A physiologically-based population model of *Philaenus spumarius*

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INTRODUCTION

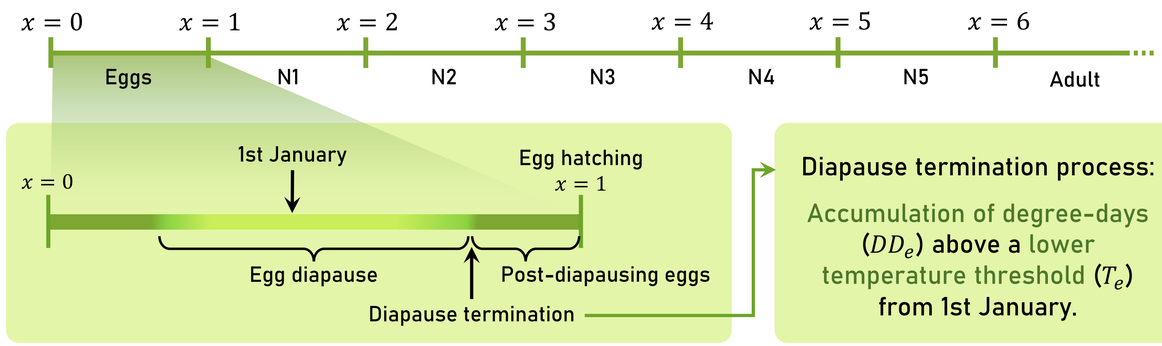
The meadow spittlebug, *Philaenus spumarius* L. (1758) (Hemiptera: Aphrophoridae), is the main vector of the plant pathogen bacterium Xylella fastidiosa (Xf) in Europe. The design and implementation of vector control strategies can take advantage of properly calibrated physiological-based models describing and predicting the phenology of *P. spumarius* populations in agroecosystems.

We developed a temperature-driven physiological-based model to predict the phenology dynamics of *P. spumarius*. We parametrized model functions describing the diapause termination and age-distribution of overwintering individuals, and the temperature-dependent development rates by integrating data collected in lab experiments and literature. The model has been calibrated and validated with field data collected in Northern and Southern Italy (in the Liguria and Apulia regions, respectively).

The model can provide useful information for the conceptualization and implementation of survey programs and Integrated Pest Management (IPM) strategies to control *P. spumarius* populations and support Xf containment by farmers and decision-makers.

METHODS

The phenological dynamics of *P. spumarius* are simulated through a mechanistic, stage-structured demographic model based on the system of Kolmogorov partial differential equations considering two dimensions: time t and physiological age x. The physiological age of an individual in the ith stage, $x^i \in [0,1]$, is defined as the proportion of individual development within its stage:



$$\frac{\partial \phi^i(t,x)}{\partial t} + \frac{\partial}{\partial x}\left[v^i(T(t))\phi^i(t,x) - \sigma^i \frac{\partial \phi^i(t,x)}{\partial x}\right] = 0, \quad t > 0,\ x \in (0,1)$$

$$\left[v^i(T(t))\phi^i(t,x) - \sigma^i \frac{\partial \phi^i(t,x)}{\partial x}\right]_{x=0} = F^i(t)$$

$$\left[-\sigma^i \frac{\partial \phi^i(t,x)}{\partial x}\right]_{x=1} = 0$$

$$\phi^i(0,x) = \hat{\phi}^i(x)$$

Development functions

Defined by the Brière function, composed of three parameters specific for each stage i:
a^i – an empirical constant;
T^i_{inf} – lower temperature threshold;
T^i_{sup} – upper temperature threshold.

Model parameterization

The parameters a^i, T^i_{inf} and T^i_{sup} of the temperature-based development rate functions, as well as the distribution of physiological age of diapausing eggs are estimated minimizing the differences between the simulated and observed cumulative phenological curves.

The observed data was obtained from a climatic chamber experiment, in which the development of the preimaginal stages of *P. spumarius* were evaluated at constant temperatures (10, 18, 24 and 30 °C). The eggs used in the experiment were collected during the autumn from microcosm (cages) in open-air conditions in Turin, Northern Italy.

Model calibration

The parameters of the diapause termination process (DD_e and T_e) and of the development rate functions were calibrated with data on preimaginal stages dynamics of *P. spumarius* collected in four olive orchards in Italy: in 2016 and 2017 at Arnasco and Finale (Liguria region, Northern Italy), in 2017 and 2018 at Locorotondo and Valenzano (Apulia region, Southern Italy) (Di Serio, 2019).

Model evaluation

The performance of the calibrated phenological model was evaluated based on phenological dynamics observed in field conditions, from a dataset different from those used in the calibration procedure.

We used data collected in the Apulia region during the monitoring survey in 2019. We focus on three olive groves in Castellano Grotte, Martina Franca and Surbo, and one cherry grove in Castellano Grotte.

RESULTS

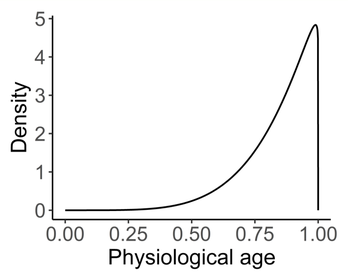


Figure 1. Estimated physiological age distribution of overwintering eggs of *Philaenus spumarius* collected in a mesocosm in Turin, Northern Italy.

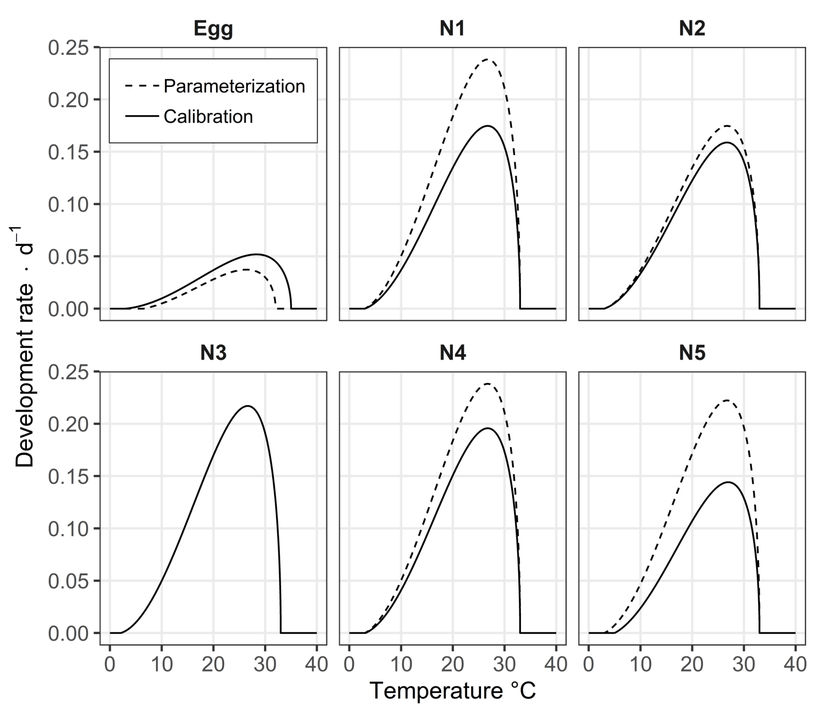


Figure 2. Development rate functions of post-diapausing eggs and the nymphal stages (N1 to N5 in the charts) of *Philaenus spumarius*, defined by the Brière function. The results of parameterization procedure are based on climatic chamber experiments (dotted lines), and the results of the calibration procedure are based on fields data (continuous lines).

Figure 3. Results of the calibration studies. The sampled (asterisks) and estimated (lines) cumulative emergences (%) of *Philaenus spumarius* stages considering the field experiments performed at Arnasco in 2016 (A) and in 2017 (B), at Finale in 2016 (C) and 2017 (D), at Locorotondo in 2017 (E) and 2018 (F), at Valenzano in 2017 (G) and 2018 (H). N1–N5 correspond to the 1st–5th nymphal instars, respectively. The estimated emergence curves of the 1st and 2nd instars were unsatisfactory and thus not considered. The temperature threshold T_e and cumulative degree days DD_e for diapause termination were estimated at 6.5 °C and 120 DD, respectively

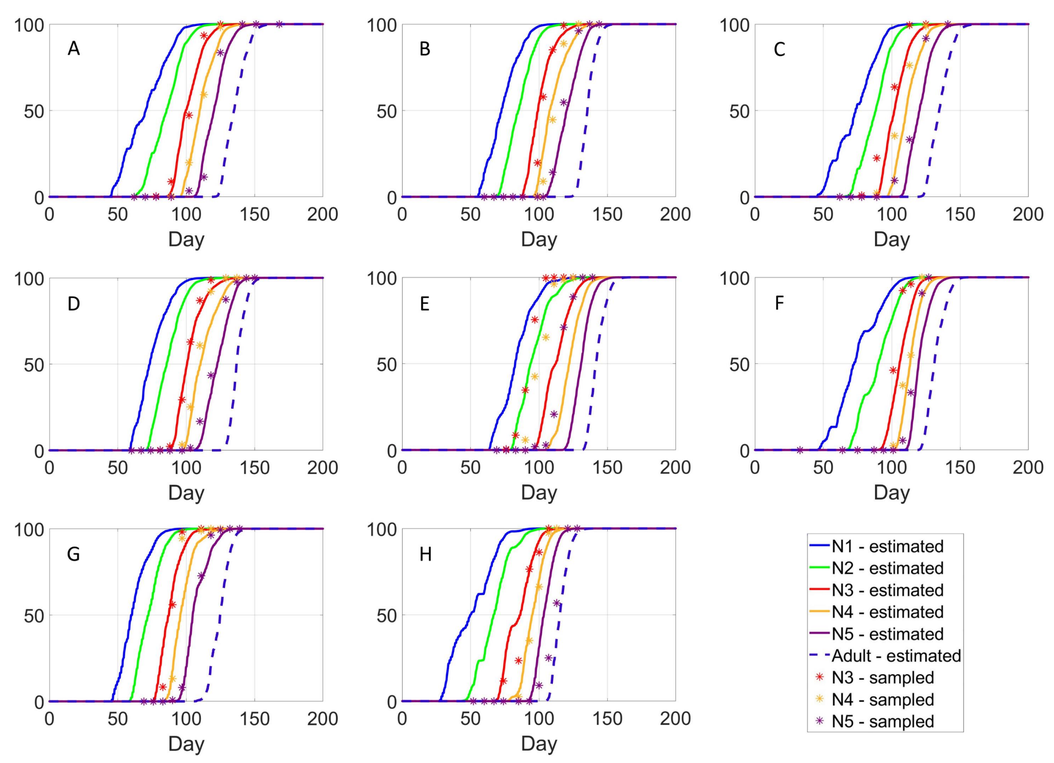
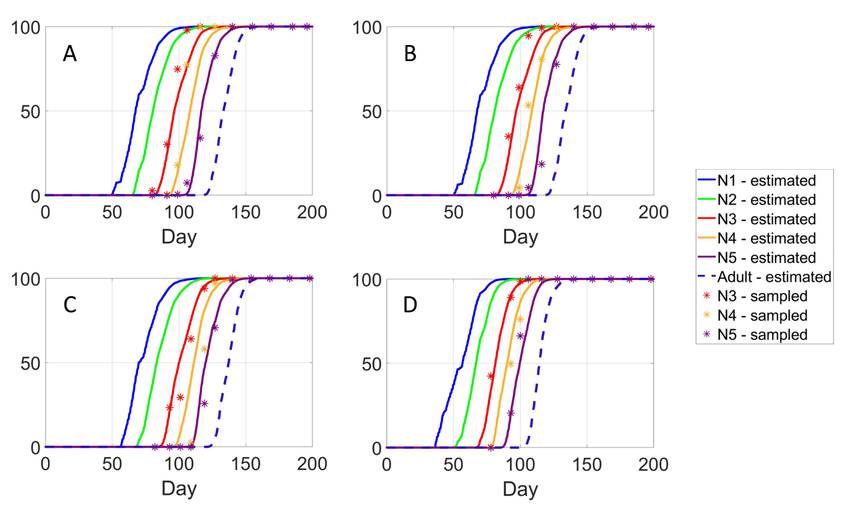


Figure 4. Results of the evaluation procedure: comparison of the sampled (asterisks) and estimated (lines) cumulative emergences (%) of *Philaenus spumarius* stages in cherry grove in Castellano Grotte (A), and in olive groves in Castellano Grotte (B), Martina Franca (C), and Surbo (D), in Apulia region (Southern Italy) in 2019. N1–N5 correspond to the 1st–5th nymphal instars, respectively. The results presented a great fit of the model to the sampling data for the 3rd, 4th, and 5th nymphal instars (differences between the estimated and observed curves ranging between ~0–9 days).



CONCLUSIONS

- The developed phenological model is a useful rational decision-tool that provides reliable quantitative information to support scheduling monitoring and control actions against the late nymphal stages of *P. spumarius*, for the Italian region.
- Despite the attempt to optimize the diapause termination processes, the model could not properly estimate the emergence curve of the 1st and 2nd instars compared to the field observations, due to the very limited knowledge on the processes involved.