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Update of the Scientific Opinion on the risks to plant health posed by *Xylella fastidiosa* in the EU territory

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Abstract

EFSA was asked to update the 2015 EFSA risk assessment on *Xylella fastidiosa* for the territory of the EU. In particular, EFSA was asked to focus on potential establishment, short- and long-range spread, the length of the asymptomatic period, the impact of *X. fastidiosa* and an update on risk reduction options. EFSA was asked to take into account the different subspecies and Sequence Types of *X. fastidiosa*. This was attempted throughout the scientific opinion but several issues with data availability meant that this could only be partially achieved. Models for risk of establishment showed most of the EU territory may be potentially suitable for *X. fastidiosa* although southern EU is most at risk. Differences in estimated areas of potential establishment were evident among *X. fastidiosa* subspecies, particularly *X. fastidiosa* subsp. *multiplex* which demonstrated areas of potential establishment further north in the EU. The model of establishment could be used to develop targeted surveys by Member States. The asymptomatic period of *X. fastidiosa* varied significantly for different host and pathogen subspecies combinations, for example from a median of approximately 1 month in ornamental plants and up to 10 months in olive, for *pauca*. This variable and long asymptomatic period is a considerable limitation to successful detection and control, particularly where surveillance is based on visual inspection. Modelling suggested that local eradication (e.g. within orchards) is possible, providing sampling intensity is sufficient for early detection and effective control measures are implemented swiftly (e.g. within 30 days). Modelling of long-range spread (e.g. regional scale) demonstrated the important role of long-range dispersal and the need to better understand this. Reducing buffer zone width in both containment and eradication scenarios increased the area infected. Intensive surveillance for early detection, and consequent plant removal, of new outbreaks is crucial for both successful eradication and containment at the regional scale, in addition to effective vector control. The assessment of impacts indicated that almond and *Citrus* spp. were at lower impact on yield compared to olive. Although the lowest impact was estimated for grapevine, and the highest for olive, this was based on several assumptions including that the assessment considered only *Philaenus spumarius* as a vector. If other xylem-feeding insects act as vectors the impact could be different. Since the Scientific Opinion published in 2015, there are still no risk reduction options that can remove the bacterium from the plant in open field conditions. Short- and long-range spread modelling showed that an early detection and rapid application of phytosanitary measures, consisting among others of plant removal and vector control, are essential to prevent further spread of the pathogen to new areas. Further data collection will allow a reduction in uncertainty and facilitate more tailored and effective control given the intraspecific diversity of *X. fastidiosa* and wide host range.

Keywords: *Xylella fastidiosa*, long-range spread, short-range spread, potential establishment, risk reduction options, asymptomatic period

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Summary

The European Food Safety Authority (EFSA) was requested to update the 2015 EFSA Scientific Opinion on the risk of *Xylella fastidiosa* to the territory of the European Union (EU). *X. fastidiosa* is vectored by xylem sap-feeding insects and is regarded one of the most dangerous plant bacteria worldwide. At the time of the writing of this Scientific Opinion, the only confirmed vectors of *X. fastidiosa* in Europe were *Philaenus spumarius* (Hemiptera: Aphrophoridae), and in experimental conditions, *Neophilaenus campestris* and *Philaenus italosignus* (Hemiptera: Aphrophoridae). *X. fastidiosa* causes damage on many plant species which are listed and frequently updated in the EFSA *Xylella* spp. host plant database (EFSA, 2018a), and is associated with numerous diseases including Pierce's disease, olive quick decline syndrome, citrus variegated chlorosis, almond leaf scorch and various other leaf scorch diseases. *X. fastidiosa* was historically confined to the Americas, where it is endemic, and is also present in Iran. However, in 2013, the pathogen was reported for the first time in the EU, on olive trees in the south of the Italian region of Apulia. Subsequent discoveries were made in the EU in Corsica, in the Provence-Alpes-Cote d'Azur region in France as well as in the Autonomous region of Madrid, the province of Alicante and the Balearic Islands in Spain, Tuscany in Italy and Porto district in Portugal. These outbreaks represent multiple host plant species as well as different *X. fastidiosa* subspecies including *pauca*, *fastidiosa* and *multiplex*, together with the identification of several Sequence Types (STs). The pathogen is regulated under Council Directive 2000/29/EC and through emergency measures under Decision (EU) 2015/789 (as amended Decision (EU) 2017/2352) to prevent further introduction and spread of *X. fastidiosa* in the EU. These measures include establishing a demarcated area around infected areas with specific requirements associated with surveillance, plant removal and other management measures including agricultural practices to control vector populations.

EFSA published a full pest risk assessment on *X. fastidiosa* in 2015 (EFSA PLH Panel, 2015a). The current mandate involved a request to update the previous pest risk assessment with the main objective of preventing further spread within the EU and included requests to assess: (i) the potential establishment of *X. fastidiosa* within the EU, (ii) the probability of short- and (iii) long-range spread, (iv) the length of the asymptomatic period (i.e. the period from infection to expression of symptoms), (v) the impact of *X. fastidiosa* and (vi) an update of available risk reduction options. EFSA was also asked to take into account the different subspecies and STs of *X. fastidiosa* during this assessment. However, it was only possible to partially fulfil this latter request due to data limitations at subspecies and ST levels.

Potential establishment

X. fastidiosa is known to occur over a wide range of climatic zones in tropical countries and subtropical areas (e.g. Brazil, Costa Rica and southern California) and also in more temperate or even continental climate regions (e.g. British Columbia, southern Ontario and Saskatchewan in Canada, the north-eastern regions of the USA and Argentina), in addition to the aforementioned outbreak areas across the EU. To assess the risk of potential establishment within the EU, firstly, the distribution records of *X. fastidiosa* were intersected with Köppen–Geiger climate zones to identify the climate types present in the EU where *X. fastidiosa* is known to occur (Peel et al., 2007; Beck et al., 2018). This illustrated that most of the EU territory consists of climate types where the pathogen is known to occur. Next, the potential for establishment was modelled using ensemble predictions encompassing different species distribution model (SDM) techniques that assessed the effects of climate on the distribution of the species (Naimi and Araújo, 2016). This revealed areas in southern EU to be most at risk from *X. fastidiosa*. The models were also applied at subspecies and ST levels, although with considerably greater uncertainty due to data limitations (e.g. many older records of the pathogen were only reported at species level). *X. fastidiosa* subsp. *multiplex* showed particular differences and demonstrated areas of potential establishment further north in the EU compared to other subspecies. Information on risk of establishment could be used as the basis of risk-targeted surveys to optimise survey intensities to attain a required level of statistical significance and increase the probability of new detections. EFSA is currently developing risk and statistically based survey guidelines on *X. fastidiosa* as part of its mandate on Survey Guidelines to EU Member States (EFSA, 2018c).

Asymptomatic period

X. fastidiosa is known to exhibit a long asymptomatic period (i.e. the time from infection of a plant to expression of symptoms). This has epidemiological significance and also is a key determining factor

on the design of effective detection and control strategies given that the pathogen may have spread during the asymptomatic period. A literature review was undertaken using the EFSA Update of the *Xylella* spp. host plant database (EFSA, 2018a) which was filtered to include all papers which included artificial inoculation and which included information on the time of first symptom expression and which quantified the number of individuals. The data from these studies were categorised by *X. fastidiosa* subspecies and host plant. The absence of data on the time of symptom development for all individual hosts led to the application of two modelling approaches (parametric and non-parametric) to determine the distribution of the asymptomatic period for each combination of host–subspecies. The asymptomatic period of *X. fastidiosa* varied significantly for different host and pathogen subspecies combinations, for example from a median of up to 1 month in ornamental plants and up to 10 months in olive, for subsp. *pauca*. This variable and long asymptomatic period is a considerable limitation to successful detection and control, particularly where surveillance is led by visual inspection.

Short- and long-range spread modelling

The probability of spread was assessed using two distinct modelling approaches due to the epidemiological processes that occur at different spatial scales and the computational burden that would be encountered by capturing these processes in a single epidemiological model with sufficient detail. Models were thus developed for short-range spread (e.g. within an orchard) and long-range spread (e.g. regional scale) separately.

The short-range spread model is a fully mechanistic epidemiological model describing the spatial–temporal pattern of disease spread and assessing the effectiveness of eradication measures for new outbreaks in a free area. Based on available data from spread of *X. fastidiosa* in olive orchards in Apulia and the results of an EFSA expert knowledge elicitation (EKE), the model was parametrised to describe the epidemics of the disease at high spatial resolution in homogeneous host plant orchards characterised by a regular planting distance. The model was used to explore different scenarios in terms of host susceptibility and vector abundance and to assess the outcome of application of different detection and control strategies. Model simulations showed that the application of highly effective vector control of nymphs and adults, reduction in the delay from infection to detection and from detection to implementation of control measures (e.g. removing plants) are the key factors for a successful local eradication. Simulations also showed that with a smaller cut radius (50 m) it was possible to achieve an effective eradication of the disease provided there was high efficacy of nymph and adult vector control. A cut radius of 100 m was more efficient for eradication but eradication could still fail if the vector was poorly controlled and detection and instigation of control were too slow. Thanks to the structure and the flexibility of the epidemiological model a wide range of conditions can be explored parameterising the model to account for different scenarios to support risk assessment and the design of emergency plans.

The long-range spread model describes the spread of a pest through a landscape of susceptible hosts and was parameterised primarily based on *X. fastidiosa* subsp. *pauca* spread in Italy. The model simulates spread by coupling a generic epidemiological model with a dispersal-kernel model, similar to approaches used to successfully model spread for a range of different pest types from fungal to vector-borne disease. Available data on the epidemiology and spread of *X. fastidiosa* in Apulia, Italy, were used to parameterise the model but the influence of changing the epidemiological and landscape parameters were also assessed. The model illustrated the effectiveness of the current measures in limiting further spread, and in some cases, reversing the expansion of infected areas and even eradicating *X. fastidiosa* outbreaks. Reducing buffer zone width in both containment and eradication scenarios increased the area infected. In agreement with the short-range spread model, the importance of early detection of new outbreaks was key to successful control, demonstrating the importance of surveillance and detection capabilities. Further data on the magnitude and pattern of long-range movements is needed due to their significant impact on success of control. The model is flexible in nature and could be applied to other outbreak areas specifically given availability of observed data on spatial and temporal spread.

Impact

The wide range of host plant species for *X. fastidiosa* includes cultivated plants, forest species and ornamental plants with significant potential impacts for agriculture, nurseries and other sectors as well as the environment. Following the request included in the Mandate, the Panel analysed the impact on

plant species concerned with a focus on the hosts with higher economic values found attacked by *X. fastidiosa* in the EU: *Olea europaea* (i.e. olive), *Prunus dulcis* (i.e. almond), *Vitis vinifera* (i.e. grapevine), *Prunus avium* L. (i.e. cherry), and *Prunus domestica* and *Prunus salicina* (i.e. plum). In addition, the Panel also included in the assessment *Citrus* spp. for their economic importance in the EU and as recognised important hosts in other areas of the world. The Panel also considered the potential impact on tree and ornamental nurseries, and on forest species. Impact was assessed using a combination of EKE where information allowed (i.e. for olive, almond and *Citrus* spp.) and by literature review for other areas (i.e. nurseries, forest species, cherry and Japanese plum). In the case of the impact estimated with the EKE process, the assessment was done under the general scenario assumption that the entry, establishment and spread of the pest had already occurred. This corresponds to a scenario where the pest is already present throughout the area of potential distribution in the EU (i.e. it has spread to its maximum extent) (EFSA Working Group on EU Priority Pests[1]). In addition, the only vector that was considered in this scenario was *Philaenus spumarius*, the most common and widespread currently known vector of *X. fastidiosa* in the EU. As stated in the previous Scientific Opinion (EFSA PLH Panel, 2015a), should other xylem-feeding insects act as vectors of *X. fastidiosa*, the impact could be different.

Almond and *Citrus* spp. were estimated to have lower impact on yield compared to olive. However, the lowest impact was estimated for grapevine. As already mentioned, this was based on the specific scenario assumptions of the assessment. The introduction or spread of *X. fastidiosa* to forest areas within the EU could lead to impact on oaks, elms, maples and other tree species known to be affected in North America. The uncertainty to the level of this impact is high, however, primarily since it is not known whether tree species within those genera that are native to Europe, but absent in North America, may serve as hosts and their level of susceptibility. Moreover, there is a lack of quantitative information on the impact of *X. fastidiosa* on forest tree species generally. The impact may also differ depending on the environment of the tree e.g. urban, peri-urban, amenity tree or forest. Impacts on nurseries are highest in southern EU where outdoor nurseries coincide with the areas of highest climatic suitability for the pathogen, and for indoor nurseries throughout the EU territory. The lack of information on the impact of *X. fastidiosa* on plant nurseries prevents a quantitative assessment. Nurseries that could be affected are mainly those producing plants for planting of fruit trees and shrubs, forest and landscape trees and ornamentals. Production under screenhouse of healthy mother plants and seedlings together with vectors control are options to reduce such impact. Hot water treatment is also an efficient tool but so far tested only on grapes and pecan for *X. fastidiosa*. Should *X. fastidiosa* become widespread in the EU, an indirect impact can be expected on trade through limitations on plants for planting toward countries where *X. fastidiosa* is listed as absent or a quarantine pest.

Risk reduction options

Risk reduction options were assessed through a literature review updating the information already available in previous EFSA scientific opinions. So far, no treatment has been found able to eliminate the bacteria from the plant. At EU level field surveys and experimental studies have identified tolerant/resistant cultivars of olive that can be used to mitigate the effect of *X. fastidiosa* subsp. *pauca*. In agreement with the spread models, efficient vector control is important for controlling and slowing down the spread of *X. fastidiosa*. In Italy, some insecticides approved for use in EU territory were shown to be effective (75–100% mortality), especially neonicotinoids (i.e. acetamiprid) and pyrethroids (deltamethrin). Incorporation of *X. fastidiosa* vectors in Integrated Pest Management (IPM) programmes in Mediterranean countries is currently missing and should be mandatory to include xylem-sap feeding insects. Further research is needed to assess the effectiveness and implementation of biological and cultural control methods, which have been shown to be successful but with the majority of studies in Apulia and thus uncertain as to their efficacy in other outbreak areas. As far as common agricultural practices, experiences from the US report that if on the one hand water stresses can accelerate disease progression, on the other fully irrigated plants could be subjected to longer and more frequent feeding events by the vectors. Low levels of plant water stress could reduce vector transmission efficiency. Recent research from the US on infected grapevine showed that pruning does

[1] Mandate M-2017-0136 available online in the EFSA Register of Questions at http://registerofquestions.efsa.europa.eu/roqFrontend/

not remove *X. fastidiosa* from infected plants to an extent that would justify its adoption for disease management.

Short-range and long-range spread modelling showed that an early detection and rapid application of phytosanitary measures are essential to prevent further spread of the pathogen to new areas.

The intraspecific diversity of *X. fastidiosa* is an important piece of information for the application of phytosanitary measures in outbreak situations. For each new outbreak, it is important that the decision whether to work at *X. fastidiosa* species, subspecies, ST or at the strain levels is taken based on the available knowledge on the diversity of the bacterial population and on the host range. Although control measures should be applied expediently, experimental studies and intensive sampling and testing should be conducted on plant species in the outbreak area to identify possible new host plants.

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1. Introduction

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

This Scientific Opinion for *Xylella fastidiosa* was requested to EFSA by the European Commission DG SANTE, pursuant to Article 29(1) of Regulation (EC) No 178/2002, as per letter to EFSA's Director, dated 22 December 2017, reference ARES(2017)6346828. The opinion has as deadline of 15 months after the requested date.

EFSA was requested to 'update the Scientific Opinion on the risks to plant health posed by *Xylella fastidiosa* in the EU territory, published on 6 January 2015.[2] That update should take into account the subspecies and Sequence Types (STs) of *X. fastidiosa* and the susceptible plant species detected so far in the Union territory since the first outbreak notified by Italy in October 2013. The probability of short and long distance spreading and establishment in the rest of the Union territory should be assessed, together with their consequences on the plant species concerned. In addition, based on recent scientific developments, EFSA should identify and evaluate relevant risk reduction options to prevent further spread of those subspecies and STs into the rest of the Union in order to allow, if needed, the update of the EU control measures as laid down under Decision (RU) 2015/789. EFSA should also assess the latency period of those isolates, taking into account the different climatic conditions of the Union territory, with the aim to provide an indication about the minimum number of years needed before lifting the demarcated area after the implementation of the eradication measures.'

1.2. Interpretation of the Terms of Reference

The Terms of Reference (ToR) specified that the requested opinion should update the previous EFSA Scientific Opinion, published on 6 January 2015, addressing establishment, spread and risk reduction options (RROs) (EFSA PLH Panel, 2015a). Therefore, this scientific opinion will not include entry, also because the pathogen is already established in parts of the EU territory. Since the publication of the first Scientific Opinion in 2015, when within the EU only *X. fastidiosa* subsp. *pauca* ST53 was observed in Apulia, Italy, new outbreaks of different *X. fastidiosa* subspecies and STs were observed in other limited parts of the EU (Section 1.4). Therefore, the main source of expansion in the EU territory is considered to be represented by the spread of the pathogen from the reported outbreaks.

Considering the pathogen diversity described above and its host plants, the Mandate requested to consider *subspecies and Sequence Types (STs) of X. fastidiosa.* However, there are limited data in literature so far at subspecies and ST levels; therefore, the Panel addressed this request only when the assessment could be supported by the currently available scientific and technical knowledge. In particular, considering the available scientific literature, data and the current level of information, the Panel considered that the analysis could be conducted at:

- species, subspecies and ST levels for the assessment of the establishment, depending on data available. The assessment of climate suitability for establishment was conducted also at the subspecies level (*pauca*, *fastidiosa* and *multiplex*) and at the STs' level for some of the ST detected in EU (ST1, ST53, ST6 and ST7) but with a higher level of uncertainty due to a comparatively lower level of positive and negative reports of different subspecies and STs in different environments, than for species level.
- species level for the assessment of the short/long-distance spreading due to a lack of data on the temporal and spatial dynamics of different subspecies, environments and host combinations to inform an analysis of spread beyond this level. The spread models are pest generic in nature and parameterised based on available spread data from the current EU outbreak (which are so far predominantly available from the Apulian outbreak) but sensitivity analysis was performed to examine potential consequences to other outbreak situations.
- subspecies level for the assessment of the latency (i.e. asymptomatic period, see below) period, due to the availability of controlled environment studies at subspecies level. Some of the studies also report information at ST level.
- species level for the evaluation of impact. However, the assessment of impact was based on evidence from specific host–subspecies/STs situations
- As far as the RROs, since the update was based on literature review, the analysis was at different taxonomic levels according to the considered works.

[2] https://www.efsa.europa.eu/it/efsajournal/pub/3989

As far as the assessment of consequences of short- and long-distance dispersal on the spread, after further clarification with the European Commission DG SANTE, the Panel understood that the requested analysis was not aiming at studying the expansion of the disease from a specific outbreak area to project scenarios of invasion to other Union territories. EFSA demonstrated the risk of expansion of *X. fastidiosa* within the EU (EFSA PLH Panel, 2015a). The assessment in current update to EFSA (EFSA PLH Panel, 2015a) was aimed at analysing and comparing the effectiveness of the phytosanitary emergency measures included in the EU Decision 2015-789[3] and exploring alternative options for containment and eradication based on current situation in the EU territory.

As far as the potential establishment in the EU territory, the Panel applied different techniques to assess the potential establishment including the Köppen–Geiger climate types, and a multimodel ensemble approach based on widely known and extensively used species distribution models (SDMs). The uncertainty of the assessment was properly evaluated and consequences on results discussed.

As far as the consequences on the plant species, based on data available, the Panel considered the hosts with higher economic values found attacked by *X. fastidiosa* in the EU: *Olea europaea* L., *Prunus dulcis* (Miller) Webb, *Vitis vinifera* L. and *Prunus avium* L. In addition, the Panel also considered in the assessment *Citrus* spp. for their economic importance in the EU and as recognised important hosts in other areas of the world. Starting from the analysis of potential establishment in the EU territory, the Panel decided to estimate the potential consequences on the plant species under a set of assumptions simplifying the assessment. They included the situation of the pest being present in all the areas of potential establishment in the EU territory. In addition, the Panel reviewed the available information related to the impact on *Prunus domestica* and *Prunus salicina,* on forest species and on tree and ornamental nurseries in the assessment area.

As far as the *identification and evaluation of relevant risk reduction options (RROs)*, the Panel updated the information included in the previous Scientific Opinion considering also: (i) the results of Bosco et al. (2019) in relation to vector control, (ii) the EFSA statement on the susceptibility of olive cultivars (EFSA, 2017) and (iii) the recent update of the pest categorisation of *X. fastidiosa* (EFSA PLH Panel, 2018b).

As far as the request related to the *assessment of the latency period* of *X. fastidiosa*, after discussion with European Commission DG SANTE, the Panel intended that what was of interest is the assessment of the asymptomatic period (i.e. period from first infection to the appearance of first symptoms on the host).

An updated pest categorisation for *X. fastidiosa* was published in July 2018 (EFSA PLH Panel, 2018b) and so not required in the current mandate.

1.3. Summary of the emergency phytosanitary measures relevant for spread analysis

Decision (EU) 2015/789 sets up the EU emergency measures to prevent the introduction into and the spread within the Union EU of *X. fastidiosa*. Since its adoption, the EU Decision has been updated on several occasions based on new scientific and technical developments.

The regulated plants for planting susceptible to *X. fastidiosa* are defined as 'Specified plants', while some of them as 'Host plants'. Specified plants, including host plants, are all plants for planting listed in Annex I of the EU Decision (i.e. plant species known to be susceptible *X. fastidiosa* worldwide). Host plants are instead plants for planting belonging to genera and species listed in the Commission database of host plants having been found to be susceptible to *X. fastidiosa* in the EU territory.

To contextualise the work done for the assessment of the short- and long-range spread within the current Opinion, here follows an overview of the EU emergency measures as taken into account in the assessment of the short- and long–range spread with the aim to achieve eradication or containment of the pest from the outbreak area. Other measures listed under Decision (EU) 2015/789 such as movement requirements into or within the EU of specified plants, etc., were not considered.

In terms of general surveillance obligations for the presence of *X. fastidiosa* in the EU territory, the current Decision sets up general requirements, providing flexibility to Member States (MS) as regards a number of elements which should be decided based on the national risk assessment (e.g. intensity and sensitivity of inspections and sampling). As regards the survey obligations in the demarcated area, a grid based approach is set up within the buffer zone (BZ) (e.g. 100 m × 100 m squares within the

[3] Commission Implementing Decision (EU) 2015/789 of May 2015 (and further amendments) as regard measures to prevent the introduction into and the spread within the Union of *Xylella fastidiosa* (Wells et al.).

1 km, while 1 km × 1 km squares in the remaining part of the BZ) and in some parts of the infected zone (IZ) subject to containment measures (e.g. last 20 km strip adjacent to the BZ where surveillance activities shall be carried out in the 100 m × 100 m squares). Also, in this case, specific details of the implementation are left to MS based on the level of risk, climatic conditions, the presence of specified plants and relevant insect vectors. Therefore, in the absence of specific indications, in the modelling of the short- and long-distance dispersal and of the application of the phytosanitary measures, the Panel considered a scenario of intensive surveillance, depending on the particular demarcated zone, and simulates detection as described in the conceptual and formal models (Sections 2.1.4 and 2.1.5). This was informed by information on surveillance, inspection and sampling procedures in the Apulian demarcated area (Sections 2.1.4 and 2.1.5).

1.3.1. Demarcated area

According to Decision EU/2015/789, where the presence of *X. fastidiosa* is identified, the MS shall demarcate a 'demarcated area' (Article 4, 'Establishment of a demarcated area') (Figure 1). A demarcated area consists of an IZ and of a BZ. The IZ includes all plants known to be infected, the ones showing symptoms and all other plants liable to be infected due to their proximity to infected plants. The BZ is an area of a width of at least 5 km surrounding the IZ in case of an outbreak subject to eradication measures. It can be decreased to 1 km in case of isolated finding where no natural spread occurred. For areas under containment, the BZ has a width of 10 km.

If an area is found infected with one *X. fastidiosa* subspecies, the area may be demarcated for the specific subspecies and related recognised host plants. If an area is found infected with more than one *X. fastidiosa* subspecies, the area is demarcated for all subspecies and all related host plants.

By way of derogation from Article 6, and only in IZs listed in the Annex II of the Decision, a MS may decide to set up a containment area (CA) where 'containment measures' are applied. At the time of writing this Scientific Opinion, the only CAs in the EU territory were Balearic Islands (Spain), Corsica (France) and the demarcated area in Apulia (Italy).

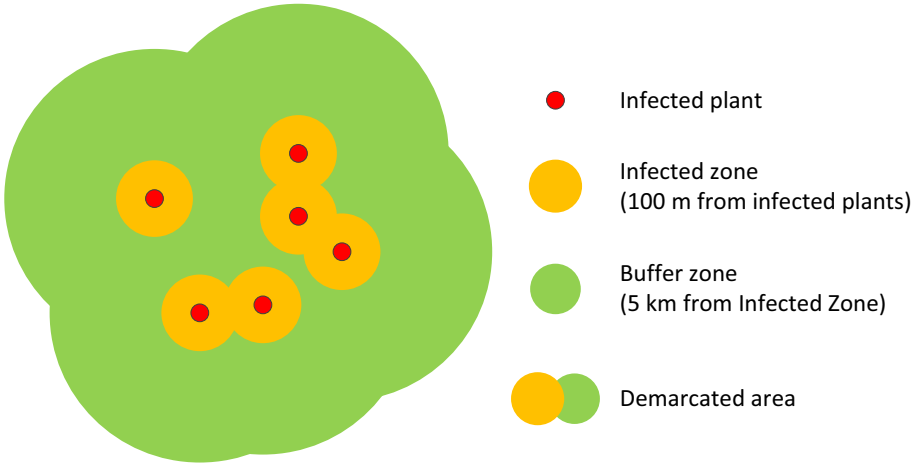

Figure 1: Schematic representation of a demarcated area according to Decision EU/2015/789

1.3.2. Eradication measures (Art. 6)

The MS shall, within a radius of 100 m around the infected plants, immediately remove the plants known to be infected, the host plants (regardless their health status) and symptomatic plants indicating possible infection by *X. fastidiosa*. Moreover, the MS shall sample and test all the specified plants within a radius of 100 m around the infected plants and shall carry out appropriated phytosanitary treatments against the vectors and plants that may host those vectors. The MS shall plan annual surveys including visual inspections of the specified plants, sample and test of symptomatic plants and asymptomatic plants in the proximity of the symptomatic ones. Appropriate agricultural practices shall be applied for the management of *X. fastidiosa* and its vectors.

1.3.3. Containment measures (Art. 7)

By way of derogation from Art. 6, the MS shall immediately remove all plants found to be infected by *X. fastidiosa* where an official survey has taken place. According to the EU Decision, MS shall monitor the presence of the specified organism by annual official surveys, at least within an area measuring at least 20 km from the border of the IZ with the rest of the EU territory, around production sites authorised to move specified plants out of the IZ, and around sites with particular social, scientific or cultural values. The MS shall sample and test all host plants within a radius of 100 m around the infected plants, at regular intervals of time and at least twice a year. The MS shall apply appropriate phytosanitary treatments against the vectors and plants that may host those vectors, and shall apply appropriate agricultural practices for the management of the pest and its vectors. The main difference with the eradication measures is that only the infected plants are cut.

1.4. Current distribution of *X. fastidiosa* outbreaks in Europe and known vectors

The first identification of *X. fastidiosa* in open field in the EU was reported in diseased olive trees in Apulia, Italy, in fall 2013 (Saponari et al., 2013). Since then, the pest was identified in 2015 in several plant species in France (Corse and then in Provence-Alpes-Côte d'Azur (PACA) region) (Denance et al., 2017) and in 2016 in Spain (Balearic Islands, and afterwards in the province of Alicante and in the Autonomous Region of Madrid) (Olmo et al., 2017). The presence of subspecies *pauca*, *fastidiosa* and *multiplex* was reported, together with the identification of several STs (Table 1). A detailed description of the current pest distribution in the EU is reported in the updated pest categorisation of *X. fastidiosa* (EFSA PLH Panel, 2018b).

More recently, in October 2018, the presence of *X. fastidiosa* subsp. *multiplex* (ST87) was reported in Monte Argentario (Tuscany, Italy) (Saponari et al., 2019), and in January 2019, the subsp. *multiplex* (ST7) was identified in Portugal (Vila Nova de Gaia, Área metropolitana do Porto) (EUROPHYT, online).

At the time of the writing of this Scientific Opinion, the only confirmed vectors of *X. fastidiosa* in the EU were *Philaenus spumarius* (Hemiptera: Aphrophoridae), and in experimental conditions, *Neophilaenus campestris* and *Philaenus italosignus* (Hemiptera: Aphrophoridae) confirmed their physiological ability to transmit the bacteria (Cavalieri et al., 2018). However, as reported in the previous Scientific Opinion (EFSA PLH Panel, 2015a), any xylem sap-feeding insect is a potential *X. fastidiosa* vector.

Table 1: Current distribution of *X. fastidiosa* subspecies and ST in EU (only confirmed cases listed in EUROPHYT were considered)

Country	Region	*X. fastidiosa* subspecies	Sequence type (ST)
France	Corse, PACA Region	*multiplex*	ST6
France	Corse, PACA Region	*multiplex*	ST7
France	PACA Region	*pauca*	ST53
Italy	Apulia	*pauca*	ST53
Italy	Tuscany	*multiplex*	ST87
Portugal	Área metropolitana do Porto	*multiplex*	ST7
Spain	Balearic Islands	*fastidiosa*	ST1
Spain	Balearic Islands, Alicante province, Autonomous Region of Madrid	*multiplex*	ST6
Spain	Balearic Islands	*multiplex*	ST7
Spain	Balearic Islands	*pauca*	ST80
Spain	Balearic Islands	*multiplex*	ST81

2. Data and methodologies

2.1. Methodologies

2.1.1. Overview

The methodological approach was designed to assess the Terms of Reference regarding the update of the previous EFSA Scientific Opinion on *X. fastidiosa* (EFSA PLH Panel, 2015a). This update refers to specific requests as described in the Interpretation of the ToR, specifically:

- Potential establishment of *X. fastidiosa* in the EU
- Assessment of the length of the asymptomatic period of *X. fastidiosa*
- The probability of short-range spread and its consequences
- The probability of long-range spread and its consequences
- The impact of *X. fastidiosa* in the EU
- An updated review of RROs.

Note this included two separate sections on spread to adequately cover mechanisms of short- and long-range spread. We followed the EFSA Guidance on quantitative pest risk assessment (EFSA PLH Panel, 2018a) in our methodology. We followed the two-tiered approach for the use of both expert knowledge elicitation (EKE) and modelling. The first tier has been adopted for the estimation of the impact under the specific assumption of the EKE (Appendix E). The second tier approach was used for assessing the short- and the long-range spread of the disease developing two spread models. The second tier was also used for assessing the potential establishment.

Due to the nature of some aspects of the mandate, we analysed a single baseline scenario. No alternative scenarios were addressed. Moreover, the risk reduction review component of the Scientific Opinion necessitated a description of existing literature and studies. This approach was also taken for the specific issue of impact of *X. fastidiosa* on forest species. EKE was applied to the probability of short- and long-range spread and impact. Modelling was applied to the assessment of the potential establishment, probability of short-range spread (SRS), probability of long-range spread and the length of the asymptomatic period (although with limited mechanistic detail). Impact of *X. fastidiosa* was also informed by modelling on the potential establishment.

To assess the potential establishment two modelling approaches were adopted, the Köppen–Geiger system of climate classification and an ensemble of SDMs. The Köppen–Geiger system is an effective approach to identify and map climate types where species are known to occur. SDMs are based on statistical approaches which analyse the relationship between geographical occurrences of species and the associated environmental variables. Climate data was obtained from Chelsa Climatology (Karger et al., 2017) and pest information and distribution was obtained from the update of the *Xylella* spp. host plant database (EFSA, 2018a) and from local data sets provided by National Plant Protection Organizations with *X. fastidiosa* outbreaks in the EU (Osservatorio Fitosanitario Regione Puglia, Italy; Servicio de Sanidad Vegetal, Generalitat Valenciana, Spain; Bureau de la Santé des Végétaux, Ministère de l'Agriculture et de l'Alimentation, France).

The length of the asymptomatic period was assessed using a literature review of the EFSA update of the *Xylella* spp. host plant database (EFSA, 2018a) which was filtered to include all papers which included artificial inoculation and which included information on the time of first symptom expression and which quantified the number of individuals. The data from these studies were categorised by *X. fastidiosa* subspecies and host plant. The absence of data on the time of symptom development for all individual hosts led to the application of two modelling approaches (parametric and non-parametric) to determine the distribution of the asymptomatic period for each combination of host–subspecies.

It should be noted that in this Scientific Opinion SRS and long-range spread were analysed separately. This was due to the differing biological mechanisms driving spread at these two spatial scales and the impracticalities for the necessary level of detail, and associated computational burden, to be handled by a single model capturing processes at both spatial scales. The 'short-range' model essentially models spread processes occurring within a large orchard (i.e. within an orchard, or small number of consecutive orchards) and the 'long-range' spread model considers spread within a region (i.e. between different areas of orchards at a regional scale).

SRS was modelled using a fully mechanistic epidemiological model describing the epidemics of the disease at high spatial resolution in a homogeneous spatial grid with maximum extent 10 $\times$ 10 km, characterised by a regular planting distance. The short-range model explicitly modelled the local

dispersal of the infected vectors, the interaction between the vectors and the susceptible plants and the disease growth within the infected plants. The dynamics and impact of different RROs were modelled including efficacy of nymph and adult vector control, variation in time to detection and in the delays in implementation of vector control and host cutting measures, and cut radius of plants. The RROs are evaluated considering the achievement of eradication, the change in the disease spread rate and in the infected vector density, and the number of cut trees.

For long-range spread, the effectiveness of different eradication and containment measures was investigated using a pest-generic spatially explicit, stochastic simulation model parameterised for *X. fastidiosa*. The landscape was at a larger spatial scale to the short-range model (150 × 150 km) and captured small-scale dynamics of the disease using a spatially implicit model within each 200 × 200 m grid cell. To do this, *X. fastidiosa* outbreaks were simulated in generic landscapes. The simulations included algorithms that emulate the emergency measures described in Decision (EU) 2015/789, in which demarcated eradication and/or containment zones (CZs) are established around detected *X. fastidiosa* occurrences, and surveillance and disease control measures are applied within these zones. The sizes of simulated outbreaks after 5 years of demarcation were outputted in order to test the effectiveness of the disease control measures.

Impact was assessed for olive, almond, grapevine and *Citrus* spp. using the EKE process (EFSA, 2014) and in terms of yield losses. For cherry, plum, forest species and nurseries, where less specific information was available, a literature review approach was taken. The update of the RROs compared to the previous *X. fastidiosa* Opinion (EFSA PLH Panel, 2015a) also followed a literature review approach.

Maps for potential establishment and impact on forest species and crops were developed considering EU MS (EU28), countries of the European Free Trade Association (EFTA; i.e. Iceland, Liechtenstein, Norway and Switzerland), the EU candidate countries (i.e. Albania, North Macedonia, Montenegro, Serbia and Turkey) and the EU potential candidate countries (Bosnia and Herzegovina, and Kosovo[4]).

2.1.2. Establishment

2.1.2.1. Data and methodology

Pest information and distribution was obtained from the EFSA Update of the *Xylella* spp. host plant database (EFSA, 2018a) and from the local data sets provided by the Regional Authorities and/or National Plant Protection Organizations of Italy, France and Spain (i.e. Osservatorio Fitosanitario Regione Puglia, Italy; Servicio de Sanidad Vegetal, Generalitat Valenciana, Spain; Conselleria de Medi Ambient, Agricultura i Pesca del Govern de les Illes Balears, Spain; Bureau de la Santé des Végétaux, Ministère de l'Agriculture et de l'Alimentation, France).

The potential for establishment of *X. fastidiosa* in the EU was modelled using two different approaches: identification of climate types suitable for *X. fastidiosa* occurrence based on the Köppen–Geiger climate classification (Peel et al., 2007) and predictions from an ensemble of SDMs (Guisan and Zimmermann, 2000; Peterson et al., 2011).

An analysis was also performed at the level of STs. However, due to the low number of records to conduct this analysis it is subject to substantial uncertainty (Appendix D).

The Köppen–Geiger system uses monthly data of temperature and precipitation to classify climate into five main classes and 30 subtypes (Peel et al., 2007). Thus, it provides a simplified but ecologically meaningful climate classification to assess species distribution (Beck et al., 2018) or growth behaviour of a species.

SDMs investigate how the geographic distribution of a species could be related to the environmental conditions prevalent in the locations in which the species is known to occur (Guisan and Zimmermann, 2000; Peterson et al., 2011). Applications of SDMs are found in ecology, biogeography, evolutionary biology or conservation biology, among others disciplines (Araújo and Peterson, 2012). In the field of invasive species, SDMs can be used to predict the spatial spread of the species and detect areas at risk (Vaclavik and Meentemeyer, 2012). Several SDM approaches have been developed based on different techniques, and their choice represents a major source of variability (Meller et al., 2014; Naimi and Araújo, 2016). SDM ensembles aggregate the results of different SDMs and allow finding areas that are classified as suitable for the species across models, giving more consistent estimates (Early et al., 2018).

[4] This designation is without prejudice to positions on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence.

A widely known limitation of SDM approaches is that they rely on the availability of records across a representative sample of environmental conditions for the modelled species or subspecies. If records are not available, or are under-represented, in areas where a species occurs, this will impact on the validity of the final model outputs.

2.1.2.2. Conceptual model

Environmental data

The potential distribution of *X. fastidiosa* has previously been analysed, in particular for the strains that are present in the USA. Feil and Purcell (2001) determined the relative risk of Pierce's disease on grapes using isotherms of January minimum temperature to classify zones as severe (4.5°C), occasional (1.7°C) or rare (−1.1°C) risk for grapes. Hoddle (2004) estimated the potential distribution for *X. fastidiosa* and its vector *Homalodisca vitripennis* in California using the bioclimatic niche model CLIMEX parametrised with data from Feil and Purcell (2001). They found out that regions with tropical, semitropical, mild-temperate and moderate Mediterranean climates are suitable for both organisms. There is evidence that suggests that the climatic limits for diseases caused by *X. fastidiosa* largely depend on the pathogen–host combination. In North America, Pierce's disease on grapes and phony disease of peach are restricted to the mild winter regions in eastern and western USA and are only present in northern latitudes when close to the coast in which winter temperature is warmer (Purcell and Hopkins, 1996). In contrast, diseases characterised by leaf scorch as those occurring in some forest species as oaks can be found in northern latitudes associated with cold winters (Hartman et al., 1995). This could also explain the differences in the distribution of almond leaf scorch (ALS) and Pierce's disease in California (Purcell, 1980). On the other hand, the capacity of *X. fastidiosa* to support high summer temperatures is poorly understood. Nevertheless, the severity of the epidemics of citrus variegated chlorosis (CVC) caused by *X. fastidiosa* subsp. *pauca* in Brazil suggests that hot temperatures occurring in tropical climates are not limiting (Lee et al., 1992).

X. fastidiosa is a mesophilic organism. The optimum temperature for growth *in vitro* was observed to be around 28°C for *X. fastidiosa* subsp. *fastidiosa*, and it was not able to grow *in vitro* at 12°C (Feil and Purcell, 2001). Anas et al. (2008) observed the occurrence of Pierce's disease as occasional in south-east of the USA, in areas previously classified as at low risk. Based on data on the occurrence of the disease in this area, they constructed new maps of risk based on the number of winter days with minimum temperatures below −12.2°C and −9.4°C. These temperature values were also used for creating a risk map for *X. fastidiosa* in the USA using the NAPPFAST system (Engle and Magarey, 2008). In a recent study, Godefroid et al. (2018) estimated the potential distribution of *X. fastidiosa* in Europe. They identified the Mediterranean regions in southern Europe, as well as the Atlantic coastal regions of France and Portugal as those most suitable for *X. fastidiosa*. The sensitivity of *X. fastidiosa* to cold temperatures has been described mostly on grapes. Hopkins (1976) observed how the severity of Pierce's disease epidemics tends to be lower after a cold winter. This was confirmed by Purcell (1977) exposing grapevine plants in pots to subfreezing temperatures. Reduction on xylem moisture caused by deeper dormancy induced by cold temperature is suggested as the cause rather that a direct detrimental effect on the bacteria (Hopkins, 1976; Purcell, 1980). In contrast, when *X. fastidiosa* subsp. *fastidiosa* is inoculated in almonds in the spring in California, only some trees are found infected after winter (Davis et al., 1980).

Climate data was obtained from Chelsa Climatology (Karger et al., 2017). Chelsa climate data are for the time period 1979–2013 and are based on the downscaled ERA-interim global circulation model with GPCC (Global Precipitation Climatology Centre) and GHCM (Global Historical Climatology Network) bias correction, and a resolution of 30 arc seconds (approximately 1 km) (Karger et al., 2017). Bioclimatic variables were derived from monthly temperature and precipitation values and are intended to approximate climate dimensions meaningful to biological species. We used climate data at 5 arc-min spatial (approximately 10 km grid cell). We used the 19 bioclimatic variables proposed by Hijmans et al. (2005) to estimate the potential distribution of *X. fastidiosa*. These bioclimatic variables are derived from the monthly temperature and rainfall values and represents annual trends, seasonality and extreme or limiting environmental variables (Hijmans et al., 2005). Multicollinearity of climate variables may violate statistical assumptions and cause over-fitting in SDMs, thus we removed the highly correlated variables. The variance inflation factor (VIF) was used to compare collinearity between regression predictors. The VIF quantified the expected amount of variance in a regression coefficient that is due to collinearity in the predictors. A VIF greater than 10 (as a rule of thumb) is a signal that the model has a collinearity problem (Chatterjee and Hadi, 2012); therefore, a threshold of 10 was used.

Background selection

Since limited information is available on confirmed *X. fastidiosa* absence, particular attention must be given to the identification of the 'background' area which represents those areas in which an absence of a positive detection likely indicates the absence of the species (VanDerWal et al., 2009; Barve et al., 2011). Different procedures have been proposed to estimate the extent of the background but those based on bioclimatic methods are recommended for their simplicity (Barve et al., 2011) and practicality (Soberón, 2010). Two background extent were tested: (1) The distribution records of *X. fastidiosa* were intersected with the 30 Köppen–Geiger climate zones identified worldwide (Beck et al., 2018) at the spatial resolution of 5 arc-min, selecting the geographic extent of the climate types in which *X. fastidiosa* is known to be present; and (2) the geographic extent of the current known distribution of *X. fastidiosa* territory records were selected as background. This extent was estimated by the area delimited by the geographic coordinates of the presence data used in the analyses. The second extent was then used as background based on preliminary analyses that showed more consistent results across data sets comprising the global *X. fastidiosa* distribution. This extent was determined by selecting the geographic extent of the presence data used in the analysis.

Pathogen distribution data and pseudo-absence generation

The presence records for *X. fastidiosa* were obtained from two sources: (1) the EFSA Update of the *Xylella* spp. host plant database (EFSA, 2018a); (2) Local data sets provided by Regional Authorities and National Plant Protection Organizations listed above including *X. fastidiosa* outbreaks in the EU, i.e. of Italy, France and Spain. The presence records used were filtered by: (1) selecting only records from infection observed under natural inoculum pressure either during surveys or research activities on natural habitat, omitting records from greenhouse, screenhouse or interceptions; (2) selecting records with precise geographic coordinates and (3) records with confirmed positives. In order to reduce spatial autocorrelation, i.e. the tendency of closer locations being more similar than those further apart, the presence records were submitted to a spatial filtering approach. In this procedure, the presence records are randomly selected according to a minimum nearest neighbour distance greater than or equal to 10 km between each locality. This distance is equal to the spatial resolution used for the climatic data resulting in sets of 540 presences for *X. fastidiosa* as a whole, 43 for *X. fastidiosa* subsp. *fastidiosa*, 104 for subsp. *multiplex* and 63 for subsp. *pauca*, 26 for subsp. *fastidiosa* ST1, 11 for subsp. *multiplex* ST6 and 18 for subsp. *pauca* ST53. This procedure was performed using the spThin package in R (Aiello-Lammens et al., 2015). The procedure was repeated four times obtaining four different spatially filtered data sets.

As mentioned, SDMs estimate potential distribution of a species based on their associated environmental information. When only the presence data are available, the pseudo-absence data are estimated from the background, adding yet another source of uncertainty through less informative response variables (VanDerWal et al., 2009). Different number and weighting schemes for pseudo-absences generation were tested including: equal weight for presences and absences (prevalence 0.5) or weighted to simulate a prevalence of 0.1. This later pseudo-absence scheme generation was selected to account for the different number in the presence data across data sets, in particular for models fitted to *X. fastidiosa* subspecies and STs. In addition, to reduce the uncertainty of the random sampling, we repeated this process four times to generate four pseudo-absence data sets per model replication and spatially filtered data set for *X. fastidiosa* (as species) as well as for each subspecies and ST.

Species distribution modelling

The potential for establishment of *X. fastidiosa* in Europe was modelled using ensemble predictions generated with the 'sdm' R package encompassing different SDM techniques that assessed the effects of climate on the distribution of the species (Naimi and Araújo, 2016; R Core Team, 2018). In SDM, when several models are used to estimate the potential distribution of a species, commonly no single model could be considered as the optimum model. Different models could account for specific characteristics of the interactions between species and the environment. In ensemble modelling, a consensus model that combines the prediction from several models and algorithms is selected (Strubbe et al., 2015; Naimi and Araújo, 2016). The consensus model minimises bias due to model selection and optimises estimation of suitable areas across models (Guisan et al., 2017).

An ensemble SDM was developed, which included 10 modelling techniques: bioclim, boosted and regression trees (BRT), classification and regression trees (CART), domain, generalised additive models (GAM), multivariate adaptive regression splines (MARS), maximum entropy (MaxEnt), random forest

(RF), recursive partitioning and regression trees (RPART) and support vector machines (SVM). Default parameters of the dependent R package of each algorithm that were used. All models were evaluated using a fivefold cross-validation procedure in which the data were split into five roughly equal-sized parts, four of which were used for model fitting and one for model validation (Naimi and Araújo, 2016). This process was repeated five times.

Model performance was evaluated using several widely established threshold-dependent statistics: specificity, sensitivity and the True Skill Statistics (TSS), as well as threshold-independent statistics: the area under the curve (AUC) of the Receiver Operating Characteristic (ROC) plot and Cohen's Kappa. The AUC represents the relationship between the sensitivity and the specificity of the classification method as the threshold is varied (Jiménez-Valverde, 2011). It ranges between 0 and 1, with a value of 0.5 indicating no predictive ability of the classification method. Cohen's Kappa (κ) also ranges from 0 to 1 and gives a quantitative measure of the agreement between observed and predicted values. However, unlike the AUC, it is affected by the prevalence of the outcome of interest (Cohen, 1960). The TSS is prevalence independent and is calculated as:

$$\text{TSS} = \text{sensitivity} + \text{specificity} - 1$$

It ranges from -1 to $+1$, and 0 indicates a random performance (i.e. no predictive performance). TSS compares the number of correct predictions minus those attributable to chance (Allouche et al., 2006). In addition, we evaluated each variable importance by calculating the improvement of the model performance (AUC) over inclusion of each variable comparing to when the variable is excluded through a cross-validation procedure (Naimi and Araújo, 2016).

We ran a total of 800 single models (i.e. 4 spatially filtered data sets, 4 pseudo-absence sampling replicates, 10 single modelling techniques and 5 cross-validation runs). For building the model ensemble, we chose the weighted average method to combine all single models with TSS values greater than or equal to 0.7 (Guisan et al., 2017). The output of this process is a continuous variable that ranges from 0 to 1, which may need to be classified into dichotomous predictions of species presence and absence for practical application and validation (Jimenez-Valverde and Lobo, 2007). This requires the specification of a threshold value. Since no single threshold can be considered the most accurate we compared five different thresholds: (a) two thresholds set to be the suitability value at which sensitivity, i.e. true positive rate, was 95% and 90%, respectively; (b) the suitability value that maximises the sum of sensitivity and specificity; (c) the suitability value that minimised the difference between sensitivity and specificity and (d) a four levels threshold was applied ranging the suitability index (SI) as follows: (1) SI < 0.1; (2) 0.1 > SI < 0.3; (3) 0.3 > SI < 0.6 and (4) SI > 0.6. Thresholds 1 and 2 represent a fixed proportion of sensitivity and are particularly informative for models based on presence-only data to ensure a correct prediction of at least 90% or 95%, respectively, of *X. fastidiosa* presences to be suitable. Thresholds 3 and 4 are designed to produce the most accurate model predictions (Jimenez-Valverde and Lobo, 2007). We should take into account that both, sensitivity and specificity are interdependent, and if sensitivity is maximised (thresholds 1 and 2), this could result in a reduction on the specificity. In this context, threshold 4 was designed to equally balance, both sensitivity and specificity.

2.1.3. Asymptomatic period

2.1.3.1. Data collection and processing

A literature review was undertaken using the EFSA Update of the *Xylella* spp. host plant database (EFSA, 2018a). At the time of search, this database included 853 papers. All papers which described studies using artificial inoculation of plants (including insect transmission, grafting with infected material and mechanical inoculation of a bacterial suspension) were selected (n = 413). Information on the following was recorded:

- The species of host plant and the source of *X. fastidiosa*.
- The bacterial incubation conditions and the inoculation procedure.
- Whether plant infection was confirmed using laboratory testing.
- The time of first appearance of symptoms (in relation to inoculation time) and the number of symptomatic and asymptomatic plants at this time.
- The time of the end of the study and the number or proportion of symptomatic and asymptomatic plants at this time.

All papers which did not record the timing of first symptom expression were then removed, leaving a total of 127 papers (Figure 2). All papers which did not record the numbers of individuals in the studies, which were considered unreliable, or which contained duplicated data were also removed. This left a total of 35 papers describing a total of 124 different individual studies (i.e. where a 'case-study' is considered a set of data from a paper and a given combination of a strain on a plant genotype). These studies were then categorised according to subspecies and host as shown below and in Table 2:

- *X. fastidiosa* subspecies:
  - *X. fastidiosa* subsp. *fastidiosa*
  - *X. fastidiosa* subsp. *multiplex*
  - *X. fastidiosa* subsp. *pauca*
  - *X. fastidiosa* subsp. *morus*
  - *X. fastidiosa* subsp. *sandyi*
- Host plant:
  - Grape (*Vitis vinifera* and *Vitis rotundifolia*)
  - Almond (*Prunus dulcis*)
  - Sweet orange (*Citrus sinensis*)
  - Olive (*Olea europaea*)
  - Tree (*Ulmus americana* and *Platanus occidentalis*)
  - Ornamental (*Catharanthus roseus*)
  - Blueberry (*Vaccinium corymbosum*)
  - Mulberry (*Morus rubra* and *Morus alba*)

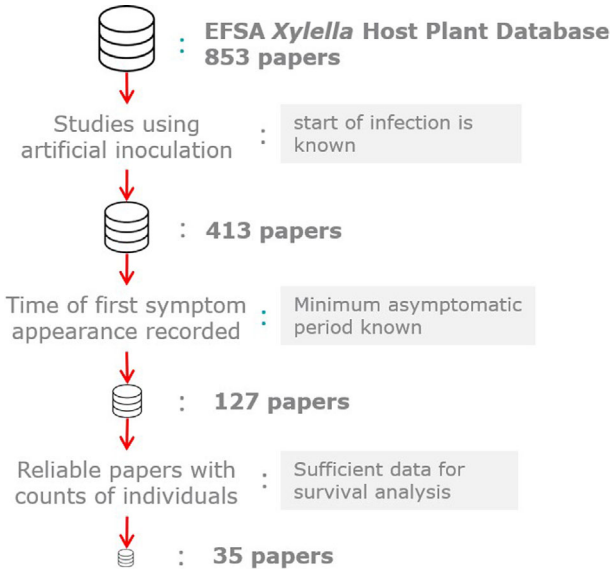

Figure 2: Protocol for the selection of the scientific papers for the estimation of the asymptomatic period of *X. fastidiosa* from the EFSA Update of the *Xylella* spp. host plant database (EFSA, 2018a)

Data on the subspecies of *X. fastidiosa*, the host plant, the timing of infection, the timing of first symptom expression and the numbers of individuals at both these time points were available for a total of 86 case studies. The subspecies–host combinations of these case studies are shown in Table 2. All subspecies–host combinations covered by only a single study were not considered for further analysis. The asymptomatic period data table is available in Appendix J.

2.1.3.2. Data analyses

Since data on the time of development of symptoms for each individual host in each study were not available, it was not possible to estimate the duration of the asymptomatic period for each subspecies–host combination directly from the data. Instead, data on the number of symptomatic and asymptomatic individuals at two post-infection time points were available: the time of first recorded

symptom expression and the time of the end of the study. As a result, the data are 'censored', meaning that the exact timing of symptom expression is unknown in the following three cases:

- Hosts which exhibited symptoms before the time of first observation ('interval censored' data).
- Hosts which developed symptoms between first symptom observation and end of the study ('interval censored' data).
- Hosts which had not developed symptoms by the end of the study ('right censored' data).

The issue of censored data is addressed by using two distinct methodologies to estimate a 'survival function', which in the current study describes the probability that a host will not have developed symptoms at any given time point following infection. In order to account for the relatively low number of observations, the survival function was first estimated using a maximum likelihood method under the assumption that symptoms develop at a fixed rate over time. These results were then compared with a non-parametric method using the Kaplan–Meier estimator, which makes no such assumption.

Table 2: Subspecies–host combinations for which data are available

Subspecies	Host	Number of case studies
X. fastidiosa subsp. *fastidiosa*	Almond	14
	Grape	10
X. fastidiosa subsp. *multiplex*	Shade Tree	2
	Almond	2
	Grape	1
	Plum	1
X. fastidiosa subsp. *pauca*	Orange	23
	Grape	18
	Olive	4
	Ornamental	2
X. fastidiosa subsp. *morus*	Mulberry	4
	Blueberry	3
X. fastidiosa subsp. *sandyi*	Grape	1
	Almond	1

Maximum likelihood estimation

The survival function was first estimated by fitting the data to an explicit mathematical model of symptom development using a maximum likelihood approach (Leclerc et al., 2014). This model assumes that the instantaneous rate of development of symptoms (the 'hazard') is fixed over time, and therefore that the probability of symptom development at any time follow an exponential distribution (with a rate parameter equal to the inverse of the mean asymptomatic period). In order to account for interval censored observations and the numbers of inspected hosts, symptom appearance was modelled as a binomial process, with the probability equal to the cumulative probability of symptom expression according to an exponential distribution. A 'lag period' (which could take any positive number up to the earliest timing of observed symptom development for the subspecies–host combination in question) was included in order to allow the start of symptom development to be delayed for a fixed period after initial infection, and thus account for any temporal lags before symptoms are able to develop. We then used the optim function (R Core Team, 2018) in the base stats package of R to run a simulated annealing algorithm in order to identify the exponential rate parameter and lag period which maximised the log likelihood of the observed data.

Kaplan–Meier estimation

The Kaplan–Meier estimator estimates the proportions of available hosts which did not develop symptoms at each time of symptom expression and calculates the survival function at any time as the product of these over all previous time points. As a result, this is a non-parametric method which makes no assumptions regarding the rate of symptom development over time, and therefore is derived solely from the data. The survival function was estimated using the surv and survfit functions in the R survival package (version 2.43-3) (Therneau, 2015), assuming that any symptoms developed in the interval prior to observation, and that all asymptomatic hosts at the end of the study were right

censored. The survival function was then visualised by creating Kaplan–Meier curves using the ggsurvplot function from the survminer package (version 0.4.3) (Kassambara and Kosinski, 2018).

2.1.4. Short-range spread

2.1.4.1. Data

The SRS model describes the epidemics of the disease at high spatial resolution in a homogeneous host plant orchard characterised by a regular planting distance. The model is used to derive the spatial–temporal pattern of disease spread and to assess the effectiveness of eradication measures for a new outbreak in a previously free area. The SRS model considers only the local spread (i.e. within the orchard) of the disease due to the dispersal behaviour of the infected vectors. Long jumps of the vectors due to human-assisted spread or passive dispersal through strong winds are excluded in the SRS model, while they are considered in the long-range spread model (Section 2.1.5). The limited amount of quantitative data on the disease does not allow the estimation of the biological and epidemiological parameters in the model. Therefore, to produce most of the required parameters, the Panel relied on the EFSA EKE methodology (see Appendix F), in line with the related guidelines EFSA (2014), the Guidance on Uncertainty (EFSA Scientific Committee, 2018b) and the Guidance on Quantitative Pest Risk Assessment (EFSA PLH Panel, 2018a). The information used for model development and calibration refers to the ongoing spread of *X. fastidiosa* subsp. *pauca* in olive groves in the Apulia region given the availability of data but different scenarios of vector abundance and host susceptibility are explored. The sources of information are reported below:

- Most of the biological information used for model parameterisation were derived from the EKE on *Xylella* biological/epidemiological parameters for modelling purposes (Appendix F).
- Information included in the deliverable 2.1 of the H2020 PONTE Project was used for the estimation of the growth curve of the disease in the plant.
- Dr. M. Saponari and Dr. D. Boscia (IPSP, CNR, Italy) provided information on the disease growth in the plant, and on molecular and visual detectability of the disease.
- The estimation of the asymptomatic period reported in this Opinion has been used for disease growth in the plant.
- Information in the final report on Collection of data and information on biology and control of vectors of *Xylella fastidiosa* (Bosco et al., 2019) is used for the specification of the scenario on population abundance and phenology of the vector.
- The data in spatial and temporal dynamics of Olive Quick Decline Syndrome in orchards in Apulia, southern Italy, by Montes-Borrego et al. (2017) were used for model calibration.

2.1.4.2. Specification of the scenarios

Scenario for the epidemiological dynamics

The landscape for modelling the SRS of *X. fastidiosa* outbreak and control is a simplified representation of a large olive grove with the maximum extent of 10 × 10 km with reflecting boundary conditions (Neumann homogeneous boundary conditions). The susceptible plants are in the nodes of a regular grid 10 × 10 m. Each node represents a cell of 10 × 10 m in which there is a susceptible olive plant at the centre. The spatial and temporal epidemiological dynamics was followed considering the establishment on a new outbreak in the centre of a free area. The disease dynamic was analysed for a maximum period of 5 years, the temporal resolution was one day. Environmental conditions were those typical of a Mediterranean area. Environmental driving variables were not explicitly included in the model, however the role of climate was considered by assigning different patterns in the year to the disease growth in the plant and to the phenology and the density of the vectors. The same patterns were repeated every year of the simulation.

The following biological and epidemiological processes and assumptions were considered and explored in the scenario analysis:

- The local infection in a free area started with the inoculation of a small number of trees in an area of about 30 m radius. The pathogen was carried in the new area by a small number of infected vectors (propagule population) arriving in the free area and able to infect a small number of trees in an area of about 30 m radius.
- An adult vector feeding on an infected plant becomes infected and immediately infectious, and it can transmit the pathogen to a susceptible plant or to an infected plant (increasing the

disease level). Hereinafter, the status of the vector carrying the pathogen is equivalently defined as infected or infectious. The possibility that vectors take and spread the disease in the olive grove is influenced by the bacterial titre in the host plant. The disease agent is propagated only by the feeding activity and the dispersal movement of infected vectors.

- Successful transmission of the pathogen to the host plant is described by a transmission function which takes into account: (i) the vector feeding behaviour (including also the vector preference for the target host), (ii) the capacity of the vector to transmit the pathogen and (iii) the susceptibility of a specific host plant (species or cultivar) to the pathogen.
- In an infected plant, the bacterial load titre growths due to the multiplication of the bacterial population within the plant based. A plant can receive multiple successful inoculums of the pathogen due to the feeding of the infected vectors. They also contribute to the bacterial population growth (details reported in Table A.1).
- The growth of the bacterial population in the plant only occurs during a period of the year when favourable environmental conditions and suitable plant physiological conditions are verified (details reported in Table A.1).
- Vector phenology is characterised by two stages: disease transmitting adult stage and non-transmitting pre-imaginal stages. The transition from pre-imaginal stages to adults (emergence) and from adult to pre-imaginal stages (oviposition) occurs in two fixed points in time during the year (in spring and autumn, respectively).
- Vectors move in the spatial domain. Only the individuals in the adult stage are able to disperse and the dispersal behaviour is modelled by means of a random walk motion.
- The survival pattern of the vector population is described by a suitable function.

The spatial–temporal dynamics of the disease in the new infected area is described considering the combination of a set of initial conditions related to vector density and host plant susceptibility. The scheme is reported in Table 3.

Table 3: Variables and values used to define the scenario analysis for the epidemiological dynamics

Parameter	Level	Values	Justification
Maximum vector density	High	20 adults/m^2	Data on vector abundance (Bosco et al., 2019)
	Low	1 adults/m^2	
Susceptibility of the host plant	High	See parameters r_H and r_L in Appendix A – Table A.1 (cultivar of reference: Ogliarola)	Data on growth of symptoms severity and the dynamics of the incidence from Montes-Borrego et al. (2017)
	Low	See parameters r_H and r_L in Appendix A – Table A.1 (cultivar of reference: Leccino)	

Based on the variable and values used to assess the epidemiological dynamics, four scenarios were defined:

1) Epidem-ShVh: high susceptible plants and high vectors population density;
2) Epidem-ShVl: high susceptible plants and low vectors population density;
3) Epidem-SlVh: low susceptible plants and high vectors population density;
4) Epidem-SlVl: low susceptible plants and low vectors population density.

Scenario for detection, eradication and control

To explore the scenario on the efficacy of the eradication strategy we take into consideration the worst-case scenario for the epidemiological dynamics, namely the Epidem-ShVh.

Bases on the variables and values used to define the detection and the eradication strategy (shown in Table 4), eight scenarios are defined:

1) Contro-ChRhDe: high efficacy in vector control (both adult vector and weed control), high cutting radius for plant removal (100 m), early detection (3 years after the inoculum, i.e. in the 4th year of simulation),
2) Contro-ChRhDl: high efficacy in vector control (both adult vector and weed control), high cutting radius for plant removal (100 m), late detection (4 years after the inoculum, i.e. in the 5th year of simulation),

3) Contro-ChRlDe: high efficacy in vector control (both adult vector and weed control), low cutting radius for plant removal (50 m), early detection (3 years after the inoculum, i.e. in the 4th year of simulation),
4) Contro-ChRlDl: high efficacy in vector control (both adult vector and weed control), low cutting radius for plant removal (50 m), late detection (4 years after the inoculum, i.e. in the 5th year of simulation),
5) Contro-ClRhDe: low efficacy in vector control (both adult vector and weed control), high cutting radius for plant removal (100 m), early detection (3 years after the inoculum, i.e. in the 4th year of simulation),
6) Contro-ClRhDl: low efficacy in vector control (both adult vector and weed control), high cutting radius for plant removal (100 m), late detection (4 years after the inoculum, i.e. in the 5th year of simulation),
7) Contro-ClRlDe: low efficacy in vector control (both adult vector and weed control), low cutting radius for plant removal (50 m), early detection (3 years after the inoculum, i.e. in the 4th year of simulation),
8) Contro-ClRlDl: low efficacy in vector control (both adult vector and weed control), low cutting radius for plant removal (50 m), late detection (4 years after the inoculum, i.e. in the 5th year of simulation).

Table 4: Setting used to define detection and control scenario for disease eradication. Scenario components refer to a homogeneous olive grove characterised by a regular planting distance

Parameter	Level	Values	Justification
Efficacy of the weed treatments for nymph control	Low	60% of nymph mortality	Data in Appendix D
	High	80% of nymph mortality	
Efficacy of chemical control of the adults	Low	50% of adult mortality	
	High	90% of adult mortality	
Period of efficacy of chemical control	One	25 days	
Cutting radius in the infected area	Low	50 m	Scenario hypothesis
	High	100 m	Current legislation
Time to detection	Early	3 years after inoculation	Scenario hypothesis
	Late	4 years after inoculation	Scenario hypothesis
Time to cutting hosts into the infected area	Recommended	30 days from the detection	Interpretation of current legislation
	Late	65 days from the detection	Scenario hypothesis
Time to apply adults vector treatment in the infected area (the year in which the detection is carried out)	One	5 days before the cut	Interpretation of current legislation
Buffer zone	One	5,000 m divided in: – 1,000 m high surveillance area – 4,000 m low surveillance area	Current legislation
Efficacy of detectability in the buffer zone	One	99% in the high surveillance area (grid 100 m × 100 m) 95% in the high surveillance area (grid 1,000 m × 1,000 m)	Hypothesis of maximum efficacy
Time horizon for assessing the eradication	One	5 years since the first detection Resolution: daily	

2.1.4.3. Conceptual model of the short-range spread model

The conceptual model for describing the SRS of the disease in the olive grove and the outcome of the control measures is reported in Figure 3.

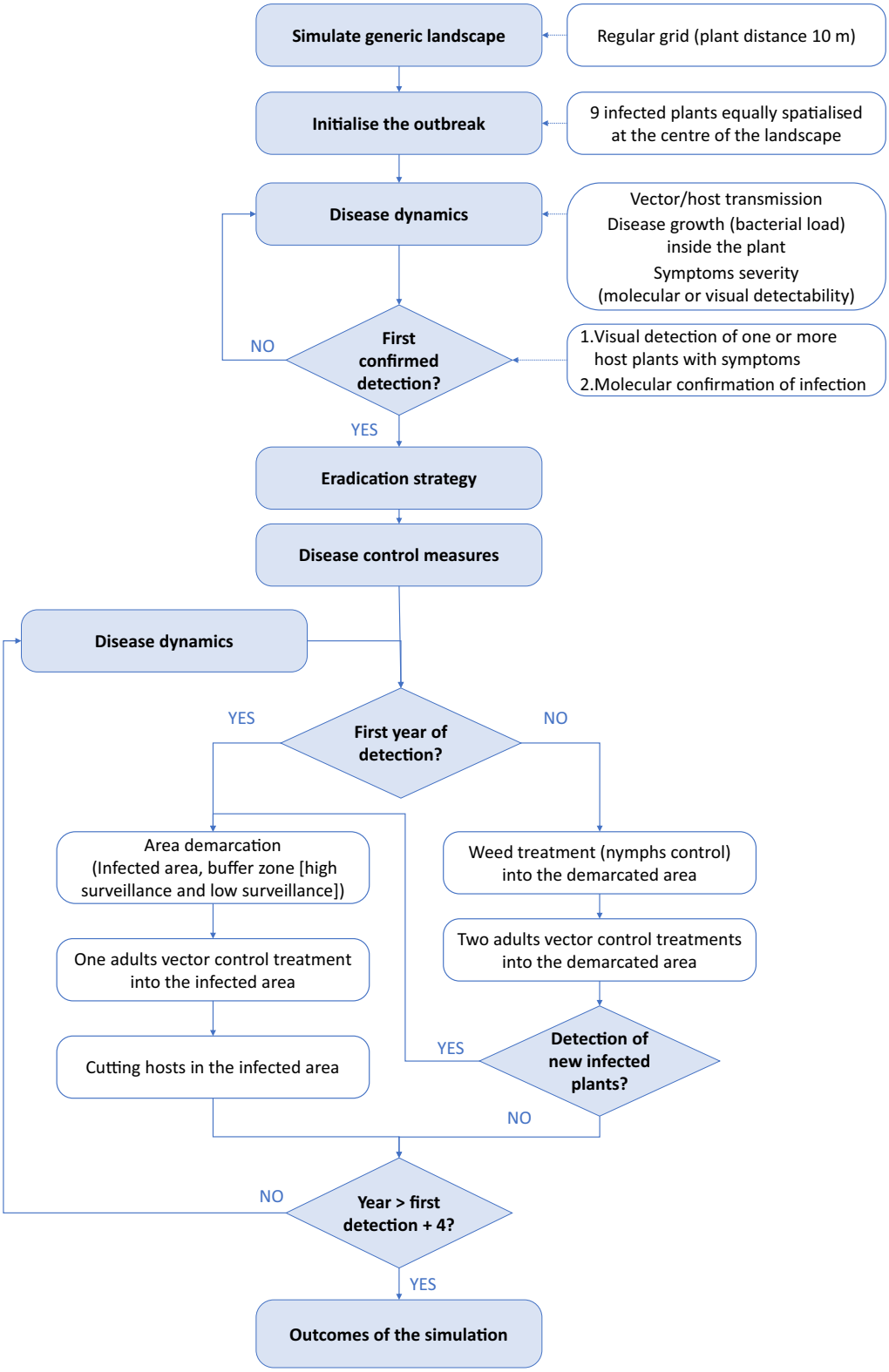

Figure 3: Flow chart overview of the short-range spread model

2.1.5. Long-range spread

2.1.5.1 Conceptual model

The *X. fastidiosa* simulation model was developed based on knowledge of the epidemiology and pattern of spread of *X. fastidiosa* subsp. *pauca* in olive trees in Apulia, Italy, between 2013 and 2018. The spatial scale of spread described by the model is termed 'long range' in that it represents spread over regional scales (e.g. provinces, countries, etc.) rather than between individual host plants (i.e. 'short-range' spread). Figure 4 shows an overview of the simulation algorithm. Descriptions of each sub model are given below.

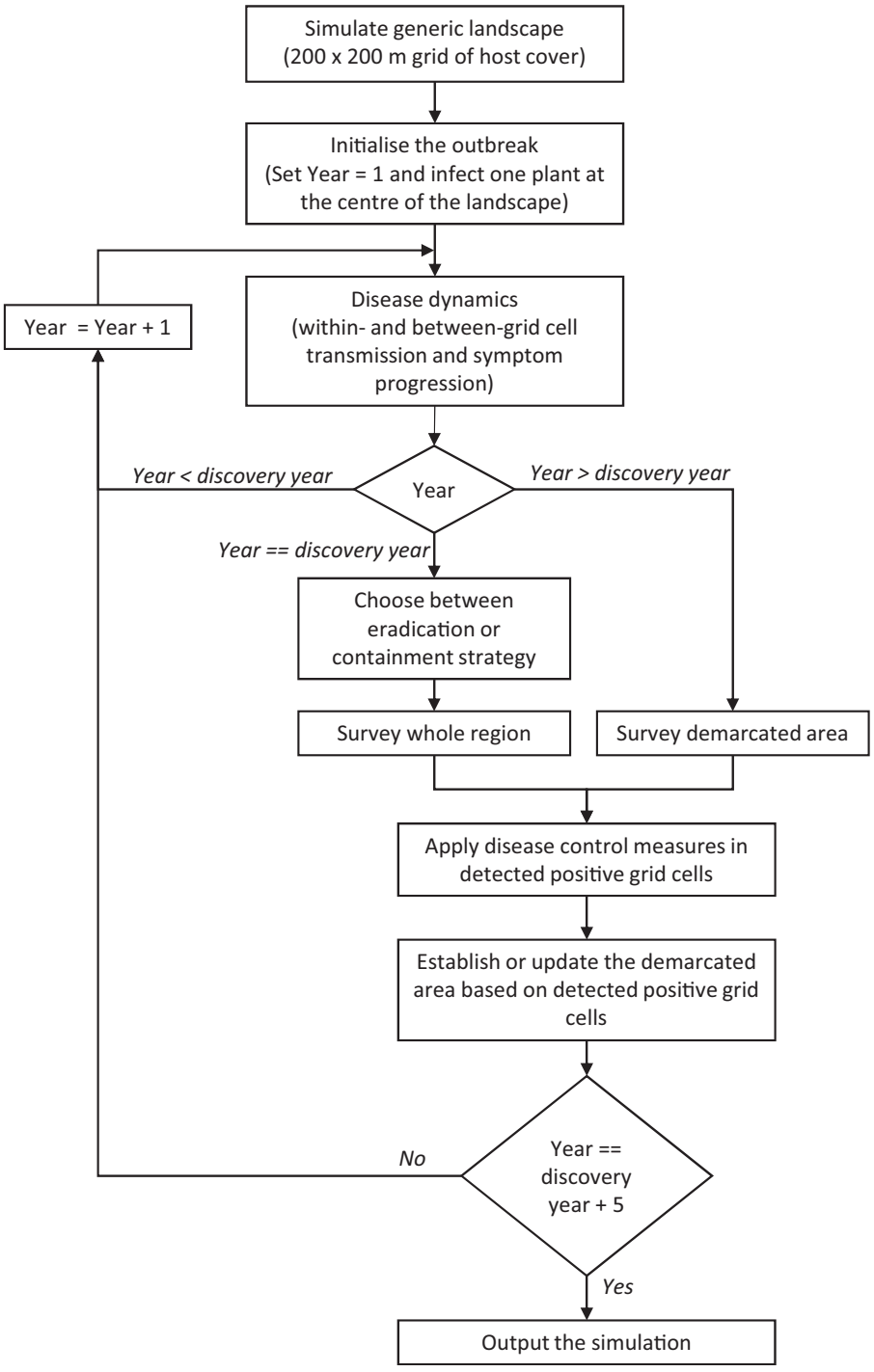

Figure 4: Flow chart overview of the long-range spread model for testing alternative eradication or containment measures on *X. fastidiosa* outbreaks

Simulation of generic landscapes

The landscapes for the modelled *X. fastidiosa* outbreaks were 150 × 150 km squares, divided into a 200 × 200 m resolution grid with absorbing boundaries. The grid resolution approximated the 100 m buffer for felling around infected plants specified in Decision (EU) 2015/789. Within each grid cell, a certain proportion of the land is occupied by susceptible host cover (i.e. a habitat in which there is a high density of susceptible host plants). The distribution of susceptible host cover is simulated in such a way as to produce generic landscape patterns with similar spatial properties to the major outbreak areas in Italy (Apulia), France (PACA) and Spain (Alicante) (Appendix A). These landscape types were selected to span a range of different landscape configurations in which *X. fastidiosa* outbreaks have occurred in mainland Europe. However, because of this the model may not be representative of all potential outbreak situations, for example those in islands such as Corsica and the Balearics that are substantially smaller than the modelled landscapes.

Spatial disease dynamics

X. fastidiosa dynamics in infected grid cells was approximated with a standard deterministic compartmental model (Brauer, 2008) in discrete annual time steps. The modelled host plant population was divided into four compartments – uninfected susceptible plants (*S*), infected asymptomatic plants (*A*), infected symptomatic plants (*I*) and infected plants that have been killed or otherwise removed from the infective population (*R*) (Figure 5). The *S* proportion of the population moves into the *A* compartment at a rate that is proportional to the current population size of infective plants (*A* and *I*, with *A* assumed to be less infective than *I* due to lower bacterial titre). Once infected, plants then progress through the *A* and *S* compartments at a constant rate, finally moving into the *R* compartment (Figure 6). Transmission and progression parameters were estimated through expert knowledge about typical times for symptom development and canopy cover loss in olive groves (Donato Boscia and Maria Saponari, pers. comm.) and analysis of infection growth in olive grove monitoring plots from Apulia.

The model also includes between-grid cell disease transmission as a stochastic process whereby infective plants in one grid cell transmit *X. fastidiosa* to plants in other uninfected grid cells and spread the disease to new locations. This implicitly represents *X. fastidiosa* dispersal via the movements of infected vectors that may spread the disease, as well as the possibility of human-assisted movement of infected plant material. To model between-grid cell transmission, the transmission rate used for the within-grid cell model is scaled by a distance–decay function, termed a transmission kernel. Using this kernel, new infections mostly appear in the neighbourhood of large infective populations, reflecting disease transmission through diffusive-like local scale movements of infected vector insects. However, the transmission kernel is also specified to produce rare long-distance transmission events. No specific mechanism for these long-range jumps is modelled, but they may occur through wind or human-assisted long-distance dispersal of infected vectors or through long-range human movement of infected plants. The kernel parameters were estimated by tuning the spread model to produce approximately the correct rate of spread and spatial pattern of disease observed in Apulia from 2013 to 2018.

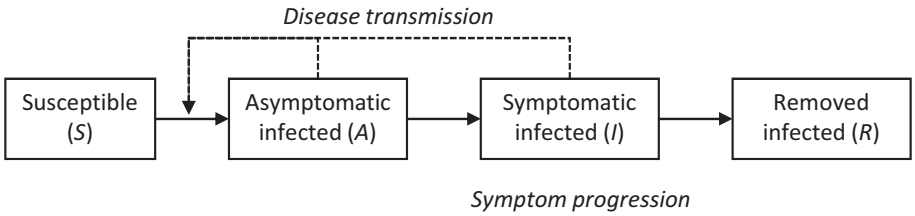

Figure 5: Schematic showing the compartmental epidemiology model for *X. fastidiosa* dynamics. Solid arrows show movements of individuals between compartments and the dashed arrows show how the infection transition depends on the density of infective compartments

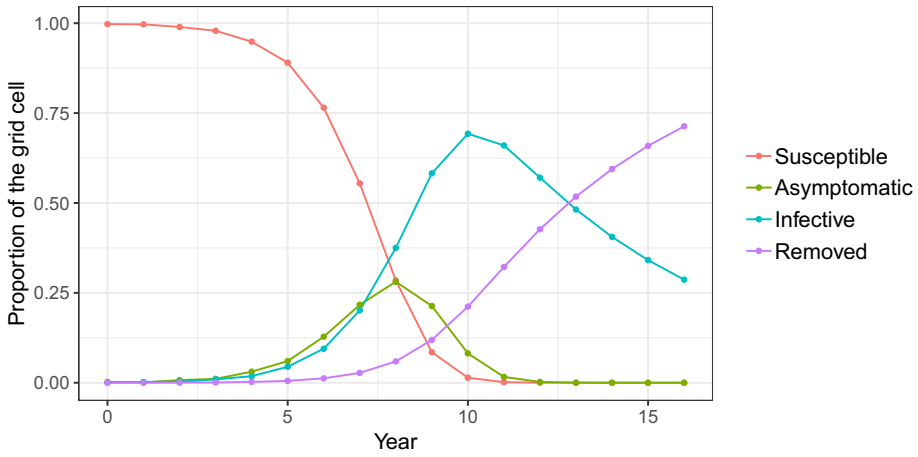

Figure 6: Example modelled *X. fastidiosa* dynamics in 200 × 200 m grid cell completely covered by susceptible habitat. Note that 'removed' refers to dead host plants killed by *X. fastidiosa* rather than plants deliberately felled during disease management

Surveillance and management

The model was used to investigate both eradication and containment strategies for managing *X. fastidiosa* outbreaks. The two modelled strategies mainly differ in terms of the way demarcated zones were delimited and in the actions taken after detection (Figure 7, Table 5). In a modelled eradication strategy, the demarcation consists of a fixed radius BZ around all known *X. fastidiosa* positive locations, as described in Decision (EU) 2015/789. The default BZ width of 5 km was varied in the model scenarios (see below). In a modelled containment strategy, the BZ is established around the periphery of the known infected region by buffering the minimum convex polygon bounding all known positive locations. In addition, a CZ is defined as the most peripheral part of the IZ, bordering the BZ (and forming an internal buffer to the BZ). This approximates the strategy being employed in Apulia. The BZ and CZ are assumed to represent the focus of both preventative vector control measures (modelled as a uniform reduction in transmission rates in these zones) and surveillance to locate and remove infected plant material (Table 5).

To model surveillance in the BZ, CZ and elsewhere, each of the 200 m × 200 m grid cells was divided into four 100 m × 100 m squares, forming the units for inspections under Decision (EU) 2015/789. Visual inspection for symptoms was modelled in each of these. The probability of detecting symptomatic host plants during the inspection increases with the symptom prevalence in the population and the fraction of the grid cell that is inspected. In all simulations, greater inspection effort (higher fraction inspected) is applied in the first 1 km of the BZ and all of the CZ, compared to the outer part of the BZ. This is based on the description of surveys in Decision (EU) 2017/2352 (Decision 2015/789 requests the same inspection effort in the whole BZ, but has been modified in December 2017). Furthermore, a very low surveillance effort was applied in the rest of the landscape to account for detection of disease foci beyond the demarcated zones.

If the modelled visual inspection of a 100 m × 100 m square locates symptomatic hosts, then the model selects one random symptomatic host for laboratory testing. If no symptomatic hosts are detected, the model assumes that a randomly selected asymptomatic host is tested. Test accuracy rates for infected symptomatic and asymptomatic host plants were estimated from the monitoring data from Apulia, suggesting a significant level of false negatives between around 5–10% but negligible false positive rates. In the model, the visual inspection and laboratory testing combine into an overall probability of detecting *X. fastidiosa* in each grid cell during surveillance. These are converted stochastically into detection events through Bernoulli trials ('coin tosses') using the overall detection probabilities.

When the surveillance results in *X. fastidiosa* detection in the model, demarcation of the model BZ and CZ are updated accordingly (Figure 4) and disease control measures are implemented at the positive locations, based on Decision (EU) 2015/789. The 200 × 200 m resolution of the model is approximately equivalent to the 100 m buffer around positive host plants specified in the Decision (EU) 2015/789. In the BZ, when a positive is detected all the host plants (infected and uninfected) in the 200 × 200 m grid cell are permanently removed from positive locations. In the CZ, when a positive is

detected only the infected host plants are permanently removed from the 200 × 200 m grid cell, but uninfected host plants are allowed to remain. For simplicity, we assumed this was done without false negatives in the laboratory testing.

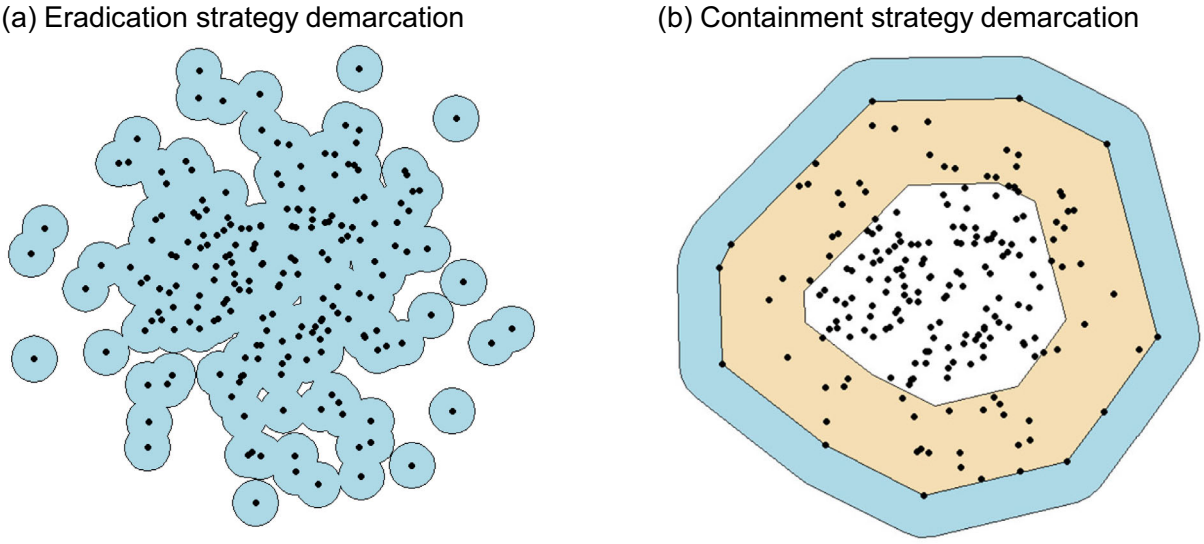

Figure 7: Illustrations of the modelled demarcations of a buffer zone (BZ, blue) and containment zone (CZ, light brown) for (a) an eradication strategy and (b) a containment strategy. Points show the known positive locations. The BZ and CZ form the focus for disease surveillance and management

Table 5: Summary of the modelled disease management strategies for the long-range spread model. These approximate the measures in Decision (EU) 2015/789 and Decision (EU) 2017/2352, but with some simplification of the real management approach and not the full list of emergency measures

	Eradication	**Containment**
Demarcation	Buffer zone (BZ) around known infected locations (see Figure 7a)	Buffer zone (BZ) around the edge of the known infected region. Containment zone (CZ) established at the edge of the infected region, twice as wide as the BZ) (see Figure 7b)
Surveillance	Inspections of all 100 m × 100 m squares. Inspections are most thorough in the first 1 km of the BZ and less thorough in the remaining BZ. A very low inspection rate is applied in the disease-free area to pick up new foci	Inspections of all 100 m × 100 m squares. Inspections are most thorough in the CZ and first 1 km of the BZ and less thorough in the remaining BZ. A very low inspection rate is applied in the disease-free area and core of the infected area to pick up new foci
Host plant removal	Removal of all host plants in the 200 m × 200 m grid cells in which infections are detected (approximating a 100 m cut radius)	In the BZ and disease-free area, removal of all host plants in the 200 m × 200 m grid cells in which infections are detected (approximating a 100 m cut radius). In the CZ, removal of all infected host plants in the 200 m × 200 m grid cells in which infections are detected
Vector control	Applied throughout the demarcated area	Applied throughout the BZ and CZ

Specification of the scenarios

All combinations of the following scenarios were run 50 times, each with a different random draw from the model parameter distributions (Appendix A, Table A.5).

To standardise the assessment of the simulated management strategies, the infected area ($\sum$ (A + I + R)) after 5 years of management was divided by the infected area from equivalent simulations with no management intervention. In other words, the model outputted the proportionate

change in the size of the infected area as a result of management. Smaller proportions therefore indicate more effective disease management

Table 6: Scenario settings used in the simulation experiment. All combinations of scenarios were modelled

Variable	Scenarios	Justification
Landscape type	Apulia-like, Alicante-like or PACA-like	Three of the major European mainland infected areas
Management goal	No management, eradication or containment	Based on Decision (EU) 2017/2352
Buffer zone widths (km)	2.5, 5, 10 or 15 km	Based on Decision (EU) 2017/2352
Disease discovery	Early (5 years after the initial inoculation) or late (10 years after the initial inoculation)	Model fitting to the spread in Apulia suggests *X. fastidiosa* may have been present for 10 years prior to detection
Inspection efficiency (v)	High (v = 0.990 in the first 1 km of the BZ and the whole CZ, 0.368 in the outer BZ and 0.086 in the 'disease-free' area) or low (v = 0.3689 in the first 1 km of the BZ and the whole CZ, 0.0448 in the outer BZ and 0.009 in the 'disease-free' area)	Based on ISPM 31 inspection rates for 1% detection of 0.1% prevalence in populations of 1,000 or 10,000 host plants, respectively
Vector control (υ)	No control (υ = 1 everywhere) or effective control in the demarcated area (υ = 0.1 in the demarcated area, causing a 90% reduction in disease transmission, υ = 1 elsewhere)	To include scenarios with not or effective control

CZ: containment zone; BZ: buffer zone.

2.1.6. Impact

Xylella fastidiosa is the causal agent of the diseases of several plant species including cultivated plants, forest species and ornamental plants. The economic impact for agriculture is huge and influencing different sectors. Direct impacts are on farms and nurseries with cascaded impacts on other sectors such as processors, traders, garden centres, retailers, landscapers.

Following the request included in the Mandate, the Panel analysed the impact on plant species concerned with a focus on the hosts with higher economic values found attacked by *X. fastidiosa* in Europe: *Olea europaea* (i.e. olive), *Prunus dulcis* (i.e. almond), *Vitis vinifera* (i.e. grapevine), *Prunus avium* L. (i.e. cherry), and *Prunus salicina* and *Prunus domestica* (i.e. plum). In addition, the Panel also included in the assessment *Citrus* spp. for their economic importance in the EU and as recognised important hosts in other areas of the world. The Panel also considered the potential impact on tree and ornamental nurseries and on forest species.

Impact was analysed adopting two different approaches according to the available information for the considered hosts.

For olive, almond, grapevine and *Citrus* spp., for which at least some information/data on impact was found in the scientific and/or technical, and/or grey literature, the EKE process was applied (EFSA, 2014). A short description of the EKE process is given in Appendix E. For the EKE on the impact on this hosts, the Panel adopted the general scenario assumptions applied by the EFSA Working Group on EU Priority Pests[1] and which assume that the entry, establishment and spread of the pest had already occurred. This corresponds to a scenario where the pest is already present throughout the area of potential distribution in the EU (i.e. it has spread to its maximum extent). In addition, the only vector that was considered in this scenario was *Philaenus spumarius*, the most common and widespread known vector of *X. fastidiosa* in Europe. The full list of scenario assumptions is given in Appendix E. Impacts was expressed in terms of yield losses and not in monetary terms, whereas 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). Finally, the Panel also overlapped the areas of distribution of the hosts (based on statistical data of cultivated areas at NUTS 2 level) to the area of potential establishment of *X. fastidiosa* according to Section 3.1 to show the overlap between growing areas and areas of climate suitability of *X. fastidiosa* (Appendix I).

For cherry, plum, forest species and for the impact on nurseries, due to lack of specific information on impact, the Panel adopted a literature review approach. The result of the literature review is presented in Section 3 Assessment.

For forest species, the Panel overlapped the area of potential distribution of the bacterium based on the SDMs described in Section 3.1 and Appendix B (which offers a finer level detailed compared to the Köppen–Geiger approach) with the distribution area of host tree species to analyse the potential impact in terms of areas potentially affected.

For nurseries, the Panel reviewed the potential impact with regard to the type of productions (outdoors vs protected cultivation) and plant species grown.

2.1.6.1. Data

Statistical data of productions areas for olive, almond, grapevine and *Citrus* spp. were collected at NUTS 2 level from the websites of the national statistical institutes of each country. If data were not available in the websites, the statistical institutes were contacted, or the EUROSTAT database was consulted (Appendix H). In general, statistical data referred to year 2015, with few exceptions due to availability of data for specific countries.

Statistical data (year 2015) on cherry and plum area and production were collected at NUTS0 level from EUROSTAT.

Forest species chorological maps mapping their native distribution range for the EU were obtained from Caudullo et al. (2018).

Quantitative evidences on *X. fastidiosa* impact on olive, almond, grapevine and *Citrus* spp. were mainly provided by the experts invited to the EKE. The list of all the evidences and the respective references are available for each crop in Appendix E.

2.1.6.2. Scenario assumptions and questions for EKEs on olive, almond, grapevine and *Citrus* spp.

The EKEs on olive, almond, grapevine and *Citrus* spp., were conducted on the basis of a set of general scenario assumptions that were the same for all the crops. In addition, a set of specific scenario assumptions for each crop were developed during the EKE. On the basis of the scenario assumptions, specific questions to be elicited were developed. The full set of scenario assumptions and the questions can be found in Appendix E.

2.1.7. Risk reduction options

Risk reduction options were assessed through a literature review updating the information already available in the previous EFSA Scientific Opinion on *X. fastidiosa* (EFSA PLH Panel, 2015a) and in the more recent EFSA *X. fastidiosa* Pest Categorisation (EFSA PLH Panel, 2018b). Therefore, the review was focused on the most recent information since 2015 and on research activities that are ongoing in EU.

3. Assessment

3.1. Establishment

3.1.1. Assessment of establishment

3.1.1.1. Köppen–Geiger climate zones for *X. fastidiosa*

Xylella fastidiosa is known to occur over large areas in different climatic zones, in tropical countries and subtropical areas such as Brazil, Costa Rica and southern California and in more temperate or even continental climate regions such as British Columbia, southern Ontario and Saskatchewan in Canada, the north-eastern regions of the USA and Argentina (EFSA PLH Panel, 2015a). In the EU, it is reported in southern Apulia in Italy, on the island of Corsica and in the Provence-Alpes-Côte d'Azur region in France, as well as in the province of Madrid, the province of Alicante and the Balearic Islands in Spain (EFSA PLH Panel, 2018b). Recently, it was reported also in the Argentario, Tuscany, Italy and in the district of Porto in Portugal.

To determine the climate zones in which *X. fastidiosa* is known to occur (as a species as a whole), the distribution records of *X. fastidiosa* were intersected with Köppen–Geiger climate zones (n = 30)

(Beck et al., 2018) at the spatial resolution of 5 arc-min for the period 1980–2016 derived from an ensemble of four high-resolution, topographically corrected climatic maps (Beck et al., 2018).

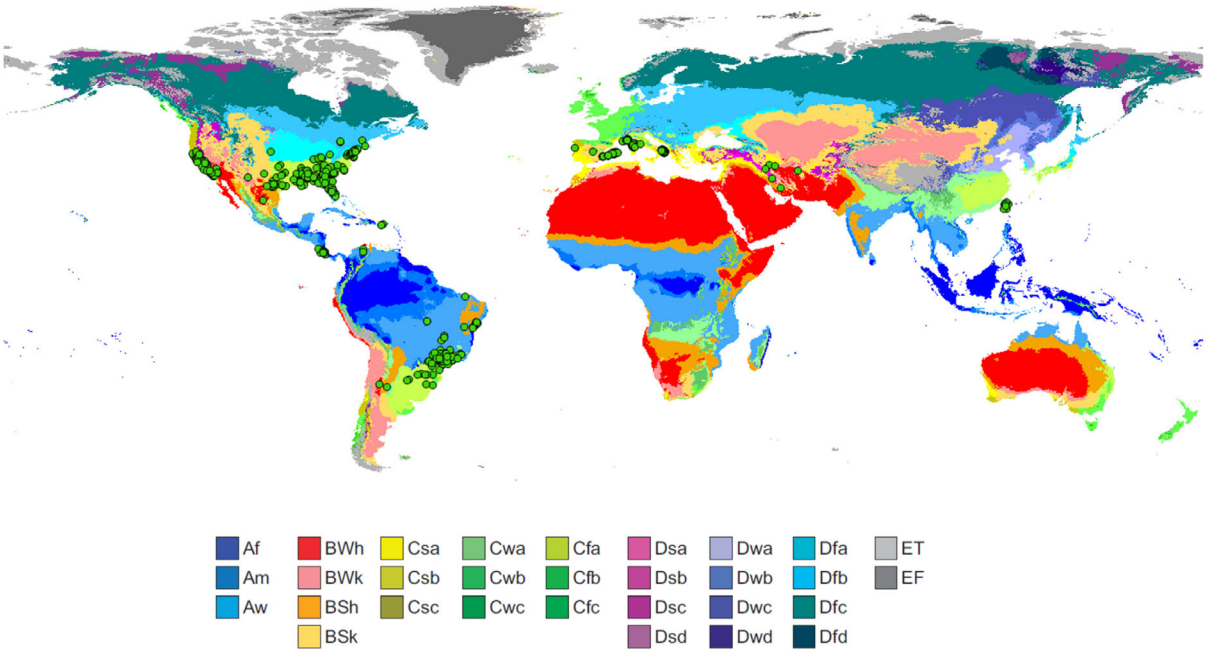

Figure 8: Köppen–Geiger climate type map from Beck et al. (2018). Green points represent locations where *X. fastidiosa* was reported in open field conditions (EFSA, 2018a)

X. fastidiosa was reported over large areas in different climatic zones characterised by different Köppen–Geiger climate types (Peel et al., 2007) (Figure 8) including four of the main climate types: tropical (A), arid (B), temperate (C) and cold (D). Of these, the dominant climate type by number of localities with the presence of *X. fastidiosa* is temperate, followed by tropical, arid and cold, respectively (Figure 8). The prevalent climate subgroups in which *X. fastidiosa* have been recorded are: Csa (temperate with dry-hot summer), Cfa (temperate without dry season and hot summer) and Aw (tropical, savannah). At lower frequency, other subgroups with *X. fastidiosa* presence include BSk (arid, steppe, cold), Cwa (temperate with dry winter and hot summer) and BWh (arid, desert, hot) (Figure 8). In the EU MS, large areas of the southern countries are characterised by BSk, Csa, Csb and Cfa climate types, while Cfb and Dfb (cold, without dry season and warm summer) are prevalent in central Europe (Figure 9). Therefore, most of the climatic types occurring in the EU are suitable for the establishment of *X. fastidiosa*.

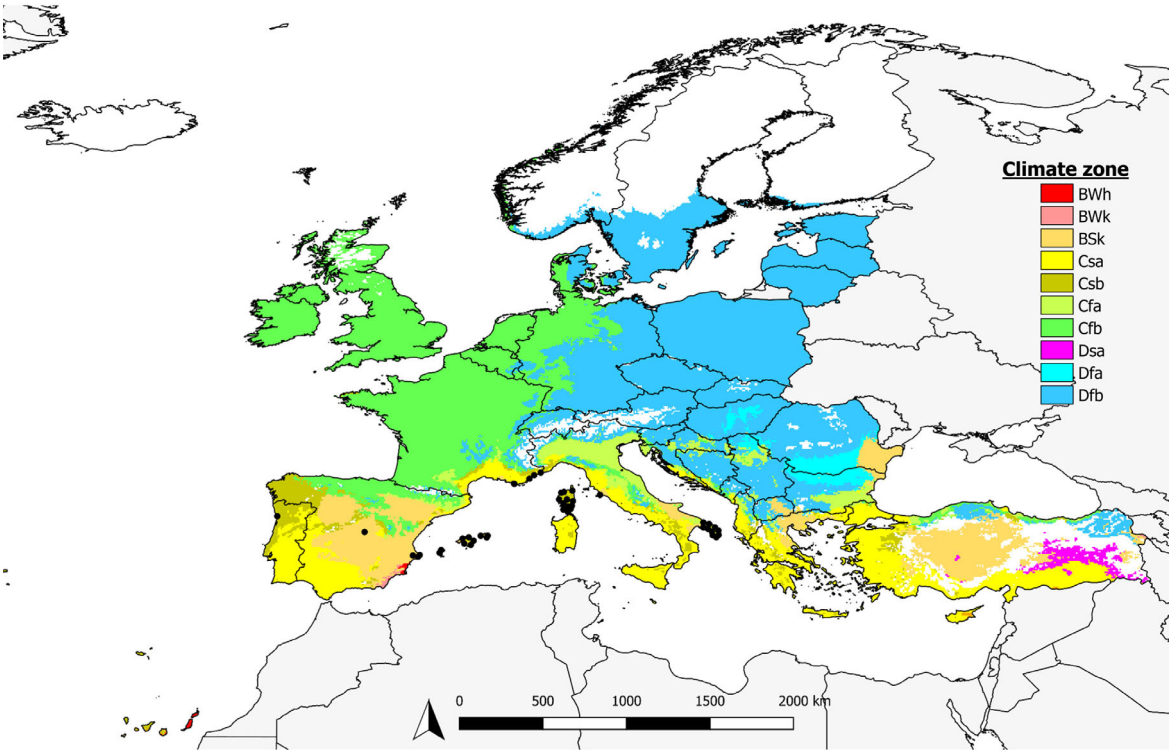

Figure 9: Köppen–Geiger climate type map from Beck et al. (2018). Black dots represent locations where *X. fastidiosa* was reported in the EU in open field conditions. Coloured areas are areas corresponding to Köppen–Geiger climate zones of locations worldwide where *X. fastidiosa* was reported; white areas are climate zones where at the time of writing this Opinion *X. fastidiosa* had not been reported (EFSA, 2018a)

3.1.1.2. SDM ensemble modelling for *X. fastidiosa* and subspecies

SDM ensemble modelling for X. fastidiosa

Overall 800 models were generated for *X. fastidiosa* using SDM ensemble modelling. The performance of the models was high although varied according to the different algorithms (Table 7). For the 10 different models used, AUC ranged from 0.88 to 0.98 (average 0.93 ± 0.039), the sensitivity ranged from 0.78 to 0.94 (average 0.88 ± 0.067), the specificity ranged from 0.71 to 0.94 (average 0.87 ± 0.085), the TSS from 0.62 to 0.89 (average 0.75 ± 0.085) and the Cohen's kappa from 0.34 to 0.74 (average 0.55 ± 0.147).

Table 7: Summary of performance statistics for SDMs for *X. fastidiosa*

Modelling methods[(a)]	AUC	Sensitivity	Specificity	TSS	Kappa
domain	0.87 ± 0.013	0.90 ± 0.045	0.75 ± 0.051	0.65 ± 0.025	0.34 ± 0.045
bioclim	0.92 ± 0.012	0.89 ± 0.045	0.83 ± 0.046	0.71 ± 0.028	0.44 ± 0.060
BRT	0.88 ± 0.013	0.91 ± 0.063	0.71 ± 0.056	0.62 ± 0.031	0.30 ± 0.057
CART	0.90 ± 0.026	0.78 ± 0.053	0.94 ± 0.022	0.72 ± 0.050	0.64 ± 0.064
GAM	0.96 ± 0.007	0.92 ± 0.027	0.90 ± 0.027	0.82 ± 0.024	0.60 ± 0.057
MARS	0.95 ± 0.009	0.88 ± 0.034	0.89 ± 0.031	0.77 ± 0.032	0.56 ± 0.064
MaxEnt	0.96 ± 0.008	0.90 ± 0.028	0.91 ± 0.023	0.81 ± 0.026	0.62 ± 0.053
RF	0.98 ± 0.006	0.94 ± 0.021	0.94 ± 0.020	0.89 ± 0.023	0.74 ± 0.060
RPART	0.90 ± 0.024	0.78 ± 0.051	0.94 ± 0.021	0.72 ± 0.050	0.64 ± 0.059
SVM	0.94 ± 0.015	0.90 ± 0.034	0.91 ± 0.023	0.81 ± 0.032	0.61 ± 0.054

SDM: species distribution model; AUC: area under the curve; TSS: True Skill Statistics.
(a): Modelling methods: bioclim, boosted and regression trees (BRT), classification and regression trees (CART), domain, generalised additive models (GAM), multivariate adaptive regression splines (MARS), maximum entropy (MaxEnt), random forest (RF), recursive partitioning and regression trees (RPART) and support vector machines (SVM).

In particular, the model sensitivity (an essential measure in models based on presence-only data) reached a mean value of 0.88 – indicating a mean false negative proportion (i.e. locations in which *X. fastidiosa* is known to occur but the model predicts these locations as unsuitable for the species) of 12%. Among the models, RF, MaxEnt and GAM showed the best performances, while domain, BRT and CART were those with the lowest values for the statistics used. However, as a TSS > 0.7 criteria was used to include a given model in building the ensemble, most of these models were not included in the consensus model. Thus, our results allow projections of observed patterns into other areas and minimises overfitting of data (Araujo and Guisan, 2006). In general, machine-learning methods (i.e. RF and MaxEnt) showed higher performance.

The map with the continuous suitability scores for the *X. fastidiosa* in the EU territory drawn from the consensus model is presented in Figure 10 with areas classed as climatically suitable for *X. fastidiosa* mainly located in the southern regions in Portugal, Spain, France, Italy, Greece and Cyprus (Figure 10).

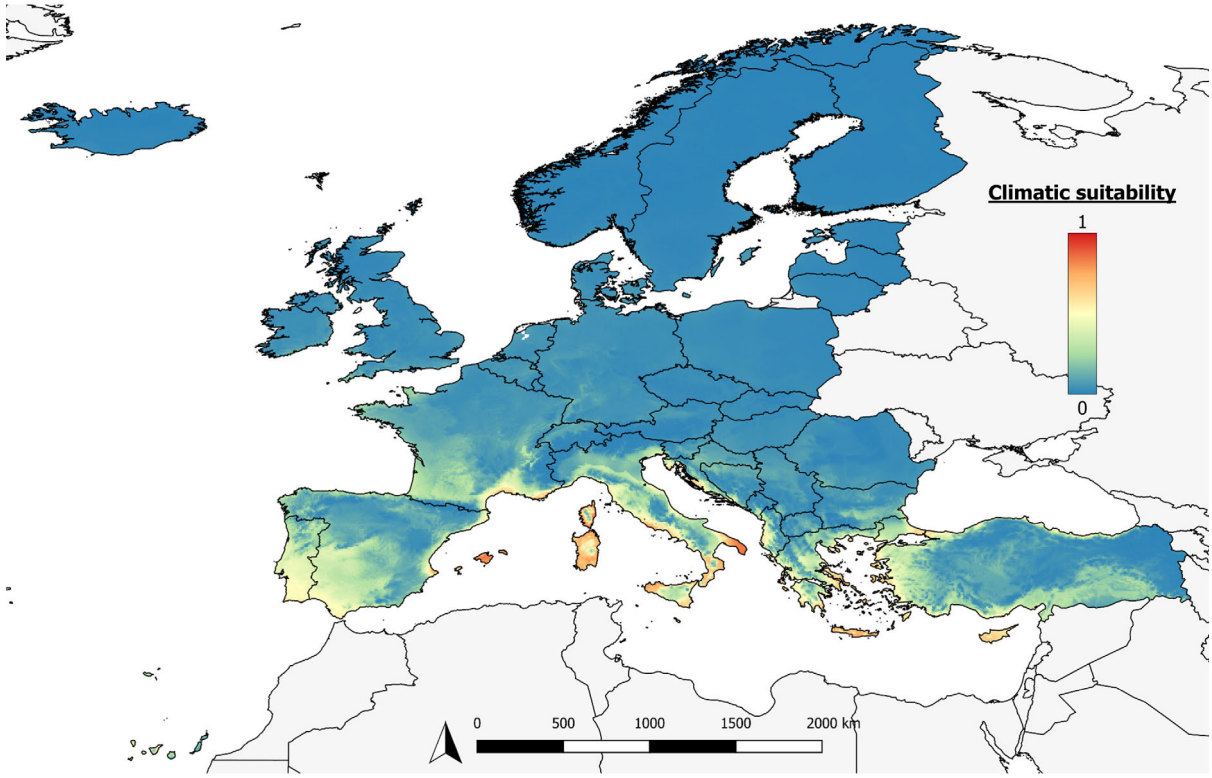

Figure 10: Estimated climatic suitability map for *X. fastidiosa* according to the SDM ensemble model

SDM ensemble modelling for X. fastidiosa *subspecies*

At the time of writing this Opinion, there were four accepted subspecies of *X. fastidiosa*: *fastidiosa*, *pauca*, *multiplex* and *sandyi*, although only two, subsp. *fastidiosa* and *multiplex*, were considered valid names by the International Society of Plant Pathology Committee on the Taxonomy of Plant Pathogenic Bacteria (ISPP-CTPPB) (Bull et al., 2012).

For the three considered subspecies (*fastidiosa*, *multiplex* and *pauca*), the SDM models showed high levels of performance, with AUC, sensitivity and specificity being higher than 0.90. While TSS and Cohen's kappa was higher than 0.83 and 0.63, respectively (Table 8).

Table 8: Summary of performance statistics for SDMs for *X. fastidiosa*

***X. fastidiosa* subspecies**	**AUC**	**Sensitivity**	**Specificity**	**TSS**	**Kappa**
fastidiosa	0.93 ± 0.046	0.93 ± 0.079	0.90 ± 0.066	0.83 ± 0.082	0.63 ± 0.152
multiplex	0.95 ± 0.036	0.93 ± 0.070	0.93 ± 0.044	0.86 ± 0.070	0.69 ± 0.110
pauca	0.94 ± 0.041	0.92 ± 0.071	0.94 ± 0.050	0.86 ± 0.071	0.72 ± 0.132

SDM: species distribution model; AUC: area under the curve; TSS: True Skill Statistics.

SDM ensemble modelling for X. fastidiosa *subsp.* fastidiosa

X. fastidiosa subsp. *fastidiosa* has its origins in Central America (Schuenzel et al., 2005; Nunney et al., 2010). Major hosts of this subspecies include grapevine, almond and alfalfa (EFSA PLH Panel, 2018b). *X. fastidiosa* subsp. *fastidiosa* is currently present in Central America (Costa Rica and Mexico), Taiwan, and California and southern USA (California, District of Columbia, Florida, Georgia, Louisiana, Maryland, North Carolina and Texas). In the EU it is present only in Spain in Mallorca Island, infecting *Vitis* spp., *Prunus avium* and *Prunus dulcis* (EFSA PLH Panel, 2018b; EPPO, 2019).

The map with the continuous suitability scores for the *X. fastidiosa* subsp. *fastidiosa* in the EU territory drawn from the consensus model is presented in Figure 11. The model predicts areas with suitable climatic conditions for *X. fastidiosa* subsp. *fastidiosa* in the southern regions of Portugal and Spain and the Balearic Islands, Cyprus and Crete, with decreasing suitability values along the coastal Mediterranean regions and southern France and Corsica, in that order.

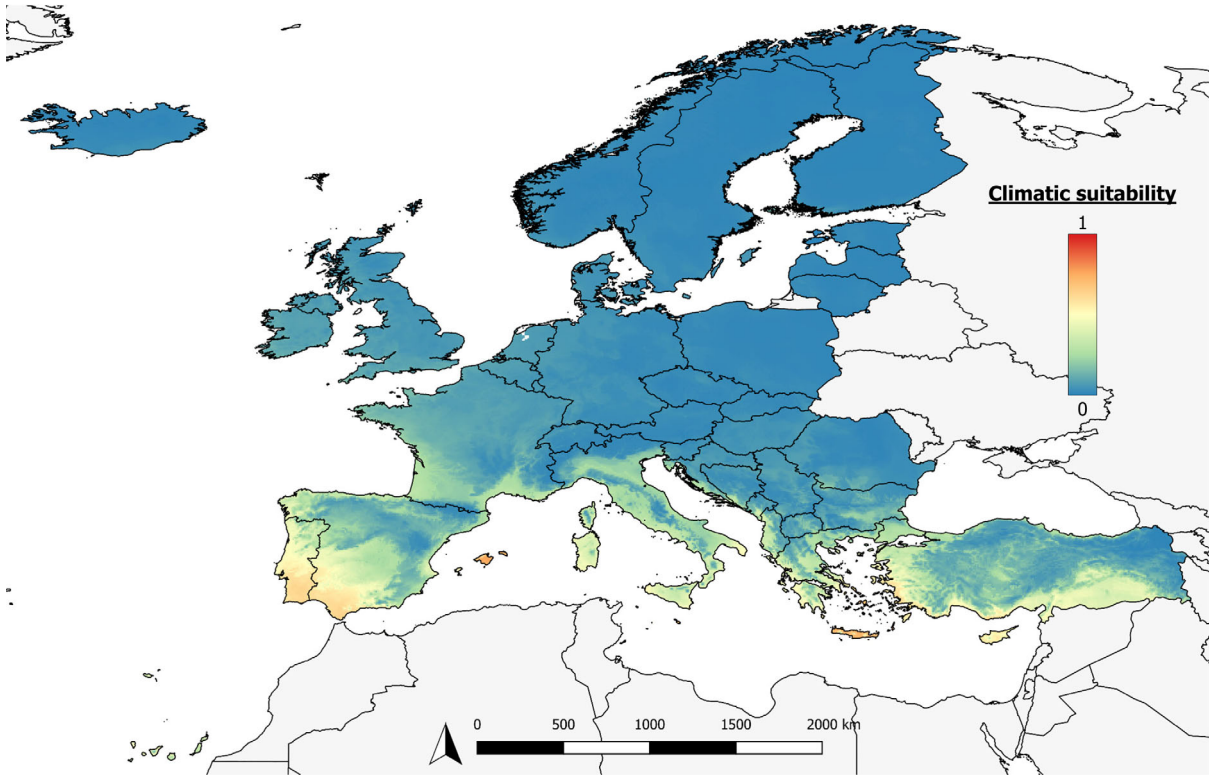

Figure 11: Estimated climatic suitability map for *X. fastidiosa* subsp. *fastidiosa* according to a SDM ensemble model

SDM ensemble modelling for X. fastidiosa *subsp.* multiplex

X. fastidiosa subsp. *multiplex* has its origins in North America and is mainly distributed in South America (Argentina, south-east Brazil and Paraguay) and in California, and southern and eastern USA (EPPO, 2019). In the EU it is the subspecies with the widest geographic distribution as has been recorded in Corsica and the PACA region in France, Tuscany in Italy, near Porto in Portugal and in Alicante and the Balearic Islands in Spain (EFSA PLH Panel, 2018b; EPPO, 2019).

The map with the continuous suitability scores for the *X. fastidiosa* subsp. *multiplex* in the EU territory drawn from the consensus model is presented in Figure 12. This subspecies had the highest extent compared with that predicted for subsp. *fastidiosa* and *pauca*. With the exception of central Europe this subspecies could find suitable climatic conditions in the EU territory. The highest suitability is found in along the coastal line of the Mediterranean, including Corsica, Sardinia and Sicily. Suitability decreases in the central and southern regions in the Iberian Peninsula and Italy, and southern Greece and lower values are present in France, Belgium, the Netherlands, and along the coastal regions in the UK and Ireland.

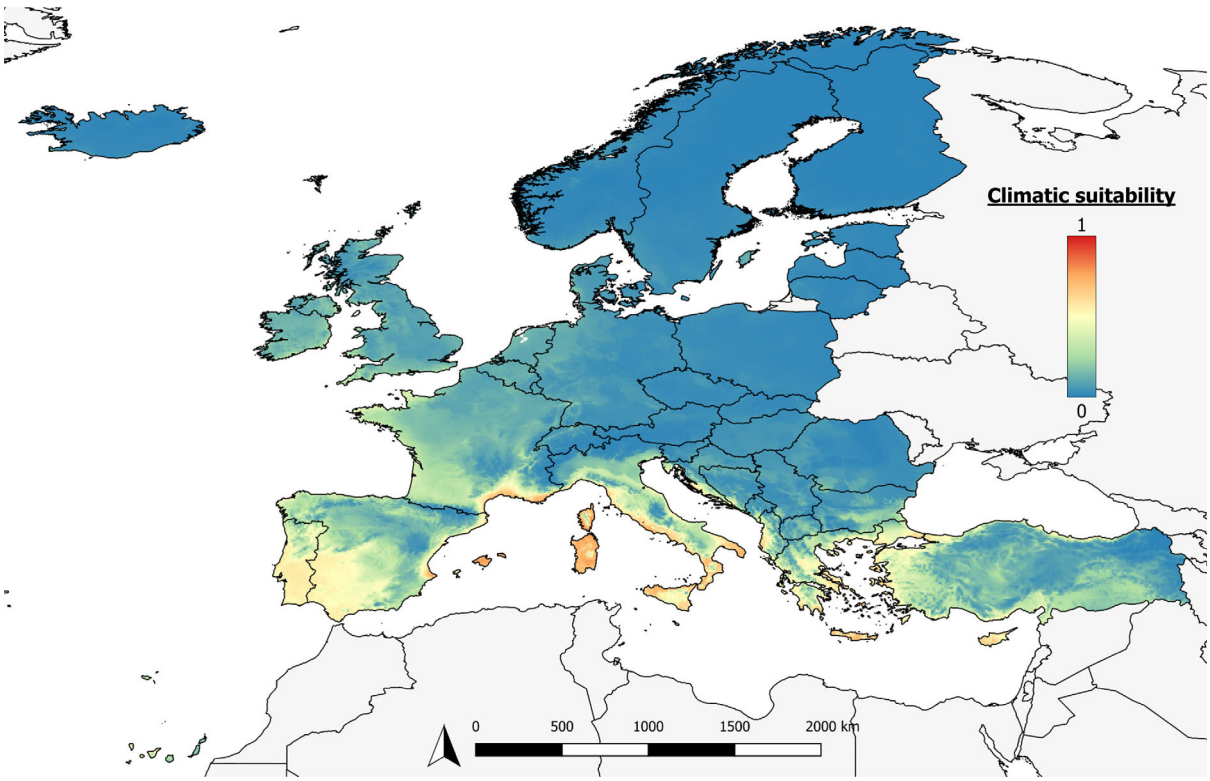

Figure 12: Estimated climatic suitability map for *X. fastidiosa* subsp. *multiplex* according to a SDM ensemble model

SDM ensemble modelling for X. fastidiosa *subsp.* pauca

X. fastidiosa subsp. *pauca* has its origins in South America (Sicard et al., 2018). Major hosts for this subspecies includes: *Citrus* spp., coffee and olives (EFSA PLH Panel, 2018b). *X. fastidiosa* subsp. *pauca* is currently present in Argentina, Brazil, Costa Rica and Ecuador (EPPO, 2019). In the EU, it has been found in Italy, France and Spain (EFSA PLH Panel, 2018b; EPPO, 2019).

The map with the continuous suitability scores for the *X. fastidiosa* subsp. *pauca* in the EU territory drawn from the consensus model is presented in Figure 13. The model predicted the lowest extent of suitability compared with the two other subspecies that would establish in well delimited areas in southern Italy, and along coastal areas in the Mediterranean, as well as the Atlantic coast of Spain, Portugal and France.

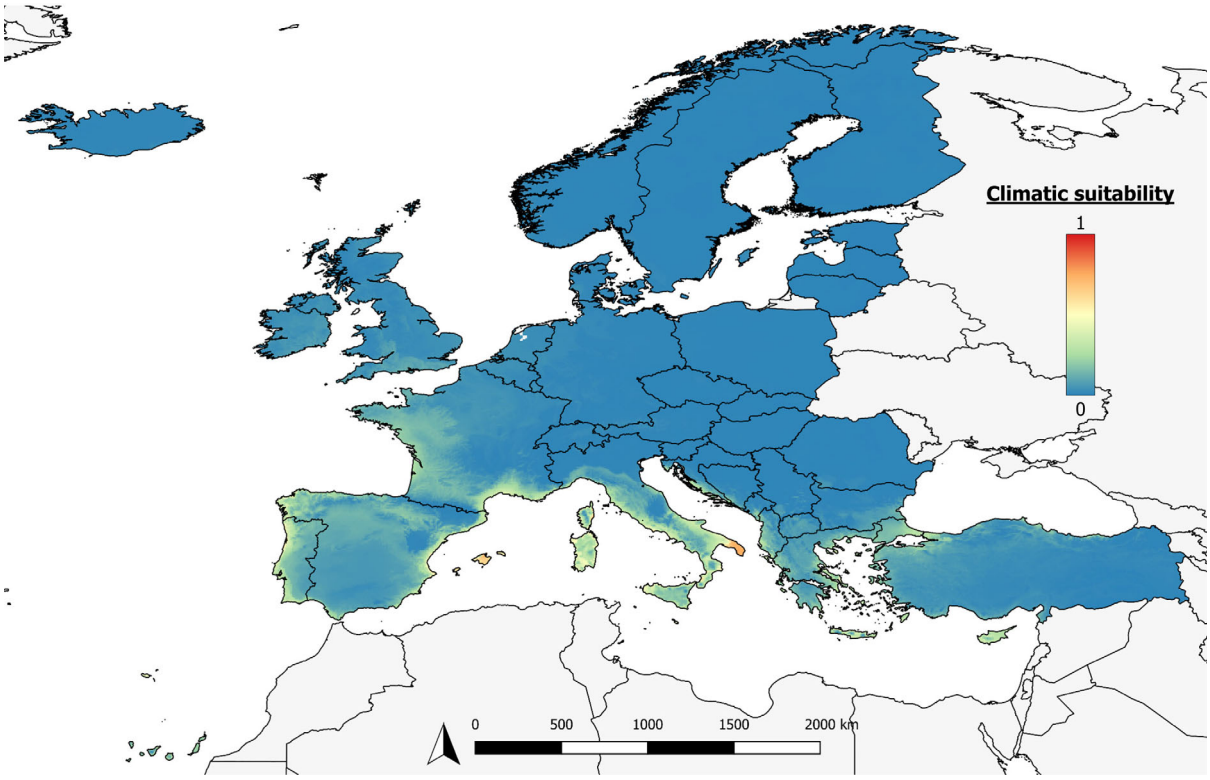

Figure 13: Estimated climatic suitability map for *X. fastidiosa* subsp. *pauca* according to a SDM ensemble model

3.1.1.3. Environmental factors related to establishment of *X. fastidiosa* and subspecies

Environmental factors for X. fastidiosa

Climate suitability was estimated based on bioclimatic variables representing annual trends (e.g. mean annual temperature, annual precipitation) seasonality (e.g. annual range in temperature and precipitation) and extreme or limiting environmental factors (e.g. temperature of the coldest and warmest month, and precipitation of the wet and dry quarters). Ten non-correlated bioclimatic variables were selected based on VIF for model fitting. These variables included: isothermality (bio3); minimum temperature of coldest month (bio6); mean temperature of wettest quarter (bio8); mean temperature of driest quarter (bio9), mean temperature of warmest quarter (bio10); precipitation in wettest month (bio13); precipitation in driest month (bio14); precipitation seasonality (bio15); precipitation in warmest quarter (bio18) and precipitation in coldest quarter (bio19). Variable importance values for each bioclimatic predictor showed similar values for all models (Table 9). The contribution of these bioclimatic variables assessed by their variance importance based on AUC, indicated that the potential geographic distribution of *X. fastidiosa* is mostly influenced by five bioclimatic variables: mean temperature of driest quarter (bio9), minimum temperature of coldest month (bio6), mean temperature of warmest quarter (bio10) and precipitation in coldest quarter (bio19). Thus, suitable areas in the EU for *X. fastidiosa* establishment are mainly characterised by warm temperatures during the summer-dry period (high values for bio9 and bio10), mild winter temperatures (high values for bio6) and regions with well-defined rainy season (bio15). Maps representing these bioclimatic variables for the EU are shown in Appendix C, Figure C.1. In this context, bio6 and bio19, highlight the importance of minimum temperature on the potential establishment of *X. fastidiosa* that generally occur in geographical areas with mild winter climates (Hopkins, 1976; Purcell, 1980). Feil and Purcell (2001) determined the minimum threshold temperature for growth of *X. fastidiosa* in plants to be between 12 and 18°C. On the other hand, bio9 and bio10 could be related with the ability of the bacterium to support water stress or warm conditions, respectively, in agreement with results of Martinetti and Soubeyrand (2019).

Table 9: Variable importance of bioclimatic predictors included in model the SDM for *Xylella fastidiosa*

Modelling methods[(a)]	bio6	bio9	bio10	bio15	bio19
domain	0.27 ± 0.023	0.32 ± 0.030	0.17 ± 0.026	0.17 ± 0.021	0.01 ± 0.001
bioclim	0.27 ± 0.024	0.32 ± 0.034	0.19 ± 0.048	0.16 ± 0.022	0.02 ± 0.001
BRT	0.27 ± 0.038	0.33 ± 0.041	0.17 ± 0.025	0.17 ± 0.018	0.02 ± 0.001
CART	0.26 ± 0.032	0.32 ± 0.020	0.18 ± 0.040	0.16 ± 0.022	0.02 ± 0.001
GAM	0.26 ± 0.019	0.31 ± 0.028	0.17 ± 0.044	0.16 ± 0.018	0.02 ± 0.001
MARS	0.38 ± 0.026	0.37 ± 0.024	0.33 ± 0.024	0.14 ± 0.024	0.18 ± 0.018
MaxEnt	0.38 ± 0.025	0.35 ± 0.026	0.32 ± 0.031	0.14 ± 0.023	0.20 ± 0.034
RF	0.37 ± 0.029	0.35 ± 0.033	0.32 ± 0.024	0.13 ± 0.015	0.20 ± 0.042
RPART	0.37 ± 0.026	0.35 ± 0.025	0.33 ± 0.030	0.13 ± 0.011	0.19 ± 0.036
SVM	0.35 ± 0.024	0.33 ± 0.026	0.31 ± 0.028	0.13 ± 0.022	0.20 ± 0.031
Mean	0.32 ± 0.060	0.33 ± 0.033	0.25 ± 0.080	0.15 ± 0.024	0.11 ± 0.092

SDM: species distribution model.
(a): Modelling methods: bioclim, boosted and regression trees (BRT), classification and regression trees (CART), domain, generalised additive models (GAM), multivariate adaptive regression splines (MARS), maximum entropy (MaxEnt), random forest (RF), recursive partitioning and regression trees (RPART) and support vector machines (SVM).

Environmental factors for subspecies

For the subspecies models, the non-correlated bioclimatic variables that were selected based on VIF for model fitting are presented in Table 10. Although a distinct set of bioclimatic variables was selected for each subspecies, mean temperature of driest quarter (bio9), precipitation seasonality (bio15) and precipitation in coldest quarter (bio19) were selected irrespective of the subspecies. Models for subspecies *fastidiosa* and *multiplex* shared three predictors: isothermality (bio3), mean temperature of wettest quarter (bio8) and precipitation in driest month (bio14). Similarly, models for subspecies *fastidiosa* and *pauca* included maximum temperature of warmest month (bio5) and precipitation in warmest quarter (bio18) as predictors. Finally, annual mean temperature (bio1) for subspecies *fastidiosa*; mean temperature of warmest quarter (bio10), mean temperature of coldest quarter (bio11) and precipitation of wettest month (bio13) for subspecies *multiplex*; and minimum temperature of coldest month (bio6) and annual precipitation (bio12) for subspecies *pauca*. This indicates that the geographic distribution of these three subspecies is linked to specific climatic conditions. In fact, models for subspecies *fastidiosa* were mainly linked to prevalent mean temperature and water stress (bio1 and bio9) being particularly suitable areas with warm temperatures all over the year and particularly during the dry season; subspecies *multiplex* is mainly linked to water and cold stress (bio11 and bio9) and found more suitable areas with warm temperatures during the dry season but also particularly sensible to cold temperatures in winter; and subspecies *pauca* is linked to extreme temperatures and water stress (bio5, bio6 and bio9) being particularly suitable in warm-hot climates with mild winters. Maps representing bioclimatic variables importance are shown in Appendix C, Figure C.1.

Table 10: Variable importance of bioclimatic predictors included in model the SDM for *Xylella fastidiosa* subspecies

Bioclimatic variable	*X.f.* subsp. *fastidiosa*	*X.f.* subsp. *multiplex*	*X.f.* subsp. *pauca*
bio1	0.36 ± 0.115	---	---
bio3	0.02 ± 0.022	0.14 ± 0.045	---
bio5	0.10 ± 0.062	---	0.39 ± 0.098
bio6	---	---	0.49 ± 0.072
bio8	0.08 ± 0.052	0.10 ± 0.053	---
bio9	0.33 ± 0.108	0.39 ± 0.064	0.48 ± 0.071
bio10	---	0.22 ± 0.086	---
bio11	---	0.51 ± 0.072	---
bio12	---	---	0.09 ± 0.088
bio13	---	0.12 ± 0.050	---

Bioclimatic variable	*X.f.* subsp. *fastidiosa*	*X.f.* subsp. *multiplex*	*X.f.* subsp. *pauca*
bio14	0.02 ± 0.018	0.04 ± 0.025	---
bio15	0.09 ± 0.049	0.14 ± 0.044	0.25 ± 0.103
bio18	0.05 ± 0.039	---	0.06 ± 0.064
bio19	0.11 ± 0.113	0.19 ± 0.153	0.09 ± 0.071

X.f.: *Xylella fastidiosa*; SDM: species distribution model.

3.1.2. Uncertainties affecting the assessment of potential establishment

A number of caveats should be considered for the analyses performed to estimate potential establishment:

- SDMs correlate the presence data of a species with climatic conditions prevalent in those locations, and then predict suitable climatic areas outside the species native geographic range. However, other factors, particularly host distribution would have also an effect. Unfortunately, no global database is available mapping geographic distribution of potential hosts at the spatial resolution need for the analyses.
- When the model classifies a certain location as suitable, it indicates that climatic conditions prevalent in this location could allow the establishment of *X. fastidiosa*, but it would establish only if a susceptible host to this particular strain of the bacterium is present, vectors are present and no control measures are applied.
- Models are based on current known global distribution of *X. fastidiosa;* however, a key consideration is the limitation of data and potential bias of data towards current outbreak areas; in general, areas associated with colder climates are thought to be underrepresented due to reduced survey effort due to different reasons such as limited impact of the disease or affecting non-economically relevant hosts.
- New or unknown strains of *X. fastidiosa* could have a different reaction to climate.

As an alternative to SDMs, process based mechanistic models could also be used to determine climatic suitability, however these models require detailed information on how the behaviour of the species is related mechanistically with environmental factors that are not currently available.

3.1.3. Conclusions on the potential establishment

X. fastidiosa is known to occur over large area in different climatic zones across tropical, temperate and continental regions (EFSA PLH Panel, 2018b). The Köppen–Geiger climate matching revealed most parts of the EU to be suitable for potential establishment of *X. fastidiosa*, excluding only some higher altitude and northern regions (Figure 9). Species distribution ensemble modelling revealed areas in southern Europe to be at more risk (Figure 10). Differences in areas of potential establishment were evident between *Xylella* subspecies, particularly *X. fastidiosa* subsp. *multiplex* which demonstrated areas of potential establishment further north in Europe compared to other subspecies. The *multiplex* subspecies is also more common on forest species and the estimated area of potential establishment may be influenced by positive records from the northern America. The area of potential establishment of the *pauca* subspecies on the other hand was restricted largely to coastal regions in southern Europe. This may be significantly influenced by data limitations, since most identifications of this subspecies are within a small number of outbreak areas within the EU. An effort was made to estimate distributions below species level. At the time of writing this Opinion, the current distribution in the EU is heterogeneous in terms of subspecies and host affected in the different outbreaks. This could be related at least in part to specific climatic conditions and/or host distribution in the different territories. Therefore, models at subspecies level could help to estimate how the different genotypes of the bacterium already present in the EU could establish outside their current known distribution. However, model analyses below species level are restricted by increased data limitations since many records of *X. fastidiosa*, particularly older records, do not list subspecies or ST types. Further information from model projections and field data, balanced evenly across different regions, is needed to reduce uncertainty in the assessment of the potential establishment.

The models developed could be used in surveillance programmes for *X. fastidiosa* in the EU territory. Suitability maps can be particularly useful for targeted surveys in which samples are selected from areas where *X. fastidiosa* is most likely to establish, by prioritising areas to be inspected based on

their climatic suitability (FAO, 2018). EFSA is currently mandated by the European Commission to facilitate MS in the planning and execution of survey activities, including appropriate design of risk-based surveys (EFSA, 2018c). As part of this request, EFSA is producing a Pest Survey Card for *X. fastidiosa* as well as detailed survey guidelines, of which climate suitability as well as host plants distribution and vectors presence and abundance are among the factors that could be considered.

3.2. Asymptomatic period

3.2.1. Assessment

Figures from 14 to 17 show the non-parametric and parametric survival functions estimated from the data for each subtype–host combination. The non-parametric Kaplan–Meier curves are shown as stepped solid curves, and the parametric exponential model as a smoothed dotted curve. Estimates from the parametric model are shown in Table 11.

As can be seen in Figures from 14 to 16 and in Table 12, the parametric and non-parametric methods gave qualitatively similar results in most cases, with *X. fastidiosa* subsp. *fastidiosa*, *X. fastidiosa* subsp. *multiplex*, *X. fastidiosa* subsp. *pauca* and *X. fastidiosa* subsp. *morus* showing a relatively rapid development of symptoms in grapes, almonds, ornamental and mulberry, respectively. *X. fastidiosa* subsp. *multiplex* had a longer asymptomatic period in shade trees, and *X. fastidiosa* subsp. *pauca* had an even longer asymptomatic period in both oranges and olives. These qualitative conclusions correlate with what we already know about these different pathosystems. In the case of *X. fastidiosa* subsp. *morus* infection of blueberry, insufficient number of plants developed symptoms over the course of the experiments to be able to determine a median survival time using the Kaplan–Meier estimator (Figure 17), and therefore care should be taken when interpreting these results. The analysis suggests that grapevine infected with *X. fastidiosa* subsp. *pauca* developed symptoms relatively rapidly (Table 12, Figure 16). These results derive from a single report describing the artificial inoculation of strains of the subsp. *pauca* associated with the citrus disease CVC into plants of different grape cultivars (Li et al., 2002). There have been no reports of infection of grapevines with strains of subsp. *pauca* under natural conditions. Experimental inoculation of three grapevine cultivars with the strain of the *X. fastidiosa* subsp. *pauca* associated with olive quick decline syndrome (which is genetically distant from the CVC strain) found no evidence of colonisation, as reported in the EFSA Scientific Opinion on '*Vitis* sp. response to *Xylella fastidiosa* strain CoDiRO' adopted in November 2015 (EFSA PLH Panel, 2015b).

Table 11: Parameter estimates obtained from the parametric model of the survival function, along with the predicted mean time until symptom development derived from this model. The sigma parameter is the rate parameter of the exponential distribution describing symptom development over time, and the lag is the duration of the period before symptoms start to appear

Subspecies	Host	Sigma (per day)	Lag (days)	Mean time until symptoms (days)
X. fastidiosa subsp. *fastidiosa*	Almond	0.004	0	224
	Grape	0.015	0	66
X. fastidiosa subsp. *multiplex*	Shade Tree	0.003	0	314
	Almond	0.012	0	81
X. fastidiosa subsp. *pauca*	Orange	0.003	0	361
	Grape	0.011	0	93
	Olive	0.002	0	452
	Ornamental	0.023	5	49
X. fastidiosa subsp. *morus*	Mulberry	0.006	2	166
	Blueberry	0.001	0	981

As mentioned above, subspecies–host combinations that were not covered by more than a single quantitative study (Table 2) were not taken into account in the survival analyses. This represents a total of four case studies of *X. fastidiosa* subsp. *multiplex* on grape and plum, and *X. fastidiosa* subsp. *sandyi* on grape and almond (Table 2), which will be qualitatively described here. (i) Plums infected

with *X. fastidiosa* subsp. *multiplex* have been found to remain asymptomatic over a 4-month period (Raju et al., 1982), but little more is known on the timing of symptom development. (ii) Infection of grapes with *X. fastidiosa* subsp. *multiplex* strains from almond resulted in low bacterial titres and few symptoms. Despite this, asymptomatic overwintering was also reported, resulting in an asymptomatic period of more than 1 year (Almeida and Purcell, 2003) (iii) *X. fastidiosa* subsp. *sandyi* failed to establish in grapes, as determined by molecular testing and culture, suggesting that grapes are not natural hosts of this strain of *X. fastidiosa* subsp. *sandyi*. (iv) Almonds infected with *X. fastidiosa* subsp. *sandyi* had low bacterial titres and remained asymptomatic over a 4-month period (Almeida and Purcell, 2003), suggesting that survival is limited in this host, similar to *X. fastidiosa* subsp. *multiplex* in grape. However, overwintering of *X. fastidiosa* subsp. *sandyi* in almond has not been reported.

Table 12: Percentile estimates of the time until symptoms appearance from the parametric (maximum likelihood) and non-parametric (Kaplan-Meier) models

Subspecies	Host	Median time from parametric method (days)	Median time from non-parametric method (days)	Time until 95% chance of symptoms from parametric method (days)
X. fastidiosa subsp. *fastidiosa*	Almond	155	57	671
	Grape	46	29	197
X. fastidiosa subsp. *multiplex*	Shade Tree	218	308	941
	Almond	56	57	242
X. fastidiosa subsp. *pauca*	Orange	250	169	1,080
	Grape	64	29	278
	Olive	313	141	1,354
	Ornamental	35	29	138
X. fastidiosa subsp. *morus*	Mulberry	115	126	493
	Blueberry	680	N/A	2,939

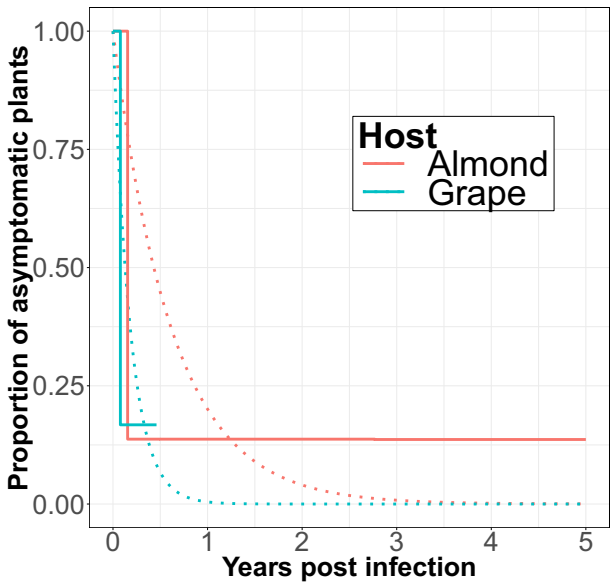

Figure 14: Survival curves for *X. fastidiosa* subsp. *fastidiosa* in *Prunus dulcis* ('almond') and *Vitis vinifera* or *Vitis rotundifolia* ('grape'). Solid lines show the Kaplan–Meier curve and dotted lines show the predictions from the parametric model (assuming a fixed rate of symptom development following a lag period)

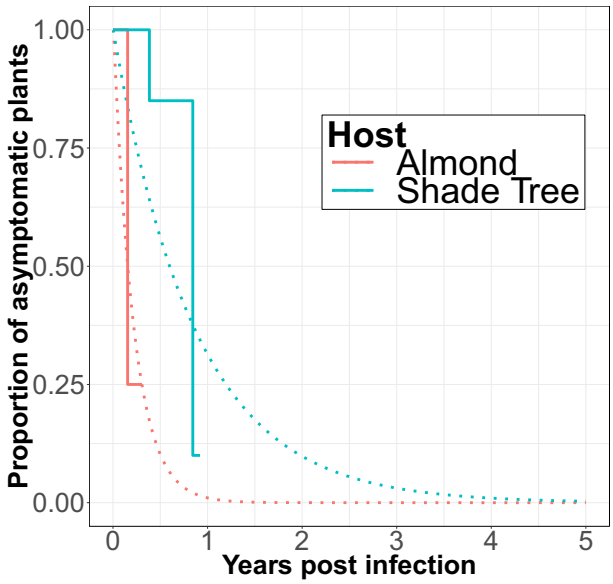

Figure 15: Survival curves for *X. fastidiosa* subsp. *multiplex* in *Prunus dulcis* ('almond') and *Ulmus americana* or *Platanus occidentalis* ('tree'). Solid lines show the Kaplan–Meier curve and dotted lines show the predictions from the parametric model (assuming a fixed rate of symptom development following a lag period)

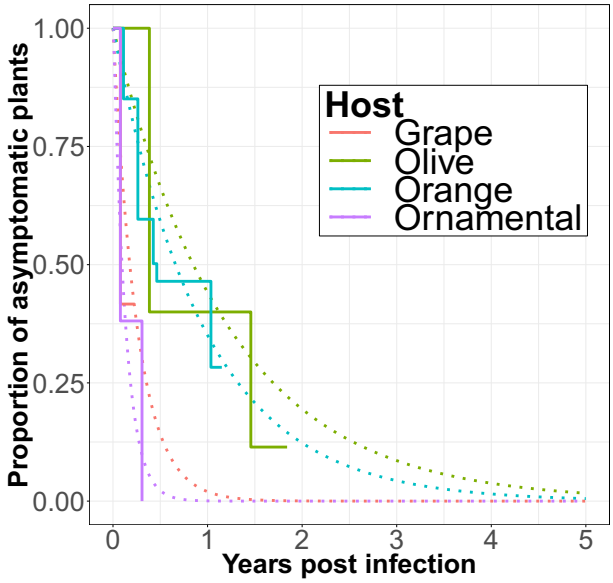

Figure 16: Survival curves for *X. fastidiosa* subsp. *pauca* in *Vitis vinifera* or *Vitis rotundifolia* ('grape'), *Olea europaea* ('olive'), *Citrus sinensis* ('sweet orange') and *Catharanthus roseus* ('ornamental'). Solid lines show the Kaplan–Meier curve and dotted lines show the predictions from the parametric model (assuming a fixed rate of symptom development following a lag period)

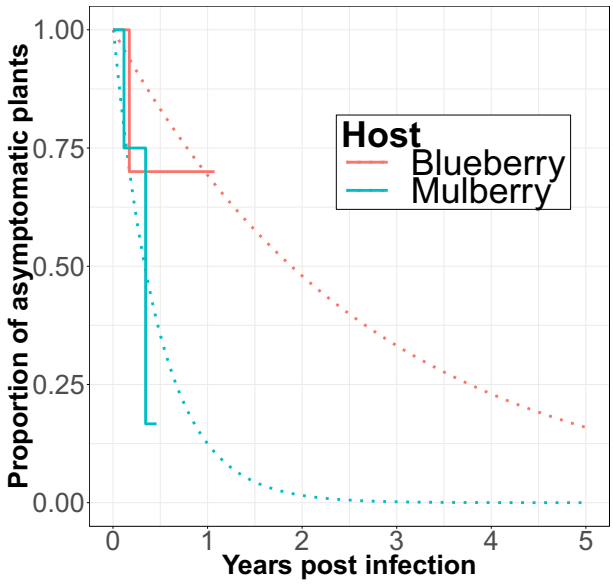

Figure 17: Survival curves for *X. fastidiosa* subsp. *morus* in *Vaccinium corymbosum* ('blueberry') and *Morus alba* and *Morus rubra* ('mulberry'). Solid lines show the Kaplan–Meier curve and dotted lines show the predictions from the parametric model (assuming a fixed rate of symptom development following a lag period)

3.2.2. Uncertainties

A number of caveats should be considered for both survival analysis approaches used in the current analysis. Being a non-parametric method, the Kaplan–Meier curves are derived completely from the available data, of which only two data points were available for each study. As a result, the 'steps' in the curves can only take place at one of these time points – and, by extension, any percentile of the curve can only exist at one of these time points. Also, the available calculable percentiles are constrained by the numbers of asymptomatic hosts at the end of the studies – with more than 10% of hosts remaining uninfected for most subspecies–host combinations (meaning that percentiles of 90% or more cannot be calculated), and a 50th percentile not being calculable in the case of blueberry infection with *X. fastidiosa* subsp. *morus*. Although these issues are remedied to some degree in the parametric analyses, this is achieved by assuming that symptoms develop at a fixed rate over time. The limitations of this assumption are shown most clearly in the case of *X. fastidiosa* subsp. *fastidiosa* in almond, for which the parametric model predicted a considerably longer median asymptomatic period than the non-parametric method (Figure 14, Table 12). This results from the fact that although most host plants developed symptoms within around 6 months of infection, some host plants failed to develop symptoms after 5 years of study. It is not possible to replicate this pattern of symptom development under the assumption of a constant rate of symptom development, and therefore, the best fitting survival function lies between the initial curve (where symptoms developed rapidly) and the end of the experiment (where some hosts remained asymptomatic). In this particular case, it is likely that those trees that did not show symptoms at the end of the experiment will never develop symptoms (possibly due to differences in susceptibility, as described below), but the analysis was not able to capture cultivar-specific factors. Although factors such as these are undoubtedly important, the limitations of the available data make it unrealistic to capture all of these characteristics in the current study. We note in particular the following factors which may invalidate the underlying assumption that all hosts will ultimately develop symptoms:

- The potential for some hosts to clear infection under certain climatic conditions such as cold temperatures (Purcell, 2013).
- The fact that infection does not always results in disease (Purcell, 2013), for example, in tolerant or resistant cultivars (Martelli, 2016; Luvisi et al., 2017), or in particular environmental conditions (Lopes et al., 2005).
- The fact that inoculation is not always successful even in susceptible plants (Almeida et al., 2001; Prado et al., 2008). Since not all studies considered in the analysis used bacterial

isolation to confirm infection, it is not possible to exclude the possibility that inoculation did not result in establishment and subsequent infection of the host. To counter this limited infection efficiency, two series of inoculations are sometimes made (Lopes et al., 2000, 2003), but this practice is infrequent.

It is also important to note that the estimates are based on studies of young hosts, which may differ from more mature hosts in the timing of symptom expression. Because the exact age of the host was inconsistently recorded, this information was not included as a variable in the model.

3.2.3. Conclusion on the asymptomatic period

The aim of this analysis was to quantify the asymptomatic period of isolates of *X. fastidiosa* currently found in the EU. At the current time, there are insufficient data on isolates present in the EU to be able to quantify this, and data were therefore collated from the literature on previous experimental case studies of different subspecies–host combinations worldwide. Although these case studies were conducted in a range of different environments and controlled conditions, climatic conditions were not explicitly included as a variable in our model since they will be strongly associated with particular combinations of *X. fastidiosa* subspecies and host. However, all studies came from warm regions – generally in the southern states of the USA, Brazil and southern Europe. Studies of infection in almonds, olives and grape were generally conducted in regions with a Mediterranean climate, whereas studies of oranges were generally from humid subtropical climates, and those of shade trees, mulberry and blueberry were generally from humid temperate climates. Studies of infection of ornamental hosts with *X. fastidiosa* subspecies *pauca* were divided between the two climate types.

For each subspecies–host combination considered, the survival function (with the outcome being the appearance of symptoms) was estimated using both non-parametric and parametric methods.

The asymptomatic periods were highly variable (Table 12), reflecting the multiple biological processes involved. Almond infected with *X. fastidiosa* subsp. *multiplex* and orange or olive infected with *X. fastidiosa* subsp. *pauca* remained asymptomatic for the longest durations after infection (up to 5 years post-inoculation). Differences in the length of the asymptomatic period in these hosts has been linked to rootstock type in almonds (Krugner and Ledbetter, 2016) and tolerant and/or resistant sweet orange or olive cultivars (Coletta-Filho et al., 2007; Garcia et al., 2012; Saponari et al., 2018). Ornamentals infected with *X. fastidiosa* subsp. *pauca* and grapevine with *X. fastidiosa* subsp. *fastidiosa* displayed the shortest asymptomatic periods (Table 12). Plants from susceptible cultivars may also remain symptomless while being infected up to 18 months after pinprick inoculation. Discounting these differences, the current analysis supports the following general conclusions regarding the subtypes present in the EU:

- The median time until the development of symptoms of *X. fastidiosa* subsp. *multiplex* infection in almond trees is around 2 months, with a 95% chance of symptoms developing within about 8 months. Infection of shade trees with the same subspecies had a median asymptomatic period of less than 11 months, with a 95% chance of symptom development within about 30 months.
- The median time until symptom development in olive trees infected with *X. fastidiosa* subsp. *pauca* was less than 11 months, with a 95% chance of symptoms developing within 4 years. In *Catharanthus roseus* ('ornamental' in the results), the median time of symptom development was around 1 month, with a 95% chance of symptoms developing within around 5 months.

The rapid development of symptoms of *X. fastidiosa* subsp. *fastidiosa* infection amongst some almond trees, but the lack of symptoms in others after 5 years makes parametric estimation of the duration of the asymptomatic period challenging. Further work should consider the impact of different cultivars and rootstocks on symptom development in this host. In conclusion, the length of the asymptomatic period following infection with *X. fastidiosa* is of considerable importance to the epidemiological dynamics of infection (due to the impact of symptoms on vector preference), and on surveillance and control measures. In particular, long asymptomatic periods make declaration of absence (including those involved in lifting demarcated areas), early detection surveillance and estimation of the incidence of infection more challenging. The current results suggest that the use of visual inspection for detection of infections of sweet orange or olive with strains of *X. fastidiosa* subspecies *pauca*, or shade tree infection with strains of *X. fastidiosa* subspecies *multiplex*, may be problematic due to the duration of the asymptomatic period in these hosts. This is a particular problem

for early detection surveillance and delimiting surveillance, since it may take up to 3–4 years for symptoms to manifest in individual plants. In these cases, alternative methods of detection which are able to identify infection during the asymptomatic period should be considered when planning surveillance. Where there is known variation in disease susceptibility within particular hosts (such as olive, sweet orange and almond, as described above), this should also be taken into consideration during surveillance planning, since visual detection may be appropriate if targeted towards more susceptible varieties or cultivars of the hosts. The length of the asymptomatic period is one consideration in determining an appropriate length of time before lifting a demarcated area. This must be combined with appropriately intensive, statistically based and risk targeted surveys. EFSA is currently mandated to provide survey guidelines to EU MS, for multiple pests, including *X. fastidiosa,* which is ongoing (EFSA et al., 2018c).

As well as the points above, consideration should also be given to factors such as the expected rate of pathogen transmission and the numbers of expected infected hosts, which were not considered in the current analysis. Additionally, further experimental work, including field observations, quantifying the development of symptoms over time for European isolates, and further evaluating differences between host cultivars, would be beneficial in refining and improving these estimates in the future.

3.3. Short-range spread

3.3.1. Assessment of short-range spread

3.3.1.1. Epidemiological dynamics without management

Infected vector pressure

Considering the information on vector population density available in Bosco et al. (2019), the vector carrying capacity in the node was set equal to 2,000 vectors (20 adults/m^2) in the scenario with high vector density and 100 vectors (1 adult/m^2) in the low vector density scenario. To describe the epidemiological dynamics, the model is run for 10 years without control measures. In Figure 18, the change in the infected vectors density with respect to the distance from the first inoculated plants in the outbreak area at different years of the simulation is reported.

In all the scenarios, the density of infected vector population significantly increases only from the 6th year of simulation (y = 6) and continues the growth up for the whole period of simulation (y = 10). The percentage of infected vectors over the total vector population reaches a maximum value of 60% for the scenario Epidem-ShVh in agreement with observation in highly diseased olive groves where the highest value of infected vectors is maximum 70% (D. Bosco, personal communications). The percentage of infected vectors over the total vector population is significantly lower in the other scenarios, reaching a minimum level of 12% in Epidem-SlVl.

The infected vector population pressure decreases with a common pattern over the spatial dimension. The pressure is sustained at high level in the scenario Epidem-ShVh in an area of few km. The pressure remains relatively high only in the first 100 m in the case of low density and low plant susceptibility (scenario Epidem-SlVl).

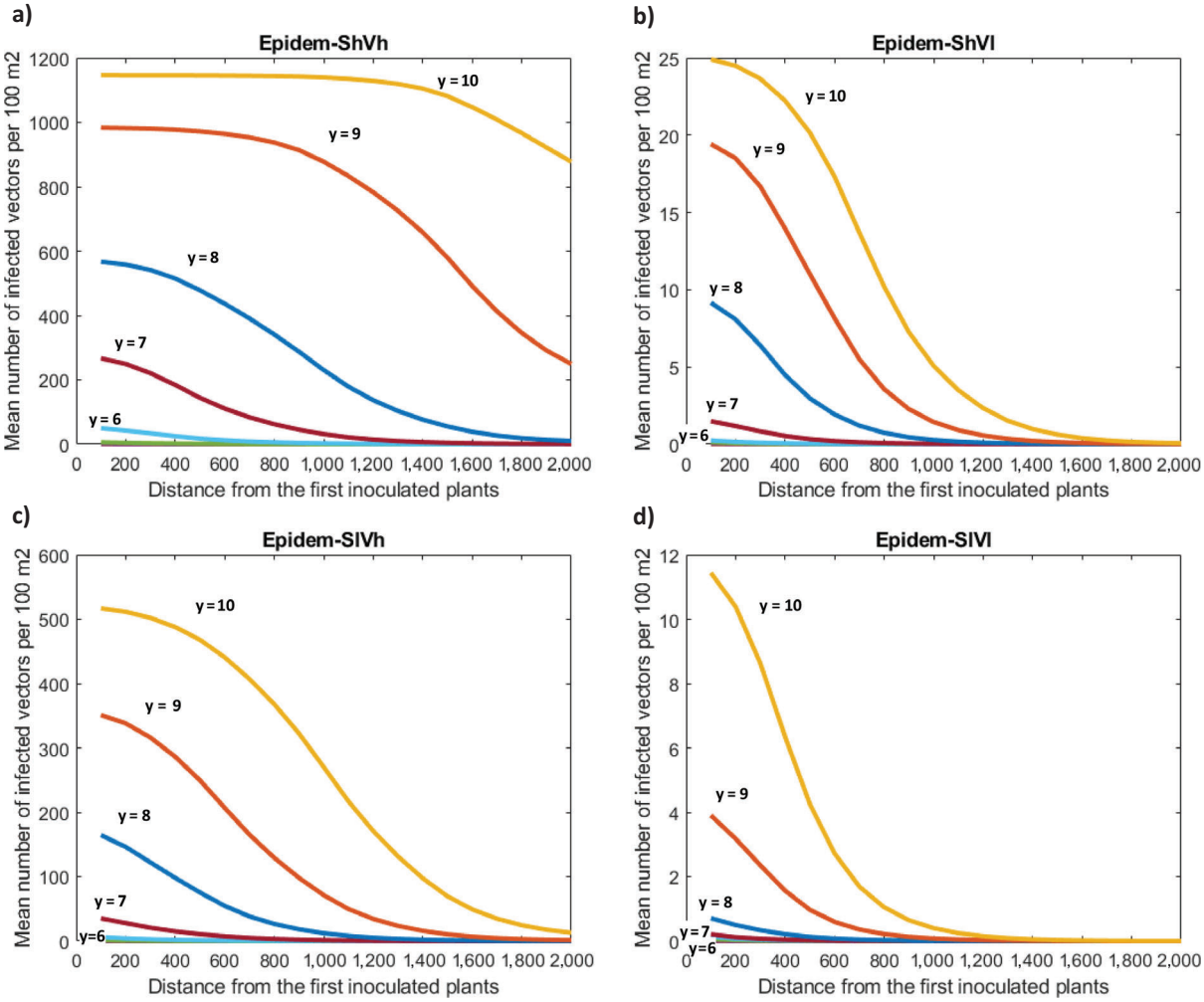

Figure 18: Distribution of the mean infected vector density (adults/100 m^2) in relation to the distance (metres) from the first inoculated plants in the 10 years of simulation (inoculum at year 1). Frame (a) referred to the Epidem-ShVh scenario, frame (b) to the Epidem-ShVl scenario, frame (c) to the Epidem-SlVh scenario and frame (d) to the Epidem-SlVl scenario. The scales on the y-axis are adapted to the maximum value of each graph

Disease level in the infected host plants

The spatial–temporal dynamics of the disease is represented in Figure 19. In the scenario Epidem-ShVh, the disease epidemic reaches high level of severity (level 4, Appendix A.1.3.3, Table A.2) at the 6th year of simulation (y = 6) and increases rapidly both in space and time being able to expand at the maximum level of severity at year 10. In the scenario Epidem-SlVl, the level 3 is reached almost 2 years later, level 4 the following year (y = 9), and the spatial spread is much more contained.

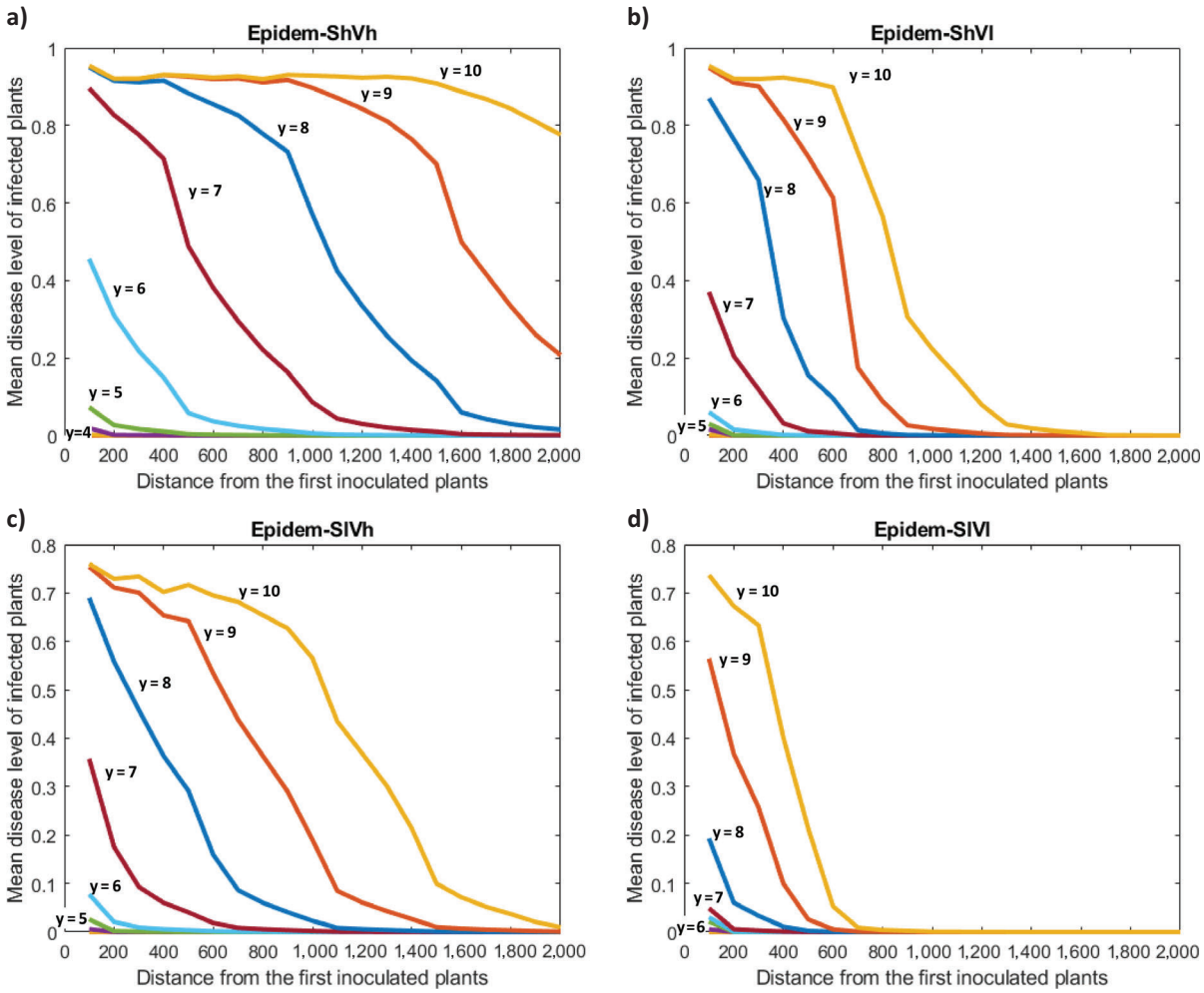

Figure 19: Distribution of the mean disease level in the infected plants in relation to the distance from the first inoculated plants in the 10 years of simulation (inoculum at year 1 of the (a) Epidem-ShVh scenario, (b) Epidem-ShVl scenario, (c) Epidem-SlVh scenario, (d) Epidem-SlVl scenario

Spread of the disease

Results obtained for the disease spread are represented in Figure 20. Based on the maximum distance separating the farthest infected plants from the first inoculated plants, the spread rate of the disease in kilometres per year can be derived. The spread rate of the disease increases over time with a non-linear pattern depending on the scenario. In the initial phase of the new outbreak, the diseased area is almost constant, then it starts increasing after y = 2 in the Epidem-ShVh scenario. For this scenario, the rate of increase changed over the years with rates that are higher than in other scenarios. In Epidem-ShVh after y = 5, the rate is 0.65 km/year. The spread rate of the disease is only 0.28 km/year at y = 5 in the scenarios Epidem-SlVh and Epidem-SlVl. The simulation of the disease spread focused on the initial build-up of an invasion front. Note that the time period considered in the simulation is too short to investigate the long-term pattern of the radial expansion process and the short-range model presented here considers a spatial scale that does not include long-range jumps (i.e. dispersal events at a spatial scale beyond the orchard), which of course lead to faster rates of spread at the regional scale (as considered in the long-range model, Section 3.4).

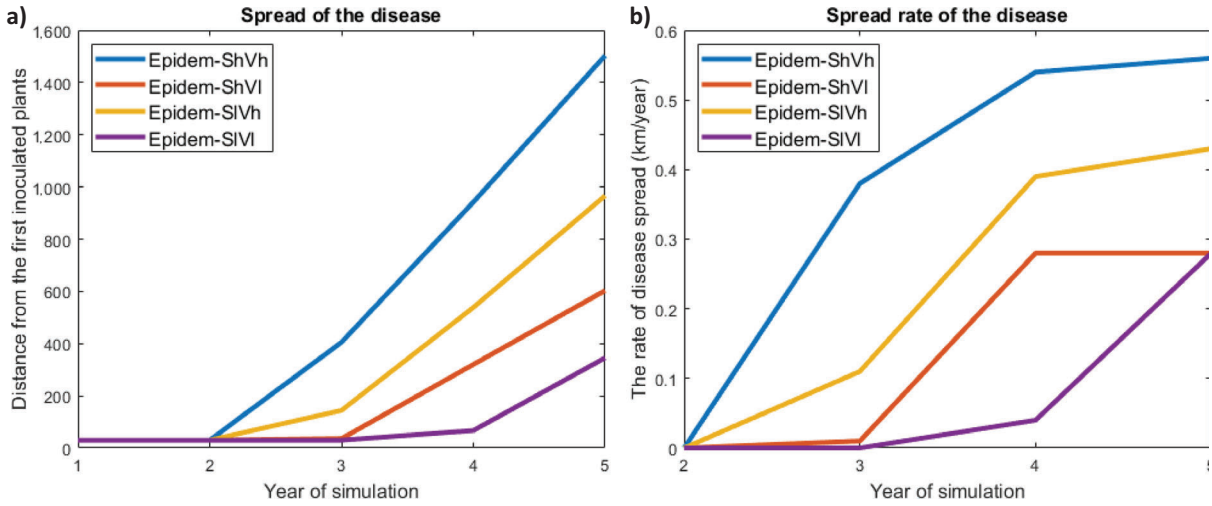

Figure 20: Spread of the disease measured in terms of (a) maximum distance of the infected plants from the first inoculated plants and (b) rate of spread (km/year) in the four scenarios

Number of infected plants

In Figure 21, information on the magnitude of the disease in terms of number of infected host plants per year (bacterial titre greater than 0), molecular detectable infected host plants per year (bacterial titre greater than the threshold for molecular detectability) and visually detectable infected host plant is reported (bacterial titre greater than the threshold for visual detectability, see Appendix A.1.3.3 – Table A.2). As a consequence of the differences in the spread rate of the disease among the scenarios (Figure 20), the number of infected plants in the scenario Epidem-ShVh after y = 5 from the inoculum is seven times higher than in the scenario ShVl and 30 times higher than in the scenario Epidem-SlVl. As for the detectability, in the scenario Epidem-ShVh almost one third of the infected plants are detectable, with a small proportion of plants that are visually detectable. The proportion of detectable plants is much smaller in all the other scenarios, with comparable number of molecular and visually detectable host plants.

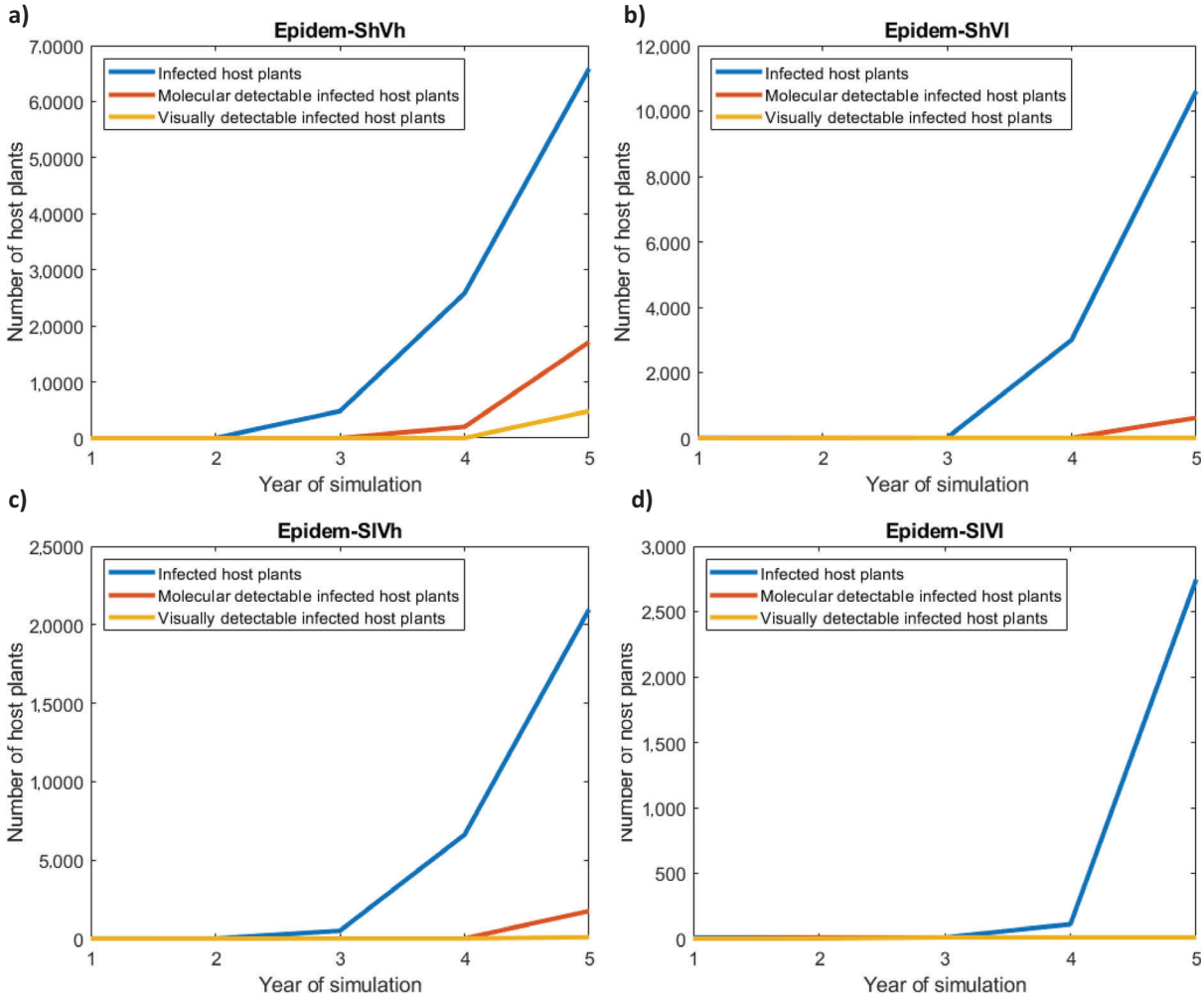

Figure 21: Distribution of the number of (i) infected host plants (bacterial titre greater than 0), (ii) molecular detectable infected host plants (bacterial titre greater than the threshold for molecular detectability), (iii) visually detectable infected host plants (bacterial titre greater than the threshold for visual detectability, see Appendix A.1.3.3 – Table A.2). Frame (a) referred to the Epidem-ShVh scenario, frame (b) to the Epidem-ShVl scenario, frame (c) to the Epidem-SlVh scenario and frame (d) to the Epidem-SlVl scenario. The scales on the y-axis are adapted to the maximum value of each graph

3.3.1.2. Evaluation of risk reduction options

Results in Section 3.3.1.1 confirmed that Epidem-ShVh (high susceptible plants and high vectors population density) represents the epidemiological worst case scenario. On this scenario eradication measures are applied. To explore the efficacy of eradication strategy, scenarios based onto two levels of efficacy of the control for the adults and the nymphs (high and low, Appendix F.2.5), two different cutting radii (100 m and 50 m) and two times to detections (at year 4 and year 5 since the inoculation) are considered. Furthermore, two times of intervention after the detection have been considered: 30 days, in accordance with the 'immediate felling' reported in the current legislation, and 65 days, a plausible scenario describing a delay in the intervention. Outcomes of the simulation scenarios in which eradication measures are applied are shown in Table 13.

From the results, a clear picture of the roles played by the control efficacy, the cut radius, the time to detection and the delay of the intervention emerges.

The efficacy of nymphs and adult control treatments is of major importance. In all the scenarios where efficacy is high, the disease is eradicated. When there is a low efficacy in vector control, the disease is eradicated only with an early detection, a prompt intervention (30 days after the detection) and a cut radius of 100 m. In all the other cases with low vector control efficacy, eradication is not achieved.

In all the scenarios, an early detection (3 years after the inoculation) limits the impact of the disease in terms of the dimension of the infected area and the number of cut trees.

The delay of the intervention is a key factor to eradicate the disease. In the scenarios with high efficacy of treatments, when a cut delay of 30 days is applied eradication is achieved 1 year before with respect to cases with a cut delay of 65 days, removing on average 11.2% less plants than the cases with late cut. Furthermore, in the Contro-ClRhDe scenario, the recommended time of intervention results in the disease eradication, while the eradication is not achieved if a late intervention is applied. In the scenarios where eradication is not achieved, a prompt intervention limits the impact of the disease.

The dimension of cut radius has not influence if vector control is applied with high efficacy, since eradication is achieved both with a high cutting radius (100 m) and with a low cut radius (50 m). A cut radius of 100 m is required for eradication in the scenario with low treatment efficacy, early detection and prompt intervention. In all the other cases of low efficacy of vector controls, eradication is never achieved.

Table 13: Major outcomes of the simulation scenarios for the comparison of eradication measures (in green the scenarios that resulted in an eradication of the diseases, in orange the scenarios that did not resulted in an eradication of the disease)

Scenario components					Scenario outcomes			
Scenario	**Control efficacy**	**Cut radius**	**Time to detection (years after inoculation)**	**Delay of the intervention (days from the detection)**	**Outcome of the control**	**Infected area (in km^2) at the end of the simulation period**	**Infected plants in the buffer zone at the end of the simulation period**	**Maximum distance of plants removed (in m from the point of initial outbreak)**
Contro-ChRhDe	H	100	3	30	Eradicated at year 4	2.97	0	1003.2
				65	Eradicated at year 5	3.03	0	1024.9
Contro-ChRhDl	H	100	4	30	Eradicated at year 4	6.99	0	1591.8
				65	Eradicated at year 5	7.05	0	1595.2
Contro-ChRlDe	H	50	3	30	Eradicated at year 4	2.48	0	957.7
				65	Eradicated at year 5	2.73	0	976.37
Contro-ChRlDl	H	50	4	30	Eradicated at year 4	5.91	0	1544.3
				65	Eradicated at year 5	6.92	0	1644.4
Contro-ClRhDe	L	100	3	30	Eradicated at year 5	3.07	0	1037.0
				65	Not eradicated	4.35	896	1247.8
Contro-ClRhDl	L	100	4	30	Not eradicated	8.59	176	1772.0
				65	Not eradicated	10.40	856	1905.0
Contro-ClRlDe	L	50	3	30	Not eradicated	3.36	7292	1198.7
				65	Not eradicated	4.10	12,104	1328.3
Contro-ClRlDl	L	50	4	30	Not eradicated	8.52	17,052	1926.3
				65	Not eradicated	8.85	32,128	1998.3

In Figure 22, the spatial distribution of the infected vector density in relation to the distance from the first inoculated plants is reported for the five simulation scenarios in which eradication is achieved for the 5 years of application of eradication strategy. Both the pressure of the infected vectors (Figure 22) and of the disease (Figure 24) rapidly decreases over time. Since the first year of application of the eradication measures, the density of the vector population is reduced to less than 0.025 vectors/m^2.

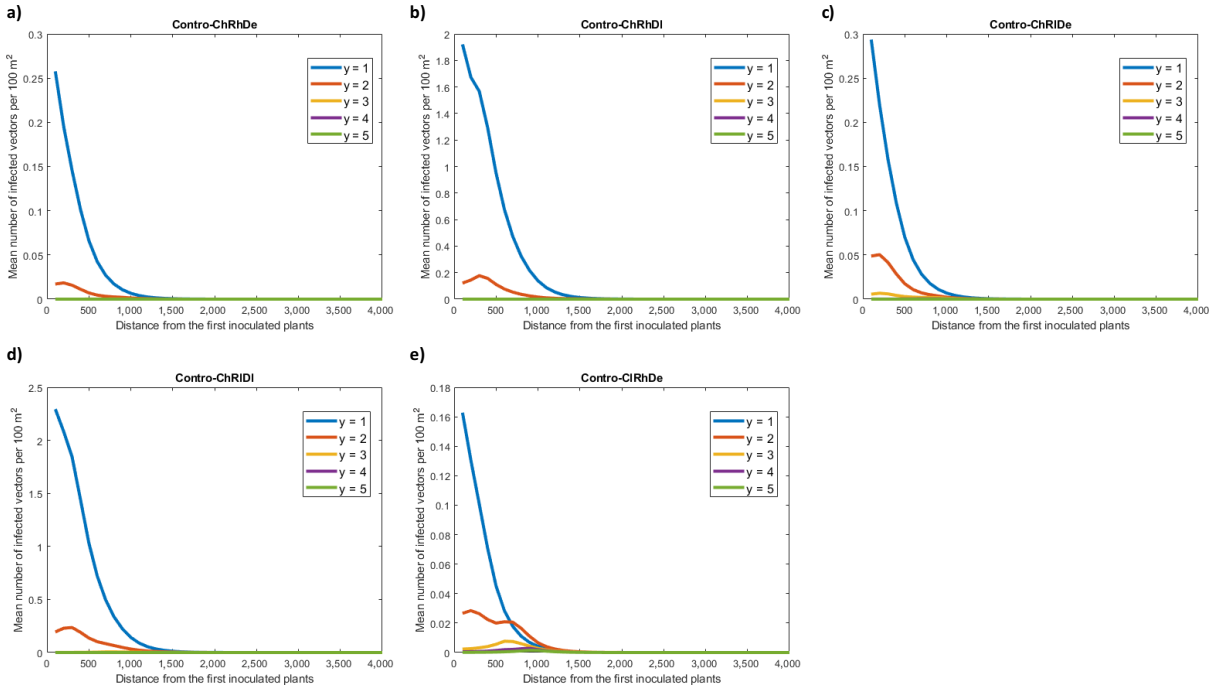

Figure 22: Spatial distribution of the mean infected vector density (adults/100 m^2) in relation to the distance (metres) from the first inoculated plants in the 5 years of application of eradication strategy (detection at year 1 in the five scenarios in which eradication is achieved: (a) Contro-ChRhDe, (b) Contro-ChRhDl, (c) Contro-ChRlDe, (d) Contro-ChRlDl and (e) Contro-ClRhDe. The scales on the y-axis are adapted to the maximum value of each graph

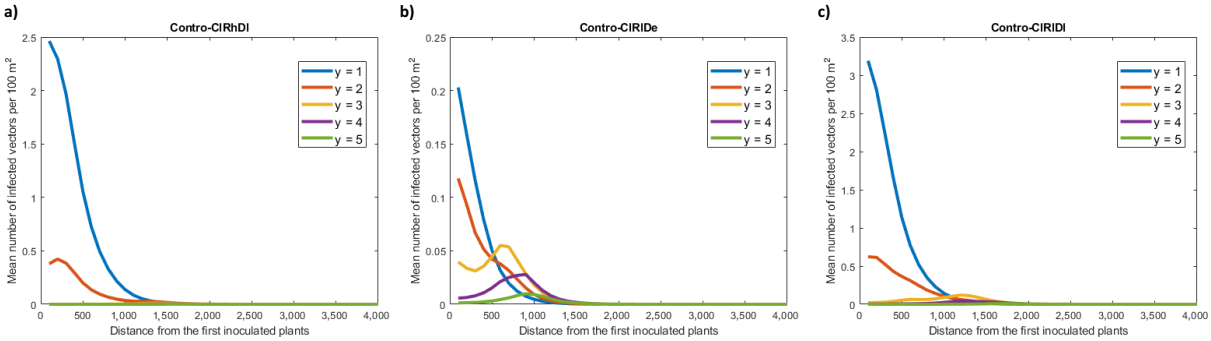

Figure 23: Distribution of the mean infected vector density (adults/100 m^2) in relation to the distance (metres) from the first inoculated plants in the 5 years of application of eradication strategy (detection at year 1). The three scenarios in which eradication is not achieved are considered: (a) Contro-ClRhDl, (b) Contro-ClRlDe and (c) Contro-ClRlDl. The scales on the y-axis are adapted to the maximum value of each graph

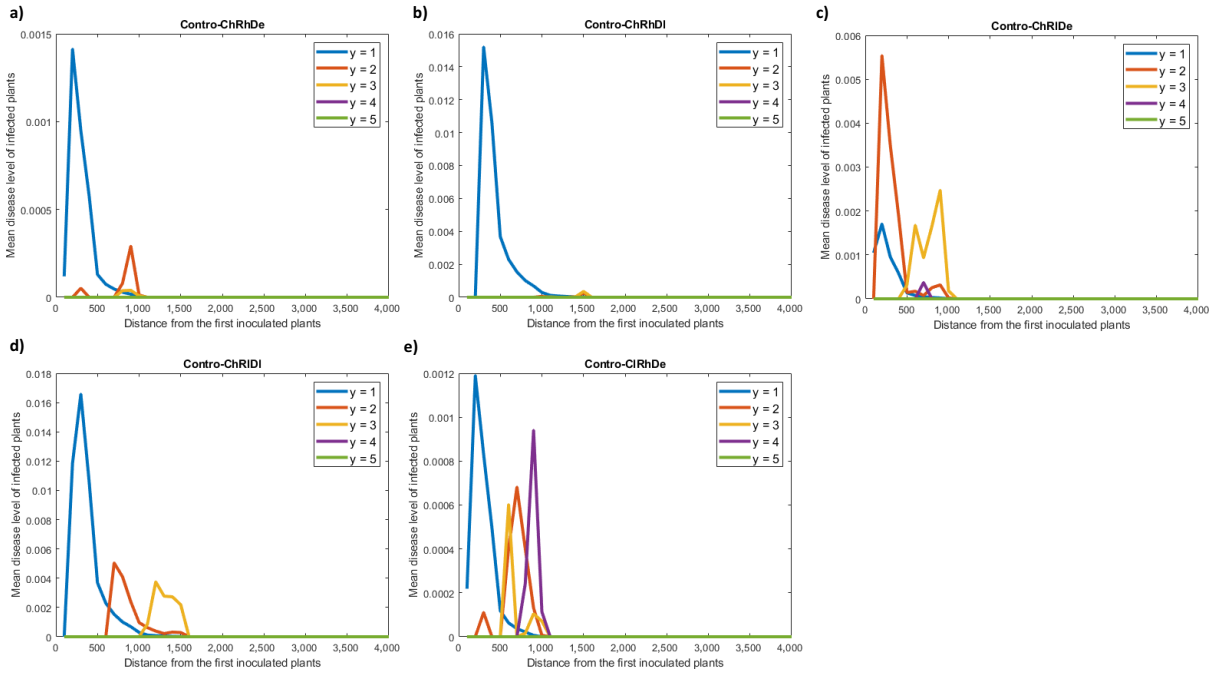

Figure 24: Distribution of the mean disease level in the infected plants in relation to the distance from the first inoculated plants in the 5 years of application of eradication strategy (detection at year 1) in the five scenarios in which eradication is achieved: (a) Contro-ChRhDe, (b) Contro-ChRhDl, (c) Contro-ChRlDe, (d) Contro-ChRlDl and (e) Contro-ClRhDe. The scales on the y-axis are adapted to the maximum value of each graph

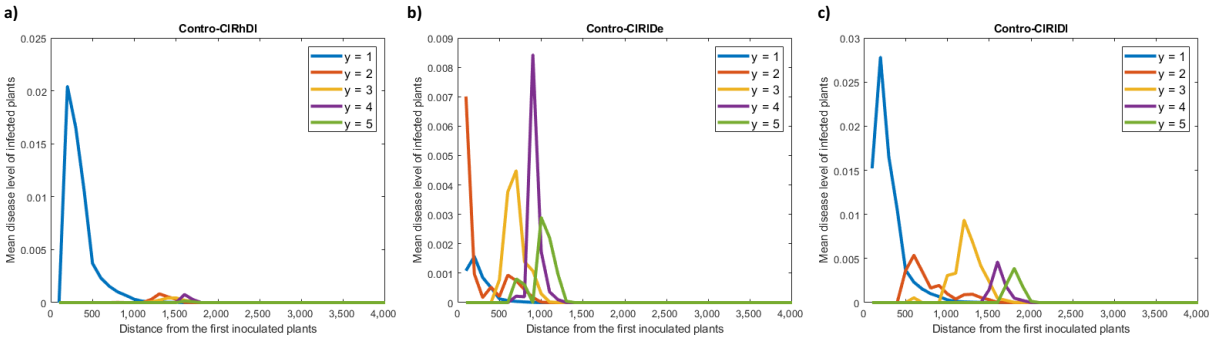

Figure 25: Distribution of the mean disease level in the infected plants in relation to the distance from the first inoculated plants in the 5 years of application of eradication strategy (detection at year 1). The three scenarios in which eradication is not achieved are considered: (a) Contro-ClRhDl, (b) Contro-ClRlDe and (c) Contro-ClRlDl. The scales on the y-axis are adapted to the maximum value of each graph

In the scenarios in which eradication is not achieved, the application of control measures strongly reduces the pressure of the infected vectors and the level of the disease as well. In all the scenarios, the infected vectors density (Figure 23) is lower than the one in the epidemiological scenario with no control measure in place (Figure 19a). Due to the application of control measures, infected vectors density is reduced to less than 0.035 vectors/m^2 since the first year of application of the control measures.

Figure 25 shows that the application of the eradication measures strongly reduced the pressure of the disease (in terms of mean disease level in the infected plants, see Appendix A.1.4) by a factor ranging from 250 (Contro-ClRlDl) to 6,700 (Contro-ClRhDl) with respect to the epidemiological scenario with no control measure (Figure 19a). When eradication measures are applied (Figure 25), we noticed the presence of a spatial–temporal pattern for the disease pressure similar to travelling waves. This pattern was not present in the case of epidemiological scenario with no control measure. The presence

of travelling waves could be explained by the presence of the asymptomatic infected plants that are not detected and in which the disease grows and spreads outside the cutting zone. This pattern was not present without control measure (Figure 19a).

The main results obtained from the model exploration of the eradication scenarios are:

- In the model simulation, only high efficacy in adults and nymphs control and early detection make possible the disease eradication. Eradication is achieved also in the case of low efficacy in adults and nymphs control, but only with early detection, 30 days of intervention delay and the 100 m cut radius.
- A prompt intervention is a key factor to eradicate the disease and to limit the impact of the disease when eradication is not achieved. In the scenarios with high efficacy in vector control, the eradication is achieved 1 year in advance applying a cut delay of 30 days with respect to cases in which the cut delay is 65 days.
- Considering the cut radius, results showed that with high efficacy of vector controls, the eradication is achieved both with a cut radius of 100 m and 50 m. In cases with low treatments efficacy even with a cut radius of 100 m, the eradication is not achieved, apart from the only exception of the scenario with very fast detection and very fast implementation of control measures.
- Considering the impact of the control measures in terms of the number of removed plants, the most efficient strategy is the one with high efficacy in vector control, low cut radius, early detection and prompt intervention
- When vector control is applied with low efficacy and control measures are not effective in eradicating the disease, prompt intervention, large cutting radius and early detection are however effective in reducing the pressure of the disease in the BZ
- In the scenarios in which eradication is not achieved, the control measures are able to reduce the pressure of the disease by a factor ranging from 250 to 6,700 with respect to the disease epidemiological dynamics without management.

3.3.2. Uncertainties affecting the assessment of short-range spread

Model results are affected by limitations related to assumptions and hypotheses introduced to define the scenario and the model. Uncertainty also affects model parameters values. Furthermore, the model is fully deterministic and this explains part of the regularity and homogeneity in the patterns of the simulation outputs. However, thanks to model structure and flexibility a wide range of conditions and options for management can be explored. Different conditions can be tested by the model including vector species, *X. fastidiosa* subspecies and strains, host plant species, mixed plant communities (with species with different susceptibility) and different landscape (homogeneous, heterogeneous but continuous, patchy). The model can also be extended to a stochastic version to account for all sources of variability and uncertainty affecting the spatial and temporal dynamics of the biological and epidemiological processes. The main sources of uncertainties in the assessment are listed and discusses in Table 14 showing the main limitations affecting the assessment results and the way in which the model could address them.

Table 14: List of the main source of uncertainty and a short discussion on their consequences for the assessment and the possibility for the SRS model to evaluate the impact of uncertainty

Source of uncertainty	How to evaluate the impact of uncertainty and expected consequences
Variability in the spread rate of the vector and the pattern of the vector dispersal movement	An uncertainty distribution for the vector dispersal kernel is available and can be explored by the simulation model. Variation in the spread rate could influence the growth rate, the spread of the disease, and the effectivity of control measures. Inhomogeneity in the pattern of the vector dispersal could lead to inhomogeneity in the distribution of the disease, affecting the uncertainty in the assessment of the cut radius
Vector acquisition rate of the bacteria	The vector acquisition rate could be affected by within- and between-species variability in the feeding rate and preference. This could result in increasing the spatial variability of the disease. The model can include element of stochasticity in the feeding behaviour of the vectors and the consequences be explored

Source of uncertainty	How to evaluate the impact of uncertainty and expected consequences
Vector population density that is known to be highly variable in a given area	This factor resulted one of the most important drivers for the spread of the disease. The spatial and temporal variability of vector density could affect the risk of disease spread in an area as well as the temporal dynamics of the symptom appearance. The density also affects the possibility of eradication of the disease. Also, the phenology of the vector could have large impact on disease spread and control. The model can account for variability in the density and the phenology of the vector
Susceptibility of the host plant	Together with vector density this is the most important factor influencing disease spread and control. Variability in the host susceptibility highly affect the growth rate of the disease in the plant with consequences on the spatial and temporal pattern of the disease. Susceptibility influences also the asymptomatic period, the detectability of the plants and the severity of the symptoms. These factors are explicitly represented in the model
Diseased plant detection	The deterministic nature of the model produces regularity and homogeneity in the temporal and spatial patterns of the disease level and symptoms severity. This also makes the pattern of detection homogeneous for small areas. The role of spatial variability in disease presence and severity was not explored in its consequences on the probability of detection. Only the stochastic formulation of the model could allow a full exploration of a probabilistic approach to plant detection
Vector control	Vector control for both adults and nymphs were applied at two levels of efficacy as they are reported in Appendix F. The availability of uncertainty distribution of vector control efficacy could allow the model to explore uncertainty related to this factor. Some important aspects related to vector control were not explored like, for example the long-term impact of chemical control and weed removal, the difficulty to access or doing vector control in some areas (private gardens, forestry areas or urban areas). These factors could affect the outcome of the control measures. The role of uncertainty in the vector control efficacy and in the availability of refugees for the vector population can be explored by the model considering suitable parametrisation of the mortality function and appropriate definition of the landscape structure
Option for cutting	The adoption of a cutting strategy applied to all the plants was the most effective option. An alternative option could consider only the cutting of the infected plant only. This should provide the advantage of saving potentially healthy plants. However, this strategy is at risk of saving from cutting plants that are infected but not molecularly detectable
Time horizon of the simulation	The simulation scenarios considered only a period of control of 5 years from detection as it represents a reasonable time horizon for eradication measures. No information is reported regarding the long-term behaviour of the system after the 5 years of simulation. However, the model can easily explore longer period of control evaluating them in term of effort of controlling the vectors, impacts in terms of plant removed and final outcome of the interventions (i.e. disease eradication or not)
Outcome of the eradication process	With respect to eradication indications emerging from model simulations, they showed dichotomous system behaviour: disease eradicated or not eradicated. Since there is a stochastic component in the detection of infected plants the level of confidence associated to the outcome of control was not the same for all the scenarios. For the scenarios where the transition from eradication to non-eradication occurs, there is a possibility of a random variation in the outcome of the control (e.g. scenario Contro-ClRhDe in Table 13). The level of confidence in this case was lower than for the remaining scenarios where a clear outcome is observed for all the realisations (i.e. repeated simulations for the same scenario). To account for this uncertainty, the model was run several times, particularly for the scenarios characterised by a significant level of uncertainty and the most probable outcome was considered

3.3.3. Conclusions on short-range spread

In a homogeneous structured landscape considering a large olive grove with the maximum extent of 10 × 10 km, local spread rate of the disease was estimated around 0.7 km/year (in the 5 years simulation of the epidemiological dynamics without management). Longer simulation period showed an increase in the movement range. The disease spread rate was in the order of magnitude of the vector spread rate and anyway less than 1 km/year. These results were obtained under the assumption of short-range dispersal of the vector. Higher spread rate of the disease are expected when jumps of the vectors are considered due to both human activity and passive dispersal through strong winds;

Under an eradication strategy, model results indicated that:

- high efficacy in both nymphs and adults vector control is the most important factor for effective eradication of an outbreak in a free area;
- early detection, and the consequent host plants removal, is a key factor for effective eradication, reducing the time from the initial infection to when eradication is achieved;
- eradication measures (in the year of detection: one adult control and the cutting of all susceptible hosts in the infected area; in the following years: one weed treatment and two adult vectors control per year in the whole demarcated area) are effective if implemented before or in the first period of adult flight (just after adults emergence) as they limit the density of infected vectors that rapidly increase over the favourable season. These results highlight the importance of limiting the delay in the application of control actions;
- early detection and prompt intervention are also important for limiting the impact of eradication measures in terms of number of cut trees and size of the infected area;
- the cut radius for the host plant removal proved to be important only in the case of low efficacy of nymphs and adults control, early detection and prompt intervention. In this case, eradication is achieved only by applying a 100-m cut radius and not with a 50-m cut radius. When the nymphs and adults control efficacy is high, eradication is achieved also with a cut radius of 50 m. There is no eradication if the effectiveness of the treatments is low and there is late detection even with a cut radius of 100 m;
- even when the eradication is not achieved, the application of control measures results in a reduction of the disease pressure and the infected vector population density limiting the disease spread. The level of the disease is reduced by a factor ranging from 250 to 6,700. When eradication measures are applied a spatial–temporal pattern similar to travelling waves appeared for both the vectors and the disease. The main sources of uncertainty are related to the vector movement range, the vector acquisition rate of the bacteria, the susceptibility of the host plants and the delay in the disease detection. The rate of successful transmission of the disease agent from the infected vector to the host plant and from an infected plant to the vector are the two most important parameters affecting model results;
- Thanks to model structure and flexibility a wide range of conditions can be explored parameterising the model to account for different vector species, *X. fastidiosa* subspecies and strains, mixed plant communities (species with different susceptibility). Scenarios on landscapes (homogeneous, heterogeneous but continuous, patchy) and combinations of management options can also be assessed. The exploration of new conditions and scenarios requires availability of data on biological and epidemiological parameters as well as the precise definition of the elements characterising the agricultural landscape and the options for management;
- The model was parametrised based on the Apulian data, since it is the only case where there are sufficient data, however differences in vector abundance and host susceptibility were explored. The model is generic in nature and can be specifically applied to other outbreak areas where data becomes available. This makes the model suitable not only for the exploration of theoretical scenarios but also a tool able to support decision making for the definition and management of emergency plans related to new outbreaks.

3.4. Long-range spread

3.4.1. Assessment of long-range spread

Example simulation outputs showing the effect of simulated management on infected area growth are shown in Figure 26. Section 3.3 demonstrated the conditions where local eradication of outbreaks is feasible. In this section on long-range spread, we focus on regional-scale spread and control. In the

examples in this section, implementation of eradication measures limited the growth of the infected area, even switching it to long-term decline. Containment measures also limited the rate of growth when implemented early (i.e. implemented 5 years after introduction), and especially when implemented with large BZs (> 5 km).

Across all the replicate simulations, there was wide variability between different simulations of the same management scenario. This is attributable to parameter uncertainty, variation in simulated generic landscape patterns (especially whether *X. fastidiosa* is introduced at a highly susceptible or low susceptibility location) and the inherent stochasticity in simulated epidemics driven by rare long-range dispersal events.

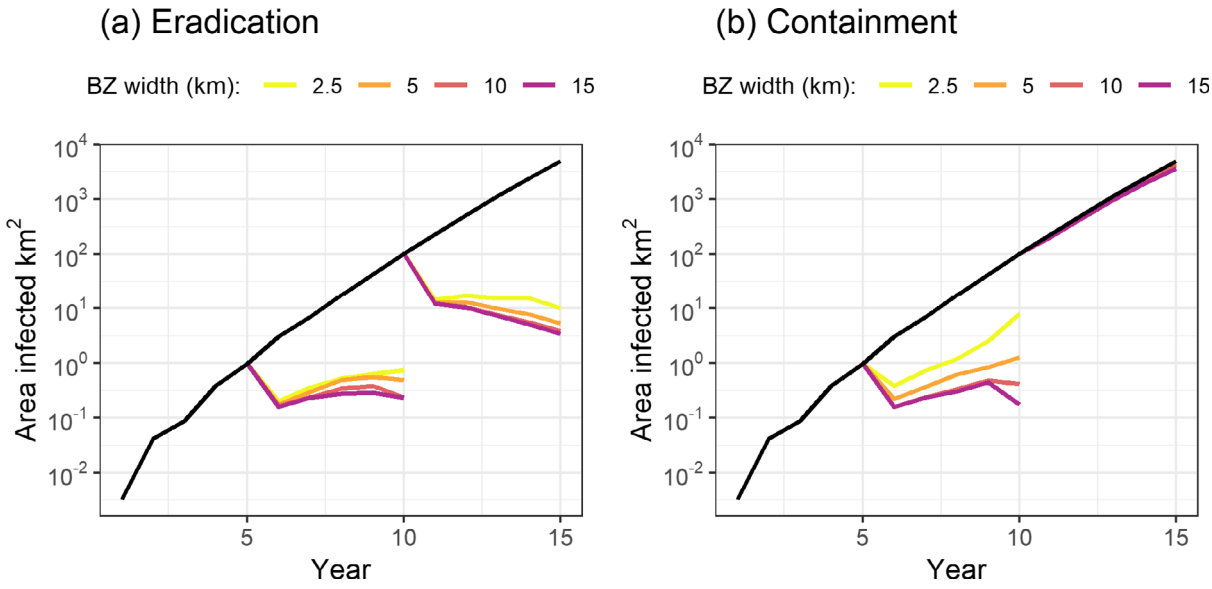

Figure 26: Example simulation outputs showing growth of an unmanaged *X. fastidiosa* epidemic in an Italy-like landscape over 15 years (black line) and the effect of 5 years of surveillance and (a) eradication or (b) containment management starting in either year 5 or year 10 with different sized buffer zones (BZ). Lines show the median values from all 50 replicate simulations (note that the lines for containment after 10 years nearly overlap the black line for no management). Simulated management involved the high inspection effort and effective control scenarios (see Table 6). Note the logarithmic scaling of the *y*-axis, meaning that each labelled division represents a 10-fold change in the size of the infected area

Management effectiveness

To estimate the effects of simulated management on *X. fastidiosa* spread, the relative sizes of modelled infected areas were calculated as a proportion of the equivalent simulated infected areas with no management (Figure 27). This provides a standardised measure of management effectiveness, with small values meaning management caused a large proportionate reduction in the size of the infected area after 5 years. In this context, infected area means the area currently holding infection, so infected grid cells in which all hosts are felled are not included in the infected area.

As shown in Figure 27, there was wide variability between different simulations of the same management scenario and large effects of the overall strategy and year of discovery. Simulated eradication strategies reduced the size of the infected area after 5 years by a median of 98.7% compared to its unmanaged size, across all management scenarios and parameter uncertainty (Table A.5). In general, containment strategies were less effective and resulted in infected areas that were a median of 65% of the unmanaged size. However, the results of containment varied strongly according to the modelled scenario (Figure 27b–d). As expected, the wider the BZ the higher the effectiveness of the control. In fact, as the BZ width increases it will eventually asymptote at a maximum reduction in infected area corresponding to a width which ensures capturing even the occasional very long-distance dispersal events. However, it should be noted that in general the gain in effectiveness diminished as the BZ increased. For example, in the case of an early discovery and application of containment strategy, the gain achieved by increasing the BZ from 10 to 15 km, is substantially lower than the gain achieved by increasing the BZ from 5 to 10 km (Figure 27b). In

addition, early detection is crucial for effectiveness as well as high inspection rates and stringent vector control. By contrast, the same containment strategies starting after discovery of the disease in year 10 resulted in the median infected area being 68% of the unmanaged size. This demonstrates the sensitivity of containment strategies to the discovery year and highlights the need for early detection of new disease foci in a disease-free area.

For eradication strategies, the model suggested that smaller infected areas relative to no management were achieved when then disease was discovered later (after 10 years of spread) rather than early (after 5 years) (Figures 27 and 28). However, it is important to note that the absolute size of the remaining infected area was much larger at the end of management simulations with late discovery (Figure 26). We identify three reasons why the model predicts better relative control (proportionate reduction in the size of the infected area) for late discovery. First, upon late discovery the infected area consisted of more well-developed disease foci, which were easier to detect by the simulated surveillance programme, facilitating eradication management. Second, unmanaged infections exhibited near exponential growth in the model (Figure 26) so the unmanaged baseline was much larger in the late discovery scenario, making the managed infected areas relatively smaller. Third, as a consequence of the first two, a much larger area was demarcated causing a much larger number of trees and bacterial inoculum to be removed when the disease was discovered later. Indeed, the simulated area under management was approximately 10 times larger in the late discovery scenario than the early scenario. Therefore, combining these effects results in a large relative eradication initially after later discovery.

Interestingly, there were relatively little differences between landscape types in terms of the relative areas infected compared to no management, despite their variation in host density and spatial structure (Figure 27a). BZ widths had a relatively small effect on the effectiveness of eradication, which may have been because the most intense surveillance and host plant clearance occurred in the first 1 km of the BZ and this was retained in all of the BZ width scenarios. However, BZ widths were more important for the effectiveness of containment strategies for which wider BZs resulted in better containment (Figure 26b). This may reflect the greater size of the CZ, which was always set twice as wide as the BZ and in which intense surveillance and removal of detected infected plants was applied. High inspection effort and vector control contributed to effective management, except that they made little difference to containment measures initiated after 10 years of *X. fastidiosa* spread (Figure 27c,d).

The simulations therefore suggest that for eradication strategies it may be better to use resources to increase inspection effort and reduce vector populations, rather than to increase the size of the BZ. However, for containment of large outbreaks, maintaining a large BZ is important.

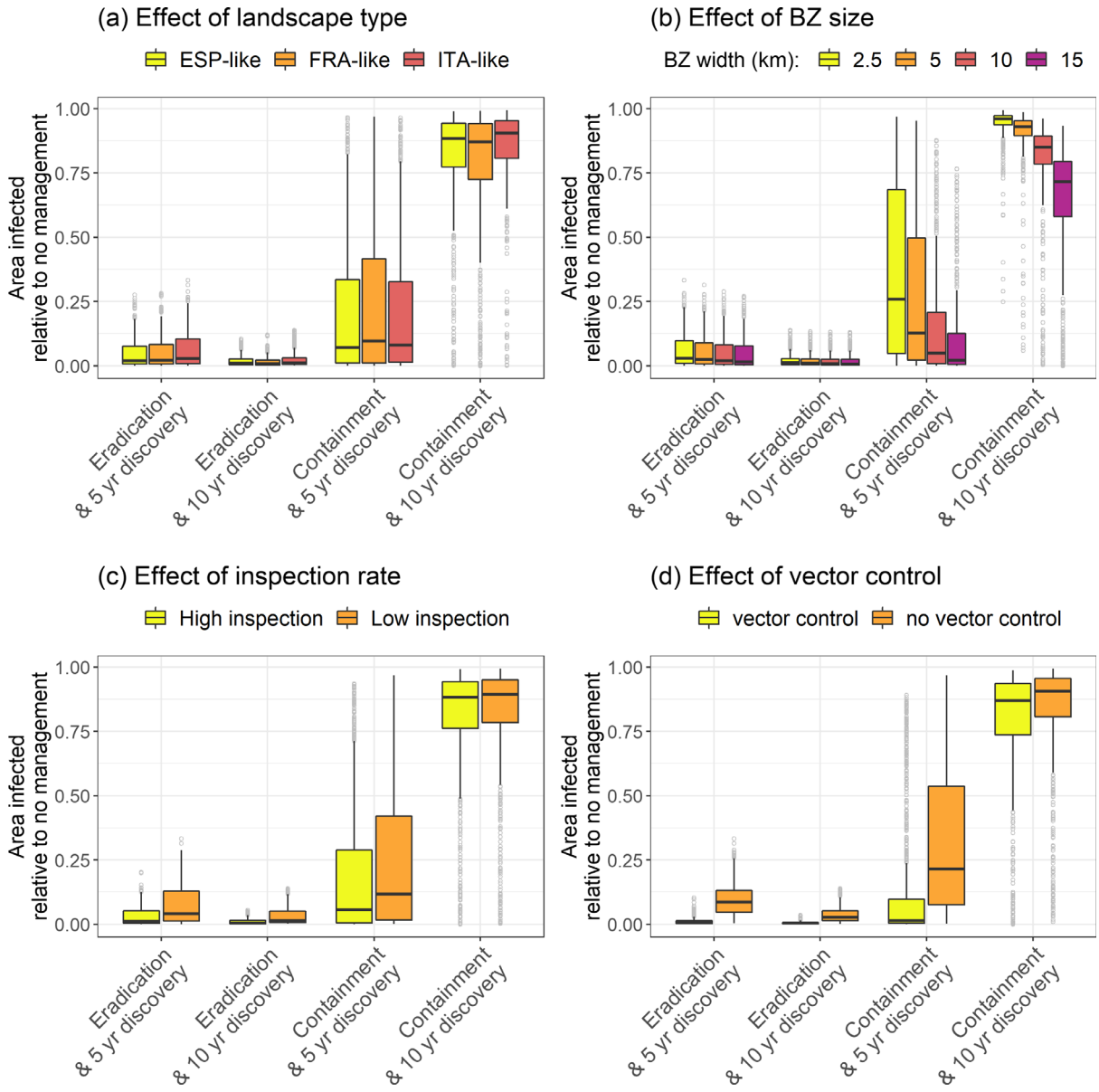

Figure 27: Boxplots for how (a) landscape type, (b) buffer zone (BZ) width, (c) inspection rate and (d) vector control affect the size of the infected area after 5 years of management, relative to the sizes of simulated outbreaks with no management. The boxplots differentiate between different management goals (eradication or containment) and disease discovery times (after 5 or 10 years of spread) and aggregate across all replicate simulations with all values of the other model parameters and settings. Note that the scenario for discovery after 5 years is compared to unmanaged spread in year 10, while the scenario for discovery after 10 years is compared to unmanaged spread in year 15, explaining the differences between the two discovery scenarios

Effect of changing the size of buffer zone

To estimate the effect of changing BZ widths, relative infected areas after 5 years of management were expressed as proportions of the infected areas after 5 years of management with the current BZ sizes (5 km for eradication and 10 km for containment) (Figure 28). As such, values less than one show cases that improve on the current strategy, and values greater one indicate worse performance.

For eradication strategies, halving the BZ width from 5 to 2.5 km caused the median area infected after 5 years of management to increase by a median of 5% for infections discovered 5 years after inoculation, and by 16% if the disease was discovered 10 years after inoculation (Figure 28). Doubling the BZ width to 10 km led to around 7% smaller infected area in both discovery scenarios.

For containment strategies, halving the BZ width from 10 to 5 km caused the median infected area after 5 years of management to increase by 54% if the disease was discovered in year 5 and by 9% with discovery in year 10 (Figure 28). Increasing the current BZ width to 15 km led to 17% or 15% smaller infected area with discovery in years 5 and 10, respectively.

Although the simulations produced a large variability, they suggest that the most likely consequence of reducing BZ widths would be to increase the size of *X. fastidiosa* infected areas. These effects may be more pronounced for containment strategies rather than eradication.

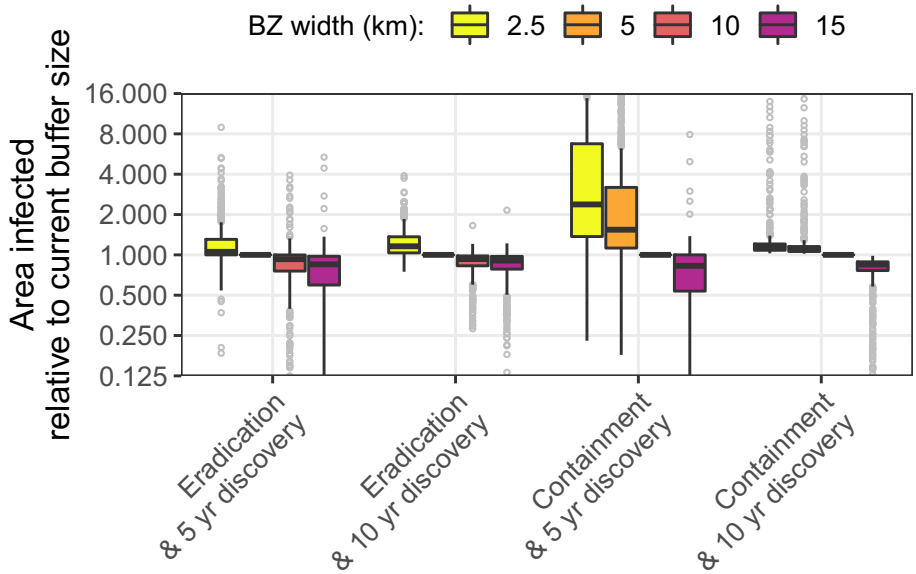

Figure 28: Boxplot showing the effect of changing the size of the buffer zone (BZ) in the model. The relative area infected is expressed as a proportion of the infected area after 5 years of management with the currently used BZ sizes (5 km for eradication and 10 km for containment). As such, the *y*-axis shows the relative change in the expected infected area if the BZ was changed. The *y*-axis is displayed on a logarithmic scale and has been truncated to improve clarity

Comparison to previous long-range spread modelling

Previous modelling work suggested that with dispersal range of only 1 km, *X. fastidiosa* may spread through the network of olive groves in southern Italy (Strona et al., 2017). The long-range spread model presented here extends the earlier model through a more realistic representation of *X. fastidiosa* epidemiology and the inclusion of long-range jumps as well as local dispersal. The model presented here confirms Strona et al. (2017) prediction of spread through habitat networks similar to those in olive orchards in Italy and extends their findings to other types of landscape with sparser habitat cover. They also investigated the effect of 'immunising' orchards, i.e. strategies aimed at identifying and removing specific orchards from the network in order to break it apart into small and isolated fragments and so restrict spread. From this, they concluded that a large proportion of orchards must be 'immunised' to substantially slow the spread. Because the model presented here includes long-distance jumps, calibrated to the observed spread in Italy, we would expect an even more pessimistic result from the new model. Furthermore, their model was not used to investigate eradication and containment management strategies, so their findings are not directly relevant to the main findings presented here.

The model used here is similar to that of White et al. (2017), which also showed the importance of long-distance dispersal on the effectiveness of containment in slowing the spread of *X. fastidiosa* in the real landscape of Apulia, Italy. Similarly, the model presented here agrees with their findings that whilst increasing BZ/CZ widths may reduce the spread of disease, they may fail to halt the spread altogether. Moreover, the authors showed that when control budgets are limited, increased BZ/CZ widths should be favoured over increased surveillance.

3.4.2. Uncertainties affecting the assessment of long-range spread

The model used in this assessment was developed from a generic epidemiological model original designed for *X. fastidiosa* subsp. *pauca* infecting olive trees in Apulia, Italy. In this region, eradication is no longer considered possible and there were problems with implementing management measures (for example a long time between detection and felling of infected plants). As such it may not capture the full variability in epidemiology in other EU MS arising from the presence of different *X. fastidiosa* subspecies, host species and asymptomatic periods, host density within susceptible land cover types, vector ecology, climate and other factors not accounted for in the modelling.

Geographic barriers (e.g. mountains or coastlines) specific to particular outbreaks were not considered but they may influence spread depending on how they influence landscape connectivity, i.e. for onward spread.

The model necessarily simplifies the real-world epidemiology in Apulia and does not explicitly represent processes such as vector population dynamics or highly specific details of the epidemiology such as potential host plant regrowth after 'removal', as happens after canopy loss in heavily infected olive trees.

Uncertainties also arise from the relatively coarse annual temporal resolution of the model. This means the model does not represent the seasonal timing of management actions or delays in laboratory testing and implementation of management measures. The model also does not account for non-compliance or long delays in implementing management measures after disease detection. Surveillance and laboratory testing practices may vary from those implemented in the simulations. For example, there was no quantitative guidance on how survey effort should change at the outer part of the BZ. Also, the sampling model differs from practice in Apulia where sampling and laboratory analysis are done for all symptomatic host plants detected by visual inspection, as well as for the asymptomatic plants in their immediate vicinity.

Finally, we assumed false negatives during laboratory testing did not interfere with management in CZs, in which only infected plants are removed after detection. Including this in the model may have further reduced the effectiveness of the containment strategies.

3.4.3. Conclusions on long-range spread

- The model for the landscape-scale spread of *X. fastidiosa* is based on our understanding of the epidemiology of *X. fastidiosa* subsp. *pauca* in Apulia, Italy. However, the model is flexible and pest generic in nature and the sensitivity of the results to different epidemiological and landscape parameterisations was evaluated.
- In the model, spread was driven by stochastic and rare long-range jumps as well as the local-scale diffusive spread represented in the SRS model. In order to reproduce the observed pattern and spread rate in Apulia, it was necessary to include long-range jumps in the model. Because the modelled spread rate is very sensitive to these long-range jumps, any measures aimed at reducing their frequency are likely to be effective at slowing large-scale disease spread. Potential measures might include restrictions on movements of infected plants and plant material that may harbour vector insects, as well as vector control to reduce the population sources from which long-distance dispersers arise.
- The long-range jumps included in the dispersal model also impede management because they are difficult to predict and allow *X. fastidiosa* to escape from the BZs and spread into new areas. Better understanding of the range of long-distance dispersal may be used to increase the widths of the BZs.
- Despite this, simulations of eradication and containment management typically limited growth of the infected area, often very effectively. However, total landscape-scale eradication was rarely achieved after only 5 years of simulated management.
- Early discovery of the outbreak and the consequent application of phytosanitary measures was critical for restricting disease spread while also limiting the area under management and therefore the resource needs for disease management. Although good disease control was achieved by the eradication strategy after late detection, this required an approximately 10-fold increase in the area under management, the area to be surveyed and the number of host plants to be felled. Furthermore, cases where the model did achieve total eradication occurred when the disease was discovered after 5 years rather than 10, emphasising the need to detect new *X. fastidiosa* outbreaks and implement phytosanitary measures as early as possible.

- When the outbreak was discovered later, containment strategies limited the growth of the infected area by a much smaller degree than eradication or containment after early discovery. However, the simulations considered spread in a 'mainland' type landscape and may not indicate the success of containment when the disease spreads through narrow or bounded landscapes, such as the peninsular infected area in Apulia, Italy.
- As expected, the larger the BZ widths the lower the infected area sizes under both eradication and containment strategies. However, in general, the gain in effectiveness diminished as the BZ increased. The effect of increasing the BZ width was least pronounced in the eradication scenarios, which may even be because simulated surveillance was concentrated in the first 1 km of the BZs and this region was maintained when the BZs were made smaller. It is likely that more intensive surveillance throughout the whole BZs would have improved disease control and increased model sensitivity to BZ width. BZ width had a bigger effect on containment than eradication, suggesting that larger BZs may further slow *X. fastidiosa* spread in large outbreaks under containment.
- Vector control and efficient surveys to trigger an early application of phytosanitary measures in the infected area are fundamental to effective disease control at regional scale. Modelled vector control in the infected areas, manifesting in a substantial reduction in disease transmission rates, increased the extent to which management reduced disease prevalence. Furthermore, total eradication was usually achieved when the simulated management included both vector control and high inspection effort. However, simulation of vector control and efficient surveys did not substantially improve the effectiveness of containment strategies implemented after late discovery of the infection. These were the least effective management strategies in the model, and so vector control and efficient surveys did not provide a large benefit.
- These findings were not qualitatively affected by the different landscape types analysed, suggesting that control strategies are robust across the different landscape types where outbreaks are most likely in the EU. However, this is subject to the caveat that the model is based on *X. fastidiosa* subsp. *pauca* epidemiology and dynamics in Apulia.
- Uncertainty in these conclusions arises from incomplete knowledge of *X. fastidiosa* epidemiology and the relatively small set of epidemiological, landscape and management scenarios selected for analysis.

3.5. Impact

3.5.1. Assessment of impact for different hosts

3.5.1.1. Olive, almond, grapevine and *Citrus* spp.

The full results of the EKE on the potential impact of *X. fastidiosa* on olive, almond, grapevine and *Citrus* spp., including the list of evidences evaluated, are included in Appendix E.

Importantly, to understand the results of the EKE, are the assumptions of the assessment. In fact, the assessment was done under the general scenario assumption that the entry, establishment and spread of the pest had already occurred. This corresponds to a scenario where the pest is already present throughout the area of potential distribution in the EU (i.e. it has spread to its maximum extent) (EFSA Working Group on EU Priority Pests). In addition, the only vector that was considered in this scenario was *Philaenus spumarius*, the most common and widespread currently known vector of *X. fastidiosa* in the EU (more information in Appendix E). As stated in EFSA PLH Panel (2015a), should other xylem-feeding insects act as vectors of *X. fastidiosa*, the impact could be different.

The main results are reported in Table 15. As far as olive, two age classes were considered, > 30 years trees, which were assumed to be mainly cultivated in traditional olive orchards, and < 30 years trees, assumed to be cultivated mainly in more modern olive orchards. For grapevine, EU production was divided in three classes based on production systems and geographic areas different for their climatic conditions: wine grape in southern Europe, table grape in southern Europe, and wine grape in northern Europe. Both almond and *Citrus* spp. were estimated as a unique class.

According to the EKE, the most impacted crop was olive with an estimated median yield loss going from 34.6% for trees younger than 30 years to 69.1% for older trees. The three classes of grapevine production were estimated to be the least impacted under the considered scenario.

Table 15: Estimated yield losses for the considered crops and uncertainty range: main assumption included that the pest is already present throughout the area of potential distribution in the EU (i.e. it has spread to its maximum extent), and the only considered vector was *Philaenus spumarius*. No other potential vectors were considered

Crop	Estimated yield loss (median)	90% uncertainty range (confidence interval)	
		5th percentile	95th percentile
Olive trees younger than 30 years	34.6%	14.9%	59.0%
Olive trees older than 30 years	69.1%	36.3%	91.9%
Almond	13.3%	3.9%	22.8%
Wine grape in southern EU	2.1%	0.5%	5.6%
Table grape in southern EU	1.0%	0.1%	3.7%
Wine grape in northern EU	0.5%	0.1%	1.4%
Citrus spp.	10.9%	0.7%	30.2%

Maps showing the crops growing areas and the climate suitability of *X. fastidiosa* on the growing areas are in Appendix I. In general they show that all the considered crops are grown in areas characterised by a good climate suitability for *X. fastidiosa*, with the exception of the grapevine cultivated in central and northern Europe characterised by low levels of climate suitability.

3.5.1.2. Cherry and plum

Cherry (*Prunus avium*) and plum (*Prunus salicina* and *Prunus domestica*) are known to be susceptible to *X. fastidiosa* infection. Records from USA, Italy, Spain and France report infection of both cherry trees and plum (Hernandez-Martinez et al., 2007; Yuan et al., 2010; Nunney et al., 2013; Loconsole et al., 2016; Olmo et al., 2017).

In USA, data available about the cherry and plum infection is scarce and it is mainly from survey activities (Hernandez-Martinez et al., 2007; Yuan et al., 2010; Nunney et al., 2013). Wild plum and cherry are also considered symptomless reservoirs of the bacterium (Janse, 2011) and although the confirmed susceptibility of *Prunus avium* and *Prunus salicina*, the disease seemed to be a problem for the commercial production in the USA (Hernandez-Martinez et al., 2007).

The situation is different in Brazil for what concern plum production. Cultivation of plum has a great economic importance (Schneider et al., 2017) and the plum leaf scald (PLS) disease, caused by *X. fastidiosa*, represents a limiting factor for plum production (Dalbo et al., 2018). Symptoms are characterised by leaf scorch and brown rot but the disease produces low fruit quality affecting negatively the weight, the firmness and the size of the fruits (Kleina et al., 2018). The spread of the PLS in Brazil is due to the presence of alternative hosts and efficient and widespread vectors (sharpshooters) (Dalbó et al., 2016). In the state of Santa Carolina, where the PLS disease caused damages to the 90% of plum orchards from 1975 to 1982 (Ducroquet and Mondi, 1997), was developed an intensive breeding programme using some cultivar selections from Florida (Dalbo et al., 2018). However, plum orchards usually have short-life term and the common used strategy is to plant healthy material and spray insecticides for the vector control (Dalbo et al., 2018). It has to be considered that in Brazil the commercial orchards are based on *Prunus salicina* and its hybrids while in EU the most common species is *Prunus domestica*. In addition, vectors belong to different families with different lifestyles (sharpshooters in Brazil and spittlebugs in EU).

In EU, infection of *X. fastidiosa* on *Prunus avium* (cherry) was first reported in 2014 in South Italy (Saponari et al., 2014). In the infected area of the Apulia region, cherry trees showing leaf scorch symptoms and bud failure resulted infected by *X. fastidiosa* subsp. *pauca* (Saponari et al., 2014). Symptoms appear and develop faster in the summer season (Loconsole et al., 2016) and such as other plants (e.g. almond, oleander and broom), *Prunus avium* is considered a source of inoculum for *X. fastidiosa* (Martelli et al., 2016). In Spain, a case of infected cherry trees is reported in Olmo et al. (2017), where in a garden centre three cherry trees out of four showing symptoms were polymerase chain reaction (PCR) positive to *X. fastidiosa* subsp. *fastidiosa* (Landa et al., 2018).

The plum species cultivated in EU are *Prunus domestica* (mostly in northern regions) and *Prunus salicina* (in southern Europe) but no data are available about natural infection. The lack of susceptibility of these species to *X. fastidiosa* subsp. *pauca* ST53 is confirmed by experimental studies using mechanical inoculation (Saponari et al., 2016).

In the EU, the main production areas of cherries are located in Poland, Italy, Spain, Hungary and Greece, while the plum production is greater in Romania, Spain, Italy and France. The potential area of climate suitability of *X. fastidiosa* (Section 3.1.1.2), suggests that *X. fastidiosa* could have a substantial impact in the Mediterranean areas of southern Europe, i.e. Italy, Greece, Spain, France, Croatia, Portugal and Cyprus. Poland, Hungary and Romania, are located in an areas characterised by low climatic suitability for the pathogen, according to the results presented in Section 3.1.1.2.

3.5.1.3. Forest species

Observed impact

X. fastidiosa has been found associated with leaf scorch and decline syndromes on a variety of broad-leaved tree species (Barnard, 2009). Symptoms may include marginal leaf tissue necrosis, premature leaf abscission, decrease in fruit production, decline in vigour, stunting and/or reduced growth, delayed bud break, dieback and eventually death (Sinclair et al., 1987; Barnard, 2009).

Sinclair et al. (1987) noted that leaf scorch diseases caused by *X. fastidiosa* are known mainly in landscape and orchard trees, while their incidence and importance in forests remain to be learned. However, since the beginning of 2000 the disease has been detected in several state forests in Delaware and New Jersey in oak trees (*Quercus* spp.) observed dying from leaf scorch (Griffiths, 2013). In addition, *X. fastidiosa* has been shown to cause typical leaf scorch symptoms on red oak and box-elder (*Acer negundo*) in a commercial nursery in Maryland (Huang, 2007).

X. fastidiosa has been reported to cause great economic impact from an aesthetic or commercial point of view especially on oak, elm and sycamore (Lashomb et al., 2002), although mulberry, red maple and other tree species may also be attacked (Sinclair et al., 1987). Infected trees do not die immediately but tree life is shortened and the aesthetic quality is reduced (Sherald and Kostka, 1992). In general, affected trees may decline to the point where they must be removed (Hearon et al., 1980).

In a survey conducted in 2011–2012 in the District of Columbia, D.C. (USA), on over 20 species of urban trees, the occurrence of crown dieback was found significantly associated with *X. fastidiosa* infection on *Quercus palustris*, *Quercus rubra*, *U. americana* and *Platanus occidentalis* (Harris et al., 2014).

In some New Jersey municipalities, leaf scorch was reported to affect up to 35% of oaks planted as street trees and in landscapes (Lashomb et al., 2002; Gould et al., 2004; Gould and Lashomb, 2005). Loss of value plus replacement costs for older trees affected by this disease was estimated at $8,000 per tree (Gould and Lashomb, 2005). An analysis of economic impact of *X. fastidiosa* indicated that the affected communities in New Jersey would sustain, and must plan for, losses ranging from $0.7 to 1.6 million during the following 10 years (Gould et al., 2004). In addition, it was noted that landowners and tree care professionals in these locations must plan for the loss of property values and high costs of replacement as shade trees in landscapes, wood lots, and golf courses affected by leaf scorch decline and must be removed (Gould and Lashomb, 2005).

In a study conducted in Florida, shoot measurements on *Quercus laevis* revealed significant differences in the shoot growth of the year 1992 between leaf scorched trees and asymptomatic trees, as well as between paired *Xylella*-positive and *Xylella*-negative trees (Barnard et al., 1998). Yearly shoot growth on trees with leaf scorch symptoms was approximately 29% less than that on asymptomatic trees, and shoots on *Xylella*-positive trees were approximately 38% shorter than those on paired *Xylella*-negative trees (Barnard et al., 1998). Based on the above results, *X. fastidiosa* was deemed related to, if not a cause of, growth decline in *Q. laevis* (Barnard et al., 1998).

Bacterial leaf scorch of elm has been reported as particularly troublesome in the mid-Atlantic US (Gould and Lashomb, 2005). For example, 30% of 3,000 elm trees planted in the area around the Washington monument in Washington D.C. were found to be affected by the disease in 2001 (Lashomb et al., 2002). In a survey conducted over 6 years on approximately 600 elm trees (*U. americana*) in the same area as above in Washington D.C., leaf scorch caused by *X. fastidiosa* affected trees in all diameter classes (Sherald et al., 1994). The 20–30 cm diameter class was the most affected with approximately 50% of the trees showing symptoms of leaf scorch (Sherald et al., 1994).

Although leaf scorch on elm is not deemed in itself lethal, it has been reported to predispose elms to attacks by elm bark beetles, which are vectors of the Dutch elm disease (DED) pathogen (Stipes and Campana, 1981). DED is the usual reason such trees die and are removed (Gould and Lashomb, 2005). DED in an elm population surveyed for several years in District of Columbia was about 12 times as common in scorch-affected elms as in others. Overall, over 40% of all cases of DED occurred in trees already affected by bacterial leaf scorch (Sinclair et al., 1987).

On sycamore (*Platanus occidentalis*) leaf scorch caused by *X. fastidiosa* is a chronic disease and it may take years before the affected tree die (Gould and Lashomb, 2005). *X. fastidiosa* -infected trees subsequently attacked by secondary pathogens (e.g. *Botryosphaeria* spp.) have been reported to display cankers and xylem discoloration similar to that caused by the serious canker stain pathogen *Ceratocystis platani*. Hence, it has been suggested that some of the reported significant canker stain mortality in sycamore plantations could have been misidentified, and could therefore be associated with *X. fastidiosa* (Harrington, 2013).

In East Potomac Park, Washington D.C., 80% of trees in a sycamore tree planting were reported to be affected by the disease in 2001 (Lashomb et al., 2002; Gould and Lashomb, 2005). Many sycamore trees growing close to the Capitol building, Washington D.C., were reported to be reduced in size because of the disease, and a lot of dead wood was subsequently removed (Lashomb et al., 2002). Furthermore, sycamore seedlings inoculated with *X. fastidiosa* were reduced in growth and exhibited dieback (Lashomb et al., 2002). Another report refers to the monitoring of a planting of 2,000 London planetrees (*Platanus* × *hybrida*) in Charlotte, North Carolina. The first tree died from *X. fastidiosa* within 7 years after planting, and the disease incidence increased up to 75% (Lashomb et al., 2002).

Bacterial leaf scorch of red mulberry affects trees of all ages, from seedlings to mature individuals (Sinclair et al., 1987). Little is known on the impact of *X. fastidiosa* on mulberry trees. However, in a pathogenicity assay of white mulberry (*Morus alba*) with one strain of *X. fastidiosa*, 3 months after inoculation the pathogen was recovered from 21 out of 25 inoculated plants. Mulberry plants started showing leaf scorch symptoms approximately 5 months after inoculation. After 6 months, leaves dropped and the new shoots and leaves were chlorotic and malformed, and 5 out of 25 plants were dead within a year of inoculation (Hernandez-Martinez et al., 2006).

A leaf scorch on California buckeye (*Aesculus californica*) has also been reported, but trees remain alive (Sinclair et al., 1987). The pathogen has been detected in other tree species, including ashes (*Fraxinus* spp.) (McGaha et al., 2007; Nunney et al., 2013), *Alnus rhombifolia*, *Carya* spp., *Cercis* spp., *Juglans* sp. and *Nerium oleander* (Purcell and Saunders, 1999; Wichman et al., 2000; Wong et al., 2004; Hernandez-Martinez et al., 2007; Yuan et al., 2010; Melanson et al., 2012; Nunney et al., 2013; Hilton et al., 2017; Sanderlin, 2017) as well as in *Fagus crenata* bonsai (Huang et al., 2003). The pathogen has also been detected in a few gymnosperms, including *Ginkgo biloba*, *Pinus taeda* and *Juniperus ashei* (Wong et al., 2004; McGaha et al., 2007), although it was suggested that pines and junipers may harbour non-multiplying bacterial populations inoculated during sharpshooter feeding because conifers lack the vessels that *X. fastidiosa* typically colonises (McGaha et al., 2007). *Eucalyptus* spp., *Populus fremontii* and *Salix* spp. have been documented as potential hosts through artificial inoculations (Purcell and Saunders, 1999; Wistrom and Purcell, 2005).

Most of the above reports on the impact of *X. fastidiosa* on forest trees were based on pathogen identification at the species level rather than at the subspecies level. However, all lines of evidence point to an involvement of *X. fastidiosa* subsp. *multiplex* in the decline of oak, elm, sycamore and ash (Hernandez-Martinez et al., 2006; Morano et al., 2008; Yuan et al., 2010; Behringer et al., 2012; Hopkins et al., 2012; Behringer and Kobayashi, 2013; Nunney et al., 2013; Harris et al., 2014; Harris and Balci, 2015), while white mulberry was reported to be associated not only with *X. fastidiosa* subsp. *multiplex* but also with *X. fastidiosa* subsp. *sandyi* (Harris et al., 2014), or with the newly proposed subspecies *morus* (Nunney et al., 2014b). There is one report of maple (*Acer* sp.) associated with *X. fastidiosa* subsp. *fastidiosa* (Yuan et al., 2010). However, most of the reports on maples refer to *X. fastidiosa* subsp. *multiplex* (Nunney et al., 2013).

X. fastidiosa subsp. *multiplex* has been recently detected in Corsica, France, in sycamore maple (*Acer pseudoplatanus*), cork oak (*Quercus suber*), *Cercis siliquastrum* and *Myrtus communis* (Ministère de l'Agriculture et de l'Alimentation de la République Française, 2018). In the Balearic Islands, Spain, the subsp. *multiplex* has also been detected on *Fraxinus angustifolia*, and the subsp. *fastidiosa* ST1 has been detected on *Juglans regia* (Boletín Oficial de las Islas Baleares, 2018). However, to date, little information is available on the impact of *X. fastidiosa* on these tree species in the EU.

Potential impact in the EU

Should *X. fastidiosa* spread or be introduced to forest areas in the EU, impact could be observed on oaks, elms, maples, and other tree genera known to be affected by the disease in North America. However, there is a high level of uncertainty related to this impact since it is not known whether tree species in those genera that are native to the EU and absent in North America may serve as hosts for *X. fastidiosa* and their levels of susceptibility to the disease.

An analysis of the EFSA Update of the *Xylella* spp. host plant database (EFSA, 2018a) combined with information on the distribution of tree species in the EU reveals that several confirmed hosts of *X. fastidiosa* are widely present in the EU either as native tree species or as non-native planted tree species. Confirmed hosts widespread in the EU include the native *Quercus robur*, *Q. suber*, *Ulmus glabra* and *Acer pseudoplatanus*, and the non-native *Q. palustris*, *Q. rubra*, *Ulmus pumila* and *Acer negundo*; this latter group planted in the EU either for amenity or other purposes (CABI, 2019; EUFORGEN, 2019). Some non-native host tree species became invasive in the EU (Krumm and Vítková, 2016; CABI, 2019; EUFORGEN, 2019). The list of confirmed hosts widespread in the EU also include *Fraxinus angustifolia* (Boletín Oficial de las Islas Baleares, 2018). London planetree (*Platanus* × hybrida) is reported as a host in North America by a report of the USDA (Lashomb et al., 2002) and is widely distributed as an urban and amenity tree species throughout the EU.

The overlap between host distribution range and the map with the continuous suitability scores for *X. fastidiosa* in the EU territory (Section 3.1 on Potential Establishment) suggests that *X. fastidiosa* could have an impact on oaks (*Quercus* spp.) mainly in southern Europe, in particular in southern Portugal, southern Spain, southern France, coastal areas of Italy, Croatia, Cyprus and Greece (Figure 29).

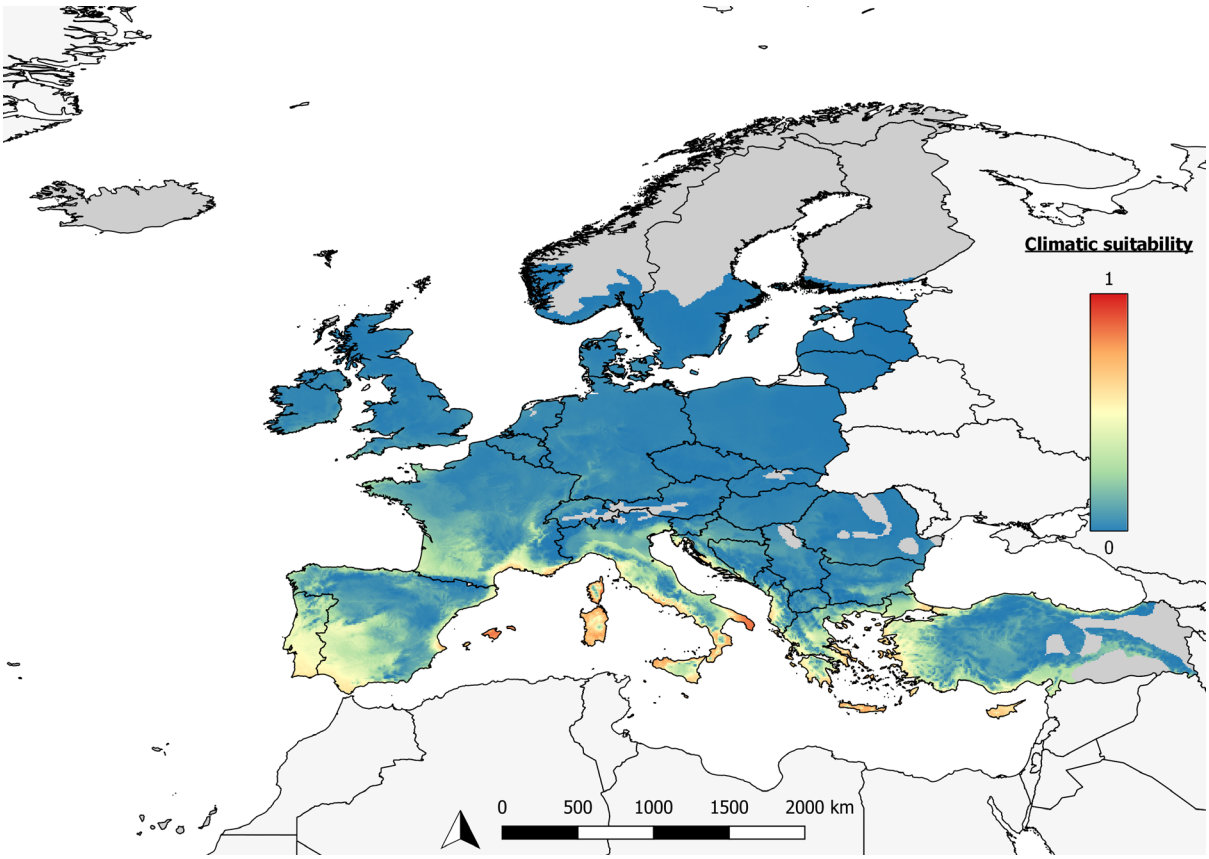

Figure 29: Native distribution range of *Quercus* spp. in the EU (all coloured areas) and levels of climatic suitability of *X. fastidiosa*. Host distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the native distribution range of *Quercus* spp. are mapped

X. fastidiosa is expected to have marginal impact on *Q. robur* as there is only a small overlap between host native distribution range and the climatic suitability area of the pathogen at the EU scale (Figure 30); the overlap is limited to some areas of the Tyrrhenian coast in central Italy (Figure 30). Conversely, most of the natural distribution range of *Q. suber* overlaps with areas characterised by suitable conditions for *X. fastidiosa* (Figure 31), including southern Portugal and Spain, Cote d'Azur and Corsica in France, Sardinia as well as southern Tyrrhenian and Adriatic coasts in Italy. These patterns suggest that *X. fastidiosa* might have a greater impact on *Q. suber* than *Q. robur*.

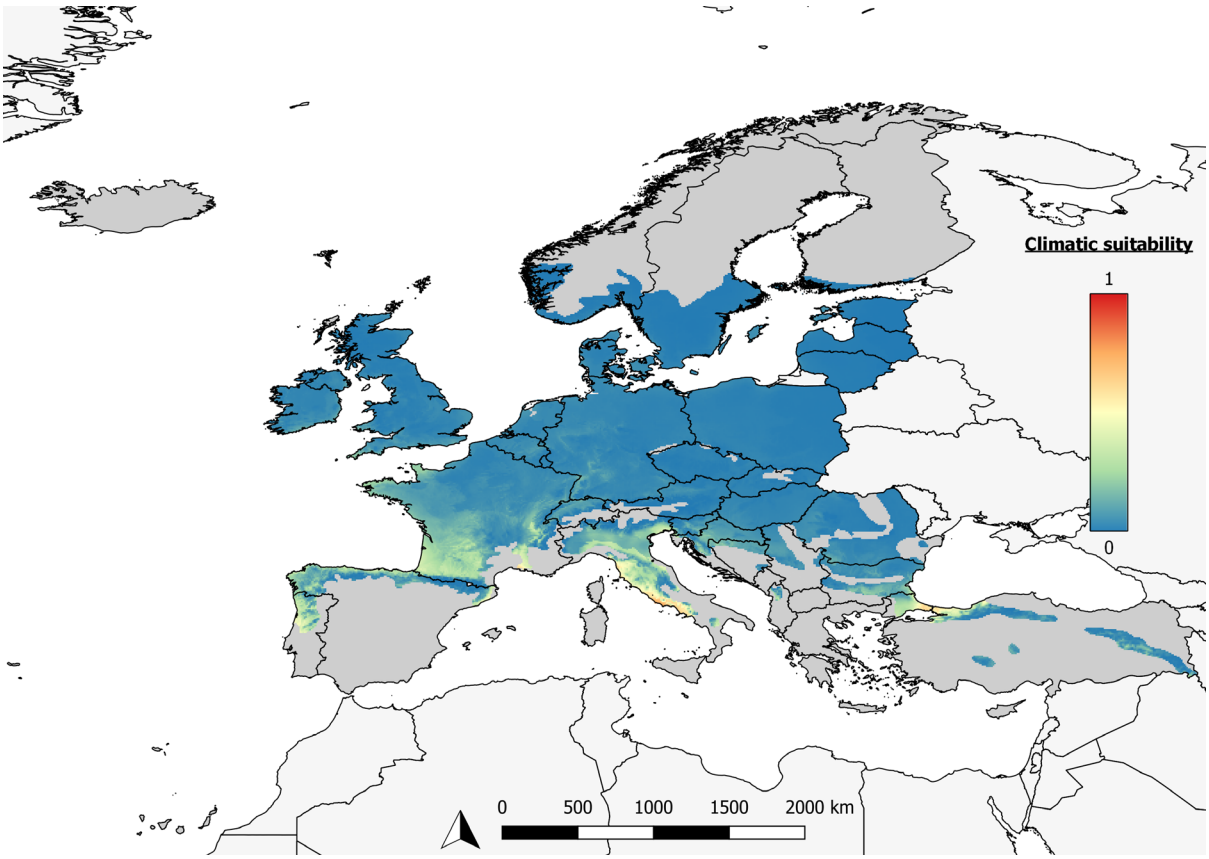

Figure 30: Native distribution range of *Quercus robur* in the EU (coloured areas) and levels of climatic suitability of *X. fastidiosa*. Host native distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the distribution range of *Q. robur* are mapped

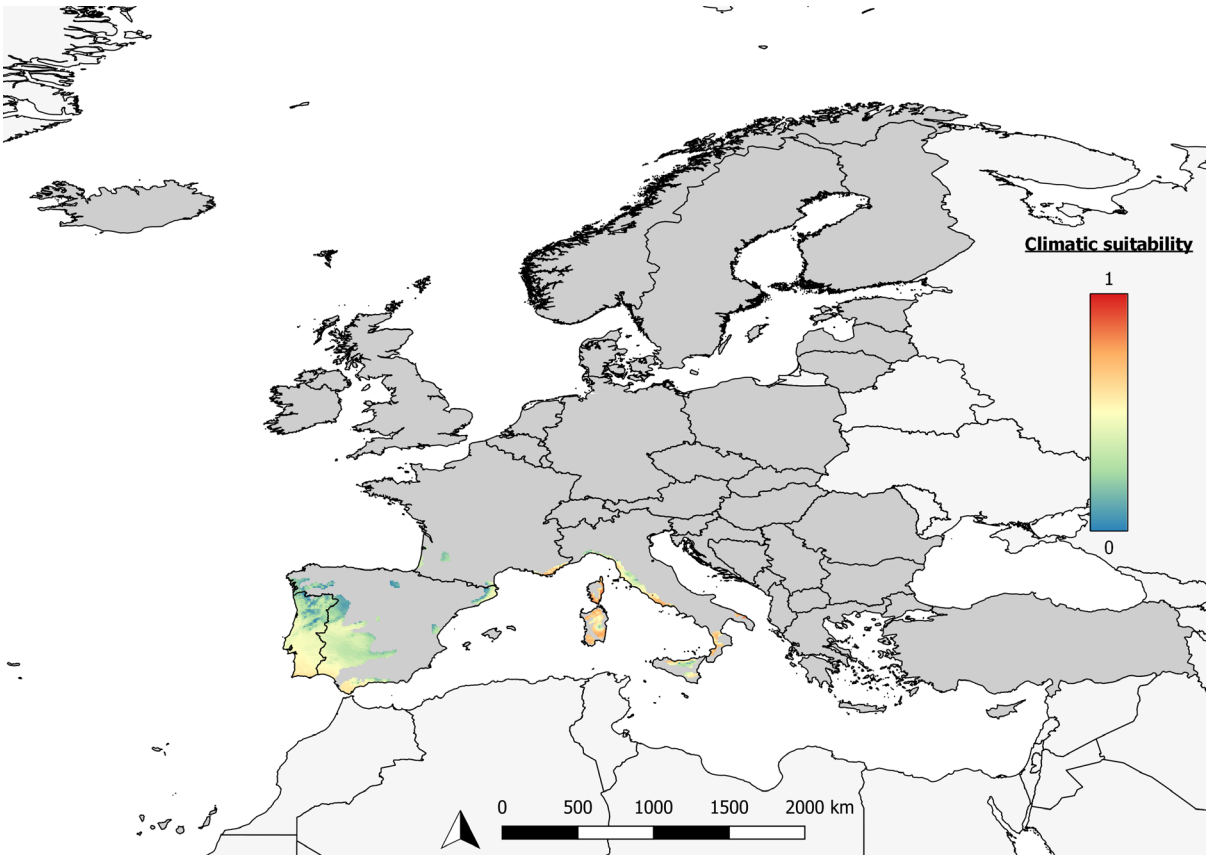

Figure 31: Native distribution range of *Quercus suber* in the EU and levels of climatic suitability of *X. fastidiosa*. Host native distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the native distribution range of *Q. suber* are mapped

A potential impact of *X. fastidiosa* could be expected on elms (*Ulmus* spp.) mainly in southern Europe (Figure 32). Climatic suitability value for the pathogen in the presence of elms is highest (over 0.6) in the proximity of the Mediterranean sea in Portugal, Spain, France, Italy, Croatia and Greece (Figure 32). The map shows that a very limited overlap could occur between the native distribution range of *Ulmus glabra* and pathogen climatic suitability area at the EU scale (Figure 33), suggesting that *X. fastidiosa* could only marginally threaten this tree species. However, other *Ulmus* spp. are present in the Mediterranean area (Figure 32), including *U. minor*, which could be susceptible to the disease, and the confirmed host *U. pumila*. In addition, impact on elms susceptible to DED could also arise from the interaction between *X. fastidiosa*, DED pathogens and their insect vectors, since DED is present in the EU (Kirisitis, 2013).

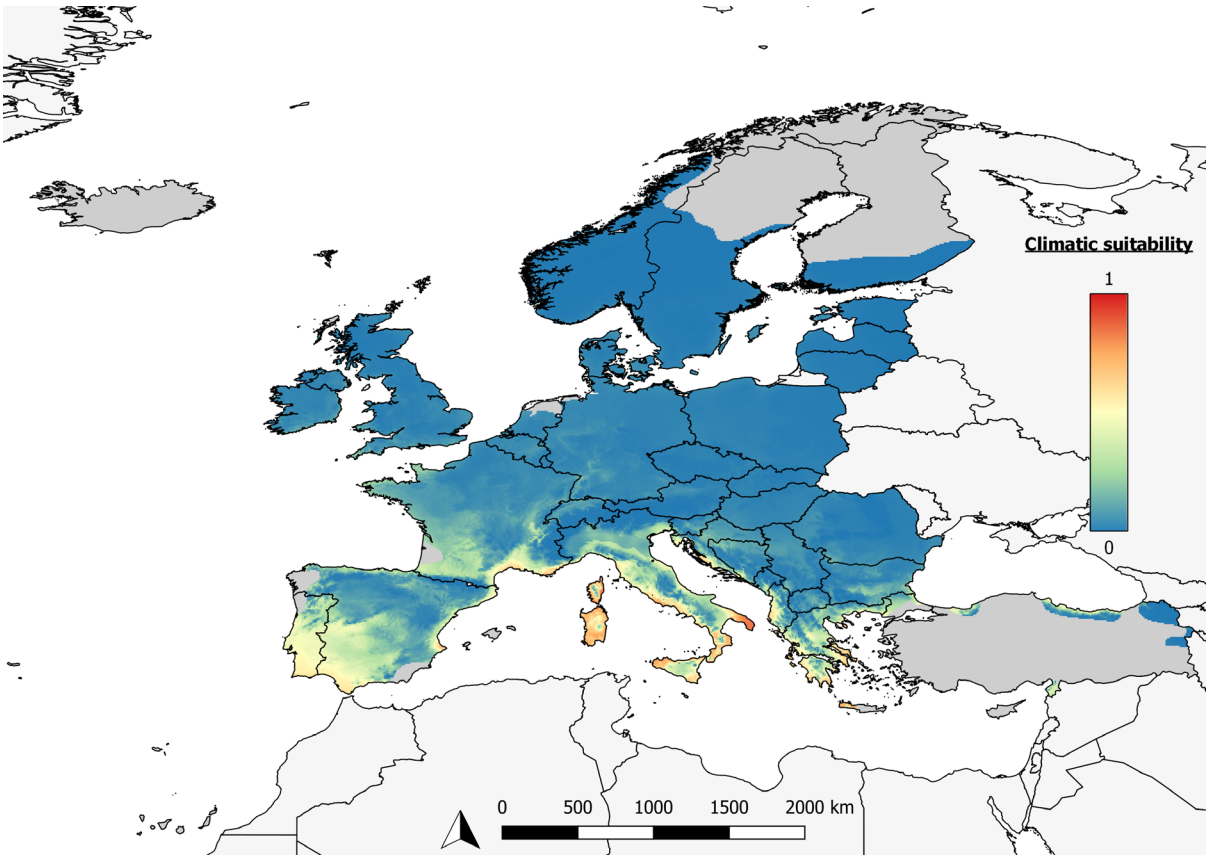

Figure 32: Native distribution range of elms (*Ulmus* spp.) in the EU and levels of climatic suitability of *X. fastidiosa*. Host distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the native distribution range of *Ulmus* spp. are mapped

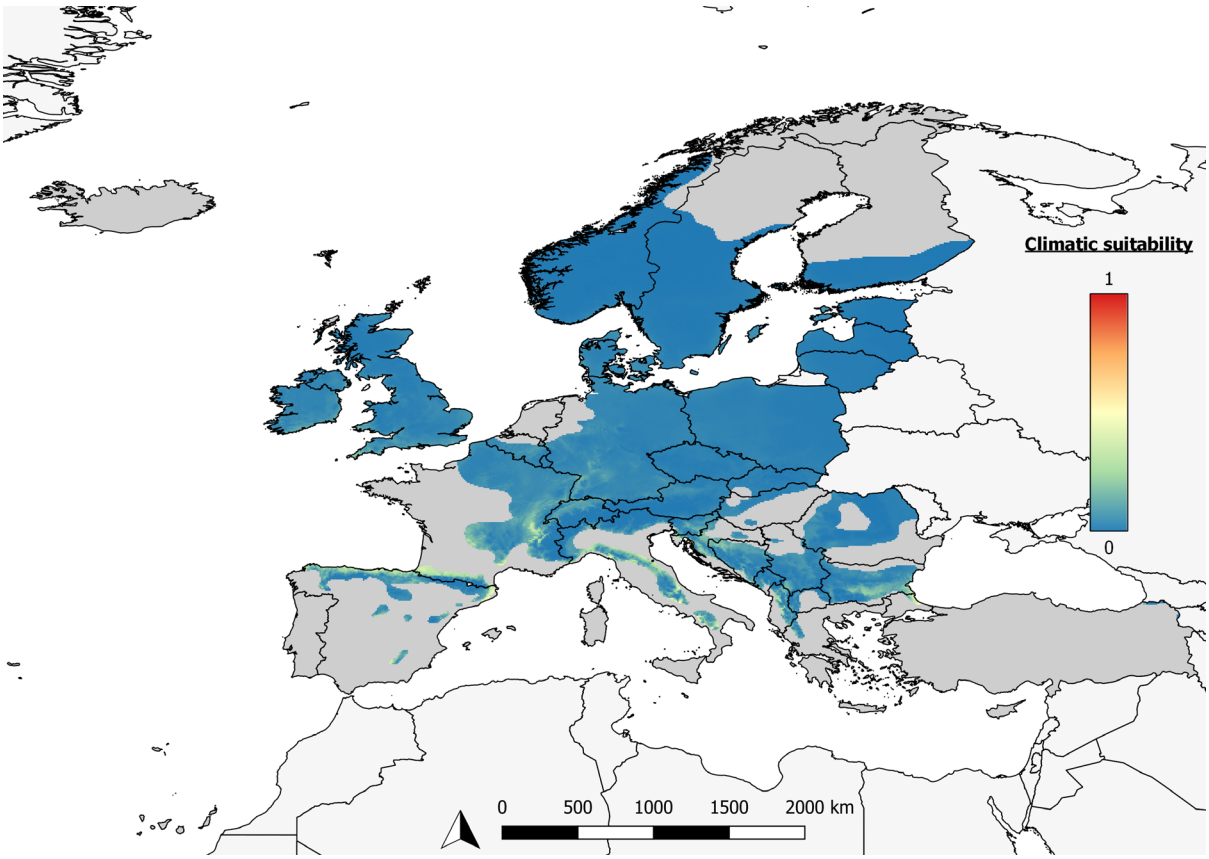

Figure 33: Native distribution range of *Ulmus glabra* in the EU (coloured areas) and levels of climatic suitability of *X. fastidiosa*. Host native distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the native distribution range of *U. glabra* are mapped

X. fastidiosa could impact maples (*Acer* spp.) mainly in southern Europe in particular in the proximity of the Mediterranean sea in Spain, France, Italy, Croatia and Greece (Figure 34). A very limited overlap, which is restricted to the southern Italian Apennine and Sicily (Figure 35) occurs between the native distribution range of *Acer pseudoplatanus* and pathogen climatic suitability area at the EU scale (Figure 35), suggesting that *X. fastidiosa* could only marginally threaten this tree species. However, other *Acer* spp. are present in the Mediterranean area (Figure 34).

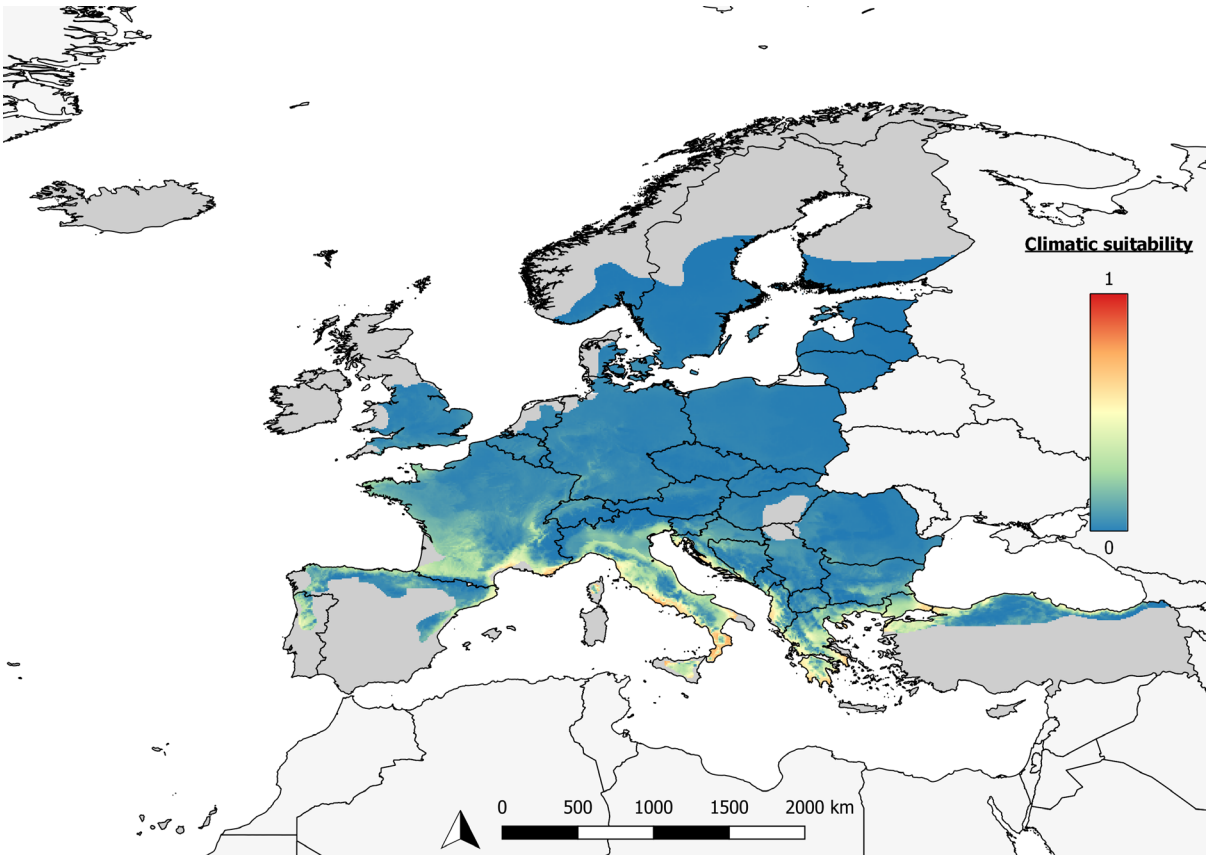

Figure 34: Native distribution range of maples (*Acer* spp.) in the EU (coloured areas) and levels of climatic suitability of *X. fastidiosa*. Native host distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the native distribution range of *Acer* spp. are mapped

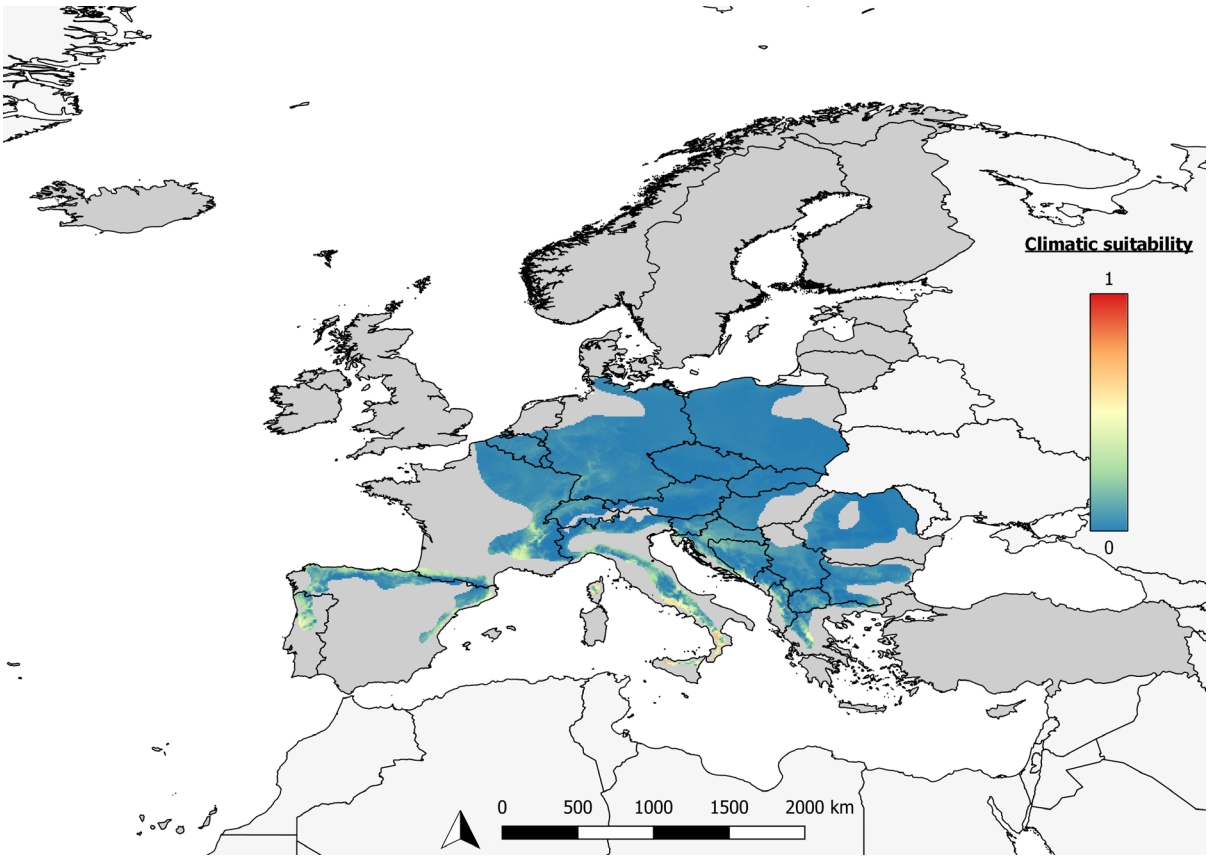

Figure 35: Native distribution range of *Acer pseudoplatanus* in the EU (coloured areas) and levels of climatic suitability of *X. fastidiosa*. Host distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the native distribution range of *A. pseudoplatanus* spp. are mapped

Overlap also occurs in southern Europe between the climatic suitability area of the pathogen and the native distribution range of ashes (*Fraxinus* spp.) (Figure 36), including that of *Fraxinus angustifolia* (Figure 37), although the effects of *X. fastidiosa* on this tree species as well as on other *Fraxinus* spp. are almost unknown.

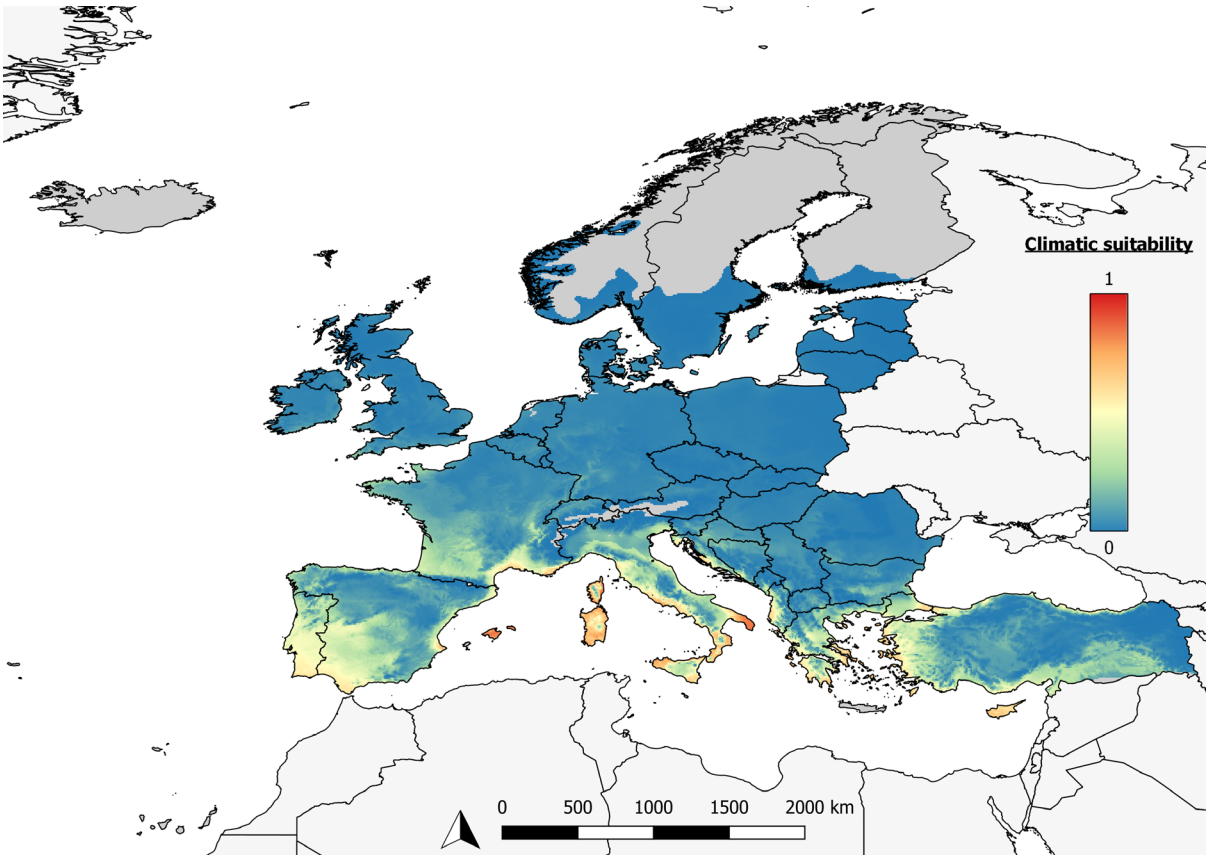

Figure 36: Native distribution range of ashes (*Fraxinus* spp.) in the EU (coloured areas) and levels of climatic suitability of *X. fastidiosa*. Native host distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the native distribution range of *Fraxinus* spp. are mapped

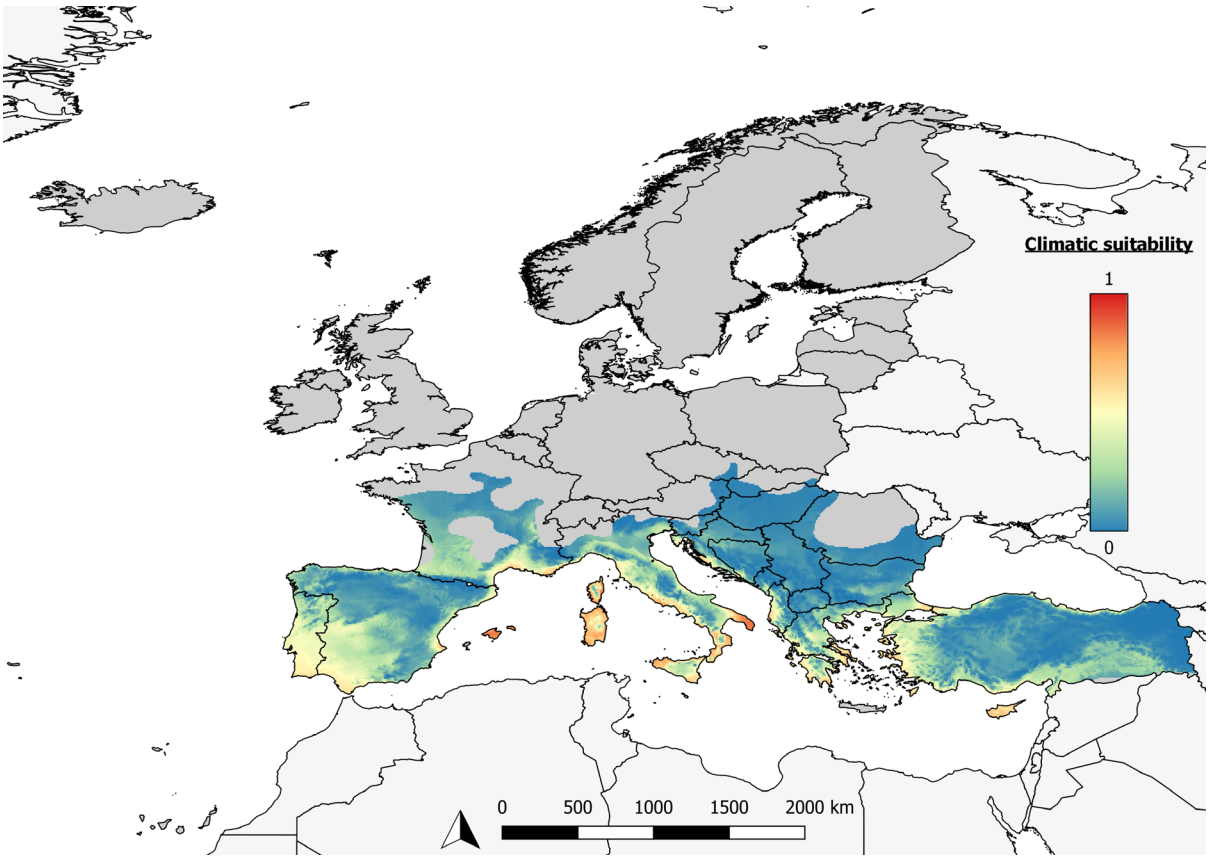

Figure 37: Native distribution range of *Fraxinus angustifolia* in the EU (coloured areas) and levels of climatic suitability of *X. fastidiosa*. Native host distribution maps from Caudullo et al. (2018) and *X. fastidiosa* climatic suitability map according to Section 3.1. Only areas of climatic suitability that overlap with the native distribution range of *F. angustifolia* are mapped

3.5.1.4. Nurseries

X. fastidiosa is able to infect a large number of ornamental, landscape, forest and fruit tree and shrub plant species which are commonly propagated and grown in nurseries. Out of 316 plant taxa reported so far to be naturally infected by *X. fastidiosa* based on at least two different detection methods (EFSA, 2018a), more than 80% of these plant taxa are trees, shrubs or perennial plant species, often vegetatively propagated. These taxa include ornamentals, landscape and forest plants as well as fruit trees and shrubs.

Fruit tree and shrub genera potentially affected by *X. fastidiosa* include *Citrus, Ficus, Morus, Olea, Persea, Prunus, Pyrus, Rubus, Vaccinium* and *Vitis*.

Forest and landscape tree genera potentially affected by *X. fastidiosa* include *Acer, Aesculus, Alnus, Carya, Cercis, Eucalyptus, Fagus, Fraxinus, Ginkgo, Ilex, Juglans, Pinus, Platanus, Populus, Quercus, Salix* and *Ulmus*.

Other ornamental and landscape plant genera potentially affected by *X. fastidiosa* include *Acacia, Albizia, Asparagus, Callicarpa, Catharanthus, Chitalpa, Cistus, Cytisus, Fatsia, Genista, Grevillea, Hebe, Hedera, Hemerocallis, Hibiscus, Jacaranda, Lagerstroemia, Laurus, Lavandula, Ligustrum, Lonicera, Magnolia, Malva, Metrosideros, Myrtus, Nerium, Pelargonium, Phoenix, Polygala, Rhamnus, Rosa, Rosmarinus, Salvia, Sambucus, Spartium* and *Westringia*.

Potential impact on nurseries can be due to direct damage (from leaf scorching to reduced growth, decline and dieback) that reduces the production and the commercial quality of plants for planting in nurseries, however it is also possible that many nursery plants would show limited or no symptoms when they are produced under optimal growth conditions. It is expected that the impact on nurseries growing plants for planting outdoors would be proportional to the climate suitability, whereas the production of plants for planting indoors, under protected cultivation, would generally provide suitable

climatic conditions for *X. fastidiosa* infections. Vectors control practices in nurseries by insecticide treatments is generally more intensive than in agriculture farms or in forests, thus providing an efficient option to reduce the spread of *X. fastidiosa* in nurseries of plants for planting. As shown by the control of CVC in Brazil (Gonçalves et al., 2011), the combination of healthy mother plants use of screenhouse protection for mother plants and seedlings and vectors control are key elements for production of *Xylella*-free plants for planting, particularly for crops which are vegetatively propagated. Hot water treatment for dormant plants for planting is another tool for nursery production of pathogen-free plants, however so far it has been tested for control of *X. fastidiosa* only on grapes and pecan walnut (EFSA PLH Panel, 2015a).

The main impact of *X. fastidiosa* on nurseries is however not linked to the direct damage to the plants but to effect on trade. A simple indicator to estimate this indirect impact is given by the trade flows of plant for planting towards countries where *X. fastidiosa* is not yet present (Appendix G) or is a quarantine pest. Trade of plants for planting towards such countries would encounter limitations if *X. fastidiosa* would become widespread.

3.5.2. Uncertainties affecting the assessment of impact

3.5.2.1. Olive, almond, grapevine and *Citrus* spp.

Uncertainties considered for the EKEs on the impact of *X. fastidiosa* on olive, almond, grapevine and *Citrus* spp. are available in Appendix E.

3.5.2.2. Forest species

The main uncertainty is related to the lack of specific quantitative information on the impact of *X. fastidiosa* on forest species. In addition, there is a high level of uncertainty related to this impact since it is not known whether tree species in those genera that are native to the EU and absent in North America may serve as hosts for *X. fastidiosa* and their levels of susceptibility to the disease.

3.5.2.3. Uncertainties affecting the assessment of impact on nurseries

The main uncertainty is related to the lack of specific quantitative information on the impact of *X. fastidiosa* on nurseries

3.5.3. Conclusions on impact

3.5.3.1. Olive, almond, grapevine and *Citrus* spp.

Among the considered crops and under the considered scenario assumptions (Appendix E), olive was estimated to be the most sensitive crop to *X. fastidiosa*, with estimated median yield losses of 34.6% (90% uncertainty range between 14.9% and 59%) in the case of olive trees younger than 30 years, and of 69.1% (90% uncertainty range between 36.3% and 91.9%) in the case of trees older than 30 years. The main elements that drove the assessment included that most of the EU olive production is based on plants older than 30 years (more sensitive) and conducted with traditional farming systems. *Philaenus spumarius* populations are correlated positively with olive groves in the landscape where high densities are found (Santoiemma et al., 2019). So far impact on olive has been reported by *X. fastidiosa* subspecies *pauca* in Italy (ST53), Brazil (ST16) and Argentina.

Almond and *Citrus* spp. were estimated to be at lower risk compared to olive. The estimated median yield loss on almond was estimated to be 13.3% (90% uncertainty range between 3.9% and 22.8%), while for *Citrus* spp. 10.9% (90% uncertainty range between 0.7% and 30.2%). One of the main factors driving the experts' estimates on almond was the fact that most of the almond production area in the EU (85%) relies on rainfed traditional systems with very low or absent management. Only the remaining 15% is represented by modern, highly productive and well managed plantations. Information is still little on the effect of different varieties. The impact on *Citrus* spp. considered mainly oranges, because mandarins, limes and lemons are resistant, tolerant, or show very little symptoms. The assessment was mainly driven by the fact that in Mediterranean areas citrus plantations are irrigated, there is almost no ground cover in summer, and high densities of the known European vectors have not been reported on citrus. So far impact on citrus has been reported in Brazil by CVC strains of *X. fastidiosa* subsp. *pauca*.

Regarding grapevine, this is the crop for which the lowest impact was estimated. In fact, for the three classes that were estimated, the estimated median yield losses were between 0.5% (wine grape in northern EU) and 2.1% (wine grape in southern Europe). Like almond and *Citrus* spp., in grapevine

high densities of *Philaenus spumarius* populations are not found. In fact their population levels are negatively correlated with vineyards in the landscape (Santoiemma et al., 2019). In addition, the window of time in which infectious vectors can effectively transmit the diseases (determining a systemic infection) is short, just 2 or 3 months and late infections would be removed by pruning. In fact, modern vine training systems include seasonal heavy pruning which lower the probability of systemic infections. In general, pest control is well applied in grapevine. This is particularly true for table grape where pest control is more intense throughout the whole season. The assessment for grapevine production in central Europe is lower than southern Europe because of the impact of the freezing winter temperatures that would eliminate the bacterium from grapevine infected in spring. The assessment did not consider the impact of other potential vectors of *X. fastidiosa*. In case other xylem-feeding insect species would prove to be efficient vectors in grapevines in the EU, this assessment would need to be repeated taking into consideration the new vectors. A much higher impact is expected in case new exotic and efficient vectors are introduced in the EU. So far impact on grapevine has been reported in North America by Pierce's disease strains of *X. fastidiosa* subsp. *fastidiosa.*

3.5.3.2. Forest species

Due to the limited information on the impact of *X. fastidiosa* on forest trees in North America, the level of impact in the EU should the pathogen be introduced or spread from current infested areas cannot be quantified. However, considering the plants detected infected so far, the distribution of the hosts, and the area of potential establishment of the disease, impact is likely to be expected mainly in southern Europe. However, considering that the most important subspecies for forest species seems to be *X. fastidiosa* subsp. *multiplex*, the range of potential impact could be wider and extended to other areas of central and northern Europe (Section 3.1.1.2 on the potential establishment of *X. fastidiosa* subspecies).

The impact of *X. fastidiosa* on forest tree species may be different depending on whether the tree is planted in urban and peri-urban environment as an amenity tree or if it is found in forests. In the former case, a direct impact of the disease on the aesthetic of the tree, hence on one of its major functions, is to be expected. In the latter case, the disease may cause reduced shoot growth (Barnard et al., 1998), and possibly a reduction in the production of wood. Leaf scorch, dieback and mortality may occur both in urban and forest environments, although they might have more impact in the former environment, due to the necessity of removing and replacing the diseased tree with a new one.

3.5.3.3. Nurseries

Due to the very limited published information on the impact of *X. fastidiosa* on plant nurseries, the level of impact in the EU should the pathogen be introduced or spread from current infested areas could not be quantified by an expert elicitation. However, considering the plants detected infected so far, the distribution of the nurseries and the area of potential establishment of the disease, impact is likely to be expected outdoors more frequently in southern Europe, and indoors in all the EU. Nurseries that could be affected are mainly those producing plants for planting of fruit trees and shrubs, forest and landscape trees and ornamentals. Production under screenhouse of healthy mother plants and seedlings together with vectors control are options to reduce such impact. Hot water treatment is also an efficient tool but so far tested only on grapes and pecan for this pathogen.

In case *X. fastidiosa* would become widespread in the EU, an indirect impact can be expected in terms of trade limitations for plants for planting toward countries where *X. fastidiosa* is absent or is listed as a quarantine plant pest.

3.6. Risk reduction options

In this section, the Panel reviewed and updated the control measures available by vectors control (Section 3.6.1), available resistant or tolerant germplasm (Section 3.6.2) and agriculture practices (Section 3.6.3), whereas risk reducing options for control *in planta* are assessed in a separate scientific opinion (EFSA PLH Panel, 2019). The phytosanitary measures were considered and reviewed within the analyses of the asymptomatic period (Section 3.2), the SRS (Section 3.3) and the long-range spread (Section 3.4). The taxonomic level in phytosanitary measures is discussed in Section 3.6.4.

3.6.1. Vector control[5]

Control measures against insect vectors of plant pathogens should be considered as part of an integrated approach of disease management. Strategies should take into account the interactions of the vectors with other disease elements, such as the pathogen (transmission characteristics), the host plants (of the pathogen and vector) and the environment, as well as the inoculum sources and types of spread (primary and secondary) (Almeida et al., 2005; Lopes et al., 2016). In Italy (Apulia) and other southern regions of the EU now invaded by *X. fastidiosa*, spittlebugs (Hemiptera: Aphrophoridae) are recognised as important vectors (or potential vectors) based on their wide distribution in different habitats and crops currently affected by *X. fastidiosa*. The most abundant spittlebug species, *Philaenus spumarius*, has been well studied with respect to its biology and ecology, and confirmed as a vector of *X. fastidiosa* to many different plant species (Severin, 1950; Purcell, 1980; Cornara et al., 2016, 2017). It is a highly polyphagous and univoltine species that overwinters in the egg stage, and the nymphs develop mostly on herbaceous plants (Weaver and King, 1954), which are commonly found in the ground vegetation and surrounding areas of orchards. In the Mediterranean region, nymphs develop during March and April and adults start emerging in April and May (Cornara et al., 2018). Over late spring and early summer (coinciding with senescence of ground vegetation in dry regions), adults move to woody hosts that include olives and a number of evergreen or deciduous trees and shrubs (Bodino et al., 2017; Cornara et al., 2017). At the end of summer and early autumn, adults return to herbaceous plants for egg laying and overwintering (Weaver and King, 1954; Cornara et al., 2018). The CoDiRO strain of *X. fastidiosa* subsp. *pauca*, which causes the olive quick decline syndrome (OQDS) in Italy, has a known host range (including crops and ornamental plants) that overlaps with that of *Philaenus spumarius* (Weaver and King, 1954; Cornara et al., 2017), suggesting that some of these host species may serve as natural reservoirs and possibly as inoculum sources for primary spread of the pathogen to the affected crops. There is also evidence from transmission studies in Apulia that secondary (tree-to-tree with active role of vector) spread of *X. fastidiosa* occurs within infected olive orchards (Cornara et al., 2017, 2018). Studies on transmission mechanisms of *X. fastidiosa* show that vectors can efficiently acquire the pathogens either as nymphs or adults, but nymphs loose the infectivity after moulting (non-transstadial passage), whereas adults remain infective for life (Purcell and Finlay, 1979; Hill and Purcell, 1995; Almeida and Purcell, 2003). This information applied to the OQDS pathosystem suggests that primary and secondary spread by *Philaenus spumarius* most likely occur by adults, which move from weeds to olives and other woody hosts and will be able to carry the pathogen among trees within and between orchards. In fact, a high frequency of field-collected adults in Apulia is shown to be naturally infected with *X. fastidiosa* by quantitative polymerase chain reaction (qPCR) (Cornara et al., 2017).

Considering the available information on transmission, vector ecology and disease epidemiology, management strategies should be established to reduce adult vector population density and to avoid or mitigate both primary (from alternative hosts or between orchards) and secondary (tree-to-tree spread within an orchard) spread. In the case of olives in Apulia, primary spread can be reduced by combining vector control in the ground vegetation of the orchards and surrounding areas with other phytosanitary measures aimed at reducing pathogen inoculum outside the crop (e.g. eradication of alternative hosts of the pathogen). Secondary spread can be avoided by controlling the vector on the crop at specific times of the year when spittlebug adults visit the crop tree canopy more often (e.g. May–July), combined with other measures aimed at reducing the inoculum within the crop (e.g. planting healthy nursery trees and roguing of infected trees).

An extensive review of the available chemical, biological and cultural control methods that can be used to suppress vector populations in orchards or surrounding areas, depending on the target (nymphs and/or adults), ground vegetation, season and environmental conditions, is available in Bosco et al. (2019).

[5] The Panel wishes to highlight that the scope of this opinion is to present and discuss possible vector control measures retrieved from the scientific literature, that may have efficacy controlling insect vectors of *X. fastidiosa*. The control measures mentioned in this opinion may have referred to pesticide active ingredients contained in products that no longer have current authorisations for plant protection in the EU. The use of plant protection products in the EU is regulated by Regulation (EC) No 1107/2009. The competent regulatory authorities of Member States for pesticides should be consulted to obtain the latest information on pesticide product authorisations. The European Commission's data base of pesticide active substances approved for use in pesticide products (http://ec.europa.eu/food/plant/pesticides/eu-pesticides-database/public/?event=homepage&language=EN) is also a resource that it is important to consult.

Chemical control

Regarding chemical control, Bosco et al. (2019) includes:

- a list of active ingredients tested on *X. fastidiosa* vectors and potential vectors approved for use in the EU territory (Bosco et al., 2019, Annex 1),
- a list of the available reports regarding the efficacy of insecticides towards xylem-sap feeding insects in different countries (Bosco et al., 2019, Annex 9)
- an inventory table of Good Agricultural Practices, country by country, applicable to the active ingredients allowed for use in the EU (Annex 9).

In summary, the most effective active substances to control adults of *Philaenus spumarius* on olive trees are neonicotinoids and pyrethroids (Dongiovanni et al., 2018a) with mortality rates ranging from 76.7% to 100% at 3 day after treatment; although pyrethroids are by far much less persistent than neonicotinoids. Data on organophosphates are conflicting, however they show very low persistency. Application of insect growth regulators (buprofenzin and spirotetramat) against spittlebugs nymphs showed very low efficacy and was judged as not promising (Dongiovanni et al., 2018a). However, data are very scarce. Preliminary data suggest that, among substances screened for use in organic farming, essential citrus oil is more effective than pyrethrins, however both products are not persistent. Similarly, for the control of the juveniles, the neonicotinoids and pyrethroid products cause significant reduction in nymphs on the sprayed vegetation.

In Italy, some insecticides approved for use in EU territory were shown to be effective (75–100% mortality), especially neonicontinoids (i.e. acetamiprid) and pyrethroids (deltamethrin) (Dongiovanni et al., 2016, 2018a). Organophosphates (e.g. chlorpyrifos and dimethoate) cause significant mortality of adults, but were less effective and persistent than neonicotinoids (Dongiovanni et al., 2018a).

According to Bosco et al. (2019), Integrated Pest Management (IPM) programmes ongoing in most if not all the Mediterranean countries still do not consider *X. fastidiosa* vectors as pests, and a revision of these programmes will be mandatory in order to include xylem-sap feeding insects' control.

Biological control

Information regarding natural enemies of *X. fastidiosa* vectors is very limited. Parasitoids of eggs (Hymenoptera: Eulophidae and Mymaridae), nymphs and adults (Diptera: Pipunculidae) of spittlebugs are reported in the USA and other parts of the world (Weaver and King, 1954; Harper and Whittaker, 1976), but there are still few studies on their natural rates of parasitism and effectiveness in reducing the pest populations. In addition, the introduction of non-indigenous parasitoid species in classical biological control programmes have several constraints, including regulatory issues (EPPO, 2014, 2018) because of their possible polyphagia. In the EU, the pipunculid fly *Verralia aucta* is perhaps the only parasitoid of *Philaenus spumarius* whose impact has been investigated (Harper and Whittaker, 1976). Preliminary results from Reis et al. (2018) indicate that beneficial organisms such as parasitoids could be effective in controlling eggs of *Philaenus spumarius*. The lack of knowledge on other potential natural enemies hampers the effective implementation of biological control measures (Bosco et al., 2019).

Entomopathogenic fungi (e.g. *Metarhizium anisopliae*), if proven effective against *Philaenus spumarius*, could be used to target developing nymphs on ground vegetation in early spring. Entomopathogenic micro-organisms have the advantage of being more selective than insecticides to other natural enemies, not toxic to humans and other vertebrates and may be used in areas where insecticides would pose serious risks to humans or wildlife. Interestingly, *M. anisopliae* was shown to be compatible with neonicotinoid insecticides in integrated control of spittlebugs in sugarcane (Kassab et al., 2014). No data or information on the use of entomopathogenic fungi is available for the EU.

Cultural and other control options

The immature life of most, if not all, *X. fastidiosa* vectors and potential vectors are associated with herbaceous host plants and weeds. This observation was verified also for *Philaenus spumarius* in the particular case of the olive groves in Apulia where the elimination of weeds within and around the olive groves may help in reducing the vector populations. Cultural methods usually involve vegetation management by removal of vector host plants (Linnane and Osgood, 1976) and elimination of straw on the soil, which provides a preferred oviposition site (Weaver and King, 1954) and favourable microclimate for nymphal development (Koller and Valerio, 1988). Removal of ground vegetation of olive orchards (by tillage, mowing or herbicides) has been suggested as a method to control *Philaenus spumarius* nymphs developing on herbaceous plants (Cornara et al., 2018). Field trials carried out in

olive groves in Apulia confirmed the possibility to mitigate the spread of the bacterium through mechanical weed control methods. Specifically, a 2-year (2017–2018) field trial conducted in olive orchards in Apulia showed that tillage performed in winter and spring significantly reduced (almost to zero) the abundance of both *Philaenus spumarius* and *N. campestris* on olive trees and ground vegetation, with an efficacy (Abbott's index – Abbott, 1925) of 99.6% compared to control plots. Conversely, tillage performed in winter only reduced the *N. campestris* population (efficacy from 50% to 60%), but not the *Philaenus spumarius* population when compared to control plots (Dongiovanni et al., 2018b). Sowing of *Lolium* spp. and *Hordeum vulgare* as a cover crop in winter decreased *Philaenus spumarius* juvenile populations, with an efficacy of 60% and 40% compared to control plots, respectively. Whereas, in the same plots surveys for the juveniles of *N. campestris* produced inconsistent results between the two experimental years: high efficacy (from 58% to 86.5%) during the first year and no efficacy at all (0%) during the second year (Dongiovanni et al., 2018b).

Another selective and potential control method is the application of particle film technology (e.g. kaolin) to interfere with vector host plant selection; when applied on grapes, kaolin particles change the colour of the tree canopy, inhibiting landing by sharpshooter vectors and reducing pathogen transmission (Puterka et al., 2003; Tubajika et al., 2007). However, preliminary results from field trials aimed to test the effect of kaolin on vector transmission in olive trees in the infected are in Italy did not show effective results compared to controls (Dongiovanni et al., 2018b).

Application of RROs in different areas

Research is needed to investigate the efficacy of these vector control methods individually and in combination in different regions, since the results may vary substantially depending on climate, vegetation and vector species, among other factors.

In the EU, most of the vector control experiences come mainly from Apulia. Other areas, like e.g. Alicante where small orchards are surrounded by natural and semi natural vegetation, options for cultural control or chemical spray could be rather limited. However, although the biological cycle and the population dynamics can slightly change according to the ecological and climatic conditions, the tools for the control rely mainly on the same pillar: i.e. juveniles would be the most vulnerable stage to control by soil tillage, and chemical products tested against the adults may be effective despite the crop.

3.6.2. Available germplasm

The plant varietal resistance or tolerance to *X. fastidiosa* infection have been studied on different host plant species (He et al., 2000; Krivanek et al., 2005a; Ledbetter and Rogers, 2009; Cao et al., 2011; Sisterson et al., 2012). Various degrees of resistance, tolerance and susceptibility have been observed in economically relevant crops such as grape, citrus, almond, and more recently, olive.

Field observation and experimental studies carried out in southern Italy in the last 5 years evidenced the possibility to mitigate the impact of *X. fastidiosa* through the use of olive germplasm that carry tolerant/resistant genetic traits. The recent discovery of severe susceptibility of *Olea europaea* to *X. fastidiosa*, as demonstrated by the epidemic of OQDS reported from Italy in the fall of 2013 (Saponari et al., 2013; Boscia et al., 2017a), stimulated the search for tolerant/resistant olive accessions in germplasm collections. Extended surveys and experimental infectivity studies designed to evaluate olive cultivar response to *X. fastidiosa* infection (subsp. *pauca*, ST53, strain CoDiRO) identified cv. Leccino as being tolerant to *X. fastidiosa* based on lower incidence, bacterial population, and symptom severity when compared to cv. Ogliarola salentina (Figure 2) (Boscia et al., 2017a).

A global quantitative transcriptome profiling of cv. Leccino and cv. Ogliarola salentina revealed the presence of differentially expressed genes in plants of the two cultivars, and that cv. Ogliarola salentina response to *X. fastidiosa* infection resembled the response to drought stress, as shown by the up-regulation of several genes known to be differentially expressed in other plant species. The lower pathogen concentration in cv. Leccino compared to other cultivars suggests that cv. Leccino may have genetic constituents and/or regulatory elements that suppress population growth of *X. fastidiosa* (Giampetruzzi et al., 2016; Saponari et al., 2018). EFSA (2017) concluded that, from experimental infectivity studies and from surveys in olive orchards, converging lines of evidence indicate tolerance of the olive variety Leccino to *X. fastidiosa* subsp. *pauca* ST53 infections, although no long-term observations on yield are available yet (EFSA, 2017).

Preliminary results show that tolerance or resistance traits can also be found in other olive varieties (EFSA., 2017). In observations conducted in a severely affected multivarietal olive orchard, another

cultivar, FS17®, exhibited satisfactory phenotyping (i.e. absence or mild development of symptoms) and reduced prevalence of *X. fastidiosa*. None of the FS17® olive trees showed OQDS symptoms, contrary to Ogliarola salentina and Leccino plants that exhibited severe and mild symptoms, respectively (Boscia et al., 2017a; Technical report by POnTE et al., 2017). Quantitative PCR assays showed that *X. fastidiosa* population density in FS17® plants was 50% lower than in Leccino plants from the same grove. The bacterial population detected in Ogliarola salentina trees was 100-fold higher compared to Leccino olive plants (Boscia et al., 2017a; Technical report by POnTE et al., 2017).

Figure 38: Olive grove in the *X. fastidiosa* -affected area in Apulia (Italy). The row of severely affected olive trees of cv. Ogliarola (left) is compared with the symptomless row of cv. Leccino (right)

With the aim to extend the panel of olive germplasm with promising characters of resistance/tolerance to *X. fastidiosa*, a larger screening was initiated in 2015 and progressively extended in the following years. The screening trials include hundreds of cultivars/accessions and feral olive seedlings that have been mechanically inoculated under controlled greenhouse conditions and/or exposed to natural inoculum pressure in experimental plots in Apulia. Although this approach is currently considered an ongoing long-term research programme, preliminary data already show differences in the incidence of infection among different olive candidates, representing a promising approach to identify tolerant and resistant plants (Technical report by POnTE et al., 2017). Due to the lower bacterial population, a very low percentage of spittlebugs were able to acquire and inoculate the bacterium after feeding on infected Leccino plants, indicating that olive cultivars may have implications in vector transmission efficiency.

Efforts have been made to identify genetic traits that confer resistance/tolerance to Pierce's disease of *Vitis* spp. in California. In 2006, Krivanek et al. (2006) identified a quantitative train locus (QTL), PdR1, as a primary resistance gene region to Pierce's disease in *Vitis*. An intensive conventional breeding programme using marker-assisted selection was developed to introgress the PdR1 region in commercial *V. vinifera* cultivars (Riaz et al., 2009). Walker and Tenscher (2012) succeeded in the selection of 97% *V. vinifera* cultivars harbouring the PdR1 gene region. Those populations have been tested for agricultural and organoleptic characters and screened for the highest level of resistance. To date, some advanced selections have been pre-released to grapevine nurseries for propagation and should become available for commercial use in the coming years (Walker et al., 2017). However, it is possible that the pathogen may overcome resistance. Therefore, the ongoing breeding programmes in California are searching for alternative sources of resistance. Three resistant accessions with phenotypic data that do not correlate with the genetic markers linked to PdR1 QTL were selected (Riaz

et al., 2018). The availability of additional resistance sources is crucial for developing *V. vinifera* cultivars with a more durable resistance to Pierce's disease.

In the US, the production of genetically transformed grapevines has also been considered as an option to control Pierce's disease. Recently, transgenic grapevine rootstocks expressing a pear polygalacturonase inhibitory protein (PGIP) or a chimeric antimicrobial protein (CAP) were obtained (Aguero et al., 2005; Dandekar et al., 2012) and showed resistance to *X. fastidiosa*. Those transgenic rootstocks efficiently prevented symptom expression on grafted wild-type scions (Dandekar et al., 2019). Dandekar et al. (2017, 2012) genetically transformed grapevines to produce a chimeric antimicrobial protein containing cecropin B, a lytic peptide that targets bacterial membranes. Transgenic lines expressing such chimeric protein showed promising results in controlling *X. fastidiosa* infection (Dandekar et al., 2017).

As reported above, almond (*Prunus dulcis*) is a sensitive crop to *X. fastidiosa*, with an estimated yield loss over 10% (Table 15); however, different levels of susceptibility of almond (*Prunus dulcis*) cultivars have been reported (Sisterson et al., 2008, 2012) and the use of a rootstock immune to *X. fastidiosa* has been proposed to control ALS disease in nurseries (Krugner et al., 2012) and orchards (Krugner and Ledbetter, 2016). The search for resistant rootstocks continues and *Prunus* hybrids have been developed and trialled for *X. fastidiosa* resistance. Differences in susceptibility have been reported among traditional *Prunus persica* × *Prunus dulcis* hybrids (peach–almond hybrids), that appear non-hosts of *X. fastidiosa* (Ledbetter and Rogers, 2009), and non-traditional *Prunus webbii* × *Prunus dulcis* hybrids showing susceptibility to the pathogen (Rogers and Ledbetter, 2015; Ledbetter and Lee, 2018).

Citrus is another industry to which *X. fastidiosa* may cause a substantial yield loss (Table 15). Within *Citrus* spp., all *C. sinensis* cultivars are susceptible to *X. fastidiosa* infection, except cv. Navelina ISA 315, which is resistant (Fadel et al., 2014). Different levels of resistance/tolerance were observed in *Citrus* spp. and hybrids, with mandarins (*C. reticulata*), tangors (*C. sinensis* × *C. reticulata*) and lemons (*C. limon*) generally considered resistant (Laranjeira et al., 1998a,b; Laranjeira and Pompeu Junior, 2002; Coletta-Filho et al., 2007; Garcia et al., 2012).

3.6.3. Agricultural practices

Common agricultural practices, usually applied to both healthy and diseased plants, include pruning, irrigation and fertilisation.

Irrigation

The effects of irrigation and plant water stress on pathogen and vector behaviours have been investigated. However, all these studies are limited to North America and the main vector found in this area. Plant water stress can accelerate disease progression and increase symptom severity (McElrone et al., 2001, 2003). Changes in xylem-fluid tension caused by water stress play a relevant role on vector feeding behaviour leading to conflicting effects on pathogen acquisition and inoculation processes. An experiment conducted with citrus and almond plants showed that longer and more frequent feeding events by the glassy-winged sharpshooter, *Homalodisca vitripennis* (Hemiptera: Cicadellidae) (the most efficient vector of Pierce's diseases in the USA), occurred on fully irrigated plants, suggesting that even low levels of plant water stress could reduce transmission efficiency of *X. fastidiosa* (Krugner and Backus, 2014). Grapevines, though, show a different response. Acquisition efficiency of *X. fastidiosa* by *H. vitripennis* increased as water stress increased in source grapevines, whereas inoculation efficiency was not affected by water status of recipient grapevines (Del Cid et al., 2018).

Fertiliser application

Fertilising infected plants may temporary reduce disease severity. The effect of some products containing copper and zinc was extensively discussed in the EFSA scientific opinion on 'Effectiveness of *in planta* control measures for *X. fastidiosa*' (EFSA PLH Panel, 2019).

Pruning

The only case reporting successful elimination of *X. fastidiosa* infection and disease symptoms by pruning was reported from sweet oranges in Brazil (Amaral et al., 1994), but only in very specific conditions and at the early stages of the infection of individual branches (before a systemic infection). There are no other examples of elimination of *X. fastidiosa* from diseased plants by pruning described

in literature. Hopkins and Purcell (2002) reported that summer and autumn pruning of grapevines may eliminate recent bacterial infections occurring on the outer canopy of grapevines (cane tips). However, a recent study tested the effects of severe pruning on Pierce's disease grapevines. Results showed that this practice does not remove *X. fastidiosa* from infected plants to an extent that would justify its adoption for disease management (Daugherty and Almeida, 2018).

3.6.4. Taxonomic level in phytosanitary measures

The plant pathogenic bacterium *X. fastidiosa* is currently listed as EU quarantine plant pest in the Directive 2000/29/EC. This means that all subspecies and strains of *X. fastidiosa* are quarantine plant pests, whereas the other described species of the genus *Xylella*, *Xylella taiwanensis*, is not. Although this species in only reported currently in Taiwan, a further specific pest categorisation and pest risk assessment are recommended for *X. taiwanensis*.

With regard to the intraspecific diversity of *X. fastidiosa*, information from literature and official reports on host range at subspecies and ST levels are available in the EFSA Update of the *Xylella* spp. host plant database (EFSA, 2018a) and in the updated *X. fastidiosa* pest categorisation (EFSA PLH Panel, 2018b). This is particularly important for application of phytosanitary measures in outbreak areas, to allow focusing the measures on the hosts of the specific subspecies or STs identified in that location. However, whereas the host range of some subspecies and STs have been extensively studied, little is known for other subspecies or STs (EFSA, 2018a). Biological diversity within an ST (two strains of *X. fastidiosa* subsp. *multiplex* ST7 were shown to have different host ranges under experimental conditions) was recently demonstrated on *X. fastidiosa* (Nunney et al., 2019) and this is generally observed for other bacterial pathogens (Jaureguy et al., 2008; Nicolas-Chanoine et al., 2014; Newberry et al., 2019). In addition, generation of novel strains with specific host range has been evidenced for *X. fastidiosa* (Nunney et al., 2014b). Very often new host plants are reported during the expansion of the outbreak (e.g. in Apulia the number of reported host plant species increased from 3 in 2013 to 32 in 2018) (EFSA, 2018a) or in other cases completely new STs have been reported at the onset of a new outbreak (e.g. the identification at the end of 2018 of the new ST87 belonging to subspecies *multiplex* in Monte Argentario, Italy). In conclusion, for each new outbreak, it is important that the decision whether to work at *X. fastidiosa* species, subspecies, ST, or at the strain levels is taken based on the available knowledge on the diversity of the bacterial population and on the host range. Although control measures should be applied expediently, experimental studies and intensive sampling and testing should be conducted on plant species in the outbreak area to identify possible new host plants.

3.6.5. Uncertainties affecting the assessment of RROs

Many scientific reports came from areas outside the EU, mostly from Americas where environmental conditions and vectors are very different from the EU.

3.6.6. Conclusions on the assessment of RROs

The main results of the literature review are summarised here. Since 2015, studies on available germplasm have identified tolerant/resistant cv of olive that can be used to mitigate the effect of *X. fastidiosa*. Preliminary results from US showed (i) advances in the multiplication of resistant cv of grapevine and (ii) significant etiological heterogeneity and differences in incidence of ALS disease depending on rootstock type. Apart from the studies on the identification of tolerant/resistant cv of olive, the indications that can be extrapolated from the recent literature substantially confirm previous knowledge:

- So far, no treatment has been found able to eliminate the bacteria from the plant (EFSA PLH Panel, 2019). Once a plant gets systemically infected, it remains infected. The effect of some products containing copper and zinc was extensively discussed in the EFSA scientific opinion on 'Effectiveness of in planta control measures for *X. fastidiosa*' (EFSA PLH Panel, 2019)
- An efficient vector control is fundamental for controlling and slowing down the spread of the *Xylella*-induced diseases. Field trials carried out in olive groves in Apulia confirmed the possibility to reduce the vector population through mechanical weed control methods, or, in the case of *Philaenus spumarius*, by sowing of *Lolium* spp. and *Hordeum vulgare* as a cover crop in winter

- As far as common agricultural practices, if on the one hand water stresses can accelerate disease progression, on the other fully irrigated plants could be subjected to longer and more frequent feeding events by the vectors. In some cases (i.e. in almond and citrus), plants under mild water stress were less prone to vector transmission, however opposite behaviour was observed in grapevine.
- Results from a recent study from the US on grapevine showed that pruning does not remove Pierce's disease from infected plants to an extent that would justify its adoption for disease management
- As far as the intraspecific diversity of *X. fastidiosa*, for each new outbreak, it is important that the decision whether to work at *X. fastidiosa* species, subspecies, ST or at the strain levels is taken based on the available knowledge on the diversity of the bacterial population and on the host range and that an intensive sampling and testing is conducted on plant species in the outbreak area to identify possible new host plants.
- Short-range and long-range spread modelling showed that an early detection and rapid application of phytosanitary measures are essential to prevent further spread of the pathogen to new areas.
- Studies have shown the possibility to mitigate the impact of *X. fastidiosa* through tolerant/resistant varieties. The acquisition efficiency of *X. fastidiosa* is known to be correlated with bacterial load (Hill and Purcell, 1997) and thus focus should be on varieties that reduce pathogen load as well as limit disease severity.

4. Conclusions

The assessment of the potential establishment area of *X. fastidiosa* within the EU demonstrates that, although most of the EU territory is estimated to have some level of risk, based on available data, southern Europe is most at risk. This however, covers considerable uncertainty due to a potential underrepresentation of reporting from northern latitudes in North America. Models at the subspecies level could help to estimate how the different genotypes of the bacterium already present in the EU could establish outside their current known distribution. The model for *X. fastidiosa* subsp. *multiplex* estimated areas of potential establishment further north in the EU, compared to other subspecies. However, uncertainty is higher at subspecies level since many published data only involve reports at species level. Given the wide host range of *X. fastidiosa*, climate suitability mapping could represent an important tool in the design of targeted detection surveys for *X. fastidiosa* for MS. Spatially referenced data on positive, and importantly negative reports, from representative, i.e. unbiased monitoring surveys are crucial to further refine estimates of potential establishment.

Data on the asymptomatic period of isolates currently found in the EU were not available for a quantitative assessment so data were collated from the literature on experimental studies of different subspecies–host combinations. Studies were mainly available from warm regions of the world e.g. southern states of the US, Brazil and southern Europe. Asymptomatic periods were highly variable depending on the subspecies and host combination; almond infected with *X. fastidiosa* subsp. *multiplex* and orange or olive infected with *X. fastidiosa* subsp. *pauca* remained asymptomatic for the longest durations after infection (e.g. *pauca* on olive had a median of approximately 10 months and a 95% chance of developing symptoms within 4 years). The long length of the asymptomatic period in some host-subspecies combinations means that visual inspection will lead to detections only after a considerable period from infection and thus methods that can detect the pathogen earlier in the infection period should be utilised, e.g. sampling and diagnostic testing of vectors and asymptomatic host.

The SRS modelling indicated that dispersal of the vector leads to spread rates of less than 1 km/year but this is expected to increase at large spatial scales when long-range jumps of the vectors are considered as a result of human activity and passive dispersal through strong winds. Under a scenario including the measure of plant removal, the modelling suggested that reduction of transmission through control of vector populations is the most important factor for effective eradication of an outbreak in a previously free area. However, there can be landscape constraints to the efficacy of vector control in specific condition (e.g. unaccessible areas, steep hill sides). Early detection (i.e. the time from infection to detection), and consequent removal of plants, through intensive surveillance and prompt implementation of interventions (i.e. the time from detection to implementation of control measures) are also crucial for effective eradication and control of spread. Model simulations showed that if nymph and adult vector control efficacy is high and detection and implementation of measures are quick, local

eradication can be achieved with a 50-m cutting radius. However, not even a 100-m radius can achieve eradication if vector control, detection time and the delay in implementation of measures are poor.

Reducing the BZ width increased the infected areas. Because long-distance jumps drive large-scale spread of *X. fastidiosa,* as expected the long-range spread model suggested that the increases in the sizes of BZs and CZs are likely to increase the success of disease control, although the gain in effectiveness diminished as the BZ increased. The long-range model also reinforced the importance of early detection surveillance as concluded in the short-range model. Better understanding and quantification of the mechanisms and ranges of long-distance dispersal could be used to adjust the BZs and to base surveillance in the disease-free area on risk of long-distance dispersal (e.g. survey on major roads if human vehicle transport is important). Using some surveillance resources to better quantify spread and dispersal patterns in infected areas could provide this information (i.e. randomised representative surveys that report negative data, in addition to targeted detection surveys). As also found with the short-range model, the long-range spread model suggested that maintaining effective vector control in the infected and uninfected areas, in combination with surveys and prompt application of measures to slow the growth of disease foci, are recommended. The models suggest vector control plays an important role in disease management; better data on the effect of vector control on disease transmission should be collected to develop more accurate model assessments.

The assessment of impact was done under a set of assumptions including *Philaenus spumarius* as the only vector of *X. fastidiosa.* Should other xylem-feeding insects act as vectors of *X. fastidiosa*, the impact could be different. The assessment indicated that almond and *Citrus* spp. have lower impact on yield compared to olive. However, the lowest impact was estimated for grapevine and the highest for olive. The introduction or spread of *X. fastidiosa* to forest areas within the EU could lead to impact on oaks, elms, maples and other tree species known to be affected in North America. The uncertainty in the level of this impact is high however, primarily since it is not known whether tree species within those genera that are native to Europe, but absent in North America, may serve as hosts and their level of susceptibility. The lack of information on the impact of *X. fastidiosa* on plant nurseries prevents a quantitative assessment. Nurseries that could be affected are mainly those producing plants for planting of fruit trees and shrubs, forest and landscape trees and ornamentals. Production under screenhouse of healthy mother plants and seedlings together with vector control are options to reduce such impact. Hot water treatment is also an efficient tool but so far tested only on grapes and pecan for *X. fastidiosa*. Should *X. fastidiosa* become widespread in the EU, an indirect impact can be expected on trade through limitations on plants for planting toward countries where *X. fastidiosa* is listed as absent or a quarantine pest.

A review of RROs from the literature reinforced that efficient vector control is important for controlling and slowing down the spread of *X. fastidiosa*. In Italy, some insecticides approved for use in EU territory were shown to be effective (75–100% mortality), especially neonicontinoids (i.e. acetamiprid) and pyrethroids (deltamethrin). Incorporation of *X. fastidiosa* vectors in IPMs programmes in Mediterranean countries is currently missing and should be mandatory to include xylem-sap feeding insects. Further research is needed on the effectiveness and implementation of biological and cultural control methods, the latter of which have been shown to be successful but with the majority of studies in Apulia and thus uncertainty as to their efficacy in other outbreak areas. As far as common agricultural practices, if on the one hand water stresses can accelerate disease progression, on the other fully irrigated plants could be subjected to longer and more frequent feeding events by the vectors. Low levels of plant water stress could reduce transmission efficiency. Recent research showed that pruning does not remove *X. fastidiosa* from infected plants to an extent that would justify its adoption for disease management. Short-range and long-range spread modelling showed that an early detection and rapid application of phytosanitary measures are essential to prevent further spread of the pathogen to new areas.

The intraspecific diversity of *X. fastidiosa* is an important piece of information for the application of phytosanitary measures in outbreak situations. For each new outbreak it is important that the decision whether to work at *X. fastidiosa* species, subspecies, ST or at the strain levels is taken based on the available knowledge on the diversity of the bacterial population and on the host range. Although control measures should be applied expediently, experimental studies and intensive sampling and testing should be conducted on plant species in the outbreak area to identify possible new host plants.

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Abbreviations

AAP	acquisition access period
ALS	almond leaf scorch
AUC	area under the curve
BF	buffer zone
BRT	boosted and regression trees
CA	containment area
CAP	chimeric antimicrobial protein
CART	classification and regression trees
CFU	colony forming unit
CNR	Italian National Research Council
CSIC	Spanish National Research Council
CVC	citrus variegated chlorosis
CZ	containment zone
DAS-ELISA	double antibody sandwich enzyme-linked immunosorbent assay
DED	Dutch elm disease
EKE	Expert Knowledge Elicitation
ELISA	enzyme-linked immunosorbent assay
EFTA	European Free Trade Association
GAM	generalised additive models
GRF	Gaussian random field
IAP	inoculation access period

IPM	Integrated Pest Management
ISPP-CTPPB	International Society of Plant Pathology Committee on the Taxonomy of Plant Pathogenic Bacteria
IVIA	Valencian Institute for Agricultural Research
IZ	infected zone
MAR	multivariate adaptive regression splines
MaxEnt	maximum entropy
MLST	multilocus sequence typing
MS	Member State
OQDS	olive quick decline syndrome
PACA	Provence-Alpes-Côte d'Azur
PCR	polymerase chain reaction
PD	Pierce's disease
PDE	Partial differential equation
PGIP	pear polygalacturonase inhibitory protein
PLH	EFSA Panel on Plant Health
PLS	plum leaf scald
QTL	quantitative train locus
qPCR	quantitative polymerase chain reaction
ROC	Receiver Operating Characteristic
RF	random forest
RPART	recursive partitioning and regression trees
RRO	risk reduction option
SDM	species distribution model
SRS	short-range spread
SI	suitability index
ST	Sequence Type
SVM	support vector machines
ToR	Terms of Reference
TSS	True Skill Statistics
USP	University of São Paulo
VIF	variance inflation factor

Appendix A – Model formalisation

A.1. Formal model for short-range spread

A.1.1. Short-Range Spread Eco-epidemiological Model

For investigating the SRS dynamics of the disease and evaluate the different eradication measures under the set of initial conditions defined in the scenario analysis, we define a spatial explicit eco-epidemiological model (SRS model). The model describes a region Ω densely populated with host plants arranged in regular grid. In the region are present vectors feeding on host plants and transmitting the disease agent. Fixing a time interval [0,T], we define γ (x, y, t) as the abundance of infected adult vectors in the point (x, y) of Ω at time t in [0,T], and φ (x, y, t) as the disease level of the plant in the point (x, y) of Ω at time t in [0,T]. φ lies between 0 and 1, where φ = 1 and φ = 0 correspond to a fully diseased plant and to a healthy plant, respectively.

Under the set of processes and assumptions defined in the scenario, we describe the space-time spread of the disease induced by *X. fastidiosa* bacteria by means of the following evolutionary PDEs (Partial differential equations) system

$$\dot{\gamma} = \alpha\Delta\gamma - M\gamma + b\ (P(t)\ k(t) - \gamma)\varphi$$

$$\dot{\varphi} = (s\ l\ y + F(t)\varphi)(1 - \varphi)$$

where

α is a positive scale parameter for the diffusive Laplacian operator Δ acting on γ. It depends on the biological properties of the vector species. The spread rate of the vectors increases with the increase of α,

b is a positive scale parameter describing the disease acquisition rate of the vectors,

M is a vector natural mortality rate,

P is a mortality rate due to vector control actions, k(t) is vectors carrying capacity at time t,

s is a plant susceptibility (related to the specific vector–host disease association),

F(t) is a growth rate of the disease level in the infected plant.

A.1.2. Model parameters

The biological and epidemiological parameters used in the model, their values and the source of information used for their estimation are reported in Table A.1.

Table A.1: Biological and epidemiological parameters for the eco-epidemiological model (SER model). For each parameter, its definitions, the numerical value and the information and data used for the estimation are given

Parameter	Meaning	Estimated values	Justification
α	Coefficient of the diffusive Laplacian operator for the vectors	1500 m^2/day	The uncertainty distribution of the median value of the adult vectors dispersal kernel is used to define the parameter for the diffusive Laplacian operator (Section A.1.3). The median value of the distribution (800 m) allowed to derive the parameter a in the model
M	Natural mortality rate of the adults	0.015 1/day	Fitted to data on vector survival (Bosco et al., 2019)
F(t) = r_H	Bacteria population growth rate during the most favourable period for bacterial growth	0.02 (for high susceptible host plants) 0.017 (for low susceptible host plants)	Fitted to the symptoms severity and incidence data reported in Montes-Borrego et al. (2017). Ogliarola is taken as example of a high susceptible cultivar and Leccino for a low susceptible cultivar
F(t) = r_L	Bacteria population growth rate during the less favourable period for bacterial growth	0.01 (for high susceptible host plants) 0.009 (for low susceptible host plants)	Fitted to the symptoms severity and incidence data reported in Montes-Borrego et al. (2017). Cultivar Ogliarola is taken as example of a high susceptible host plant and cultivar Leccino for a low susceptible host plant

Parameter	Meaning	Estimated values	Justification
b	Bacteria acquisition rate	0.0995	The value has been estimated by running the model in the same conditions as in the scenario of the EKE for the vector acquisition rate. The median value in the uncertainty distribution was considered
S	Host susceptibility	0.14 (for high susceptible host) 0.09 (for low susceptible host)	It represents the probability that a single susceptible olive tree becomes systemically infected as a consequence of the feeding activity of one infected adult vector during an average day during the period where vector–host interaction occurs. The value corresponds to the median of the uncertainty distribution on host susceptibility The value for a non-susceptible (tolerant or resistant) variety has been set equal to the 25th percentile of the elicited uncertainty distribution
l	Bacterial load inoculated per vector per day	1.4286e-05	The value has been estimated starting from the information reported in the Appendix F on the transmission rate of an infected vector

A.1.3. Model implementation

A.1.3.1. Phenology and population dynamics of the adult vectors

In Figure A.1, the essential elements of the phenology and the population dynamics of the adult vectors as they are considered in the SRS model are reported. The reference period is a year in the simulated scenario that starts at t_i. Adult emergence occurs at t_{V_i}, this moment also represents the beginning of adult feeding activities.

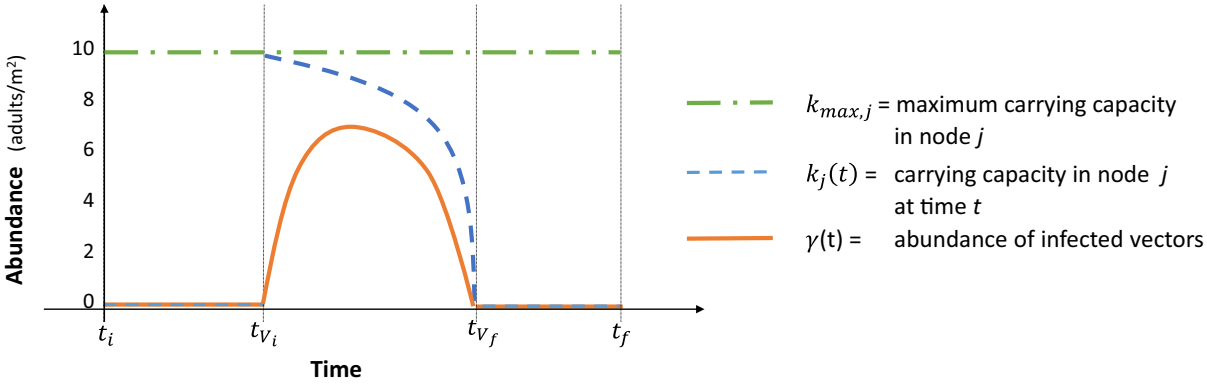


Figure A.1: Phenology and population dynamics of the adult vectors in a generic year of the simulated scenario

To summarise, the phenology of the adults is characterised by the following points in time:

t_i initial time of the simulation period,
t_{V_i} time of adult vectors emergence (beginning of period of vector feeding activities),
t_{V_f} time at which adult vectors disappear (the end of period of vector feeding activities),
t_f final time of the simulation period.

In each year, the number of adults emerging in a node j is equal to $k_{max,j}$, a parameter that is defined as the maximum carrying capacity in the node (10 × 10 m). The adult abundance in the node ($k_j(t)$) decreases to 0 at the end of the period in which adults are present (t_{V_f}) according to a parabolic survival pattern

$$k_j(t) = \begin{cases} 0 & t_i \le t \le t_{V_i} \text{ or } t_{V_f} \le t \le t_f \\ 5 \times \sqrt{\frac{t_{V_f} - t}{t_{V_f} - t_{V_i}}} & t_{V_i} \le t \le t_{V_f} \end{cases}$$

In the period from t_i to t_{V_i} and from t_{V_f} to t_f, only pre-imaginal stages of the vector are present in the system.

A.1.3.2. Bacterial population growth into the host plants

In the SRS model, the bacterial population growth follows a typical pattern reported in Figure A.2. Due to the physiology of the plant and the environmental conditions, two periods in the year are considered. A favourable period in which the bacterial population grows and an unfavourable period in which bacterial growth does not occur.

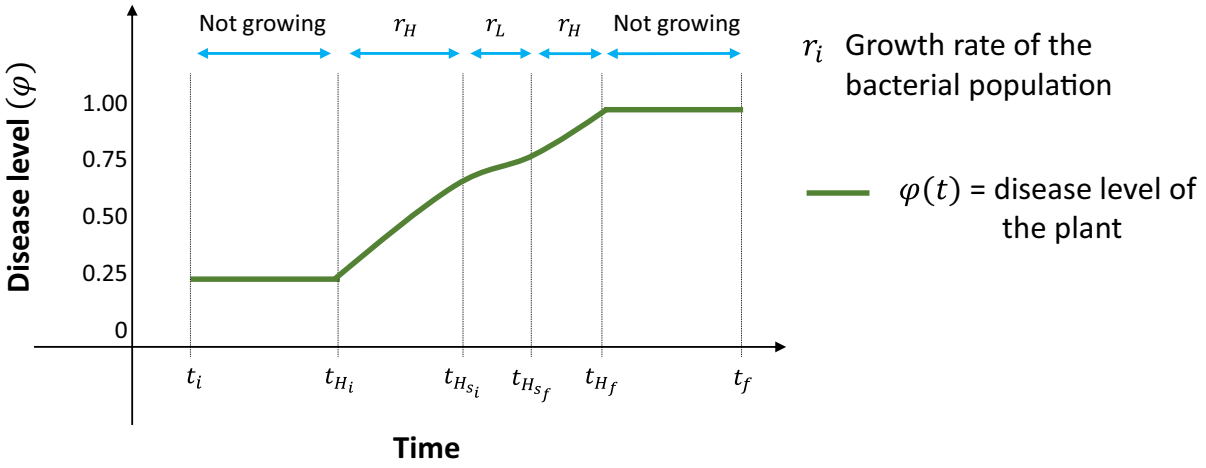


Figure A.2: Pattern of bacterial population growth curve into the plant during the year

More in detail, for the bacterial population growth the following elements are considered:

t_i is the initial time of the simulation period;
t_{H_i} is the initial time in which bacterial population starts to growth (with high growth rate, $F(t) = r_H$) due to favourable temperatures and plant physiological conditions;
$t_{H_{s_i}}$ is the point in time in which bacterial population, due to high temperatures and environmental stressing conditions, switch to a lower growth rate ($F(t) = r_L$);
$t_{H_{s_f}}$ is the point in time in which, due to the return of favourable environmental conditions, bacterial population switches again to high growth rate;
t_{H_f} is the time in which bacterial population stop growing due to unfavourable environmental and plan physiological conditions;
r_H high growth rate of the bacterial population;
r_L low growth rate of the bacterial population.

A.1.3.3. Symptoms severity and thresholds of detectability

In the POnTE project (deliverable 2.1), investigations on the relationship between the severity of the symptoms and the concentration of *X. fastidiosa* (bacterial load, LogC) are reported. These data were interpolated and the estimated function was used to determine the disease level thresholds for detectability and the possible value identifying the upper threshold for each category of severity of the symptoms shown by the plant. The thresholds used in the model are reported in Table A.2.

Table A.2: Relevant values of the disease level related to threshold for detectability and categories of symptoms severity

Phi value	Bacterial load (LogC)	Severity	Meaning
1×10^{-4}	3.000	0	Threshold for molecular detectability with high sensitive techniques
3.78×10^{-3}	4.578	0	Upper threshold for the absence of symptoms
6.61×10^{-3}	4.820	0.5	Threshold for visual detectability
1.15×10^{-2}	5.062	1	Upper threshold for symptoms severity = 1
3.52×10^{-2}	5.547	2	Upper threshold for symptoms severity = 2
1.07×10^{-1}	6.031	3	Upper threshold for symptoms severity = 3
3.28×10^{-1}	6.516	4	Upper threshold for symptoms severity = 4
1	7	5	Upper threshold for symptoms severity = 5 Maximum bacterial load

A.1.3.4. Implementation of eradication measures

Following the first detection of a host plant infected by *X. fastidiosa* in a free area, the following actions are undertaken:

1) definition of the demarcated area (infected area and BZ),
2) if the detection occurs in the period in which the adult vectors are present, a chemical treatment is carried out for the vectors control of in the infected area,
3) all host plants are cut in the infected area.

In the demarcated area, the eradication strategy is applied which includes:

4) weed control in the whole demarcated area during the period in which only the pre-imaginal stages of the vector are present;
5) a chemical treatment in the whole demarcated area at the emergence of the adult vectors, followed by a second treatment a month later;
6) monitoring of the BZ for the detection of new infected host plants;
7) if new infected host plants are detected, the demarcated area is updated, the chemical control of the vectors (if the adult vectors are present) and the cutting of all the host plants in the infected area are applied.

A flow chart describing the implementation of eradication strategy is shown in Figure A.3.

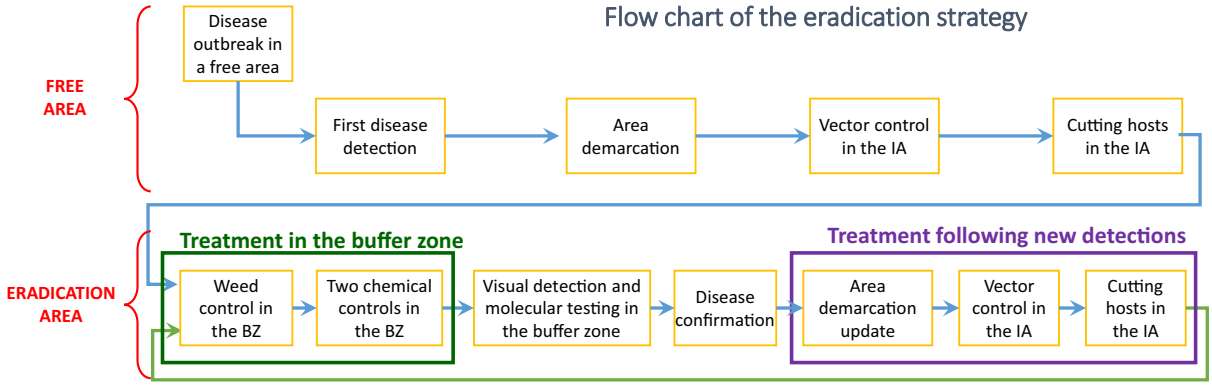


Figure A.3: Flow chart representing the action following a disease outbreak in a free area and the action considered in the eradication strategy (IA: infected area; BZ: buffer zone)

A.1.3.5. Timing

The implementation of the SRS model requires the definition of the timing of the events related to the biology and the epidemiology of the vector and the host plants and the implementation of the control measures.

Table A.3: Timing of the events related to biology and epidemiology of the vectors and the host plants and the implementation of the control measures

Parameter	Meaning	Defined values (day in the year)	Justification
t_i	Initial time of the simulation period	1	
t_{H_i}	Initial time in which bacterial population starts to growth at high growth rate	129	D. Boscia, M. Saponari (personal communications)
t_{H_i}	Initial time in which bacterial population starts to growth at high growth rate	129	Idem
$t_{H_{s_i}}$	Initial time in which bacterial population growths with a low growth rate ($F(t) = r_L$) due to high temperatures	212	Idem
$t_{H_{s_f}}$	Final time in which bacterial population growths with a low growth rate due to high temperatures	212	Idem
t_{H_f}	Final time in which temperatures allow the growth of bacterial population	287	Idem
t_{v_i}	Time of vectors emergence (beginning of period of vector feeding activities)	130	Idem
t_{v_f}	Time at which vectors disappear (the end of period of vector feeding activities)	300	Idem
	Time at which the first adults vector treatment is performed in the demarcated area	142	Idem
	Time at which the second adults vector treatment is performed in the demarcated area	172	Idem

For the weed control, there is not a specific timing in the model. The mortality due to the weed control on the nymphal stages is directly translated in a reduction of the emerging vector abundance.

A.1.4. Output variables

The following model output variables (i.e. assessing variables) are considered to evaluate the epidemiological dynamics of the infection and the outcome of the measures implemented to eradicate the disease.

Infected vector pressure: Mean value of γ computed, in each year, in the period where adults vectors are present.

Disease pressure: Mean value of φ at the end of the year computed for the infected plants.

Spread of the disease: maximum distance of the infected plants from the first inoculated plants.

Number of infected plants: Number of infected host plants ($\varphi > 0$) at the end of the year.

Number of molecular detectable plants: Number of infected host plants with a disease level $\varphi \geq \pi_m$ at the end of the year, where $\pi_m = 0.0001$ is the disease level threshold for molecular detectability.

Number of visually detectable plants: Number of infected host plants ($\varphi \geq \pi_v$) at the end of year, where $\pi_v = 0.0066$ is the disease level threshold for visual detectability (which correspond to a severity of 0.5)

Total number of plants removed: Number of cut plants at the end of the year.

A.2. Model for long-range spread

A.2.1. Formal model for long-range spread

To simulate generic landscapes with similar spatial properties to each region, the spatial pattern in each real landscape was characterised by calculating empirical variograms for the spatial distributions of the main susceptible habitat types (Table A.4). For an aggregated landscape, the variogram

quantifies the increasing variability in cover values between pairs of locations at increasing distance (Figure A.4b). Simulated cover patterns with similar variograms to the real data were simulated as follows. First, Gaussian random fields (GRFs) were simulated on the model grid using the RandomFields R package (Schlather et al., 2015) and powered exponential autocorrelation models. The GRFs are normally distributed spatially autocorrelated random numbers arranged on the model grid. Next, GRF values were transformed into actual cover values from the real landscapes by a rank order transformation (Figure A.4d,e). Finally, a variogram was calculated for the simulated landscape, to compare the simulated and real landscapes. The parameters of the powered exponential model, controlling the simulated spatial pattern, were tuned so that the resulting variograms closely matched the real landscapes (Figure A.4f). Any simulated landscape in which the central grid cell did not contain any susceptible cover was rejected, as the modelled epidemics were initiated from the centre of the simulated landscapes (see below). See Figure A.5 for some example generic landscapes.

Table A.4: Settings used for simulating generic host plant cover landscapes with similar spatial properties to three of the major outbreak areas in the EU

Region	Land cover data source and main susceptible land cover types	Per cent susceptible	Gaussian random field autocorrelation parameters	
			Range (km)	Exponent
Apulia, Italy	Olive grove polygons (provided by InnovaPuglia SpA, https://www.innova.puglia.it/), in which 82% of *X. fastidiosa* positives occur	38.3%	10	0.7
Alicante, Spain	Spanish Land Parcel Identification System (SIGPAC): nut orchards (FS), fruit orchards (FY), olive groves (OV), in which 82% of *X. fastidiosa* positives occur	15.0%	6	0.75
PACA, France	CESBIO 2017 land cover map (Inglada et al., 2018): diffuse urban (code 42) and industrial and commercial (code 43) in which 84% of *X. fastidiosa* positives occur	12.4%	55	0.5

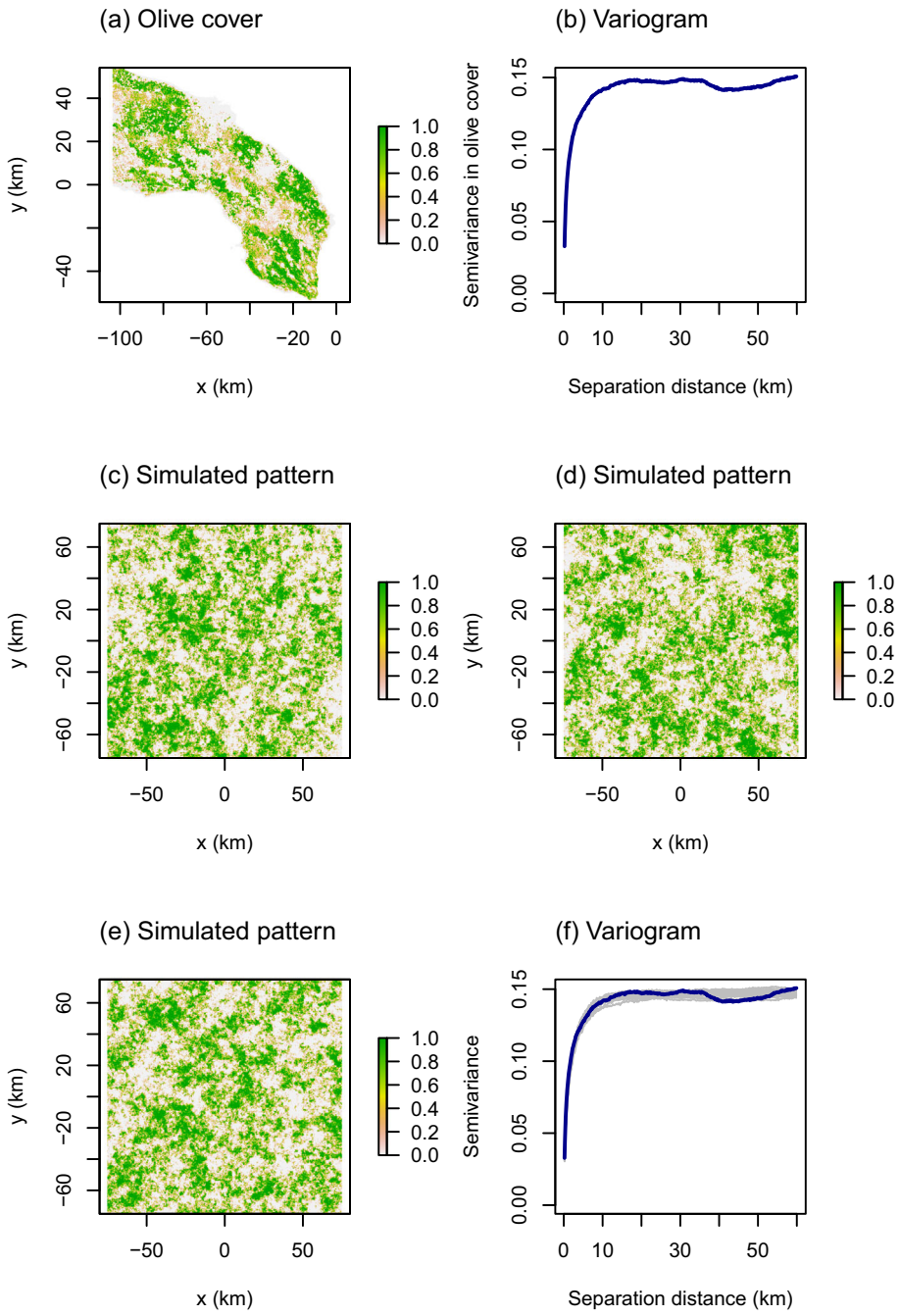


Figure A.4: An example of the generic landscape simulations. (a) Proportion cover of olive groves in Apulia, southern Italy, representing the real outbreak region. (b) The spatial pattern in real olive cover quantified as its empirical variogram. (c–e) Generic landscapes simulated to have similar spatial properties to the real data. (f) Empirical variograms for 20 simulated landscapes (grey lines) plotted against that for the real landscape (dark blue)

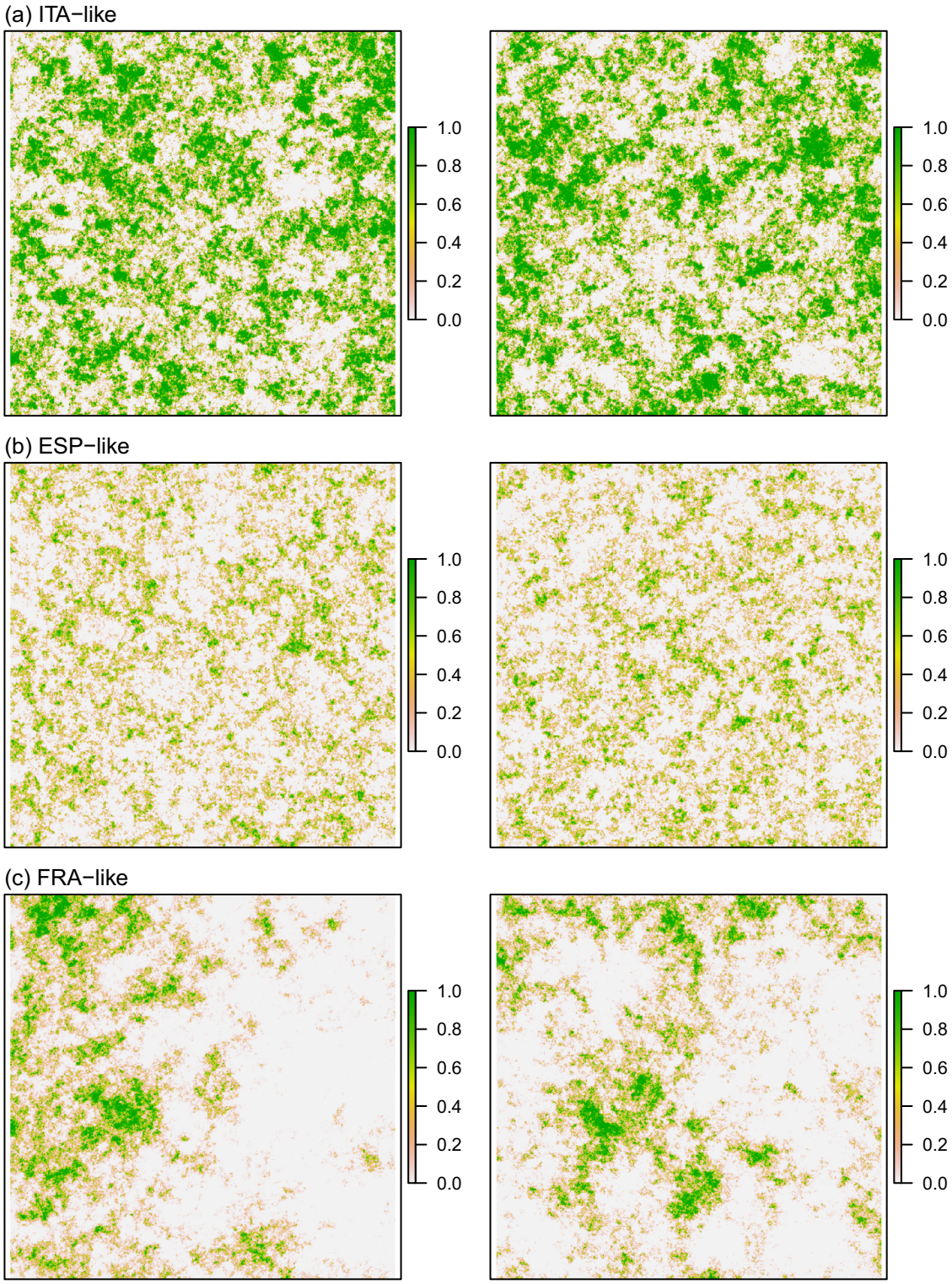


Figure A.5: Example generic landscapes for simulating *X. fastidiosa* infection dynamics. The grids are 150 x 150 km and have similar spatial properties to three of the major mainland infected regions in the EU

Model parameters

Parameters used in the simulations are defined in Table A.5.

Table A.5: Estimated parameter values of the *X. fastidiosa* spread model used in the simulations. The model was designed for the spread of *X. fastidiosa* subsp. *pauca* in olive groves in Apulia, Italy so parameter ranges reflect our understanding of the epidemiology in that system, and its uncertainty. Parameter values used were 50 samples from posterior distributions obtained by fitting the spread model to the monitoring data from Apulia. Model fitting was done using approximate Bayesian computation (Beaumont, 2010), in which prior parameter distributions were estimated, then 200,000 simulations were performed with random draws from the prior distributions and the 50 best fitting parameters retained as an approximate posterior distribution. These posteriors are expressed as their median and 95% range. Some other model parameters were not estimated but varied in the simulation experiment (see Section 2.1.5.1) so are not included here

Parameter	Meaning	Values	Justification
b_0	Transmission rate at low host cover (yr^{-1})	1.830 (1.625–1.959)	Prior estimated by fitting a simple transmission model to progression of symptoms in Italian monitoring plots of varying size
b_1	Decline in transmission rate with increasing host cover	−0.0152 (−0.0198 to 0.0098)	Prior estimated by fitting a simple transmission model to progression of symptoms in Italian monitoring plots of varying size
τ	Proportion of transmission achieved by asymptomatic hosts	0.050 (0.005–0.098)	*Xylella* concentrations are lower in asymptomatic hosts and bacterial acquisition rates by vectors on asymptomatic hosts is lower than on symptomatic hosts
α	Symptom development rate (yr^{-1})	2.898 (2.317–4.111)	These values give 90–98% of infected hosts showing symptoms after one year, consistent with symptom development in olive trees (D. Boscia and M. Saponari, pers. comm.)
γ	Infection removal (canopy collapse or host plant death) rate (yr^{-1})	0.194 (0.176–0.230)	These values give median removal times of 3.0–3.9 years, consistent with expert opinion on time for canopy collapse in infected olive trees (D. Boscia and M. Saponari, pers. comm.)
d_{short}	Median of short-distance dispersal kernel (km)	0.151 (0.043–0.431)	Fitted to the spread rate in Apulia and consistent with limited mark recapture data on vector movement range (D. Bosco, pers. comm.)
d_{long}	Median of long-distance dispersal kernel (km)	10.7 (8.0–20.1)	Fitted to the spread rate in Apulia
L	Proportion of long-distance dispersal	1.95×10^{-4} (1.18×10^{-5} to 2.91×10^{-4})	Fitted to the spread rate in Apulia
ϕ	Proportion of uninfected host plants exhibiting scorch-like symptoms	7.72×10^{-4} (7.54×10^{-4} to 7.91×10^{-4})	Prior estimated by latent class analysis on agreement between tests (inspection, ELISA and qPCR) on olive trees in Apulia
f_A	False negative rate of infected samples from asymptomatic host plants	0.109 (0.077–0.142)	Prior estimated by latent class analysis on agreement between tests (inspection, ELISA and qPCR) on olive trees in Apulia
f_S	False negative rate of infected samples from symptomatic host plants	0.087 (0.062–0.114)	Prior estimated by latent class analysis on agreement between tests (inspection, ELISA and qPCR) on olive trees in Apulia

Spatial disease dynamics

Deterministic disease dynamics within *X. fastidiosa* -infected grid cells are described by the following discrete-time versions of standard differential equations used in epidemiological compartmental modelling:

$$S_{t+1} = S_t - S_t(1 - e^{-\beta v(I_t + \tau A_t)/N})$$

$$A_{t+1} = A_t + S_t(1 - e^{-\beta v(I_t + \tau A_t/N)}) - A_t(1 - e^{-\alpha})$$

$$I_{t+1} = I_t + A_t(1 - e^{-\alpha}) - I_t(1 - e^{-\gamma})$$

$$R_{t+1} = R_t + I_t(1 - e^{-\gamma})$$

where the compartments *S*, *A*, *I* and *R* are defined as in Figure 5, t is the time step (year) and $N = S + A + I + R$ is the total number of host plants in the grid cell. Ancient Olive groves in Apulia have a typical density ranging around of 10,000 trees km^2, so we used this value to calculate N. Since grid cells were 200 × 200 m, the maximum N = 400 trees. This model was developed considering infection of olive trees, but for application to other settings, the compartmental model can be interpreted as modelling the fraction of the grid cell in each compartment out of 400.

The transmission rate β represents the average number of transmissions from an infective plant. However, the transmission rate may be modified by vector control (parameter υ quantifies the reduction in transmission if vector control is applied) and the differential infectiveness of different compartments (parameter τ quantifies the relative infectivity of asymptomatic plants compared to symptomatic ones). Lower bacterial concentrations in asymptomatic host plants probably means they have lower infectivity than symptomatic plants (particularly in olive). The remaining parameters are the rates of symptom development (α) and removal (γ) where removal is defined as canopy loss or host plant death.

In data from monitoring plots in olive groves in Italy, we observed faster relative disease progression in smaller plots, which may reflect spatially limited disease transmission at very local scales. Assuming infection dynamics in grid cells with low susceptible cover are similar to the dynamics in small plots (which will be true if the susceptible cover is aggregated into monocultures such as olive groves) we made β a function of the area of susceptible habitat (H) in the grid cell as:

$$\beta = b_0 + b_1\sqrt{H}$$

Scaling parameters b_0 and b_1 were estimated to the plot disease progression.

Infection of new grid cells by dispersal is modelled stochastically using a mixture of short- and long-distance exponential transmission kernels, to represent local diffusive-like movements of vectors as well as the rarer and less predictable jumps across large distances that can spread the disease rapidly to new regions. The mixture kernel is:

$$K(d_{ij}) = \frac{(1 - L)e^{\frac{d_{ij}\ln 0.5}{d_{short}}} + Le^{\frac{d_{ij}\ln 0.5}{d_{long}}}}{2\pi d_{ij}}$$

where d_{ij} is the distance between two grid cells i and j, L is the proportion of long-distance dispersal and d_{short} and d_{long} are equivalent to the median short- and long-distance dispersal distances.

In the model, the dispersal kernel scales a decline in transmission rate with increasing distance from sources of infection. As such we adapt the equation for infection of susceptible individuals in the compartmental model to formulate the probability that a susceptible host plant in a currently uninfected grid cell i becomes infected from any source of infection in the modelled landscape is

$$\rho_{i,t} = 1 - e^{-\sum_j K(d_{ij})\beta_j(I_{t,j} + \tau A_{t,j})/N_j}$$

where j indexes over all other grid cells for summing the product of the dispersal kernel and the source transmission rate (see the equations of the compartmental model).

Potential infection of each plant in the uninfected grid cell is simulated by drawing random numbers of new infections from the binomial distribution with probability $\rho_{i,t}$. If any plants become infected, they are moved to the asymptomatic (A) compartment triggering subsequent growth of a new disease foci in that grid cell.

Surveillance model

The surveillance model is based on our understanding of practice in Apulia, in which visual inspection is followed by laboratory testing. The equations defining the probability of detecting *X. fastidiosa* in an inspected grid cell are as follows.

The probability of detecting symptomatic hosts during the visual inspection of a 100 m × 100 m square is:

$$P = 1 - (1 - \Psi)^{v}$$

where v is the visual inspection rate (proportion of the square inspected) and Ψ is the proportion of the population with symptoms, calculated as:

$$\Psi = \frac{\phi(S + A) + I + R}{N}$$

where ϕ is the (low) proportion of uninfected and asymptomatic trees displaying scorch like symptoms in the general population.

Note that we used different visual inspection rate parameters *v* in different parts of the landscape. Decision (EU) 2017/2352 describes higher surveillance effort in the first 1 km of the BZ and in the containment zone (if used) compared to the outer part of the BZ. Therefore, we apply the highest values for *v* in the first 1 km of the BZ and containment zone. Although Decision (EU) 2017/2352 does not specify survey procedures in the 'disease-free' area beyond the demarcated region, we implemented a low level of surveillance (lower v) in the 'disease-free' area to account for the probability that large disease foci would be noticed by growers or the public.

If symptoms are detected during the simulated visual inspection of a 100 m × 100 m square, then the model assumes that one random symptomatic plant is taken for laboratory testing. Note that greater sampling rates are applied in Apulia. In the model, the probability that the sampled symptomatic plant is infected with *X. fastidiosa* is:

$$P_2 = \frac{\phi A + I + R}{\phi(S + A) + I + R}$$

If no symptoms are detected during the simulated visual inspection of a 100 m × 100 m square, then the model assumes that a random asymptomatic plant is taken for laboratory testing. The probability that the sampled asymptomatic plant is infected with *X. fastidiosa* is:

$$P_3 = \frac{A}{S + A}$$

During laboratory testing, we assume no false positive results occur but some false negatives occur. This is based on Latent Class Analysis (Linzer and Lewis, 2011) of the agreement between symptoms, ELISA and PCR in the Apulian monitoring data and assessment of the rates at which negative ELISA results from symptomatic and asymptomatic trees are re-tested with the more accurate qPCR. Based on this analysis, false negatives occur in the model with rates f_A and f_S for asymptomatic and symptomatic samples, respectively.

The overall probability of getting a positive test result from an inspection of a 100 m × 100 m square is therefore:

$$P = P_1P_2(1 - f_s) + (1 - P_1)P_3(1 - f_A)$$

which represents the probability of getting a positive sample from a symptomatic or asymptomatic host plant.

This probability is then scaled up to the overall probability of detection in the 200 × 200 m grid cell, in which four 100 m × 100 m inspections occur, as:

$$P_{det} = 1 - (1 - P)^4$$

Appendix B – Uncertainties affecting the assessment of establishment for *Xylella fastidiosa* and subspecies

B.1 SDM ensemble modelling

B.1.1. Variability of model projections for *X. fastidiosa*

The variability on model projections estimated by the standard deviation of the suitability index (SI) for the 800 individual models used in the SDM ranged 0.000467–0.089953 and tended to be higher in areas with high suitability values (Figure B.1).

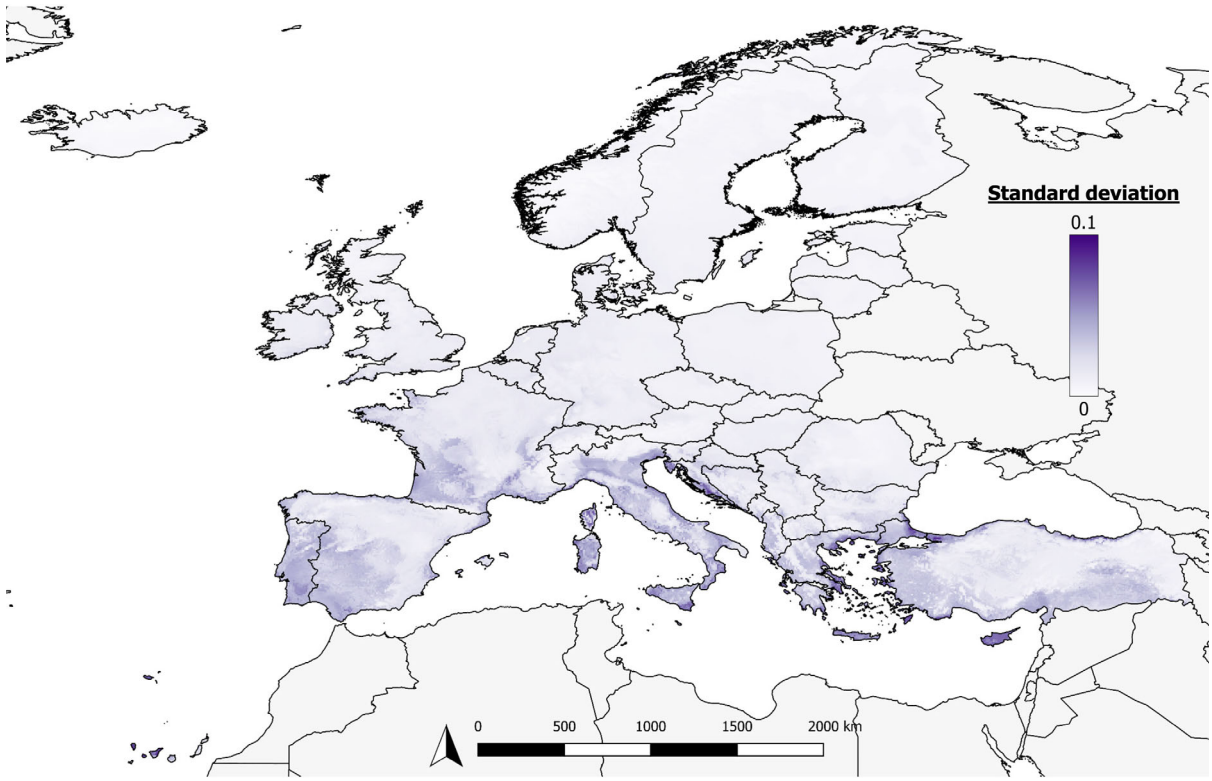


Figure B.1: Uncertainty in the projections of climatic suitability for *X. fastidiosa*, estimated by the standard deviation among models used to build the SDM ensemble

The variability on model projections, estimated by the standard deviation of the SI for the 800 individual models used in the SDM, was positively correlated with the suitability value (Figure B.2). The higher variability was found for subsp. *fastidiosa* (range 0.0011–0.1231), while similar range was estimated for subsp. *multiplex* (0.0011–0.0948) and *pauca* (0.0005–0.0967).

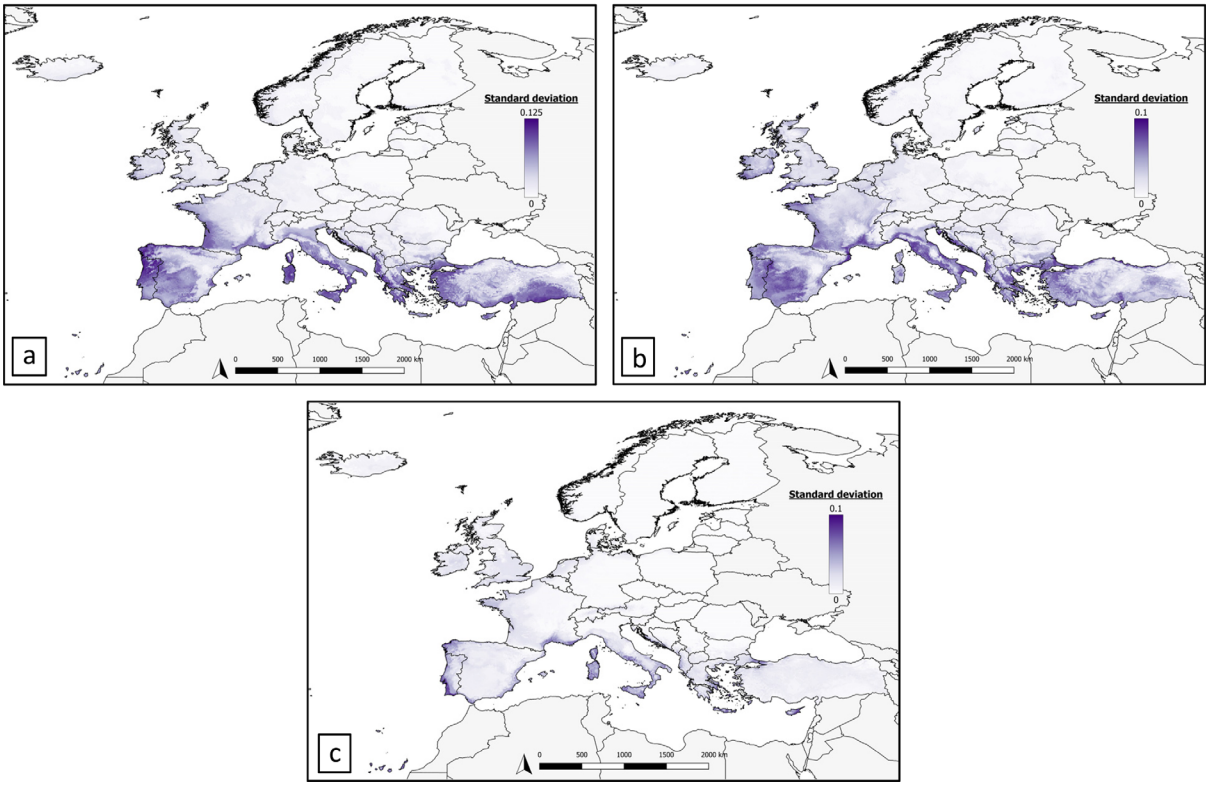


Figure B.2: Uncertainty in the projections of climatic suitability for *X. fastidiosa* subspecies estimated by the standard deviation among models used to build the SDM ensemble. (a) subsp. *fastidiosa*; top-left (b) subsp. *multiplex*; top-right (c) subsp. *pauca*; bottom

B.2. Uncertainty on the lower limit of climatic suitability for *X. fastidiosa* and subspecies

B.2.1. Lower limit for *X. fastidiosa*

The output of SDMs is a continuous variable that range 0–1 that indicates the relative suitability of a given location. However, for a practical application of these models on risk management, a discrimination between suitable and unsuitable areas is more convenient. But, as indicated in Section 2.1.2.2, a fixed threshold value, such as 0.5, does not usually correspond to the threshold above which the species is more likely to be present (Jimenez-Valverde and Lobo, 2007). Moreover, it is broadly accepted that no single threshold can be selected as the most accurate (Liu et al., 2005; Jimenez-Valverde and Lobo, 2007; Nenzen and Araujo, 2011); consequently, we applied five different values of the climatic SI as thresholds above which a given location is categorised as suitable for the establishment of *X. fastidiosa*. In a precautionary action, the highest threshold, i.e. that which estimate the widest suitable area for potential establishment, should be applied; however, the risk to overestimate the extent of *X. fastidiosa* establishment is highest.

Five different thresholds were applied: (a) two thresholds set to be the suitability value at which sensitivity, i.e. true positive rate, was 95% and 90%, respectively; (b) the suitability value that maximises the sum of sensitivity and specificity; (c) the suitability value that minimised the difference between sensitivity and specificity and (d) a four levels threshold was applied ranging the SI as follows: (1) SI < 0.1; (2) 0.1 > SI < 0.3; (3) 0.3 > SI < 0.6 and (4) SI > 0.6.

Thresholds 1 and 2 are used to ensure that the model correctly predicts at least 90% and 95%, respectively, of the locations in which *X. fastidiosa* is confirmed to be present as suitable, but at the expense of a risk to overestimate the extent of potential establishment. We should consider that in presence-only models, as is our case, only presences are confirmed while absences are estimated from a background and are not real observations. Thresholds 3 and 4 are designed to optimise model accuracy and usually results in lower extent of the area of potential establishment accounting for maximising predictions of both, presences (suitable) and absences (unsuitable).

Threshold values applied to determine the lower limit for the climatic suitability of *X. fastidiosa* in the EU (Figure B.3) are shown in Table B.1. Thresholds 1 and 2, for which the sensitivity was fixed at 95% and 90%, respectively, estimated the lowest specificity of 81% and 82%, respectively. Thresholds 3 and 4, designed to optimise model performance showed similar values for both, sensitivity and specificity of ca. 90%. The models used are based on the presence data with generation of pseudo-absences and therefore sensitivity, that is true positive rate, should be prioritised, however the important reduction on specificity suggest that either thresholds 3 or 4 could be more appropriate. Thresholds 1 and 2 could underestimate the extent for *X. fastidiosa* establishment.

All four thresholds identify areas of southern Europe to be climatically suitable for the establishment of *X. fastidiosa*, in an area covering from 7,759 5 arc-min grid cells for threshold 2, to 15,443 5 arc-min grid cells for threshold 4. Irrespective of the threshold used, the model estimate grid cells being climatically suitable for *X. fastidiosa* in the Atlantic regions of southern Portugal and southern-west Spain, as well southern regions in the Mediterranean, particularly those close to the coast in southern France, Italy and Croatia. Threshold 1 extends this area to some territories in southern France close to the Spanish border, and thresholds 3 and increase northward most previous areas in particular in, central Spain, central France and some territories in northern Italy. Is important to indicate that all islands and archipelagos in the Mediterranean are estimated as suitable areas for *X. fastidiosa* establishment, as currently known for Corsica and the Balearic Islands.

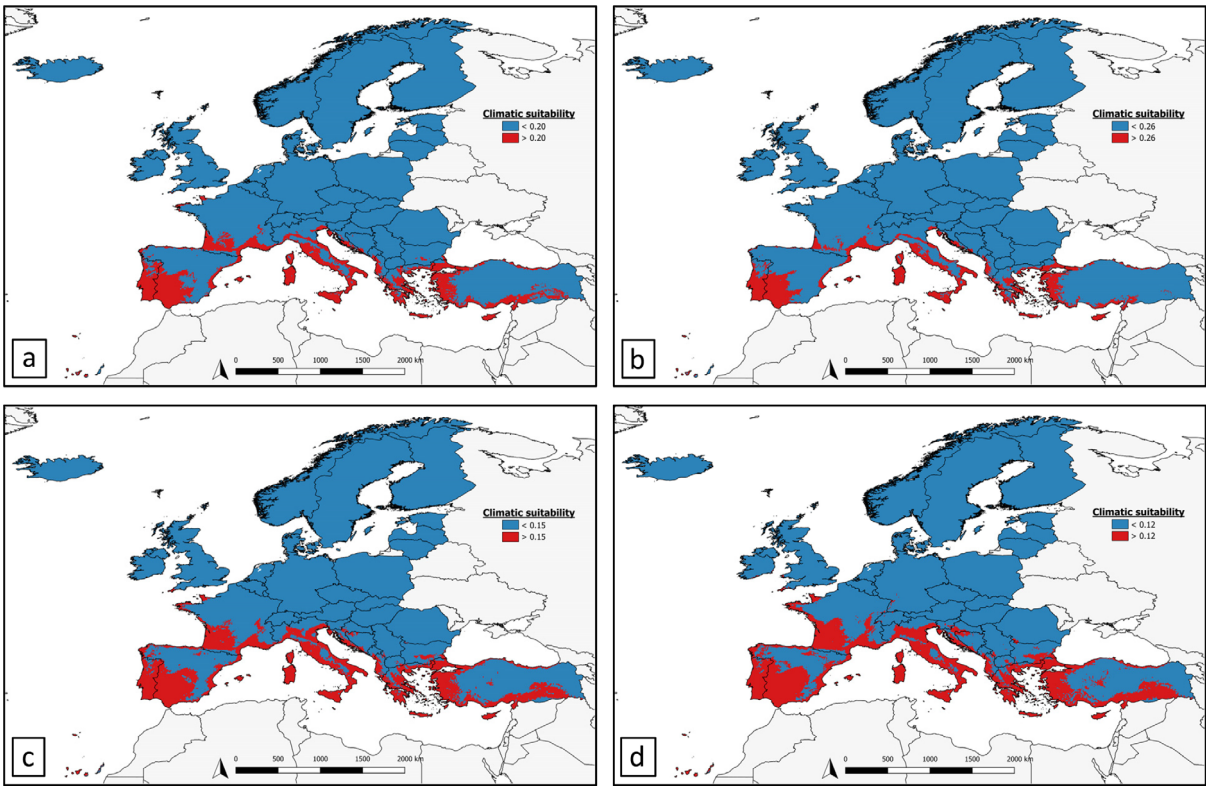


Figure B.3: Estimated climatic suitability maps for *Xylella fastidiosa* according to a SDM ensemble model with different thresholds indicated in Table B.1. (a) Threshold 1 (0.20), (b) threshold 2 (0.66), (c) threshold 3 (0.15), (d) threshold 4 (0.12)

Table B.1: Comparison between percentage of *X. fastidiosa* presences and pseudo-absences that are correctly predicted by different thresholds

Threshold number	Rationale	Threshold	% of known *X. fastidiosa* presences predicted to be suitable (sensitivity ± sd)	% of *X. fastidiosa* pseudo-absences predicted to be unsuitable (specificity ± sd)	No. of EU28 5 arc-min grid cells predicted to be suitable for establishment
1	Predicts all but 5% of *X. fastidiosa* presences to be suitable	0.20 ± 0.022	95%	80.7 ± 2.66%	10,109
2	Predicts all but 10% of *X. fastidiosa* pseudo-absences to be suitable	0.26 ± 0.022	90%	81.9 ± 2.61%	7,759
3	Maximises the sum of the accuracy of predicting occupied sites to be suitable and unoccupied sites to be unsuitable (i.e. sum of sensitivity and specificity)	0.15 ± 0.022	89.0 ± 5.51%	90.8 ± 4.16%	13,116
4	Minimises the difference between the accuracy of predicting occupied sites to be suitable and unoccupied sites to be unsuitable (i.e. minimum difference between sensitivity and specificity)	0.12 ± 0.008	89.6 ± 2.90%	89.9 ± 2.67%	15,443

Finally, Figure B.4 shows the climatic SI categorised in four classes In this figure, areas in the EU territory in which *X. fastidiosa* is known to be present, i.e. Apulia and Tuscany in Italy, Corsica and PACA region in France, and the Balearic Islands and Alicante in Spain are coincide with climatic SI > 0.6 or those located in Madrid (Spain) and northern Portugal with a climatic SI between 0.3 and 0.6 (Figure B.4).

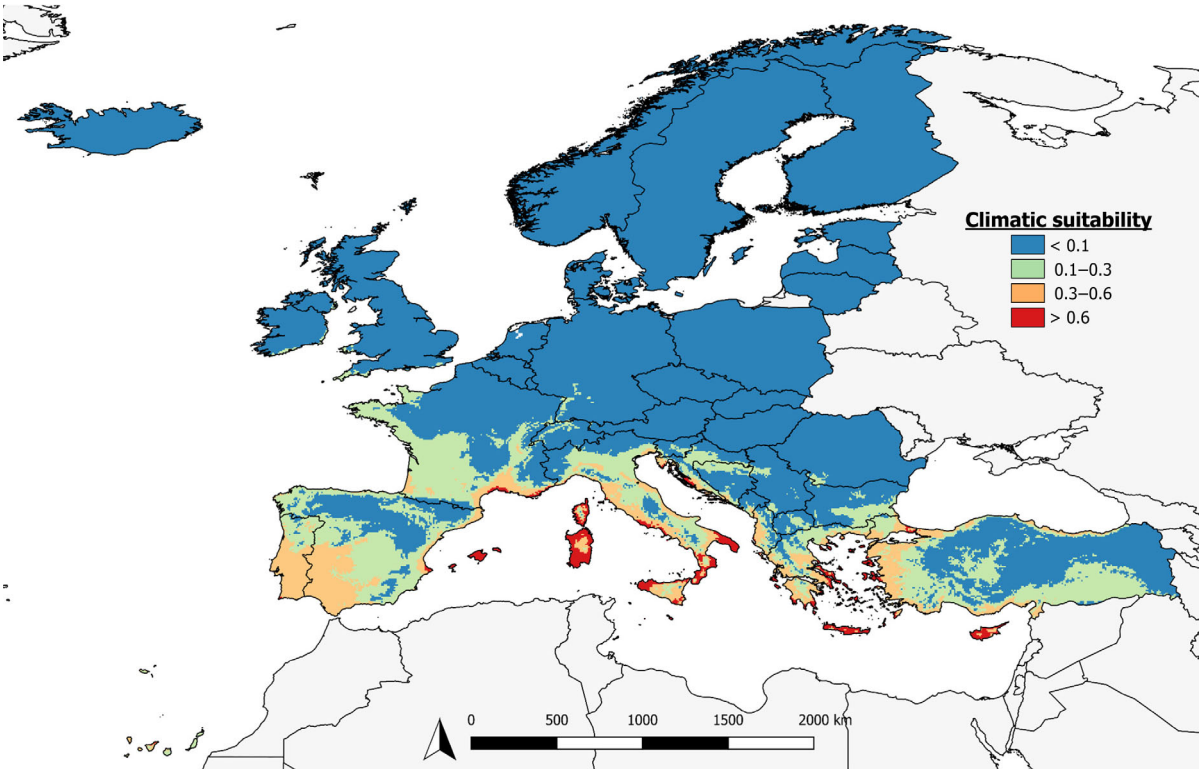


Figure B.4: Estimated climatic suitability map for *X. fastidiosa* according to a SDM ensemble model with four thresholds

B.2.2. Lower limits for *X. fastidiosa* subspecies

The statistics associated to each threshold as well as the area estimated as suitable for establishment of *X. fastidiosa* subspecies are indicated in Table B.2 and from Figures B.5 to B.7. Above these thresholds, and according to the likelihood values associated to these thresholds, we are confident that *X. fastidiosa* subspecies can establish in the EU territory.

Table B.2: Comparison between percentage of *X. fastidiosa* presences and pseudo-absences that are correctly predicted by different prevalence thresholds for subsp. *fastidiosa*, subsp. *multiplex* and subsp. *pauca*

Threshold number	Rationale	Threshold	% of known *X. fastidiosa* presences predicted to be suitable (sensitivity ± sd)	% of *X. fastidiosa* pseudo-absences predicted to be unsuitable (specificity ± sd)	No. of EU28 5 arc-min grid cells predicted to be suitable for establishment
X. fastidiosa* subsp. *fastidiosa					
1	Predicts all but 5% of *X. fastidiosa* presences to be suitable	0.30 ± 0.032	95%	87.8 ± 3.51%	6,628
2	Predicts all but 10% of *X. fastidiosa* pseudo-absences to be suitable	0.36 ± 0.033	90%	88.6 ± 3.39%	4,802
3	Maximises sum of sensitivity and specificity	0.25 ± 0.037	92.7 ± 7.90%	90.0 ± 6.57%	8,975
4	Minimises the difference between sensitivity and specificity	0.21 ± 0.031	89.5 ± 4.97%	89.8 ± 4.09%	11,322
X. fastidiosa* subsp. *multiplex					
1	Predicts all but 5% of *X. fastidiosa* presences to be suitable	0.30 ± 0.021	95%	91.9 ± 2.00%	10,313
2	Predicts all but 10% of *X. fastidiosa* pseudo-absences to be suitable	0.36 ± 0.022	90%	92.7 ± 2.02%	7,956
3	Maximises sum of sensitivity and specificity	0.19 ± 0.020	93.4 ± 6.96%	92.6 ± 4.37%	16,337
4	Minimises the difference between sensitivity and specificity	0.17 ± 0.016	91.3 ± 4.45%	92.2 ± 3.43%	18,206
X. fastidiosa* subsp. *pauca					
1	Predicts all but 5% of *X. fastidiosa* presences to be suitable	0.31 ± 0.026	95%	91.5 ± 2.04%	2,012
2	Predicts all but 10% of *X. fastidiosa* pseudo-absences to be suitable	0.38 ± 0.026	90%	92.3 ± 1.82%	1,019
3	Maximises sum of sensitivity and specificity	0.28 ± 0.023	92.5 ± 7.06%	93.5 ± 4.97%	2,454
4	Minimises the difference between sensitivity and specificity	0.21 ± 0.015	91.1 ± 5.10%	93.0 ± 3.12%	3,764

As described for *X. fastidiosa* as a species, the estimated area that could be explored by *X. fastidiosa* subspecies in the EU territory was related to the threshold level used, increasing with the decrease in the threshold value. Of the three subspecies, subspecies *multiplex* showed the higher potential area for establishment, followed by subsp. *fastidiosa* and *pauca*, in that order. Thus, the estimated area that could be explored for each subspecies ranged from 4,802 to 11,322 5 arc-min grid cells for threshold 2 (0.36) and threshold 4 (0.21), respectively, for subsp. *fastidiosa*; from 7,956 to 18,206 5 arc-min grid cells for threshold 2 (0.36) and threshold 4 (0.17), respectively, for subsp. *multiplex*, and from 1,019 to 3,764 5 arc-min grid cells for threshold 2 (0.38) and threshold 4 (0.21), respectively, for subsp. *pauca* (Table B.2 and from Figures B.5 to B.7).

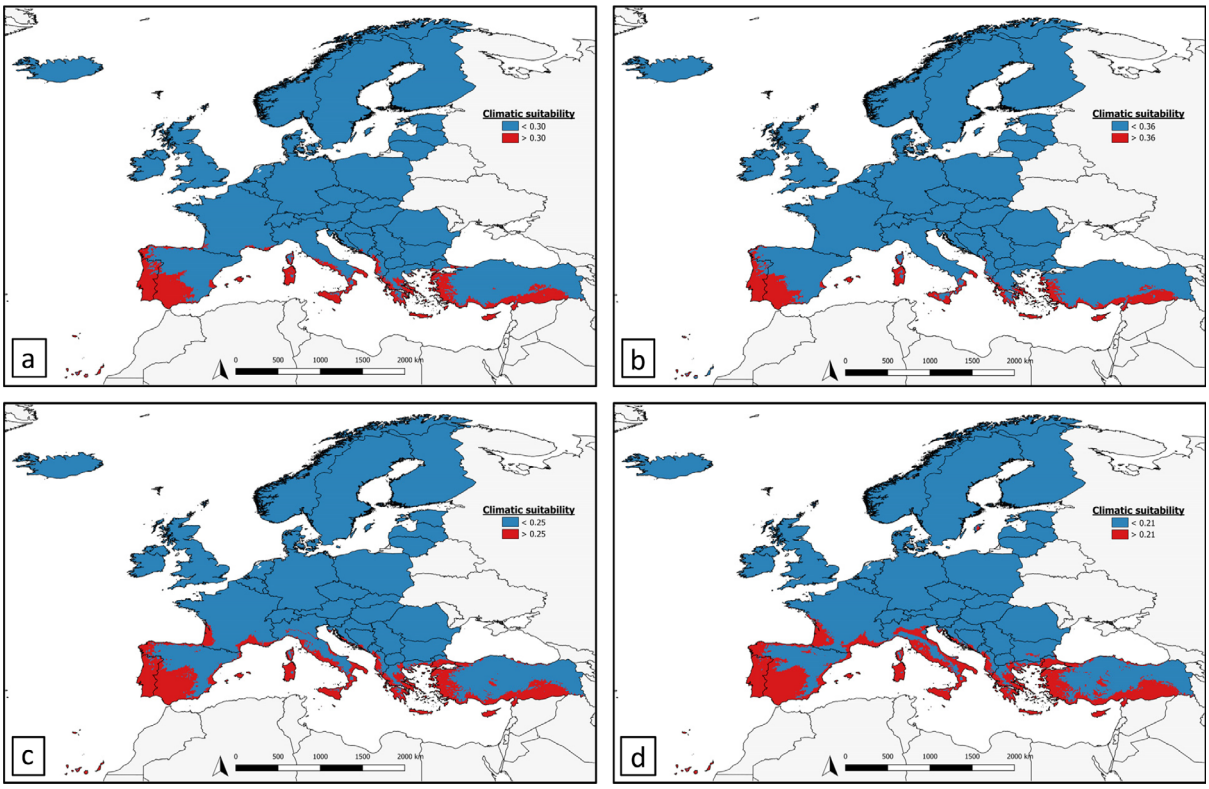


Figure B.5: Estimated climatic suitability maps for *X. fastidiosa* subsp. *fastidiosa* according to a SDM ensemble model with different thresholds indicated in Table B.2. (a) Threshold 1 (0.30), (b) threshold 2 (0.36), (c) threshold 3 (0.25), (d) threshold 4 (0.21)

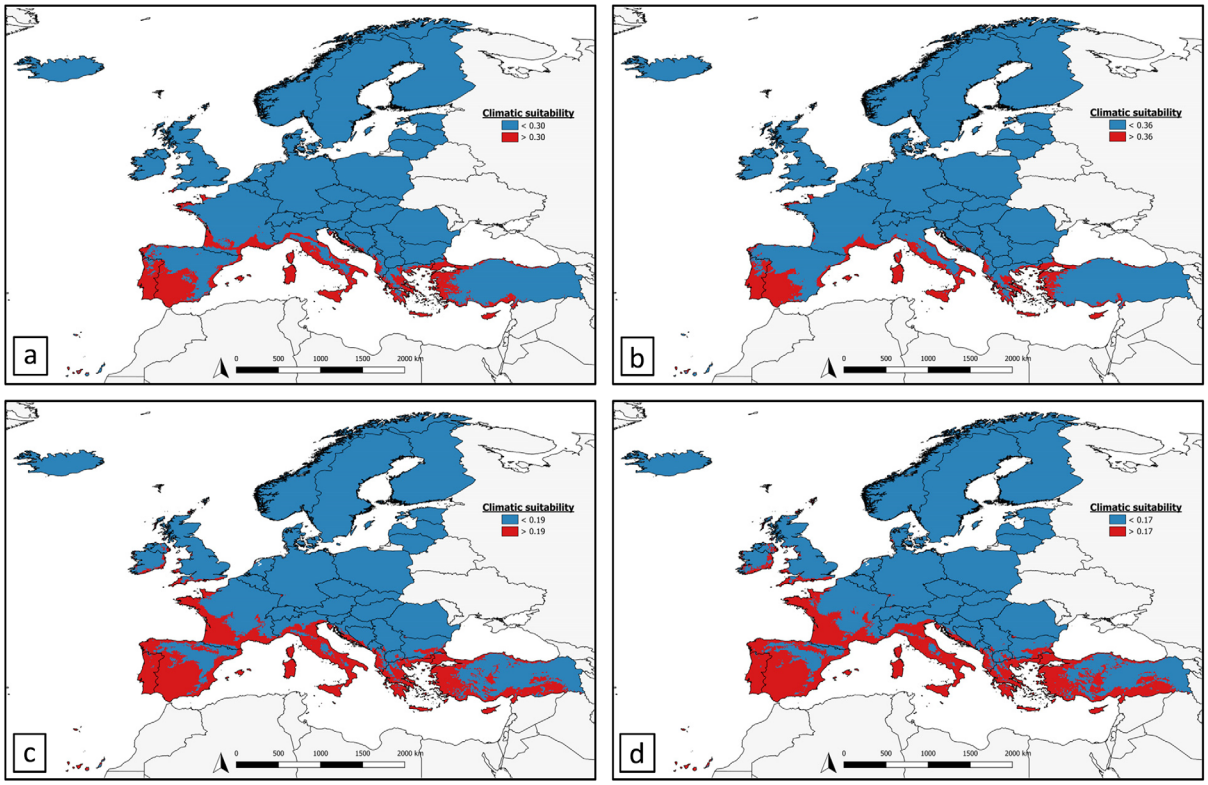


Figure B.6: Estimated climatic suitability maps for *X. fastidiosa* subsp. *multiplex* according to a SDM ensemble model with different thresholds indicated in Table B.2. (a) Threshold 1 (0.30), (b) threshold 2 (0.36), (c) threshold 3 (0.19), (d) threshold 4 (0.17)

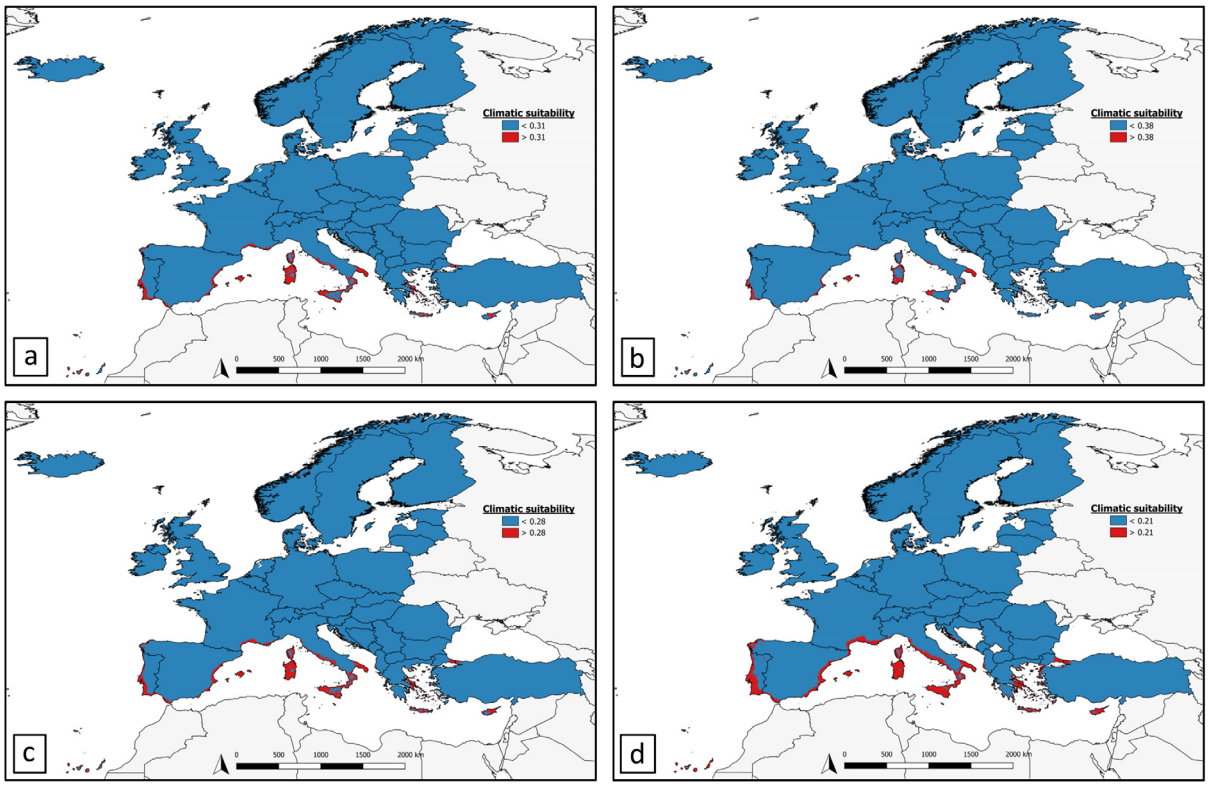


Figure B.7: Estimated climatic suitability maps for *X. fastidiosa* subsp. *pauca* according to a SDM ensemble model with different thresholds indicated in Table B.2. (a) Threshold 1 (0.31), (b) threshold 2 (0.38), (c) threshold 3 (0.28), (d) threshold 4 (0.21)

Figures B.8–B.10 show the categorised climatic suitability maps for *X. fastidiosa* subsp. *fastidiosa*, *multiplex* and *pauca*. For subsp. *fastidiosa*. the most suitable areas for this subspecies are found in the southern regions of Portugal and Spain and the Balearic Islands, Cyprus and Crete (climatic SI > 0.6), with lower suitability values along the coastal Mediterranean regions (climatic SI 0.3–0.6) with values lower than 0.3 in southern France and Corsica (Figure B.1). Subsp. *multiplex* had the highest extent compared with that predicted for subspecies *fastidiosa* and *pauca*. With the exception of central Europe subsp. *multiplex* could find suitable climatic conditions in many areas of the EU territory. The highest suitability is found in along the coastal line (SI > 0.6) of the Mediterranean, including Corsica, Sardinia and Sicily. Suitability values between 0.3 and 0.6 are present in the central and southern regions in the Iberian Peninsula and Italy, and southern Greece. Lower values (0.1–0.3) prevails in France, Belgium, the Netherlands, and along the coastal regions in the UK and Ireland (Figure B.1). Subsp. *pauca* would have the lowest extent of suitability compared with the two other subspecies. Suitability values above 0.6 is only estimated for the Apulia region in southern Italy and the Balearic Islands, while limited areas along the Mediterranean coast and southern Portugal show suitability values between 0.3 and 0.6 (Figure B.10).

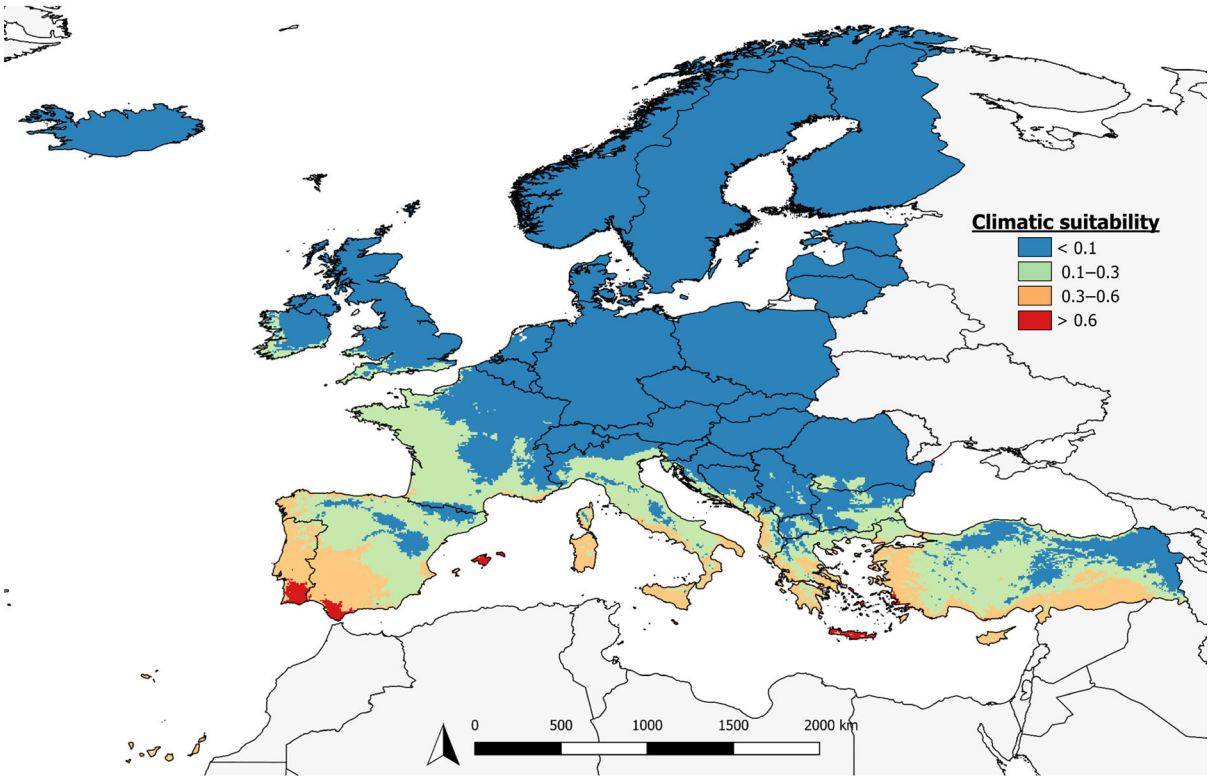


Figure B.8: Estimated climatic suitability maps for *X. fastidiosa* subsp. *fastidiosa* according to a SDM ensemble model with four thresholds

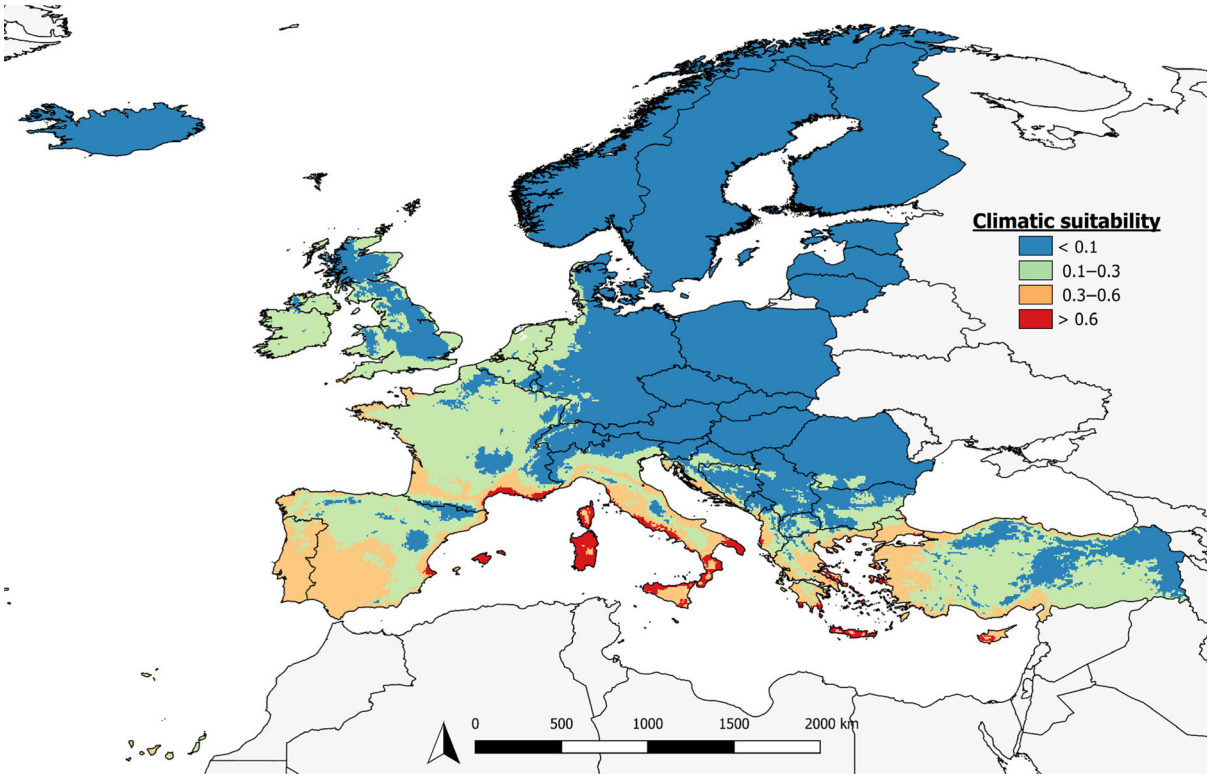


Figure B.9: Estimated climatic suitability maps for *X. fastidiosa* subsp. *multiplex* according to a SDM ensemble model with four thresholds

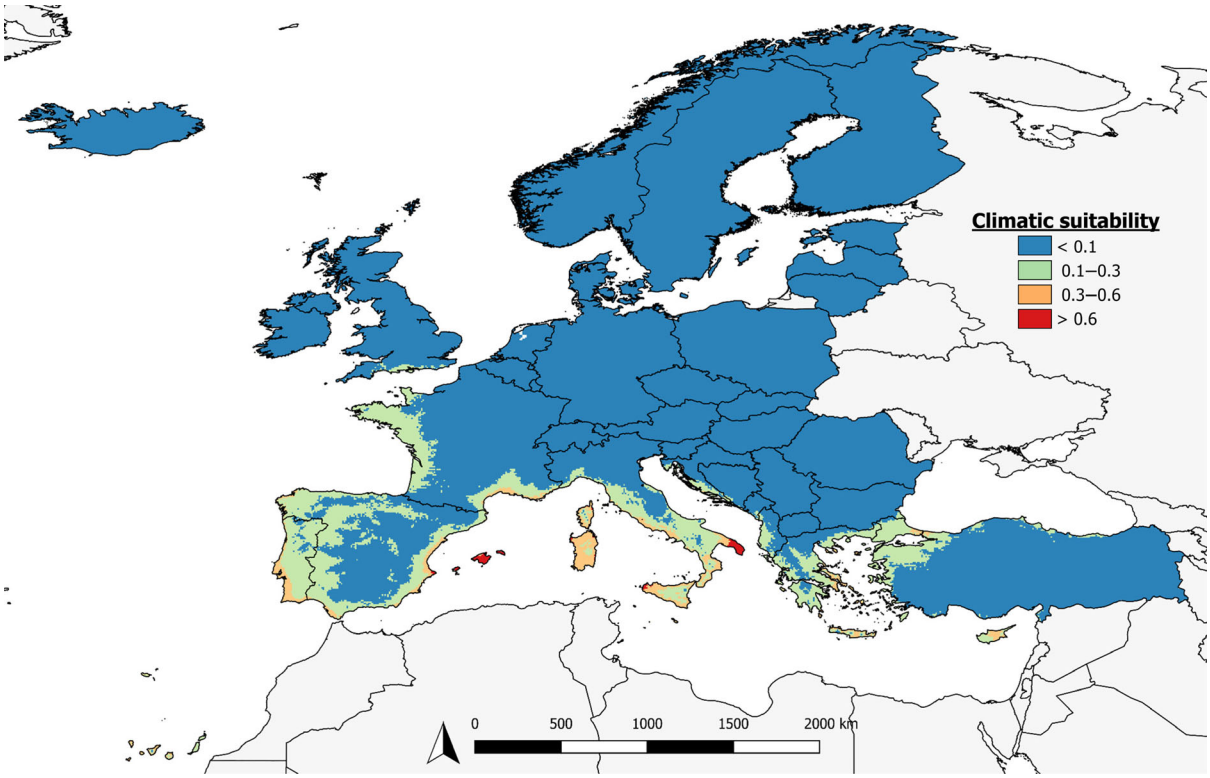


Figure B.10: Estimated climatic suitability maps for *X. fastidiosa* subsp. *pauca* according to a SDM ensemble model with four thresholds

Appendix C – Maps of bioclimatic variables related to establishment of *Xylella fastidiosa* and subspecies

Figure C.1 shows the bioclimatic variables that contribute to models to predict the potential for establishment of *X. fastidiosa* and subspecies described in Section 3.1.1.3 and Table 9.

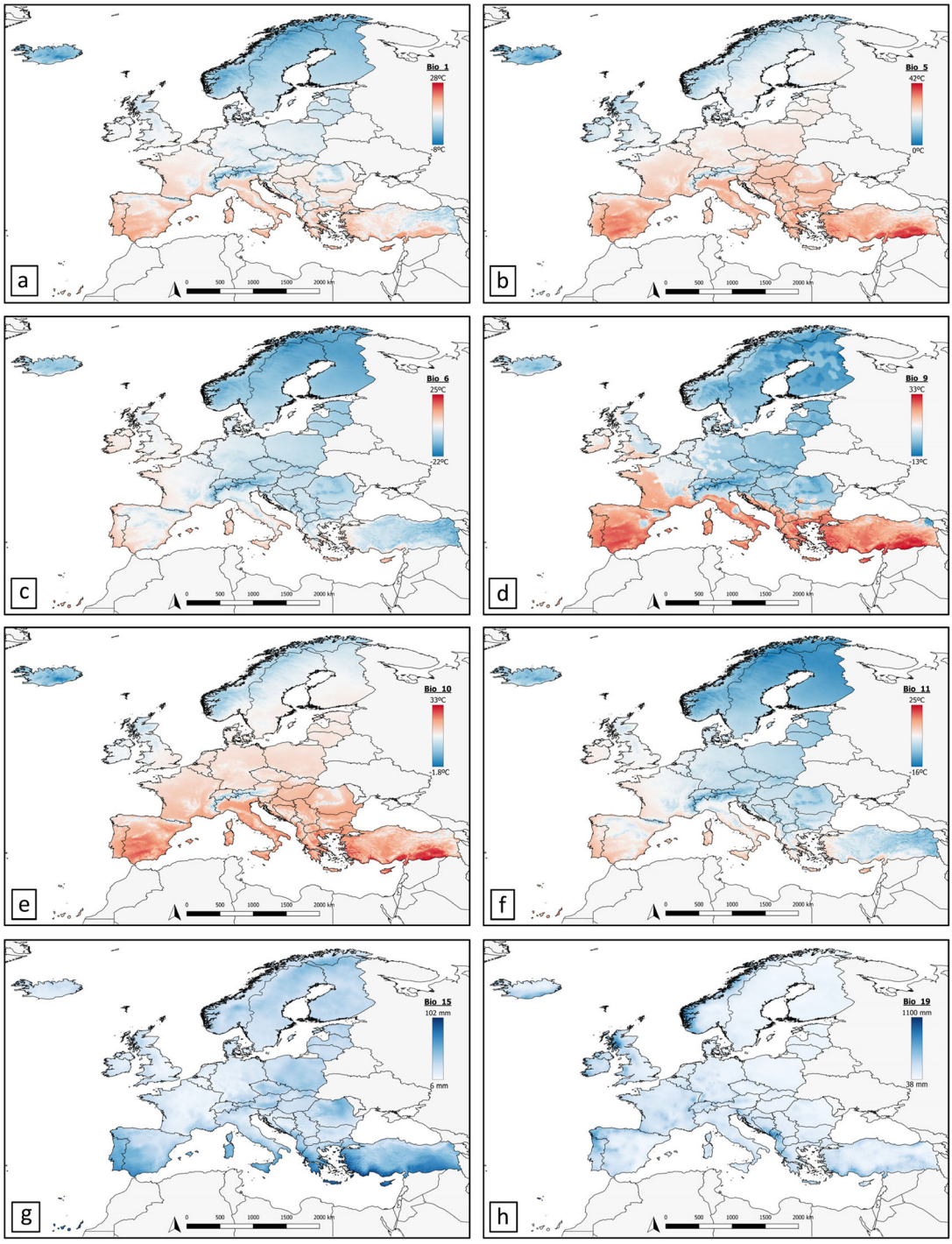


Figure C.1: Maps for bioclimatic variables related to suitability models predicted for *X. fastidiosa* and subspecies. (a) bio1: annual mean temperature; (b) bio5: maximum temperature of warmest month; (c) bio6: minimum temperature of coldest month; (d) bio9: mean temperature of driest quarter; (e) bio10: mean temperature of warmest quarter; (f) bio11: mean temperature of coldest quarter; (g) bio15: precipitation seasonality; and (h) bio19: precipitation of coldest quarter. Climate data was obtained from Chelsa Climatology (Karger et al., 2017)

Appendix D – Assessment of establishment for *Xylella fastidiosa* Sequence Types by SDM ensemble modelling

Multilocus sequence typing (MLST) (Maiden et al., 1998) is largely accepted as a very useful genetic typing methodology. This method is based on the sequence of a set of seven housekeeping genes for *X. fastidiosa*. Each sequence of a given housekeeping gene is assigned to a distinct allele. For a given *X. fastidiosa* isolate, the alleles at each of the seven genes define the Sequence Type (ST). MLST allows for the grouping of genotypes that are biologically distinct within the various *X. fastidiosa* subspecies. To date, there are up to 81 different recorded types worldwide (EFSA, 2018a). Up to eight different STs are recorded in the EU, belonging to the subspecies *fastidiosa* (ST1), *multiplex* (ST6, 7, 79, 81), *pauca* (53, 80) and *sandyi* (76) (EFSA PLH Panel, 2018b).

D.1. Ensemble modelling for *X. fastidiosa* Sequence Types

For the three subspecies ST combinations, the SDM models showed high levels of performance, with AUC, sensitivity and specificity being higher than 0.92. While TSS and Cohen's kappa was higher than 0.77 and 0.72, respectively (Table D.1).

Table D.1: Summary of performance statistics for the ensemble SDMs for *X. fastidiosa* ST1, ST6 and 7, and ST53

***X. fastidiosa* subspecies and ST**	**AUC**	**Sensitivity**	**Specificity**	**TSS**	**Kappa**
fastidiosa ST1	0.95 ± 0.045	0.95 ± 0.084	0.92 ± 0.070	0.88 ± 0.090	0.72 ± 0.170
multiplex ST6	0.96 ± 0.049	0.99 ± 0.010	0.93 ± 0.082	0.93 ± 0.082	0.77 ± 0.220
pauca ST53	0.98 ± 0.046	0.97 ± 0.080	0.98 ± 0.038	0.95 ± 0.085	0.92 ± 0.128

D.1.1. *X. fastidiosa* subsp. *fastidiosa* ST1

X. fastidiosa subsp. *fastidiosa* ST1 is linked to Pierce's disease of grapevines. In the EU, this ST has been found only infecting cherry trees, grapevine and almond in Mallorca Island in the Balearic Islands, Spain (EFSA PLH Panel, 2018b).

The map with the continuous suitability scores for the *X. fastidiosa* subsp. *fastidiosa* ST1 in the EU territory drawn from the consensus model is presented in Figure D.1. Overall the predicted model is similar to that shown for the subspecies *fastidiosa* as a hole. The model predicts areas with suitable climatic conditions for *X. fastidiosa* subsp. *fastidiosa* ST1 in the southern regions of Portugal and the Balearic Islands, with lower suitability values in southern-western Spain and Apulia, Sardinia and Sicily in Italy.

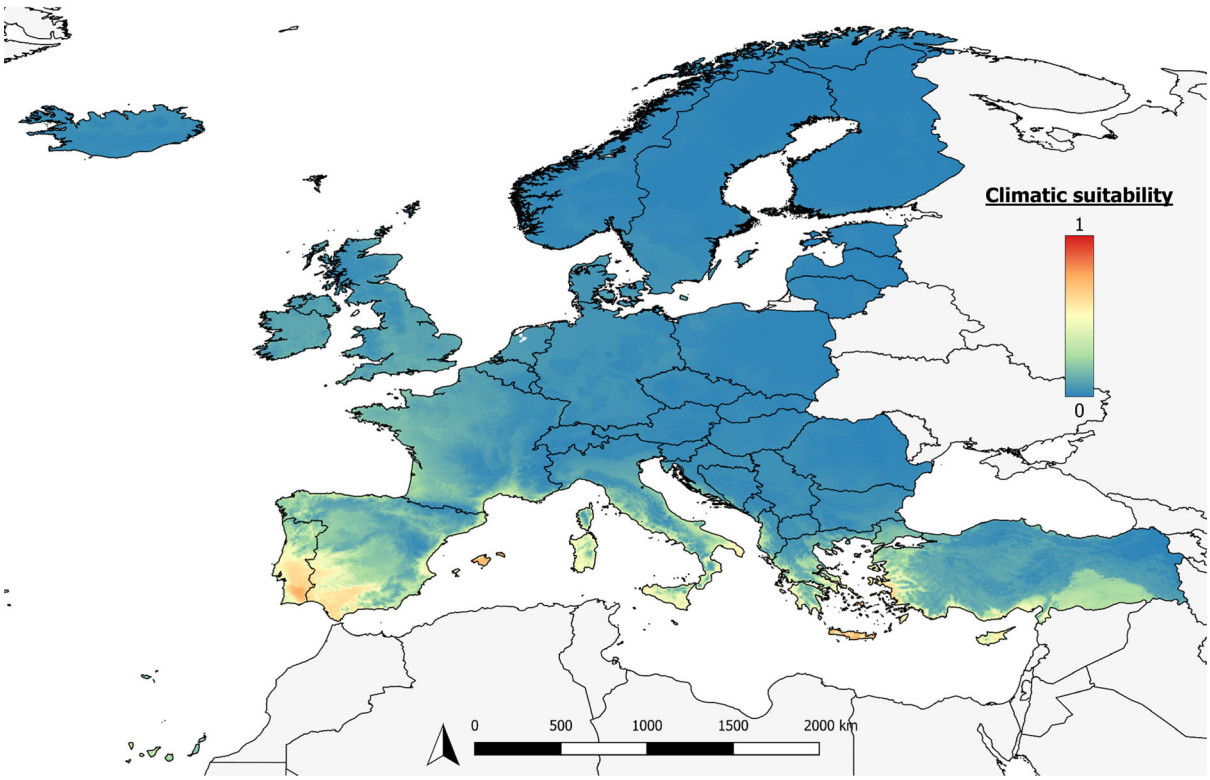


Figure D.1: Estimated climatic suitability map for *X. fastidiosa* subsp. *fastidiosa* ST1 according to a SDM ensemble model

D.1.2. *X. fastidiosa* subsp. *multiplex* ST6

The subsp. *multiplex* has the highest number of STs identified. ST6-ST7 are widespread in Corsica (Denance et al., 2017) and PACA region in France, Mallorca island in the Balearic Islands (ST7) (Olmo et al., 2017), and more recently, in mainland Spain, both in the province of Alicante (ST6) and Madrid (ST6) (Giampetruzzi et al., 2019).

The map with the continuous suitability scores for the *X. fastidiosa* subsp. *multiplex* ST6 in the EU territory drawn from the consensus model is presented in Figure D.2. According to model predictions, this particular ST of *X. fastidiosa* subsp *multiplex* would be essential restricted to the southern regions, particularly in the southern half of the Iberian Peninsula, southern Italy and Greece and particularly the south-east of Spain and Portugal and all the archipelagos in the Mediterranean.

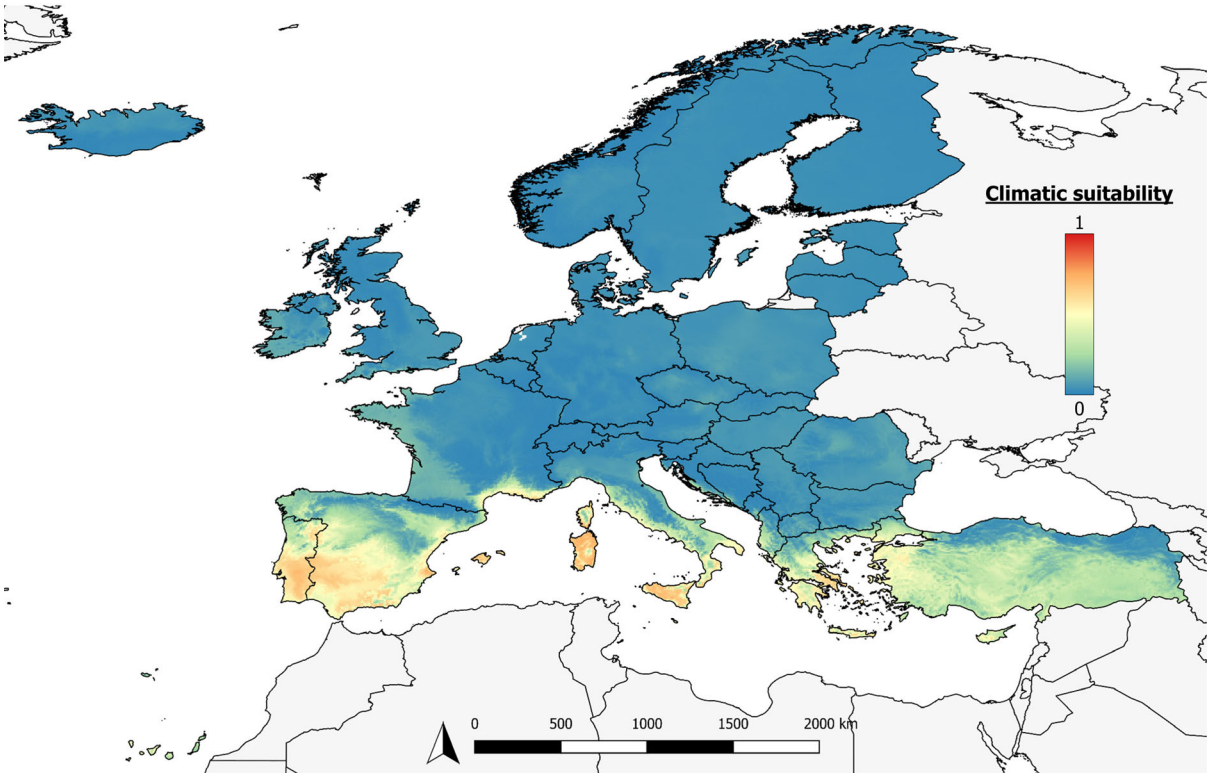


Figure D.2: Estimated climatic suitability map for *X. fastidiosa* subsp. *multiplex* ST6 according to a SDM ensemble model

D.1.3. *X. fastidiosa* subsp. pauca ST53

X. fastidiosa subsp. *pauca* ST53 is the causal agent of the Olive quick decline syndrome in Apulia region, being olive, widely cultivated in the area concerned, is by far the most commonly infected and severely affected host in all the Apulian outbreaks. However, searches for susceptible plant species identified a list of 31 plant species naturally infected with the ST53 isolate (Saponari et al., 2018). Isolates harbouring ST53 were concomitantly described in 2014 in Central America by Nunney et al. (2014a). In the EU, this genotype has been identified in the PACA region in Polygala myrtifolia (Denance et al., 2017) and in *Prunus persica* and *Quercus ilex* in Corsica (EFSA PLH Panel, 2018b).

The map with the continuous suitability scores for the *X. fastidiosa* subsp. *pauca* ST53 in the EU territory drawn from the consensus model is presented in Figure D.3. Only limited areas in the Atlantic coast of Portugal and southern Spain, together with Apulia region would have a high climatic suitability. Lower suitability is predicted for southern Italy, Sicily, Corsica and the Balearic Islands.

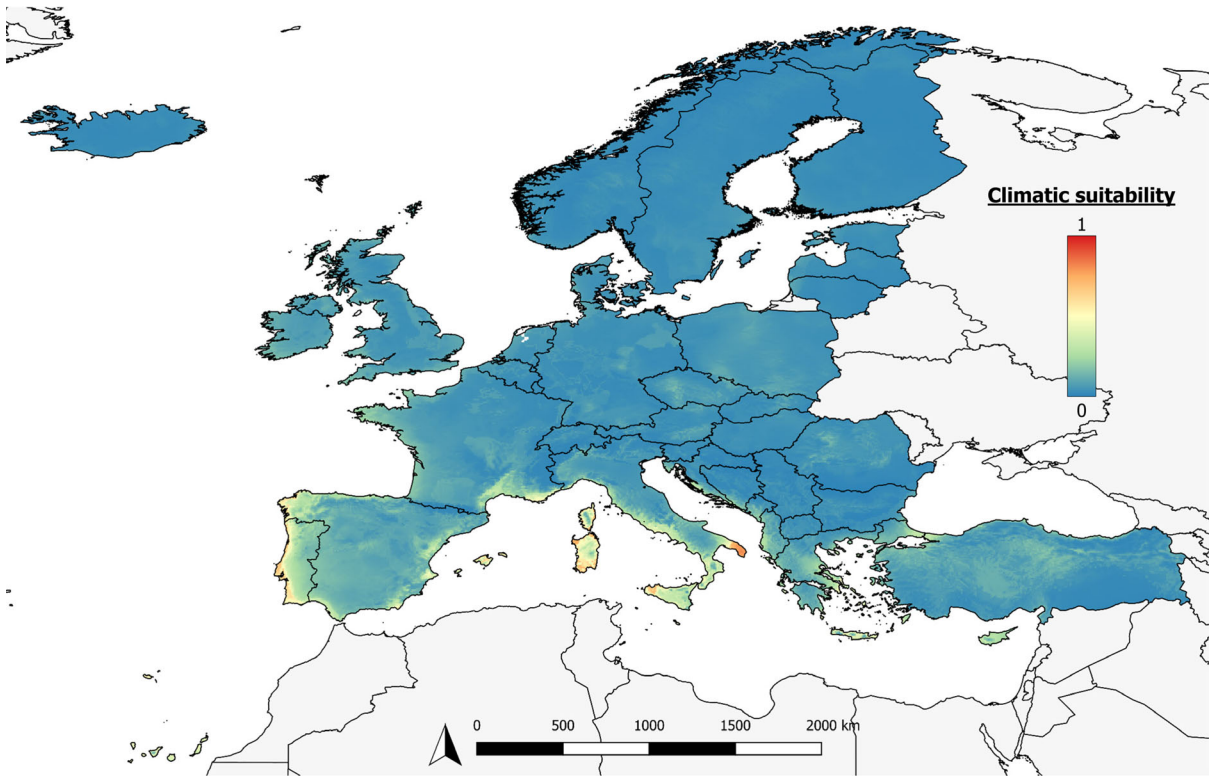


Figure D.3: Estimated climatic suitability map for *X. fastidiosa* subsp. *pauca* ST53 according to a SDM ensemble model

D.1.4. Uncertainty affecting the assessment of establishment for *X. fastidiosa* Sequence Types

D.1.4.1. SDM ensemble modelling

The variability on model projections estimated by the standard deviation of the SI for the 800 individual models used in the SDM was positively correlated with the suitability value (Figure D.4), The higher variability was found for subspecies *pauca* ST53 (range 0.00018–0.12888), while similar range was estimated for subspecies *multiplex* ST6 (0.0014–0.0919) and *fastidiosa* ST1 *pauca* (0.0014–0.0919).

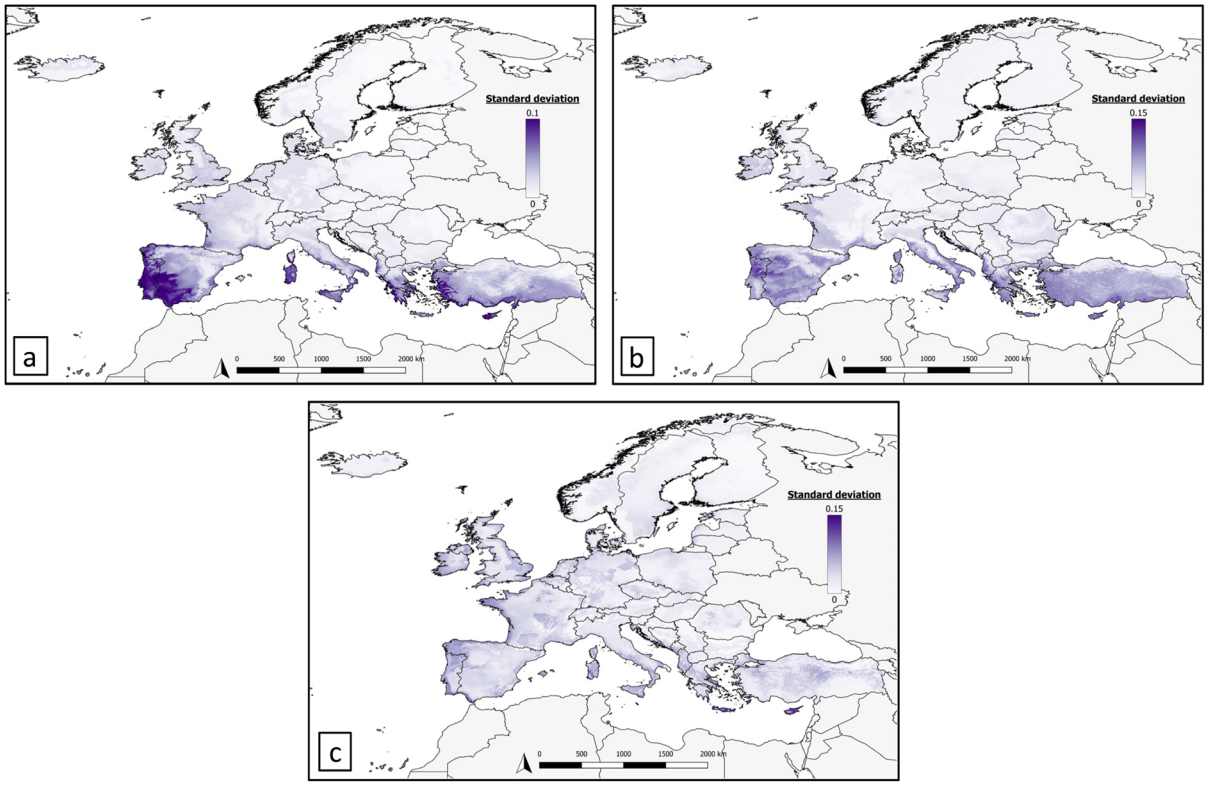


Figure D.4: Uncertainty in the projections of climatic suitability for *X. fastidiosa* Sequence Types estimated by the standard deviation among models used to build the SDM ensemble. (a) subspecies fastidiosa ST1; (b) subspecies multiplex ST6; (c) subspecies pauca ST53

D.1.4.2. Uncertainties on the lower limit of suitability for the establishment of *X. fastidiosa* Sequence Types

As previously described, five different thresholds as follows: (a) two thresholds set to be the suitability value at which sensitivity, i.e. true positive rate, was 95% and 90%, respectively; (b) the suitability value that maximises the sum of sensitivity and specificity; (c) the suitability value that minimised the difference between sensitivity and specificity and (d) a four levels threshold was applied ranging the SI as follows: (1) SI < 0.1; (2) 0.1 > SI < 0.3; (3) 0.3 > SI < 0.6 and (4) SI > 0.6 (Table D.2).

The statistics associated to each threshold as well as the area estimated as suitable for establishment of *X. fastidiosa* STs are indicated in Table D.2 and from Figures D.5 to D.7. Above these thresholds, and according to the likelihood values associated to these thresholds, we are confident that *X. fastidiosa* STs can establish in the EU territory.

Table D.2: Comparison between percentage of *X. fastidiosa* presences and pseudo-absences that are correctly predicted by different prevalence thresholds for ST1, ST6 and ST53

Threshold number	Rationale	Threshold	% of known *X. fastidiosa* presences predicted to be suitable (sensitivity ± sd)	% of *X. fastidiosa* pseudo-absences predicted to be unsuitable (specificity ± sd)	No. of EU28 5 arc-minute grid cells predicted to be suitable for establishment
***X. fastidiosa* subsp. *fastidiosa* ST1**					
1	Predicts all but 5% of *X. fastidiosa* presences to be suitable	0.34 ± 0.43	95%	87.3 ± 3.91%	4,400
2	Predicts all but 10% of *X. fastidiosa* pseudo-absences to be suitable	0.36 ± 0.044	90%	87.9 ± 3.58%	4,005
3	Maximises sum of sensitivity and specificity	0.33 ± 0.031	95.1 ± 8.44%	92.4 ± 6.98%	4,563
4	Minimises the difference between sensitivity and specificity	0.37 ± 0.056	95.0 ± 8.36%	95.3 ± 3.40%	3,938
***X. fastidiosa* subsp. *multiplex* ST6**					
1	Predicts all but 5% of *X. fastidiosa* presences to be suitable	0.35 ± 0.040	95%	89.9 ± 2.90%	7,804
2	Predicts all but 10% of *X. fastidiosa* pseudo-absences to be suitable	0.35 ± 0.040	90%	89.9 ± 2.90%	7,804
3	Maximises sum of sensitivity and specificity	0.39 ± 0.075	99.9 ± 0.01%	92.7 ± 9.22%	7,123
4	Minimises the difference between sensitivity and specificity	0.40 ± 0.073	99.9 ± 0.01%	93.9 ± 6.95%	6,861
***X. fastidiosa* subsp. *pauca* ST53**					
1	Predicts all but 5% of *X. fastidiosa* presences to be suitable	0.36 ± 0.047	95%	83.4 ± 3.69%	1,771
2	Predicts all but 10% of *X. fastidiosa* pseudo-absences to be suitable	0.42 ± 0.049	90%	83.7 ± 3.665	1,228
3	Maximises sum of sensitivity and specificity	0.58 ± 0.046	97.1 ± 7.98%	98.2 ± 3.82%	412
4	Minimises the difference between sensitivity and specificity	0.58 ± 0.048	98.3 ± 6.26%	98.5 ± 3.02%	408

Overall, the estimated area that could be explored by *X. fastidiosa* STs in the EU territory was inversely related to the threshold level used. Of the three subspecies/ST combinations, subspecies *multiplex* ST6 showed the higher potential area for establishment, followed by subspecies *fastidiosa* ST1 and subspecies *pauca* ST53 in that order. For *X. fastidiosa* subsp. *fastidiosa* ST1, all the four thresholds were similar, ranging from 0.33 to 0.37, consequently, the estimated area that could be explored for this genotype differed only in 625 5 arc-min grid cells, i.e. 3,938–4,563 5 arc-min grid cells for threshold 4 (0.37) and threshold 3 (0.33), respectively. For *X. fastidiosa* subsp. *multiplex* ST6, fixed sensitivity thresholds, i.e. 1 and 2 were estimated in 0.35, that resulted in an estimated area for potential establishment of 7,804 5 arc-min grid cells. Similarly, for thresholds 3 and 4, 0.39 and 0.40, respectively, the area for potential establishment could reach at least 7,123 and 6,861 5 arc-min grid cells. For *X. fastidiosa* subsp. *pauca* ST53, thresholds ranged from 0.36 and 0.42, respectively, for fixed sensitivity thresholds 1 and 2, to a much higher threshold value of 0.58 for thresholds 3 and 4. These thresholds values resulted in an estimated area of potential establishment for this genotype of 408–1,771 5 arc-min grid cells for thresholds 4 and 1, respectively.

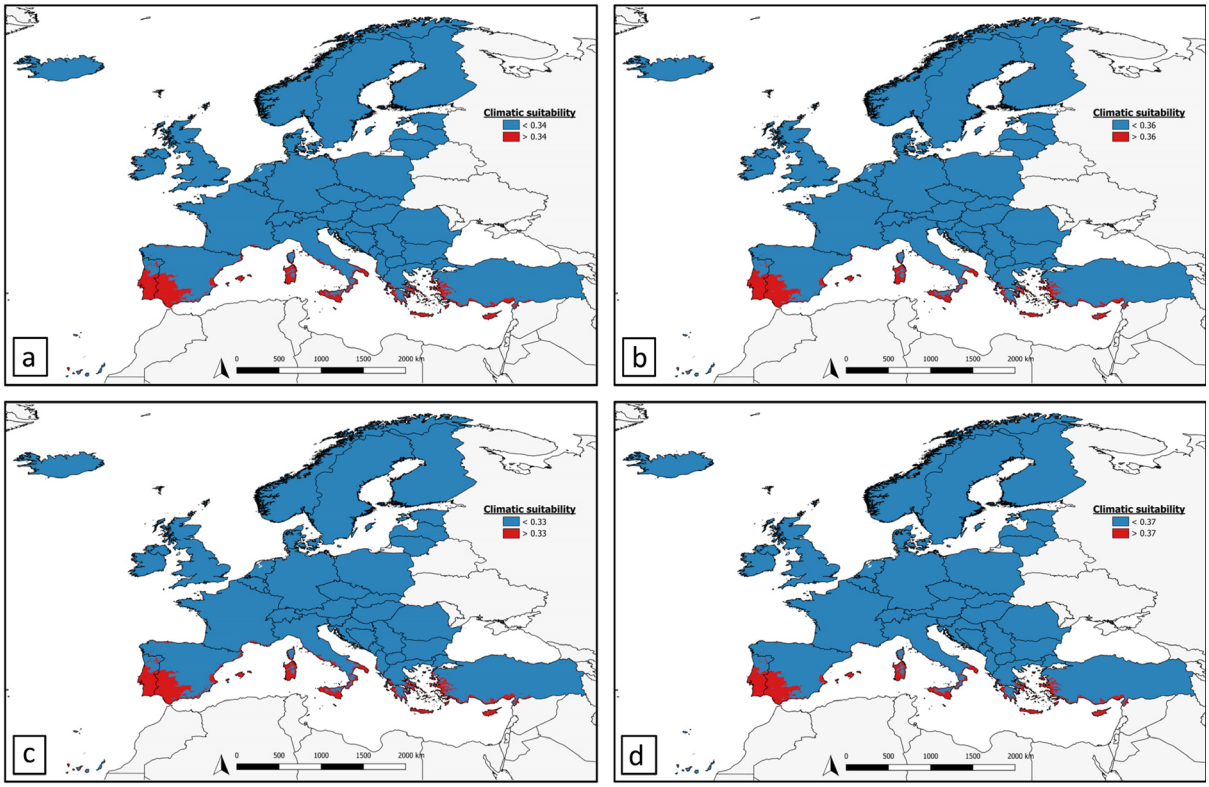


Figure D.5: Estimated climatic suitability maps for *X. fastidiosa* subsp. *fastidiosa* ST1 according to a SDM ensemble model with different thresholds indicated in Table D.2. (a) Threshold 1 (0.34), (b) Threshold 2 (0.36), (c) Threshold 3 (0.33), (d) Threshold 4 (0.37)

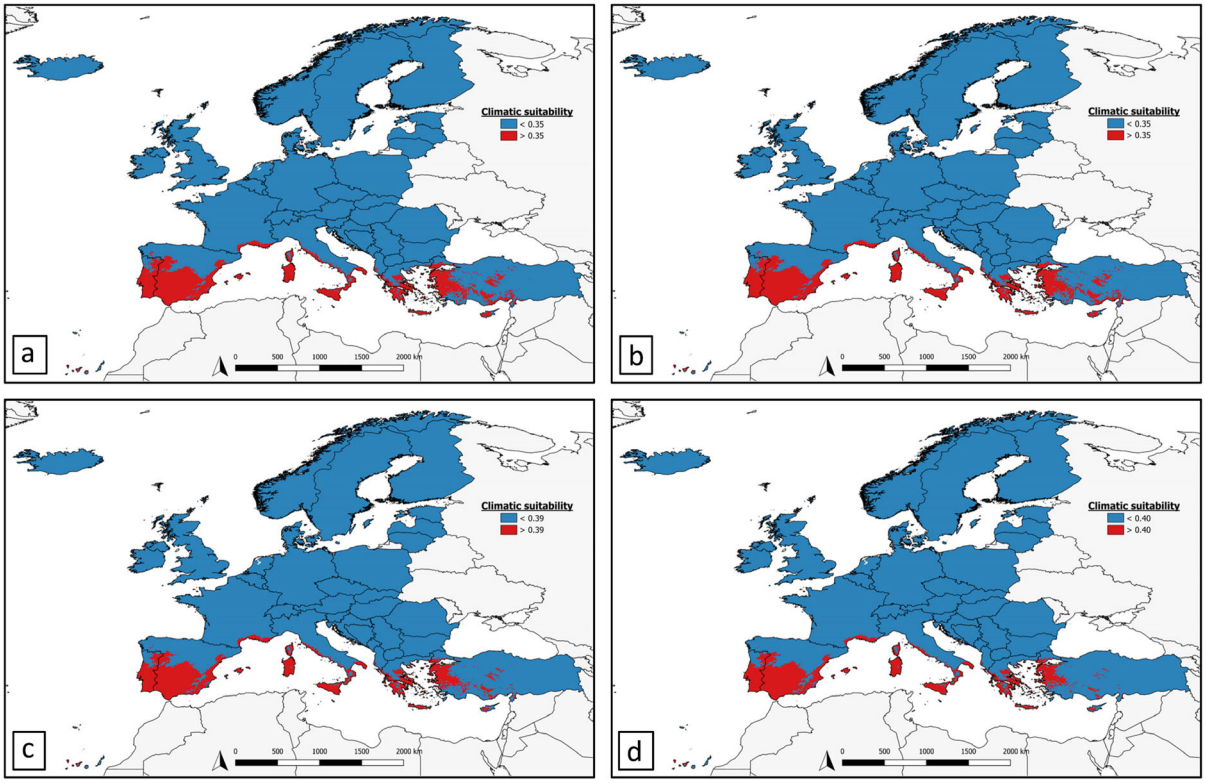


Figure D.6: Estimated climatic suitability maps for *X. fastidiosa* subsp. *multiplex* ST6 according to a SDM ensemble model with different thresholds indicated in Table D.2. (a) Threshold 1 (0.35), (b) Threshold 2 (0.35), (c) Threshold 3 (0.39), (d) Threshold 4 (0.40)

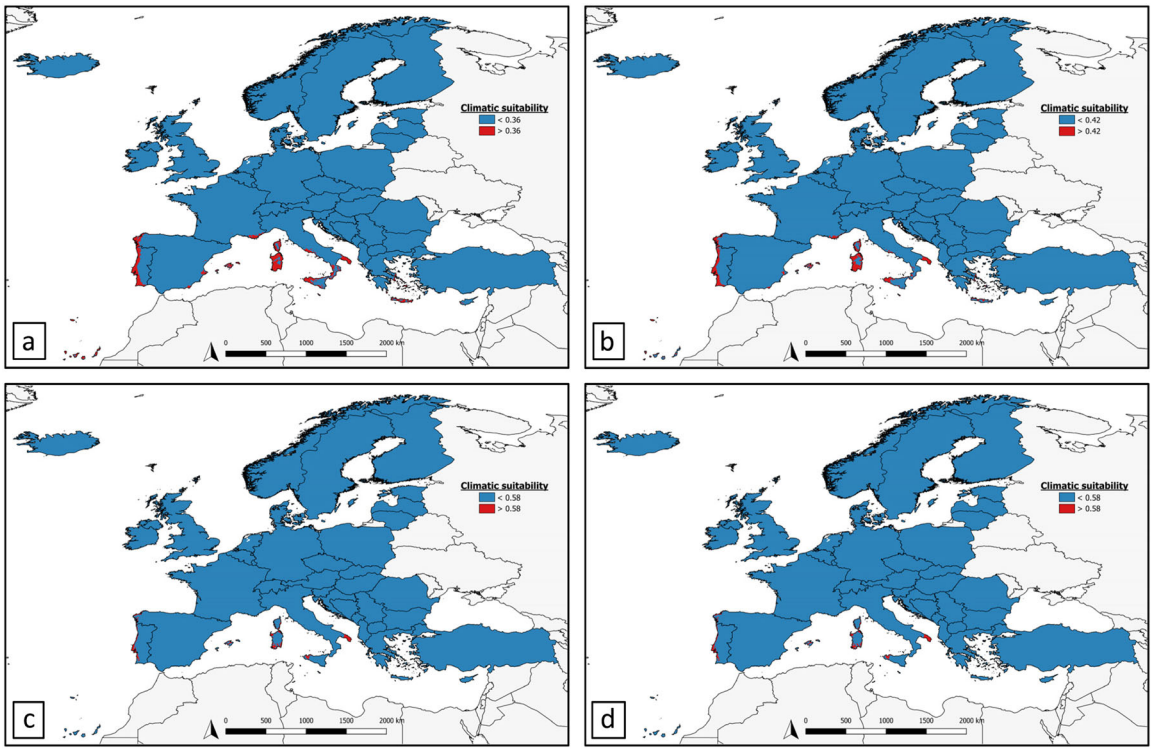


Figure D.7: Estimated climatic suitability maps for *X. fastidiosa* subsp. *pauca* ST53 according to a SDM ensemble model with different thresholds indicated in Table D.2. (a) Threshold 1 (0.36), (b) Threshold 2 (0.42), (c) Threshold 3 (0.58), (d) Threshold 4 (0.58)

Figures D.8 to D.10 show the categorised climatic suitability maps for *X. fastidiosa* subsp. *fastidiosa* ST1, *X. fastidiosa* subsp. *multiplex* ST6, and *X. fastidiosa* subsp. *pauca* ST53. For the *X. fastidiosa* subsp. *fastidiosa* ST1 the model predicts areas with high suitable climatic conditions (climatic SI > 0.6) in the southern regions of Portugal and the Balearic Islands, with lower suitability values in southern-western Spain and Apulia, Sardinia and Sicily in Italy (climatic SI 0.3–0.6). The rest of the Iberian Peninsula, western France, Corsica, and central Italy are categorised with a lower SI (0.1–0.3). For *X. fastidiosa* subsp. *multiplex* ST6 would be restricted to the southern regions, particularly in the southern half of the Iberian Peninsula, southern Italy and Greece (SI 0.3–0.6), being particularly suitable (SI > 0.6) the south-east of Spain and Portugal and all the archipelagos in the Mediterranean. In addition, the south-west area in France and some coastal areas in Ireland wold be considered suitable but with a SI of 0.1–0.3. For *X. fastidiosa* subsp. *pauca* ST53 only limited areas in the Atlantic coast of Portugal and southern Spain, together with Apulia region would have a high climatic suitability (climatic index > 0.6). Suitability values between 0.3 and 0.6 would be also restricted to southern Italy, Sicily, Corsica and the Balearic Islands. Lower values are expected for most the rest of the Iberian Peninsula and south-west France.

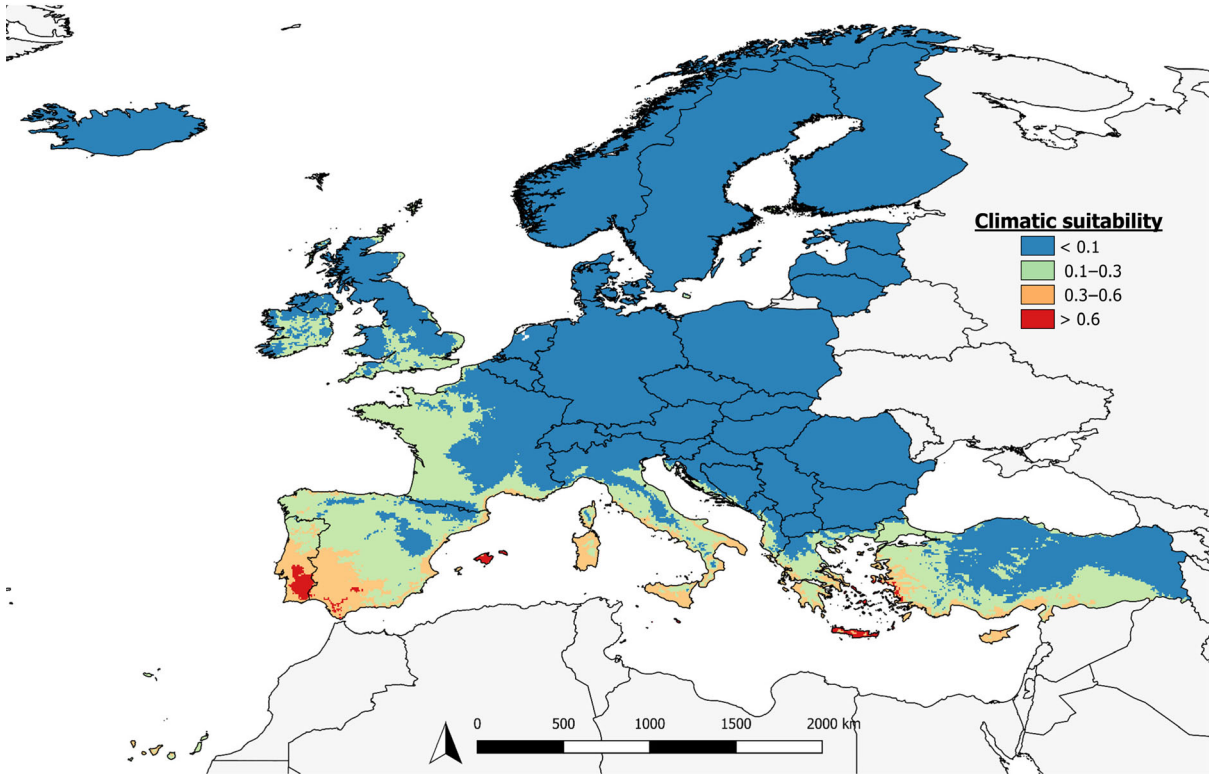


Figure D.8: Estimated climatic suitability maps for *X. fastidiosa* subsp. *fastidiosa* ST1 according to a SDM ensemble model with four thresholds

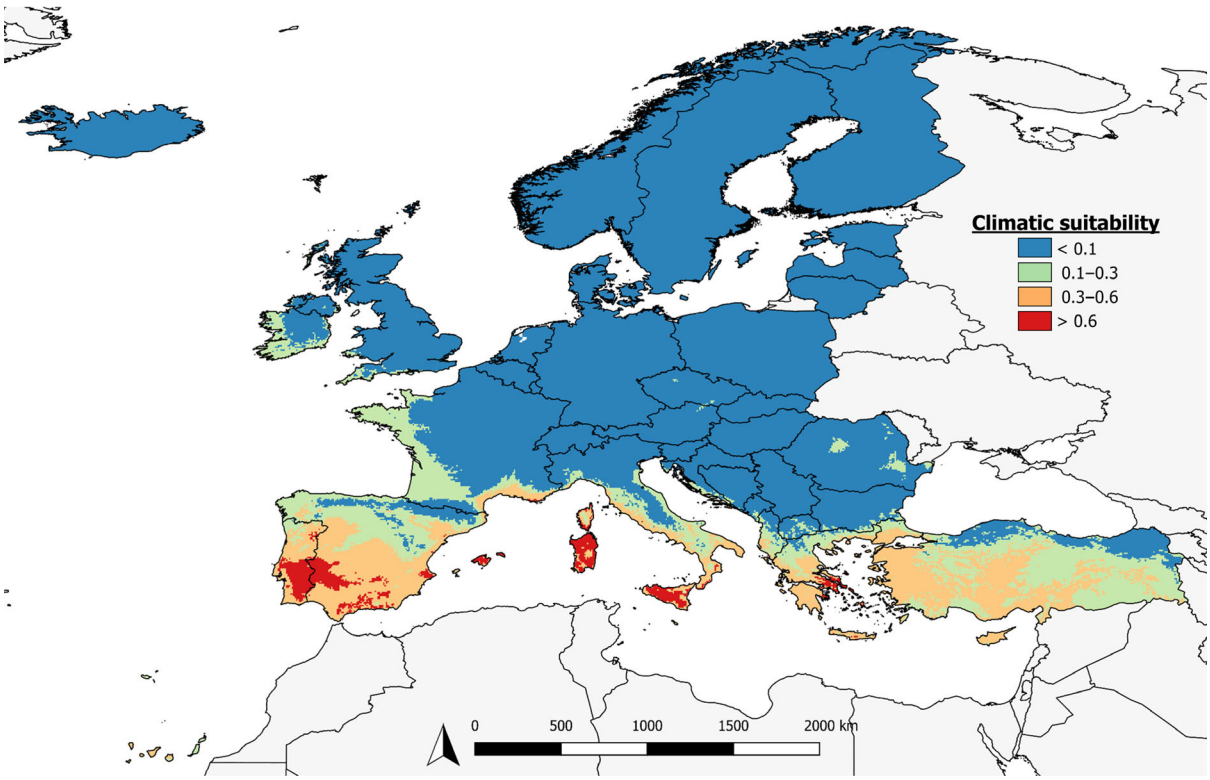


Figure D.9: Estimated climatic suitability maps for *X. fastidiosa* subsp. *multiplex* ST6 according to a SDM ensemble model with four thresholds

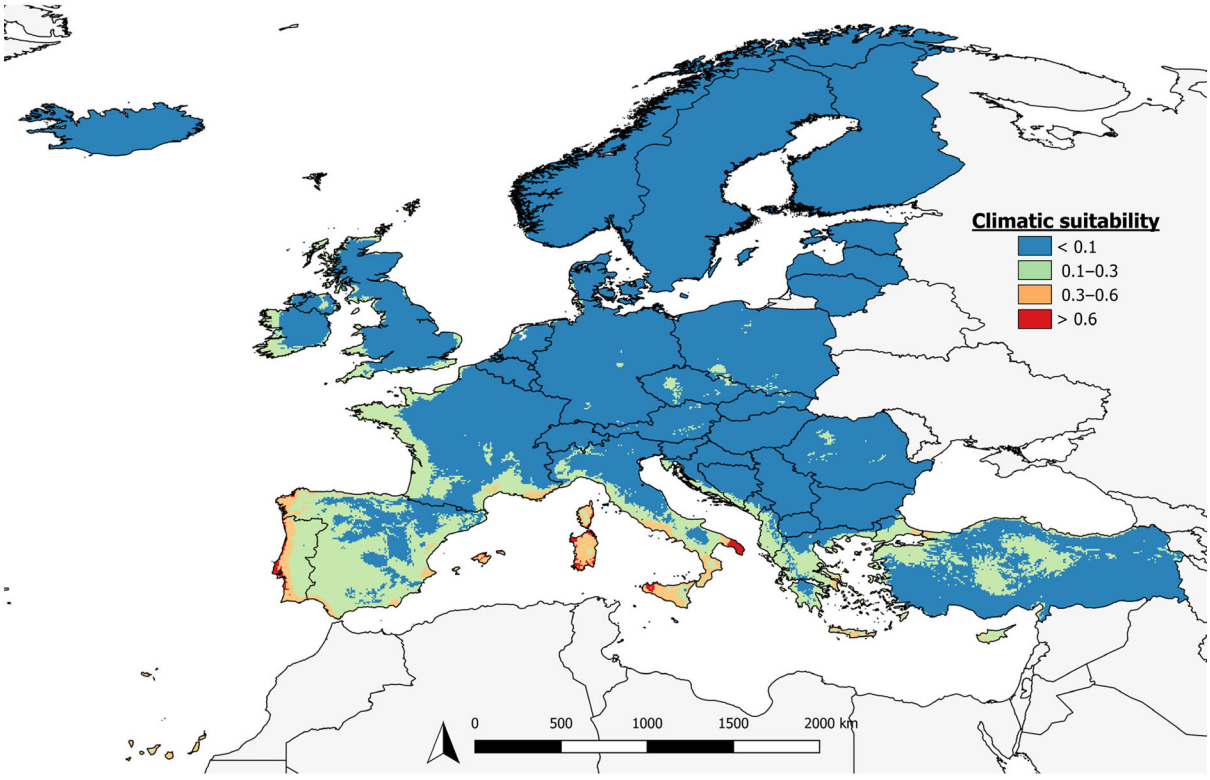


Figure D.10: Estimated climatic suitability maps for *X. fastidiosa* subsp. *pauca* ST53 according to a SDM ensemble model with four thresholds

D.1.5. Environmental factors related to establishment of *X. fastidiosa* Sequence Types

The non-correlated bioclimatic variables that were selected for model fitting for each subspecies are presented in Table D.3. A distinct set of bioclimatic variables was selected for each ST with the only exception of precipitation seasonality (bio15) that was selected irrespective of the ST. Models for subspecies *fastidiosa* ST1 and subspecies *multiplex* ST6 included four common predictors: mean temperature of warmest quarter (bio10), mean temperature of coldest quarter (bio11), precipitation in driest month (bio14) and precipitation in coldest quarter (bio19). On the other hand, subspecies *fastidiosa* ST1 and subspecies *pauca* ST53 also included the mean temperature of wettest quarter (bio8). Moreover, each ST included specific predictors that included isothermality (bio3), the mean temperature of driest quarter (bio9) and precipitation of wettest month (bio13) for subspecies *fastidiosa* ST1 and maximum temperature of warmest month (bio5) and minimum temperature of coldest month (bio6) for subspecies *pauca*.

Table D.3: Variable importance of bioclimatic predictors included in model the SDM for *X. fastidiosa* for ST1, ST6 and ST53

Bioclimatic variable	*X. fastidiosa* subsp. *fastidiosa* ST1	*X. fastidiosa* subsp. *multiplex* ST6	*X. fastidiosa* subsp. *pauca* ST53
bio3	0.14 ± 0.045	---	---
bio5	---	---	0.38 ± 0.125
bio6	---	---	0.55 ± 0.168
bio8	0.10 ± 0.053	---	0.38 ± 0.148
bio9	0.39 ± 0.064	---	---
bio10	0.22 ± 0.09	0.27 ± 0.15	---
bio11	0.51 ± 0.072	0.46 ± 0.21	---
bio13	0.12 ± 0.050	---	---
bio14	0.04 ± 0.025	0.18 ± 0.12	---
bio15	0.14 ± 0.044	0.17 ± 0.13	0.50 ± 0.128
bio19	0.19 ± 0.153	0.08 ± 0.08	---

Appendix E – Factsheet and report of the expert knowledge elicitation on the impact of *Xylella fastidiosa*

E.1. General information

E.1.1. Scope of the expert knowledge elicitation (EKE)

In the framework of the European Commission Mandate M-2018-0020 to EFSA about the update of the Scientific Opinion on the risks to plant health posed by *Xylella fastidiosa* in the EU territory, EFSA was requested to assess the '[...] consequences on the plant species concerned. [...]'. On the basis of this request, the Panel considered the hosts with higher economic values found infected by *X. fastidiosa* in the EU: *Olea europaea* L. (Section 2.1), *Prunus dulcis* (Miller) Webb (Section 2.2), and *Vitis vinifera* L. (Section 2.3) In addition, the Panel also included in the assessment *Citrus* spp. (Section 2.4) for their economic importance in the EU and as recognised important hosts in other areas of the world (consult Terms of Reference of the present Scientific Opinion). To assess the potential impact on the above-mentioned crops, considering the limited amount of quantitative data on the observed impact, the Panel adopted the EFSA EKE methodology, in line with the related guidelines EFSA (2014) and guidance on Uncertainty (EFSA Scientific Committee et al., 2018b). In this specific case, the EKE was conducted in line with the approach defined by the EFSA Working Group on EU Priority Pests[1] for assuring the consistency of results among different projects dealing with the same pest.

E.1.2. Selection of experts

Experts were selected considering their expertise on the crops identified as the most relevant for the EKE.

The experts who participated to the EKE were:

- Antonio Vicent, Head of the Mycology Unit at the Valencian Institute for Agricultural Research (IVIA), expert in epidemiology, control of fungal diseases of citrus and epidemiological and risk models. Involved in the EKE for *Citrus* spp.
- Domenico Bosco, Full Professor in Agricultural Entomology at the University of Turin, Associate scientist at the Institute for Sustainable Plant Protection of the Italian National Research Council (CNR), expert in plant pathogen-vector interaction, transmission biology and epidemiology of insect-transmitted plant pathogens. Involved in the EKE for grapevine.
- Donato Boscia, Head of the operative unit of Bari of the Institute for Sustainable Plant Protection of the Italian National Research Council (CNR), expert in plant virology and plant molecular biology and expert in the 'Olive quick decline syndrome' associated to *X. fastidiosa* in the Apulia region. Involved in the EKE for olive and almond.
- Federico Dicenta López-Higuera, Researcher at the Spanish National Research Council (CSIC), plant genetic and fruticulture. Involved in the EKE for almond.
- Gianni Gilioli, Associate Professor in the Dept. of Molecular and Translational Medicine at the University of Brescia, expert in risk analysis and food safety, models and management schemes in eco-epidemiology, parameter estimation for ecological models. Involved in the EKE for olive, almond, grapevine and *Citrus* spp.
- João Roberto Spotti Lopes, Full Professor in the Dept. of Entomology and Acarology at the Luiz de Queiroz College of Agriculture, University of São Paulo (USP), expert in vector ecology, behaviour and transmission of phytopathogenic bacteria (e.g. *X. fastidiosa*) and viruses. Involved in the EKE for olive, almond, grapevine and *Citrus* spp.
- Juan Antonio Navas Cortés, Head of the Phytopathology for Sustainable Agricultural Systems at the CSIC, expert in quantitative models to facilitate prediction of plant diseases and spatiotemporal dynamics of plant disease epidemics. Involved in the EKE for grapevine and *Citrus* spp.
- Miguel Ángel Miranda, Associate Professor of Zoology at the Universitat de les Illes Balears (UIB), expert in vector and plant pests biology. Involved in the EKE for olive, almond and grapevine.

- Nicola Bodino, postdoctoral researcher at the University of Turin, project on the 'Collection of data and information on biology and control of vectors of *Xylella fastidiosa*'. Involved in the EKE for olive.
- Panagiotis Milonas, Researcher in Entomology at the Benaki Phytopathological Institute, expert in insect biology and biological control. Involved in the EKE for olive and almond.
- Pierfederico La Notte, Researcher at the Institute for Sustainable Plant Protection of the Italian National Research Council (CNR), expert in virology, epidemiology of phytoviruses, viticulture and oenology. Involved in the EKE for grapevine.

E.1.3. Short description of the EKE methodology

The existing evidence was reviewed by the experts of the working group. To describe the existing evidence and remaining uncertainties, the working group performed an expert elicitation to judge on the parameter following the Quartile method of the Sheffield protocol:

- Each member of the group of experts were individually judging on the quartiles of the uncertainty distribution in the following queuing:
  1) The lower and upper limit of the credibility range (98% uncertainty range: 1st and 99th percentile).
  2) The median value (2nd quartile) as central estimate, which equally likely over- or underestimates the unknown parameter.
  3) The lower and upper limit of the interquartile range (50% uncertainty range: 1st and 3rd quartile), which describes the precision of the central value.
- The judgements on the credibility range was discussed and agreed in consensus by the group before the other values were judged. The reasoning was summarised.
- The judgements on the median and interquartile range were discussed and agreed in consensus. The reasoning was summarised.

Finally, a smooth distribution curve was fitted to the consensus, and additional percentiles were calculated. The final distribution was reviewed and agreed by the group of experts.

E.1.4. Evidence on the pest in support to the EKE

According to the EFSA methodology on EKE, invited experts received in due time a factsheet with general information regarding the biology of the pest, list of hosts, geographical distribution of hosts and pest, area of potential establishment. Since this information is provided in the main body of this Scientific Opinion and in the most recent EFSA outputs regarding *X. fastidiosa* (e.g. EFSA pest categorisation, EFSA Update of the *Xylella* spp. host plant database), it is not repeated here in the Appendix.

In addition, for each estimated parameter, a specific table possibly including quantitative evidences on the observed impact in a given host was prepared and used during the EKE procedure. These tables are included in Appendix E.4.

E.1.5. Scenario assumptions common to all crops

The general scenario assumptions are the following and reflect those applied by the EFSA Working Group on EU Priority Pests:

- Impacts are assessed by assuming that the entry, establishment and spread of the pest had already occurred. This corresponds to a scenario where the pest is already present throughout the area of potential distribution in the EU (i.e. it has spread to its maximum extent) and there are no ongoing eradication or containment programmes.
- It is assumed that the pest is not only present throughout the area of potential distribution but also that the limits to this area do not change. Within the area of potential distribution, pest presence depends on the heterogeneity of the patches where the host occurs. It is therefore not necessarily the case that the pest is present in all suitable patches.
- Where the pest occurs, it has reached its maximum potential abundance based on current environmental conditions (including climate, ecosystem resistance and resilience) and current crop production practices, e.g. pest control such as the efficacy of the pesticides targeted at other pests and current quarantine measures.

- The maximum potential abundance is considered as the driving factor for the estimation of yield/quality loss and it is evaluated in a time frame long enough to take into account the possible effects of the temporal variation in pest population dynamics (e.g. population cycles), impacts, and cropping practices (e.g. the crop replacement time). Yield/quality losses due to quarantine measures are also included (e.g. rejection of full lots, downgrading of final product).
- Cropping practices and management options are those currently in place in the area of potential distribution, taking into account the fact that these may differ from those in places where the pest is currently present and thus from where the data on impacts have been published.
- The effect of currently applied control against other pests is taken into account while the effect of this pest is evaluated in the absence of other pests
- Future changes in agricultural practice have not been taken into account; only already existing pest control measures have been evaluated.

E.2. Results of the expert knowledge elicitation

E.2.1. Olive

Scenario assumptions for the assessment of yield loss on olive:

Scenario assumptions for olive crop are:

- Considering that the scenario assumptions common to all crops, which include among others that the pest is present everywhere in EU in the areas of potential establishment, and that no clear evidence is available concerning the damage produced on the same host/cultivar by different bacterial subspecies, in areas different from the ones of the observed outbreaks, the impact was evaluated at species (*X. fastidiosa*) level, clarifying in the rationale the main subspecies on which the evidence is based.
- The focus, however, was on *X. fastidiosa* subsp. *pauca,* as the observations on strains of *X. fastidiosa* subsp. *multiplex* in California (Krugner et al., 2014) did not clearly correlate infection of olive plants by those strains with disease symptoms. Data and observations analysed in this assessment regard the outbreaks of *X. fastidiosa* subsp. *pauca* on olive trees in Italy, Brazil and Argentina, with most evidence related to the outbreak of *X. fastidiosa* subsp. *pauca* ST53 in Apulia (IT).
- The impact was estimated in the most suitable climatic conditions for the EU.
- The endangered area corresponds to the EU olive production area and the area of potential distribution takes into account climate suitability for pest potential establishment at species (*X. fastidiosa*) level, to account for the strong uncertainties on climate suitability for subspecies *pauca* and ST53 levels discussed in Section 3.1 (Potential establishment).
- Considering the main areas of production, climate is not expected to represent a major limiting factor for the estimation of the impact.
- Insect vector distribution does not represent a limitation to pathogen distribution. The only vector that was considered in this scenario was *Philaenus spumarius*, the most common and widespread currently known vector of *X. fastidiosa* in the EU (Section 1.4). No other insect vectors, were considered in the assessment. Such insect vector is present throughout the area of potential establishment of the pathogen and their direct impact on the host plants is not assessed. In addition, the proportion of overwintering adult vectors is considered irrelevant for this assessment.
- Olive fruit is harvested from mature trees, which are assumed to reach their full production 25 years after planting. Therefore, economic losses due to tree removal/replacement have to take into account the initial unproductive (or very little productive) phase (from 5 to 8 years) of newly planted olive trees.
- Proportion of replanting, mortality rate, reduction of production are all aspects related to yield losses.
- Olive productions for table olives and for oil production are considered together.

- Rationale for yield loss calculation from a dead tree: the reduction considers the productive period lost after infection and the less-productive phase of the newly planted olive tree substituting the previous one.
- The assessment takes into account the two main olive farming systems (namely traditional and intensive) and their relative weight at EU level dividing the EKE in two values: impact on olive orchards less than 30 years (intensive farming) and more than 30 years (traditional farming). As such, the first estimation is mostly based on the impact expected in former farming systems and the second in latter farming systems, respectively.
- No evidence is available regarding the effects of pathogen infection on fruit quality.

Questions for expert knowledge elicitation:

- What is the annual % of loss (in weight) in olive production in EU averaging the different countries, production systems, olive varieties in the long-term situation under the condition of the general scenario for olive orchards younger than 30 years?
- What is the annual % of loss in olive production in EU averaging the different countries, production systems, olive varieties in the long-term situation under the condition of the general scenario for olive orchards older than 30 years?

E.2.1.1. Evidence and uncertainty in the assessment of yield loss for olive crop

In this section, the main components of the identified evidence and the overall uncertainties of the assessment are listed.

Main evidences:

- Traditional farming systems with trees up to 100 years old (20 years needed to be fully productive); Intensive farming systems with trees up to 30 years (5–8 years needed to be fully productive).
- Monumental olive trees infected by *X. fastidiosa* subsp. *pauca* ST53 collapse in 2–3 years in areas with high olive tree density and susceptible olive cultivar.
- The impact is more severe on old than young olive orchards.
- Currently, in the presence of *Xylella*-infected olive trees, in Apulia people react differently: some do severe pruning, light pruning, or no pruning. Some very preliminary observations suggest that the lightly pruned trees tend to tolerate longer the infection before dying.
- Pruning frequency in Apulia: Southern zone every 6–7 years; Central zone more regular activity (i.e. biennial) associated to tillage and other agricultural practices.
- Current treatments for other pests in olive orchards do not affect *X. fastidiosa* vector.
- 50% more production in irrigated orchards.
- *X. fastidiosa* impact is on the number of fruit and not on the quality.
- Coletta-Filho et al. (2016): relevant evidence proving that cultivar Arbequina can express symptoms under field conditions.
- Boscia et al. (2017b): 70% incidence is for Ogliarola and Cellina di Nardò.
- Leccino is less susceptible due to the lower infection, bacterial load and symptom expression than the other varieties studied by Saponari et al. (2017). The reduced infectivity of Coratina compared to other cultivars was probably due to the specific experimental circumstances and would be better not to be pointed out as a sign of resistance.
- Olive varieties are many in the EU with a limited overlap from country to country. Most of the information available is related to Italian varieties.
- Best eco-climatic conditions for olive production: sufficient rainfall, flat not mountainous. In each EU MS where olive is grown (around 5–6 million ha in the EU) there are hotspots with very good suitable conditions.
- More than 50% of EU olive production is based on plants older than 50 years (EUROSTAT) (i.e. the majority of the EU olive production is based on plants older than 30 years).
- Symptoms can appear months after the infection. Extreme cases include some years after the infection.
- 22% production in Spain is intensive (Fernandez Escobar et al., 2013)
- Control of weeds is a crucial aspect in limiting vector population densities.
- Vectors and environment have a crucial role in symptoms expression.

- The vector is wherever olive production is (e.g. Cruaud et al., 2018).
- Adults appear in May, are present in orchards from May to September-October with a population peak in late-May or June. In some areas of EU (Spain, Greece) vectors are not found in olive orchards during summer. They return in autumn.
- Vectors are not adapted to very dry areas, so they perform better in northern areas of olive production. On the other hand, in northern areas olive trees show less symptoms, as they are less stressed by drought.
- Vector pressure is an important factor that contributes to accelerate the infection of host plants and spread due to an increase in the likelihood of repeated inoculation events. However, vectors are not a limiting factor to disease spread and development: they are ubiquitous. A similar level of infection of plants with same susceptibility is expected to be reached during their productive period even with low density of the vectors.
- Inoculum presence and availability at level of single plant or orchard plays a role in disease spread.
- Treatments against the olive fruit fly (which could have an impact on the *X. fastidiosa* vectors). In northern Mediterranean regions, e.g. Tuscany, treatments apply in July (and August, depending on the year). In Spanish intensive olive orchards treatments apply in July, when also vectors have the peak. In Greece treatments are applied from July to September according to regions and climate.

Table E.1: Summary of differences among traditional and intensive olive orchards

	Traditional	**Intensive**
Cycles	It can easily reach 100 year cycles	25–30 year cycles
Productivity	1.5 t/ha	8–10 t/ha
Irrigation	In most of the cases rainfall only. In Greece applied in most of not intensive plantations	Irrigation can be used
Labours	Infrequent (also marginal productions are included in this group)	Regular and intensive
Pruning	Not regular, infrequent, or extreme from time to time	Light and regular
Treatments against olive flies	Less treatments in organic production	Threshold based
Control of weeds	Low	High

Overall uncertainties:

- No clear evidence is available concerning the different damage produced on the same host by different *X. fastidiosa* subspecies, in environments different form the ones of the observed outbreaks.
- Role of cultivars is still not very well known. Limited knowledge on the different sensitivity of different olive germplasm.
- Effectiveness of treatments against olive fruit fly in controlling *X. fastidiosa* vectors.
- Newly planted traditional orchards will be included in the first category (i.e. orchards less than 30 years) but the weight is minor.
- The proportion of classes of ages in the EU is not known.
- Not known the tendency in varietal selection for new plantations.
- Regional variations of management practices can influence the expected yield particularly for traditional orchards.
- Existence of fully latent infections cannot be excluded.

E.2.1.2. Elicitation outcomes of the assessment of yield loss on olive trees younger than 30-years

Reasoning for a scenario which would lead to a high yield loss (99th percentile/upper limit)

The upper value of 60% yield losses includes the two main olive farming systems and their relative weight at EU level for plants younger than 30 years. Varieties are more susceptible and impact occurs at the beginning of the productive period: after the first five non-productive years, at around the 7th year the tree will start showing symptoms compromising the remainder of the productive cycle: the

tree will still probably yield some fruit until the 10th year, with the effect that out of the 25 years of productive cycle there will be 10 years of production and 15 years of full loss.

This scenario considers conditions of irregular pruning, limited or null weed control, non-irrigated orchards. The abundance of vectors is high, as observed in Apulia.

Young olive plants represent less than 20% of the total EU production and not all of them could be necessarily grown under intensive systems. Under this scenario, it is expected that traditional farming systems will suffer full losses while the practices of intensive farming systems could mitigate yield losses.

Reasoning for a scenario which would lead to low yield loss (1st percentile/lower limit)

The lower value of 10% yield losses is mainly driven by the intensive farming system, by the use of less susceptible olive varieties and the application of agricultural practices less favourable to the disease development, such as regular and light pruning, tillage, irrigation, and weed control, which would limit vector population densities.

In these conditions, an olive tree intensively grown could survive during the whole productive cycle (30 years).

Reasoning for a central scenario equally likely to over- or underestimate the yield loss (50th percentile/median)

The median value of 35% yield loss is mainly supported by the production system and the age of the plants which does not favour *X. fastidiosa* infections.

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The distribution of intermediate values is reflecting the maximum uncertainty with a bit more confidence on the lower values.

Table E.2: Fitted values of the uncertainty distribution on the yield loss (%) on olive trees younger than 30 years

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	10					25		35		45					60
Expert 1	10					20		25		30					70
Expert 2	10					20		30		45					65
Expert 3	40					30		45		50					50
Expert 4	5					22		30		40					40
Expert 5	10					30		40		50					80
Expert 6	20					20		40		50					60
Fitted distribution	9.4%	12.1%	14.9%	18.5%	22.0%	25.6%	28.7%	34.6%	40.9%	44.5%	48.9%	53.6%	59.0%	63.5%	68.5%

Fitted distribution: BetaGeneral(4.1534,7.5543,0,1), @RISK7.5.

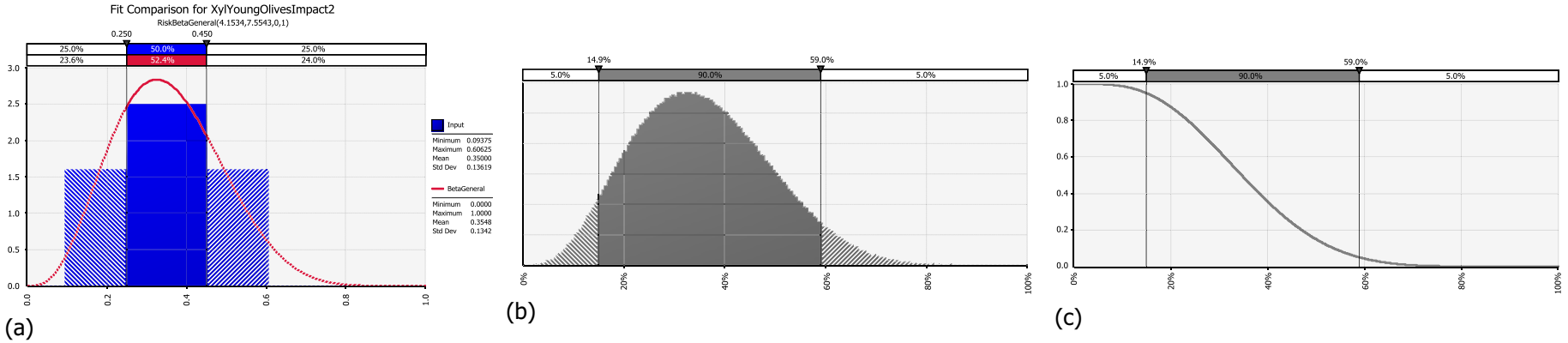


Figure E.1: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

E.2.1.3. Elicitation outcomes of the assessment of yield loss on olive trees older than 30-years

Reasoning for a scenario which would lead to a high yield loss (99th percentile/upper limit)

This scenario represents the worst conditions in the EU: very old olive trees of susceptible varieties grown in a traditional farming system without irrigation and minimal agricultural interventions, causing, for example, high probability of having weeds and other reservoir crops in the surroundings. High vector population densities. Probably low presence of tolerant/resistant germplasm. Apulia is the reference for this scenario.

Most of the losses are expected in the case of olive orchards with centuries-old olive trees.

Reasoning for a scenario which would lead to low yield loss (1st percentile/lower limit)

The lower value of 25% losses reflects a condition of less susceptible cultivars, low amount of pathogen inoculum, limited vegetation on the ground, low density of vector population.

In traditional systems, even in the best-case scenario, around 30% of the production could be lost.

The expected impact is lowered to 25% in order to extend the scenario and increase the uncertainties given the effect of regional variations in management practices.

Reasoning for a central scenario equally likely to over- or underestimate the yield loss (50th percentile/median)

The median value of yield loss is expected to be the double than what observed on young trees. This scenario reflects the Apulian situation.

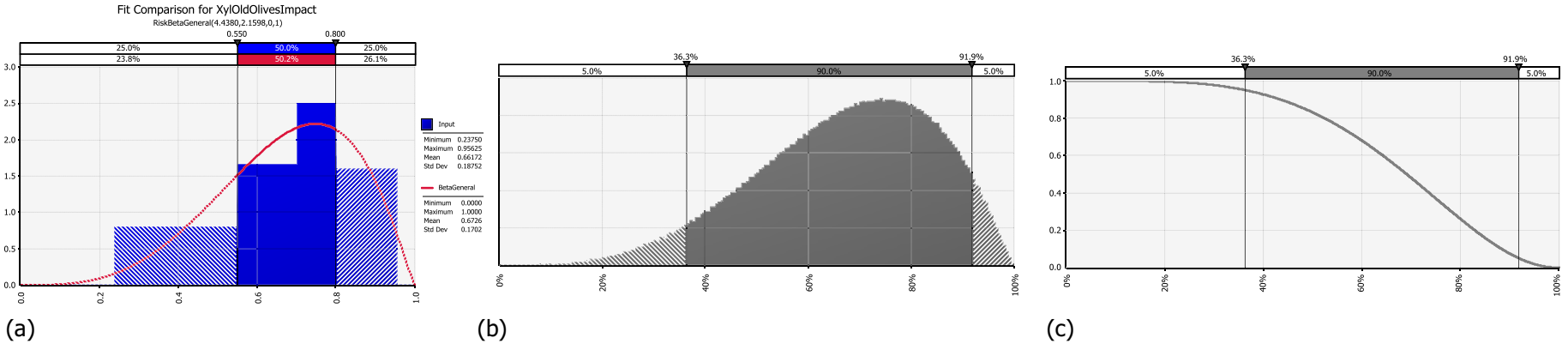
Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

Almost maximum uncertainty for the whole distribution in order to take into account the effect of different old varieties susceptibility, climatic conditions, agricultural practices.

Table E.3: Fitted values of the uncertainty distribution on the yield loss (%) on olive trees older than 30 years

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	25					55		70		80					95
Expert 1	30					35		60		75					85
Expert 2	35					40		65		75					90
Expert 3	60					50		75		80					95
Expert 4	20					50		65		75					90
Expert 5	50					65		70		85					95
Expert 6	10					50		75		80					80
Fitted distribution	24.4%	30.6%	36.3%	43.4%	49.8%	55.8%	60.7%	69.1%	76.7%	80.5%	84.6%	88.4%	91.9%	94.3%	96.3%

Fitted distribution: BetaGeneral(4.438,2.1598,0,1), @RISK7.5.



(a) (b) (c)

Figure E.2: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

E.2.2. Almond

Scenario assumptions for the assessment of yield loss on almond:

Scenario assumptions for almond crop are:

- Considering that the scenario assumptions common to all crops, which include among others that the pest is present everywhere in EU in the areas of potential establishment, and that no clear evidence is available concerning the damage produced on the same host/cultivar by different bacterial subspecies, in areas different from the ones of the observed outbreaks, the impact was evaluated at species (*X. fastidiosa*) level, clarifying in the rationale the main subspecies on which the evidence is based.
- The focus, however, was on *X. fastidiosa* subsp. *multiplex* and *fastidiosa* which are the subspecies that have been found associated with the almond leaf scorch so far.
- 25-year productive lifespan including the first 3 non-productive years.
- According to Sisterson et al. (2012), yield loss of an infected plant is significant only after 6 years of infection. However, after 6–7 years, the tree is still alive and productive.
- Consider a density of 200–270 trees ha^{-1}.
- The only vector that was considered in this scenario was *Philaenus spumarius*, the most common and widespread currently known vector of *X. fastidiosa* in the EU (Section 1.4). No other insect vectors, were considered in the assessment.

Questions for expert knowledge elicitation:

What is the annual % of loss in almond production in EU averaging the different countries, production systems, varieties in the long-term situation under the condition of the general scenario?

E.2.2.1. Evidence and uncertainty in the assessment of yield loss for almond

In this section, the main components of the identified evidence are listed and the overall uncertainties of the assessment are listed.

Main evidence:

- 85% of total EU area is represented by traditional plantations with low or absent management. Only the remaining 15% is represented by modern, well managed, highly productive plantations.
- In all the main European producing countries (Spain, Italy, Portugal and Greece) more than 80% of almond orchards are rainfed.
- Density of 200–270 trees ha^{-1}.
- Sisterson et al. (2012) gives some figures on susceptibility.
- Differently from US where peach rootstock is commonly used (Krugner and Ledbetter, 2016), rootstocks used in Spain are usually almonds or peach × almond hybrids.
- Main EU producers: Spain (85%) > Italy > Portugal > Greece.
- Traditionally marginal culture with no irrigation and low prices (situation is changing above all in Spain).
- For some cultivars, Sisterson et al. (2012) observed that a non-infected tree in the proximity of an infected one, produce more than an almond tree in a non-infected area.
- Trees suffering from drought conditions are less attractive to vectors
- Price payed around 2–3 € kg^{-1} kernels have increased in the last years to 5 €/kg and it has become recently an economically relevant crop. Therefore, area and cropping practices have changed a lot in the last years (> 30% surface increase).
- 20–25 years of production before removing the tree (values from US).
- 3 years from planting to first harvest.
- The modern plantations are irrigated (drip irrigation). In areas with > 500 mm/y rain, without irrigation there is still a reasonable production.
- Around 28% of symptomatic almonds are actually confirmed for infection by PCR in Balearic Islands.
- In Alicante, in 2017, 8% of the infected plants were asymptomatic. In 2018, 4%

- Young EU plantations have comparable growing conditions with US: high number of treatments, cleaned soils.
- Almond trees already infected seem to be able to still provide 6 years full production.

Overall uncertainties:

- Potential effect of spatial coexistence of *X. fastidiosa* subsp. *fastidiosa*, *pauca* and *multiplex* in almond plantations.
- Consequences of coinfection by different subspecies in the same plant.
- Only preliminary observations are available from EU concerning the different level of susceptibility of almond varieties (more evidence coming from US).
- Effect of secondary spread in almond.
- Effect of infectivity and transmission capacity of vectors in almond.
- Yield loss of an infected plant.

Potential *X. fastidiosa* vectors look not very common in almond orchards. In general the abundance of vectors in almond orchards is not very well known.

E.2.2.2. Elicitation outcomes of the assessment of yield loss for almond

Reasoning for a scenario which would lead to a high yield loss (99th percentile/upper limit)

The upper value of yield loss is expected in conditions of non-management, non-clean environment. Older trees (> 25 years, assumed to be more sensitive). More heterogeneous environment including alternative hosts. Use of sensitive varieties. No pest control.

During the first 6–7 productive years 9% mortality can be expected (Sisterson et al., 2012). During the whole productive time around 30% loss.

This scenario reflects the empirical observations from Balearic Islands.

Reasoning for a scenario which would lead to a low value for yield loss (1st percentile/lower limit)

The lower value of yield loss can be given by well conducted cultivations: pest control (particularly against aphids), low water stress, use peach × almond hybrid rootstocks with resistance. Production cycles of 25 years. Monoculture. Use of resistant varieties.

The prevalence comes from the observed average prevalence during a production cycle multiplied by the reduction in yield coming from the American observations with a high uncertainty component.

Reasoning for a central scenario equally likely to over- or underestimate the yield loss (50th percentile/median)

The median value of yield loss is based on the fact that most of the almond production areas in the EU (85%) relies on traditional systems with very low or absent management, and rainfed.

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The shape of the curve indicates high uncertainty around the median. The distribution is slightly skewed to the left.

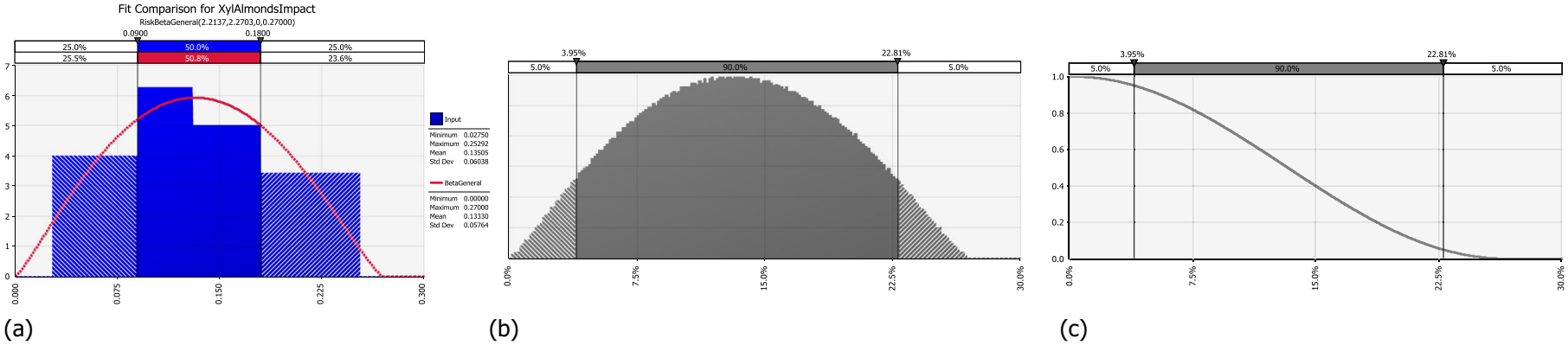
Summary of scenarios

Low impact	High impact
Low water stress	High water stress
Good management (pest control aphids, fertiliser)	Not managed, no pest control, no fertilising
Production period 25 years	Older trees (older than 25 years)
Less susceptible varieties, resistible rootstock	Susceptible varieties, rootstocks
	No big monocultures, scattered smaller orchards, proximity of other hosts

Table E.4: Fitted values of the uncertainty distribution on the yield loss (%) on almond

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	3					9		13		19					25
Expert 1	5					9		14		19					20
Expert 2	5					12		15		18					50
Expert 3	20					13		16		21					66
Expert 4	5					7		12		20					50
Expert 5	2					5.5		8		16.5					20
Expert 6	3					6		8		14					25
Fitted distribution	1.8%	2.8%	3.9%	5.5%	7.2%	8.9%	10.4%	13.3%	16.2%	17.7%	19.5%	21.2%	22.8%	24.0%	25.0%

Fitted distribution: BetaGeneral(2.2137,2.2703,0,0.27), @RISK7.5.



(a) (b) (c)

Figure E.3: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

E.2.3. Grapevine

Scenario assumptions for the assessment of yield loss on grapevine:

Scenario assumptions are:

- Considering that the scenario assumptions common to all crops, which include among others that the pest is present everywhere in EU in the areas of potential establishment, and that no clear evidence is available concerning the damage produced on the same host/cultivar by different bacterial subspecies, in areas different from the ones of the observed outbreaks, the impact was evaluated at species (*X. fastidiosa*) level, clarifying in the rationale the main subspecies on which the evidence is based.
- The focus, however, was on *X. fastidiosa* subsp. *fastidiosa* which is the subspecies that have been found associated with Pierce's disease in grapevine so far.
- Replacement is taken into account in terms of 3.5 years of loss of production on a total of around 25–30 years for wine grapes and on around 20 years for table grapes.
- Two estimates: one for southern EU and the other for central EU.
- In southern Europe: high temperatures, no chilling effect, some dry out during summer period; incidence of severely infected wine plants, that will not recover the next year.
- For southern Europe, estimation of impact on wine grapes and table grape. Climate conditions are good for the pathogen and less suitable for the vector. % of plants dying every year. Recovery due to low winter temperatures is not relevant/likely in these climatic conditions.
- The only vector that was considered in this scenario was *Philaenus spumarius*, the most common and widespread currently known vector of *X. fastidiosa* in the EU (Section 1.4). No other insect vectors, were considered in the assessment.

Questions for expert knowledge elicitation:

- What is the annual % of loss in grapevine production devoted to wine production in southern EU countries, averaging the different production systems, varieties in the long-term situation under the condition of the general scenario?
- What is the annual % of loss in grapevine production devoted to table grape production in southern EU countries, averaging the different production systems, varieties in the long-term situation under the condition of the general scenario?
- What is the annual % of loss in grapevine production devoted to wine production in Central EU countries, averaging the different production systems, varieties in the long-term situation under the condition of the general scenario?

E.2.3.1. Evidence and uncertainty in the assessment of yield loss for grapevine

In this section, the main components of the identified evidence are listed and the overall uncertainties of the assessment are listed.

Main evidences:

- In central Europe, freezing winter temperatures would eliminate the bacterium from grapevine infected in spring.
- Very low density of *Philaenus spumarius* is found in grapevine, as confirmed by D. Bosco from observation in Piedmont organic vineyard.
- Most of the vectors in a vineyard feed on ground cover, inter-rows or alternative hosts.
- Since grapevine is not a preferred host, the probability of secondary spread is very low.
- *Philaenus spumarius* is hard to spot all over season. This phenomenon was observed in Spain, south Italy, and Greece above all in summer time inside vineyards.
- Most of the vineyards in southern EU are not irrigated.
- A recent publication (Santoiemma et al., 2019) reports that population levels of *Philaenus spumarius* negatively correlates with vineyards in the landscape.
- One of the most used vine training system (i.e. Guyot) is based on seasonal heavy pruning which could determine a lower probability of systemic infection. In general plants are pruned at the end of the season.

- The window of time in which infectious vectors can effectively transmit the diseases (determining a systemic infection) is short, just 2 or 3 months (late infections would be removed by pruning).
- Table grape production only in Mediterranean regions.
- Plant cover almost absent during summer in southern EU grapevine.
- Compared to almond, in grapevine lower vector densities are found. In addition weed management is more intense.
- In general, pest control in vineyards is high. Vines are protected until harvest. In table grape vineyards, pest control is more intense compared to wine grapes (multiple spray treatments, clean soil, fertilisers, irrigation).
- Productive period: 20 years for table grapes (to have new varieties), 30 years for wine grapes. Relatively small number of 60 years for old, special, vineyards.
- Production area for main table grape producers in 2016 (EUROSTAT): Greece 15,840 ha, Spain 13,930 ha, Italy 46,160 ha (mainly in the South of Italy) are the main producers.
- In Italy, 1/10 of grapevine is table grape.
- There are some concentrations in certain regions/areas for both table and wine grapes (e.g. Burgundy, Champagne, Barolo, etc.).
- Italy, Portugal, Romania have high number of varieties; differences in terms of varieties concern more wine grape than table grape.
- Yield changes a lot from top quality wines to industrial productions.
- Hot water treatments: not a common practice, only in some parts of Italy (nord, not table wine) and France. Now in South Italy hot water treatment is compulsory against *X. fastidiosa* and it is applied to both table and wine grapevines.
- For old varieties, it is preferred to buy only rootstocks and then graft them in-house.
- More care in table grape industry than wine grape in choice of rootstock.
- The effect on quality is due to the replanting with plants of a different age and of resistant varieties.
- Hot water treatment is applied against 'bois noir' and 'Flavescence dorée' on wine grapes but rare on table grapes. It is however relevant only for secondary spread and therefore not suitable to the scenario.
- Recovery from *X. fastidiosa*: in the US it has been observed that low winter temperatures (central California conditions, north US) favour plant recovery.
- Until now Pierce's disease in natural conditions has been observed caused by *X. fastidiosa* subsp *fastidiosa* only.
- Ground vegetation is present in most of EU vineyards located in non-warm Mediterranean conditions.
- Cornara et al. (2016): EU *X. fastidiosa* vector is efficient in transmission to grapevine.
- In general, vegetative development starts in April, flowering around May–June, ripening around June, harvest up to December depending on varieties.
- According to Feil et al. (2003), the infection should take place by June to be effective otherwise high probability of winter recovery.
- In general, grapevine is grown mostly from sea level up to 500 m.
- Treatments against pests are done (e.g. against moths, leafhopper vector of Flavescence dorée where the disease is present).
- Compared with olive and almond, grapevine get more treatments.
- Temperature favouring the growth of the bacterium and chilling are the main climatic factors affecting the disease. Also important is the phenology of the vector.
- In America sharpshooter, vectors overwinter as adults outside the vineyards. EU spittlebug vectors overwinter as eggs. After nymphal development on herbaceous hosts in late winter and early spring, spittlebug adults emerge and move to woody hosts (including grapevines) over the spring (starting in April) and early summer in South Italy.
- If the plant is systemically infected, disease becomes chronic (no winter recovery) and replanting is only solution.
- Quality loss can derive from replanting: replanting creates heterogeneity in the field, different level of maturation at harvest time.
- If the conditions are favourable, the establishment of an infection within the plant is fast and in that case the plant can die within 2–3 years.
- Winter chilling can have a strong effect in stopping the disease.

- From 3 to 4 years are needed for a plant to become productive (wine production) after a replanting. In relation to productive lifespan this corresponds to around 10% loss.
- For very susceptible varieties (Barbera, Chardonnay, Pinot) if conditions are favourable to the disease, they can be systemically infected already during the first year.
- Costello et al. (2017) evaluated incidence in Sonoma County (California): from 0.02% to 37.1%. Sonoma County has very hot summer. Winter is a bit warmer than northern Italy. Considering the different vector situation in EU, the expected incidence in EU is expected to be lower: few vectors feeding on grapevine and short time for infection.
- Experts report that in Balearic Islands on average 0.002 adults are captured per swept in August. In May 0.09 adults per swept. In the Piedmont region (northern Italy) from 0.2 to 0.5 adults per swept in grapevine canopy, while in shrubs close to the grapevines it can be from three to five times more.

Overall uncertainties:

- Higher density of vectors does not necessarily mean higher incidence of disease.
- Very limited evidence on impact.
- Proportion of symptomatic plants out of the infected plants in Balearic Islands observations.
- The chilling effect in limiting *X. fastidiosa* inoculum on grapevine in EU conditions.
- Effect of rootstock.
- Importance of different varieties.
- Not clear effect of resistance: longer life with lower yield?
- Most European varieties can be considered susceptible.
- Recovery rate unknown under EU viticultural conditions.

E.2.3.2. Elicitation outcomes of the assessment of yield loss for wine grapes in southern EU

Reasoning for a scenario which would lead to high yield loss (99th percentile/upper limit)

The upper value of yield loss is linked to relatively high abundance of vectors. Vectors are very competent for transmission. Long time for transmission. Incidence 40% (value corrected from American values). High proportion of infectious vectors.

The incidence in Sonoma (Costello et al., 2017) was taken into account. *Philaenus spumarius* population can be abundant in summer season and could be in any case able to transmit to grapevine for a couple of months/year. Alternative hosts are expected to be available in the surroundings.

However, even considering the favourable elements described above, the experts took into account that low densities of vectors are found in grapevine, that not all vectors become infected, and a low probability of secondary infection.

Reasoning for a scenario which would lead to a low value for the parameter (1st percentile/lower limit)

The lower value of yield loss can be given by the low abundance of vectors. Very few vectors are present during the hot summer months. Vectors are not very efficient in transmitting the disease. Short time for transmission. Incidence 2%. Low proportion of infectious vectors.

The population of putative vectors is very low in vineyards. 0.2 insect/swept roughly corresponds to 0.2 vector/plant, not all vectors are infectious and not all are able to transmit the disease.

Reasoning for a central scenario equally likely to over- or underestimate the parameter (50th percentile/median)

The main elements that were taken into account were:

- Population levels of *Philaenus spumarius* is negatively correlated with vineyards in the landscape.
- The probability of secondary spread is very low (in consequence of low acquisition and low transmission).
- *Philaenus spumarius* is hard to spot all over season especially in summer (ground cover almost absent in southern Europe).
- Most used vine training system is based on heavy pruning which would determine lower probability of systemic infection.

– The window of time in which infectious vectors can effectively transmit the diseases (determining a systemic infection) is short, just 2 or 3 months (late infections would be removed by pruning).

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The precision is mainly affected by the high uncertainty on the whole distribution, although for higher value the experts are more supportive for values close to median.

Table E.5: Fitted values of the uncertainty distribution on yield loss (%) on wine grape in southern EU

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	0.3					1.2		2		3.5					6
Expert 1	0.1					0.5		0.8		3					5
Expert 2	0.75					1		3		4					2
Expert 3	0.5					1		2.5		4.5					15
Expert 4	0.3					2		3		3.5					6.7
Expert 5	1.5					0.6		3.6		4.8					6.3
Expert 6	0.65					0.8		1.2		3					4.5
Fitted distribution	0.2%	0.3%	0.5%	0.7%	0.9%	1.2%	1.5%	2.1%	2.8%	3.3%	3.9%	4.7%	5.6%	6.8%	8.1%

Fitted distribution: Gamma(2.0511,0.011956), @RISK7.5.

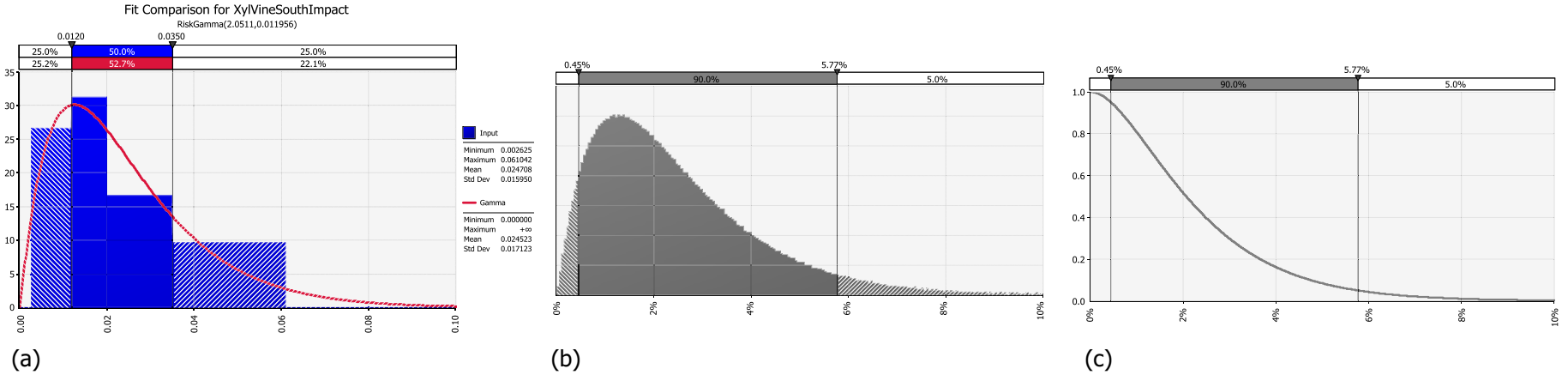


Figure E.4: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

E.2.3.3. Elicitation outcomes of the assessment of yield loss for table grapes

Reasoning for a scenario which would lead to high yield loss (99th percentile/upper limit)

The more care and agricultural practices taken in this type of crops could limit the impact. More sprays, more monoculture, more pruning, more fertilisers. More anthropic environment. Also productive cycles are shorter (20 years). This is an irrigated crop, therefore, on the one side it is more attractive to spittlebugs (due to the higher xylem pressure, turgor of plant tissues), on the other side the limited water stress would also limit the disease development, i.e. symptoms expression.

Reasoning for a scenario which would lead to a low value for the parameter (1st percentile/lower limit)

The same above-mentioned reasons apply as reducing factor to the lower limit of the curve.

Reasoning for a central scenario equally likely to over- or underestimate the parameter (50th percentile/median)

The same above-mentioned reasons apply as reducing factor to the median value.

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The uncertainty is high but the curve is skewed to the right side.

Table E.6: Fitted values of the uncertainty distribution on yield loss (%) on table grape in southern EU

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	0.1					0.5		1.0		2					4
Expert 1	0.1					0.5		1		2					3
Expert 2	0.1					0.3		0.5		1					2
Expert 3	0.1					0.3		0.7		1.4					2
Expert 4	0.2					1		2.5		3					7
Expert 5	0.1					0.2		0.6		1.2					1.8
Expert 6	0.1					0.4		0.7		1.2					2
Fitted distribution	0.0%	0.1%	0.1%	0.2%	0.4%	0.5%	0.7%	1.0%	1.5%	1.9%	2.3%	2.9%	3.7%	4.4%	5.4%

Fitted distribution: Gamma(1.3469,0.010083), @RISK7.5.

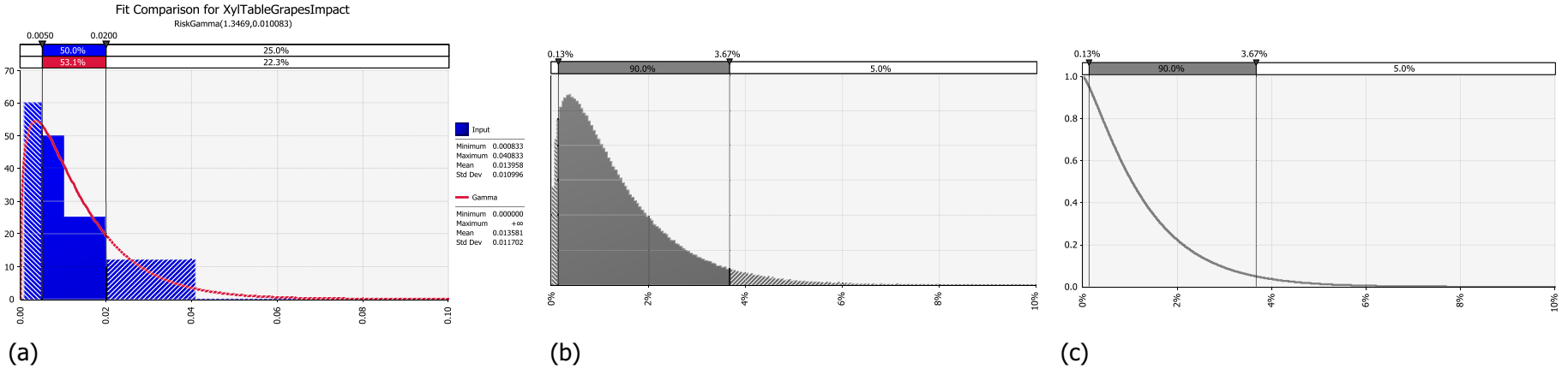


Figure E.5: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

E.2.3.4. Elicitation outcomes of the assessment of yield loss for wine grapes in Central EU

Reasoning for a scenario which would lead to high yield loss (99th percentile/upper limit)

Some main differences compared to Mediterranean vineyard apply to the whole scenario: the presence of adult vectors all through the summer, no drought stress, high vector abundance. The chilling effect is uncertain, while the recovery due to freezing winter temperature is the main difference. The pathogen will have a smaller time window to systemically infect the plant.

Even in case of high inoculum *X. fastidiosa* will need to survive each winter. Divide by a factor of 3, the value from southern EU.

Reasoning for a scenario which would lead to a low value for the parameter (1st percentile/lower limit)

In winter time, the bacterium will survive with very high difficulty. Even in the presence of systemic infections, the low bacterium load could hamper acquisition by vector. *X. fastidiosa* could be present but not causing symptoms, could remain undetected. Divide by a factor of 3, the value from southern EU.

Reasoning for a central scenario equally likely to over- or underestimate the parameter (50th percentile/median)

Divide by a factor of 4, the value from southern EU.

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

According to the experts, the uncertainty is more on the upper values.

Table E.7: Fitted values of the uncertainty distribution on yield loss (%) on wine grape in central Europe

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	0.05					0.3		0.5		0.8					2
Expert 1	0					0.25		0.5		0.75					2
Expert 2	0.4					0.8		1.5		3					4
Expert 3	0.1					0.3		0.5		1					2
Expert 4	0					0.1		0.2		0.4					1
Expert 5	0.6					0.24		0.4		0.7					1.2
Fitted distribution	0.1%	0.1%	0.1%	0.2%	0.2%	0.3%	0.4%	0.5%	0.7%	0.8%	0.9%	1.1%	1.4%	1.6%	1.9%

Fitted distribution: Gamma(2.1598,0.0027498), @RISK7.5.

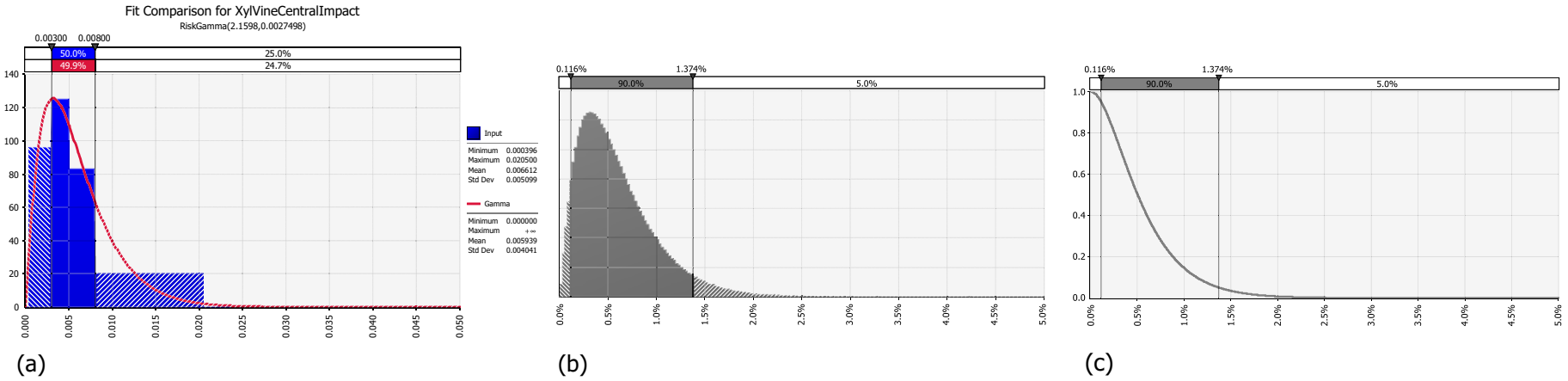


Figure E.6: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

E.2.4. *Citrus* spp.

Scenario assumptions for the assessment of yield loss on *Citrus* spp.:

Scenario assumptions are:

- Considering that the scenario assumptions common to all crops, which include among others that the pest is present everywhere in EU in the areas of potential establishment, and that no clear evidence is available concerning the damage produced on the same host/cultivar by different bacterial subspecies, in areas different from the ones of the observed outbreaks, the impact was evaluated at species (*X. fastidiosa*) level, clarifying in the rationale the main subspecies on which the evidence is based.
- The focus, however, was on *X. fastidiosa* subsp. *pauca* which is the subspecies that have been found associated with citrus variegated chlorosis (CVC) so far.
- Lemons and limes excluded.
- Mandarins less susceptible than sweet oranges.
- Yield loss: % of reduction in production weight including lower number of fruits, size of fruit below the marketable threshold (e.g. 5 cm sweet oranges), lower productivity of plants.

Questions for expert knowledge elicitation:

What is the annual % of reduction in citrus production weight including lower number of fruits, size of fruit below the marketable threshold (e.g. 5 cm for sweet oranges), lower productivity of plants, in the long-term situation under the condition of the general scenario?

E.2.4.1. Evidence and uncertainty in the assessment of yield loss for *Citrus* spp.

In this section, the main components of the identified evidence are listed and the overall uncertainties of the assessment are listed.

Main evidence:

- Navel oranges are susceptible. Just one exception: Navelina cultivar.
- Limes and lemons: most are resistant, some tolerant, probably all symptomless. Confirmed by (Cordeiro et al., 2014). They were not considered in EKE due to no or very minor expected impact.
- Tangelos: resistant or tolerant.
- Mandarins (*C. reticulata*) presents a range of susceptibility. It can be considered moderately resistant.
- Grapefruits are not widely cultivated in the EU. Considered together with sweet orange.
- Difficult to distinguish sensitivity at cultivar level, and data in official statistics aggregated at species level.
- In general, in the Mediterranean Basin new shoots and leaves in citrus trees appear in 3 different seasons: spring (80%), summer and autumn the remaining 20%.
- Sour orange (*C. aurantium*) used mainly as a rootstock or ornamental, not susceptible.
- All studies on impact are about sweet orange, no data on mandarins.
- On average, 25-year productive cycle.
- Affected plants grow less and produce smaller fruit.
- Younger the plant, faster the infection.
- In an orchard, it is possible to switch from 10 to 100% affected branches in 3–5 years.
- Cure by pruning is possible but only when systematic visual inspection is done: when detecting the infection, 1 m below the symptoms on the branch should be cut.
- Data on disease incidence is available.
- Climatic and irrigation differences between EU and Brazilian situation.
- Observations on disease severity at tree level in terms of proportion of canopy area expressing symptoms.
- Replacement: in modern plantations replacement is generally for all the plants, not just one tree, they remove the entire orchards, since it is not practical to have plants of different ages in the same orchard.
- Productive lifespan: from the 5th to the 30th year.

- *X. fastidiosa* does not kill the plant during the productive lifespan, the plant has dieback, tree is smaller, stressed, extensive symptoms, smaller fruits (impact of the disease). Quality impact due to fruit size. There is reduction of yield and of quality of the fruits. Some changes in sugar and other parameters can be observed, but no significant change in taste. The problem for juice industry is that small fruits do not fit in the crushing machine, so they are discarded. Juice quality is not severely affected, but the fruits are discarded.
- Standard for sweet orange for trade: diameter 50 mm is the minimum, best class from 92 to 110 mm, complete loss for fruits below 50 mm (OECD, 2010).
- *X. fastidiosa* can infect all branches of a citrus tree not before 4–5 years.
- In southern São Paulo State, Brazil less symptoms are observed due to more water availability. In northern São Paulo State, more symptoms due to the opposite situation (longer dry season).
- In Mediterranean area citrus is irrigated. Irrigation might mitigate effect on production and reduce symptoms. However, even with irrigation, dry summers typical of the Mediterranean Basin may stress the trees to a certain level.
- In Spain grass cover in citrus orchards, but not in summer for dry conditions.
- Young trees decline faster.
- Pruning looks like an effective measure only if inspections are frequent and symptoms detected early. Pruning is regularly done in the Mediterranean area, at least once a year and manually, favouring the early observation of symptoms. However, these symptoms are very difficult to link with the specific disease, for which specific training would be required. When symptoms become evident, then it is already too late and you should cut the tree.
- Goncalves et al. (2012) reported 23% loss after 8 years (no information on % symptoms in tree) in northern São Paulo State, Brazil, where plants are more water stressed. This is an ideal area for disease, where CVC is most important in Brazil.

Overall uncertainties:

- No information concerning host preference by *Philaenus spumarius*: In the EU, adults were found in citrus orchards, but only in the ground cover.
- No observation on disease severity at orchard level.
- No information on susceptibility of citrus cultivars in the EU.
- Not clear whether the climate in the EU plays a relevant role in favouring disease development and symptoms expression
- Vectors are present but their preference for feeding on *Citrus* spp. is unknown, neither the transmission efficiency.

E.2.4.2. Elicitation outcomes of the assessment of yield loss for *Citrus* spp.

Reasoning for a scenario which would lead to high yield loss (99th percentile/upper limit)

The upper value of yield loss is driven by high disease prevalence, early infection (on young plants), high disease severity, high impact on fruit (many small fruits, lighter fruits), EU cultivars more susceptible, EU vectors more active and efficient than South American vectors.

The 35% losses could be the result of a scenario with:

- Disease incidence 80% of infected plants.
- Disease severity 80% of symptoms expression.
- Number of affected plants 40%.
- Yield loss 75%.
- The resulting 20% losses could be increased to 35% taking into account the potential susceptibility of EU varieties, and the additional losses at the market.

Reasoning for a scenario which would lead to low yield loss (1st percentile/lower limit)

The lower value of yield loss is driven by overall low disease prevalence, late infection, low disease severity, low impact on fruit, EU cultivars less susceptible, EU vectors less active and efficient.

Reasoning for a central scenario equally likely to over- or underestimate the parameter (50th percentile/median)

The median value of yield loss is due to the fact that EU vectors are not expected to perform better than in Brazil, while EU citrus cultivars could be susceptible. Low vector diversity compared to Brazil. *Philaenus spumarius* could be affected by some weed management. This situation could lead to late infection. Mandarins are less susceptible than sweet oranges.

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The precision is mainly affected in the upper part: experts are more convinced about lower side of the curve.

Table E.8: Summary of low and high impact scenarios

Low	High
Prevalence in EU orchards (compared to Brazil)	Prevalence in EU orchards (compared to Brazil)
Late infection	Early infection
Low severity (% of the plant affected)	High severity
Low impact on fruit (marketable fruit, size)	High impact on fruit
Susceptibility of European cultivars	Susceptibility of European cultivars
Vector preference, different vectors, the presence of weeds, lower management, average size of the orchards are smaller in EU, some secondary infection	
Climatic conditions – low precipitation in EU compensated by irrigation	

Table E.9: Fitted values of the uncertainty distribution on the yield loss (%) on *Citrus* spp.

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	0					5		10		20					35
Expert 1	0					4		7		15					20
Expert 2	0					5		15		25					25
Expert 3	0.4					4		10		22					28
Expert 4	0					5		10		22					80
Fitted distribution	0.1%	0.3%	0.7%	1.5%	2.8%	4.5%	6.4%	10.9%	16.2%	19.4%	23.1%	26.7%	30.2%	32.5%	34.4%

Fitted distribution: BetaGeneral(0.85391,1.6537,0,0.37), @RISK7.5.

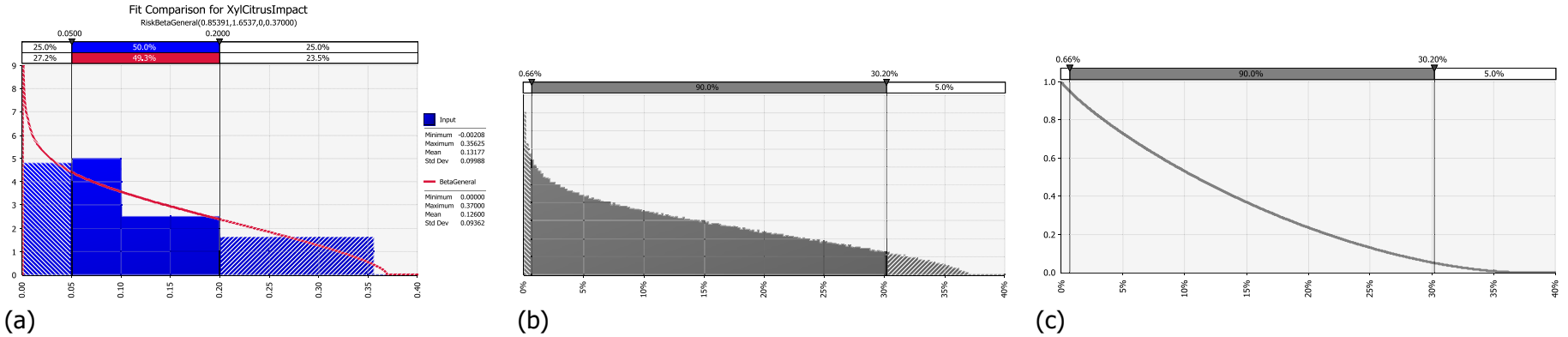


Figure E.7: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

E.3. Conclusions

Under the hypothetical scenario that *X. fastidiosa* is already present throughout the area of potential establishment in the EU and reached a stable spatial distribution with maximum abundance, the proportion (%) of yield losses, for different crops, and applying the agricultural management options currently used in EU (excluding emergency phytosanitary measures) were estimated (Table E.10).

Table E.10: Estimated yield losses for the considered crops and uncertainty range

Crop	Estimated yield loss (median)	90% uncertainty range (confidence interval)	
		5th percentile	95th percentile
Olive trees younger than 30 years	34.6%	14.9%	59.0%
Olive trees older than 30 years	69.1%	36.3%	91.9%
Almond	13.3%	3.9%	22.8%
Wine grape in southern EU	2.1%	0.5%	5.6%
Table grape in southern EU	1.0%	0.1%	3.7%
Wine grape in northern EU	0.5%	0.1%	1.4%
Citrus spp.	10.9%	0.7%	30.2%

The assessment on olive crop was divided in two assessments, taking into account the broad assumption that the olive farming systems can be divided into traditional systems, including plants older than 30 years and century-old plants, and more modern intensive systems, including mainly plants up to 30 years. As a result of the EKE, traditional plantations resulted more at risk than more modern olive productive systems.

Regarding the assessment on almond, one of the main factors driving the experts' estimates was the fact that most of the almond production area in the EU (85%) relies on rainfed traditional systems with very low or absent management. Only the remaining 15% is represented by modern, highly productive and well managed plantations. Information is still little on the effect of different varieties.

Regarding grapevine, this is the crop for which the lowest impact was estimated. *Philaenus spumarius* population level is negatively correlated with vineyards in the landscape. The window of time in which infectious vectors can effectively transmit the diseases (determining a systemic infection) is short, just 2 or 3 months and late infections would be removed by pruning. In fact, modern vine training systems include seasonal heavy pruning which lower the probability of systemic infections. In general pest control is well applied in grapevine. This is particularly true for table grape where pest control is more intense throughout the whole season. The assessment for grapevine production in central Europe is lower than southern Europe because of the impact of the freezing winter temperatures that would eliminate the bacterium from grapevine infected in spring. The assessment did not consider the impact of other potential vectors of *X. fastidiosa*.

The impact on *Citrus* spp. considered mainly oranges, because mandarins, limes and lemons are resistant, tolerant, or show very little symptoms. The assessment was mainly driven by the fact that in Mediterranean areas citrus plantations are irrigated, there is almost no ground cover in summer, and low level of the known EU vector is found on citrus.

E.4. Evidence Tables

E.4.1. Olive

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Ogliarola salentina	Survey carried out in olive orchard in Taviano (Lecce) revealed that nearby 80% of the plants showed OQDS symptoms			Ogliarola salentina is one of the most sensitive cultivar, together with Cellina di Nardò	Bleve et al. (2016)	
	The finding of diseased olive trees with positive diagnosis for the same ST16 in two localities distant 130 km from each other (Maria da Fé and São Bento do Sapucaí), indicate that the bacterium is spreading through orchards in the Mantiqueira Mountain Range region	The diseased olive trees found in Brazil displayed branches that were either entirely desiccated, or had basal and apical leaves expressing different degrees of scorching, starting at the leaf tips. Additional symptoms included pale green leaves, partial defoliation and death of shoots and branches. The symptoms were identical to those recently described for olive plants infected with *X. fastidiosa* in southern Italy, and in Argentina		First study in Brazil, the bacterium is spreading. A New paper (Safady et al., in press) confirms those findings in Brazil: 43% of symptomatic (leaves with desiccation, scorch, yellowing, etc.) plants were positive to *X. fastidiosa*	Coletta-Filho et al. (2016)	
		In December 2013, in Aimogasta (La Rioja province) and Cruz del Eje (Córdoba province) (Argentina) olive trees older than 50 years of age were observed in six orchards of cv. Arauco, which showed symptoms recalling those induced by *X. fastidiosa.* Some branches displayed desiccated leaves at the top and basal leaves with apical scorching. Additional symptoms were slow decay, dull green coloration, curling and necrosis of the leaves, partial defoliation and rapid death of shoots and branches			Haelterman et al. (2015)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Several cultivars		Orchard in Lecce province. Disease progression in four olive cultivars, expressed as mean disease severity scores based on a visually assessed scale from 0 to 3. Observations reported were assessed 2 and 8 months after pruning Cellina di Nardò: 0.73–2.10 Ogliarola di Lecce: 0.73–2.17 Frantoio: 0.10–1.38 Leccino: 0.08–1.33		Score 0 = symptomless. Score 1: few branches. Score 2: some branches, production is probably affected. Score 3 is zero production. Ogliarola di Lecce and Cellina di Nardò are the most sensitive. Leccino is the less diseased. Frantoio is intermediate	Table 1 in Luvisi et al. (2017)	
	Survey in California on olive trees: 17% of the diseased trees tested positive for *X. fastidiosa* subsp. multiplex by PCR				Krugner et al. (2014)	Pathogenicity test in greenhouse showed that symptoms cannot be attributed *to X. fastidiosa* subsp. *multiplex* infection. Olive may contribute to epidemiology
Leccino, Cellina di Nardò, Ogliarola salentina	Survey in Lecce province, ELISA test: Leccino: 15 positive/100 plants Cellina di Nardò: 145/150 Ogliarola salentina: 341/350	Cellina di Nardò and Ogliarola were symptomatic, while Leccino plants were almost all asymptomatic		PCR test on Leccino plants showed 35% positive instead of 15% (ELISA test), probably because the bacterium was erratically distributed Bacterial concentration in Leccino was lower compared to the other cultivars	Boscia et al. (2017b)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
	The infected area extended from approximately 8.000 ha in 2013, to approximately 715.000 in 2018. The infected area covers 36% of Apulia region, with approximately 21 million of trees under threat				Saponari et al. (2018)	
	Leccino plants harbour less bacterial concentration compared to Ogliarola salentina and Cellina di Nardò cultivars Even lower incidence was found in FS-17 cultivar	Leccino plants show less symptoms compared to Ogliarola salentina and Cellina di Nardò cultivars		Leccino is less susceptible cultivar (less infection, less symptoms, less bacterial concentration)	Saponari et al. (2018)	

OQDS: olive quick decline syndrome; ST: Sequence Type; ELISA: enzyme-linked immunosorbent assay; PCR: polymerase chain reaction.

E.4.2. Almond

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Prunus dulcis	183 (ALSD)-affected trees out of 4,193 tested		Extension of yield evaluations from 3 to 5 years demonstrated that yield loss due to ALSD was consistent over 5 years, with yields of ALSD-affected trees reduced by 20% and 40% compared with unaffected trees for 'Nonpareil' and 'Sonora', respectively 9 of 183 (ALSD)-affected trees died after 5 years		Sisterson et al. (2012)	
Prunus dulcis		Severe leaf stunting and death tree	*X. fastidiosa* killed almond trees both under field and greenhouse conditions		Amanifar et al. (2016)	
Prunus dulcis		Severity of leaf scorching symptoms was highest on trees grafted on Nonpareil rootstock, intermediate on Okinawa and Y119, and lowest on Nemaguard	Trunk cross-sectional areas of *X. fastidiosa* - infected trees grafted on Nemaguard and Nonpareil rootstocks were significantly smaller than non-infected trees, whereas trunk size of trees grafted on Okinawa and Y119 was not affected by infection status		Krugner and Ledbetter (2016)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Prunus dulcis		Newly infected trees usually develop leaf symptoms in a single terminal branch and then in adjacent branches; within 2–5 years, the entire tree develops leaf scorch			Mircetich (1976)	

ALSD: almond leaf scorch disease.

E.4.3. Grapevine

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Vitis vinifera cv. Chardonnay	Samples that tested positive for *X. fastidiosa*: 56 positive out of 120 using ELISA 65 positive out of 120 using PCR	Samples were taken from symptomatic (leaf scorch) and asymptomatic plants		Comparison of *X. fastidiosa* detection in whole tissue samples with xylem fluid samples Both whole-tissue and xylem fluid samples were collected from 30 grapevines from a commercial vineyard in Temecula, CA and from the University of California, Riverside campus	Bextine and Miller (2004)	
Vitis vinifera Cultivars: Site 1 – Merlot Site 2 – Merlot Site 3 – Cabernet Sauvignon Site 4 – Merlot Site 5 – Sauvignon Blanc Site 6 – Grenache Site 7 – Zinfandel Site 8 – Zinfandel	Incidence in all 8 sites: Tabella 3 Site 1 – 23.7% of 500 Site 2 – 0.02% of 500 Site 3 – 0.02 of 500 Site 4 – 37.1% of ,1179 Site 5 – 26.2 of 1,448 Site 6 – 5.5 of 6,056 Site 7 – 25.8% of 4,021 Site 8 – 0.2% of 3,192			Collection in vineyard field sites located in the Knight's Valley (Sonoma County, northern California) Data collected on over 30 environmental variables	Costello et al. (2017)	
Grapevine	In 2011, 21 vines were positive out of 61 sampled In 2012, 43 vines were positive out of 61 sampled			Grapevine growing provinces of Iran were visited, and plants exhibiting PD symptoms were sampled in 2011 and then in 2012. The samples were tested by DAS-ELISA for infection by *X. fastidiosa*	Amanifar et al. (2014)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Vitis vinifera	16 plants tested positive out of 24 sampled			In 2003, symptomatic plants from three vineyards in Costa Rica (locality of Santa Ana, La Uruca and La Garita) were collected and tested by DAS-ELISA for infection by *X. fastidiosa*	Aguilar et al. (2008)	
Resistant genotypes: *Vitis aestivalis* subsp. *smalliana* and *V. simpsonii* *V. cinerea* and *V. berlandieri* *V. aestivalis* subsp. *smalliana* *V. aestivalis* subsp. *smalliana* and *V. simpsonii* *V. arizonica* *V. shutttleworthii* Susceptible genotypes: *V. vinifera* (Chenin blanc) *V. vinifera* (Chardonnay)		Leaf scorching was quantitatively measured by taking the mean percentage of scorched area on four leaves above the point of inoculation 12 weeks post-*X. fastidiosa* inoculation the mean percentage of scorched area ranged from 25% to 91%		Six field-resistant and two field-susceptible Vitis genotypes were evaluated in this study Greenhouse experiment Four to five *X. fastidiosa* -inoculated replications were used per genotype Two to four water-inoculated replicates of each genotype served as controls	Krivanek et al. (2005b)	Leaf scorch could be due to background environmental stresses (greenhouse)

PD: Pierce's Disease; DAS-ELISA: double antibody sandwich enzyme-linked immunosorbent assay.

E.4.4. *Citrus* spp.

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Citrus sinensis Cultivars: Hamlin, Natal and Pera	55.7% out of 1,171 samples were PCR positive for the presence of *X. fastidiosa* The incidence of *X. fastidiosa* increased with the tree age (Figure 3b) Percentage of infected plants according to variety and tree age (Table 5) 0–2 years: Pera 5.9% Natal 5.0% Hamlin 0.0% 3–5 years: Pera 36.0% Natal 18.8% Hamlin 19.0% 6–10 years: Pera 72.5% Natal 50.8% Hamlin 47.3% > 10 years: Pera 65.8% Natal 65.1% Hamlin 57.4%	40.9% symptomatic		Sweet orange samples were collected from commercial groves in northern, central and southern regions of São Paulo State (Brazil) A total of 1,117 samples, one each from the 1,117 commercial blocks surveyed, were collected in 2005 Each block has a population equal to or greater than 200 citrus trees of the same botanical species (sweet orange) and age, grown under the same management at the same density. Each sample consisted of 10–20 leaves taken from one tree randomly selected in the block	Coletta-Filho et al. (2013)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Citrus *sinensis* Cultivar: Pera	In the LN region 26.9% of 93 groves were affected in 2003 and 54.2% of 253 groves were affected in 2004 Mean CVC incidence per age class in LN: 0–2 years: 5% 3–5 years: 8% 6–10 years: 21% > 10 years: 20% In the RB region were not found plants with CVC symptoms			A series of surveys were performed in two regions of Bahia State: Recôncavo Baiano and Litoral Norte (Brazil) Sampled groves were sorted into the four age classes Percentage of groves per age: 0–2 years: RB 0% LN 2.4% 3–5 years: RB 5% LN 3.3% 6–10 years: RB 29.7% LN 36.5% > 10 years: RB 65.3% LN 57.8%	Laranjeira et al. (2008)	
Citrus sinensis			Study from 2006 to 2008 The disease reduced the weight of fruits with symptoms by 50% The expected yield in the absence of CVC is 114 kg/plant. A CVC severity of 10 or 20% of branches would reduce yield by 18.3 and 33.8 kg/plant, respectively	This study was carried out in a citrus grove located at an Experimental Station in the northern region of São Paulo State, Brazil Inoculation made by grafting and tested by PCR after 6 months	Goncalves et al. (2012)	
Citrus sinensis			After 8 years, 23.8% of difference between yield of trees from healthy seedlings and trees from seedlings artificially inoculated with *X. fastidiosa* This difference represents a gain of approximately 203 boxes of 40.8 kg each, considering a planting density of 550 plants/ha	Healthy nursery plants and artificially inoculated plants with *X. fastidiosa* Inoculation was made by grafting and the plants were tested by PCR after 6 months Each plot was composed of 24 plants, six of which were evaluated Orchad in São Paulo State, Brazil	Gonçalves et al. (2011)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Citrus sinensis	From 1987 (when the disease was observed the first time in São Paulo) to 2000, the disease affected already 34% of the 200 million sweet orange trees. By 2005, the percentage had increased to 43%, and CVC was present in all citrus growing regions of Brazil	From 1996 to 2005, the percentage of trees with mild symptoms decreased from 16 to 6%, while the percentage of trees with severe symptoms increased from 6 to 37%, indicating that trees with mild symptoms turned into trees with severe symptoms	Yield losses of severely affected sweet orange trees can be as high as 60–80%. In 1996, when CVC was still mild, 270 fruits were required to fill one box, while in 2006, when CVC was more severe and fruits were smaller, 300 fruits were needed per box. The difference of 30 fruits per box represents a loss of 10%, meaning that CVC decreases the number of boxes produced by 10%	Review of three citrus diseases in Brazil	Bové and Ayres (2007)	
C. sinensis – 15 cultivars		No correlation between symptoms and fruit damage	Trees planted in a high inoculum area (São Paulo State, Brazil). Considering results of PSF (percentage of small fruits) and PED (percentage of estimated damage), the varieties can be distinguished in three different groups: highly susceptible (PED between 72 and 98%: Barao, Pera, Lima, Rubi, Cadenera 17 and 51, Berna, Valencia), susceptible (PED between 60 and 70%: Gardner, Pineapple, Sunstar, Folha Murcha, Baianinha), mildly susceptible (Lue Gim Gong 43% PED and Westin 22% PED)	Citrus cultivars not cultivated in EU	Laranjeira and Pompeu Júnior (2002)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Tangelo (*Citrus tangelo*)		Intensive screening was launched in 1990 to detect some degree of CVC tolerance. Symptoms were observed in sweet oranges. No symptoms were observed in most tangelo varieties (yield and fruit quality were not affected)			Laranjeira et al. (1998a)	
Several *Citrus* spp.		Plants of genera *Citrus*, *Fortunella* and *Poncirus* were evaluated under field conditions in order to evaluate symptomatic and asymptomatic host range of *X. fastidiosa*. All *Citrus sinensis* varieties showed symptoms. Some mandarins, tangors, tangelos and one sour orange (*C. aurantium*) had symptoms. Pathogen detection was negative in *Poncirus trifoliata, Fortunella margarita, Citrus yuzu, Citrus limettoides, Citrus latifolia* and *Citrus paradisi*. Eureka, Feminello and Monachello lemons (*C. limon*) were non-hosts even under high inoculum pressure, but Camargo, Sanguino 2 and amber lemons were positive. Comprida citron (*C. medica*) and Periforme pummelo (*C. grandis*) were symptomless hosts			Laranjeira et al. (1998b)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Citrus sinensis (Valencia, Pêra, Caipira, and Natal) *C. limonia* (Rangpur lime and Cravo lime) *C. aurantifolia* (Mexican lime) *C. limettioide* (Persian lime) *C. sunki* (Sunki mandarin) *C. reshni* (Cleopatra mandarin) *C. reticulata* (Ponkan mandarin)		12 months post-inoculation the percentage of symptomatic plants reached 63% of a total of 27 seedlings in Caipira, followed by Natal (55.6% of 54), Pêra (58.6% of 58), Valencia (53.8% of 52) and Sunki (40.7% of 59) Pêra showed the highest percentage of symptomatic leaves at 45.9% per plant, followed by Caipira (39.1%), Valencia (33.9%), Natal (30.1%) and Sunki (15.9%) No symptom developed on Ponkan mandarin, Cleopatra mandarin, Cravo mandarin, Mexican lime, Persian lime and Rangpur		The resistance of 11 commercial citrus varieties to *X. fastidiosa* infection was characterised based on the percentage of seedlings that expressed leaf symptom 6, 8, 10, and 12 months after inoculation; populations of cultivable bacteria from symptomatic and asymptomatic seedlings; and the percentage of apparently obstructed xylem vessels Plants inoculated by injection	Garcia et al. (2012)	

Host plant (cultivar, variety)	Incidence	Severity	Losses	Additional information	Reference	Uncertainties
Citrus sinensis (Natal) *C. reshni* (Cleopatra mandarin)			In 1991, the average production of the citriculture of apparently healthy plants was 532.2 fruits/plant, with a mean weight of 21,720/kg per 100 fruits, and the average production of CVC plants was 501.6 marketable fruits (with a higher diameter to 50 mm) per plant, with an average weight of 14,700/kg per 100 fruits In 1992, apparently healthy plants had a mean yield of 813.8 fruits/plant, with an average weight of 22,678/kg pe 100 fruits, and diseased plants produced an average of 319.5 marketable fruits per plant, with an average weight of 14,575/kg per 100 fruits	Estimation of losses caused by CVC in Colina, State of São Paulo	Palazzo and Carvalho (1993)	

Appendix F – Factsheet and report of the expert knowledge elicitation on *Xylella fastidiosa* biological/epidemiological parameters for modelling purposes

F.1. General information

F.1.1. Scope of the expert knowledge elicitation (EKE)

In the framework of the European Commission Mandate M-2018-0020 to EFSA about the update of the Scientific Opinion on the risks to plant health posed by *Xylella fastidiosa* in the EU territory, EFSA was requested to assess the probability of short- and long-distance spreading of the bacteria in relation to the EU emergency phytosanitary measures included in the EU Decision 2015-789. To perform this task, the Panel used two modelling approaches based on different approaches and assumptions. These models include biological and epidemiological parameters related to the disease for which, at the time of the development of the Scientific Opinion, there was very little information and knowledge. To assess the parameter values, considering the limited amount of quantitative data, the Panel adopted the EFSA EKE methodology, in line with the related guidelines EFSA (2014) and guidance on Uncertainty (EFSA Scientific Committee et al., 2018b).

F.1.2. Selection of experts

Experts were selected considering their expertise on the crops identified as the most relevant for the EKE.

The experts who participated to the EKE were:

- Domenico Bosco, Full Professor in Agricultural Entomology at the University of Turin, Associate scientist at the Institute for Sustainable Plant Protection of the Italian National Research Council (CNR), expert in plant pathogen-vector interaction, transmission biology and epidemiology of insect-transmitted plant pathogens.
- Gianni Gilioli, Associated professor, Dept. of Molecular and Translational Medicine, University of Brescia, expert in risk analysis and food safety, models and management schemes in eco-epidemiology, parameter estimation for ecological models.
- Miguel Ángel Miranda, Associate Professor of Zoology at the Universitat de les Illes Balears (UIB), expert in vector and plant pests biology.
- Davide Martinetti, Ecodevelopment Research Unit, French National Institute for Agricultural Research (INRA), expert in statistical analysis and modelling.
- Maria Saponari, Researcher at the Institute for Sustainable Plant Protection of the Italian National Research Council (CNR), expert in invasive plant pathogens of woody crops (olive and citrus).
- Crescenza Dongiovanni, Researcher at the Institute of Centre for Research, Education and Experimentation in Agriculture 'Basile Caramia' (CRSFA), expert in phytosanitary products and pest management.
- Michael Maixner, Senior Scientist at the Institute for Plant Protection in Fruit Crops and Viticulture of the Federal Research Institute for cultivated plants (JKI), expert in epidemiology and control of vector transmissible grapevine diseases and biology of insect vectors of grape diseases.

F.1.3. Short description of the EKE methodology

The existing evidence was reviewed by the experts of the working group. To describe the existing evidence and remaining uncertainties, the working group performed an expert elicitation to judge on the parameter following the Quartile method of the Sheffield protocol:

- Each member of the group of experts were individually judging on the quartiles of the uncertainty distribution in the following queuing:
    - The lower and upper limit of the credibility range (98% uncertainty range: 1st and 99th percentile)
    - The median value (2nd quartile) as central estimate, which equally likely over- or underestimates the unknown parameter

  - The lower and upper limit of the interquartile range (50% uncertainty range: 1st and 3rd quartile), which describes the precision of the central value.

- The judgements on the credibility range was discussed and agreed in consensus by the group before the other values were judged. The reasoning was summarised.
- The judgements on the median and interquartile range were discussed and agreed in consensus. The reasoning was summarised.

Finally a smooth distribution curve was fitted to the consensus, and additional percentiles were calculated. The final distribution was reviewed and agreed by the group of experts.

F.1.4. Evidence on the pest in support to the EKE

According to the EFSA methodology on EKE, invited experts received in due time a factsheet with general information regarding the biology and epidemiology of the pathogen and the vector (i.e. *Philaenus spumarius*), list of hosts, area of potential establishment. Since this information is provided in the main body of this Scientific Opinion and in the most recent EFSA outputs regarding *X. fastidiosa* (e.g. EFSA pest categorisation, EFSA Update of the *Xylella* spp. host plant database), it is not repeated here in the Appendix.

In addition, for each estimated parameter, a specific table possibly including quantitative evidences on the observed impact in a given host was prepared and used during the EKE procedure. These tables are included in Section 4 of this Appendix.

F.1.5. Elicited parameters

Elicited parameters included:

- Vector local spread (Section F.2.1)
- Mean distance of disease spread (Section F.2.2)
- Transmission efficiency on susceptible hosts (Section F.2.3)
- Acquisition rate of the vector (Section F.2.4).

Due to lack of time, the following parameters, that were initially included in the EKE, were not discussed:

- Growth rate of bacteria/disease in the host
- Natural mortality
- Prevalence of infected vectors.

Due to lack of time, the parameter 'Adult mortality due to chemical and weed control', initially included in the EKE, was not elicited following the formal procedure (i.e. Quartile method of the Sheffield protocol) but following a simplified approach based on expert judgement. The results are reported in Section F.2.5.

F.2. Results of the expert knowledge elicitation

F.2.1. Vector local spread

Scenario assumptions for vector local spread:

Vector local spread scenario assumptions are:

- Olive orchard with herbaceous cover present among trees.
- Mean density of host plants for an olive orchard (considering that in a secular olive orchard the mean distance from olive trees is 10 × 10 m, in 25–40 years old olive orchards the mean distance is from 5 × 6 m to 7 × 7 m, depending on farmer choices).
- No border effects.
- Human-assisted movements (e.g. no hitchhiking) were not considered.
- Rare events were not considered.
- Extreme winds were not considered.
- No other strong source of attractions were considered.

- Vector move on random walk in all direction with no preference.
- Influence of competing hosts was not considered.
- Time span: lifespan of adult (from 4 to 6 months according to different conditions observed in EU).
- Temperatures are favourable, trees available, no water stress.

Questions for expert knowledge elicitation:

Considering a large number of adult vectors emerging in the centre of a large area (e.g. 10 km × 10 km) with no border effects, which is the radial distance (m) of dispersal by the 50% of the initial population of adult vectors during their lifespan. Excluded are human-assisted movements, e.g. hitchhiking; rare events, e.g. extreme winds. Consider a homogeneous landscape with tree hosts (orchard), no specific stimulus/source of attraction determine jumps. Consider an average value covering all EU conditions.

F.2.1.1. Evidence and uncertainty in the assessment of vector local spread

In this section, the main components of the identified evidence are listed and the overall uncertainties of the assessment are listed.

Main evidences:

- Experiment (3 weeks) conducted in Apulia and Piedmont based on insect release and recapturing. During first day vectors recaptured at a distance between 24 (in Apulia) and 35 m (in Piedmont). Extrapolation from data fitting gave from 251 to 675 m after 170 days (taken as mean adult lifespan) for the 50th percentile. 98th percentile up to around 3,000 m (data owned by one of the expert and not yet published or publicly available).
- Output of a model based on data. Results showed roughly a front velocity of 1,860 m/year. Spread could be underestimated as results are based on monitoring programme based on plant symptoms (data shared by an expert from a manuscript under revision, not yet published).
- *Philaenus spumarius* can travel for more than 30 m in a single flight. Observation of marked specimens revealed around 90 m in 24 h. Adults usually flight within 60 cm from ground but can as high as 6 m (Weaver and King, 1954).
- Monitoring data set from Apulia indicate that the majority of the new infections occur close by the infected sources (e.g. Montes-Borrego et al., 2017 showing that the majority of the infections in the susceptible olive cultivars has an aggregate spread pattern).

Overall uncertainties:

- Potential underestimation of adult population due to the method of sampling by sweeping nets (e.g. in the case of orchards with big trees) both in seasonality studies and marked-release recapture studies.
- Movement of vectors in different periods of the year (i.e. seasons) due to drivers that are not fully understand such as climate, innate behaviour, the presence of sheltering vegetation nearby crops (i.e. forest) and that make difficult to collect insects from their 'refuges'.
- There are situations in which vectors disappear (Spain, France, and Greece). Main driver for this event is dryness of hosts in given environmental conditions. In Apulia, the vector fly to trees.
- Effect of climate conditions (e.g. wet season = richness in ground vegetation = less vector dispersal) and of innate behaviour of the insect moving seasonally from ground cover to tree and vice versa independently from the plant cover.
- The presence of forests nearby crops, may represent sites where populations are abundant, or suitable 'refuges' for vectors when conditions are not favourable in the crops.
- The presence of various plant species with different attractiveness.
- Seasonality (e.g. prolonged winter, spring or summer seasons).

F.2.1.2. Elicitation outcomes of the assessment of vector local spread

Reasoning for a scenario which would lead to a high value for the parameter (99th percentile/upper limit)

The upper value of vector local spread was justified under the following assumptions:

- Data from the marked-release recapture experiments are underestimations: considering the low efficiency of the recapture of marked insects, longer flights could be not excluded.
- Areas of EU with environmental conditions favourable for the movement of vector.
- Prolonged favourable climatic conditions and no substantial limitations to vector movement.
- Areas subjected to frequent winds (excluding strong winds).
- The absence of local attracting factors reducing the movement of the vector.
- *Philaenus spumarius* is an active insect, probably on a daily basis in favourable climatic conditions.
- In areas with low vector density the vector could move more for mating.
- Competition for free areas.

Reasoning for a scenario which would lead to a low value for the parameter (1st percentile/lower limit)

The lower value of vector local spread was justified under the following assumptions:

- Based on experiments, after 15 days vectors were still collected within 20 m.
- High vector density: the vectors do not have to move for long distances for mating.
- The presence of factors limiting movement.
- All area in the EU were considered to be very close to experimental conditions.

Reasoning for a central scenario equally likely to over- or underestimate the parameter (50th percentile/median)

Judgement was mainly based on experimental observations from Italy, but taking into account that the experimental results could represent an underestimation (around 400 m).

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The precision was mainly affected by lacking of clear argumentation and evidences.

Table F.1: Fitted values of the uncertainty distribution on the vector local spread (m)

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	100					400		800		1,200					2,000
Expert 1	100					200		400		1,000					1,000
Expert 2	100					300		600		1,000					1,000
Expert 3	300					1,200		1,500		1,800					2,500
Expert 4	75					400		850		950					2,000
Expert 5	200					500		600		800					1,000
Expert 6	105					300		1,100		1,500					800
Expert 7	200					450		650		900					2,000
Fitted distribution	53	95	148	234	335	441	543	767	1,032	1,189	1,388	1,637	1,933	2,204	2,536

Fitted distribution: Weibull (1.5845,967.23), @RISK7.5.

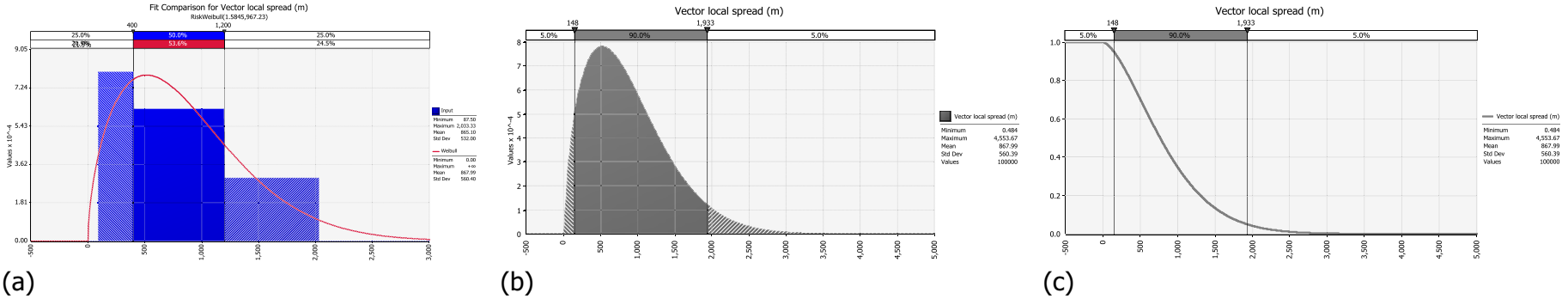


Figure F.1: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

F.2.2. Mean distance of disease spread

Scenario assumptions for the mean distance of disease spread:

The mean distance of disease spread scenario assumptions are:

- Human-assisted movements (e.g. hitchhiking, movement of machineries, current agricultural practices, shaking trees for harvesting) were considered.
- Delivery of fruits to packing houses was not considered.
- Rare events are considered.
- Extreme winds are considered.
- Plant movements for trade were not considered.
- Only a small % of whole pop able to big jumps or transported over very long distances. Likelihood of secondary spot.
- Mainly the continuity of the spread was considered, not isolated infrequent jumps: i.e. the expansion of the area include the time needed to fill all the gaps of the advance of a disease front.
- Focus on the vectors, not on the disease, i.e. the interest is in disease brought by infected vectors.
- Considered plants that are hosts for the adults.
- The vector population dimension was not considered.
- Optimal conditions for disease transmission.
- Infected area not able to be eradicated.

Questions for expert knowledge elicitation:

The mean distance (km) which will comprise 90% of the area containing the newly infected plants around an infected area within 1 year.

F.2.2.1. Evidence and uncertainty in the assessment of mean distance of disease spread

In this section, the main components of the identified evidence are listed and the overall uncertainties of the assessment are listed.

Main evidence:

- Infected area expansion in Apulia (monitoring programme). The data related to the outbreak appeared in 2015 in the municipality of Oria (Brindisi) were considered since the affected territories were monitored for three consecutive years.

Overall uncertainties:

- Level of bacterium load in an area
- Climate conditions
- Weather effects (e.g. wind)
- Level of human activities
- Density of vectors.

F.2.2.2. Elicitation outcomes of the assessment of mean distance of disease spread

Reasoning for a scenario which would lead to a high value for the parameter (99th percentile/upper limit)

The upper value of mean distance of disease spread was justified under the following assumptions:

- High level of human activities (including tourism).
- High population of bacteria in the hosts.
- High number of infected hosts/High susceptible hosts.
- High weather effects (e.g. wind favouring spread of vectors).
- Very suitable climate.
- High abundance of vector.

- Considered that the spread detected in one of the new foci in Apulia (approx. 8 km/year) represented an underestimation since the monitoring programme is based on sampling symptomatic trees.

Reasoning for a scenario which would lead to a low value for the parameter (1st percentile/lower limit)

The lower value of mean distance of disease spread was justified under the following assumptions:

- Less susceptible host plants.
- Low level of human activities.
- Considered mostly insect active movements and transmission processes efficiency.
- Low efficacy of hitchhiking.
- Less weather effects (e.g. less wind or not effectivity of transportation by wind).
- Low abundance of vectors.

Reasoning for a central scenario equally likely to over- or underestimate the parameter (50th percentile/median)

Apulia should be considered a worst case as:

- in the outbreak area the vector population density appear to be very high compared to other part of the same region, thus many other EU area may be characterised by lower vector density.
- in the outbreak area the contiguous presence of olives (highly susceptible to the specific bacterial strain occurring in Apulia) allow for high rates of infection spread.

However, it was also considered that Apulia is not an extreme situation for human activities in terms of agricultural practices and tourisms.

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The precision is mainly affected by uncertainty on the factor (vector abundance, intensity of human activities) that has the most impact in the disease spread.

Table F.2: Fitted values of the uncertainty distribution on the mean distance of disease spread (km)

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	1.0					3.0		5.0		8.5					12.0
Expert 1	0.5					4.0		8.0		10.0					8.0
Expert 2	1.2					1.5		3.0		6.0					8.0
Expert 3	0.5					2.0		4.0		7.0					15.0
Expert 4	2.0					4.0		7.0		9.0					20.0
Expert 5	2.0					4.0		6.0		8.0					10.0
Expert 6	3.0					3.0		6.0		9.0					15.0
Expert 7	0.5					1.7		3.0		7.0					15.0
Fitted distribution	0.42	0.73	1.10	1.69	2.37	3.07	3.74	5.18	6.85	7.82	9.05	10.57	12.35	13.98	15.10

Fitted distribution: Weibull (1.6840,6.4398), @RISK7.5.

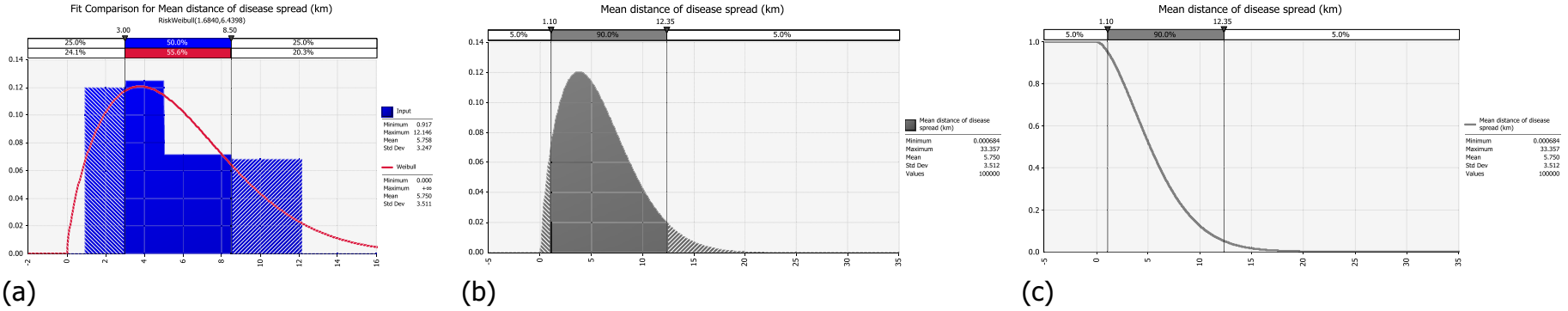


Figure F.2: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

F.2.3. Transmission efficiency on susceptible hosts

Scenario assumptions for transmission efficiency

Transmission efficiency scenario assumptions are:

- A single olive tree caged with infected vectors (no vegetation ground was considered to occur).
- Olive cultivar does not represent an important factor in vector transmission efficiency.
- Transmission was considered successful only if the host gets systemically infected.
- Not significant plant reactions are expected in relation to infection.
- Climatic conditions occurring in southern Europe where all the known outbreaks currently occur. For the climatic conditions, we refer to the season when the vector (particularly the adults) are present (from spring to autumn).

Questions for expert knowledge elicitation:

Probability (%) that a single susceptible olive tree becomes systemically infected as a consequence of the feeding activity of one infected adult vector during an average day occurring in the period when vector–host interaction occurs.

F.2.3.1. Evidence and uncertainty in the assessment of transmission efficiency

In this section, the main components of the identified evidence are listed and the overall uncertainties of the assessment are listed.

Main evidence:

- In Cornara et al. (2017) (Figure 3), roughly 30% of the recipient plants exposed to single insects were infected. Although periwinkle was considered an host plant significantly different from olives, comparing the data obtained on periwinkle (Cornara et al., 2017) and on olives (Cornara et al., 2017) the rate of transmission were quite similar.
- In Cornara et al. (2017) (Figure 1), 5 insects per plant in 2 periods (prevalence of infected vectors around 50%). Period for feeding activity was 4 days in first year, 7 days second year with no difference from 1 year to other (asymptotic value reached quickly).
- In Cornara et al. (2016), time-course transmission experiment carried out using grapevine (1 insect/plant) showed that after 24 h transmission efficiency was slightly below 20%.
- Preliminary results from an experiment conducted by one of the experts (not yet published). Transmission efficiency in summer was on average 35%, obtained with 20% of prevalence of infected insects. In a second experiment, plant infection rates ranged from 20% to 100% obtained with 50% of prevalence of infected insects (5 insects caged with one plant for 3–4 days). In early summer lower probability of infected vectors compared to late summer/early autumn.
- From the data presented by Cornara et al. (2016), it appears that most of transmission events occur in the first 24 hours, as shown by the tendency to have a plateau level (the experts questioned the significance of the exponential curve presented by the authors, conversely the trend is more toward a plateau).

Overall uncertainties:

- Duration of interaction vector–host (vary during the season).
- Potential effect of host attractiveness.
- Potential underestimation of infected vectors (e.g. the level of the bacterium harboured by the vectors is below the threshold of detection).
- Prevalence of infected vectors not considered.
- Number of insects used in experiments vs vector abundance in the field.
- Experiments are done using young olive plants/trees (highly susceptible to the infections), a condition that differs from the trees under field conditions; indeed, in general transmission tests are carried out under optimal conditions (temperature, vegetative status of the plants, avoiding water stress, etc.).

- Effects of water stress may reduce the susceptibility of the host or the propensity of the vectors to feed on a plant under stresses.
- Effects of temperature stresses: apparently high temperatures determine higher death rate of vector.

F.2.3.2. Elicitation outcomes of the assessment of transmission efficiency

Reasoning for a scenario which would lead to a high value for the parameter (99th percentile/upper limit)

The upper value of transmission efficiency considering:

- The scenario included the assumption that all the individual insects caged on the olive trees were infected, thus an higher prevalence than the situation occurring under field/experimental conditions.
- Favourable weather conditions during the season (e.g. reduced stresses on the plants, higher probability that the event of transmission results in a systemic infection).
- A single feeding event is already able to originate a successful systemic infection.
- During the full period it is possible to have systemic infection.
- One feeding event is already effective (plateau model for experimental data).
- Long period vector–host interaction.
- High susceptible olive cultivar.
- Favourable physiological conditions of the plants for bacterium infection and vector feeding.
- Plant conditions more likely to produce successful infection (conditions similar to experimental conditions performed using very young olive trees kept in optimal condition, e.g. no winter season, no water stress).

Reasoning for a scenario which would lead to a low value for the parameter (1st percentile/lower limit)

The lower value of host susceptibility can be given by:

- Conditions not suitable for systemic infections (i.e. a low number of feeding event originates then systemic infections).
- Vector–host interactions limited to a short period.
- Physiological status of plant not suitable for insect to feed or to infection to progress effectively (e.g. water stress).
- Transmission is limited by low vector presence and low establishment of a persistent infection.
- Less susceptible olive cultivar.
- Long periods of unfavourable weather during the seasons may impact establishment of bacterial infection.
- Results from experiments represent an overestimation as performed on young plants.

Reasoning for a central scenario equally likely to over- or underestimate the parameter (50th percentile/median)

The main reason for the median value of transmission was the experts' agreement that in general terms the experimental settings could bring to overestimations but not dramatically higher than in natural conditions where other factors could influence the transmission.

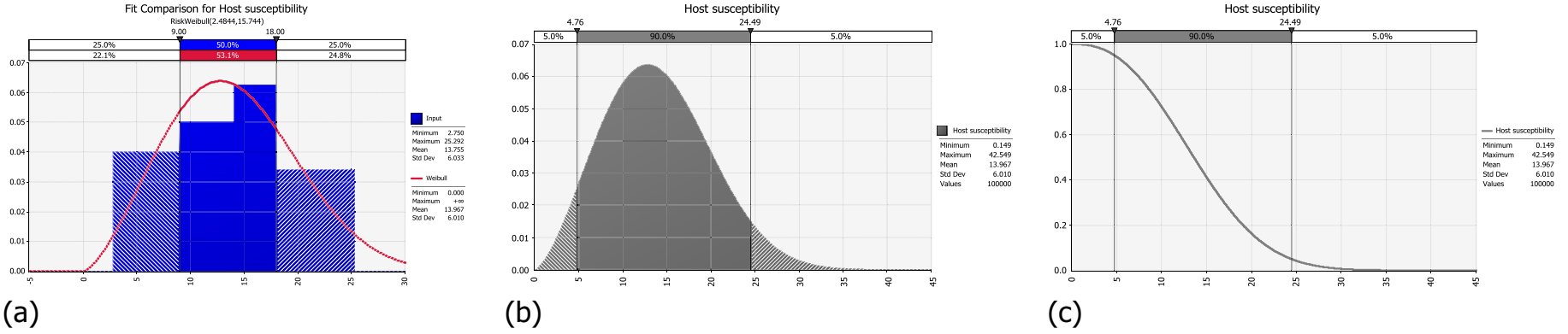
Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The precision is mainly affected by the experts' shared opinion that the upper limit is a high value. Therefore, Q3 was fixed closer to median.

Table F.3: Fitted values of the uncertainty distribution on the transmission efficiency (%)

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	3					9		14		18					25
Expert 1	5					8		15		18					25
Expert 2	7					5		10		20					25
Expert 3	10					10		15		20					35
Expert 4	6					5		10		12					20
Expert 5	5					10		18		20					20
Expert 6	3					5		15		20					15
Expert 7	3					8		12		16					35
Fitted distribution	2.47	3.58	4.76	6.36	8.01	9.54	10.89	13.58	16.41	17.96	19.82	22.02	24.49	26.63	29.11

Fitted distribution: Weibull (2.4844,15.744), @RISK7.5.



(a) (b) (c)

Figure F.3: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

F.2.4. Acquisition rate of the vector

Scenario assumptions for acquisition rate of the vector:

Vector local spread scenario assumptions are:

- Assessment is done considering olive as host.
- Vector is feeding on an infected olive plant.
- Bacterial load is not a limiting factor.
- 75% should be considered the maximum threshold for prevalence.
- Acquisition rate is assumed constant.

Questions for expert knowledge elicitation:

Probability (%) of acquisition of the bacteria per day by a vector feeding exclusively on an infected olive plant at a time when the bacterial load is not a limiting factor.

Note on the selection of host for the EKE exercise: the EKE is done for olive, in the modelling approach it will be scaled for other hosts.

F.2.4.1. Evidence and uncertainty in the assessment of acquisition rate of the vector

In this section, the main components of the identified evidence are listed and the overall uncertainties of the assessment are listed.

Main evidence:

- In Cornara et al. (2016), acquisition efficiency of spittlebugs was tested in grapes (inoculated grapevine with optimal bacterial concentration). Efficiency of acquisition per individual per day was 15%. Experts' shared opinion is that this represents a very good optimal condition and might represent an overestimation).
- In Cornara et al. (2017) (Figure 3), 75% of the specimens collected from olive trees in the infected olive groves (i.e. under natural infection conditions) tested positive for the bacterium (qPCR assay). Assumptions: considering that 75% as the max prevalence of infected vectors (in Apulia), and it is reached between end of June and beginning of July (i.e. around 40 days from the appearance of adult vectors), this would bring to an acquisition rate of approx 2% day-1. Nevertheless, bacterial load is increasing during the season (from May to July), so 2% could be an underestimation.
- Experimental data from experts (not published). Experiment caging insect in infected olives. According to the season acquisition rates ranged from < 20% up to 50 upon 4 days of acquisition access period (AAP). These experiments were conducted under field conditions, thus the variations recorded include the strong effect of the climatic and growing conditions of the plants in the field.
- In experiments, insects are caged on infected branches (i.e. forced to feed on infected tissues), and this could overestimate the acquisition.

Overall uncertainties:

- Effect of high temperature on transmission.
- Effect of water stresses, acquisition is more difficult.
- Host preference and suitability for feeding activity.
- Estimation of the infected vectors may be affected by some false negatives results (bacterium in the vector lower than the detection threshold), i.e. the insect test negative but it is still capable to transmit the bacterium.
- Host preference.

F.2.4.2. Elicitation outcomes of the assessment of acquisition rate of the vector

Reasoning for a scenario which would lead to a high value for the parameter (99th percentile/upper limit)

The upper value of acquisition rate of the vector if:

- Acquisition takes place at high rate during the first day (assumption from exp data) then reach a plateau.
- Prolonged favourable vegetative conditions, i.e. prolonged autumn season when plants are still in good conditions and level of bacteria in plant is high.
- Considered the highest experimental values (i.e. the rates of AAP) obtained under experimental conditions are most likely those that occur in the field).
- Short period in which plant physiological status is not suitable for vector feeding and bacterial acquisition.

Reasoning for a scenario which would lead to a low value for the parameter (1st percentile/lower limit)

The lower value of acquisition rate of the vector can be given by:

- Acquisitions occur mainly early in the season when the level of the bacterium in the plant is low.
- Acquisition more likely follows a linear trend (i.e. constant acquisition); thus, in 1 day, the rate of acquisition during AAP is significantly lower than what was experimentally demonstrated with 3 or 4 days of AAP.
- Considered the lowest experimental values, i.e. the experimental conditions were much favourable for the acquisition than the field conditions.
- Long period in which plant physiological status do not allow efficient bacterial acquisition by the vector.
- Assumed that grape experiment (Cornara et al., 2016) need to be downscaled since olive is a different source of bacteria than grape, and most likely grapes harbour a higher bacterial concentration than olives. In addition, grape was inoculated with optimal bacterial concentration).

Reasoning for a central scenario equally likely to over- or underestimate the parameter (50th percentile/median)

Experts agreed that the experimental settings could bring to overestimations but not dramatically higher than in natural conditions. Some evidences are based on grapevine where a higher bacterial concentration can be observed, so the acquisition by the vector is higher compared to olive.

Reasoning for the precision of the judgement describing the remaining uncertainties (1st and 3rd quartile/interquartile range)

The precision is mainly affected by the experts' shared opinion that the upper limit is a high value. Therefore, Q3 was fixed closer to median.

Table F.4: Fitted values of the uncertainty distribution on the acquisition rate of the vector (%)

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert agreement	5					9		13		18					30
Expert 1	5					7.5		10		15					15
Expert 2	5					8		13		18					15
Expert 3	5					10		15		20					15
Expert 4	5					8		12		20					20
Expert 5	8					10		12		20					35
Expert 6	15					8		15		20					60
Expert 7	5					9		13		18					25
Fitted distribution	4.40	5.14	5.90	6.95	8.09	9.24	10.34	12.08	15.87	17.80	20.39	23.87	28.34	32.78	38.65

Fitted distribution: InvGaussian (14.399,56.735), @RISK7.5.

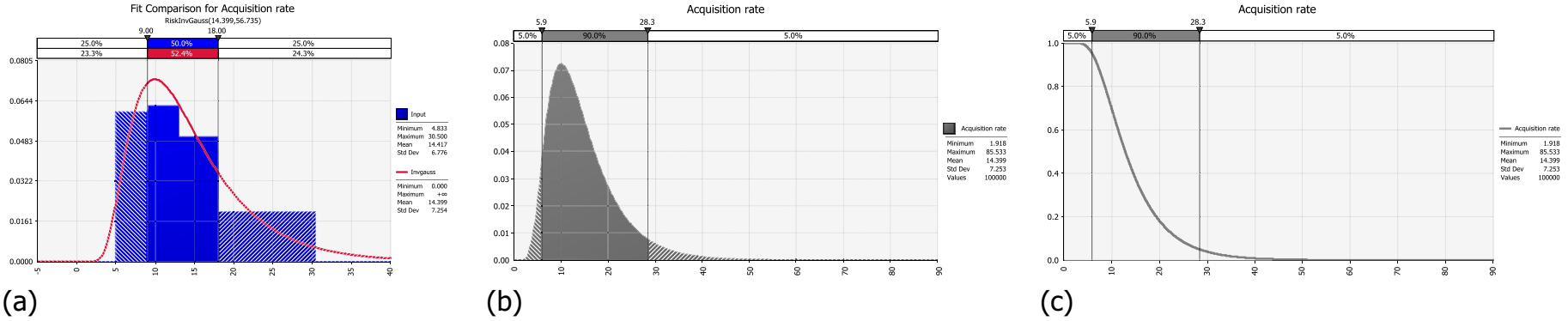


Figure F.4: (a) Comparison of judged values (histogram in blue) and fitted distribution (red line); (b) fitted density function to describe the uncertainties with 90% uncertainty interval; (c) fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded

F.2.5. Adult mortality due to chemical treatment and weed control

Preliminary note on the parameter

Due to lack of time, this parameter was not elicited following the same formal procedure (i.e. Quartile method of the Sheffield protocol) applied for the parameters above. A simplified approach was applied based on an open discussion with the experts.

Scenario assumptions for adult mortality due to chemical treatment and weed control

Scenario A: Weed control, low efficacy

- Mulching
- Extended to large area

Scenario B: Weed control, high efficacy

- Soil tillage or herbicide application
- Performed when a peak of the fourth instar is recorded
- Performed ensuring removal in whole plot (including between/among rows, and borders)
- Mechanical interventions at wide-scale area

Scenario C: Chemical control of the adults of the vector, low efficacy

- Appropriate dosage and spray volume of 1000–1500 l ha^{-1}
- 2 applications as suggested by phytosanitary services
- First treatment: 10–15 days after adult emergence. Second treatment 20–25 days after first treatment
- Organic insecticide (citrus extract oil)

Scenario D: Chemical control of the adults of the vector, high efficacy

- Appropriate dosage and spray volume of 1,000–1,500 l ha^{-1}
- First treatment: 10–15 days after adult emergence. Second treatment 20–25 days after first treatment
- Formulates based on pyrethroids (deltamethrin) or neonicotinoids (acetamiprid) if and when allowed
- Wide area of control strategy (not farm level).

Questions for expert knowledge elicitation:

What are the mean efficacies (% vector population mortality) of the four different scenarios of vector control in an olive orchard?

F.2.5.1. Evidence and uncertainty in the assessment of vector control

In this section, the main components of the identified evidence are listed and the overall uncertainties of the assessment are listed.

Main evidence:

- Among agricultural practices, tillage is more effective than mulching, which is more effective than mowing (not considered in the scenarios).
- No available data for mulching.
- Best moment for nymphs treatment is when the fourth instar appear (can vary according to climate conditions). The fifth instar is already too late.
- Although efficacy can be high, consider that you can only apply mulching and till only in crop area and surrounding but vector is everywhere and move.
- Spray volume of chemical treatment against adults vary from 1,000 to 1,500 L/ha, according to crop size and to ensure a good and uniform distribution on the canopies.
- Although efficacy of chemical treatment against the vector can be high, application can only be applied to olive canopy.

Overall uncertainties:

- Proper application of mulching/tillage
- Vector movements.

F.2.5.2. Elicitation outcomes of the assessment of vector control

Regarding the different scenarios, the experts agreed the following:

- Scenario A has an efficacy of around 60 ± 20%.
- Scenario B has an efficacy of around 90 ± 5%.
- Scenario C has an efficacy of around 50 ± 5%.
- Scenario D has an efficacy of around 90 ± 5%.

The values refer to a single application of the treatments.

F.3. Conclusions

F.3.1. Vector local spread

Under the hypothetical scenario described in Section 2.1 *Vector local spread*, the mean radial distance of dispersal by the 50% of a population of adults of *Philaenus spumarius* during their lifespan is 767 m with a 90% uncertainty range of 148–1,933 m. The estimate was mainly based on experimental results from Apulia, and Piedmont regions in Italy.

F.3.2. Mean distance of disease spread

Under the hypothetical scenario described in Section 2.2 *Mean distance of disease spread*, the mean distance which will comprise the 90% of the area containing the newly infected plants around an infected area within 1 year is 5.18 km with an estimated 90% uncertainty range of 1.10–12.35 km. The main evidence considered was the infected area expansion in Apulia (information from monitoring programme).

F.3.3. Transmission efficiency on susceptible hosts

Under the hypothetical scenario described in Section 2.3 *Transmission efficiency on susceptible hosts*, the probability (%) that a single susceptible olive tree becomes systemically infected as a consequence of the feeding activity of one infected adult vector during an average day during the period where vector–host interaction occurs is 13.58% with an estimated 90% uncertainty range of 4.76–24.49%.

F.3.4. Acquisition rate of the vector

Under the hypothetical scenario described in Section 2.4 *Acquisition rate of the vector*, the probability (%) of acquisition of the bacteria per day by a vector feeding exclusively on an infected olive plant at a time when the bacterial load is not a limiting factor is 12.08% with an estimated 90% uncertainty range of 5.90–28.34%.

F.3.5. Adult mortality due to chemical treatment and weed control

Following the discussion among the experts, the efficacy (% vector population mortality) of the following scenarios of vector control in an olive orchard is:

- Not efficient weed control: around 60 ± 20%.
- Efficient weed control: 90 ± 5%.
- Not efficient chemical control of the adults: 50 ± 5%.
- Efficient chemical control of the adults: 90 ± 5%.

The values refer to a single application of the treatments.

F.4. Evidence tables

F.4.1. Vector local spread

Data	Uncertainties	Reference
Under artificial conditions (laboratory flight mill) movement of 1 km within 1 h	Maximum potential, only 1 insect, upper limit, lab conditions	Lago et al. (2018)
Within 15 days after release, recapture within 60 m from release point. In a second experiment, recapture up to 100 m within 30 days	Preliminary data	Plazio et al. (2017)
The authors assumed an exponential dispersal mode of vector; have chosen mean dispersal distance of 100 m based on paper by Blackmer et al. (2004) dealing with *H. vitripennis*	Information from *H. vitripennis* and not *Philaenus spumarius*	White et al. (2017)
Olive grove: • Maximum distance 100–155 m in 7–12 days • The majority of the marked-insects were captured within 60 m from the release point • In summer population, more stationary than autumn (80% of the marked insects were found within 18 m from the release point) • Thus, in Apulia > dispersal capacity in autumn than in summer (favoured by the emergence of the weeds and ground vegetation)		Plazio et al. (2017)
Spread velocity of vector and disease combined is, on average of 2×10^5 m^2/month, (median = 1.8×10^5, sd = 0.7×10^5), that corresponds roughly to a front velocity of 155 m/month (spread is circular and isotropic)		Preliminary data (Abboud et al., 2018)
Active migration by flight is probably limited to distances of about 40–80 m	Only observation	Halkka et al. (1971)
Philaenus spumarius move 30 m in a single flight, marked adults 100 m in 24 h. Adults usually fly within 60 cm from the ground, can fly as high as 60 m		Weaver and King (1954)

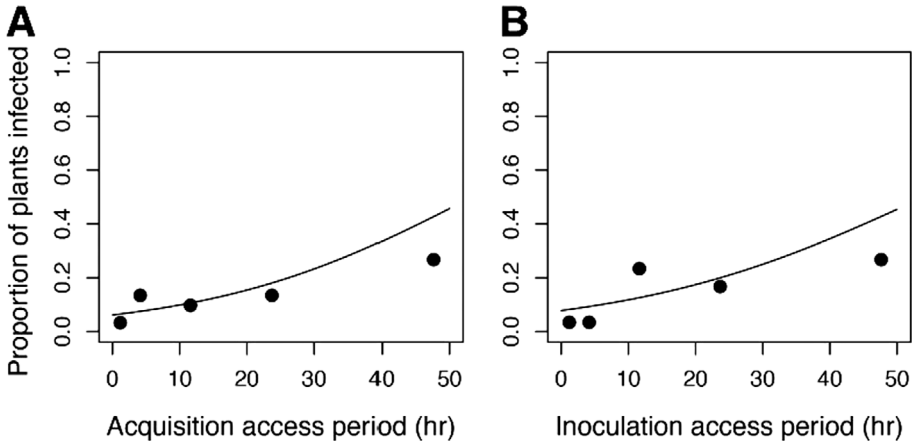
F.4.2. Mean distance of disease spread

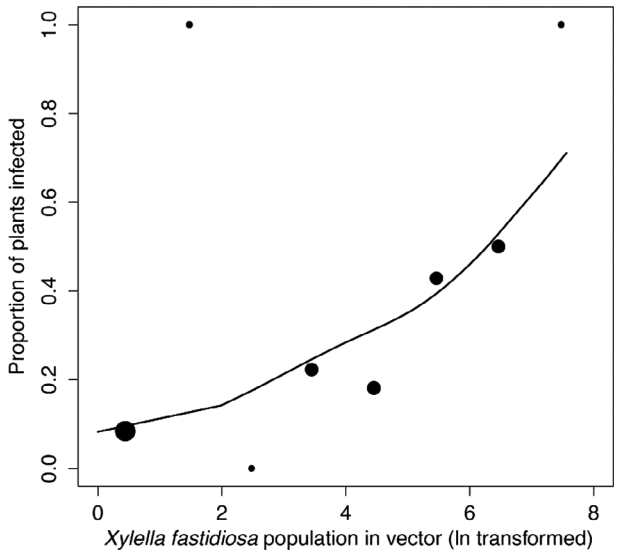
Data	Uncertainties	Reference
Philaenus spumarius can be transported by wind currents and is potentially capable of long-distance migration. Passive dispersal over great distances is mediated by wind and human activities (Weaver and King, 1954)		Cornara et al. (2018)
Passive dispersal due to transportation by cars has been observed		Expert empirical observation
Philaenus spumarius dispersal by floating on water: Of 1,510 marked specimens released on the sea surface, 10 specimens were found alive on the shore of an island in 1.1 km distance from the release point		Halkka et al. (1974)
Philaenus spumarius on car windshield (outside) travels > 150 km with highway speed (> 100 km/h)		Expert empirical observation
Detection of *Philaenus spumarius* in sea cargo containers		Stanaway et al. (2001)
Model assumption. Parameter d = 20 km		White et al. (2017)
In Apulia, new foci in Oria: in 3 years the disease spread 20–30 km (probably underestimated). In Cisternino: in 1 year diseases spread a radius of 5 km		Data provided by expert

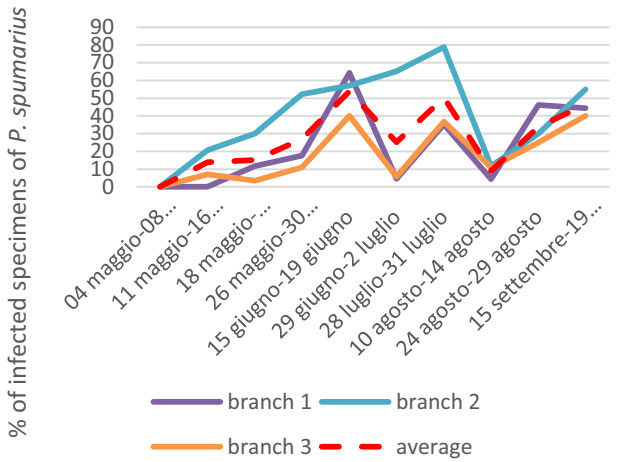
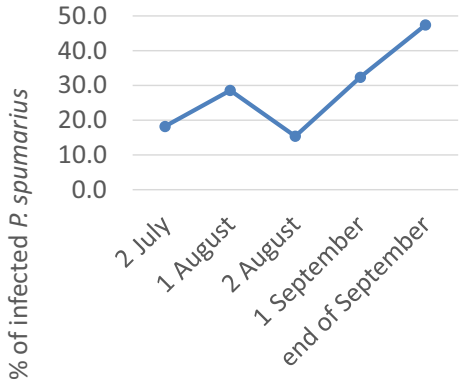
F.4.3. Transmission efficiency

Data	Uncertainties	Reference
Two of four olive plants inoculated with *Philaenus spumarius* were infected with *X. fastidiosa*, while none of the two olive plants inoculated by *Neophilaenus campestris* tested positive		Cornara et al. (2017)
Conference presentation. Preliminary results presented by expert. Transmission efficiency in summer was on average 35%, obtained with 20% of prevalence of infected insects. In a second experiment, plant infection rates ranged from 20% to 100% obtained with 50% of prevalence of infected insects (5 insects caged with one plant for 3–4 days). In early summer, lower probability of infected vectors compared to late summer/early autumn		Bodino et al. (2018)

F.4.4. Acquisition rate of the vector

Data	Uncertainties	Reference
 **Figure 1:** Relationship between *X. fastidiosa* transmission and spittlebug pathogen, **A** acquisition access period and **B** inoculation access period on plants. In both panels, the line indicates the model-predicted (marginal) probability of transmission, and the points indicate the proportion of test plants testing positive for *X. fastidiosa* at each time point. Sample size n = 30 for each time point	15% per day on grapevine	Cornara et al. (2016)

Data	Uncertainties	Reference
 **Figure 2:** Relationship between the modelled probability of *X. fastidiosa* transmission and populations of *X. fastidiosa* in *Philaenus spumarius*, for the entire data set (PCR-positive and PCR-negative vectors). Points indicate the proportion of test plants infected binned in intervals of 1 natural log of numbers of *X. fastidiosa* cells; points are placed at the median of intervals. The size of points represents their respective sample size: smallest points $1 \leq n < 10$, medium points $10 \leq n < 100$, and largest point $n \geq 100$. *X. fastidiosa* populations were natural log transformed to meet assumptions of linear models		

Data	Uncertainties	Reference
Acquisition rate recorded on a selected field tree (96 h AAP) – 2017 (months name in Italian: maggio = May; giugno = June; luglio = July; agosto = August; settembre = September) **Field A**  Acquisition rate recorded on a selected field tree (96 h AAP) – 2017 **Field B**  		Data on vector acquisition under different conditions, provided by the experts and not yet published or publicly available

Data	Uncertainties	Reference
Experiments on acquisition and transmission of *X. fastidiosa* by *Philaenus spumarius* in olive orchards Semi-field condition AAP = 3–4 days Field 1 = severely infected trees (30 years) Field 2 = new plantation (3 years) Trees bacterial populations (average): Cellina di Nardò and Ogliarola Salentina 10^5 CFU/mL Leccino 10^3 CFU/mL		Cavalieri et al. (2017)
Acquisition rates determined by testing individual insects in quantitative PCR assays, ranged from 4.9% in *N. campestris* to 22% in *Philaenus italosignus*, whereas no acquisition was recorded for *L. tunetana*		Cavalieri et al. (2018)
IAP and AAP had equivalent effect on transmission probability with acquisition and inoculation efficiencies of approximately 15% per individual per day	This value was lower than those observed in previous study, probably because the bacterial population in the plant was not very high	Cornara et al. (2016)
Olive-olive transmission: After the 4-day AAP on olive branches in the field, 16 *Philaenus spumarius* and 6 *N. campestris* were found dead; of these 5 *Philaenus spumarius* and 1 *N. campestris* individual tested positive for *X. fastidiosa*. At the end of the IAP, 11 of 35 *Philaenus spumarius* and 1 of 16 *N. campestris* individuals were *X. fastidiosa* positive		Cornara et al. (2017)
Data provided by expert, yet unpublished, show significant differences in the feeding activity of *Philaenus spumarius* on different host plant species		Data provided by expert, yet unpublished
Two sets of experiments have been performed, in order to describe (i) the kinetics of the bacterial multiplication and persistence in the spittlebug *Philaenus spumarius* and in the sharpshooter *C. viridis*; (ii) the influence of environmental factors (temperature, season) and insect age on simulated epidemics progression on olive plants under controlled and natural climatic conditions (indoor-outdoor). Both experiments have repeated in 2017 and 2018, twice a year (June–July and September–October) Although the results from 2018 have to be collected yet, preliminary results from 2017 indicate for *Philaenus spumarius*: (a) an higher acquisition efficiency in September as compared to July; (b) a lower acquisition efficiency when periwinkle was used as source plant compared to olives, conversely transmission was higher on periwinkle plants compared to olives. Very low acquisition efficiency and no transmission ability were recovered for *C. viridis*		Bodino et al. (2018)

Data	Uncertainties	Reference
Transmission rate was highest for oleander (72.00 ± 8.00), decreasing significantly ($p = 0.0484$) for olive seedling (44.00 ± 13.27) and olive cv. Coratina ($p = 0.0060$) (32.00 ± 14.97). There was no difference in overall transmission rate related to the period when transmission tests were carried out in 2014 ($p = 0.356$), except for that performed in August that showed a significantly lower value than those sampled in April ($p = 0.0026$) or September ($p = 0.0242$). In 2015, treatments with *X. fastidiosa* infection were statistically different ($p < 0.05$). Transmission to GF677 rootstock, with only one plant infected in mid-June 2015, was significantly lower than to olive cv. Ogliarola ($p = 0.0012$), olive seedlings ($p = 0.015$), oleander ($p < 0.0001$) and periwinkle ($p = 0.0010$), but not differed for sweet orange ($p = 0.1295$). For those hosts, transmission rate was significantly higher for oleander (72.00 ± 8.00) and periwinkle (50.00 ± 11.79), decreasing significantly for olive cv. Ogliarola (43.64 ± 10.02) and olive seedling (42.22 ± 8.46) with no significant differences among them ($p \geq 0.05$), being lowest ($p < 0.0015$) for sweet orange (12.00 ± 5.33). There were no significant differences ($p \geq 0.05$) in transmission rate related to the period when experiments were carried out, except for samples taken in mid-May and early June that showed a significantly lower transmission rate ($p < 0.05$). The increment in IAP from 4 days in 2014 to 7 days in 2015 had no effect on infection rate for olive seedlings ($p = 0.8855$), oleander ($p = 0.7473$) or sweet orange ($p = 0.6320$)		Cornara et al. (2017)
Philaenus spumarius transmit the bacterium to host plants from May to October		Cornara et al. (2017)
For *H. vitripennis* (causal agent of vector dissemination of Pierce's disease in southern California on vineyards), '[…] there is a threshold below which acquisition rarely occurs: i.e. < 104 CFU/g of plant.'		Daugherty and Almeida (2018)

CFU: colony forming unit; IAP: inoculation access period; AAP: acquisition access period.

Appendix G – Data extraction of exported live plants to trade partners

Data extraction of exported live plants (including their roots, cuttings and slips; mushroom spawn (excl. bulbs, tubers, tuberous roots, corms, crowns and rhizomes, and chicory plants and roots)) from EU28 to trade partners (Eurostat Comext, accessed 18 March 2019).

For each trade partner, the pest free country/pest free areas/pest free production sites status is reported, together with literature data reporting the presence of *Xylella* species (EFSA, 2018a).

Trade partner	Mean export 2013–2018 (quantity in 100 kg)	*X. fastidiosa* pest free countries (+++) or countries with pest free areas (++) or pest free production sites (+) according to articles 16 or 17 of Commission Implementing Decision (EU) 2015/789[(a)]	Trade partners with literature reports of *X. fastidiosa* from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)	Trade partners with literature reports of other *Xylella* species from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)
SWITZERLAND (incl. LI→1994)	1,827,551.83			
RUSSIAN FEDERATION (RUSSIA)	1,264,926.17			
TURKEY	1,262,818.33	(+++)		
NORWAY (incl. SJ, excl. 1995, 1996)	553,410.67	(+++)		
BELARUS (BELORUSSIA)	480,578.17			
UKRAINE	208,649.50	(+++)		
LEBANON	150,012.00			
MOROCCO	122,225.83	(+++)		
BOSNIA AND HERZEGOVINA	109,621.33	(+++)		
UNITED ARAB EMIRATES	103,550.17			
AZERBAIJAN	92,370.33			
ISRAEL (GAZA and JERICHO → 1994)	88,515.00	(+++)		
KAZAKHSTAN	84,704.67			
JAPAN	81,013.83	(+++)		
OMAN	77,643.00			
SERBIA (EU data from 1/6/5 ex CS)	77,426.33	(+++)		
QATAR	74,845.17			
UNITED STATES	71,872.00	(++), (+)	(x)	

Trade partner	Mean export 2013–2018 (quantity in 100 kg)	*X. fastidiosa* pest free countries (+++) or countries with pest free areas (++) or pest free production sites (+) according to articles 16 or 17 of Commission Implementing Decision (EU) 2015/789[a]	Trade partners with literature reports of *X. fastidiosa* from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)	Trade partners with literature reports of other *Xylella* species from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)
NORTH MACEDONIA	68,032.00	(+++)		
CHINA (PEOPLE'S REPUBLIC OF)	63,048.83	(++)		
ALBANIA	62,648.00	(+++)		
IRAQ	47,181.50			
JORDAN	46,713.50	(+++)		
UZBEKISTAN	40,031.83			
MOLDOVA, REPUBLIC OF	37,058.50	(+++)		
KOREA, REPUBLIC OF (SOUTH KOREA)	33,428.17	(+++)		
SAUDI ARABIA	33,408.17			
ALGERIA	29,396.83			
GEORGIA	25,282.67			
TAJIKISTAN	24,507.50			
COSTA RICA	23,452.00		(x)	
KUWAIT	23,231.00			
ECUADOR	22,383.17	(+++)	(x)	
MONTENEGRO	20,366.67	(+++)		
KOSOVO[b] (EU data from 1/6/5)	19,499.67			
MALAYSIA	19,257.50			
ARMENIA	15,865.17			
TURKMENISTAN	13,129.67			
CANADA	13,011.50		(x)	
TUNISIA	12,954.83	(+++)		
PANAMA (excl. CANAL → 1980)	11,921.50			
ICELAND	8,839.83			
EGYPT	8,242.17	(+++)		

Trade partner	Mean export 2013–2018 (quantity in 100 kg)	*X. fastidiosa* pest free countries (+++) or countries with pest free areas (++) or pest free production sites (+) according to articles 16 or 17 of Commission Implementing Decision (EU) 2015/789[(a)]	Trade partners with literature reports of *X. fastidiosa* from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)	Trade partners with literature reports of other *Xylella* species from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)
THAILAND	8,081.50	(+++)		
INDIA	6,712.17	(+++)		
HONG KONG	6,678.17			
CHILE	6,294.83	(+++)		
BAHRAIN	6,280.50			
ANDORRA	5,636.33			
DOMINICAN REPUBLIC	5,279.33			
LIBYAN ARAB JAMAHIRIYA (LIBYA)	4,836.67			
LIECHTENSTEIN	4,419.50			
KYRGYZ, REPUBLIC (ex KYRGYZSTAN → 2005)	4,021.67			
MEXICO	3,946.50		(x)	
ARUBA	3,733.67			
EQUATORIAL GUINEA	3,252.33			
IRAN, ISLAMIC REPUBLIC OF	3,230.50		(x)	
SINGAPORE	3,091.33			
NEW ZEALAND	2,805.00	(+++)		
BRAZIL	2,786.67	(+)	(x)	
MELILLA	2,747.33			
ETHIOPIA (incl. ERITREA →1993)	2,673.33	(+++)		
SOUTH AFRICA (incl. NA →1989)	2,662.17	(+++)		
COLOMBIA	2,588.50	(+++)		
VIETNAM (excl. NORTH → 1976)	2,503.33	(+++)		
CEUTA (incl. MELILLA → 1998)	2,447.83			

Trade partner	Mean export 2013–2018 (quantity in 100 kg)	*X. fastidiosa* pest free countries (+++) or countries with pest free areas (++) or pest free production sites (+) according to articles 16 or 17 of Commission Implementing Decision (EU) 2015/789[(a)]	Trade partners with literature reports of *X. fastidiosa* from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)	Trade partners with literature reports of other *Xylella* species from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)
FAROE ISLANDS	2,123.17			
PAKISTAN	1,739.83			
ARGENTINA	1,739.33	(++)	(x)	
GIBRALTAR	1,691.67			
AFGHANISTAN	1,586.00			
KENYA	1,563.67	(+++)		
PERU	1,377.67	(+++)		
PHILIPPINES	1,353.83	(+++)		
SYRIAN ARAB REPUBLIC (SYRIA)	1,007.00			
ANGOLA	946.33			
TAIWAN	931.83			(x)
TANZANIA, UNITED REPUBLIC OF	891.50	(+++)		
SURINAME (ex DUTCH GUIANA)	823.17			
NIGERIA	800.67			
MAURITANIA (incl. Sp SAH. from 1977)	785.50			
COTE D'IVOIRE	685.83			
MALDIVES	578.33			
AUSTRALIA	577.33	(+++)		
INDONESIA (ID + TP from 77, excl. TP→2001)	574.67	(+++)		
URUGUAY	519.33			
GUATEMALA	489.50			
MADAGASCAR	447.67			
BANGLADESH	341.67			
SRI LANKA (ex CEYLON)	300.33	(+++)		

Trade partner	Mean export 2013–2018 (quantity in 100 kg)	*X. fastidiosa* pest free countries (+++) or countries with pest free areas (++) or pest free production sites (+) according to articles 16 or 17 of Commission Implementing Decision (EU) 2015/789[(a)]	Trade partners with literature reports of *X. fastidiosa* from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)	Trade partners with literature reports of other *Xylella* species from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)
CAPE VERDE	292.83			
SENEGAL	283.83			
CAMEROON	278.67			
SINT MAARTEN (DUTCH PART)	273.33			
ZIMBABWE (RHODESIA → 1980)	261.33			
BARBADOS	251.67			
GUINEA	250.50			
CURACAO	220.83			
MACAO	210.50			
BOLIVIA	156.17			
MAURITIUS	147.67			
BRUNEI DARUSSALAM (BRUNEI)	133.50			
OCCUPIED PALESTINIAN TERRITORY (WEST BANK -INCLUDING EAST JERUSALEM AND GAZA STRIP)	131.67			
PARAGUAY	128.67		(x)	
UGANDA	119.83	(+++)		
GHANA	119.50	(+++)		
GREENLAND	113.83			
SOMALIA	112.83			
NEPAL	111.00			
ERITREA	89.67			
TOKELAU	85.00			
CONGO	74.33			
VENEZUELA	60.50		(x)	

Trade partner	Mean export 2013–2018 (quantity in 100 kg)	*X. fastidiosa* pest free countries (+++) or countries with pest free areas (++) or pest free production sites (+) according to articles 16 or 17 of Commission Implementing Decision (EU) 2015/789[(a)]	Trade partners with literature reports of *X. fastidiosa* from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)	Trade partners with literature reports of other *Xylella* species from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)
MYANMAR (BURMA)	55.67			
MONGOLIA	49.17			
SAINT BARTHELEMY	43.17			
CONGO, DEMOCRATIC REPUBLIC OF (ZAIRE → 1997)	42.00			
ZAMBIA	41.00			
NEW CALEDONIA	39.50			
EL SALVADOR	37.67	(+++)		
ANTIGUA AND BARBUDA	37.33			
BONAIRE, SINT EUSTATIUS AND SABA	34.00			
SUDAN	29.50			
TRINIDAD AND TOBAGO	29.33			
CAMBODIA (ex KAMPUCHEA)	23.17			
GABON	17.67			
YEMEN (excl. SOUTH → 1990) (ex NORTH YEMEN AND SOUTH YEMEN)	13.50			
BAHAMAS	12.83			
FRENCH POLYNESIA	12.67			
MALI	11.83			
DOMINICA	11.17			
BURKINA FASO (UPPER VOLTA → 1985)	10.50			
VIRGIN ISLANDS, BRITISH (and MONTSERRAT → 1994)	10.50			
HAITI	8.33			

Trade partner	Mean export 2013–2018 (quantity in 100 kg)	*X. fastidiosa* pest free countries (+++) or countries with pest free areas (++) or pest free production sites (+) according to articles 16 or 17 of Commission Implementing Decision (EU) 2015/789[(a)]	Trade partners with literature reports of *X. fastidiosa* from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)	Trade partners with literature reports of other *Xylella* species from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)
NAMIBIA	7.33			
NIGER	7.17			
SAN MARINO	5.00			
GUYANA	4.67			
JAMAICA	4.67			
MOZAMBIQUE	4.67			
KOREA, DEMOCRATIC PEOPLE'S REPUBLIC OF (NORTH KOREA)	2.50			
NICARAGUA	2.33			
CENTRAL AFRICAN REPUBLIC	2.17			
CHAD	2.17			
SAINT PIERRE AND MIQUELON	2.17			
BERMUDA	2.00			
RWANDA	2.00			
GUINEA-BISSAU	1.67			
FRENCH SOUTHERN TERRITORIES	1.50			
LAO PEOPLE'S DEMOCRATIC REPUBLIC (LAOS)	1.50			
DJIBOUTI (AFARS ISSAS → 1977)	1.33			
HONDURAS	1.33		(x)	
SOUTH GEORGIA AND SOUTH SANDWICH ISLANDS	1.33			
TOGO	1.33			

Trade partner	Mean export 2013–2018 (quantity in 100 kg)	*X. fastidiosa* pest free countries (+++) or countries with pest free areas (++) or pest free production sites (+) according to articles 16 or 17 of Commission Implementing Decision (EU) 2015/789[(a)]	Trade partners with literature reports of *X. fastidiosa* from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)	Trade partners with literature reports of other *Xylella* species from EFSA Update of the *Xylella* spp. host plant database, excluded dubious reports and eradicated outbreaks (x)
FIJI	0.83			
SAO TOME AND PRINCIPE	0.83			
AMERICAN SAMOA	0.67			
CAYMAN ISLANDS	0.67			
BENIN (DAHOMEY → 1976)	0.50			
GRENADA	0.50			
MALAWI	0.33			
MARSHALL ISLANDS	0.33			
BRITISH INDIAN OCEAN TERRITORY	0.17			
GUAM	0.17			
SAMOA (ex WESTERN SAMOA)	0.17			
SOUTH SUDAN	0.17			
ST LUCIA	0.17			
ST VINCENT AND THE GRENADINES	0.17			
TONGA	0.17			
VANUATU (NEW HEBRIDES → 1980)	0.17			

(a): https://ec.europa.eu/food/plant/plant_health_biosecurity/legislation/emergency_measures/xylella-fastidiosa/declarations-non-eu_en
(b): This designation is without prejudice to positions on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence.

Appendix H – Source of data for crop statistics

Country	Source	Year
Austria	Wein-Online of the BMNT	2015
Bulgaria	MAF, Agrostatistics Department	2015
Croatia	Croatian Bureau of Statistics	2015
Cyprus	Eurostat	2015
Czech Republic	Czech Statistical Office (CZSO)	2012
France	Ministère de l'Agriculture et de l'Alimentation Agreste – Statistique agricole annuelle (SAA)	2015 2016 (Almond)
Germany	Eurostat	2015
Greece	Hellenic Statistical Authority (ELSTAT)	2015
Hungary	Eurostat	2013
Italy	Italian National Institute of Statistics (ISTAT)	2015
Kosovo[(a)]	Eurostat	2015
Luxembourg	National Institute of Statistics and Economic Studies of the Grand Duchy of Luxembourg	2015
North Macedonia	Farm register in the Ministry of Agriculture, Forestry and Water economy of North Macedonia	2015
Malta	Eurostat	2015 2016 (Olive and Citrus)
Montenegro	Statistical Office of Montenegro (MONSTAT)	2015 2016 (Olive and Citrus)
Poland	Eurostat	2010
Portugal	Instituto Nacional de Estatística Portogal (INE)	2015 (Olive and Grapevine) 2016 (Citrus and Almond)
Romania	Romania National Institute of Statistics	2015
Slovakia	Statistical Office of the Slovak Republic	2015
Slovenia	Minister of Agriculture, Forestry and Food – Republic of Slovenia	2015
Spain	Ministerio de Agricultura, Pesca y Alimentación	2015
Sweden	Swedish Board of Agriculture	2017
Switzerland	Contrôle officiel de la vendange des cantons	2015
Netherlands	Statistics Netherlands (CBS) – Dutch Central Bureau of Statistics	2013/2015
Turkey	Turkish Statistical Institute (TURKSTAT)	2015 2017 (Citrus and Olive)

(a): This designation is without prejudice to positions on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence.

Appendix I – Crops growing areas and areas of *Xyllela fastidiosa* climatic suitability

I.1. Olive

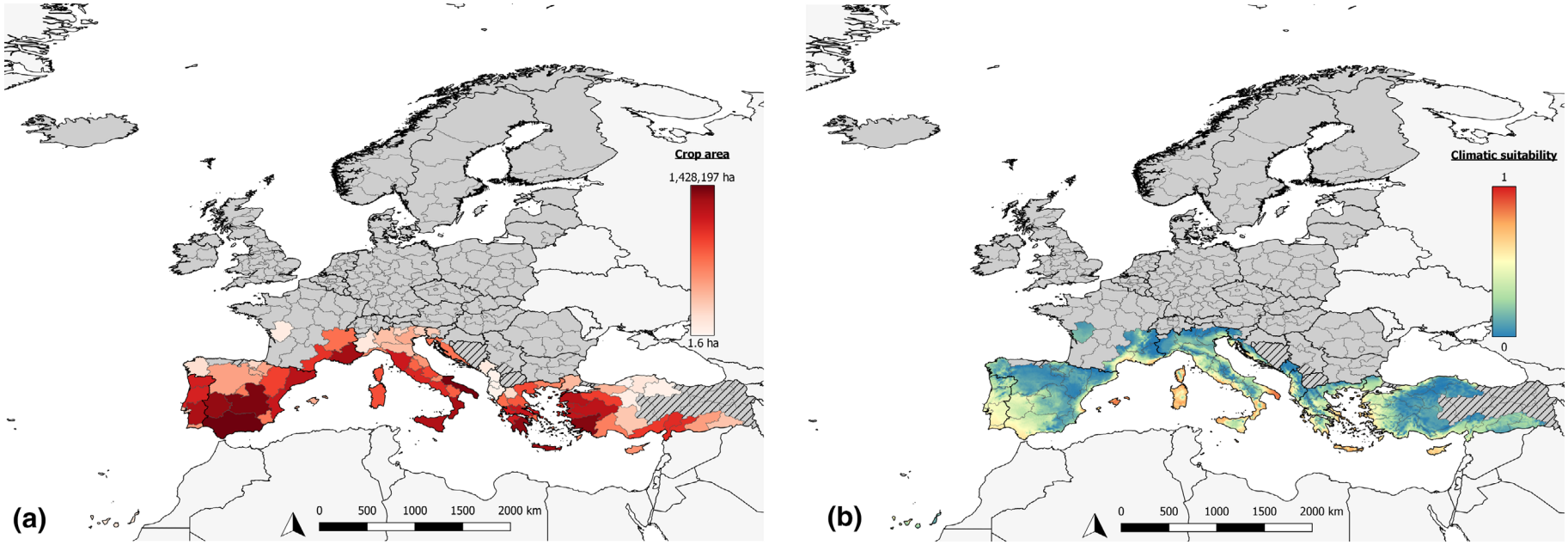


Figure I.1: Olive growing areas (left map) and levels of climate suitability of *X. fastidiosa* in the olive growing areas (right map). Statistic data of crop area at NUTS 2 level. In dark grey the regions and countries included in the analysis (see Section 2.1.1) but with no olive growing areas. Areas with lines indicate areas with no data. Areas in light grey are neighbour countries not included in the analysis

I.2. Almond

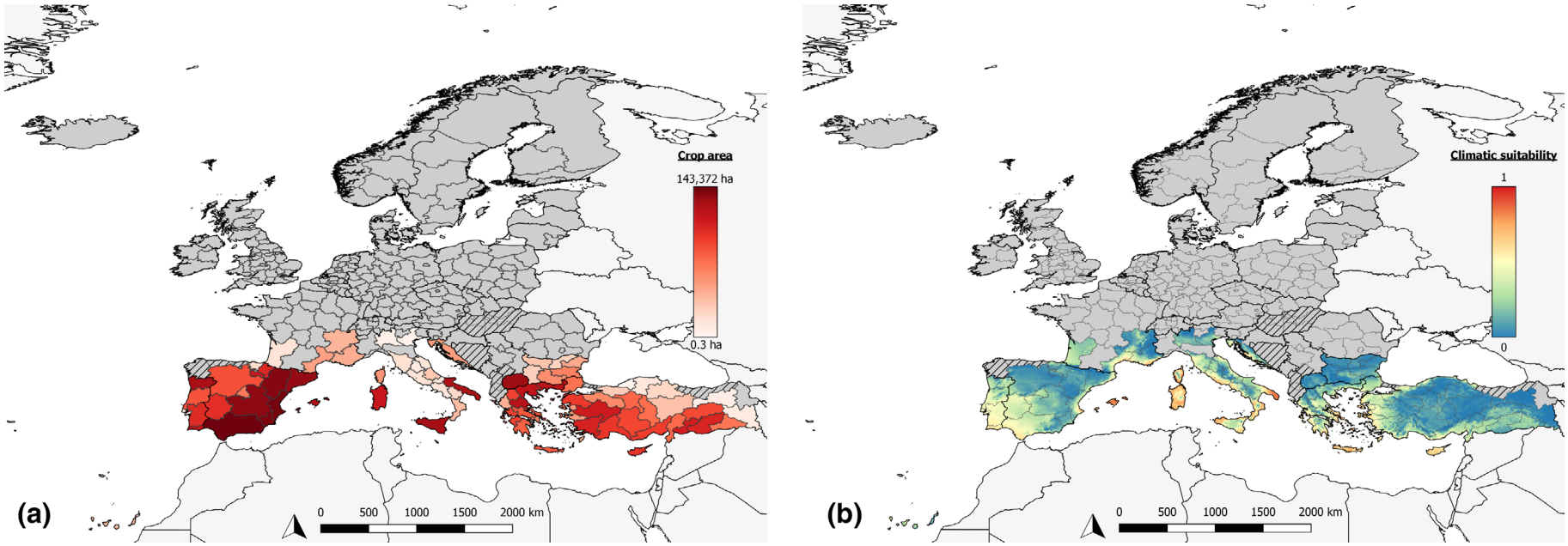


Figure I.2: Almond growing areas (left map) and levels of climate suitability of *X. fastidiosa* in the almond growing areas (right map). Statistic data of crop area at NUTS 2 level. In dark grey the regions and countries included in the analysis (see Section 2.1.1) but with no almond growing areas. Areas with lines indicate areas with no data. Areas in light grey are neighbour countries not included in the analysis

I.3. Grapevine

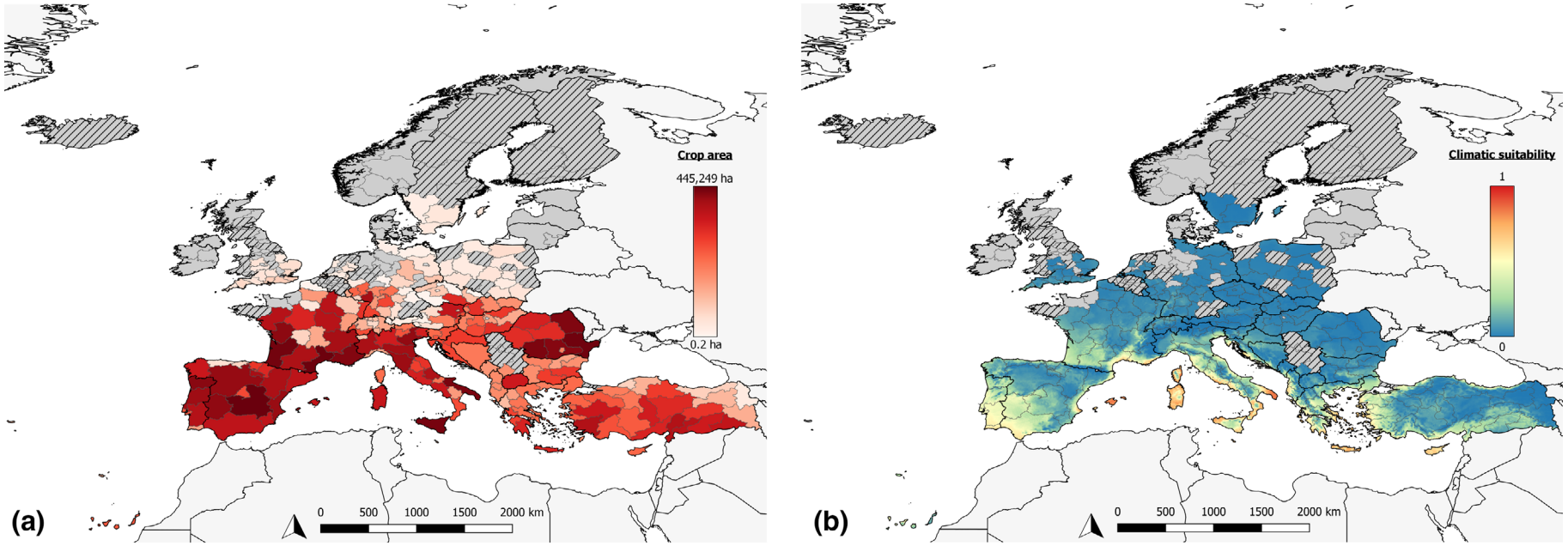


Figure I.3: Grapevine growing areas (left map) and levels of climate suitability of *X. fastidiosa* in the grapevine growing areas (right map). Statistic data of crop area at NUTS 2 level. In dark grey the regions and countries included in the analysis (see Section 2.1.1) but with no grapevine growing areas. Areas with lines indicate areas with no data. Areas in light grey are neighbour countries not included in the analysis

I.4. *Citrus* spp.

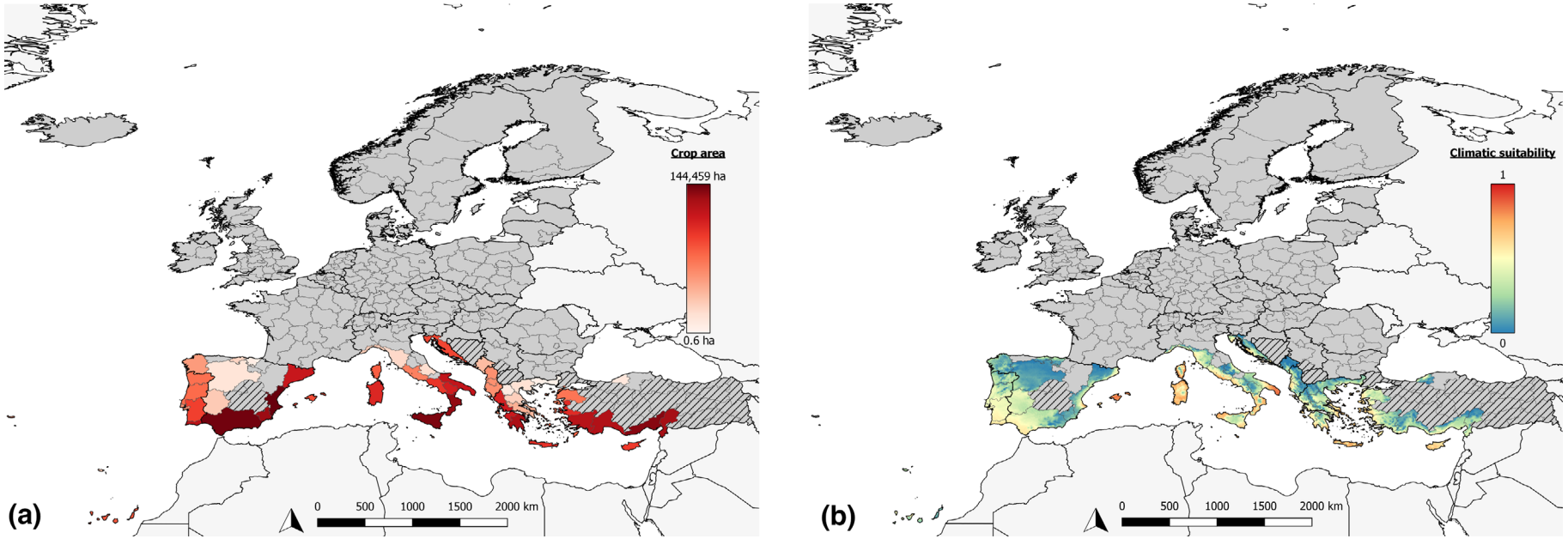


Figure I.4: *Citrus* spp. growing areas (left map) and levels of climate suitability of *X. fastidiosa* in the *Citrus* spp. growing areas (right map). Statistic data of crop area at NUTS 2 level. In dark grey the regions and countries included in the analysis (see Section 2.1.1) but with no *Citrus* spp. growing areas. Areas with lines indicate areas with no data. Areas in light grey are neighbour countries not included in the analysis

Appendix J – Asymptomatic period data table

Annex J can be found in the online version of this output ('Supporting information' section): https://efsa.onlinelibrary.wiley.com/doi/10.2903/j.efsa.2019.5665