PROGETTI DI RICERCA DI RILEVANTE INTERESSE NAZIONALE – Bando 2022- (CUP) Title: GREening Food by RESHaping feed: a comprehensive approach to upcycle agro-industrial by-products in ruminant feeding (REFRESH).

O340

Projections of the temperature humidity index for the Italian territory

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The accelerating pace of climate change poses a significant threat to livestock production systems, with heat stress (HS) emerging as a critical challenge to animal health and performances. Understanding the temporal and spatial impacts of climate pressures is thus crucial for developing effective preventive and adaptive strategies. This study aims to characterise heat stress patterns across Italy using the Temperature-Humidity Index (THI) as an indicator. A multi-model approach was adopted, drawing on 27 climate models from the Coupled Model Intercomparison Project Phase 6 (CMIP6), which also feature in the latest Intergovernmental Panel on Climate Change (IPCC) Assessment Report. These models provided global daily temperature and humidity data at a high spatial resolution (0.25° × 0.25°) for both historical (1985–2014) and projected (2026–2100) periods. Daily THI values for Italy were computed and then aggregated into monthly means, which were further averaged by season (winter, spring, summer, autumn). The resulting seasonal THI values were thus calculated for both the historical Climatological Normal (CliNO, 1985–2014) and future conditions under four Shared Socioeconomic Pathways (SSP1-2.6, SSP2-4.5, SSP3-7.0, SSP5-8.5) from 2026 to 2100 at 25-year interval. By mid-century (2026–2050), under the most optimistic low-emission scenario (SSP1-2.6), annual THI anomalies relative to CliNO are projected to rise by about 1 unit in winter and up to 4 units in summer. Based on thresholds established for dairy cattle, large portions of Italy may be thus characterised by

summer THI (72 ≤ THI <75) associated with discomfort conditions or, with reference to southern regions, with alert conditions (75 ≤ THI <79). By the end of the century (2076–2100), under the high-emission/worst case scenario (SSP5-8.5), northern regions appear especially vulnerable, with THI anomalies reaching up to 6 units in winter and up to 11 units in summer. Danger conditions (79 ≤ THI <84) are expected to become widespread in summer across southern regions, coastal zones, and the Po Valley. Moreover, the same scenario shows a progressive temporal expansion of the mild discomfort conditions (68 ≤ THI <72), which extends into the autumn months. In conclusion, HS is anticipated to become a significant challenge across all SSP scenarios. Therefore, even under the lower-emission pathways (SSP1-2.6), substantial adaptation efforts will be required to avoid severe health problems and production losses by mid-century.

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O287

Relationship between cows' milk performances and dry period length in Italian cattle breeds

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In conventional dairy cows' management, about eight weeks of dry periods between two successive lactations are routinely considered optimal. For high yield producing cattle, partial or total suppression of dry period have been tested in literature. The present study is aimed at testing retrospectively the effect of dry period length on successive lactation performances investigating AIA datasets. After quality control, the datasets included 166,223 records of dry period length (days) and the successive cumulative lactation for 87,848 cows of 4 breeds in 1,040 farms (F): 5,259 Italian Brown (100 F), 75,184 Holstein (660 F), 5,515 Simmental (74 F), 112 Jersey (13 F) and 1,778 crossbred cows (193 F). The milk production and quality were analyzed by applying a within-breed linear mixed model that fitted the fixed effect of dry period length (3 level), year of parturition (4 classes of three years length), parity order (4 level), dry-off season (4 levels), the interaction between dry period length × dry-off season and the random effect of the farms. Six milk traits were analyzed: 305-days milk, fat and protein yield (305MY, 305FY and 305PY) and effective daily average (dMY, dFY and dPY). The random effect of the farm explained a large proportion of variance across all breeds and traits (from 0.43 ± 0.06 Simmental to 0.53 ± 0.05 of Brown). Among the 5-breed ×6-traits combinations, the dry period length was highly significant ($p < 0.001$) in 14 combinations out of 30, significant ($0.001 < p < 0.05$) in 8/30 (mostly in Holstein, Simmental and Brown), whereas the last 8/30 were not significant ($p > 0.05$) (mostly in Crossbred and Jersey). As examples, in Holstein MY305 (dMY) slightly decreased from 10,769 ± 71 kg (35.17 ± 0.23 kg/d) to 10,529 ± 72 kg (34.34 ± 0.22 kg/d) passing from conventional (50–65 d) to short (<50 d) dry period. 305FY and 305PY experienced a drop from 399.7 ± 3.23 kg and 351.7 ± 2.4 kg (conventional dry period) to 390.5 ± 2.25 kg and 347.2 ± 2.4 kg (short dry period), respectively. In some cases, significant interactions between dry off period and season were observed. In conclusion, the analysis of a large sample of Italian dairy farm showed a significant effect of dry periods on milk yield and composition for all the considered breeds.

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O111

Study of the variation in the distribution of wild and domestic ungulates in an extensive livestock farm in Central Apennine during the seasons through trapping rate

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Understanding the seasonal distribution patterns of wild and domestic ungulates is essential for fostering coexistence and sustainable management in extensive livestock systems. This study was conducted on a 2,330-hectare farm in Central Italy (Lazio Region, 42.4846 N, 11.6445 E), comprising 565 hectares of pastureland and 1,765 hectares of forested areas. The farm supports 430 cattle and 60 equines of the Maremmana breeds, raised in semi-wild conditions, alongside wild ungulates such as red deer (Cervus elaphus), roe deer (Capreolus capreolus), and wild boar (Sus scrofa). Seventeen camera traps were deployed using a systematic sampling approach across five silvo-pasture

sections and operated continuously for 12 months, recording 14,620 detection events. Data analyses integrated Kendall's Tau correlation and spatio-temporal analysis performed with specific R packages to assess activity rates, overlap indices and the effect of environmental and anthropogenic factors. Temporal activity analyses indicated clear diel patterns, with wild boar being primarily nocturnal and red deer showing crepuscular peaks. Spatial analyses showed wild boar concentrated in forested areas during summer (42% of detections) and red deer in pasture zones during autumn (37%). Roe deer maintained stable activity across seasons. Overlap indices (Δ) between domestic and wild ungulates highlighted moderate spatial coexistence, ranging from 0.42 (cattle vs. roe deer) to 0.56 (cattle vs. wild boar), and temporal overlap indices from 0.37 (cattle vs. red deer) to 0.62 (cattle vs. wild boar). Kendall's Tau correlation coefficients revealed that proximity to water sources positively influenced wild boar presence, while red deer activity correlated negatively with distance from fences. In winter, overlapping habitat use between cattle and red deer increased due to reduced forage availability. Conversely, during summer, wild species adjusted spatial distributions when cattle were introduced, confirming interspecific competition for resources. This study demonstrates the efficacy of camera trapping as a non-invasive method to collect continuous, high-resolution data on wildlife-livestock interactions. The findings provide actionable insights for sustainable management, such as zoning and adapting practices to seasonal dynamics, while emphasising the potential of integrating artificial intelligence and drones to enhance future monitoring efforts.

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O208

Cost of buffalo milk: an analysis pre and post Covid

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Global agriculture is evolving rapidly due to shifting international food markets, agricultural globalisation, policy changes, societal demands, and environmental challenges. In Italy, the dairy sector accounts for over a third of the livestock sector's economic value, focusing on high-quality cheeses, many with EU Protected Designation of Origin (PDO) status. Over three decades, the sector has faced significant changes driven by EU policy reforms, milk quota elimination, and sustainability efforts like the Farm-to-Fork strategy. Intensification, larger herds, fewer farms, and advancements in genetics have boosted productivity. Yet, global integration and trade liberalisation have raised input costs, while milk prices remain volatile, especially during crises like the COVID-19 pandemic.

In 2020, Italy's lockdown halted industrial activities, causing severe sales declines in livestock sectors. Labor shortages disrupted milk collection and processing, collapsing spot market prices. These challenges underscore the need for accurate data and cost management, particularly for farmers bearing the highest supply chain costs. The Italian buffalo sector, pivotal for producing Mozzarella di Bufala Campana DOP, also endured these structural shifts. In 2019, the buffalo farming value chain contributed €600 million directly and €2 billion indirectly, supporting over 11,000 jobs. Most buffaloes are intensively reared in Southern Italy's PDO areas for mozzarella production, which grew 26.1% from 2013–2017 due to rising demand. Selective breeding has enhanced production efficiency, ensuring year-round milk supply. The economic environment calls for renewed focus on efficiency in the dairy sector. Benchmarks such as milk yield, unit costs, and price competitiveness are essential. Cost analysis highlights sustainability and competitiveness, influencing policies and helping producers set fair milk prices. It connects producers and consumers, guiding investments and strategies while ensuring sector viability. Despite buffalo farming's importance, it has received limited research attention, particularly in Western contexts. This study aims to fill that gap by analyzing production costs, milk prices, and economic trends in Italy's buffalo sector from 2018–2022 using FADN database, with a focus on COVID-19's impacts. Understanding these trends will provide policymakers and stakeholders with crucial insights to support the sector's sustainability and resilience in a dynamic global market.

O183

Management of extended lactation: effects on milk production and reproductive parameters

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In dairy cows, a 305 days lactation length is traditionally suggested in order to have a one-year calving interval to maximise the number of production peaks during the cows' career. However, a high calving frequency can lead to a significant number of health risk periods such as drying-off, calving and transition during cows' life span. Moreover, at drying-off, milk yield might be still very high.

To reduce the frequency of these problematic events it is possible to extend the voluntary waiting period (VWP) for first insemination and lengthen the lactation. Through this strategy the insemination occurs when the energy balance is more positive and the cow is more fertile. In addition, the cow can be dried off at a reduced milk yield. The aim of this study is to assess the actual length of lactation (DIM) and VWP in Northern Italian farms and to study their possible relationship with milk yield, number of inseminations (FEC) and days open (DO). Data from seven farms (676 cows in total) were considered. The sample has been divided in three groups based on milk production level: 0–32 kg/d (LP); 32–41 kg/d (MP); >41 kg/d (HP) at the first control. The average milk yield at last control was 27.4 kg/d in LP 32.9 kg/d in MP 42.5 kg/d in HP. The average DIM was 347 ± 63 d, with 71 ± 50 d of dry-off period, the VWP was 90 ± 28 d and FEC for pregnancy was 2.9 ± 2.3. Therefore, the entire cycle appeared to be well beyond the year. The cycle was even longer in the HP group: VWP was pared to 99.5 d in HP, compared to 87.7 d in MP and 86.5 d in LP. DO was 163 d in HP, 130 d in MP and 129 d in LP. Finally also the length of lactation was higher in HP group (373 d) compared to 340 d in MP and 335 d in LP. A possible explanation might be found in the higher FEC needed to have a pregnancy: 3.8 in HP, 2.7 in MP and 2.6 in LP. A reduced reproductive efficiency of HP cows is shown also by the time interval between first insemination and conception: 63 d in HP and 43 d in LP. Milk LS was significantly lower in HP compared to the other groups. In conclusion, data from the sample suggested that many farmers are already (deliberately or not) extending the lactation by delaying insemination. Especially in most productive cows (where milk yield at last control before drying-off was still over 40 kg/d) there is potential to postpone insemination even more without compromising udder health.

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O392

Survey on the management of cattle farms in two municipalities located in the park area of the Campania Region

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The survey aimed to improve farm management through the use of digital techniques in extensive cattle farming. To understand the potential of Precision Livestock Farming System (Virtual fencing; use of portable NIR to estimate quality pasture; animal tracking with GPS), we first analyzed the evolution of cattle farming in the two municipalities where the project farms operate: Senerchia (AV) in the Monti Picentini Regional Park and Piaggine (SA) in the Cilento National Park, using the National Livestock Registry Database (BDN). Subsequently, interviews were conducted with the farmers to identify structural conditions, problems, and their perception of some ecosystem services. The Campania Region holds 10% of Italian cattle farms; of these, 15% are in the province of Avellino and 35% in the province of Salerno. The cattle farms in the municipality of Senerchia are 16, of which 13 specialised in meat production and 3 in both milk and meat production. The genetic types bred are 54% Podolica breed, followed by crossbred (38%), with 54% of the farms raising cattle outdoors all year round, but only 3 farms have more than 50 heads. The cattle farms in the municipality of Piaggine are 25, all specialised in meat production. The genetic types are 98% crossbred, with 92% of the farms raising cattle outdoors all year round, but only 6 farms have more than 50 heads. All farmers, when asked what it means to manage a farm in a park area, highlighted an increase in bureaucracy with stricter constraints even on improvements that could be positive for the park, such as finding water and creating fountains on Monte Polveraccio (Senerchia) instead of bringing water every day with a tanker, or allowing the use of electric fences at a suitable height to keep cattle separate from horses on Monte Vivo (Piaggine). Additionally, they pointed out that the park regulations should be updated every two years, involving the farmers as well. All the farmers, when asked if they would change their farm productions, answered that, although they could consider producing cereals or aromatic herbs, they prefer to continue with animal production. All farmers are aware of their value in protecting the territory but, only one farmer was immediately willing to apply Virtual fencing, while the others prefer to first see the results and problems in real application of such techniques.

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O338

Mother-offspring management in different dairy farm animal species as guidance for the implementation of cow-calf-Contact systems?

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Cow-calf Contact (CCC) systems are beneficial for both cow and calf welfare by promoting udder health and maternal behaviour, calf growth and social learning and by reducing abnormal behaviour. Despite these advantages and increasing public pressure to convert to CCC systems, dairy farmers are reluctant to adopt this practice. Their concerns relate to financial performance, staff wellbeing, lack of suitable barn facilities, scarce know-how, and animal health. In addition, farmers that have converted to CCC systems often report some difficulties, like stress during separation of cow and calf and less saleable milk. Finding best CCC practices by ensuring animal welfare and farmer viability is essential for a successful implementation of CCC systems. Aim of this contribution was a systematic literature review on mother-young management to find strategies used in other dairy farm animal species that could be used in dairy cattle farming. A total of 381 records on mother-young management in sheep, goats, buffaloes, and equids was found using Web of Science and Scopus. After manual screening using specific inclusion/exclusion criteria, 24 records were included in this review. Records overview shows that dairy calves spend the shortest time (minutes to a few hours) with their dams compared to intensively farmed dairy sheep and goats (1–2 days), buffaloes (up to 6 days) and dairy equids (7–10 months). A major challenge in mother-young management is separation stress. Suggested strategies to reduce this stress are gradual separation (8 records) and avoiding a simultaneous occurrence of weaning and separation (7 records). These strategies are not evenly supported by evidence and more research is needed to provide best practices to farmers and to improve the effectiveness of CCC systems in different farm settings. Other potential strategies to reduce separation stress include Contact with (familiar) peers and positive handling by stock people. Farmers are also often concerned about milk yield loss due to the presence of the offspring: to reduce this loss and shorten the period of anoestrus, restricted suckling is often proposed. The overview of strategies that this review provides could help to solve problems that CCC farmers may experience. Combined with research into economic viability, governmental support through incentives and effective communication and education strategies, these practices could allow the implementation of CCC systems by dairy cattle farmers.

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O220

Genomic characterisation and diversity assessment in endangered Italian sheep breeds

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Despite the growing diffusion of some cosmopolite specialised breeds, several autochthonous populations are still reared in marginal areas of Italy. Today, many of these populations encounter the threat of extinction due to factors such as small population size, geographic isolation, limited economic viability, and declining interest in breeding. Assessing their genetic diversity is important to enhance these breeds and their unique traits.

Although the Italian ovine diversity has been already investigated, this work aimed to explore the genomic structure of endangered local sheep breeds, never analyzed before, to provide information on their conservation status, essential for managing their genetic variability. A total of 164 animals (15–30 per breed) belonging to eight breeds (Cornella Bianca, Cornigliese, Garfagnina, Nostrana, Pecora dell'Amiata, Pomarancina, Turchessa and Zerasca) were genotyped with the Illumina OvineSNP50 v3 BeadChip array. The raw data were integrated with genotypes from 25 other Italian breeds that had been previously characterised. A total of 824 individuals genotyped for 38,723 markers were used for the analysis. Moderate levels of heterozygosity were observed among the studied populations. Coefficient of inbreeding varied from 0.015 in Zerasca to 0.049 in Cornella Bianca. Multi-dimensional scaling, admixture, and Treemix analyses consistently highlighted the separation of populations based on their genetic origin or geographical proximity between breeding areas. The endangered breeds showed more spread clusters and different levels of admixture. Some breeds (Cornella Bianca, Zerasca and Garfagnina) shared genetic ancestry with Leccese breed. Nostrana showed an internal substructure probably linked to different family lines. Our study provides, for the first time, a consistent overview of population structure, genetic diversity and inbreeding of minority Italian sheep breeds. They highlight the need for a careful monitoring of these populations in accordance with their status of endangered breeds. In this regard, genomic information may significantly contribute to the optimal management of these small populations.

O252

The rediscovery of a forgotten breed: the genomic characterisation of the Fasanese sheep and investigation of its Eastern European origins

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In recent years, an unrecognised sheep breed has been identified in the Apulian territory, located in the municipality of Fasano within the province of Brindisi. It is a large animal with white wool of 30 µm and typical black spots around the eyes and muzzle. It is intended to be a double purpose animal. This breed was named 'Fasanese' sheep, although local shepherds also referred to them as the 'Turkish' or 'Montenegrin' sheep. This breed likely originated from the importation of animals from the former Yugoslavia in the early 1930s. To uncover the history and genetic characteristics of this breed, interviews, bibliographic research, and high-density genome analysis were conducted. Samples from 45 individuals were genotyped using the Illumina OvineSNP50K. Data obtained were merged with other European and Balkan sheep breed from previously published work. Genomic analyses revealed that the Fasanese sheep exhibits a moderate level of inbreeding, with an average FROH of 0.20, placing it in an intermediate position compared to breeds such as Valais Blacknose (FROH = 0.45) and Lesvos (FROH = 0.10). Biodiversity metrics showed an observed heterozygosity (Ho) of 0.36 ± 0.02, an expected heterozygosity (He) of 0.38 ± 0.02, and a mean inbreeding coefficient (Fis) of 0.07 ± 0.01, indicating balanced genetic diversity. Principal Component Analysis (PCA) provided further insight into the genetic relationships of the Fasanese sheep. The results positioned the Fasanese closer to Altamurana and Gentile di Puglia, Italian breeds historically raised in the same geographical region. Moreover, the Fasanese clustered near breeds from the Croatian Isles, such as Dalmatian and Istrian, suggesting potential historical gene flow or shared ancestry with populations across the Adriatic Sea. Despite these affinities, the Fasanese maintained distinct genomic features, underlining its unique status as a locally adapted breed. Future analyses will need to focus on dating the divergence time to confirm the time elapsed since the importation of this genetic group. This study is part of the activities financed by the BIO.ZOO.CARE project: 'PSR Puglia 2014–2022. Misura 10 – Pagamenti agro-climatico-ambientali. Sottomisura 10.2 – Operazione 10.2.1'.

0424

Mapping the phenotypic and genomic landscape of Montanina cattle

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In 1927, the Italian zoologist Mascheroni classified cattle from the Italian island of Sicily into three varieties based on geographical location: the Modicana (plains), the Mezzalina (hills), and the Montanina (mountains) ecotype. These varieties were described to differ in size, horn length, and production traits. Modicana and Mezzalina (the latter currently known as Rossa Siciliana) were described for having good milking ability, whereas the small sized Montanina presented limited milk production but superior fattening potential. Currently, Montanina is reared in the Nebrodi mountains (northeastern Sicily) using extensive farming systems. Although no official estimate of the current Montanina population size exists, the most recent estimate suggests ~1,500 individuals. Montanina cattle have a characteristic red coat with black shades and a reddish stripe on the back, and white horns with black tips. To date, limited information exists on the Montanina ecotype. Here, we combined phenotypic and genomic investigations to provide a first assessment of this neglected local population. Phenotypic evaluation involved 32 adults Montanina from three farms in the Nebrodi region, recording body weight and ten morphometric traits. We recorded an average body weight of 495 kg and exhibit variability in body conformation, classified as mesomorphic or dolichomorphic, which aligns with their adaptation to mountainous environments. A genomic investigation, performed using the Affymetrix 65k SNP array on 61 Montanina and 1,036 animals from 35 Italian and French breeds, revealed moderate heterozygosity (0.33) and low inbreeding (0.04). Neighbour-Net analysis grouped Montanina with Sicilian breeds but on a separate branch. Admixture, haplotypes sharing, Treemix and f3-statistics highlighted introgressions from Limousine and Modicana. Notably, introgression patterns varied across farms, reflecting differences in breeding practices. Some farmers crossbreed Montanina with Limousine to enhance meat yield, while others preferred crossbreeding with Modicana for its recognised breed status. Selection analysis applying the nSL approach identified 18 genes associated with productive and reproductive traits. Finally, demographic reconstruction clarified the genetic hierarchy among Sicilian autochthonous cattle populations, further supporting the phenotypic and genetic distinctiveness of the Montanina cattle.

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0358

A genomic perspective on the Agerolese autochthonous cattle breed

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Autochthonous livestock breeds are a reservoir of unique gene pools shaped by the interplay of natural environmental factors (such as climate, flora, photoperiod, and infectious agents) and artificial influences (including breeding systems and production needs). Therefore, their conservation ensures the availability of genetic resources capable of addressing future challenges, including climate change and evolving human needs. The Agerolese cattle is a local dual-purpose (milk and meat) breed native to the Lattari Mountains and the Sorrento Peninsula (Naples, Italy). Historical reports suggest that this breed underwent crossbreeding with Bretonne, Brown Swiss, Jersey, and Friesian cattle. Over time, the population size of Agerolese has experienced significant fluctuations, the current genealogical registry includes only ~300 lactating individuals. This study aims to provide a more precise genomic assessment of the Agerolese cattle population to support and enhance existing conservation plans. To this end, 95 Agerolese cattle were genotyped at 777k SNPs using the BovineHD Genotyping BeadChip and analysed together with 527 animals from 16 cosmopolitan breeds. A genomic investigation revealed moderate heterozygosity (0.326) and moderate-low inbreeding (0.068) in Agerolese. Both Neighbour-Net and PCA analysis clustered Agerolese with Brown Swiss. Similarly, admixture and haplotypes sharing analyses showed introgressions with Brown Swiss and Holstein. nSL selection signature analysis identified 50 SNPs under putative selection intercepting 16 genes known to be associated with obesity, tumour suppression, neural development. These preliminary results provide a first in depth genomic analysis of the Agerolese local cattle population. We reconstructed the genomic background of the breed and identified localised events of introgression from Jersey cattle and determined its current selection trajectories. Such information will be instrumental in educating conservation plans and shaping future breeding strategies for these peculiar local cattle. In conclusion, these first genomic results confirm the historical reports suggesting that this breed has been crossed with Brown Swiss, Jersey, and Holstein breeds.

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O335

Structural Variants shaping the aptitude of local cattle breeds

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Structural variants (SVs) and copy number variants (CNVs) represent a critical but underexplored source of genetic variation in livestock. Unlike single nucleotide polymorphisms (SNPs), SVs can profoundly influence both monogenic and complex traits, impacting immunity, fertility, production, and environmental adaptability. Despite their significance, research on SVs has primarily focused on cosmopolitan breeds, often overlooking local breeds uniquely adapted to challenging environments.
In this study, we investigated the genomic diversity of three autochthonous cattle breeds from the Aosta Valley (Aosta Red Pied – ARP, Aosta Black Pied – ABP, and Aosta Chestnut – ACH) in comparison with cosmopolitan breeds. The Aosta breeds are pivotal to the region's economy, contributing to the production of Fontina cheese, a PDO-certified product, and hold considerable cultural significance through traditional events like the Bataille de Reines. Their seasonal farming system, which includes altitudinal grazing up to 2500 meters, underscores their remarkable adaptation to the harsh Alpine environment.
To elucidate the role of SVs in these breeds, we analyzed 45 Illumina paired-end whole-genome sequencing (WGS) datasets, with a read depth of 20–30x, using the nf-core pipeline Sarek. Reads were aligned to the ARS-UCD1.2 reference genome using BWA-mem2, and SVs were identified with Manta and CNVkit using default parameters. Preliminary results from Manta revealed an average of 3800 breakends (BND), 6864 deletions (DEL), 855 duplications (DUP), and 2492 insertions (INS) per breed, while CNVkit identified 5649 deletions and 2372 duplications. Shared and breed-specific SV and CNV regions were identified using custom Python scripts, focusing on regions shared by at least 10 samples. Among these, approximately 1200 regions were common across all breeds, while 635, 775, and 746 regions were specific to ABP, ACH, and ARP, respectively. Gene annotation was conducted with BCFtools, and associated QTLs were identified using the Cattle QTL Database, and the functional annotation was performed with the DAVID database.
This research highlights the importance of studying SVs in local cattle breeds to gain deeper insights into their environmental adaptability. These findings could support conservation strategies and promote sustainable breeding practices for these invaluable genetic resources.
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O468

Genetic diversity and evolutionary history of Baroque horse breeds: insights from genome-wide data

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The Baroque horse breeds, originating from Southern Europe, are known for their unique characteristics and roles in classical dressage and ceremonial contexts. These breeds have been shaped by centuries of selective breeding, geographic isolation, and interactions with other equine populations. This study explores the genetic diversity and population structure of Baroque breeds, including Lipizzan (LIP), Murgese (MUR), Lusitano (LUST), and Spanish Purebred Horse (PRE), alongside eleven other relevant equine populations. PRE samples were genotyped with GeneSeek® Equine Genomic Profile and publicly available samples/breeds were included. After datasets merging (plink1.9), quality control and subsampling (BITE v2), the final cohort included 440 genotyped individuals from fifteen populations with 24,677 markers. Genetic diversity was assessed using PCA, ADMIXTURE and neighbor-network analysis using Reynolds' genetic distances. The results show that the Baroque breeds form a cohesive genetic group but exhibit subtle genetic differences due to their distinct breeding histories and geographic origins. The PCA highlighted the separation of Baroque breeds from other horse populations, demonstrating unique genetic signatures compared to non-Baroque breeds like

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the Exmoor and Thoroughbred. ADMIXTURE analysis showed progressive clustering, with LIP and MUR forming distinct groups at K = 4, and LUST and PRE emerging as separate clusters at K = 8. The neighbor-network analysis confirmed the genetic uniqueness of these breeds, with LIP showing divergence likely due to selective breeding, while LUST and PRE, sharing Iberian origins, grouped closely. These findings underscore the individual genetic identities of Baroque breeds, shaped by selective pressures and isolation, while linking them within the broader equine genetic landscape. This study contributes to understanding the genetic structure of Baroque horses and their historical development, emphasising their importance as models for genetic diversity and conservation.

O313

Signatures of selection in Mora Romagnola, a highly inbreed autochthonous pig breed

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Mora Romagnola is an Italian autochthonous pig breed, characterised by a blackish coat with lighter shades on the abdomen and a distinctive dorsal line of thick, dense hair known as the 'Sparta line'. Historically, pigs with similar phenotypic traits have been found in various areas of Northern Italy, but currently, they are only raised in the eastern part of the Emilia-Romagna region, originating the pig population of this breed. The Mora Romagnola breed experienced a significant population decline, putting it at risk of extinction, due to the introduction of cosmopolitan breeds. Its conservation program began in the 1990s. Products from Mora Romagnola pigs are part of a breed-specific branded value chain that provides a profitable economic gain to farmers, crucial for the sustainable conservation of this animal genetic resource. This study aimed to characterise the genomic features of Mora Romagnola and evaluate the level of inbreeding in the breed population. Approximately 250 Mora Romagnola pigs were genotyped for a total of 68516 SNPs using the GGP Porcine HD single nucleotide polymorphism array. Using this genomic data, several inbreeding parameters were calculated and runs of homozygosity (ROH) islands were identified. These analyses revealed a high level of inbreeding in this breed and suggested that the population had recently experienced a bottleneck. The inbreeding coefficient based on the deviation from observed versus expected heterozygosity, F_{HOM}, had an average value of 0.18 ± 0.13, and reached a maximum of 0.64. The F_{ROH} coefficient resulted in values ranging from 0.036 to 0.632, with an average value of 0.292 ± 0.095. The average number of ROH per animal was 92.2 ± 20, with a minimum of 17 and a maximum of 130. Additionally, 12 genomic regions showed evidence of selective pressure, as indicated by the high frequency of homozygous regions in the population. These homozygosity hotspots were present in more that 75% of the analysed animals and the most relevant were located on SCC1 between 208.9Mbp and 277.2Mbp and on SCC15 between 104.7Mbp and 105.0Mbp, encompassing several QTLs related to production traits, such as weight gain or number of vertebrae. Integrating this genomic information into the Mora Romagnola herd book will help improve breed conservation programs for this autochthonous genetic resource.

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O074

A multivariate approach to investigate mutual relationship among milk fatty acids across different ruminant species

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Understanding the metabolic pathways of fatty acids (FA) and the factors influencing their modulation is essential for defining and modifying the nutritional properties of milk. The complex correlations between individual milk FA make it challenging to interpret lipid metabolic pathways in the mammary gland (MG). In such cases, it may be more informative to access the metabolic or feeding status of the animal by examining simultaneous variations in groups of FA, rather than focusing on individual FA. Through Multivariate Factor Analysis (MFA), it is possible to study complex multivariate systems by extracting a small number of latent variables with clear technical and biological significance. Many studies have focused on lipid profiles of single species, but this approach has overlooked interspecific differences, leading to an incomplete understanding of mammary metabolism. The goal of this study was to explore mammary lipid metabolism across multiple ruminant species simultaneously, using MFA, defining a set of factors as new variables for assessing the relationship between the FA profile of different species, breeds and diet composition. The study included 3,431 animals: 770 cows (550 Holstein Friesian and 220 Brown Swiss); 1,151 sheep (307

Massese and 844 Sarda); 830 buffalo and 690 goats (Saanen). All animals were pluriparous and in mid-lactation. The data were cross-validated to assess whether the extracted factors are actually linked to the associated biological processes. MFA extracted 11 latent factors that explained 72% of the original variance, elucidating several pathways: synthesis of odd and branched-chain FA (Factor 1), medium-chain FA synthesis (Factor 2), biohydrogenation of C18:2n-6 (Factor 3), milk fluidity control (Factor 4), b-oxidation of FA (Factor 5), biohydrogenation of C18:3n-3 (Factor 6), ruminal elongation of FA (Factor 7), cellulolytic (Factor 8) and amylolytic (Factor 9) bacteria activity, elongation of C18:2n-6 (Factor 10) and short-chain FA synthesis (Factor 11). These 11 factors confirm that FA originate both from de novo synthesis in the MG (Factors 2, 4, 5, 10, 11) and from ruminal activity (Factors 1, 3, 6, 7, 8, 9). Some factors were identified only in cattle, others in sheep, and some across all species. Additionally, two factors (Factor 5 and Factor 7) had not been identified in previous studies. The results of this work emphasise that using milk from different species in the same MFA allows for a comprehensive definition of mammary lipid metabolism, with the potential to generate factors useful for studying genetic, nutritional, and physiological effects.

O023

Dietary black soldier fly oil reduces oxidative stress in dairy cows without affecting blood nutritional parameters

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Some lipid sources traditionally used in ruminant nutrition pose concerns due to their negative effects on the environment. Therefore, nutritionists are looking for innovative and sustainable feedstuffs to be included in ruminant diets. The oil extracted from black soldier fly (*Hermetia illucens*) larvae (HIO), being rich in lauric and palmitic acids, could replace conventional lipid sources characterised by high saturation levels. This study aimed at assessing the effects of replacing hydrogenated palm fat (HPF) with HIO in the diet of dairy cows on their blood nutritional parameters and oxidative stress. Twenty-six Valdostana Red Pied cows fed mixed hay *ad libitum* were divided into two balanced groups that received isonitrogenous and isoenergetic concentrates containing HPF or HIO at 3% as fed (162 g/head × day). Individual blood samples were collected from the jugular vein, before the morning milking, at the beginning (d0, the day before starting the experimental diets administration), middle (d26) and end (d50) of the trial. Plasma collected at d0 and d50 was assayed using colorimetric enzymatic reactions with a multiparameter analyzer (Kone Instruments Corporation) to determine non-esterified fatty acids, cholesterol, glucose, triglycerides, urea, and β-hydroxybutyrate concentrations. Serum collected at d0, d26 and d50 was analyzed for blood oxidative stress using the OXY-Adsorbent Test and the d-ROMs Test (Diacron International, Grosseto, Italy). Data was statistically analyzed with SAS software using a mixed model, considering as factors the sampling period (repeated), the dietary treatment, their interaction (fixed), the animal (random), and the values of each parameter at d0 as a covariate. All the considered plasma metabolites did not differ between the two experimental groups ($p > 0.05$). Serum antioxidant capacity was not affected by dietary treatment ($p > 0.05$). However, lower d-ROMs concentrations were observed in the HIO-fed cows when compared to the HPF-fed ones (73.70 *vs.* 110.84 UCARR, respectively; 1 UCARR = 0.08 mg H_2O_2/dL; $p < 0.001$). The interaction between diet and time was never significant. These results show that the dietary replacement of HPF with HIO increased the resistance to oxidative stress in dairy cows, which is known to weaken the animals and cause several diseases and metabolic disorders during lactation. The HIO naturally possesses antioxidant activity, suggesting its potential use as a novel energy source in ruminant nutrition.

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O026

Relationship between oral microbiome and performance traits in Angus bulls

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Microbial composition of the gastrointestinal tract is an important factor affecting the variation in feed efficiency in ruminants. However, the collection of biological samples such as rumen fluid is an invasive process that could be stressful to animals. Recent studies on the oral microbiome have suggested possible relationships between its composition and performance traits in livestock such as residual feed intake (RFI). The advantage in using the oral microbiome is that it can be easily collected using noninvasive buccal swabs. The aim of this study was to identify possible relationships between oral microbiome composition and RFI. To achieve this aim, oral samples from 526 Angus bulls were collected and analyzed for their microbial composition. A total of 797 bacterial families (BF) were identified. For each animal, the RFI was computed and bulls were divided in two groups: 270 animals with positive RFI (PRFI) and 256 animals with negative RFI (NRFI). From the BFs identified, those whose abundance was zero for more than 95% of the involved animals were excluded from the analyses, which resulted in 304 BFs retained. The canonical discriminant analysis (CDA) was applied to test whether BFs were able to separate the two RFI groups. The results of the CDA showed a highly significant separation between the two groups (Hotelling's *T*-test, *p*-value <0.001) with an Euclidean distance, between groups, of 11.60. Moreover, the CDA was able to assign each animal to their proper group with an accuracy of around 94% and an error rate of around 6%. These results suggest the existence of a strong association between the oral microbiome and feed efficiency. However, further studies combining data collected from both oral and rumen microbiome could help to support these findings.

O196

Is black soldier fly oil a good alternative to replace palm distillate fatty acids in the diet of lactating sheep? Animal performance, feed efficiency and ruminal fermentation responses

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Interest in finding alternative feed resources is driven by concerns about the environmental impact of the animal feeding industry and the increasing feed-food-fuel competition. In this context, the use of insect oils as a replacement for conventional energy sources in ruminant diets is of great interest due to their local, efficient, and sustainable production. Among these conventional feeds, those obtained from the cultivation of oil palm would stand out because of the contribution of this crop to deforestation, biodiversity loss, and the high carbon footprint of its transport. Therefore, the aim of this study was to evaluate the effects of replacing palm distillate fatty acids with *Hermetia illucens* oil (HI oil) in the diet of dairy ewes. To this purpose, 14 lactating Assaf ewes were used in a replicated 2 × 2 change-over design with 2 periods of 25 d each and 2 experimental diets: total mixed ration containing either 2% dry matter (DM) of palm distillate fatty acids or 2% DM of HI oil. Individual milk yield and DM intake were recorded daily and individual milk samples were collected 3 times a week for chemical composition analysis. Feed efficiency was estimated through feed conversion ratio (FCR) and residual feed intake (RFI). At the end of each period, individual samples of ruminal digesta were collected using an oesophageal probe and employed to analyse *in vivo* ruminal fermentation parameters (pH, ammonia, and volatile fatty acids). Ruminal fluid samples were also used as the inoculum in *in vitro* batch cultures of ruminal microorganisms to examine gas production and DM disappearance after 20 h of incubation. Results of body weight, DM intake, FCR, RFI, and milk yield were not significantly different, nor were milk fat, protein, and lactose concentrations and yields ($p > 0.10$). Ruminal pH values and ammonia concentration were similar for both diets, as were total and individual volatile fatty acids concentrations ($p > 0.10$). *In vitro* incubations showed that the oil replacement did not affect gas production and DM disappearance ($p > 0.10$). Palm distillate fatty acids are included in the diet of dairy animals to obtain high production yields. Our results suggest that this energy source can be replaced by HI oil in the diet of dairy ewes without adverse effects on milk production and composition or ruminal fermentation. Therefore, at the tested dose (2% of diet DM), this alternative energy source could be considered as a suitable ingredient in the diet of dairy ewes.

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O185

Gut health effects of hazelnut skin dietary supplementation in Limousine bulls

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Polyphenol supplementation in bovine diets has been shown to significantly influence the fatty acid composition of milk and meat by modulating rumen microbiota. Hazelnut skins (HS) are a promising coproduct as they are rich in bioactive compounds, especially polyphenols. The aim of this study was to evaluate the impact of a HS-supplemented diet on gut health and rumen and cecum microbiota in beef cattle. A total of 34 Limousine beef cattle bulls were randomly assigned either to a control ($n = 17$) or a treated ($n = 17$) group, replacing cornmeal and beet pulp with hazelnut skins (12% of the diet). Both diets were supplemented with *ad libitum* straw. After 120 days the bulls were slaughtered and samples of rumen (dorsal and ventral sac), reticulum, omasum and abomasum were submitted to histomorphometry (papillae density, length and width, absorption area, and thickness of mucosa, submucosa, and muscular layers of both ruminal sacs) and histopathological evaluation using a semi-quantitative scoring system based on severity, pattern and type of inflammation, and epithelium degeneration. Ruminal fluids and cecal contents were analyzed for microbiota composition through the V3-V4 hypervariable region of 16S rRNA gene sequencing. Ruminal morphometric indexes and epithelial degeneration were not affected by diet. Despite the absence of significant differences in morphometric indices, a decrease in the severity of inflammation in the dorsal sac of rumen, reticulum and abomasum was observed in the HS animals compared to the controls ($p < 0.05$). Significant differences in alpha and beta diversities for the cecal microbiota emerged, while the HS effect on rumen was milder. Differential abundance analysis for cecum identified many bacterial genera participating in carbohydrate fermentation and volatile fatty acids production, such as *Anaerovibrio*, *Succinivibrio*, *Prevotella*, *Bifidobacterium*, *Roseburia*, *Faecalibacterium* and *Alloprevotella*. Some of these beneficial bacteria (*Eubacterium*, *Anaeroplasma* and *Clostridium*) increased in HS rumen samples. The HS dietary inclusion can be an effective strategy to support a healthy microbial community within the gastrointestinal tract of beef cattle. The rumen appears to be more resilient in response to dietary changes due to its buffering capacity, while the cecum is probably more susceptible to persistent microbial community shifts over time. HS supplementation seems to have a positive impact on gut health inflammation even if further research is needed.
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O291

Evaluation of udder health status using bacteriological culture and somatic cell count after calving and at drying-off, and effects of antibiotic therapy

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Until selective dry-cow antibiotic therapy (SDCT) has been mandatory in 2022 in the EU, a significant proportion of antibiotics (AB) in dairy farming was used to prevent and cure intramammary infection (IMI) at drying-off (DO). Somatic cell count (SCC) threshold at the last test-day before DO is commonly used as a practical and cheap indicator of mastitis to select cows for DCT. With the aim to support farmers during the transition period from blanket DCT to SDCT protocol, a study was performed on 4 commercial dairy farms to compare bacteriology (BAC) and SCC test results in relation to cure or new IMI rates. Between 2021 and 2024 9689 quarter milk samples were aseptically collected for BAC and 2423 cow composite milk samples for SCC analysis from 710 clinically healthy Italian Friesian cows once before the planned DO and twice in the early post-partum (PP), in parity 1 (PRI) and parity 2 and 3 (PLU). Milk samples were analyzed at the laboratory of IZSLER of Brescia using standard methods and results were shared with farmers. At DO cows were assigned to SDCT or not (NoDCT), according to the procedures adopted in each farm. For data analysis, cows with at least one infected quarter or high SCC (≥ 100.000 and 200,000 cells/mL for PRI and PLU, respectively) were categorised as positive (POS) for IMI or mammary inflammation, whereas

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those with a full set of bacteriologically negative quarters or low SCC as negative (NEG). Results indicated 20% of quarters were positive for pathogens at samples taken at PP and 29.7% at DO; overall, 61% of quarter samples were negative and 15% contaminated. The most prevalent pathogens isolated at DO and PP were environmental staphylococci (47%), corynebacteri and streptococci (30%). Cows categorised as POS were 58% at PP and 72% at DO when based on BAC, but 28% and 39%, respectively when based on SCC. Considering cows POS at DO (only SDCT), cows classified as NEG at PP were 38% when based on cow-level IMI cure and 73% on recovery from mammary inflammation; on the contrary, for cows NEG at DO, the rate of POS cows at PP varied from 51 to 20% in the SDCT group and from 53 to 23% in the NoDCT one, for the BAC and SCC tests, respectively. The percentages of cured or infected cows were statistically different at χ^2 test ($p < 0.01$) using BAC or SCC. It is concluded that different selection criteria could affect untreated IMI cows or use of unnecessary AB at DO, so as the evaluation of DCT efficacy for curing and preventing mastitis.

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O497

Individual risk factors for intramammary infections affecting dairy herds in Western Alps

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Mountain dairy farming plays a vital role in preserving landscapes and biodiversity, socioeconomically supporting local communities, but is threatened by intramammary infections (IMIs), the main cause of mastitis and economic losses. While IMI risk factors are well documented in lowland farms, little is known for mountain herds. This study aimed to identify the risk factors for IMIs caused by contagious pathogens in transhumant dairy cows. Eight herds from the Lanzo Valleys, western Alps (Italy), were studied: 6 transhumant and 2 sedentary. Milk was sampled from up to 30 dairy cows per herd thrice between April and August 2024: T0 in spring before transhumance; T1 within five days after transhumance, and T2 approximately one month later. Composite milk samples ($n = 488$) were analyzed for composition (fat, protein, lactose) and somatic cell count. Quarter milk samples ($n = 1{,}956$) underwent bacteriological analysis for detecting major contagious pathogens (*Staphylococcus aureus*, *Streptococcus agalactiae*, *Corynebacterium bovis*). Data on cow breed, parity, days in milk, body condition score (BCS), litter hygiene, and cleanliness of cows were also collected. We tested the same cows repeatedly and used a mixed-effects logistic regression model to assess risk factors for IMI. Transhumant cows had nearly threefold the odds of IMI at T1 compared to sedentary cows (odds ratio: 2.74, 95% CI: 1.05–6.16), likely due to stressors associated with transport, walking and environmental changes. Additional findings included a 1.2% daily increase in IMI odds likely due to advancement in hot season and lactation stage (95% CI: 1.0–2.5%), a 32.6% decrease in IMI odds per BCS point increase (95% CI: 5.3–52.1%), and 27.2% higher odds per lactation rank increase (95% CI: 11.8–44.6%). A 0.1% rise in milk fat increased IMI odds by 2.5% (95% CI: 0.3–5.2%), probably due to the advancement of lactation stage.

This study emphasizes the need for targeted strategies for transhumant dairy cows to protect udder health and sustain this traditional practice.

O385

Effect of subclinical intramammary infection on blood biochemical parameters in susceptible and resistant Holstein cattle

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Mastitis is one of the most common and challenging diseases in high producing dairy farms, especially in its subclinical form, as it is difficult to detect due to the absence of symptomatic immune responses. In this study, we aimed at evaluating the effect of subclinical intramammary infection (sIMI) by *Staphylococcus aureus* on a detailed panel of hematochemical parameters including metabolic, immune-response, oxidative stress, and liver function traits in Holstein cows from a commercial farm. Based on genetic (estimated breeding values for somatic cell count, SCC) and phenotypic data from previous lactations (SCC and previous mastitis episodes), we selected 400 multiparous cows

which were divided into two groups according to their attitude to develop mastitis: TOP (resistant; $n = 200$) and BOTTOM (susceptible; $n = 200$) animals. A bacteriological screening of 373 cows was performed by single quarter milk culture at time 0 (T0) to define experimental groups: (i) negative for bacteriological examination ($n = 43$) and ii) positive for *S. aureus* ($n = 24$). Blood and milk samples were subsequently collected at T1 (2 weeks after T0; $n = 67$) and T2 (2 weeks after T1; $n = 67$), to confirm the health status and analyze hematochemical indicators. A linear mixed model including the cows' fixed effect, days in milk, parity, SCC in classes, bacteriological status (BACT, positive and negative) and group type (BOTTOM and TOP), was used to analyse the detailed panel ($n = 35$) of hematochemical indicators. Results showed that TOP animals had higher beta-hydroxybutyrate (BHB) levels compared to BOTTOM ones at T2 ($p < 0.01$). This finding might be attributable to a more efficient energy metabolism in TOP animals, as BHB, being an alternative energy source, might be used by neutrophils, which require energy for their activity. Concerning the BACT effect, positive animals have higher aspartate aminotransferase (AST) values ($p < 0.01$) in respect to the healthy ones at T1, suggesting hepatic stress potentially linked to the infection. Moreover, we observed higher levels of creatine kinase (CK) in positive animals at T1 ($p < 0.01$) and a tendency for higher levels at T2 ($p < 0.1$). CK is an enzyme that serves as a source of reversible energy, which could be used by animals with IMI to activate the immune response. This study highlighted changes in blood biochemical indicators which provide useful information for the prediction and/or detection of sIMI and udder inflammation in Holstein cows.

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O383

Associations of body condition score and body weight changes with milk composition and fatty acids during the transition period in dairy cattle

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The transition period represents a critical challenge for dairy cows, as high-producing animals often experience negative energy balance. This phase is characterised by the mobilisation of energy reserves, particularly fat and protein, to support the demands of elevated milk production. The extent of body condition score (BCS) and body weight (BW) changes (ΔBCS, ΔBW) during this period may influence milk composition, which can reflect the metabolic status of cows. This study aimed to investigate the associations between ΔBCS and ΔBW during the transition period and their effects on milk composition and fatty acid profiles. A longitudinal study was conducted on a commercial dairy farm, where 107 cows, which were in their first or second parity, were assessed from the day before the cows' dry period (T0) up to 30 days postpartum (T3). Body condition scores were evaluated by a trained technician, while BW was measured using an automated weighing system positioned at the exit of the milking parlor. ΔBCS and ΔBW were calculated as the absolute differences between T3 and T0. Milk composition, and fatty acids measured at T3 were analyzed as functions of ΔBCS and ΔBW and categorised into quartiles (Q). At T0, BCS and BW averaged (± SD) 3.20 (± 0.58) and 704.53 kg (± 73.36), respectively, while they were 2.56 (± 0.35) and 658.44 kg (± 56.31) at T3. The average ΔBCS values across quartiles were as follows: –1.54 (± 0.36) for Q1, -0.89 (± 0.13) for Q2, -0.50 (± 0.00) for Q3, and –0.13 (± 0.17) for Q4. For ΔBW, the average values were –96.09 kg (± 26.15) for Q1, -53.86 kg (± 6.27) for Q2, -33.41 kg (± 7.33) for Q3, and –8.70 kg (± 25.76) for Q4. Results revealed significant effects ($p < 0.05$) of ΔBCS and ΔBW on protein and casein percentages, the fat-to-protein ratio, and fatty acid profiles. Cows with greater losses in BCS and BW (i.e. those within the first Q) exhibited reduced protein and casein percentages, along with elevated fat-to-protein ratios (> 1.3), suggesting an increased risk of ketosis. Furthermore, these cows displayed higher levels of unsaturated fatty acids, monounsaturated fatty acids, and preformed fatty acids, indicating greater fat mobilisation. These findings highlighted the importance of managing BCS and BW during the transition period to mitigate negative effects on milk composition and metabolic health.

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O156

Multi-omic data integration for the identification of molecular drivers of subclinical intramammary infection in dairy cows

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In this study, we integrated the RNA-Seq profiling of milk somatic cells with Methyl Binding Domain (MBD)-Seq data, and immune cells population obtained with flow cytometry from cows naturally affected by subclinical intramammary infection (sIMI), to gain deeper insights on the molecular response driving the animal infection and the identification of molecular drivers for its detection. Bacteriological screening was performed on 188 Holstein cows reared in one herd in order to identify the experimental groups, which were defined as follows: (i) animals with no history of mastitis and negative at the bacteriological examination (NEG; $n = 9$) and (ii) animals positive at the bacteriological examination for different pathogens (sIMI; $n = 22$). The Data Integration Analysis for Biomarker discovery using Latent Components (DIABLO) algorithm was adopted to identify highly correlated transcriptomic and epigenetic information capable of discriminating between NEG and sIMI animals. Then, only interaction among variables with $r \geq 0.9$ were visualised in a network using CIRCOS. This integration analysis displayed a strong correlation between the differentially expressed genes (DEGs) and the differentially methylated regions (DMRs) ($r = 0.92$), as well as between immune cells population and DMRs ($r = 0.74$) and DEGs ($r = 0.78$) variables. Among the most informative DEGs identified by DIABLO, we observed the upregulation of the *SAMD9* gene, involved in cell proliferation and apoptosis, and the downregulation of *GNA11*, encoding for a type of guanidine nucleotide-binding receptor, recently implicated in energy-related pathways, especially fat metabolism. Concerning DMRs, one of the most informative methylated regions was co-located within the *ADAM11* gene, which encodes for a member of the disintegrin and metalloprotease protein, involved in cell-cell and cell-matrix interactions.Total leucocytes were found to be negatively correlated with the *EMC3* gene, involved in the transport of proteins within the endoplasmic reticulum, and with a DMR co-located within the angiopoietin 4 gene (*ANGPTL4*), which seems to be implicated in the mediation of inflammatory processes. This study provided a deeper understanding of the regulatory mechanisms governing subclinical mastitis. Moreover, the identification of potentially informative candidate features could pave the way for their development as biomarkers in mastitis control strategies.

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O505

Addressing antibiotic resistance in dairy herds: the role of platelet rich plasma in mastitis treatment

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Mastitis is a major problem in dairy farming due to its economic and health impact, compounded by the overuse of antibiotics and the emergence of antimicrobial resistance (AMR). This issue, which is becoming increasingly critical for both human and animal health, is driving research into alternative solutions to antibiotics in livestock management. Platelet-rich plasma (PRP), a biologic preparation rich in growth factors and bioactive molecules, has shown potential as an alternative regenerative therapy. This study aimed to evaluate the efficacy and safety of autologous PRP as a treatment for acute bovine mastitis compared to conventional antibiotic treatment. A randomised controlled non-inferiority trial was conducted in 100 lactating dairy cows reared in 6 herds diagnosed with clinical mastitis. The animals were randomised into two groups (50 animals/group): one treated with PRP and one treated with antibiotic therapy (ethical approval: PROT. N. 11/CESA/2023). The PRP was prepared using a standardised double centrifugation process and administered in five 10ml doses over two and a half days (one dose every 12 hours). Monitoring included clinical signs, somatic cell count (SCC, expressed as $\log_2(SCC/1000) + 3$), differential SCC (DSCC), milk composition (fat, protein, lactose and total solids) and bacterial prevalence at four time points within 21 days. Both PRP and antibiotic treatments achieved a complete resolution of clinical symptoms (e.g. pain, redness, and altered milk appearance) by the third monitoring point (14 days-post treatment). Statistical analysis showed no significant differences in SCS and DSCC trends between the two

treatments ($p > 0.05$). Similarly, milk composition showed no significant differences. The PRP demonstrated comparable efficacy in modulating bacterial load with no adverse effects, confirming the non-inferiority of this treatment compared to conventional antibiotics. Our results suggest that PRP could represents a sustainable and feasible alternative treatment to antibiotics for acute bovine mastitis, with comparable clinical and microbiological outcomes. Its application aligns with the need to reduce antibiotic dependency in dairy farming, following a One Health perspective and contributing to mitigating AMR issues. Future studies should address long-term outcomes, larger datasets, and practical scalability, as well as a more detailed investigation of milk quality and cheese-making properties when comparing the two treatments.

O188

Proteome characterization of milk extracellular vesicles isolated from cows that experienced hyperthermia

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With climate change the impact of hyperthermia on dairy cows' welfare, health status and performance has been demonstrated by a significant drop in milk production and fertility. The molecular background of the effects of hyperthermia in dairy cows is still elusive.
Extracellular vesicles (EVs) are particles of a size ranging from 30 to 5000nm, distinguished by their cargo housing several molecules such as proteins, metabolites and nucleic acids. This cargo can vary based on the physiological state of one organism, which is now being utilised as a tool to understand different pathological and physiological conditions. Milk EVs can carry important information contributing to mother-calf communication and play an important role in processes such as immunity transfer and calf intestine maturation. The molecular variations that can occur to milk EVs during hyperthermia is still to be elucidated. Our project seeks to gain a deeper knowledge on the proteome changes in milk-EVs. 7 Holstein and 7 Brown Swiss lactating cows experienced hyperthermia during a natural heat wave by switching off the fans for 4 days (THI >84). Sampling was conducted in 5 time points, each at 3pm: one day before (T-1), at day 0 (T0), 1 (T1) and 4 (T4) and at day 11 (T11).EVs were isolated and characterised from 72 milk samples, proteins were extracted for a subsequent identification and semi-quantification by nanoscale liquid chromatography coupled to tandem mass spectrometry (nanoLC-MS/MS). Raw data of peptides were analyzed with the Progenesis QI software. The initial results allowed the identification of 400 unique proteins exhibiting dynamic changes in EVs composition. These proteins could show a temporal pattern of differential abundance across the time points, indicating that hyperthermia induced distinct phases of biological responses and putative adaptations in cows. In-depth biostatistical analysis are currently in progress to target the most responsive proteins and further investigate their potential roles in key heat-stress-related pathways.

O199

Effects of dietary commercially processed former foodstuffs on the gut ecosystem in broilers

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Feed-food competition is a significant challenge in livestock production, requiring the development of sustainable feed alternatives to address this issue. Thus, there is an ongoing study for sustainable and circular ingredients to substitute conventional raw materials in animal feed. This study aimed to evaluate the effects of substituting commercially processed former food-stuffs (cFF) for corn, soybean meal, and soybean oil in broiler diets on the gut ecosystem, focusing on intestinal histomorphology, gut microbiota composition, caecal volatile fatty acids (VFA) and ammonia levels. A total of 200 one-day-old male ROSS-308 broiler chicks were allocated into four dietary groups based on average body weight (38.0 ± 0.11 g), with five replicates of ten chickens per group. The diets were formulated to be isonitrogenous and isoenergetic, meeting the nutritional needs of broilers. The nitrogen-corrected apparent metabolisable energy (AMEn) levels and crude protein (CP) percentages were set at 3000 kcal/kg and approximately 23% for the starter phase (days 1–12), and 3100 kcal/kg and approximately 21% for the grower phase (days 12–33), respectively. The control group (cFF0) received

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a standard commercial diet, while other three groups were fed diets in which cFF partially replaced for corn, soybean meal, and soybean oil at substitution levels of 6.25% (cFF6.25), 12.5% (cFF12.5), and 25% (cFF25) for 33 days. At the end of the experimental study (day 33), 60 chickens (15 per dietary group) were slaughtered for analysis. Results showed no differences in gut histomorphometry and histology of liver, spleen and bursa of Fabricius across the dietary groups. In the gut microbiota, alpha diversity indices, such as observed features and Shannon entropy, showed no variation among dietary groups. However, at the genus level, *Faecalibacterium* abundance increased ($p < 0.05$) in the cFF25 group compared to the control group (cFF0). Additionally, there were no differences in VFA concentrations among dietary groups. A linear decrease in ammonia concentration ($p < 0.05$) was observed as cFF levels increased in the diet, from cFF0 to cFF25. These results suggest that the substituting of up to 25% cFF in broiler diets did not negatively impact gut histomorphometry or microbiota diversity, nor did it compromise broiler performance.

O172

Dietary supplementation with hazelnut skin polyphenols affects growth performance and intestinal microbiota in broiler chickens

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Polyphenol supplementation in animal diets has been shown to influence several metabolic pathways and the gastro-intestinal ecosystem. Hazelnut skins (HS) represent an agro-industrial co-product rich in bioactive compounds, including polyphenols. Three dietary dosages of HS polyphenols (D1-D2-D3: 200–400–800 mg/kg, respectively) were used to study broiler chicken growth performance, ileum/cecum histomorphometry and microbiota during the finisher phase (22–42 days of age). Additionally, the influence of supplemented diets on *Campylobacter* spp. shedding was evaluated. A total of 72 subjects (18 per group) were used. Birds of group D3 showed higher ($p < 0.05$) final body weights (2452 ± 84 g) when compared to groups D1 (2312 ± 77 g) and control (2346 ± 77 g). Feed conversion rate (2.01) of the D3 group was lower ($p < 0.05$), while average daily gain (83 ± 4) was higher ($p < 0.05$) than those observed in groups D1 and control (2.16 and 75–77 g, respectively). Digital histological analysis revealed a general trend of improved histological metrics for both intestinal tracts in the treated groups. A significant decrease in cecum epithelium height was observed in D3 when compared to all the other groups. Differences in microbial community structure were observed across diets for both cecal and ileal contents. Fourteen, 15, and 18 differentially abundant (DA) species in cecum, and 19, 14, and 19 DA species in the ileum (for D1, D2 and D3, respectively), were found compared to the C group. As for cecal microbiota composition, group D3 showed the highest number of DA species, with *Megasphera*, *Dusulfovibrio*, and *Anaerobiospirillum* being the most abundant genera. Among key bacterial genera in the ileum, D3 showed a marked difference with both D1 and control. *Weissella,* a genus known for its probiotic effects in chickens, was found increased in all supplemented groups when compared to control. *Bacteroides*, *Helicobacter*, and *Clostridium* spp., known to have controversial effects in the intestinal ecosystem, increased in the D3 diet. The supplementation had no influence on *Campylobacter* spp. fecal shedding. This study evaluated for the first time the impact of HS polyphenols on chicken growth and gut health. Much remains to be clarified, including the role of the bacterial species identified, many of which are unknown or have roles that are not yet clearly defined in the chicken microbiota.

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O202

Microbiota characterization of four autochthonous Italian chicken breeds

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The gastrointestinal tract (GIT) plays a vital role in animal productivity by performing key functions such as pathogen defence, nutrient breakdown and absorption, and the development of the host immune system. The microbiota is crucial for enhancing animal resilience, particularly in the face of climate change. Autochthonous

animal genetic resources represent a valuable component of biodiversity and the characterisation of their caecal microbiota could be an interesting tool for understanding host-microbe-environment interactions. The microbiota composition of four autochthonous Italian chicken breeds (Ancona, Ermellinata di Rovigo, Pepoi, Robusta Lionata, 120 subject in total) was characterised using a metagenomics approach to explore the potential influence of breed and environmental factors on microbial diversity. The chickens were reared in two distinct environments (both outdoor but with different climate influences), aiming to monitor the effects of genetic background and rearing conditions on the gut microbiota. Morpho-functional measurements were taken throughout the entire growth period (120 days) to integrate microbiota data with physiological development and performance traits. DNA was extracted using a commercial kit and a microbiome profiling techniques was used. The profile identified resulted similar among breeds, but we observed significant variations in microbial communities between the breeds in the same environmental settings. The most abundant genus was *Phocaeicola* (6.02% Ancona; 3.41% Ermellinata di Rovigo; 1.64% Pepoi; 3.08% Robusta Lionata), which exhibited great variability. *Enterococcus* results more abundant in the Pepoi group (1.25%) than in the other breeds (0.85% Ancona; 0.90% Ermellinata di Rovigo; and 0.81% Robusta Lionata). The abundance of *Escherichia/Shigella* was higher in Ancona (3.29%) and Pepoi (2.54%) than in Ermenllinata di Rovigo (1.72%) and Robusta Lionata (1.15%). Whilst *Ligilactobacillus* genus has the highest abundance in Ermellinata di Rovigo (3.66%), followed by Pepoi (2.47%) and Ancona (2.11%) groups, and at last by Robusta Lionata (0.93%). These findings highlight the interplay between breed and environmental factors in shaping the gut microbiome, offering valuable insights into sustainable poultry farming and breed-specific management practices.

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O277

Replacing vegetable oils with *Hermetia illucens* (Black Soldier Fly) larvae oil in broiler chicken diets: impacts on growth performance, meat quality, and caeca microbiome

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Protein from poultry, particularly meat-type (broiler) chickens, is crucial to future global food security. Although poultry production already shows higher efficiency and lower environmental impacts than other livestock, the use of feed lipid sources such as soybean oil can significantly affect sustainability due to their production footprint. Black Soldier Fly (*Hermetia Illucens*, HI) larvae oil has emerged as a promising alternative among cultivated insect species due to its relatively rapid development and preference for organic waste as a growth substrate, contributing to a reduced environmental footprint. This study investigated how replacing soybean oil with HI larvae oil affects broiler chicken growth performance, meat quality, fatty acid profiles, and caeca microbiome. A total of 552-day-old male Ross 308 broilers were allocated to three dietary treatments ($n = 184$ birds/group, 8 replicate pens/group and 23 birds/pen): 100% soybean oil (CON), 50% soybean oil +50% HI larvae oil (MIX), and 100% HI larvae oil (HIO). Diets were isoenergetic and with the same amino acid profile. Growth performance parameters were recorded at the end of each feeding phase (14, 28 and 42 d). On day 42 all birds were processed in a commercial facility, n. 10 breast muscles and thighs per group were collected for meat quality assessment (pH, color, and water-holding capacity), while ceca content samples were obtained from 8 birds/group (1 bird/pen) for caeca microbiome analysis. Data were analyzed using one-way ANOVA, with significance set at a p-value of ≤0.05. Growth metrics revealed improved feed conversion ratios in HI-fed groups during the starter phase (1.536 vs. 1.454 vs. 1.460, for CON, MIX and HIO, respectively; $p < 0.01$) and comparable productive performance in the overall trial period (0–42 d). Overall meat quality traits were not affected ($p > 0.05$). Although fatty acid analysis revealed increases in saturated fatty acids (lauric, myristic, palmitic) and reductions in PUFA (linoleic acid, omega-6), a more balanced omega-6: omega-3 ratio in HI-fed groups was observed (16.5 vs. 15.2 vs. 11.6, for CON, MIX and HIO, respectively; $p = 0.0001$). Caeca microbiome profiling demonstrated minimal microbial shifts, with stable diversity across treatments. Overall, results suggest that the inclusion of HI larvae oil as a partial or complete replacement for soybean oil supports production traits effectively and comparably to traditional vegetable lipid sources while enhancing feed efficiency during the starter phase and promoting a more balanced omega-6: omega-3 ratio in breast meat.

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– D.D. 1032 17/06/2022, CN00000022). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

O388

Egg-laying performance of hens fed diets containing former food products

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One of the most relevant global issues is the reduction in food loss and waste, a challenge that undermines environmental sustainability. Around 30% of the food produced globally is estimated to be wasted, causing social, economic and environmental issues. In addition, feed cost takes up to 60% of the total cost of poultry production and the competition between feed and food is supported by the large use of cereals in poultry rations. In this context, the concept of circular feeding can effectively support sustainability in the poultry sector and the former food products (FFP; processed bakery products) could play a pivotal role. The present study aimed to evaluate the application of FFP in laying hen diet. Lohmann Brown® laying hens ($n = 180$), were housed in furnished cages from 17 to 34 weeks of age. Hens were randomly distributed (12 hens/cage; 5 replicates/treatment) and fed one of the following dietary treatments: (1) control group (T0), standard commercial feed; (2) T20 group, standard commercial feed with 20% inclusion of FFP; (3) T40 group, standard commercial feed with 40% inclusion of FFP. The diets were isonitrogenous and isoenergetic (CP: 17.0%; AME = 12.47 MJ/kg) and *ad libitum* fed. The FFP utilised in the present study was the Primo® product, provided by a private feeding company. The effect of dietary treatments has been biweekly evaluated on productive performance, egg quality parameters (whole egg, yolk, albumen and shell weight, shape index, shell thickness, yolk and shell color) and proximate egg composition (week 19, 26, 34 of age). Egg mass was significantly higher ($p < .0001$) in T0 and T20 group (4.86 and 4.88 kg respectively) than in T40 group (4.66 kg). The daily feed intake was significantly lower ($p < 0.0002$) in T0 (111.59 g/d) than in T20 and T40 (119.43 and 116.46 g/d respectively), and FCR/egg mass was lower ($p < .0001$) in T0 (1.91) than in T20 and T40 (2.04 and 2.06 respectively). No significant differences were observed in quality parameters and proximate egg composition.
In conclusion, including 20% FFP in the laying hen diet did not affect egg production or quality, despite an increase in FCR. FFP shows potential as a sustainable strategy, but further research is needed to optimise inclusion rates for balancing performance and feed efficiency. Life Cycle Assessment studies are crucial for evaluating sustainability in the poultry industry, and an economic analysis of production costs should be conducted to complete the assessment.

O078

Application of YOLOv8 for analyzing social dynamics in dairy cows within Automated Milking Systems

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Cattle form structured groups with well-established hierarchies in the herd. Within these hierarchies, cows develop strong and lasting social bonds that significantly influence group dynamics, welfare, and productivity. Understanding these social interactions is essential for improving management practices, reducing stress, and enhancing productivity. Traditional methods for monitoring such interactions rely on manual observation, which is labor-intensive, prone to errors, and difficult to scale. The primary objective of the study was to map and analyze the social interactions within this herd using advanced computer vision techniques. Specifically, we leveraged the YOLOv8 deep learning model to automatically identify and track individual cows. This study was conducted on a commercial farm in Northwestern Italy, housing 240 Holstein Friesian dairy cows in a cubicle-free stall system. The barn, composed of two sections measuring 45 × 30 meters each, was equipped with two Automated Milking Systems (AMS) per section. Eight strategically positioned wide-angle cameras were installed at a height of 7 meters, outside the animal-occupied areas. This configuration provided complete visual coverage of the barn and milking robots, enabling non-invasive monitoring of cow movements while allowing routine checks and cleaning operations without disrupting the cows' daily activities. The YOLOv8 model demonstrated robust performance in detecting and tracking cows under real-world conditions. Specifically, the model achieved a mean Average Precision (mAP) of 0.75 at an Intersection over Union (IoU) threshold

ranging from 0.5 to 0.95, along with precision and recall values of 0.88 and 0.90, respectively. These metrics highlight the model's ability to accurately detect individual cows while minimising false positives and negatives. Moreover, the system maintained an inference speed of 7.57 milliseconds per image, making it suitable for real-time applications on commercial farms. The findings underscore the transformative potential of computer vision systems in monitoring and improving the welfare of dairy herds. This study represents a significant advancement in integrating non-invasive, scalable monitoring technologies in Precision Livestock Farming, paving the way for data-driven interventions that enhance both animal welfare and economic sustainability.

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O046

Computer vision for monitoring feeding behavior of dairy cow

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Monitoring the feeding behavior of dairy cows is an important aspect of managing herd health and optimising productivity. This study investigates the application of computer vision techniques to analyze the time dairy cows spend at the feeding lane. Using an artificial vision system, 19 Holstein dairy cows were monitored continuously in an experimental barn located in Ozzano, Bologna. RGB images were captured using a camera connected to a personal computer. The video was annotated by assigning unique IDs to each cow based on their morphological characteristics. The dataset adopted in the study consisted of 7,200 frames, used 70% for training, 10% for validation, and 20% for testing. Before training the model, data augmentation techniques including changes in geometry and alterations in lighting and contrast have been applied. For this study, the pre-trained YOLO(v.8) weights were used and then has been refined with a training process of 100 epochs applied to the collected dataset. The codebase was developed using Python 3.10.12 with OpenCV 4.8.0 for image processing. PyTorch(v2.2.1) serves as the fundamental deep-learning framework. The trained model was used to identify the region of interest (ROI) at the feeding lane. The feeding behavior was analyzed by comparing the times spent by individual cows at the feeding lane, as predicted by the model, with the ground truth annotations. This comparison validated the approach's accuracy and demonstrated its potential for practical livestock managements applications. Key metrics such as Precision, Recall and mAP50 were calculated, revealing an average accuracy of about 67% for animal identification. The outcomes highlight the potential of automated systems for providing accurate and continuous monitoring of certain activities which can be used as indicators of individual animal health and welfare. Moreover, the research uses computer vision technology to demonstrate an innovative method for advancing precision livestock farming and offers a system for improving dairy herd management practices.

O068

Environmental changes and hen spatial distribution in cage-free systems: A preliminary study

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This study aimed to evaluate hen distribution and changes in environmental conditions within a multi-tiered aviary system, considering the effects of tier height and hen genotype. Additionally, the relationships between hen distribution and environmental conditions were assessed. Environmental variables, including CO_2, NH_3, and particulate matter (PM_1, $PM_{2.5}$, PM_4, PM_{10}), as well as hen distribution at the different levels, were monitored at three heights, i.e. ground floor (10 cm), mid-tier (180 cm), and upmost tier (270 cm). Data were collected in winter over a three-week period (31 to 33 weeks of hen age) in two aviary pens (225 hens per pen), each housing a different genotype (white or brown; Novogen Layers). Hen distribution (% of observed hens through video-recordings) was influenced by genotype, with a higher proportion of white hens observed on the mid-tier (13% vs. 8%; $p < 0.001$) compared to brown hens, while a lower proportion of white hens were observed on the ground floor (26% vs. 28%; $p < 0.05$). Environmental conditions changed with genotype and tier height. Higher air values of CO_2, NH_3, $PM_{2.5}$, PM_4, and PM_{10} (ranging from +9% to +38%; $p < 0.001$) were recorded in the pen with brown hens compared to the pen with white hens. Then, significantly higher CO_2 and particulate matter (ranging from +17% to +48%; $p < 0.001$) were observed on the mid-tier compared to the upmost tier and ground floor, whereas NH_3 concentration were highest on the ground floor (+53%; $p < 0.001$) compared to

the tiers. The concentrations of CO_2 and NH_3 showed weak correlations with hen distribution on the ground floor ($r = 0.16$; $p < 0.05$) and at the tiers ($-0.09 < r < -0.28$; $p < 0.05$). In contrast, concentrations of $PM_{2.5}$, PM_4, and PM_{10} were moderately correlated with hen presence on the ground floor ($r = 0.37$; $p < 0.001$) and mid-tier ($-0.43 < r < -0.40$; $p < 0.001$), while weaker correlations were found at the upmost tier ($-0.29 < r < -0.25$; $p < 0.001$). In conclusion, hen genotype and tier height significantly influenced hen distribution and environmental conditions within the aviary. Brown hens showed a preference for the ground floor, where higher NH_3 concentrations were recorded, while white hens primarily occupied the aviary tiers. Elevated levels of CO_2 and particulate matter were observed in the mid-tier.

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O184

Development of an image analysis system at the slaughterhouse to assess laying hens' welfare on farm

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In the poultry sector, artificial intelligence could be a valuable means to ensure better farm welfare conditions and meet consumers' demands, which are increasingly directed towards the choice of 'welfare-friendly' products. Much of the research in the field is focused on farm welfare where systems have been developed to detect behaviours, health or sounds automatically. However, some evaluations conducted directly on animals at the slaughterhouse may be iceberg indicators of poor on farm welfare conditions. The slaughterhouse represents a crucial and strategic point where evaluations can be carried out efficiently and quickly as it receives many animals daily, processed under standardised conditions. Last but not least, technological innovation and automation could support and facilitate veterinary inspection in monitoring such large numbers. In farmed laying hens, one of the main animal welfare consequence is bone lesions, including keel bone fractures, which, in addition to causing pain and suffering in the animals, can affect production performance and consequent economic damage. The causes for keel bone lesions are many and complex. Despite commonly linked to high egg production, husbandry systems, genetic lines and management practices also play fundamental roles in the onset and frequency of this problem. To gain an understanding of the welfare conditions on the farm and hypothesise corrective actions in the situations of most significant risk, the present research project focused on the development of an image analysis system that allows the automatic recognition and classification of keel bone lesions in laying hens. To this purpose, laying hens of brown genotypes in the slaughter line of a commercial plant in north-eastern Italy were filmed using a smartphone. 600 frames containing approximately five hens each were extracted from the videos obtained. On video, keel bone detection and lesion assessment were carried out by three different annotators using a three-score scale (0;1;unclassifiable). A total of 1443 images were obtained by applying the preprocessing and data augmentation steps. Finally, a YOLO11 model was trained. A mAP@50 value of 0.74 was obtained for the keel bone detection phase and an F1-score of 0.71 for the classification phase. The results obtained are preliminary and subject to improvement. The following steps will involve improving of the image dataset.

O495

Evaluating infrared thermography for early detection of subclinical mastitis in dairy cows: the impact of *Staphylococcus aureus* infections on udder skin temperature

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Mastitis is regarded as the most significant technopathy affecting the overall sustainability of dairy cow farms, as it causes economic losses and is a common cause of antibiotic consumption in dairy cows. Early detection of subclinical intramammary infections is essential to mitigate antibiotic dependency, reduce milk loss, and enhance animal welfare. Among the new technologies that are seen with increasing interest is infrared thermography as its application may help identify early changes in superficial skin temperature in the mammary gland that could predict the occurrence of clinical mastitis. In this study, we aimed at evaluating the effect of intramammary infection by

Staphylococcus aureus on the superficial skin temperature of the rear udder quarters. We monitored 400 multiparous Holstein Friesian cows, with 200 exhibiting genotypes favorable for mastitis resistance and 200 with genotypes considered unfavorable. Bacteriological screening through single quarter milk culture was conducted at T0 to select approximately 100 animals for subsequent monitoring at two additional time points, T1 and T2, each spaced two weeks apart. At T1 and T2, 44 cows consistently negative for *Staphylococcus aureus* and 24 consistently positive were identified. In addition, thermographic imaging, using a portable FLIR E76 thermocamera, was conducted at a 1-m distance from the udder rear quarters before milking in a carousel milking system. Results showed that at both sampling times, cows infected by *Staphylococcus aureus* had significantly higher somatic cell counts (170 000 *vs*. 983 000 cells/ml at T1, 242 000 *vs*. 571 000 cells/ml at T2, for uninfected vs. infected cows). Udder superficial skin temperature at T1 was significantly associated with somatic cell counts ($p < 0.05$), though this association diminished at T2. These findings suggest that rear udder quarters may have limitations in reliably detecting subclinical and clinical mastitis through infrared thermography, warranting further investigation into the technique's diagnostic reliability.

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O457

Detection of livestock site-use intensity at fine-scale in mountain grazing systems using Sentinel-2 time series

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The monitoring of livestock site-use intensity is essential to preserve the productivity, quality, and ecosystem services of mountain grasslands. While GPS collars provide detailed quantification of site-use intensity, their high costs often limit their use. Proxies like terrain slope and distance from buildings can estimate site-use intensity but cannot capture seasonal variability in grazing patterns, which is driven by forage and climatic conditions, management practices, and individual animal behavior. Recent advancements in remote sensing offer free, accessible, and high-resolution spatio-temporal data to overcome these limitations. This study aimed to predict livestock site-use intensity in alpine pastures using Sentinel-2 satellite time series data, validated against site-use intensity measured with GPS collars. The research was conducted across four alpine pastures in the NW Italian and Swiss Alps from 2019 to 2024. Since GPS collars were used in some pastures for multiple years, the study included a total of 12 case studies. Using Google Earth Engine, vegetation indices (VIs) such as NDVI, GNDVI (Green Normalised Difference Vegetation Index), NDII (Normalised Difference Infrared Index), and GVMI (Global Vegetation Moisture Index) were computed at a 10-m resolution. An R algorithm was developed to analyze temporal changes in VIs and identify the significant reduction in forage yield related to grazing events. We assumed that the sum of significant reductions could estimate seasonal forage consumption. To optimise accuracy, 110 combinations of parameters were tested per each VI, varying time series interpolation intervals (5– 15 days) and VI reduction thresholds (0.01– 0.10), resulting in 440 total combinations. Each parameter combination was analyzed with GLMM to assess its relationship with site-use intensity measured by GPS collars. According to model AIC and RMSE, GVMI and NDII were identified as the best indices, both showing significant positive relationships ($p < 0.05$) between grazing consumption estimated by satellite data and site-use intensity measured by GPS collars. This research shows the potential of high-resolution satellite imagery to estimate livestock site-use intensity in mountain grasslands, facing interannual forage variability, offering a cost-effective alternative to GPS for large-scale use.

O048

Preliminary analyses on the identification of horse behaviors using deep learning techniques

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Horse behavior can provide meaningful insight into their current subjective state, thus being a good indicator of their welfare and the daily time spent for the different behaviors can be a useful monitoring strategy. For example, among the different daily routinary behaviors, sleep plays a fundamental role for animal welfare due to its significant biological function of restorative properties and its cognitive role in memory consolidation. In fact, horses, as a prey species, usually have a daily total sleep ranging from 3 to 5 hours. The lack of sleep, known as sleep deprivation, is a common problem and a major stressor

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for horses, causing changes in both behavior and affective state. Lying has been reported as an effective animal-based indicator of the welfare of stabled horse. Moreover, the monitoring of the access to the drinking trough or evaluating the feeding time can be useful measures for the establishment of the welfare state. However, measuring this behavior in animals by direct or video observations can be time-consuming, especially in horses which spend a relatively small proportion of their day lying down or drinking. To help the daily management, computer vision allows automated systems to interpret and understand visual information in animal environments. By drawing on methodologies from image processing and machine learning, computer vision facilitates the analysis, interpretation, and extraction of valuable information from visual data. This study investigates a deep learning-based computer vision system to identify the behaviors of individual stabled horses. The initial phase involves the fine-tuning of a pre-trained YOLO architecture to recognise different behaviors, i.e. lying, active standing, non-active standing, drinking of a single horse housed in a closed box. Object detection techniques were applied to identify behaviors like lying and standing, while pose estimation was used to detect drinking. To differentiate between active and non-active standing, we set a pixel-based threshold. Subsequently, the model was used to predict the horse's behavior for one month of continuous monitoring, in order to provide the 24-hour budget time for the animal. Performance evaluation of the network involves the use of precision-recall curves, and accuracy of identification by comparison with the human labelling performed on the same video. The system achieved 86% accuracy in behavior classification compared to manual annotation. This technology provides real-time insights into the welfare of monitored horses, highlighting it value for behavior monitoring. In fact, it is possible to detect any abnormal signs of the horse's behavior using computer vision. This means that it may be a useful help to assist breeders in practicing horse care.

O225

Performance of Italian Dairy Heard Information (DHI) milk laboratories assessed through three years of proficiency tests

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Producing reliable and consistent Mid-Infrared data across laboratories is essential for accurate and comparable results in analytical and diagnostic applications. Aligned methodologies and well-calibrated devices are crucial for maintaining data integrity, reducing variability, and enhancing collaboration. Blind proficiency tests (PT), where laboratories independently analyze the same sample set without knowing the expected outcomes, are invaluable for identifying discrepancies in lab performance or device calibration. These tests objectively assess alignment, detect systematic errors, ensure robust data quality, and foster trust in multi-laboratory collaborations. Laboratorio Standard Latte (LSL) of Italian Breeders Association leads 'DHI milk laboratories' in analyzing milk samples to monitor dairy species' performance. LSL ensures nationwide analytical uniformity by organising PTs for cows, sheep, buffalo, and goats, in compliance with ISO 17043. Statistical analyses follow ISO 13528 and UNI ISO 5725-2 standards. This study presents the performance outcomes of DHI milk laboratories monitored over a three-year period (2022–2024). Analysis focused on fat content in raw milk from various species, a key parameter for milk quality and among the most critical due to its well-documented variability. A total of 12 PTs was conducted for raw cow milk, involving about 80 analytical instrument lines per test. For raw buffalo, goat, and sheep milk, 6 PTs were conducted for each species, with about 25 analytical instrument lines participating per test. Overall, DHI milk laboratories showed improved analytical performance during the monitoring period. Repeatability (r) and reproducibility (R) metrics were equal to or better than those of external labs, especially for sheep milk, where reproducibility significantly improved (R = 0.09 vs 0.18). The proportion of participants with satisfactory Z-Score classifications ranged from 87% to 99%. In conclusion, PTs have been vital in enhancing milk laboratory accuracy. The outstanding performance of DHI milk laboratories, with improved r, R, and alignment with assigned values, underscores the importance of PTs for analytical excellence. These tests have driven continuous improvement and quality control, enabling superior results, especially in challenging analyses like sheep milk fat content. This highlights the essential role of structured PT programs in maintaining high-quality analytical standards in the dairy industry.

O106

Terpene transfer from hemp (*Cannabis sativa L.*) and savory (*Satureja hortensis L.*) to milk of dairy cows supplemented with fresh leaves

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This study investigates the transfer of terpenes from aromatic plants, hemp (*Cannabis sativa L.*) and savory (*Satureja hortensis L.*), to the milk of dairy cows supplemented with fresh leaves. The aims were to quantify terpene transfer efficiency and explore their dynamics in milk. Three groups of 2 dairy cows each were fed in 3 consecutive periods of 14 days each, following a 3 × 3 Latin Square Design to test the effects of 3 experimental diets: a conventional diet (CTRL) and the same diet supplemented with hemp (CS) and savory (SH) leaves. Fresh leaves were administered from day 4 to day 9 of each period, with quantities increasing from 0.2 to 0.8 kg/d of dry matter. Milk samples were collected daily during the first period and mixed (evening of the previous day with the morning of the following day) to evaluate transfer kinetics. Samples from day 9 (evening) and day 10 (morning) of each period were used to analyze terpene content in milk, at peak supplementation. Terpenes were quantified using Headspace Solid-Phase Microextraction coupled with Gas Chromatography-Mass Spectrometry (HS-SPME/GC-MS). A total of 24 terpenes were identified in feed and milk. The CTRL diet contained 228 µg/kg of total terpenes, while CS and SH leaves had 85,962 and 11,313 µg/kg, respectively. Consequently, the CS diet was 378 and 7.6 times richer in terpenes than the CTRL and SH diets. These differences were reflected in milk concentrations, with terpene levels reaching a total of 50.8, 388.8 and 48.7 µg/L for CTRL, CS and SH diets, respectively. The carryover of terpenes from feed to milk was higher in cows fed CTRL diet compared to CS and SH diets (15.4 vs 8.7 and 6.2%, respectively). Key terpenes, including *Cis, trans-α-Farnesene*, *β-caryophyllene*, and *Trans-α-Bergamotene* from hemp, and *O-Cymene* from savory, were identified in milk. The day-by-day milk analysis revealed the presence of terpenes on day 5, following initial leaf supplementation. Peak concentrations were observed on day 10 at maximum supplementation, after which terpene levels declined, falling below detection limits by day 14, four days post-supplementation. These findings highlight the dynamic nature of terpene transfer from feed to milk and demonstrate hemp's greater potential compared to savory in enriching milk with terpenes. This research provides insights into enhancing milk quality through plant supplementation and lays the groundwork for optimising aromatic plant use in dairy systems.
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O479

Effect of dietary linseed on milk fatty acid profile, coagulation properties, and methane emission in local Sardo-Bruna cows

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The Sardo-Bruna is one of the three local cattle breeds of Sardinia, together with the Sardo-Modicana and Sarda breeds. Similar to other local species and breeds, the Sardo-Bruna is considered at risk of extinction. The production of typical products represents a strategy to preserve the genetic biodiversity, and the social, economic and cultural implications related to the local breeds farming.
The farming system of the Sardo-Bruna is mostly extensive, and the derived products are influenced by the pasture characteristics. During the summer season, the low availability and quality of pasture can negatively affect the quality of products. The aim of this study was to evaluate the differences in milk yield and quality, cheesemaking properties, resulting from the inclusion of extruded linseed in the diet of Bruna and Sardo Bruna cattle. Another objective was to determine possible reduction of enteric methane emissions related to the use of extruded linseed. This research was conducted in a private farm, specialised in the production of Casizolu del Montiferru cheese. Eighteen lactating cows of the Sardo Bruna and Bruna breeds were selected and allocated to two experimental groups: a control group (CON), receiving a basal diet, and a treatment group (LIN), receiving the diet where 1kg of concentrate was replaced by 1.2 kg/head of extruded linseed. Individual milk yield was recorded, and samples were collected weekly during two daily milkings. Milk samples were analyzed for the determination of chemical characteristics by mid infrared spectroscopy, coagulation properties by formagraph and milk fatty acids profile by gas-chromatography. Methane emissions were measured by using a Laser Methane Mini Smart (Tokyo Gas Engineering Solutions). Data were

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analyzed by a mixed model including the fixed effects of diet, time and their interaction, and the random effect of animal. No differences in terms of milk yield and composition were detected between groups, except for the fatty acid profile: the milk of LIN group had a significantly higher content of polyunsaturated fatty acids, lower content of saturated fatty acids than CON group. From the perspective of cheesemaking properties, no negative effects were observed, either in the laboratory parameters measured or during processing in the dairy. Additionally, the use of linseed resulted in a reduction in methane emissions. In conclusion, the use of extruded linseed in the diet of Sardo Bruna and Bruna cattle could be useful to improve the quality of dairy products and to reduce the environmental impact of the farm.

O231

Stabilized bovine milk extracellular vesicles as anti-inflammatory and immunomodulatory agent on human macrophage-like cells

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Milk represents a natural resource of bioactive components, including extracellular vesicles (EVs). EVs are micro and nano-sized structures enclosed in a phospholipidic double-layer membrane, mainly functioning as message delivery vectors of a plethora of molecules from producing to recipient cells. Milk is a promising scalable EV source and milk EVs (mEVs) have been recently explored as an alternative therapy for human inflammatory bowel disease (IBD). Our preliminary results on bovine mEVs applied in a 2D in vitro model of IBD demonstrated anti-inflammatory and immunomodulatory properties by reducing proinflammatory cytokine production and improving enterocyte homeostasis. Despite the promising results, the primary challenge associated with mEV utilisation lies in their conservation; low-temperature storage (–80 °C) is indeed the most effective preservation method but its application in clinical and medical fields is challenging. The aim of this research was to develop a prototype formulation obtained by transforming mEV suspensions into microparticle powders with the unique and essential feature of stabilising mEVs to be stored at room temperature and easily applied in clinical therapies. mEVs were isolated through differential centrifugations and ultra-centrifugations adding an EDTA cleaning step and then processed for transformation into dry powders. Isolated mEVs and powdered mEVs were observed at scanning electron microscopy and measured in terms of size distribution (AccuSizer Optical Particle Sizer M770) and concentration (Malvern Panalytical NanoSight NS300). The presence of EV markers was assessed by western blot testing CD81 and TSG101 as well as the absence of cellular contamination markers such as calnexin. Finally, both fresh mEVs and dry powders were used to treat a human macrophage cell line (THP-1) to evaluate whether the powdered mEVs maintained the same effects as fresh mEVs. First, the gene expression of naïve THP1 cells was assessed at two endpoints of treatment (6h and overnight), evaluating also the shelf life of the powder (18 months from production), then the same treatment was applied on cells pretreated with an inflammatory stimulus. The powders demonstrated a comparable effect than fresh mEVs and overall, the study highlighted the considerable stability of mEVs stored as dry powders at room temperature for 18 months.

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O025

Comparison of machine learning algorithms to trace the geographical origin of raw milk using infrared spectra

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Sarda breed represents the most important dairy sheep in Italy, accounting for approximately 90% of the Italian dairy sheep stock. In the case of sheep milk cheeses, geographical traceability of their raw material is essential since the quality components are strictly related to the environment. Originally, this breed was divided into three subpopulations (plain, hill, and mountain) with differences in body size and milk yield and composition. Infrared spectroscopy is a valid alternative to collect information on milk origin and are widely used for identification and classification of food products. Thus, the aim of this study was to trace milk origin using the differences in

the milk spectra of Sarda dairy ewes raised at different altitudes. A total 455 milk samples were collected in plain (≤ 200 meters; 176 samples), hill (201–500; 139 samples), and mountain (> 500 meters; 142 samples). The dataset was randomly divided 1,000 times in training (90% of observations, to train the models) and validation (10% of observations, to predict the zone). Six models were tested: linear discriminant analysis (LDA), stochastic gradient boosting machine (GBM), support vector machines (SVM), recursive partitioning robust tree (RPART), random forest (RF), K-Nearest neighbors (KNN). The largest accuracy (0.90 ± 0.01) in the training dataset was observed for GBM. The same model had also the highest balanced accuracy in the validation dataset, with hill showing a lower value compared to the other two zones. LDA had the second-best accuracy in training, and it was much faster than GBM (2 seconds for LDA vs 5 minutes for GBM). Hill and mountain were closer compared to the plain group. Because of the high accuracy and low computing time, LDA could be a good option to routinely assign simple samples to the correct zone of origin in Sarda dairy sheep breed.
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O305

A comparative analysis of milk fat globule size and distribution in Holstein-Friesian and Reggiana cattle breeds

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The size range and complex composition of bovine milk fat globules (MFGs) affects the technological and nutritional characteristics of milk and adds unique sensory and nutritional attributes to the dairy products. For these reasons, the aim of this study was to investigate the effect of animal-related factors [e.g. breed, days in milk (DIM) and parity] on variability of MFG in bovine milk. Individual milk samples were collected from 627 dairy cows balanced between Holstein-Friesian and Reggiana breeds reared in six mixed commercial farms located in the Emilia-Romagna region. The MFGs size distribution was measured using a Malvern Mastersizer 3000 via light scattering that provided the following traits: the volume-weighted mean diameter (d4,3), surface-weighted mean diameter (d3,2), the specific surface area (SSA) and the distribution variability of MFGs (span).The variability of MFG traits was analyzed using a linear mixed model that included breed, DIM and parity as fixed factors and day of sampling as random factor. The mean values of d4,3, d3,2, SSA and span were 1.71 µm, 1.01 µm, 5830.4 cm^2/ml and 2.14, respectively. Among the assessed animal-related factors, the results demonstrated that breed ($p < 0.001$ for all the MFG), and DIM ($p < 0.001$ for all the MFG) effects were the most influential in determining milk fat globule size, while the parity was less important ($p < 0.01$). Specifically, regarding the breed effect, Reggiana cows showed larger average fat globule sizes (d4,3, d3,2 and SSA with the values of 1.73 µm, 1.02 µm and 5808.53 cm^2/ml, respectively), while Holstein-Friesian cows exhibited a greater variability with a span value of 2.16. In the case of DIM, it was observed that, during the early lactation phase (approximately 60 days after calving), fat globules were smaller compared to those produced after the peak of milk production. The study highlights the complex interplay of animal-related factors in shaping the size distribution of fat globules and reveals significant breed-specific differences. These findings underline the importance of such factors in optimising milk quality and suggest their potential inclusion in future breeding selection programs.
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O400

Promoting a circular bio-economy: use of wine cellar by-products as feed supplement for dairy cows and evaluation of the chemical and microbiological effects on dairy products

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In the Trentino Alto Adige region, grape stalks (GS) residues disposal is one of the main costs for wine cellars. The development of strategies to valorise agricultural waste, within different supply chains, can serve as a viable and more profitable management approach. Specifically, GS are known to contain nutritional and functional compounds like phenols and tannins that can affect rumen microbiota. This study aimed to assess if supplementing cows with GS could highlight any variation in milk and cheese composition. GS of 3 red grape varieties were collected from a local wine cellar: Lagrein, Cabernet Sauvignon and Merlot. GS were stored at -20 °C until the start of the experiment, then dried at 45 °C, ground and analyzed for their microbial and chemical safety. Total polyphenols and tannins content were also analyzed. The average content of GS total polyphenols was about 15 g/Kg of dry matter (DM). Following the results obtained, 3 Holstein cows, already fed with hay and concentrates, were selected by a local dairy farm, for the test of daily supplementation with GS at 2% DM of the diet. The study consisted of a one-week control period (CTRL), when no GS supplementation was added to the cows' diet, followed by a week of GS supplementation, for a total of 7 weeks of experimental study (4 CTRL and 3 GS diet weeks). Every week, individual milk samples were collected on the first and last day of the week and analysed for microbiological and chemical composition. Additionally, at the end of each week, 3L of individual milk were collected for experimental mini-cheeses production. A total of 42 milk samples were collected and 21 cheeses were produced. Mini-cheese were processed starting by 2.5 L of milk, ripened for 28 days and analyzed for sensory properties. For milk, routine chemical analyses were performed. Milk and cheese samples were also analyzed for microbial counts. For cheese samples, total polyphenol content, water activity and NMR analysis were performed. Preliminary results showed no correlation between milk microbiological count and the diet: mean values of coliforms in milk samples were always in the range 2.3–2.4 log UFC/mL and mean values of bacteria total count were always in the range 5.0–5.1 log UFC/mL. Total polyphenols mean in cheese samples were always in the range 203–211 mg/Kg. Other test and statistical analysis are under progress.
This study was carried out within the Interconnected Nord-Est Innovation Ecosystem (iNEST) and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.5 – D.D. 1058 23/06/2022, ECS00000043). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

O533

Genetic evaluation of climate effect on Maremmana young bulls reared in test station

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The Maremmana cattle breed is typically raised in free-range or semi-free-range systems due to its distinctive resilience and hardiness. These systems expose animals to various environmental conditions influenced by several climate factors and their combinations. The aim of this study is to evaluate the potential presence of genotype-by-environment interactions (GxE) for different climatic variables and a composite index of these variables with respect to average daily gain (ADG). Phenotypic data from 596 young bulls were collected over 27 years of performance testing at the Alberese test station, where bulls are tested outdoors. Animals were monthly weighted, and ADG was calculated for a first period (first four weighings), a second period (from the fourth weighing on), and the total testing period. This resulted in the datasets P1 ($n = 596$), P2 ($n = 506$), and TOTAL ($n = 572$). Climatic data as temperature (TEMP), humidity (HUM), wind speed (WIND), and solar radiation (RAD), were extracted from NASA databases and used to calculate the adjusted Temperature-Humidity Index (THI_adj). Mean values for each

climatic variable and for THI_adj were estimated for each ADG. Multiple trait models (MTM) were performed to investigate possible GxE interactions, and ADGs within each dataset were partitioned based on the median values of the climatic variables and treated as two traits to correlate. The presence of GxE interactions was assessed using the 90% posterior maximum density interval for a right tail (HDP90) of the genetic correlation. In addition to genetic effects, the fixed effect of test group was included in the models. The average ADG values were 1.33, 1.50, and 1.43 kg/day for the P1, P2, and TOTAL datasets, respectively. MTM revealed HDP90 values below 0.8, indicating GxE interactions, for P1 with THI_adj (0.60) and WIND (0.79), and for TOTAL with HUM (0.78) and RAD (0.64). In contrast, no significant values were found for P2. The results for P1 suggest a better genotype expression in environments with higher THI values, while higher WIND limits expression. For the TOTAL dataset, higher HUM positively affects genotype expression, while higher RAD negatively impacts it. In conclusion, the study highlights GxE interactions for ADG in different environments. The availability of genomic data opens the way for further investigations into specific environmental variables of interest for Maremmana, such as solar radiation.

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O316

Describing Reggiana cattle farms using genomic information from the breed population

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Reggiana is an autochthonous cattle breed mainly raised in the province of Reggio Emilia, located in the Emilia-Romagna region, in the North of Italy. Reggiana cattle are closely associated with the production of the unique mono-breed branded Parmigiano-Reggiano cheese, which provides the economic support that is needed for the sustainable conservation of this animal genetic resource. The breed population consists of approximately 4500 cattle registered in the herd book, distributed in 60 farms. This study investigated the breed structure by combining genomic data obtained from high-throughput genotyping arrays (GGP Bovine 150k single nucleotide polymorphism chip) and whole genome sequencing, which provided genomic information for 4026 animals of this breed from 45 farms, including 280 sires. Pedigree information available in the herd book was corrected using these genomic datasets. Population genomic structures were investigated using admixture analysis and multi-dimensional scaling plots. Some differences in farm clustering profiles were observed suggesting varying degrees of genetic stratification between farms. The mean Fst value, when comparing a single farm with the global population, ranged from 0.00076 to 0.006. However, the Fst values calculated for specific genomic regions had a higher average of 0.018 ± 0.043, with some comparisons between individual farms reaching a maximum value of 0.648. Genomic inbreeding patterns were determined using runs of homozygosity (ROH). The average inbreeding level, based on Runs of Homozygosity, was 0.066 ± 0.038, ranging from 0.003 to 0.128 when considering specific farms. Farm-specific information was gathered and used to monitor breeding practices and suggest corrections in the genetic management of the herds. The results of this study will be useful in designing more effective genetic improvement and conservation programs for the Reggiana breed, enhancing the sustainability of this animal genetic resource.

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O114

Genomic basis of Bovine Respiratory Disease resistance in preweaned dairy calves

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Bovine Respiratory Disease (BRD) is a leading cause of illness and death in preweaned dairy calves, representing a major concern for cattle farming. As a multifactorial disease caused by various pathogens, BRD affects both animal health and farm productivity, prompting research into strategies for enhancing disease resistance. Despite its importance, genome-wide association studies (GWAS) targeting genetic resistance to BRD in preweaned calves remain scarce. This study combined two diagnostic methods—thoracic ultrasonography (TUS) and the Wisconsin respiratory score (WISC)—to improve the accuracy of BRD phenotyping and classify calves as either resistant or susceptible. A cohort of 240 calves was evaluated, resulting in 47

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calves being identified as resistant (TUS ≤1 and WISC ≤4) and 47 as susceptible (TUS ≥5 any WISC score). Using a selective genotyping approach combined with DNA pooling approach, we conducted a GWAS to uncover Quantitative Trait Loci (QTL) associated with BRD resistance and susceptibility. Genotyping was performed with NEOGEN's GGP Bovine 100K SNP chip, and allele frequency comparisons between the resistant and susceptible groups led to the identification of 28 QTL regions (QTLRs) associated with BRD resistance. Within these QTLRs, 141 genes were annotated and functionally classified into four major categories: (i) regulation of systemic arterial blood pressure, (ii) fertility, (iii) immune function, and (iv) filament cytoskeleton structure. These classifications highlight potential biological pathways involved in disease resistance. Notably, 61 of the 141 genes had already been associated with BRD resistance in previous GWAS studies on dairy cattle, reinforcing the reliability of our findings. Among these, ASB9, BMX, EPSTI1, and OLFM4 emerged as particularly relevant, appearing in four prior BRD-related GWAS studies, supporting their potential role in mediating resistance in preweaned calves. This study demonstrates the utility of combining TUS and WISC for precise phenotyping in GWAS investigations of BRD. By identifying critical QTLs and candidate genes, our findings provide valuable insights into the genetic basis of BRD resistance, paving the way for targeted breeding programs to improve dairy cattle health and productivity over the long term.
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O330

GWAS analysis of fitness traits in autochthonous dual-purpose breeds

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In this study, we investigated the genomic architecture of fitness traits in autochthonous cattle breeds using a Genome-Wide Association Study approach (GWAS). The focus was on the genetic basis of traits like days open (DO), longevity (LONG), and somatic cell score (SCS), which are critical indicators of fertility, mammary health, and overall robustness, but are often overlooked compared to production traits. The autochthonous breeds studied, the Alpine Grey and the Rendena, are local to the Alpine region of Northern Italy. These breeds exhibit unique adaptations to challenging environments and contribute significantly to genetic diversity. GWAS identified 830 significant quantitative trait loci (QTLs) across the three traits in Rendena and Alpine Grey cattle, linked to 23 genes. Only QTLs located within 0.5 Mb genomic windows and explaining over 1% of the additive genetic variance for each phenotype were considered significant. For LONG, key genes in Rendena included ZNF644, LCORL, and CPEB4, while CDC42SE2 and RAPGEF6 were significant in Alpine Grey. Genes like PRMT8, TSPAN11, and TSPAN9 were associated with LONG in both breeds. For SCS, LCORL, CPEB4, and PRMT8 were significant in Rendena, while LEMD3, TOX, and DSC1-3 were unique to Alpine Grey. Regarding DO, XKR4 emerged as significant in Rendena, while DSC2 was important in Alpine Grey. PRMT8, predominantly expressed in the nervous system, is essential for dendritic growth and synaptic plasticity, linking it to traits like longevity. TSPAN9, known for its role in cell signalling and lactation persistency, influences longevity through productivity traits. LCORL, which regulates body size and growth, enhances structural resilience, supporting also longevity. RAPGEF6 is associated with fertility and fatty acid metabolism, affecting reproductive success and productivity. Further significant genes were C5orf47 and CPEB4, both involved in reproductive processes, while NKX2-5, essential for cardiac development, is linked to health and longevity traits. This study underscores the importance of local breeds in sustainable breeding programs, highlighting key genes associated with traits critical for productivity, health, and longevity.
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O304

On the use of antibody responses as selection criteria to improve disease resistance in sheep

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The individual infectious status (IS), inferred from antibody response levels measured through an ELISA test, is widely used in prevalence studies to design control strategies. Genetic selection based on IS may represent a promising approach for improving sheep health and resilience. However, implementing effective selective breeding programs based on IS requires designing data-recording protocols mainly considering that IS may depend on the age at infection and delays in seroconversion. The genetic

basis of IS for Paratuberculosis (PTB) and Maedi Visna (MV) was investigated in an experimental flock of Sarda sheep. The flock, consisting of an average annual population of 800 ewes, involved a total of 5,583 ewes born from 1999 to 2022. All pedigrees were recorded and ewes were genotyped using the Illumina 50K chip. Annual sampling from all animals for PTB started in 2001 and ended in 2012. Two variables for genetic analyses were derived from ELISA tests: a binary variable indicating animal IS over its productive lifetime and a continuous one representing the level of antibodies recorded over time. In 2016, all ewes were tested for MV. Subsequently, every 6 months until 2022, ewes with negative IS were re-tested, while those with positive IS were excluded from further testing. Two variables were defined for genetic analyses: a binary variable representing the last animal's IS and a pre-adjusted variable, where the last IS was adjusted for age at sampling to account for age-related prevalence. PTB prevalence increased from 9% at 1 year to 27% at 4 years of age. For MV, prevalence rose dramatically, from 45% at 1 year to 93% at 3 years of age. Both PTB and MV produced promising results in terms of h^2 (0.20 and 0.46). However, pre-adjusting IS data for MV produced a more correct ranking of the animals, especially for the youngest ones. Results demonstrate that selective breeding based on IS data is a feasible strategy to enhance PTB e MV resistance. However, considering the evolution along the lifetime of the prevalence, a reliable large scale genetic evaluation can not be based on a single IS determined early in life. This implies that recording protocols need either several tests along or a single test late in the lifetime. Alternatively, dynamic models including pre-adjustments for the age at sampling of IS of young animals should be implemented.

O348

Prion protein gene polymorphisms in two Sicilian goat populations

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Scrapie is a fatal disease affecting small ruminants and is classified as a transmissible spongiform encephalopathy (TSE). Polymorphisms in the prion protein (*PRNP*) gene has an important role in susceptibility or resistance to scrapie. Previous studies identified several amino acid substitutions related with susceptibility/resistance to classical or atypical scrapie in goats: G127S, I142M, N146D/S, R154H, R211Q and Q222K. According to the Regulation EU 2020/772 polymorphisms K222, D/S146 could function as resistance alleles in the genetic management of disease prevention in goat. Estimating the frequency of candidate alleles is a preliminary step in understanding the feasibility of a breeding program, aimed at controlling this disease. The aim of this study was to assess the presence of polymorphisms within the *PRNP* gene in two Sicilian local populations: Girgentana and Mascaruna goats. A total of 48 samples were genotyped using the Illumina Goat SNP65K array. This chip contains 26 SNPs within the *PRNP* gene region. Among them, four and five were in the upstream and downstream regions, respectively, while 17 were in the coding region. Of these 17 SNPs, three were synonymous variants while the remaining 14 positions correspond to missense variants and therefore valuable for identifying potential mutated alleles associated with scrapie resistance. Out of 17 SNPs located in the coding region, our results showed only four polymorphic sites which led to amino acid substitutions. The K222 resistant allele occurred in both populations, with overall frequency of 20%. No animals carried the D/S146 resistance allele. On the other hand, H154 allele, responsible for atypical scrapie, showed a low frequency of 4%. Furthermore, although not involved in resistance/susceptibility to scrapie, the amino acids Q101R and P240S showed frequencies of 3% for Q101 and 70% for P240, respectively. Out results are in agreement with previous studies, that reported a higher frequency of K222 allele in Southern than in Northern goat breeds (~20% *vs*. ~5%). Though the absence of D/S146 allele in any animals could represent a limitation for eradication program, the presence of K222 allele in both Sicilian goat breeds suggest the possibility to investigate the effects of all other codon mutations on a wider sample whit the final goal to control and eradicate this disease.

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O070

Investigation of interaction between sheep and soil microbiota

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The animal microbiota plays a key role in animal health and productivity, yet the characterisation of the fecal microbiota in grazing sheep remains a largely unexplored topic. In this study, lactating sheep were sampled across different seasons (winter/summer). The farm is located in Tuscany, Italy. Simultaneously with the collection of individual fecal animal microbiota samples

(83 in winter, 76 in summer), soil samples were gathered from grazing (G, n.=15) and areas inaccessible to the animals (NG, n.=15). The aim is to assess the interaction between animals and soil, seeking to understand the extent to which the presence of animals alters soil biodiversity. The first step involved detecting potential differences between seasons and among animals. The 16S rDNA gene has been sequenced, and bioinformatic analyses were conducted using the DADA2 R package. α diversity and β diversity indices were calculated, as well as richness and dominance values, and a non-parametric test was applied to highlight differences between seasons and grazing conditions. Regarding soil microbiota, the averaged values of Chao1 αdiversity were slightly higher in winter in both grazing and not grazing samples, while Shannon index resulted close to 7 in G during summer and higher in NG and generally during winter. Regarding animal microbiota, the averaged αdiversity ranged from 2002 to 1898, and from 6.5 to 5.9 for Chao1 and Shannon indices during winter and summer, respectively. The most abundant bacteria genera in animal fecal samples were *Ruminococcus*, *Porphyromonas* and *Treponema*, while in soil samples were *Sphingomonas*, *Candidatus Udaeobacter* and *Bacillus*. The month of sampling affected the relative abundance of fecal samples, especially relating to *Moraxella*, *Clostridium*, *Butyrivibrio*, *Aestuariispira*, and *Prevotella* (p-value $\leq 5 \times 10^{-11}$). G and NG soil differed for *Pontibacter*, *Pseudoduganella*, *Luteimonas,* and *Planomicrobium*, while the month effect caused a statistically significant difference in relative abundances of *Candidatus Ovatusbacter*, *Silvanigrella,* and *Micromonospora* ($p \leq 0.001$). These preliminary results suggested that animals affect soil biodiversity, and it is fundamental to quantify and characterise grazing sheep's impact on the environment.

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O384

Metabolomics identified new biomarkers to help describing feed efficiency in Italian Large White pigs

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Improving feed efficiency in the swine industry is a key strategy for enhancing the sustainability and cost-effectiveness of this sector. In fact, as the pig grows toward market weight, it becomes less efficient at converting feed into body weight gain, as more energy is required from the organism to manage the basic biological functions. This is particularly relevant for the Italian heavy pig sector that is characterised by high slaughter weights and significant feed costs. This study applies untargeted metabolomics to explore feed efficiency in Italian heavy pigs. Here, feed conversion ratio (FCR) and average daily gain (ADG), the two primary metrics of efficiency, were evaluated using plasma metabolomics. Over 700 Italian large White pigs, with random residuals retrieved from genetic indexes routinely collected for selection purposes was used to generate two distinct pools (one for FCR and one for ADG). Each pool contained animals with extreme and divergent values for the trait of interest. Using untargeted metabolomic profiling of plasma, 722 metabolites were identified, with 662 of endogenous origin. Machine learning approaches (i.e. Boruta algorithm) identified discriminant metabolites within groups associated with FCR and ADG. For FCR, 11 key metabolites spanning lipid, amino acid, and peptide pathways were highlighted. For ADG, eight metabolites were identified, with notable changes in lipids and amino acids. Only one unknown metabolite was detected for both groups. The heritability of the selected metabolites ranged from 0.08 to 0.33. Functional analysis revealed metabolic pathways linked to energy production, lipid metabolism, and amino acid turnover as key drivers of feed efficiency. Principal component and random forest analyses further underscored the predictive power of these metabolites for differentiating high and low efficiency groups. The findings provide a foundation for integrating metabolomic biomarkers into precision breeding and selection strategies, ultimately enhancing the efficiency and sustainability of Italian heavy pig production.

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O494

Development of a genetic index for heat stress tolerance in dairy sheep

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Heat stress (HS) is becoming a concern for livestock systems of temperate countries due to the effects of climate change. The mediterranean area, where a large number of dairy sheep is farmed, represent a particularly fragile hotspot for the negative effects of climate change. The improvement of HS tolerance can be therefore of great interest for the dairy sheep industry. However, selection for HS tolerance is constrained by the lack of consensus for a suitable phenotype that could be recorded at population scale. Moreover, an antagonistic genetic correlation between HS tolerance and production level has been reported in cattle and sheep. In the present study, an index of HS tolerance for dairy sheep is developed using principal component analysis (PCA). Data were 2,695 TD records for milk yield, fat and protein percentage, SCS and milk coagulation properties (MCP) of 555 Sarda breed ewes. Animals were genotyped with the 50K Illumina ovine beadchip. After edit, 45,813 SNPs were available. Data were analyzed with a mixed linear model that included the fixed effects of days in milk class, parity, production month and THI max class (6 classes), and the random effects of farm and animal. The random effect of the animal was fitted with an Unstructured (UN) 6x6 covariance structure (corresponding to the 6 levels of THI_class). PCA was then carried out on the estimated UN covariance structure. For all the considered traits, first two principal components represented the general level (PC1) and the slope of production across different THI levels (PC2), respectively. Scores of the two principal component for all the animals were calculated and then variance components were estimated using a GBLUP. The estimated heritability values ranged from 0.08 to 0.47 and from 0.12 ± 0.24 for PC1 and PC2, respectively. The two variables were analyzed also in a bivariate model and the estimated genetic correlation was not significantly different from zero. The PC2, even characterised by a low heritability, could represent a valid tool to improve heat resistance in sheep. The absence of a significant genetic correlation with the level of production may allow for selecting for HS tolerance without modifying production level.

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O270

Individual variability of tolerance to heat stress of Sarda ewes raised in the Mediterranean region

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This study investigates the variability of tolerance to heat stress of Sarda ewes. The data consisted of 179,943 test-day (TD) milk yield records pertaining to 16,249 lactations of 4,940 ewes, collected from 2000 to 2022 in an experimental farm located in the South of Sardinia. All animals were genotyped by the OvineSNP50 Beadchip. The ewes were managed according to the typical Sardinian system, with adult ewes lambing mainly between November and December and primiparous ewes between January and March. Milking was carried out daily from weaning until early July. During the summer, dry ewes had free access to water and shaded areas. The climatic parameter considered was the temperature-humidity index (THI), derived from the temperature and humidity recorded at meteorological stations located within or near the farm. The effects of heat stress on production were estimated at different levels: (i) short-term, where TD yields were analyzed with a random-regression animal model that included the linear systematic and random (genetic and non-genetic) effects of the average THI in the 4 days preceding the TD (THI_{4d}); (ii) medium-term, where lactation yields were analyzed with a random-regression animal model that included the linear systematic and random (genetic and non-genetic) effects of the average THI in the 50 days preceding the lambing (THI_{50d}). In both models, random regression coefficients represented genetic and non-genetic individual heat stress tolerance. Genetic effects and corresponding variances were estimated using a genomic relationship matrix. At the short-term, a systematic effect on daily

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milk yield of -0.074 liters per unit of $THI_{4d} > 22$ was identified. At the medium-term, a systematic effect on lactation milk yield of -3.1 liters per unit of $THI_{50d} > 17$ was identified. Genetic standard deviations of heat tolerance were 0.022 liter/THI_{4d} and 2.3 liter/THI_{50d} and the proportion between genetic and total individual variance were 0.52 and 0.62 for short-term and medium-term respectively. The genetic correlation between milk yield and heat tolerance was strongly negative (–0.72) for the short-term and negative but modest (–0.02) for the medium-term. Our results demonstrate that despite the seasonal organisation of the Sardinian farming system, the adverse effects of heat stress are not negligible. However, the observed individual variability suggests the possibility of genetically improving the tolerance of Sarda ewes to heat stress.

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O498

Heat stress modifies the miRNA cargoes carried by small extracellular vesicles isolated from Holstein and Brown Swiss milk

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Heat stress (HS) is one of the main causes of economic losses in dairy industries and affects welfare and performance. The molecular mechanisms enabling the metabolic adaptation of dairy cows to hyperthermia are not fully elucidated. Whether bovine breeds differentially cope with HS in sustaining productive performance remains elusive. The aims of this study were (a) to profile the microRNA cargoes of milk-derived small extracellular vesicles (sEVs) isolated from 2 dairy breeds, Holstein and Brown Swiss; (b) to compare the different effects of HS on the miRNome delivered by milk-derived sEV of the 2 breeds in thermal comfort conditions (TC) and HS. The study was carried out on 36 dairy cows, 18 per breed. Each animal experienced TC and HS. The HS was induced by switching off the cooling system during a natural heat wave for 4 days. Animal stress was confirmed by measuring temperature-humidity index, respiratory frequency, and rectal temperature twice daily at 4 am and 3 pm. The HS affected the 2 breeds differently. The rectal temperature increased with HS in both breeds. Milk yield recording and sampling were performed at d 1 (at 4 am) and d 4 (at 5 pm). Productive parameters were different: milk yield, Fat-Corrected Milk, Energy-Corrected Milk, protein and casein content, and renneting parameters were decreased in Holstein cows but remained unaffected in Brown Swiss cows. sEV were isolated by ultracentrifugation and size exclusion chromatography and were characterised by Western blot, Nanoparticle tracking analysis, and transmission electron microscopy. No differences were identified in size or concentration; the shape and integrity analysis showed the presence of whole, undamaged small sEVs, and markers were identified. Comparing the milk-sEV profiles in Brown Swiss in TC and HS, 132 miRNAs were significantly altered, among which 80 increased and 52 decreased after HS. The milk-sEV profiles in Holstein in TC and HS identified 32 altered miRNAs, among which 25 increased and 7 decreased after HS. Comparing milk-sEVs after HS, 23 miRNAs were dysregulated in both breeds. PCA analysis demonstrated that the separation between TC and HS is clear (effect of HS); and Holstein is characterised by a higher distribution than Brown Swiss (effect of breeds). Gene Ontology analysis showed that dysregulated miRNAs may modulate the cell cycle, insulin signaling pathway, reproduction, fatty acid synthesis, and pain and stress. In conclusion, milk-sEV miRNA profiles are influenced by HS, and Holstein and Brown Swiss responded differently.

O546

Assessing the impact of climate factors on the growth performance of Podolica bulls during Pre-Performance Phases

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The Podolica breed (PO) is renowned for its adaptability to the challenging mountainous environments of Basilicata, Calabria, Puglia, Campania, and Molise. Known for thriving on marginal resources like shrubs and undergrowth, this breed has transitioned from draft purposes to being valued for its high-quality meat and milk, used in traditional products. While the PO is typically well-suited to extreme conditions, recent studies have highlighted significant variability in individual responses,

even among animals adapted to specific environments. Moreover, early developmental phases, particularly those preceding entry into performance evaluation centers, are often overlooked in breeding programs despite their potential impact on reproductive success. In this study, data from 868 male calves selected for performance testing at the Laurenzana performance station (Basilicata) and born between 2021 and 2023 were analyzed. To assess the impact of environmental factors on growth performances, 21 environmental variables were initially evaluated using Mixed Models, incorporating the fixed effect of age in days and the random effect of herd-year. Using AIC parameter relative humidity (RH) emerged as the most important variable influencing both entry weight and average daily gain from birth to performance (ADG). Although Temperature-humidity index (THI) was not the most significant variable it was evaluated as it is the most used in these kinds of studies. Results revealed that high RH negatively impacted growth performance, with ADG decreasing from 0.92 to 0.70 kg/day (~24% reduction) and entry weight dropping from approximately 300 kg to 240 kg (~20% reduction), likely due to increased thermoregulatory stress in cooler climates. Conversely, moderate THI levels improved growth performance by supporting metabolic efficiency within tolerable thermal limits. Seasonal trends indicated that most births occurred in winter (January-March), while weight assessments began in autumn, coinciding with cold, humid conditions that hinder early growth. These findings emphasise the critical influence of RH on livestock performance while demonstrating the complementary insights gained from analyzing THI. Aligning management practices with environmental conditions—such as adjusting breeding schedules to warmer periods, improving housing ventilation, and monitoring THI to maintain thermal comfort—can mitigate stress and optimise productivity. This study underscores the importance of environmental adaptation in sustaining the productivity and welfare of PO cattle in marginal areas.

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O040

A meta-analysis on the relationship between agro-industrial byproducts supplementation and milk production traits in dairy sheep

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Agro-industrial byproducts (BP) generated from the processing vegetables and fruits could be interesting for animal nutrition because they still contain important amounts of nutrients and are also source of bioactive compounds as polyphenols. The effects of supplementation in dairy sheep of agro-industrial BP containing polyphenols on milk production and milk composition has been investigated. A systematic search of scientific papers was performed using PubMed, Scopus and WOS. Only studies with sheep were considered. The keywords used to search in all databases were sheep, milk, by-products, tomato, grape, citrus, olive, pomegranate, coffee and cocoa. The data were extracted from 26 papers that included byproducts from citrus, cocoa, coffee, grape, olive and tomato processing. The effects of BP were analyzed using random effects statistical models. The standardised mean difference between BP and control treatments was examined. A metaregression was carried out to test the effect of the byproducts dose (g polyphenols/kg diet), whereas differences among byproduct sources were investigated using a second metanalysis. The results showed that the addition of byproducts in the diet of sheep did not modify the milk yield and the main milk components (fat, protein, lactose and urea). The effects of each byproduct on milk production and composition have been also determined. The source of polyphenol influenced significantly fat and protein percentage and the SCC. Specifically, adding cocoa-BP to sheep diet increased milk fat content, while grape BP had no effect both on fat and protein percentage. Tomato-BP significantly lowered fat and protein contents. Coffee-BP increased milk fat and protein content, while pomegranate increased SCC. Overall, all BP evidenced

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positive effects on the fatty acid composition of milk fat as showed by the reduction of saturated fatty acid (FA) and the enhance of unsaturated FA, specifically on vaccenic and rumenic acids, that have healthy promoting properties. In conclusion, the meta-analysis performed to the published studies regarding the inclusion of agro-industrial by-products in the diet of dairy ewes showed no effect on milk yield and exerted moderate effect on the main components and improve the nutritional quality of milk fat.
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O210
Destoned olive cake as an alternative feed and ruminal fermentation modifier for dairy ewes

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In recent years, there has been an increased interest in the use of agro-industrial by-products produced from vegetable processing because of their nutritional characteristics for use in dairy ruminant diets. In the Mediterranean region, olive by-products, such as olive cake rich in polyphenolic compounds, represent a valuable low-cost feed supplement. Therefore, this study aimed to investigate the dietary effects of incorporating destoned olive cake (OC) in the concentrate diet on milk yield, milk composition, and ruminal fermentation parameters of Valle del Belice ewes. The chemical composition of the olive cake was as follows: DM (93.9%), CP (12%), EE (22.1%), aNDFom (64.3%), ADFom (48.75%), and ADL (22%). A total of 124 ewes that were homogeneous for parity (< 3rd lambing), days in milk (60 DIM), and milk yield (1.48 ± 0.4 kg/d) were randomly divided into control (CTR) and experimental (EXP) groups, each consisting of 62 ewes. The experimental trial lasted for 14 weeks, including 14 days of dietary adaptation. Individual milk yield was recorded every 2 weeks during the trial. Bulk and individual milk was analyzed for chemical composition. The experimental ewes were fed fresh grass from pasture and 0.5 kg/d/ewe a commercial concentrate supplemented with 17% OC (To ensure concentrate iso-energetic) on fresh matter, whereas the control ewes were fed the same diet without OC supplementation. At the end of the experiment, a total of 10 ewes were slaughtered (5 CTR and 5 EXP ewes), and rumen fluid was sampled. The data were analyzed with the PROC GLM mixed model (SAS, 9.2, 2010). The results showed that ewes consumed the entire amount of concentrate (OC supplemented) without any leftovers. The daily milk yield did not change among the groups. However, the milk composition of the EXP group resulted in higher somatic cell counts ($p < 0.05$) and lower milk urea levels ($p = 0.07$) than those of the control group. Ruminal fermentation parameters, such as ruminal ammonia, volatile fatty acid concentration, and protozoa (*Entodininae*, *Holotricha*) counts, were also not affected by diet. The present study confirms that destoned OC is a valuable feed supplement for ewe nutrition. Further research incorporating destoned OC at different levels into the concentrate diet of dairy ewes could be evaluated.
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O116
Effects of feeding prickly pear by-product silage on dairy ewes

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Prickly pear fruit processing generates large quantities of fibrous by-products (peels, pulp and seeds) with high content of water-soluble carbohydrates and bioactive compounds such as polyphenols. This study investigated the use of prickly pear by-products silage to replace other conventional ingredients for Valle del Belice sheep, assessing its effects on body weight, milk yield and composition, nutrient utilisation and degradability, as well as its impact on rumen microbiota. A total of 12 ewes were randomly divided into three experimental groups homogeneous for days in lactation, parity, live weight and milk yield. Each group was fed for 14 days (9 days for diet adaptation +5 days to record milk yield, composition and nutrients intake), with one of the three experimental diets based on a Latin square design. The diets, characterised by same crude protein and NDF contents, were: (1) control (CTR): 900 g/d per head of commercial concentrate +3,000 g/d per head of sulla hay; (2) peels (PPP): 1,500 g/d per head of PPP silage (prickly pear peels +12% wheat bran) + 500 g/d per head of commercial concentrate +2,700 g/d per head of sulla hay; (3) peels, pulp, seeds (PPS): 1,000 g/d per head of PPS silage (prickly pear peels, pulp, seeds +12% wheat bran) + 500 g/d per head of

commercial concentrate +2,300 g/d per head of sulla hay. 16S rRNA amplicon sequencing was used to investigate the rumen bacterial communities in the rumen liquid of the three experimental groups. The data were analysed with GLM and mixed models (SAS 9.2, 2010). Daily milk yield resulted to be lower in ewes fed the PPP and PPS diets than in those fed the CTR diet, probably due to lower intake of dry matter, crude protein and net energy for lactation. However, no differences were found for fat and protein corrected milk among the diets. Milk from ewes on the PPP diet had higher protein and casein levels ($p \leq 0.05$) than CTR diet. Additionally, milk urea concentration in PPP-fed ewes was 15% lower compared to those on the CTR diet. Comparisons of PPP vs. PPS and PPP vs. CTR revealed significant differences in species composition of rumen microbiota, while PPS and CTR showed no significant differences. The dry matter degradability was lower ($p < 0.01$) in the PPS diet (736 g/kg) than in PPP (858 g/kg) and CTR (841 g/kg) diets. These findings suggest that PPP silage can be partially included in dairy ewe diets to lower feeding costs and enhance milk nitrogen efficiency.

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O365

Sesame seed meal as alternative protein source in growing lambs

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The feedstuff market faces significant challenges due to price volatility and frequent availability issues. These challenges are particularly pronounced for high-protein feed sources like soybean meal, and other feed ingredients. This situation has led to a growing demand for local alternative protein sources that are affordable and readily available, without compromising animal health or productivity, while reducing the environmental impact of the feedstuff supply chain. To this purpose, this study aimed to assess the effects of including sesame (*Sesamum indicum* L.) seed meal, grown in Mediterranean area, in lamb diet on animal performances and meat quality. Sixteen male weaned lambs (40 days old; 15.3 ± 0.51 kg live weight) were selected from the native farm and randomly allocated to two experimental groups. The 1st group was fed a conventional diet (CON), including maize (43%), alfalfa hay (32%), soybean meal (20%), molasses (3%), and vitamin-mineral premix (2%). The 2nd group received the same diet but 10% of sesame seed meal (SES) replaced soybean meal. After 50d of the trial all lambs were slaughtered in a local slaughterhouse, then carcasses were weighed and stored at 4 °C for 24h. Subsequently, *Longissimus dorsi* muscle samples were collected for further analyses. The replacement of 10% of soybean meal with SES meal did not affect voluntary feed intakes (821, and 778 g day for CON and SES, respectively). Ruminal pH and carcass traits revealed no significant differences between the two experimental groups. Similarly, also meat quality attributes concerning the moisture retention (water holding capacity, drip loss, and cooking loss) and color parameters revealed no significative differences between the two diets. Therefore, SES meal is a valuable protein source that can replace traditional feed in growing lamb diets without causing any detrimental effects on their performance. This suggests that substituting 10% of soybean meal with SES results in comparable nutritional values between the two diets. Further analyses are in progress to investigate meat quality as well as quantify possible decrease in feed cost.

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O364

Characterization of lamb rumen and cecal microbiota in response to hazelnut skins and linseed dietary supplementation using 16S rRNA sequencing

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Lamb meat is highly valued in Italy, with consumers displaying a strong preference for local products. The Italian lamb production

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sector is characterised by diverse organisational systems and varied production strategies, often linked to dietary supplementation. Numerous studies have highlighted that dietary linseed can affect the levels of polyunsaturated fatty acids in meat, which enhance the meat's nutritional profile and provide health benefits for consumers. Moreover, polyphenol supplementation has been shown to influence the rumen microbiota, which plays a critical role in fatty acid biosynthesis. The aim of this study was to characterise the lamb gastrointestinal microbiota using hazelnut skin, linseed, or a combination of both. Forty 2-month-old lambs were assigned to 4 dietary treatments and fed for 60 d with: a conventional cereal-based diet (a), the same diet with 8% of extruded linseed (b), or 15% of hazelnut skin (c), or 4% of linseed plus 7.5% of hazelnut skin (d) as partial replacement of maize. Individual ruminal and cecal contents were collected within 10 min of slaughter and immediately frozen with dry ice and then stored at – 80 °C. A total of 40 samples were analyzed (10 per group). The microbiota was assessed through 16S rRNA gene sequencing, targeting the V3-V4 hypervariable regions (metabarcoding), and bioinformatic analysis using the QIIME2 pipeline and custom R scripts. Results revealed differences in alpha diversity in the cecal microbiota, with a trend toward greater diversity in rumen bacterial communities of animals supplemented with hazelnut skin. However, no alpha-diversity differences were observed for the rumen microbiota. In terms of beta diversity, differences in microbial community structure were observed across all four diets. Differential abundance analysis identified key cellulolytic bacterial genera in the rumen content, which were abundant in all diets with hazelnut skins and/or linseed addition compared to the conventional diet, including *Ruminococcus*, *Prevotella* and *Blautia*. Similar results were also observed for the cecal content. These bacteria play a crucial role in the metabolism of carbohydrates and proteins in the rumen, potentially affecting digestive efficiency and animal performance. This study highlights the potential of dietary hazelnut skin, either with or without linseed, to modulate the microbiota, laying the groundwork for further investigations.
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O203

Effects of guanidinoacetic acid levels on growth performance and feed efficiency of finishing lambs

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Guanidinoacetic acid (GAA) is a natural precursor of creatine that plays a crucial role in energy metabolism and muscle development. Recent studies highlight its positive effects on the performance of beef cattle and sheep-fed moderate-energy diets supplemented with variable GAA dosages ranging from 500 to 1000 mg/kg DM. However, further research is needed to determine optimal dosages for lambs under feedlot conditions. This study evaluated the effects of increasing levels of GAA supplementation on the growth performance of Suffolk × Dorset crossbred finishing lambs fed high-energy diets based on wheat straw, corn, and soybean meal. Forty lambs (20 males and 20 females) with an initial body weight (IBW) of 21.9 ± 4.4 kg were randomly assigned to four dietary treatments containing different levels of GAA (0, 1000, 1500, and 2000 mg/kg DM). The study was conducted using a completely randomised design with initial body weight as a covariate. The fixed effects of GAA dose (linear and quadratic) and sex were evaluated. Growth performance parameters were monitored over a 56-day feeding period. Results showed that initial body weight was similar across GAA levels (21.47 to 22.29 kg; $p = 0.976$). No differences were observed in final body weight (FBW: 40.82–42.39 kg; $p = 0.580$) , average daily gain (ADG: 0.35–0.36 kg/d; $p = 0.864$), and daily feed intake (DFI: 1.16–1.25 kg/d; $p = 0.431$). However, a significant quadratic effect was observed for feed conversion ratio (FCR; $p = 0.021$), and feed efficiency (FE) tended to show a quadratic response ($p = 0.052$), with optimal values observed at 0 and 2000 mg/kg GAA treatments. Mathematical modeling indicated that the optimal GAA doses were 1000.45 and 976.59 mg/kg to minimise FCR and maximise FE, respectively. Males outperformance females in FBW (+3.18 kg; $p = 0.001$), ADG (+0.5 kg/d; $p = 0.001$), FCR (–0.38 kg; $p = 0.007$), and FE (+0.04 kg; $p = 0.006$). These findings suggest that while GAA supplementation did not affect growth rate, it had significant effects on feed utilisation parameters in finishing lambs.

O463

Mitigation of the milk fat depression in ewes, caused by ryegrass herbage rich in water-soluble carbohydrate, by sodium bicarbonate: effects on milk fatty acid profile

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Herbage rich in water soluble carbohydrates (WSC) can cause subacute ruminal acidosis in ewes, resulting in a decrease in milk fat content. With the aim to mitigate these effects, the use of sodium bicarbonate as rumen buffer was tested in sheep fed fresh ryegrass (*Lolium multiflorum* Lam., var. westervoldicum) rich in WSC (mean of 27.7% DM). Ten lactating Sarda ewes were divided into two homogeneous groups: control (CNT) and bicarbonate (BIC). The animals were fed indoors with automatic Biocontrol AS (Rakkestad, Norway) feeders, which recorded continuously the individual intake of grass of the ewes. The ewes received ad libitum freshly cut grass from 1:00 PM to 7:00 AM of the subsequent day. In addition, they received in two meals a total of 400 g/d of soybean meal and 550 g/d of whole corn grains (as fed values). The BIC group also received a supplement of 25 g/day/ewe of sodium bicarbonate just before the ryegrass supply. Daily intake of grass, particularly high in the first hours after its supply, was higher in BIC than in CNT (1488 and 1340 g DM/d, respectively; $p = 0.03$). Milk yield was not affected by the treatment. Milk fat concentration of afternoon (BIC 6.52%, CNT 6.01%; $p < 0.001$) and morning (BIC 5.39%, CNT 5.06%; $p = 0.03$) milking was higher in BIC than CNT. Moreover, the milk fat yield of afternoon milking was higher in BIC than CNT (42.2 and 38.7 g/d, respectively; $p = 0.03$) but there were no differences in morning milking. The milk fatty acids (FAs) profile (g/100 g of total FAME) was affected by the treatment. The concentrations of C17:0 ($p = 0.04$), C17:1 cis-9 ($p = 0.07$), their sum ($p = 0.04$), anteiso C17:0 ($p = 0.003$) and anteiso FAs group ($p = 0.007$), indicators of high-concentrate diets and/or biomarkers of ruminal acidosis, were higher in CNT than in BIC. The C18:2 n-6 ($p = 0.02$), the C18:3 n-3 ($p < 0.001$), as well as the levels of polyunsaturated FA (PUFA; $p = 0.002$), n-3 PUFA ($p < 0.001$) and n-6 PUFA ($p = 0.01$), were higher in CNT than in BIC probably due to a higher rate of rumen biohydrogenation process, in the latter. Indeed, the de novo fatty acids group (g/100 g of milk), derived from ruminal acetate and butyrate, tended to be higher in BIC than in CNT ($p = 0.086$), confirming improved ruminal conditions in the BIC group. In conclusion, the milk FA profile suggested that sodium bicarbonate improved ruminal environment, ruminal pH, microbial activity and consequently ruminal fermentations, thus reducing milk fat depression from WSC overload.

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O414

Summer dairy cows: THI-Heat_Load model for development of an alert-based cooling protocol

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Heat stress impairs milk yield, reproduction and welfare of dairy cows. The study was aimed to develop a real-time tool that collects temperature and humidity of barn, computes the Temperature Humidity Index (THI), and models the heat load of the cows (THI-HL) based on THI and cooling treatments (on or off) at a point in time. If THI is below 77, the THI-HL falls and the decline is faster if cooling is activated. In contrast, when THI is above 77, the THI-HL falls or rises depending on whether cooling is turned on or off. When THI-HL rises above 10, a value indicative of a body temperature of 39.5 °C, the tool alarms for emergency cooling treatment. In the three-day trial, twenty-four lactating Holstein cows were divided into control (CG) and experimental (EG) groups homogeneous for parity, DIM and milk yield. The CG was cooled (sprinklers + fans) three times in the holding area of the milking parlour for approximately 30' before milking, while at the feed bunk, fans worked all day and sprinklers approximately from 8:00 AM until midnight. The EG received the same cooling treatments in the holding area of the milking parlour, while at the feed bunk fans were working all day, whereas sprinklers were activated only approximately 45' after milking. The two groups were housed in separate sections of the same barn, divided by a gate. Two wireless datalogger were installed in the CG and EG pens, and temperature and humidity data were gained every 15 minutes to calculate THI-HL. When the THI-HL exceed 10, the EG cows were locked and cooled for 1 hour. All procedures were computed by Python. Vaginal temperature (VT) was monitored in continuous every 15' by mini temperature dataloggers. Variation of VT were evaluated by GLM, the differences were analysed by the Tukey test and the significances were set for $p < 0.05$. The average THI was 74.2 ± 6.5 and 74.3 ± 6.1 in the pens hosting CG and EG, respectively. The THI-HL

exceeded the critical threshold approximately at 8:00 PM in the first two days, and twice, at mid-day and at 6:00 PM, in the third day. The VT was lower ($p = 0.023$) in EG (39.0 ± 0.3) compared with CG (39.1 ± 0.2) cows. These preliminary results showed the tool's ability to evaluate cows' thermal balance in real time and identify critical conditions requiring immediate cooling treatments. Compared to cows with extended free access to cooling facilities, the tool reduced more effectively the heat loaded by less-cooled cows, resulting also in significant water savings.

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O458

Combination of PLF and omics to characterize heat stress response in Marchigiana breed

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Precision livestock farming (PLF) allows continuous real-time monitoring of animals behavior, health and welfare using IoT sensors. The aim of the study was to assess cattle animal welfare in heat stress conditions to identify biomarkers associated to resilient animals useful for breeding. Marchigiana (MAR, 30), Holstein (HOL, 20) and Limousine (LIM, 30) cattle were enrolled, measuring key physiological parameters through wearable IoT sensors. Blood samples for hematological and transcriptomics (total RNA and circulating small-RNAs) were collected at the heat peak in condition of suspected heat-stress (HS – end of July) and in thermoneutrality (TN – end of November). The collection day was chosen based on the Temperature Humidity Index (THI), calculated using meteorological stations data. The hourly standard deviation of the resultant vector of accelerometric data collected by the IoT sensor were related to the THI value over the 15 days before the blood sampling. The results shown a general increase in activity during the HS but a better correlation (–0.97 in TN vs -0.73 in HS, Spearman correlation) between the two parameters in TN because in HS the animals rest for a longer time, compared with TN. Complete blood count results showed higher total white blood cells (WBCs) in HS with respect to TN in both MAR and HOL, presumably due to a seasonal immune response, while WBCs slightly decreased in LIM. Neutrophiles increases for HOL in HS probably as an inflammatory response led to stress whereas eosinophilia observed in MAR and LIM in HS may be due to summer parasites. Red blood cells and hemoglobin substantially increased in MAR in HS and tend to increase in HOL, probably as an adaptation to improve oxygen transport under heat stress. Hematocrit increased in both MAR and HOL breed in HS, while it slightly decreased in LIM. For transcriptomics, differentially expressed genes (DEGs) and miRNAs between HS and TN conditions were identified. A protein-protein interaction network for DEGs and DE miRNA targets was built and submitted for a gene ontology enrichment analysis. Enriched biological processes for DEGs were related to response to stress, inflammatory and immune response; while for DE miRNA targets, transcriptional modulations, DNA and RNA packaging were found. Overall data confirm the animal response to thermal stress allowing a better evaluation of cattle's physiological responses and their ability to adapt and cope with heat stress.

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O071

Comparative evaluation of subclinical ketosis risk in Lombardy using two methods based on DHI data

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In recent decades, the milk fat-to-protein ratio (F-to-P), exceeding the breed-specific threshold (1.4 for Italian Holstein Friesian)

within the first 60 days in milk (DIM), has been used to assess the risk of subclinical ketosis (SCK). The development of Fourier-transform infrared (FTIR) mid-infrared (MIR) spectrometry has enabled the precise quantification of milk acetone (mACE) and beta-hydroxybutyrate (mBHB), offering more specific and reliable markers for SCK. The aim of this study was to compare the assessment of SCK risk at the herd level in Lombardy using either the F-to-P ratio or a combined approach involving mACE and mBHB, considering herd size and milk yield performance. A total of 3,799,352 Dairy Herd Improvement records from three years were analyzed. Herds were classified by size (<100, 101–200, 201–300, >301 lactating cows), milk yield during the first 60 DIM (≤28, >28–33, >33–38, >38 kg/cow), and annual SCK prevalence (<10%, 10–20%, 20–30%, >30%). Using a two-step approach in R (v3.6.3), mACE and mBHB thresholds associated with milk yield reductions were identified in 241,399 cows within 15 DIM, then compared to the F-to-P ratio (≥1.4) to assess SCK risk distribution. Chi-square tests and mosaic plots visualised herd-level SCK prevalence by herd size and milk yield classes. Our findings reveal that mACE and mBHB exhibit distinct postpartum patterns: mACE peaks during the first week, while mBHB peaks in the second week. This complementary behavior enhances the accuracy of estimating SCK prevalence at the herd level when both markers are used. Within our database, herds with the lowest average daily milk yield during the first 60 DIM showed a higher-than-expected prevalence of SCK, whereas more productive herds exhibited a lower-than-expected prevalence. Smaller farms, often less productive, likely contribute to this trend due to uniform diets that overlook variations in yield, parity, lactation stage, or dry phase. This approach may result in overfeeding during the late lactation period, predisposing cows to enter the dry phase in an over-conditioned state and increasing their susceptibility to SCK and clinical ketosis in the subsequent lactation.

This study was part of a collaborative agreement between Associazione Italiana Allevatori, AIA, and Centro di ricerca Zootecnia e Acquacoltura del Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria (CREA).

O064

Meta-analytical study on feeding behavior and daily time budget management of dairy cows in free-stall housing using ChatGPT

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This study explores the integration of artificial intelligence (AI) in dairy cow behavioural research, evaluating the potential of ChatGPT-4 to extract and categorise time-activity data from scientific literature. Traditional behavioural analyses often require extensive manual effort and are prone to observer bias. By applying ChatGPT-4 to a dataset of 55 studies focusing on eating, ruminating, and lying behaviours, the research assesses AI's capacity to streamline these processes. Significant differences were observed between AI and human analyses for eating and ruminating times, while lying time estimates showed strong alignment. AI exhibited a moderate-to-high level of reliability in data extraction and a reasonable consistency in behavioural categorisation, with variability influenced by input data formats and contextual nuances. AI demonstrated reliability in processing inferred and ambiguous data, despite challenges in interpreting explicit information. The findings highlight the potential of combining AI with human expertise to enhance the efficiency and precision of behavioural meta-analyses. Advancing AI algorithms and promoting standardised reporting in the literature will be crucial to optimising AI applications in this field. This work underlines the transformative role of AI in animal science and its implications for improving welfare and management practices.

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O092

Antimicrobial use in buffalo farm and dynamic of correlation with animal welfare and biosecurity evaluated by ClassyFarm system

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Antimicrobial usage (AMU) is a very critical driver for the One Health approach. Future scenario models aimed at reducing multi-drug-resistant bacteria represent a challenge for AMU control systems. Animal Welfare (AW) and Biosecurity are also essential tools to achieve this goal. ClassyFarm (CF) is an integrated system for categorising farms according to the risk assessment methodology. CF collects and processes data related to AMU, AW and biosecurity. It can be applied to several livestock species, including water buffalo. In CF, AMU is estimated using the Defined Daily Dose Animal for Italy (DDDAit). The AW assessment for water buffalo includes 62 non-animal-based measures (N-ABMs) and 17 animal-based measures (ABMs). The N-ABMs were divided into 'management' (32 items) and 'housing' (30 items). Biosecurity is assessed using 15 items. AW and Biosecurity scores are expressed as percentages.
DDDAit, AW and Biosecurity were assessed on 382 buffalo farms with an average size of 374 heads. The mean overall DDDAit was 0.40 ± 0.04, with 43% of the farms scoring DDDAit = 0, while the mean of the only farms that have DDDAit ≠0 was 0.7 ± 0.07. The AW score was $76.9 \pm 9.8\%$ and the Biosecurity score was $68.9 \pm 15.3\%$. Statistical analysis was performed using Spearman's rank correlation in GraphPad Prism 8.0.1. Biosecurity and AW were positively correlated ($\rho = 0.42$; $p < 0.001$). A positive correlation was also observed between Biosecurity and both Management ($\rho = 0.61$; $p < 0.001$) and Housing scores ($\rho = 0.36$; $p < 0.001$). No significant correlation was found between AMU, Biosecurity and AW, likely due to the low levels of AMU found. Contrary to the linear narrative often suggested between AMU, Biosecurity and AW, the dynamic system we described is far more complex and articulated. Knowing the level of biosecurity and AW, their relationship and critical points, in livestock farms, is a tool for planning strategic priorities in human resources and investments. It also helps raise farmers' awareness and animal health. However, while these tools are necessary but not sufficient for a significant reduction in AMU; other socioeconomic drivers must be considered to achieve this goal. Achieving good levels of biosecurity and AW reduces exposure to pathogens and improves host natural immunity, respectively. In our view, it is essential to integrate the mitigation actions with decision-making processes for appropriate diagnostic and treatment protocols involving breeders, vets and farm employees.

O521

Risk factors for *Toxoplasma gondii* seropositivity and DNA detection in raw milk on dairy buffalo farms in Southern Italy

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The aim of the present study was to assess the prevalence of *T. gondii* on buffalo farms in the Campania Region through serological screening using blood samples collected during state prophylaxis and analysed with an indirect ELISA kit (ID Screen®, Indirect Toxoplasmosis Multi-Species, Innovative Diagnostics, Garbles, France). The number of adult buffaloes serologically tested was $n = 13{,}649$ on 184 farms between Caserta and Salerno. Of the tested animals, $n = 2{,}693$ tested positive for *T.gondii* with a seroprevalence of 19.7% and of the 184 farms, 179 tested positive with a seroprevalence of 97.3%. In addition, a specially designed questionnaire was administered for risk assessment, which took into account several factors such as number of animals, presence of cats and rodent control measures) and possible clinical symptoms in adult buffaloes. Of the farms that tested positive for *T. gondii*, 97% were found to have cats on the farm and 85% did not apply rodent control measures. A further phase of the study involved milk sampling for parasite DNA on the farms that tested serologically positive. The

milk was taken on the farms that volunteered to participate in the research project, the number of milk samples taken was $n = 43$ from two buffalo farms, one located in the province of Salerno and the other in the province of Caserta. Total DNA was extracted using a QIAamp DNA Mini kit, according to the manufacturer's instructions. The ddPCR reaction was performed in a QX200 system to amplify the 529 bp repeat element. Of the samples analysed, 63% (27/43) tested positive for T.gondii, Toxoplasmosis is a parasitosis that is considered the fourth leading cause of illness within the foodborne diseases and the third leading cause DAILY (Disability-Adjusted Life Year) in Europe. Buffalo milk, although consumed less fresh than cow's milk, could become a source of infection for humans. So far, *T. gondii* DNA and *anti-T. gondii* antibodies have already been detected in the milk of some types of animals, such as goat, sheep, cow, and buffalo. It is therefore believed that transmission of can occur through the milk of all animals if consumed raw. The results obtained from our study highligh that there are risk factors in buffalo farms that do not perform proper monitoring by applying appropriate biosecurity plans and that vertical transmission of the parasite through milk can become a form of foodborne transmission if consumed raw.

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O159

Blood metabolite profile in Italian Mediterranean buffalo: effect of parity, lactation stage, and calving season

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Monitoring blood metabolites in lactating buffaloes is essential for detecting metabolic imbalances, thereby improving health and productivity. This study evaluated the metabolic profile of 855 clinically healthy Italian Mediterranean buffaloes from 19 farms in Italy, sampled between December 2021 and August 2023. Blood samples were analyzed to assess key metabolic profiles, including protein, energy, and hepatic markers. The protein profile included albumin (ALB), creatinine (CRE) and their ratio (A/G), globulin (GLO), total protein (TP), and urea. The energy profile comprised cholesterol (COL), glucose (GLU), triglycerides (TRI), non-esterified fatty acids (NEFA), alkaline phosphatase (ALP), alanine aminotransferase (ALT), and aspartate aminotransferase (AST). The hepatic profile included creatine kinase (CK), lactate dehydrogenase (LDH), gamma-glutamyl transferase (GGT), total bilirubin (TBIL), and high- and low-density lipoproteins (HDL and LDL). A generalised linear mixed model was used to assess blood metabolite variations by parity, lactation stage, and calving season. First-lactation buffaloes exhibited significantly higher protein (ALB, GLO, A/G, TP), energy (COL, ALP, ALT, AST), and hepatic markers (LDH, HDL) compared to multiparous buffaloes, reflecting increased energy demands and body reserve mobilisation. Moreover, lactation stage influenced metabolite levels, with significantly higher protein (ALB, GLO, CRE, TP, urea), energy (COL, TRI, NEFA, ALT, AST), and hepatic markers (GGT, TBIL, LDL) observed during early lactation (5–75 days in milk), coinciding with peak milk production and greater metabolic stress. While calving season showed limited effects, CRE levels were higher in autumn and winter compared to summer and spring. These findings highlight the metabolic challenges faced by buffaloes during early lactation and underscore the importance of tailored herd management strategies to enhance productivity and animal welfare.

O027

Evaluation of the impact of the dietary inclusion of salty and sugary former food products on the liver and the plasma profile of pigs through OMICS approaches

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Former food products (FFPs) are industrial bakery and confectionery food leftovers no longer intended for humans due to commercial or manufacturing defects, although being still suitable as feed. FFPs have more energy, fats and sugars than cereals and have been studied in monogastric. Here, we replaced 30% cereals with FFPs in growing to finishing pig diets and evaluated growth performance, meat quality, and impact on metabolism. Thirty-six Swiss Large White male pigs were assigned to three groups (12 animals/group): (i) CTR, control diet (cereals); (ii) SA, 30% cereals replaced with salty FFPs; iii) SU, 30% cereals replaced with sugary FFP (SU). The trial lasted around 110 d from growing phase (22.4 ± 1.7 kg, 60 ± 3.8 d) to slaughter (110 ± 3 kg, 159 ± 7.42 d), with growth performance monitored throughout. Liver tissue and blood samples were collected at the end and nano-LC HR-MS-MS was applied on liver proteome (6 samples/group, 18

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samples in total) and plasma peptidome (1 sample/animal, 36 samples in total) to assess the potential metabolic impact of FFPs. Growth performance was analysed with MIXED procedure by SAS software. Meat quality, fatty acid profile and sensory data (1 sample/animal, 36 samples in total) were analysed by ANOVA after checking normality and homoscedasticity using R software. For omics data, MaxQuant software was used to process raw data and Perseus software for data interpretation. Results were statistically significant when $p < 0.05$. FFP-fed pigs showed no difference in growth performance compared to CTR group. The SA and SU diets slightly modulated muscle and backfat fatty acid profile as well as meat sensory traits, but meat quality was not altered. The SA and SU diets significantly upregulated (log2 FC >0.57) and down-regulated (log2 FC < –0.57) a limited number of proteins (125 out of 2881) mostly related to lipid metabolism and cell structure with no metabolic interaction among them, indicating a limited impact of FFPs diets on liver function. Plasma peptidomes were not significantly different among groups, although three peptides related to vascular homeostasis and anti-hypertension were exclusively identified in the SA group, suggesting a potential self-regulating response to face the higher Na content of the SA diet. Overall, FFPs inclusion was safe for pig welfare, with no unintended effect on metabolism, thus supporting the idea of a wider application of FFPs as feed ingredients to reduce feed-food competition and food waste.

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O462

Multi-omics characterisation of pig colostrum and association of its bioactive compounds and gut microbiota with the survival of piglets

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Colostrum is recognised as the 'golden elixir of health' due to its optimal chemical, immunological and nutraceutical properties for newborns, but little is known about its nature in the pig. This study aims to provide a multi-omics characterisation of pig colostrum from different parities to identify the most relevant bioactive compounds associated with piglet survival and faecal microbiota, with the ultimate goal of providing information for the production of artificial colostrum. 20 colostrum samples from gilts (6), second (7) and adult (6) sows, individual piglet performance data were collected at farrowing (d0), day 7 (d7) and day 24 (d24). Colostrum was analysed for metabolomic and lipidomic profile. Piglet faeces (11 litters) were collected and analysed for microbiota (V3-V4, 16S rRNA gene). Litters were categorised into survival classes at d0-d7 and d0-d24. Data were analysed using orthogonal and sparse partial least squares discriminant analysis and Data Integration Analysis for Biomarker discovery (DIABLO). 950 metabolites (108 chemically confirmed) and 72 fatty acids (FAs) were characterised in colostrum. Parity class was the main driver for piglet survivability ($p < 0.001$; highest at 2° parity), metabolomics ($R^2 = 0.97$; $Q^2 = 0.52$; >200 discriminated metabolites) and lipidomics profile (22 discriminated FAs) and piglet faecal microbiota (beta diversity $p < 0.05$ at d7 and d24). Colostrum composition allowed clustering for piglet mortality from d0-d7 ($Q^2 > 0.50$). Mortality class was discriminated by 177 metabolites and 5 FAs; alpha-tocopherol acetate, monolinolein, cholest-4,6-Dien-3-One (3-hydroxyhexadecanoyl) glycine (Variable importance in projection [VIP] scores: 3.50, 3.24, 3.39, 2.10) and conjugated linoleic acid (CLA) 8t10c (VIP score 1) discriminated for higher survivability. The DIABLO model reveals that the variables most associated with a lower morality were a higher faecal abundance of Lachnospiraceae FCS020, *Holdemania*, *Roseburia*, and a higher colostrum abundance of CLA 8t10c, and the oleic acid isomers *t5* C18:1 and metabolites related to benzoic acid. In conclusion, this study suggests the importance of parity order in determining colostrum composition and highlights the presence of several bioactive compounds in colostrum that may be associated with improved piglet survival and maturation of the gut microbiota. The results of the present study may also be of interest for the development of future artificial colostrum supplements.

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O558

EU Circles Project: multi-omics analysis reveals distinct microbial networks linked to a blend of chestnut and quebracho extract supplementation in weaned pigs under different Farming conditions

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Weaning is a critical transition in pig production, often accompanied by significant physiological and microbial changes that can compromise growth and health. Tannins, are known for their antimicrobial, antioxidant, and anti-inflammatory properties, making them potential candidates for improving gut health. This study investigated the effects of a blend of tannins derived from chestnut and quebracho (Silvafeed Nutri P/ENC for Swine, Silvateam, Italy) on growth performance, health status, and fecal metagenomic and metabolomic profiles of weaned pigs raised under two different farming conditions. A total of 160 pigs (24 ± 2 days old; T0) were allocated into two weaning units categorised as high (H) or low (L) performance, based on body weight and litter origin. Within each unit, pigs were further divided into two dietary groups: a Control group (CON; 40 pigs) fed a standard weaning diet, and a Treated group (TRT; 40 pigs) fed the standard diet supplemented with 2 g/kg of a tannin blend. Body weights were recorded at days 35 (T1), 49 (T2), and 76 (T3) post-weaning, while fecal samples were collected at the same time points for metagenomic profiling and metabolomic analysis (Metabolon, Inc. platform). Growth performance data were analyzed to using a linear model including group (TRT vs. CON) and farming condition (H vs. L), while metabolomic data were evaluated using Sparse Partial Least Squares Discriminant Analysis (sPLS-DA), microbial species were identified using a multi-kingdom approach. Results indicated that at T2, the diarrhea index was significantly lower in the TRT group compared to the CON group in farm L ($p = 0.02$). Microbial alpha diversity at T2 and T3 was reduced in farm L ($p < 0.05$) and in the TRT group compared to CON ($p < 0.01$). Beta diversity for microbial species and functions was influenced by the interaction between farming conditions and diet at all time points ($p < 0.05$). At T2, sPLS-DA identified Urolithin B and Isourolithin A, metabolites associated with tannin metabolism, as being linked to the TRT group in farm H. Weighted gene correlation network analysis revealed species and functions, such as *Corynebacterium* and *Pseudomonas* subspecies with tannase activity, correlated ($r > 0.5$) with Urolithin metabolites. In conclusion, dietary tannin blend supplementation reduced diarrhea under suboptimal sanitary conditions by fostering a microbial network capable of metabolising tannins and producing metabolites that support gut health.
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O246

Metataxonomic characterization of fecal microbiota of heavy pigs fed with different levels of *Arthrospira platensis*

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Protein is recognised as the most crucial nutrient in pigs' diets, both from an economical and environmental perspective. This encourages the exploration of alternative protein sources for the nutrition of growing pigs. Among these, *Arthrospira platensis* has been recognised as a promising candidate due to its high protein content and ability to be cultivated in a way that does not involve agricultural land use. The present study aimed to analyze the fecal microbiota of 60 pigs, which were randomly allocated to one of four isoenergetic, isoproteic, and iso-amino acid dietary treatments. The control diet comprised cereals and soybean meal, while the experimental diets replaced 33%, 66%, and 100% of soybean meal with *A. platensis* nucleus (CTR, SP33, SP66 and SP100, respectively). Fecal samples were collected at two different times: T1, during the mid-late feeding period (168 d of age, 117.1 ± 5.9 kg as mean weight), and T2, before slaughter (230 d of age, 174.5 ± 7.3 kg as mean weight). DNA was extracted using the commercial kit QIAamp PowerFecal Pro DNA (Qiagen, Hilden, Germany), while libraries were produced using QIAseq 16S Region Panels kit for the amplification of V3-V4 regions. The samples were sequenced using Illumina MiSeq platform

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(Illumina, San Diego, USA). Bioinformatics analyses showed differences in the relative abundances of phyla and genera both for sampling time and diet effect. In particular, at phylum level Bacillota was the most present (80% at T1 and 85.4% at T2), followed by Bacteroidota (11.4% at T1 and 10.6% at T2) and Spirochaetota (5.3% at T1 and 2.1% at T2). For dietary treatments, Bacillota phylum exhibited a decline from 84.8% in the CTR group to 81.1% in the SP100 group, while Bacteroidota increased from 9% in the CTR group to 12.4% in SP100, and Spirochaetota rose from 3.3% in the CTR group to 4% in SP100. The α-diversity analysis showed no differences among diets within sampling times, while the results of the perMANOVA on β-diversity showed differences between sampling time and diet effect on the structure and composition of the microbiota. In particular, the CTR group differed from the SP66 and SP100 groups at both sampling times. In conclusion, soybean substitutions with *A. platensis* led to differences in the pigs' fecal microbiota.

Further studies will assess whether the different dietary treatments may be associated with favorable or unfavorable changes in the microbial ecosystem and the host physiology.

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O519

Effect of dietary microbial muramidase supplementation on weaned pigs' performance, health status and intestinal microbiota

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Microbial muramidase (MM) has recently been introduced as a feed additive for swine. However, limited research has investigated its effects, particularly on intestinal microbiota. This study evaluated the effects of dietary MM on growth performance, health status, and fecal microbiota profiles of weaned pigs. A total of 96 weaned pigs (28 ± 0.2 days old) were assigned to two groups based on body weight (BW): (1) Control (CTR), fed a standard diet; and (2) Treated (TRT), fed a standard diet supplemented with MM at 65,000 LSU(F) (muramidase activity units)/kg feed. Diets were provided from day (d) 0 (weaning) to d44. Body weight, and feed intake (FI) were measured weakly, while antibiotic use and diarrhea occurrence were measured thought the trial. Fecal samples were collected on d9 and d28 for microbial profile, NH_3 and calprotectin quantification. Supplementing MM increased FI ($p = 0.05$) and ADG ($p = 0.02$), leading to a BW gain of up to 2.1 kg ($p = 0.05$) by d44 in the TRT group. From d7 to d14, MM reduced the feed conversion ratio ($p = 0.05$), while antibiotic treatments decreased ($p < 0.01$) until d28 in the TRT group. MM supplementation had no significant effect on fecal scores, calprotectin levels (an inflammatory marker), or mortality. Microbiota analysis revealed that at d9, alpha diversity (Chao1 index) was lower in the TRT group compared to CTR ($p = 0.02$), but no differences were observed at d28 or for other alpha indices. Beta diversity differed significantly at both d9 ($R^2 = 0.05$, $p = 0.002$) and d28 ($R^2 = 0.05$, $p = 0.05$), indicating distinct microbial community structures between groups. LEfSe analysis identified reductions in specific bacterial taxa, including *Turicibacter* and *Colidextribacter*, in the TRT group. Despite these changes, MM did not alter fecal concentrations of volatile fatty acids or NH_3, indicating that microbial fermentative activity remained intact. This study demonstrates the effectiveness of microbial muramidase at the recommended dosage in improving growth performance and reducing the need for antibiotic treatments in weaned pigs. The reduction in APP treatments suggests that MM was able to improve piglets health, those improving nutrient utilisation. Moreover, MM influenced fecal microbial composition by reducing rare species and altering beta diversity, while preserving fermentative activity.

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O381

Effect of complete maize replacement by sorghum on health, welfare, performance and faecal microbiota of post-weaning piglets

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Sorghum, due to its nutritional value and lower environmental impact, especially in terms of water use, could be a viable substitute for maize in pig diets. This study evaluated the effects of replacing maize with sorghum or extruded sorghum on the performance, intestinal health, and behavior of post-weaning piglets. From weaning (d0) to 4 weeks, 522 pigs were assigned to one of 3 diets: Control (CTR), sorghum

(SO), and extruded sorghum (EX_SO). Pigs were fed 2-phase diets: phase I (d0-d6) and phase II (d7-d28). CTR included 7% and 10% maize in phases I and II and it was fully replaced with sorghum and extruded sorghum in SO and EX_SO groups. Diets were isoenergetic and isoaminoacidic. At d0, d7, and d28, pigs were weighed, and ear and tail lesions were scored. Feed intake (FI) and behavior measurements (BMs) were recorded on d7, d14, and d28. Faecal samples collected on d7 and d28 were analyzed for microbiota (16S rRNA gene V3-V4), metabolomics (NMR), NH_3, and dry matter content. Data on body weight, average daily gain, NH_3 and dry matter faecal content were analysed using a 'linear mixed effects' model including the diet, litter and sex as factors; pigs were considered as the experimental unit. FI, feed conversion ratio, lesions index and BMs were analysed using a linear model including the diet as factor; pen was used as experimental unit. Metabolomics and microbiota data were analyzed using a multivariant approach. Results showed no significant differences in growth performance, FI or BMs among groups. At d7, NH_3 and faecal dry matter were not affected by the diet. At d7, *Oscillospira* ($p < 0.01$), was more abundant in the CTR than EX_SO, 2-Oxogutarate, Acetoin, 2-Methyl 3-Ketovalerate, 3-Methyl 2-Oxovalerate was more abundant in the EX_SO than CTR. At d28, faecal dry matter content tended to be higher in the SO compared to the CTR group ($p = 0.08$) and the diet affected the beta-diversity ($p = 0.05$); *Olsenella* was more abundant in the CTR than in the SO ($p < 0.01$). Additionally, *Olsenella* ($p = 0.01$) and *Ligilactobacillus* ($p = 0.01$) were more abundant, while *Anaerovoracaceae_Family XIII UCG-001* ($p = 0.01$) was less abundant in the CTR group than in the EX_SO; *Shuttleworthia* ($p = 0.02$) and *Syntrophococcus* ($p < 0.01$) were more abundant in the SO than in the EX_SO, Butyrate, Propionate and Valerate were more abundant in the EX_SO than CTR. In conclusion, sorghum can replace maize in weaned pig diets, maintaining growth performance, behavioral welfare, and intestinal health.

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O483

Postbiotic supplementation in gestating and lactating sows and its effects on piglets health and performances

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Hyper-prolific sows, genetically selected to increase piglets per farrowing, face physiological and management issues that affect both their welfare and piglet growth. Postbiotics, consisting of inanimate microbial cells and/or their components, are a promising solution to improve the piglet's gut health and overall performance. This study investigates the impact of a postbiotic (heat-inactivated *Lactobacillus fermentum* and *Lactobacillus delbrueckii*) (GutServTM Biotix, dsm-firmenich, Switzerland) administered to sows in late gestation and lactation at different doses, on the growth and health of their piglets. The last three weeks of gestation, 200 sows were divided into two groups: (i) a control group (G0; 40 sows) fed a standard gestation diet, (ii) a postbiotic group (G20; 160 sows) fed the same gestation diet with the on top addition of 20 g/t of postbiotic. After farrowing, the G20 group was further divided into 4 subgroups receiving different doses of postbiotic during lactation: 0 (G20-L0), 10 (G20-L10), 20 (G20-L20), or 100 (G20-L100) g/t. Productive performances of the sows, as well as piglets body weight (BW) and mortality, were recorded at days 0, 6, 14, and 28. Colostrum samples were collected to analyse the immunological profile. Data were analysed using a linear model, including diet, batch, and parity as factors, and litter size and initial BW as covariates for piglet growth performance. Results showed that piglets born from G20 sows had a higher BW at birth than those from G0 ($p < 0.05$). Piglet BW and ADG from day 0 to day 6 were significantly greater for piglets born to sows supplemented with postbiotics during gestation ($p < 0.001$). Mortality rates during the suckling period were lower in groups receiving the postbiotic, particularly in G20-L0 and G20-L100, compared to G0-L0 ($p < 0.01$). Sow's feed intake and weight loss was not influenced by the lactation diet. Colostrum immunological profile was not affected by the experimental diets. In conclusion, supplementing the gestation diet with postbiotics proved to be an effective strategy for enhancing piglet survival and growth performance during the suckling period. However, it did not appear to influence the immunological profile of colostrum. The observed benefits are likely attributable to other, as yet unidentified, mechanisms that warrant further investigation to better understand their effects and optimise the application of postbiotics in the management of hyper-prolific sows.

O102

Modeling dairy production under microclimatic variability in Automatic milking systems using TSMixer

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Heat stress induced by climate change presents a significant challenge to the dairy industry. This phenomenon arises from a combination of environmental factors, including temperature, relative humidity, and airflow. Heat stress adversely impacts animal well being, milk production, and quality, leading to substantial economic consequences for the global dairy sector. Among its most recognised effects on dairy cows is a reduction in milk production and dry matter intake, which directly translates into financial losses for dairy farmers. Recent advancements in Artificial Intelligence (AI) have introduced innovative tools capable of leveraging historical data to forecast future conditions, providing valuable insights for addressing heat stress challenges. This study focuses on evaluating and predicting the impact of microclimatic conditions on milk production within an Automatic Milking System (AMS). From 2016 to 2023, milk production and quality data, as milk protein, fat, yield, and temperature, were collected from AMSs on a commercial dairy farm, while meteorological information was sourced from the nearest ARPA (Agenzia Regionale per la Protezione Ambientale) station. Temperature and relative humidity data were combined to calculate the Temperature Humidity Index (THI). Statistical analysis were performed using Python software. Our analysis identified a significant negative Pearson correlation (P value < 0.01) between milk protein content and THI, with a peak correlation of -0.66 observed at a lag of five days. This underscores the strong relationship between milk quality and environmental conditions, particularly temperature and humidity. Understanding both current and historical microclimatic conditions is thus crucial for predicting future trends in milk related data. To this end, we employed a state of the art Neural Network model known as TSMixer to forecast protein content, fat content, milk production, and milk temperature over a two month horizon. The model was trained and validated using data from 2016 to 2021 and tested with data from 2022 and 2023. TSMixer leverages input data from the preceding three months to generate predictions. Test results demonstrated the model ability to accurately predict linear trends, achieving R^2 values of 0.83, 0.81, and 0.80 for protein, fat, and milk production, respectively.

O406

Effect of Automatic Milking System on udder health in Holstein breed

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As the global and national prevalence of Automated Milking System (AMS) installations continues to rise, evaluating their impact on key productive and health parameters has become essential. The objective of this study is to evaluate the impact of Automated Milking Systems (AMS) on somatic cell count, expressed as Linear Score, to determine their effect on udder health and milk quality in dairy cows. The analysis draws on a seven-year (2018–2023) longitudinal DHI records, encompassing milk yield, fat and protein percentages, SCC, Linear Score (LS), and milking system type (AMS or conventional parlor). It focuses on farms in the Lombardia region that transitioned to AMS at least 18 months before the last test day in 2023. To ensure the cows were exclusively milked with AMS following its implementation, only farms with an average herd size up to 70 were included. Baseline LS representing conventional milking were derived from the three test days immediately preceding the first recording under AMS. To assess the short-, medium-, and long-term effects of AMS adoption on LS, data were analyzed across three intervals post-AMS implementation: the 4th to 6th test days, the 7th to 9th test days, and the 13th to 15th test days. The study included 17 farms and data from 1,340 individual cows. A linear mixed-effects model incorporating AMS versus conventional milking, parity, test month, and DIM class as fixed effects, while Farm ID and Cow ID were treated as random effects was used. Marginal means for LS associated with AMS were calculated and their differences assessed by p-values. The results indicate that AMS has a slight negative impact on LS, with a significant effect observed in the short time after its introduction (LS AMS= 3.46, LS conventional milking = 3.36; $p = 0.0213$). However, this effect diminishes approximately six months post-adoption, as the differences in LS between AMS and conventional milking are no longer statistically significant during the medium-term period (LS AMS = 3.30, LS conventional milking = 3.38; $p = 0.222$). One year after AMS implementation, a reduction in LS compared to traditional milking systems was observed (LS AMS= 3.21, LS conventional milking = 3.37 $p = 0.013$), suggesting a potential improvement in udder health over time. These findings are based on limited data from a single breed, emphasising the need for larger, multi-breed studies to confirm and generalise the results.

O492

Substitution rate between partial mixed ration and robotic supplemental concentrate in high-producing dairy cows

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Optimising feeding strategies in automatic milking systems (AMS) is key to improving dairy cow performance and farm profitability. Adjusting AMS concentrate levels influences feeding behavior, intake patterns, and milk production, enhancing feed efficiency and yield while supporting animal health. This study investigated the effects of different robot concentrate levels on feed consumption, milk production, and composition in dairy cows ($n = 24$). Two levels of AMS concentrate, 1.5 kg as fed (AF) and 4.5 kg AF per day, were compared in a double crossover design (4 × 7-day periods). The basal TMR was the same throughout the trial and based on dry hays and non-fermented components. The milk yield was recorded daily while quality was tested weekly ($n = 288$). Data were analyzed using a Mixed Model procedure (JMP Pro 18). Results showed that increasing the robot concentrate intake significantly increased the intake of robot feed (1.40 vs. 3.82 kg DM, $p < 0.01$) while reducing TMR intake (28.99 vs. 27.00 kg DM, $p < 0.01$), with a substitution rate of 0.82 kg DM TMR per kg DM AMS concentrate. Despite these changes, the total DMI showed only a marginal increase (30.39 vs. 30.82 kg, $p = 0.05$). Milk yield was significantly higher with the 4.5 kg level (45.64 vs. 47.01 kg/day, $p < 0.01$), while milk protein content also showed a slight increase (3.20% vs. 3.23%, $p < 0.01$). Other milk composition parameters, including fat (3.46% vs. 3.34%, $p = 0.10$), lactose (4.91% vs. 4.92%, $p = 0.60$), and urea content (19.11 mg/dL vs. 18.93 mg/dL, $p = 0.80$), were not significantly affected. These findings suggest that increasing AMS concentrate intake alters feed substitution dynamics and enhances milk yield and protein content, though with limited effects on other milk components. The results can be useful in enhancing rationing program equations, enabling more precise calculation of substitution rates (robot concentrate–TMR) on dairy farms using AMS.
Research supported by PRIN: PROGETTI DI RICERCA DI RILEVANTE INTERESSE NAZIONALE – BANDO 2022 PROT. 2022 PBS32M. Development of nutritional mechanistic models to predict the effects of asynchronous feed supply and intake in dairy ruminants'.

O389

New insights of climate effects on dairy production

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Climate change affects the entire world in many ways, and the livestock sector is not immune to it. On dairy cows the effects are on milk quality and quantity, together with udder health. It's essential to enhance our understanding of how climate conditions affect milk production, helping breeders and stakeholders mitigate the impact of global warming on animal production. Longitudinal data (milk yield, fat, protein and somatic cell count—SCC, as a proxy for udder health status) from functional control (FC) from 'Pezzata Rossa Italiana' cattle breed were combined with historical climatic data, in particular with the Temperature Humidity Index (THI). The data are from 1994 to 2020 from Friuli-Venezia Giulia region. For each phenotype, for each FC in each farm the percentage variation in comparison with the annual average value was calculated. Data with low representativeness (eg less than 5 animals per FC, less than 24 FC per farm on the entire dataset) were removed. More than 85,000 entries were analyzed. Firstly, we evaluate how many heat days (max daily THI passed 79) are necessary to impact milk production. For all the phenotypes even just one heat day before the FC, also in 90 days windows, significantly reduces the performance. The greatest effect was identified in protein and fat, where a reduction of ~3% in percentage variation was observed within a 15 days window. Secondly, the THI level effect was evaluated. For milk yield, when the max daily THI passed 50 at around 60 or 90 days before the FC, the production started to drop significantly. For the quality, the change is in the short term (around 15 and 30 days before the FC): for fat the value is 50, while for protein and SCC is 60. Finally, a Machine Learning algorithm was developed to predict the impact on animal production and welfare of climatic variables, in short (days) and long (decades) periods. The selected algorithm was a Gradient Boosting Machine (GBM) optimised for the dataset. The model outperformed naïve benchmark models. For milk yield the max daily THI at long period (60 days) was most significant then short period. To conclude, even at low levels of THI (50), for limited time (1 day) and distant periods (60 and 90 days before the FC) we can have impacts on milk quantity and quality. For this it is fundamental to have accurate prediction algorithms that help the livestock sector to react on time and prevent the global warming impact of animal production.

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O200

Feedback thinking in the dairy supply chain: system dynamics modelling of cheese factory

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Systems perspectives and system dynamics have been widely used in decision-making for agricultural problems. However, their use in the dairy sector remains limited. This work demonstrates the use of systems approaches in modelling cheese making factory management. The scope was to create a dynamic digitalised instrument of decision support for the whole Grana Padano PDO chain, helping their evolution and resilience. A stock and flow diagram was created to simulate the flux of milk, cheese and other milk derived products (i.e. whey, cream) in a Grana Padano PDO cheese plant by applying a dynamic model with a time-horizon of 5 years. The model has been applied to a commercial dairy plant that has an income of milk of approximately 3200 ton/month. The model predicted a production of 6500 forms/month and a repartition of forms per aging stock of 34% 9-month, 39% till 20-month, 27% over 20-month aging. The evaluation of fitting between observed and predicted values was computed with Lin's concordance correlation coefficient (CCC), being equal to 0.83 in the case of milk transformed and 0.75 for cheese forms produced. Some of the potential predictions of the cheese factory model are presented. The model can be used for policy formulation and testing simulating productive scenario analysis of stock and flow dynamics aimed to improve the resilience of the Grana Padano PDO chain in the medium-long term or similar supply chains and consortia. It might also be used to consider the current situation of production limits, raw material prices, marketing costs, sales performances, dairy plant investments and a systemic vision of the dairy chain system and behavior.

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O345

Quality of milk and cheese from cows grazing on mountain pasture from italian Alps

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Over the past few years, there has been growing interest in milk and dairy products from pasture grazed livestock, driven by their perceived health benefits for consumers. Notably, grazing in mountainous areas such as Alpine pastures, has been shown to significantly enhance the quality of milk and cheese by improving fat composition and fatty acid profiles. The wide variety of botanical species in these pastures are rich in bioactive compounds such as terpenes, fatty acids, carotenoids and antioxidants, which contribute to the natural color, flavors, aromas, and nutritional qualities of dairy products. Compositional and nutritional properties of milk and cheese produced from a herd of Bruna cows reared in the alpine area of Lombardy were analyzed. Bulk milk and corresponding cheese samples ($N = 30$) were collected during 2024, both in the mountain pasture (late June to August) and at valley farm, where cows were fed conserved forages (mid-May, October and November). During the summer, whole pasture samples were collected in correspondence to milk sampling in order to analyse the terpenes profile. Raw milk analysis revealed an average protein content of 3.2%, lactose at 4.8% and 3,7% fat. Milk from the pasture-based system showed a healthier fatty acids profile compared to the farm-based system, with lower levels of saturated fatty acids (56 vs 64 g/100g), higher content of monounsaturated fatty acids (35 vs 27 g/100g) and a more favorable n-6/n-3 ratio (3.9 vs 5.06) due to the higher presence of n-3, derived from fresh grass. Alpine cheese exhibited 29% protein,

32% fat and 4.2% ash (1–2% NaCl). Alpine cheese showed higher amounts of beneficial fatty acids compared to farm-produced cheese (1.19 vs 0.5 g/100g c9t11-CLA, 35 vs 28 g/100g MUFA, 3.78 vs 5.13 n-6/n-3 ratio).The volatile compounds profile of the cheese highlighted a notable aromatic richness due to the presence of volatile compounds such as ketones (e.g. 2-heptanone) and esters (e.g. ethyl acetate), which contribute to its distinctive aroma. Cheese samples were further analyzed for their colour and rheological properties. Valley-cheese showed a higher L* value (81.04) compared to pasture cheese (76.06). No significant differences were identified in rheological properties (hardness, chewiness, adhesiveness, cohesiveness, gumminess). This study confirms that grazing on alpine pastures enhances the chemical composition and physical properties of milk and cheese, supporting strategies to promote alpine dairy products and increase their economic value in the mountain area.

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O543

Effect of grazing season on quality traits of cow ricotta cheese

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In recent years, pasture-based dairy products have become increasingly popular among consumers, driven by growing interest in healthy, natural and local production, as well as animal welfare.

Several studies demonstrated the impact of grazed herbage in feeding systems on the fatty acid (FA) and organoleptic profile of several dairy products, with increasing yellowness related to β-carotene content, that provides also beneficial effects. However, relatively little attention has been paid to these aspects for ricotta cheese. Typically produced in several parts of Italy, especially in the south, ricotta cheese is an artisanal dairy production, obtained from heat-acid aggregation of whey proteins. To this purpose the present study aimed to assess the effect of pasture availability on the FA, color properties, and β-carotene content of artisanal cow ricotta cheese. The trial was split into two different seasons: when animals were fed indoors in the barn during the dry season (DS), and when animals grazed on green forage during pasture season (PS). For each period, ricotta cheese samples were collected in triplicate from 5 different farms and analyzed for color, β-carotene and FA contents. Data were statistically analyzed using mixed model. Pasture season ricotta cheese showed a significantly higher ($p < 0.001$) b* index compared to DS samples (9.64 vs 6.52), indicating that PS samples were more yellow in color than DS, which directly correlates with β-carotene results, significantly higher ($p < 0.001$) in PS compared to DS Ricotta (5.03 vs 0.66). The total PUFA and MUFA contents were significantly higher ($p < 0.001$) in PS than in DS samples (5.02 vs 4.13 g/100g FA and 30.32 vs 29.54 g/100g FA). Whereas SFA content was significantly lower in PS than DS sample. Among the PUFA, α-linolenic acid and the sum of n-3 FA resulted in a significantly ($p < 0.001$) higher concentration in PS sample compared to DS (0.87 vs 0.47 g/100g FA and 1.25 vs 0.74 g/100g FA). The ratio n-6/n-3 FA was significantly lower in PS compared with the DS (3.10 vs 4.74). Consequently, also the atherogenicity and thrombogenicity indexes were significantly lower ($p < 0.001$) in PS compared to DS ricotta cheese. These findings highlight the beneficial effects associated with pasture feeding, leading to a product beneficial for human consumption. Moreover, both carotenoids and favorable FA could serve as potential biomarkers for grazing production systems for ricotta cheese.

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O399

Exploring natural additives for cheese preservation

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Fresh cheese is a common highly perishable dairy product due to its composition and storage conditions, which promote fungi and bacteria's growth on its surface, leading to quality reduction, economic losses and health risks. To address these challenges, the dairy industry is focusing on extending shelf-life and enhancing quality and safety, with natural additives that are in high demand by consumers. The project aimed to develop essential oil (EO)/plant extract (PE) with antimicrobial and antifungal activity for application as a protective coating on fresh cheeses. Given the instability and sensitivity of EO and PE to light, moisture and air, nano-emulsions represent a promising protective solution to stabilise these compounds, preserve their activity during storage and improve solubility in fresh cheese formulations. Commercial sunflower oil was selected as the reference oil due to its cost-effectiveness, widespread availability, neutral taste and odor. Their stability was evaluated up to 72 h after preparation at room temperature. Four types of coating based on monoglycerides, sodium alginate, isolated soya proteins and cheese-making whey proteins were tested with 3 oil concentrations. The coating solutions were characterised in terms of total soluble solids content, viscosity, surface tension, and pH. Mini-cheeses were produced using 2 L of milk and coated via 3 different methods: electrostatic spray, immersion (for 60 seconds) and brushing. Coating thickness and microstructure were measured in the 24 h post-application, and texture, color, weight loss, and hardness were assessed over 30 days of ripening. Preliminary results indicated the stability of emulsions across the different coating types. Only monoglycerides-based emulsions containing 0.5% and 1% oil, and pH 7.5 and 7.49, respectively, displayed constant viscosity. Sodium alginate-based emulsions containing 1%, 3% and 5% oil, with 1% alginate and 5% whey protein were evaluated as stable, exhibiting a pseudoplastic viscosity trend and neutral pH. Soy protein-based emulsions behaved like Newtonian liquids with constant viscosity, stable at oil concentrations of 1%, 3% and 5%, and pH 7.5–7.7. Similarly, whey protein-based emulsions 1%, 3% and 5% oil were stable, with constant viscosity and Newtonian liquids behavior. In conclusion, a total of eleven stable emulsions were identified as viable for use in cheese coating, offering promising potential to enhance cheese preservation during ripening.

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O446

Impact of different enzymatic coagulants and doses on the cheese-making ability of milk from different dairy species

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This research tested the impact of different enzymatic coagulants (commercial rennets) with 3 increasing doses on the cheese-making ability of milk from dairy cows and dromedary camels. A total of 20 individual milk samples were collected from 10 Simmental dairy cows reared in the 'Lucio Toniolo' experimental farm of the University of Padova in Italy and 10 dromedary camels from a commercial farm in the province of Biskra in Algeria. For each sample, 6 rennets with 3 increasing doses (25.5, 51, and 102 IMCU/L of milk) were used (360 experimental units in total). Rennets were distinguished by origin and enzymatic makeup as follows: one microbial rennet consisting of pure mucorpepsin; 2 natural rennets derived from calf stomach, with chymosin to pepsin ratios of 80:20 and 95:5, respectively; and 3 microbial rennets from genetically modified microorganisms, including one pure bovine chymosin and 2 pure camel chymosins from different commercial lines. All experimental units were subjected to the same cheese-making protocol (9-MilCA protocol) and milk coagulation analysis (lactodynamography). In bovine milk, both dose and rennet type showed important effects. Higher doses improved fresh cheese yield by enhancing nutrients retention. Differences among rennet types were less pronounced and mainly limited to better cheese-making ability of other rennets compared to pure mucorpepsin. More evident differences were observed in coagulation properties. Doubling the dose halved the coagulation time, increased curd-firming and syneresis rates, and improved the maximum curd firmness, also reached in less time. Concerning rennet type, coagulation properties improved progressively from mucorpepsin to natural rennets (with 95% bovine chymosin rennet surpassing the 80% one) and further to microbial chymosins, with camel chymosin outperforming the bovine one. In dromedary milk, increasing rennet doses similarly enhanced cheese-making outcomes. In this milk, mucorpepsin performed comparably to both natural and microbial rennets. The 80% chymosin natural rennet outperformed the 95% one. Among microbial chymosins, camel chymosin again demonstrated superior results compared to bovine one. In conclusion, in both species, camel chymosin showed better results than the other rennets on milk cheese-making ability whereas, for other rennets, in bovine milk, the increase of bovine chymosin and, in dromedary milk, the increase of bovine pepsin and the use of mucorpepsin were more suitable.

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Extra 1000 NB as 95:5 natural rennet, CHY-MAX® Extra as pure microbial bovine chymosin rennet, CHY-MAX® M 1000 and CHY-MAX® Supreme 1000 as pure microbial camel chymosin rennets).

O091

Dietary supplementation with by-products from olive oil mill wastewater processing in dairy cows affected the aromatic fingerprint in cheeses

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This study aimed to evaluate the effects of incorporating varying levels of polyphenols, extracted from olive mill wastewater using spray drying technology, into the diets of lactating dairy cows on the volatile organic compounds of Caciotta cheese. Thirty dairy cows were divided into 3 groups balanced for milk yield, parity and day in milk and fed with three dietary treatments, containing increasing levels of polyphenols: 0% (C), 0.1 % (T 0.1), and 0.2% (T 0.2) of dry matter. A total of 3 cheesemaking sessions were carried out using bulk milk for each group, collected for three consecutive weeks. 27 samples of Caciotta cheese, at 21 days of ripening, were collected in triplicate from 3 different cheesemaking and used for volatile compound contents analysis. Extraction of volatile compounds from cheese samples was performed by solid phase microextraction (SPME) coupled with mass spectrometry. In addition, the odour fingerprint analysis on cheese was evaluated using an electronic nose (PEN3). Dietary integration of biophenols, recovered by spray-dried from olive mill wastewater, significantly influenced the aromatic profile of Caciotta cheese after 21 days of ripening. A total of 45 compounds, including ketones, alcohols, aldehydes, esters, lactones, hydrocarbons, and fatty acids, were identified. Cheese samples from the T 0.2 group showed a significant increase in the proportions of alcohols and esters ($p < 0.0001$) compared to the control (C) and T0.1 samples. Conversely, cheese samples from the T0.1 group exhibited significantly higher aldehydes ($p < 0.01$) content and showed reduced levels of lactones ($p < 0.01$) compared to the C and T 0.2 samples. The most abundant compounds identified in all experimental cheeses were carboxylic acids, indicating that lipolysis was the primary process during cheese ripening. Furthermore, results from the electronic nose demonstrated that the LD algorithm effectively distinguished three distinct groups based on the different dietary treatments, suggesting that the dietary inclusion of polyphenols influences the differing odour patterns in the cheese. In conclusion, the production of new feed for animal nutrition, enriched with natural polyphenols from olive oil mill wastewater can be an effective strategy for modifying the volatile characteristics of dairy products, valorising the by-products from the oil industry, reducing environmental impact and promoting waste reuse in line with the principles of a circular economy.

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O474

Exploration of hyperspectral imaging for the discrimination of Parmigiano Reggiano and Grana Padano PDO cheeses and ripening time

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Parmigiano Reggiano (PR) and Grana Padano (GP), both of which are Protected Designation of Origin (PDO), are significant contributors to the global dairy market. The high demand and premium price for PR and GP have led to widespread fraudulent practices. The economic value for PR and GP is also strongly linked to the maturation process of the base cheese. To combat fraud and ensure the accurate determination of both the PDO status and age of PR and GP, advanced analytical techniques such as Hyperspectral Imaging (HSI) is increasingly being employed. The use of HSI and other similar non-destructive methods is becoming an essential tool in the fight against cheese fraud, helping to protect the economic value of genuine PR and GP products and ensuring that consumers receive the quality they expect. Therefore, the aims of this study were to: (i) discriminate between PR and GP, and (ii) classify them according to their ripening time. HSI images in the Visible and Near Infrared spectral range were recorded on 18 cheese samples slices, sourced from six dairy plants, equally divided between GP and PR consortia. Three different aging periods for each cheese type were considered: 12, 20, and ≥34 months of aging for GP, 12, 24, and ≥34 months of aging for PR. The image processing and chemometric were carried out as follow: (1) selection of the Region of Interest (ROI) represented by the entire slice; (2) calculation of the average spectrum for each entire ROI; (3) calculation of the average

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spectra of three specific selected areas on each ROI; (4) Partial Least Squares Discriminant Analyses (PLSDA) using separately the data from step 2 and 3; (5) Visual and statistic validation of the models, predicting all the spectra available for each ROI. In this exploratory study, HSI has proven its potential and efficiency for applications on heterogeneous samples providing also space of actions in terms of chemometric practices and accurate validation processes. Although, further studies are needed to develop more efficient models using larger sample sets which include more cheese categories and aging times.

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O191

Evaluating Italian butter quality: a preliminary study of chemical and rheological factors across production sites

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Recent research indicates an increasing consumer preference for dairy products derived from pasture-fed livestock, attributing this trend to perceptions of more natural and ethical animal husbandry practices. This study aimed to elucidate Italian consumers' attitudes towards butter through an online survey and to differentiate national butter samples based on their geographical origin. The methodology encompassed an anonymous online observational study that involved a cohort of 1,200 voluntary participants from June to August 2024. Additionally, 94 butter samples were collected from diverse production sites and subjected to comprehensive analysis, including moisture content, fatty acid profile, colour assessment and melting test. The sampling period spanned from October 2023 to September 2024, and considered monthly samples from 4 mountain ($n = 47$), and 3 lowland cheese factories ($n = 36$). Eleven samples were collected from 5 alpine summer farms during the grazing season. The results of the survey indicated that over 80% of respondents were butter consumers with half of them expressing a preference for an undifferentiated product of national origin having price as the driving choice. Forty percent of butter consumers declared a preference for a mountain product, citing superior organoleptic and nutritional attributes. Analytical findings revealed that mountain butter had significantly higher concentrations of PUFAn3 and CLA, a more favorable n3:n6 fatty acid ratio, an enhanced pigmentation, and a lower melting point than lowland counterparts. A comparative analysis restricted to the summer samples from lowland, mountain, and alpine summer farms sites demonstrated that butter from alpine pastures contained high levels of unsaturated fatty acids, superior spreadability, and a more intense pigmentation. Conversely, lowland butter presented higher saturated fatty acid content, less favorable n6:n3 ratio, and reduced spreadability. Samples from mountain cheese factories occupied an intermediate position, distinguishing from standardised lowland products while not fully attaining the characteristics of alpine pasture butter. In conclusion, this study corroborates consumer perceptions regarding the superior quality of mountain-sourced butter, highlighting significant variations attributable to geographical origin of the product.

O157

Identification of functional variants leading to alternative splicing associated with subclinical intramammary infection in dairy cattle

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Functional variants (FVs) like SNPs and INDELs occurring in the splice junction can lead to alternative splicing, resulting in different mRNA isoforms and, consequently, proteins that may be functionally impaired. This can increase susceptibility to certain diseases, including mastitis. To investigate this phenomenon, MGISeq RNA-Sequencing was conducted on milk somatic cells collected from Holstein cows with no history of mastitis ($n = 9$, Neg) and with subclinical intramammary infection (IMI) due to *Streptococcus agalactiae* ($n = 11$, Sa+) or *Prototheca* spp. ($n = 11$, P+). Using the CLC Genomic Workbench (Qiagen), raw data were aligned to the *Bos Taurus* ARS-UCD1.3 to generate a unique alignment for each condition and to finally identify group-specific FVs within the transcriptome which contributed to splice site events (SSEs). Additional analysis of the functional consequences was performed using *Variant Effect Predictor* (Ensembl). A total of 273 uniquely fixed FVs causing SSEs were identified in the Neg group (122 SNPs, 97 insertions, 54 deletions), 252 in the P+ (90 SNPs, 99 insertions, 63 deletions), and 185 in the Sa+ (94 SNPs, 45 insertions, 46 deletions). Furthermore, four INDELs unique of the Neg group overlapped the regions of specific mRNA isoforms encoded by *KRT78*, *CSN1S1*, and *MYBPC1*, which were observed to be down regulated in P + when compared to Neg group

(FDR >0.05, Fold Change <2) in a previous study on the same population. In particular, the one-base insertion overlapping *MYBPC1* was predicted as a frameshift and splice region variant with *high impact* on the functionality of the final protein. The observed FVs may promote a splicing pattern that results in the expression of specific mRNA isoforms and proteins associated with potential resistance/susceptibility traits. In fact, keratins help protect the teat canal acting as a barrier to pathogens, while a deregulation of myosin protein may contribute to pathogen invasion, as host cell myosin is often exploited by pathogens to enhance their pathogenicity. After a validation on an independent population, these results could help to enhance the understanding of IMI resistance and susceptibility leading to the development of targeted breeding strategies.

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O308

Predicting mastitis follow-up using time series on automatic milking system data and machine learning methods

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Bovine clinical mastitis (CM) is one of the most important diseases in the dairy industry, affecting both animal welfare and farm profitability. Therefore, early and accurate detection of the disease allow a prompter and more adequate intervention. The Automatic Milking System (AMS) daily monitor the health status of dairy cows recording numerous parameters, including the Somatic Cell Count (SCC) and the Electrical Conductivity (EC), the two most studied phenotypes related to mastitis. The objective of this study was to use data obtained from AMS to predict the mastitis follow-up within 24 hours after an increase of SCC above 400,000. For this study data from 420 clinical mastitis were collected in nine farms of Piedmont region and classified based on clinical sign and follow up. Data were divided into training and test dataset to have balanced information based on the farm of origin and mastitis follow-up. Data augmentation technique was used in the training data to balance the prediction classes. Row data from AMS were first elaborated as time series data using the mini rocket algorithm with the aim to identify time series patterns in the data. Thereafter, six different machine learning algorithms were used for the follow-up prediction and compared to detect the best performing models. Sixteen milk parameters were initially included for the modelling and four of them were identified as the most informative for the prediction: SCC, EC, milk lactose, and milk time flow. The models were tested on two different mastitis classification: a two-classes mastitis classification (mild and severe mastitis), and a three-classes mastitis classification (mild, moderate, and severe mastitis). The best prediction was obtained for the two classes categorisation using the gradient boosting classifier method (accuracy: 0.91; precision: 0.90; recall: 0.91; f1-score: 0.90), and for the three classes classification with the random forest method (accuracy: 0.76; precision: 0.75; recall: 0.76; f1-score: 0.76). Although the performances of the three classes categorisation were lower compared to the two classes categorisation, none of the sever mastitis was classified as mild, and therefore all the animals that needed attention were correctly identified. The results from this study demonstrated the ability of this method to identify all the animals that were developing a severe mastitis within 24 hours from the brake out, permitting an early detection of the animals to be treated.

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O403

Genetics and bioindicators of mammary health in Agerolese cattle: an integrated analysis

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According to Taste Atlas, Provolone del Monaco PDO (PMPDO) is ranked as the 21st most renowned cheese globally, generating a turnover of approximately 4 million euros in 2023. The Production Specification mandates that at least 20% of the total milk used comes from Agerolese cattle, a dual-purpose (milk and meat) autochthonous breed from the Lattari Mountains and the Sorrento Peninsula (Naples, Italy). Consequently, the number of lactating

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Agerolese cows registered in the Herdbook, along with their production parameters, constitutes a critical factor limiting PMPDO production. To ensure the sustainability of PMPDO production, it is essential to protect Agerolese cattle from both numerical decline and health issues, particularly, mammary health, as these directly influence milk quality and quantity. This study, for the first time, investigates the relationships between milk composition and mammary health in Agerolese cows by analyzing data from functional controls. The objective is to identify significant associations between milk composition and mammary gland health and to compare these findings with data from other commercial breeds raised under similar conditions. We investigated phenotypic sources of variation and genetic factors, namely: variance components and heritability of differential somatic cell count (DSCC). Data from lactations spanning 2020 to 2024 were analyzed, encompassing 14,500 test-day (TD) records from ~500 animals across 30 farms, along with environmental data from the sampling area. A minimum of four TD per lactation was applied, and outliers were excluded. The fixed effects included in the model were: farm, lactation length, parity, year and date of calving and sampling, production level, and climatic variations based on Temperature Humidity Index (THI). Significant differences in average DSCC were observed among farms, with values ranging from 51.7% to 76.3%. DSCC levels were also analysed concerning lactation stage and parity. DSCC shows a positive correlation with fat content (+0.172) and a negative relationship with lactose (–0.048) and urea (–0.050), suggesting a potential link between milk quality and the inflammatory status of the mammary gland. Genetic analyses revealed that DSCC exhibits a measurable level of heritability. The findings provide the preliminary step toward developing genetic management programs tailored to this native breed, aiming to enhance its productivity and sustainability.

O430

Mastitis treatments and somatic cell count in lactating dairy cows: a resilience perspective

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Mastitis remains a significant challenge in dairy farming, impacting both cow health and farm profitability due to reduced milk yield and quality. Somatic cell count (SCC) is a primary indicator of mastitis, reflecting the immune response to udder infections. In recent years, resilience—the ability of cows to maintain production and recover quickly from stressors—has emerged as a key factor for improving herd health and sustainability. However, resilience is complex to quantify, requiring longitudinal data analysis. This study examines the relationship between mastitis treatments, SCC, and productive resilience in a herd of 1,088 genotyped Holstein cows, equipped with nine automatic milking systems. The dataset includes 528,368 milking records across multiple lactations, allowing a detailed analysis of phenotypic and genetic factors influencing resilience. Detailed information of pharmacological treatments of mastitis were available for all cows. A 7-day pre- and post-treatment window was applied to assess impact of mastitis event and consequent treatment on production. Key resilience indicators were calculated, including: ΔProd (milk yield variation), T_rec (time to recovery), Slope_Drop and Slope_Recov (rate of decline and recovery), Pre_Treat_Var (pre-treatment production variability). Variation across cows in resilience was identified for the parameters here used: in contrast to cows exhibiting rapid recovery after the stressful event, others failed to regain pre-treatment production levels. On the other hand, SCC values did not significantly change before and after treatment, and many cows received treatment despite having low SCC values, indicating that SCC alone was not a reliable indicator for resilience assessment in this context. As genotyping of herds is becoming a widespread practice, an interesting perspective is to identify QTL associated with resilience indicators. These findings were obtained based on accurate longitudinal information and offer new insights to dissect resilience and improve overall profitability in dairy herds. Funding: Research supported by Agritech National Research Center and funded by the European Union Next-Generation EU (PNRR – MISSION 4 COMPONENT 2, INVESTMENT 1.4 – D.D. 1032 17/06/2022, CN00000022). This manuscript reflects only the authors' views and opinions, and neither the European Union nor the European Commission can be considered responsible for them.

O152

Analysis of long non-coding RNAs in dairy cows with subclinical mastitis caused by *Streptococcus agalactiae* and *Prototheca spp.*

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Long non-coding RNAs (lncRNAs) have recently emerged as key regulators in immune responses during mastitis infection. In this

context, investigating lncRNA expression in subclinical mastitis may provide insights into the molecular mechanisms of infection and host defense. The aim of this study was to compare the lncRNAs expression in milk samples from healthy cows and cows affected by subclinical mastitis from *Streptococcus agalactiae* and *Prototheca* spp. Three experimental groups were established based on bacteriological analyses of 188 Holstein cows from a single farm: healthy animals (H, $n = 15$), animals infected with *Streptococcus agalactiae* (Sa+, $n = 10$), and animals infected with *Prototheca* spp. (P+, $n = 9$). MGISeq RNA-Sequencing was conducted using a paired-end approach. After mapping with Hisat2, Cufflinks was used to assemble the transcriptome. The individual GTF files were then merged into a single transcriptome and compared to the reference annotation using Cuffcompare. Cuffdiff tool was used to identify differentially expressed genes between healthy and subclinically infected cows. In parallel, a stringent stepwise filtering pipeline was used to detect candidate lncRNAs by excluding low-expressed transcripts and potentially coding transcripts using coding potential prediction tools such as CNCI, CPC2 and FEElnc. In total, we detected 34,750, 37,226, and 28,997 intergenic transcripts in H, Sa + and P + groups and 20,113, 19,288, and 23,961 intronic transcripts in H and Sa + and P + groups. After filtering steps, we obtained a total of 703, 754, and 567 lncRNAs in H and Sa + and P + groups, respectively. This study identified novel potentially functional lncRNAs and their putative role in mastitis development in dairy cows. Further functional validation is necessary to confirm their role in immune response regulation and their potential application within breeding strategies to improve udder health.

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O346

Blood epigenetic patterns in mastitic buffaloes

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In buffalo farming, genetic selection has increasingly focused on enhancing traits such as disease resistance, reproductive efficiency, and milk production. Despite these advances, mastitis remains a major challenge in the dairy industry, negatively affecting both the quality and quantity of milk yield. This is particularly significant for the Mediterranean Italian River Buffalo, which is primarily bred for the production of *Mozzarella di Bufala Campana* PDO. Mastitis, therefore, is one of the main causes of economic losses in this livestock sector. The role of epigenetic regulation, particularly DNA methylation, has recently emerged as a key area of interest in understanding mastitis and its impact on mammary gland health. This study aimed to investigate DNA methylation alterations associated with mastitis in the Mediterranean Italian River Buffalo. Blood and milk samples were collected from a dairy herd in southern Italy. Based on somatic cell counts (SCC), differential somatic cell count (DSCC) and bacteriological culture, animals were classified as healthy or mastitic. Sequencing was performed using the PromethION 2 (P2) Solo device. The analysis showed 22 differentially methylated cytosine sites (DMCs) and one differentially methylated region (DMR) between healthy and mastitic groups. A substantial proportion of hypomethylated DMCs were located in distal intergenic regions, suggesting the involvement of distant regulatory elements such as enhancers or silencers. Additionally, 15% of hypermethylated DMCs were found in the promoter region, located 1–2 kb upstream of the transcription start site (TSS). The enrichment analysis identified genes linked to cellular processes, cell proliferation and differentiation regulation, and immune response mechanisms. Future research with a larger sample size is needed to validate these findings. Expanding the investigation to include other diseases may further shed light on DNA methylation dynamics and aid in developing gene panels for early disease detection. Such biomarkers could enhance disease management strategies and improve genetic selection in buffalo breeding programs.

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O245

Evaluation of different additives to improve soybean silage quality

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Soybean meal is the main protein feed source used in the EU, mainly imported and connected to environmental problems due to

land use change and transportation. Hence, there is the need for a higher protein production in dairy cattle farm. Among forages, whole plant soybean silage (SS) might be an interesting crop for its chemical composition. Moreover, as a legume, it increases the N soil content and can be inserted in a flexible rotation with maize silage. The objectives of the research were: (1) to improve the SS quality; (2) to reduce the ammonia production in the rumen due to the high degradable SS protein. The study was thus divided into two experiments. In exp. 1, four soybean varieties (Avril, Daring, Victorious, Warrior) were ensiled in 2 L micro-silages with four treatments: negative control (C), C + sugar 4% on DM (S), C + 1.25 × 106 CFU/g of Lactobacillus plantarum (L), and C + S + L. For exp. 2, Avril was ensiled also with hydrolysable tannins (HT) at 2 or 4% on DM (HT2 and HT4) and in combination with all the other previously listed treatments. For each treatment, 4 replicates were produced for a total of 96 micro-silages. All the micro-silages were analyzed for aerobic stability, chemical composition, fermentation parameters, and fiber degradability. Statistical analysis was performed using proc. mixed of SAS. The four varieties were harvested at stage R6 (31% of DM) and Warrior resulted in the highest yield (9353 kg DM/ha) while Avril had the lowest DM content (26.7%) and yield (7330 kg DM/ha). Victorius had the highest protein and lipid contents (21.3 and 9.60%) and the highest NDF digestibility (46.5%), while Avril had the lowest NDF (39.0%) and ADL (8.73%), although its fiber digestibility (45.8%) was not the highest. As regards to treatments, the addition of sugars (S and SL) significantly reduced the pH (4.5 vs 5.2), increased the contents of DM and NFC and diluted those of ash, fiber and lipids, but not of protein, since proteolysis was reduced with lower NH3 production (7.52 vs 11.1 NH3 as % of total N). Regarding the second aim, the inclusion of HT linearly reduced the pH (5.09, 4.91, and 4.86, for C, HT2, and HT4) and NH3 (% of total N) (13.9, 10.9, and 9.26, for C, HT2, and HT4), without affecting fiber degradability. In conclusion, SS resulted to have good protein and lipid contents and a low quality fiber. Sugars and HT can improve silage quality, particularly HT can reduce proteolysis and thus NH3 production.

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O336

Chemical composition and nutritive value of leaves and stems of poplar clones in an innovative Mediterranean agroforestry system

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The use of fodder trees has been proposed as a viable solution to increase fresh biomass availability in Mediterranean areas, where climate change has intensified droughts in recent decades, limiting pasture growth. In southern Tuscany, an agroforestry plot trial was conducted on two commercial farms to evaluate the suitability of poplar (Populus spp.) for producing high-quality fresh forage in late spring and summer. In this study, we examined the variation in chemical composition of poplar clone leaves and stems from a one-year coppice hedgerow system. This study investigated the effects of harvest period (HP) and clone (C) on the nutritive values of poplar during late spring and summer.

A plot trail, according to a randomised block design composed by three plants per block and replicated three times was conducted in two farms with five clones. In 2024, four Populus × canadensis Moench clones (IMOLA, TUCANO, ORION, I214) and one Populus nigra L. clone (JPT) were harvested on June 6th and July 18th. Per each clone, a sample was dried at 60 °C for 48 hours, ground to 1 mm, and analysed for dry matter (DM), neutral detergent fibre (aNDFom), acid detergent fibre (ADF), acid detergent lignin (ADL), crude protein (CP), neutral detergent-insoluble crude protein (NDICP), ether extract (EE), and ash content. A linear mixed-effect model was used to assess the effects of HP and C and their interactions on chemical composition and nutritive value.

CP content in leaves significantly ($p = 0.03$) changed between clones in June, showing values from 11.5% ± 0.7 to 16.3% ± 0.7, and declined significantly ($p = < 0.001$) in July varying from 10.8% ± 0.8 to 12.3 ± 0.9. Conversely, the aNDFom content showed no significant differences. The ADF content in leaves increased significantly ($p = 0.002$), and JPT showed the highest variation, 36.4% ± 1.07 in June to 48.1% ± 2.5 in July. The content of ADL showed significative differences ($p = 0.002$) only among clones, with the lowest value of 14.13% ± 1.3 and the highest of 17.0% ± 3.4. Moreover, stems exhibited significant differences in CP ($p = 0.002$), and ADF content increased significantly ($p = 0.02$) from 51.2% ± 0.6 and 53.4% ± 0.8, in June and July, respectively. ADL content increased significantly ($p = < 0.001$). These preliminary findings confirm that C and HP influenced poplar chemical composition and nutritional value. Protein content showed slight seasonal declines while ADF increased with minimal seasonal impact on lignification.

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O469

Use of functional silage in the feeding of Sardinia dairy sheep

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Antimicrobial resistance, which renders antibiotics ineffective against bacterial diseases, is one of the most critical global health challenges. The One Health approach, emphasising prevention and surveillance through interdisciplinary collaboration, is crucial for understanding the complex epidemiology of antibiotic resistance. In livestock production, the urgent need for antibiotic alternatives highlights probiotic microorganisms as a promising solution. This study aimed to evaluate two potentially probiotic lactobacilli strains, isolated from milk and ewe rumen fluid, as inoculants for corn ear silage (snaplage) to feed Sarda dairy sheep. The objective was to analyze not only the impact on the quality of the final product but also its effects on the animals' health. The trial lasted 35 days, with an additional 15-day adaptation period, and was conducted on lactating Sarda sheep. The animals were divided into two homogeneous groups of 144 each: the treated group (TRT), fed inoculated maize silage, and the control group (CNT), fed non-inoculated silage. The basal diet was formulated to be isoenergetic and isoproteic to highlight only the effect of the probiotic bacterium. As expected, there was no difference in the chemical-nutritional composition between the inoculated and non-inoculated snaplages. Feed intake was estimated daily using Lely Horizon Software (V. 4.15.3), and the total milk production of each group was measured twice a day, after the evening and morning milking. No statistically significant differences were observed for daily dry matter intake (329.02 ± 29.04 *vs*. 321.11 ± 33.74 kg/d for the CNT and TRT groups, respectively) and daily total milk production (281.6 ± 15.8 *vs.* 276.2 ± 21.1 L/head for the CNT and TRT groups, respectively) between the two groups. The preliminary results of this study demonstrate that the inoculum used for snaplage inoculation rapidly decreased the pH of the mass and completed the fermentation process, significantly reducing the number of *Clostridia* and yeast ($p < 0.05$). Moreover, the sheep that received the inoculated feed showed a higher milk lactose content ($p = 0.033$), a lower NaCl content ($p = 0.01$), and a numerically lower somatic cell count. Regarding blood parameters, the inoculated snaplage significantly influenced only plasma urea content ($p = 0.03$). However, ruminal ammonia levels, which were generally low, were higher in the group fed inoculated snaplage compared to the non-inoculated group (33.03 vs. 27.14, respectively). Based on these last two results, a greater efficiency in nitrogen recycling can be hypothesised. In conclusion, the results obtained so far indicate that inoculated snaplage might positively influence mammary gland health and improve ruminal-hepatic urea recycling.

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O397

Impact of green forage on milk yield and quality, digestibility, and feeding behavior in Italian Mediterranean buffaloes during the hot season

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Hot conditions can cause negative output in livestock. Various strategies can be adopted to alleviate heat stress, which includes the adoption of sprinkles and fans, and nutritional interventions. For dairy buffaloes, one effective nutritional strategy is to modify their diet composition. This work aimed to evaluate the impact of green sorghum (GS) on dairy buffaloes' production parameters, apparent digestibility, and feeding behavior. A group of 33 lactating buffaloes (DIM = 198 ± 22, milk yield = 7.7 ± 0.5) was enrolled in the experiment. From the beginning of July, for three weeks (P1) experimental animals received the control diet, after that, they received the test diet containing GS (5 kg/head/d) and more corn flour (+0.4 kg/head/d) for six weeks (P2). Fortnightly, sampling of total mixed ration (TMR) and feces were collected to calculate apparent digestibility, and individual milk samples were obtained through an automatic milk sampler. The automatic milking system (DeLaval, Tumba, Sweden) continuously registered milk yield, and feeding behavior was monitored and recorded thanks to the ear tag (DeLaval, Tumba, Sweden) with which each animal was equipped. Feed intake was obtained by subtracting the amount of

residue after 24 hours from the amount of TMR distributed. Ambient temperature and relative humidity were registered by a datalogger and then used to calculate the temperature-humidity index. Data were analyzed using a GLM with ID (random), diet period (fixed), and days in milk (continuous) as factors. Results showed that climate conditions were similar in both periods (THI = 74.7 ± 2.1 and THI = 76.4 ± 1.7 for P1 and P2, respectively) and that changes in the diet caused an increase ($p < 0.01$) in TMR intake. Starch ($p < 0.05$) and lipid ($p < 0.01$) digestibility increased in P2, whereas no differences were found for dry matter, protein, and NDF digestibility. Surprisingly, after GS was introduced, milk data indicated a significant worsening ($p < 0.01$) of clotting parameters, despite a similar chemical composition and no statistical difference in milk yield. However, a positive tendency in the reduction of somatic cells was observed. Regarding feeding behavior, data showed an increase ($p < 0.001$) in the time spent eating and ruminating. Therefore, the inclusion of GS in dairy buffaloes' diet had both positive and negative effects on the parameters evaluated. Further studies are needed to deepen the effects of diet change during heat stress in dairy buffaloes.

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O531

Comparison of NIR chemical predictions for alfalfa hay using portable and benchtop systems

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Widely recognised for its speed and cost-effectiveness, Near Infrared spectroscopy (NIRs) technology is crucial in evaluating feed and diets, ensuring optimal nutritional balance, and improving overall herd management. This study aims to compare portable and benchtop instruments by evaluating NIRs performance to predict the chemical composition of alfalfa hay. Eighty-five samples of alfalfa hay were collected from 40 dairy farms in northern Italy and analysed for chemical traits by AOAC methods and for NIRs data acquisition (three replicates). NIRs data were collected using three handheld devices MicroNIR Pro (JDSU, 900–1700 nm, resolution 6.2 nm), LabSpec 2500 (Malvern Panalytical, 350–1830 nm, resolution 1.0 nm), and UV-Vis-NIR *i*-trometer (B&WTEK, 160–2050 nm, resolution 0.47 nm) and one benchtop instrument DS_{2500} (FOSS, range 400–2500 nm, resolution 0.5 nm). The NIRs datasets were distinctly used to develop predictions for the chemical compounds (mean ± SD; DM: 90.65 ± 0.84, Ash: 9.87 ± 1.50, CP: 17.90 ± 1.71, EE: 2.07 ± 0.36, CF: 30.12 ± 4.02, NDF: 48.18 ± 4.98, ADF: 33.29 ± 4.00, ADL: 7.80 ± 1.09, AIA: 0.69 ± 0.59, aNDFom: 43.75 ± 5.38 expressed as % of DM). The best prediction model for each parameter and spectral range was selected based on cross-validation's highest determination coefficient (R^2CV) and lowest standard error (SECV). The DS_{2500} benchtop instrument achieved higher R^2CV values (0.56–0.89) compared to MicroNIR Pro (0.40–0.87), LabSpec 2500 (0.40–0.82), and UV-VIS-NIR (0.00–0.60). To evaluate performance, the prediction models were classified into two levels of prediction capability based on R^2CV: low (0.66–0.81) and medium (0.82–0.90). Medium prediction performance was observed with DS_{2500} for DM, Ash, CP, NDF, ADF, and aNDFom, while both MicroNIR and LabSpec 2500 achieved medium performance only for aNDFom prediction. Low performance was observed for DS_{2500} in CF, AIA predictions, MicroNIR Pro in DM, Ash, CP, CF, NDF, and ADF, and LabSpec 2500 in DM, CP, NDF, and ADF predictions. All instruments showed inadequate predictions (R^2CV <0.66) for EE and ADL and UV-VIS-NIR device could not provide reliable predictions for any parameter. These preliminary results suggest that portable instruments can predict aNDFom on-site and in real-time, offering valuable support to optimise feed intake and herd productivity. The rapidity of analysis improves the decision-making time, enabling diet adjustments tailored to herd requirements while optimising farm feed resources.

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O223

Impact of endogenous ruminal lipopolysaccharides on functional activity in rumen mixed microbial communities

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Subacute ruminal acidosis (SARA) is a well-recognised digestive disorder of high yielding dairy cows that has a negative impact on both animal health and herd profitability. It is associated with increased ruminal lipopolysaccharide (LPS). Our previous data showed that LPS from *E. coli* (LPS-E) increased the starch-digesting and lactate-producing ruminal bacteria. However, it is not known if LPS-E would be representative of LPS from ruminal

bacteria (LPS-R) to evaluate its effect on the pathogenesis of SARA. Therefore, the objectives of this study are to 1) collect LPS released from the rumen bacteria by inducing SARA nutritional model in batch culture; 2) and compare the effects of LPS-R with the LPS-E on bacterial function by using short-read RNA sequencing.
The SARA was induced by cultivating rumen mixed bacteria with TMR contained 40% starch in 1/12 Menke & Steingass's buffer, which was able to maintain the pH <5.6 for more than 180 min. LPS-enriched culture media (LPS-R) were collected 20 hours post-incubation using centrifugation and 0.22 µm filtration, aligning with peak LPS concentration (22,172 EU/mL) during a 24 h incubation, which was ~7 times higher than non-SARA group (3,244 EU/mL). LPS-E and LPS-free (LPS-F) media were adjusted to match the LPS, VFA, and lactic acid concentrations of LPS-R. All media were prepared with a TMR substrate, essential minerals, vitamins, and adjusted to a final pH of 6.8. Each medium was dispensed into 8 ml aliquots within Hungate tubes. The rumen mixed bacteria 20% of the cultivated volume inoculated in these media. Bacterial samples were taken at 24 h after inoculation for the RNA sequencing.
Metabolic pathways were identified using DIAMOND and the UniRef90 database. Differential pathway analysis across treatments was conducted with DESeq2. We identified 22 significantly altered metabolic pathways between LPS-R and LPS-F, and 17 between LPS-E and LPS-F, classified at KEGG level 3. Among these, three pathways—energy metabolism and ribosome biogenesis—were shared and downregulated in both LPS-R and LPS-E compared to LPS-F. Nitrogen metabolism was upregulated in LPS-E but downregulated in LPS-R compared to LPS-F. Additionally, 71 significantly altered pathways were identified between LPS-R and LPS-E.This study demonstrates that LPS-E and LPS-R distinctly impact ruminal bacterial functions, emphasising the need to evaluate LPS-R's specific role in SARA pathogenesis through our further gene expression analysis.
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O171

Welfare issues in cow-calf Contact

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Cow-calf Contact could be an opportunity to meet the growing consumer sensitivity of early calf separation from its mother at birth. In 2023 the EFSA report indicated to keep the calf with the dam for a minimum of 1 day after partum. A possible alternative approach is the use of foster cows that could reduce the calves stress from mother separation. Anyway, it is necessary to understand whether a short or long period of Contact has positive or negative effects on calf and cow, in terms of welfare. Cortisol hormone can be a good indicator of physiologic status after a potential stressful event.
In the present study, cows and calves were kept together for three days after birth, before being separated. 20 minutes after separation saliva samples were collected from 16 mother cows and 26 female calves. At weaning, after 100 d of rearing with foster cows, saliva sample were collected from 16 calves and 15 foster cows. Hair samples were collected from dorsal area of calves at birth and at weaning and from dorsal area of mother cows and foster cows at calves' birth (zero point) and two months later, to analyse weaning period and the differences between cows and foster career, in terms of chronic stress. An enzyme immunoassay (SALIMETRICS ASSAY #1-3002) was performed to assess cortisol concentration in saliva samples and hair, after an extraction procedure. The average cortisol concentration in saliva at three days' separation was 0.20 ± 0.14 µg/dl for cows and 0.22 ± 0.23 µg/dl for calves while at weaning was 0.26 ± 0.14 µg/dl for foster cows and 0.32 ± 0.24 µg/dl for calves. The average cortisol concentration in hair samples for calves was 37.4 ± 15.2pg/mg at birth and 8.77 ± 3.69pg/mg at weaning, for mother cows and foster cows respectively was 10.5 ± 8.23 pg/mg and 14.2 ± 16.8pg/mg at calves' birth and 11.5 ± 9.45pg/mg and 10.7 ± 10.5 pg/mg two months later. The results show an increased acute stress (saliva) at separation both in young and adult animals when they spend more time together. The high content of hair cortisol in calves at birth suggests that this hormone might play an important role in foetal development. With growth, the level of hair cortisol in calves dropped to the same level as adult animals and this may reinforce the hypothesis. However, specific studies would be useful to investigate this topic. The high variability shows the individual influence of different susceptibility to stress, which highlights the need for relative comparisons.
Research supported by Gruppo Operativo VISION – OPERAZIONE 16.1.01 'Gruppi Operativi PEI' del Programma di Sviluppo Rurale 2014-2020 della Regione Lombardia.

O311

Current management of calves in Italian dairy farms: preliminary overview on the welfare of calves

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Consumers are increasingly concerned about the welfare of animals, especially for categories perceived as 'neglected' by the sector, such as dairy calves. Nowadays, compared to the past, dairy farmers are more aware of the fact that the calves are the future of their farm. However, the European Food Safety Authority (EFSA) published in 2023 a scientific opinion about welfare of calves, a document that provides experts' recommendations, which may represent guidelines for future European regulations. The primary objectives of this study were to obtain an overview of the Italian calf management practices from birth to weaning and to document the background of Italian dairy farmers. An online questionnaire about calf-rearing procedures was administered to farmers, via distribution of the link and QRcode through various social platforms, web magazines and during Italian livestock exhibitions. Although the questionnaire is still accessible and data collection is ongoing, 175 responses were collected. This study includes preliminary responses ($n = 112$) due to a modest completion rate (64%). In general, about half of the respondents have more than 10 years of experience in the sector (50.4%), most of the respondents have read about or heard about EFSA scientific opinion at least once (78.8%) and regularly attend continuing education/training courses (71.7%). Moreover, cow-calf separation occurs in 82% of herds within 6 hours post calving and calves are accommodated in a facility dedicated to them only in 43.7% of the farms. In about 51.2% of the farms, they are housed in boxes or hutches without enclosure, but only in 57.6% of cases they are exclusively housed individually. In fact, it is worth noting that calves are socially housed with their mothers/nurses or with peers just in 17.6% of the farms. In addition, most of the respondents (80.9%) answered that they administer a quantity of milk equal to approximately 12% of the calves' body weight or more and most of the participants (91.8%) provide it in 1 or 2 meals a day. Most commonly (63.2%), age is used as the criterion to initiate the weaning process, and half of the farmers tend to start weaning calves between 8 and 9 weeks of age (50%). To conclude, this study provides a preliminary overview of the current calf management practices in Italy. Further analysis will be conducted to identify areas for improvement of management and welfare of calves.

O271

Application of Qualitative Behaviour Assessment on cows before and after their separation from their calf in a cow-calf Contact system

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Cow-calf Contact (CCC) systems are attracting increasing interest as alternatives to early separation and offer great potential to improve animal welfare by promoting species-specific behaviours. Allowing prolonged Contact is beneficial for both cow and calf by promoting growth and social competence in calves and maternal behaviors in cows. However, pair management and stress at separation may be challenging, and tackling these issues is essential to guarantee their welfare. A Qualitative Behavior Assessment (QBA) was applied to evaluate the dairy cows' attitudes and emotions before and after separation from their calf on a commercial CCC dairy farm in northern Italy. Ten Italian Friesian cows giving birth to female calves were assessed from May to July 2024 at approximately 7 and 14 days post-partum (before (BS) and after separation (AS), respectively). Two lists of fixed terms developed in previous studies were used before (BS, 14 terms) and after separation (AS, 20 terms). Inter-observer reliability of 4 assessors was achieved through 6 online trainings before on-farm assessments that were done after joint cow observations in the two contexts.
For each QBA list, scorings were submitted to a Principal Component Analysis (PCA) in XLSTAT and summarised in main components PC1, PC2 and PC3. Eigenvalues were above 1.5 with 59.9% of the total variability explained for BS and above 2.3 with 50.2% of the total variability explained for AS. Before separation, PC1 summarised the terms *relaxed* and *calm* with positive loadings (≥0.67) and *frightened, agitated, attentive* and *worried* with negative loadings (≥–0.65). *Active* and *indifferent* cross-loaded on PC1 and PC2. *Irritated* and *aggressive* had negative high loadings on PC3 (≥–0.72). After separation, PC1 summarised the terms *active, friendly, lively* and *sociable* with positive loadings (≥0.68) and *indifferent* with a negative loading (–0.65). *Calm* had a positive loading (0.67) and *uneasy* a negative loading (–0.75) on PC2. *Inquisitive* loaded positively on PC3 (0.63). The results confirmed QBA as a reliable method to evaluate cows' attitudes and emotions, however the use of two different lists for before and after separation did not allow a direct comparison of a cow's state with and without the calf. This underlines the need for either a single list of fixed terms applicable to different contexts or for further developments of approaches to integrate and compare QBA fixed lists.
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O052

Effects of dietary concentrate level on protein feed-food and land use competition indicators

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The capacity of dairy cows to use both land and feeds potentially competing for direct human use or not challenges what is their optimal use to maximise milk output and related efficiency. To assess the relationships between these resources and milk output, this study evaluated the effects of dietary concentrate level on efficiency of conversion of dietary protein into bovine milk. Data originated from 336 northern Italy dairy farms, with a wide range in intensification degree, diet composition, milk yield (MY) and milk protein content (MPc), acquired through farm visits and official databases. The net energy requirement of cows and the dietary net energy content were used to estimate dry matter intake (DMI). The crude protein intake (CPI) was computed as DMI × dietary CP content, whereas the milk protein yield (MPY) as MY × MPc. The following protein conversion ratios (PCR = CPI/MPY) of dietary CP into milk were used as indicators of efficiency: (a) PCRwd, using the CPI of the whole diet; (b) PCRmp, using the CPI from main products of arable land, with exclusion of byproducts; (c) PCRco, using the CPI from concentrates; (d) PCRhe, CPI from potentially human-edible foods. The PCRs were analyzed with a mixed model testing the fixed effect of the quintile of the percentage of CPIwd covered by CPIco (CPc_p, with average values of 6, 15, 20, 26, and 37% for quintiles from 1 to 5) and the random effect of the dairy system. Herd size averaged 101 lactating cows (range: from 3 to 1009), MY 25.7 kg/cow/d (8.5–44.5), MPY 0.83 kg/cow/d (0.27–1.43). Efficiency indicators (mean ± standard deviation) averaged 4.38 ± 0.71 (PCRwh), 2.58 ± 1.15 (PCRmp), 0.85 ± 0.41 (PCRco) and 1.12 ± 0.52 (PCRhe). The CPc_p significantly affected MPY, which increased from 1st to 4th quintile. Similarly, at increasing CPc_p we observed a nearly linear decrease of PCRwd (from 4.97 to 3.74 for quintile 1 to 5), whereas PCRmp exhibited best values for CPc_p comprised between 15 to 26%. Increasing CPc_p linearly increased PCRco, with value ≤1 kg CPI/kg MPY for CPc_p ranging from 6 to 26%, and quadratically affected PCRhe, with best values for CPc_p ≤ 15%. In conclusion, the use of human-competitive resources has complex interactions with the capacity of dairy cows to convert dietary CP into MP. Anyway, diets with CPc_p close 25% resulted in the best trade-off between MPY and conversion of dietary protein into milk protein, thus supporting the efficiency of dairy farming as source of protein for humans.

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O280

The effect of feeding strategies on enteric and manure methane emissions in dairy cows: evidence from Italian farms

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The dairy sector faces increasing environmental challenges, with methane being a major concern due to its role in enteric emissions from livestock. This study explores the impact of various feeding strategies on methane emissions from lactating Holstein cows fed TMR silage-based diets. Data were collected from 36 dairy farms in Northern, Central, and Southern Italy. Four equations for estimating methane emissions were compared to assess whether they behave differently in response to diet variability and sensitivity to dietary changes. The Global warming Potential (GWP) of the diet was calculated as the sum of each feed's GWP in the TMR. The study also investigated how feeding strategies affect the excretion of volatile solids and methane emissions from manure. A hierarchical cluster analysis categorised diets into homogeneous groups based on (i) their nutritional profile, including feed type, inclusion level, and nutritional characteristics, and on (ii) feed composition. The four diets groups based on feed composition showed no significant differences in methane emissions. Clustering by nutrient composition revealed three categories: 'High quality', 'Medium quality', and 'Low quality' diets. Only the Mills equation detected differences between these nutrient-based clusters. According to this equation, average CH_4 emissions were 460.36 ± 46.95 g/d, 18.90 ± 1.57 g/kg DMI, and 12.89 ± 2.83 g/kg FPCM, corresponding to a 5.93% loss of gross energy intake. The low-quality cluster showed the highest emissions, with methane production reaching 485.85 g/d. Notably, this cluster had the lowest methane emissions, equal to 19.47 kg CO_2eq/kg DMI and 14.82 kg CO_2eq/kg FPCM. Despite variations in diet GWP across clusters, ranging from 0.45 to 1.17 kg CO_2eq/kg DMI, no significant differences were observed. The choice of feed type had no significant impact on emissions or GWP in this context. However, the type of equation used influenced the evaluation of feeding strategies. Empirical equations based on single intake variables identified differences in methane intensity but not production, while the Mills equation accounted for both factors. This highlights the importance of accurately estimating enteric methane emissions to improve national greenhouse gas

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inventories and develop context-specific models for effective mitigation strategies in dairy farming.

O158

Effects of two commercial additives on pollutant emissions from dairy cow manure

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CH4 and NH3 emissions from dairy manure represent a relevant part of the environmental impact of agriculture. NH3 emissions from manure come from microbial ureolysis and the subsequent volatilisation of NH3, which can affect human and animal health and is involved in the production of fine particulate. CH4 is a greenhouse gas, and it is produced by microbial fermentations. Aim of this *in vitro* experiment was to evaluate the effect of two products added to dairy cow manure on NH3 and CH4 emissions. The first commercial product (MIN) is mainly based on calcium sulphate and other minerals; the second product (MA) is a microbial starter based on bacteria, yeasts and fungi. Both products are claimed to reduce NH3 and CH4 emissions. A mix composed by 63 % feces and 37 % urine, as such basis, was used for the experiment, with biweekly additions of the same material. Three theses were replicated thrice, using 2 l glass jars and 1 kg of manure: unsupplemented manure (CTR), manure added of MIN, manure added of MA. Both additives were supplemented at the doses suggested by producers. CH4 and NH3 emissions were measured at 1, 3, 7, 14, 28, 60, 90 days after the beginning of the experiment. Data were analyzed with repeated measures mixed models. No evidence for group differences was found for CH4 production expressed as mg m^{-2} h^{-1}, although it tended to be lower in MA (–24.92 %, $p = 0.09$) than CTR and -12.09 % *vs*. MIN, when cumulated emissions are considered. A significative effect ($p = 0.01$) of the treatment was observed for NH3 emissions, with MIN that had the lowest NH3 production (–11.29 % *vs*. CTR) but an opposite trend was observed with MA, that emitted more NH3 *vs*. CTR (+ 11.01 %, $p = 0.01$). These results suggest a tendential positive impact of the microbial additive on CH4 production, whereas the MIN additive limited NH3 emissions. A combination of the two additives would be worth to be tested.

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O189

Ammonia and greenhouse gases emissions during storage of excreta from poultry fed with 15% *Spirulina* dietary inclusion

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Microalgae, such as Spirulina, are sustainable and nutrient-rich alternatives for broiler feeding. Conversely, animal manure management significantly contributes to greenhouse gas (GHG) and ammonia emissions (NH_3), with nitrogen (N) losses influenced by storage conditions and manure characteristics. To assess the impact of these practices on GHG and NH_3 emissions during the storage of excreta, two broiler strains (Naked Neck vs Full Feathered) at two different temperature conditions (23 vs 30 °C) were fed under control conditions and with 15% Spirulina dietary inclusion. Excreta were collected during two trials conducted by Fernandes et al. (2024) in winter and summer 2022. Each trial included two dietary groups: a control diet (under thermoneutral (CTNZ) or heat stress conditions (CHS)) and a diet with 15% Spirulina inclusion (under thermoneutral (SPTNZ) or heat stress conditions (SPHS)), for 12-weeks. After each trial, excreta were collected and frozen before starting the storage experiment. The measurement of GHG and NH_3 emissions during storage, followed the methodology described by Prado et al. (2020). The storage experiment lasted 60 days at room temperature (23.5 ± 3.5 °C) and per treatment three replicates were used. The cumulative emissions were compared using multivariable regression models in R environment considering the fixed effects of diets and environmental temperatures. Animal strain was not significant and therefore was not considered in the multivariable model. During excreta storage, N losses (%) via NH_3 emissions were higher ($p < 0.001$) when excreta were collected at 30ºC (CHS = 26.381and SPHS = 20.781) compared to 23ºC (CTNZ = 8.623 and SPTNZ = 15.732). Additionally, incorporating Spirulina into the diet significantly increased NH_3 emissions (3.174 g/kg in CTNZ, 6.719 g/kg in SPTNZ, 9.859 g/kg in CHS, $p < 0.05$), except in chickens under heat stress with Spirulina inclusion (7.781 g/kg in SPHS). Spirulina increased

also nitrous oxide (N_2O) emissions at both temperatures ($p = 0.05$), with excreta collected under heat stress releasing more N_2O than those from normal conditions (8.187 mg/kg in CTNZ, 9.197 mg/kg in SPTNZ, 12.140 mg/kg in CHS and 14.518 mg/kg in SPHS). Methane emissions remained consistently low and unaffected by the treatments. Overall, including Spirulina in broiler diets substantially raised atmospheric N losses via NH_3 and N_2O emissions, amplifying nitrogen and carbon footprint of broiler manure.

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O518

EU CIRCLES project: on-farm wastewater treatment with bioactivators reduces air pollution and modulates slurry microbiota in pig growing units

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Mitigating ammonia (NH_3) emissions is critical for pig production, as high NH_3 can be harmful for the environment and the health and welfare of pigs and farmers. This trial investigated the impact of applying bacterial-enzymatic bioactivators to slurry on gas emissions, wastewater characteristics, pig welfare, and slurry microbiota during the growing phase. A total of 980 pigs (47.14 ± 3.82 kg) were randomly assigned to two groups: (i) Control group (C), with no intervention applied to the slurry, and (ii) Treated group (TR), which received a combination of interventions to treat the slurry which included: (1) Tablets supplied through the slatted floor into the wastewater tank (1 tablet/week per 2 m^3 of slurry pit); (2) Powder sprinkled on the floor (1 kg/week per 10,000 kg of animal weight); and (3) Liquid dispersed via an automatic sprinkler system. The trial lasted 63 days. Wastewater samples were collected before each draining (d21, d42, d63) for quality and microbiota analyses, while air quality measurements and lesion scores on ears and tails were recorded. A factorial design was used to assess the effects of treatment, sampling time, and their interaction. The TR group showed improved wastewater quality by reducing pH ($p = 0.03$), total nitrogen ($p = 0.02$), ammonium (NH_4, $p = 0.04$), and organic nitrogen ($p < 0.001$), while increasing total potassium oxide (K_2O, $p < 0.001$). In addition, treatment reduces the wastewater biological oxygen demand and chemical oxygen demand at T3 ($p < 0.05$), environmental NH_3 levels were significantly reduced in the TR group ($p < 0.001$). Microbiota analysis revealed that the TR group exhibited lower Shannon and InvSimpson indices at T1 ($p < 0.01$) and a higher Shannon index at T2 ($p < 0.05$), with no differences at T3. Beta diversity analysis showed significant differences between the TR and C groups at T1 ($R^2 = 0.61$, $p < 0.01$), T2 ($R^2 = 0.46$, $p < 0.05$), and T3 ($R^2 = 0.57$, $p < 0.05$). Taxa such as *Lactobacillus* and *Sphaerochaeta* were enriched in the TR group (LDA score >3, P.adj <0.05), while *Clostridium sensu stricto* and *Christensenellaceae R-7 group* were enriched in the C group (LDA score >3, P.adj <0.05). No effect was observed on the lesion incidence. In conclusion, the on-farm application of bacterial-enzymatic bioactivators improved wastewater quality and mitigated NH_3 emissions by favoring the presence of *Lactobacillus* in the slurry, which reduced the pH and subsequently decreased NH_3 volatilisation.

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O442

The effect of increasing H_2SO_4 on NH_3 and NMVOC emissions from pig slurry application to permanent grass

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Slurry acidification with concentrated sulfuric acid (H_2SO_4) is an effective and established technique to reduce ammonia (NH_3) emissions from animal slurry. Acidification can be performed at various stages of the slurry management chain, such as inside animal houses, in storage tanks, and during field application. In Denmark, the regulation sets the quantity of concentrated H_2SO_4 (96%) required to achieve a reduction in NH_3 emissions of 25% compared to non-acidified slurry applied by trailing hoses. Dosages vary depending on slurry type and slurry management stage. For pig slurry acidification during filed application, the legally required nominal dose is 2.9 kg H_2SO_4 ton^{-1} slurry. Besides

the positive effect of NH_3 emissions mitigation, slurry acidification could negatively impact emissions of non-methane volatile organic compounds (NMVOC), by enhancing the release of volatile fatty acids after slurry distribution. Additionally, release of H_2S can be increased by lower pH. This study evaluated the effect of increasing H_2SO_4 dosages beyond the legal requirement on NH_3 and emissions of NMVOC and H_2S following pig slurry application in a grass field. The experiment was carried out at Campus Viborg, Aarhus University (Tjele, Denmark). The tested dosages were 2.9 (legal dose), 5.3, 10.5, and 0 kg H_2SO_4 ton^{-1} slurry. Emissions were measured using the dynamic flux chambers method, using cavity ring down spectrometry (CRDS, Picarro CA, USA) to monitor NH_3 concentrations, and proton transfer reaction-mass spectrometry (PTR-MS, IONICON Analytik, Innsbruck, Austria) for NMVOC and H_2S concentrations. All treatments were tested in triplicates. The slurry was collected the day before the start of experiment, and H_2SO_4 was added with the corresponding dosage using a micropipette. Slurry was applied using a water can connected to a hose, simulating trailing hose application at a rate of 35 tons ha^{-1}. Immediately after slurry application, the chambers were placed on top of the applied area and measurements started. Fluxes of the target compounds were monitored for 5 consecutive days. H_2SO_4 dosage effects on cumulative NH_3 emissions were analyzed by linear regression. Emissions averaged 5.4% of applied ammoniacal nitrogen, with high variability between treatments. Acidification had no significant effects, likely due to the low slurry dry matter content, causing rapid infiltration and limiting volatilisation from all the plots. NMVOC results are still under elaboration.

O133

Does Virtual Fencing affect cattle behaviour and pasture utilization as compared to traditional grazing management?

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Virtual fencing (VF) is an innovative technology for grazing management which relies on GPS collars. Herd containment is ensured by a paired stimuli released by collars. In detail, when animals cross the VF, the collar activates, and an audio tune is played. If the animal turns back, the audio tune stops; otherwise, if the animal keeps walking, at the end of the audio tune the collar delivers a slight electrical pulse. The sequence of audio cues and the electrical pulse can be repeated at most three times, then, a notification of escape is delivered, and only GPS positioning is maintained active. The study aimed to assess whether VF could affect the behavior of a herd of Limousine cows during seasonal grazing. Cows were divided in a control group (C, $n = 15$) handled according to the traditional grazing management, letting the animal grazing along 15 ha for 6 weeks, and an experimental group (VF, $n = 15$) handled using VF collars (Nofence® Norway), on incremental surfaces according to biomass availability and consumption rate. For the VF testing group, five virtual fencing changes (VF1 to VF5) were performed, starting from 4.5 ha, and reaching 15 ha after 6 weeks. Each animal was provided with smart ear-tags (Allflex®, USA) registering time spent ruminating, resting, and eating. Data were analyzed using R software and GLM procedure setting Group (C, VF), Period (VF1-VF5), Time (00–04 am, 04–08am, 08–12am, 12–16 pm, 16–20pm, 20–00pm), as fixed factors, Distance and Temperature as covariates, and Animal within Group and Day as random. Results showed that VF did not affect any of the studied behaviors, indeed, total time spent ruminating, resting, and grazing was similar between C and VF cows. The three-way interaction between Period, Group, and Time resulted always significant for each examined behavior. VF cows showed an increase in time spent ruminating during night and the early afternoon for each Period, whereas grazing occurred during the late afternoon and the early evening. C cows preferred to eat during night and early afternoon and to ruminate in the late afternoon. In conclusion VF seems a promising PLF application to enhance pasture utilisation in extensive grazing systems by reducing farmers' labor without affecting animal behavior.

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O162

GPS as a tool to monitor grazing behavior of Sarda dairy ewes

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Understanding the spatial pattern of a grazing animal is crucial for ecology and conservation. A highly concentrated space use may lead to overgrazing and degradation in some areas. A more uniform use results in less pressure on specific resources and a more balanced impact on the environment. The Camargo's index of evenness (CI) quantifies the uniformity of space use in grazing contexts, whether an animal distributes its time evenly across a grazing area or concentrates its activities in specific zones. Values of CI are between 0 (extremely concentrated) and 1

(uniform space use). During 2023 and 2024 at the Bonassai farm of AGRIS Sardegna, an experiment (funded by the Horizon 2020 TECHCARE project GA N. 862050) was conducted. Two groups of dairy Sarda ewes, homogeneous in age, days in milk, milk yield, and body condition, were subjected to two different grazing access times: 3 hours/day (group 3h) and 6 hours/day (group 6h). The groups have grazed two paddocks comparable in quality and quantity of grass per animal with identical stocking rate. The hypothesis of the study was that the different grazing duration affects grazing behavior of the animals. The animals were equipped with GPS collars (igotU GT-600®), collecting locations, date, and time once per minute, for a total of 5 days. Values of CI were calculated for different phases at a grid resolution of 5 m using R. The data were analyzed according to a General Additive Model. During the first 3 hours of grazing, both groups showed an increase in the uniformity of grazing distribution since entering the pasture, reaching a maximum in the middle phase, then a decrease in the final phase. The two groups exhibited different behaviors, with similar CI values in the initial phase (0.14 ± 0.02), 3h group showed higher values during the intermediate phases (0.30 ± 0.03 vs 0.13 ± 0.02 and 0.30 ± 0.03 vs 0.18 ± 0.02, respectively) and grazed least evenly (0.07 ± 0.03 vs 0.17 ± 0.02) in the final phase. Ultimately, the different grazing durations have led to varying behaviors, with the 3h group showing a spreading after entering the pasture, almost as if they know they won't have much time to explore it. In contrast, the 6h group demonstrates greater consistency in the CI value, as if they are aware that they will have more time available to explore the entire pasture.

O470

Virtual fencing vs. traditional grazing: impacts on dairy cows' milk yield and behavior assessed with an automatic milking system

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Virtual fencing (VF) is an innovative livestock management system that uses GPS-enabled col-lars to guide animal movement within defined boundaries, eliminating the need for traditional physical fences. When an animal approaches a virtual boundary, the collars emit an audio warning. If the animal continues toward the boundary, an electrical pulse is delivered, training the animal to avoid crossing the virtual border. Studies have demonstrated VF's effectiveness in grazing cows systems. However, its application for managing dairy cows in small paddocks and integrating VF with automatic milking systems (AMS) remains underexplored. In this study, 13 lactating Pezzata Rossa grazing dairy cows were on pasture for 90 days, alternating VF management with traditional grazing systems. Initially, cows grazed by means of VF collars (Nofence®, Norway) for 24 days (VF1). They were then moved to a new continuous grazing pasture for 13 days (CG1), setting perimetral borders only. This sequence was repeated for two additional periods, resulting in four experimental phases: VF1, CG1, VF2, and CG2. During the experiment, data on milk yield and cow behavior were collected using AMS software (Lely, Maassluis, the Netherlands). Generalised mixed models were used, with fixed effects including the experimental phase, day within phase, and their interaction, as well as lactation stage and the number of lactations as covariates. Additionally, the total number of stimuli emitted by the collars during the VF periods was modeled to assess the animals' learning adaptation to VF. Results showed that the highest daily milk yield was recorded during VF1, with no differences in milk protein content across phases. VF did not affect cow routing, as there were no differences in AMS failure rates between periods. However, feeding time differed significantly: cows spent more time feeding during CG1 compared to VF2 and CG2, while no differences were observed in ruminating time. Importantly, cows demonstrated good learning adaptation to VF, with the number of electrical pulses significantly higher in VF1 than VF2. Conversely, the total daily number of audio warnings was higher in VF2 than in VF1. These findings highlight VF as a promising tool for managing dairy herds on pasture, supporting efficient grazing management, promotes animal welfare, and contributes to sustainable dairy farming practices. Future studies with a larger sample size are needed to validate and expand upon our results.

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O098

Smart livestock grazing: GPS serving the extensive Marchigiana breeding system

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The optimisation of efficiency in Marchigiana cattle semi-extensive farming still poses significant challenges. Monitoring of

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animal behavior during grazing is the most investigated aspect to optimise the use of pastures by animals. Smart collars with GPS and accelerometer technology are currently proposed to improve animal management. The present study aims to: (1) analyze the suitability of smart collars for managing Marchigiana cattle; (2) investigate the consistency between smart collar data and animal behavior. The study was conducted on a 9-ha pasture divided into 3 paddocks. Animals were weighed using a wireless scale (Gallagher™, Epping, VIC, Australia) at each paddock entrance and trial end. 11 cows and 1 bull have been fitted with smart collars (SmartPaddock™, Moorabbin, Victoria, Australia) equipped with GPS trackers and triaxial accelerometers for 45-days period. Cattle behaviors were observed and recorded to correlate smart collar data with animal behavior. Collar data were aggregated at 15-s intervals, while the triaxial accelerometer raw data were recorded at 0.05-s intervals. Dedicated statistical software was used to explore behavioral models and correlations. During the monitoring period, a positive variation in animals' mean weight (cows: from 577.36 ± 72.39 kg to 596.00 ± 63.97 kg; bull: from 717 to 721 kg) was observed. The smart collars facilitated the monitoring of Marchigiana cattle grazing, enabling the early identification of some anomalies related to both animals and technology. Besides the high initial cost and the continuous need for maintenance and technical control of collars, some critical issues, such as data variability in different environmental conditions and data loss due to hardware problems, occurred in the 45-days trial. GPS and accelerometer have registered data relating mainly to grazing and resting behaviors, while others occurred occasionally, such as mating and allogrooming. Trusting in a rapid overcoming of technological difficulties, smart collars could be useful to monitor Marchigiana cattle in grazing systems by optimising their management. However, further research is needed to address technical and operational challenges of deploying such technologies on a large scale.

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O100

Traceability for a grazing equine system in inner areas of Centre-South Italy

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The marginalisation and depopulation phenomena which afflict inner areas of Centre-South Italy represent a significant issue for the socio-economic and environmental sustainability of those areas increasingly threatened by soil degradation, hydrogeological risks, and biodiversity loss. The study aims to evaluate the introduction of Global Positioning System (GPS) and Geographic Information System (GIS) as valid tools both for monitoring grazing equines and, consequently, for a better characterisation of the nutritional value of resilient grazed areas. The study was conducted on the Apennine pastures of Capracotta municipalities (41°50′N 14°16′E, Isernia province), a Special Area of Conservation (SAC, IT7218215) located between 1150 and 1500 m of altitude, characterised by the widespread presence of rock outcrops. A total of twelve heavy horses, reared in extensive conditions from July to December, were fitted with GPS collars (Digitanimal®, Spain) which detect horse temperature and position every 30-min. The temporary alarm system was triggered when either the animals get across the predetermined fences or exhibit rapid behavioral changes. The GPS tracking showed that horses remained within the virtual fences, so that the study assessed the variation in land use according to the season. During summer and autumn, the animals were observed to extensively explore the entire pasture area. However, in summer equines came down to the valley at night for drinking, while they spent the hottest hours of the day at the top or on the edge of the woods. During winter, horses spent less time grazing and gathered between the woods and drinking area. Data from the GPS tracking system will be combined with data on pasture productivity and quality to optimise animal nutrition and

welfare. This integration is expected to improve animal management in extensive farming systems of marginal inner areas.
The study has been approved by the Bioethics Committee of the University of Molise. The research was supported by project PRIN 20224L4WSR, funded by Next Generation EU (CUP: H53D23005120).

O112

Factors affecting fat globules size of sheep milk

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The milk fat globules in sheep are characterised by a wide range of sizes and a complex composition that varies by diameter, influencing both the nutritional and technological properties and contributing to the distinct nutritional and sensory qualities of dairy products. For these reasons, 270 individual milk samples were collected from Comisana e Massese breeds reared in two commercial farms and in the genetic nucleus of the Italian sheep and goat breeders Association, all located in Tuscany region. The size distribution was measured in triplicate using a laser diffraction-based particle size analyzer. The instrument calculates the particle size distribution by measuring the angular pattern of light scattered by the particles. The following traits were provided: d4,3 (volumetric average diameter), d3,2 (volume-surface average diameter), d2,1 (the surface-weighted average diameter), specific surface area (SSA) and span (the variability of the distribution of the fat globules). Animal related-factors (e.g. parity), major milk components (e.g. casein) and udder health-related minerals (e.g. Mg, Cl) were tested on the size distribution of milk fat globules. A mixed model with bootstrap resampling was used to estimate the variability and confidence intervals of the statistical relationships between the factors included in the model and traits related to the size distribution of fat globules. Results showed that both SSA and span increased with the parity of the ewes. This effect was attributed to the production of smaller, more uniform globules, which increased the surface area relative to mass. Correspondingly, the d4,3 and d3,2 values decreased, reflecting the smaller average size of the fat globules produced by older ewes. These changes could be associated to the alterations in mammary gland function with age. Conversely, higher casein levels resulted in larger, more uniform fat globules, as casein stabilises the globules and prevents aggregation. Larger fat globules resulted in a decreased surface-to-volume ratio, which in turn lowered the SSA. Magnesium and Cl affected the size distribution, suggesting that their presence influences the stability and emulsification of fat globules. Overall, the study highlights the complex relationships among animal-related factors and milk composition in modifying the size distribution of fat globules, emphasising the importance of these factors for optimising milk quality and its functional properties.
Research supported by University of Parma through the action 'Bando di Ateneo 2023 per la Ricerca'.

O309

Effect of fat globules size on the technological properties of sheep milk

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Sheep milk is known for its high solids content and advantageous coagulation properties. However, despite its great cheese-making characteristics and the continuous growth of dairy product production, scientific research mainly focuses on cattle, leaving diverse characteristics of ovine milk still unexplored. Milk fat globules (MFGs) play a crucial role in curd firming and can also significantly impact cheese yield. Therefore, in this study we aimed to better understand the fat-related factors influencing coagulation and cheese-making traits. A total of 270 individual sheep from Comisana and Massese breeds were milk-sampled, and composition, MFGs, coagulation properties and cheese-making traits were characterised. Sheep were reared at the genetic nucleus of the Italian sheep and goat breeders Association, and in two commercial farms, all located in Tuscany. Coagulation properties [rennet coagulation time (RCT), k_{20}, a_{30}, a_{60}] and cheese-making traits [weight of the curd ($\%CY_{CURD}$), and water ($\%CY_{WATER}$) and solids ($\%CY_{SOLIDS}$) in the curd as percentages of the weight of the processed milk, and curd content of solids

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($\%REC_{SOLIDS}$), fat ($\%REC_{FAT}$) and protein ($\%REC_{PROTEIN}$) recoveries as percentages of the corresponding nutrients in the processed milk] were assessed in duplicate with the 9-MilCA method. MFGs size distribution was measured via light scattering providing the following traits: volume-weighted mean diameter (d4,3), surface-weighted mean diameter (d3,2), the specific surface area (SSA) and the distribution variability of MFGs (span). A linear mixed model was used to assess the effect of fat-related factors (fat content and MFG traits) on both traditional and modelled coagulation and cheese-making traits. Additionally, animal-related factors, day of sampling and analysis conditions were added as random factors. Results showed that, among the MFG traits, the interaction between d3,2 and casein was significant for $\%REC_{PROTEIN}$ ($p < 0.01$) and $\%CY_{SOLIDS}$ ($p < 0.05$), while the single factor d3,2 was relevant for $\%REC_{PROTEIN}$ ($p < 0.05$) and $\%REC_{FAT}$ ($p < 0.1$). It emerged that MFGs with higher d3,2 were associated with a general improvement of nutrients recovery in the curd, particularly for milk with the highest content in casein. This study underlines the influence of MFGs' physical characteristics on cheese-making traits, emphasising the potential of MFGs not only as milk quality indicators, but also as predictors of cheese yields.
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O432

Animal performance and milk quality in grazing ewes supplemented a concentrated phenolic extract from olive-milling wastewaters

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Dairy sheep farming usually exploits graze. Animal performance and products quality can be affected by seasonal variations of pasture characteristics. Bioactive compounds from olive by-products, such as polyphenols, can influence ruminant metabolism, thus having potential to mitigate the impact of pasture variability. This study assessed the effect of feeding lactating ewes a concentrated phenolic extract from olive-milling wastewaters during two grazing seasons. Animal performance, milk clotting parameters, fatty acids and antioxidant capacity were evaluated. Twenty-four Comisana ewes were divided in two groups. During the two daily milkings the animals individually received 500 g/head of a commercial (CTR) or a concentrate added with 11% phenolic extract (PHN). Both groups grazed 8h/d in a native pasture during May-June (fresh pasture, FRH) or July-August (dry pasture, DRY). After 7-day experimental period, individual milk was sampled every 7 days during 4 consecutive weeks of FRH and DRY period. Data from FRH and DRY period were analyzed separately using a Mixed model, considering the fixed effect of diet (D; CTR and PHN), sampling time (T; 1 to 4), and their interaction (D × T), animal was the random effect. Despite the grazing periods, milk yield was similar between groups ($p > 0.05$), whereas urea was lower in PHN than CTR group ($p < 0.002$). For both the periods, clotting parameters improved over sampling time for the CTR group and remained stable for PHN. The antioxidant capacity of milk was not affected ($p > 0.05$) by D or T. Regarding milk fatty acids, during FRH period C18:1 *t*6-8, C18:1 *t*11, C18:2 *c*9*c*12; C22:0, C24:0, and C20:5 ω-3 were lower in PHN than CTR milk ($p \leq 0.05$). Similarly, PHN milk showed a lower odd- and branched-chain fatty acids and thrombogenic index than CTR ($p \leq 0.05$). A D × T effect ($p < 0.001$) was observed for total and ω-3 PUFA during FRH period, both decreasing over sampling time only in the CTR group. Regarding DRY period, C18:2 *c*9*t*11 was higher for PHN milk ($p < 0.001$), whereas it showed lower C18:2 *c*9*c*12 and odd- and branched-chain fatty acids than CTR milk ($p \leq 0.05$). Dietary phenolic extract lowered milk urea and affected milk clotting parameters similarly across grazing seasons. Its effects on milk fatty acids was lower than expected and varied by grazing season. It could be supposed that bioactive compounds in pasture may have partially masked the phenolic extract effect during both the periods.
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O570

Effects of Sulla Flexuosa hay as alternative feed resource on goat's milk production and quality

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Sulla flexuosa (*Hedysarum flexuosum* L.) is an endemic legume growing in some Mediterranean areas in rainfed and cold mountainous conditions. It could be used in goat diets as an alternative feed resource to supplement forest rangeland. This study aimed to test the effects of incorporating Sulla flexuosa (SF) hay into the diet of Beni Arouss goats on their milk production and quality. The hay was introduced at two levels, i.e. 35 or 70% (SF70), on a DM basis; it partially or totally replaced the alfalfa hay in the control diet. Sulla flexuosa incorporation did not affect milk production or physicochemical composition (pH, acidity, protein, fat, ash, solids non-fat, total solids, and net energy of milk). However, milk FA content varied in proportion to the SF incorporation percentage. The SF70 diet was associated with increased milk levels of healthier FA, such as oleic (C18:1n-9), linolenic (C18:2n-6), α-linolenic (C18:3n-3), docosahexaenoic (C22:6n-3), and total monounsaturated, polyunsaturated, and omega-3 fatty acids, which was mainly due to the inhibition of ruminal biohydrogenation. As a consequence, atherogenic and thrombogenic indices improved. Additionally, the incorporation of Sulla flexuosa, reaching 70 %DM, improved milk polyphenols, which probably increased the antioxidant capacity (FRAP and DPPH) of milk. Therefore, Sulla flexuosa can be used as an interesting alternative forage in goat diets.

O441

Feasibility of mid-infrared spectroscopy for the prediction of milk coagulation properties in the Alpine and Saanen goats breeds

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Milk coagulation process is typically monitored using lactodynamography, which measures rennet coagulation time (RCT, min), curd-firming time as the time to reach a curd firmness of 20 mm (k_{20}, min) and curd firmness after 30 minutes (a_{30}, mm). However, this method has practical limitations, including reliance on skilled personnel, long analysis times, and rennet availability and costs, making large-scale phenotyping challenging. In this context, mid-infrared (MIR) spectroscopy may offer a valuable alternative as a rapid predictive technique. While effective models have been developed for cattle, buffaloes, and sheep, research in goats is limited. This study evaluated the potential use of MIR spectroscopy to predict milk coagulation properties and pH in goat milk. A total of 405 individual milk samples were collected during monthly official milk testing from Saanen and Alpine goats farmed in 8 commercial herds of the Veneto region (Italy). Each sample was divided in two aliquots. The first aliquot was analyzed using CombiFoss™ 7 system for milk quality assessment and MIR spectrum acquisition. The second aliquot was used for the determination of pH (through pH meter) and RCT, k_{20} and a_{30} (through lactodynamographic analysis). Milk spectra were matched with their corresponding measured values of pH, RCT, k_{20} and a_{30} and a partial least squares analysis was performed. The model was fine-tuned using leave-one-out cross validation; spectral data points were centered and scaled. The number of latent variables was set automatically but limited at a maximum of 15 to avoid overfitting. The data set was randomly split into a calibration set (including 70% of the samples) and a validation set (including 30% of the samples), ensuring similar means and standard deviations across both the sets. The average values recorded were 10.60 min for RCT, 2.87 min for k_{20}, 41.18 mm for a_{30}, and 6.64 for pH. In external validation, the coefficients of determination were 0.62 for k_{20}, 0.67 for RCT, 0.68 for a_{30} and 0.82 for pH, while the ratio of prediction to deviation ranged from 1.50 (k_{20}) to 2.36 (pH). In conclusion, MIR spectroscopy demonstrated potential as a tool for predicting milk coagulation properties in goat milk and might be implemented in genetics and breeding.

O144

Fennel seed powder in the diet of dairy buffalo affects milk VOCs profile, antioxidant activity and SCD1 mRNA level

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The aim of this study was to assess the influence of dietary fennel seed powder (FSP) supplementation on milk production, antioxidant properties, volatile organic compounds (VOCs), and gene expression in dairy buffaloes. Twenty animals, homogenous for parity (2.6 ± 1.7), days in milk (DIM: 41.1 ± 7.17), body condition score (BCS: 6.8 ± 0.2) and daily milk yield (DMY: 13.6 ± 1.8 kg), were randomly assigned to two groups fed total mixed ration (TMR): a control group (CON) and a treated group

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(FEN), which received an additional 100 g/day of FSP to the diet. Over a four-week period, the milk yield, composition (Milkoscan), fatty acid (FA) profile (Gas Chromatography), antioxidant activity (superoxide dismutase: SOD, catalase: CAT, glutathione peroxidase: GPx, total antioxidant capacity: TAC, 2,2-diphenyl-1-picrylhydrazyl: DPPH), and volatile organic compounds (Gas Chromatography -Mass Spectrometry) were analyzed, along with the gene expression related to lipid metabolism and antioxidant responses (Real time-qPCR). The treatment had no effect on milk yield or chemical composition. However, FSP supplementation resulted in alterations of the milk FA profile. The milk of the FEN group exhibited significantly higher ($p < 0.05$) mixed FA content (C16:0-C16:1), particularly C16:1 and also C18:1 isomers, accompanied by a significant reduction ($p < 0.05$) in de novo synthesised FA (< C16:0). Gene expression analysis revealed a reduction in the expression of stearoyl-CoA desaturase 1 (SCD1) in the treated group ($p < 0.05$). The milk cholesterol content was found to be significantly lower ($p < 0.001$) in the FSP group milk, while antioxidant parameters demonstrated enhanced oxidative stability, with significantly higher ($p < 0.001$) levels of SOD, CAT, TAC, DPPH observed in the treated group. The analysis of VOCs revealed higher levels ($p < 0.001$) of fennel-derived compounds, such as limonene, fenchone, estragole and anethole, and significantly ($p < 0.001$) lower concentrations of acids, including acetic and butanoic acids, in the milk of the FEN group. The findings of this study indicate that FSP has the potential to enhance the nutritional and functional properties of buffalo milk by increasing its antioxidant capacity and modulating its FA and VOC profiles, while maintaining the yield and cheese-making potential of the milk. Further research is required to investigate the sensory and health implications of this dietary treatment.

O477

The North being cold, the South warm: genome-wide assessment of local sheep breeds in contrasting environmental conditions

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Local breeds are an important source of genetic diversity, being adapted to diverse environmental conditions. The aim of the study is to investigate the molecular basis of resistance to diverging environmental conditions in sheep. Three Italian local breeds Comisana ($n = 531$), Sarda ($n = 445$), and Valle del Belice ($n = 431$) reared in Southern Italy, facing harsh summers and mite winters have been genotyped using the Illumina 50kOvine Beadchip. The genotypes have been merged with other 1339 sheep from 46 breeds originating from Northern and Eastern Europe, which are adapted to extreme cold in winter and mite summers. A case-control GWAS and an FST analysis were performed in order to identify genomic regions underlying adaptive traits. Eighteen SNPs located on 11 chromosomes were identified as the most significant in both approaches. All genes falling within 250 kbp upstream and downstream from the significant SNPs were annotated and used as training to test the genes intersected by significant SNPs using the Gene prioritisation utility in the TopGene tool. This analysis identified 12 functional pathways significantly enriched (FDR <0.05), and having a role in the response to oxidative stress, inflammation, cell ion homeostasis, and protein repair mechanisms, which are important mechanisms related to climate adaptations. A single QTL associated with tail fat deposition was identified through the QTL enrichment analysis carried out using GALLO. The results obtained emphasised the polygenic nature of resistance to opposite environmental conditions suggesting the physiological processes involved. This study can be a starting point to identify gene mutations that could have a useful role with respect to climate change and environmental adaptations.

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O539

Uncovering the architecture of production-driven introgression in Cinisara cattle

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Local livestock breeds play a pivotal role in maintaining agricultural sustainability, biodiversity conservation, and cultural heritage. They often possess unique genetic traits tailored to local environments including rusticity, heat tolerance, and digestive efficiency. Cinisara is a dual-purpose local cattle breed of Podolian ancestry mostly farmed in western Sicily, Italy, and is an integral part of Sicilian agriculture. However, spurious crossbreeding with cosmopolitan breeds aimed at improving meat or milk yield has been reported. To better understand the conservation status and ongoing selection of this unique breed, we investigated and detailed the current depth of cosmopolitan breeds introgression in Cinisara through local ancestry inference (LAI). We genotyped 71 unrelated Cinisara cattle at 65k SNPs, subsequently merging the dataset with genotype data of publicly available cosmopolitan cattle breeds, such as Holstein, Brown Swiss, Limousine, Modicana and Podolica. After quality checks, Cinisara recorded moderate levels of heterozygosity (0.359) and low levels of inbreeding (0.040). Global ancestry analysis confirmed the Podolian origin of the breed while highlighting significant introgression from Holstein and Brown Swiss, contributing 27% and 15%, respectively, to the ancestry composition of the Cinisara population. The Treemix analysis confirmed the migration events from Holstein and Brown Swiss. Local genomic ancestry was inferred using three reference populations: Podolica cattle, representing the ancestral origin of the Cinisara, and the two sources of cosmopolitan introgression: Holstein and Brown Swiss. Among the SNPs identified as highly introgressed (top 1%), 258 and 257 were associated with the Holstein and Brown Swiss reference populations, respectively. Gene-annotation enrichment analysis revealed 52 and 48 candidate genes within the regions defined by the Holstein and Brown Swiss references, respectively. These genomic regions exhibited high to complete substitution by the genomes of the two cosmopolitan breeds, predominantly overlapping with known QTLs associated with milk production traits. These findings align with the historical use of cosmopolitan breeds to enhance the production performance of local breeds. However, they also raise significant concerns regarding the preservation of traditional breeds, livestock biodiversity, and their cultural and economic value. The results underscore the importance of developing informed breeding strategies to balance production improvements with the conservation of genetic heritage.

O293

Black boxing impacts of selection in alpine cattle breeds

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Local cattle breeds from the Alpine region provide valuable case studies on selection's mechanisms, evolution, and impacts. These populations are significant for three reasons. First, selection began recently, preserving much of their ancestral genetic background with data available from its onset. Second, they have been selected for antagonistic traits, such as milk and beef production. Third, their small populations make them susceptible to genetic drift and inbreeding. The breeds studied included Alpine Grey, Rendena, and Aosta Red, with genomic data spanning 3,500–7,000 animals per breed and 65,305 to 564,472 pedigree records. The study aimed to assess how genetic selection shaped these breeds across three dimensions: The first dimension involved estimating population dynamics. Pedigree and genomic data were used to analyze changes in population size, inbreeding coefficients, and genetic relationships. This provided context for broader population trends. The second dimension focused on changes in heritability and genetic correlations for four key traits. Four traits—milk production, protein/fat percentage, fertility, and carcass yield—were analyzed over time, from 1980 to 2017. Results indicated declining heritability for milk production form 2 to 11 % and increasingly antagonistic correlations between milk production and fertility (+20% on average). However, correlations with fat percentage showed no clear patterns, suggesting a non-linear trade-off between milk production and fertility. The 'Bulmer effect', rather than genetic drift, was identified as the primary driver of heritability decline. The third dimension evaluated the genomic footprint of selection: Runs of homozygosity (ROH) were compared between 'young' (born after 2015) and 'old' (born before 2000) animals. This analysis confirmed trends from the other dimensions, exploring biological signatures of recent selection. The findings revealed several key trends. A decline in heritability, particularly for milk production traits, was observed over time. Genetic correlations between milk production and fertility became increasingly antagonistic, indicating that higher milk production had a progressively detrimental effect on fertility. Despite some loss of ancestral genomic footprints closely associated with milk production, these breeds have largely retained their original genetic backgrounds.

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O215

A genome-wide scan to identify signatures of selection in Sarda and Valle del Belìce sheep breeds in relation to their geographical origin

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Natural and artificial selection have shaped the genome of livestock breeds. Sarda (SAR) and Valle del Belìce (VdB) are two important dairy sheep breeds in Italy. In the present study, we genotyped about 900 individuals from both breeds, reared under different agro-climatic conditions (plain, hill and mountain), using medium (MD) and high density (HD) Illumina BeadChip, to investigate the effect of the selection on the genomic architecture of these breeds. When analyzing the three ecotypes from each breed collectively using a within-population statistic (iHS), we identified three clear signals in SAR, located on chromosome (OAR) 19 (35–40 Mb) and on OARX (40–45 Mb and 52–53 Mb), and two clear signals in VdB on OAR03 (209–211 Mb) and on OARX (77–78 Mb). All five candidate regions were detected with both arrays. In VdB, several top 0.1% of the most significant SNPs detected with the HD array were located within candidate regions for milk production traits previously identified in the breed. By comparing the three ecotypes within each breed using Rsb approach and both arrays, we identified a distinctive genomic region on OAR03 (166.9–168.7 Mb) in the mountain ecotype of SAR, which mapped the *ANKS1B,* a candidate gene associated with high-altitude environmental adaptation for hypoxia tolerance. In the VdB breed, we identified a signal on OAR01 (75.5–78 Mb) putatively under selection in the hill and mountain ecotypes but not in the plain ecotype. Most of the significant SNPs in this region are located within *CDC14A*, a gene associated with milk protein percentage. In general, moving from plain to mountain, the animals tend to reduce their milk production and for the dilution effect, the quality traits tend to improve, for fat and protein. When contrasting the extended haplotype homozygosity (EHH) profiles between the mountain and the plain ecotypes from each breed, we identified several highly significant regions on chromosomes 1, 3, 8, 18 and X in SAR and on chromosomes 2, 6 and 25 in VdB. At least, 20% of the SNPs present in these regions exceed the significance threshold (*P*-value = 0.001). Our results highlight several differentially selected regions between the three ecotypes from each breed, confirming the role of environmental adaptability. A further investigation of the candidate genes in the identified regions is needed to refine and validate these results.

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O236

Preliminary study of the Caprera goat: an ancient feral population?

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A preliminary characterisation of the Caprera goat population was conducted through phenotypic assessment and genomic analyses in collaboration with *Associazione Allevatori della Regione Sardegna* and *Parco Nazionale Arcipelago di La Maddalena*. The Caprera goats, a feral, free-roaming, and unmanaged population, have inhabited the island of Caprera -part of the Maddalena Archipelago near Sardinia- since ancient times: according to early written records, they were introduced to the island in the latter half of the 1600s by Corsican shepherds from Bonifacio.

Nine adult individuals (3 females, 6 males) were examined for morphological traits and genotyped using the Illumina IGGC 65K SNP chip. The resulting genomic data were compared to a public dataset from the Italian Goat Consortium, which includes over 1,000 individuals spanning more than 30 Italian goat breeds. After quality control, population structure, genomic background, and inter-population relationships were assessed.

Phenotypically, Caprera goats are large animals, with most individuals exhibiting long hair and predominantly red or red-and-white coat colouration. All individuals were horned, with males displaying greater homogeneity in their appearance compared to females.

Genomic analyses, including multidimensional scaling analysis, genomic distance-based phylogenetic trees, and admixture analysis, revealed a clear genetic originality of the Caprera goats. The population forms a well-separated cluster, distinct from all known Italian breeds. The closest genomic affinities were observed with Sardinian breeds, as expected, and the Montecristo goat, another insular wild goat population. The investigation of runs of homozygosity also uncovered extremely high levels of inbreeding.

These preliminary findings underscore the originality and uniqueness of the Caprera goat population. However, further studies involving a larger sample size and comparisons with other Mediterranean breeds that may have historically influenced these

goats are needed. In addition, in-depth investigations into the Caprera goats' wild behaviour and population dynamics are essential. Such efforts will support the development of effective conservation strategies aimed at preserving this ancient and unique genetic resource, ensuring its long-term survival and valorisation.

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O486

Exploring climate adaptation in European Merino sheep: a landscape genomics approach

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In the context of climate change, it is essential to comprehend the genetic underpinnings of environmental adaptation in livestock. This study investigates the landscape genomics of 24 European Merino sheep populations, examining the associations between 50K SNP chip genotyping data and 19 bioclimatic variables, predominantly related to precipitation and temperature. Following the implementation of quality control filtering, a dataset was obtained, comprising 38,381 SNPs and 736 animals. In order to study the genotype-environment association, five independent runs of the Auxiliary covariate model – implemented in the Baypass software—were performed for each of the 19 bioclimatic variables. The median Bayes Factors (BF) were then calculated. The application of the filtering criteria, which included a median BF exceeding the threshold of 15 and a BF above 10 in each individual run, resulted in the detection of 168 outlier SNPs, which were significantly associated with one or more bioclimatic variables. A total of 232 unique genes were further identified within the 100-kilobase windows around each significant SNP. Based on the highest number of loci with high BF, the variable BIO18, representing precipitation of the warmest quarter, was found to play a major role in driving selective pressure on Merino sheep. Moreover, three main genomic regions mapping on chromosome 1 and two on chromosome 14, respectively, showed exceptionally high BF values. In order to investigate the potential biological functions and pathways of the identified candidate genes associated with environmental adaptation, a Gene Ontology (GO) enrichment analysis was performed using g:Profiler tools. The analysis revealed pathways associated with immune response (GO:0006957), system development (GO:0048731) and keratin filament (GO:0045095). Key genes found in candidate genomic regions from our analyses, including *STAT1*, *COL11A1*, *ATP6V1A* and *COL6A3*, were previously identified as being related to thermoregulation, hair follicle development, lipid metabolism and altitude adaptation, suggesting a possible role in environmental adaptation.

O243

Detection of homozygosity and heterozygosity regions in Southern Italian sheep breeds revealed by high-density SNP array

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Runs of homozygosity (ROH) provide information about the demographic evolution of a population over time and can highlight selection signals related to functional traits. Runs of heterozygosity (ROHet), associated with balancing selection, offer valuable perspectives on the adaptive evolutionary processes of domestic animals. In this study we investigated the ROH and ROHet patterns in four different Italian peninsular sheep breeds: Barbaresca ($n = 48$, BAR), Noticiana ($n = 48$, NOT), Valle del Belice ($n = 142$, VDB), and Sarda ($n = 144$, SAR). The animals were genotyped using the Illumina Ovine SNP600K array. ROHs and ROHet were detected through the R package *detectRUNS*. After quality control, 465,236 SNPs from 372 sheep were retained for the analysis. The Multidimensional Scaling Plot (MDS) showed a clear separation between breeds. The endangered breeds (NOT and BAR) showed the highest mean number of ROH per individual (92.38 and 83.71, respectively), whereas the SAR (60.38) and VDB (58.49) had the lowest one. All the breeds showed similar values for the mean ROH length (~2.50 Mb). A total of 15 ROH islands have been detected.

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These genomic regions mapped genes associated with economically important traits such as reproduction (*ZDHHC21, FSIP2* and *TRNAC-GCA*), milk (*FAM13A, HERC3,* and *HERC6*), meat production (*ABCG2, PKD2, LAP3, NCAPG, SPP1,* and *FAM184B*), and body size (*GRID2* and *LCORL*). Regarding the ROHet, the mean number of segments for individuals ranged from 4.65 (BAR) to 6.50 (VDB); similar values have been identified for the mean length (from 0.15 Mb to 0.17 Mb). The 17 ROHet islands (6 for NOT, 4 for BAR and VBD and 3 for SAR) mapped genes related to reproduction (*CAPSPERB* and *TC2N*) and climate adaptation (*VPS13B* and *NUP37*). Our results showed the usefulness of ROH and ROHet in investigating genomic regions containing genes associated with important traits consistent with the phenotypic characteristics of these involved breeds, which present differences in both morphology and production traits and show excellent adaptability to the local environments. These findings may help in designing effective breeding or conservation programs for these sheep breeds.

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O118

Omic technology to monitoring resilience and adaptation to exercise and heat stress in athlete horses

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In horses heat led to a modulation in hypothalamic–pituitary–adrenal axis, autonomic nervous system and hypothalamic-pituitary-thyroid axis to maintain body temperature and to prevent excessive heat accumulation. However, following strenuous exercise under hot and humid conditions, the accumulation of body heat exceeds dissipation and horses can suffer from heat stress leading to anhidrosis, heat stroke or brain damage. Incremental field standardised exercise tests (fSETs) are valuable systems to evaluate the horse training and fitness. The aim of this research was to address molecular features of resilience and adaptation combining heat and exercise-induced stresses in horses. Six Arabian horses stabled at Italia Endurance Stable and Academy were enrolled for the study and monitored during fSETs in summer and winter, collecting blood samples before and after each fSET. Differences in blood parameters were tested through two-way ANOVA and Student's T test for post-hoc pairwise comparisons. Lactatemia and hematocrit were significantly increased in summer vs. winter and GPT, creatinine, Mg, CK, total bilirubin were increased in summer post vs. pre fSET ($p < 0.05$); urea was significantly increased post vs. pre fSET in winter ($p < 0.05$). Moreover, total RNA was isolated from serum and sequenced through the Illumina® NGS approach. A set of differentially expressed small RNAs (|log2 fold change| >1 and adjusted $p < 0.05$), were obtained with DESeq2 software, including eca-myomir-206, eca-mir-301, 36133p, 142 and 144 that were modulated in response to temperature and exercise; a protein-protein interaction (PPI) network for targets of miRNAs was built and submitted for a gene ontology (GO) enrichment analysis. In post vs. pre fSET, enriched terms were related to transcriptional regulation, glucose and LDL response, intracellular trafficking and cytoskeleton organisation, cardiac conduction, ions channels and immune regulation. In summer post vs. pre fSET, terms for positive regulation of dendritic cell cytokine production, negative regulation of inflammatory response, negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathways, were enriched. In conclusion, no serious signs of decompensation were highlighted. The differences in the circulating transcriptome between the two comparisons early trigger homeostasis restoration systems and could be useful to understand the mechanism of successful adaptation to stress and plan personalised training.

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O525

From wastes to resources: using construction and demolition wastes to develop sustainable horse footing layers

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Nowadays, the horse industry is knowing a growing economic importance as well as an increasing environmental impact in the European Union. One of the aspects that could be addressed to increase the sustainability of the horse industry is related to the equestrian footing surfaces. In fact, they still demand non-renewable resources such as sand and water. The present study aimed to apply a circular economy approach by using materials deriving from construction and demolition wastes (CDW) and extractive waste (EW) to develop sustainable and safe horse footing layers. The study was carried out for three weeks (from the 22nd of July to the 9th of August). Five wooden boxes of 1.2 m × 1 m were built to simulate equestrian arenas. Each box was filled with a three-layer mixture; the drainage and the stabilizer layers, made from CDW materials, were common to all boxes, while footing layers were different: natural sand commonly used in the equestrian arenas (Box 1, control box), recycled granite sand from EW (Box 2), CDW sand (Box 3), 50% recycled granite sand from EW and 50% CDW sand (Box 4), stabilised soil from granite EW (Box 5). The footing layers were tested for the five technical criteria specified by the Fédération Equestre Internationale (FEI). In particular, the uniformity was evaluated according to granulometric analysis. The grip, the cushioning and the responsiveness were tested with a *Traction Tester* that was equipped with two different horseshoes (i.e. plastic and iron). The impact firmness was tested with a soil penetrometer. Moreover, the water holding capacity (WHC) was tested according to literature methods. Data were recorded for five days and repeated three times. Data were statistically analyzed (JMPpro v17, SAS Institute) by constructing a linear mixed effects model considering the following fixed effects: footing layer, horseshoe type, and their interaction. Our results highlighted significant differences ($p < 0.05$) among the footing layers tested in terms of impact firmness, cushioning, grip, and WHC. In particular, Boxes 2 and 4 could represent sustainable alternatives as they exhibited characteristics similar to the control box made of natural sand. The data obtained represent a positive outcome and point out the attention on the use of CDW as resources. Further tests on field are needed exploring the use of these materials in real conditions.

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O516

Towards a higher level of welfare in pasture-kept horses: development and application of a new welfare protocol

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Nowadays, horses are most commonly stabled in individual loose boxes. However, more ethological alternatives have been applied in recent decades. In particular, pasture-based systems have become increasingly popular. In Italy, this type of housing is widely used for meat production horses, including the Italian Heavy Draft Horse (IHDH). Although the pasture better meets horses' needs, it is not free from welfare risks. No method exists to assess the welfare of pasture-kept horses and only protocols to assess horses kept in boxes, such as the AWIN, have been developed. Hence, this study aims to develop and apply a new objective and feasible protocol to assess the welfare of pasture-kept horses. Considering that the risks associated with pasture are different from those associated with stabling, the authors developed the protocol selecting from the literature the most indicative parameters for this type of husbandry. The protocol was structured around the Welfare Quality® principles of good feeding, housing, health and behaviour. Different parameters were selected to assess each of these principles, including some positive welfare indicators, such as the assessment of positive interactions with humans and the environment. This first protocol was tested on 26 IHDHs (21 adults, 5 foals) kept in 3 different herds with a space allowance of about 1 hectare/horse in the Apennines of central Italy. The preliminary results served to revise the protocol and its feasibility. As expected, some parameters that are fundamental in this context were not present in the AWIN. These included the distance from water sources, which was more than 1 km in 42.3% of cases (11/26); the presence of shelter, which was formed only by trees in all the horses assessed (26/26); and the presence of predators, which farmers reported as a common risk, especially for foals.

These preliminary results will be followed by the protocol application on a large scale in the coming months. In particular, the project aims to assess a representative sample of IHDHs across Italy to define the welfare status of this breed. Although these data are preliminary, they highlight the need for an *ad hoc* protocol for the assessment of pasture-kept horses and the limited applicability of protocols developed for other types of husbandry. The ultimate aim would be to promote pasture-based systems for other categories of horses and give the horsemeat consumer a greater guarantee of the welfare of the product consumed.

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O404

Animal welfare assessment of urban carriage horses in Malta

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The Maltese urban carriage horses have been a part of the country's cultural heritage for centuries. However, nowadays the use of horses for urban carriage is losing its social license to operate. The aim of this project was to evaluate the welfare of urban carriage horses in Malta using a new bespoke protocol by analyzing both animal-level and owner-level factors to enhance horse welfare The welfare assessment was performed on 60 urban carriage horses and 43 owners, during summer, when the high temperature (30°C–35°C) and the number of tourists increase could have an impact on the welfare of the horses. This new protocol was created following a structured and comprehensive approach to evaluate both animal-level and owner-level factors based on the four principles of animal welfare, the AWIN protocol, literature review and 5 experts' opinions. Owner-level evaluations included face-to-face interviews to all the 43 owners addressing feeding, health management, housing, and human-animal interactions. At the animal level 30% were assessed during the breaks at the place of work 70% were assessed at the stable depending on the availability of the owners. On average, horses used to work three times weekly, 6 hours each day. Welfare indicators such as housing, feeding, and behavior were recorded. Observations were complemented by health checks, behavioral assessments, and an approach test to estimate the horses' responses to human interaction by the same assessor. Results highlighted positive welfare practices, such as body condition scores of 3 (92%) and cleanliness (97%), though areas for improvement can include providing better shade areas during work, feed, and water ad libitum. 100% of horses inspected had no access to feed during working time and rationed feed at the stable (91% fed twice a day and 9% three times per day). Moreover in 100% of horses inspected during working time water was provided by buckets. Most horses exhibited no behavioral issues, injuries, or lameness. However, minor health concerns, such as skin disorders (7%) and respiratory issues (2%), were observed. The study emphasised that caretakers have accumulated extensive experience in this role over the years. They primarily relied on veterinarians for health care but faced challenges due to limited availability. Overall, the assessment provided valuable insights into the welfare of urban carriage horses in Malta, identifying strengths and opportunities for targeted welfare improvements through the creation of guidelines and policy.

0224

Exploring the nutritional value of *Mytilus galloprovincialis* from the Gargano area (Apulia Region)

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Mussels' aquaculture provides food products with high quality proteins that represent an important part of the Mediterranean diet, especially in health conscious consumers. Being filter-feeding organisms, mussels exhibit dynamic and cyclic changes in the concentration of nutritional compounds, especially due to geographical location, reproductive cycle, seasonal changes, and seawater composition, even when cultured in nearby the same coastal ecosystem or in sites within the same embayment. The Gargano Peninsula, located in Southern Italy along the Adriatic coast, represents an ideal environment for mussel cultivation due to its favorable climate, nutrient-rich waters, and extensive coastline. Therefore, the objective of this study was to assess the nutritional characteristics of *Mytilus galloprovincialis* cultivated in three offshore farming sites located in the Northern Coastal Area of Gargano. The mussel farms were characterised by different dropper ropes distances: extensive dropper ropes farming (EDR: 70 m distance between backbones, 90 cm distance between dropper ropes), intensive dropper ropes farming (IDR: 30 m distance between backbones, 60/70 cm distance between dropper ropes) and semi-intensive dropper ropes (SIDR: 70 m distance between backbones, 50/60 cm distance between dropper ropes). Mussels' chemical composition, fatty acids, and amino acids profiles were investigated at monthly intervals, from April to June 2023. Data were analyzed by two-way ANOVA with farming system and sampling time as fixed effects by using the GLM procedures of SAS. The results revealed that the fat content of mussels from EDR and SIDR sites was lower than values observed for mussels of the IDR in both, April and June sampling months. An increase of the main saturated fatty acids (C15:0; C16:0; C17:0 and C18:0; $p < 0.001$) and polyunsaturated fatty acids (C18:2c9c12, C18:3n3, C20:2n6, C20:4n6, and C22:6n3; $p < 0.001$) was found in the mussels collected in June from all farms analyzed. Refers to farming systems, mussels from the EDR and SIDR sites exhibited the greatest content of n3 fatty acids ($p < 0.05$) and conjugated linoleic acids isomers ($p < 0.001$) compared to the IDR farming site. Mussels collected from EDR and SIDR sites evidenced higher values of glutamic acid ($p < 0.05$), serine ($p < 0.05$), tryptophan ($p < 0.001$), hydroxyproline ($p < 0.05$) and proline ($p < 0.01$) amino acids. This study suggests that EDR and SIDR farming

methods are able to modulate the nutritional composition of mussels reared in the Gargano area.
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O408

Flesh quality, shelf-life, and sensory properties of Sea Bream reared in a Mediterranean coastal Integrated Multi-Trophic Aquaculture (IMTA) system

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Integrated Multi-Trophic Aquaculture (IMTA) is an emerging system that combine the farming of aquatic species from different trophic levels in an integrated approach enhancing efficiency while minimising waste. This study investigated the flesh quality, shelf-life, and sensory properties of sea bream (*Sparus aurata*) reared in the REMEDIA Life IMTA system, located in the Mar Grande of Taranto (Northern Ionian Sea, Southern Italy). The Mar Grande, a semi-enclosed basin connected to the Gulf of Taranto, is characterised by significant anthropogenic activity, including commercial and military ports, and extensive mussel farming. The research was conducted at the 'Maricoltura Mar Grande' (MMG) aquaculture facility. Since 2019, half of the MMG plant has been transformed into an innovative IMTA system as part of the EU REMEDIA Life project. This system incorporates bioremediator organisms: sponges, polychaetes, bivalves, and macroalgae, supported by artificial vertical collectors to enhance the settlement of sessile macroinvertebrates and improve environmental quality. A total of 48 fishes (18 months old) collected from MMG farm were analysed: of which 24 belong to IMTA system and 24 to the control group (C) reared without bioremediators. Both groups receive the same commercial feed. For each group, 8 fishes were analysed after +24 h, 1 and 2 week of storage at 2 ± 1 °C. IMTA fishes showed a significantly longer tail, probably due to the reduced cannibalism occurring in this system. The total (331.44 ± 34.06) and fillet (107.19 ± 10.22) weights were markedly greater for IMTA group ($p < 0.05$). On average, IMTA fishes showed significantly lower pH value and moisture content of flesh, but higher fat content. In all the storage times, the content of total saturated fatty acids was markedly higher in the C group in turn of a lower concentration of polyunsaturated fatty acids ($p < 0.05$). The quality index method, a sensory test performed using odor, color, texture, clarity and shape of the eye, and color of the gill, showed better results for IMTA fishes, particularly after 2 weeks of storage with better scores for skin brightness, flesh texture, eyes clarity and shape, gill colour and odour and total score ($p < 0.05$). In conclusion, sea bream reared in the IMTA system showed better flesh quality, extended shelf-life, and superior sensory properties, highlighting the potential of the IMTA system to enhance sustainable aquaculture productivity while mitigating environmental impacts.
Research founded by the European Commission, Life Environment program: REMEDIA Life project (LIFE16 ENV/IT/000343): Remediation of Marine Environment and Development of Innovative Aquaculture: exploitation of Edible/not Edible biomass.

O122

Substitution of fishmeal with an insect meal blend and the effects on the intestinal microbiota of European seabass

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In recent decades, aquaculture research has increasingly focused on alternative protein sources, like insect meal (IM), as replacements for fishmeal (FM), which is in growing demand in aquafeed industry. This study examined the impact of a blend of black soldier fly larvae (BSFL) and yellow mealworm larvae (YML) on the growth performance and gut microbiota of European seabass (*Dicentrarchus labrax*). Seabass juveniles were fed a control and two treatment diets for 75 days. Diets in which 25% and 50% of FM were replaced with IM, referred to as IM25 and IM50, respectively, showed no negative impact on feed intake or fish health. BSFL and YML were added at a 50:50 ratio, with an inclusion level of 2.15% (IM25) and 4.20% (IM50) each. At the end of the trial,

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key indicators like voluntary feed intake, feed conversion ratio, and daily growth index were consistent across all groups, confirming that this IM blend supports growth performance effectively. Gut microbiota analysis revealed some significant differences between the feeding groups. While there were no significant changes in alpha diversity indices (Chao1 and Shannon), an increasing trend appeared to be associated with the IM blend. Analysis of beta diversity revealed an overall stability in mucosa-associated microbiota and notable shifts in digesta-associated microbiota in the IM25 and IM50 groups. This reflects the higher sensitivity of the transient microbiota to dietary changes compared to the stable microbiota. Beneficial bacterial genera, including *Bacillus* ($p = 1.21 \times 10^{-6}$ mucosa; $p = 2.61 \times 10^{-8}$ digesta), and *Paenibacillus* ($p = 1.30 \times 10^{-6}$ mucosa; $p = 0.0002$ digesta), were enriched in fish fed with the IM blend, likely due to their chitinolytic activity. *Oceanobacillus* ($p = 0.0002$) and *Brevibacterium* ($p = 0.0002$) were more abundant in the digesta of IM-fed fish but not in the mucosa, suggesting that they are more responsive to changes in diet than to a stable mucosal environment. Our findings highlight the potential of this BSFL-YML blend to successfully maintain fish health and growth performance, and at the same time foster a beneficial gut microbiota in the short term. This study does not investigate the long-term effects of IM inclusion in aquafeeds. To assess whether IM stands as a feasible replacement for FM, further research is needed.

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O031

Employing a natural microencapsulated antioxidant to mitigate dietary microplastic accumulation and oxidative stress response in juvenile European seabass (*Dicentrarchus labrax*)

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The potential contamination of aquafeeds by microplastics (MP) exposes farmed fish to this widely distributed contaminant, posing a risk for their health and consumers' concerns. Dietary MP smaller than 20 µm can be absorbed at fish intestinal level, leading to a consequent translocation to other tissues, among which liver acts as a retaining organ. This prevents the accumulation in other sites but causes the triggering of oxidative stress. The present study aimed to implement fish feeds with a strong antioxidant molecule (natural astaxanthin; AX) included in microcapsules made of an organic wall matrix able to preserve it and, at the same time, to exert a crucial role in limiting the MP absorption at fish intestinal level. European seabass juveniles were fed diets containing commercially available fluorescent MP microbeads (1–5 µm; 50 mg/kg feed) alone or in combination with microencapsulated AX (7 g/kg feed; tested for half or whole feeding trial – 30 or 60 days, respectively). MP were localised in fish tissues with confocal microscopy and were quantified by a KOH-mediated digestion of tissues samples followed by a MP count on filters through epifluorescence microscopy. Fish welfare was assessed with histological and molecular analyses. Fish from the different dietary treatments did not evidence variations in survival and growth performance as well as gut pathological alterations. However, the fluorescent MP microbeads were absorbed at the intestinal level with a consequent translocation to the liver, leading, when provided solely, to an upregulation of oxidative stress markers (*sod1*, *sod2*, and *cat*). Interestingly, the dietary implementation of microencapsulated AX significantly mitigated the oxidative stress response. Additionally, the microcapsules promoted MP coagulation in the fish gut, limiting their absorption and accumulation in all the tissues analyzed (intestine, liver, blood, muscle, and adipose tissue), resulting in a higher detection in fish feces. In fact, the wall matrix was mainly composed of starch that promoted the formation of MP coagula too large to be absorbed by the enterocytes; a process favored by the transition through the stomach acidic environment. These results can be of great interest for the aquaculture sector in light to promote fish welfare and quality product.

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O054

Estimation of protein and fat requirements for greater amberjack (*Seriola dumerili*) juveniles

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The farming of greater amberjack (*Seriola dumerili*) in Europe is limited by the lack of suitable diets, requiring an optimal protein-to-energy balance for its sustainable production. Thus, this study investigates optimal dietary protein and fat levels in greater amberjack juveniles by testing six experimental diets formulated according to a bifactorial arrangement combining three crude protein (50%, 55%, 60% as fed) and two crude fat levels (14%, 17% as fed). Trials were conducted at ICTA facilities in RAS systems (temperature 22 ± 1.6 °C; DO 7.5 ± 0.5 mg/L; salinity 28 ± 1.8 g/L; pH 8.1 ± 1.2; NO_3^- 32 ± 9.4 mg/L; NO_2^- and NH_4^+ not detectable) with fish initially stocked at 1.3 kg/m^3 and fed to visual apparent satiation. Digestibility and postprandial nitrogen excretion assays followed a Latin square experimental design (5 replicates per diet) by feeding 20 fish (65g on average) randomly distributed in 5 tanks for 90 days. The growth trial used 720 fish (58 g on average) randomly allocated in 18 tanks (3 replicates per diet) and fed experimental diets for 84 days. Data were analysed using ANOVA with initial weight as a covariate and differences were tested via Newman-Keuls test ($p < 0.05$). Apparent digestibility coefficients of protein and fat increased as dietary CP decreased from 60% to 55% and 50% (+8% for both nutrients) and when CF decreased from 17% to 14% (+8% and +6%, respectively for protein and fat; $p < 0.05$). No differences were observed in hourly nitrogen excretion either related to CP or CF level. Daily nitrogen excretion decreased (−49%) as CP decreased from 60% to 55% and 50% ($p < 0.05$), whereas no differences were observed respect to CF level. Survival rate was lower in fish fed diets with 60% CP compared to those fed diets with 50% (52% vs. 83%, respectively) and in fish fed diets with 17% CF compared to 14% (57% vs. 79%; $p < 0.05$). Final weight and specific growth rate were lower (−17% for both variables; $p < 0.05$) in fish fed the diet formulated with 60% CP and 17% CF compared to other diets. No differences were found in body composition and somatic indexes of fish according to the dietary CP or CF levels. Overall, diets exceeding 55% CP and 14% CF impaired productive performance, likely due to surplus protein being metabolised for energy and surplus fat limiting nutrient utilisation, which increased nitrogen excretion. Future studies aimed at optimising protein-to-energy ratios are needed for eco-friendly and cost-effective greater amberjack aquaculture.

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O248

Monitoring water temperature during the growth of gilthead sea bream juveniles in sea cage aquaculture

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Mediterranean Sea is showing an increase in water temperature with effects on mariculture cage systems especially on growth of euryhaline fish species altering feeding behaviour and causing physiological stress. Gilthead sea bream is able to tolerate a moderate increase in temperature and feeding regimes need to be reduced. Innovations in digital systems applied to the record temperature trend and water quality can help mitigate risks on the environment and improve farm management.

In this context, a study was conducted to investigate the application of a digital water monitoring system in a sea cage farm in the South Adriatic Sea. The study aimed to analyse the mean body weight and growth trend of gilthead sea bream (initial mean body weight: 12.75 g) in relation to water temperature, from mid-June 2024 to mid-December 2024.

A digital water monitoring system was installed in a cage equipped with a water temperature sensor to record this parameter in real time and store the data in the cloud. The mean body weight was sampled monthly and compared to that of sea bream juveniles (initial mean body weight: 12.1 g) reared in a cage at the same stocking density during a previous production cycle in the same fish farm (2022). During that earlier cycle, water temperature was only recorded occasionally.

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The growth model of the two productive cycles were studied and data were submitted to unpaired *t*-test statistical analysis using GraphPad Prism 10.4.0 (621).
In the summer of 2024, sea bream had a mean body weight that was 23% lower than those reared in the same season in 2022, when water temperatures had higher average values (>29 °C) for a prolonged time than those recorded in 2022 (26 °C).
Thanks to real-time water temperature monitoring, fish growth was recovered by adjusting the feeding rate more accurately. As a result, after six months, no significant differences were observed between the mean body weight recorded in 2022 (119.8 ± 3.38 g) and in 2024 (121.3 ± 2.07 g).
This trial demonstrated that the application of a digital system for water temperature monitoring improved the feeding strategy and the fish growth also with benefits for the environment.
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O082

Aquaculture in the Mediterranean region: key factors and future trends

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This study is based on the analysis of Mediterranean aquaculture value from 1984 to 2017 and on aquaculture production data from 1950 to 2017, obtained from the FAO databases, which are the largest existing aquaculture databases. In this research the economic value of all farmed species in the region have been analyzed, in all the countries. Univariate and descriptive statistics, regression analysis including polynomial models, cluster analysis and Shannon diversity index have been used in the statistical elaboration of the data. Both functional and geographical expansion of aquaculture is investigated, considering two main complementary aspects of aquaculture: farmed species and farming countries. The calculated models on Mediterranean global value of aquaculture foresee that it is in a stationary phase and that in the next future it will keep constant about 4.8 US$ billions. Aquaculture diversity is a crucial factor for future expansion, but the current aquaculture economic impact is based on a few successful species and countries. In the future the 80% of economic value of aquaculture will be provided by 4 or 5 species and the 99% of value by 20 to 22 species. The most relevant species of aquaculture economic value are Nile tilapia, gilthead seabream and European seabass. Even if the first Mediterranean country is Egypt, which aquaculture is based on extensively farmed tilapia, the analysis of relative aquaculture growth and the geographical expansion of aquaculture indicate that leading countries are Malta, Israel, Greece and Cyprus. These countries should be taken as possible models for country aquaculture development, with the exception of Malta where intensive aquaculture has reached the sustainability limit. The balance between aquaculture and capture fishery has been largely surpassed in some representative countries (Malta, Israel and Egypt). In these countries the aquaculture/fishery ratio in 2017 was higher than 3, with Israel where the production of aquaculture more than 8 times that of fishery. Up to our knowledge, this study represents the most extensive research on the economic value of aquaculture in the Mediterranean, based on its evolution in a period of 33 years. This study shows aquaculture economic models and productive traits that can be used as a powerful reference point for a sustainable aquaculture policy and management in the Mediterranean.

O526

Reduction of amylose-amylopectin ratio in low-protein diets for fattening pigs: performance, health, behavioral, and environmental implications

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To improve the environmental sustainability, the reduction of dietary crude protein (CP) coupled with the inclusion of amino acids (AAs) is a common strategy; however, it can raise issues related to the synchronisation between glucose and AAs blood availability with negative effect on the growth performance. A low amylose-to-amylopectin ratio (AM:AP) in the diet with synthetic AAs modulate nutrients synchronisation to optimise protein synthesis. This study aim to evaluate the effect of a low CP and AM:AP diet on the performance, welfare, and faecal microbiota of growing-finishing pigs.
1,544 pigs (36.76 kg) were assigned to a control diet (CO) or a treated diet (TRT) blocked for sex and initial body weight (BW). The TRT diet reduced CP by 1.5%, 1.4%, and 0.7% across 3-feeding phases and included waxy maize, characterised by a low AM:AP ratio (CO, AM:A*p* = 16.97; TRT AM:A*p* = 7). A group of 398 pigs were individually tagged and weighed at housing, on d36 and d160, when faecal samples (20 pigs/group) were collected to analyse

microbiota diversity (V3-v4 16S rRNA gene sequencing), calprotectin concentration and ammonia. Behavioural indices and pen-level air gases were monitored monthly. Average daily gain and BW were not influenced by the diet. Faecal microbiota alpha diversity was affected by diet-time interaction ($p < 0.0001$), time (Chao1 and Shannon, $p < 0.001$; InvSimpson, $p = 0.02$), and sex (Chao1, $p = 0.01$; Shannon, $p = 0.02$; InvSimpson, $p = 0.04$). At d36 and d160, the TRT group showed increased abundance of *Clostridium sensu stricto* 1 and *Terrisporobacter*. While some studies associate these genera with intestinal inflammation, others link *Clostridium sensu stricto* to improved feed efficiency. Microbiota may also have been influenced by the inclusion of waxy maize, but there is a lack of studies linking low AM:AP with microbiota composition. Fecal calprotectin and ammonia concentrations did not differ between groups. On d71, the TRT group have higher environmental CO_2 ($p < 0.02$) and H_2S ($p = 0.10$) concentrations. Although literature suggests a link between low CP diet and increased aggression, tail and ear scoring indicated no exacerbation of aggressive behaviours. However, TRT pigs exhibited greater activity and restlessness at d11 ($p = 0.01$) and d50 ($p = 0.03$). This study suggested that a low CP and AM:AP diet can maintain Italian heavy pigs performance and welfare, highlighting the possibility to design a diet that minimise environmental impact.

O360

Growth performance and nutrient balance of pigs fed low protein diets without mineral phosphate supplementation

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To combat issues of nitrogen (N) and phosphorous (P) runoff and reliance on imported protein feed sources and mineral phosphate (MP) in Swiss pig production, a feeding experiment on growing-finishing pigs was conducted. The 48 pigs were blocked by gender, body weight (BW), and litter, assigned to 1 of the 4 treatments (C = control, N = low crude protein (CP) with amino acid (AA) addition, P- = no MP, and N-P- = combination of N- and P-), fed ad libitum, and all housed in one pen. Grower and finisher diets with C contained respectively 15.5% and 13.5% CP, 0.47% and 0.41% P, and 0.29% and 0.26% digestible P (dP), diets with N- contained 10% and 15% less CP, and diets with P- contained 20% and 22% less P, leading to 24% and 21% less dP than C. Diets with N- were optimised to use minimal amounts of imported soybean meal, replaced by Swiss-origin protein beans and rapeseed meal, and synthetic AAs to reach minimal CP but equal digestible AA contents as in C. In P-, phosphate was removed and calcium:dP ratios were fixed as in C by adjusting calcium carbonate. Individual feed intake and weekly BW were recorded. Average daily feed intake and gain, and feed conversion ratio (FCR) were calculated. Over grower and finisher phases (47 ± 4.0d and 40 ± 8.2d, respectively), nutrient balance data were derived by differences between nutrient intake and body nutrient accretion which was derived from body composition assessment by dual X-ray absorptiometry at the start (22.3 ± 3.35kg BW), middle (≈60kg BW at diet change from grower to finisher), and end (BW ≥100kg) of the experiment. Spot samples of urine ($n = 1$) and feces ($n = 4$ over 4 consecutive days) were collected within the end of the grower and finisher phases, respectively. There were no interactions ($p > 0.05$) between N- and P- effects on any measured parameter. No differences ($p > 0.10$) were observed in growth performance due to N- or P- effects, except finisher pigs with P- had a higher FCR ($p < 0.05$, 2.66 vs 2.60). In grower, finisher, and overall periods, the intake and excretion of N and P were reduced ($p < 0.01$) in pigs fed respectively diets N- and P-, and female pigs had better nutrient utilisation rates ($p \leq 0.001$) regardless of treatments.
The findings suggest replacing imported soybean meal with local protein sources and AA supplementation while simultaneously reducing CP contents and the MP removal in growing-finishing pig's diet can maintain animal growth and reduce N and P excretion into the environment.

O187

Feeding low-protein or standard diets to growing-finishing pigs reared under environmental stressors: effects on growth and carcass composition

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This study investigated the effects of low-protein (LP) diets on growth, nutrient digestibility, and carcass composition in pigs reared under environmental stressors (ES). LP diets are a well-established strategy for enhancing the sustainability of pig production. However, when only partially balanced for essential amino acids and fed in the presence of ES, these diets may fail to sustain efficient growth. Forty-eight Swiss Large White female pigs, with an initial body weight (BW) of 20 ± 2.2 kg, were used. Pigs were allocated within BW and litter to pens cleaned daily (D) or twice a week (W). Pigs ($N = 12$) assigned to either the D or W pen, had ad libitum access to isocaloric grower and finisher standard (ST) or a LP diets. The ST diets were formulated according to the Swiss feeding recommendations for pigs and contained 16.4 and 12.5% crude protein (CP), respectively. In the

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LP diets, CP, digestible Lys, Met, Thr, Trp and Val levels were on average 20% lower than the ST diets. The individual BW and feed intake (FI) was monitored weekly and at each feeder visit, respectively. Energy and nitrogen (N) digestibilities were determined from fecal samples collected at 41.9 ± 2.5 and 71.5 ± 2.3 kg BW. Carcass composition was assessed with dual-energy x-ray absorptiometry. Data were analyzed with linear models (R, v4.4.1), with diet, cleaning protocol and the interaction as main effects, and litter as a random effect. Compared to pigs in D pens, average daily FI and average daily gain of pigs in W pens were 8.4 and 8.7% higher ($p < 0.01$), respectively, but total FI did not differ. The latter was due to pigs in D pens spending 5.6 more days on feed ($p < 0.05$), resulting in comparable gain-to-feed ratios. Pigs fed the LP diets were 7.5% less efficient, with 9.0% higher feed intake and 5.1% lower growth rate ($p \leq 0.02$ for each). In LP pigs, gross energy and N digestibilities were on average 2.4 and 3.1% lower than ST pigs, respectively ($p \leq 0.04$ for each). Pen cleaning status as well as dietary CP level had an impact on carcass fat content. Pigs in W pens and LP pigs had 6.3 and 10.7% higher carcass fat content ($p \leq 0.03$ for each). In conclusion, partly balanced LP diets impaired growth traits, nutrient digestibility and carcass quality. Pigs reared in W pens exhibited improved growth without compromising efficiency but showed also increased carcass fatness. This suggests a trade-off between enhanced growth performance and increased carcass fat under less strict hygiene conditions.

O264

Growth performance and carcass quality of heavy pigs fed *ad libitum* diets with decreasing SID lysine contents

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This study aimed to define the lysine requirements of a pig population (Goland C21 × Cambor-ough-43) for dry-cured ham production, using animal growth performance and carcass quality as evaluation criteria. Ninety-six pigs (44.5 kg initial body weight, BW), housed in 8 pens homogeneous in initial BW, were allotted to 4 feeding treatments (2 pens/treatment) differing for the dietary standardised ileal digestible (SID) lysin contents: Low (L), Medium-low (ML), Medium-high (MH), and High (H). The pigs of each treatment received feed with decreasing SID lysine content with increasing age in growing (90–118 days of age), early finishing (119–132 days), and late finishing (133–233 days). The dietary SID lysine content in the three periods were 6.9, 6.0, and 4.2 g/kg for the L group; 7.8, 6.9 and 5.2 g/kg for the ML one; 8.3, 7.8 and 6.0 g/kg for the MH; and 9.3, 8.3 and 6.9 g/kg for the H group. Daily feed intake was measured using automated feeding stations, while BW and backfat thickness (BF) were recorded every two weeks. The data were analysed using a model that included the effects of treatment, sex, and their interaction. Orthogonal contrasts were employed to compare the ML diet with the other treatments. Over the entire experimental period, the ML group exhibited significantly greater final BW ($p < 0.01$; 197 *vs*. 175 kg), and average daily gain (ADG) ($p < 0.01$; 985 *vs*. 859 g/d) compared to L, but L and ML did not differ for feed intake and final BF depth. In addition, the ML treatment did not evidence differences for these traits when compared to MH and H. The ML also exhibited greater carcass weight ($p < 0.01$; 164 *vs*. 145.5 kg), lean cuts ($p < 0.01$; 82 *vs*. 73 kg), and fat cuts ($p = 0.02$; 38.4 *vs*. 32 kg) compared to L, but there were no differences when compared to MH and H. The four treatments evidenced little or no difference for carcass quality traits such as carcass yield (0.834), proportion of lean meat (478 g/kg), total cuts (731 g/kg), lean cuts (507 g/kg), and trimmed ham (189 g/kg). The only exception was for the proportion of fat cuts, which was lower for L compared to ML ($p = 0.047$; 219 *vs*. 234 g/kg). Based on these results, the optimal dietary SID lysine content for this pig population is 7.8, 6.9 and 5.2 g/kg in growing (44 to 75 kg BW), early finishing (76 to 108 kg BW) and finishing (108 to 194 kg BW) period, respectively.

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O101

Effects of a partial to total replacement of soybean meal with spirulina powder in the diets for growing pigs on fatty acid profile of loin, lard, ham trimming and liver fat

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This study investigated the effects of replacing soybean meal (SBM) with *Arthrospira platensis* (AP) in the diets for growing pigs on fatty acid (FA) profile of lard, ham trimming, liver and loin fat. The study involved 88 gilts and barrows (52.4 ± 4.2 kg initial body weight – BW) randomly allocated to one of the following four dietary treatments (2 groups/treatment): a control diet, based on cereals and SBM, and 3 experimental diets formulated by replacing 33%, 66% or 100% SBM with a nucleus based on AP (640 g/kg), sugar beet pulp (308 g/kg) and soft wheat (40 g/kg). After 138 days on feed pigs were slaughtered at 174.9 ± 6.4 kg BW, and samples of lard, trimming fat from hams, liver and loin were individually collected to be analysed for FA profile. Data were analyzed with a mixed model including the effects of tissue, sex and diet and the random effect of animal. Ten saturated FA (SFA), 8 monounsaturated FA (MUFA), and 13 polyunsaturated FA (PUFA) were identified, of which 3 were exclusive to the liver (C22:1n-9, DPA C22:5n-6, DHA C22:6n-3), 2 were present only in the liver and loin (C8:0 and C20:5n-3 EPA), and 1 was absent in the liver (CLA c9,t11). Tissue significantly influenced FA composition ($p < 0.05$). SFA were highest in the liver (43.02%) compared to other tissues, which ranged between 36.98% of loins to 32.13% of ham's fat. MUFA were predominant in loin and ham fat, whereas PUFA were most abundant in the liver (32.17%) and lowest in loin (10.16%). Sex influenced only few FA, the most notable was C18:2n-6, more abundant in females. Diet affected mainly PUFA and SFA content, but no consistent pattern in FA profile variation emerged with increasing levels of AP supplementation, and differences compared to control were limited to specific experimental groups. Concerning interaction effects, only the tissue × diet interaction exhibited notable significance for most FA, mainly due to the different behavior of liver fat compared to other tissues. Indeed, the increase of AP in the diets tended to linearly increase the SFA and decrease the PUFA content in the liver. Conversely, no systematic variation in the FA profile appeared to be associated with the progressive increase of AP in the diets in the other tissues. This study adds new knowledge about the feasibility of using AP as main protein source in the diets of growing pigs, evidencing neutral effects of the replacement of SBM with AP on the quality of fat composition of the carcass tissues obtained.

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O110

Increasing the energy and lysine content of sow transition diets can improve litter performance and modulate colostrum composition

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The transition period from 7 days pre-parturition to 4 days post-parturition is a critical phase for the sow due to physiological changes and nutritional requirements. A balanced diet for energy and amino acid (AAs) requirements could improve reproductive performance, colostrum quality and piglet growth. The aim of this study was to verify the efficacy of a diet designed to improve the coverage of the energy and AAs requirements of the sow during the transition period, compared to a standard diet, on the composition and qualitative characteristics of colostrum and of sows and piglet's performance. Two diets were compared: a standard farm diet (CO) with 2950 kcal of metabolised energy (ME) and 0.70% of SID lysine (Lys) and a treated diet (TRT), characterised by 3100 kcal of ME and 0.85% SID Lys. The ration between the AAs and SID Lys was maintained in both diets. A total of 100 sows, balanced for to body condition score (BCS) and muscle and backfat depth and parity, were divided into the CO and TRT groups, on upon entry into the farrowing room. The diet was administered from day 6 pre-parturition to day 4 post-parturition. Duration of farrowing, timing intervals between born piglets and their vitality were recorded on 12 sows/group. Data on performance and colostrum (20 sows/group) were collected at farrowing (d0), day 6 (d6) and weaning (d24). Colostrum was analysed for its proximal, immunoglobulin (Ig) and metabolomic composition (NMR analysis). The diet did not affect the feed intake, BCS, backfat and muscle loss of the sows. The farrowing duration and piglets-born intervals were not affected by the diet. The TRT group tended to have a higher number of live births ($p = 0.066$), a lower number of stillbirths ($p = 0.002$) and an increase in piglets' weight at weaning ($p = 0.032$) and average daily gain d0-d24 ($p = 0.080$)

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compared to the CO group. Colostrum from the TRT group had a higher percentage of fat ($p = 0.036$) and a different metabolomic profile, mainly characterised by a higher concentration of UDP-gluconate and carnitine and a lower concentration of citrate ($p < 0.05$). In conclusion, the results suggest that a transition diet consisting of 3,101.08 Kcal EM and 0.85% SID Lys is capable of improving sow parturition performance (fewer stillbirths) and lactation performance by modifying sow energy metabolism and colostrum quality.

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O214

Effects of a combination of the active form of Vitamin D and natural triterpenes on sows health and productivity

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Productive sows are susceptible to vitamin D deficiency, resulting in reduced calcium bioavailability, decreased offsprings growth and altered immune functions. We hypothesised that a supplementation of a premix containing glycosylated calcitriol (Active D) combined with triterpenes, able to bypass liver and kidney hydroxylation processes, may enhance sows' productivity and health. The present trial was performed in a conventional commercial farm in which 24 multiparous sows (320.08 ± 26.21 kg) were divided into 3 homogenous groups from one-week prior to farrowing to the end of lactation: Control (CTR) fed a standard basal diet (1800 IU of cholecalciferol), Treatment 1 (T1) and Treatment 2 (T2) fed the basal diet +400 mg/kg and 600 mg/kg of premix corresponding to 0.64 µ/kg and 0.96 µ/kg of calcitriol respectively. Sows body weights (BW), back fat thickness (BF) and body condition score (BCS) were registered during the trial. Farrowing time (FT) was monitored through dedicated cameras. Litters growth performances were evaluated. Blood samples were collected from each sow at the start, farrowing and end of lactation to determine plasma pro-inflammatory cytokines (TNF-α, IL1-β and IL1-α), parathormone (PTH) and calcitriol levels through ELISA tests. Data were analyzed through a general linearised model (GLM) followed by Tukey's test. T1 and T2 sows displayed reduced FT in comparison to CTR (176.25 ± 32.92 min. and 181.25 ± 24.16 min vs 236.25 ± 28.88 min.; $p < 0.05$). T1 litters revealed a higher livability in comparison to CTR at the end of the trial (0.13 ± 0.35 vs 1.25 ± 1.16 lost piglets; $p < 0.05$). Both T1 and T2 piglets revealed better BW at weaning when compared to CTR (10.63 ± 1.06 kg and 10.50 ± 1.07 kg vs 9.38 ± 1.30 kg; $p < 0.05$). No differences in terms of sows BW and BCS were detected ($p > 0.05$). At the end of the lactation, T2 sows revealed lower BF in comparison to CTR ($p < 0.05$). Calcitriol levels were stably higher in T1 and T2 after farrowing (15.83 ± 4.63 pg/ml and 17.49 ± 4.48 pg/ml vs 7.12 ± 3.45 pg/ml; $p < 0.01$) and at the end of lactation (16.79 ± 5.00 pg/ml and 18.61 ± 4.39 pg/ml vs 10.58 ± 3.01 pg/ml; $p < 0.05$). PTH revealed the opposite trend ($p < 0.05$). TNF-α, IL1-β and IL1- α were markedly lower at the end of the trial in T1 and T2 sows ($p < 0.05$).

In conclusion, the tested solution based on glycosylated calcitriol improved sows productivity and health in a critical phase of the production cycle due to its enhanced bioavailability.

O209

Leveraging 3D accelerometer data to predict heat stress in dairy cows

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Collar-based activity sensors are increasingly recognised as effective tools for monitoring cow behavior and identifying potential indicators of heat stress. This study evaluated the use of a 3D accelerometer-based neck-mounted collar (AfiCollar, Kibbutz Afikim, Afimilk, Israel) to investigate the associations between feeding, rumination, and panting behaviors under varying stress conditions, as defined by the daily average temperature-humidity index (THI). The study was conducted on 1,295 Holstein cows housed in four commercial farms across Lombardy, Emilia-Romagna, and Tuscany (Italy) from September 2023 to October 2024. Behavioral data, captured at 0.01-second intervals by the accelerometer, included feeding, rumination, and panting activities, resulting in a raw dataset of 273,851,259 records. Average (± SD) daily values for feeding, rumination, and panting were 7.82 ± 0.99 hours, 8.23 ± 0.82 hours, and 2.49 ± 0.81 hours, respectively. Climatic data were sourced from NASA POWER and validated against continuous measurements

from a data-logging weather station installed on one farm ($r = 0.98$ for temperature; $r = 0.97$ for THI). Hourly NASA POWER data were used for the entire study period. Statistical analyses were performed using generalised additive mixed models (GAMMs) with integrated smoothness estimation, implemented via the mgcv package in R. A GAMM with repeated measurements was applied to assess the effects of daily mean THI and heat stress conditions, with restricted maximum likelihood (REML) estimation. Fixed effects included days in milk (DIM), parity, season, and farm. Least squares means of behavioral metrics across DIM, parity, and season aligned with established physiological patterns. Results showed that rumination time decreased as the THI increased, particularly above a threshold of 52 (until ~73), likely because heat-stressed cows prioritise thermoregulation over digestive activities. Feeding time decreased with increasing THI, likely due to reduced feed intake as a response to heat stress. Conversely, panting behavior increased with higher THI. The study demonstrates the effectiveness of 3D accelerometer collars in detecting heat stress-related behaviors. These findings are particularly relevant for managing dairy cows in moderate climates, highlighting the importance of implementing strategies such as adjusting feeding schedules or enhancing cooling systems to mitigate the adverse effects of heat stress.

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O273

Evaluation of feeding behaviour in growing bulls with an ear-tag accelerometer

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Precision farming relies on the availability of data collected automatically by sensors to increase the overall farm production efficiency. Feeding behaviour in cattle is one of the most monitored aspects, and many studies associate this trait with production, welfare, and health parameters. This study aimed to evaluate whether the CowManager ear sensor (CowManager B.V.) is suitable for monitoring the eating time of growing bulls. For this purpose, 23 Italian Simmental bulls were equipped with an ear-tag accelerometer and video recorded for 5 days (HDR-AS50, Sony Corp.). For each day and for each pen, the three non-consecutive hours with the highest number of accesses to the feed bunks were selected. A trained operator visualised roughly 350 hours of records and annotated eating behaviour using Boris software (Behavioral Observation Research Interactive Software, v.8.19.1), an appropriate tool for live observation. The data recorded by the accelerometer were compared with visual observations with a 2-sided paired *t*-test, and a significant difference ($p < 0.001$) was found with an average difference of 1.83 min/h. The Pearson coefficient (0.55, $p < 0.01$) denoted a moderate positive correlation between the ear-tag accelerometer and visual observation according to the manual 'Applied Statistics for the Behavioural Science' (5th edition). The concordance correlation coefficient of 0.52 confirmed this finding, suggesting that the results seem promising despite the difference between the data recorded with the two approaches. However, a more thorough evaluation of CowManager is needed to detect accurately the eating behaviour in growing bulls. Research supported by PRIN2022 M4C2 Inv.1.1 'Improvement of assessment at individual level of feed efficiency and methane emissions: From research to cattle breeding' 2022KSFEKE. Funded by the European Union – NextGenerationEU.

O439

Detection of on-farm indicators for early signals of lameness in dairy cows using generalized additive models

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Lameness is one of the main diseases in dairy farming. The consequences of lameness are reduced milk production, decreased fertility, and early animal culling. The usual method for the evaluation of lameness is the visual observation by farmers, but when the lameness becomes evident it's too late to prevent the milk loss and the consequent economic impacts. This study aims to understand whether on-farm data (milking and behavioral parameters) could be used as early indicators of lameness. The study involved a dairy farm in Northern Italy, with more than 500 Holstein cows. Throughout 2023, data on milking and behavior for each cow at both daily milking sessions were collected using on-farm pedometers and sensors integrated into the rotative

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milking parlor (Afimilk Agricultural Cooperative Ltd). Lameness was visually detected by the farmer. The starting dataset included 13,432 observations from 71 lame cows in the 60 days before and after the day of lameness detection and treatment. Generalised Additive Mixed Models (GAMMS) were used to model the evolution of both milking and behavioral parameters before and after the lameness detection, using days in milk (DIM) and days distance from lameness detection (DDL) as smooth terms. Parity class, milking session, and season were included as fixed effects, while the effect cow was considered random (*mgcv* R package). Moreover, on the model outputs for DDL, derivatives were calculated to identify the changing points of the milking and behavioral parameters around the lameness event (*gratia* R package). Results showed significant changes in all parameters starting from -58 to -18 DDL. Small decreases (<10%) were detected for milk conductivity (mS/cm), average milking flow (kg/min), and average milking time (min). For milk production, there was a decrease (–2 kg, –11%) between –18 DDL and +7 DDL, followed by a recovery. All the behavioral parameters showed significant variations before the lameness detection (from around -40 DDL), especially resting time (from 47% to 55% of the total time), average resting time per bout (+5 min), and hourly steps (+ 4%). The results highlighted that milking and behavioral parameters could be used as early indicators of lameness, with significant changes occurring up to 18 days before visual lameness detection. However further investigations are needed to develop prediction models for early lameness detection.

This study was carried out within the Agritech National Research Center and received funding from the European Union NextGenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022).

O562

Integrated sensor data for monitoring calves' condition

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Calves are essential resources for dairy farming, and preserving their health helps reduce economic and environmental costs. Precision Livestock Farming (PLF) technologies for monitoring young animals can improve herd efficiency and management. The study aimed to integrate data from multiple sources to evaluate the potential for early diagnosis of health and welfare issues, enabling a more comprehensive approach to monitoring dairy calves. The study was conducted between November and May, on a farm located in Northern Italy, involving 37 dairy female calves monitored from birth to weaning. For the first 20 days, they were housed in individual cages, then moved to a multiple pen equipped with automatic feeding systems (AFS). Through the AFS, milk and feed intake, number of visits, sucking speed, and body weight were recorded. In addition, time budget and environmental conditions were collected with HOBO sensors. Those data were integrated with others coming from visual assessment, namely calf health scoring and rectal temperature. Statistical analysis was performed by using the JMP software through OLS – Ordinary Least Squares test and principal component analysis. The results revealed that 30% of calves developed respiratory diseases. Sick calves showed a significant increase in the time spent lying down (%), starting from 5 days before the diagnosis, persisting up to 10 days after diagnosis and treatment. Sick calves were lying for around 75% of the time, 5 days before diagnosis, compared to a lying period of less than 70% for 10 days before the diagnosis. At the same time, a significant reduction in sucking speed (ml/min) and daily concentrate intake (kg/head) was observed in the 5 days prior to the diagnosis, whereas no statistical differences were observed for daily milk intake (l/head). The individual concentrate intake dropped from 1.0 to 0.7 kg/head. Results showed a variation in animal behavior corresponding to the environmental temperatures alert of <10 °C, with lower drinking speed, reduced milk intake and higher respiration rate. The study demonstrated that the integration of sensor data and traditional evaluations improves the early identification of health issues in calves. Changes in lying behavior, concentrate intake, and sucking speed were observed days before respiratory disease diagnosis, highlighting the value of PLF technologies for proactive management, improved calf welfare and reduced economic losses.

This study was carried out within the Agritech National Research Center and received funding from the European Union NextGenerationEU (PIANO NAZIONALE DI RIPRESA E RESILI-ENZA (PNRR) – Missione 4 Componente 2, Investimento 1.4 – D.D. 1032 17/06/2022, CN00000022).

O420

Use of Precision Livestock Farming technologies on dairy cows in a mountain environment

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The preservation of alpine pastures is important for maintaining biodiversity and landscape quality and supporting local economies and traditions, reducing the risk of mountain abandonment. Proper management of grazing cows is crucial to ensure grass quality and availability, as well as animal welfare and productivity. Sustainable grazing practices, supported by Precision Livestock Farming (PLF) technologies, offer a potential solution for optimising herd and pasture management in mountain regions. Sensors can monitor pasture quality and quantity, assessing how dietary changes affect milk yield (MY) and quality, animals' body condition and welfare, enabling improvements in herd management through targeted actions. The study aimed to assess the impact of alpine grazing on productive efficiency, milk quality and animal welfare in an alpine environment through PLF technologies. The study was conducted during summer 2024 on 20 Brown Swiss cows grazing an alpine pasture in Valchiavenna (>1,700 m asl). Milk samples were collected every 2 weeks and analyzed for chemical composition and somatic cell count (SCC). Pasture biomass was measured using a plate meter and grass composition was assessed by identifying plant species and analyzing samples using near-infrared spectroscopy. Cows wore collars, equipped with accelerometers and GPS, and pedometers to record activity, while 10 of them were additionally fitted with RumiWatch halters for monitoring feeding behavior. Body Condition Score (BCS), Locomotion Score (LS), Hygiene Score (HS) and Respiratory Rate (RR) were evaluated. Data analysis was conducted using RStudio for the Principal Component Analysis (PCA), and SAS for the General Linear Model (GLM) procedure. Pasture cover varied across different grazing areas, ranging from 533 to 3,044 kg/ha of biomass, due to the presence of trees, shrubs and rocks. Individual MY decreased over the season ($p < 0.0001$) from 9.9 to 5.8 kg/milking, with average fat and protein content of 4.64% and 3.77% (SD 0.73 and 0.44 respectively). Differences ($p < 0.0001$) in MY, milk fat and protein, as well as HS and RR, were found across different pasture areas. Higher MY levels were associated with areas with higher pasture cover and biodiversity, as identified by PCA. Continuous monitoring and targeted actions are necessary for mitigating the effects of alpine grazing on MY and animal welfare during summer season. PLF technologies may help the management of grazing cows in mountain areas, especially regarding different pasture zones in the alpine systems.
This study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – Missione 4 Componente 2, Investimento 1.4 – D.D. 1032 17/06/2022, CN00000022).

O029

Monitoring the time of calving in dairy cows by means of vocalizations

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Acoustic monitoring is minimally invasive; sounds can be detected in the absence of light, providing information even during night hours. Therefore, bioacoustics represents a potentially interesting tool in various areas of animal production, as automatic systems may be developed to decode information emitted by the animals, depending on the context of emission. The moment of calving is crucial for farm productivity and for ensuring animal welfare. The aim of this study was to investigate the possibility of early detection of calving time by monitoring dairy cows' vocalisations. Ten cows were fitted with individual microphones (Song Meter Micro) attached to a collar and were video recorded from 7 days before the expected calving date until delivery, to identify the precise calving time. One calving required assistance and two were dystocic. The Audacity software was used to label vocalisations during the three hours before calving (1060 labeled vocalisations retained after data cleaning of the original 1226 vocalisations). Vocal rate and duration of vocalisations were calculated, and 15 acoustic features were extracted using MATLAB. Results showed a wide range of individual variation in the rate of vocalisations (min 32–max 340) and a significant increase of the vocal rate as calving approached ($R^2 = 0.75$; $p < 0.05$). Principal Component Analysis did not reveal clear trends in acoustic features relative to the time of calving. However, a general increase of Energy Q25 (amount of energy in the 25th quartile of the spectrum, Hz) was observed, and this was significant for three cows ($p < 0.05$; Kruskal-Wallis test).

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Statistically significant differences were observed for nine variables (duration (s), Peak Frequency (Hz), Energy Q50 (Hz), Amplitude Modulation (dB), Frequency Modulation (Hz), Wiener Entropy, i.e. geometric mean/arithmetic mean of spectrum) between normal and assisted/dystocic deliveries. This suggests that it might be possible to identify calvings requiring special attention, based on the acoustic features of the vocalisations emitted by the cows. Our results confirm that individual monitoring of pre-calving vocalisations of dairy cows is feasible and that the increase in frequency of vocalisations around birth may provide an early warning of the calving time. This paves the way for the future development of automated systems that support farmers in detecting calving and providing timely assistance, especially in case of difficult deliveries.

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O302

Variation of faecal microbiota of bitches during pregnancy and lactation on development of faecal microbiota of puppies during lactation and at weaning

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Microbiota plays a paramount role in the newborn, shaping not only digestive processes but also immunity and behaviour. The composition of microbiota of bitches during pregnancy primes the colonisation of bacteria in utero and affects the microbial population during the early stages of life. The aim of the study was to investigate the faecal microbiota of bitches from mating to 48 days of lactation and that of the corresponding puppies during lactation and at weaning. Faecal samples were collected from 5 Siberian Husky bitches (mean age 6 years), named as family, at mating, within 12 hours from delivery, 48 hours from delivery, after 24 days and 48 days of lactation. Bitches were fed kibble diets, specifically designed for gestation and lactation. Faecal samples were collected from puppies at 24 days and 48 days of lactation and after weaning, at 72 days from delivery. The number of litters ranged from 4 to 7, for a total of 22 puppies. Faecal samples from bitches and puppies were collected in a tube with a preservative and were stored at –20 °C until analysis. After DNA extraction, the V3-V4 hypervariable regions of the 16s rRNA gene were sequenced in a 250 PE mode with Illumina Novaseq platform. FASTQ files were uploaded in QIIME2 and the taxonomic annotations were based on the greengene database using a classifier trained on the amplified regions. The Shannon alpha diversity index significantly differed ($p < 0.001$) between family and also the beta diversity index varied significantly ($p < 0.001$). The Shannon alpha diversity index of bitches decreased ($p < 0.001$) from pregnancy to delivery and increased during lactation. A linear increase of Shannon alpha diversity index was recorded for puppies from lactation to weaning ($p < 0.001$). The linear discriminant analysis effect size identified 64 taxa affected by family (FDR <0.001 and LDA >2) and the relative abundance of Firmicutes increased from early lactation to weaning in puppies (from 78% to 87%, $p < 0.05$), whilst the relative abundance of Bacteroidota 36% to 30% ($p < 0.05$) and that of Enterococcaceae from 4,11% to 1.53% ($p < 0.05$). The results indicated that the microbiota of puppies is primed from the mother, either in relation to pregnancy and during lactation.

O069

Analysis of BRCA gene SNPs in dogs with mammary tumor

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Canine Mammary Tumor (CMT) is the most common cancers in female dogs. CMT has a multifactorial etiopathogenesis, due to the interaction of genetic, hormonal and environmental factors. Among the hormonal factors, steroid hormones, particularly estrogens and progesterone, play a crucial role in promoting mammary epithelial proliferation and creating a favorable environment for neoplastic transformation. Additionally, advanced age, early-life obesity, and dietary factors contribute to the onset of the disease. In recent years, given the relevance of CMT as a model for comparative oncology in human breast cancer, scientific interest in the genetic factors involved in its development has been steadily increasing, particularly regarding the *Breast and Ovarian Cancer Susceptibility Gene 2* (*BRCA2*). Mutations in this gene have been widely associated with breast and ovarian cancers in humans, and recent studies suggest a potential correlation in CMTs as well. *BRCA2* plays a fundamental role in DNA repair processes and the prevention of genomic instability. Consequently, its mutations may result in genomic instability, promoting tumor initiation and progression. The aim of this study is to identify potential single nucleotide polymorphisms (SNPs) in the *BRCA2* gene and the evaluation of their possible correlation

with the malignancy grade of the CMT and the prognosis of the patient. SNP analysis was performed on DNA extracted from blood samples collected from five healthy dogs and five dogs affected by CMT. DNA amplification was conducted via polymerase chain reaction (PCR) employing primers specific to exons 11, 23, 24, and 27 of the BRCA2 gene. The amplified products were subsequently subjected to Sanger sequencing, and the resulting sequences were examined for the identification of SNP variants. Tumor tissue samples were subjected to histopathological analysis to evaluate the malignancy grade of the neoplasm. Based on the anticipated results, we expect to observe a correlation between the identified SNPs and the tumor's malignancy grade. Characterising potential mutations in the *BRCA2* gene has important clinical and practical implications. Genetic screening could become a diagnostic tool for identifying at-risk individuals, improving preventive management, such as early sterilisation, and guiding personalised therapeutic strategies.

O160

Functional ingredients in cats' nutrition

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Many pet owners regard their animals as family members, and consequently pay a lot of attention to their dietary and health-related considerations. As a consequence, there is a growing interest to probiotics due to their beneficial effects on pets' health. The aim of this study is to investigate the impact of *Bacillus clausii*, a strain with established antimicrobial and immunomodulatory properties, on the gut health of cats, since a healthy gut impacts host physiology and well-being, influencing nutrient absorption, metabolism and protective functions. A total of 14 healthy adult neutered Chartreux cats (mean age 6.2 ± 2.8 years; 4 males and 10 females; body condition score_ BCS 5.64 ± 0.69/9 points) were recruited for a double-blind trial. The cats were randomly divided into two groups, which received 10 g/d of supplementation: control (CTR_maltodextrin) and treatment (TRT_B.clausii, 1.00×10^6 CFU) in their diet. The trial lasted 6 weeks (1 of adaptation and 5 of administration). Individual feed intake, body weight, BCS, and faecal quality parameters (faecal score_FS on 7 points scale, IgA, pH, D- and L-lactic acids, short-chain fatty acids_SCFA and calprotectin) were weekly monitored. The results indicated a significant increase ($p < 0.001$) in feed intake in the TRT group (from 13.9 to 14.3 g/d/Kg) in comparison to the CTR group (from 13.0 to 13.2 g/d/Kg). No significant differences in body weight and BCS were discerned. Furthermore, after 5 weeks of treatment the TRT group showed improved stool quality, reduced FS (from 4.29 to 3.0) and high DM content (from 32.4 to 58.0%), no variations were observed in CTR group. Moreover, faecal aspecific and specific inflammatory biomarkers levels were significantly ($p < 0.001$) affected by *B. clausii* supplementation (IgA increased from 5.87 to 6.61 mg/dl; Calprotectin decreased from 12.4 to 7.8 µg/dL) no significant time effect variations were observed in CTR group. *Bacillus clausii* administration also resulted in an increase in butyrate (from 37.8 to 44.9 µmol/g) while in CTR group butyrate progressively decreased (from 38.8 to 25.3 µmol/g). No statistical differences were observed between the groups and along the trial about D- and L-lactic acids. These preliminary results suggest that *B. clausii* supplementation may improve gut health in cats, potentially leading to better health and well-being probably due to an increase of beneficial microbial population.

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O329

Homemade diets for dogs: owner's motivation and management

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There has been an increasing trend among dog owners in the use of homemade diets (HD) globally. A cross-sectional study was conducted to investigate the motivations of Italian dog owners for using HD, along with the ingredients they use. The survey was carried out from April 2022 to June 2023 via Google Forms distributed over social media. Only owners who fed their dog a HD were invited to participate and those with multiple dogs were instructed to respond only for one dog. Voluntary responses ($n = 141$) were collected and descriptive statistics applied. Most dogs were reported as mixed breed (33%) and healthy (60%). Currently, gastrointestinal diseases (23%) and adverse food reactions (19%) were the most frequently reported health problems. More than half of the participants (64%) reported applying HD as advised by nutritionists (31%) or non-nutritionist (28%) veterinarians, although some used online sources and magazines (29%). Reported main motivations for HD were 'being healthier than commercial food (CF)' (48%) and 'being a treatment option (32%)'. Compared to previous

CF, HD was more satisfying according to 90% of the participants whose dog showed fewer episodes of diarrhea (66%) and vomiting (74%), increased activity (75%), and enjoyed more food (71%). As protein sources, white and red meat (88%; among which 29% chicken and turkey, 26% beef, 19% pork), fish (83%; among which 34% codfish, 15% salmon, 11% whiting) and eggs (38%) were used. The carbohydrate source used in HD was starchy food and/or potatoes (63%; among which 40% bread, 30% potatoes, 22% pasta), and cereals (37%; mostly rice, 68%). Generally, vegetable oils (87%; among which 42% sunflower oil, 14% coconut oil, and 13% olive oil) and animal fats (59%; 59% salmon oil, 11% butter, and 10% lard) were used. Additionally, 91% of the participants included vegetables (23% carrots, 23% zucchini, and 15% pumpkin) in HD. The majority of the owners (80%) reported using vitamin-mineral supplements (VMS) for balancing HD.
In conclusion, our survey indicates that the primary reasons for using HD are its perception as a healthier alternative to CF and its recommendation by veterinarians as a treatment option for dogs. HD includes a variety of ingredients; however, some crucial ones, such as vegetable oils rich in essential fatty acids and VMS are not always included in HD. This finding highlights the crucial role of specialised veterinary nutritionists in ensuring adequate and balanced HDs for dogs.

O294

Genetic evaluation of Sarda sheep for milk protein content based on genomic information and a female reference population

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Genomic selection relies on reference animals with genomic and phenotypic data to train models linking DNA markers to traits. These models may enable accurate genetic predictions for no phenotyped animals. In dairy cattle, the reference population has traditionally included many bulls with progeny tests based on extensive daughter records, ensuring high prediction accuracy. In dairy sheep, however, the smaller size of sire families, limited phenotypic data, and pedigree inaccuracies make reference populations less reliable. This study evaluates the consistency of the first genomic evaluation for lactation protein content (PC) using a female reference population (FRP) raised in a nucleus flock. FRP included 5,583 ewes, born between 1999 and 2023, from 253 rams selected to represent most of the genetic variability in the Herd Book (HB). Over this period, 214,921 test days were recorded, producing 16,835 lactation records for 5,120 ewes. The selection candidates were 2,236 rams from the HB of which only 10% had progeny in FRP. All ewes and rams were genotyped using the OvineSNP50 Beadchip by Illumina Inc. Variance components estimates were obtained using a GBLUP method with a repeated measures animal model. The average number of lactations per ewe was 3.3 ± 0.9, with a mean PC of 5.14 ± 0.8 g/dL. Repeatability and heritability were 0.72 and 0.61, respectively. The genomic predictions of rams ranged in an interval of 1.28 g/dL of PC, with an average expected accuracy of 0.40 (ranging from 0.11 to 0.90). These results showed that using nucleus flocks as reference populations may be a promising approach to trigger the genomic selection of dairy sheep breeds. However, since accuracies are strongly related to the proportion of the rams' genomes represented in the nuclei and the corresponding amount of recorded phenotypic data, careful planning of the size of the nuclei as well as an accurate choice of the used rams is crucial to increase both the average accuracy and the number of rams with a sufficient accuracy.
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O219

Genetics and meat quality: challenges and perspectives in Vitellone Bianco dell'Appennino Centrale

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The 'Vitellone Bianco dell'Appennino Centrale' is a PGI (Protected Geographical Indication) product that encompasses three famous Italian cattle breeds: Chianina, Marchigiana, and Romagnola. Research on the Vitellone Bianco primarily focuses on analyzing the genetic, environmental, and management factors that influence meat quality, with particular attention to traits such as tenderness, color, pH, cooking loss, water holding capacity and fat composition. This study investigates how genetic variability among the three breeds contributes to the final meat quality. One of the main factors analyzed is the age at slaughter, which ranges from 12 to 24 months. Age affects parameters such as tenderness and water holding capacity, with younger animals generally producing more tender meat and showing

a better ability to retain moisture. Three breeds showed significant differences in carcass traits and meat quality; the study also highlights the role of external factors, such as stress during transport and slaughter, and meat aging conditions. These factors have a significant impact on the final product quality. To estimate the effect of breed on these traits, a general linear model (GLM) was applied, with breed as a fixed effect. The methods used for meat evaluation, such as pH, color, and shear force measurements, have been standardised. However, some variability was noted between slaughterhouses and aging times, which can affect data reliability. The heritability of the traits was estimated using BLUPF90+ software through a mixed model that included sex as a fixed effect and the covariates age at slaughter and carcass weight. The estimated values range from 0.41 (Lightness) to 0.78 (Cooking loss). Genetic correlations showed the same trend as phenotypic ones; particularly noteworthy are those between lightness and cooked meat hardness (–0.69), raw meat hardness (–0.51), and pH (–0.57). It would be useful to introduce more consumer-relevant traits in the production disciplinary, such as red index (a*), water holding capacity and caloric intake.
The study highlights the potential for genetic improvement to enhance meat quality while preserving the unique traits of the three breeds, acknowledging the challenges of managing their distinct genetic and productive characteristics.

O262

Phenotypic and genetic study of hair whorls in the Maremmano horse and their correlations with the temperament index

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Temperament, a component of behavior describing an animal's personality, is challenging to measure, often delaying evaluations and hindering genetic progress an alternative approach is to identify morphological indicators, such as hair whorls, variations in hair growth patterns potentially linked to behavior. The present study investigates the phenotypic and genetic traits of hair whorls in Maremmano horses, focusing on their distribution and number in relation to the temperament index.
Data from 1,032 horses, provided by the National Association of Maremmano Horse Breeders (ANAM), were analyzed using GLM to assess the factors influencing the position and the number of hair whorls: coat color (bay, black, and chestnut); sex (male and female); birth period (animals born between 1983 and 2001, between 2002 and 2008, and >2009) and the inbreeding coefficient (<0.0320, between 0.0321 and 0.0560; and >0.0560). Head and neck positions were analyzed on a dichotomous scale, indicating the presence or absence of vortices at specific head (A–I classes) and neck (N–L classes) positions; the number of vortices was analyzed on a discrete linear scale (n_head and n_neck). Phenotypically, 35% of the examined horses presented a hair whorl below the orbital line in the central region of the head (H class), 70% exhibited whorls in the central head region (B, E, H classes), and 80% had a single whorl on the head. Regarding the neck, it was observed that 64% of animals showed whorls on the lateral neck regions (L, N classes) rather than the central area (M class). The results from the binomial and multinomial GLZ models revealed a significant association with inbreeding ($p \leq 0.05$), indicating that the number and position of hair whorls are influenced by inbreeding. The estimates of h^2 coefficients with Gibbs sampling for dichotomous traits ranged from 0.011 (F class) to 0.62 (L class); for the discrete trait, estimates ranged from 0.13 (n_head) to 0.36 (n_neck). Head whorls showed weak correlations with temperament, though Class B (–0.09) and Class D (–0.07) had significant negative associations. Neck whorls showed significant correlations (0.09; -0.09), while the number of head whorls (–0.06) showed a weak negative correlation.The findings indicate that hair whorls are potentially linked to equine temperament and serve as non-invasive markers to streamline temperament assessments and improve breeding strategies. Further research is needed to validate these associations and uncover their mechanisms.

O237

Genetic parameters of horse international longitudinal show jumping results

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Show jumping performance in horses are complex traits influenced by genetic, environmental, and management factors. Traditional animal models provide valuable insights into the genetic architecture of show jumping traits. However, these methods rely on assumptions of linearity and homogeneity, which may oversimplify the dynamic nature of longitudinal performance data. Therefore, we aimed to estimate the genetic parameters of international longitudinal show jumping results using univariate and multi-trait animal models, as well as Random Regression Models (RRM) and Generalised Additive

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Mixed Models (GAMMs). The RRM approach enables modelling repeated measurements as a continuous function, accounting for the hierarchical structure of the data. Meanwhile, GAMMs might extend regression frameworks by capturing non-linear relationships between predictors and response variables, thereby uncovering trends that may be obscured by linear models. The dataset comprised 20,968 horses with at least 10 competition results, spanning 11 height categories (1.10 m to 1.60 m). Horses competing in at least five height categories were included, with an average of 73 results per horse. Performance traits included clear round count and ratio, victory count and ratio, podium count and ratio, and prize money won in each category. In both univariate and multi-trait animal models, the following fixed effects were considered: date of birth, sex, studbook of origin, and the number of riders per horse. Heritabilities estimated by univariate models ranged from 0.02 for placement ratio in the 1.55 m category to 0.15 for clear round ratio at 1.40 m. When multi-trait animal models, most heritabilities increased benefiting from genetic correlations among traits. Interestingly, a variety of patterns emerged in the genetic correlations among traits. For most traits, correlations between adjacent height categories were positive, ranging from +0.26 to +0.99. High positive genetic correlations were observed between traits recorded from 1.10 m to 1.35 m, ranging from 0.84 to 0.99, but these correlations dropped from the 1.40 m category onwards. Conversely, genetic correlations between 1.40 m and 1.60 m categories remained positive, ranging from +0.34 to +0.98. Further research is ongoing to implement RRM and GAMMs to better capture the dynamic nature of show jumping performance over time across different height categories.

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O193

Selective breeding for Varroa Sensitive Hygiene (VSH) behavioral trait in honey bee (*Apis mellifera*) colonies: initial results of four years of selection

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The *Varroa destructor* mite is one of the main causes of honey bee colony losses. To combat infestations, beekeepers commonly use chemical treatments. An alternative to control varroa infestations is genetic selection and development of honey bee populations with inherent resistance to the mite. Since 2021, within the Beenomix 3.0 project, a breeding program has been created with the final aim of selecting bees based on improvement of the Harbo test scores, a key measure of varroa sensitive hygiene. Each year, forty colonies were phenotyped, and the five best-performing were used as breeders. The colony with the highest resistance score was selected for the paternal side, while four other top-performing colonies were used to produce virgin queens to mate with the best colonies through single-drone insemination. Over the course of the years Harbo test scores progressively increased with yearly means of 22%, 23%, 30%, and 41%, reflecting a steady improvement in resistance. However, significant variability remains among the colonies. In all years, the minimum score of Harbo test consistently remained at 0%, with 28% of colonies showing values of zero in 2021 to 16% in 2024. Nevertheless, a clear trend of improvement is evident in the maximum scores observed over time. In 2021, the highest score recorded was 58%, which increased to 90% in 2022. By 2023, one colony achieved the maximum score of 100%, and in 2024, this number rose to three colonies, demonstrating progress in enhancing varroa resistance. Future research will aim to identify key genes linked to varroa resistance in this honey bee population.

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O088

The use of a fitness tracker to analyze heart rate variability in show jumping horses during standard exercise test in warm and cold environment

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Heart rate variability (HRV) analysis is a method for assessing the state of the autonomic nervous system and the neuroendocrine system. In horses, heat stress determines an upregulation of those systems and the accumulation of body heat results in hyperthermia and in the reduction in cardiac vagal modulation of heart rate (HR). The influence of exercise heat stress on HRV in horses has not been reported. This study aims to evaluate how temperatures might influence HR responses and autonomic regulation in 15 clinically sound horses during a field exercise test. A fitness tracker (Equimetre™) was used to collect electrocardiograms for HRV and HR data. Eight horses completed the test in temperatures between 0 and 10 °C (group C), the remaining seven in temperatures between 20 and 35 °C (group W). The heat index of group W was between 123 and 125, classifying the training conditions as slightly risky. The exercise test consisted of 15 minutes of flat work, 4 jumps and 5 minutes recovery at walk. HRV analysis was performed to assess autonomic regulation between group C and W and during the different phases of the training. Student's *t*-test was used to assess the effect on the HR data between groups, and repeated measure ANOVA was used to assess HRV data among the training phases and groups as 'between subject factors'. Significance was set at $p < 0.05$. The HR and HRV data did not differed between groups. Significant differences were detected in RR intervals and sympathetic nervous system (SNS) activity between walk and jump phases, and between jump and recovery phases, highlighting increased sympathetic activity during maximal effort. The analysis of parasympathetic nervous system (PNS) values showed significantly higher values at walk and recovery, compared to jump; however, recovery value remained significantly lower than walk indicating presence of stress components. Exercise intensity drives autonomic shifts in horses, with maximal stress during jumps and incomplete recovery post-effort, independently of temperature in this study group. Limitations included the small sample size and ethical limitations, since all horses were trained under safe conditions, with a heat index <130. Furthermore, differences in the athletic conditioning of the horses may have an impact. Future research should focus on analyzing HRV in the same horses exposed to both cold and warm environments conditions to better assess the impact of temperature on autonomic regulation.

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O478

Strides to success: How gait and technique shape performance in show jumping

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The quality of a performance in equestrian sports, and especially in show jumping, is influenced by several intrinsic (e.g. morphology, attitude) and extrinsic (e.g. rider experience, surface) factors. In recent years, significant research has focused on the jumping technique and biomechanics of show jumping horses, aiming to enhance their training and selection processes. However, the type and quality of gait performed during the show jumping course (e.g. canter, gallop, rotary gallop) can also significantly influence the final performance outcomes. Accordingly, this study aimed to investigate the relationship between faults incurred during a show jumping course, the type of gait performed, and other factors, including the rider's level of experience.

This study analysed high-definition footage of 49 elite riders and their horses competing in an international 5-star show jumping event. All participants completed the same course, which consisted of 13 obstacles, each 155 cm in height. For each horse-rider-pair gait video evaluation was performed using Kinovea an open-source software. A trained operator analysed each video to evaluate the gait between each obstacle: gallop (G), canter (C), negative diagonal advanced placement (NDAP), rotary gallop (RG). In addition, data about riders and horses (e.g. age, horse studbook) were recorded together with the competition results (e.g. ranking, faults, time), since all of them are registered to the Fédération Equestre Internationale (FEI). Statistical analysis was performed with the aim to find possible correlation between the faults occurred during the show jumping course and intrinsic/extrinsic factors.

Our findings highlighted a significant and positive correlation between the presence of NDAP and the occurrence of obstacle faults ($r = 0.37, p = 0.01$). Additionally, a significant negative correlation was observed between the number of starts in FEI events

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and the faults incurred ($r = -0.34$, $p = 0.02$), underscoring the influence of rider experience on horse performance.
These findings emphasize the importance of further exploring the relationship between rider and horse. Investigating the mutual impact of rider experience and horse biomechanics on performance could provide deeper insights into optimising training strategies. Moreover, the application of video analysis tools should be implemented and supported to better understand biomechanics and characteristics of sport horses.

O488

Open cage farrowing system: balancing welfare and productivity

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The transition to cage-free farrowing systems represents a pivotal advancement in improving animal welfare in pig production. This shift responds to increasing societal and legislative demands for more ethical livestock management. However, it introduces significant challenges for farmers and animals, requiring re-evaluating traditional management practices. This study investigates the management of sows in cage-free farrowing systems, focusing on welfare, productivity, and practical implementation. The key areas of exploration include housing design to balance sow freedom and piglet safety, addressing sows' behavioural and physiological needs, and mitigating health risks such as crushing and hygiene concerns. The study monitored farrowing outcomes in 40 sows divided into two groups: (a) Control group (C), where sows were housed in crates from farrowing to weaning, and (b) Free Sows group (FS), where sows were released from the crate on day 3 postpartum. Data collection included litter weight measurements at days 1, 8, 15, and 22 postpartum, health indicators for piglets (e.g. diarrhoea, limb disorders), sow dry matter intake, and sow health. The findings revealed a higher incidence of piglet crushing in the FS group compared to the C group after cage opening (10.2% vs. 2.4%; $p < 0.01$), with a more significant proportion of sows involved in crushing episodes (60.0% vs. 25.0%; $p < 0.05$). At weaning, while the average number of piglets per litter was higher in the C group (13.1 vs. 12.0; $p < 0.001$), the average piglet weight was more significant in the FS group (7.69 kg vs. 6.64 kg; $p < 0.001$). These results emphasise the trade-offs in cage-free farrowing systems: while increased sow mobility may elevate the risk of piglet crushing and slightly reduce the number of piglets weaned, it also improves piglet growth and weaning weights. From an economic perspective, the higher growth rates and weaning weights in the FS group may help offset losses in piglet numbers, offering a potential pathway to greater confidence in the economic sustainability of alternative farrowing systems. The results provide a critical foundation for addressing farmer concerns about open cage Farrowing Systems, proving that such systems, while challenging, can align animal welfare improvements with economic viability through careful management practices.
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O506

Effectiveness of Fe (II) supplementation in Italian honey bee (*Apis mellifera ligustica* Spin.) under laboratory conditions

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The western honey bee (*Apis mellifera* L.) (HB) is a crucial species for global crop pollination and the economy, but the apiculture sector faces significant challenges, notably colony decline caused by the *Varroa destructor* mite, leading to substantial economic losses for beekeepers. Ferrous fumarate (FeFum) has been suggested as a potential management strategy for honey bees, offering pre-winter nutritional benefits and possibly reducing Varroa mite infestation levels. This study evaluated FeFum's effectiveness through three consecutive laboratory trials on *Apis mellifera* L. workers. Young workers (0–1 day old), sourced from colonies managed under controlled temperature conditions at the Teaching and Experimental Farm of the University of Tuscia (Viterbo, Italy), were divided into cages containing 30 bees each and treated with 8 increasing concentrations of FeFum (from 0.4 to 2.5 mg/kg) chelated with vinasse (DV) 1:100 in sugar syrup (SS50). The trials, carried out under controlled conditions (30.2 ± 1.1 °C; 70.6 ± 1.4% RH), lasted 21 days and included controls (SS50 and SS50 + DV), using 4 cages as replicates per treatment/control. Varroa mite fall (VMF), HB mortality rate (MR), daily wax production (DWP), average daily weight gain (ADG) and daily sugar syrup intake (SSI), were monitored every day. The acaricidal effect of FeFum was not observed, as the VMF values of FeFUM treated bees were lower than those of the

controls ($p < 0.05$) (91.00% in the treatments and 57.38% in the controls). Across all FeFum treatments, the DWP was lower than the SS50 control, albeit not significantly. Regarding the ADG, only the 2.2 mg/kg FeFum treatment showed a positive effect ($p < 0.05$) if compared to other treatments and controls (0.41 ± 3.56 mg/day *vs.* −0.99 ± 1.95 mg/day). A significant interaction ($p < 0.05$) between treatment and time for SSI suggests that treatment levels and experiment duration may influence bees' behavior and physiology. These preliminary findings indicate that FeFum at high dosage (i.e. 2.2 mg/kg) can have positive effects on the worker bees even though such effect was not confirmed at the highest treatment level considered (2.5 mg/kg). The contradictory result on the VMF of bees treated with FeFum are not easily explainable and deserve further investigation. Long-term field studies are needed to evaluate FeFum supplementation's impact on colony productivity and determine its suitability as sustainable pre-winter nutritional support for honey bee colonies.

O030

Effects of coconut oil-enriched diet administration on honey bees' survival and health

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Administration of supplemented artificial diets is a wide management practice in beekeeping to face honey bees' nutritional deficiencies and mortality in critical periods. Among nutrients, lipids play a significant role in insect nutrition as structural components in cell membranes, energy sources and reserves, and are involved in many physiological processes. Lipids are the major components of the fat body organ with the function of storing energy and with great biosynthetic and metabolic activity. Bees appear to regulate their fat intake by an unknown mechanism and lipid restriction has been reported to affect the social organisation, health, hive duties and productivity of the whole colony. This study aimed to investigate the effects of 0.5% and 1% fat-enriched diet administration on summer newly emerged and forager bees' survival rate, feed intake and health (i.e. immune and antioxidant system, fat and vitellogenin content). In newly emerged bees, diet supplementation with both 0.5% and 1% coconut oil determined an increase in survival rate from the 3rd to 14th day of feeding compared to control. Moreover, an overall increase in fat content over longer times (i.e. 20th day of rearing) was recorded. Feed consumption and phenoloxidase activity only decreased in newly emerged bees fed 1% enriched diet, while no differences in vitellogenin content occurred. An increase in fat content was also recorded in forager bees fed both 0.5% and 1% coconut oil-enriched diet. Therefore, low percentages of coconut oil inclusion in honey bee diets results in enhanced newly merged bees' survival and lipid content in summer bees. This result suggests that coconut oil inclusion in bee nutrition could play a role in preventing lipid deficiency. However, winter bees have a longer life expectancy and a slightly different physiology compared to summer bees. This arises the necessity to further investigations to assess the suitability of the use of such supplement feed to prevent fat loss in weak families during winter.

O041

How nutritional programming and genotype shape the gut microbiota and influence growth of Atlantic salmon

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Nutritional programming (NP) induces adaptive changes through early nutritional stimuli that can potentially enhance adult traits. This study investigated the interactions of NP with the genotype and gut microbiota of Atlantic salmon (*Salmo salar*) to optimise feed efficiency and health. Approximately 5100 eggs from six families with high (HP) or low pigment retention (LP) were assigned to a marine (M: 61% fishmeal and 8% fish oil) or vegetable (V: 5% fishmeal, vegetable proteins and rapeseed oil) stimulus diet and formed four groups (HPM, HPV, LPM, LPV). After a three-week stimulus phase, the fish underwent a 49-week freshwater phase with a commercial feed and a seawater phase with a plant-based challenge diet until 101 weeks of age. Survival rate, specific growth rate and feed conversion ratio were monitored. Samples for microbiota analysis were collected at T0 (post-stimulus), T1 (pre-challenge), T2 (challenge, post-challenge diet) and T3 (end of feeding trial). The gut microbiota was analyzed using next-generation sequencing on the Illumina platform.
The composition of the microbiota changed with age, largely independent of NP or genotype, highlighting the importance of developmental stage. Early diet affected beta diversity and specific bacterial populations, but the effects diminished over time.

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NP influenced the microbiota during the stimulus phase, but was overshadowed by current diet during the challenge phase. Interactions between genotype and diet affected microbial genera and metabolic potential, but these changes did not correlate with growth or feed conversion. The results suggest that plant NP has transient effects on gut microbiota and growth, with long-term growth more likely to be determined by pigmentation genotype. Future research should further investigate the interactions between genotype, diet and microbiota.

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O222

Optimising stocking density of Largemouth bass (*Micropterus salmoides*) in coupled aquaponic systems

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Maintaining optimal water conditions and nutrient balance is crucial in coupled aquaponic systems, with fish stocking density playing a key role, impacting both fish and plant health and growth.

This study evaluated the effects of three initial stocking densities, i.e. very low (VLD: 3.1 kg/m^3), low (LOD: 4.1 kg/m^3), and moderate (MOD: 6.2 kg/m^3) on the growth performance, mortality rate, and slaughter traits of largemouth bass (*Micropterus salmoides*), as well as on the yield of lettuce (*Lactuca sativa*), sweet basil (*Ocimum basilicum*), and Swiss chard (*Beta vulgaris*) in a coupled aquaponic system utilising vertical farming techniques. A total of 184 largemouth bass (initial body weight: 109 ± 28 g) were randomly allocated to nine 500 L tanks (three replicates per stocking density) and monitored for 176 days. A commercial diet was provided until apparent satiety twice daily from Monday to Saturday. At the end of the trial, the fish were slaughtered to evaluate carcass and fillet yield, as well as to assess morphometric and hepatosomatic indices. Data were analysed using ANOVA in SAS software, with stocking density included as a fixed effect. Water temperature (22.4 ± 1.6 °C) and dissolved oxygen (8.31 ± 1.28 mg L^{-1}) were monitored daily and were not affected by the experimental treatment. Fish final live weight (233 g vs. 219 g vs. 200 g for VLD, LOD, and MOD, respectively) and specific growth rate (0.43%/day vs. 0.39%/day vs. 0.34%/day) decreased as stocking density increased ($p < 0.001$), whereas mortality did not differ among groups. The daily feed intake was significantly lower in the MOD group compared to the LOD and VLD groups ($p = 0.01$), and the feed conversion ratio increased with stocking density (1.76 vs. 1.45 on average; $p = 0.01$). Total fish biomass gain over the experimental period was similar among groups (approximately 1007 g per tank). Fish morphometric and hepatosomatic indices, as well as carcass and fillet yield were not affected by stocking density. Lettuce yield was higher in the LOD and MOD groups compared to the VLD group ($p < 0.001$), whereas sweet basil and Swiss chard yields showed no significant differences among groups. In conclusion, fish stocking density is confirmed as a critical factor in aquaponics. The findings of the present study suggest that very low to low fish stocking densities represent the optimal conditions for maintaining high production efficiency in coupled aquaponic systems with largemouth bass and leafy vegetables.

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O425

New genomic tools for the conservation and management of native brown trout (*Salmo trutta*) in the Valle d'Aosta regio

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In Italy, in recent decades, native populations of brown trout have been modified by introgressive hybridisation with commercial farmed strains. The purpose of this study is analyze the genetic structure of the brown trout populations found in the North West Alpine area. Approximately 200 brown trout were sampled by electrofishing at thirteen stations in streams of the Valle d'Aosta region during the period from October to December 2022. Samples taken from the Ripa and Chisone streams (Po basin, Piedmont region) and Petit Buech (Durance basin, France) were added as reference groups. DNA was extracted from dorsal fins using the MagAttract HMW DNA kit. The nuclear LDH-C1* locus and a mtDNA control region genes were analyzed. ddRAD libraries were prepared and sequenced by IGA technology services s.r.l. (Udine, Italy). Bioinformatic analysis was performed using the following software: Stacks v2.0, Admixture, Adegenet, NewHybrids, SNPhylo and SNPRelate. To explore the degree of native brown trout population structure and introgression, we performed a

cross-validation analysis using the Admixture software. According to the results, the number of clusters that best describes the population structure is a sub-sample of four groups (K = 4). These results support the idea that, the long-standing practice of river restocking (in the North West Alpine regions) using the Atlantic lineage, has led to a substantial erosion of the native genetic pool. Genetic traces of the marble trout (*Salmo trutta marmoratus*) lineage were found (with varying percentages) in almost all samples of the Valle d'Aosta region (Vargno and Stuba streams showed an estimated percentage of assignment of more than 30%).

In the light of recent studies, confirming the autochthony of the Mediterranean lineage of brown trout in the Alps (from Liguria to Lake Garda), it is believed that these populations re-colonised the suitable Alpine streams in the North West alpine area during the post-glacial period. It is reasonable to assume that the 'Po valley trout' set up of a dynamic and diverse group of populations has largely disappeared due to the human activities.

O450

Effects of dietary microelements supplementation on growth performance and fillet quality of Largemouth bass (*Micropterus salmoides*) in a coupled aquaponic system with lettuce (*Lactuca sativa*)

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Freshwater fish species are valuable sources of protein and vitamins, but provide lower levels of bioavailable microelements compared to marine fish species. Biofortification strategies, increasing the content of microelements in fish diets, can enhance the nutritional quality of fish fillets, while optimising the nutrient flow in aquaponic systems. This study aimed to evaluate the effects of supplementing a mineral pre-mix containing iron, iodine, manganese, selenium, and zinc at three inclusion levels (M1: 0.7%, control diet; M2: 1.4%; and M3: 2.1%) on the growth performance and fillet quality of Largemouth bass (*Micropterus salmoides*) and on the yield of lettuce (*Lactuca sativa*) in a coupled aquaponic system using vertical farming techniques. The trial utilised nine experimental units (3replicates per treatment), composed by a fish tank (500 L volume), a settling and a biofilter vessel, nine Nutrient Film Technology towers for vertical crop cultivation, and a water storage tank that recirculated water back to the fish tank. A total of 174 Largemouth bass (initial live weight: 129 ± 29 g) were monitored over a 171-day trial period. Water temperature (20.2 ± 2.7 °C) and dissolved oxygen (8.09 ± 0.57 mg L^{-1}) were monitored daily. Data were analysed using ANOVA in SAS software, with minerals inclusion set as a fixed effect. Mortality was 5.75%, with no significant differences among treatments. Similarly, final live weight (237 g on average), daily weight gain (0.50 g day^{-1}), specific growth rate (0.36% day^{-1}), and feed conversion ratio (1.58) were unaffected by dietary treatments (PROC GLM, SAS). Morphometric indices, slaughter traits, proximate composition, and fatty acid profiles of fish fillets also showed no significant changes between groups. However, increasing dietary levels of iodine and selenium resulted in a linear increase in their concentrations in fish fillets (M3 > M2 > M1: 4.10, 3.29, and 1.90 mg kg^{-1} for iodine; 0.42, 0.38, and 0.35 mg kg^{-1} for selenium; $p < 0.01$). Iron, manganese, and zinc content remained unchanged. Lettuce yield was consistent across treatments, averaging 3.00 kg m^{-2} over four crop cycles. In conclusion, growth performance of Largemouth bass and lettuce yield in a coupled aquaponic system did not reach optimal levels. Nevertheless, dietary supplementation with the mineral pre-mix effectively increased the iodine and selenium contents in fish fillets, achieving biofortification of the final product.

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O057

Role of the dietary supplementation of arginine and valine: health status, digestibility, and performances of growing rabbits

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Arginine is a semi-essential amino acid that plays an important role on protein synthesis and immune response of growing rabbits. Valine is an essential branched-chain amino acid involved in the stimulation of protein synthesis and in the reduction of structural protein catabolism. The study aimed at evaluating the effects of the dietary supplementation with synthetic L-arginine and L-valine on health status, diet digestibility, growth performance, carcass and meat quality of growing rabbits. To this aim, 336 Hyplus Grimaud crossbred rabbits of both sexes, weaned at 32 d of age, were divided into 4 experimental groups with 12 replicates (pen) each (7 rabbits/pen) fed 4 experimental diets (Diet C, not supplemented with the tested amino acids; diet A, with 0.4% L-arginine; diet V, with 0.4% L-valine; diet AV, with 0.4% L-arginine and 0.4% L-valine), offered *ad libitum* during the whole trial. At 73 days of age, all animals were slaughtered in a commercial slaughterhouse and 144 carcasses were selected and submitted to dissection and meat quality assessment. The supplementation of arginine and valine, individually or in combination, did not affect final live weight (2771 g on average), growth rate (49.5 g/d), feed intake (146 g/d) and feed conversion (3.00 g/g) during the trial. Nutrients digestibility was scarcely affected by the dietary treatment apart from the digestibility coefficients of NDF and ADF, which were higher in rabbits fed diet V compared to other rabbits (+17% and +21% on average, respectively; $p < 0.05$). The health status of the animals was affected by the appearance of epizootic rabbit enteropathy, and a mortality rate equal to 13.1% on average was reached in the whole trial. The mortality rate tended to be higher in rabbits fed diet AV than in those fed diet C (16.7% vs. 10.7%; $p = 0.07$). Slaughter weight and dressing out percentage averaged 2643 g and 61.9%, respectively, without significant differences among dietary treatments. Meat quality was not affected by valine supplementation, whereas rabbits fed the diet supplemented with arginine showed lower pH values in the *biceps femoris* muscles with respect to those fed the other experimental diets ($p < 0.01$).

In conclusion, under the conditions of the present study, neither growth performance nor mortality rate or carcass and meat quality were substantially improved by the dietary supplementation with synthetic arginine and valine, and then their dietary supplementation cannot be recommended.

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O120

Dietary supplementation with Lauraceae and Chlorellaceae in growing rabbits: effects on meat quality parameters

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In recent years, following the official ban on growth promoters, there has been a significant shift in research towards using dietary natural substances to support animal health and performances. The present study evaluated the effects of *Laurus nobilis* leaves (LAU) and *Chlorella vulgaris* (CHLO) dietary supplementation in rabbits on meat quality parameters. The trial was conducted at the National Agricultural and Food Centre (Luzianky, Slovak Republic) on 75 weaned New Zealand rabbits (35 days old, average body weight 1.1 kg), randomly divided into three groups: the control group (CTR) received a commercial pellet diet, the CHLO group received the same diet supplemented with 0.1% dried *Chlorella* algae powder and the LAU group received the control diet supplemented with 0.1% dried bay leaves powder. After 60 days, rabbits were slaughtered at about 2.8 kg of live weight and *Longissimus dorsi* (LD) muscles were collected (10 animals per treatment) for determination of meat quality parameters. The chemical composition and the fatty acid composition were determined using the Fourier Transformed Infrared Spectroscopy (FT-IR) method. No differences ($p > 0.05$) in dry matter, protein and ash content were observed. The ether extract of LD muscle resulted lower ($p < 0.001$) in CHLO (0.70 ± 0.04%) than in CTR (0.94 ± 0.04%) and LAU (0.94 ± 0.05%) groups. The LD muscle fatty acid composition was influenced by dietary treatments. The LAU group showed a higher percentage ($p < 0.05$) of saturated (36.2 ± 0.21 CTR *vs* 37.1 ± 0.10 LAU *vs* 36.5 ± 0.15 CHLO), monounsaturated (37.4 ± 1.85 CTR *vs* 44.3 ± 0.25 LAU *vs* 36.6 ± 1.8 CHLO), polyunsaturated (6.8 ± 0.19 CTR *vs* 7.6 ± 0.25 LAU *vs* 6.7 ± 0.29 CHLO) and omega 6 fatty acids (6.2 ± 0.19 CTR *vs* 7.0 ± 0.24 LAU *vs* 6.0 ± 0.29 CHLO) compared to the CTR and CHLO groups.

Omega-3 fatty acids ($p < 0.05$) were higher in both CHLO (0.53 ± 0.01) and LAU (0.51 ± 0.01) groups than in CTR (0.48 ± 0.01). The health-promoting atherogenic and thrombogenic indices were lower in the LAU group than the other two experimental groups. Supplementation with *Chlorella vulgaris* powder affected the fat content of the meat. *Laurus nobilis* had a positive effect on the fatty acid composition of the LD muscle, enhancing its health benefits. Further studies are required to confirm the present data and evaluate the effect of these supplements on meat sensory profile.

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O217

Grazing behaviour and meat quality in different rabbit genotypes reared in outdoor conditions

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The rabbit organic farming rules in the EU are relatively new and only a few scientific evidences are available. Theoretically outdoor systems can offer benefits for animal health and welfare, such as the expression of natural behaviors; however, their effectiveness depends on the management of resources and environmental conditions, including group handling, feeding and genotype adopted. 16 rabbits of Leprino di Viterbo (LV) and 16 commercial New Zealand White (NZW) rabbits were reared outdoors. The rabbits were fed a commercial diet (Martini), supplemented by pasture grazing. Feed and grass intake were evaluated weekly by weighing the feed provided minus the residues and by measuring grass height using a herbometer. The trial was carried out from July to September 2024 at the experimental farm of the University of Tuscia. Animal behavior was evaluated by day and night video recordings by camera traps. Six videos per day were analyzed each with a recording duration of one minute using a continuous sampling method. Both grazing and eating behaviors were registered. Carcass and meat quality were assessed according to standard laboratory protocols. Meat color (*Longissimus dorsi*) was also estimated using the Minolta Chroma Meter (CIELAB). The aim of this study was to evaluate the differences between two genotypes reared in outdoor conditions in terms of animal welfare, growth performance and meat quality.

Data were analyzed by ANOVA ($p < 0.05$). Behaviors varied according to environmental conditions (hour of observation, weather and season). Anyway, results showed that LV had a higher frequency of grazing and other active behaviors (1.125 vs 1.000, $p = 0.0405$), while the eating frequency was the same in both genotypes. At the same time, the intake of feed and grass were respectively lower and higher for LV compared to NZW.
Carcass and meat quality were also affected by the genetic strain. Specifically, LV showed lower live and slaughter weight and lower lipid content both in the carcass and in meat. Meat quality was further differentiated by genetic strain: LV had a lower pH likely due to higher glycogen stores and higher water-holding capacity. The effect of kinetic activity on muscle fibers is confirmed by the higher estimated value of myoglobin. In conclusion, LV rabbits appear to be more adapted to outdoor conditions as showed higher capacity of pasture utilisation. Further investigation into the complete behavior repertoire and nutritional traits of meat should be conducted.

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O216

Effects of *Euglena gracilis* supplementation on growth performance, antioxidant status, meat quality in broiler chickens

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The current growth in global demand for animal products poses significant challenges in terms of environmental, economic and nutritional sustainability. The search for sustainable alternatives has become a priority. Innovative sources, such as microalgae, fungi and agro-industrial by-products, offer opportunities to improve the nutritional quality of feed, animal welfare and the resilience of livestock supply chains, contributing to a more circular and sustainable agriculture. The purpose of this project was to evaluate the performance, health status, and meat quality of broiler chickens that had been supplemented with *Euglena gracilis*. In particular, a 0.019% supplementation of *Euglena gracilis* was administered to 240 Ross 308 male broiler chickens for 42 days. Animals were housed in two identical rooms equipped with

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temperature and humidity control systems. Each room contained 120 chicks, divided into 12 boxes (10 chicks/pen), with 6 boxes allocated to each treatment group. The experimental groups are as follows: CTR (Control group) and TRT (Treatment group). At the end of the test, two animals per pen were slaughtered for analysis. Subsequently, performance, meat quality and antioxidant capacity of plasma and liver were evaluated. Key parameters evaluated for performance were Average Daily Gain (ADG), Average Daily Feed Intake (ADFI) and Feed Conversion Ratio (FCR). Meat quality parameters included color, pH, Water-Holding Capacity (WHC) and myoglobin content. Antioxidant capacity was assessed by T-AOC (Total Antioxidant Capacity) and Glutathione Reductase (GR) assays. Data (mean ± SEM) were analyzed with one-way Anova using GraphPad Prism 9 ($p < 0.05$). Performance in TRT with *Euglena gracilis* supplementation in the broiler diet showed no significant differences compared to the control group. The animal oxidative status in TRT resulted in an enhanced liver antioxidant capacity (6.64 ± 3.34 U/ml) and plasma GR activity (5335.43 ± 107 2.78 nmol/min/ml) compared to the CTR (4.01 ± 0.92 U/ml and 382 4.74 ± 695.86 nmol/min/ml, respectively). Meat quality parameters showed no significant differences in TRT. These preliminary findings emphasise the role of *Euglena gracilis* as a sustainable and functional feed ingredient in livestock production systems, addressing challenges related to animal health and stress resilience.

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O299

Effect of zinc-enriched *Camelina sativa* supplementation in broiler diets on meat quality and sensory properties

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Camelina sativa (L. Crantz) is an oilseed crop of the Brassicaceae family; it is a short-seasoned (85–100 days) annual crop that can be grown under different climatic and soil conditions, needing minimum water and nutrient requirements and being able to grow in low fertility or saline soils. Camelina cake, seeds and oil have been thoroughly used in poultry feeding due to the high quality of the fatty acids, rich in α-linolenic and linoleic acid. Different fertilisation methods have been experienced over time in order to improve the plant productivity and the properties of the oilseeds. Fertilisation with zinc (Zn) may exert positive effects on the nutritional properties of the plant. In broiler chickens, it has been reported that Zn plays important functions such as catalytic, structural, and regulatory, acting as a cofactor to several enzymes, thus improving growth performance, health, blood chemistry, tissue and faecal Zn concentration, immune responses, and intestinal histomorphology. Zinc is a potent antioxidant, thus it may positively affect meat quality and shelf-life. The aim of the study was to evaluate the effect of dietary supplementation with camelina seeds obtained from conventional farming or fertilisation with zinc on broiler meat quality and sensory properties. 45 one-day-old male R-7 broilers obtained from a commercial hatchery were used and fed a starter diet for two weeks.; afterwards, the chicks were weighed and randomly allotted to 35 m^2 floor pens in an environmentally controlled coop. Three homogeneous groups of chicks (n.=15) were fed *ad libitum* the following diets for 7 weeks: a control feed (C), or a feed containing 10% of conventional (Cam) or Zn-enriched (Zn-Cam) seeds. The Zn-Cam diet showed a lower slaughter body and hot carcass weight($p < 0.05$). The C broilers showed the lowest carcass refrigeration loss ($p < 0.05$). The Cam diet led to a significantly greater incidence of the breast and thigh as compared to the Zn-Cam group ($p < 0.05$). The immune organ index was significantly lower following the Zn-Cam diet, thus showing a positive effect of Zn on the immune function ($p < 0.05$). Furthermore, this diet led to an increased tenderness of meat and lower concentration of malondialdehyde ($p < 0.05$). Meat from the Zn-Cam group showed a better succulence and juiciness, though the tenderness and overall acceptance were better in broilers fed the Cam diet. In conclusion, meat from broilers fed the Zn-Cam diet showed better quality traits.

O459

Donkey feeding behavior in shrub- and tree-encroached pastures in Gran Paradiso National Park

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Since the 1950s, land abandonment has caused widespread encroachment of Alpine grasslands by woody species (shrubs and trees), resulting in a decrease in forage quality and quantity. Silvopastoral systems with livestock hardy species able to consume woody plants, such as donkeys, could represent a suitable option for the management and recovery of encroached grasslands. In this study, the feeding behaviour of a herd of 18 donkeys was analysed by direct observations (15-seconds record, 20-second pause) in a 11 ha pasture in Gran Paradiso National Park during summer 2023. Available and consumed plants were recorded in the feeding station of donkeys, spatially identified as a volume extending 2 m in height from the ground surface, with a radius of 0.5 m around animal mouth. Research questions were: (1) do donkeys feed on a mixture of herbaceous and woody plant species, following a mixed diet? (2) Are some plants preferred and others refused? (3) Is the relative consumption of woody species influenced by their abundance in the environment? A total of 6472 observations were carried out by two to nine observers throughout the grazing season. The available-consumed relationships (modeled with GAMs) were analyzed with cluster analysis and three groups of plants were identified: preferred, indifferently consumed, and rejected. The results showed a preference of donkeys for herbaceous forages (66–96% of the diet), although they were able to browse woody species and ferns (0–22%), making this livestock species effective in contrasting encroaching species. Donkeys preferred *Fraxinus excelsior* and *Rubus idaeus*, whereas *Hypericum perforatum* and *Betula pendula* were refused. Furthermore, the consumption of many species – particularly, *Alnus viridis* and *Athyrium filix-femina* – was influenced by their availability in the environment and increased proportionally to it. These results suggest that the integration of donkeys into the grazing pasture management systems could be a promising strategy for maintaining grassland biodiversity and improve forage quality of Alpine pastoral ecosystems.
Research supported by Gran Paradiso National Park.

O256

InnovaRE: Research and application of innovative tools to improve resilience in ruminants

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InnovaRE project introduces cutting-edge tools and methodologies to enhance the sustainability and resilience of ruminant production systems. By integrating precision livestock technologies and novel phenotypic data, the project facilitates the selection of animals with superior adaptability to environmental and management challenges. This innovative approach intends not only advances animal welfare but also fosters sustainable livestock production by minimising environmental impacts and optimising resource use. Funded under the Spoke 5 Agritech initiative 'Sustainable Productivity and Mitigation of Environmental Impact in Livestock Systems', InnovaRE is a collaborative effort involving public and private stakeholders, including breeders' associations, universities, and industrial partners. Through this multidisciplinary partnership, InnovaRE aims to transform livestock farming practices in response to the increasing challenges posed by climate change and resource limitations. The project is structured around several key actions. A network of pilot farms and an integrated IT system will be established to collect and manage data. Wearable sensor technologies will be developed to monitor physiological and environmental parameters, such as behavior, body temperature, heart rate, and location, which serve as indicators of resilience phenotypes. Advanced data analytics and machine learning models will be organised to extract insights from these datasets, identifying traits linked to adaptability. This phenotypic data will be used to enhance genetic and genomic evaluation programs, supporting the selection of robust, adaptable animals. Further, InnovaRE includes a focus on the Beef-on-Dairy program, aimed at improving productivity and market efficiency by leveraging crossbreeding strategies to produce high-value beef offspring from dairy cattle. InnovaRE targets both ovine and bovine species across a range of production systems, including intensive and semi-extensive management practices. Expected outcomes include the development of novel wearable sensors, the identification of resilience-related phenotypes, and the creation of advanced genetic improvement. Through its holistic and technology-driven approach, InnovaRE paves the way for adaptiveness, efficient, and environmentally sustainable livestock systems, addressing critical challenges in contemporary agriculture.

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O178

An application of system thinking approach to study complex problems in animal nutrition: a case study of feeding behavior

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Daily feed intake of dairy cows is influenced by nutrients and diet characteristics and by several conditions related to animal farming systems, such as environment, management, animal health, metabolic and physiological condition of the animal. In particular, the feeding behavior (FB) can be described by number of meals, time spent to eat and intake per meal. Understanding how FB influences intake over time allows to predict the amount of substrate that can be degraded by digestive enzymes in gastro-intestinal tract improving dry matter intake prediction resulting in more efficient diet formulation. Dynamic models and in particular the use of a system thinking approach is useful to improve the understanding of interactions among elements of a system, with the purpose of modelling complex biological phenomena. Animal FB is complex and dynamic. A system thinking approach allows for better understanding this complexity by analysing the relationships and interaction between feeding and the animal's biological variables. Aim of this work was to develop a conceptual model, characterised by feedback structure describing the complexity of factors influencing the FB. A Casual Loop Diagram (CLD) representing a preliminary system model of the dynamic system behaviour was thus developed and presented. Key variables that are considered most influential on animal FB and that often can be represented by data have been identified from experimental trials and expert consultation. All variables considered were grouped into fifteen feedback loops describing the potential causal effect among variables by using appropriate direction of arrows and their polarity. Main loops representing endogenous drivers of animals FB are relate to animal characteristics and rumen capacity, health status and requirements, farming structure, environment, animals management, social interaction, sorting behaviour and biochemical satiety signals. A more detailed analysis of the variables that influence number of meals, ingestion per meal, and time spent eating were added on the basis of the literature review. This allowed to identify feedback loops and endogenous control systems of intake regulation changes over time. Therefore, no empirical data or numerical simulations are presented. Identified feedback loop can provide a framework for understanding FB dynamics and to highlight that system thinking can be used as the first step to modelling several aspects related to animal science.
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O395

Technical and practical aspects of using PLF tools in a buffalo farm: the SensorHost software

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Research shows that Precision Livestock Farming (PLF) is not as widespread as it should be, due to the initial investment costs and difficulties in managing, consulting, and interpreting the data by farmers. Moreover, one of the main issues related to PLF's application is the heterogeneity of the sensors used and the data obtained. At CREA-ZA, we have a digitalised dairy buffalo stall equipped with the following devices and sensors: rumen boluses for individual identification (RFID), ear tag accelerometers (nutrition, reproduction, and health), the Zoometer® (live weight and body condition score), the laser methane detector (LMD) for individual gas emissions, lactometers (milk yield and other lactation parameters), and a weather station (Temperature Humidity Index). All these tools provide different data, based on different units of measure and timing slots. Therefore, it is essential to gather all this information in a single dashboard from which the user can extract indications for more efficient herd and farming activity management. In this perspective, we have developed the first version of the SensorHost software, which can automatically extract, sort, store, and merge data from sensors, providing patterns, predictions, alerts, and comparisons among animals, groups, and periods for the recorded parameters. The dashboard has been created within a dedicated development environment, specifically a graphical programming environment used to develop automated production, validation, and research test systems. Additionally, a stand-alone tool, fully integrated with SensorHost, has been designed to specifically manage data from the LMD, which presents some challenges. The LMD generates large datasets (120 files/min) that are not automatically attributed to a single animal, as they cannot be connected to the RFID. This tool can read and correctly catalog the CH_4 data, which can then

be imported by SensorHost, saving significant labor. Hence, the SensorHost environment provides real-time data that would otherwise require a lot of time to process and dramatically reduces human errors. In conclusion, our system represents a free and easy-to-use tool, simple and intuitive, which can help overcome the lack of familiarity and, in some cases, distrust of 'basic' users towards technical, digital, and computational tools and big databases. Therefore, this can help overcome one of the major limitations to the large-scale adoption of PLF.

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O440

Comparing two different weighting systems to improve whole-plant corn silage quality in the top layer of a farm bunker

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Management practices such as decreasing the porosity of the ensiled mass and keeping the plastic cover weighed down are critical during storage and feed-out periods to prevent aerobic deterioration. The effect of weighting the plastic cover on the aerobic deterioration of whole-plant corn silage (WPCS) in the upper layer of a bunker silo was investigated. Specifically, we compared a weighting system placing in 50 m^2 300 silo-net bags [SNB; high-density polyethylene (HDPE) 27 × 120 cm, 200 µm mesh pores) filled with 16 ± 1.4 kg of gravel to achieve a weighting action of 100 kg/m^2 (WP) and a control system without placing any SNB (NoWP). A bunker silo was divided lengthwise into two equal parts with a 2-m buffer zone between treatments (i.e. NoWP and WP). For each system, 6 SNBs were filled with approximately 6.9 kg of freshly chopped forage, and then buried at a depth of 0.30 m in different regions of a bunker silo. Once completed the packing operations, the bunker was sealed using a combined (2 in 1) oxygen-barrier film (actual thickness 115 + 40 µm) 15 months ultra-violets (UV) stabilised, and a security net in HDPE 8 years UV stabilised. After 8 months of storage, the SNBs were removed from the ensiled mass, weighted, and subsampled to analyze chemical, fermentative, microbiological parameters. Data were analyzed through a mixed linear model considering the weighting system as fixed effect. The WP group had higher lactic acid (45.0 ± 10.0 *vs* 31.6 ± 10.0 g/kg DM; $p < 0.05$), lower propionic acid (0.2 ± 0.1 *vs* 0.6 ± 0.1 g/kg DM; $p < 0.05$), lower butyric acid (0.04 ± 0.01 *vs* 0.3 ± 0.01 g/kg DM; $p < 0.05$), and lower DM losses (1.4 ± 0.6 *vs* 2.9 ± 0.6 % DM; $p < 0.05$). On the other hand, the NoWP group had lower ethanol (2.2 ± 0.6 *vs* 5.1 ± 0.6 g/kg DM; $p < 0.05$), lower methanol (0.4 ± 0.1 *vs* 0.7 ± 0.1 g/kg DM; $p < 0.05$), lower total alcohols (3.6 ± 0.6 vs 7.0 ± 0.6 g/kg DM; $p < 0.05$), lower 1,2 propanediol (23.5 ± 5.0 *vs* 44.3 ± 5.0 g/kg DM; $p < 0.05$), lower ethyl lactate (27.5 ± 8.3 *vs* 73.2 ± 8.3 mg/kg DM; $p < 0.05$), and lower total esters (39.6 ± 13.7 *vs* 87.0 ± 13.7 mg/kg DM; $p < 0.05$). Keeping the plastic cover weighed down is crucial to decrease the air penetration. Notably, the WP system allowed to obtain a well-fermented product reducing the DM losses. The practical aspect of using SNB filled with gravel instead of placing soil or tires may allow farmers to achieve a proper weighting action avoiding to contaminate silage and damage the plastic film during the feed-out operations.

O569

Precision livestock farming with APPàre, a digital platform for feeding and management of sheep farming in Sardinia

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Precision livestock farming (PLF) plays an important role in technological innovation of farms. PLF involves innovative tools regarding management feeding and milking aimed at improving the productivity and economic sustainability of the livestock industry. PLF technologies are mostly used in dairy cattle farms, thanks to the intensive management that is particularly suitable for the implementation of innovative tools. However, dairy sheep farmers could also benefit from the introduction of PLF. In this work, the APPàre platform was presented. It consists of an informative system of the Sardinia sheep sector that collects data at farm and animal level, uploading and collecting records from national databases and farm software or from farmer direct data entry. The platform is able to calculate series of partial indicators, allowing the storage and elaboration of farm records in order to present in user friendly dashboards and proper graphical interfaces the flock profile, crop plans, nutritional information of the animal categories, reproduction records of ewes, milk and meat productivity, farm income and environmental performances of the farm. It directly aimed at increasing the farmer awareness for the farm performances and at improving technical efficiency and profitability by stimulating a supported decision-making process. It also might stimulate demand for knowledge and skills in farm management. Through the platform, each breeder can:

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view the performance of his farm and compare it with regional averages; – visualise animal intake, milk production, weight, and Body Condition Score and monitor flock efficiency; – rank the ewes for production, reproductive and health data; monitor crop productivity indicators and environmental parameters of the farm. The application of this platform at large scale may promote open innovation and digitalisation of the sector provide useful insight and guidelines to promote the efficiency of the dairy sheep farms in Sardinia.

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O451

Advantages of precision livestock data sharing platforms in the genomic era

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Extracting high-quality information from the farm is crucial during database creation, leading to more accurate genetic evaluations. Despite the genomic era we are in, phenotypic information is still necessary for creating reference groups, which are essential for calculating SNP effects. Synergy and IDDEN have implemented an efficient structure for collecting information from Italian dairy farms. This system facilitates the real-time retrieval of large and diverse amounts of farm and animal data, ensuring continuity and standardisation. The process is based on API-based protocol for livestock data through an IDDEN Hub service with a data processing center (Synergy). The data exchange service follows the ICAR Animal Data Exchange (ADE) standards (version 1.3), which are part of a public project on GitHub. These standards define the API data contract schema and URL specifications. The Synergy database has developed a service compatible with the ICAR ADE standard for data acquisition and integration. This innovative service is available exclusively to farms registered on Synergy that request activation. To enable this functionality, each farm undergoes a registration (authentication) process to validate access to the APP/interface. Data synchronisation occurs automatically through farm sensors (e.g. robotic milking, feeding troughs, etc.), with integrated quality control protocols. As a result, the system performs this task without manual intervention from farmers or specialised technicians, effectively reducing both the time and costs associated with data collection. After each event, a response message is generated to monitor the process status. The system collects diverse data types from Italian farms, including individual milking events, milking events supplemented by sensor data, teat coordinates, milk weights and time by quarter, animal body condition scores, artificial insemination/embryo transplant events, heat observation events, pregnancy diagnosis events, calving events, calving difficulties, and additional livestock-related parameters. The data is currently stored only in the Synergy database. However, it is expected that in the coming months, genetic evaluations will incorporate this data into phenotypic information. Furthermore, this data collection and classification mechanism enables the development of new, innovative indexes, with the first applications targeting reproductive traits and milk production.

O228

Exploring the genomic basis of dental agenesis in Labrador Retrievers

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Dental anomalies, which frequently have a genetic basis, are well-studied in humans but remain largely unexplored in dogs. Among these, tooth agenesis or hypodontia -the congenital absence of one or more teeth- is particularly common and is considered a fault by several -but not all- breed standards. In humans, non-syndromic tooth agenesis is associated with mutations in genes such as MSX1, PAX9, and WNT10A. In dogs, studies on this topic are scarce: research on the Kerry Blue Terrier confirmed a genetic basis for tooth agenesis, though no genomic studies have identified the associated regions in this species. This study aimed to investigate the genomic basis of tooth agenesis in the Labrador Retriever, whose standard requires full dentition. We analysed 23 Labrador Retrievers, including 21 from a three-generation family. Of these, 12 had complete dentition, and 11 exhibited dental agenesis, primarily on the superior arch ($n = 8$), involving the first, third, and/or fourth premolars. DNA was genotyped using the Canine SNPchip 230K (Illumina), and the groups were compared with multiple analyses: Wright's Fst (top 1% SNPs retained), XP-EHH (top 1% SNPs retained), runs of homozygosity (top 1% delta between groups retained), and logistic regression incorporating the results of a principal component analysis as covariates to account for family structure. Genomic analyses identified multiple candidate regions, though none overlapped with the genes most commonly associated with non-syndromic familial tooth agenesis in other species. However, some genes mapped within these regions are linked to syndromes

involving dental anomalies in humans or with key roles in odontogenesis. Notably, two genes were highlighted across three analytical approaches. Among these, one is a coactivator of *NOTCH1* and a tooth-specific target of *RUNX2*, a gene critical for dental development and previously associated with tooth agenesis in other species. This study offers the first genomic insights into dental agenesis in dogs, identifying candidate genes and regions that deserve further investigation. Expanding this research to larger cohorts and additional breeds will be crucial for more accurately identifying the genomic regions involved in hypodontia in dogs, thereby improving our understanding of its pathogenesis and mode of inheritance.

O312

Genomic study of idiopathic epilepsy in dogs: a natural model for human epilepsy

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Most dog breeds are derived from a small number of founders and have undergone intense selection, resulting in limited genetic diversity within each breed. This leads to a high degree of homozygosity and the presence of large genomic regions in linkage disequilibrium. Intense selection has also contributed to genetic susceptibility to various diseases, including neurological disorders.
The objective of this study was to conduct a genomic analysis of dogs with idiopathic epilepsy, categorised into treatment-sensitive (S), treatment-refractory (R), and control (C) groups. Blood samples were collected from 90 dogs (C = 32, S = 39, R = 19), and DNA was extracted. These samples were analyzed using the Axiom™ Canine HD array (700K SNPs). The filtering criteria applied included excluding the individuals with a low genotype call rate (< 0.90), the SNPs with a genotype call rate <0.90, a minor allele frequency (MAF) < 0.01 and those deviating from Hardy-Weinberg equilibrium (HWE) ($p < 10^{-6}$). A total of 708,782 SNPs were used for further analysis. Genetic diversity was assessed using homozygosity and inbreeding coefficient (F) with PLINK. Homozygosity regions (ROHs) and the genomic inbreeding coefficient (Froh) were analyzed using DetectRUNs, where ROHs were declared based on a minimum length of 1 Mb. Although the number of animals in each group was limited, a GWAS analysis was conducted using a multiple loci mixed model with the GAPIT3 program. Among the functional SNPs associated with diseases included in the high-density array, no genotypes associated with diseases were found, however, associations were found with morphological phenotypes such as size, coat color, or hair type. As expected, since the animals came from different breeds, multidimensional scaling analysis revealed that the population was structured. Epileptic dogs had a higher inbreeding coefficient ($F = 0.169 \pm 0.14$) compared to controls ($F = 0.098 \pm 0.10$), but no significant genomic differences were observed (Froh controls = 0.141 ± 0.114; Froh epileptics = 0.151 ± 0.156). The ROH lengths were similar in epileptic (333.508 Mb ±343.963) and control dogs (310.972 Mb ±250.508), though some regions with higher ROH incidence (ROH hotspots) were detected in epileptic dogs. The GWAS analysis identified 8 significant SNPs at the chromosomal level with a false discovery rate (FDR) < 5%. This study provides initial insights into the genetic basis of canine idiopathic epilepsy and is ongoing to expand the sample size.
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O255

Insights into history and phenotypical traits of the maltese hunting dog (Kelb tal-Kacca ta' Malta)

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The Maltese Hunting Dog (Kelb tal-Kaċċa ta' Malta, KTKM) has long been intertwined with Malta's history and cultural heritage. Historical records, such as the 1773 edict by Grand Master Ximenes, reference a 'Braque'-type dog, highlighting the pivotal role of hunting dogs in rural Maltese life dating back to the 16th century. However, despite its historical significance and continued presence, the KTKM remains under-researched and lacks official recognition as a distinct breed. In 2019, the Federation for Hunting and Conservation – Malta (FKNK) estimated the total population of this breed to count approximately 600 individuals. This study examines the phenotypic characteristics of the evaluated canine population, focusing on cranial biometrics and overall body structure. Assessment of morphological traits, evaluated using a standardised protocol on 24 adult specimens (all at least one year old), revealed a mean cephalic index of 55.24

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and a mean body index of 83.09, values indicative of a predominantly mesocephalic and mesomorphic morphotype. The breed, possessing appearance traits reminiscent of 'Bracco' breeds, predominantly features large, pendulous ears and a 'Braque'-type face, often complemented by a pink-coloured nose and flews. Their short-haired, smooth coat usually displays a combination of colours, with patches ranging from light lemon to deep orange on a white background, giving it a unique appearance. In conclusion, the Maltese Hunting Dog is a historical breed for the Maltese territory and still plays a hunting role today. Its numbers and phenotypic uniformity give cause for hope that, together with genomic investigations, there are all the elements for the drafting of a breed standard and the subsequent application for the opening of a studbook by the competent Maltese authorities.

O221

Genetic characteristics for a breed standard definition of the Maltese Hunting Dog (Kelb tal-Kacca ta' Malta)

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The Maltese Hunting Dog (Kelb tal-Kacca ta' Malta, KTKM) is deeply rooted within the Maltese historical and cultural landscape. This breed can be traced back to the 16th century with the edict of Grand Master Ximenes in 1773 referencing the use of a 'braque'-type dog, underlining the significant role of hunting dogs in Maltese rural life. Despite its presence and historical importance, the KTKM population is not well studied, nor is it officially recognised as a breed. To define the genetic structure of the KTKM and determine its genetic uniqueness and phylogenetic relationships, genomic data of 24 KTKM were compared with 46 dog breeds, comprising hunting dogs (spaniels, hounds, and pointers), Italian (Cirneco dell'Etna) and Maltese primitive dogs (Kelb tal Fenek, also known as Pharaoh Hound), as well as terriers, herding and guardian shepherd breeds included to exclude possible introgressions. Multidimensional scaling analysis placed the KTKM within the hunting pointing dog cluster, aligning with its phenotypic and functional characteristics, but closer to Kelb tal Fenek than the rest of the group. A phylogenetic tree constructed using Reynolds distances grouped the KTKM with Italian and Maltese breeds, positioned in between the hounds and pointing dogs, whereas the identity-by-state analysis confirmed that the closest association of the KTKM is with the pointing breeds, further highlighting its intermediate genetic position. The treemix analysis identified migration events from the spaniel lineage to the KTKM and from the KTKM to the Cirneco dell'Etna and Kelb tal Fenek, suggesting possible historical genetic exchanges between these groups. In the admixture analysis, the KTKM have a high degree of uniformity and originality, with a unique genetic identity already evident before K = 8. Haplotype sharing analysis revealed modest levels of sharing but identified specific connections of the KTKM with the Kelb tal Fenek and some pointer breeds. In conclusion, the KTKM appears to be a distinct and genetically uniform population, closely aligned with the functional group of pointing dogs to which it belongs. Remarkably, this goes along with encouraging results related to inbreeding, with this breed presenting moderate levels of inbreeding and heterozygosity, despite its small size and geographic isolation. This study highlights the importance of conservation efforts to safeguard the KTKM's gene pool and its place in Maltese cultural heritage.

O333

Preliminary genomic analysis of an autochthonous dog population from the San Pietro Island

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Isolated animal populations present significant genetic challenges. These populations often experience a genetic bottleneck, where the reduced number of founders limits genetic diversity. Furthermore, inbreeding can further amplify this effect over time, leading to an accumulation of deleterious alleles and a loss of adaptive potential. On San Pietro Island (Sardinia, Italy) lives an example of these isolated populations: formerly domestic dogs that have been abandoned in the past, become feral, and bred in the wild. Recently, to reduce the risks related to stray dogs, these mongrel dogs have been captured and the puppies have been adopted by locals on the island and colloquially named 'Volpette Tabarkine'. A total of 41 owned dogs from different litters were sampled during routine visits by veterinary practitioners and blood was gathered for each animal. The dogs were evenly distributed between females and males (20 and 18, respectively) and had an average age at sampling of 4.7 ± 2.3 years. To investigate the population genetics, the Illumina Canine 230K SNP

array was employed. After quality control pruning, a total of 109,749 SNP was kept for further analyses. Average Minor Allele Frequency in the population was 0.23 ± 0.16, while the average observed heterozygosity was 0.32 ± 0.06. Principal Component Analysis was employed to observe the presence of stratification in the analysed population. A total of 4 clusters were observed by plotting PC1 versus PC2 (the two principal components representing 15% and 7.4% of the total variability, respectively). Furthermore, Nei's genetic distances were calculated and then plotted in dendrogram plots to better highlight the observed clusters. Further analyses are ongoing to expand the understanding of the sampled population genetics and to compare it with other dog breeds.

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O429

Phenotypical and genomic analysis of Sila Sheepdog (*Canis lupus familiaris*)

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The aim of the present research is to describe the Sila Sheepdog, one of the Italian livestock guarding dog breeds originating in the Calabria region, through phenotypic and genomic parameters. According to the official ENCI breed standard the Sila Sheepdog has been bred since time immemorial in the mountainous regions of the Calabrian Apennines. Its origins can be traced back to flock-guarding dogs that arrived in Calabria with the Indo-European peoples, as well as to shepherd dogs that accompanied the Greek populations during the colonisation of the Sila Plateau. The original type of the breed developed and was maintained thanks to the rugged and impenetrable terrain of the Calabrian Apennines, where the Sila Shepherd Dog has always been used to guard livestock, goats in particular, from wolves. Genomic analysis was carried out on 38 unrelated samples using Axiom™ Canine HD Array (20 females and 18 males; age >12 months, unrelated). Morphometric measures included: height at withers (HWH, cm), Total body length (TBL, cm), TBL/HWH ratio (BPR, ratio), total head length (THL; cm), Skull Length (SKL; cm), Muzzle Length (MZL; cm), MZL/SKL ratio (HPR, ratio). Additionally, bite type and coat colour were recorded. Data were analysed by sex using the PROC MEANS procedure in SAS® software. Genomic analysis revealed the uniqueness of the breed, reduced inbreeding and good variability. Morphometric analysis showed measurements consistent with those reported in the official breed standard. For males and females, respectively, HWT was 66.44 ± 0.74 cm and 60.10 ± 0.63 cm; BPR was 1.05 ± 0.01 and 1.07 ± 0.01 and HPR was 0.74 ± 0.05 and 0.75 ± 0.02. The main part of the samples presented a scissor bite (84.21%) and a black and tan coat (65.79%). Our findings provide solid scientific support for breed characterisation and offer the possibility to define effective selection plans and communication strategies aimed at conserving the biodiversity of Italian canine breeds.

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P125

Evaluation of the physico-chemical stability of cricket meal and dried whole cricket during storage at room temperature

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Compared to conventional farming, insect production for human food and animal feed generates significantly less greenhouse gas emissions and uses less soil and water, making it a livestock perfectly in line with sustainable development goals. In this study, two commercial products of domestic cricket (*Acheta domesticus*) were analysed in duplicate during a long-term storage test. A meal obtained from dried crickets (MEAL) and dried whole crickets (DRIED) were stored at room temperature (25 °C). The experiment lasted four months during which intermediate samplings were carried out at 0, 15, 30, 45, 60, 90, and 120 days of storage. The values of pH, colour parameters (L^*, a^* and b^*), water content, fatty acid classes, and oxidation products of the lipid component were monitored during storage. GLM proc of SAS was utilised to conduct a one-way ANOVA with storage time as fixed effect run separately for each commercial product (MEAL or DRIED). Furthermore, a two-way ANOVA was used to evaluate product and storage time as fixed effects. The results showed that the groups exhibited significantly different values of initial moisture levels and colour. Specifically, DRIED was darker than MEAL, with the lightness (L^*) values being 49.86 and 51.73, respectively; DRIED had the highest content of water (11.43 g/100 g of sample *vs* 4.29 g/100 g at day 0). During storage, the groups behaved differently, especially in terms of water content, which was lost in the DRIED and gained by the MEAL group. Specifically, for both groups the first variations occurred after 15 days of storage; then, DRIED continued to lose water until 60 days of storage, and this trend was followed by the stabilisation of the water content till the end of the trial. Regarding the MEAL group, it significantly

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increased its water content until day 90, reaching the value of 7.37 g/100 g. Substantial instability of the lipid oxidative markers was also observed despite the limited differences in fatty acid classes. Both formulations were found to be highly oxidised since the early beginning of the trial, probably due to the heat treatment they were subjected to. Based on the obtained results, 45 days of storage at room temperature seemed the threshold of storage of both meal and dried whole crickets; the drying procedure should be optimised to limit lipid and protein oxidation. Modified atmosphere packaging should also be considered to increase the shelf life of crickets, as meal or as dried whole.

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P545

Yellow mealworm (*Tenebrio molitor*) rearing on different substrates affects feed intake in captive sardinian partridges (*Alectoris barbara barbara*)

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This study evaluates the effects of Yellow Mealworm (YM) reared on different substrates used as supplemented feed on captive Sardinian partridges' nutrition. YM larvae (YML) were reared on four feed substrates: wheat bran, dried tomato peels and seeds, dried brewer's spent grains, and hemp seed cake. Approximately 1.5 kg of frozen YML per substrate was obtained as follows. Over four months, six plastic trays (30 × 40 × 10 cm) were used for each substrate, each containing approximately 70–100 g of 8-week-old larvae sourced from a stock colony. The larvae were reared for 3–5 weeks until they reached maturity (200–400 g/tray). The mature YML were then separated from the feed substrate, fasted for 24 hours, frozen, and stored at -20 °C before being used in the partridge feeding trial. The partridge trial involved 60 adult breeder partridges (30 pairs, sex ratio 1:1) divided into five groups, with six replicates per group and 2 birds/replicate. Four groups received 10 g of thawed YML daily (from each substrate group) supplementing 50 g of pelleted feed per bird, while the control group received only pelleted feed. The YML amount was established based on literature review evaluating larvae acceptance in poultry species. To prevent moisture transfer from larvae to pellets, feed components were served in separate metallic feeder. The feeding trial lasted three weeks. Feed intake was calculated daily based on the difference between the feed offered and the residual amounts after 24 hours both for pelleted feed and YML. Pelleted feed intake was not influenced by YML supplementation. Larvae consumption differed significantly among groups. Partridges showed the highest intake for YML reared on brewer's spent grains (6.15 g/day – fresh weight), followed by larvae reared on wheat bran (5.35 g/day), larvae on hemp seed cake (4.87 g/day), and larvae on tomato peels and seeds (4.53 g/day) ($p < 0.05$). Partridge dry matter intake followed a similar trend, with YML reared on brewer's spent grains at 2.10 g/day, larvae on wheat bran at 1.89 g/day, larvae on hemp seed cake at 1.52 g/day, and larvae on tomato peels and seeds at 1.43 g/day ($p < 0.05$). This study demonstrates that the YM feed substrate influences larval intake in captive Sardinian partridges. In fact, YML reared on brewer's spent grains emerged as the most favored among those reared on the four feeds, yielding larvae with the highest consumption rates by birds.

P253

Impact of sex ratio manipulation on reproductive output in *Tenebrio molitor*

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Manipulating the sex ratio is a valuable strategy for influencing the fertility and reproductive success of a population. However, this approach has not been extensively investigated in *Tenebrio molitor* breeding. This study investigated the effects of sex ratio manipulation on reproductive outcomes in *Tenebrio molitor* beetles, specifically examining the number of larvae produced per crate and per female. Pupae were sexed, and after metamorphosis, 14-day-old beetles were visually selected and assigned to nine experimental groups, each with 4 replicates. The groups were organised based on female-to-male sex ratios: 5:1, 4:1, 3:1, 2:1, 1:1, 1:2, 1:3, 1:4, and 1:5. Beetles were housed in 36 plastic cups (9.3 cm in diameter and 8.2 cm in height) with feed for future larvae growth. An oviposition grid (7.5 cm in diameter) was placed above the feed, and beetles were positioned on the grid to breed for four weeks. Every seven days, the grid and beetles were transferred to a new cup with fresh feed, marking the beginning of a

new oviposition week. Sixteen batches of larvae were obtained each oviposition week from each group, totaling 144 batches of larvae over the study period. When larvae reached three weeks of age, their number was recorded. Data were analysed using two-way ANOVA, with sex ratio and breeding week as fixed effects. Results indicated that groups with a higher proportion of females to males produced more larvae per crate, with significantly higher yields observed at the 5:1 and 4:1 female-to-male ratios ($p < 0.01$). Among groups with multiple males, the 1:5 ratio resulted in the highest productivity per crate ($p < 0.01$). However, when productivity was measured per female, significantly fewer larvae were produced at the 5:1 and 4:1 ratios. In fact, within groups with multiple females-, productivity per female increased at sex ratio of 3:1 and 2:1. Overall, the highest number of larvae per female was observed at the 1:5 ratio. In conclusion, this study demonstrated that increasing the number of females per crate enhances the total reproductive output per crate. However, the number of larvae produced per female increases when each female has the opportunity to mate with multiple males, underscoring the polygynandrous nature of *Tenebrio molitor* beetles and the positive effects of multiple mating on reproductive output.

P136

Hermetia illucens as functional feed for laying hens: effect on productive performance

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The growing global population and increasing pressure on natural resources require innovative solutions to promote sustainability in the livestock sector. The larvae of *Hermetia illucens* (HI), reared on substrates derived from agricultural waste produce biomolecules of high biological value, including chitin. This study aimed to evaluate the effects of integrating this bioactive molecule, extracted from HI larvae, into the diets of laying hens to enhance their productive performance and improve the physical and organoleptic quality of eggs. The experiment involved 120 Isa Brown laying hens, 28 weeks old and homogeneous for body weight (1.77 ± 0.107 kg), divided into three experimental groups (each consisting of 4 replicates of 10 birds): control (CTR) fed a basal diet; exuviae (ESU) fed a basal diet supplemented with HI exuviae powder and chitin (CHI) fed a basal diet enriched with chitin derived from HI. Both experimental diets were formulated to administer 1g/hen/day of the respective dietary supplement. At the end of the trial, at 39 weeks of age, 2 hens/replicate were slaughtered, and a total of 180 eggs per group (45 eggs/ replicate), were analyzed. During the experimental trial and post-slaughter evaluation, various productive parameters were assessed, including organ development, and reproductive traits. Feed conversion ratio (FCR) improved significantly in ESU and CHI groups compared to CTR ($p < 0.05$), reflecting improved feed efficiency. Organ development showed adaptations influenced by dietary treatments. The percentage weight of the muscular stomach was significantly lower ($p < 0.05$) in CHI and ESU groups compared to CTR one. Similarly, the percentage of weight of the glandular stomach decreased in CHI and CTR compared to ESU ($p < 0.05$). Regarding intestinal parameters, jejunal weight was significantly lower in ESU compared to CTR ($p < 0.05$), while ileal weight percentage followed a similar trend, with significantly lower values in CHI and ESU compared to CTR ($p < 0.05$). Colon length was significantly longer in CHI group while rectal length was longer in ESU group ($p < 0.05$). In addition, uterine weight was significantly higher in ESU group compared to CHI and CTR ($p < 0.05$). These findings suggest that diets containing chitin and exuviae from *Hermetia illucens* influence the digestive morphology and metabolic function of laying hens, leading to improvements in feed efficiency and digestive morphology.
Research supported by grant n: P2022SN3M9, University of Naples Federico II.

AQUACULTURE

Po76

Nature-based solutions for wastewater management towards a sustainable aquaculture: the CARDIMED case study

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Over the last decade, growing evidence has supported the use of Nature-based Solutions (NBS) to tackle crucial environmental and societal issues. NBS are founded on the principle that healthy

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ecosystems provide numerous benefits. This condition is achieved by safeguarding, sustainably managing, and restoring both natural and human-modified environments, ultimately enhancing biodiversity and improving human well-being. These solutions serve multiple purposes, offer no downsides, and address critical challenges such as climate change adaptation, disaster risk reduction, emissions reduction, improved air, food, and water security, biodiversity conservation, and human health, besides being essential for sustainable economic growth. Within this context, CARDIMED project, funded by the Horizon Europe Programme, is focused on boosting Mediterranean climate resilience through widespread NBS adoption across regions and communities. The NBS approach of CARDIMED will be tested in 9 selected Demonstration Sites, distributed among Portugal, Spain, France, Italy, Greece, Turkey, and Cyprus, covering a diversity of Mediterraean region framework, challenges and technologies. Particularly, the Demonstration Site located in Sardinia (Italy) will be focused on the decarbonisation of agricultural practices and the reduction of agriculture-derived pollution by connecting crop field cultivation with different types of aquaculture techniques. In Sardinia, agriculture is one of the most important sectors in terms of economy and employment, but still heavily rely on irrigation, leading to substantial greenhouse gas emissions. In addition, this area is drained into a delicate water body frequently experiencing eutrophication. To achieve the targets of water quality, energy and carbon footprint, the NBS in this Demonstration Site will include microalgae cultivation, crop rotation, precise irrigation methods, constructed wetland system and buffer strips, and aquaculture practices linked together within a strictly connected flow chart. Particularly, in the rural/peri-urban area of Alghero, phyto-depurated water coming from the crop field will be firstly collected in a free surface constructed wetland that will serve as a water basin for a tank-based aquaculture system intended for a fish species of commercial interest, the common carp. Differently, in the Calich lagoon, mussel farming will be exploited to depurate agricultural-derived river runoff before entering the sea.

Research supported by the 'Climate Adaptation and Resilience Demonstrated In the MEDiterranean region (CARIMED)' project, HORIZON-MISS-2022-CLIMA-01-06

P240

The RESILTROUT project: identifying genetic markers associated to disease resistance and heat stress resilience in farmed rainbow trout (*Oncorhynchus mykiss*)

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Starting from the '80 of the last century, the fish aquaculture sector has experienced a continuous growth and is now providing about half of the fish-based food products consumed globally. Its role is thus crucial to meet the increasing demand for food of the growing human population, which cannot be satisfied by fishing alone. In fact, currently most species are heavily overfished and fish availability is rapidly decreasing, with factors like pollution and climate change impacting further on marine ecosystems. In this context, aquaculture can contribute twofold by mitigating the overfishing on the one hand and by providing an invaluable source of proteins for human consumption on the other hand. However, intensive aquaculture requires a shift to more sustainable and climate-smart practices to mitigate its impact on natural ecosystems and to deal with the increasing temperatures caused by climate change. The RESILTROUT project is funded by the Italian National Recovery and Resilience Plan [PNRR] with the goal of enhancing the competitiveness and sustainability of the Italian trout farming sector. The study will target genetic traits associated to heat stress-resilience, resistance to lactococcosis and to proliferative kidney diseases (PKD) through case-control Genome-Wide Association Studies (GWAS). Within each of these three case-control studies 1,000 individuals (500 cases and 500 controls) will be genotyped with a SNP (single nucleotide polymorphism) array of about 50,000 markers. The same array will be used to screen 5000 candidate trout to identify carriers of resilience/resistance genetic variants to be used as breeders of the next generation. The results of this study will provide important contributions to improve the sustainability and competitiveness of the Italian aquaculture sector.

The project «RESILTROUT – aquaculture resilient to global change: research in support of Italian trout farming» (code 6-CFP) is supported by the Italian Ministry of Agriculture, Food Sovereignty and Forestry (MASAF).

P481

Dietary effects on growth, gut health and immune response of flathead grey mullet fed black soldier fly meal

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The diversification of farmed fish species, with the focus on the development of sustainable aquafeeds with a low dependency on marine-derived ingredients is one of the main goals of the modern aquaculture. Low-fish meal diets, in which with black soldier fly (*Hermetia illucens* HI) meal was used to partially replace conventional ingredients, were formulated to assess the effect on growth, gut health and immune status of flathead grey mullet (*Mugil cephalus*). Three isoproteic, isolipidic and isoenergetic diets were formulated with 10, 15 and 20 % HI meal (HI10, HI15 and HI20, respectively) and tested against a control diet (HI0). For the feeding trial, 360 juvenile grey mullets (initial weight = 40.2 ± 0.5 g) were randomly distributed in 12 experimental tanks connected to an open recirculating system (Temperature, 22,05 ± 9,12 °C; O_2, 66.5 ± 8.1 mg L^{-1}; Salinity=, 39.07 ± 0.41 PSU; pH, 8.62 ± 0.42). Fish were assigned to the four dietary treatments, in triplicate and fed the experimental diets (1–3% body weight, according to the water temperature) for 138 days. At the end of the experiment, fish were individually weighted and gut, liver and spleen were sampled and processed for histological and immunohistochemistry analyses. As far as growth and somatic indexes is concerned, only final weight and Fulton condition factor showed significant differences. In particular fish fed HI15 and HI20 diets recorded a significant lower ($p = 0.003$) final weight compared to those fed H0 and HI10 diets and a lower ($p = 0.026$) Fulton condition factor was recorded in fish fed diet HI20 compared to the other groups. These differences could be ascribed to an increasing chitin content in the diets with a higher HI content considering that chitin can reduce the nutrients digestibility of the diets. Investigations performed to assess gut health did not show major negative effects related to HI meal inclusion, except from changes in villi thickness ($p = 0.01$) and increased mucous cells abundances ($p = 0.001$) in fish fed HI15 and HI20 diets. Remarkably, as revealed by immunohistochemical analyses, a significantly higher ($p = 0.001$) proliferation of TNFa + cells was observed in anterior intestine of fish fed HI10 diet, suggesting a potential role of supplementing feed with low percentage of HI meal, in boosting gut immune defenses, without compromising growth indexes.

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P573

Technology transfer for *Haliotis turberculata* farming in Sicily: evaluation of adaptive responses to culture conditions

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Abalone (*Haliotis tuberculata*) is a commercially valuable, globally overfished herbivorous marine mollusk that is gaining great interest in aquaculture, also in Sicily (Italy). Since abalone is highly sensitive to environmental changes such as temperature, salinity, dissolved oxygen, and pH, this study aimed to identify optimal culture conditions by monitoring stress-related molecular markers. A first experiment was conducted in January 2023, on ten specimens for three conditions: before transport (control), immediately after transport (T0) and after 48 hours of acclimatisation (TF), in a tank with open-circuit seawater (pH 8.3, salinity 37.5 ‰, dissolved oxygen 4.17 ppm, and temperature 23.04 °C). The gene expression of heat shock proteins (Hsps), showed overexpression of Hsp71 and Hsp84 at T0 ($p < 0.05$), indicating acute stress from transport. At the end of the acclimation period (TF), a recovery phase was observed, suggesting the activation of adaptation mechanisms. The second experiment (March-June 2023) was aimed to evaluate the adaptation to pH changes (8.3, 7.8 and 7.3). A total of 100 abalones (37.93 ± 1.2 mm) were stocked in cages (1130 L ×

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1130 W × 760 H mm) and placed in 3 × 16 m tanks supplied with seawater, fed a commercial pellet diet (9 g/day). Three culture conditions were tested: a control group (Cnt) in a tank with open-circuit seawater (pH 8.3, salinity 37.5 ‰, dissolved oxygen 4.17 ppm, and temperature 23.04 °C), a groundwater tank (GW) (pH 7.3, salinity 35.3 ‰, dissolved oxygen 6.29 ppm, and temperature 21.39 °C), and a mix group (50/50 seawater and groundwater) (pH 7.8, salinity 36.4 ‰, dissolved oxygen 5.53 ppm, and temperature 23.42 °C). Six specimens from each cage were sampled at zero and after 1, 3, 6, 30 60 and 90 days. Results showed a significant increase ($p < 0.05$) in Hsp70, Glut4 and Nrf2 protein levels during the first six days of culture at pH 7.3 (GW), suggesting an adaptive response to environmental stress. The assessment of biochemical-nutritional parameters showed that changes in pH did not lead to changes in abalone composition. Overall, the obtained results showed that *H. tuberculata* can adapt to different culture conditions through the activation of specific metabolic pathways, providing insights for optimising procedure for cultivation.

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P061

Reducing food losses by developing an automated hatching system prototype for early stage embryos of rainbow trout (Oncorhynchus mykiss)

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A consolidated knowledge currently relies behind the management aspects of rainbow trout production cycle, ensuring high productivity rates and quality standards. However, the very early embryonic development (from fertilisation to the achievement of the eyed egg stage) still represents the most vulnerable phase due to egg infections by ubiquitous Oomycete species (*Saprolegnia* sp.), and other pathogens, as well as due to poor eggs management, causing the loss of entire egg batches. This phase is conducted in upwelling incubators subjected to visual check, manual removal of dead embryos, and use of chemicals for disinfection to prevent the spreading of infections. The present research aimed to develop and validate a technological automatic system, equipped with a set of multi-spectral cameras and specific tools, able to gently lift the embryos and to recognise and remove the non-developing ones. In a preliminary stage, acquisitions in the visible (VIS) and near infrared (NIR) spectrum were performed with XIMEA multi-spectral cameras, with or without water, on 50 batches composed by good (orange) and bad (white) rainbow trout eggs, obtained from an Italian supplier. The collected images (3 images per batch) were labelled by domain experts and then used to train a deep learning model able to detect eggs and assign label based on reflectance data. Then, a prototype of the vertical incubator was developed and equipped with: (*i*) 45° inclined cochlea to gently lift the embryos from the bottom of the system to the sorting area where multi-spectral cameras can discriminate embryos; (*ii*) probes for pH, temperature, dissolved oxygen and CO_2 all connected to a data collection and transmission system; (*iii*) a water flow meter. The prototype efficiently lifted the embryos without affecting their integrity and the cameras discriminated them with an overall accuracy of 94%. It will be further improved with a device able to remove bad eggs according to cameras-derived data. This device could improve up to 5% the number of embryos that achieve the eyed stage (less delicate), thus improving the productivity of trout farms. The main limitation of this technology may be the immediate large-scale application in a farming scenario.

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P249

Preliminary set-up of a digital system for the fish welfare improvement in cage aquaculture

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Recent technology based on interconnection among sensors, devices and computer tools aimed at improving productive

efficiency, fish welfare and environment. It has been recognised that the calibration of these systems remains a sensitive aspect because it can take a long time before starting to work.
In order to better understand the optimisation of the set-up of a digital system, an innovative apparatus to monitor water quality and record fish was installed in a cage fish farm in the South Adriatic Sea. The apparatus was set-up in two cages: one to rear gilthead sea bream and the other for European sea bass. Both the fish species had been introduced, as juveniles, before the assembly of the equipment. A multi-parameter real-time system and an underwater video monitoring were tested. Water quality was determined by means of five sensors: Temperature; Salinity; Oxygen Dissolved and saturation; Dissolved solids; pH; Chemical Oxygen Demand; Biochemical Oxygen Demand; Turbidity. A platform was created to collect data. The video monitoring consisted of three cameras positioned inside the cage at a depth of 1 m and 3 m from the edge of the cage. Two stereoscopic cameras were synchronised, placed at a focal distance of 27 cm, for 3D analysis and another camera was placed in the opposite direction to the others, towards outside of the net cage. The video streams were set to 10 sec in length and stored on files in HEVC format to be sent via network to a repository. In sequence, each video had 3 frames (1/camera). A thermal camera was pointed towards the farm area to record marine currents. The first part of the set-up study was spent to identify the most suitable position to locate the digital system and wirings. Sensors and video cameras were installed on a horizontal, lift and rotate bracket in a side of each cage. This resulted strategic because it did not interfere with farmers routine activities. Several sessions of calibration of the probes and videos were performed per cage. For the video cameras, the checkboard based-method was used. The images acquisition was considered suitable in both the cages although the length of the frames resulted as too short to show fish abnormalities. The monitoring system by thermal camera integrated data of the environmental parameters well. Exporting data in worksheet format was also optimised. Data collected from all the systems were related by algorithm to evaluate fish welfare.
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COMPANION ANIMALS

P073

Breed-specific hematological phenotypes in dogs apparently healthy but infected by zoonotic pathogens: the case of Fonnese and Cirneco dog breeds

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Fonnese (FO) and Cirneco dell'Etna (CE) are Mediterranean dog breeds, indigenous to Sardinia and Sicily (Italy), although they differ in morphology and function (guarding livestock and hunting respectively), they have a similar health management. This study analyses the prevalence of *A. phagocytophylum (AP), E. canis (EC)*, *L. infantum (LI)* and *R. rickettsii (RR)* infections, and the hematological parameters associated in FO and CE dogs. Sixty dogs (30 FO and 30 CE) apparently healthy were used. Epidemiological data were collected, and the animals were grouped as puppy (< 9 months), young (between 9 to 24 months), adults (between 2 and 8 years old) and senior (≥8 years). Serological testing was performed to *AP, EC*, *LI* and *RR*, and hematological parameters analysis was realised. Data were analyzed using the Mixed Model procedure. Prevalence of *AP, EC* and *RR* were similar (33.3%, 33.3% and 38.3%, respectively) and higher than *LI* infection (13.3%). The most common coinfection was *EC* with *RR* (six dogs, all FO), followed by *AP* with *EC* (five dogs, 4 FO and 1 CE). *RR* infection is higher in adults than in other age. Prevalence of infections was similar between canine breeds for *AP*, *LI* and *RR*, but the prevalence of *EC* was statistically higher in FO than in CE dogs (60.00% and 6.67%, respectively; p-value <0.05). Sex and age do not affect the prevalence of other infective pathogens evaluated. Related to hematological features, sex and age affects cholesterol (COL). The last one affects glucose (GLU) and phosphorus (P), being higher in puppies than in other aged groups. COL is higher in females than in males, and in senior and puppies than in young and adults' dogs. Creatinine (CRE) levels are higher in males of CE, whereas these difference between sex is not observed in FO dogs. Differences in albumin (ALB), alkaline phosphatase (ALP), and other biochemical parameters showed between canine breed, being higher in CE than in FO, whereas calcium (CAL) and urea (UR) were higher in FO than in CE. *AP* and *LI* infection increases ALP in CE canine breed, whereas this parameter decreases in FO infected by *LI*. Similar results were observed for bilirubin (BT) values in *RR* dogs infected. Levels of CAL and P were higher in FO dogs infected by *LI* and *RR* respectively than in other groups. EC infection decreases ALP levels in two canine breeds evaluated. Higher values of ALB, ALP, and BT were found in CE than in FO dogs, whereas the values of CAL and UR were higher in FO than in CE.
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P128

Hydrolyzed Feather Meal in dog nutrition: dry food proximate composition, amino acid content, and biogenic amines

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The use of animal by-products from the human food industry to produce commercial pet foods is considered a sustainable practice. This study aimed to characterise the chemical properties of two maintenance diets for adult dogs, achieved by substituting 7% of poultry meal with hydrolyzed feather meal (HFM). Two extruded diets were formulated to be isoenergetic, isonitrogenous, and isolipidic. The control diet (CTR) contained poultry meal as the sole source of animal-derived protein (160 g/kg of feed), whereas the experimental diet (TRT) included 90 g/kg of poultry meal and 70 g/kg of a commercial HFM product. Both diets contained the same ingredients, nutritional additives, and antioxidants. Triplicate food samples were analyzed for proximate composition, soluble dietary fiber (SDF) and insoluble dietary fiber (IDF) using AOAC (Association of Official Analytical Chemists) methods. Total dietary fiber (TDF) was calculated as the sum of SDF and IDF. Amino acid analysis was performed by gas chromatography, and biogenic amines by high-performance liquid chromatography. Statistical differences between diets were evaluated using a two-sample *t*-test in R ($p \leq 0.01$). The HFM contained approximately (g/100g, as-fed): 5.59 moisture, 82.64 crude protein (CP), 7.07 crude fat, 0.91 crude fiber (CF), 5.63 starch, 1.83 ash, 2.38 TDF, 0.35 SDF, 2.03 IDF. No significant differences were found between the CTR and TRT diets (g/100g, as-fed) for moisture (9.16 vs. 8.08), CP (19.07 vs. 19.20), fat (15.24 vs. 15.00), CF (2.10 vs. 2.00), starch (40.59 vs. 40.80), ash (5.45 vs. 5.01), TDF (7.51 vs. 6.97), SDF (1.37 vs. 1.00), IDF (6.14 vs. 5.98), respectively. Additionally, similar values were observed for the amino acid profiles between the two diets. Among the non-essential amino acids, however, serine was present at a significantly higher concentration in the TRT diet compared to the CTR diet (2.20 vs. 2.13 g/100g, as-fed; $p = 0.002$). The biogenic amine profile showed no significant differences between the two diets, except for cadaverine, which was significantly higher in the TRT diet compared to the CTR diet (0.124 vs. 0.082 mg/g, as-fed; $p = 0.009$). Nonetheless, recent studies on the in vitro toxicity of cadaverine to intestinal cells have shown that the cytotoxic levels in food are four times higher than those observed in the diet containing hydrolyzed feather meal.

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P323

Hydrolyzed Feather Meal in dog nutrition: application of electronic senses on extruded diet

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The acceptability of food is a critically important factor. Color, odor, and taste can influence dogs' food preferences. Therefore, the aim of this study was to assess the acceptability, and consequently the palatability, of an extruded dog food containing hydrolyzed feather meal using sensory instrumentation. Two extruded isoenergetic (calculated metabolizable energy of 3680 kcal/kg, as-fed), isonitrogenous (19 %, as-fed) and isolipidic (15 %, as-fed) commercial diets were formulated to meet the nutritional requirements of adult dogs. The control diet (CTR) contained poultry meal as the sole source of animal-derived protein (160g/Kg of feed), while the experimental diet (TRT) included 90 g/kg of poultry meal and 70 g/kg of hydrolyzed feather meal (GOLDMEHL® FM, Gepro, Diepholz, Germany). The color, odor and taste of the diets were analyzed using E-Eye (Alpha M.O.S., Toulouse, France), E-Nose (FOX 4000, Alpha M.O.S., Toulouse, France) and E-Tongue, (αAstree, Alpha MOS, Toulouse, France), respectively. The data were subjected to Principal Component Analysis (PCA). In addition, the color, the odor and taste characteristics of the hydrolyzed feather meal (HF) were also considered in the evaluation. Regarding color, expressed through the RGB method, the PCA results indicate that both TRT and HF are characterised by lighter color codes. Specifically, a medium light shade of yellow (color code 2711) is present exclusively in HF (33.3%) and TRT (5.2%), but absent in CTR ($p = 0.0001$). This outcome is attributed to the high sensitivity of the E-Eye in detecting the presence of hydrolyzed feather meal in TRT feed, a difference that may not be perceptible to the naked eye. The volatile profile of the CTR and TRT feeds were very similar, as evidenced by the P and T sensors, with no significant effect from the presence of HF, as indicated by the LY sensors. Regarding the taste profile, the E-tongue results revealed no differences between the two groups. In conclusion, the partial replacement of poultry meal with hydrolyzed

feather meal did not affect the odor or taste of the dog food. The only noticeable difference in color, which was detectable exclusively with powerful tools such as the E-Eye, does not influence the food's acceptability and could prove valuable in the future for traceability purposes.

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P455

Effects of *Saccharomyces cerevisiae* DSM 34246 var. *boulardii* supplementation on nutritional status, fecal parameters, and overall well-being in healthy adult breeding cats and dogs

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This study evaluated the efficacy of Saccharomyces cerevisiae DSM 34246 (Canobios-BL) var. boulardii as a dietary supplement to improve intestinal health and maintain optimal physiological conditions in cats and dogs. Two separate randomised controlled trials were conducted, one involving 14 adult Chartreux cats and the other including 53 adult dogs (28 West Highland White Terriers and 25 German Shepherds). In both trials, animals were divided into a control group (CTR) receiving a placebo and a treated group (SACC) supplemented with S. boulardii at 5×10^9 CFU/kg of food. Both groups were fed a dry commercial diet, and the trials lasted 35 days, with six evaluation time points. Parameters assessed included Body Weight (BW), Body Condition Score (BCS), Fecal Score (FS), FS measured with a penetrometer (FSp), Fecal Dry Matter (DM), Fecal Humidity (UM), and Fecal IgA (IgA). The parameters BW, FSp, IgA, DM and UM were analysed using analysis of variance (ANOVA) based on a repeated measures model ($p < 0.10$). Kruskal-Wallis test and multiple comparison analysis based on pairwise two-sample Wilcoxon comparisons were used for the BCS and FS parameters ($p < 0.10$). In cats, supplementation significantly ($p < 0.10$) improved BCS, FS, FSp, DM, UM, and IgA, indicating better gut health and physiological status in the SACC group. Similarly, in dogs, the SACC group demonstrated significant ($p < 0.10$) improvements in BCS, FS, FSp, DM, UM, and IgA across both breeds. These findings support the positive effects of S. boulardii supplementation on gut health and overall physiological and biological conditions in healthy cats and dogs living in breeding environments.

P487

Genome-wide characterization of a local heeling dog population from Northern-Apennines

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Over the centuries, dogs accompanied humans as they moved seasonally in search of grazing land for their livestock in the practice of transhumance. The subject of this study is a population of heeling dogs, which has been identified in the Apennine area stretching from the Tuscan-Romagna Apennines to the Monte Vettore massif. These dogs, to which we'll refer as Apennine heeling dogs, have been reared by various sedentary and transhumant shepherds, who have selected individuals with homogenous physical and behavioural characteristics. The population is morphologically characterised by a long, trotter-like body, a dolichocephalic head with a pronounced stop, a broad and strong muzzle, erect ears, round eyes, a muscular neck, thick and adherent skin, strong limbs, powerful muscles, a low-set tail, and a rough coat with various colors and patterns. The aim of this study is the genomic characterisation of the population and the investigation on his relations with other shepherd and heeling dog breeds both from neighboring areas and the international context. To achieve our goal we sampled 16 dogs with recorded pastoral ancestry, a group of 6 dogs from the same area and with similar morphological features, but with uncertain ancestry. The samples have been genotyped through the Embark™ SNP chip which is based on the Illumina CanineHD™ BeadChip. Our samples have been merged with the consortial dataset of the LUPA project. Additionally we retrieved genotypes from other 9 heeling and shepherd breeds. Genetic diversity indices (Ne, He, Ho, and F_{ROH}) have been calculated. Then, the genetic structure of the

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population has been assessed through ADMIXTURE, TREEMIX and an MDS analysis. Our results showed genetic diversity indices suggesting the necessity of management of inbreeding and genetic drift. The results of the three genetic structure analyses are consistent and indicate that the population possesses a distinct genomic identity. Furthermore, we observed a shared ancestry between the investigated population and the group of six dogs originating from the same area. The results of this study emphasise the significance of utilising genomic data in conjunction with morphological observations for the characterisation of dog breeds. Furthermore, this approach may assist in the management of local dog populations' genetics by identifying animals that can be used to increase the breeding stock using molecular information.

P138

Effects of a hepatoprotective supplement on liver function, inflammation markers, and gut microbiota in overweight dogs

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Overweight dogs often experience metabolic dysfunction, inflammation, and impaired liver functions, possibly linked to gut microbiota dysbiosis and interaction with the gut-liver axis. This study evaluated the effects of a hepatoprotective supplement containing *Silybum marianum*, prebiotics, probiotics, n-3 polyunsaturated fatty acids, vitamins, and minerals on metabolic health in 10 overweight dogs over 35 days. The dogs, aged between 8 and 13 years, with body weight range of 9 to 38.1 kg and a body condition score of 6 to 8. Dogs were recruited from a veterinary clinic and remained in their home environment throughout the study ensuring minimal disruption of their daily routines. Clinical and laboratory assessments were conducted at baseline (T0) and on days 7, 14, 21, 28, and 35 (T1–T5). The supplement significantly reduced markers of metabolic dysfunction from T3 to T5, including alkaline phosphatase ($p = 0.043$), glucose ($p = 0.027$), and direct bilirubin ($p = 0.038$). C-reactive proteins (CRP), an important marker of inflammation, decreased from 1.2 mg/L at T0 to 0.5 mg/L from T3 onward ($p = 0.046$). However, no significant variations were observed for total Short-chain fatty acids ($p = 0.091$), alpha diversity ($p = 0.77$), and beta diversity ($p = 0.45$) in the fecal samples concerning the administration of the supplement. Notably, high inter-individual variability was observed in the alpha diversity analysis.These results indicate that the supplement may support metabolic health and reduce inflammation in overweight dogs. However, more research is needed to further understand the effective contribution of the supplement in clinical situations, especially to further understand the considerable individual variability observed in the microbiome.

FOOD QUALITY

P339

Inclusion of extruded linseed and grape derived antioxidants in the diet of Apulo Calabrese × Goland pigs: effects on animal performance and meat quality

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Supplementing pigs' diets with linseed increases polyunsaturated fatty acids (PUFA) in meat, enhancing consumer health benefits. To mitigate the meat's increased oxidative instability due to higher PUFA content, research is actively exploring natural and sustainable antioxidants for feed supplementation. This study assessed the impact of adding extruded linseed and a grape-derived antioxidant to pigs' diets on growth performance and meat quality. A total of 31 male (M) and female (F) Apulo Calabrese × Goland pigs (121 ± 3 d, 58 ± 8,3 kg) were assigned to the three dietary treatments: Control (CTR) diet ($N = 11$; 6 M, 5 F); SL diet, with 5% of linseed ($N = 10$; 5 M, 5 F); SLXI diet, with 5% of linseed and 0.2% of a powdered grape pomace rich in polyphenols (12,200 mg GAE/100g) ($N = 10$; 5 M, 5 F). After 13 d of adaptation, the 97-day feeding trial took place, during which body weight (BW) was measured biweekly. At slaughtering, hot carcass weight (HCW), carcass yield (CY%), pH45, pHu and backfat thickness (BF) were measured. *L. thoracis* of each carcass was subjected to physicochemical analysis (drip and

cooking losses, lipid content, FA profile, and lipid and color stability in 6 d of storage). BW, meat lipid and color stability were analyzed by Mixed effects model with diet, time and their interaction as fixed effects. A 2-way ANOVA with diet, sex and their interaction as fixed factors was applied to evaluate the carcass and other meat traits. Means were separated by Tukey HSD test ($p \leq 0.05$). Carcass and meat traits, except CY%, were not influenced by sex. BW, HCW and BF were not affected by diet, while CY% was higher for SLXI than for CTR ($p < 0.01$) and was greater in M than in F ($p < 0.05$). The pH45 was higher in SL than in the other groups ($p < 0.01$), while the pHu was not affected by diet. SLXI had greater drip loss than the other groups ($p < 0.01$) and CTR showed the highest cooking loss ($p < 0.01$); in both cases, the values were acceptable except for the SLXI drip loss, which exceeded 5%. Content and lipid stability of SL meat were higher and lower ($p < 0.05$), respectively, than those of the other groups. The FA profile was improved by SL and SLXI diets compared to CTR, thanks to the higher percentage of C18:3 n-3 ($p < 0.05$) and total n-3 FA ($p < 0.05$) and the lower n-6/n-3 FA ratio ($p < 0.05$). In conclusion, feeding linseed and grape-derived antioxidants to pigs improves pork nutritional value without compromising its technological traits or growth performance and carcass quality.

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P201

Effect of microencapsulated *Yucca schidigera* extract on milk production and composition in dairy goats

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Several studies have evaluated the effects of adding plant extracts rich in saponins to the diet of ruminants and their impact on production levels in these animals. However, these secondary metabolites face challenges that degrade them quickly, such as digestive processes and attacks by ruminal microbiota, which can limit their benefits for animal health and production. This study aimed to evaluate the effect of microencapsulation of Yucca schidigera extract (YE) through spray drying in a double matrix of mesquite gum and whey protein on milk production and composition in dairy goats. The experiment was conducted over 45 days with a group of 24 Saanen female goats recently postpartum (55 ± 5.0 kg body weight, multiparous, and over 2 years old). The goats underwent a 15-day acclimatisation period to adapt to the total mixed ration (TMR) diet, fed at a rate of 3 kg/day, which began 10 days before parturition. Daily leftovers were weighed to assess feed refusal. Five days after parturition, the first milk sample was taken, followed by a second sample midperiod (day 22) and a third at the end of the experiment (day 45). The samples were analyzed using a MilkoScope Julie C3 Automatic™, which measures parameters such as fat, non-fat solids, protein, lactose, density, solids, freezing point, and added water. The study used a completely randomised design, with goats randomly assigned to three groups: one fed the basal diet without YE (NYE, control), another with microcapsules at 0.5 g/animal/day (MYE), and a third with crude YE extract at 0.5 g/animal/day (CYE), however, data were analyzed using ANOVA. The MYE goats showed a nonsignificant increase in milk production (kg/head/day) than the CYE goats (1.450 *vs*. 1.380) and the NYE goats (1.450 *vs*. 1.400), and there were also no significant differences between CYE and NYE (1.380 *vs*. 1.400). Feed intake revealed a significant difference ($p < 0.05$) between the groups. The MYE goats showed higher feed intake (kg/head/day) compared to the CYE goats (1.900 *vs*. 1.566; $p < 0.05$), although they also outperformed the NYE goats (1.900 *vs*. 1.800; $p < 0.05$), this difference was not statistically significant. The data analysis reveals that the YE capsule additive positively impacts the milk quality of dairy goats. Significant differences were observed in fat, lactose, and non-fat solids when comparing the groups. For example, on Day 1, the MYE goats showed a fat content of 4.44%, slightly lower than the NYE goats (4.54%) but higher than the CYE goats (4.36%). In terms of lactose, the MYE goats reached 5.39%, surpassing the NYE (5.13%) and CYE (4.97%) goats. Additionally, the non-fat solids were 9.11% in the MYE goats, compared to 9.34% in the NYE goats and 8.97% in the CYE goats. These results are encouraging, as they suggest that the encapsulation of YE extract not only preserves its beneficial properties but also improves milk quality. Encapsulation allows for controlled release of the additive, maximising its effectiveness in the goats' bodies, which enhances nutrient digestibility and absorption, as well as optimises milk production. The data suggest that the use of *Yucca schidigera* in microcapsule form can be an effective strategy for improving milk quality in goats, presenting significant advantages that justify its inclusion in the diet of these animals.

P267

Effect of replacing corn silage with alternative crops on milk yield and quality in Italian Simmental dairy cows

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The substitution of corn silage in dairy cows' diets is considered crucial for the economic and environmental sustainability of the livestock sector due to its price fluctuation, high irrigation water requirements and susceptibility to mycotoxin contamination. However, knowledge about the effects of using alternative crops to replace corn silage on milk yield and composition remains limited. In a group of 20 Italian Simmental cows raised in a free stall farm of Northern Italy, 6 animals in the lactation phase (DIM: 145 ± 80; Parity: 3.2 ± 1.7; Milk yield: 24.7 ± 4.7 kg/d) for the entire duration of the trial were identified. The trial consisted in four consecutive periods using four isonitrogenous and isoenergetic diets: a control diet (CTR), a diet based on corn silage (P1) being replaced by sorghum-soy silage (P2), and then by sorghum silage (P3). The duration of each period was of 21 days, with transition periods of 12 days in between to gradually change the diet. Milk yield was recorded daily and samples were analyzed for chemical composition and coagulation properties for each individual cow at the last week of each period. For the statistical analysis, a mixed model was applied, using the cow, diet and parity as fixed effects and the days in milk as a covariate. Milk yield (25.6 ± 6.09 kg/d) was not affected by the diets. The fat content was similar for the CTR and P2 groups, but higher than P1 and P3 (4.21, 3.94, 3.24 and 3.48% resp.; $p < 0.01$). While, non-adverse effects on any of the other parameters (protein: 3.6%, casein index: 78.3, urea: 26.6 mg/100ml, lactose: 4.5%, Somatic Cell Score: 3.4, RCT: 20 min, K20: 7.0 mm, a30: 23.1mm, a45: 24 mm, a60: 20.8 mm in average) were observed. To conclude, the replacement of corn silage with sorghum-soy silage had increased the fat content in milk without affecting milk yield or any other milk quality parameters suggesting to be a good alternative as an alternative crop for dairy cows.

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P051

Effect of High-Pressure Processing on texture of gilthead sea bream (Sparus aurata) fillets

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Conventional food processing technologies often rely on thermal methods which can negatively affect nutritional value, texture and freshness of the product. In raw fish, high-pressure processing (HPP) is an effective non-thermal preservation technique that extends the microbiological shelf life, minimises the loss of desirable compounds, and preserves freshness and nutritional values. Texture is one of the most important parameters that determines the overall quality perception of fish and Texture Profile Analysis (TPA) is a widely used physical method to evaluate the textural properties of fish such as hardness (H), springiness (S), adhesiveness (A), cohesiveness (C), gumminess (G), and chewiness (Ch). The aim of this study was to evaluate the effect of two different high-pressure treatments on the texture of gilthead sea bream fresh fish fillets. Fish farmed in Turkey were individually vacuum packed and immediately subjected to HPP treatment. The samples were placed in a 350 L chamber, filled with water and subjected to 5930 bar for 290 s or 6000 bar for 300 s at 4 °C, respectively. An untreated group was used as a control (CTRL). Following the HPP treatment, all the samples were stored at 4 °C for 2 days until TPA. Five sea bream fillets for each group, average weight 95 ± 38 g, were randomly selected and subjected to TPA. Texture parameters were measured with a TA.XTplus Texture Analyzer equipped with a 10-kg load cell. The whole experiment was performed at room temperature, applying a spherical probe ∅ 12.7 mm. Samples were compressed twice to 50% of their original height at a constant speed of 1 mm/sec. Data were analysed by ANOVA followed by Tukey HDS test ($p \leq 0.05$) of XLSTAT. Samples treated at 5930 bar exhibited a significant change in all the parameters compared to the CRTL group, except for C. More specifically, H, S, A, G, and Ch showed higher values than CRTL group ($p < 0.01$). The comparison of 6000 bar samples with those of CTRL group was significant for S and A ($p < 0.01$), while the values of H, G and Ch were between those of 5930 bar and CTRL group. These results demonstrate that HPP, when applied under appropriate conditions, has a

noticeable effect on texture parameters. Since fish muscles undergo excessive and rapid post-mortem softening due to weak connective tissue and the activity of endogenous proteolytic enzymes, HPP improves the texture (firmness) of fish muscle as opposed to thermal processing that result in brittle and flaky product.

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P117

Discriminant analysis to classify two fish species based on geographical origins and farming systems using FT-NIRS

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Aquaculture supplies 51% of the global seafood market, surpassing the quantity of wild products. Despite this milestone, the European Union remains heavily reliant on imports to meet domestic demand for seafood products, making it the largest importer worldwide. Widely produced euryhaline finfish species in Italy are the European seabass (*Dicentrarchus labrax*) and gilthead seabream (*Sparus aurata*). Because of the strong relationship between farming conditions, feed composition, and the quality of the final aquaculture products cannot be considered homogeneous. Therefore, it is essential to identify markers of traceability, and to develop rapid techniques for assessing product quality. This preliminary study aimed to classify different geographical origins and farming systems of the two fish species, applying the qualitative approach of discriminant analysis based on principal components of the near-infrared (NIR) spectra. Fish samples ($n = 30$) of *S. aurata* were collected from three Italian farms located in different geographical areas of Tuscany (two in Piombino, Livorno, equipped with inland tanks or sea cages), and Apulia (Manfredonia, Foggia, equipped with sea cages). Other 40 specimens of *D. labrax* were purchased from the previous mentioned farms, plus a farm located in Castiglione della Pescaia, (Grosseto) equipped with ponds. For each fish, two intact portions from the epaxial part of fillet were acquired by Antaris II FT-NIRS instrument (Thermo Fisher Scientific) considering the infrared region ranged from 3999 to 9999 cm^{-1} with a resolution of 4 cm^{-1}. Thirty-two continuous scans for each replicate was collected as log 1/R. After a pre-processing on raw spectra, on average spectra a multivariate exploration was applied on 3112 wavenumbers by discriminant analysis of principal components (DAPC) using the factoextra R package. A cross-validation was applied for class assignment where the full dataset was used for model training, and the discriminant functions were extracted based on all samples for fish classification. The first two components explained 99% of the total variability of the dataset (82.7 PC1 and 16.7 PC2 as % of variance). The DAPC model resulted in an overall assignment success rate of 75.7% for the farming systems, and 81.4% for geographical origin using one discriminant function.

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P121

Nutritional characterization of a fermented beverage from donkey milk

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The present work is part of the Tool4MEDLife project (PRIMA program), which aims to increase awareness about the Mediterranean diet thanks to the production of innovative foods and educational toolkits. Donkey milk, due to its potential hypoallergenic properties, has been suggested as a good alternative for feeding young children affected by cow milk protein allergy (CMPA) when it is not possible to breastfeed. Furthermore, thanks to the presence of nutraceutical molecules with antioxidant, anti inflammatory, antimicrobial, antiviral, and antitumor activities, donkey milk is interesting also for elderly people. Considering the high-quality characteristics associated with fermented milk, the aim of this work was the production of fermented donkey milk by selected Lactic Acid Bacteria (LAB) able to synthesise folates (vitamin B_9). The final product was also fortified with vitamin D_3 and calcium. The levels of folates of natural origin represent an optimal alternative to synthetic folate-fortified products, which have limited bioavailability, and possibly lead to the accumulation of unmetabolised folic acid. Five fresh pasteurised donkey milk samples, added with vitamin D_3, calcium carbonate, *Streptococcus thermophilus, Lactobacillus delbrueckii ssp. bulgaricus* and *Lactobacillus plantarum* IMC 509 (Synbiotec), were fermented at a constant temperature of 38–40 °C for 5 hours. Folate content on the final product was determined by RP HPLC (Agilent 1260 Infinity LC system), using a column C18 HiQSil HS, 5 µm, 4.6 mm i.d., 250 mm (Kya Tech Corporation, Tokyo, Japan). The fermentation process led to the production of a fermented beverage with a final pH value of 4.4. The determination of folates by RP HPLC indicated mainly the

presence of tetrahydrofolate (5.3 ± 0.081 µM) which is a form of folate with high bioavailability. Other water soluble vitamins found in the final fermented donkey milk were vitamin C (110.16 ± 13.5 µM), nicotinic acid, and nicotinamide (52.7 ± 0.05 µM and 7.36 ± 0.15 µM respectively), and also vitamin B_{12} (1.69 ± 0.022 µM). Comparing the above results with the water soluble vitamin content of donkey milk present in the literature, it can be noticed that the vitamin content found in the fermented donkey milk beverage is considerably higher. These preliminary results indicated that the LABs used in these experiments are very promising to produce fermented donkey milk with enhanced nutraceutical properties.

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P137

Hermetia illucens as functional feed for laying hens: effect on egg quality

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Insect-derived products are part of many animal feeding programs because they provide a sustainable way of recycling waste into nutrient-rich ingredients. Additionally, the nutrient content and accessibility of ingredients derived from insects are typically much higher compared to the required levels and formulation demands, and components such as chitin, provide additional benefits. The aim of this study was to evaluate the physical characteristics of eggs produced by laying hens fed exuviae and chitin functionalised feeds produced by larvae of *Hermetia illucens* reared on substrates derived from agricultural waste. A total of 120 ISA Brown laying hens were randomly divided into 3 groups (40 hens per group): CTR, fed a basal diet (16.6% CP; 2714 kcal/kg); CHI, basal diet enriched with chitin extract (1g/head/day); and ESU, basal diet integrated with exuviae in terms of 1 g/head/day of chitin. The trial lasted 70 days, and a total of 252 eggs (126 at the start and 126 at the end of the trial) were sampled to assess their quality. Physical parameters were determined on each egg (42 eggs per group) using a texturometer (TA.XTPlusC). Yolk color was determined using a Yolk Color Fan (dsm-firmenich). All data were subjected to the ANOVA model of XLSTAT software, using diet as fixed effect. No significant differences were found in eggs weight and shell thickness among the 3 groups, but the CHI group (54.09N) showed greater shell breaking strength compared to the ESU (46.99N) and CTR (40.24N) groups, while the ESU group evidenced greater shell deformation (0.81mm) than CH (0.77mm) and CT (0.63mm) groups ($p = 0.032$). In a farm context, both parameters are very important to prevent damage due to handling and to preserve eggs during transport from farm to market. Regarding egg freshness indicators such as albumen height, Haugh Unit, yolk width, yolk index and yolk color, no significant differences were found. However, experimental feeding significantly improved vitelline membrane strength ($p = 0.0001$) with the highest value in the CHI group (CHI 0.18N; ESU 0.17N; CTR 0.17N). No significant differences were observed in the length, width, circumference of the egg, weight and percentage of the components (shell, yolk and albumen). In conclusion, the supplementation of exuviae and chitin in laying hen diets, highlighted the positive effect of these functional components derived from *Hermetia illucens* on improving egg quality.

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P148

Alfalfa and linseed oil in rabbit diet to improve sustainability and healthiness of the meat

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Rabbit farming represents an interesting livestock resource for meat production, both for Western and for emerging countries. However, the sector has crucial difficulties also due to the dependence on conventional feed ingredients responsible for price volatility, competition between feed and food and environmental impacts. In recent decades there has been a strong reduction in the use of forage in rabbit diets in order to improve performance and reduce feed costs. In a previous experiment we compared a commercial diet with one based on alfalfa, finding a significant improvement in the nutritional characteristics of the meat but, at the same time, a worsening of growth performance. For this reason, the aim of the present study was to verify the efficacy of an enrichment with linseed oil added to alfalfa-based diet. The trial was carried out at a commercial rabbitry, where at weaning age three hundred hybrid rabbits of both sexes were divided into three homogeneous groups and fed with commercial feed based on 18% wheat +17% alfalfa hay+ 8% dehydrated alfalfa (Control), experimental feed based on 40.4% alfalfa hay +35.0% dehydrated alfalfa (Alfalfa) and another experimental feed based on 40,4% alfalfa hay +35.0% dehydrated alfalfa +2% of linseed oil (Alfalfa + Linseed). A linear

model was used to evaluate the effect of diet; to define the significance, the Turkey post-hoc test was used. The different formulation determined different chemical characteristics of feeds, in particular an increase of the fiber fractions and a decrease of lipid and protein contents and metabolizable energy. A reduction ($p < 0.05$) in slaughtering weight was observed only in the Alfalfa group, while the addition of linseed oil eliminated the gap with the Control. The lipid content of the *Longissimus dorsi* muscle was significantly lower in the Alfalfa group compared to the Control and Alfalfa + Linseed ones ($p < 0.05$). Significant changes were observed in the fatty acid composition with higher levels of α-linolenic acid in the Alfalfa + Linseed group followed by Alfalfa and Control ($p < 0.001$). The Eicosapentaenoic and Docosahexaenoic acid levels also followed the same trend, although the differences between the two experimental groups became less pronounced ($p < 0.05$). In conclusion, it can be stated that this dietary proposal represents an interesting non-competitive strategy which allows obtaining rabbit meat with a high nutritional profile, without reducing productive performance.

P150

Meat quality of breast and drumstick of different ECC-approved chicken genotypes

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Poultry meat is considered less expensive and 'healthier' than other meats due to its high protein, low fat (with high unsaturation level), and low cholesterol content. To fulfill the increasing demand for chicken meat, poultry breeding companies have hardly selected genetic lines with high growth performance, often despite health and meat quality. In this context the current market is strongly directed toward the use of slow growing chicken genotypes (SG), as demonstrated by the European Chicken Commitment (ECC) challenge: the use of only SG in all poultry productions by 2026. In this regard, some chicken genotypes are selected. To evaluate the meat (breast and drumstick) quality of some of these novel chickens, two ECC approved genotypes presenting intermediate (MG, 40–50 g/d; Ranger Gold) and slow (SG: 30–40 g/d, Kabir) growth were chosen and compared to a fast-growing genotype (FG >65 g/d, Ross 308). A total of 180 chickens (15 birds per replicate for each genotypes) were reared in experimental conditions following ECC-standard management practices (bird density: ≤ 30 kg live weight/m^2). The animals were fed with a commercial starter diet from 1 to 20 d and a finisher from 21 until slaughtering (2759 ± 174 g final body weight). At slaughter 3 chickens/replicate/genotype ($n = 12$) were sampled and qualitative evaluations on breast and drumstick (physico-chemical, oxidative status and antioxidants profile) were performed. The analysis was done with post-hoc Bonferroni test $p > 0,05$. The SG showed lower water holding capacity (WHC) and higher cooking loss both in breast and drumstick and low lightness (L), redness (a*) and yellowness (b*), whereas the pHu showed higher value than MG and FG. Furthermore, the SG showed the highest lipid content followed by FG and MG (3.6 vs 0.91 and 1.45 in breast; 5.2 vs 1.52 and 2.06 in drumstick), and the lowest (breast) or not significantly different (drumstick) tocopherols concentration ($p > 0.05$). Accordingly, a higher lipid oxidation of breast was observed in SG than other genotypes, but not for the protein ($p > 0.05$). Concluding, despite the slow growing rate of SG genotype, it showed a higher meat fat concentration, probably due to an intrinsic metabolism of the birds. This highlights that the ECC-approved chickens may exhibit very different qualitative profiles, and should be studied in depth before being in the ECC list.

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P169

Impact of dietary hemp seeds in an agroecological farming system (HappyHens): functional and nutritional features of eggs from different layer breeds

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The aim of the HappyHens project is to support the use of alternative protein sources for animal nutrition for more sustainable production, in a socio-cultural context where human wellbeing animal welfare relationship is centre-oriented and integrated within One Health concept. HappyHens joins the framework of a community chicken coop project launched in 2023 by the association Soulfood Forestfarms Hub Italia with the support of more than 150 citizens. This regenerative peri-urban agroforestry system is located between the Corvetto and Vigentino neigh-borhoods, planted on land owned by the City of Milan in the Vettabbia Park assigned under agrarian lease to CasciNet – Società Agricola Impresa Sociale. In this context, laying hens are bred according to the agroecological principles of rational grazing. The central theme of the project is the use of hemp to promote hemp

co-products in animal nutrition. Hemp plays key roles within the industrial sector, for the production of paper, textile fibre, biodegradable plastic, alternative energy and as a construction material, as well as being widely used within the pharmaceutical sector. Within food and feed sectors, hemp seed (HS) is becoming a key element due to its nutritional and functional properties. The project involves 4 target breeds and eggs are being sampled over a 10-month period. Hens are allocated in mobile hen houses equipped with covered tunnels considering their breed (n.30): Lohmann Brown, Livornese, Milanino and Marans. The diet administered to laying hens includes 20% of HS. Productive performance and egg quality parameters (whole egg, yolk, albumen and shell weight, shape index, shell thickness and yolk color) are evaluated. Furthermore, proximate composition, fatty acid profile of total lipids, healthrelated lipid indices and antioxidant compounds are analysed and compared with commercial eggs. This research is coordinated by the Department of Veterinary Medicine and Animal Sciences and the Department of Cultural and Environmental Heritage of the University of Milan. Following a multidisciplinary approach, the project promotes a sustainable solution in animal production in an innovative socio-cultural context.

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P235

Nutritional properties of Podolian meat: the impact of dietary forage to concentrate ratio

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Beef nutritional properties are very notable in purchasing behaviour, because consumers are interested about health warnings. Improving meat nutritional properties through animal feeding strategies is crucial in order to meet the current human nutritional recommendations. Therefore, the present study aims to assess the effects of two different forage to concentrate ratio on nutritional properties of beef. Twenty Podolian young bulls were randomly assigned to two groups: high forage to concentrate (HF:C) receiving a forage to concentrate ratio of 65:35, low forage to concentrate (LF:C) group receiving a forage to concentrate ratio of 45:55. Fatty acid profile, bioactive compounds, α-tocopherol content and oxidative stability were evaluated on *Longissimus thoracis muscle* vacuum-packaged and aged at 2 °C for 11 and 18 days, respectively. Results showed that feeding the highest forage to concentrate ratio improved fatty acid profile with a decrease of saturated fatty acids ($p < 0.01$) and an increase of monounsaturated ($p < 0.05$) and n-3 polyunsaturated fatty acids ($p < 0.001$). In particular, the percentages of linolenic acid (C18:3n-3), eicosapentaenoic acid (EPA-C20:5 n-3), DPA (C22:5 n-3), and docosahexaenoic acid (DHA-C22:6 n3) were significantly higher ($p < 0.01$) in the HF:C group than LF:C group. As consequence, meat from animals fed with higher forage to concentrate ratio showed better qualitative and nutritional indices with higher P/S ($p < 0.05$), EPA + DHA percentage ($p < 0.01$), unsaturation index ($p < 0.05$), hypocholesterolemic/hypercholesterolemic ratio ($p < 0.05$) and lower n6/n3 ($p < 0.01$), atherogenic and trombogenic indices ($p < 0.05$) than meat from LF:C group. In addition, the highest forage-to-concentrate ratio also increases the content of bioactive compounds such as creatine ($p < 0.001$), carnosine ($p < 0.01$) and anserine ($p < 0.05$). Our results suggest that the diet including 65% DM of forage improves the sustainability of Podolian beef production systems providing healthy meat with a great oxidative stability that is fundamental for a meat that need of an aging time longer than two weeks. This may help to preserve and to promote this native breed, contributing to the proper management and conservation of semi-natural habitats as well as to healthy meat production.

This study was carried out within the Agritech National Research Center and received funding from the European Union NextGenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022).

P290

Sustainable rabbit production: carcass traits, physical meat quality, and shelf-life of three local breeds

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The present study is a part of a wide project proposing a multidisciplinary approach to design a new strategy to valorise rural rabbit meat chain, by using national genotypes, thus

protecting biodiversity, promote free-range system, and meet consumer's expectations for innovative, sustainable and welfare-friendly products. The first experiment, conducted at the University of Turin, studied three different breeds (Bianca Italiana – B, Grigio Piemontese – G, Leprino di Viterbo L) farmed in a free-range system, aiming at selecting the most suitable one for the second experiment (test an innovative and low-input diet). Fifty weaned rabbits/breed were allocated into five replicated indoor pens with outdoor access (accessible after rabbits were 60 days old) and fed *ad libitum* with a commercial diet. After slaughter (90 days of age) and carcass chilling (24 hours), $n = 10$ rabbit carcass/breed were transported to the MAPS Department (LabCNX Laboratory; University of Padova) for carcass dissection and meat quality evaluations. Data were analyzed by a one-way ANOVA with breed as fixed effect. Least square means were obtained, and post-hoc pairwise comparison was carried out applying the Bonferroni correction (significance: 5% confidence level). Overall, carcass traits were comparable in the three breeds, with some exceptions such as fore leg weight (77.6 *vs* 69.6 *vs* 64.4 g for B, L and G, respectively; $p < 0.05$), *longissimus thoracis e lumborum* (LTL) weight (72.1 *vs* 57.0 *vs* 55.9 g for B, G and L, respectively; $p < 0.05$) and liver incidence on the chilled carcass (6.29 *vs* 5.50 *vs* 4.77 % for G, B and L, respectively; $p < 0.05$). Redness value of the *biceps femoris* muscle was the only trait differing among breeds for physical meat quality traits (0.32 *vs* 1.19 *vs* 1.17 for B, G and L, respectively; $p < 0.05$). Meat cooking loss (LTL and hind leg) and Warner-Bratzler Shear Force were similar in the three breeds. Differently, femur fracture toughness was higher in the B rabbits than in G ones, with L being intermediate (424 *vs* 349 *vs* 309 kg for B, L and G, respectively; $p < 0.01$). From results obtained for the present experimental part it did not emerge a clear indication regarding the best breed to be selected for the second experiment. To make the right choice, a careful consideration of growth curves and welfare aspects of the three breeds is necessary, together with a nutritional meat quality evaluation and sensory profile.

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P297

Milk microbiota composition in Girgentana goat breed

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The characterisation of microbiotas has shifted from culture-dependent methods to culture-independent approaches, leveraging 16S rRNA sequencing and analysis for phylogenetic and compositional insights. Understanding the microbial composition of milk is increasingly important for product quality, safety, and as a reflection of animal health. In this study, NovaSeq (Illumina) technology was used to sequence the V3–V4 regions of 16S rRNA from 44 milk samples of Girgentana goats, a Sicilian breed known for its resilience and high-quality dairy niche products. Milk samples were collected during early-morning milking, alongside bulk milk representative of the whole farm. Additionally, microbial analysis was extended to 'Ficu' a traditional cheese made from the same bulk milk. DNA was extracted and amplified via PCR-method. Reads were processed with MICCA and QIIMEv1.9 in-house pipelines, with adapters, primers, and low-quality bases removed to ensure data integrity. Alpha diversity metrics assessed richness, evenness, and overall diversity, while taxa composition was analyzed to characterise microbial structure. Sequencing yielded 8'135'944 high-quality reads after filtering, identifying 2'210 distinct OTUs. The alpha diversity metrics highlighted a rich and balanced microbial composition. Observed OTUs averaged 1460.0, while Chao1 (1718.1) and ACE (1715.1) estimates indicated the presence of additional rare taxa. Shannon (4.2) and Simpson (1.0) indices showed a moderately diverse and evenly distributed community, with Fisher's index (218.1) highlighting overall complexity. Firmicutes (51%) was the most abundant phylum, followed by Proteobacteria (27%) and Actinobacteria (21%), representing the 99% of the total taxa composition. At the family level, *Lactobacillaceae* (54%) and *Bifidobacteriaceae* (22%) dominated. Notably, bulk milk composition aligned with individual milk samples, while microbial analysis of 'Ficu' cheese revealed an increase in *Actinobacteria* (27%), accompanied by a decrease in both Firmicutes (48%) and Proteobacteria (26%). This study is the first to unravel the milk microbiota composition of the Girgentana breed, using advanced sequencing technologies to provide detailed microbial profiling. The findings establish a baseline for microbial diversity, offering insights into artisanal dairy systems and enabling future comparisons with other breeds.

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P301

Olive residues as a cost-effective feed supplement: effects on milk quality in small dairy farms

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Two cross-over trials were carried out on two small farms in the Sorrento peninsula to evaluate the use of olive tree biomass residues as feedstuff for lactating cows: pruning residues (OlPr) and olive mill leaves (OlLe). In each trial, two homogeneous groups of four cows (160.7 ± 42.5 and 74.5 ± 28.9 DIM respectively for the two trials) were formed: one receiving a ration supplemented with either OlPr or OlLe and the other receiving a control diet. Each trial lasted 6 weeks and consisted of 2 treatment periods, each consisting of a 15-day adaptation phase followed by a 6-day measurement phase during which milk production, and intake of the single dietary component were recorded daily for each cow. Data were analyzed by repeated measures mixed ANOVA model with diet, period, and interaction as factors, and cow as a random effect. Limited to milk fatty acid (FA) composition, a GLM ANOVA was used with diet, period and interaction as factors. Both OlPr and OlLe by-products had a significant lignin and lipid content, a remarkable concentration of polyunsaturated and monounsaturated FA (PUFA and MUFA) and moderate saturated FA. The incidences of OlPr and OlLe in the diets (%DM) were respectively 15.69 and 23.13. This resulted in an increased overall dry matter intake (17.13 vs 18.18 SE 0.15 and 17.27 vs 18.93 SE 0.14 kg/d respectively for the two trials), and CP, NDF and fat supply ($p < 0.001$), with greater increases observed in cows fed OlLe. A slight but significant reduction in energy intake was observed in the OlPr group. Milk yield was unaffected by the treatments (17.84 vs 17.74 kg/d SE 0.70 and 18.51 vs 18.49 SE 0.24). The use of OlPr slightly influenced only the milk FA composition with an increment of oleic acid ($p < 0.01$). In contrast, OlLe supplementation significantly ($p < 0.01$) increased milk fat percentage and fat/protein ratio, while no significant effects were observed on milk yield, SCC, or milk protein content. Milk from cows fed OlLe also exhibited significant shifts in FA profile compared to the control group with a decrease in saturated FA and an increase in PUFA and MUFA resulting in a decrease in both the atherogenic index ($p < 0.001$) and the saturated-to-unsaturated ratio. In conclusion, the use of OlLe in dairy cow feeding appears to be a promising strategy for improving sustainable and economically viable dairy farming in the Sorrento Peninsula.

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P341

Milk production of ewes fed diets integrated with encapsulated or non-encapsulated lemon essential oil

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The exposure to heat stress (HS) is known to affect the physiological functions of livestock animals, with negative effects on their welfare, health and productivity. Among the various strategies for mitigating the negative effects of HS, addition of bioactive plant extracts, such as citrus essential oils (EOs), to the diet of dairy ewes, showed to improve milk and cheese production, also enhancing animals' resilience to HS. This research aimed to evaluate the performance of dairy ewes fed diets supplemented with EOs in non-encapsulated (EO) or microencapsulated (EOM) form. Since some bioactive components of EOs are unstable, the encapsulation was assessed for its ability to coat and protect them. The experimental activities were carried out in a farm during the hot season (from June to August) over 40 days. Forty primiparous dairy ewes were divided into 5 homogeneous groups based on live weight, days in milk and milk yield (on average, 41 kg, 82 days and 1100 g/day per head, respectively). One group was fed a control diet (C), while the other groups received the same diet supplemented with EO or EOM at low (L = 400 mg/day per head) or high (H = 800 mg/day per head) dosage. The research examined several aspects, including environmental parameters, feeding resources, and ewes' behavior, physiological and immune responses, and milk production. This note exclusively reports the results related to milk and cheese produced during the experiment. A significant increase in live weight was observed in all groups from the start to the end of the trial, primarily due to the ongoing growth of the primiparous ewes. The milk yield of ewes was affected only at a level of tendency; in

particular, the LEOM and HEO groups tended to have a production higher ($p < 0.10$) by about 50 g/day in comparison with the other groups. Regarding milk quality, the effects of EOs supplementation emerged exclusively in the somatic cell count (SCC), which was found to be tendentially higher in the group C compared to HEOM group (5.45 *vs* 5.25 $\log_{10}$ n/ml, $p < 0.10$). Finally, the diet had no significant effect on cheese yield, color and texture. Overall, the findings from the experiment demonstrate that the EOs supplements had negligible effects on the main parameters of sheep milk production, except for a slight positive impact, observable only as a tendency, on milk yield and SCC. Research supported by PRIN 2022 PNRR grant – P202283T2J – Ceo-SUSTAINSHEEP.

P398

Effect of grape pomace in the diet of ewes during the mid-lactation period on milk fatty acid profile and methane emissions

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Grape pomace (GP), a byproduct rich in bioactive compounds, could be included in animal diet to improve the animals' performances and the quality of the livestock products. The aim of this study was to evaluate the effect of including GP in the diets of ewes during mid-lactation on milk composition, milk coagulation properties (MCP), and methane emissions (ME), using a Laser methane Detector (LMD). Twenty-four Sarda dairy sheep, homogeneous in body weight (BW; 59.1 ± 0.75 kg), milk yield (MY; 2.4 ± 0.007 kg/day), and days in milk (DIM; 101 ± 1 days), were allocated into three treatment groups. The control group (CTR) received no GP supplementation, the GP100 group was supplemented with 100 g/day per head of GP, and the GP150 group with 150 g/day per head of GP. The trial lasted six weeks, including one week for adaptation and five for sampling. Feed intake was recorded daily using an individual automatic feeding system (Biocontrol AS, Rakkestad, Norway), and individual milk samples were collected weekly. Methane emissions were measured during the final week of the trial over three consecutive days during both morning and evening milkings, with two-minute measurements per ewe. Data were analyzed with a mixed model in which the diet, the time and their interaction were used as fixed effects and the animals as random. The inclusion of GP, at both dosages, did not affect milk yield, fat content, or protein content. The SCC tended to be lower for animals fed the highest doses of GP compared to the other two groups (2.32, 2.41 and 1.95 for CON, GP100 and GP150, respectively, $p = 0.09$). This parameter had impact on milk pH, that is higher in CON and GP100 compared to GP150, and also on MCP. However, GP reduced the concentration of saturated fatty acids (SFA) while increasing monounsaturated fatty acids (MUFA) and total unsaturated fatty acids (UFA) in the milk. Notably, GP150 significantly increased the levels of CLA cis-9, trans-11 and C18:1 trans-11 compared to the CTR and GP100 groups. Methane emissions, expressed as ppm-m, were not affected by GP supplementation. The means of concentration of methane during eructation events were 1030, 1312 and 983 ppm for CTR, GP100 and GP150, respectively. These results suggest that including 100 to 150 g of GP per day in the diet of lactating ewes can improve the fatty acid profile of milk without negatively impacting production traits, offering potential benefits for milk quality.
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P401

Determination of κ-casein B in bovine milk through HPLC and ELISA techniques

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Among milk casein fractions, κ-casein (κ-CN) plays a central role in cheese making process since it is the target compound of rennet. The κ-CN exists in different genetic variants, with κ-CN B being the most reactive toward coagulant activity, thus leading to greater cheese making efficiency and improved cheese quality. Therefore, there is great interest in the application of analytical techniques which are able to quantify κ-CN B. High pressure liquid chromatography (HPLC) is the reference analytical method for both qualitative and quantitative determination of κ-CN variants, being characterised by high sensitivity and accuracy but also by high labor demand and analytical costs. On the other hand, enzyme-linked immunosorbent assay (ELISA) is an alternative technique for fast and cheap quantification of κ-CN B. On this background, the aim of this study was to gauge the agreement between HPLC and ELISA techniques for the quantification of κ-CN B in bovine milk. Individual milk samples ($n = 975$) of Italian Brown Swiss cows were collected during evening milking in 50 herds located in the north-central area of Italy. Samples were analyzed through reverse phase HPLC to identify and quantify κ-CN B. The same samples were analyzed through ELISA

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commercial kit for the quantification of κ-CN B. The agreement between the two methods was estimated through Pearson's correlation coefficients and z-score (z). According to the latter indicator, results from 2 experimental conditions may be considered equal when $|z| \leq 2$, similar when $2 < |z| \leq 3$, and different when $|z| > 3$. Chromatographic analyses highlighted that 68% and 4% of the cows were homozygous for the allele of κ-CN B (genotype BB) and κ-CN A (genotype AA), respectively. The remaining 28% of the cows were heterozygous (genotype AB). Pearson's correlation coefficients (z-scores) calculated for concentrations of κ-CN B measured through HPLC and ELISA techniques were 0.88 (0.29) when considering BB and AB genotypes together, 0.60 (0.59) when considering only BB genotypes, and 0.40 (4.11) when considering only AB genotypes. Results indicate that ELISA is consistent with HPLC technique when κ-CN B is represented in relatively great concentrations (i.e. when including BB genotypes). Poor agreement was observed for milk samples with low concentrations of κ-CN B (i.e. AB genotypes). Research supported by the project 'Dalla genomica ai minerali del latte: un migliore utilizzo delle proteine nel processo di caseificazione – GENETOCHEESE', funded by MIPAAF (DM n. 16830, 11/04/2019 – Fondo per gli investimenti nel settore Lattiero Caseario).

P402

Microbiological, nutritional, and sensorial characterization of bottarga of *Mugil cephalus* produced in the east and west coast of Sardinia

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Bottarga, called also avgotaracho in Greece or karasumi in Japan is the product arising from the process of drying and salting of mullet ovaries (*Mugil Cephalus*). The different condition of fish rearing and bottarga manufacturing could have an impact on physic-chemical characteristics and on quality of the final product. For this reason, the nutritional, microbiological, and sensory qualities of the bottarga from two different location of Sardinia were investigated. The samples of bottarga were collected from two fishing companies located in the east (EC) and west coast (WC) of Sardinia Island. The samples were analysed for water activity (aw), fat, protein, sodium, and cholesterol concentration. The microbiological and sensory analysis were carried out to assess the safety of the products and the consumer acceptance. The protein concentration was 40.5 % ± 1.73 and 38 % ± 0.46 for the bottarga of WC and EC, respectively, without any difference between the two areas. The overall fat concentration was 18.6%. The bottarga had also a good concentration of calcium, equal to 455 and 413 mg/kg for WC and EC, respectively. The cholesterol found in the samples was 417 and 389 mg/100 g of edible part for bottarga from WE and EC, respectively. Both mesophilic and psychrophilic microbial count were approximately 4 log CFU/g in all bottarga samples analysed. The spoilage microorganism indicative of environmental contamination, such as Clostridia, yeasts and moulds, were not found in the samples. The potential pathogens coagulase positive staphylococci were not determined in the EC samples and in very low concentrations in the WC samples, meeting the safety criteria. No significant differences were observed in bottarga colour uniformity, suggesting a homogeneity in the raw material quality and preliminary processing phases. The texture attributes (greasiness, adhesiveness, friability) did not show significant differences between the two samples. The global odour and the sea odour were higher for WC compared to the EC, suggesting a more pronounced aromatic profile. The WC evidenced also a significantly higher score for global flavour and sea flavour, probably due to the natural biochemical composition of the roe due to differences in mullet environmental condition. Overall, these preliminary results indicate that the food product of both areas is microbiologically safe, chemically sound, and sensorially appealing.

P452

iSafe-Graze: selection of probiotic lactic acid bacteria as starter cultures to enhance Conjugated Linoleic Acid content in sheep's milk cheese

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A significant interest has emerged in the effects of conjugated linoleic acid (CLA), which is naturally present in the meat and dairy products of ruminants. CLA exerts numerous health benefits, and certain lactic acid bacteria (LAB) have the ability to convert linoleic acid found in foods into CLA. This study aimed to select LAB strains for their capacity to produce CLA to be used as starter cultures in

the cheese-making process of sheep cheese. A total of 45 LAB strains were screened using 0.5 mg/ml of pure linoleic acid in broth cultures incubated at 30 °C for 48 hours. Fatty acids were extracted with 2-propanol and hexane, followed by spectrophotometric analysis at 233 nm. Two strains belonging to Lacticaseibacillus rhamnosus were further evaluated for their cheese-making aptitude (coagulation properties, acidifying power, and survival in different salt concentrations). These strains were subsequently blended and inoculated as starter cultures in the traditional cheese-making process of a raw milk sheep cheese known as 'Canestrato'. Microbiological and fatty acids (FA) profile (GC-FID, Fatty acids were separated using a CP-Sil 88 fused-silica capillary column (100 m × 0.25 mm i.d. × 0.2 µm film thickness) were performed on the milk and then on the cheeses after 24 hours, 15 days, and 30 days of aging. Data were processed by ANOVA. The experimental cheese exhibited a higher abundance of Lactobacillus spp. (8.24 vs. 6.5, log CFU/g) and Lactococcus spp. (7.69 vs. 7, log CFU/g) compared to the control cheese, along with a significant reduction in Enterococci (4.1 vs. 5.5, log CFU/g), Staphylococci (4.4 vs. 5.4, log CFU/g), and Enterobacteriaceae (4 vs. 5, log CFU/g). FA of nutritional interest (g/100g identified FA), compared to the control cheese, the total PUFA content was higher in the experimental cheeses (5.72 vs. 5.39; $p < 0.05$), as were the n-3 (1.20 vs. 1.08; $p < 0.01$) and n-6 fatty acids (3.36 vs. 2.91; $p < 0.01$). The oxidised fatty acids (OFA) index was also higher in the experimental cheese (42.04 vs. 41.14; $p < 0.01$). The CLA (C18:2 cis9trans11) content showed no significant differences between the two cheeses (0.67 vs. 0.70). Although the produced cheeses did not exhibit significant differences in CLA content, the experimental cheese demonstrated a better acidic and microbiological profile.

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P460

Effect of feeding olive mill wastewater (*Olea europaea* L.) on meat quality of Podolian young bulls

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This study aimed to evaluate the effect of dietary olive mill wastewater supplementation on the meat quality traits of Podolian young bulls. Ten young bulls were randomly assigned to two dietary treatments: a control diet (C: $n = 5$ at an average weight of 294.5 ± 29.2 kg) composed of cereal flour and legume hay and a diet supplemented with 30g/die/animal of spray-dried olive mill wastewater (OMW: $n = 5$; at an average weight of 278.7 ± 42.3 kg). The daily dry matter intake was 2% of each bull's body weight. The finishing trial lasted 40 days, preceded by a 2-week adaptation period. Each animal was weighed individually at the beginning and end of the trial. After an on-farm fasting period of 8 h, the animals were transported to the abattoir (animals were slaughtered in two stages 4 days apart). At slaughter, the hot carcass weight was recorded, and the dressing percentage was calculated. After 15 days of aging (3 °C), the *Longissimus thoracis* (LT) muscle was removed from each left-side carcass, vacuum packaged, and stored frozen (–20 °C) until chemical analysis. Data were processed by one-way ANOVA. Diet did not affect ($p > 0.05$) final live weight, carcass weight, and yield. The OMV group showed a higher ($p < 0.01$) dry matter and protein content. Lipid, ash, cholesterol, and vitamin E were not affected by the supplementation OMW. Concerning the fatty acid (FA) profile of LT muscle, total saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), and polyunsaturated fatty acids (PUFA) contents were similar ($p > 0.05$) between the two dietary treatments. Considering the composition of single MUFA, palmitoleic acid was lower ($p < 0.05$) in the OMV group than in C. A higher amount ($p < 0.05$) of α- linoleic (C18:3 n-3), eicosapentaenoic acid (EPA, C20:5 n-3) and docosapentaenoic acid (DPA, C22:5 n-3) was found in OMV group, with a lower ($p < 0.05$) n-6/n-3 ratio in comparison with C group. The PUFA/SFA ratio, atherogenic and thrombogenic indices were not influenced by diet ($p > 0.05$). Dietary OMW supplementation in young bulls did not adversely affect growth and carcass traits but improved the FA profile. Further studies are needed to validate the optimal level of inclusion and the timing of administration.

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P490

Towards sustainable beekeeping: Warrè (people's) *vs* Dadant-Blatt hives. Evaluation of chemical and aromatic profile of Sicilian Acacia (*Robinia pseudoacacia*) Honey

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Organic and sustainable beekeeping practices have gained global attention for their positive impact on honey products, bee health, and environmental conservation. These practices ensure high-quality bee products and support bee population well-being. Warré hives are designed for minimal inspections and are considered bee-friendly, simple, and cost-effective. However, no studies have evaluated the impact of this hive type on honey quality. Thus, the main goal of our work was to compare the quality of honey produced by bees in Warré hives (WH) and Dadant-Blatt hives (DB). Black Sicilian honey bees (*Apis Mellifera Siciliana*) were used, and four WH and four DB hives were set up in an apiary in Sicily, in an area known for producing monofloral honey during the acacia (*Robinia pseudoacacia*) flowering in May. Three honey samples per hive were taken and analyzed for pH, electrical conductivity (mS/cm), soluble solids content (brix %), Baumé degree (°B), moisture (g/100g), total polyphenols (mg GAE/100g), free acidity (meq/kg), combined acidity (meq/kg), total acidity (meq/kg), mineral content (Na, Ca, P, K, Mg) (mg/100g), heavy metals (As, Hg, Cd, Pb) (mg/kg), and sugar content (fructose, glucose, sucrose, maltose, total sugars) (g/100g). Free volatile components were determined by GC-MS (µg/kg). Most results showed no significant differences. However, honey from WH had higher K content (67.09 mg/100g vs. 62.71 mg/100g in DB, $p = 0.008$) and lower sucrose (1.07 g/100g vs. 0.90 g/100g in DB, $p = 0.003$). Some variations were also observed in the volatile compounds, likely due to differences in bee fumigation treatments or the wood used for the hives. DB honey contained vanillin and 4-vinylguaiacol (2 and 9 µg/kg), typical of lignin degradation during wood toasting. WH lacked vanillin, but methyl vanillate (516– 13 µg/kg in DB) indicated prolonged toasting. Furfural (33 µg/kg) in WH, absent in DB, supports this hypothesis. Wax extraction differences may also exist: DB had higher levels of palmitic acid (1143 vs. 541 µg/kg) and lauric acid (182 µg/kg), absent in WH, where oleic, octanoic, and stearic acids were present (5776, 79, and 252 µg/kg). While further research is necessary, this study provides valuable insights for guiding sustainable beekeeping practices.

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P514

Unveiling the unique microbiome and nutritional profile of milk from the caprine Nera di Verzasca local breed

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The Nera di Verzasca (NV) goat, native to Lombardy, is essential for sustainable farming and high-quality dairy production, often raised alongside commercial breeds. This study analyzes the nutritional profile and microbiome of NV milk, comparing it with Camosciata delle Alpi and Saanen. Individual milk samples (n. 266) were collected from 4 mixed-breed farms: n. 50 from Camosciata delle Alpi, n. 104 from NV and n.112 from Saanen (each of them present in three farms). Analyses covered composition, somatic cell count, minerals, milk fat globules, coagulation properties, modeled curd-firming over time parameters, cheese-making traits and microbiome. Milk composition was determined via infrared spectroscopy (Mastersizer 3000). Milk cream was used for lipid extraction and fatty acid (FA) transesterification with FA methyl esters (FAME) analyzed in hexane using an Agilent 7890 GC system (CP-Sil88 column, 100 m × 0.25 mm ×25 µm) with pure methyl ester standards peak identification. Microbiological analyses included total aerobic counts and lactic acid bacteria enumeration using standard methods. Bacterial DNA was extracted and sequenced via 16S rRNA-metabarcode sequencing on NextSeq 2000 (Illumina), with data processed through a pipeline involving quality filtering, clustering into zero-radius Operational Taxonomic Units (zOTUs), and taxonomic classification against the SILVA 138 database. NV milk exhibited excellent cheese-making efficiency due to low somatic cell counts, large fat globules, ideal mineral profile, and good curd firming traits. Polyunsaturated fatty acids, including α-linolenic and c9 t11 conjugated linoleic acid, varied by farm, reflecting differences in diet and management. Total bacterial counts ranged from 2.00 to 3.23 Log10 cfu/mL with minimal variability across breeds, producers, and grazing periods, while lactic acid bacteria remained below 2.00 Log10 cfu/mL. Microbiota analysis revealed a strong influence from the producer and, to a lesser extent, the breed on biodiversity and composition. Grazing periods significantly reshaped microbiota due to dietary and environmental changes. These findings emphasise NV dairy products' quality and role in traditional farming. Differences among producers and grazing effects on microbiota highlight the product's role in preserving biodiversity. Integrating local and commercial breeds supports genetic diversity and traditional practices in modern livestock, offering economic and conservation benefits.

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P517

Influence of cattle breeds on microbiota and quality of Valtellina Casera PDO Cheese

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Valtellina Casera PDO is a key cheese designation in the Valtellina region, utilising over 30% of the milk produced by livestock farms in Sondrio. Its production is governed by a Production Specification Document (PSD), which emphasises the cheese's link to its territory but lacks clarity in some aspects. This study evaluates the impact of cattle breeds on the cheese microbiota to inform PSD revisions that better represent production methods and preserve the unique traits of Valtellina Casera PDO. Milk from specific cattle breeds influences cheese profiles. The current PSD permits traditional breeds, including Brown Swiss, Holstein Friesian, Simmental, and their crossbreeds. Differences in cheese from these breeds may result in organoleptic variations. Brown Swiss milk could enhance the cheese's market value, promote sustainable farming, and justify a differentiated labeling for cheese made exclusively from Brown Swiss milk. To explore these differences, 12 cheese samples from Brown Swiss milk and 31 from mixed breeds were analyzed across three ripening stages. Microbiological analyses included lactic acid bacteria enumeration (rods and cocci, heterofermentative lactic acid bacteria and enterococci) using standard methods. DNA sequencing (16S rRNA) was performed using Illumina MiSeq, and fatty acid profiles were analyzed with an Agilent GC system. Microbiological results showed more homogeneous microbial levels in mixed-breed cheese compared to Brown Swiss cheese, which had higher heterofermentative bacteria and rod-shaped lactic acid bacteria. These differences persisted during ripening but were not statistically significant. Fatty acid profiles also showed no significant differences between the two groups. Sequencing produced an average of 45,056 reads per sample. Alpha and beta diversity analyses revealed no significant differences in microbiome richness or biodiversity between the two groups (Observed species index p-value = 0.9859, Chao1 p-value = 0.9953, Shannon p-value = 0.2901). In both cases, 90% of the core microbiota consisted of *Streptococcus spp.* and *Lactobacillus spp.* The findings confirm that microbiota composition is stable across breeds, and microbial or fatty acid profile differences are minimal. Nonetheless, a differentiated branding strategy for Brown Swiss milk cheese could enhance the cultural and economic value of Valtellina Casera PDO while maintaining its traditional identity.
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P524

Lysozyme and total antioxidant capacity in raw milk of Ragusano donkey: effect of lactation stage and seasonal period

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Donkey milk is a niche product and can be considered as a functional food, due to its high lysozyme and antioxidant content. The present sudy, performed in Sicily on milk of *Ragusano* donkeys, was aimed to evaluate the effect of both different lactation stages (namely: <3 months; between 3 and 6 months; >6 months) and environmental temperature, as moderate or high temperatures (M: mid-January to mid-May and mid-September to mid-October, and H: mid-May to mid-September) respectively, on lysozyme content (LYS), lysozyme activity (LA) and total antioxidant capacity (TAC). Individual milk samples were collected from 20 animals every 2 weeks from mid-January to mid-October at a farm in South-Eastern Sicily. Milk samples were frozen and stored until analyses. LYS content was determined according to the ISO 27105:2016 protocol by reversed-phase HPLC and LA using *Micrococcus lysodeikticus* cells as the substrate. TAC was determined by an electrochemical method using a portable e-BQC NI instrument (Bioquochem, Spain). The statistical model included lactation stage, period, and lactation stage × period as fixed effects. Significance level was set up at 0.05. Results showed that lactation stage only affected LYS and TAC. In particular, LYS and TAC were higher in milk at short lactation stages and decreased throughout the lactation stage over 6 months from 0.82 to 0.5 g L^{-1} ($p < 0.001$) and from 621.1 to 397.8 e-BQC mL^{-1} ($p < 0.001$), respectively. Moreover, the production period affects all the considered variables, with higher values in the M periods with lower ambient temperatures compared to the H period. Specifically, LYS, LA and TAC were 0.66 vs. 0.50 g L^{-1} ($p < 0.01$) 9460 vs. 7810 U mL^{-1} ($p < 0.01$) and 500.2 vs. 396.5 e-BQC mL^{-1} ($p < 0.05$), respectively. The nutraceutical properties of donkey milk are higher when produced at moderate ambient temperatures compared to summer. However, restricting the production period should only be considered if sustainable and adequate preservation methods

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are available. Additionally, the nutraceutical properties of milk vary throughout lactation. Therefore, to ensure consistent milk quality, foaling should be evenly distributed throughout the year. Research supported by the Rural Development Program 2014-2022, sub-measure 16.1 of the Sicilian Region Government.

P565

Photo-electrocatalytic water remediation for sustainable fish farming: effect on rainbow trout microbial contamination and shelf-life

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Aquaculture requires innovative technologies to improve water quality, fish health, and sustainability. This study addresses these challenges by applying a smart purification system in Rainbow trout (*Oncorhynchus mykiss*) farming using TiO_2-based photo-electrocatalytic treatment (PET) for the remediation of nitrogen compounds in water and control microorganisms. The effectiveness of the PET was assessed through microbiological analysis to ensure the high-quality aquaculture production. Rainbow trout were reared during the winter at the Istituto Spallanzani (Milan, Italy) in six tanks: three equipped with a photo-electrocatalytic system (PET) and three serving as controls (C), with low fish density as the primary rearing condition. The fish after 4 weeks of rearing were euthanised, slaughtered, gutted, and processed into fillets. A total of 12 samples (6 fish per 2 theses) were analyzed fresh to assess initial contamination levels. The shelf-life of 40 fillets (4 fillets per 2 theses were assessed 5 times) was evaluated every 4 days over a 15-day storage period. The fillets were stored in trays covered with commercial polyvinyl chloride film, simulating large-scale distribution under standard atmospheric conditions. The major foodborne pathogens (e.g. *Listeria monocytogenes*, *Salmonella spp.*, *Staphylococcus aureus*, enteropathogenic *Vibrio spp.*) and spoilage bacteria were examined after slaughtering (T0). Specific spoilage indicators (SSI), including total viable count, total psychrotrophic count, *Enterobacteriaceae*, *Pseudomonas spp.*, and H_2S-producing bacteria, were monitored throughout during the shelf-life study. Sensory evaluation of the fillets focused on attributes such as appearance, colour, odour, texture, and drip loss, was based on a 5-point hedonic scale for panel training and overall acceptability. Considering both microbiological and sensory descriptors, no statistically significant differences were observed between PET and C samples. The study of Pseudomonas as SSI determined the shelf-life to be 305.4 (12.7 days) and 306.7 h (12.8 days) for the C and PET groups, respectively. In alignment with microbiological data, sensory rejection occurred after 12 days of storage, with 16% of the fillets scoring below 9 points. The use of PET in trout farming ensured microbiological safety and did not affect the fillets' shelf life. However, its impact on microbial contamination and potential fish pathogens requires further investigation.

P062

High pressure processing and cryogenic treatments to kill Anisakis in fish fillet and near infrared spectroscopy to verify their application

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The ingestion of viable Anisakis spp. larvae, through the consumption of raw infected seafood products, can have serious consequences on consumers' health. Therefore, it is essential to determine the conditions that can kill these parasites to establish effective methods for their inactivation. To date, European legislation (Regulation 853/2004 and 1276/2011) mandates that fish intended for raw consumption must undergo freezing treatment to ensure product safety. Low temperatures have indeed proven effective in controlling this health hazard. Moreover, the high-pressure processing (HPP) has been identified by the European Food Safety Authority (EFSA) as a valid method for inactivating Anisakis spp. larvae. The aim of our research is to study the actual effectiveness of two treatments: cryogenic

freezing (CF), and HPP in killing these parasites. In addiction we explored whether coupled with chemometrics approach can discriminate between fish fillets subjected to the treatments and untreated fillets. The experimental study was carried out on 20 fillets of farmed sea bream (Sparus aurata) contaminated with three larvae each. Ten contaminated samples were subjected to HPP for 290 sec at 5930 bar and ten to cryogenic freezing 30 min at -70 °C. NIR spectra acquisitions were performed with a portable NIR device (VIAVI, 908–1676 nm), PRE and POST treatments. Statistical data elaboration has been performed with Unscrambler X software. All larvae extracted from fish fillets subjected to HPP or CF treatments died, while larvae taken from a sample infested and not subjected to treatments were still alive. As far as concern HPP, good classification between the samples PRE and POST treatments was found with both principal component analysis (PCA) and linear discriminant analysis (LDA). In detail, the PCA score plot showed that, as expected when considering continuous variables in the near infrared range, PC1 and PC2 explained a large percentage of the variance (respectively, 94% and 4%), and it was able to efficiently distinguish PRE and POST samples based on PC1 and PC2. The LDA classification model adopted showed 100% classification accuracy (considering, as variables, the 1300–1440 nm wavelength range). As for the discrimination between cryogenically frozen samples and untreated samples, the analysis is still in progress. Our results indicate that both cryogenic freezing and HPP can ensure product safety, opening new perspectives for their adoption as approved methods to ensure raw fish safety.

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P351

In vitro production of bovine hepatocyte growth factor

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The process of cultivating animal cells in vitro relies on the strategic use of growth factors (GFs) to specifically stimulate cell proliferation and differentiation, which are essential elements for the development of complex tissues. Among these, hepatocyte growth factor (HGF) stands out for its crucial role in muscle tissue formation and regeneration. The main challenge lies in efficiently and cost-effectively producing recombinant HGF, a fundamental step for implementing large-scale bovine cell cultivation processes. To obtain recombinant HGF, mRNA was extracted from MDBK (Madin-Darby Bovine Kidney) cells and placenta. The cDNA synthesised from the mRNA was amplified via PCR (Polymerase Chain Reaction), and cloned into pBKCX. The expression vectors were transfected into CHO (Chinese Hamster Ovary) cells potentially capable of expressing HGF. The expression of HGF mRNA in transfected cells was analyzed using RT-qPCR (Reverse Transcription Quantitative Polymerase Chain Reaction). Chinese hamster ovary clones with the highest expression levels were identified and tested in an MTT assay using untrasfected CHO cells as a control. The recombinant CHO clones HGF2 and HGF7 grew significantly more than the control ($p < 0.01$), demonstrating that the presence of HGF in the culture medium promotes cell proliferation. This in vitro production of bovine-derived growth factors represents a first step toward developing bovine-specific reagents, which are currently lacking on the market.

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P415

Effects of brewer's spent grain in dairy sheep diet on yield, nutritional quality and volatile organic compound profile of cheese

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The use of local agro-industrial by-products represents a promising strategy to enhance the efficiency of livestock farms within a framework of circular economy principles. By integrating these by-products into animal feeding systems, it is possible to reduce environmental impacts, promote the sustainability of rural areas, and support the local economy. Brewer's spent grains (BSG), a by-product of beer production, offer a valuable example of how such materials can be repurposed as a feed ingredient, contributing to resource efficiency and reducing waste. This study evaluated the impact of using local BSG on the quality of ewe cheese. Specifically, the effects of the introduction of BSG in ewe diets on the cheese's fatty acid profile and volatile organic compounds

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(VOCs) were assessed. The experiment involved 24 dairy sheep divided into two groups of twelve animals each: a control group (CT) and a treatment group (TR). Over a 28-day period, the TR group was fed a diet in which commercial concentrate feed was completely replaced with BSG, provided at a rate of 0.460 kg DM per day per head. During the trial, three cheesemaking sessions were conducted on days 14, 21, and 28. From each session, six cheese wheels were produced and analyzed after two ripening periods: 30 and 60 days, respectively. At the end of the experimental period, no statistically significant differences were recorded between the groups in terms of milk yield, fat content, and protein content. Regarding cheese quality, significant differences were observed in saturated fatty acids (SFA), unsaturated fatty acids (UFA), polyunsaturated fatty acids (PUFA n3), and the n6/n3 ratio. The TR group exhibited higher SFA levels (over 16%) and a greater n6/n3 ratio (over 60%) compared to the CT group. Conversely, the CT group showed higher levels of UFA (over 13%) and PUFA n3 (over 61%). Furthermore, a canonical discriminant analysis of VOCs revealed distinct profiles for each treatment and ripening stage, demonstrating that the use of brewer's spent grains in sheep diets significantly altered the aromatic characteristics of ewe cheese.

P435

Influence of pig dietary supplementation with hazelnut skin (HS) or hazelnut skin green extract (HSE) on live performance, carcass characteristics, and meat quality of heavy pigs

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In light of growing concerns about the sustainability of production processes, the environmental impact of intensive farming has been at the center of public debate for several years, highlighting the urgency of making this food supply chain more eco-sustainable. The use of agro-industrial by-products for animal feed not only aids in the ecological transition of livestock production but also offers numerous functions within a feed due to the composition and substances contained in various by-products. One example is the high content of bioactive substances such as phenolic compounds whose metabolites, with strong antioxidant properties, could make meat particularly susceptible to oxidation, such as pork, more stable. The Italian agri-food sector has a wide availability of by-products, such as hazelnut skin (HS) rich in phenolic compounds. This work aimed to evaluate the effects of dietary addiction of HS in two different forms: raw hazelnut skins or their green polyphenolic extract (HSE) on growth performance, carcass traits, and meat quality of heavy pigs. A total of 72 pigs were allotted to 3 dietary treatments (each $n=24$): control group (C) fed a conventional diet and two groups with a similar diet supplemented with 0.6% of HS or 0.1% of HSE, respectively. After the live performance evaluation, 36 subjects, balanced for gender and treatment, were slaughtered for carcass and meat quality evaluation. Dietary treatments did not significantly impact growth performance or carcass yield, demonstrating nutritional adequacy. However, HSE showed an increased thigh yield ($p<0.01$), suggesting a potential beneficial effect on lean cuts yield. Negligible effects on meat quality were observed; oxidative stability of the meat was slightly enhanced in the HS group, after 7 days of storage ($p<0.08$). Moreover, HSE reduced cooking loss, enhancing water retention. HS also slightly improved omega-3 levels and reduced the omega-6/omega-3 ratio ($p<0.05$), showcasing its potential for improving the nutritional value of meat. The subtle improvements observed and the absence of interference with growth performance, carcass characteristics, and final meat quality indicate for HS and HSE the possibility of notable commercial advantages in sustainable livestock systems. Future research should focus on refining supplementation levels to maximise benefits and fully exploit the bioactive properties of hazelnut by-products, paving the way for broader adoption in commercial pig farming.

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P566

Effect of aging facility on chemical-physical and microbiological characterization of Limousine dry aged meat

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Interest in dry aged meat has been steadily increasing, yet there is a notable lack of standardisation in the process parameters

employed for its production. This study aimed to compare the effects of aging time and aging facility, either in a dry aging cabinet or a dry aging room, on beef quality. Twelve loins from six Limousine steers were assigned to two aging facilities: the 6 right loins were aged in a dry aging room (R), while the 6 left loins were aged in a dry-aging cabinet (C). The loins were aged for 38 days, and at each experimental time point (0, 10, 17, 24, 30, and 38 days), a steak approximately 30 mm thick was collected for analysis. The collected samples were analyzed to evaluate their physico-chemical, microbiological, oxidative, colorimetric, and textural profiles. Data were tested for normal distribution using the Shapiro-Wilk test and analyzed using analysis of variance (ANOVA), considering the aging facility and aging time as independent variables. No Listeria spp., Salmonella, or Staphylococcus aureus were detected in the analysed meat samples. Fresh beef showed good microbiological quality in both meat samples aged in C and in R groups, with total mesophilic counts (TMC), lactic acid bacteria (LAB), coagulase-negative staphylococci (CNS), Enterobacteriaceae, and yeast and mould levels recorded as 3.4 ± 0.18, 2.6 ± 0.24, 2.2 ± 0.29, 1.81 ± 0.39, and 2.10 ± 0.22 log10 CFU/g respectively. The numbers of bacteria increased notably during the first 2 weeks of storage; later on the counts did not change greatly. A greater increase in the TMCs were observed during the first 17 days in C compared to R meat samples. The R samples reaches TMC values >7 log10 CFU/g at 24 and 38 days. Whereas the C samples reaches values >7 log10 CFU/g only at 17 days. At the other sampling points, the count remains consistently below 7 log10 CFU/g. According to Regulation No. 2073/2005, meat with these TMC values is not considered satisfactory. On average, the lactic acid bacteria count is higher in R compared to C samples (5.20 ± 1.5 *vs* $4.73 + 1.5$ log10 CFU/g). Oxidation parameters were exclusively affected by aging time, with no impact from the aging facility. TBARS levels increased at 17 days of aging compared to day 0 and further increased at 24 days in both experimental groups ($p < 0.05$). Conversely, protein carbonyl content rose at 30 days in R group ($p < 0.01$) and at 38 days in C group ($p < 0.01$). Lightness did not show differences, while redness tended to increase and yellowness decreased at 17 days of aging compared to previous days ($p < 0.01$). Texture decreased at 17 days ($p < 0.01$) and then remains constant. In conclusion, the results highlight that aging time significantly influences the microbiological, oxidative, and textural characteristics of the meat, while the impact of the aging facility is more evident on microbiological parameters. This underscores the need to standardise protocols to ensure the quality and safety of the final product.

P572

Chemical composition of camel meat: a meta-analysis and meta-regression study

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Compared to ruminants, camels are a promising protein resource in arid and semiarid regions. However, the results published in the literature vary according to several factors. This study aimed to evaluate the physicochemical quality of camel meat using a meta-analysis and meta-regression approach. Four search databases and bibliographies were used from January 1991 to August 2024, and the parameters were analyzed using a random-effects meta-analysis model. The live body weight (LBW) of fattened camels averaged 379.79 kg. After slaughtering, the chemical composition was 5.77 for meat pH, 32.52% for dry matter, 70.06% for moisture, 4.75% for intramuscular fat, 20.30% for protein, and 1.39% for ash. Concerning physical quality, the expressed juice, cooking loss, and shear force averaged 36.09%, 34.50%, and 7.75 kg/cm², respectively. Meta-regression and subgroup analysis showed that the moderators employed (species, breeding system, and age), affected some parameters. Indeed, for crossbreeds, there was a significant decrease in LBW and an increase in protein, ash, fat, and cooking loss. Camels subjected to the extensive system were characterised by higher LBW but lower fat, expressed juice, and lightness (L^*). Concerning camel age, animals aged >6 years were characterised by high FBW, ash, fat, low L^*, and expressed juice content. Future studies should consider these results and continue to evaluate these factors in detail to determine production practices and to improve the quality of camel meat on a global scale.

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GENETICS

P239

BCO2 allele frequencies in many rabbit breeds and populations: insights from the spread of a genetic defect

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Carotenoids are essential compounds crucial for many biological processes, including vision, immune function, and antioxidant activity. Animals are unable to synthetise carotenoids *de novo*, relying entirely on their diet as a source. In animal tissues, β-carotene, a precursor of vitamin A, can accumulate, leading to yellow fat pigmentation. The metabolism of carotenoids is regulated by genes like *SCARB1*, *BCO1* and *BCO2*. Mutations in these genes disrupt carotenoid breakdown, resulting in tissue accumulation and causing a yellow-fat phenotype observed in various species. In rabbit, a deletion of the AAT triplet at codon 248 of the *BCO2* gene causes a recessive yellow-fat phenotype, which is expressed only in homozygous animals. Yellow-fat is considered a defect in meat production. This study aimed, for the first time, to investigate the presence and frequency of the *BCO2* mutation in over 40 rabbit breeds and commercial lines. Genomic DNA was extracted from hair follicles from more than 500 rabbits, amplified by PCR, and Sanger sequenced. Genotyping revealed the mutation in both heterozygous and homozygous forms, with significant variation in allele frequency across breeds. Companion breeds showed a higher frequency of heterozygous rabbits, likely due to relaxed selection pressures and aesthetic preferences, while meat breeds exhibited lower frequencies, reflecting efforts to remove this genetic defect. The Lynx breed had the highest frequency of the mutated allele. This study highlights the widespread distribution of the *BCO2* mutation in rabbits. Further studies should explore additional genetic factors affecting carotenoid metabolism in rabbits.

The research was supported by the PSRN (Programma di Sviluppo Rurale Nazionale) Cun-Fu and Cun-Fu 2 projects (co-funded by the European Agricultural Fund for Rural Development of the European Union and by the Italian Ministry of Agriculture, Food Sovereign and Forestry (MASAF).

P315

BECH.GRIS Project: genetic characterization, conservation and management of the Grigia delle Valli di Lanzo local breed

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The Grigia delle Valli di Lanzo, also known as *Fiurinà*, is an endangered goat breed from Piedmont, with only 446 individuals recorded. Due to its limited population size and the risk of abandonment, there is an urgent need for a project dedicated to conserving this breed to ensure its survival and preserve livestock biodiversity. Therefore, the BECH.GRIS project was established to genetically characterise the breed and set up a breeding center at the Veterinary Special Teaching Structure of the University of Turin. Each year young bucks are gathered from the farms, evaluated for their genetic and morphological traits, and reassigned to suitable farms before the beginning of the breeding season. The project initially involved 13 farms, where a total of 245 individual blood samples collected. For now, 192 animals were genotyped using the GGP Goat 70K chip, and nine young bucks were introduced into the breeding center. To characterise the breed and analyze the differences among farms the following analyses were conducted using the PLINK program: multi-dimensional scaling (MDS), inbreeding coefficient estimation, runs of homozygosity (RoH), identity by descent (IBD), and genomic kinship matrices. Moreover, the admixture software was used to compare *Fiurinà* with five other goat breeds potentially involved in gene flow: Camosciata, Saanen, Roccaverano, Vallesana, Valdostana. Inbreeding and RoH analyses highlighted significant variability across farms, whereas IBD analysis revealed genetic relationships between farms, and the obtained information were used for the strategic distribution of bucks to minimise inbreeding. Admixture results confirmed the *Fiurinà* distinct breed characteristics and showed genetic affinities with the Valdostana breed. The results highlight the need for further genetic monitoring of the breed to optimise mate planning and selection to minimise inbreeding effects and support its conservation. By combining genetic and morphological evaluations, the BECH.GRIS project provides a model for preserving endangered livestock breeds,

supporting biodiversity, sustainability, and the cultural heritage associated with local agriculture, ensuring a viable future for the Grigia delle Valli di Lanzo goat.
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P242

Honey bee genetics from honey samples: monitoring the diffusion of *Apis mellifera* mitochondrial DNA lineages in Emilia Romagna over seven years

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Growing interest has emerged in the need to monitor the genetic integrity of the European *Apis mellifera* subspecies. Honey contains environmental DNA (eDNA) traces from all organisms that directly or indirectly were involved in its production, including the DNA of the honey bees that produced it. Specific mitochondrial DNA (mtDNA) lineages (known as mitotypes) characterise several *A. mellifera* subspecies. Different mitotypes can be detected using honey as a source of honey bee DNA, providing approximate population genetic information useful for estimating the diffusion and frequency of honey bee mitotypes. In 2019, the Emilia-Romagna region became the first Italian regional authority to issue a law specifically addressing the protection of the native *A. m. ligustica* subspecies. In this study we present an overview of the diffusion of the main *A. mellifera* mtDNA lineages in the Emilia-Romagna region over a seven-year period (2018–2024). DNA was extracted from more than 1000 honey samples produced by many beekeepers across the region. PCR products were analysed using a fragment size-based assay. Results confirmed that the C mtDNA lineage, which characterises *A. m. ligustica*, was the most prevalent mitotype: its frequency increased over the years, from 82% in 2018 to 94% in 2024. The presence of the A and M mtDNA haplotypes was always in combination with the C lineage in the honey samples and their frequencies decreased over the seven years. Metadata about the geographical origin, the altitude of the production site and beekeeper information were collected and used to produce a distribution map of the main honey bee mitotypes. The results obtained in this study can be useful for designing and evaluating the potential effectiveness of conservation policies aimed at maintaining the integrity of honey bee genetic resources in this region. We further demonstrated that eDNA from honey can be exploited to design cost-effective non-invasive and simple methods to obtain information on the genetic distribution of honey bee genetic information.
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P260

Meta-analysis on early traits genetically correlated with later performance in life in horses

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Compared to other animal industries, horse sector lags in genetic selection due to challenges in describing phenotypes, understanding the environmental factors influencing them, and identifying early traits genetically correlated with later performances. Horses are late-maturing animals, with initial performance evaluations occurring at 5–6 years. Identifying early measurable phenotypes correlating with performance traits could accelerate selection and reduce the generation interval. This meta-analysis aims to identify what has been known in the literature on early traits in horses genetically correlated with later performance. A list of 130 keywords was developed, divided into the following categories: 38 related to phenotypes, 10 to early development, 27 to horses, 39 to performance, 16 to genetics, and 9 exclusion terms. The search has been performed in Web of Science, resulting in 941 papers published between 1985 and 2024; of these, 430 were relevant. A systematic review and abstract screening were conducted on the first 150 selected papers. Data on analyzed phenotype, breed, number of horses/records, and presence of genetic parameter estimations have been extracted. Phenotypes were categorised as conformation, movement, jumping ability, dressage, race performance, disease, or others. Breeds were classified as coldblood, warmblood, or hotblood. Most papers focused on conformation and movement traits, followed by performance traits like jumping and racing. Only 20 papers discussed disease and 7 other traits. A median of 2863 horses were studied per article, ranging from 5 to 475077. Breed-wise, 42% of the studies focused on warmblood horses, where research was equally distributed across conformation, movement, and jumping traits, followed by dressage. The 16% of studies involved hotblood horses, with 62% focusing on racing ability. Finally, 23% of the studies involved coldblood horses, primarily exploring

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conformation traits. The systematic literature search will be extended to Scopus using the same keywords. Preliminary results show that research focuses on conformation traits in coldblood horses, while mainly performance traits are studied in warmblood and hotblood breeds. A full-text screening will be conducted and the analyses will be performed in R. The final expected outcome is to identify which traits can be measured early in life and the most heritable ones, enabling the identification of traits most suitable for predicting horse performance.

P020

Veterinary treatment data from the electronic recording system for genetic selection in the alpine grey cattle breed

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In cattle breeding, emphasis has traditionally focused on productive traits, while health and fitness traits were often overlooked due to their low heritability and negative genetic correlations with productivity. Challenges in recording phenotypes, stemming from high costs or lack of quality data, further exacerbated this issue, leading to increased fertility and health problems, economic losses, and consumer concerns about animal welfare and food safety. This study investigates the potential use of veterinary diagnoses, collected through Italy's electronic veterinary treatment recording system, for breeding decisions in the Alpine Grey cattle breed. The dataset included 97,821 records from 8,273 individuals and 18,110 lactations (2021–2023), documenting treatments for mammary, respiratory, and urogenital pathologies, after data editing unique datasets were then generated for each pathology with a final dataset of 5 233 cows. Heritability estimates for these traits were calculated using univariate linear animal models and Gibbs sampling algorithms after data editing. Results showed that mammary pathologies affected most cows (11%), followed by urogenital (5%) and respiratory (4%) issues. Heritability estimates were low across all traits, ranging from 0.01 to 0.04. Respiratory pathologies had the highest heritability (0.04 ± 0.04), followed by mammary (0.03 ± 0.01) and urogenital (0.01 ± 0.01) pathologies. These findings align with literature reports, highlighting the limitations of using health traits for genetic selection. Despite these constraints, veterinary diagnoses hold potential for improving health and welfare in Alpine Grey cattle breeding. Refining the diagnostic criteria in the Italian electronic system could improve the utility of health data in genetic evaluations. To enhance breeding strategies, future research should include larger datasets and additional indicators, such as somatic cell counts, to increase the precision of genetic evaluations and promote sustainable cattle production.

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P035

Investigation of genetic polymorphisms in Estrogen and Prolactin gene receptors in the autochthonous Greek black pig breed

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One of the major goals in the pig breeding industry is the improvement of the most important economic traits, including the reproductive rate and especially litter size. Furthermore, this is also important for the improvement of autochthonous local pig breeds, which, although very important for the maintenance of genetic diversity, are now in danger of extinction. Many studies have underlined the importance of the estrogen receptor gene (*ESR*) as a candidate gene in studying its relationship with the litter size of pigs because steroid hormones and their receptors are essential in the process of reproduction. Furthermore, the prolactin hormone is involved in several endocrine functions, especially in the reproductive processes, and the action of this gene is mediated by its receptor (*PRLR*). However, although genetic studies regarding these two genes have been performed in many pig breeds, little is known about the effects of these genes in local breeds, and more specifically in the autochthonous Greek black pig breed. This breed, which was raised locally and is well known for the high quality of its meat, is the only traditional indigenous pig breed reared in Greece and is able to adapt to different and harsh environmental conditions. Therefore, the objective of this study was to study the potential use of estrogen and prolactin gene receptors as a genetic marker to improve the reproductive traits of this breed and to investigate the existence of polymorphisms in the ESR and PRL gene receptors within autochthonous Greek black pig breed.

One hundred eighty pigs raised in Greece were included in the study. DNA was extracted and genotyping was performed using RFLP – PCR. The molecular results showed that for ESR, the genotype GG had a frequency of 0.54, GA 0.35 and AA 0.11, while the frequency of allele G was 0.72 and of A 0.28. For PRLR, the genotype AA had a frequency of 0.46, AB 0.31 and BB 0.23, with frequencies of alleles A and B being 0.61 and 0.39, respectively. These data revealed that all genotypes of the two genes were present in the investigated population, indicating that these genes could be used for Marker-Assisted Selection programmes for the genetic improvement of reproductive characteristics of this breed.
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P063

Genetics of temperament in five Italian beef cattle breeds

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Cattle temperament is often defined as the behavioral expression of animals, or fear response, to humans' interaction or novel environments; also, it is usually an indicator to evaluate cattle welfare. However, animals' social behaviors are also expressions of temperament, e.g. attitudes of dominance, or response to predator's presence in an open pasture system. This study aimed to estimate genetic parameters for temperament trait in Marchigiana (M), Chianina (C), Romagnola (R), Maremmana (M) and Podolica (P) beef cows and heifers. Traits were evaluated on heifers and cows in 7686 herds (3316 for M, 2074 for C, 733 for R, 309 for MM, and 1254 for P), from 1994 to 2022 using a linear scoring including a 1–5 point scale: 1 – Aggressive, 2 – Less docile than average, 3 – Average disposition, 4 – More quiet than average and 5 – Very quiet & gentle. This trait is influenced by several environmental factors (mostly farming system in case of heifers), age, parity and reproductive phase for cows. Because of possible culling of aggressive heifers, two separated analyses were carried out for heifers (48,346 M, 47,524 C, 15,078 R, 8,243 MM, and 24,247 for P, total heifers) and for cows (30,514 M, 24,490 C, 9,111 R, 6,401 MM, and 26,922 for P, total cows). A preliminary GLM allowed the identification of 2 main non-genetic factors affecting the scores in heifers, i.e. herd-year-classifier and the age; otherwise, for cows, herd-year-classifier and parity resulted significant factors affecting temperament scores. These factors were all accounted in genetic analysis carried out through single trait animal model-REML. Heritability (h^2) estimates ranged from very low (0.02 in M) to low values (0.09 in P) in heifers, and from 0.01 in MM to 0.11 in P cows. Despite the low h^2 values, temperament trait, especially in beef cattle reared in loose housing system or at pasture, is interesting to be used in selection, also because it can be related to other important traits, such as fertility, longevity, meat quality, etc.

P075

Environmental factors affecting the quality of boar semen for AI

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Aim of the research was to identify some environmental factors that can influence the quality of boar semen to be used for AI (motile, morphologically normal, motile and morphologically normal, useful spermatozoa). The data relating to the analyses carried out with ISASp SUS PROiSER software (https://proiser.com/) on 8087 semen samples collected over two years from 205 boars (number of samples from 1 to 137, mean 38.2 ± 34.7) were used. Data were analyzed with SPSS (ver. 29.0.1.0, 2023) with ANOVA according to a model that included the fixed factors of year (2 levels), boar breed (3 levels: Duroc, Large White, commercial hybrid), month of collection (12 levels), time of collection (7 levels: <7.00, 7.00–8.00, 8.00–9.00, 9.00–10.00, 10.00–11.00, 11.00–12.00, >12.00), the covariates age at collection (d) and distance from the previous collection (d), both in linear and quadratic form, and the random effect of the boar within breed. The model explained very low variability rates for the values expressed as a percentage of total spermatozoa (from 0.3% to 1.0%), while for those expressed in absolute value (M/ml) they reached the maximum value of 17.5% (for motile and useful spermatozoa). Large White subjects showed significantly lower values ($p < 0.05$) for all parameters compared to other breeds. Furthermore, commercial hybrids were better than Durocs for % and number of morphologically normal spermatozoa (resp. 86.75% vs 85.15% and 172 M/ml vs 138 M/ml; $p < 0.05$). The effect of the high temperature of the central summer months (July and August) manifested itself with a delay of about one month (August and September: $p < 0.05$ compared to the other months). Samplings taken before 7.00 and after 10.00 showed lower values for all parameters, compared to samplings taken between 7.00 and 10.00 ($p < 0.05$). Overall, the significantly lowest values were those of the afternoon samples. Semen quality deteriorated linearly in relation to age at sampling, both in terms of percentage

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and absolute values. Instead, the quadratic component was always positive. The increase in distance from the previous sampling had a negative linear impact on percentage values and a positive impact on absolute values. In this case, the quadratic component had an opposite effect, improving percentage values and worsening absolute values. The results confirm the need to monitor environmental aspects related to boar semen collection, to avoid situations that could result in a reduction in farm fertility.

P113

Local pig and chicken breeds: weaknesses, strengths and challenges by Italian stakeholder concept

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Two broad surveys were conducted addressing actors and stakeholders (breeders, advisers, veterinarians, technicians) involved in the conservation of pig and chicken locally as part of the European multi-actor project GEroNIMO (Genome and Epigenome eNabled breeding in MOnogastrics). The objective was to identify stakeholder perceptions about the future of local breeds, recording information on productivity, economic viability, sanitary situation and breeding programs for pigs and chicken sectors, focusing here on Italian participants. In Italy, the principal difference concerning the cosmopolitan breeds was that the local breeds were almost all reared in a closed-cycle farming system (94%). Results showed that the local population were mainly raised in small farms by a free-range system, which for pigs lasted from weaning to the fattening phase for ≥70%, while for poultry was partly (48% for chicken and 42% for hens) or fully outdoor (44 % for chicken and 50% for hens). Locally available food resources were used and integrated with co-product feed and raw feed ingredients. Natural mating was the sole reproduction system used; however, preserving standard characteristics and genetic diversity emerged as the primary objective pursued by the surveyed stakeholders. As regards economic activities, breeders identified feed as the highest cost (mentioned by 88% and 93% for pig and poultry farmers, respectively), followed by installations for the sanitary protection of the herd, such as fences or locks (67% and 45%, for pig and poultry responses). Sanitary costs were cited by 43% and 38% of the pig and poultry farmers, with a newly identified expense for welfare. Nevertheless, increasing concerns emerged among pig farmers for the possible costs needed to contrast health crises (i.e. ASF). Products from local pig breeds were often marketed under a quality label (85%), which is considered a strength in adding value to these products. In contrast, a quality label did not appear necessary for Italian chicken farmers. Considering the practical differences in perspectives and management between local and cosmopolitan breeds, new policies should provide specific support to ensure these farms are up to the challenges.

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P130

Mapping the biodiversity in small ruminants. The LOCAL project in Apulia Region

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The biodiversity protection represents a challenge included in the Agenda ONU 2030 for Sustainable Development Goals. It is considered of great importance, apart from as genetic reservoir of native breed, strictly connected to cultural land heritage, for future breeding options, but especially for preserving the environment, the landscape, the human presence in marginal areas. Apulia region, its geographic position and topography, from coastal plains to mountainous areas, provide distinct ecological niches where sheep and goats contributed significantly to the genetic richness of the Mediterranean livestock pool. Over time, this selective breeding, combined with the influence of natural selection, led to the emergence of local breeds adapted to specific agro-climatic conditions and capable of utilising marginal lands. Small ruminant farms are particularly widespread and very

diverse (sheep or goat, local breeds, different production purposes and degrees of intensification) reflecting the adaptability of sheep and goats to different geographic and socioeconomic conditions. The LOCAL project, which intends to promote, characterise and valorise the goat and sheep genetic resources of Apulia region through the study of genomic and reproductive features, milk production and dairy products. The project has implemented historical data collection, identification, mapping and characterisation of the genetic heritage of local sheep (Gentile Moretta) and goat (Capra Capestrina, Capra Antica della Murgia, Capra Grigia del Sub-Appennino) populations of Apulia region. Integration and management of data in Apulian and national databases, creation of maps by using a Geographical Information System (GIS) has been performed. Furthermore, the characterisation of genetic heritage lead to *ex situ* and *in situ* conservation of the genetic material with the creation of Animal Germplasm Cryobank for the storage of embryos and other genetic material. The LOCAL project aims to valorise sheep and goat populations as bioconverter of the food resources of grazing areas into high quality dairy products and for their cultural, anthropological and socio-economic value in rural communities. Enhancing the knowledge of small ruminant local breeds is crucial for developing effective strategies for their conservation and genetic improvement.

Research supported by LOCAL grant (Regione Puglia, Misura 10; Sottomisura 10.2 – 'Sostegno per la conservazione, l'uso e lo sviluppo sostenibili delle risorse genetiche in agricoltura').

P143

Exploring genetic variability at goat *CSN2 locus* using novels PCR based methods

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The calcium-sensitive beta-casein (β-Cn), encoded by *CSN2* gene, is the major protein in goat milk comprising up to 50% of the total casein content. At least ten alleles have been identified at this *locus*: the strong alleles A, A1, B, C, C1, D, E, and F, associated with a normal amount of casein in goat milk (about 5–6 g/L per allele), and the 0 and 01 alleles, associated with a non-detectable amount of this protein in milk. Recently, two less expressed β-Cn variants, C2 and F1, were found. In this study, we report the characterisation of an unclassified allele at the goat *CSN2 locus*, that we name A2, in Cilentana breed reared in Campania region (Italy). The already known mutational event responsible for its formation is a transversion AJ011019:g.3794A > C at 52th nucleotide of exon 2 responsible for the Ile > Leu substitution at position 14 of leader peptide. The presence of Leu14 represents the ancestral condition of β-Cn because it has been found in all mammalian species. However, from the comparison of the sequences available in GeneBank, it is interesting to note that this polymorphism also characterises the ovine species, which could indicate the identification for the first time of a Trans-Specific Polymorphism at this *locus*. To evaluate the genotype distribution and allelic frequencies of this polymorphism, a genotyping method based on restriction fragment length polymorphism (*Eae*I PCR-RFLP) was set up. The survey, conducted on 98 Cilentana goats allowed the identification of all three genotypes at the *CSN2 locus* with a higher frequency (0.6) of the A2 allele. Identifying new alleles and mutations requires continuous updating of genotyping protocols useful for association study. Therefore, in addition, new efficient and specific PCR-based genotyping protocols have been developed to detect the remaining alleles with known mutations at this *locus*. Consequently, for the first time, it was possible to propose an evolutionary pathway of the goat *CSN2* gene, as it was already published for other caseins encoding genes, with the A2 allele the original one from which all known alleles originate. Thanks to the application of these protocols, a preliminary association study between the different *CSN2* genotypes and some milk traits, without an effect on the milk yield, was carried out. The results of this research add new knowledge about the genetic variability of goat *CSN2* and may contribute to the genetic improvement of milk productions for this species.

P147

Genetic variability characterization of the 'Leprino di Viterbo' rabbit breed

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Analysis of genetic variability is a useful investigative tool for finding strategies for proper management of the genetic heritage of populations. Especially in livestock breeding, the regional and

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local dimensions have the greatest importance in biodiversity issues. Investigating the biodiversity of these species allows us to have a better understanding of them, to know if and how endangered they are, and to implement the necessary tools to preserve them. The aim of this research was the characterisation for conservation purposes of the 'Leprino di Viterbo' rabbit breed reared on the 'Nello Lupori' University of Tuscia experimental educational farm. The Leprino di Viterbo is a synthetic breed, developed from a genetic base comprising 70% New Zealand White, 10% Belgian Hare, 5% English Lop, 5% Dutch, and 10% local rural grey rabbits. Through subsequent selection and crossbreeding, the desired morphological and productive traits were stabilised. DNA extraction was performed from blood of 12 specimens, 4 males and 8 females. Their yield was evaluated with DTX880 Multimode Detector (Beckman Coulter) and quality and integrity with Bioanalyzer 2100 (Agilent). One sample was discarded due to low DNA yield. Genomic libraries were prepared with 'Nextera XT DNA Library Preparation Kit' (Illumina). Both quantification and quality control were performed and 10 out of 11 libraries (one failed due to low concentration) were shipped to Novogene Co. for ~20X NGS sequencing analysis (shotgun method) with the aim of reconstructing the whole genome of the individuals analyzed and assessing their variability. The raw data were processed by bioinformatics analysis in a Linux environment. Assessment of read sequencing quality and accuracy was performed before the quality control where adaptors and low-quality reads or a portion of them were removed. Reads were aligned on OryCun2.0 reference sequence, and the variants were called and annotated. Variants with an effect on the protein coding were identified on *CAPN13*, *CAPN5*, *CAPN8* and *CAST* genes, related with growth and meat quality, and *GDF7* gene, responsible for the follicular development of oocytes. The inbreeding analysis identifies a very low value due to the recent history of the breed (i.e. crossing with parental populations); at least in the short term, there is no risk of inbreeding depression.

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P204

Phenotypic characterization of ram's reproductive system: preliminary investigation for the development of a fertility index

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The use of artificial insemination in sheep farming is still not widely used, due mainly to economic and management reasons. Regular health checks of the animals are essential in order to ensure adequate reproductive efficiency, as infertility can result in significant costs for the breeders. Breeding Soundness Evaluation (BSE) of males must include biometric measurements as head width (HW), chest circumference (CC), and particularly those of the testicles scrotal circumference (SC), right testicle length (TL), and right testicle diameter (TD). These features provide important information about sexual maturity and fertility, as they are directly related to sperm production and to the reproductive capacity of the breeder. Biometric and testicular measurements were carried out once on a total of 309 rams (with an age ranged from 6 to 54 months) of several breeds as Comisana, Massese, Merinizzata Italiana, Gentile di Puglia, and Appenninica. The results show that the correlations among scrotal traits are all positive (0.78 SC with TL; 0.89 SC with TD), while correlations between biometric and testicular measurements are lower and sometimes negative (–0.37 HW with TL; 0.55 CC with SC). The results showed that, among rams older than 12 months (the ideal age for mating), only 31% of dairy breeds and 14% of meat breeds met the classification standards defined by the Breeding Soundness Examinations of Rams and Bucks, for instance, the achievement of a minimum of 30 cm of scrotal circumference at the age of 12 months. This suggests that nonconforming rams should be excluded from reproduction, in order to optimise genetic selection, highlighting the need to establish specific biometric standards for each breed. The potential of these data as a criterion to improve male fertility, already applied in cattle, should also be implemented in sheep genetic centers. It will be crucial to establish a targeted protocol based on the collection of morphological data, mainly testicular biometrics, combined to clinical examinations and to semen collection and analysis.
Based only on this clinical approach, it will be possible to effectively select rams intended for reproduction purposes.

P227

Phenotypic characterization of two native Italian turkey breeds: a comparative study

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Romagnolo (RO) and Ermellinato di Rovigo (ER) are native Italian turkey breeds. RO is a small-sized breed from Emilia-Romagna region and is well known for its hardiness, cold resistance, and disease resilience. ER is a medium-sized breed from Veneto's Rovigo province appreciated for early maturity and rapid feathering. Since the 1970s, intensive production systems favoring commercial hybrids have led to a decline in native poultry breeds, risking extinction and reduced genetic diversity. In response, conservation projects, like TuBAvI, aim to safeguard Italy's poultry heritage and provide new knowledge and tools for the implementation of effective conservation activities. The phenotypic characterisation of autochthonous breeds aims to expand and consolidate knowledge about Italy's poultry heritage. In this context, the aim of this study was to evaluate the phenotypic traits of RO and ER turkey breeds, focusing on laying rate, growth performance, egg quality, morphological characteristics, and the assessment of innate immunity markers. The study involved 20 RO turkeys and 15 ER turkeys raised in outdoor pens. Males and females of both breeds were regularly weighed from day one until they reached 180 days of age. Growth rate was significantly slower in ER compared to RO turkeys after the third month onwards, resulting in lower final growth performance in ER compared to RO. Egg laying in both breeds began in January, with the peak of production occurring in the second half of March. The average number of eggs produced per female was 65 and 70 in ER and RO respectively. Results on egg characterisation showed that a significantly higher total egg and yolk weight (80.6 ± 5.3 g; 27.2 ± 2.5 g) was found in RO compared to ER (72.6 ± 8.8 g; 18.9 ± 3.6 g). Regarding morphometric parameters, no significant differences were observed between the two breeds for either sex. However, RO males and females exhibited a higher average live weight and greater body length compared to ER turkeys. Innate immunity was assessed by measuring lysozyme (LYZ), complement C3, and IgY levels. The results showed that ER males had higher LYZ concentrations (694.4 ± 82.1 ng/mL) compared to other groups ($p > 0.05$). However, no significant differences were found in complement C3 and IgY levels between the breeds. These findings contribute valuable insights to the conservation efforts aimed at preserving Italy's native poultry breeds and enhancing their role in sustainable agricultural systems.

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P233

Constitution of a semen cryobank for the conservation of the Italian small ruminant local breeds

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In Italy a national gene bank for animal genetic resources has not yet been established, and efforts to develop such initiatives are still in their early stages. Recently, through various PSRN and PSR Project (SHEEP&GOAT and CHEER coordinated by ASSONAPA, and BIODIVAL and BIO4VERBA coordinated by IBBA-CNR), specific actions have been dedicated to the cryopreservation of small ruminant germplasm. In this framework, the Genetic Reserve of Italian Sheep and Goat Breeds (GRISGB) was developed over the years, becoming the most important section of the IBBA-CNR Farm Animal Cryobank, officially recognised in 2023, by the National Network of Biodiversity of Agricultural and Food Interest. To identify donors and maximise genetic variation, pedigree and historical information about animal flows across herds were used. Semen collection was performed on farm following health status verification. The collected semen was diluted with a commercial extender, cooled to 5 °C, and transported to the laboratory for semen analysis (volume, sperm concentration/ml, and total motility) and cryopreservation in nitrogen vapour. GRISGB currently includes 4017 cryopreserved semen doses collected from 190 donors across 17 italian local breeds, including: GOAT – Bionda dell'Adamello (2 donors, 70 doses), Cilentana (4 donors, 92 doses), Frisa Valtellinese (32 donors, 601 doses), Garganica (6 donors, 84 doses), Jonica (1 donor, 47 doses), Orobica (32 donors, 391 doses), Rossa Mediterranea (2 donors, 34 doses), Nicastrese (18 donors, 294 doses) and Verzaschese (26 donors, 933 doses); SHEEP – Brianzola (17 donors, 437 doses), Ciuta (12 donors, 207 doses), Comisana (4 donors, 179 doses), Delle Langhe (4 donors, 92 doses), Gentile di Puglia (16 donors, 171 doses), Leccese (1 donor, 54 doses), Massese (3 donors, 126 doses). Semen volumes of

samples collected ranged from 0.19 to 4.70 ml (goats) and 0.8 to 4.90 ml (sheep). Sperm concentrations varied from $0.32x10^9$ to $4.5x10^9$/mL (goats) and $0.21x10^9$ to 2.5×10^9/mL (sheep), with fresh semen motility ranging between 60% and 90%. In the near future semen quality of the cryopreserved samples will be assessed using computer-assisted sperm analysis and flow cytometry to identify potential breed-specific differences. GRISGB represents a cornerstone in safeguarding Italy's rich livestock biodiversity.
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P265

Implementation of sheep production system through genomics and phenomics: preliminary results

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Small ruminant breeding supports rural development, cultural traditions, and environmental sustainability. However, ovine milk production in Europe has significantly declined over the past 20 years. Italy, where dairy sheep represent 75% of the national sheep population, is the major European sheep-milk cheese exporter despite the low profitability of the sector. Increased milk production and quality is needed to meet the rising demand for high-quality animal products. Breeders aim to increase milk yield and quality but face challenges such as inbreeding and limited resources for evaluating milk characteristics. Recently some projects were funded for the characterisation of milk quality through the use of easy to use and cost-effective analysis, and genomic information for the verification of pedigrees, inbreeding levels, and availability of genetic markers for favourable traits. The separation and quantification of major protein fractions in milk are crucial in dairy sheep research. Therefore, accurate, high-throughput and fast techniques are essential. The Agilent Protein 80 kit with the 2100 Bioanalyzer system is faster, easier to use and consumes substantially fewer chemicals and materials than traditional methods. Therefore, this study aimed to analyse sheep milk protein fractions using the Agilent Protein 80 kits on the 2100 Bioanalyzer. A total of 569 milk samples collected from Comisana and Massese breeds were evaluated for major milk proteins content. Data analysis was performed using Agilent 2100 Expert software, which determines the molecular weight, concentration and percentage of total individual proteins in the sample. In our study we succeeded in identify α-lactalbumin, β-lactoglobulin, β-casein, and κ-casein, whereas α_{S1}- and α_{S2}-casein co-migrates and had to be considered together as α-casein. Other minor protein fractions were not included in the analysis. Results showed that the sheep milk contains the overall mean values of 6.46% α-lactalbumin, 10.87% β-lactoglobulin, 42.03% β-casein, 34.25% α-casein, and 6.34% κ-casein. No significant variation was observed in the protein composition between the two sheep breeds. The findings obtained in this study align with the data reported in the existing literature.

P300

European turtle dove (*Streptopelia turtur*) in Apulia: preliminary estimate of the breeding population abundance

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The European Turtle Dove (TD, *Streptopelia turtur*) is a bird with Euro-Central Asian and Mediterranean corology, characterised by four subspecies distributed in an area of about 10 million km^2 across Eurasia and North Africa. In Italy, the TD is a regular migratory species widely distributed, except for the Alps and the highest peaks of the Apennines; its presence is lower in the Eastern part of the Po plain, in the Lower Tyrrhenian coast and in the central-southern areas of Apulia, probably due to the reduced presence and extension of woods and hedges. TD arrives in Apulia in Spring to nest. According to BirdLife International (2017), TD is classified as SPEC 1 being in an unfavourable state of conservation. Recently, action plans have been implemented to improve its conservation, in balance with sustainable hunting, allowed in September. So far, limited information is available on the TD's abundance in each Italian region; therefore, this study aimed at providing preliminary information on the distribution and abundance of the TD in Apulia. The methodology adopted for the Farmland Bird Index (FBI) project was further intensified to obtain a more homogeneous coverage of the sampling points; for this purpose, in addition to the 34 UTM squares monitored within the FBI project, other 17 grid squares of 10 km of length were analysed. The count technique used for the FBI project is based

on listening points without limits of distance lasting 10 minutes. The counts were carried out during May 15th-June 15th, starting shortly after dawn until 12:00, visiting each station only once. During 2023, 59 specimens of TD were recorded in 39 listening points. Only in one cell a maximum of 6 TDs were observed; followed by 4 birds in another point of survey, 3 specimens observed in 2 cells and 2 observed in 8 cells. When a single bird was observed, it was considered as part of a pair, while a pair number of birds was divided by two; in case of sightings of 3 individuals, they were considered as 2 pairs. The total estimate of the registered pairs resulted between 41 and 59. The estimated density for TD in Apulia was 0.64/km^2, while that of pairs is 0.44–0.64/km^2. When the estimated census area was compared to the total area of the region, without islands, an abundance of TD was estimated at about 12,333, with a minimum number of pairs ranging from 8,570 to 12,333. These results are similar to those found in Tuscany, unique Italian region in which TD abundance was detected.

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P307

Heterozygosity-rich regions survey in Sicilian and worldwide horse breeds using genome-wide imputed data

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Heterozygosity-rich regions (HRR) are sections of the genome often associated with important traits such as immune response, adaptation, and fertility. Despite their biological significance, studies characterising HRR in livestock species remain scarce. SNP arrays are a common tool for assessing genomic diversity, but whole-genome sequence data and imputation techniques offer an improved resolution. This study aimed at extending the use of imputation to HRR detection, comparing pre- and post-imputation results and evaluating two different detection methods: consecutive runs (CR) and sliding windows (SW). We analyzed SNP array data (~40K markers) from 281 horses representing twelve breeds. These data were imputed to sequence level using a reference panel of 327 sequenced individuals, yielding ~7M markers after quality control. HRR were investigated using CR and SW methods in both the original (SNP) and the imputed (IMP) datasets. The results demonstrated high consistency between CR and SW methods, with strong correlation coefficients for descriptive parameters such as HRR number, length, and diversity rate ($r > 0.968$ for SNP and >0.964 for IMP datasets). However, comparisons between SNP and IMP datasets within each method revealed lower correlations for HRR length (0.191 for CR and 0.134 for SW), indicating significant variation introduced by imputation. A total of 6218, 6126, 11369, and 8832 HRR were detected using SNP_CR, SNP_SW, IMP_CR, and IMP_SW, respectively. While breed contributions to HRR counts were consistent across datasets, filtering for the top 0.1% of markers revealed substantial differences in HRR islands: 135, 142, 2,060, and 1,996 for SNP_CR, SNP_SW, IMP_CR, and IMP_SW, respectively. Notably, three HRR islands were shared across all datasets: ECA1 (118.6–118.9 Mb) and ECA7 (50.4–50.5 Mb, 52.9–53.3 Mb). the island on ECA1 comprised the candidate genes *PSTPIP1*, *TSPAN3*, and *PEAK1* which have been linked to growth rate in chickens and adaptation and resilience in cattle. These results demonstrate the effectiveness of integrating the imputation approach and the diverse detection methods to refine HRR analysis. Identification of HRR islands and candidate genes highlights their useful role in exploring genetic diversity and functional traits, providing a basis for future research on adaptation and resilience in horse species.

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P318

Phenotypic and genetic characterization of the Spanish *Gallina Murciana* chicken breed

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The *Gallina Murciana* (GM) is an indigenous poultry breed from the Region of Murcia (southeastern Spain), classified as

endangered and included in the protected species section of the Official Catalogue of Livestock Breeds of Spain (Royal Decree 1682/1997). Indigenous livestock breeds are granted special protection by Spanish administrations to preserve biodiversity and support rural sustainability. At present, approximately 650 animals are registered in the breed's Genealogical Book. The GM is a Mediterranean-type, dual-purpose slow-growing breed, with two recognised color varieties: salmon and silver. Conservation efforts are centralised at the Universidad Politécnica de Cartagena (UPCT) in Spain. The objective of this study was to phenotypically and genotypically characterise adult birds (over 10 months of age) housed at the UPCT conservation center, following the FAO protocol. To achieve this, 13 males and 45 females selected for reproduction were evaluated. Phenotypic measurements included live weight, body length (from the tip of the beak to the base of the tail), wingspan, tarsus length, tarsus diameter, and thoracic circumference. The comparison between males and females yielded the following results: live weight: 3166 ± 288 g vs. 2446 ± 297 g; body length: 46.0 ± 1.8 cm vs. 41.7 ± 1.5 cm; thoracic circumference: 40.1 ± 2.7 cm vs. 35.2 ± 1.9 cm; tarsus length: 10.8 ± 0.5 cm vs. 8.9 ± 0.4 cm; tarsus diameter: 5.4 ± 0.4 cm vs. 4.1 ± 0.2 cm; wingspan: 58.5 ± 2.4 cm vs. 51.2 ± 2.6 cm. For genetic characterisation of GM, DNA extracted from feathers was genotyped using 26 microsatellite markers. For each individual, heterozygosity index (H), total number (Na), and effective number (Ne) of alleles, observed (Ho) and expected (He) heterozygosity, and F (Wright's inbreeding coefficient) indexes were calculated. The individual heterozygosity across loci ranged between 0.15 and 0.77, with an average of 0.48. A total of 85 alleles were identified with only one locus not polymorphic. The average Na was 3.27, and Ne was 2.09. The Ne resulted lower due to the presence of low-frequency alleles that can be easily lost by genetic drift, thus reducing the genetic variability of the breeds, and increasing their risk of extinction. Observed and expected heterozygosity were both 0.48, with F = 0.003. The phenotypic measurements confirmed GM as a medium-sized chicken with clear sexual dimorphism. Meanwhile, the genetic characterisation emphasised the breed's value as a valuable genetic resource.

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P328

A study on diversity and pathway signals in Ragusano donkey microbiome

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In Italy, the Ragusano donkey is one of the most productive breeds originated from the Mediterranean island of Sicily. This animal is employed in specialised farms for milk and meat production as well as for recreational activities, trekking and onotherapy. Currently, this breed is included among the native Sicilian breeds at risk of extinction. The comprehension of the complex interactions of microbial communities correlated with states of good health or disease represents an expanding research field both in human and veterinary medicine. The objective of the study was to construct the functional map of the bacterial community by calculating the different gene families and the different metabolic and functional 'pathways' found within the gut microbiota of the Ragusano donkey. 18 female Ragusano donkeys officially registered in the Registry of Equine and Donkey Breeds were considered. For a study on the functional profiles of microbial communities, we extended our sampling to a cohort of adult and clinically healthy donkeys with a live weight between 300 and 350 kg. All donkeys came from two farms, reared under similar management conditions. Genomic DNA was extracted from each faecal sample taken directly from the rectal ampoule. The V3-V4 region of the bacterial 16S rDNA gene was sequenced using a paired-end strategy on an Illumina Miseq platform. Sequences obtained were processed using QIIME2 software. In addition, metabolic pathways were predicted by using the PICRUSt2 bioinformatic tool. In this metagenomic study, a total of 23 phyla, 190 families and 350 bacterial genera were identified using an identity threshold of 74%, 85% and 95% respectively; of these, only 11 phyla, 69 families and 125 genera showed a relative abundance greater than 0.1%. The most abundant phylum was *Bacteroidetes* (~44%) followed by *Firmicutes* (~40.8%), *Spirochaetes* (~8.9%), *Fibrobacteres* (~3.2%) and *Proteobacteria* (~2%). The complex function of Ragusano donkey microbiota is further supported by prediction of thousands of enzymatic classes involved in several biochemical and molecular pathways. In fact, in this study over 2000 enzymatic classes and 404 metabolic pathways were identified. Pentose phosphate, gondoate and cis-vaccenate biosynthesis were the most enriched pathways in our metagenomes, that promote the health and general well-being of the host. The results are encouraging and may serve as a starting point for future microbiome investigations in Ragusano breed.

P331

EpiC Fun: A project investigating the epigenetic diversity and functional adaptation in local and cosmopolitan Italian cattle breeds

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Our research group has recently characterised breed-specific epigenetic diversity in cattle blood, comparing Angus and Nellore breeds, likely driven by long-term selection for morphological, adaptive, and quantitative traits. Building on this foundation, we extended our analysis to the male germline using publicly available data from the NCBI database, focusing on Holstein and Montbéliarde breeds. Our findings reveal that epigenetic diversity exhibits partial consistency between somatic tissues and germline cells, suggesting potential implications for embryonic development and adult tissue homeostasis. In EpiC Fun project we aim to investigate epigenetic diversity in both autochthonous and cosmopolitan Italian cattle breeds by analyzing DNA methylation profiles in somatic tissues (blood) and germ cells (sperm). Our study encompasses 10 cattle breeds representing diverse productive purposes: dairy breeds – Frisona Italiana (F); dual-purpose breeds – Modenese (MO), Valdostana Pezzata Rossa (VPR), and Varzese (V) and Pezzata Rossa Italiana (PR); and beef breeds – Blu Belga (BB), Chianina (C), Marchigiana (MA), Piemontese (P), and Romagnola (R). DNA has been successfully extracted from blood and cryopreserved semen samples collected from 79 bulls representing the 10 cattle breeds included in the study, with varying levels of representation ranging from 10 individuals in some breeds (Piemontese, Chianina, Marchigiana, and Romagnola) to 4 in Modenese. Reduced Representation Bisulfite Sequencing (RRBS) and Genotyping by Sequencing (GBS) will be applied to investigate epigenetic variation both within and between breeds and to assess the relationship among epigenetic variation, genetic polymorphisms and phenotypic/morphological traits. The expected output is a DNA methylation map of Italian cattle breeds, the exploration of candidate heritable methylation patterns and of epigenetic variation contribution to traits associated with beef and dairy production.

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P359

Genetic polymorphism of the PAX7 minisatellite region in italian chicken breeds

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In local chicken breeds primarily raised for meat production, growth performance must be economically viable to ensure their sustainable utilisation. However, it is crucial to maintain a balance with the preservation of biodiversity. Investigating polymorphisms in the Paired Box 7 (PAX7) gene—proposed as a candidate marker for growth and meat quality—could provide a valuable tool for genetic improvement. This study investigated the genetic polymorphism of the *PAX7* gene's region in 1,131 individuals from 17 Italian poultry breeds, comprising 28 populations from different origins or generational lineages. Analysis of the minisatellite region identified eight alleles (222, 243, 253, 259, 281, 283, 301, and 315). Among these, the most prevalent were 253 and 283, which accounted for 96% of the observed variability and resulted in an effective allelic richness of two alleles. Although up to six alleles were detected in some populations, the average number of alleles per population was 2.6, with a mean allelic richness of 1.7. Observed and expected heterozygosity were 0.36 ± 0.04 and

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0.37 ± 0.04, respectively. The alleles 253 and 283 were observed in almost all populations potentially linked to improved fitness: the locus was monomorphic in the Livorno Argento (allele 283) and the allele 253 had the highest frequency in the Mericanel della Brianza (98%), where the private allele 222 (2%) was detected. Allele 315 was observed in nine populations, with frequencies from 3% to 23%. Four populations had the allele 259 and two of them completely lacked the allele 283. In the Pisa conservation centre, a high allelic diversity with the identification of some low frequency allele (243,281 and 301) was observed, probably maintained by genetic conservation strategies. Genotype distribution highlighted the prevalence of three genotypes: homozygotes 253 (41%) and 283 (21%), and heterozygote 253/283 (31%), with an excess of homozygosity. Among Piedmontese breeds, Millefiori Piemontese had the highest polymorphism, with three alleles (253, 283, 315) and five genotypes, unlike Bionda Piemontese and Bianca di Saluzzo which lacked allele 315. The dominance of alleles 253 and 283 may reflect past selection for desirable traits, as these variants correlate with growth performance in literature. Low-frequency genotypes observed may be due to the application of genetic variability-preservation mating plan and also to the introduction of breeders from local farms into conservation centres.

P362

Exploring signatures of selection in the indigenous Nero Siciliano pig breed

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The Nero Siciliano, an autochthonous black pig breed reared mainly in the Nebrodi Mountains of Sicily, represents a valuable cultural and genetic resource for the valorisation of the region's traditional agroecosystems due to its resilience and adaptability to harsh environments. This study aimed to detect potential signatures of selection in Nero Siciliano (NER) characterised by a medium-density SNP array. Data from the local breeds Calabrese, Casertana and Cinta Senese, from the cosmopolitan breeds Landrace, Large White and Pietrain, and wild boars were retrieved from public databases. The analysis combined four statistical approaches (iHS, ROH, Rsb and F_{ST}) and compared NER against local (LOC), cosmopolitan (COS) and wild boar (WBI) groups. Multidimensional scaling analysis showed a clear homogeneous pattern for NER, which occupies an intermediate position between the COS and WBI groups and partially overlaps with the LOC group. The iHS approach revealed 20 genomic regions across seven chromosomes under positive selection in the NER breed. The Rsb approach identified 17, 10, and 14 candidate regions under selection in the comparisons of NER vs COS, NER vs LOC, and NER vs WBI, respectively. Notably, four overlapping regions between the two extended haplotype homozygosity (EHH) approaches were detected on chromosomes 1, 6, and 8, including genes linked to key reproductive traits and efficiency (*ALDH1A3*, *LRRK1*), meat and carcass production traits (e.g. subcutaneous fat thickness and average daily gain), and health-related parameters (e.g. blood markers). The window-based F_{ST} approach identified 8, 6, and 6 hotspot regions comparing NER vs COS, NER vs LOC, and NER vs WBI, respectively. Nine ROH (Runs of Homozygosity) islands distributed across seven chromosomes were detected in the NER breed. ROH and F_{ST} analyses showed seven overlapping regions under potential selection on chromosomes 8, 13, and 14, which harbored genes associated with growth regulation and body conformation traits (*JADE1*), reproductive (*SMTNL2*), and exterior traits, such as susceptibility to umbilical hernia (*OSM*). None of these signals overlapped with regions identified with the two EHHderived statistics. This study provides valuable insights into the genomic regions under selection in the Nero Siciliano pig, enhances the knowledge of the genomic make-up of meat production traits and thus might support future breeding strategies for preserving and improving this local breed.
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P363

Does inbreeding cause a decrease in lifetime milk production?

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Over the last decades, selective pressure has aimed at maximising production causing the increase of inbreeding,

especially in high-production dairy cattle. The potential side effects of reduced genetic diversity might impact at both population and individual levels causing inbreeding depression. This study aimed to estimate the impact of inbreeding on total lifetime milk production using an animal model. The dataset included 16,379 Italian Holstein-Friesian dairy cows with lifetime production records, including lifespan milk yield (LMY), lifespan kg of fat (LFY) and lifespan kg of protein (LPY), and productive lifespan expressed in days. All dairy cows included in the analysis were born between 2002 and 2017, ensuring that only those that had completed their productive careers were considered. The inbreeding coefficient for each dairy cow was calculated using two approaches: pedigree-based coefficients (FPED) and genomic data, assessing the stretches of homozygosity (FROH). Specifically, FPED, was defined as the probability that an individual has two identical alleles by descendant and were computed using the OptiSel R package. The ROH segments were detected using the DetectRUNS package in R and defined as follows: at least 15 SNPs in a run, a minimum length of a run equal to 1 Mb, a maximum distance between consecutive SNPs in a window 500 kb, a lower density limit of 1 SNP per 100 kb and allowing for a maximum of one missing and one heterozygous SNP in a run. The FROH were calculated as the proportion of individual genome size covered by ROH. The presence of inbreeding depression was evaluated by regressing phenotypes on FPED and FROH implementing an animal model in ASReml-R correcting for herd and birth year. As expected, FPED (mean = 6.41% ± 1.75) was lower than FROH (mean = 15.0 % ± 3.0). A 1% increase in FROH was associated with a decrease in LMY of 270 kg ($p < 0.01$) whereas FPED was not significant in the model. A similar trend was found when evaluating LFY and LPY ($p < 0.01$) for FROH, with a LFY decrease of 7.56 kg and of 8.59 kg for LPY. This study underscores the importance of monitoring inbreeding levels in breeding programs highlighting the impact of inbreeding on lifetime production traits. Further research is ongoing to evaluate the role of recent and ancient inbreeding based on ROH length classes on lifetime production.

P368

Variability survey at meat production loci in Nero Siciliano pig breed

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The local breeds represent a rich patrimony of livestock biodiversity, an important reserve of rare alleles and allelic combinations linked to adaptative traits. Nero Siciliano is an autochthonous pig breed reared mainly in extensive systems in the mountainous area of Nebrodi in northeastern Sicily. Meat products of Nero Siciliano pigs have been appreciated since the Roman era, but this breed is endangered despite its ecological and economic importance. Structural and scientific actions to promote production performance and genetic improvement are essential to preserve this resource and meet the market challenges, climate change and production sustainability. The genetic characterisation of the livestock populations is the basis for designing conservation strategies towards local breeds at risk and for more effective selection programs. This study aimed to evaluate the genetic variability at 9 loci within candidate genes involved in feed intake, growth rate, fattening and back fat deposition: Melanocortin 4 Receptor (*MC4R*), Ryanodine Receptor 1 (*RYR1*), Class 3 Phosphoinositide 3-Kinase (*PIK3C3*) and Leptin (*LEP*) to provide useful information for the conservation and exploitation of Nero Siciliano pig. Distribution of the genetic variants was assessed in a representative sample of 87 pigs (18 boars and 69 sows) collected in 8 farms located in the original breeding area of the breed. Genotypes have been determined using different PCR-RFLP methods. DNA sequencing was used to genotype MC4R c.-135 (C > T) and *MC4R* c.707 (G > A) loci. Furthermore, direct DNA sequencing was used to confirm the results of the PCR-RFLP methods. Alleles linked to slow growth rate and high fattening and back fat deposition were observed at high frequencies (*MC4R c.175C* – 0.93; *LEP g.3469T* – 0.91) in the whole sample. Genetic disequilibrium and different distribution in boar and sows were also observed in some loci (*MC4R c.-780 C > G; MC4R c.175 C > T; LEP g.2728 G > A; PIK3C3 g.2604 C > T*). The presence of the *RYR1 g.1843T* allele associated with Malignant Hyperthermia and Pale Soft Exudative meat defect has been reported in 7 heterozygote pigs (0.04). In particular, this allele was found at a quite high frequency (0.29) in a farm. Our results suggest the need for continuous monitoring of the genetic variants in this local pig breed to maintain high meat quality and eradicate the *RYR1g.1843T* allele, which might cause significant economic losses.

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P374

Filling the gaps in the genomic management of italian dog breeds

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The canine sector holds significant cultural, economic, and social importance, reflecting the historical ties between nations and their native dog breeds. The Fédération Cynologique Internationale officially recognises 356 dog breeds, classified into 10 groups based on their morphology and function. In Italy, the Ente Nazionale della Cinofilia Italiana (ENCI) is the authority responsible for managing the herd books of purebred dogs. It sets breed standards, monitors breeding practices, and promotes the cultural and functional value of breeds also through zootechnical evaluation through national and international dog shows. Despite this robust framework, this research seeks to develop advanced tools for the conservation, enhancement, and valorisation of the Italian canine breeds, which are 18. Despite ENCI's robust structure, some limitations persist, as in any other kennel club. Underrepresented breeds with small populations could face genetic bottlenecks and diversity loss. Although the registration of litters is compulsory for entry in the specific herd book and the issuing of pedigrees, there is no free access to all advanced and hereditary health information on breeding animals, only the results of official orthopaedic tests such as hip, elbow and patella dysplasia. Integrating genomics tools into the management system will help in breed conservation, genomic data can provide precise inbreeding coefficients, uncover hidden genetic relationships, and offer real-time insights into genetic health. This study addresses genomic management gaps in Italian dog breeds, focusing on refining genetic metrics to preserve populations. As a first survey, we focussed on the Sicilian Mastiff. For this breed, records of 693 dogs were available through ENCI's Sicilian Mastiff database. This population recorded an average inbreeding coefficient of 0.023. However, the inbreeding coefficients currently available are computed exclusively using pedigree data, whose accuracy depends heavily on the depth of the pedigree. Indeed, based on our database, 58% individuals are classified as LA in the 'Libro delle Origini Italiano', referring to pedigrees with no recorded generations, and only 3% are classified as LO, documenting three or more generations. This shows limitations in the depth of available pedigrees and the need to supplement pedigree analyses with genomic data to more accurately assess genetic diversity, reduce inbreeding risks, safeguard breeds, and promote ecotypes.

P378

Exploring head morphology and exterior traits in Nero dei Nebrodi pig

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The Nero Siciliano pig also known Nero dei Nebrodi (NN), is an autochthonous Italian breed from Sicily. The origin of the NN breed is controversial. The well-defined characteristics suggest this breed descends from various breeds and pig populations. The NN breed is considered an expression of ethnic–genetic heterogeneity, showing an evident polymorphism influenced by the natural living environment, the rearing systems, and the type of targeted production system. This pig is a good grazer, characterised by large, long, and drooping ears. Its head shows a remarkable development, a long and straight profile, and a narrow and inclined muzzle, while the nasal profile of the forehead shows a tendency to be straight, sometimes presenting keloidism. In 2001, the NN breed received official recognition as a native breed, and the standard characteristics of the breed were defined. The ears are small and obliquely turned upwards, with the tips carried horizontally forward. The limbs are of medium length and sturdy and present dry joints and strong nails. Current field observations indicate that the animals exhibit morphological features of the head that deviate from those reported in the literature. This study aims to analyze the morphological traits of the NN breed, with particular emphasis on the head, to identify any changes that may have occurred in recent decades to the established breed standards. This study considered 96 animals (50 males and 46 females) over 12 months old. The morphological measures considered were fronto-nasal length (FNL), skull length (SL), snout length (SNL), snout width (SNW), ear length (EL), and ear width (EW). Moreover, records were also taken on the tail length (TL), presence/absence of wattles (W), snout bearing (SB) and ear bearing (EB). The mean FNL, SL, SNL, SNW, EL and EW of females were 24.32 ± 2.17 cm, 7.9 ± 1.60 cm, 16.35 ± 2.00 cm, 6.1 ± 1.00 cm, 16.01 ± 2.04 cm and 12.72 ± 1.61 cm. The corresponding values for males were 24.8 ± 2.09 cm, 7.6 ± 1.53 cm, 15.99 ± 1.95 cm, 5.98 ± 0.88 cm, 15.72 ± 2.45 cm, 12.07 ± 2.36 cm. Considering qualitative traits, all individuals had a long tail (18.50 ± 2.3), approximately 94% and 96% were without wattles and had a convex SB, respectively; and finally, all but one animal had a small forward EB. The average values for EL and EW were found to be lower than those reported in the literature. These results could be used to define better morphological traits linked to the head of the NN breed.

P379

Simulation of mating plans by optimal contribution selection in Camosciata delle Alpi goats

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The selection strategies in Italian small ruminant breeds focus on estimating breeding values and managing matings. Optimal contribution selection (OCS) method allows to elaborate mating plans effectively, balancing genetic gain while controlling inbreeding and preserving genetic variation. Developing a new mating plan is one of the aims of SHEEP&GOAT project, managed by the Italian Sheep and Goat Breeders Association (Asso.Na.Pa.). This study presents the results of applying OCS using EVA software on data from 18 farms, with more than 1,200 Camosciata delle Alpi goats. The farms were selected for their participation in the artificial insemination (AI) program managed by Asso. Na.Pa. over the past 5 years. We hypothesised three simulated scenarios: i) 100% natural mating (NM100), ii) 100% AI with French bucks (AI100), and iii) a combination of 50% natural mating and 50% AI (NM50AI50). For NM100 scenario, it was assumed that Asso.Na.Pa. centralised male management, allowing males to be shared among farmers. The analyses were conducted twice for each scenario, testing two different mating plans: one aimed at maximising genetic merit and the other at minimising the genetic relatedness in the offspring. The mating plans were formulated using the official pedigree data and the selection index (Quality Index composed of protein-kg and fat-kg with 4:1 weight). We compared the results in terms of average ± SD of estimated breeding value (EBV), genetic relatedness (REL), and inbreeding coefficient (INB) in the offspring. When prioritising genetic merit, the results showed similar EBV values, across the three scenarios, ranging from 203 ± 41 for AI100 to 231 ± 40 for NM100. However, AI100 exhibited higher REL (0.033 ± 0.006) and INB (0.015 ± 0.01) compared to NM100 and NM50AI50. Conversely, when minimising relatedness was prioritised, NM100 produced higher average values for EBV (144 ± 10), REL (0.016 ± 0.002), and INB (0.008 ± 0.004) than AI100 and NM50AI50. This could be attributed to the higher genetic relatedness between NM males and females compared to AI males, as well as the different selection strategies applied for AI bucks. These findings emphasise the importance of tailoring mating strategies for a specific population structure and of harmonising data collection and sharing among countries to achieve a sustainable improvement of goat breeding.
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P387

Genomic characterisation of Varzese: an iconic dual-purpose autochthonous cattle breed

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The Varzese cattle breed is an autochthonous breed native to Lombardy and is mainly reared in mountainous areas of the 'Appennino Lombardo'. This breed has experienced a significant population decline due to competition from advancements in agricultural mechanisation and higher-yielding cosmopolitan breeds. By the 1990s, the breed had reached critically low numbers, but efforts to preserve biodiversity and the recognition of its high-quality meat and milk products have led to its revival. This study aimed to assess the population structure and detect selection signatures of the Varzese breed ($n = 82$), comparing it with two closely related Italian autochthonous breeds: Reggiana ($n = 196$) and Modenese ($n = 92$). Using high-density single-nucleotide polymorphism (SNP) chip data, we conducted population structure analyses, including Multidimensional Scaling, genetic admixture analysis and Linkage disequilibrium decay. Selection signatures were identified through various methods, including Runs of Homozygosity (ROH), Fixation Index (FST), Integrated Haplotype Score (iHS), and Cross-Population Extended Haplotype Homozygosity (XP-EHH). Our findings reveal a close genetic relationship between Varzese and Reggiana breeds, with significant selection sweeps on chromosome 3. Annotation of these selected regions identified genes associated with key traits for dairy and beef production, highlighting opportunities for genetic improvement and conservation of the Varzese breed. This study provides a comprehensive genomic characterisation that can inform future breeding and conservation strategies for this endangered cattle breed.
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P502

Behavioural and productive traits of Italian honey bee *(Apis mellifera ligustica* Spin.) colonies: results of a survey among beekeepers in some Central Italy regions

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Apis mellifera ligustica Spinola is a honey bee subspecies endemic to Italy. The preservation of its genetic heritage is essential to maintaining biodiversity, ensuring adaptability to environmental stressors, and supporting agricultural productivity through pollination. This study, involved 28 beekeepers operating in five central Italy regions. The participants collectively manage 6,503 colonies across 288 apiaries. Through the administration of expertise-knowledge structured questionnaires, between March and April 2024 the beekeepers were asked to contribute to the identification of potentially high-performing colonies by providing structured data subsequently organised into a georeferenced database. Eight behavioral and productive traits were evaluated for each colony: swarming tendency, calmness on the comb, gentleness under beekeeper manipulation, nest stores, orderly wax construction, brood vitality, queen laying rate, and honey production. Each trait was scored on an ordinal scale from 1 to 3, with a minimum of 8 and a maximum of 24 possible total points per colony. Data on a total of 112 colonies distributed across 33 locations were recorded and analysed. The average overall score assigned per colony was 18.2 ± 3.5 (13–22). The 68.8% of colonies were classified as 'potential performers', being ranked above the established minimum threshold of 18 points. Honey production received the lowest score (1.48 ± 0.71, 1 min-3 max), reflecting the challenges in honey yields experienced in recent years in Italy, exacerbated by adverse climatic conditions. However, the levels of satisfaction for traits such as 'calmness on the comb', 'orderly wax construction', and 'brood vitality' were relatively high (2.49 ± 0.5; 2 min-3 max). All the traits investigated were submitted to an association study (Spearman Rank Test) from which resulted that the colony total score was strongly associated ($R > 0.5$; $p < 0.05$) with the traits 'gentleness', 'calmness on the comb', and 'low swarming tendency'. This suggests that these traits were prioritised in selective breeding performed by the beekeepers and or queen breeders. The prioritised traits merit further investigation in the light of the ongoing climate change scenario. These findings provide a semi-quantitative foundation for future selective breeding initiatives aimed at the conservative valorisation of endemic subspecies of honey bee.

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P544

Architecture and function of ancestral genomic components in hybrid livestock populations: the Sardo-Modicana case

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The Italian livestock sector is characterised by a rich diversity of local breeds, which play a fundamental role as reservoirs of genetic variability, making their conservation a priority for biodiversity preservation. In this context, the Sardo-Modicana cattle breed represents a unique genetic resource, resulting from the crossbreeding of Modicana bulls imported from Sicily in the late 19th century with Sarda cows native to Sardinia. This study explores, for the first time, the genetic structure of the Sardo-Modicana population using a local ancestry inference (LAI) approach. This methodology enables the chromosomal-level identification of ancestral contributions from the parental populations (Sarda and Modicana), providing new insights into the genetic composition of this breed. Our results revealed that the Sardo-Modicana breed exhibits moderate levels of heterozygosity (0.344) and low levels of inbreeding (0.023), likely reflecting its hybrid origin. Admixture analysis indicated that the Sardo-Modicana genome is predominantly derived from Sarda (75%) compared to Modicana (25%). Similar proportions were detected through local ancestry inference (LAI). Noticeably, the ancestry distribution appeared to be uneven across the genome, with occurrences of near-fixed ancestry from one or the other parental breeds. Highly introgressed regions (top 1%) from both ancestral populations included a total of 357 SNPs intercepting 46 and 71 genes of Sarda and Modicana ancestry, respectively. To determine their potential roles in the breed's genetic

architecture, a functional enrichment analysis was performed to group these genes into functional clusters. In the regions with higher Sarda ancestry, a single significant cluster including the genes *SPEF2, HOOK1* and *SPTBN2,* was obtained; whereas in the ancestral component sourcing from Modicana, the genes were grouped into three clusters: the first including *HERC3, HERC5, HERC6* and *FEM1A*; the second including *CD83, EBI3, CNTN1, FSD1, PHYHIP* and *PTPRT*; the third containing *GIPC3, PDLIM5, PDZRN4* and *TJP3*. Many of the identified genes are related to milk (*SPEF2, HERC3, HERC5, HERC6*), or meat (*RLF, FEM1A, IBSP*) production, and reproduction (*NDUFAF1, SHANK2, ROR1*). Our results reconstruct the architecture of hybridisation and selection in the Sardo-Modicana cattle, emphasising the importance of genomic approaches in providing the detailed knowledge required to effectively describe and manage livestock populations.

P547

Quality control procedures in biobanca nazionale zootecnica Biobanking: scope and outcomes

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ConsDABI has played a key role in the creation and management of the National Livestock Biobank ('Biobanca Nazionale Zootecnica' BNZ). To date, BNZ has collected over 630,000 biological samples from 376 livestock breeds spanning more than 30 years. The repository is continuously expanding thanks to collaborations with national labs and new initiatives targeting native breed sampling, contributing to the achievement of Strategic Priority 9 of the FAO Global Plan of Action for Animal Genetic Resources. According to ISO 20387:2018, biobanks must establish quality control measures to maintain the suitability of biological materials and associated data for research purposes. This continuous monitoring guarantees the optimal preservation of biological samples (tissues, blood, hair bulbs, DNA, semen straws) over time. Regular quality analyses, especially of cryopreserved semen and biological samples, are a key component of BNZ's standardised internal protocols, ensuring proper and transparent management. These ongoing quality check ensure the long-term integrity of the samples but also uphold high-quality standards. Until 2024, a total of 4,907 quality control analyses were conducted, focusing on two different matrices. The first one involved a randomised selection of 4,704 hair bulb samples, stratified by year of storage. Their quality was assessed based on suitability for high-throughput genomic analysis using Affymetrix platform. From a total of 3072 DNA samples processed on SNP array, 75% showed call rate values >0.90. The other samples subject to quality control were cryopreserved semen straws stored in liquid nitrogen, originating from multiple cryogenic banks. Data from qualitative and quantitative testing using the Makler chamber confirmed the presence of viable spermatozoa, with an average sperm concentration of 29.4×10^6/ml and an average motility of 25%. These straws, derived from bulls of 10 different Italian native breeds, preserve genetic lines from 2002 to 2013, representing individuals no longer active in breeding programs. They constitute a critical resource for conserving breeds at risk of extinction and with high genetic relatedness. The results of these analyses allow for the classification of semen into viable and motile samples, suitable for reproductive purposes and preservation in liquid nitrogen, and non-viable samples, stored at -20 °C as biological material intended for research purposes.

P575

Characterization of the Cinisara chain in northwest Sicily

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Cinisara (CNS) is a dual purpose cattle breed reared in small farms of Northwest Sicily. Within the frame of the Italian 'Piano di Sviluppo Rurale 2014–22, sottomisura 16.1 (PSR)', a project has arisen with the aim of valorising this genetic resource that remarkably represents a sustainable breeding model. Target of the project is the analysis of the different factors that play a relevant role in the supply chain of CNS to defining a production's policy.. To achieve this goal the project points to characterising the territorial typology of the enrolled farms, with precise reference to dimension and conformation, and to investigate the genetic structure of the CNS, with a specific glance to inbreeding level. To characterise CNS farming systems, a sample of 10 farms, located in northwest Sicily and belonging to the Consorzio Allevatori per la Tutela della Razza Bovina Cinisara was selected. For each farm, the agricultural surface was georeferenced in a GIS environment using cadastral data and intersected with the Corine Biotopes Habitat Map of Sicily. Based on the identified habitats, 10 land use categories were defined, and farms were classified using a cluster analysis. Three groups were identified: farms dominated by mesotrophic pastures, farms dominated by

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dry pastures, and farms dominated by arable crops. The genetic investigation of CNS, still a work in progress, is carried out on a total of 175 animals that were sampled in the 10 enrolled farms and subsequently genotyped using the Neogen GGP Bovine 100k SNP array. Further analyses are being performed on the obtained genotypes to investigate the level of inbreeding both in the population under exam and in the different farms. Runs of homozygosity will be analysed using the detectRuns package in R environment. A moderate-to-high inbreeding is expected in the sampled animals, due to the common use of the farm-owned bull for calves breeding in this area. Clustering based on the genotypes will be performed to further observe the existence of population stratification in the sampled animals. The obtained results will allow the setting up of meeting schemes aimed to a better genetic management of the CSN population.
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P576

How alternative models affect resilience indicators in dairy cattle

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In this study, the observations of 1200 dairy cows reared in a single Northern Italian farm were used to evaluate how alternative models affect the resilience indicators. Fourteen models were implemented to obtain the deviations and eight already established resilience indicators were calculated upon the deviations between the observed and model-estimated (unperturbed) milky yield curves. The models comprehend Wood, Wilmink, Ali&Schaeffer, and polynomials as parametric models, moving average and moving median for the non-parametric ones. Customised models were included to reach fourteen. The principal component analysis (PCA) of the models, run within each indicator, indicated high correlation and a similar pattern of the loadings across model classes, but the first PCs were not able to cluster the scores. As reflection of the high correlation among the models, almost the totality of the variance (60–80%) was absorbed by the first component. A different analysis revealed that model choice significantly influenced the ranking of individual cows across resilience indicators. In comparing the Ali & Schaeffer lactation model with the 4th degree polynomial, 76% of the cows were placed in the same top 2% and bottom 2% tails of their LnVar indicator distribution (logarithm of the variance of the deviations), compared to 21% when comparing the spline regression with the Wilmink lactation curve. When comparing the consistency of rankings, LnVar was the most robust indicator across models, while the least robust were those based on negative deviations, such as the DPert (the daily perturbations) and WFPert (weighted frequency of the perturbations) indicators. In these cases, the percentage of overlapping rankings among models ranged from 1% to 62%. Starting from a better understanding of the dynamics of model trait combination we performed a simulation study, which incorporated signal from general physiological variability, random technical error, and resilience related perturbations. Findings of the current study highlight the need for careful consideration of model selection in resilience studies, suggesting that while model-specific results may vary, underlying patterns of resilience may be consistent across different modeling approaches. This study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

P107

Evaluation of genetic parameters for milk composition and technological properties in Podolica cattle breed

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Podolica is an autochthonous rustic Italian beef cattle breed exclusively selected for meat pro-duction. Its milk is however commonly used to produce the typical Italian Caciocavallo cheese. The aim of this study was to evaluate the genetic components for seven traits related to cheesemaking. More specifically, the chemical composition (as percentage of fat, proteins, lactose, and

casein), and the coagulative properties (a_{30}, K_{20}, coagulation time – r) were inferred with near infrared spectroscopy from 427 milking cows from 27 different farms, and the respective pedigree of 1,735 animals was retrieved. Heritabilities, phenotypic and genetic correlations (r_p and r_g), genetic and residual variances and covariances were obtained by Gibbs sampling with Gibbsf90+ software (100,000 cycles, 5,000 burnin, 10 thinning interval) using parity and farm of origin as fixed effects. Results highlighted strong r_p between the coagulative traits (a_{30}-K_{20} = –0.95 ± 0.01; a_{30}-r = –0.80 ± 0.02; K_{20}-r = 0.75 ± 0.02) and, as expected, between proteins and casein percentage (0.99 ± 0.001). Other moderate r_p were observed between all traits, except between fat and a_{30} and r, proteins with lactose and r, and casein with r. The same correlations within the coagulative traits were observed for r_g (–0.95 ± 0.02 a_{30}-K_{20}; -0.83 ± 0.07 a_{30}-r; 0.78 ± 0.08 K_{20}-r), alongside between proteins and casein percentage (0.99 ± 0.003). Moreover, strong r_g resulted between fat and a_{30} (0.95 ± 0.03), K_{20} (–0.82 ± 0.08), r (–0.80 ± 0.09). Moderate genetic (and phenotypic) correlations between proteins and casein with a_{30} (r_g 0.56–0.59 ± 0.16–0.18) and K_{20} (r_g –0.56 both ± 0.16–0.18) and finally r_g between fat and proteins (0.42 ± 0.20), and casein (0.46 ± 0.18) were also observed. Regarding genetic correlations, fat percentage showed strong positive correlation with a_{30}, and negative with K_{20}, which were not observed in the phenotypic correlations. Apparently, the environment has a particular influence on fat content in the milk. This is also confirmed by the fact that the heritability for fat percentage resulted the lowest (0.14 ± 0.03) compared to all the other traits that showed moderate to high heritabilities (proteins 0.43 ± 0.11; lactose 0.40 ± 0.15; casein 0.42 ± 0.11; a_{30} 0.47 ± 0.10; K_{20} 0.48 ± 0.11; r 0.52 ± 0.12). Our results suggest the feasibility of genetic selection for chemical and technological properties in Podolica milk.

P229

Performance evaluation of the new SNPs array designed for Mediterranean river buffalo breed

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The domestic buffalo (*Bubalus bubalis*) plays a pivotal role on a global scale. This species is categorised into two main types: the river buffalo, primarily raised for milk production, and the swamp buffalo, predominantly used for draft work. In the context of river buffaloes in Europe, the Italian Mediterranean buffalo (IMB) breed represents 95% of the buffalo population. Among the most renowned products derived from this breed is 'Mozzarella di Bufala Campana', a typical Italian product certificated by the European Protected Designation of Origin (PDO). As part of the Genobu project, a new version of Axiom Buffalo Genotyping Array (BUF2) has been developed, specifically designed to enhance genomic selection in IMB. This new array marks an evolution from the original SNP chip (BUF1, ~90k SNPs), which was initially created to characterise the genetic biodiversity of both river and swamp buffalo. The new array features a total of 122,017 SNPs. About 57.45% of the BUF2 markers came from the BUF1, because they were already associated with genomic selection and linked to important characteristics in IMB. The remaining were identified using short- and long-read sequencing technologies, to enhance array performance, including functional and chromosome Y markers. To validate the new array 480 were genotyped, with almost 51% male and more than 96% from IMB. Almost the 98% of the samples passed the Affymetrix Quality Control (QC). After the QC processes more than 91% (almost 115k) SNPs were classified as high-precision markers, improving the BUF1 performance (i.e. below 75%). About them, the minimum SNP call rate exceeds 97%. About the Minor Allele Frequency (MAF), 97.66% and 95.36% of the markers present a MAF greater then 0.01 and 0.05, respectively. About the functional markers, for example, almost 60% of the Y chromosome ones passed the QC. This represents a significant advancement compared to the previous array, both in terms of quantity and quality of SNP markers retained after QC. Genetic analyses will be more accurate and reliable, making the new array a highly effective tool for genomic studies and genomic selection evaluation focused on the IMB. Additionally, thanks to the inclusion of Y-markers, the new array is suitable for sex-specific genomic analyses.

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P247

An initial genome-wide association study for haematological and blood clinical-biochemical parameters in Italian Duroc pigs

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Blood-related traits, such as haematological and clinical-biochemical parameters, are key indicators of the physiological and health status of animals. These parameters can be considered intermediate phenotypes useful for dissecting more complex traits, such as resilience and disease resistance. In this study, we measured 15 haematological and 18 clinical-biochemical parameters in about 200 Italian Duroc pigs, using blood collected after slaughtering at the end of their production life, at 9 months of age. These pigs were also genotyped using the 60K single nucleotide polymorphism (SNP) panel. Blood parameters were first normalised using Box-Cox transformation, accounting for sex, weight and slaughtering date, as well as environmental and technical factors, which were then removed with a linear regression model. After SNP filtering and haplotype reconstruction, single-marker and haplotype genome-wide association studies were carried out. The single-marker analysis identified associations for 21 out of 33 blood traits. The most significant QTL was identified on porcine chromosome 3, associated with the level of LDL-cholesterol. This region contains the *APOB* gene known to affect this parameter in other pig breeds and other species. The results provide an initial genetic characterisation of several blood parameters in Italian Duroc pigs. Further studies are needed to refine these results and evaluate if blood parameters can be used as proxies for other economically relevant traits. The research was supported by: (1) the Horizon Europe Re-Livestock project that has received funding from the European Union's Horizon Europe research and innovation programme under the grant agreement No. 01059609 (for the elaboration and analysis of the data); (2) the Italian PRIN2022 project FEEDTHEPIG, CUP J53D23018310001; (3) the Italian PRIN2022 HamCapture, CUP J53D23009570001; (4) the Agritech National Research Center (Agritech Spoke 1) and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022).

P250

CHAMP: Combining Horse Athletic Measurements with Precision Genomics

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Europe stands as a global hub for equestrian activities, hosting over 70% of worldwide events and fostering a thriving industry with an annual turnover exceeding one hundred billion euros. Despite this, the equine sector lags behind other livestock industries, particularly in the application of genomics within breeding programs for sport performance.
Therefore, this project aims to address two critical gaps in the horse breeding sector that have hindered the integration of genomics. These gaps are mainly the lack of tools for objectively measuring phenotypic traits on a large scale among Warmblood studbooks and the absence of a robust dataset of horses genotyped with high-density SNP chips and matched with objectively measured phenotypes. Through a multidisciplinary approach combining molecular genetics, computer science, morphometry, and biomechanics, the CHAMP project aims to provide a starting point to integrate novel phenotyping tools and genomics into the horse breeding scheme. Specifically, the project has three main objectives:

1. Apply artificial intelligence (AI) techniques for the non-invasive collection of large-scale phenotypic data in horses using image and video analysis.
2. Establish an international dataset of Warmblood horses genotyped with high-density SNP chips and phenotyped using the proposed AI-based strategy.
3. Evaluate the feasibility of using genomics to enhance genetic progress for sport traits in horses.

The primary expected outcomes of the project are: i) The development and implementation of an automated pipeline for extracting objective traits from images and videos of Warmblood horses; ii) A comprehensive phenotypic characterisation of genotyped Warmblood horses with high-density SNP chip (670K) with the developed pipeline; iii) The estimation of genetic parameters for at least 20 novel traits, along with Genome-Wide Association Study (GWAS) results and predictive equations based on Genomic

Best Linear Unbiased Prediction (GBLUP). By achieving these outcomes, the project aims to advance the use of genomics and AI tools in equine research, paving the way for more efficient horse breeding practices. These efforts are expected to facilitate more informed selection decisions and accelerate genetic progress for sport traits.

This research was funded by the University of Parma through the 'Bando di Ateneo 2024 per la ricerca' initiative and received additional support from Scuderia 1918, serving as the industry advisory board for the project.

P263

Focus on genetic diversity within the InnoVaDiv project

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Italy is one of the richest countries in terms of biodiversity. The diverse climates and environments across the country have fostered the development of a wide variety of species and breeds. However, a significant loss of biodiversity is occurring as local breeds are increasingly replaced by cosmopolitan and more productive ones. These local breeds are essential for conserving local traditions and environments, as they exhibit resilience, adaptability, and serve as reservoirs of genetic diversity. Preserving these breeds is therefore critical, and implementing concrete measures to safeguard them is urgent. This project focuses on the characterisation of three endangered Italian local breeds: the Nero di Parma swine, the Cornigliese sheep, and the Parma and Piacenza turkey. These breeds are considered at risk due to their low population sizes. Genomic data will be analyzed from a total of 300 swine and sheep, carefully selected to capture the highest possible genetic variability in the population, along with 96 turkeys, representing the entire population available at the project's start. Due to recent outbreaks of Bluetongue and swine fever in Italy, not all samples for sheep and swine have been collected yet. Samples will be genotyped using species-specific SNP chips: Illumina® PorcineSNP60v2 for swine, OvineSNP50v2 for sheep, and Axiom® Turkey Genotyping Array, covering 643,845 SNPs, for turkeys. The genotype data will undergo quality control using PLINK and further analyses will be performed in R. This includes calculating inbreeding coefficients from genotyped data, studying population structure, and identifying selection signatures. Preliminary analysis of 70 Cornigliese sheep samples revealed an average inbreeding level of 9%, with a minimum of 3.4% and a maximum of 18.8%. These values are significantly higher than the 2% inbreeding level estimated from pedigree data. For the 96 Parma and Piacenza turkey, inbreeding coefficients from genotype data ranged from 0% to 47%, with an average of 16.3%. Genotype data for the Nero di Parma swine samples are not yet available for analysis. These preliminary results highlight that the inbreeding levels obtained from genomic data are often much higher than those derived from pedigree data. This underscores the importance of genomic tools in accurately assessing genetic variability, particularly in small breeds where inbreeding is frequently underestimated.

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P266

In silico functional polymorphisms analysis for milk-related genes in *Camelus dromedarius* species

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Dromedary camels (*Camelus dromedarius*) are among the most important livestock animals in arid and semi-arid regions of Africa and Asia, and provide basic needs to millions of people assuring the production of milk, meat, wool, leather, transport, and workforce. In recent years, the interest in camels and their products (mainly dairy and dairy-derived products) has rapidly grown, even in countries without a tradition of breeding this species, due to the known or assumed health properties of camel products. Thus, several camel dairy farms have been established worldwide and are currently supplying local and international markets. Among the possible strategies to meet the growing demand for camel milk and dairy products, genetic improvement may play a prominent role. However, the investigation of polymorphisms for milk-related genes in camels, which is fundamental for implementation of marker-assisted selection schemes, is still in its infancy in this species. In this context, the 11th Illumina® Agricultural Greater Good Initiative was activated with the main goal of developing the commercially available Illumina® CamelSNP60 BeadChip for dromedary camels, achieved by whole-genome sequencing more than 350 camel samples worldwide using the Illumina® NovaSeq platform. This approach generated a wealth of data that is being thoroughly *in silico* analyzed in order to investigate sequence polymorphisms in milk-related genes and their potential functional effects on milk-related proteins. Overall, the results of this study could contribute to obtaining a wider knowledge of the sequence variation at the *C.*

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dromedarius milk-related loci, including functional polymorphisms, which could be useful to possibly assist selection for milk production in this species via the large-scale genotyping of validated genetic markers.

P356

Identification of SNP markers associated with carcass trait and meat quality in Italian slow-growing chicken breeds using targeted next-generation sequencing (NGS)

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Bionda Piemontese (BP) and Bianca di Saluzzo (BS) are two local chicken breeds native to the Piedmont region (North-west Italy). Known for their slow-growing nature, these breeds are traditionally raised in extensive farming system. However, the slow production rate poses challenges in meeting demand while maintaining high meat quality. To address this issue, a molecular analysis approach has been employed. Extensive research has been conducted to identify quantitative trait loci (QTL) associated with economically important traits in chickens. This has enabled the identification of single nucleotide polymorphism (SNP) variants in specific genes linked to these traits. This study involved 100 BP and BS chickens. For each individual, key parameters related to carcass traits (e.g. the weight of the entire carcass, eviscerated carcass, carcass without organs, breast and thigh weight) and meat quality (e.g. ph, color, crude protein and ether extract content) were evaluated. A total of 29 genes were selected for the analysis. Among these, ten genes—ADSL, CDKN3, CD36, DGAT2, MC4R, PAX7, PIXT2, POU1F1, PTH2R and SIX1—have been identified in prior studies as having SNPs and/or indel regions related to the parameters evaluated; the remaining 19 genes—ACOX1, AOAH, APOA1, CASP6, CAT, CYP26B, ENPP6, FABP1, FADS2, GLA, HSPA2, LPL, NEU2, NUDT19, PLA2G4F, PLA2G10, PLBD1, SOD1, and SREBF2—where found to be differentially expressed in the liver of BP and BS chickens. However, no information on polymorphisms is currently available for these genes in poultry. A custom panel targeting all these genes was designed using Illumina Design Studio (Illumina, San Diego, CA, USA) and achieved a total coverage of 98% of all genomic targets over a span of 20 kilobases (kb). This custom panel was then sequenced with next-generation sequencing (NGS) technology, enabling high-resolution identification of SNP variants linked to carcass traits and meat quality. The potential outcomes of this study, including new identified SNPs and their correlations with key meat quality and carcass parameters, are in progress and will be presented at the Congress. These insights have the potential to contribute to the genetic improvement of these breeds while preserving their unique characteristics.

P412

Effect of breed and season on productivity, quality and dairy efficiency of two Italian dairy sheep breeds

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The low level of innovation, high production costs (due to the difficulty in supplying feed, especially in marginal areas) and high variability of production (related to season and its impact on cheese yield and characteristics) are leading the dairy sheep industry (DSI) to face a period of crisis. The DSI represents a complex system, involving biological, technological, economic, ecological and social aspects. For this reason, critical points need to be identified and the biological mechanisms underlying milk production need to be investigated, so that new selection targets can be included (such as resilience, sustainability and feed efficiency). The aim of this study was to evaluate factors affecting the variability of production and quality traits on a total of 243 animals belonging to two Italian sheep breeds: Comisana ($n = 60$) and Massese ($n = 183$). Phenotypes were collected on a commercial farm in central Italy in different seasons and included traits of production (kg of milk/day), components (fat, protein, caseins, lactose, total solids, casein index, pH and somatic cells), cheese making efficiency, in terms of cheese yield (%CY) and individual milk components recovered in the curd (%REC). Phenotypic records ($n = 778$) were validated based on information provided by Asso.Na.Pa. and analysis of variance was used to assess the impact of different effects on analysed traits. Season, breed, parity, stage of lactation and interaction between breed and season were considered as fixed effects, while animal effect was

considered as random. The breed showed a significant effect on casein index ($p < 0.05$), pH ($p < 0.001$) and urea level of milk ($p < 0.01$). Indeed, milk produced by Massese ewes showed higher casein index and lower levels of urea and pH than Comisana ewes. Season and interaction between breed and season have impacted most traits (fat, protein, lactose, casein, total solids, dry matter cheese yield, recovery of total solids in the curd, milk yield, pH and urea), along with stage of lactation. Results suggest that differences among sheep breeds may be exploited in the search for better adaptable herds in determined environmental conditions, with further studies still ongoing within the project.

P418

WGCNA analysis elucidates pathways involved in fatty acids biosynthesis in local chickens

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The worldwide increase in chicken production is primarily attributable to commercial lines. However, local breeds are of increasing significance as they are recognised for their unique products. The Robusta Maculata (RM) and Bionda Piemontese (BP) are two local chicken breeds that represent a valuable and endangered domestic heritage resource in Italy. Conventional poultry products contain lower *n*-3 fatty acids compared to products from local breeds. Therefore, the objective of this study was to evaluate the modulation of expression of genes involved in long-chain polyunsaturated fatty acids (PUFA) biosynthesis pathways according to genetic background and sex. The RM and BP chickens of both sexes were reared until commercial maturity. At slaughtering, liver tissue from a subset of reared animals (3 males and 3 females per breed) was sampled. The liver fatty acid composition was determined using a Varian Gas Chromatograph (CP-3800), resulting in the identification of 29 fatty acids. The RNA was extracted from liver and sequenced using the RNAseq method. A weighted gene co-expression network analysis (WGCNA) was conducted using the R package *WGCNA* to identify gene expression patterns significantly associated with the fatty acids. About the five groups of co-expressed genes (modules) significantly associated with PUFA, the red one was the most associated ($r = –0.70$; $p < 0.01$) and encompassed a total of 676 genes, of which 17 were involved in fatty acid metabolism. Gene ontology analysis identified three triggered biological processes: fatty acid elongation, unsaturated fatty acid biosynthetic process, and long-chain fatty acid transport. The first and second biological processes shared common genes such as *FADS1*, *FADS2*, *ELOVL2*, *GPAM*, and *ACSBG2*, and the long-chain fatty acid transport process was led by *FABP1* and *FABP2* genes. As for *n*-3 fatty acids, the most notable module was honeydew1 ($r = 0.70$; $p < 0.05$), in which *ABCD3* and *HACD4* genes were included in the very long-chain fatty acid biosynthetic process. The brown4 module significantly correlated with *n*-6 ($r = –0.80$; $p < 0.01$), encompassing genes of interest such as *FADS6*, in addition to the modules previously identified for PUFA. Local breeds can modulate gene expression in PUFA biosynthesis pathways, involving key genes and biological processes, thus enhancing *n*-3 and *n*-6 fatty acid profiles.

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P426

Genomic insights on the history and selection trajectories of the local goat breed Comune di Sicilia

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The 'Capra Comune di Sicilia' (CCS), also known as 'Mascaruna' due to its typical black 'badgerface' markings, is a Sicilian local goat population described since 1870 and currently subjected to a recovery project for its characterisation and ethnic recognition. This study details the ancestral genetic components and selection trajectories of CCS. We analysed the genotypes of 78 CCS goats using the Goat 60k SNP BeadChip along with data from 1,920 individuals of 66 goat breeds of Mediterranean and African origin.

The CCS recorded relatively high levels of heterozygosity (0.408) and moderate inbreeding (0.04), with an effective population size ranging from 96 to 185. Genetic ancestry analysis identified gene flow signals with Maltese, Girgentana, Rossa Mediterranea and Saanen populations, along with a putative Greek ancestry shared with most of the Mediterranean breeds in our dataset, reflecting Sicily's deep historical and cultural links with Greece. In order to understand the evolutionary trajectories of this population and exploit the potential ancestry sourcing from Greek populations, we investigated selection signatures within CCS through iHS and ROH analysis, identifying 76 and 31 SNPs falling within 38 and 12 genes, respectively, under putative selection. Then, we applied XP-nSL and ROH using Greek populations as ancestors, and identified 21 and 431 SNPs, associated with four and 157 genes, respectively, under putative selection. Overall, all selection signature analyses highlighted genes under positive selection linked to milk (*MGFGE8, ANPEP, POLG, AXIN2*) and meat (*MRPL46*) production, body size and growth (*FAM184B, LCORL*), fertility (*PFOXic, FANCA, NTRK3, CPEB1, BLM, SPP1, MGFGE8*), coat colour (*AP3B2*), fat deposition (*KLF5, COPS8*), and ear and horn development *(PFOXic, ORC6, LCORL, MEPE, FAM184B, ISBP*). Our results shed light on the history of CCS, emphasising its genetic uniqueness and providing essential information about its background, which is crucial for informed efforts to recognise it as a distinct and valuable breed.

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P428

Genomic characterization of the Maltese cattle breed

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Maltese cattle, known locally as 'il baqra maltija', is a native population of Malta, with the earliest historical detailed text giving evidence of its presence and use of the oxen on the island dating back to 1240, with more specific reference going back to the 1400's. The breed was described phenotypically in 1915 as having two coat color variations (light brown and blue/brown), with an average height at the withers of 170 cm and having a carcass weight of 630 to 800 kg. The current population, less than 50 animals, retains some ancestral traits similar to North Africa cattle. During the 1930s, a breeding program was implemented with the intention to transform this breed into a dual-purpose one with the compulsory used stud bulls imported from UK (e.g. Brown Swiss, Ayrshire, Jersey), by the Department of Agriculture. Thus, corrupting the true genetic heritage of the population. This breed was ignored as it never proved to yield an adequate quantity of milk, and this fact contributed towards the almost total disappearance of this bovine population. The aim of this work is to analyse and characterise the genomic health of the current Maltese cattle population to initiate a reconstruction process of this unique genetic pool. The conservation of this breed would be crucial to maintaining Mediterranean biodiversity, particularly within the context of Malta's small and isolated environment. The genotypes of 8 Maltese individuals were analysed using the Affymetrix 65K SNPChip together with the data of 830 individuals from 30 different cattle breeds of European and African origin. The Maltese cattle showed high levels of inbreeding (0.57) with a very low effective population size (8). In the principal component analysis, Maltese grouped together with Italian beef breeds of Podolian origin, such as Chianina, Podolica, Romagnola and Marchigiana. Although small sample size and high consanguinity could have an influence on the results, the analysis of global ancestral components indicates an ancestral link with African breeds (NDama, Nelore and Lohani) cannot be excluded, while more obvious are ancestral components related to European breeds. In conclusion, while the results reflect the zootechnical ancestry of this population, they highlight the urgency of implementing a zootechnical recovery program, which could include cryopreservation of semen after genotyping, to avoid complete loss of this genetic pool.

P500

A study on instrumental insemination in *Apis mellifera ligustica* Spin. as a tool for conservation strategies of the Italian honey bee

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The Italian honeybee (Apis mellifera ligustica Spinola) is a subspecies of great importance to Italian apiculture but increasing pressure of hybridisation with other subspecies and/or commercial breeds ask for valuable strategies of conservation. As a first step, however, the consistency of selection made within the subspecies phenotypic descriptors should be ensured. This study

aimed to produce laying queens of A. m. ligustica through instrumental insemination (II), with the objective of generating F1 colonies derived from parent colonies exhibiting morphotypes in line with the national reference standard for wings' size and morphology, tergites' banding, and legs' size. The experimental activities were repeated in two consecutive years: the first year (2022) at the University of Tuscia experimental apiary (Viterbo, Italy), and the second year (2023) at the BeeHive Farm (Gennazzano, Rome). Advanced and tailored protocols were adopted for the selection of parental colonies, queen management, and morphometric analysis of parental colonies and their progeny. In 2022, adverse climatic conditions, including delayed spring and extreme summer temperatures, hindered queen production and then the II operations. Out of a pool of 11 selected colonies, only three queens were inseminated, with just one resulting in a surviving F1 colony exhibiting a phenotypic membership of 33% that was lower than the expectations and values of the mother colonies (61.1% and 50.0%). In 2023, more favourable weather conditions led to significantly better outputs. Eleven instrumental inseminations were performed with an overall II efficiency of 36.4%, and the resulting F1 colonies showed phenotypic membership levels above 50% (from 50.0% to 64.7%), approaching the standards for the A. m. ligustica subspecies. However, overwintering survival of F1 colonies remained a critical issue, with 50% of F1 colonies lost during the winter. The results confirmed the potential and feasibility of II as a tool for ensuring further breeding programme dedicated to the Italian honey bees, even though the unexpected morphotype observed in 2022 deserves further investigation especially in the control of drones' drift among neighbouring hives. These preliminary findings can provide foundation for future advancements in sustainable apiculture, contributing to the conservation of endemic honey bee subspecies and the resilience of the Italian apiculture sector.

MONOGASTRIC NUTRITION

P044

Horehound (*Marrubium vulgare* L.) as a feed additive affects the productive traits, serum antioxidants, digestive enzymes, intestinal bacterial counts, and gut morphology of growing rabbits

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The present study was conducted to assess the effects in rabbit diet of Marrubium vulgare L., belonging to Lamiaceae family, one of the most useful plant families in the Mediterranean area. Marrubium vulgare L. is a perennial herb which is commonly known as 'white horehound' in Europe. This plant is widely used in folk medicine against various ailments such as gastrointestinal disorders, intestinal infections, and inflammatory processes. The wide range of bioactive compounds found in this plant have suggested the possible inclusion as a feed supplement in animal diet. Therefore, this study aimed to investigate the effect of horehound powder (HP) as a natural feed additive on productive traits, serum antioxidants, digestive enzymes, intestinal bacterial counts, and gut morphology in growing rabbits. Horehound aeral parts were collected during spring season at early flowering stage, then air-dried at room temperature and ground into a fine powder, in order to be included into the pellet. A total of 40 male Bianca Italiana breed rabbits, weaned at 42 days, were allotted to two dietary treatments: a control diet without any supplement, or a test-diet including HP at 0.15% of diet, for 6 weeks. The rabbits were housed as one rabbits per cage in galvanised wire single cages. No medication was included in feed or drinking water and rabbits' health status was checked through the trial. At slaughter age (84 days), meat, blood and intestinal samples were collected. From findings, dietary inclusion of HP improved the rabbit final body weight ($p < 0.05$) and feed efficiency as well as carcass yield ($p < 0.01$), whereas no effect was observed for meat composition. Feeding HP led to higher ($p < 0.05$) meat total PUFA and n-6 concentrations, and improved ($p < 0.05$) n-6/n-3. Serum lipids were not affected by dietary treatments, but serum antioxidant capacity (GPx, MDA and SOD) was improved ($p < 0.01$) by HP. The herb also similarly increased ($p < 0.001$) the activities of duodenal α-amylase, maltase, lipase, and trypsin. Both rabbit caecal characteristics and microbial populations were not affected by treatments, whereas rabbit duodenal histomorphometry was positively affected by HP diet showing higher villi and deeper crypts ($p < 0.001$). The results suggest that HP supplementation in rabbit diet could efficiently improve production traits, with a beneficial regulation on health status, antioxidant capacity and gut histology.

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P142

Preliminary assessment of chemical and nutritional value, and biomass production of an area in Centre-South Italy grazed by equines

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Grazing ecosystems can be affected by several factors, including territory and herbivorous species reared and managed, which could influence plant diversity and pastures' nutritional value and quality. The study of Apennine pastures in Capracotta municipalities (41°50′N 14°16′E, Isernia province), a Special Area of Conservation (SAC, IT7218215) in a mountainous area (1150–1500 m of altitude), investigated dynamics in pasture areas characterised by widespread presence of rock outcrops. During spring and summer grazing season 2024, pasture biomass was evaluated in six sampling sites, grazed by Italian Heavy Draught breed horses, by 24 representative sub-areas. In each sub-area, biomass was manually collected at 3 cm above ground to simulate grazing. The dried biomass underwent chemical analyses including dry matter (DM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF) and ash. Antioxidant activity, as mg of ascorbic acid equivalents (AAE)/g DM, was assessed by 2,2′-azinobis-(3-ethylenebenzothiazoline)-6-sulfonic acid (ABTS) assay. Total phenolic content (TPC), as mg of gallic acid equivalents (GAE)/g DM, was quantified by the Folin-Ciocalteu method. The average (± SE) turf production was 2.82 (± 0.19) t DM/ha. The pasture, mainly composed of grass and legume plants, was characterised by DM 34.3 (± 5.75) g/100g, CP 6.43 (± 0.41) g/100g DM, ash 8.82 (± 0.17) g/100g DM, NDF 48.1 (± 1.73) g/100g DM, and ADF 30.6 (± 0.93) g/100g DM. The average (± SE) ABTS content was 3.17 (± 0.06) mg AAE/g, and TPC 2.32 (± 0.09) mg GAE/g. Antioxidant activity varied significantly ($p < 0.001$) among sites: sites 2 and 3 recorded in spring the highest values at 3.62 ± 0.07 and 3.75 ± 0.07 mg AAE/g, respectively, according to the highest TPC content (3.03 ± 0.04 and 2.97 ± 0.11 mg GAE/g). Overall, both antioxidant activity (3.40 ± 0.04 mg AAE/g) and TPC (2.63 ± 0.05 mg GAE/g) were higher ($p < 0.001$) in spring than in summer (2.48 ± 0.07 mg AAE/g and 1.41 ± 0.08 mg GAE/g). Results suggest the impact of site and season variations on pasture value. Assessing pasture characteristics with a comprehensive evaluation of equine breeding systems will improve breeding models to enhance the resilience of marginal areas, especially in Centre-South Italy.
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P342

Functional activity and anti-inflammatory response of *Fucus vesiculosus* on mouse peritoneal macrophages

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The necessity to enhance animal health, growth, and productivity while addressing environmental and ethical concerns led zootechnical sector to explore innovative and functional ingredients that can be beneficial to animal production. Seaweeds have emerged as a promising component in livestock feed due to their nutritional benefits and potential to mitigate environmental impacts. Considering this, the objective of this study was to investigate the functional properties of *Fucus vesiculosus* and their behavior after *in vitro* digestion. Following the bromatological characterisation, according to the official AOAC methods, digestion process was simulated through INFOGEST protocol. Extract and products of digestion were analyzed for polyphenol, flavonoid, and phlorotannin content through colorimetric assays, as well as for antioxidant properties with ABTS assay and growth inhibition capacity against *Escherichia coli* with microdilution methods. Subsequently cytotoxic activity and anti-inflammatory property of *F. vesiculosus* was evaluated on mouse peritoneal macrophages by crystal violet assay and gene expression assessment of IL-1β, IL-6, TNFα and iNOS, respectively. Bromatological characterisation confirms its nutritional values with a high content of dietary fiber (47.36 ± 0.54%) and protein (13.99 ± 0.21 %). Polyphenols, flavonoid, and phlorotannin were equal to 6428.98 ± 7.37 µg TAE/g sample, 5171.31 ± 51.50 µg CE/g sample, and 2.10 ± 0.01 mg PGE/g sample, respectively, and were maintained after digestion process ($p > 0.05$). The high values of bioactive molecules are reflected in the functional properties exerted. Concentration of

50 mg/ml of *F. vesiculosus* can show an ABTS$^{\bullet+}$ scavenging effect (%) equal to 85.96 ± 2.95 %. Additionally, it can reduce the growth of *E. coli* by 17%. Finally, *F. vesiculosus* extract (50 and 100 µg/ml) exhibits a protective effect in peritoneal macrophages stressed with H_2O_2. The gene expression evaluation revealed a down-regulation of IL-1β, IL6, and TNFα. Results highlight the functional capacity of *F. vesiculosus* also after the digestion process, allowing the foundation to be laid for the introduction of *F. vesiculosus* into the diet as they ensure that the known functional properties of this alga are maintained even following digestive processes.

P043

Red lentil screening by-product inclusion in rabbit diet: effects in growth traits, meat quality and gut health

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Lentils, widely consumed as part of traditional diet, are well-known for their health-promoting properties. However, their industrial processing generates many by-products, such as red lentil screening (RLS), identified as promising animal feed. A total of 120 male Bianca Italiana breed growing rabbits, aged 42 days, were allotted to three dietary treatments containing different levels of RLS: 0 (RLS0), 5 (RLS5) or 10% (RLS10), respectively, for 6 weeks (4 rabbits/cage). At 84 days, meat, plasma and intestinal samples were collected. The rabbits were housed under identical environmental and sanitary conditions throughout the trial. No medication was included in feed or in drinking water, and rabbits' health status was checked through individual observations. The RLS inclusion showed no adverse effects on growth performance. However, significant differences were found on meat fatty acid profile, where both RLS5 and RLS10 groups showed reduced C18:0 percentage and higher MUFA content owing to an increase in C18:1 n-9; moreover, RLS5 showed a significant increase in C16:1 *trans*. On the other hand, only RLS10 recorded a significant reduction of the PUFA total content due to decreased single unsaturated fatty acid. Dietary RLS significantly decreased serum total cholesterol, LDL and HDL along with an enhancement of serum antioxidant capacity ($p < 0.05$). Rabbit caecal characteristics and microbial population were found to be similar among groups. However, referring to histomorphometric measurements, both RLS5 and RLS10 groups displayed a significant increase in villus height and in an improved villus height to crypt depth ratio ($p < 0.01$). In conclusion, RLS in rabbits diet up to 10% can be considered an effort-effective feeding strategy to modulate rabbit meat fatty acid profile, to enhance endogenous antioxidant capacity, and to im-prove serum lipid profile and intestinal morphology.

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P066

Bioactive compounds from *Silybum marianum* L. and *Cynara cardunculus scolymus* L. improve the well-being of laying hens: preliminary data

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This study was designed to assess the effectiveness of *Silybum marianum* L., and *Cynara scolymus* L. association extract (PHYTO-LAYER™) expressed in silibinin (>2.4g/L), and chlorogenic acid (>2.2g/L) content respectively, provided during 8 weeks (wk) to laying hens raised in enriched cages to improving the liver health and egg quality.
A total of 792 Lohmann LSL-White hens at 41 wk of age, randomly assigned to 2 replicated groups, control (Cr) and treated (Tr), 396 each were used. The PHYTO-LAYER™ treatment (*TRT*) was supplied in drinking water at different time points (T) at a dose of 1 mL/L day, as follows: 1st day (d) of the 41st wk (T0), before the *TRT* administration for 7 d (T1); 14 d of withdrawal period (T2); other 7 d of *TRT* (T3); other 14 d of withdrawal period (T4); other 7 d of *TRT* (T5, end of the trial). At T0, T3 and T5, 13 hens

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per group were sampled for blood analysis, and 60 eggs per group were evaluated for quality parameters. At T5, the same hens were sacrificed for gut and liver weight, gut pH and liver histological evaluations. The body weight (BW) was recorded at different time points, and the mortality daily. One-Way MANOVA followed by Duncan's post hoc test was applied to assess the effects of the *TRT*, time (*t*), and their combination (*TRT-t*), fixing the statistical significance at $p < 0.05$.

Preliminary results showed that the *TRT* reduced the serum ALT ($p < 0.005$), and improved the red blood cell ($p < 0.01$), hematocrit ($p < 0.05$) and haemoglobin levels ($p < 0.005$), with a lower increase in BW in the Tr hens (Cr, 1.67 ± 0.13 kg-BW; Tr, 1.69 ± 0.14 kg-BW, $p < 0.05$). The egg quality (egg, yolk, albumen weight, and thickness) was improved after the *TRT* ($p < 0.001$). However, the Haugh Unit was lower in the Tr group, compared to the Cr ($p < 0.001$). Furthermore, some effects by *t* and *TRT-t* were evidenced ($p < 0.05$). At T5, the Tr hens showed a high pH in the proximal tenue tract ($p < 0.05$), and lower liver weight (Cr, 44.61 ± 6.97 g; Tr, 39.91 ± 3.62 g, $p < 0.05$). Liver steatosis was significantly less severe to absent in Tr hens compared to Cr ($p < 0.05$). No mortality was recorded in both groups.

From these results, the PHYTO-LAYER™ can support the raised-cage laying hens' health at the late production phase, with a positive influence on blood indices and liver health, with an improvement of the egg quality parameters, also important for commercial purposes.

P127

Effect of cannabidiol dietary supplementation on the fatty acid profile of rabbit liver

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Rabbit meat, valued for its exceptional nutritional profile and lower environmental impacts than other livestock species, is gaining renewed recognition as a sustainable alternative to conventional meats. Its production offers a viable solution to meet rising consumer demand for health-conscious and eco-friendly protein sources. Incorporating natural additives, such as phytobiotics, further enhances its appeal by improving both animal welfare and meat quality. Cannabidiol (CBD) is a psycho-inactive phytocannabinoid derived from hemp (*Cannabis sativa*) that shows anti-inflammatory, antioxidant, and stress-relieving effects, thus interesting as a feed additive in animal feeding. This study assessed the impact of CBD dietary supplementation on the lipid content and fatty acid composition of rabbit liver, a key organ in lipid metabolism where the additive's effects were expected to be more pronounced than in other tissues, such as muscle. Forty-two hybrid New Zealand White × California rabbits (21 males, M, 21 females, F) were assigned to two groups at 65 days of age. The control group (CTRL; 10 M, 11 F) received a basal diet, while the CBD group (10 M, 11 F) was supplemented daily with 0.1 mL of hemp extract in coconut-based oil, providing 10 mg of CBD per animal. All rabbits were slaughtered at 92 days of age. Two-way ANOVA (factors: sex (S) and diet (D), with interaction S × D) was performed using SAS/STAT (2021). CBD did not significantly alter the fatty acid family composition in the liver. Nonetheless, quantitatively, saturated and n-6 polyunsaturated fatty acids dominated in both sexes, while monounsaturated fatty acids were lower. This trend was consistent across diets. At the individual fatty acid level, isoC14:0 was influenced by diet ($p = 0.017$), being more present in the CBD livers, and higher palmitoleic acid (C16:1n-7) concentrations were found in the CBD group. The n-6/n-3 ratio was affected by sex, being higher in males, as well as the eicosadienoic acid (C20:2n-6). A significant S × D interaction was noted for C20:0 fatty acid ($p = 0.050$). The values were as follows: F in the CTR group (0.143 g fatty acid/100 g fatty acid methyl esters), M in the CBD group (0.136), F in the CBD group (0.127), and M in the CTR group (0.125). Further research is warranted to explore the potential sex-dependent effects of CBD on lipid metabolism in rabbits and its broader role in enhancing animal welfare and the nutritional quality of rabbit meat as a functional food.

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P151

Larch wood waste: a functional fiber for late gestating and lactating sows

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Larch wood chips or sawdust is a fiber waste product that deserves attention as a functional fiber ingredient. In the first part of the study, the bioactive compounds and antioxidant potential of larch fiber waste from five Italian woodworking companies ($n = 3$ each) were evaluated to verify possible differences in their composition. Hexane, methanol and water extracts were analysed by UPLC-PDA, to quantify the presence of target flavonols (taxifolin, TXF; dihydrokaempferol, DHK), and terpenoids (larixol, LX; larixyl acetate, LXA). The antioxidant activity (expressed as EC_{50}) was determined by the ABTS assay.

In the hexane extract, LX and LXA were quantified up to 15.7 % and 14.50 % w/w $_{dry\ extract}$ respectively, while in the methanol extract, TXF and DHK were present up to 23.20 % and 24.00 % w/w $_{dry\ extract}$, respectively. The water extract had an EC_{50} of 0.012 mg/mL. The second part of the study was a preliminary evaluation of larch fiber supplementation in sows during late gestation and lactation. Twenty sows were randomly divided into two groups (10 sows/group) from 10 days (d) before the expected farrowing until the end of lactation (28 d). The treatments were as follows: Treated (Trt) 4% larch fiber in the basal diet during late gestation and lactation; Control (Ctrl) diet with an appropriate fiber level to ensure the same fiber level in both groups. Blood samples were collected from the jugular vein 10 d before the expected farrowing, within the first 24h after farrowing, and at the end of lactation for metabolic profile evaluation. On the same days, the feces consistency was evaluated from 0 (very hard, dry) to 5 (unshaped and liquid feces), and pH was evaluated in urine and feces. The data were analyzed by a MIXED procedure of SAS for repeated measures, and the faecal scores using the Wilcoxon rank sum test, fixing the significant differences at $p < .05$. The results showed that Trt sows had lower serum ALT ($p < .05$) at the end of lactation (28. 4 vs 40.1 IU/L, SEM 2.2) while GGT tended to be lower at farrowing (18.2 vs 41.4 IU/L, SEM 4.2). Total cholesterol and HDL cholesterol were lower at farrowing ($p < .05$), and urea was lower at the end of lactation (5.16 vs 3.94 mmol/L, SEM 0.03, $p < .05$). The Trt group showed an improvement in faecal scores (3.3 ± 0.2 vs 2.4 ± 0.4, $p < .05$) with lower pH. The study revealed that larch fiber may have some impacts on periparturient sows which deserve to be further investigated.

This study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR)–MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4–D.D. 1032 17/06/2022, CN00000022). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

P282

In vitro two-step evaluation of pineapple, cashew and mango waste for pig nutrition

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Pineapple (*Ananas comosus* L.), cashew (*Anacardium occidentale* L.), and mango (*Mangifera indica* L.) are among the main cultivated plants in tropical and subtropical regions which generate a huge amount of waste during harvesting and processing. At the same time, farmers in these areas face scarcity, feed costs, and provide feeds not competing with humans. The current study, in this context, aims to propose alternative feeds for pigs by cashew, pineapple, and mango fruit by-products characterisation through an *in vitro* two-step (enzymatic and microbial) study to provide feeds not competing with humans and promoting eco-sustainable livestock. To achieve this aim, No. 10 by-products [i.e. pineapple peel and pomace; cashew nut testa, cashew (var. yellow) whole fruit and pomace; cashew (var. red) whole fruit and pomace; mango peel, kernel, and testa] were sampled in republic of Benin. In addition, corn meal, soybean meal, and beet pulp were considered as referenced feed in pig nutrition. The samples were analyzed for proximate chemical composition and *in vitro* two-step digestion method (enzymatic + microbial digestibility). The microbial fermentation was stopped at 48 h for all cashew by-products and corn meal whereas others were stopped at 72 h. The software JMP® (Version 14 SW, SAS Institute Inc., Cary, NC, USA, 1989–2019) was utilised for analyse the data. Digestibility data and *in vitro* fermentation data separately for the two incubation times, were analysed using Student's *t*-test. The result reports a low dry matter (DM) content specifically in the pomace, peel, and whole apple (13.0–27.2 %) while higher lipids were observed for cashew nut testa (26.4 % DM) and mango kernel (11.2 % DM). The by-products investigated fall within the interval of referenced feeds for structural carbohydrates (NDF: 7.6–47.1 % DM) and protein (7.65–51.2 % DM) except mango by-products with low protein content (2.51–4.69 % DM). The total dry matter digestibility, short chain fatty acid, and gas production were low for cashew by-products stopped after 48 h of incubation while the same parameters for other by-products stopped at 72 h were not so far compared to the referenced feeds. Specifically, the results suggest that pineapple pomace, cashew whole apple, pomace, and testa can be considered as feedstuff in fattening pigs, presenting characteristics partially similar to beet pulp. To feed pigs, mango peels and kernels should be combined with a protein feed source, such as soybean meal. However, in the future it will be necessary to investigate the issue of by-product conservation, such as pelleting, to carry out *in vivo* studies and propose using cashew, pineapple, and mango by-products in pig nutrition.

P447

Intestinal microbiota evaluation in finishing pigs fed hazelnut skins

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Dietary polyphenols possess antimicrobial and antioxidant properties and can enhance swine meat quality and gut health by shaping microbiota. Hazelnut skins (HS), a by-product of hazelnut processing, are rich in polyphenols such as flavonoids, phenolic acids, and tannins. Green extraction technologies, such as microwave-assisted subcritical water extraction (MASWE), recover bioactive compounds reducing environmental and energy impacts. The aim of this study was to evaluate HS and HS extracted polyphenols (HSE) effects on small intestine and cecum microbiota composition in finishing pigs. A total of 36 Italian Landrace × Italian Large withe pigs (12 per treatment) balanced per gender and live weight (117.8 ± 11.2 kg), fed with HS (0.6% of feed) or HSE extract (0.1% of feed) were compared to a control group fed a conventional diet. Pigs were selected from 9 pens of 8 subjects each (3 replicates). The HS and HSE diets contained the same amount of total polyphenols. Data deriving from sequencing of the 16S rRNA gene V3-V4 hypervariable region were analyzed through the QIIME2 pipeline and custom R scripts. Microbiota composition and structure were similar between dietary treatments as indicated by the absence of differences in alpha and beta diversity indexes. A total of 402 amplicon sequence variants (ASVs) grouped in 102 species and 68 genera and 37 families, were found in the small intestine while the ASVs in cecum were 729 comprising 140 species, and 106 genera and 42 families. Differential abundance (DA) analysis revealed a few DA genera (|log2 Fold Change| > 1 and adjusted $p < 0.05$) between treatments in cecum, while in the small intestine HS and HSE diets differed significantly from the control. Several species, such as *Prevotella, Alloprevotella, Romboutsia_B, Eubacterium_R*, decreased in HS and HSE diets compared to the control, while others including *Butyricicoccus* and *Faecalibacterium* increased. Some potentially pathogenic genera including *Fusobacterium* and *Erysipelatoclostridium* increased, while others such as *Desulfovibrio*, *Rothia,* and *Actinobacillus* decreased in both HS and HSE diets when compared to control. Moreover, other poorly known bacteria were found to be influenced by diet, requiring further studies. Under the present experimental conditions, the dietary treatment induced a modulation in the intestinal microbiota of finishing pigs, although further studies can allow a better tuning of the treatment timing and dosages.

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P538

Effets of larch wood waste supplementation on fecal microbiota of late gestating and lactating sows

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Larch sawdust is a fiber waste product that deserves attention as a functional fiber ingredient for its bioactive compounds and antioxidant potential. Sows experience challenges during late gestation and lactation, including the important problem of constipation. Adding functional fiber to their diet can help to improve sows' health and possibly change the microbiota community. In a preliminary evaluation, larch fiber was administered in sows during late gestation and lactation to evaluate the possible modification of the intestinal microbiota. Twenty sows were randomly assigned into 2 groups (10 sows/group) from 10 days before the expected farrowing until the end of lactation (28 days). The treatments were as follows: Treated (T) 4% larch fiber in the basal diet during late gestation and the whole lactation period; Control (C) diet with an appropriate fiber level to ensure an isofibrous diet in both groups. At the start and at the end of the trial (days 28), fecal samples from 5 sows of each group were collected in a 50 mL sterile Falcon tube and stored at –80 °C to investigate their fecal microbiota. Bacterial DNA extraction was performed with the QIAamp Fast DNA Stool Mini Kit. The final yield and quality of extracted DNA were determined by using a NanoDrop ND-1000 spectrophotometer and Qubit Fluorometer 1.0. 16S amplification was performed and each PCR reaction was assembled according to Metagenomic Sequencing Library Preparation. Samples were subjected to cluster generation and sequenced on MiSeq platform (Illumina, San Diego, CA) in a 2x250 paired-end format. For each dataset, the matrix of abundances of OTUs were considered. For data analysis and visualisation, differential abundance analysis as well as hierarchical clustering were performed. The results

showed that there were no substantial differences in microbial communities in the treated sows from late gestation to piglets' weaning. However, the fecal microbiota at the end of lactation showed a lower relative abundance of Cyanobacteria and Desulfobacterota phylum in treated sows compared to the control. These results deserve to be further investigated.

This study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR)–MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4–D.D. 1032 17/06/2022, CN00000022). This manuscript reflects only the authors' views and opinions, neither the European Union nor the European Commission can be considered responsible for them.

P119

Exploring the impact of alternative dietary proteins on growth performance, gut health and microbiota in Bianca di Saluzzo chickens

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Population growth and increasing resource consumption make it essential to evaluate and mitigate the environmental impact of animal feed, particularly by reducing soybean meal use due to its considerable ecological footprint. This study examines the effects of completely replacing soybean meal with alternative protein sources in the diet of a slow-growing native chicken breed, focusing on growth performance, intestinal health, and gut microbiota and volatile fatty acids (VFAs) composition. Ninety-six birds were divided into two groups: a control group (C) fed a conventional soybean meal-based diet, and an experimental group (EXP) fed a diet replacing soybean meal completely with protein from field beans, pea protein, sunflower meal, and maize gluten. In terms of growth performance, there were no significant differences between the EXP and C groups. Moreover, regarding intestinal morphology, or organ health, no differences were highlighted between the experimental groups indicating that these alternative proteins support normal growth and gut integrity. However, microbiota analysis revealed notable compositional shifts, with the EXP group showing higher concentrations of *Bacteroides*, *Odoribacter*, and *Prevotellaceae*, while *Christensenellaceae* and *Lactobacillus* were more abundant in the C group. These changes suggest that alternative proteins may promote a microbiota composition that is more favorable for gut health. Regarding fermentation products, VFAs profiles significantly differed between the diets, with higher levels of citric, succinic, and valeric acids observed in the EXP group. These acids are indicative of enhanced microbial fermentation. The results suggest that while alternative proteins alter microbiota and VFAs profiles, they do not negatively impact poultry performance and may enhance gut health and energy metabolism. This underscores the potential of alternative proteins in promoting sustainable poultry nutrition. These findings support the growing demand for environmentally friendly poultry nutrition and provide valuable insights into optimising poultry health and performance through dietary adjustments, further emphasising the viability of alternative proteins in reducing the environmental footprint of poultry farming.

P394

The use of sieve fecal particle separator to evaluate dry matter digestibility in horses

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The present study aimed to evaluate the amount and quality of fecal particle fractions as estimators of dry matter digestibility in horses. Eight healthy mares (11.87 ± 4 years; BCS 5-6; BW 511 ± 60 kg) were fed a hay-based diet (CP 11.6%; NDF 61%; ADL 4.5% DM) at 2% BW for 10 days. After 8 days of adaptation, fecal samples were collected twice daily for 2 days, pooled, and processed. For each pool, a subsample was dried for DM and acid-insoluble ash (AIA) content determination, while another was wet sieved into six fractions (S1-S6, 6.7–0.15 mm mesh). Residues on each sieve were oven dried, weighted and analyzed for uDM content via a 240-hour in vitro fermentation, using a cecal inoculum. Dietary and fecal AIA were used to estimate *in vitro* total tract dry matter digestibility (ttaDMD). Correlations and regression coefficients were performed between ttaDMD and sieve residues; additionally, a REML model was employed to assess the differences in uDM concentration across individual sieves, and a *t*-test was applied to compare the ΣS1-3 and ΣS4-6 mean uDM values. Correlations and regression coefficients between ttaDMD and sieve residues showed weak and not significant positive

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relations of S1, 2 and 3 and negative relation of S4, 5 and 6 residues' amounts, indicating a shift in the relationship between particle size and ttaDMD. Thus, correlations were studied between ΣS1-3 and ΣS4-6 amounts, and ttaDMD. The uDM concentration varied significantly across single sieve ($p = 0.0011$), with higher values for S6. A moderate, significant negative correlation ($r = -0.41$, $p = 0.017$) was found between ΣS4-6 residues and ttaDMD, with better regression coefficients compared to ΣS1-3 ($R^2 = 0.17$ vs. 0.036), suggesting that the occurrence of this particle size range may be more indicative of digestive inefficiency; on the other hand, smaller fecal particles showed higher uDM content, theoretically indicating a deeper digestion if these fractions. These findings highlight the need for further studies to explore whether particle size distribution could serve as a marker of digestive efficiency, as well as the related accuracy.

P192

In vitro and *in vivo* nutrient digestibility of a pig diet enriched with *Yucca schidigera* extract

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Saponins are considered antinutritional factors which impair nutrient absorption. However, lately, it has been demonstrated that they improve performance and health status. In order to better understand their mechanism of action, an *in vitro* and an *in vivo* study were performed to assess the effects of a dietary *Yucca schidigera* extract (YE, 10.8% saponin richness) on the fermentations in the large intestine and the apparent total tract digestibility (ATTD) of nutrients (organic matter, OM; and crude protein, CP) in fattening male and female lean pigs. In the *in vitro* trial, three doses of inclusion of YE were tested (0, 150 and 300 mg/kg of feed). The feed was pre-digested performing a two-phase digestion, and then incubated to simulate the large intestine digestion. In the third phase four samples of cecal content, from two boars and two gilts of 115 kg of body weight (BW), were used as inoculums in 40 bottles (10 per inoculum, of which 3 bottles per treatment and one bottle used as blank). The gas produced (ml/g of incubated dry matter, DM) was measured through the first 10 h. For the in vivo trial, a total of 40 Pietrain × (Landrace × Large White) animals, with 76.1 ± 5.2 kg of BW, were allocated in 20 pens (2 pigs per pen) and randomly distributed in a factorial design 2 × 2, with two sexes (boars and gilts) and two diets (0 mg/kg and 300 mg/kg of YE). The study lasted 42 days and acid-insoluble ash (AIA) was used as internal marker for nutrient digestibility. In the *in vitro* trial YE reduced linearly the cecal pH in males (5.75 vs 5.85; $p < 0.05$), but not the DM digestibility or the gas production ($p > 0.10$). Also, female inoculum reduced the cecal DM digestibility (13.4 vs 23.8; $p < 0.05$) and generated an earlier gas concentration peak than the male one (4 h vs. 6 h of fermentation, $p < 0.05$), with no effect on total gas production. In the *in vivo* trial YE reduced the ATTD of OM (90.2 vs 92.1) and CP (87.7 vs 89.9; $p < 0.05$). In addition, the ATTD of nutrients did not differ between the two sexes. In conclusion, in the *in vitro* trial, dietary YE increased the acidity in the male cecal contents but did not alter the fermentation process that occur in large intestine. However, in the *in vivo* trial, the YE diet reduced the ATTD of OM and CP. The sex affected the fermentation pattern in the *in vitro* study, and females showed a lower cecal DM digestibility, while the ATTD of nutrients resulting from the *in vivo* trial was similar in both sexes.

PHYSIOLOGY AND REPRODUCTION

P449

Heat stress impacts metabolism and milk quality of Ragusano donkey

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Ragusano donkey is a Sicily native breed and is actually classified at risk of extinction. Hence, evaluating the relationship between heat stress and metabolism of lactating donkeys represent an opportunity for implementing management strategies. Ten mid-lactating Ragusano donkeys (age: 13 ± 5; parity: 6.3 ± 3.6; days in milking: 102.7 ± 49.7 d) were monitored between June and October 2024 (Asilat, Giarre, Sicily, Italy). Milk and blood samples were collected every 3 weeks. Ambient temperature and relative humidity to calculate the Temperature Humidity Index (THI) were recorded every 15 min by a probe installed in the barn where the donkeys were housed. THI classes were established to compare milk and blood data at different THI values. All data were subjected to PRINCOMP and GLIMMIX procedures of SAS for the principal component analysis (PCA) and for the analysis of variance, respectively. From the PCA, metabolism and milk quality significantly differed between THI values below 68 and THI values above 68. Thus, the GLIMMIX model included as fixed effect the classes of THI: THI >68 (TH-H) and THI <68 (THI-L). Overall, at

THI-H there were greater ($p < 0.05$) levels of milk urea (43.65 vs. 29.94 mg/dL) and somatic cells count (75.7 vs. 14.7 x103/mL) than THI-L. Serum data showed that at THI-H there were greater ($p < 0.05$) urea (14.29 vs. 11.36 mg/dL), GGT (43.95 vs. 34.71 UI/L), and magnesium (1.72 vs. 1.49 mg/dL), while there were lower ($p < 0.05$) glycemia (40.76 vs. 71 mg/dL), triglycerides (28.33 vs. 46.64 mg/dL), cholesterol (51.67 vs. 63.64 mg/L), lipase (44.19 vs. 66.07 UI/L), albumin (2.14 vs. 3.19 g/dL), albumin-to-globulin ratio (0.75 vs. 0.83), calcium, chloride, and phosphorus than THI-L. Donkeys at THI-H had lower ($p < 0.05$) white blood cells (5.06 vs. 4.58 x103/µL), lymphocytes (4.38 vs. 3.99 x103/µL), and hemoglobin (10.62 vs. 9.68 g/dL) than THI-L. These preliminary findings indicate that higher temperature-humidity index (THI) values adversely affect milk quality and blood chemistry, suggesting that heat stress negatively impact energy, protein, and mineral metabolism together with liver functionality and immunity. This research therefore emphasises the usefulness, even for low-yielding and notoriously hardy and resistant species such as the donkey, of THI monitoring for the implementation of appropriate zootechnical management strategies to mitigate heat stress and improve metabolic well-being.

P089

Quality control in boar semen production

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The boar Semen Production Centre (SPC) of the National Pig Breeders Association (ANAS) makes it possible to enhance the association's genetic selection activities through the production and dissemination of doses of the best boars. Therefore, it is essential to manage the SPC with maximum efficiency in terms of both the quantity and quality of the doses produced. To this end, statistical quality control (SQC) techniques represent valuable tools at various levels of the production chain. Once the production target was defined in terms of refrigerated boar semen doses (80 mL volume with 1.7 billion sperm), the following steps were taken: stability of the production process, evaluation of the reproducibility of analytical measurements, and documentation of the qualitative attributes of the doses. The main critical point was the qualitative evaluation of semen (before and after dilution); therefore, the CASA system (CEROS Hamilton Thorne USA) was optimised in terms of settings for motility and morphology, while concentration was done with a more accurate and precise spectrophotometer specifically calibrated ($R^2 = 0.97$; $p < 0.001$), with verification of measurement reproducibility (using only two cuvettes to eliminate the operator effect; $p < 0.001$). It has been verified, via DIC microscopy, that the most reliable parameter for evaluating morphology with CASA was the percentage of intact spermatozoa. Process control was implemented through daily lot sampling (at least 5), with concentration evaluated using the CASA (which for diluted semen was more accurate and precise than the spectrophotometer). The stability of the production process was carried out through average control charts. The characterisation of the qualitative attributes of the doses was done by verifying the preservability up to four days (via CASA motility). The experiment lasted eight weeks (44 batches with 41 boars) and a mixed general linear model was used, which included the boar random effect, and the following fixed effects: day (1–4), operator (1,2) and season (summer vs fall). The doses on the fourth day of storage were similar to those on the first day (with an estimated decrease in motility of 5.3 with SE = 0.8), and the operator effect was not significant ($X^2 = 1.69$; $p = 0.1933$). The reproducibility of the concentration was tested because the 4 days of conservation represent 4 measurements for the same lot: the operator and the day of analysis showed significant ($p = 0.032$ and $p = 0.002$) but very low effects. In conclusion, the use of SQC allows the monitoring and optimisation of an SPC and the production of the maximum number of doses with high quality.

P094

Feasibility of using frozen semen in rabbit breeding

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Thanks to their high feed conversion rate, rabbits represent an important species for meeting the nutritional needs of the growing global population. This has led to a demand for breeding programs focused on improving genetic selection, primarily for prolificacy and meat quality. To this end, the development of cryopreservation protocols for semen from selected males would simplify the introduction of new genetics into farms and facilitate the creation of cryobanks for genetic preservation. The objectives of this study included: the development of a cryopreservation protocol starting from refrigerated semen and the establishment of a cryobank aimed at preserving genetics of interest. The samples used were pools consisting of semen from five mature male breeders of two female genetic lines raised at the Martini Genetic Centre. These animals were housed in cages at an ambient temperature of approximately 22.5 °C and subjected to a photoperiod of 8 hours of darkness alternating with 16 hours of light. Sperm was collected by an artificial vagina, diluted at a ratio of 1:6 with Galap extender (IMV, France), refrigerated at 5 °C, and

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transported to the laboratory within three hours. The samples were analysed for total motility (TM) using a CASA system (IVOSII Hamilton Thorne, USA) and membrane integrity (MI) using a Nucleocounter SP100 (Chemometec, Denmark). Pools deemed suitable for cryopreservation, with TM >60%, were further diluted 1:1 with Galap extender supplemented with 0.1 M sucrose and 16% DMSO, equilibrated at 4 °C for 45 minutes, packaged in mini straws 0,25 ml and frozen using a programmable freezer (Micro-Digitcool, IMV). After thawing at 42 °C for 20 seconds in a thermostatic water bath and incubation at 37 °C for 15 minutes, the semen was evaluated for concentration (CONC), TM, and MI to calculate the number of viable sperm per straw (NSV), calculated as CONC × the lowest value between TM and MI/100.The protocol was artificial insemination(AI) tested using five pools of semen with an average NSV of 2.8 × 10^6 per straw (min 0.63, max 9.07) on 37 synchronised females. Pregnancy diagnosis revealed that 33 females (80%) were pregnant, 32 of which completed gestation. A total of 329 offspring were born, of which 318 were live births (an average of 9.93 live births per doe). Given these results, which were comparable to those obtained in farms using refrigerated semen, the creation of the cryobank was initiated. To date, the cryobank consists of 5,700 straws belonging to 23 pools.

P289

Lipid profile in chicken sperm of Italian chicken breeds

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Lipids are a basic component of sperm, involved in its highly specialised membrane structure and functions. Sperm lipid composition is species-specific and differences have been also reported among poultry breeds or strains. The aim of the present study was to characterise sperm lipids and quality in 5 Italian chicken breeds: Bionda piemontese (BP), Bianca di Saluzzo (BS), Mericanel della Brianza (MB), Pepoi (Pe), Robusta maculata (RM). Birds were housed in individual cages in controlled environment and fed *ad libitum* a standard chicken breeder diet and fresh drinking water. Ejaculates were routinely collected twice per week and the following quality parameters were assessed: volume, concentration, sperm membrane integrity and motility parameters (CASA). Pooled semen samples were centrifuged to separate sperm pellets, then stored at -20 °C until lipid analyses. After total lipid extraction, major lipid classes were fractionated by thin-layer chromatography on silica gel and fatty acid (FA) composition of phospholipid (PL) was determined by gas-chromatography; free cholesterol was assessed by colorimetric kit. Sperm membrane integrity (range 75–92%) and sperm motility (range 78–98%) did not show significant variability between breeds. In contrast, significant breed differences were found in progressive motility and the majority of kinetic parameters. RM and BP sperm were characterised by the highest and lowest values, respectively, in progressive motility (40.3% vs 22.3%, $p < 0.05$), linearity (49.0% vs 29.2%, $p < 0.001$) and straightness (68.3% vs 52.9%, $p < 0.001$). Variability in sperm lipid components was also found in the same breeds. RM sperm showed the lowest total lipid content (182 µg/10^9 sperm), significantly lower compared to all other breeds, and a significant higher proportion of phospholipid (46%) compared to BP sperm (33%); as a consequence, the free cholesterol/phospholipids ratio was significantly lower in RM sperm (0.52) compared to BP sperm (1.00). Furthermore, PL-FA composition of RM and BP sperm showed significant differences in total saturated fatty acids (RM 58% *vs* BP 69%, $p < 0.05$), n-6 polyunsaturates (RM 34% *vs* BP 14%, $p < 0.001$) and n-3 polyunsaturates (RM 0.84% *vs* BP 5.81%, $p < 0.001$). In conclusion, a peculiar association between quality and lipid components in sperm of Italian chicken breeds was found. Sperm biological differences between breeds may contribute to improve reproductive and conservation strategies.

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P503

Relationship between residual energy intake in Holstein calves, their performance, and milk yield during the first lactation

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Dairy cattle systems aim to enhance feed efficiency by selecting animals that convert less feed into more products. While residual feed intake (RFI) is the primary metric for selection, studies typically focus on growing heifers and lactating cows, neglecting pre-weaning efficiency's impact on profitability and subsequent milk production. This study explored the relationship between residual energy intake (REI) in pre-weaned dairy calves and their milk performance in first lactation. Twenty-one Holstein female

calves were housed individually, fed milk replacer (MR) and *ad libitum* starter, and weaned at 60 d. Feed intake was recorded until 70 d, and body weight (BW) measured until 160 d. Blood samples were collected until 70 d. During their first lactation, daily milk yield for the first 100 d was recorded. Retrospectively on pre-weaning calves, predicted energy intake was calculated based on metabolizable energy of the MR and starter intake (Mcal/kg), and REI coefficients were derived as residuals from a regression model regressing the average energy intake (MR + starter) on average ADG and mid-test metabolic BW (28 d of age). Thus, calves were categorised into high-efficient (HI, $n = 11$; negative REI residues) and low-efficient (LOW, $n = 10$; positive REI residues) groups. The mean REI was −0.12 Mcal/d for HI and 0.13 Mcal/d for LOW. Data were analyzed using repeated measures (PROC GLIMMIX, SAS). No difference in milk intake was observed between groups, but the HI group had lower starter intake (1.65 vs. 1.97 kg DM/d for HI and LOW, respectively; $p < 0.01$). At weaning, BW was similar (81.4 vs. 84.1 kg for HI and LOW; respectively), but the LOW group had a higher BW at 160 d (186 vs. 177 kg for LOW and HI, respectively; $p < 0.1$). The LOW group also showed higher ADG between 60 and 70 d (1.36 vs. 1.13 kg/d for LOW and HI, respectively; $p < 0.05$) and higher plasma urea levels at 60 and 70 d, indicating greater protein intake ($p < 0.05$). During the first 100 days of lactation, HI cows produced less milk than LOW cows (35.8 vs. 37.6 kg/d for HI and LOW, respectively; $p < 0.01$). The use of Residual Energy Intake (REI) is not a valid system for evaluating calf performance, as it heavily penalises higher starter intake levels, which instead represents a crucial factor that influences both the calves' development during early stages and the productive performance of the future dairy cow.

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P179

Conception influences reproductive dynamics and lactation characteristics in primiparous Mediterranean buffalo

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The age at first calving (AFC) is a pivotal parameter in dairy herd management, directly affecting feeding costs, genetic progress, and farm profitability. In recent years, advancements in reproductive strategies have aimed to optimise AFC in Italian buffalo herds. This study evaluates how AFC influences reproductive dynamics and lactation characteristics in primiparous Mediterranean buffaloes, using 362,703 first-lactation test-day records from 50,661 buffaloes across 115 herds collected between 2013 and 2023. Milk yield data were used to monitor lactation dynamics on an individual basis, allowing for the identification of peak milk production. Reproductive traits analyzed included calving interval (CI), days open (DO), and days to peak milk production (DMP), which were calculated based on the calving date. A repeated mixed linear model was applied to assess the effects of AFC, accounting for days in milk, calving year, season, and their interactions. Results indicated a significant reduction in AFC (from 36 to 35 months), CI (from 460 to 435 days), and DO (from 150 to 125 days) from 2013 to 2023. Buffaloes that calved between 34 and 37 months exhibited the most favorable CI and DO values. While DMP remained stable across AFC categories ($p > 0.05$), it varied significantly across seasons, reaching the lowest values in spring ($p < 0.01$). As expected, buffaloes calving in winter and spring showed significantly longer CI and DO compared to those calving in summer or autumn ($p < 0.01$). Younger heifers calving in winter exhibited significantly higher DO than older buffaloes calving during the same period ($p = 0.01$). Conversely, older buffaloes calving in summer tended to have longer CI and extended DO compared to their younger counterparts. These findings underscore the critical role of seasonally targeted reproductive management strategies to optimise reproductive outcomes in buffalo herds. Primiparous buffaloes calving at an optimal AFC of 34–35 months achieved the best balance of CI, DO, and overall reproductive performance across seasons.

PRECISION FARMING

P131

Virtual Fencing learning retention in dairy cows after 3 months of non-use

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Virtual Fencing (VF) is an innovative technology for grazing management which relies on GPS-based collars to track and control the animals. Collars emit a paired stimulus sequence (i.e. an acoustic warning (AT) of increasing pitch, followed, if necessary,

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by an electrical pulse (EI)) to confine animals within pre-set virtual boundaries. VF can provide several benefits to farmers: (a) reduce the labor for installing and maintaining physical fences; (b) improve system efficiency by promoting rotational grazing; (c) offer higher flexibility to remotely modify fences at any time. It has been shown that animals learn the system within 2 to 4 days. However, it is unclear whether they can retain this learning after a period of non-use. A mixed dairy herd consisting of Grigia Alpina ($n = 14$), Pezzata Rossa ($n = 3$), and Jersey ($n = 4$) lactating cows was managed with VF collars on a lowland pasture for 11 days as learning period (L), changing virtual boundaries daily. The animals were then moved to a mountain pasture for 3 months without using VF. This was followed by a VF re-learning period (RL) of 11 days, following the same scheme of L period. The study aimed to evaluate the retention of the learning capacity of the animals by assessing the differences in the emission of AT and EI between the two periods (L vs. RL). Data were analyzed using generalised mixed-effects models. Results showed that the total number of both AT and EI was significantly higher ($p < 0.01$) in L than in RL. The EI released during L showed a decreasing trend, whereas in RL they were constant since day 1. This resulted in a significantly higher probability ($p < 0.001$) of receiving an EI during the first 6 days of L compared to RL. In conclusion, the results demonstrated that animals could retain learning after a period of non-use. This enables farmers to avoid the training phase whenever collars are worn again by the same animals. VF provides farmers with an off-the-shelf management system characterised by higher flexibility in choosing the extension of each allotted pasture area which can be quickly modified as biomass availability changes. VF can also promote the practice of rotational grazing in those situations where the workload of moving physical fencing is not affordable by farmers. These characteristics can be very useful during seasonal grazing, where biomass availability, pasture surfaces, and overall herd management can vary largely over time and staff availability is often a limiting factor.

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P083

Variations in individual feed intake predicted by a 3D accelerometer in dairy cows

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A 3D accelerometer is a promising tool for the automated monitoring of feeding behavior and feed intake in dairy cows, offering significant potential to improve farm management and support selective breeding for efficiency and sustainability in dairy farming. This study aimed to explore the 3D accelerometer-based neck collar (AfiCollar, Kibbutz Afikim, Afimilk, Israel) to predict individual dry matter intake (DMI, kg DM/d) and evaluate potential sources of variation. The study was conducted on 1,295 Holstein cows housed in four commercial farms across Lombardy, Emilia-Romagna, and Tuscany (Italy) from September 2023 to October 2024. Predicted DMI data were obtained for all cows, resulting in 44,074 records. The average (± SD) weekly DMI was 24.03 ± 5.74 kg DM/d. To validate the method, the individual DMI values (x; DIM >284 d) from one farm were regressed with the DMI predictions (y) based on the net energy requirement for maintenance and milk yield and the net energy contents of the rations computed according to the National Academies of Sciences, Engineering, and Medicine (NASEM, 2022), with good results: y= 0.985x; $R^2 = 0.987$ Climatic data for the study period were sourced from NASA POWER. Statistical analyses were performed using generalised additive mixed models (GAMMs) with integrated smoothness estimation, implemented via the mgcv package in R. A GAMM with repeated measurements was used to assess the effects of daily mean temperature-humidity index (THI) and heat stress conditions, with restricted maximum likelihood (REML) estimation. Fixed effects included days in milk (DIM), parity, season, and farm. Least squares means of DMI across DIM, parity, and season were consistent with expected physiological patterns. Specifically, DMI began at low values (~18 kg DM/d) immediately after calving, increased until the peak of lactation (~26 kg DM/d), and progressively declined until the next calving. As expected, the season effect was a significant source of variation, with the lowest DMI observed in summer compared to winter. These findings highlight the potential of 3D collar-based sensors for accurate DMI monitoring, offering a valuable tool for enhancing farm management and supporting data-driven decision-making in dairy farming.

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P268

Adaptation and growth performance of buffalo calves in an automatic feeding system with individual pens

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This study evaluated the adaptation, functionality, and efficiency of an automatic milk feeder (AMF) system for buffalo calves during the pre-weaning period. On a Mediterranean dairy buffalo farm, fifty-three female calves, aged 4 days, were housed in straw-bedded individual pens that allowed visual, auditory, and limited physical interaction with neighboring calves. Calves were introduced without prior feeding training, relying on social learning from older neighboring calves. A robotic arm delivered freshly prepared milk to each pen four times daily at six-hour intervals, adjusted according to the calf's age. Eighteen pens were monitored daily over a pre-set 40-day pre-weaning period or until the calves' body weight exceeded 80 kg, across three consecutive pre-weaning cycles per pen. Data on feeding behavior, milk intake, and health status were collected daily using AMF management software and visual examination. Growth performance was assessed by weight gain. All data were analyzed using descriptive statistics and regression analysis. No major health problems or mortalities occurred during the study, with clinical signs observed on only 4.44% of the observation days. Calves showed a high rate of adaptation to the AMF, with 73.3% of feeds accepted in the first 72 hours. Refusal rates decreased progressively, and by the end of the pre-weaning period, 80.8% of offered feeds were consumed. Daily feeding frequency averaged 3.02 sessions per calf, with an average milk intake of 6.65 ± 1.14 L/day, supporting optimal growth rates (average daily gain 1.0 ± 0.06 kg/day). The average suckling rate (0.31 ± 0.04 L/min) and feeding duration (6.82 ± 1.35 min/meal) were consistent with natural feeding behavior observed in buffalo and cattle calves. The AMF system facilitated labor efficiency, operating for an average of 18 hours per calf, with estimated electricity costs of €11.70 per calf. Results indicate that the AMFs based on individual pen allotment may be a viable solution for buffalo calf rearing, promoting efficient feeding, reducing labor demands, and supporting calf health and growth. Future research should focus on optimising feeding schedules and milk allowances specific to the developmental stages of buffalo calves and evaluating the long-term impacts on heifer productivity and welfare.

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P370

Effect of fertiliser variable rate control on quality of wheat forage

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In agricultural and livestock production there is more and more talk about environmental sustainability, efficient use of natural resources and reduction of pollutant emissions. To enhance the efficiency and sustainability of nitrogen (N) fertilisation with precision agriculture, considering spatial and temporal variability, a comparison of different wheat fertilisation strategies was conducted on a cereal farm in the Po Plain, on shallow and loam-sandy soil. A wheat field (cv. Bandera) of adequate size and variability was selected and divided in 12 plots (15 × 100 m), where alternatively was applied N fertiliser to fix (FR) and variable (VR) rate, respectively. Physical and chemical characteristics of the soil were mapped, and vegetation indices were monitored through remote (ViGIS digital platform, Pioneer Hi-Bred Italia Srl) and proximal sensing (Maia M2 multispectral camera). The prescription map was obtained based on NDRE index measured at wheat stem elongation. An average of 128 kg/ha of N was distributed for both FR and VR thesis using a spreader with electronic control (Sulky x40+). The wheat forage production and quality and its suitability for ensiling were evaluated at the milk-dough ripeness stage by means of the following parameters (NIRS Dairyland Lab Inc): biomass (t/ha and t DM/ha), dry matter (DM), crude fibre (CF), neutral detergent fibre (a-NDF), acid detergent fibre (ADF), acid detergent lignin (ADL), NDF digestibility, nonfibrous carbohydrates (NFC), starch (ST), soluble carbohydrates (WSC), crude (CP) and soluble proteins (SP), total nitrogen (TN), non-protein nitrogen (NPN), ether extract (EE), crude ash (CA), biogas (BP) and methane potential (MP), and net

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energy (NE Mcal/kg). The relative forage quality (RFQ) index and the biomass production on N fertiliser (t DM/ha / kg N/ha) were calculated. Collected data were analysed by GLM ANOVA procedure (IBM SPSS Statistics 28.0). FR showed higher DM, SP, NFC, ST, and WSC than VR ($p < 0.01$), but VR showed higher CP, aNDF, NDF digestibility and BP than FR ($p < 0.01$). These differences lead to a higher RFQ of the wheat forage obtained from RV than FR ($p < 0.05$), with a higher biomass production and efficiency in N utilisation. In conclusion, with the same overall N rate, but with a more accurate distribution of the macronutrient within the field in accordance with the crop nutritional status, the N variable rate fertilisation technique can improve the quality of the forage.

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P484

Use of remote images for natural pasture biomass prediction in sheep pre-grazing

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Precision Livestock Farming (PLF) applications, such as the estimation of biomass pasture by Normalised Difference Vegetation Index (NDVI) using unmanned aerial vehicles (UAVs), ena-ble farmers to collect objective and continuous data. For assessing the biomass of natural pastures in sheep pregrazing, the aims of this study were:(i) compare and evaluate two assessment methods (field sampling vs NDVI index), (ii) develop an equation using NDVI index, and the green biomass production from individual plots. The trials were conducted in the CREA-ZA farm's natural pasture (1.7 ha) in October and November 2024. Field surveys and drone remote sensing reliefs were performed three times, and both were done on the same day. Field sampling provided 231 biomass data points, then used to develop a model. The productive characteristics of the natural pasture were measured using an integrated DroneGisGPS (DGP) technique, and a drone equipped with a multispectral camera. The estimation method of biomass (kg DM ha-1) by UAV included the following steps: extraction of pasture geospatial reflectance with UAV mounted sensor; calculation of NDVI from pasture reflectance data; development of calibration equation to convert NDVI values to kg DM ha-1 of pasture. The correlation coefficient and significance of the Bonferroni test between NDVI and green biomass data were calculated. The effect of the sampling period was assessed using the ANOVA procedure, and the means were compared with the Tukey test. The field sampling was labour-intensive but provided accurate vegetation data, while the NDVI method was more effective for large-scale vegetation monitoring. The results indicated that the ideal flight altitude is 70 m above the ground, which provided a maximum ground resolution of 5 × 5 cm, optimal for identifying variations in the vegetative characteristics. NDVI data collected during three periods for each plot were positively correlated with the respective measurements of green biomass production ($r = 0.51$; $p < 0.001$; $n = 231$). Significantly higher NDVI and green biomass yields were observed in November than in October ($p < 0.01$). During the survey periods, an interesting exponential equation was derived that relates NDVI to the green biomass measured per unit of surface area. Although extending the surveys to a longer observation period is necessary, the use of UAVs and information technologies appears to be a useful tool for estimating a natural pasture's green biomass.

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P507

Use of Infrared thermography to monitor calf health and welfare

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Infrared thermography (IRT) has shown potential as a non-invasive tool for detecting pathological states in animals. However, its application to identify enteric diseases remains poorly understood. Developing reliable and non-invasive indicators is crucial to improving early diagnosis and promoting calf health and welfare, especially in intensive farming systems. This study aimed to evaluate whether lacrimal caruncle temperature, measured via IRT, could serve as an indicator of the onset of enteric pathologies in dairy calves. A total of 22 Holstein-Friesian calves from 2 dairy farms in Northern Italy were included. At either 7 or 21 days of age, each calf underwent a comprehensive clinical examination, including fecal scoring and temperature measurement. Infrared thermographic images (at least 3) were captured for both eyes using a FLIR Thermal Camera, and the hottest point within the lacrimal caruncle area was recorded. The mean temperature value was calculated for each eye (left and right). Eleven calves showing clinical signs of enteric disease (based on fecal

consistency) were compared to 11 clinically healthy calves, defined as having a negative fecal score and no fever, sampled during the same period. Kruskal-Wallis tests and two-way ANOVA were conducted to analyze the effects of health status (healthy/sick), fever (present/absent), and side (left/right). No significant differences in lacrimal caruncle temperature were found based on health status ($p = 0.347$) or fever ($p = 0.473$). Similarly, ANOVA revealed no significant effects of health status ($F(1, 40) = 0.349$), side ($F(1, 40) = 0.660$), or their interaction ($F(1, 40) = 1.747$). These findings suggest that lacrimal caruncle temperature alone is insufficient as an indicator of enteric pathologies in calves. Possible reasons include the variability in thermal response or the limited sensitivity of this anatomical site to enteric conditions. Future research should explore alternative anatomical sites that might exhibit more pronounced thermal changes and assess how etiological agents and disease severity influence body temperature dynamics. Additionally, incorporating larger sample sizes and diverse environmental conditions could help refine the application of IRT in the diagnosis of calf diseases.

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P529

InnovaRe: exploring innovative phenotyping for a smarter flock

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The InnovaRe Project aims to introduce cutting-edge tools and methodologies to enhance the sustainability and resilience of ruminant production systems, with a particular focus on less developed contexts, such as sheep farming. By integrating advanced animal monitoring technologies—like satellite collars and sensors for detecting physiological, behavioral, and environmental parameters—the project seeks to optimise the selection of animals with superior adaptability to environmental and management challenges. Satellite collars play a pivotal role by providing real-time geolocation data, enabling continuous tracking of grazing patterns, movement behaviors, and environmental conditions. By monitoring space-time usage patterns, such as pasture utilisation and mobility, the collars also improve resource management and grazing system optimisation, reducing the environmental impact of livestock farming. InnovaRe focuses on identifying phenotypic traits like climate resilience, resource use efficiency, and metabolic health—key factors for the long-term sustainability of sheep and goat farming. The project will study three local sheep breeds from Sicily—Comisana, Pinzirita, and Valle del Belice still managed through extensive or semi-extensive farming systems. The breeds will be monitored for at least two months during grazing periods, with data on behavior, movement, and environmental interactions. Real-time data collection on feeding behavior, activity levels, and well-being supports personalised and efficient management, leading to improved flock performance. By optimising the use of natural resources such as forage and water, and minimising greenhouse gas emissions from farming practices, InnovaRe promotes a more sustainable and eco-friendly livestock sector. Additionally, continuous health and performance monitoring using satellite collars and sensor technologies facilitates timely interventions, enhancing disease resistance and productivity. By integrating satellite collars with precision livestock monitoring, the project addresses challenges posed by climate variability and resource constraints, creating a data-driven foundation for the future of sustainable livestock production.

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P542

Exploring novel phenotypes in cattle within extensive farming systems: the InnovaRe project

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The InnovaRe Project aims to enhance livestock farming sustainability and resilience by developing novel phenotypes and advanced monitoring technologies. A key focus is on extensive cattle farming systems, where sensor technologies are traditionally absent. The project addresses challenges such as vast landscapes, variable climates, and resource limitations by introducing tools designed for these environments. The main objective is to provide novel phenotypes to understand critical traits for sustainability in extensive farming, such as climate resilience, resource-use efficiency, and metabolic health. The project will study two local cattle breeds from Sicily—Cinisara and Modicana—still managed through extensive or semi-extensive farming systems. The breeds will be monitored for at least two months during grazing periods, with data on behaviour, movement, and environmental interactions recorded in at least 120 individuals. Genotyping will assess their ancestry to allow factoring in the potential introgression with cosmopolitan breeds in the behavioural metrics. Data will be gathered using wearable collars and multi-sensor platforms. New sensors will be developed to work in field conditions, ensuring durability, accuracy, and energy efficiency. Collars will provide real-time geolocation data, enabling continuous monitoring of grazing patterns, movement, and environmental conditions, helping optimise grazing, improve herd management, and reduce environmental impacts such as overgrazing. Differential performances in rumination, observed through sensors, will be further explored via ruminal fluid analysis, offering insights into metabolic processes and cattle health. By integrating precision monitoring into extensive farming, the project facilitates tailored management strategies, improving productivity and animal welfare. Real-time insights into feeding behaviour, activity levels, and well-being allow for adaptive management suited to the unique demands of extensive systems. The project also aims to reduce the environmental footprint of cattle farming by promoting efficient use of resources like forage and water, and minimising greenhouse gas emissions. Continuous monitoring enables timely interventions, enhancing disease resistance and productivity. The InnovaRe Project bridges the gap between extensive farming systems and modern precision livestock technologies to tackle the challenges posed by climate variability and resource scarcity, advancing sustainable cattle farming practices. Research supported by the 'Centro Nazionale – CN00000022 – Agritech' CUP: J83C22000830005, 'InnovaRe (Ricerca e applicazione di strumenti innovativi per migliorare la resilienza nei ruminanti)' grant.

P564

Across breeds variability of resilience indicators based on daily automatic milking system data

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For dairy cattle, resilience can be defined as the ability of a cow to address environmental stressors. Indexes of resilience are often based on data-driven approaches including daily precision livestock farming (PLF) activity data and/or longitudinal milk records. A dairy cow is considered resilient, whether it is either unaffected by stressors or when quickly recovers after the temporary instability. Cows with less fluctuating production are likely less affected by environmental disturbances. Phenotypic and genetic individual variation were reported for these kinds of resilience indicators. The aim of this study was to test a phenotypic indicator of resilience based on quantification of the fluctuations of models' residuals from the lactation curves fitted on automatic milking system (AMS) daily records. The raw data were

provided by AIA and included about 50 million data points on 22573 cows in 82 dairy farms. The cows with at least 1500 datapoints were selected for this study. After quality control 9477 lactations of 5188 cows (3.5 million daily records) from parity <3 born from 2010 to 2021 of 4 breed were selected: Italian Holstein, Brown, Simmental and Jersey. Respectively, 4597, 3229 and 1641 first, second and third lactations were considered across breeds. For each individual lactation both the Wood function and the fourth order Legendre polynomial were fitted. The residuals of the actual yield vs the predicted curves were used to study perturbance and to compute a resilience indexes: the natural logarithm-transformed variance (LnVar). The correlation between Wood coefficients and LnVar were also analyzed. Across breed (and parity) differences in the LnVar phenotypic variation were observed. Correlations between individual Wood curve parameters were significantly different from zero. This study evaluated the LnVar resilience indicator from longitudinal milk yield records, confirming the value of PLF data for assessing cows' ability to cope with environmental disturbances.

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P571

APPàre, sensors and software in decision support systems for the Sardinian dairy sheep farmers

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The lack of digital tools and infrastructure limits innovation and management improvements in the sheep farms. The PNRR e.INS project 'Innovation Ecosystem for Next Generation Sardinia' involves farms and milk to cheese processors working in the dairy sheep sector. As part of the project, SPOKE03: 'APPàre: smart and secure applications in the livestock sector to promote digital innovation along the food chain', aims to boost data-driven innovation through the implementation of a digital information platform, to transfer and improve the technical knowledge and skills in the supply chain employers. The aim of this work was to evaluate the use of data, from sensors and software, as input for decision making tools developed within the APPàre platform. The data were collected at the experimental barn of the University of Sassari. For this purpose, 40 dairy ewes were monitored by collecting daily intake data through the Biocontrol software (Biocontrol AS, Rakkestad Norway) and milk production data twice daily through the Afimilk software (AFIMILK® System). All the data were uploaded into the platform to implement the platform and to test its operation by returning outputs. The variability of intake, the milk yield and the feed efficiency of dairy ewes were considered among the outputs. Values of these variables were:1.636 kg, 1.123 kg and 0.73, for dry matter intake, milk yield and feed efficiency, respectively. Data visualisation from collected records showed that farm inputs can help decisions making of farmer to identify the best performing ewes to be selected for replacement of less efficient ewes with individually selected lambs. Collected record from these instruments and sensors might support phenotyping of dairy sheep flocks especially in relation to nutritional intake and feed efficiency. The APPàre platform is powered using sensors that specifically aim to facilitate the data storage and analysis, related to feed efficiency, milk and meat productivity, and farm incomes to promote productivity and efficiency on dairy sheep farms in Sardinia.

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P324

Using smart collars to assess heat stress impacts on dairy cows

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The Mediterranean region is a climate change hotspot, where rising temperatures and increased frequency of heat waves negatively impact animal welfare and performance. Sensor technologies are increasingly adopted in dairy farming to monitor cow behavior and activity, providing valuable insights into animal welfare under heat stress conditions. Collar-based activity sensors are widely used to measure behaviors such as ruminating, eating, and panting. These sensors incorporate accelerometers that continuously record and transmit data with variable timing, according to manufacturing features. The continuous monitoring enables daily overviews of animal welfare, with the data analyzed to estimate the time allocated to each detected behavior over defined periods. Such information offers critical insights into stress levels, particularly during episodes of heat stress. This study aimed to investigate changes in daily behavior of dairy cows under varying heat stress conditions. The experiment was conducted during the summer of 2024 at the Centre for

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Agri-environmental Research 'Enrico Avanzi' (CIRAA) of the University of Pisa. Fifty lactating cows were equipped with activity-monitoring collars (AfiCollar, Kibbutz Afikim, Afimilk, Israel), and a weather station was installed in the barn to measure air temperature, humidity, and black globe temperature. Two heat stress indices were calculated using these parameters: the Temperature-Humidity Index (THI) and the Black Globe-Humidity Index (BGHI). Data analysis revealed clear behavioral patterns, including two peaks in eating behavior corresponding to the distribution of the total mixed ration. These peaks were followed by an increase in ruminating behavior. The rise in both THI and BGHI was associated with a significant increase of panting behavior during the hottest hours of the day and a reduction in feeding activity, high-lighting the effectiveness of collars to identify heat stress conditions. The findings highlight the importance of sensor implemented into collars aimed to monitor animal-based welfare parameters.

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P344

Study of alpine pasture exploitation by coupling GPS trackers and accelerometers

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Mountain livestock and grazing provide services for the community as maintenance of the landscape, conservation of biodiversity, and protection of resources. They also offer excellent opportunities to enhance cow welfare through natural feeding, extensive freedom of movement, and engagement in species-specific behaviours. Furthermore, mountain grazing allows the production of high-quality food. In this study, 20 milking cows from different breeders were monitored for two months during their summer stay in high mountain pasture. The study was conducted in a 200 ha fenceless alpine pasture near Madesimo (Lombardy, Italy), located at altitudes between 1850 and 2050 meters. This pasture area is recognised for its naturalistic importance, being characterised by a mosaic of calcareous, acidic soils and peatlands, resulting in highly diverse pastures (limestone and lush pastures, and four types of Nardus grassland) and complex soil-vegetation patterns. The milk produced by cows grazing on the pasture involved in this study has peculiar properties in terms of lipid composition and aromatic profile and is used to produce the characteristic PDO alpine raw milk cheese called 'Bitto'. Cow grazing behaviour was monitored using accelerometer-equipped collars to quantify resting, feeding, and rumination periods, coupled with GPS sensors to track animals' movements. The GPS devices were validated by comparison with a RTK GNSS receiver, achieving an accuracy of 2.14 ± 1.60 meters. Behaviour and position data were collected and processed obtaining a 15-minute interval dataset, including a categorisation of animals by breed, year of birth and lactation cycle. Animal monitoring was combined with productivity and composition data obtained through pasture biomass sampling and NIR analysis, and with floristic surveys on the grazed areas. Results allowed the identification of animal habits and grazing preferences that are influenced by pasture type, phenological stage, weather conditions, and herd membership. Digital tools proved to be effective in evaluating animal behaviour in mountainous environments, positioning themselves as potential indicators to enhance pasture management and optimise biomass utilisation.

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P471

Virtual Fencing and Remote Sensing: improve the herd management of dairy cows on alpine pasture

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Pastoral systems play a vital role in supporting mountain farmers by providing a sustainable income source while delivering several ecosystem services, such as biodiversity conservation and carbon sequestration. However, effective management of these systems is critical to preserving their ecological value and ensuring the sustainable use of natural resources. Virtual Fencing (VF) is an emerging technology that offers a promising solution for achieving these objectives. VF uses GPS-enabled collars to confine animals within grazing areas defined remotely. As animals approach the virtual boundary, the collars emit an acoustic warning, followed by an electrical pulse if necessary. This study aimed to (i) evaluate the animal response to VF and (ii) test the feasibility of

combining VF data with remote sensing (RS) imagery to estimate feed intake in alpine grazing systems. The research was conducted in the Eastern Italian Alps (Mount Zoncolan, Italy, 1600 m altitude), where the animal grazed consecutively on three diverse grazing areas: first, two summer pastures (Malga Pozof and Malga Tamai), and then on ski slopes repurposed for grazing. VF collars (Nofence®, Norway) were installed on 35 Bruna dairy cows, with grazing areas expanded daily to accommodate forage availability. The results showed that cows adapted well to VF, successfully using both natural pastures and ski slopes. In fact, the only differences were detected in the total number of acoustic warnings per day, with a lower total number emitted when animals were managed on Malga Pozof (i.e. first period). There were no significant differences in the emission of electrical pulses between the grazing areas, with an overall low average number. Furthermore, the integration of VF with RS techniques provided valuable insights into forage consumption. By analyzing vegetation spectral responses, by means of the Normalised Difference Red Edge Index (NDRE), feed intake estimates were derived by comparing pre- and post-grazing images acquisition (PlanetScope), when cows grazed the ski slopes. This study highlights the potential of coupling VF technology with RS data for sustainable pasture management in mountain environments, where in-situ monitoring can be logistically challenging and costly. The findings also suggest that VF can support the preservation and productive use of these areas, helping to mitigate the abandonment of alpine pastures during the summer season.

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P536

Assessing the potential of portable NIR spectroscopy to evaluate the net energy content for lactation of hay forages for dairy cattle

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Near-infrared spectroscopy (NIRS) offers a rapid and non-invasive method for forage quality evaluation in the context of precision feeding. This study assesses the potential of a portable NIR device for the rapid on-farm main analysis needed for the calculation of the net energy for lactation (NEL) in hay forage for dairy cattle. A total of 147 forage samples, 75 alfalfa hays (AAH) and 69 mixed hays (MH), were analyzed using both NIRS and wet chemistry methods. Parameters acquired included dry matter (DM), crude protein (CP), ether extract (EE), neutral detergent fiber (aNDF), acid detergent fiber (ADF), and ash content. Based on the NRC 2001 database, the acid detergent lignin (ADL), neutral detergent insoluble crude protein (NDICP) and acid detergent insoluble crude protein (ADICP) were calculated as fixed proportion of NDF (0.16 for ADL and 0.83 for NDICP) and ADF respectively (0.48 for ADICP), while fatty acids were calculated as EE-1. The NEL was then calculated based on the NRC 2001 equation for forages. A multivariate GLM analysis was performed using SPSS software (IBM SPSS Statistics for Windows, Version 29.0; IBM Corp., Armonk, NY) to compare the nutrient contents and the calculated NEL determined through wet chemistry and NIRS analysis. For AAH, differences were found in the prediction of DM with 85.79 ± 3.03 vs 87.89 ± 1.31 % as-is ($p = 0.003$), ash content with 10.75 ± 1.91 vs 12.88 ± 1.35 % DM ($p < 0.001$), and ADF with 34.65 ± 4.1 vs 37.09 ± 4.6 % DM ($p = 0.050$) respectively for chemical and NIRS analysis. Similarly, for MH, differences were highlighted in the prediction of DM with 85.81 ± 2.03 vs 91.51 ± 1.97 % as-is ($p < 0.001$), ash content with 8.98 ± 1.12 vs 6.94 ± 0.94 % DM ($p < 0.001$), and ADF with 38 ± 2.97 vs 32.80 ± 3.4 % DM ($p < 0.001$). Regarding NEL, differences emerged when considering the type of forages with values of 1.60 ± 0.10 (ranging from 1.31 to 1.83) vs 1.52 ± 0.13 (ranging from 1.35 to 1.81) Mcal/kg for AAH ($p = 0.002$) and 1.72 ± 0.07 (ranging from 1.58 to 1.86) vs 1.80 ± 0.09 (ranging from 1.59 to 1.97) Mcal/kg for MH ($p < 0.001$) for wet chemistry and NIRS analysis respectively. Although the differences in the prediction of the nutrients content of forages, the NEL values calculated starting from the two analytical techniques appears within the same ranges, indicating the potential of portable NIR for the field application in forage nutritional value assessment, despite the need for further refinements to improve its accuracy.

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PRODUCTION SYSTEMS

P085

Two different feeding systems in fattening heavy pigs: performance and nitrogen balance

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Considering the production of the Italian heavy pig, the introduction of the new guidelines for the PDO ham allows the application of new feeding strategies in the fattening phase. In this perspective, the aim of the work was to compare a traditional feeding plan with restricted administration (R) of the diet with a feeding level increased on average by 18% (V) with a feeding plan curve that followed the voluntary feed intake determined in previous trials with pigs fed ad libitum. A total of 56 pigs were used (commercial hybrids compatible with the production of PDO hams) divided into 14 pens of 4 pigs each: 7 with R and 7 with V feeding. The trial began with the animals weighing approximately 75 kg and the fattening cycle, lasting 120 days, was divided into 3 feeding phases with related diets. The three diets were formulated with a low protein content (14.0, 11.9, 10.9% on as fed for phases 1, 2, and 3, respectively) but respecting the amino acid requirements (e.g. SID Lys = 0.77, 0.61, 0.53%). At the beginning of each phase and the day before slaughter, the pigs were weighed individually and the thickness of the back fat and the longissimus dorsi muscle were measured in two dorsal points with calculation of the animal's lean meat. The individual daily weight gain (DWG) and the feed conversion ratio (FCR) were determined for each pen for each phase. The data were analyzed by ANOVA using the SAS GLM procedure. The two feeding regimes showed significant differences ($p < 0.001$) for DWG (g/d) in the first two phases (847 vs 1041 and 900 vs 997, for R and V, respectively), while in the third phase the DWG were similar: 838 vs 802, for R and V, respectively. The FCRs were similar in the first phase (2.88 vs 2.99 for R and V, respectively) and statistically different ($p < 0.01$) between treatments in the second (3.18 vs 3.50) and in the third (3.64 vs 4.06) phase, for R and V, respectively. Globally DWG and FCR resulted to be 866 vs 953 ($p < 0.001$), and 3.22 vs 3.47 ($p < 0.01$), for R and V, respectively. As far as nitrogen (N) balance is concerned, individual N intake for R and V pigs was on average 54.1 and 64.5 g/d, whilst the N retention was 47.6 and 42.7%. In conclusion, currently raised pigs are very efficient in growth performances and particularly in N utilisation. Growth performances were noticeably high in animals fed almost ad libitum until about 150 kg bodyweight. After this stage, generous feeding is less convenient both economically and environmentally.

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P141

Finishing of beef cattle on pasture: effects on performance and meat quality

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The trial evaluated the effects of two different finishing systems on the in vivo performance and meat quality of Limousin calves. Six calves (IN) were reared indoors and fed a unifeed mixture (16 kg/day/head), while 6 calves (OUT) were reared exclusively outdoors, fed on pasture and supplemented with unifeed (8 kg/day/head). The trial lasted approximately three months (from April to July), during which the animals were weighed at the start of the trial, midway through, and just before slaughter. Pasture samples were collected, and their productive potential was assessed. At slaughter, carcass weight was recorded. Physical and chemical analyses, as well as fatty acid composition, were conducted on the *Longissimus lumborum* muscle. Data were analyzed using ANOVA with the GLM procedure of SAS, considering the rearing system as a discrete effect. The rearing system significantly affected the final live weight ($p < 0.05$), with IN calves being heavier than OUT calves (740 kg vs 652 kg), due to differences in the average daily gain (1.37 kg/day vs 0.63 kg/day). The physical and chemical analyses did not show significant differences between the two groups, while the fatty acid profile was different. Specifically, IN animals showed higher levels of monounsaturated fatty acids (MUFA) and lower levels of polyunsaturated fatty acids (PUFA) compared to OUT calves (25.70 vs 32.76 and 30.85 vs 18.45, respectively). The results were likely influenced by the grazing component present in the OUT group. Throughout the trial, pasture quality was monitored, showing a decline due to the phenological progression of the vegetation, with an increase in lignin content and a reduction in digestibility. This resulted in lower energy availability and a decrease in the meat forage unit (UFC). The decline in pasture quality, combined with other factors such as trampling by the animals and the presence of non-consumable plant components, negatively impacted the in vivo performance, leading to the observed decrease. These preliminary results suggested that the exploitation of natural resources, such as pastures, must consider various factors related to both the quantity and quality of the vegetation present, taking into account their phenological and seasonal variations.

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P327

The potential effectiveness of innovative practices in livestock and permanent pasture management: stakeholder responses

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In October 2024, a SWOT analysis was conducted through Focus Groups to collect information supporting the objectives of SUREPASTOR, a project aimed to promote the introduction of sustainable and innovative practices to improve the resilience of the Mediterranean agro-pastoral sector to climate change. For this reason, stakeholders from local communities were involved in the meeting. Focus Group was carried out by dividing the participants into three groups. Each Group was led by a moderator and a facilitator and was formed by 10 participants, who were asked to answer questions about strengths/weaknesses and opportunities/threats for farms about the following topics: Precision Livestock technologies applied to sheep and goats farming systems, improvement of permanent grassland and eco-labelling of pastoral products. To each answer obtained for the proposed questions, it has been assigned a weight, calculated as a ratio between the number of stakeholders who shared the same opinion on a specific aspect and the total number of stakeholders who participated in the Focus Groups, showing the frequency of agreement of a certain aspect. The analysis revealed that: a. Precision Livestock technologies: the main strenghts were better spatial management and confinement of animals and improvement of animals' performances and production monitoring, while the main weakness concerns the high costs of technologies and equipment. In terms of opportunities, the main result concerns the reduction of farm's costs, while the main threats are the lack of public incentives and high costs. b. Improvements in permanent grasslands: the main strenghts concern the protection of lands and improvements in plant biomass and resilience to climate change, while the main weaknesses are the problems related to predations, climate change and costs. The main opportunity is public incentives, contrary threat is identified by an inadequate support for pastures under the CAP. c. Eco-labelling of pastoral products: strenghts are represented by product's valorisation and quality guarantee of the product and the production process, while weaknesses are high certification costs and obligations. In terms of opportunities, the main is the valorisation of the products, while threat concerns the high certification costs.
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P376

Effects of weaning strategies on the average daily gain of Dorper-Sarda F1 lambs

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The heavy lamb production represents a valuable opportunity in sheep farming and can be effectively integrated into the dairy Sarda sheep system to enhance farm profitability. This dual-purpose approach combines milk production with the growth of lambs specifically targeted for meat, offering an opportunity to diversify income streams and improve economic sustainability. A feasible strategy to achieve this integration is the introduction of meat-breed rams, such as Dorper, to young Sarda ewes at their first breeding. This crossbreeding approach improves the growth performance and carcass traits of lambs while maintaining the adaptability typical of the Sarda breed. The aim of this study was to evaluate the crossbreeding of Dorper rams with young Sarda ewes and to assess the effects of two weaning strategies on performance and average daily gain (ADG) of heavy lambs. Three Dorper sires were added to a group of 38 young Sarda ewes. Twenty-four F1 lambs, born on 20/01/2024 ± 17 days (means ± s.d), were divided into two groups, based on weaning period: early weaning group, EW (age: 21 ± 1 days , body weight (BW): 9.2 ± 1.4 kg), and traditional weaning group, TW (age:31 ± 4 days, BW: 12.4 ± 1.87 kg) Each group grazed a pasture of *Sulla coronaria* and was supplemented with concentrate and *Panicum miliaceum* hay. During the trial animals were weighed weekly and ADG was calculated. The lambs were slaughtered at 142 and 159 days of age for EW and TW, respectively.; pre- and post-slaughter weight were recorded and carcass yield (CY) was calculated. Data were analysed using a Generalised Linear Model (GLM) in SAS (ver 9.4, 2022). The fertility rate of the ewes was 86%, and no complications were observed during lambing in any of the animals. ADG did not differ between weaning groups (0.199 ± 0.020 and 0.211 ± 0.036 kg day, for EW and TW respectively, $p = 0.3527$). TW group showed higher value than EW for CY (56 ± 2.0% and 54 ± 2.3%, $p = 0.0283$) and for carcass weight (22.1 ± 3.12 kg and 17.9 ± 1.94 kg, $p = 0.0014$). The weaning period did not have a significant impact on the overall growth rate of lambs, suggesting that both weaning strategies can result in similar ADG. In particular, the early weaning does not necessarily compromise ADG,

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allowing for flexibility in weaning age. The better overall carcass characteristics achieved in TW group could be likely due to the extended period of growth and development of this trial.

P413

Challenges and opportunities in using the n-alkane technique to determine cattle diet in agrosilvopastoral systems

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The determination of herbage intake in grazing animals is a key aspect of studying animal nutrition and performance. However, due to the challenges of controlling grazing animals, accurately assessing their intake remains difficult. Various approaches, such as indirect pasture measurement, markers, and modelling, have been proposed. This study focuses on Maremma steers and heifers grazing in an agrosilvopastoral system. Its aim was to assess the contribution of forest understory vegetation to the diet of grazing animals. Using the exclusion cage technique, we estimated pasture mass intake from grassland, while n-alkanes were used to determine the contribution of understory vegetation to the diet. This technique relies on the fact that alkanes are not degraded in the rumen and that each plant species has a characteristic alkane profile. By comparing the alkane profiles of feed and faeces, it is possible to estimate diet composition. Alkane composition was analyzed for herbage, forest understory vegetation, and supplements (vetch-oat hay and maize-triticale flour). Monthly faecal samples were collected rectally, freeze-dried, and analyzed. The EAT-WHAT software (Dove and Moore, 1995) was used to calculate diet composition based on the n-alkane profiles of feed and faeces for April, May, and June 2021. This approach allowed us to estimate the intake of supplements, herbage, and forest understory vegetation. Regarding the only fresh forage portion, feed intake was composed by 48.2% grassland and 51.8% understory in April, 20% grassland and 80% understory in May, and 82.8% grassland and 17.2% understory in June. These findings revealed a changing pattern in the grassland:understory ratio of voluntary feed intake throughout the season. Specifically, understory vegetation intake decreased in late spring due to limited biomass accumulation after the grazing period, caused by competition with trees for resources such as light and water. Nevertheless, the similarity between the n-alkane profiles of hay and grazed herbage may have affected the accuracy of EAT-WHAT's estimates. Without an external n-alkane marker in the diet, intake quantification was not feasible. Nonetheless, the n-alkane technique is as a relatively simple method for grazing trials. This study provides a foundation for further research to refine and develop this approach.

P438

Integrating animal welfare and milk monitoring: a preliminary analysis of farm management and efficiency prediction

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Animal welfare assessment protocols are based on static indicators that provide an 'instant snapshot' of the farm's situation, useful for managing animal welfare and ensuring compliance with sector regulations. However, these assessments provide limited temporal data, preventing continuous monitoring by farm operators. In contrast, routine data obtained from bulk milk analysis could offer dynamic information that, when integrated into decision-making processes, could enrich farm assessment checklists. In this context, the aim of the study was to examine the influence of animal welfare on dairy production and how the production itself can assist operators in predicting efficiency or inefficiency at the farm and managerial levels. The data from the ClassyFarm checklists (Directorate General of Animal Health and Veterinary Drugs (DGSA) of the Italian Ministry of Health (MINSAL) and Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER)), collected at three distinct time points (T0, T1, and T2), along with the quantitative and qualitative bulk milk data from 21 dairy farms, were statistically analyzed to identify the areas of the protocol that most affect production. Multiple regression analyses revealed that Area A, related to farm management, had the greatest impact on milk quality and quantity, significantly influencing ($p < 0.05$) components such as fat, proteins, caseins, total bacterial count and kg/cow/day milk production. Area C, which directly assess animal well-being, showed a significant effect ($p < 0.05$) on proteins, lactose, caseins, urea, pH and kg/cow/day milk production, suggesting a strong correlation between animal welfare and milk's chemical quality. Linear regression analysis identified fat, proteins and caseins as significant predictors of farm efficiency for Area A, while urea and pH were relevant predictors for Area C. The results of this preliminary study support the hypothesis of integrating dynamic qualitative indicators, such as daily milk quality data, into the farm's operational routine. These indicators

can provide timely and direct information on farm management, improving responsiveness to both production needs and animal welfare requirements.

P557

A twenty-year dairy cattle farm evolution, technical and managerial aspect

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Over the past three decades, the dairy cattle industry has undergone significant transformations, involving various areas such as animal welfare, feeding, genetic improvement, reproduction and farm management. Particular innovation for instance, has come from the spread of automatic milking systems and management software for process data collection and analysis. However, in these innovation, economic and organisational aspect was given less importance than the technical aspect. This research aimed to understand what had been the business growth path of a dairy cattle farm currently with a high degree of technological equipment and technical innovation. The evolution of a Sardinian dairy cattle farm from 2000 to 2024 was analyzed. Farm was divided in different area: company management, reproduction, nutrition, crop and herd management. For each area was conducted a face to face interview with the farmer and was asked about what kind of changes have been implemented over the year. In particular was asked about: time of the decision, reason of decision and result obtained, in order to link this with farm evolution. Historical data for each area were collected from managerial software Dairy Comp® and Ecostalla®. Data collected from interview were associated to main farm changes took by the farmer. As result the analysis clearly revealed farmer priorities, on total of 41 farm changes, the main focus was on reproduction from 2000 to 2019 ($n = 11$) and for nutrition, crop and herd management were individued 11, 6 and 10 changes respectively. Only in 2020 the farmer started to take choices on company management area ($n = 11$). For reproduction and herd management, Pregnancy Rate (PR), has more than doubled over the years, from 11 % to 23 %. Overall, annual milk delivered increase of +111.7 % from 2000 to 2023 and N° of milking cow and milk delivered per year increase of 103% and 89 % respectively, the increase of milk yield does not correspond to a decline of fat and protein. In conclusion the main focus of the farmer in over 20 year were only for technical aspect expecially reproduction and not for organisational or economic aspect. This approach could be useful to see the gap in different area compared to latest literature, this could be extended to other different dairy cattle farm and could be adapted for sheep and goat.

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RUMINANT NUTRITION

P139

Rhizobium inoculation in forage legumes intercropped with cereal for ruminant feeding

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Intercropping is an agroecological practice that combines two or more crops simultaneously in the same field. This is particularly beneficial when cereals like wheat are combined with forage legumes, mainly under organic farming systems. Forage legumes play a vital role in sustainable agriculture by supporting livestock production and enhancing biological nitrogen fixation (BNF). BNF efficiency depends on the compatibility between legume species and their rhizobial strains. Applying exogenous rhizobial inoculants can enhance BNF and legume performance, especially in fields with limited legume cultivation history. Here the intercropping (IC) of durum wheat (*Triticum turgidum* subsp. *durum*) with three forage legumes (*Trifolium subterraneum*, *Medicago polymorpha*, and *Vicia sativa*) compared to wheat monocropping was evaluated. Crops were grown under two levels of N-fertilizer (60 and 120 kg ha^{-1}) with and without species-specific rhizobial inoculants (Visjon Exceed, USA). The field trial was conducted on an organic farm in Patti, Messina (38°11'N, 14°99'E, Italy) to improve wheat productivity and forage quality from wheat byproducts. The chemical composition of feed samples, in terms of protein and fibrous fractions, was determined using standard analytical methods. The three-way ANOVA (at $p \leq 0.05$) revealed significant effects of N-fertilisation ($p = 0.007$), rhizobial inoculation ($p = 0.009$), and legume IC ($p \leq 0.001$) on wheat grain yield. While N-fertilisation positively influenced weed biomass ($p = 0.026$), legume IC reduced it ($p \leq 0.001$). Wheat straw yield decreased with legume IC ($p = 0.015$; 3.8 Mg ha^{-1} in the control and 2.5 Mg ha^{-1} with *M. polymorpha*), but among legume species, *V. sativa* produced the highest additional forage yield (1.17 Mg ha^{-1}), outperforming *T. subterraneum* and *M. polymorpha* (0.61 and 0.49 Mg ha^{-1}). Rhizobial inoculation significantly increased legume yields than non-inoculated crops (0.64 vs. 0.50 Mg ha^{-1}). Additionally, rhizobial inoculants and N-fertilisation ($p = 0.004$ and $p = 0.001$) enhanced the protein content of forage legumes (10.4 *vs* 9.3%, and 10.5 vs 9.2%, respectively), without

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significantly ($p > 0.05$) affecting the fibrous fractions (NDF, ADF, ADL), thus contributing to the improvement of the quality of wheat straw. These findings confirm the benefits of IC in enhancing cash crop productivity and improving the quality of forage for ruminant feeding in organic, cereal-based cropping systems.
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P207

Effect of different RDP / RUP ratios on productive performances of high-yielding dairy cows

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Protein metabolism is one of dairy nutrition's most studied and debated topics. Nitrogen efficiency is also crucial because nitrogen ends up in manure spread on land, contributing to the environmental sustainability of milk production. A nutritional trial was performed to test the effect of different protein profiles on highly productive dairy cows. The study was conducted at the experimental dairy farm Cerzoo (San Bonico, Piacenza, Italy) of the Università Cattolica del Sacro Cuore di Piacenza. Eighteen multiparous Holstein dairy cows (153 ± 49 days in milk) were involved. Animals were randomly assigned to a treatment sequence in a replicated 3 × 3 Latin Square design with a 21-day treatment period. The experimental diets were fed daily ad libitum through the RIC (Roughage intake control) system. They were Control (CTR) with 16.5% CP on a DM basis and with a balanced RDP (rumen degradable protein)/RUP (rumen undegradable protein) ratio (64/36), low RDP/RUP ratio (58/42) and 14.5% CP (BY), higher RDP/RUP ratio (69/31) with 16.5% CP and high soluble protein (SOL). Data were analyzed using a mixed model with the Restricted Maximum Likelihood Method and random effect of cow-nested in the Latin Square (JMP® Pro 17.0.0). Multiple treatment means comparisons were conducted using the honestly significant difference Tukey test, and statistical differences were declared at $p < 0.05$. The amount of RUP fed to cows (gr/cow/day) was constant, whereas the RDP increased in treatment diets, moving from BY to CTR and SOL. All experimental diets were iso-energetic. Changing the protein profile did not significantly modify the cow's performance. Mainly, numerical differences appeared. When cows were fed the BY diet, the DMI increased by about 1 kg compared with CTR or SOL-fed cows. However, a numerically lower milk yield (44.1 kg/d) was observed compared with CTR (44.4 kg/d), decreasing feed efficiency (1.86 vs 1.73 kg of milk/ kg of DM, respectively). As expected, the milk urea content was higher ($p < 0.05$) when feeding the SOL diet (35.89 mg/dL) compared with CTR (31.44 mg/dL) or BY (23.61 mg/dL) diets. No differences among treatments were observed in NDF, starch, and CP total tract apparent digestibility. Feeding a diet with a lower amount of RDP leads to low milk yield and reduced feed efficiency. In contrast, an RDP/RUP ratio of 64/36 in our condition was optimal for cow production performance.
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P476

Fat formulation of cow milk replacers affects nutrient fecal excretions of dairy calves

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Oils derived from insect defatting may represent novel alternatives to expand the range of oils in ruminant nutrition, but there are only few published studies on their effects. In Europe and other parts of the world, vegetable fats such as palm, coconut, and rapeseed are the primary fat sources in milk replacers (MR). The aim of this study was to investigate the effect of MR fat formulation on fecal dry matter, nitrogen, fiber and mineral excretions in calves at weaning. Four commercial MR isoenergetic and isonitrogenous, differing only for the fat source were tested for 10 weeks. MRA included 80/20 ratio of palm/coconut oil, MRB included 80/20 ratio of palm/insect oil from black soldier fly, MRC included 60/40 ratio of palm/insect oil from black soldier fly and MRD included 80/10/10 ratio of palm/insect /coconut oil. A total of 32 calves (36 ± 3 kg of body weight) were randomly assigned to 4 treatments ($n = 8$ heifers per group): group A fed MRA, group B fed MRB, group C fed MRC and group D fed MRD. In addition, starter feed, chopped straw, and water were offered to all groups. Weaning was gradual and induced at about week 10. At the age of 65, 66, 67, 68, 69 days, feces were individually collected from each animal 8 h after the feed delivery. Data were analysed by ANOVA considering the treatment as fixed effect. The four MR differed for fatty acids profile and the main differences were: MRB and MRD had lower saturated fatty acids percentages (57,73 and 58,81% vs 60,51 and 61,74% of MRA and MRC) and lower C14:0 fatty acid (4,42 and 4,90 of MRB and MRD vs 5,76 and 5,88 of MRA and MRC). Fecal dry matter (DM) was significantly ($p \leq 0.05$) lower in A group (24.15%) compared to the others fed with MR containing insect oils (B; C; D). Nitrogen excretions (% on fecal DM) were also significantly different among the groups and B (2,56) showed higher values ($p \leq 0.01$) compared to the

other groups containing insect oil (C and D groups) (2,22 and 2,17% respectively). Fecal NDF reached minimum values in the C and D groups (39,09 and 38,74% on fecal DM). On the other hands, MR formulation did not affect fecal ash (% of DM). Finally, the different MR fat formulations influenced average daily weight gain and feed efficiency which showed the highest absolute values in the calves of D group (700 g/day and 67% respectively).

P466

Investigation of the microbiological, physico-chemical, and fermentative quality of baled silage produced in Sardinia

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Forage quality is a critical factor for improving livestock productivity and reproduction. Baled silage production represents an effective strategy to minimise forage losses caused by adverse weather conditions, especially for farms lacking access to bunker silos. However, improper fermentation processes can result in high pH levels, low lactic acid concentrations, and elevated butyric acid levels, all of which increase the risk of milk contamination by *Clostridia* spores and foodborne pathogens, such as *Listeria monocytogenes*. This study aimed to assess the microbiological, chemical-physical, and fermentative characteristics of baled silage from different farms in Sardinia. The microbiological evaluation included five microbial groups associated with silage quality, both positively and negatively, in addition to the detection of *L. monocytogenes* and *Escherichia co*li in samples collected at 30, 60, 90, 180, and 270 days after production. The results demonstrated that 66% of the analyzed samples were free from *Clostridia,* while mold and yeast contamination was minimal, with no presence detected in 76% of the samples. Neither *E. coli* nor *L. monocytogenes* were detected, confirming the effectiveness of silage preparation techniques adopted on the studied farms. The lactic acid bacteria count showed a statistically significant interaction between silage type and storage time ($p < 0.05$), with reductions over time being more pronounced in legume-based silages. Additionally, the silages exhibited low levels of NH3-N and butyric acid, indicating high fermentation quality. Lactic acid (3.5% of dry matter) and acetic acid (1.5% of dry matter) varied over the storage period, with lactic acid decreasing ($p = 0.010$) and acetic acid increasing significantly ($p = 0.001$), influenced by the interaction between silage type and storage duration. Levels of 2-propanediol, a compound important for preventing aerobic spoilage, also increased over time ($p = 0.030$). In conclusion, this study highlights that the analyzed baled silages exhibited good chemical-fermentative quality and microbiological safety. These findings underline the importance of proper silage management practices and their role in ensuring the production of high-quality forage, particularly in regions like Sardinia, where baled silage offers a practical and efficient solution to mitigate climatic challenges and enhance livestock productivity.

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P561

Effect of the weather pattern of two consecutive years on the floristic composition and on the quantitative-qualitative production of the forage phytomass of a summer pasture of the Southern Apennines

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The aim of this work was to evaluate how the weather trend of the spring-summer period over a two-year period (2023–2024) influenced the floristic composition and the quantitative-qualitative production of the forage phytomass of a pasture in the southern Apennines. The pasture, located in the municipality of Pescopagano (PZ) and situated at an altitude between 997 and 1060 meters a.s.l. The weather conditions observed during the study period showed, precipitation decreased drastically and the average temperature increased by approximately 2.4 °C in 2024. The area (120 ha) was divided into 11 plots (4m^2/plot), for each plot the floristic composition and the amount of biomass were determined. On mass samples of the entire pasture the chemical composition was determined: dry matter (DM), crude protein (CP), ether extract (EE), crude fiber (CF) and ash, the digestible component: acid detergent fiber (ADF), neutral detergent fiber (NDF) and acid detergent lignin (ADL), and the content of phenols and flavonoids (free and bound). The antioxidant activity of the samples was evaluated with colorimetric methods. The data were analyzed by monofactorial

analysis using the software R version 4.4.1. Botanical characterisation studies observed the presence of over 80 species and 23 families, the most representatives' families were Fabaceae, Poaceae, and Asteraceae. Compared to 2023, in 2024 Poaceae showed a higher incidence, while Fabaceae showed a slight decrease. In addition, new families such as Caprifoliaceae, Linaceae and Orobanchaceae were detected, while Orchidaceae and Rosaceae decreased. Some families such as Gentianacea and Cyperaceae were present only in 2023. Comparing nutritional characteristics, pasture in 2024 had significantly higher EE, CP and ash content ($p < 0.05$), while CF content (NDF, ADF and ADL), was lower than in 2023 ($p < 0.05$). The content in total phenols in 2023 had significantly higher ($p < 0.05$); while, no significant difference was found in flavonoids. The fraction of bound polyphenols in 2024 recorded a higher content ($p < 0.05$) for both phenols and flavonoids. Finally, the antioxidant activity values were higher in the pasture 2024 than in 2023 ($p < 0.05$).

P206

Addition of feed additives to stimulate alternative metabolic pathways through methane reduction

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Ruminant livestock farming accounts for about 14% of anthropogenic methane (CH_4) emissions, which also represent a loss of energy for the animal, estimated to be between 2 and 12% of gross energy intake. While feed additives can decrease methane emissions, the reduction of methanogenesis is frequently associated with an accumulation of hydrogen (H_2) ions, negatively affecting the energy efficiency. The objective of the present study is to perform a screening test on methane emissions of two categories of recently developed feed additives: (1) additives that inhibit methanogenesis, such as chitosan (CHI), lauric acid (LA), iodoform (IOD), bromoform (BRO), and 3-Nitrooxypropanol (3NOP); and (2) additives that facilitate the use of H_2 ions by ruminal bacteria to produce volatile fatty acids (VFA), like fumaric acid (FA), encapsulated fumaric acid (EFA), and phloroglucinol (PHG). Additives were individually tested with three different doses (expressed as % on DM) using an in vitro incubation system (Theodorou) for 24 hours in three incubation runs. At the end of each run, pH, gas and ruminal fluid were sampled to determine gas composition and fermentative profile. Statistical analysis was performed with a proc. mixed model of SAS. No effect on gas production (GP) was observed for FA, CHI and IOD, whereas the highest dose of EFA (12%) increased GP. The medium and highest doses of PHG (7.5% and 10%) resulted in higher GP than the control, while 3NOP and BRO significantly reduced GP at each dose tested. The production of CH_4 was not affected by FA, whereas the highest dose of EFA reduced the CH_4 content by 23%. The highest dose of PHG and IOD (0.01%) significantly reduced the CH_4 percentage by 25% and 53% respectively. The medium dose of 3NOP (0.04%) reduced methane production by 80%, while the highest dose (0.08%) completely suppressed CH_4 production. All doses of BRO reduced CH_4 by 100%. Total VFA production was only affected by 3NOP and PHG. The highest dose of 3NOP reduced total VFA by 16%, whereas the total VFA were increased by the medium and highest dose of PHG. Acetate proportion was decreased by the highest dose of all additives except for PHG, which increased it by 5%. In contrast, propionate production was increased by all additives except PHG. In the next phase, combinations of these two categories of additives will be tested to assess their ability reduce methanogenesis and direct H_2 ions towards high-energy metabolites.

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P272

Sustainable feed source from ensiled peanut crop residues

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Groundnut (*Arachis hypogea*) is primarily grown for seed, but its residual above-ground biomass remains largely unutilised despite its potential as forage. This study evaluated the potential of different methods for preserving peanut biomass, with the aim of promoting a circular economy in livestock farming within local agricultural supply chains. In a peanut field located in southern Italy, three random 1 m² sampling areas were selected at pod maturity (stage R8). All plants within the areas were uprooted, cut at 5 cm above the roots, and weighed. Two subsamples were collected per plot: one was oven-dried (65 °C) to estimate dry matter and crude protein (CP) yields (3290.3 ± 52.2 and 594.4 ± 13.2 kg/ha, respectively). The second was pre-wilted for 24 h in the open air and used to obtain five theses: (i) biomass reference samples (control); (ii) air-dried to <20% moisture to simulate haymaking; (iii) ensiled in vacuum-sealed mini-silos without additives; (iv) ensiled with the addition of residual milk whey; and (v) ensiled with the addition of a commercial lactobacilli. Three samples were prepared for each treatment, 700 g each. The ensiled samples were stored at room temperature for six weeks before analysis, while the control biomass and the hay

samples were analyzed immediately. Data were subjected to one-way ANOVA with Dunnett's post hoc test comparing wilted plant (control) with each preservation method. Ash content was high (mean 15.0 ± 0.73 SE) but consistent across treatments, probably due to biomass extraction from wet soil. Crude Protein was lower ($p < 0.001$) in hay (10.39 ± 0.20) compared to silages (11.98 ± 0.29). Soluble protein (%CP) was similar in hay and control biomass, but higher in the silages ($p < 0.05$), although silage treated with LAB had lower values ($p < 0.05$) compared to the other ensiling methods, suggesting increased acidification that reduced proteolytic activity. Neutral detergent fiber was lower in the silages (32.5 ± 0.60) than in the hay (36.9 ± 0.32), but in vitro NDF degradability was similar between treatments. Overall, except for the CP content, the silages had a nutritional profile comparable to mature alfalfa hay (21.7 ± 0.42 and 6.2 ± 0.23 respectively for ADF and ADL). Among the different silage treatments, the addition of whey and lactobacilli improved fermentation and helped preserve the nutritional value of the biomass. We conclude that peanut biomass is a forage of fairly acceptable quality, with silages of superior quality to hay.

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P275

High throughput UHPLC-HRMS method for the detection of purines derivatives as biomarkers of nitrogen efficiency in dairy cows

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Nitrogen efficiency in dairy cows remains low due to the inherent characteristics of the ruminant digestive system and the composition of typical feedstuffs and rations. Optimising dietary strategies is critical for enhancing nitrogen utilisation. While most efforts focus on improving feed nitrogen and ration formulations, a deeper understanding of the absorption and metabolism of nitrogenous purines, as the primary components of nucleic acids, could offer new strategies for improving nitrogen efficiency. In this study, we evaluated nitrogen efficiency in lactating dairy cows ($n = 20$) by measuring specific metabolites, such as allantoin, uric acid and creatinine, in urine samples. The final aim was to use these compounds as biomarkers of feed efficiency, considering that a correlation has been previously reported between their excretion and the synthesis of microbial protein. To this aim, an ultra-high-performance liquid chromatography (UHPLC) coupled with high resolution mass spectrometry (HRMS) Orbitrap platform with a resolution of 70,000 FWHM at 200 m/z was exploited for ad-hoc quantification of the previously mentioned compounds. The method was preliminary tested on representative milk samples collected in the same trial. The developed MS/MS method allowed an accurate quantification, being the linearity of the method in the range 25–1000 µg/L, obtaining a coefficient of determination R^2 always higher than 0.99. The UHPLC system consisted of a degassing system, a quaternary UHPLC pump, an autosampler device, and a thermostatically controlled Waters BEH C18 column (2.2 × 100 mm, 1.7 µm) held at 35 °C. The mobile phase consisted of (A) water with 0.1% formic acid and (D) acetonitrile with 0.1% formic acid. The duration of the method was 11 min, the injection volume was 10 µL, and the flow rate 0.2 mL/min. The mass range in the full scan experiments was set at 50–250 m/z. The isotopic profile of the parent ion was isolated, and the optimal collision energy voltage (10 eV) was used to determine the fragmentation pattern in tandem MS acquisition: for uric acid (parent ion = 167.01 Da; fragment ion = 124.01 Da; retention time = 1.25 min), for allantoin (parent ion = 157.03 Da; fragment ion = 114.03 Da; retention time = 1.18 min) and for creatinine (parent ion = 114.06 Da; fragment ion = 86.07 Da; retention time = 1.10 min). Creatinine was ionized under positive mode (ESI+), while Uric Acid and Allantoin under negative mode (ESI-).The animals followed three different types of feed rations, each varying in the amount of rumen degradable protein (RDP): one containing bypass protein, one containing soluble protein, and a control group. The trial consisted of three periods, each lasting approximately 21 days. Once estimated the concentration of purine derivatives in mmol/L in urine using equation adapted from Chen and Gomez (1995), synthesis of microbial protein was predicted using the PDC index. The PDC index is a metric used to estimate microbial protein supply in ruminants based on the concentrations of purine derivatives (PD) and creatinine in spot urine samples. It reflects the relationship between the products of microbial nucleic acid degradation (purines) and metabolic activity (creatinine) adjusted for body size. Following this equation, we found values in the range of 800 $kg^{0.75}$ to 2000 $kg^{0.75}$. Our findings demonstrated that the PDC index from spot urine samples can reliably estimate microbial protein supply in dairy cow under similar field conditions. The PDC index provides a practical, non-invasive estimate of microbial protein synthesis in the rumen, making it useful for evaluating nutritional strategies and feed efficiency. Higher PDC index values typically indicate greater microbial protein yield, which is critical for optimal nitrogen utilisation and dairy cow productivity.

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P320

Influence of Enniatin B on performance and metabolic profile in dairy cow

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An increasing occurrence of the emerging mycotoxin Enniatin B (ENNB) in livestock feedstuffs, cereals, forages and by-products has been outlined during recent years, with significant concerns from EFSA on its possible role in causing undesirable effects in ruminants such as reduced feed intake and rumination activity, immunosuppression, and impaired milk production. The aim of the study was to determine the influence of ENNB on performance and metabolic profile in lactating dairy cows. A seven days *in vivo* experiment was carried out on six third parity mid lactating Holstein Freisian cows fed a total mixed ration with a supplementation of 2.7mg/head/d of ENNB for the first three days on trial. ENNB was daily suspended in sterile PBS and consequently administered *per os* to each experimental cow. Milk production and rumination time (min/d) were daily recorded and individual milk samples were collected for milk quality assay. Whole blood and plasma samples were obtained at the beginning of the trial (T0) and on days 1, 2, 3, 4 and 7 for BHBA, NEFA, ALT, GLDH, total protein, and albumin content together with the full blood count with differential. Statistical data analysis was performed by ANOVA, applying a MIXED model for repeated measurement of SAS, including the effect of time with the cow representing the experimental unit. Significant differences were declared for $p \leq 0.05$. Milk yield ($p = 0.63$) and rumination time ($p = 0.82$) were not affected at the end of the ENNB administration (day 3), nor at the end of the trial or overall trial period ($p = 0.63$). Milk fat content and fat:protein ratio were increased on day 7 with respect to the other sampling times ($p \leq 0.05$). BHBA ($p = 0.47$), NEFA ($p = 0.76$), ALT ($p = 0.69$), total protein ($p = 0.32$), GLDH ($p = 0.87$) were not influenced by ENNB administration, but a decrease in albumin content was found on day 1, 3 and 4 ($p = 0.06$; $p \leq 0.01$; $p \leq 0.01$, respectively) compared to T0. No significant variations on full blood count with differential were outlined. ENNB official limits for dosage and time of exposure are not yet defined by a specific European regulation: our results show that 2.7mg/d of ENNB for three consecutive days does not induce variations on performance, metabolism, and immune status of animals, except for an increased milk fat content and fat:protein ratio. The obtained results may be due to the low dosage applied, the short time of administration, or to the degradation of the molecule during the *in vivo* digestive processes.

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P325

Fecal microbiota shifts in dairy cows consuming Enniatin B contaminated diets

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To date, there is an increasing concern on the occurrence of emerging mycotoxins, such as Enniatin B (ENNB), in livestock feedstuffs, cereals, forages and by products. At present, very limited *in vivo* information on the potential negative effects of ENNB is available on ruminants. ENNB, as other mycotoxins, could negatively influence the microbial populations of rumen and feces, leading to impaired health status and performance of lactating dairy cows. The aim of this study was to determine the shifts in fecal microbiota in dairy cows consuming ENNB contaminated diets. A seven days *in vivo* experiment was carried out including six third parity mid lactating Holstein Freisian cows fed a total mixed ration with a supplementation of 2.7mg/cow/d of ENNB for the first three days on trial. ENNB was suspended daily in sterile PBS and consequently administered *per os* to each experimental cow. Fecal samples were daily individually collected from the rectal ampoule during the whole trial and stored at -80 °C, pending 16S rRNA gene sequencing (V3-V4 region) for microbiota analysis (MiSeq, Illumina). The 16S amplicon sequencing data were processed using DADA2 tools (Galaxy version). After reads filtering, an amplicon sequence variant (ASV) table was generated. Taxonomy was assigned to each sequence variant employing SILVA database (version 138.2) as reference (100% of identity). MicrobiomeAnalyst platform was used to generate the community profiles and to perform the statistical analysis. At the class level, obtained results showed that the most dominant bacteria were *Bacteroidia* and *Clostridia*. According to the results, there were not significant differences in the alpha and beta diversity in the composition of microbiota during the timeline. However, the microbial community seemed to differ among samples, probably depending on the physiological characteristics of each cow. Moreover, it was observed that there was

a trend in the constant reduction of bacterial diversity in the feces after the first ENNB administration through the rest of the trial. ENNB official limits for dosage and time of exposure are not yet defined by a specific European regulation: our results show that the administration of 2.7mg/cow/d of ENNB for three consecutive days led to minor effects on fecal microbiota, probably due to the low dosage applied, the short time of administration, or to the degradation of the molecule during the *in vivo* digestive processes.

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P326

Feeding livestock with leftovers: exploring the potential of dry pasta residue

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The aim of this study was to preliminarily assess the suitability as energy feeds in ruminant diets of discarded pasta, one of the main leftover products from the dry pasta industry. Three 6-kg batches of four types of pasta leftovers (PL) were collected over three months (one batch each month) from a pasta production plant located in the Campania region, Southern Italy. Specifically, the PL types were whole wheat pasta (WMPL), semolina pasta (SPL), pasta with beetroot (BPL), and pasta with vegetables (VPL). The samples, along with whole maize meal (MM) as a control, were analyzed for proximate composition, fiber fractions, and *in vitro* rumen starch degradability (IVSD) after 7 hours of incubation in buffered rumen fluid. Data were analyzed using one-way ANOVA with substrate as a fixed factor, and significance was determined using Tukey's test at $p < 0.05$. Compared to MM, the PLs collectively exhibited significantly higher ($p < 0.001$) crude protein and starch levels, and lower fat content ($p < 0.001$). Among the PLs, SPL had a reduced ($p < 0.05$) crude protein concentration but an increased starch content, while WMPL displaying the lowest starch level ($p < 0.05$) compared to the others PLs. Neutral detergent fiber content varied considerably, with SPL and BPL showing significantly lower levels ($p < 0.001$) compared to MM and other PLs, which averaged around 11%. The metabolizable energy of MM was significantly lower than that of the PLs ($p < 0.001$). In terms of IVSD, the PLs displayed a higher starch disappearance rate (84.91%) compared to MM (82.62%; $p < 0.05$). Notably, VPL and WMPL had the lowest IVSD values (83.16% and 84.73%, respectively), while SPL (86.12%) and pasta with beetroot (BPL) had the highest (85.25%). Overall, the *in vitro* starch degradability indicates different digestibility dynamics compared to conventional corn, possibly due to alterations in starch granule structure, size, and shape during pasta processing. These findings suggest that PLs, with specific attention to their starch digestibility profiles, can serve as a cost-effective and sustainable energy source in ruminant diets, contributing to reduced feed costs, food waste, and associated environmental impacts.

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P391

Effects of the Rufo® supplement on enteric methane emissions in lactating Italian Mediterranean buffaloes, measured with a laser methane detector (LMD)

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Methane (CH_4) is a greenhouse gas linked to climate change and is released into the atmosphere by several processes including livestock breeding, particularly in the ruminant sector. Reducing CH_4 emissions is a key to sustainable agriculture, and nutrition-based strategies offer a viable solution. This study evaluates the effect of RuFO® (AHV, Piacenza, Italy), a nutritional supplement for dairy cows, on enteric CH_4 emission and nutrient digestibility in dairy buffaloes. Three groups of 19 heads each were formed: a control (C) receiving the basal diet and two treatment groups (T1, T2) receiving 100 and 200 g/head/d of RuFO, respectively. From June to September 2023, CH_4 emissions were evaluated using a laser methane detector (RLGD-100, FPI, Hangzhou, PRC), and individual apparent digestibility was assessed at the end of the trial. Methane data were analyzed in ppm × m as total average (MEAN), peak average (P_MEAN), and peak average belonging to eructation (ERP_MEAN). Moreover, data were transformed in g/head/d of CH_4 (gCH_4) and standardised for milk yield (gCH_4/MY) and energy-corrected milk (gCH_4/ECM).

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Statistical analysis included group (fixed), ID (random, nested in the group), and sampling (fixed) in a GLM. Results showed that group T1 significantly reduced ($p < 0.001$) the CH_4 emissions across all metrics compared to C and T2 and increased ($p < 0.001$) the apparent digestibility of dry matter, crude protein, neutral detergent fiber (NDF), and starch. Group T1 showed a significant ($p < 0.05$) negative correlation between starch digestibility and MEAN ($r = -0.51$), P_MEAN ($r = -0.58$), gCH_4 ($r = -0.58$), and gCH_4/MY ($r = -0.49$). Conversely, T2 exhibited intermediate digestibility and CH_4 emissions. It also showed a significant ($p < 0.05$) positive correlation between starch digestibility and MEAN (r = 0.53), P_MEAN ($r = 0.58$), and gCH_4 ($r = 0.58$). Group C was the worst in terms of both apparent digestibility and CH_4 emissions. It also showed a positive correlation between protein digestibility and gCH_4/MY ($p < 0.05$, $r = 0.63$) and gCH_4/ECM ($p < 0.01$, $r = 0.66$). To highlight that there wasn't a significant difference in the dry matter intake between the groups. In conclusion, the recommended dose to reduce CH_4 emissions is 100 g/head/d for dairy buffaloes. The double dose showed a low level of digestibility and a lower reduction in CH_4 emissions compared to T1 probably due to an excess of some components contained in RuFO® that might negatively affect the rumen fermentation process.

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P421

Total mixed ration in calf weaning: long-term effects on heifer performance

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To prepare a dairy heifer for a long and productive life, it is essential to feed her well from weaning.

The aim of this experimental trial was to evaluate the effects on the productive performance of Holstein heifers subjected to alternative weaning protocols compared to the standard starter-only protocol. These feeding protocols involved adding a total mixed ration (TMR) *ad libitum* to the pelleted starter. Thirty Holstein heifers (38.5 ± 1.96 kg at birth) were enrolled at 1 day of age and from 21 days of age were subjected to the following feeding protocols: starter *ad libitum* (CTR; $n = 10$), starter *ad libitum* and TMR *ad libitum* (TRT1, $n = 10$), and starter restricted to 50% of the CTR group's daily intake and TMR *ad libitum* (TRT2, $n = 10$). Milk administration was the same for all 3 groups. Calves were weaned at 63 days of age. After 2 years from weaning, the following information were recorded for each of the 30 heifers: age at first calving (months); newborn calf weight (kg, recorded on only 5 subjects per group); total milk production during first lactation (kg); mean daily milk production (kg/day); peak milk production; days in milk at peak; and duration of lactation (days).

The comparison of the mean values observed in each group, was performed by two-tailed one-way ANOVA for unpaired data, with Tukey's post-test. Statistical analysis was carried out with GraphPAD Prism v. 10.1.2 software, setting the significance level for $p \leq 0.05$ and tendency for $0.05 < p < 0.1$.

The age of first calving was not significantly different among the 3 groups. Data on average daily milk production showed no significant differences between the groups, although about 2 liters more milk per day was observed in the TRT1 group than in the CTR group. The TRT2 group showed a tendency for a higher peak milk production than the CTR group ($p = 0.0580$). Furthermore, a tendency towards an earlier peak lactation was observed in the TRT1 group compared to the CTR group ($p = 0.0557$). Regarding lactation duration, was similar among the groups (on average 343 days for the CTR compared to the treated groups that reported a duration of about 334 days). Body weight of newborn calves (all females) was higher in calves born to TRT1 heifers which weighed approximately 6 kg more than those born from the CTR group ($p = 0.0284$).

In conclusion, we can infer that the availability of TMR *ad libitum* during the weaning phase could improve the long-term performances of the heifers.

P528

Effect of different feeding regimens on fattening, carcass traits and meat quality of old Bergamasca sheep for arrosticini production: preliminary results

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Old Bergamasca sheep are often used for arrosticini production and are sent to slaughter when their productivity declines, resulting in a reduction of their economic value. Consequently, farmers are often forced to sell these animals at a low price, leading to financial losses. However, these sheep could be more effectively utilised and their value improved through fattening

programs aimed at producing high-quality meat. The objective of this study was to evaluate whether the use of three different feeding regimens could influence growth performance and meat quality aming at arrosticini production. Twenty-six female finishing sheep (aged 4 to 6 years) were divided into three homogeneous groups for a 60-days of experimental period. The Sugar Group (SG) was given hay ad libitum and a feed containing 8% sugar (5% in the Fat Group) from molasses (3 kg), while the Fat Group (FG) received hay ad libitum and a feed with 7.4% fat (2.7% in SG), derived from vegetable fats (4.8 kg). The Pasture Group (PG) was fed exclusively on pasture throughout the experiment. Feed intake was estimated in the SG and FG groups, while growth performance was measured in all groups. At the end of the trial, all animals were slaughtered. Body weights and pH were recorded at slaughter and 24 hours post-mortem. All data were statistically analysed using a mixed model procedure (fix and random effects, JMPpro v18).The pre-slaughter weights showed that SG had the highest weight, followed by FG, and PG had the lowest weight. Consequently, the slaughter body weight was also highest in SG (36.47 kg), followed by FG (35.73 kg), and PG (33.00 kg). The 24-hour post-mortem pH was 5.43 for FG, 5.30 for SG, and 5.40 for PG. Drip loss analysis indicated a decrease of 1.00% for FG, 1.20% for SG, and 0.90% for PG. Cooking loss values were 0.35% for FG, 0.32% for SG, and 0.30% for PG. In terms of colour analysis, the FG meat presented the highest lightness value (L* = 39.07), compared to SG (L* = 37.71) and PG (L* = 36.09). The redness (a*) and yellowness (b*) values were similar among the groups. SG had values of 19.62 (a*) and 4.48 (b*), FG had 19.09 (a*) and 4.40 (b*), and PG had 19.16 (a*) and 4.65 (b*). In conclusion, there were no differences in growth performance, but the SG group showed higher hot and cold carcass weights (36.88, $p < 0.01$; 36.02, $p = 0.03$). The FG group had higher copper (0.95, $p < 0.01$) and selenium (0.04, $p < 0.01$) levels in meat quality, while the PG group had higher α-Linolenic acid (n-3) content (0.04, $p = 0.04$).

P537

Feeding teff (Eragrostis tef) to lactating dairy sheep: a forage option in the Mediterranean basin

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Teff (*Eragrostis tef*), a C4 grass native to Ethiopia, is gaining attention as a hot-season fodder crop in the Mediterranean basin due to its good nutritional value and adaptability to arid climates. This study evaluated the effects of teff versus sorghum grazing on milk yield and composition in dairy sheep. Thirty-two Sarda breed sheep in late lactation (150 ± 10 DIM) were divided into two homogeneous groups according to pasture type: teff ($n = 16$) and sorghum ($n = 16$). Milk yield (kg/day) and compositional traits fat (%), protein (%), and urea (mg/dL) were monitored across five weekly sampling points (T0–T4). Statistical analysis was performed using a repeated measure ANOVA, including diet, time, and their interaction as fixed effects, and the animal as a random effect.

Significant main effects of diet were observed for milk fat and urea content ($p < 0.0001$). The sorghum-fed group produced a comparable milk yield (0.87 ± 0.12 kg/day) to the teff-fed group (0.81 ± 0.15 kg/day, $p = 0.3$), even though exhibited higher fat content from T1 to T4 (7.19 ± 0.3% *vs*. 5.68 ± 0.8%, $p < 0.001$). The protein content did not differ between groups but increased over time, significantly in the teff group at T4 compared to T0 (6.19 ± 0.82% *vs*. 5.12 ± 0.51%, $p < 0.0001$). The urea content was significantly higher in the sorghum group at T2 (71.11 ± 7.84 mg/dL), with differences highly significant ($p < 0.0001$) across other diet × time combinations. The differences observed in milk composition may be partially explained by variations in the intake of teff and sorghum during grazing, which are influenced by their specific nutritional characteristics. In this study, teff demonstrated similar performance to sorghum in terms of milk yield and protein content but was associated with a lower milk fat content that deserves further investigations. Teff could represent an attractive forage option due to its adaptability to arid climates and overall nutritional profile. Further researches are in progress to explore additional milk quality and sanitary traits (i.e. fatty acid profile, mineral composition, and somatic cell count) and to assess the economic and technical feasibility of teff as pasture, including feed costs, seed availability, and cultivation techniques.

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P548

Effect of starch source in finishing diets on carcass and meat quality of culling Sarda ewes

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The aim of this study was to assess the effect of starch sources (barley *vs.* corn) on the evolution of body fat deposition, carcass traits, and meat quality of culled Sarda ewes. Forty culled ewes (Body condition score, BCS: 2.58 ± 0.20; mean ± SEM) were equally allocated to two dietary groups and fed *ad libitum* diets containing different proportion of corn and barley: diet 1 (CORN group) with 25% of corn, 15% of barley, and 60% of wheat middling; diet 2 (BARL group) with 25% of barley, 15% of corn, and 60% of wheat middling. Ewes of both groups had also *ad libitum* access to straw and water for one month until slaughter. During the trial, body weight (BW) and BCS were recorded weekly. At slaughter, carcass measurements, pH and colour traits were recorded from the left side of the carcass. Proximate composition, cooking and drip losses were evaluated using the *Longissimus thoracis et lumborum* (LTL) muscle. Experimental results evidenced that dietary treatment had no effect on BCS and BW. The CORN group showed a higher ($p = 0.039$) cold carcass yield and a tendency for higher rib fat thickness (25.13 *vs.* 20.83 ± 1.28 mm; $p = 0.068$) compared to BARL group. Dietary treatments did not affect pH, colour, cooking and drip losses. The LTL of CORN animals displayed a higher moisture (70.65 *vs.* 68.73 ± 0.45%; $p = 0.032$) and lower protein (19.05 *vs.* 20.74 ± 0.39%; $p = 0.028$) content, while lipid content was unaffected by the diet. In conclusion, the implementation of a fattening program for culled dairy livestock at the end of their productive careers could be a valuable opportunity to replenish body reserves mobilised during lactation and to improve carcass conformation and meat quality. However, our results did not provide clear evidence for evaluating the best starch source to include in the diet. Therefore, further studies are needed.
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P555

Application of Near-Infrared Spectroscopy (NIR) for the compositional assessment of teff hay

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Eragrostis tef (Zucc.) Trotter (teff) is a cereal native to Ethiopia, valued for its nutritional properties, drought tolerance, ability to produce high-quality forage and its valuable genetic diversity within which interesting productive traits can be actively selected. In this context, near-infrared spectroscopy (NIR) represents an advanced tool for rapid and non-destructive analyses, particularly suitable for the forage nutritional quality phenotyping. In this study, 85 teff hay samples belonging to six different genotypes, cultivated under controlled agronomic conditions (Genetic Service Srl, Deliceto, Foggia, Italy), were collected at two successive heading stage cuts (C_1 and C_2). The samples were subjected to proximate analysis for crude protein (CP), ash, neutral detergent fiber (NDF), and acid detergent fiber (ADF). The same samples were scanned with a portable NIR (AuroraNIR, Grainit SRL, wavelenght 950–1650 nm), to develop calibration models for estimating the previously cited parameters. Each cut dataset was randomly divided in calibration ($n = 55$) and validation subset ($n = 30$). For calibration purposes, Partial Least Squares (PLS) and Multiple Linear Regression (MLR) combined with Principal Component Analysis (PCA) were employed, along with spectral pretreatments including Detrend (D), standard normal variate (SNV), and D-SNV, to optimise model accuracy. The results showed that for C_1 samples, the best coefficient of determination ($R^2 = 0.86$) was obtained for CP using the PLS method and the D-SNV spectra pretreatment, with a root mean square error of prediction (RMSEP) of 0.48%. For the NDF, the best model achieved an $R^2 = 0.82$, also with the PLS method and the D pretreatment, and an RMSEP of 1.12%. In C_2 samples, the best

result ($R^2 = 0.84$, RMSEP of 0.32%) was obtained for ash with PLS and the D pretreatment. For ADF, the best model showed an $R^2 = 0.68$ with SVN pretreatments and an RMSEP of 0.96% for C_1. Such results confirmed partly that by adopting different modelling approaches and spectral data pre-treatment, NIR spectroscopy could accurately predict the proximate composition of teff hay, allowing for the rapid phenotyping required by wide selection schemes. The difference in the predictive reliability of the used portable NIR spectrometer on consecutive cuts of teff plant material, deserves further investigation.

P241

The effect on productive performance and rumen pH of a *Saccharomyces cerevisiae* postbiotic inclusion in the finishing diet of Chianina bullocks

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Postbiotics are promising tools to enhance livestock welfare and performance. This study evaluates the effects of a liquid postbiotic based on selected, inactivated and stabilised Saccharomyces cerevisiae cells on performance and ruminal pH in Chianina bullocks during a three-month finishing phase. Twenty-two Chianina bullocks, 19 ± 2 -month-old, were divided into two groups. During the 3-month period of the trial, the control group received a typical finishing diet (wheat straw and concentrate ratio: 1:6), while the treated group received the same diet with 2% postbiotic inclusion in the concentrate. Both the groups were provided with feed ad libitum. Live body weight and dry matter intake (DMI) was recorded every 15 days. At the end of the experiment the animals were slaughtered. During slaughtering, rumen was opened, and pH was measured. Hot carcass weight data were collected to evaluate the dressing percentage. Concentrate DMI did not differ between the two groups, with an average consumption of 12.0 ± 0.9 kg/d per animal in the control group and 11.0 ± 1.1 kg/d per animal in the treated group (*P*-value = 0.55). Similarly, no differences were observed in daily forage DMI, with values of 1.8 ± 0.1 kg/d per animal in the treated group and 1.5 ± 0.1 kg/d per animal in the control group (*P*-value = 0.22). Average daily gain (ADG) was calculated from the slope of a linear regression of weight on animal age. The results showed no differences in ADG between groups, with average values of 1.25 ± 0.10 kg/d and 1.33 ± 0.11 kg/d for the treated and control group, respectively (*P-value* = 0.65). Similarly, the dietary treatment did not affect carcass yield, with both groups averaging 62%. The analysis of ruminal pH revealed only numerical differences between groups, with average values of 5.91 ± 0.16 and 6.20 ± 0.15 for the control and treated group, respectively (*P-value* = 0.19). Throughout the trial, the animals were in good health with no signs of stress, and this may have masked the effects of the postbiotic on welfare and growth performance. Furthermore, single-point measurements at slaughtering may not appropriately reflect the benefits of the treatment on the ruminal pH, which needs to be monitored in a continuous way. Further studies are needed to combine these findings with the characterisation of the ruminal bacterial populations and the produced metabolites, potentially influenced by the postbiotic.

P284

Hedysarum coronarium L.: an undiscovered forage resource for sheep feeding

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In sheep nutrition, the inclusion of leguminous forages is crucial to providing high-quality protein with environmental benefits also in terms of greenhouse gases due to their secondary metabolites. The trial was conducted to characterise Sulla forage (*Hedysarum coronarium* L.) in terms of nutritional value and environmental sustainability. The investigation involved two comparisons—preservation systems (pelleted, fresh, hay) and different plant parts (whole plant, flowers, leaves, stems) – determining chemical composition and secondary metabolites (total polyphenols and condensed tannins) content. The *in vitro* organic matter digestibility (dOM), fermentation maximum rate (Rmax), volatile fatty acids production (VFA) was studied incubating the samples with sheep rumen fluid for 120 h. The methane production (CH_4) was estimated from VFA at 24 h. As result, pelleted and fresh Sulla showed the highest protein and lipids content and the lowest fiber and lignin content (% DM): CP 15.1, 15.7 and 11.8, EE 2.32, 2.40 and 1.39, NDF 39.5, 40.1 and 54.8, ADL 5.31, 6.03 and 7.88 in pelleted, fresh and hay, respectively. The condensed tannins (g DE/kg DM) and total polyphenols (g GAE /kg DM)

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content follow the same trend: fresh > pelleted > hay (15.9, 7.17, 4.60 and 21.1, 13.6, 9.72 for tannins and polyphenols. The presence of these molecules significantly ($p < 0.05$) improved dOM (fresh 62.7 > pelleted 55.7 > hay 52.0 %) and Rmax (pelleted 9.86 > fresh 9.84 > hay 6.18 ml/h). The presence of secondary compounds in the different fresh Sulla parts influenced the *in vitro* CH_4 production: the low ($p < 0.05$) value found in flowers (20.9 % total gas) is related to the high ($p < 0.05$) tannins and polyphenols content (27.5 g DE/kg DM and 39.4 g GAE/kg DM, respectively), the high ($p < 0.05$) value found in stems (28.3 % total gas) is related to the low ($p < 0.05$) tannins and polyphenols content (7.74 g DE/kg DM and 9.35 g GAE/kg DM, respectively). The high fiber content in stems (NDF: 53.5 % DM) caused the increase of the CH_4 production (28.3 % total gas). Overall, Sulla forage showed interesting nutritional characteristics to be considered a valid forage base for sheep. Pelleted Sulla represents an effective opportunity to exploit the considerable forage potential in periods of insufficient pasture availability, reducing biomass and nutrient losses and preserving the properties of the bioactive components. The secondary metabolites confirm to reduce the *in vitro* methane production.

P464

Effect of different feeding sequences of soybean meal on lactating dairy ewes fed ryegrass rich in water-soluble carbohydrates

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Timing of feed supply may positively affect energy and protein availability, rumen synchronisation, and microbial synthesis. The aim of this study was to test two different feeding sequences of a protein source (soybean meal; SBM) to improve the efficiency of utilisation of ryegrass (*Lolium multiflorum* Lam. var. westerwoldicum) in the vegetative stage, rich in water-soluble carbohydrates (WSC; 27.4% of DM) and poor in CP (8.8% of DM). Ten lactating Sarda ewes were divided into two homogeneous groups: control (CNT) and third meal soybean meal (TMS). The CNT group received a total of 358 g DM/d per ewe of SBM subdivided in two equal meals at milkings (7.30 AM and 4.30 PM), while the TMS group received the same total amount per ewe in three meals, to improve the synchronisation of CP and WSC use: 89 g DM at morning milking (7.30 AM), 222 g DM at 12:00 AM, 30 min before the grass supply, and 45 g DM at afternoon milking (4.30 PM). The ewes of both groups received ad libitum freshly daily cut grass from 12:30 AM to 7:00 AM of the subsequent day, fed indoors with automatic individual Biocontrol AS (Rakkestad, Norway) feeders. Both groups also received 484 g of whole corn grains and 266 g DM/d of beet pulps (g/d per ewe, DM basis), divided in two equal meals (8.00 AM and 5.00 PM). Data were analyzed with an experimental design based on ANOVA which included fixed effects of treatment and day, their interaction and random effect of animal. During the trial, total DMI, grass intake and corn grain and beet pulp intake did not differ between two groups. However, the total intake of SBM was higher in CNT than in TMS group (355 and 324 g DM/d, respectively; $p = 0.004$). The difference derived from the lower intake of the TMS group observed at the 12.00 AM meal, while the SBM supplied at milkings was completely consumed in both groups. The milk yield and milk fat content did not differ between groups. However, the milk protein content of afternoon milking was significantly higher in CNT than in TMS (4.80 and 4.69%, respectively; $p = 0.05$). Conversely, the daily milk urea (TMS 27.1, CNT 23.4 mg/dl; $p = 0.02$), and milk urea of morning milking (TMS 26.1, CNT 22.3 mg/dl; $p = 0.03$) were higher in TMS than CNT. Milk urea of afternoon milking tended to be higher in TMS than in CNT ($p = 0.08$). In conclusion, the supply of part of SBM before WSC-rich ryegrass seemed to negatively affect protein utilisation efficiency, likely due to worsened nutrient synchronisation in the meals at milking.

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P491

Effect of green forage on the particle size of rations in buffaloes and its influence on sorting ability

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The particle size distribution (PSD) of the total mixed ration (TMR) influences feed intake and sorting behaviour (SB) in lactating ruminants. Previous studies demonstrated that adding green forage (GF) alters the PSD by increasing the proportion of particles retained in the first sieve and decreasing those in the second one. This study evaluated the effect of adding 5 kg/head/day of GF

(*Sorghum bicolor*) on the PSD and SB of lactating buffaloes during summer (July–August 2024). For the first 15 days, buffaloes were fed a standard TMR, and from day 16 onward, GF was added. Two groups of buffaloes were observed: Group A (33 buffaloes), managed with an automatic milking system, and group B (24 buffaloes), managed with conventional milking. The TMR was distributed twice daily using a towed mixer wagon. Daily dry matter intake (DMI) was calculated by subtracting 24-hour refusals from the total TMR provided. The PSD of TMR and refusals was analysed using the Penn State Particle Separator, which includes three sieves (19, 8, and 4 mm, respectively labelled US, MS, and LS) and a bottom collector (<4 mm, Bottom). Feed sorting (FS) was calculated based on PSD changes. Physically effective neutral detergent fiber (peNDF), geometric mean particle length (GMPL), and aNDF were determined. Statistical analysis was performed using a general linear model with group (random effect), GF inclusion (fixed effect), and their interaction. Statistical significance was declared at $p < 0.05$. Significant differences in PSD were observed for GF-TMR in both groups: values for US, peNDF, and GMPL were higher, whereas Bottom values were lower ($p < 0.001$). No PSD differences were found across groups for either diet, confirming that the rations were identical. There was no difference in DMI between groups or diets. No differences in FS were observed between diets, but significant FS differences were observed between groups. Compared to group B, buffaloes of group A demonstrated a greater FS capacity in that they discarded more US (98.60 vs. 99.36%, for A and B, $p < 0.05$) and consumed more MS (100.24 vs. 100.09%, $p < 0.01$) and Bottom (100.95 vs. 100.40%, $p < 0.05$). Therefore, while the addition of GF affected PSD, it did not influence the FS capacity of group A. However, GF reduced the FS capacity of group B for the second sieve and showed a trend for the first sieve ($p = 0.02$ and 0.05 for MS and US), suggesting a difference in feeding behaviour associated with the type of milking management.

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P520

Characterization of rumen-fecal microbiota in dairy cows with different productive performances

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Milk production in cows is influenced by microbiota, but the connection between them remains unclear. This study aimed to explore the differences in fecal and ruminal microbiota, ammonia levels, and volatile fatty acids between lactating cows with different production performances. Twenty lactating cows from the Alma Mater University of Bologna Dairy Research Farm were enrolled in the study. The cows were fed the same diet and based on their productivity, they were divided into two groups: high-producing cows (HY) and low-producing cows (LY). Rumen protozoa, ammonia (NH_3) concentration, and VFAs were analyzed. DNA was extracted from both rumen and fecal samples, purified, and sequenced using Illumina MiSeq. All samples were analyzed using a bioinformatics pipeline based on QIIME2, and the R environment was used for alpha and beta diversity analyses. For VFAs, acetic and propionic acids differed significantly between groups ($p \leq 0.05$). No statistical differences were observed in the main protozoal genera or ammonia concentrations. Fecal and ruminal microbiota compositions revealed significant differences between the two groups. In rumen samples, the HY group showed a higher abundance of Lachnospiraceae ($p \leq 0.05$) and Muribaculaceae ($p \leq 0.05$), while Eubacteriaceae ($p \leq 0.05$) and RF16 ($p \leq 0.05$) were higher in LY cows. In fecal samples, Clostridiaceae ($p \leq 0.05$), Peptostreptococcaceae ($p \leq 0.01$), Mogibacteriaceae ($p \leq 0.05$), and *Bifidobacterium spp.* ($p \leq 0.05$) were more abundant in LY cows. These microbiological differences between the two groups suggest that the microbiota of the HY cows is related to a greater efficiency in nutrient absorption and conversion and a different dry matter intake, thereby contributing to higher milk production. Further studies are needed to understand the metabolic functions of the observed taxa and their potential role in improving production efficiency.

P560

Nutritional characterization and variability of different livestock feed used in the national feed industry

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In modern livestock farming, optimising and characterising feed use presents both a challenge and an opportunity. Effective feed management can reduce waste, increase profitability, and better align nutrient supply with animal requirements. To achieve this, it is crucial to analyze the raw feed provided to livestock, such as corn, soybean, sunflower, wheat, and their by-products, to identify potential differences even within the same type of kernels. The aim of this study was to evaluate the chemical and nutritional

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properties of some of the most commonly used feed ingredients in the national feed industry. Specifically, we sought to identify variations in their composition and digestibility. For this trial, samples were collected from one of the largest feed industries in Italy, comprising five replicates of the ten most commonly used feed products and by-products. The samples included: wheat middlings (from *Triticum durum* and T*riticum aestivum),* wheat flour, soybean hulls, beetroot pulp, soybean seeds raw and roasted, sunflower and soybean meal, corn (from Italy and abroad) and barley. Each sample underwent analysis to determine its content of protein (including soluble protein, NDIP, and ADIP fractions), starch, ether extract, fiber fractions (NDF, ADF, and ADL), ash, and amino acids. Additionally, fiber digestibility was analyzed at 12, 72, and 120 hours, alongside the digestibility of protein and starch. As expected, we observed minimal differences in the basic nutritional and chemical profiles within samples of the same product, with a few exceptions. Nutrients with highest variability were starch that varied in Italian corn (50.22 ± 4.85% DM) and barley (48.54 ± 6.18% DM), and fiber fractions as ADF that as a big standard deviation in soybean hulls (54.68 ± 4.41% DM) and sunflower meal (32.27 ± 6.01% DM). The most interesting results emerged in the differences of digestibility of fiber fraction, starch and protein among the five samples of each product. These differences were particularly pronounced for protein digestibility, including ruminal, intestinal, total tract, and bypass digestibility. To be mentioned for example the intestinal digestibility of protein in wheat middling varies up to 50% between samples on an average content of crude protein of 16.44% (complete data will be provided in the poster). This study underscores the importance of precise investigations into the chemical and nutritional characteristics of livestock feed. Such analyses are vital for optimising rations, meeting nutritional requirements, reducing waste, and enhancing the profitability of livestock farms.

P115

Variation in the faecal microbiota of deer in relation to the hunting area in the Friuli Venezia Giulia region

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The gut microbiota of reed deer is a topic of growing interest in animal biology, particularly with regard to its ecological and physiological importance. The diversity and composition of these microbial communities is influenced by environmental variables, diet and genetic factors, but also by seasonal changes and interactions with other organisms in their habitat. Understanding the dynamics of the microbiota of red deer not only provides us with important information about their health and feeding behaviour, but also has far-reaching implications for species conservation. The faecal samples were collected in 2 hunting ground from 5 hunting districts in the Friuli Venezia Giulia region, Italy. The hunters were instructed to collect 5 individual samples from the ground in each hunting ground so that a total of 50 samples were available. the samples were collected in a tube with a shield from the fecal center to avoid environmental contamination on the surface and were stored at –20 °C until analysis. After DNA extraction, the V3-V4 16s rRNA region was sequenced in a 250 PE mode using the Illumina Novaseq platform. The raw data were uploaded to QIIME2 and taxonomic annotation was based on the greengene database using a classifier trained on the amplified regions. The Chao1 alpha diversity index varied between districts ($p < 0.01$) and the Bray Curtis beta diversity index also indicated variation in microbiota between hunting areas. Firmicutes were the most abundant phylum, followed by Bacteroidetes, Actinobacteria, Tenericutes, Verrucomicrobia and Proteobacteria. Significant differences between districts ($p < 0.05$) were calculated for the phyla Firmicutes and Tenericutes, specifically for the districts in the North and North-East compared to the districts in the hills. Different trophic conditions and population density in the areas may explain the observed differences, but also anthropic pressure and competition with wildlife and predators could be factors interacting with host behaviour and gut microbiota.

SUSTAINABILITY

P527

An innovative system for enteric methane recovery

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Methane (CH_4) emissions from cattle farming contribute significantly to greenhouse gas emissions and climate change. In livestock farms, CH_4 is mainly generated through enteric fermentation and manure management, with approximately 85% emitted via exhalation during burping or breathing. Mitigating these emissions requires innovative strategies. The CH_4 Livestock Emission project (CH4rLiE) focuses on developing a CH_4 capture prototype for cattle farming environments, utilising zeolite crystals known for their high adsorption efficiency, from which CH_4 can be subsequently extracted. The research includes:

- CH_4 dispersion simulation: computational models simulate CH_4 diffusion in barn environments, accounting for competition with other gases such as carbon dioxide (CO_2), nitrous oxide (N_2O) and ammonia (NH_3). These simulations are crucial for determining optimal gas capture positions, strategic sensor placement, and maximising CH_4 recovery efficiency.
- Measurement campaigns: a dairy cattle farm representative of the livestock sector in Northern Italy was selected for the study. A measurement protocol was established, comprising four monitoring campaigns over one year. Each campaign spans one month with weekly 24-hour monitoring sessions, capturing emission variations under different climatic conditions. The sampling strategy includes 5 points along the barn's symmetry line, spaced 10 m apart. A photoacoustic spectroscopy analyzer and a multipoint sampler monitored CH_4, CO_2, N_2O, and NH_3 concentrations. Experimental data provided information to refine simulation models and identify potential installation locations for the CH_4 capture system.
- Prototype development and installation: insights from simulations and measurements guide the design and installation of a CH_4 capture prototype in the barn. The system's performance is under evaluation. Initial laboratory tests have yielded promising results.

The results of CH_4 dispersion simulations and measurement campaigns, highlighting optimal gas capture positions in the barn, will be presented. CH_4 concentrations ranged from 6.94 ppm in spring to 14.5 ppm in summer, highlighting seasonal variations influenced by temperature, humidity, and ventilation. The status of research and development for the CH_4 capture prototype, including initial laboratory findings, will also be discussed.

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P232

Rethinking livestock feeds with hazelnut by-products: a life cycle thinking approach

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Hazelnuts are one of the top produced nuts in the world. Their processing generates a significant quantity of by-products, as the kernel constitutes only 45% of the fruit's weight. Although the shell is already used in energy recovery applications, the skin currently lacks an established application. The nutritional properties of hazelnut skin, such as its high content of polyphenols and fatty acids, make it suitable for applications in diverse sectors, including livestock feeding. Traditional livestock feeding is associated with a high environmental impact within the livestock production value chain, and the introduction of by-products in animal diets can help minimise the associated environmental consequences and improve economic performance. Our study aims to evaluate the environmental and economic effects of introducing hazelnut skins into livestock diets. To assess the potential effects of this introduction, eight different diets were studied. Four conventional rations for cattle, lambs and swine were compared with four novel diets that incorporated hazelnut skin and entailed the substitution of part of their ingredients while maintaining the energy, protein and lipid values of the original diets. The amount of hazelnut skin introduced varied among the livestock studied. The Life Cycle Assessment (LCA) methodology was applied to compare the environmental performance of the regular and hazelnut skin diets. The functional unit chosen was 1 Kg of feed ration. Moreover, the economic implications were analysed by comparing the prices of the diets based on the ingredients. LCA revealed positive results for the diets with hazelnut skin, showing reductions in environmental impact of between 8 and 15%, depending on diet and impact category. The economic analysis also favoured the use of hazelnut skin, indicating a reduction in rations prices between 3 and 11% compared to conventional ones. However, the swine diet did not show an improvement, due to the limited inclusion of hazelnut skin, as the phenolic compounds negatively affect monogastric digestion. Additionally, other studies have shown slight increase in the omega-3 content of the meat from livestock fed hazelnut skin, further enhancing the performance of the hazelnut skin diets based on the final meat quality. Although the integration produced positive environmental and economic outcomes, further research is required to assess the performance and effects of this by-product on the animal diets.

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P361

The Italian rabbit sector: analysis of competitive strategies

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Although Italy is Europe's third largest producer of rabbit meat, this sector is characterised by a continuous decline. This dynamic reflects the current and growing decrease in demand, mainly due to lack of acceptance by young consumers and, more in general, the growing negative perception of the rabbit as meat-producing animal. However, the rabbit sector has interesting potential: its high self-sufficiency rate and ability to adapt to sustainable farming systems. Indeed, the rabbit, in addition to having a high reproductive rate and rapid growth, can efficiently use low-input resources and with limited feed-food competition in extensive systems, producing healthy and nutritious meat. Considering the uncertainty in the industry but also the possible positive resources, an exploratory survey was conducted on the strategies applied by Italian livestock farmers to meet the challenges and take advantage of the opportunities in the current market. The objective of the research was to identify farmers' motivations and expectations regarding product enhancement, related to meat quality, animal welfare and environmental/economic issues. Specifically, twenty producers were interviewed through a structured survey in the Italian context, considering both small and large farms. The questionnaire was structured in four sections, investigating: (a) type of farming (fattening and/or breeding) and number of animals raised; (b) sales channel; (c) farm's management strategies and perception of the competitive advantage derived from these practices; and (d) communication strategies used for promotion and product enhancement. Analysis of the data revealed a high degree of variety in terms of company size and the strategies applied. The main trend is to maintain traditional farming systems, which, on the other hand, are lacking in terms of facilities, certification, nutrition and breeds raised. In addition, a lack of structured communication emerged in the sample considered. In conclusion the results obtained make it possible to identify critical issues and propose new strategies to meet the preferences of more sustainability-conscious rabbit meat consumers.

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P067

A holistic approach for monitoring the environmental sustainability of the Italian Holstein cattle population

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Enteric methane emissions from ruminants are a major contributor to atmospheric greenhouse gas accumulation. Accurate measurement of methane production in ruminants is crucial to not only develop reliable national greenhouse gas emission inventories, but also evaluate mitigation strategies for methane emissions. A holistic approach to monitor environmental sustainability is implemented by ANAFIBJ including and integrating direct methods and indirect one. In 2019 the collection of methane, carbon dioxide emissions, feed intake and water intake started into ANAFIBJ Genetic Center on Italian Holstein young bulls candidates to Artificial Insemination in Italy. In 2023 the Italian Sustainability Consortium (ISC) was founded including University, Experimental Farms, Research Centers and Private Companies to extend data collection also on Italian Holstein dairy cows in Italian dairy farms. From April 2019 to January 2025 36.653 CH_4 records from Greenfeed ®, 559.800 feed intake records,

6.491 water intake records, 2.181 BCS records, 6.543 biometric measures records and 2.315 weight records have been collected on 272 Italian Holstein young bulls. From January 2023 to January 2025 25.400 CH_4 records from Moologger®, 66.864 CH_4 records from Greenfeed®, 108.624 feed intake records, 2.997 weight records and 2.853 rumination records have been collected on 120 Italian Holstein dairy cows. Life Cycle Assessment (LCA) has been developed and integrated into the farmer tool 'Herd Up' for Holstein dairy herds. A 'green passport' report has been generated to summarise the innovative phenotype records for each animal. Each tool plays a pivotal role in enabling farmers across the country to assess the environmental impact of their herds and make informed decisions regarding herd management.

P134

Circular animal feed: environmental impact of by-products in diet of dairy animals

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Animal-based products are pivotal in global nutrition, providing rich energy sources, protein, macro and microelements, and vitamins. Agriculture and livestock currently cover approximately 38% of the world's land area and are responsible for 23% of total net anthropogenic greenhouse gas emissions. Using by-products in livestock feed can be an additional strategy for safeguarding land use in agriculture and reducing the environmental impact of animal production and human food competition. This study aimed to determine the carbon footprint (CF) of two different concentrated feeds for livestock, both with and without the inclusion of agro-industrial by-products in the formulation. The two concentrated feeds were classified as concentrate feed formulated exclusively using by-products: by-product concentrate feed (BCF) and concentrate formulated exclusively using raw feed materials (CRF). The main ingredients of the BCF feed were 49.1% wheat bran, 21.6% biscuit meal, and 19.5% corn gluten meal. CRF had the following composition: 43.6% soybean extraction meal, 26.3% maize meal, and 26.3% barley meal. Both concentrate feeds were iso-energetic and iso-proteic. The CF (expressed in kg of CO_2 eq/kg of functional unit, FU) of the two concentrated feeds under study was determined using the commercial software openLCA 2.0.1 with the Agribalyse v. 3.0.1 database. The FU was 1 kg of concentrate feed. The characterisation factors employed for CF were 1, 34, and 298 CO_2 eq for CO_2, CH_4, and N_2O, respectively. LCA analysis showed a CF of 0.29 kg CO_2 eq and 0.46 kg CO_2 eq for BCF and CRF concentrates, respectively. The main pollutants for these feeds were CO_2 and CH_4 from fossils, N_2O from fertilisers and diesel combustion. In particular, for BCF feed, CO_2 from fossil sources accounted for 63.4% of pollutants, followed by N_2O (33.1%) and fossil-derived CH_4 (3.5%). CRF feed had 71.1% of its pollutants attributable to CO_2 from fossil sources, 26.0% to N_2O, and 3.0% to fossil-derived CH_4. In conclusion, using agro-agricultural by-products could represent a more environmentally sustainable alternative to formulate concentrated feed for livestock sectors, with lower competition for human nutrition than using vegetable raw materials.

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P180

Life cycle assessment of cow milk production: carbon footprint according to different nutritional functional units

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Milk and dairy products are essential for the population's sustenance, providing protein and minerals; however, sustainability should also be encompassed. Until now, the focus in food production has been on environmental and nutritional dimensions in an independent way. Therefore, these dimensions of the dairy system need to be improved to a holistic and inclusive approach through the nutritional life cycle assessment (nLCA), using functional units (FUs) based on nutritional components. The study aimed to estimate milk's carbon footprint (CF) at the farm gate (cradle-to-farm-gate) by applying the innovative nLCA concept. Ninety-four dairy farms located in the production areas of two dairy-protected-cheese designations of origin (PDOs), Grana Padano (GP) and Asiago (AS), were investigated. Several FUs referring to the nutritional values of whole milk were considered: 100g of milk, protein (g/100g of milk), calcium (mg/100g of milk), essential amino acids (EAA; mg/10g), branched-chain amino acids (BCAA; mg/10g), standard portion of milk (125mL) and energy of milk (100 kcal). The inventory data analysis was conducted using SimaPro® 9.5.0.0 software tool by implementing the Ecoinvent database v. 3.9.1; the statistical

analysis was performed using JMP® Pro 17.0.0. No significant differences between CF of GP and AS were detected. The milk from GP farms was characterised by higher CF than AS for all the considered FUs. In detail, 0.17 *vs* 0.16 kg CO_2 eq per 100g of milk, 4.93 *vs* 4.56 kg CO_2 eq per 100g of protein, 0.14 *v*s 0.13 kg CO_2 eq per 100 mg of calcium, 1.09 *vs* 1.01 kg CO_2 eq per 10g EAA, 2.21 *vs* 2.05 kg CO_2 eq per 10g BCAA, 0.21 *vs* 0.20 kg CO_2 eq per 125mL, 0.34 *vs* 0.32 kg CO_2 eq per 100 kcal, for GP *vs* AS, respectively. The monitoring of additional milk quality variables (amino acids, minerals and vitamins), other than what is routinely checked (protein, fat, lactose, total bacterial count, and somatic cell count), is needed to further improve the estimate and interpretation of nLCA.

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P186

Impact of in-feed biochar supplementation on GHG and ammonia emission from manure produced by Holstein calves

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The increasing concern over greenhouse gas (GHG) emissions and ammonia volatilisation from agro-zootechnical systems necessitates innovative strategies for sustainable livestock management. Biochar has emerged as a promising feed supplement to enhance the environmental management and to reduce the impact of livestock. The aim of this study was to explore the effect of biochar as a feed supplement in Holstein calves on manure pit storage and GHG and ammonia emissions. At the end of a previous feed experiment (lasted 56 days) on Holstein calves, the solid manures were collected from individual boxes and pooled into dynamic chamber (30L) to simulate manure storage. We used the manure produced by pre-weaning calves randomly assigned to control group (CTRL, n calves = 12, the basal diet composed of milk and ad libitum feed) and to a treated group (CHAR, n calves = 12, the basal diet composed of milk and *ad libitum* feed +10 g/calf/day of biochar). Manure emissions of CO_2, CO, CH_4, N_2O, NH_3 were monitored by FTIR portable gas analyser (GasmetGT5000Terra) on day 0, 1, 2, 7, 14, 21, 28 and the gas fluxes were calculated (g/m_2/h). Data were analysed by PROC GLIMMIX (SAS 9.4) and presented as LS-means and standard error. Overall results showed that in experimental conditions the manure produced by the Holestein calves fed with biochar induced a change in GHG and ammonia emission profile. At day 0 carbon emission (CO_2, CH_4) were significantly lower in CHAR manure (–(–29% CO_2, – 15 % CH_4), whereas during the incubation we observed an increase in CO_2, CH_4 and CO emission compatible with organic matter decomposition and fermentation. Overall nitrogen emissions (NH_3 and N_2O) showed a reduction by 20% ($p < 0.05$) for N_2O emission and by 46% ($p < 0.001$) for NH_3 in CHAR manure compared to CTRL manure. These results showed that the biochar affected the GHG and ammonia emission, organic matter fermentation and manure stabilisation exhibiting a potential implication in agro-zootechnical systems. Further studies are essential to fully understand its long-term impacts and efficacy across different livestock management systems.

P212

Microalgae deriving from the biochemical conversion of CO_2 as innovative and sustainable sources of functional additives in laying hen diets. The GREEN-EGG project

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The European Green Deal consists of policy initiatives aimed at achieving climate neutrality by 2050. In this context, AGRITECH (Italian National Center for Technology in Agriculture) promotes the use of cutting-edge technologies to support the digitalisation and decarbonisation of agriculture's green transition. The GREEN EGG project focuses on enhancing agro-industrial by-products through innovative bio-based methods, utilising an advanced algal growth system that absorbs and converts CO_2. This system, based on the biorefinery concept, aims for decarbonisation while ensuring continuous production of selected microalgae. The approach improves plant productivity, boosts microalgae quality, reduces energy costs, and supports ecological sustainability for future scale-ups. The project will use photobioreactors where algae absorb CO_2 during photosynthesis, converting it into organic compounds such as sugars and proteins. Technologies

include CO_2 delivery systems, light and temperature control, and nutrient optimisation to enhance algae growth and CO_2 conversion. Advanced sensors and automation will monitor and adjust conditions for optimal CO_2 absorption. The microalga Haematococcus pluvialis, known for its high astaxanthin content (a potent antioxidant), will be used in the project. Specialised LEDs emitting blue (450–495 nm) and red (620–660 nm) light will trigger stress responses in the algae, stimulating natural defense mechanisms to enhance astaxanthin production. The project also aims to implement a circular economy model by incorporating Haematococcus pluvialis and its extracts as nutraceuticals in the diets of laying hens. Innovative feed formulations will improve both the production and quality of 'sustainable and enhanced' eggs. This process leverages advanced technologies such as cloud computing for data processing, AI to automate operations and monitor KPIs, and blockchain to track the entire supply chain, creating a trusted layer of real-world evidence accessible to all stakeholders. The expected outcomes focus on egg quality, antioxidant content, yolk color, and the development of a web application and trained AI model. Ultimately, the GREEN EGG project envisions a virtuous cycle that reduces environmental impact while improving animal welfare and egg quality.

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P410

Inclusion of grape pomace in dairy ewes diets: effects on milk production and methane mitigation potential

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The valorisation of winery wastes and by-products within a circular economy framework aligns with efforts to reduce the carbon footprint of the livestock industry. Utilising these by-products as dietary supplements supports sustainable and integrates high-value bioactive ingredients into the food chain, positively impacting human health through a farm-to-fork approach. Grape pomace (GP), the major residue of the viticulture industry, shows significant potential as feed for dairy sheep, particularly in reducing enteric methane (CH4) emissions. This study evaluated the effects of incorporating dried grape pomace (GP) at a 10% inclusion level (DM basis) into dairy ewes' diets on CH4 emissions both *in vitro* and *in vivo*. *In vitro*, the GP diet significantly reduced CH4 production ($p < 0.01$) to 38.5 ml/g DM compared to 48.0 ml/g DM in the control, measured with the Gas Endeavour® system; five fermentation trials were conducted, each with 4 replicates per sample (TMR, TMR +10%GP), using rumen liquor from slaughtered sheep mixed 1:4 with lab-made artificial saliva. Fermentation continued for 24 hours at 39.5 °C. *In vivo*, twenty-six pregnant Assaf dairy ewes, homogeneous in age, weight, and body condition, were randomly assigned to two dietary treatments: (1) a control diet (CON), and (2) a diet supplemented with 10% GP (DM basis). The study lasted a total of 12 weeks starting from two weeks before lambing (T0). All ewes received polyphite hay *ad libitum*, and a 1 kg/head/day of a custom-formulated concentrate, with GP ewes receiving a GP-supplemented concentrate to achieve 10% of the total diet on a DM basis. Milk yield and composition (fat, protein, casein, lactose, pH, milk urea nitrogen, and somatic cell count) were analyzed weekly. CH4 emissions were measured using a laser methane detector (LMD) at multiple time points. Preliminary results, performed through a repeated-measures ANOVA, revealed significant differences in CH4 emissions ($p < 0.01$). Post-treatment emissions showed a 20% reduction compared to pre-treatment levels, suggesting that condensed tannins in GP may have altered the rumen microbiota and reduced enteric CH4 production. Significant differences were observed in both milk yield and chemical composition between the control and treated groups. These findings suggest that GP has the potential to enhance the sustainability of ruminant nutrition by mitigating CH4 emissions. Further research is needed to explore its mechanisms and broader applications.

P511

Monitoring the greenhouse gas emissions and proposal of sustainable building systems in dairy cattle farms. The MITIgA project

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It is widely recognised that greenhouse gas (GHG) emissions from livestock are a major source of environmental impact and climate change. The agricultural sector is responsible for a significant fraction of GHG emissions in Europe and the world. According to European Environment Agency (EEA) data, agriculture contributed 10.3% of EU GHG emissions in 2019 (70%) from livestock farming, mainly due to the production of methane and nitrous oxide produced in the enteric fermentation of ruminant animals and from the management of manure. This research project named MITIgA, addresses dairy cattle farms in Sicily. To meet the current challenges of reducing the ecological footprint, it is necessary to: encourage practices that reduce GHG emissions and monitor their effects in the short to medium term; improve the sustainability of livestock facilities by building solutions that have a lower environmental impact, including the use of production waste in the logic of the circular economy and that ensure greater animal welfare, especially in marginal and/or mountainous areas where there are many extensive livestock farms. To monitor GHG emissions in livestock farms, it seems essential to develop systems for remote measurement, based on wireless sensors, transmitters and receivers, that allow real-time detection of GHG concentrations in the barn. The objectives of the MITIgA project can be ascribed to two specific areas: (a) GHG monitoring in livestock farms with multi-temporal and multi-scale approaches with the development of low-cost IoT sensors and specific software support and (b) proposal of sustainable livestock building systems for marginal and/or mountainous areas. For the first objective, specific advanced artificial intelligence-based algorithms will be developed to analyze and interpret the collected data. In the selection of machine learning models, including neural network-based algorithms, priority will be given to advanced regression techniques and deep learning algorithms to process and interpret GHG. These models will be customised to recognise and adapt to seasonal and/or daily variations in GHG emissions. Finally, for the second objective, modular building systems based on materials with a low ecological footprint (natural and/or waste from the processing of agricultural products) are proposed. We proposed sustainable building systems and materials, based on timber and other materials derived from plants and vegetable-fibers and agri-food byproducts.

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P568

In vitro evaluation of digestibility, gas and methane production from winery by-products

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The food industry generates substantial amounts of agro-industrial by-products, posing significant economic and environmental challenges for disposal. Among these, the wine industry produces large quantities of waste, including grape pomace (skin, seed and pulp) and grape skins, rich in polyphenols, with potential for valorisation in animal nutrition, as they are known to influence rumen fermentation and microbiota composition. The aim of the present study was to evaluate the nutritional properties, rumen digestibility, *in vitro* gas/methane production of Grape pomace (GP) and Grape skin (GS) at the inclusion level of 10% on DM basis in a standard sheep diet. Each by-product and experimental diets were subjected to centesimal chemical analysis: dry matter (DM), Ash, crude protein (CP), ether extract (E.E.), neutral detergent fiber (NDF), acid detergent fiber (ADF) and acid detergent lignin (ADL). For each by-product, a polyphenol characterisation was also performed. *In vitro* true dry matter digestibility (IVTDMD) was measured using the Ankom Daisy II filter bag technique, following Ankom Technology procedures. Four replicates per sample (TMR, TMR +10%GP, TMR +10%GS), were analyzed in each jar (3 total fermentation jars). The fermentation was conducted at 39,5 °C for 48h. Gas and methane production were monitored with the Gas Endeavour® system in 5 fermentation trials (4 replicates per sample) using rumen liquor (1:4 mix with lab-prepared artificial saliva) for 24 h at 39.5 °C. The results were processed

through a two-way ANOVA, considering dietary supplementation and rumen fluid used for each trial as factors of variability. A post-hoc Tukey-HSD test was then performed. The differences between the means were considered statistically significant with a p value <0.05. All the experimental diets showed no significant differences compared to the control for IVTDMD. The grape enriched diets showed a significant reduction ($p < 0.05$) of methane production: 38.5 mL/g DM (GP), 39.5 ml/g DM (GS), compared to C (48.0 ml/g DM). Preliminary results showed that condensed tannins in the GP may have altered rumen degradation by decreasing methane production without adversely affecting digestibility. These findings highlight the potential of grape pomace as sustainable feed additives in ruminant nutrition. Its inclusion in sheep diets reduced methane emissions without compromising nutrient digestibility. Further *in vivo* studies are needed to confirm its efficacy.

P173

Study of the relationship between animal welfare and environmental impact in Italian dairy cattle farms

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The growing awareness of sustainability in livestock systems highlights the need for integrated approaches to evaluate both Environmental Impact (EI) and Animal Welfare (AW). Poor integration of AW in environmental evaluations risks promoting practices that could harm long-term sustainability, considering that welfare and health benefit production efficiency. This study aims to develop a framework for evaluating dairy cattle farms by merging Life Cycle Assessment (LCA) method for EI evaluation with the ClassyFarm protocol for AW assessment, implemented by the Italian Ministry of Health. During the period 2023–2024, 20 Italian dairy cattle farms were surveyed to provide data from the years 2021 and 2022. Inputs (e.g. fuel, fertilizers, pesticides, electricity, purchased feed, etc.) and outputs (e.g. milk, waste, etc.) were collected for the implementation of a cradle-to-farm gate LCA approach. LCA was carried out using Simapro software v9.6 (PRé Sustainability, Netherlands) alongside the Ecoinvent v3.10 and Agri-footprint v.6.3 databases. The assessment was performed using the Recipe2016 Midpoint (H) method. The functional unit applied was 1 kg of fat and protein corrected milk, and an allocation factor was calculated to exclude the beef co-product. AW score (%) and antimicrobial use data (measured in Defined Daily Dose Animal for Italy – DDDAit) were obtained from the ClassyFarm system. On-farm data collection and analysis are still ongoing. For the first 7 farms, results for Global Warming Potential (GWP) showed a mean of 1.60 kg CO_{2eq} (range: 1.06–2.44). The main processes contributing to CO_{2eq} production were self-produced feed (40.21%), enteric fermentation (38.62%), and purchased feed (18.54%). The AW score resulted in a mean of 78.57% (range: 72–87), and DDDAit had a mean of 5.13 (range: 2.47–12.9). A not significant weak negative correlation was found between GWP and AW (Pearson R= –0.25), and a not significant moderate positive correlation between GWP and DDDAit (Pearson R = 0.42). Next steps involve validating the LCA model and adding additional data on co-products beyond beef (e.g. energy sold from photovoltaics and biogas, agricultural products). Additionally, including the remaining farms could help in clarifying the preliminary results on the relationship between environmental impact and animal health and welfare.

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P310

Analysis of sustainability and digitisation in member companies of the CAO Cooperative of Oristano

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This study presents the first results of the questionnaire 'Progetto Sostenibilità CAO' ('CAO Sustainability Project') administered to the members of the cooperative C.A.O. of Oristano, for the drafting of the first Sustainability Report. The document analyses the company's activities and sustainable development strategies, highlighting economic, financial, digital, social, and environmental aspects. The data collection, anonymous and in compliance with privacy regulations, was conducted on sample stables through a questionnaire, based on the Stanford Design Thinking model, with the participation of representatives of the Cooperative. The questionnaire covered aspects such as geographical location,

livestock management, labour, farm area, use of renewable energy and farm data management, also using barn software. The technical-economic-environmental data were collected using the process analysis methodology and following the Life Cycle Inventory (LCI) guidelines, which enabled the processing of information for the calculation of environmental impact and life cycle cost (LCC). The questionnaire was completed by 300 member farms for the 2023 crop year. The results, processed with descriptive statistics, show wide variability. In particular, the member farms had on average 267 sheep per farm (range: 25-4005). On average, just under 50% of the ewes on the farm were milking in December 2022 and 73% of the ewes were milking at the beginning of February 2023. Farms average 27 hectares (range: 2–650), mostly non-irrigated. There is a predominance of small and medium-sized farms. They are used for natural pasture or autumn grassland. Few farms have wind turbines (10 kW). The other plants are photovoltaic (29 kW). Most of the farms are concentrated in the hills and plains, a few in the mountains and a few adhere to the organic regime. The sheep reared are of the Sardinian breed using the 'semi-' method. Only a third rely on feed companies. The labour force is mainly family-based and the management of farm data is heterogeneous: some farms use digital tools, others paper documents, while most do not track data. The results show a heterogeneous landscape: some farms are adopting digital technologies and sustainable practices; others are in an early stage of transition. These preliminary data define a sample on which to perform GHG emissions analysis, describe the social basis for developing strategies to promote sustainability and digitisation, and optimise decision-making in dairy farm management.

P422

Enteric methane emissions in organic Brown Swiss cows

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In vivo measurement of enteric methane (CH_4) emissions is the challenge of these years due to the wide potential of the non-invasive devices developed to detect individual emissions such as the Sniffer, GreenFeed and the Laser Methane Detector. The implementation of these instruments within commercial farms may allow to easily quantify the emissive levels under specific farm managements and among different species and breeds, and provide an overview of the actual enteric emissions from ruminants. This study aimed to monitor the CH_4 and carbon dioxide (CO_2) emissions in a commercial organic farm rearing Brown Swiss cows and improve the understanding of the emissive levels of a livestock system little known in the literature. The concentrations of CH_4 and CO_2 were simultaneously recorded during the milking by using a Sniffer system (Tecnosens, IT) installed in the feeder of the automatic milking system (AMS) where animals were milked two times per day. Lactating cows were kept in the opened paddock all round year and fed Total Mixed Ration; during the spring and autumn seasons cows had access to pasture areas of the farm to graze for five hours per day. The emissions of thirty-four lactating Brown Swiss cows were monitored over two periods of one month in the spring, from May to June, and autumn, from October to November, while animals were grazing. Data from the AMS such as the cow entry and exit time, milk yield, days in milk and parity, were combined with the Sniffer records logged every 1 second. CH_4 and CO_2 concentrations per day for each cow were computed using Python scripts to standardise the measurements by removing outliers, negative data and background gas concentrations and detecting the number of peaks per milking. Preliminary results of the enteric emissions measured from the breath samples captured by the Sniffer showed an average daily concentration of 201.4 ± 83.0 ppm of CH_4 and 1537.6 ± 585.5 ppm of CO_2 during the spring period and 111.4 ± 59.9 and 1122.5 ± 631.3 ppm respectively for CH_4 and CO_2 during the autumn trial. The CH_4-to-CO_2 ratio was calculated and the average ratio was 0.13 and 0.10 respectively in spring and autumn. Additional information such as the differences in pasture composition during spring and autumn and the daily grazing activity need to be gathered to correlate the emissive levels of Brown Swiss cows under semi-extensive farming systems. Research supported by the European Union's Next-GenerationEU program (grant J83C22000830005), as part of the 'National Research Centre for Agricultural Technologies' initiative.

P493

Advancing methane detection in dairy cows during robotic milking: insights from enhanced laser and sniffer techniques

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Methane is a potent greenhouse gas, making its management crucial in cattle farming. To tackle this challenge, researchers have investigated several approaches for methane detection, such as laser methane detectors (LM) and sniffer methods (SM). Currently, no published equations exist that link the application

of these techniques to the Automatic Milking System (AMS). This research sought to assess the correlations between methane emissions measured using the SM method (Moologger, Tecnosens, Italy) and the LM method (Laser Methane Mini, Cowcron, UK) in dairy cows managed with an AMS (Merlin2, Fullwood, UK). The trial involved 24 Italian Holstein dairy cows with an average lactation number of 2.38 ± 0.58 and an average of 69 ± 15 Days in Milk (DIM). The cows were milked at fixed intervals (06:00, 14:00, and 22:00) over a two-day period. Methane emissions were measured simultaneously using both the LM and SM methods. During milking in the AMS, as the cows consumed supplementary concentrate, the LM device was aimed at the cow's muzzle, while the SM system collected air samples from the AMS feed manger. A Pearson correlation analysis was conducted to evaluate the relationship between these two measurement techniques. The LM method recorded an average of 97.11 ± 40.63 ppm*m, while the SM method measured 2.31 ± 1.11 µg/s. The analysis demonstrated a coefficient of determination (R^2) of 51% and a correlation coefficient (R) of 71% (RSQME = 26.61; $p < 0.01$) between the two methods. Although this preliminary finding is encouraging, the correlation remains relatively moderate. To improve the outcomes, two strategies could be adopted: increasing the sample size by enrolling more animals and/or collecting data at additional time points, as well as assessing the precision of the cow's muzzle positioning within the AMS feeders. Indeed, it is well known that once cows finish consuming the supplemental concentrate in the AMS feeder, they typically begin moving their heads in different directions, often distancing themselves from the SM aspirator. As a result, methane is no longer detected by the SM, while the LM operator continues to track the cow's muzzle. These strategies will be applied in the next stages of the experiment to improve the outcome. In conclusion, the results obtained indicate a degree of correlation between the LM and SM techniques. However, further development and refinement are required in the upcoming phases of the experiment.

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P563

Dynamics of greenhouse gases in central italian meadows: a high-resolution analysis using licor gas analyzers

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Managed meadows significantly impact soil-atmosphere exchanges of key climate gases: nitrous oxide (N_2O), methane (CH_4), and carbon dioxide (CO_2), influenced by environmental conditions and soil microbial activity. Although these meadows can absorb CH_4 and N_2O initially, they typically become net sources over time. This study analyzes the environmental impacts of GHG emissions from a central Italian meadow (60% ryegrass, 40% clover) through temporal and seasonal analysis to establish a baseline for sustainable land management. We conducted high-resolution monitoring to measure real-time GHG concentrations accurately. Measurements were carried out with LI-COR 7810 and 7820 analyzers over two days in Autumn at fixed GPS-mapped points, in morning from 08:00 to 11:00 and in afternoon from 15:00 to 18:00. The chambers' design, featuring automated bellows and a patented pressure vent system, ensures precise gas mixing without turbulence, crucial for capturing the dynamics of soil gas exchanges in Italy's temperate climate. Measurements revealed distinct diurnal patterns for greenhouse gases within managed meadows. In the morning, fluxes averaged as follows: N_2O at 0.035 ± 0.249 nmol m^{-2} s^{-1}, CO_2 at 4.010 ± 1.74 µmol m^{-2} s^{-1} and CH_4 at -0.410 ± 0.204 nmol m^{-2} s^{-1}. Whereas the afternoon values were N_2O at 0.039 ± 0.027 nmol m^{-2} s^{-1}, CO_2 at 4.100 ± 1.093 µmol m^{-2} s^{-1} and CH_4 at -0.445 ± 0.236 nmol m^{-2} s^{-1}, highlighting an increase in N_2O and CO_2 fluxes in the afternoon and an increase in CH_4 dynamics in the morning that was not significant (Tukey test; $p > 0.05$). The afternoon elevations in N_2O and CO_2 fluxes may be likely attributable to enhanced

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microbial metabolism and soil respiration, stimulated by the elevated diurnal temperatures. Furthermore, observed negative CH_4 fluxes are probably related to alterations in methanotrophic (methane-oxidising) and methanogenic (methane-producing) communities, driven by changes in soil physicochemical properties that favor aerobic methane oxidation, highlighting the soil's critical role as an atmospheric CH_4 sink. This study uses advanced gas flux measurements and temporal analysis to identify factors influencing GHG emissions in managed meadows. These preliminary results show that LI-COR analyzers effectively capture GHG flux variability, enhancing our understanding of land use impacts on greenhouse gas dynamics. Additional research is required to confirm the precision of the instruments and methodologies employed.

WELFARE, HEALTH AND BEHAVIOUR

P175

Effects of bovine milk extracellular vesicles on the oxidative and inflammatory status of bovine mammary and porcine intestinal epithelial cells

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Milk extracellular vesicles (mEVs) may alleviate inflammatory disease symptoms due to their antioxidant, anti-inflammatory and immunomodulatory properties. This study aimed at investigating the antioxidative and anti-inflammatory effects of bovine mEVs on bovine mammary epithelial (BME-UV1) and porcine intestinal epithelial (IPEC-J2) cell lines. Mass raw milk was collected in a commercial Holstein Friesian farm. The mEVs were isolated by a preliminary centrifugation step for removing cell debris and fat globules. Then, 0.25 M EDTA (pH 7.4) was added to precipitate contaminant proteins and centrifuged at 10.000g for 1 h at 4 °C. The supernatant was ultracentrifuged twice at 4 °C at 35.000g for 1 h and at 200.000g for 90 min to obtain the EVs pellet. Isolated mEVs were quantified through a Malvern Panalytical NanoSight NS300 and different concentrations of mEVs were tested to identify the optimal concentration that had no cytotoxic effect on both cell lines. Both cell lines grew at 37 °C until they reached confluence. To verify mEVs antioxidant or anti-inflammatory property, BME-UV1 cells were exposed to 200 µM/mL of H_2O_2 or 10 µg/mL of lipopolysaccharides (LPS) for 3 hours, while IPEC-J2 cells were treated with 200 µM/mL H_2O_2 or 1 µg/mL LPS for 2 hours. After being exposed to stressors, the medium was replaced with mEV-enriched medium (10^{10} particles/mL) for 48 hours. Cell viability, reactive oxygen species (ROS) production, intracellular malondialdehyde (MDA) levels, NADP+/NADPH concentration and mRNA gene expression of inflammatory genes were determined. In BME-UV1 cells, mEVs treatment reduced ($p < 0.01$) intracellular ROS levels and increased ($p < 0.01$) NADPH concentration, whereas no differences ($p > 0.05$) were observed in viability or MDA production. For IPEC-J2 cells, mEVs treatment decreased ($p < 0.01$) intracellular ROS and MDA levels in the H_2O_2 model, without affecting viability and NADPH concentration ($p > 0.05$). In LPS model, preliminary results on gene expressions showed an increase ($p < 0.05$) of interleukin-10 in BME-UV1 cells and a reduction ($p < 0.05$) of tumor necrosis factor gene expression in IPEC-J2 cells after LPS + mEVs treatment. These findings highlight the potential of mEVs to modulate oxidative and inflammatory responses in mammary and intestinal epithelial cells. Further research is needed to elucidate the molecular mechanisms involved in the protective effects of mEVs in bovine and porcine cells exposed to stressors.

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P319

Black soldier fly meal and oil: effects of novel feed sources on growth traits and welfare in fattening pigs

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Insect-derived products, such as Black Soldier Fly Larvae Meal (BSFLM) and Oil (BSFO), are gaining attention as sustainable alternatives to traditional feed ingredients like soybean meal and fats/oils for pigs. Beyond their nutritional role, these non-conventional feed sources have been attributed nutraceutical properties that might favourably influence the intestinal microbiota.
Due to the growing interest in the relationship between animal nutrition and behaviour through the gut-brain axis, this study aims to evaluate the effects of BSFLM and BSFO not only on growth performance but also on some welfare indicators, specifically behaviour and skin lesions, in finishing pigs. Seventy-two crossbred barrows (initial body weight, BW: 28 kg; 70 days old)

were randomly assigned to three dietary treatments: BSFLM, BSFO, and control (CNTR). Diets were isonitrogenous and isoenergetic, with 5% of soybean meal replaced by BSFLM in the BSFLM group, and 2% of conventional fats substituted by BSFO in the BSFO group. Pigs were reared for 204 days, reaching a final BW of 160 kg at approximately nine months of age. Growth performance was evaluated, including average daily gain (ADG) and feed conversion ratio (FCR). Diurnal individual behaviour (7 AM–7 PM) was recorded over four days distributed throughout the trial and analysed using the scan sampling technique (10 s of observation every 10 min of video). Body and tail lesions were assessed at the end of the trial according to the Welfare Quality® protocol. Growth and behavioural data were analysed using ANOVA, with Dunnett's tests as a post-hoc, while lesion scores were evaluated using the chi-square test. Significance was set at $p < 0.05$. The BSFLM group exhibited significantly lower BW and higher FCR compared to the control group ($p = 0.03$), while the BSFO group showed intermediate values. General behaviour was unaffected by dietary treatment, as were body and tail lesion scores. Further investigations will aim to explore the potential effects of BSFLM and BSFO on the intestinal microbiota to better clarify the underlying mechanisms behind the observed outcomes.

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P022

Effects of enriched cage design on the welfare and behavior of breeding does

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This study evaluates the impact of enriched cages on the welfare and behavior of breeding does. Traditional housing restricts movement and stimulation, increasing stress and reducing reproductive performance. We assessed cages modified with a raised shelf, curved tube (simulating a burrow), mirror, plastic footrest, chewable logs, and a hay rack to promote natural behaviors and improve comfort. Cages (70 × 62 × 64 cm) had a 25 cm-wide shelf (32 cm high), a 16 × 16 cm mirror, and a curved tube beneath the shelf. Additional enrichments included a plastic footrest, chewable poplar logs, and a hay rack. A backpack-style nesting box was attached externally before parturition. Behavioral observations included resting, grooming, climbing, and chewing, while reproductive indicators included litter size and kit survival. Does in enriched cages showed higher exploratory behavior (2.2% vs. 1.87%), increased tube use (3.09% vs. 0.0%), and fewer stereotypies (3.99% vs. 6.71%) than those in conventional cages. Feeding straw was only observed in enriched cages (5.58% vs. 0.0%). Resting behaviors were slightly reduced (47.7% vs. 53.08%), but standing upright (1.89% vs. 0.0%) and gnawing (0.4% vs. 0.0%) increased. Enriched cages encouraged diverse spatial use: does spent 37% of the time on the platform, 23% inside the tube, and 14% near the nest door. Conventional cages had greater use of the feeder area (29% vs. 12%) and lateral positions (18% vs. 22%). The footmat was used in enriched cages (33%), reducing wire Contact . Reproductive outcomes showed modest improvements in litter survival, but no significant differences in litter size, kit weight, or reproductive performance. Cage cleanliness was affected: conventional cages scored 1.75 (± 0.4), while enriched cages scored 3.75 (± 0.3), indicating increased soiling due to additional materials. Handling ease decreased in enriched cages, where does took over 22 seconds to capture versus 14 seconds in conventional cages, suggesting greater reactivity. These results indicate that targeted enrichments promote natural behaviors, reduce stress, and enhance comfort without markedly improving production. However, increased soiling and handling difficulty may require adjustments in management and maintenance.

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P163

Effects of breeding techniques on animal welfare in rural areas

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The Southern Italy, and particularly the internal areas of Campania region, are characterised by a unique agri-food heritage and often underutilised economic potential. The objective of this study was to explore innovative management strategies able to optimise local resources who can improve the animal welfare. Thirty dairy cattle farms located in internal area of Campania region have compiled a questionnaire survey to elucidate their management procedures, with a special emphasis on milking practices employed, as well as the productive and reproductive performance. Some of the best breeding techniques (straw bunk beds, WCU cooling system) extrapolated from the questionnaires have been applied in the lead company of the project. To this aim, 20 dairy cows have been involved in the trial and divided into 2 groups ($n = 10$/group), with (Trt) and without (Bsl) the implementation of the innovative breeding strategies. The trial lasted 6 months. Samples of blood serum have been collected at zero (T0), three (T1), and six (T3) months to assess the oxidative and inflammatory status in animals. The

colorimetric Total antioxidant capacity (TAC) and malondialdehyde (MDA) tests and bovine ELISA (Enzyme linked immunosorbent assay) assays for inflammatory cytokines were performed. Based on cytokines serum concentrations, tumor necrosis factor-alpha (TNF-α), IL-1β, and IL-6 were evaluated. The TAC increased statistically in the group that adopted managerial strategies (Trt; $p < 0.05$) at T3, whereas it remained unchanged for the control group (Bsl). On the other hand, MDA exhibited a statistically significant decrease in Trt group respect to the Bsl one during time ($p < 0.01$). TNF-α, together with IL-6, resulted in higher concentration in Bsl respect to Trt, especially at the last timepoint of the experiment ($p < 0.05$). The IL-1β increased its value immediately (T1) in the Trt group ($p < 0.05$), remaining stationary until the end of the experiment (T3; $p < 0.05$). The results evidence how a multidisciplinary approach, combining innovation for the enhancement of breeding techniques and the connection to the territory, could have a positive impact on the improvement of animal wellness and, consequently, on their products.

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P182

Effects of grazing adaptation on Italian Pezzata Rossa metabolism

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Despite numerous studies on dairy cow welfare in intensive farming systems, limited information exists on the effects of alpine pastures on animal welfare. This study involved two small dairy farms in Val Comelico (Belluno, Italy). The first farm is situated at 1100 m.a.s.l., with pastures at 1297 m.a.s.l. during the summer grazing period, while the second farm is located at 1300 m.a.s.l., grazing at higher pastures of 1941 m.a.s.l. For each farm, 10 healthy multiparous cows were selected. Data on air temperature and precipitation from meteorological stations near both pastures were analyzed to assess their influence on the cows' physiological responses.

The aim was to evaluate changes in stress-related parameters before, during, and after the cows moved from valley stables to alpine pastures, leveraging altitude differences to explore environmental impacts. Blood, feces, and vital parameters (body temperature, heart rate, and respiratory rate) were collected at three time points: pre-transhumance, during grazing, and prior to returning to stables. Data were analyzed using t-SNE (t-Distributed Stochastic Neighbor Embedding), an unsupervised machine learning technique, for exploratory purposes, and two-way ANOVA to evaluate the effects of time, farm, age, and their interactions. Results revealed metabolic stress immediately post-transhumance, with negative energy balance affecting immune responses. Blood glucose decreased, while cholesterol, NEFA, and total bilirubin increased. β-hydroxybutyrate declined. Heart rate, RBC, HCT, HGB, and related hematological parameters rose due to physical activity and altitude. AST and CK levels increased, while creatinine levels decreased, possibly as a result of muscle protein mobilisation. Mineral metabolism was affected, with higher calcium (Ca) and magnesium (Mg) and lower phosphorus (P), likely linked to forage composition and increased vitamin D from sunlight. Most parameters stabilised and haptoglobin decreased, after the grazing period at higher altitudes, indicating the cows' adaptation to alpine conditions. The small sample size included in this study may limit the generalizability of the findings. However, it represents a first step toward understanding animal welfare in alpine pastures, demonstrating that while transhumance initially induces significant metabolic stress, cows are capable of adapting to the challenges of high-altitude grazing.

P279

Perspectives of Citrus essential oil as feed in sheep farming

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Climate change is worsening animals'ability to cope with heat stress, heavily reducing their welfare. There is a strong need to find effective and efficient heat stress mitigation strategies. International policies are looking for substituting chemicals with natural compounds to sustain livestock health and welfare. For this reason, essential oils are gaining an increasing attention in literature. Essential oils are natural compounds extracted from vegetables, showing beneficial effects on animals' health, welfare and final products' quality. Among them, citrus essential oils (CEO) are particularly interesting for their anti-inflammatory properties. Their use can be particularly beneficial in the sheep sector. The study investigated *ex-ante* the suitability of the application of citrus essential oils to enhance sheep health and welfare, and thus the sustainability of the sector, using a SWOT-SOr approach. The Strength, Weaknesses, Opportunities, and Threats (SWOT) analysis allowes the identification of the interactions

between the key features of the analyzed project and consequently identifies the possible strategies for the development of innovation. This instrument was combined with the strategic orientation round (SOr) to weigh the resulting possible scenarios using a scoring method. The emerging strategies identified CEOs supplements as an opportunity to obtain products with the attributes the consumers are looking for. This may result in higher consumer approval, thus obtaining premium prices or greater demand for the final products. The emerging threats are the actual use of other supplements with similar benefits; the rising weakness is the high cost of CEOs-based supplements. This result is probably related to the sheep farm location. One of the main results of this study, indeed, is that there is an interest to increase animals' welfare, but there is the need to structure specific actions to answer the specific farmers' needs, that change in different locations. Certification ensuring animal welfare should be a good option for promoting the use of CEOs in the sheep sector and meeting the demand of the actual consumer, possibly shifting the market equilibrium towards a point with higher quantity and prices. In this scenario, the availability of standardised feeds and characterised supplements is crucial to guarantee the stability of production both in terms of quality and quantity. These feeds and supplements will possibly contribute to enhancing livestock welfare, as demanded by society and worldwide policies. CEOs-based supplements will be able to answer these needs, as they can be standardised, guaranteed, and trackable.

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P281

Welfare conditions of replacement calves and surplus calves in dairy farms in Northern Italy

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In recent years, concerns about the welfare of calves in dairy farms have been growing. Significant shortcomings have been recorded in the hygiene of housing environments and feeding equipment, colostrum administration, and weaning practices. Current calf-rearing management compromises animal health and leads to serious animal welfare issues, such as behavioral alterations, fear, pain, and hunger. These problems are more pronounced in surplus calves (mainly males), who often receive even lower standards of care than female calves kept for replacement. This study investigated the transfer of passive immunity (TPI) based on serum IgG levels and the presence of diarrhea symptoms in 240 replacement calves (mean age 9.3 days) and 207 surplus calves (mean age 8.1 days) from 75 dairy farms located in northern Italy. In addition, for each farm, the 3–30 day mortality rate was calculated for male and female calves using data from the national bovine identification and registration database. Serum IgG were quantified on blood samples ($n = 447$) using an automated agarose gel system (Hydrasys 2, Sebia, Italy) associated with Phoresis software. The IgG value in g/L was derived from the total protein value, measures by biuret method with an automatic analyzer (ILab 650, Instrumentation Laboratory, Italy). TPI was found to be poor (IgG <10 g/L) in 38.0% of calves, fair (IgG 10.0–17.9 g/L) in 41.8%, good (IgG 18.0–24.9 g/L) in 15.1%, and excellent (IgG ≥25.0 g/L) in 5.1%. No significant differences were found between replacement and surplus claves for TPI (chi-square test, $p > 0.05$). Diarrhea symptoms were present in 35.8% of the involved replacement calves and in the 35.7% of the involved surplus calves. The 3–30 day mortality rate averaged 9.1% for females (range 0.0%–45.2%) and 11.9% for males (range 0.0%-38.5%). Males were 1.6 times more likely to die during this time frame than females (OR = 1.6, 95% CI = 1.4–1.7, $p < 0.0001$). More attention is needed regarding calf conditions on dairy farms. This study revealed that poor colostrum practices affect both replacement and surplus calves. High mortality rates were recorded, which are a warning sign of suboptimal animal welfare and health conditions. It is therefore urgent to promote short- and long-term changes through information and training activities aimed at key stakeholders to improve calf welfare and reduce antimicrobial resistance.

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P334

MALDI-TOF mass spectrometry profiling to investigate subclinical mastitis in dairy cows

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Mastitis is currently one of most impacting health and economic issues in dairy farming due to the reduced milk yield and quality. Subclinical forms of mastitis are routinely monitored through the measurement of somatic cell count (SCC). Nowadays, it is possible to monitor the SCC levels on a daily basis, thanks to the introduction of Automatic Milking Systems (AMS) in many commercial dairy farms. However, the identification of subclinical mastitis can still be difficult, leading to economic losses for the farmer. In this study, a MALDI-TOF mass spectrometry approach was applied to milk samples collected from Italian Holstein dairy cows classified according to the SCC recorded by AMS, in order to improve the knowledge of existing differences in polypeptide/protein profiles. A total of 208 milk samples with SCC values ranging from 100,000 to 400,000 were collected from 4 dairy farms in Piedmont region between June and July 2024. For each sample, two different aliquots were collected: one for the bacteriological analysis and the other one for the mass spectrometry approach. The aliquots destined to classical bacteriological analysis were refrigerated and delivered to a dedicated lab service for the detection of the main mastitis-related pathogens. The major detected class of pathogens in the samples was coagulase-negative staphylococci (38.1%), while the 10.2% of the samples was negative to the bacteriological analysis (i.e. no pathogens detected). The aliquots for mass spectrometry analysis were defatted by centrifugation at 3,000g for 10min at 4 °C. The resulting skimmed milk was collected and stored at -80 °C. A MALDI-TOF Microflex LRF mass spectrometer was used to acquire spectral profiles through the positive linear ion mode (mass range 4,000–20,000 m/z). Further statistical analysis will be focused on the differences observed in the spectral profiles of the milk samples classified by the different detected pathogens. Expected results will involve potential protein markers to be further analysed and that could be eventually used as indicators of subclinical mastitis.

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P456

European partnership on animal health and welfare-EUPAHW

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The European Partnership Animal Health & Welfare (EUP AH&W) will provide society with a sustainable production for both terrestrial and aquatic animals, where infectious animal diseases are prevented and controlled, antimicrobials are used prudently, and a high level of animal welfare is provided in every phase of animal's life contributing to the economic growth of these sectors as well as to the rural development and vitality of many EU marginal territories and to the more sustainable use of aquatic and terrestrial resources. The objectives of the EUP AH&W fit in with the European Green Deal and its associated Farm to Fork strategy for a fair, healthy, and environmentally friendly food system. The partnership includes 56 Research Performing Organisations (RPO) that provide significant research-based advice on animal health and welfare to EU authorities and 30 Funding Organisations (FO) that will contribute to further R&I actions from the EUP SRIA not covered by internal activities, as they require other expertise or industry participations from 24 EU and non-EU European countries. To achieve these general objectives, the partnership has set 17 joint internal projects taken from 16 the EUP SRIA. Due to the close link between animal health and welfare and human well-being, the One Health-One Welfare perspective will take a prominent place in the EUP AH&W. The mobilisation of resources from both RPO and FO together with EC co-funding will allow the partnership to achieve ambitious goals for AHW at the transnational level, in Europe and beyond. New technologies develop rapidly and provide new R&I opportunities for AHW, to be included in the partnership as joint internal activities and projects initiated through external calls. The management will set up appropriate procedures and methodologies

to ensure a fair coverage of AHW, of terrestrial and aquatic animal species, the various priority areas and to ensure the uptake of the results in the midterm and long term for science, society and policy. CREA will contribute to the objectives with the developement of 5 projects which aim to collect, analyse, share and use integrated scientific and technical data on AW, assess of positive welfare defining animal-based measures, reinforce of animal resilience, promote sustainability aspects of AW in livestock systems, and to study the role of the immune system of farm animals.

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P508

Effect of Pair-Housing on the reactivity of pre-weaned dairy calves

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Breeding calves in pairs can be a valid alternative to single pen housing; several studies have highlighted that calves raised in pairs have better growth and welfare than calves housed individually. The objective of this study was to investigate the effect of pair housing on calves' reactivity to a possible stressful situation. Fifty-six Friesian female calves were enrolled since birth in 2 commercial dairy farms and housed either individually ($n = 28$) or in pairs ($n = 28$, 14 pairs). A startle test with 4 different novel objects (for example a plastic bottle filled with stones) was performed in the home pen of each animal, at 7, 21, 35 and 56 days of age. The startle test lasted 10 minutes and the following behaviours were analyzed: standing (s), lying (s), escape from the object (frequency), self-grooming (s), latency to approach the novel object (s) and time sniffing or licking the object (s). Pairwise comparison of the means with Bonferroni correction was conducted to analyze the housing effect on calves' behavior. There was no effect of the housing system on standing, lying and escaping from the object. Self-grooming was longer in individually housed calves compared to pair-housed at 7 ($p = 0.046$) and 21 days of age ($p = 0.048$). At 21 and 56 days of age, calves housed individually showed statistically shorter latency to approach the novel object ($p = 0.031$ and $p = 0.001$, respectively). At 21, 35 and 56 days of age individually housed calves showed longer time sniffing or licking the object compared to those housed in pairs ($p = 0.026$, $p = 0.043$ and $p = 0.001$, respectively). Novel objects likely served as enrichment for individually housed animals, as they showed significantly greater interaction with them. Calves housed in pairs seemed less interested in the objects but not scared, since escape attempts were very limited. These results suggest that the lack of stimulation in the home environment can be mitigated by the presence of a social companion. The behavior of pair housed calves during the test can be linked to improved adaptation, indicating that pair housing may be beneficial for enhancing their coping skills.

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P510

Effect of dietary inclusion of cocoa bean shells on behaviour indicators of animal welfare in Sardo-bruna cattle breed

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The use of agro-industrial by-product containing bioactive compounds in ruminant nutrition has been widely investigated in the last decades, evidencing positive effects in terms of reduction of diets' environmental impact, increase of derived products quality, and improvement of animal health. Few is known regarding the effect of these by products on the social behaviour and general activities of the animals. The aim of this study was to monitor the effect of dietary inclusion of cocoa bean shells on behaviour of finishing Sardo Bruna beef cattle. Animals were reared in the same optimal environmental conditions, according to CReNBA method (Classyfarm®). Thirty yearling-Sardo-Bruna beef were allocated to three experimental groups, each balanced for sex. A group was fed the basal diet without any supplementation (CON group), a group was fed the basal diet and a supplementation of 150 g/head/day of cocoa bean shells (Low Dose group), and a group was fed the basal diet and a supplementation of 300 g/head/day of cocoa bean shells (High Dose group). During the last 2 months of the feeding trial (lasting 6 months), animals were evaluated for the social ('displacement for space', 'fighting', 'butting', 'self-grooming', 'allo-grooming', 'oral behavior', 'stereotyping', 'chasing', 'chasing-up', 'flehmen', 'attempt mount', 'mounting') and general (standing', 'walking', 'feeding', 'drinking', and 'ruminating) activities. Evaluations (every 20 days) were carried out by two trained operators and consisted in observing animals, individually, for: (i) 15 min, 3 times a day, and 45 min of interval (social activities); (ii) 1 min, 6 times per day, and

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45 min of interval (general activities). The results evidenced no effect of the dietary treatment on the social and general activities of the animals. As expected, differences were observed between sex: compared to the female, male exhibited significant low number of events related to the social behaviour, and higher number of events related to fighting and sexual activity (flehmen). Butting activity was affected by the interaction between diet and sex, with the males belonging to the high dose group having higher values compared to the females of the CON group.
In conclusion, behaviour indicators of animal welfare were not affected by the supplementation of cocoa bean shells, indicating that this by-product can be used at the dose of 300 g/head/day in the diet of finishing Sardo Bruna beef cattle.

P553

Effect of different THI metrics on milk yield and quality attributes of Holstein cows using robot milking data

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Thermal discomfort, caused by rising global temperature, is one of the major challenges of intensive dairy farming, resulting in both reduced farmers profit and compromised animal welfare. The temperature-humidity index (THI) is widely used to quantify the combined effects of ambient temperature and humidity, offering a practical of heat stress in cattle. The objective of the study was to investigate the effect of different THI metrics, collected over a 3-year period, on productivity and milk quality of Holstein cows managed under robot milking systems. Animals involved were housed in the experimental farm of the University of Bologna. THI was recorded hourly using on-farm sensors, and six different metrics were derived: the daily average, minimum, and maximum THI, as well as the average, minimum, and maximum THI from the previous week. These metrics were combined with individual daily data on productivity (milk yield and number of milking events) and milk quality (fat, protein, lactose percentages, fat-to-protein ratio, and electrical conductivity) collected through milking robots. Each THI metric was stratified into 4 classes based on quartile distribution. Robot milking data were analysed through a linear mixed model which included the fixed effect of year of test, parity order, days-in-milk, THI metric, and their two-way interactions. Animal was fitted as a random term. Each metric was included in the model separately. All the fixed effects were significantly associated to the variables studied ($p < 0.05$). Independently from the THI metric employed, milk quality deteriorated as THI increased, while electrical conductivity variation suggested a heightened risk of clinical mastitis with higher THI. The number of milking events as well as milk yield tended to increase concurrently with THI, suggesting that under heat stress animals tended to yield a more diluted milk and to manifest a greater risk of udder infection. Results also indicated that thermal discomfort has both an acute a prolonged deteriorating effect on milk productivity and quality, as well as on udder health. This research provides insights into optimising cow welfare and productivity in robotic milking operations under varying climatic conditions.
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P140

Genomic analysis of *Streptococcus canis* and *S. dysgalactiae* subsp. *equisimilis* from different hosts in Italy 2004–2021: antimicrobial resistance and virulence profiles

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Streptococcus canis (SC) and *Streptococcus dysgalactiae* subsp. *equisimilis* (SDSE) are significant pathogens with implications in both human and veterinary medicine. While SC is a multi-host pathogen predominantly isolated from domestic animals and sporadically reported in severe cases of human infection, SDSE, traditionally known for its veterinary relevance, is now recognised as an emerging pathogen in humans. This study aimed to explore the genetic diversity, antimicrobial resistance (AMR), and pathogenicity of 55 SC and 57 SDSE isolates collected from animals in Italy from 2004 to 2021. Whole genome sequencing was employed to characterise sequence types (STs), virulence profiles, and AMR determinants. SC isolates frequently exhibited resistance to lincosamides, tetracyclines, and macrolides, with six isolates showing multidrug resistance. Resistance to tetracyclines was detected

in approximately one-third of our SC collection, and all isolates were susceptible to beta-lactams. The predominant ST in the SC dataset was ST9, and the most common AMR gene was lmrP which confers resistance for streptogramin, tetracycline, macrolide, streptogramin A and lincosamide. Comparison with other 46 SC genomes available in public repositories revealed that the Italian isolates clustered by the *S. canis* M-like (SCM) protein gene and ST and did not group according to their host, area or year of origin. Conversely, the maximum likelihood (ML) phylogenetic tree of the core genome of *SDSE* isolates, supported that SDSE is host-adapted, with few exceptions. Three SDSE isolates from animals belonged to the human-associated ST13. Interestingly, V539, originating from a dog, belonged to the ST20, an emerging ST in human medicine. V539 clustered with human isolates and harbored *slo*, a virulence factor associated with human SDSE. Additionally, 22 novel STs were identified in our collection of SDSE, confirming the scarcity of information on SDSE from animals in the literature. Moreover, SDSE isolates frequently showed resistance to lincosamides and tetracyclines. In conclusion, while SC isolates maintain susceptibility to beta-lactams and have not adapted to different ecological niches, SDSE isolates are able to adapt to several different host species with occasional interspecies transmission. These findings highlight the importance of continued surveillance and comparative genomic studies to understand the evolutionary dynamics of these pathogens across different hosts.

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P177

Untargeted metabolomic analysis of heat stress response in indicine and taurine cattle

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Heat stress (HS) is a significant challenge for livestock, affecting animal welfare, productivity, and sustainability. Resilient breeds like Nellore and susceptible breeds like Angus exhibit distinct metabolic adaptations under HS conditions. This study employed untargeted metabolomics (UHPLC-Orbitrap-MS) to investigate blood metabolome differences between these breeds, aiming to identify key metabolites and pathways underlying resilience to HS. Untargeted metabolomics discriminated the blood metabolomes of Nellore and Angus under HS conditions, revealing breed-specific metabolic responses. Nellore exhibited a balanced energy metabolism and efficient reallocation of purine intermediates, suggesting superior resilience mechanisms. In contrast, Angus showed a metabolic strategy characterised by lipid mobilisation, leading to the accumulation of intermediates like stearoylcarnitine and vaccenyl carnitine, which may exacerbate oxidative stress and metabolic strain. Amino acids, organic acids, phospholipids, and nucleotides emerged as the most discriminant biomarkers of HS. Additionally, pathway analysis highlighted the role of porphyrin and nucleic acid metabolism in recovery periods. DNA methylation analyses from previous findings supported our metabolomics results, showing hypo-methylation in key genes in Nellore, which likely enhanced fatty acid synthesis, stress signaling, and membrane stability. Notably, cyclic AMP and lysophospholipids were down-accumulated more prominently in Nellore, reflecting efficient signaling and reduced oxidative damage. The findings demonstrated that Nellore's superior HS resilience is underpinned by adaptive metabolic pathways, particularly purine metabolism, and epigenetic regulation of lipid biosynthesis. Identified blood metabolites and pathways could serve as biomarkers for selecting heat-tolerant breeds and designing interventions to mitigate HS effects. These results offer valuable insights into metabolic resilience, contributing to the development of strategies for sustainable cattle production in HS environments.

P321

THI as an alert tool for decline in milk production in grazing Sarda sheep

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The Temperature Humidity Index (THI) is increasingly recognised as a critical factor influencing livestock performance, particularly due to its association with production declines in sheep. The TechCare project, funded by the Horizon 2020 Programme, GA No. 862050, aims to enhance animal welfare and optimise livestock production by identifying specific alert indicators for animal health and productivity. This study investigated the relationship between THI and production drops in Sarda dairy ewes. Between April and June, forty-eight ewes were divided into two groups: one with 6 hours of daily grazing on ryegrass (6h) and the other with only 2 hours of grazing (2h), creating an underfeeding scenario in the

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latter and a subsequent drop in milk yield. Both groups received the same feed supplement consisting of *Panicum miliaceum* hay, concentrate, and corn, with milking occurring twice daily (morning and evening). Individual metabolisable energy intake (MEI, Mcal/day) and metabolisable protein intake (MPI, g/day) were estimated by SRNS (Tedeschi et al. 2010). Individual milk yield was measured weekly. Temperature and humidity were monitored daily using weather stations located approximately 400 meters in a straight line from the grazing fields. The maximum THI (Max THI) was then calculated. The reductions in milk yield (DMY) and energy and protein intake (DMPI) for each animal in the 2h group were calculated in comparison to the averages of the 6h group. Days in milk (DIM) of ewes were divided into four stages of equal duration. Data were analysed using a Generalised Additive Model (GAM), a flexible tool for evaluating non-linear relationships. The best GAM model found included DMPI, Max THI, and DIM as independent variables, with DMY as the dependent variable. The model was able to explain 85.1% of total deviance with an R^2 of 0.80 (p-value <0.001) and a RMSE = 0.08. The effect of THI varies across the four identified DIM stages and appears to have a greater impact during the first (100–125 DIM) and second stages (126–154 DIM), with a more significant decrease in milk production at THI levels above 65 in the first stage and above 63 in the second stage. In the third and fourth DIM stages, the effect of THI appears to be minimal. Further investigations are necessary to confirm the THI values mentioned as threshold values for potential alert tool in Sarda dairy ewes during the first 5 months of lactation.

P473

Horse welfare assessment: the parameters to consider in pain evaluation

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Background: Assessing pain in horses is crucial for their welfare but challenging due to subtle and subjective indicators. This meta-analysis identifies the most effective behavioral and facial parameters for pain detection. **Methods**: A systematic review of literature from Web of Science, PubMed, and Scopus was performed, analysing studies on horse pain scales published between 2003 and 2024. The analysis employed RStudio to create forest plots and evaluate variations across studies using Cochran's Q for heterogeneity and Higgins' I^2 statistic. K-Means cluster analysis was performed to identify distinct groups of parameters. **Results**: Out of 359 studies initially identified, 25 were included. High inter-observer reliability was noted for parameters like 'backward ears' (0.84; 95%CI 0.82–0.85), 'orbital tightening' (0.77; 95%CI 0.75–0.79), 'appetite' (0.86; 95%CI 0.81–0.90), 'sweating' (0.92; 95%CI 0.86–0.97), and 'focus to environment' (0.82; 95%CI 0.74–0.89), suggesting they are easily recognised and consistent across observers. Sensitivity highlighted 'backward ears' (0.71; 95%CI 0.67–0.75), 'strained nostrils' (0.58; 95%CI 0.54–0.62), 'orbital tightening' (0.58; 95%CI 0.54–0.62), 'mouth strained and pronounced chin' (0.71; 95%CI 0.67–0.75) and 'focus to environment' (0.58; 95%CI 0.54–0.62) as highly effective for detecting pain. Conversely, specificity revealed that 'backward ears' (1.00; 95%CI 0.99–1.00), 'kicking abdomen' (1.00; 95%CI 1.00–1.00), 'sweating' (0.984; 95%CI 0.979–0.988), 'focus to environment' (1.00; 95%CI 0.99–1.00) and 'teeth grinding' (1.00; 95%CI 0.99–1.00) were excellent for confirming pain-free conditions. Cluster analysis highlighted key pain-related parameters: 'head position/movements', 'backward ears', 'strained nostrils and flattening profile', 'orbital tightening' and 'mouth strained and pronounced chin'. These facial expressions are positively correlated with sensitivity due to their involuntary nature, aiding early detection of discomfort even without obvious behavioral changes. However, their lack of correlation with inter-observer reliability and negative correlation with specificity underscore the need for proper training to minimise false positives. **Conclusion**: This meta-analysis contributes to a deeper understanding of pain evaluation in horses, offering a robust framework for identifying reliable parameters that can improve the consistency of welfare assessments.

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