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Pest categorisation of Citrus leprosis viruses

EFSA Panel on Plant Health (PLH),

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Abstract

The EFSA Panel on Plant Health performed a pest categorisation of the Citrus leprosis viruses for the EU territory and identified five distinct viruses, *Citrus leprosis virus C* (CiLV-C), *Citrus leprosis virus C2* (CiLV-C2), *Hibiscus green spot virus 2* (HGSV-2), the Citrus strain of *Orchid fleck virus* (OFV) and *Citrus leprosis virus N sensu novo* (CiLV-N) as causing this severe disease, most significantly in sweet orange and mandarin. These viruses have in common that they do not cause systemic infections in their hosts and that they all are transmitted by *Brevipalpus* spp. mites (likely but not confirmed for HGSV-2). Mites represent the most important means of virus spread, while plants for planting of Citrus are only considered of minor significance. These well characterised viruses occur in South and Central America. Leprosis is currently regulated in directive 2000/29 EC and, together with its associated viruses, has never been recorded in the EU. All five viruses have the potential to enter into, establish in and spread within the EU territory, with plants for planting of non-regulated hosts, fruits of Citrus and hitch-hiking of viruliferous mites identified as the most significant pathways. Given the severity of the leprosis disease, the introduction and spread of the various viruses would have negative consequences on the EU citrus industry, the magnitude of which is difficult to evaluate given the uncertainties affecting the *Brevipalpus* spp. vectors (identity, distribution, density, transmission specificity and efficiency). Overall, leprosis and its five associated viruses meet all the criteria evaluated by EFSA to qualify as Union quarantine pests, but do not fulfil those of being present in the EU or of plants for planting being the main spread mechanism to qualify as Union regulated non-quarantine pests. The main uncertainties affecting this categorisation concern the *Brevipalpus* spp. mite vectors.

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Keywords: Citrus leprosis virus, *Brevipalpus* spp., Citrus leprosis virus C., Citrus leprosis virus C2, Hibiscus green spot virus 2, Orchid fleck virus, Citrus leprosis virus N sensu novo

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Table of contents

Abstract.....	1
1. Introduction.....	4
1.1. Background and Terms of Reference as provided by the requestor.....	4
1.1.1. Background.....	4
1.1.2. Terms of Reference.....	4
1.1.2.1. Terms of Reference: Appendix 1.....	5
1.1.2.2. Terms of Reference: Appendix 2.....	6
1.1.2.3. Terms of Reference: Appendix 3.....	7
1.2. Interpretation of the Terms of Reference.....	8
2. Data and methodologies.....	8
2.1. Data.....	8
2.1.1. Literature search.....	8
2.1.2. Database search.....	9
2.2. Methodologies.....	9
3. Pest categorisation.....	11
3.1. Identity and biology of the pest.....	11
3.1.1. Identity and taxonomy.....	11
3.1.2. Biology of the pest.....	11
3.1.3. Intraspecific diversity.....	12
3.1.4. Detection and identification of the pest.....	13
3.2. Pest distribution.....	13
3.2.1. Pest distribution outside the EU.....	13
3.2.2. Pest distribution in the EU.....	15
3.3. Regulatory status.....	15
3.3.1. Council Directive 2000/29/EC.....	15
3.3.2. Legislation addressing plants and plant parts on which leprosis is regulated.....	15
3.3.3. Legislation addressing vectors.....	16
3.4. Entry, establishment and spread in the EU.....	16
3.4.1. Host range.....	16
3.4.2. Entry.....	19
3.4.3. Establishment.....	19
3.4.3.1. EU distribution of main host plants.....	20
3.4.4. Spread.....	20
3.4.4.1. Vectors and their distribution in the EU.....	21
3.5. Impacts.....	24
3.6. Availability and limits of mitigation measures.....	25
3.6.1. Biological or technical factors limiting the feasibility and effectiveness of measures to prevent the entry, establishment and spread of the pest.....	25
3.6.2. Biological or technical factors limiting the ability to prevent the presence of the pest on plants for planting.....	25
3.6.3. Control methods.....	26
3.7. Uncertainty.....	26
4. Conclusions.....	26
References.....	29
Abbreviations.....	31

1. Introduction

1.1. Background and Terms of Reference as provided by the requestor

1.1.1. Background

Council Directive 2000/29/EC¹ on protective measures against the introduction into the Community of organisms harmful to plants or plant products and against their spread within the Community establishes the present European Union plant health regime. The Directive lays down the phytosanitary provisions and the control checks to be carried out at the place of origin on plants and plant products destined for the Union or to be moved within the Union. In the Directive's 2000/29/EC annexes, the list of harmful organisms (pests) whose introduction into or spread within the Union is prohibited, is detailed together with specific requirements for import or internal movement.

Following the evaluation of the plant health regime, the new basic plant health law, Regulation (EU) 2016/2031² on protective measures against pests of plants, was adopted on 26 October 2016 and will apply from 14 December 2019 onwards, repealing Directive 2000/29/EC. In line with the principles of the above mentioned legislation and the follow-up work of the secondary legislation for the listing of EU regulated pests, EFSA is requested to provide pest categorizations of the harmful organisms included in the annexes of Directive 2000/29/EC, in the cases where recent pest risk assessment/pest categorisation is not available.

1.1.2. Terms of Reference

EFSA is requested, pursuant to Article 22(5.b) and Article 29(1) of Regulation (EC) No 178/2002³, to provide scientific opinion in the field of plant health.

EFSA is requested to prepare and deliver a pest categorisation (step 1 analysis) for each of the regulated pests included in the appendices of the annex to this mandate. The methodology and template of pest categorisation have already been developed in past mandates for the organisms listed in Annex II Part A Section II of Directive 2000/29/EC. The same methodology and outcome is expected for this work as well.

The list of the harmful organisms included in the annex to this mandate comprises 133 harmful organisms or groups. A pest categorisation is expected for these 133 pests or groups and the delivery of the work would be stepwise at regular intervals through the year as detailed below. First priority covers the harmful organisms included in Appendix 1, comprising pests from Annex II Part A Section I and Annex II Part B of Directive 2000/29/EC. The delivery of all pest categorisations for the pests included in Appendix 1 is June 2018. The second priority is the pests included in Appendix 2, comprising the group of *Cicadellidae* (non-EU) known to be vector of Pierce's disease (caused by *Xylella fastidiosa*), the group of *Tephritidae* (non-EU), the group of potato viruses and virus-like organisms, the group of viruses and virus-like organisms of *Cydonia* Mill., *Fragaria* L., *Malus* Mill., *Prunus* L., *Pyrus* L., *Ribes* L., *Rubus* L. and *Vitis* L. and the group of *Margarodes* (non-EU species). The delivery of all pest categorisations for the pests included in Appendix 2 is end 2019. The pests included in Appendix 3 cover pests of Annex I part A section I and all pests categorisations should be delivered by end 2020.

For the above mentioned groups, each covering a large number of pests, the pest categorisation will be performed for the group and not the individual harmful organisms listed under "such as" notation in the Annexes of the Directive 2000/29/EC. The criteria to be taken particularly under consideration for these cases, is the analysis of host pest combination, investigation of pathways, the damages occurring and the relevant impact.

Finally, as indicated in the text above, all references to 'non-European' should be avoided and replaced by 'non-EU' and refer to all territories with exception of the Union territories as defined in Article 1 point 3 of Regulation (EU) 2016/2031.

¹ Council Directive 2000/29/EC of 8 May 2000 on protective measures against the introduction into the Community of organisms harmful to plants or plant products and against their spread within the Community. OJ L 169/1, 10.7.2000, p. 1–112.

² Regulation (EU) 2016/2031 of the European Parliament of the Council of 26 October 2016 on protective measures against pests of plants. OJ L 317, 23.11.2016, p. 4–104.

³ Regulation (EC) No 178/2002 of the European Parliament and of the Council of 28 January 2002 laying down the general principles and requirements of food law, establishing the European Food Safety Authority and laying down procedures in matters of food safety. OJ L 31/1, 1.2.2002, p. 1–24.

1.1.2.1. Terms of Reference: Appendix 1

List of harmful organisms for which pest categorisation is requested. The list below follows the annexes of Directive 2000/29/EC.

Annex IIAI

(a) Insects, mites and nematodes, at all stages of their development

<i>Aleurocantus</i> spp.	<i>Numonia pyrivorella</i> (Matsumura)
<i>Anthonomus bisignifer</i> (Schenkling)	<i>Oligonychus perditus</i> Pritchard and Baker
<i>Anthonomus signatus</i> (Say)	<i>Pissodes</i> spp. (non-EU)
<i>Aschistonyx eppoi</i> Inouye	<i>Scirtothrips aurantii</i> Faure
<i>Carposina niponensis</i> Walsingham	<i>Scirtothrips citri</i> (Moultex)
<i>Enarmonia packardi</i> (Zeller)	<i>Scolytidae</i> spp. (non-EU)
<i>Enarmonia prunivora</i> Walsh	<i>Scrobipalopsis solanivora</i> Povolny
<i>Grapholita inopinata</i> Heinrich	<i>Tachypterellus quadrigibbus</i> Say
<i>Hishomonus phycitis</i>	<i>Toxoptera citricida</i> Kirk.
<i>Leucaspis japonica</i> Ckll.	<i>Unaspis citri</i> Comstock
<i>Listronotus bonariensis</i> (Kuschel)	

(b) Bacteria

Citrus variegated chlorosis	<i>Xanthomonas campestris</i> pv. <i>oryzae</i> (Ishiyama)
<i>Erwinia stewartii</i> (Smith) Dye	Dye and pv. <i>oryzicola</i> (Fang, et al.) Dye

(c) Fungi

<i>Alternaria alternata</i> (Fr.) Keissler (non-EU pathogenic isolates)	<i>Elsinoe</i> spp. Bitanc. and Jenk. Mendes
<i>Anisogramma anomala</i> (Peck) E. Müller	<i>Fusarium oxysporum</i> f. sp. <i>albedinis</i> (Kilian and Maire) Gordon
<i>Apiosporina morbosa</i> (Schwein.) v. Arx	<i>Guignardia piricola</i> (Nosa) Yamamoto
<i>Ceratocystis virescens</i> (Davidson) Moreau	<i>Puccinia pittieriana</i> Hennings
<i>Cercoseptoria pini-densiflorae</i> (Hori and Nambu) Deighton	<i>Stegophora ulmea</i> (Schweinitz: Fries) Sydow & Sydow
<i>Cercospora angolensis</i> Carv. and Mendes	<i>Venturia nashicola</i> Tanaka and Yamamoto

(d) Virus and virus-like organisms

Beet curly top virus (non-EU isolates)	Little cherry pathogen (non- EU isolates)
Black raspberry latent virus	Naturally spreading psorosis
Blight and blight-like	Palm lethal yellowing mycoplasma
Cadang-Cadang viroid	Satsuma dwarf virus
Citrus tristeza virus (non-EU isolates)	Tatter leaf virus
Leprosis	Witches' broom (MLO)

Annex IIB

(a) Insect mites and nematodes, at all stages of their development

<i>Anthonomus grandis</i> (Boh.)	<i>Ips amitinus</i> Eichhof
<i>Cephalcia lariciphila</i> (Klug)	<i>Ips cembrae</i> Heer
<i>Dendroctonus micans</i> Kugelán	<i>Ips duplicatus</i> Sahlberg
<i>Gilpinia hercyniae</i> (Hartig)	<i>Ips sexdentatus</i> Börner
<i>Gonipterus scutellatus</i> Gyll.	<i>Ips typographus</i> Heer
<i>Ips amitinus</i> Eichhof	<i>Sternochetus mangiferae</i> Fabricius

(b) Bacteria

Curtobacterium flaccumfaciens pv. *flaccumfaciens*
(Hedges) Collins and Jones

(c) Fungi

Glomerella gossypii Edgerton

Hypoxylon mammatum (Wahl.) J. Miller

Gremmeniella abietina (Lag.) Morelet

1.1.2.2. Terms of Reference: Appendix 2

List of harmful organisms for which pest categorisation is requested per group. The list below follows the categorisation included in the annexes of Directive 2000/29/EC.

Annex IAI**(a) Insects, mites and nematodes, at all stages of their development**

Group of Cicadellidae (non-EU) known to be vector of Pierce's disease (caused by *Xylella fastidiosa*), such as:

- | | |
|--|---|
| 1) <i>Carneocephala fulgida</i> Nottingham | 3) <i>Graphocephala atropunctata</i> (Signoret) |
| 2) <i>Draeculacephala minerva</i> Ball | |

Group of Tephritidae (non-EU) such as:

- | | |
|--|---|
| 1) <i>Anastrepha fraterculus</i> (Wiedemann) | 12) <i>Pardalaspis cyanescens</i> Bezzi |
| 2) <i>Anastrepha ludens</i> (Loew) | 13) <i>Pardalaspis quinaria</i> Bezzi |
| 3) <i>Anastrepha obliqua</i> Macquart | 14) <i>Pterandrus rosa</i> (Karsch) |
| 4) <i>Anastrepha suspensa</i> (Loew) | 15) <i>Rhacochlaena japonica</i> Ito |
| 5) <i>Dacus ciliatus</i> Loew | 16) <i>Rhagoletis completa</i> Cresson |
| 6) <i>Dacus curcurbitae</i> Coquillett | 17) <i>Rhagoletis fausta</i> (Osten-Sacken) |
| 7) <i>Dacus dorsalis</i> Hendel | 18) <i>Rhagoletis indifferens</i> Curran |
| 8) <i>Dacus tryoni</i> (Froggatt) | 19) <i>Rhagoletis mendax</i> Curran |
| 9) <i>Dacus tsuneonis</i> Miyake | 20) <i>Rhagoletis pomonella</i> Walsh |
| 10) <i>Dacus zonatus</i> Saund. | 21) <i>Rhagoletis suavis</i> (Loew) |
| 11) <i>Epochra canadensis</i> (Loew) | |

(c) Viruses and virus-like organisms

Group of potato viruses and virus-like organisms such as:

- | | |
|----------------------------------|--|
| 1) Andean potato latent virus | 4) Potato black ringspot virus |
| 2) Andean potato mottle virus | 5) Potato virus T |
| 3) Arracacha virus B, oca strain | 6) non-EU isolates of potato viruses A, M, S, V, X and Y (including Yo, Yn and Yc) and Potato leafroll virus |

Group of viruses and virus-like organisms of *Cydonia* Mill., *Fragaria* L., *Malus* Mill., *Prunus* L., *Pyrus* L., *Ribes* L., *Rubus* L. and *Vitis* L., such as:

- | | |
|--------------------------------------|--|
| 1) Blueberry leaf mottle virus | 8) Peach yellows mycoplasma |
| 2) Cherry rasp leaf virus (American) | 9) Plum line pattern virus (American) |
| 3) Peach mosaic virus (American) | 10) Raspberry leaf curl virus (American) |
| 4) Peach phony rickettsia | 11) Strawberry witches' broom mycoplasma |
| 5) Peach rosette mosaic virus | 12) Non-EU viruses and virus-like organisms of <i>Cydonia</i> Mill., <i>Fragaria</i> L., <i>Malus</i> Mill., <i>Prunus</i> L., <i>Pyrus</i> L., <i>Ribes</i> L., <i>Rubus</i> L. and <i>Vitis</i> L. |
| 6) Peach rosette mycoplasma | |
| 7) Peach X-disease mycoplasma | |

Annex IIAI

(a) Insects, mites and nematodes, at all stages of their development

Group of *Margarodes* (non-EU species) such as:

- 1) *Margarodes vitis* (Phillipi)
- 2) *Margarodes vredendalensis* de Klerk
- 3) *Margarodes prieskaensis* Jakubski

1.1.2.3. Terms of Reference: Appendix 3

List of harmful organisms for which pest categorisation is requested. The list below follows the annexes of Directive 2000/29/EC.

Annex IAI

(a) Insects, mites and nematodes, at all stages of their development

<i>Acleris</i> spp. (non-EU)	<i>Longidorus diadecturus</i> Eveleigh and Allen
<i>Amauromyza maculosa</i> (Malloch)	<i>Monochamus</i> spp. (non-EU)
<i>Anomala orientalis</i> Waterhouse	<i>Myndus crudus</i> Van Duzee
<i>Arrhenodes minutus</i> Drury	<i>Nacobbus aberrans</i> (Thorne) Thorne and Allen
<i>Choristoneura</i> spp. (non-EU)	<i>Naupactus leucoloma</i> Boheman
<i>Conotrachelus nenuphar</i> (Herbst)	<i>Premnotrypes</i> spp. (non-EU)
<i>Dendrolimus sibiricus</i> Tschetverikov	<i>Pseudopityophthorus minutissimus</i> (Zimmermann)
<i>Diabrotica barberi</i> Smith and Lawrence	<i>Pseudopityophthorus pruinus</i> (Eichhoff)
<i>Diabrotica undecimpunctata howardi</i> Barber	<i>Scaphoideus luteolus</i> (Van Duzee)
<i>Diabrotica undecimpunctata undecimpunctata</i> Mannerheim	<i>Spodoptera eridania</i> (Cramer)
<i>Diabrotica virgifera zea</i> Krysan & Smith	<i>Spodoptera frugiperda</i> (Smith)
<i>Diaphorina citri</i> Kuway	<i>Spodoptera litura</i> (Fabricus)
<i>Heliothis zea</i> (Boddie)	<i>Thrips palmi</i> Karny
<i>Hirschmanniella</i> spp., other than	<i>Xiphinema americanum</i> Cobb <i>sensu lato</i> (non-EU populations)
<i>Hirschmanniella gracilis</i> (de Man) Luc and Goodey	<i>Xiphinema californicum</i> Lamberti and Bleve-Zacheo
<i>Liriomyza sativae</i> Blanchard	

(b) Fungi

<i>Ceratocystis fagacearum</i> (Bretz) Hunt	<i>Mycosphaerella larici-leptolepis</i> Ito et al.
<i>Chrysomyxa arctostaphyli</i> Dietel	<i>Mycosphaerella populorum</i> G. E. Thompson
<i>Cronartium</i> spp. (non-EU)	<i>Phoma andina</i> Turkensteen
<i>Endocronartium</i> spp. (non-EU)	<i>Phyllosticta solitaria</i> Ell. and Ev.
<i>Guignardia laricina</i> (Saw.) Yamamoto and Ito	<i>Septoria lycopersici</i> Speg. var. <i>malagutii</i> Ciccarone and Boerema
<i>Gymnosporangium</i> spp. (non-EU)	<i>Thecaphora solani</i> Barrus
<i>Inonotus weirii</i> (Murril) Kotlaba and Pouzar	<i>Trechispora brinkmannii</i> (Bresad.) Rogers
<i>Melampsora farlowii</i> (Arthur) Davis	

(c) Viruses and virus-like organisms

Tobacco ringspot virus	Pepper mild tigré virus
Tomato ringspot virus	Squash leaf curl virus
Bean golden mosaic virus	Euphorbia mosaic virus
Cowpea mild mottle virus	Florida tomato virus
Lettuce infectious yellows virus	

(d) Parasitic plants*Arceuthobium* spp. (non-EU)**Annex I A I I****(a) Insects, mites and nematodes, at all stages of their development***Meloidogyne fallax* Karssen*Rhizoecus hibisci* Kawai and Takagi*Popillia japonica* Newman**(b) Bacteria***Clavibacter michiganensis* (Smith) Davis et al.
ssp. *sepedonicus* (Spieckermann and Kotthoff)
Davis et al.*Ralstonia solanacearum* (Smith) Yabuuchi et al.**(c) Fungi***Melampsora medusae* Thümen*Synchytrium endobioticum* (Schilbersky) Percival**Annex I B****(a) Insects, mites and nematodes, at all stages of their development***Leptinotarsa decemlineata* Say*Liriomyza bryoniae* (Kaltenbach)**(b) Viruses and virus-like organisms**

Beet necrotic yellow vein virus

1.2. Interpretation of the Terms of Reference

'Leprosis' is one of a number of pests listed in the Appendices to the Terms of Reference (ToR) to be subject to pest categorisation, to determine whether it fulfils the criteria of a quarantine pest or those of a regulated non-quarantine pest (RNQP) for the area of the European Union (EU) excluding Ceuta, Melilla and the outermost regions of Member States (MSs) referred to in Article 355(1) of the Treaty on the Functioning of the European Union (TFEU), other than Madeira and the Azores.

'Leprosis' or 'Citrus leprosis' is an important and well characterised disease of citrus, in particular sweet orange. Five different viruses, sharing a similar biology, have been reported to be able to cause leprosis symptoms in various citrus species, *Citrus leprosis virus C* (CiLV-C, genus *Cilevirus*), *Citrus leprosis virus C2* (CiLV-C2, genus *Cilevirus*), *Hibiscus green spot virus 2* (HGSV-2, genus *Higrevirus*), *Citrus leprosis virus N* (CiLV-N, genus *Dichorhavirus*) and *Citrus necrotic spot virus* (CiNSV, genus *Dichorhavirus*). The first three viruses are responsible for the cytoplasmic form of leprosis while the last two are responsible for the nuclear form. These two forms of the disease are separated by the site, cytoplasm or nucleus, of a typical cytopathic alteration, the accumulation of electron-dense inclusion bodies.

Following a taxonomic review of the Mononegavirales order, CiLV-N and CiNSV are now considered as constituting a Citrus strain of *Orchid fleck virus* (OFV), the type member of the *Dichorhavirus* genus. Very recently, a novel *Dichorhavirus* was identified in Citrus plants with leprosis symptoms and confusingly given the same name of *Citrus leprosis virus N*. The present pest categorisation therefore addresses all the currently known viruses causing leprosis disease in citrus, CiLV-C, CiLV-C2, HGSV-2, the citrus strain of OFV and CiLV-N *sensu novo*.

2. Data and methodologies**2.1. Data****2.1.1. Literature search**

A literature search on leprosis and on the various viruses able to cause it was conducted at the beginning of the categorisation in the ISI Web of Science bibliographic database, using the scientific and synonymous names of the virus as well as the commonly used disease names as search term. Relevant papers were reviewed, and further references and information were obtained from experts, from citations within the references and grey literature.

2.1.2. Database search

Pest information, on host(s) and distribution, was retrieved from the EPPO Global Database (EPPO, 2017).

Data about import of commodity types that could potentially provide a pathway for the pest to enter the EU and about the area of hosts grown in the EU were obtained from EUROSTAT.

The Europhyt database was consulted for pest-specific notifications on interceptions and outbreaks. Europhyt is a web-based network launched by the Directorate General for Health and Consumers (DG SANCO), and is a subproject of PHYSAN (Phyto-Sanitary Controls) specifically concerned with plant health information. The Europhyt database manages notifications of interceptions of plants or plant products that do not comply with EU legislation, as well as notifications of plant pests detected in the territory of the MSs and the phytosanitary measures taken to eradicate or avoid their spread.

2.2. Methodologies

The Panel performed the pest categorisation for leprosis, following guiding principles and steps presented in the EFSA guidance on the harmonised framework for pest risk assessment (EFSA PLH Panel, 2010) and as defined in the International Standard for Phytosanitary Measures No 11 (FAO, 2013) and No 21 (FAO, 2004).

In accordance with the guidance on a harmonised framework for pest risk assessment in the EU (EFSA PLH Panel, 2010), this work was initiated following an evaluation of the EU's plant health regime. Therefore, to facilitate the decision-making process, in the conclusions of the pest categorisation, the Panel addresses explicitly each criterion for a Union quarantine pest and for a Union RNQP in accordance with Regulation (EU) 2016/2031 on protective measures against pests of plants, and includes additional information required as per the specific terms of reference received by the European Commission. In addition, for each conclusion, the Panel provides a short description of its associated uncertainty.

Table 1 presents the Regulation (EU) 2016/2031 pest categorisation criteria on which the Panel bases its conclusions. All relevant criteria have to be met for the pest to potentially qualify either as a quarantine pest or as a RNQP. If one of the criteria is not met, the pest will not qualify. Note that a pest that does not qualify as a quarantine pest may still qualify as a RNQP pest which needs to be addressed in the opinion. For the pests regulated in the protected zones only, the scope of the categorisation is the territory of the protected zone, thus the criteria refer to the protected zone instead of the EU territory.

It should be noted that the Panel's conclusions are formulated respecting its remit and particularly with regard to the principle of separation between risk assessment and risk management (EFSA founding regulation (EU) No 178/2002); therefore, instead of determining whether the pest is likely to have an unacceptable impact, the Panel will present a summary of the observed pest impacts. Economic impacts are expressed in terms of yield and quality losses and not in monetary terms, while addressing social impacts is outside the remit of the Panel, in agreement with EFSA guidance on a harmonised framework for pest risk assessment (EFSA PLH Panel, 2010).

Table 1: Pest categorisation criteria under evaluation, as defined in Regulation (EU) 2016/2031 on protective measures against pests of plants (the number of the relevant sections of the pest categorisation is shown in brackets in the first column)

Criterion of pest categorisation	Criterion in Regulation (EU) 2016/2031 regarding Union quarantine pest	Criterion in Regulation (EU) 2016/2031 regarding protected zone quarantine pest (articles 32–35)	Criterion in Regulation (EU) 2016/2031 regarding Union regulated non-quarantine pest
Identity of the pest (Section 3.1)	Is the identity of the pest established, or has it been shown to produce consistent symptoms and to be transmissible?	Is the identity of the pest established, or has it been shown to produce consistent symptoms and to be transmissible?	Is the identity of the pest established, or has it been shown to produce consistent symptoms and to be transmissible?

Criterion of pest categorisation	Criterion in Regulation (EU) 2016/2031 regarding Union quarantine pest	Criterion in Regulation (EU) 2016/2031 regarding protected zone quarantine pest (articles 32–35)	Criterion in Regulation (EU) 2016/2031 regarding Union regulated non-quarantine pest
Absence/ presence of the pest in the EU territory (Section 3.2)	Is the pest present in the EU territory? If present, is the pest widely distributed within the EU? Describe the pest distribution briefly!	Is the pest present in the EU territory? If not, it cannot be a protected zone quarantine organism.	Is the pest present in the EU territory? If not, it cannot be a regulated non-quarantine pest. (A regulated non-quarantine pest must be present in the risk assessment area).
Regulatory status (Section 3.3)	If the pest is present in the EU but not widely distributed in the risk assessment area, it should be under official control or expected to be under official control in the near future.	The protected zone system aligns with the pest free area system under the International Plant Protection Convention (IPPC). The pest satisfies the IPPC definition of a quarantine pest that is not present in the risk assessment area (i.e. protected zone).	Is the pest regulated as a quarantine pest? If currently regulated as a quarantine pest, are there grounds to consider its status could be revoked?
Pest potential for entry, establishment and spread in the EU territory (Section 3.4)	Is the pest able to enter into, become established in, and spread within, the EU territory? If yes, briefly list the pathways!	Is the pest able to enter into, become established in, and spread within, the protected zone areas? Is entry by natural spread from EU areas where the pest is present possible?	Is spread mainly via specific plants for planting, rather than via natural spread or via movement of plant products or other objects? Clearly state if plants for planting is the main pathway!
Potential for consequences in the EU territory (Section 3.5)	Would the pests' introduction have an economic or environmental impact on the EU territory?	Would the pests' introduction have an economic or environmental impact on the protected zone areas?	Does the presence of the pest on plants for planting have an economic impact, as regards the intended use of those plants for planting?
Available measures (Section 3.6)	Are there measures available to prevent the entry into, establishment within or spread of the pest within the EU such that the risk becomes mitigated?	Are there measures available to prevent the entry into, establishment within or spread of the pest within the protected zone areas such that the risk becomes mitigated? Is it possible to eradicate the pest in a restricted area within 24 months (or a period longer than 24 months where the biology of the organism so justifies) after the presence of the pest was confirmed in the protected zone?	Are there measures available to prevent pest presence on plants for planting such that the risk becomes mitigated?
Conclusion of pest categorisation (Section 4)	A statement as to whether (1) all criteria assessed by EFSA above for consideration as a potential quarantine pest were met and (2) if not, which one(s) were not met.	A statement as to whether (1) all criteria assessed by EFSA above for consideration as potential protected zone quarantine pest were met, and (2) if not, which one(s) were not met.	A statement as to whether (1) all criteria assessed by EFSA above for consideration as a potential regulated non-quarantine pest were met, and (2) if not, which one(s) were not met.

The Panel will not indicate in its conclusions of the pest categorisation whether to continue the risk assessment process, but, following the agreed two-step approach, will continue only if requested by the risk managers. However, during the categorisation process, experts may identify key elements and

knowledge gaps that could contribute significant uncertainty to a future assessment of risk. It would be useful to identify and highlight such gaps so that potential future requests can specifically target the major elements of uncertainty, perhaps suggesting specific scenarios to examine.

3. Pest categorisation

3.1. Identity and biology of the pest

3.1.1. Identity and taxonomy

Is the identity of the pest established, or has it been shown to produce consistent symptoms and to be transmissible?

YES, the identity of the five viruses analysed is well established

As indicated in Section 1.2 'Interpretation of the Terms of Reference', 'Leprosis' or 'Citrus leprosis' is an important and well characterised disease of citrus, in particular sweet orange (Bastianel et al., 2010; Roy et al., 2015a). It has been separated into two forms, cytoplasmic or nuclear, based on a typical cytopathic alteration, the accumulation of electron-dense inclusion bodies of either the cytoplasm or the nucleus of infected cells (Kitajima et al., 1974; Colariccio et al., 1995). While the aetiology of leprosis remained obscure for a long time, in recent years five different viruses, sharing a similar biology, have been reported to be able to cause leprosis symptoms in various citrus species. The viruses were initially described based on electron microscope observation of viral particles and of cytopathic inclusions and later genomic sequences were determined. The first virus to be described was CiLV-C (genus *Cilevirus*) (Kitajima et al., 1974), followed by CiLV-N (genus *Dichorhavirus*) (Colariccio et al., 1995). The complete CiLV-C genome has been sequenced and found to consist of two segments (5 and 9 kilobases) of positive sense single stranded RNA with poly-A tails (Bastianel et al., 2006a; Locali-Fabris et al., 2006; Pascon et al., 2006). The complete genomic sequence of CiLV-N, a single negative stranded RNA molecule, has also been determined (Roy et al., 2015b).

More recently, other viruses causing similar leprosis symptoms in Citrus and having the same transmission biology have been described. These include a virus related to CiLV-C identified in Colombia and termed *Citrus leprosis virus Cytoplasmic Type 2* (CiLV-C2, genus *Cilevirus*; Roy et al., 2013), a virus named HGSV-2 (genus *Higreivirus*) observed causing symptoms in *Citrus volkameriana* in Hawaii (Melzer et al., 2012) and a virus causing leprosis symptoms in citrus in Mexico and named CiNSV (genus *Dichorhavirus*, Cruz-Jaramillo et al., 2014).

CiLV-C, CiLV-C2 and HGSV-2 are responsible for the cytoplasmic form of leprosis while CiLV-N and CiNSV are responsible for the nuclear form. CiLV-C appears to be the most widespread and the most important of these agents (Bastianel et al., 2010; Roy et al., 2015a). It shares 55% nucleotide genome identity with CiLV-C2, the only other known member of genus *Cilevirus* (Locali-Fabris et al., 2012). Following a taxonomic revision of the Mononegavirales order, CiLV-N and CiNSV are now considered as constituting a Citrus strain of OFV, the type member of the *Dichorhavirus* genus in the Rhabdoviridae family (Dietzgen et al., 2014; Afonso et al., 2016).

Very recently, a novel *Dichorhavirus*, clearly distinct from OFV was identified in Citrus plants with leprosis symptoms in Brazil and confusingly given the same name of *Citrus leprosis virus N* (Ramos-Gonzalez et al., 2017). In what follows, it will be referred-to as CiLV-N *sensu novo*.

The present pest categorisation therefore addresses all the currently known viruses causing leprosis symptoms in citrus, namely CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N *sensu novo*. All these viruses are well characterised agents for which complete genomic sequences are available. There are however some uncertainties concerning the possibility that there may exist other viruses causing leprosis symptoms in Citrus that are yet to be discovered and described.

3.1.2. Biology of the pest

The five viruses associated with leprosis are all characterised by an unusual and common biology. Their most striking property is that, contrary to the vast majority of plant-infecting viruses, they are unable to systemically invade their Citrus host plants (Bastianel et al., 2010; Roy et al., 2015a). These viruses are only able to move locally, from an infected cell to immediately neighbouring cells. This process allows the development around inoculation points of the localised, centimetric infection lesions on leaves, young stems or fruits typical of the disease (Bastianel et al., 2010; Roy et al., 2015a). There

are no known systemic hosts for these viruses (Bastianel et al., 2010; Roy et al., 2015a). However, the orchid strain of OFV is known to systemically infect a few experimental hosts such as *Beta vulgaris* (Peng et al., 2000) so that there may still exist some hosts in which the five viruses analysed here may have the ability to mount a systemic infection. In this absence of a mechanism allowing the virus to infect parts of the Citrus plants distant from an inoculation point, the presence of many lesions over an infected tree reflects multiple inoculation events having taken place all over the tree canopy. This original situation is the basis of early speculations associating the leprosis disease with bacterial or fungal infections or with toxic effects of the saliva of the mite vectors (see below).

One of the consequences of this peculiar infection biology is that plant tissues away from an infection site are considered free of infection and that propagation using this material should result in virus-free progeny plants.

The second characteristic shared by all five viruses is that they are all transmitted by *Brevipalpus* spp. mites (Acari: Tenuipalpidae) (Rodrigues and Childers, 2013) (or suspected to be in the case of HGSV-2). Three mite species (*Brevipalpus californicus*, *Brevipalpus obovatus* and *Brevipalpus phoenicis sensu lato* (s.l.)) have been described as vectors of one or another of these viruses or of the leprosis disease (see Section 3.4.4). The analysis of the literature is however very complex, because in older references the identity of the particular virus under study may not be known. In addition, a recent taxonomic revision has shown *B. phoenicis* to be a complex of cryptic species (Beard et al., 2015) so that it is not possible to know which particular species of *Brevipalpus* was referred to in publications citing *B. phoenicis* and predating the taxonomic revision. There are consequently large uncertainties about which specific mite species are able to transmit which leprosis-associated virus species (see Section 3.4.4).

These mite species have a broad plant host range and are widely distributed (Childers et al., 2003). All active stages (larvae, nymph, and adult) can acquire and transmit the viruses by feeding (Bastianel et al., 2010). The specific characteristics of the CiLV-C transmission by *Brevipalpus yothersi* have been evaluated in detail recently (Tassi et al., 2017). Given the very recent discovery of some of the viruses analysed here, there are significant uncertainties about whether all the transmission properties described below for CiLV-C apply to them without any significant difference but all available information point to that direction.

In the case of CiLV-C transmission by *B. yothersi*, a minimum acquisition access period (AAP) of 4 h is needed for mites to become viruliferous. After a latent period of 7 h, mites may transmit the virus to bean plants (*Phaseolus vulgaris*) used as indicator hosts, in as short as 2 h (inoculation access period (IAP)). Viruliferous mites may transmit for at least 12 days without having new access to an infected plant and it is believed that they may remain viruliferous during their entire lifespan (Bastianel et al., 2010; Tassi et al., 2017). All mobile developmental stages of the mite (larva, protonymph, deutonymph and adult) are able to transmit CiLV-C but the virus is not transovarially transmitted to the offspring (Tassi et al., 2017). Similar AAP and IAP values were obtained when using sweet orange as the indicator plant (Freitas-Astua et al., 2010). Shorter AAP and IAP, of 30 min and 10 min, respectively, were estimated for the transmission of CiLV-C2, using sweet orange as the indicator plant (León et al., 2016). Although suggested (Roy et al., 2015a), the leprosis-associated viruses do not seem to propagate within their mite vectors (Kitajima and Alberti, 2014; Tassi et al., 2017). Taken together, the relatively short AAP and the long retention of infectivity in the absence of replication or of transovarial transmission are typical of a persistent circulative mode of transmission (Rodrigues and Childers, 2013; Kitajima and Alberti, 2014; Tassi et al., 2017).

3.1.3. Intraspecific diversity

The five leprosis-causing viruses belong to three different genera: *Cilevirus*, *Higrevirus* and *Dichorhavirus* (Locali-Fabris et al., 2006; Melzer et al., 2013; Dietzgen et al., 2014; Roy et al., 2015b; Afonso et al., 2016). The amount of information available on the intraspecific diversity of these five viruses varies from one virus to another.

The two viruses now recognised as forming the Citrus strain of OFV, and which were previously recognised as distinct species, share on the order of 10% full genome divergence (Dietzgen et al., 2014). The divergence is slightly higher with isolates belonging to the Orchid strain of OFV (Kondo et al., 2017), while there are lots of uncertainties when it comes to differences in biological properties between these two strains. In particular, there is extremely limited information as to whether isolates of the Orchid strain are able to infect Citrus hosts. An orchid strain isolate was, however, able to infect and cause symptoms in *Citrus hassaku* (a Japanese citrus hybrid) upon experimental inoculation using

viruliferous mites (Kondo et al., 2003, 2017) but natural infection of citrus by such isolates has never been reported.

CiLV-N *sensu novo* is also known to have significant intraspecific diversity at the genome level, with divergence values of between 2% and 8% reported between four Brazilian isolates (Ramos-Gonzalez et al., 2017).

Comparison of partial sequences available in Genbank for CiLV-C and CiLV-C2 shows also these two viruses to have significant intraspecific genome diversity with, for example, divergence levels of up to around 15–17% for the partial movement protein gene of CiLV-C or for the P24 gene of CiLV-C2.

There is only extremely limited information on the intraspecific diversity of HGSV-2, which was only reported from Hawaii and for which literature is extremely limited. Partial sequencing of isolates from *C. volkameriana* and from nearby symptomatic hibiscus (*Hibiscus arnottianus*) showed only limited variability, on the order of 1–2% divergence (Melzer et al., 2012).

3.1.4. Detection and identification of the pest

Are detection and identification methods available for the pest?

YES

Initially, leprosis was mainly detected through symptoms observation. To avoid confusion with the somewhat similar symptoms of citrus canker, observation of the bacilliform virus particles by transmission electron microscopy (TEM) was then the most desirable approach. In addition, TEM allowed to distinguish between CiLV-C and CiLV-N by looking for the viroplasm in the cytoplasm or nucleus, respectively.

The five viruses addressed here are now well-characterised agents for which full-length genomic sequences are available, making possible the development of specific reverse transcription polymerase chain reaction (RT-PCR) detection assays. Although there might be some uncertainties on the specificity and polyvalence of some of the published detection methods, detection and identification methods can be generally considered to be available for these agents. A few references describing such methods are listed below, without aiming at completeness.

CiLV-C: Locali et al., 2003; Kubo et al., 2011; Choudhary et al., 2015 (serological detection is also available, Choudhary et al., 2013, 2014).

CiLV-C2: Roy et al., 2013; (serological detection is also available, Choudhary et al., 2017).

HGSV-2: Melzer et al., 2012.

Citrus strain of OFV: Cruz-Jaramillo et al., 2014; Roy et al., 2014, 2015b.

CiLV-N *sensu novo*: Ramos-Gonzalez et al., 2017.

3.2. Pest distribution

3.2.1. Pest distribution outside the EU

Leprosis has been reported from North, Central and South America (Table 2 and Figure 1). Although there are old reports of its presence elsewhere in the world (reviewed in Bastianel et al., 2010), these have not been confirmed in more recent times, suggesting that these reports were erroneous or that the disease may have disappeared from these areas as it did from Florida in the 1960s. The idea of the total absence of leprosis from the other continents than the Americas should still be considered with some caution as a result of these uncertainties.

Table 2: Global distribution of leprosis virus *sensu lato*^(a) (extracted from EPPO Global Database, accessed 20 of October, 2017)

Continent	Country	Status
America	Argentina	Present, no details
America	Belize	Present, restricted distribution
America	Bolivia	Present, restricted distribution
America	Brazil	Present, no details
America	Colombia	Present, few occurrences
America	Costa Rica	Present, no details

Continent	Country	Status
America	El Salvador	Present, no details
America	Guatemala	Present, no details
America	Honduras	Present, few occurrences
America	Mexico	Present, restricted distribution
America	Nicaragua	Present, no details
America	Panama	Present, no details
America	Paraguay	Present, no details
America	Peru	Absent, invalid record
America	United States of America	Present, restricted distribution
America	Uruguay	Present, no details
America	Venezuela	Present, no details

(a): Leprosis virus sensu lato is meant here as indicating the presence of any of the leprosis-causing viruses (CiLV-C, CiLV-C2, HGSV-2, Citrus strain of OFV or CiLV-N sensu novo).

Last updated: 2017-9-13

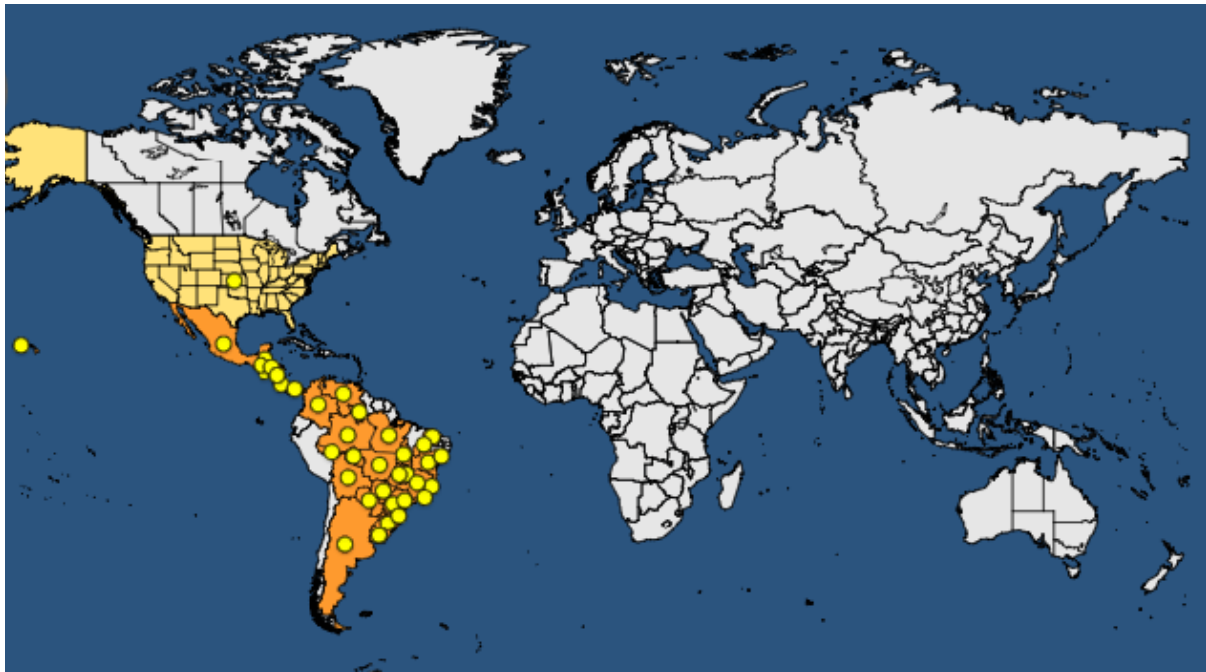


Figure 1: Global distribution of leprosis virus sensu lato (for an explanation, see footnote (a) to Table 2; extracted from EPPO Global Database, accessed 20 October 2017)

As several of the individual viruses analysed in the present opinion have been described recently, precise information on their distribution is frequently limited. CiLV-C is, however, the best known and most widely distributed of these agents. As reviewed by Roy et al. (2015a), the following distributions have been reported for the individual agents:

CiLV-C: Argentina, Belize, Bolivia, Brazil, Columbia, Costa Rica, Guatemala, Honduras, Mexico, Nicaragua, Panama, Paraguay, Uruguay, Venezuela

CiLV-C2: Colombia, USA (Hawaii) (Melzer, 2010; cited in Roy et al., 2015a)

HGSV-2: USA (Hawaii)

Citrus strain of OFV: Brazil, Colombia, Mexico, Panama

CiLV-N sensu novo: Brazil

The exact identity of the virus(es) responsible for the severe leprosis problems that occurred in Florida in the first part of the 20th century until the 1960s is not known. The partial genomic

sequences obtained by high throughput sequencing from an herbarium specimen for an isolate collected in 1948 (CiLV-N0) do not allow an unambiguous taxonomic assignment but suggest it might have represented yet another virus species in the *Dichorhavirus* genus (Hartung et al., 2015).

3.2.2. Pest distribution in the EU

Is the pest present in the EU territory?

NO

Leprosis is not known to occur in the EU and the same is true for its associated viruses (CiLV-C, CiLV-C2, HGSV-2, Citrus strain of OFV and CiLV-N *sensu novo*). As a consequence, leprosis and the associated viruses therefore do not fulfil the presence of the EU territory criterion to qualify as a Unions RNQP.

The Orchid strain of OFV has been reported from the EU (Germany, Denmark) as well as from a range of other countries in the world (Peng et al., 2013). However, its ability to cause leprosis in Citrus plants remains unknown.

3.3. Regulatory status

3.3.1. Council Directive 2000/29/EC

Leprosis is currently regulated in Directive 2000/29 EC (Table 3).

Table 3: Leprosis in Council Directive 2000/29/EC

Annex II, Part A	Harmful organisms whose introduction into, and spread within, all member states shall be banned if they are present on certain plants or plant products	
Section I	Harmful organisms not known to occur in the community and relevant for the entire community	
(d)	Virus and virus-like organisms	
	Species	Subject of contamination
8.	Leprosis	Plants of <i>Citrus</i> L., <i>Fortunella</i> Swingle, <i>Poncirus</i> Raf., and their hybrids, other than fruit and seeds

3.3.2. Legislation addressing plants and plant parts on which leprosis is regulated (Table 4)

Table 4: Regulated hosts and commodities that may involve leprosis in Annexes III, IV and V of Council Directive 2000/29/EC

Annex III, Part A	Plants, plant products and other objects the introduction of which shall be prohibited in all member states
Description	Country of origin
16. Plants of <i>Citrus</i> L., <i>Fortunella</i> Swingle, <i>Poncirus</i> Raf., and their hybrids, other than fruit and seeds	Third countries
Annex IV, Part A	Special requirements which must be laid down by all member states for the introduction and movement of plants, plant products and other objects into and within all member states
Section I	Plants, plant products and other objects originating outside the community
Plants, plant products and other objects	Special requirements
16.1 Fruits of <i>Citrus</i> L., <i>Fortunella</i> Swingle, <i>Poncirus</i> Raf., and their hybrids, originating in third countries	The fruits shall be free from peduncles and leaves and the packaging shall bear an appropriate origin mark

Section II	Plants, plant products and other objects originating in the community
Plants, plant products and other objects	Special requirements
30.1 Fruits of <i>Citrus</i> L., <i>Fortunella</i> Swingle, <i>Poncirus</i> Raf., and their hybrids	The packaging shall bear an appropriate origin mark
Annex V	Plants, plant products and other objects which must be subject to a plant health inspection (at the place of production if originating in the community, before being moved within the community — in the country of origin or the consignor country, if originating outside the community) before being permitted to enter the community
Part B	Plants, plant products and other objects originating in territories, other than those territories referred to in part A. I. Plants, plant products and other objects which are potential carriers of harmful organisms of relevance for the entire Community
	1. Plants, intended for planting, other than seeds but including seeds of ... <i>Citrus</i> L., <i>Fortunella</i> Swingle and <i>Poncirus</i> Raf., and their hybrids ... 3. Fruits of: - <i>Citrus</i> L., <i>Fortunella</i> Swingle, <i>Poncirus</i> Raf., and their hybrids.

3.3.3. Legislation addressing vectors

Brevipalpus species are not listed in Directive 2000/29/EC.

3.4. Entry, establishment and spread in the EU

3.4.1. Host range

From all viruses causing a leprosis disease in citrus, CiLV-C is the most common and found in many of the citrus production areas in South and Central America. CiLV-C2, a distinct virus species related to CiLV-C was identified in several citrus growing areas of Columbia after CiLV-C tests failed on symptomatic materials. The most sensitive hosts for CiLV-C and CiLV-C2 is sweet orange (*Citrus sinensis*). The virus is also widespread in mandarin (*Citrus reticulata*) and its hybrids, although the varieties express various degree of resistance or tolerance to CiLV-C. The Mediterranean mandarin, *Citrus deliciosa* shows high susceptibility while *C. reticulata* mandarins are less sensitive and often only leaf symptoms are expressed (Rodrigues et al., 2003; Bastianel et al., 2006b). There are a number of *C. reticulata* hybrids (e.g. *C. sinensis* x *C. reticulata* 'Murcott tangor') that show high field resistance to CiLV-C and the highly resistant Murcott is extensively used in breeding programmes. Natural infections of CiLV-C are found in many other Citrus species (Table 5), however lemons (*C. × limon*), limes (*Citrus aurantifolia*), grapefruit (*Citrus paradisi*), limette (*Citrus limetta*) and Persian lime (*C. × latifolia*) are not found naturally infected with CiLV-C and are considered resistant (Bastianel et al., 2006a,b); *C. limon* is immune to CiLV-C (Bastianel et al., 2010). The host range of CiLV-C also extends to non-citrus rutaceous (*Swinglea glutinosa*) and non-rutaceous hosts. *S. glutinosa* often used as hedgerows or *Commelina benghalensis*, growing in association with Citrus in orchards, are natural hosts of CiLV-C (León et al., 2008) and may play a role in the epidemiology of the leprosis disease as a source of virus inoculum and by harbouring mite vector populations. Similarly, *Hibiscus rosa-sinensis*, *Malvaviscus arboreus*, *Grevillea robusta* and *Bixa orellana*, often also used as hedgerows were shown to be hosts of CiLV-C by experimental inoculation (Nunes et al., 2012) (Table 5). Additionally, CiLV-C has a wide range of several hundreds of experimental hosts, ranging from *Arabidopsis* to *Phaseolus*. Many of those hosts have only experimental significance however, ornamental hosts like *Dieffenbachia* or *Hibiscus* may be subject to international trade and can constitute a pathway for introduction and spread of CiLV-C.

While mandarins, lime and grapefruit are considered resistant to CiLV-C, these citrus species, in addition to sweet orange, are susceptible to infection with the Citrus strain of OFV (Cruz-Jaramillo et al., 2014; Roy et al., 2015a,b). Lemon and sour orange have also been found naturally infected (Cruz-Jaramillo et al., 2014; Roy et al., 2015a,b) and *Dieffenbachia* and *Swinglea* are also alternative natural hosts. Sampling in non-commercial *C. sinensis* orchards in Brazil identified that a further distinct rhabdovirus species with the proposed name CiLV-N is causing there a nuclear-type leprosis disease (Ramos-Gonzalez et al., 2017). While not identified anywhere else, this finding confirms that further and diverse rhabdoviruses cause the leprosis disease. Considering that this new virus has similar biological properties as the Citrus strain of OFV, it represents a challenge to virus detection and identification.

HGSV-2 was identified in *C. volkameriana* in Hawaii (Melzer et al., 2012). It was only found in this citrus host and not in sweet orange orchards in the vicinity of the leprosis affected plants. Thus, this citrus host can be considered as an alternative host to a virus that commonly infects malvaceous hosts.

Given that some of these viruses are of recent discovery, the information on their host range (see Table 5) should be considered with care and as carrying significant if not high uncertainty.

Table 5: Host range of the five viruses causing leprosis

	Viruses causing citrus leprosis disease					Natural (nat)/ experimental (exp) infection	Reference
	CiLV-C	CiLV-C2	HGSV-2	OFV- Citrus strains	CiLV-N		
<i>Citrus sinensis</i>	X	X		X	X	nat	Ramos-Gonzalez et al. (2017)
<i>Citrus aurantium</i>	X			X		nat	Roy et al. (2015a,b)
<i>Citrus jambhiri</i>	X					nat	Roy et al. (2015a,b)
<i>Citrus medica</i>	X					nat	Roy et al. (2015a,b)
<i>Citrus reshni</i>	X			X		nat	Roy et al. (2015a,b)
<i>Citrus reticulata</i> x <i>C. sinensis</i>	X			X		nat	Roy et al. (2015a,b)
<i>Citrus sinensis</i> x <i>Poncirus trifoliata</i>	X					nat	Roy et al. (2015a,b)
<i>Citrus</i> × <i>paradisi</i>				X		nat	Roy et al. (2015a,b)
<i>C.</i> × <i>limon</i>				X		nat	Roy et al. (2015a,b)
<i>C. aurantifolia</i>				X		nat	Roy et al. (2015a,b)
<i>C. limetta</i>				X		nat	Roy et al. (2015a,b)
<i>C.</i> × <i>latifolia</i>				X		nat	Roy et al. (2015a,b)
<i>Citrus volkameriana</i>	X		X			nat	Roy et al. (2015a,b); Melzer et al. (2012)
<i>C. reticulata</i>	X					nat	Bastianel et al. (2008)
<i>C. deliciosa</i>	X					nat	Bastianel et al. (2008)
<i>C. suhuiensis</i>	X					nat	Bastianel et al. (2008)
<i>C. clementina</i> x. <i>C. reticulata</i>	X					nat	Bastianel et al. (2008)
<i>C. clementina</i> x (<i>C. reticulata</i> x <i>C. paradisi</i>)	X					nat	Bastianel et al. (2008)
<i>C. sinensis</i> x <i>C. reticulata</i>	X					nat	Bastianel et al. (2008)
<i>C. latifolia</i>	X					nat	Lovisolò et al. (2000)
<i>C. limon</i>	X					nat	Lovisolò et al. (2000)
<i>C. sinensis</i> × <i>Poncirus trifoliata</i>	X					nat	Lovisolò et al. (2000)

	Viruses causing citrus leprosis disease					Natural (nat)/ experimental (exp) infection	Reference
	CiLV-C	CiLV-C2	HGSV-2	OFV- Citrus strains	CiLV-N		
<i>Swinglea glutinosa</i>	X	X		X		nat	León et al. (2008)
Non-rutaceous host plants							
<i>Commelina benghalensis</i>	X					nat	León et al. (2008)
<i>Dieffenbachia</i> sp.		X		X		nat	Roy et al. (2015b)
<i>Hibiscus arnottianus</i>			X			nat	Melzer et al. (2015)
<i>P. vulgaris</i>	x					exp	Garita et al. (2013)
<i>Hibiscus rosa-sinensis</i>	X	X	X			exp	Nunes et al. (2012)
<i>Malvaviscus arboreus</i> Cav.	X					exp	Nunes et al. (2012)
<i>Grevillea robusta</i>	X					exp	Nunes et al. (2012)
<i>Bixa orellana</i>	X					exp	Nunes et al. (2012)
<i>Hibiscus syriacus</i>	X					exp	Garita et al. (2014)
<i>Epidendrum</i> sp.	X					exp	Garita et al. (2014)
<i>Capsicum annuum</i>	X					exp	Garita et al. (2014)
<i>Datura stramonium</i>	X					exp	Garita et al. (2014)
<i>Solanum violaefolium</i>	X					exp	Garita et al. (2014)
<i>Nicotiana benthamiana</i>	X					exp	Garita et al. (2014)
<i>Nicotiana edwardsonii</i>	X					exp	Garita et al. (2014)
<i>Solanum melongena</i>	X					exp	Garita et al. (2014)
<i>Solanum nigrum</i>	X					exp	Garita et al. (2014)
<i>Viola tricolor</i>	X					exp	Garita et al. (2014)
<i>Tetragonia expansa</i>	X					exp	Garita et al. (2014)
<i>Chenopodium quinoa</i>	X					exp	Garita et al. (2014)
<i>Gomphrena globosa</i>	X					exp	Garita et al. (2014)
<i>Galinsoga quadriradiata</i>	X					exp	Garita et al. (2014)
<i>Zinnia elegans</i>	X					exp	Garita et al. (2014)
<i>Arabidopsis thaliana</i>	X				X	exp	Garita et al. (2014)
<i>Glycine max</i>	X					exp	Garita et al. (2014)
<i>Vigna radiata</i>	X					exp	Garita et al. (2014)
<i>Abelmoschus esculentus</i>	X					exp	Garita et al. (2014)
<i>Hibiscus cannabinus</i>	X					exp	Garita et al. (2014)
<i>Portulacca oleaceae</i>	X					exp	Garita et al. (2014)
<i>Ricinus communis</i>	X					exp	Garita et al. (2014)
<i>Gomphrena globosa</i>	X					exp	Lovisol et al. (2000)
<i>Chenopodiaceae</i>	X					exp	Lovisol et al. (2000)
<i>Atriplex hortensis</i>	X					exp	Lovisol et al. (2000)
<i>Atriplex latifolia</i>	X					exp	Lovisol et al. (2000)

	Viruses causing citrus leprosis disease					Natural (nat)/ experimental (exp) infection	Reference
	CiLV-C	CiLV-C2	HGSV-2	OFV- Citrus strains	CiLV-N		
<i>Beta vulgaris</i> <i>ssp cicla</i>	X					exp	Lovisolo et al. (2000)
<i>Chenopodium album</i>	X					exp	Lovisolo et al. (2000)
<i>C. amaranticolor</i>	X					exp	Lovisolo et al. (2000)
<i>C. ambrosioides</i>	X					exp	Lovisolo et al. (2000)
<i>C. bonushenrici</i>	X					exp	Lovisolo et al. (2000)
<i>C. capitatum</i>	X					exp	Lovisolo et al. (2000)
<i>C. foliosum</i>	X					exp	Lovisolo et al. (2000)
<i>C. murale</i>	X					exp	Lovisolo et al. (2000)
<i>C. polyspermum</i>	X					exp	Lovisolo et al. (2000)
<i>C. quinoa</i>	X					exp	Lovisolo et al. (2000)
<i>Tetragonia</i> <i>tetragonioides</i>	X					exp	Lovisolo et al. (2000)

3.4.2. Entry

Is the pest able to enter into the EU territory?

YES

The pathway of Citrus plants for planting is closed by existing legislation. However the various viruses analysed in the present opinion could potentially enter in the EU using the following pathways:

- Plants for planting of non-regulated rutaceous and non-rutaceous hosts (in particular for CiLV-C and CiLV-C2, known to naturally infect *S. glutinosa*, *C. benghalensis* and *Dieffenbachia* sp.)
- Fruits of susceptible Citrus species as the viruses are known to replicate and to be efficiently acquired by *Brevipalpus* spp. vector mites from them (Tassi et al., 2017)
- Hitch-hiking viruliferous mites in consignments of plants or plant products since virus retention is known to be very long and vector species are known to have a very large host range. Moreover, these mites are minute and difficult to detect.

Uncertainties on entry are considered high but mostly affect the scale of entry along these potential pathways rather than the existence of these pathways themselves.

Between 1995 and 20 October 2017, there were no records of interception of leprosis or of the leprosis-associated viruses in the Europhyt database.

3.4.3. Establishment

Is the pest able to become established in the EU territory?

YES. Susceptible hosts and vector mites are present and ecoclimatic conditions are not limiting for the various viruses.

There are no ecoclimatic constraints known for the five leprosis-associated viruses, except for those affecting their host plants and their mite vectors present in Europe (see Section 3.4.4.1). Therefore, these viruses are expected to be able establish in areas where their Citrus hosts are able to develop. Citrus cultivation occurs widely in the Mediterranean part of Europe (see EFSA PLH Panel, 2014), while ornamental rutaceous hosts may also grow in protected cultivation in more northern regions of the EU.

3.4.3.1. EU distribution of main host plants

Citrus hosts of the five leprosis-associated viruses are widely grown for citrus fruit production (oranges, mandarins etc.) in eight MS in the Mediterranean part of the EU. In order of decreasing production, they are: Spain, Italy, Greece, Portugal, Cyprus, Croatia, Malta and France (Table 6). In addition, plants of *Citrus*, *Fortunella* and *Poncirus* are grown as ornamentals, either in the open or under protected cultivation in a number of MS.

Table 6: Area of citrus production (in 1,000 ha) in Europe according to the Eurostat database (Crop statistics apro_acs_a, extracted on 20 June 2017)

GEO/TIME	2012	2013	2014	2015	2016
Spain	310.50	306.31	302.46	298.72	295.33
Italy	146.79	163.59	140.16	149.10	141.22
Greece	50.61	49.88	49.54	46.92	44.72
Portugal	19.85	19.82	19.80	20.21	20.21
France	3.89	4.34	4.16	4.21	4.70
Cyprus	3.21	2.63	2.69	2.84	3.29
Croatia	1.88	2.17	2.17	2.21	2.18

Last update 14.6.17

3.4.4. Spread

Leprosis-associated viruses are either transmitted by or associated with mites of the genus *Brevipalpus*, known as flat mites, and more specifically as *B. phoenicis* s.l. (Geijskes), *B. californicus* s.l. Banks, and *B. obovatus* Donnadieu (Childers et al., 2003; Rodrigues and Childers, 2013; Roy et al., 2015a). Leprosis is characterised by strictly localised symptoms and viral infection because all leprosis-associated viruses are non-systemic in their Citrus hosts. Therefore, virus lesions are only associated with the *Brevipalpus* spp. vectors feeding sites. A direct consequence of this unusual biology is that vegetative multiplication practices used to produce planting materials are very unlikely to represent a major mechanism for virus spread, and that the main means of virus movement and dispersal is via the vector mites.

Symptoms of infection appear from 17 to 60 days after mite transmission, with most symptoms appearing between 21 and 30 days (Chiavegato and Salibe, 1984). Subsequently, only mites feeding on infected lesions may become viruliferous and spread the disease. The percentage of viruliferous individuals in mite colonies grown on different infected tissues ranges from 25% to 60% (Tassi et al., 2017).

Because mites only acquire the virus by feeding on infected tissues, the infective mites are directly responsible for the disease progress within a plant or orchard. Therefore, disease spread is primarily affected by the size of the mite population. The virus can be acquired from infected Citrus plants (leaves, twigs or fruits lesions) but also potentially from rutaceous (*Swinglea*) or non-rutaceous host plants (see Section 3.4.1) that may be used as windbreaks or fences in Citrus groves and may favour the development of mite populations (Ulian and Oliveira, 2002; León et al., 2008; Bastianel et al., 2010).

The typical life cycle of a *Brevipalpus* spp. mite includes the egg and four feeding stages (larva, protonymph, deutonymph and adult, mostly females due to the presence of the feminising endosymbiont bacterium *Cardinium* sp. (Weeks et al., 2001)) separated by quiescent developmental stages (protochrysalis, deutochrysalis and teliochrysalis). All feeding stages are able to transmit the viruses. Developmental rates are strongly influenced by temperature, relative humidity and host plant (reviewed by Childers et al., 2003). In general, infestation is favoured by increased photoperiod and temperature and by low relative humidity and low soil–water availability for the plants (Ferraz Laranjeira et al., 2015). It has been suggested that vector species have different climatic preferences and transmission specificities (for example in Mexico, *B. californicus* is mostly present in cooler places at higher elevations and *B. yothersi* at lower elevation in warmer places) may in part explain the distribution of the different viruses (Roy et al., 2015a).

Study of the spatial patterns of *B. phoenicis*-infested trees, as well as of plants with leprosis symptoms, in commercial orange groves showed some degree of aggregation, mainly at large scale, with higher aggregation for virus infection than for mite infestation (Bassanezi and Laranjeira, 2007). Mites move slowly and prefer to shelter in surface openings and wounds; therefore, a low

dissemination by mite ambulation, in combination with the lack of directionality observed, suggest that other 'passive' mechanisms (such as cultural practices and tools, machinery or human phoresy) should play a role in their dispersal within an orchard (Bassanezi and Laranjeira, 2007). Viruliferous mites may also be spread by wind (Alves et al., 2005) from infested groves to nearby healthy ones, thus initiating an epidemic. The absence of a clear spatial association between mite-infested and virus-infected trees is possibly due to the absence of systemic infection, the time lag between mite infestation and virus infection/symptoms development (17–60 days) and the disrupting effects of any applied acaricides or tree pruning (Bassanezi and Laranjeira, 2007).

The analysis of the literature on virus–mite relationships and on vector specificity is very complex. In older references, the identity of the particular virus under study may not be known. In addition, a recent taxonomic revision has shown *B. phoenicis* to be a complex of cryptic species (Beard et al., 2015) so that it is not possible to know which particular species of *Brevipalpus* was referred to in publications citing *B. phoenicis* and predating this taxonomic revision. There are consequently large uncertainties about which mite specie(s) is(are) able to transmit which leprosis-associated virus species.

Following this recent taxonomical revision of *B. phoenicis* s.l., *B. yothersi*, the most common species in citrus orchards in Brazil (Sanchez- Velazquez et al. 2015), is now considered as the major vector of CiLV-C (Tassi et al., 2017). CiLV-C2 has been reported to be also transmitted by *B. yothersi* (used as a synonym to *B. phoenicis* s.l.; Roy et al., 2013, 2015a). CiLV-N has recently been shown to be transmitted by *B. phoenicis* sensu stricto (Ramos-Gonzalez et al., 2017). Based on their association in the field, isolates of the Citrus strain of OFV are believed to be transmitted by *B. californicus*. Mite transmission is suspected but has not been confirmed so far for HGSV-2, nor a tentative vector species been identified (Melzer et al., 2012; Roy et al., 2015a).

In addition, it should be kept in mind that other *Brevipalpus* species may also be able to transmit these viruses (for example, leprosis has also been associated in the past with *B. obovatus* (Childers et al., 2003; Rodrigues and Childers, 2013; Roy et al., 2015a)). Overall, there are large uncertainties on the precise vector spectrum for each of the five analysed viruses.

3.4.4.1. Vectors and their distribution in the EU

Is the pest able to spread within the EU territory following establishment?

Yes. *Brevipalpus* mites that have been associated with the spread of the disease are present in the EU.

RNQPs: Is spread mainly via specific plants for planting, rather than via natural spread or via movement of plant products or other objects?

No. Due to the non-systemic nature of the leprosis-associated viruses, plant for planting are not the main means of spread.

Leprosis-associated *Brevipalpus* spp. mites are considered the most significant *Brevipalpus* species worldwide (Childers et al., 2003; Childers and Rodrigues, 2011), infesting a large number of plants (mainly perennials) including most *Citrus* species in tropical and subtropical areas throughout the world (Childers et al., 2003; Kitajima et al., 2010; Beard et al., 2014, 2015).

According to the EPPO GD *B. phoenicis* s.l. is present in the EU territory in Austria, Cyprus, France, Greece, Hungary, Italy, the Netherlands, Poland, Portugal and Spain. In the non-EU Europe, it is reported from Georgia, Ukraine and the European part of Turkey (Figure 2).

Last updated: 2017-7-20

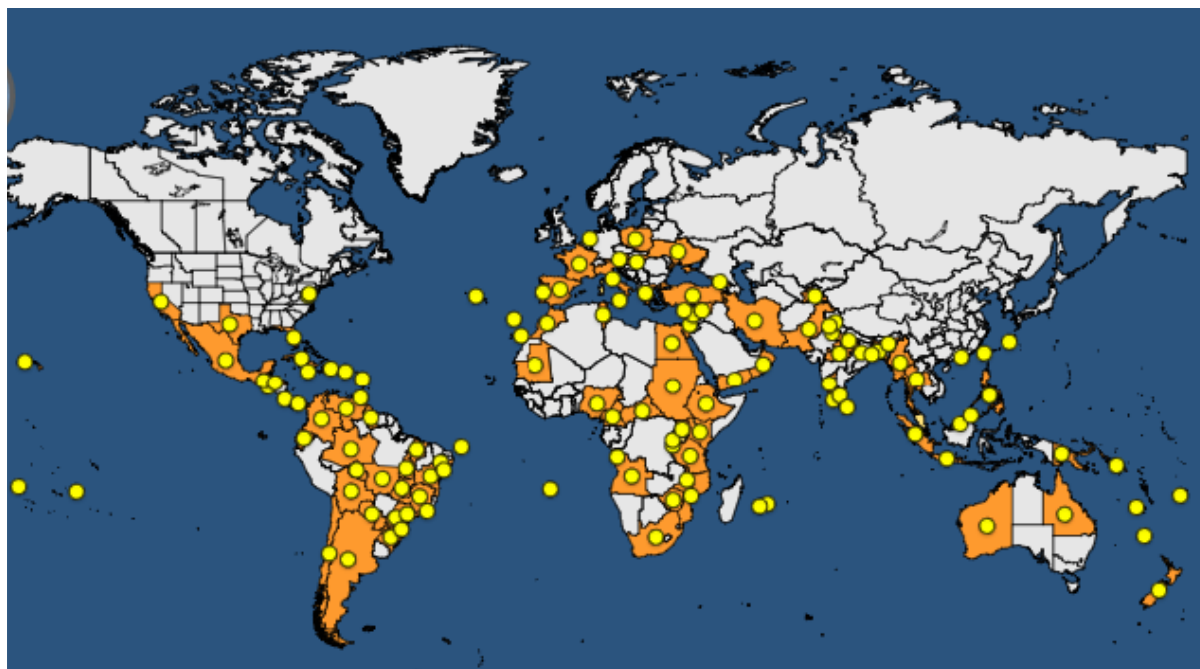


Figure 2: Global distribution of *B. phoenicis sensu lato* (extracted from EPPO Global Database, accessed 20 October, 2017)

Recently, the use of molecular markers (Navia et al., 2013) and the inclusion of additional morphological characteristics (Beard et al., 2015) revealed the existence of multiple cryptic species within *B. phoenicis* s.l. As a result, *B. phoenicis* s.l. is now considered as a species complex and its taxonomy was revised, resulting in the description of a number of new species (sp. nov.) or the re-description of other ones previously considered as *B. phoenicis* synonyms (Table 7, Beard et al., 2015). Available information on the occurrence and distribution of *B. phoenicis* s.l. in the EU mostly predates this taxonomical revision, so that information on the distribution of *B. phoenicis sensu stricto* and of the newly described species is very limited. The consequence of this situation is that the distributions of all these species should be considered as carrying large uncertainties. This is also reflected by the significant differences in distribution reported by the EPPO GD and in the Fauna Europea. These uncertainties are also reflected by the fact that the distribution of the revised species is much more restricted than that of *B. phoenicis* s.l., suggesting that these distributions may be very incomplete.

Table 7: Species comprised in the *Brevipalpus phoenicis* s.l. species complex (Beard et al., 2015), their distribution in the EU according to EPPO GD (updated on the 13 September accessed on the 7 November 2017 and the viruses they are known to transmit

Species name	Occurrence in the EU	Virus vectored
<i>Brevipalpus azores</i> sp. nov. Beard & Ochoa	Portugal, Spain	
<i>Brevipalpus feresi</i> sp. nov. Ochoa & Beard	Non-reported	
<i>Brevipalpus ferraguti</i> sp. nov. Ochoa & Beard	Spain	
<i>Brevipalpus hondurani</i> Evans	Non-reported	
<i>Brevipalpus papayensis</i> Baker	Non-reported	
<i>Brevipalpus phoenicis</i> (Geijkes) <i>sensu stricto</i>	Netherlands	CiLV-N <i>sensu novo</i>
<i>Brevipalpus tucuman</i> sp. nov. Beard & Ochoa	Non-reported	
<i>Brevipalpus yothersi</i> Baker	France*, Spain*	CiLV-C and CiLV-C2

*Reports refer to the new re-described species after *B. phoenicis* s.l. taxonomical revision.

According to the EPPO GD, *B. californicus*, the vector species associated with the Citrus strain of OFV is present in the EU in Cyprus, Greece, Italy and Portugal (Figure 3) Adding to uncertainties, it should be noted that *B. californicus* has been considered by some authors as also being a complex of cryptic species (Navia et al., 2013; Beard et al., 2015; Roy et al., 2015a).

Last updated: 2011-9-1

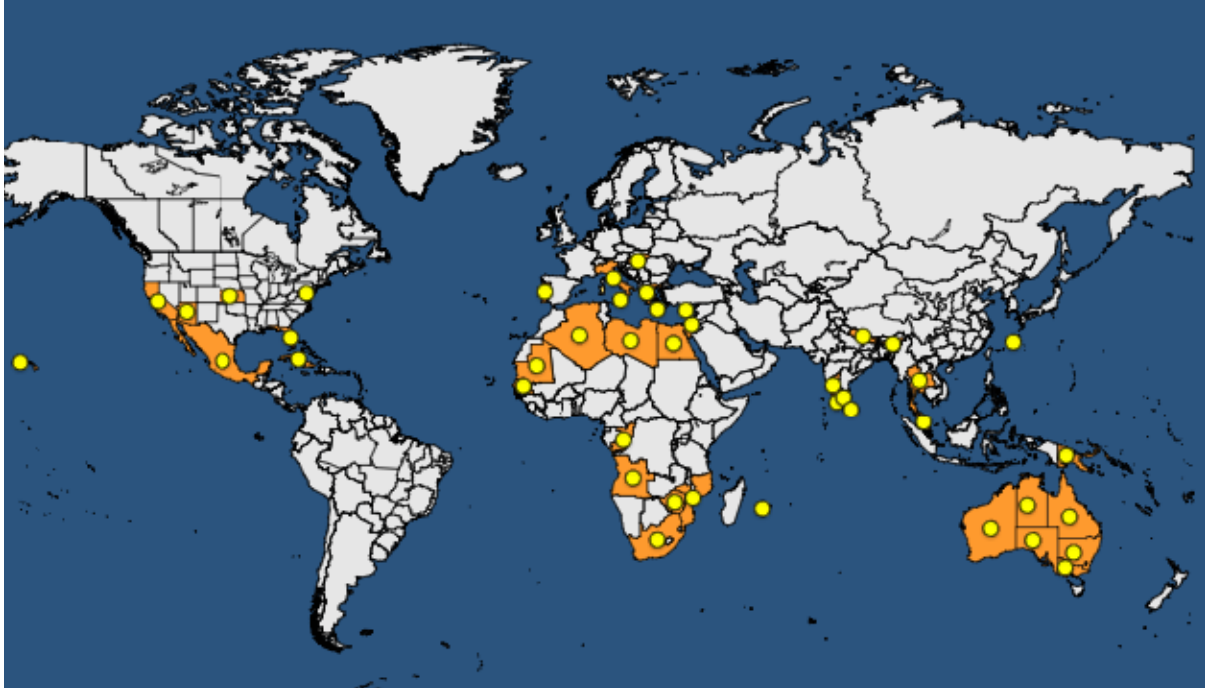


Figure 3: Global distribution of *Brevipalpus californicus* (extracted from EPPO Global Database, accessed 20 October 2017)

According to Fauna Europea (no information available in the EPPO GD), *B. obovatus*, a species associated in old reports with the spread of the leprosis disease (Frezzi, 1940; Vergani, 1945; Knorr, 1968; all cited in IOCV) is present in the EU in Cyprus, France, Greece, Spain, Italy and Portugal. In non-EU Europe, it is also present in Ukraine (Figure 4).



Figure 4: Global distribution of *Brevipalpus obovatus* (extracted from Fauna Europea on 7 November 2017)

Overall, despite the large uncertainties involved, it appears that all *Brevipalpus* species that have been associated with the spread of the leprosis disease or with that of its associated viruses are present in at least some parts of the EU territory.

3.5. Impacts

Would the pests' introduction have an economic or environmental impact on the EU territory?

YES, the introduction of one or another of the viruses analysed here would have an economic or environmental impact in the EU territory but there are large uncertainties on the magnitude of this impact

RNQPs: Does the presence of the pest on plants for planting have an economic impact, as regards the intended use of those plants for planting?⁴

YES

Citrus leprosis is a very important disease affecting various citrus species in South and Central America (Bastianel et al., 2010; Roy et al., 2015a). It causes typical circular chlorotic or necrotic lesions on leaves, stems and fruits, from light yellow to dark brown, with a diameter ranging from 5 to 12 mm. CiLV-C is the most widespread causal agent and affects many citrus species and some non-citrus Rutaceous species, such as *S. glutinosa*. Sweet orange is the most susceptible species and is severely damaged, showing premature fruit drop and low aesthetic value of fruits for fresh consumption, as well total loss of the internal fruit quality (Bastianel et al., 2010). Leaf drop causes a progressive reduction in tree canopy development and dieback. Under high inoculation pressure conditions (high mite population densities), young susceptible plants can die (Rodrigues, 2000) or totally lose their production. After adopting control methods, recovery from leprosis of a severely affected tree may take up to 2 years (Müller et al., 2005). In orchards where no chemicals are applied for the control of the mite vectors, 100% of the trees may be infected within 2–3 years (Rodrigues et al., 2000).

⁴ See Section 2.1 on what falls outside EFSA's remit.

Symptom severity may vary according to the age of the plants and to the host species and variety. In particular, there appears to be a large variability in the susceptibility of individual Mandarin and Tangor varieties to CiLV-C, which has formed the basis of resistance breeding efforts (Bastianel et al., 2006a). Lime, lemon, grapefruit, limete and Persian lime are also reported to be resistant to CiLV-C (Bastianel et al., 2006a,b) but are susceptible to some of the other leprosis-associated viruses (see Section 3.4.1).

The other viruses analysed here appear to have a more limited geographic distribution but cause similar types of symptoms so that their impact on individual affected plants are likely to be of the same order of magnitude, with some uncertainties. Evidence for this analysis comes in particular from the very severe damages incurred by the Florida Citrus industry in the 20th century as a consequence of infections by a nuclear type virus similar to the Citrus strain of OFV or to the newly described CiLV-N *sensu novo* (Hartung et al., 2015). All the five viruses analysed here therefore are likely to have the potential to cause substantial impact on a Citrus industry.

The indirect economic and environmental impacts are related to the management of the disease. Currently, growers in affected areas spray frequently (weekly) acaricides to control the vector mite populations. In this respect, it should also be considered that *Brevipalpus* spp. mites feeding on all aerial plant tissues cause some direct damages from the toxins they inject with their saliva (Childers et al., 2003; Rodrigues et al., 2003). In Brazil, 24% of production cost is attributed to the control of leprosis and an estimated \$80–100 millions are invested annually for chemical control of the mite vectors alone (Bastianel et al., 2010).

Because of the non-systemic nature of the viruses involved, impact is directly linked to the density of the mite vector populations. During this categorisation, the Panel was unable to identify precise information on the density of the EU *Brevipalpus* spp. vector populations. It is therefore difficult to assess the magnitude of the impact that could be caused by one or another of the analysed virus under the EU conditions. However given the severe aesthetic impact of the symptoms on fruits, it likely that control efforts would be implemented by the industry in case of introduction. For the same aesthetic considerations, a similar negative impact is also expected on ornamental Citrus production.

3.6. Availability and limits of mitigation measures

Are there measures available to prevent the entry into, establishment within or spread of the pest within the EU such that the risk becomes mitigated?

YES partially and at least for CiLV-C and C2, for which the control of currently non-regulated hosts would address one of the identified entry pathways

RNQPs: Are there measures available to prevent pest presence on plants for planting such that the risk becomes mitigated?

YES: Monitoring in the frame of a certification system would limit the risk of pest presence

3.6.1. Biological or technical factors limiting the feasibility and effectiveness of measures to prevent the entry, establishment and spread of the pest

- Symptoms can take weeks to months to appear.
- Wide host range of at least one of the viruses involved (and likely of the other viruses as well).
- Mite vectors may be difficult to monitor and to exclude from consignments.
- Localised nature of the viruses makes sampling for testing more complicated as the virus is only present in localised areas of the plants.

3.6.2. Biological or technical factors limiting the ability to prevent the presence of the pest on plants for planting

- Symptoms can take weeks to months to appear.
- Mite vectors may be difficult to monitor and control.
- Localised nature of the viruses makes sampling for testing more complicated as the virus is only present in localised areas of the plants.

3.6.3. Control methods

- Eradication in case of early detection.
- Pruning of symptomatic plant parts to reduce inoculum.
- Control of *Brevipalpus* spp. mite vector populations. As impact is directly linked with the inoculation pressure and with the density of *Brevipalpus* spp. populations, this is the most efficient and most widely used control strategy in affected countries.

3.7. Uncertainty

- Possible existence of additional leprosis-causing viruses that may yet be identified.
- Possible unreported presence in the EU of one of the five leprosis-associated viruses.
- Possible ability of isolates of the Orchid strain of OFV (known to be present in the EU) to infect Citrus species and cause leprosis.
- Unclear regulatory status of the various viruses given that they are not explicitly listed in Directive 2000/29/EC.
- Possible existence of yet undescribed natural hosts of the various viruses, in particular for HGSV-2, Citrus strain of OFV and CiLV-N *sensu novo*.
- Incomplete knowledge on the identity and efficiency of the *Brevipalpus* spp. mite species able to transmit the different viruses.
- Incomplete information on the identity and prevalence of the *Brevipalpus* spp. mite species present in the EU MS where Citrus are grown.

The uncertainties affecting the *Brevipalpus* spp. mite populations (identity, distribution, density, ability to transmit and transmission efficiency) are by far those that affect the most the conclusions of the present pest categorisation.

4. Conclusions

Of the criteria evaluated by EFSA, 'Leprosis' and the five viruses associated with it meet all the criteria to qualify as Union quarantine pests. They do not fulfil the criterion of being present in the EU or the criterion of plants for planting being the main spread mechanism needed to qualify as a Union RNQP (Table 8).

Table 8: The Panel's conclusions on the pest categorisation criteria defined in Regulation (EU) 2016/2031 on protective measures against pests of plants (the number of the relevant sections of the pest categorisation is shown in brackets in the first column)

Criterion of pest categorisation	Panel's conclusions against criterion in Regulation (EU) 2016/2031 regarding Union quarantine pest	Panel's conclusions against criterion in Regulation (EU) 2016/2031 regarding Union regulated non-quarantine pest	Key uncertainties
Identity of the pest (Section 3.1)	CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N <i>sensu novo</i> are all well characterised viruses able to cause leprosis symptoms and efficient detection methods exist for them	CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N <i>sensu novo</i> are all well characterised viruses able to cause leprosis symptoms and efficient detection methods exist for them	Possible existence of other leprosis-associated viruses Potential ability of the Orchid strain of OFV to cause leprosis symptoms in Citrus
Absence/presence of the pest in the EU territory (Section 3.2)	CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N <i>sensu novo</i> are absent from the EU territory	CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N <i>sensu novo</i> are absent from the EU territory	Possible unreported presence in the EU of one of these viruses
Regulatory status (Section 3.3)	Leprosis is currently regulated in directive 2000/29 EC. CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N <i>sensu novo</i> are not formally listed in directive 2000/29 EC	Leprosis is currently regulated in directive 2000/29 EC. CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N <i>sensu novo</i> are not formally listed in directive 2000/29 EC	Are all five viruses covered by the existing legislation?
Pest potential for entry, establishment and spread in the EU territory (Section 3.4)	CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N <i>sensu novo</i> have the potential to enter into, establish in and spread within the EU territory. The main identified pathways are: <ul style="list-style-type: none"> Plants for planting of non-regulated rutaceous and non-rutaceous hosts Fruits of susceptible Citrus species Hitch-hiking of viruliferous <i>Brevipalpus</i> spp. mites in consignments of plants or plant products 	Plants for planting are not considered the main pathway for spread of CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV and CiLV-N <i>sensu novo</i> .	<ul style="list-style-type: none"> Possible existence of yet undescribed natural hosts of the various viruses Incomplete knowledge on the identity and efficiency of the <i>Brevipalpus</i> spp. vector species for each of the viruses Incomplete knowledge on the EU mite vector populations (identity, distribution, density, transmission efficiency)
Potential for consequences in the EU territory (Section 3.5)	The introduction and spread of CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV or CiLV-N <i>sensu novo</i> would likely have negative consequences on the EU citrus industry	The presence of CiLV-C, CiLV-C2, HGSV-2, the Citrus strain of OFV or CiLV-N <i>sensu novo</i> on plants for planting would have a negative impact on their intended use	Incomplete knowledge on the EU mite vector populations (identity, distribution, density, transmission efficiency)
Available measures (Section 3.6)	At least for CiLV-C and CiLV-C2 closing of currently non-regulated hosts pathway	Monitoring in the frame of a certification system would limit the risk of pest presence on plants for planting	Incomplete information on the host range of the five viruses

Criterion of pest categorisation	Panel's conclusions against criterion in Regulation (EU) 2016/2031 regarding Union quarantine pest	Panel's conclusions against criterion in Regulation (EU) 2016/2031 regarding Union regulated non-quarantine pest	Key uncertainties
Conclusion on pest categorisation (Section 4)	'Leprosis' and the five viruses associated with it meet all the criteria evaluated by EFSA to qualify as Union quarantine pests.	Of the criteria evaluated by EFSA to qualify as Union RNQPs, 'Leprosis' and the five viruses associated with it do not fulfil those of being present in the EU or of plants for planting being the main spread mechanism.	
Aspects of assessment to focus on/scenarios to address in future if appropriate	The uncertainties affecting the <i>Brevipalpus</i> spp. mite populations (identity, distribution, density, ability to transmit and transmission efficiency) are by far those that affect the most the conclusions of the present pest categorisation. These uncertainties are unlikely to be resolved until further research results become available		

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Abbreviations

AAP	acquisition access period
C CiLV-C	Citrus leprosis virus
CiLV-C2	Citrus leprosis virus C2
CiLV-N	Citrus leprosis virus N sensu novo
DG SANCO	Directorate General for Health and Consumers
EPPO	European and Mediterranean Plant Protection Organization
EU MS	European Union Member State
FAO	Food and Agriculture Organization
HGSV-2	Hibiscus green spot virus 2
IAP	inoculation access period

MS	Member State
OFV	Orchid fleck virus
PLH	EFSA Panel on Plant Health
RA	Risk assessment
RNQP	Regulated non-quarantine pest
RT-PCR	reverse transcription polymerase chain reaction
TEM	transmission electron microscopy
TFEU	Treaty on the Functioning of the European Union
ToR	Terms of Reference