Risk mapping of the likelihood and impact of a *Xylella fastidiosa* outbreak in Scotland

Samantha Broadmeadow[1], Kevin Watts[1], Chris Quine[1] and Ruth Mitchell[2]

[1] Forest Research, Centre for Ecosystems, Society and Biosecurity, Alice Holt Lodge, Wrecclesham, Farnham, Surrey, GU10 4LH, UK. Tel: +44 (0) 300 067 5626, www.forestresearch.gov.uk
[2] Ecological Sciences Group, The James Hutton Institute, Craigiebuckler, Aberdeen AB15 8QH, UK. Tel: +44 (0) 1224 395231,
www.hutton.ac.uk

Plant Health Centre
C/o James Hutton Institute, Invergowrie, Dundee DD2 5DA
Phone: +44 (0)1382 568 905
Email. info@planthealthcentre.scot; Web: www.planthealthcentre.scot

Final Report

Contents

1. Introduction

Xylella fastidiosa is a bacterial pathogen not currently found in the UK but a potential threat to many sectors of the Scottish plant-based economy, and the natural environment due to a wide host range and associated mortality. The Chief Plant Health Officer Scotland and the Plant Health Centre Directorate identified the need for Scotland-specific consideration of the threat of *Xylella fastidiosa*, so that the generic UK contingency plan could be refined to accommodate the Scottish scene.

Four subspecies of the bacterial pathogen *Xylella fastidiosa* are known to cause severe disease in a wide range of plant species, including important European crops such as *Prunus*, grapes, olives, rosemary and lavender and several species native to the UK.

In the USA, *X. fastidiosa* infection causes disease in a wide variety of street trees, including American elm, American sycamore, several oak species, maples and mulberry. Bacterial Leaf Scorch (BLS) was initially overlooked, but in the early 1980s *X. fastidiosa* was recognized as the pathogenic cause of symptoms very similar to those caused by abiotic stress. In New Jersey the incidence in some urban forests is as high as 35%. Symptoms manifest in late-summer and early autumn; typically, necrotic patches form on leaf tips and margins and leaves drop prematurely resulting in reduced crown density.

The pathogen was discovered for the first time in Europe in southern Italy in October 2013, and since the initial outbreak has spread across the Apulia region affecting >23,000 ha of olive trees (White et al., 2017).

In November 2018, as shown in Figure 1, *X. fastidiosa* infection has been reported in southern France, Corsica, Balearic Islands and mainland Spain (EU, Article 4(1) of Decision (EU) 2015/789 (UPDATE 10). It has also been reported in several non-EU countries and is of great concern throughout the Mediterranean basin. Currently *Xylella* is not known to occur in the UK.

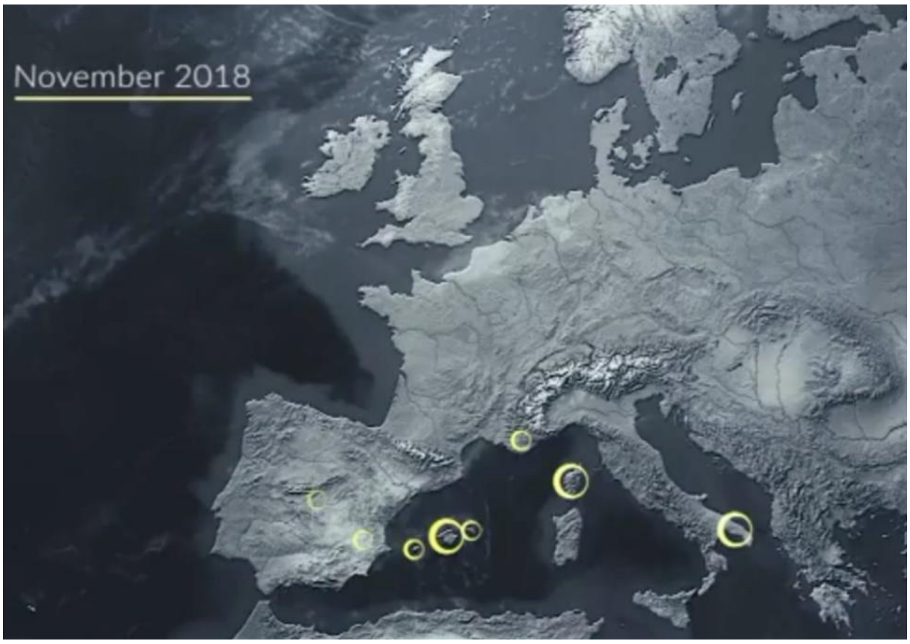

Figure 1 Distribution of demarcated areas established due to the presence of *Xylella fastidiosa*

The Scottish Government is preparing a contingency plan and preparedness measures for the possible arrival of the bacteria in the UK and is seeking information to help devise an effective response to a potential *X. fastidiosa* infection. This paper presents a broad-scale and spatially explicit risk assessment of *Xylella* infection to the key aspects of host-plant related concerns and businesses in Scotland; risk is taken to be the product of the likelihood of the event (arrival/establishment of Xylella) and the impact (on a range of values).

2. Objectives

- Consider the likelihood of arrival of *X. fastidiosa* in Scotland. Map the extent of suitable climate, host and vector species in the UK and Scotland
- Consider the potential impact of *X. fastidiosa* infection on the Scottish economy and ecology. Map the extent and distribution of vulnerable host species with high economic value and ecological significance
- Combine these maps to create a relative risk map

3 Mapping Approach

Published information on the biology of the *Xylella* pathogen, vectors and hosts were used to define potential environmental constraints on the spread of the disease. Distribution modelling for pathogen, vector and host species were applied to Scotland using the best available national spatial data, assessing the potential distribution of the species in geographical space based on their known distribution in environmental space (White et al., 2017).

Figure 2 attempts to illustrate the mapping approach used in this study. To assess the likelihood of *X. fastidiosa* infection; the climate range for *Xylella* (i) was defined using data from the USA where the pathogen has been well studied and compared to UK climate using long term meteorological data. The climate suitability for the disease in Scotland is represented by the blue circle in Figure 2. The potential host species (ii) in the UK remain highly uncertain; the extent and distribution of land cover likely to contain native species known to be susceptible was determined. The geographic range of landcover/plant communities which include potential host species is represented by the orange circle, and the extent of individual species vulnerability is illustrated by the black boxes in Figure 2. The bacterium is known to be transmitted by xylem-feeding insect vectors (iii). The common-meadow spittlebug was used as a model vector species and its environmental range in the UK was defined using records for the species in the NBN gateway. The geographic range of the vector is represented by the brown box in Figure 2. The area in which (i), (ii) and (iii) overlap defines the combined high-risk zone in which disease transmission is unlikely to be constrained by either climate or lack of insect vectors. The combined high-risk zone is represented by the yellow shaded area in Figure 2.

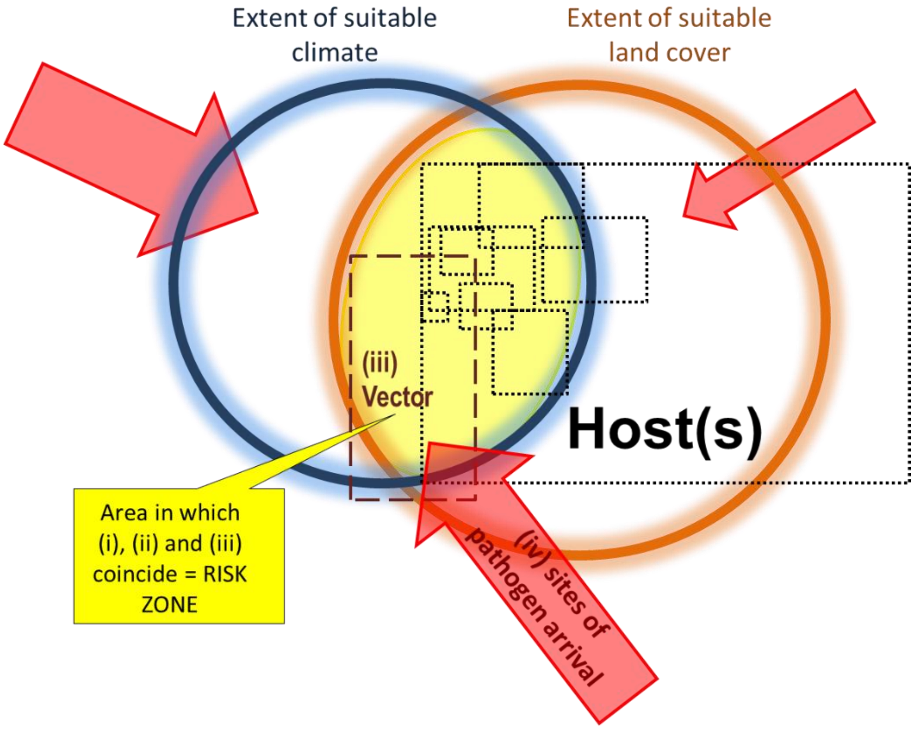

Figure 2 Representation of the mapping approach

The points of arrival and routes for distribution of potentially infected plant material (iv) are unknown at present although represented by the red arrows in Figure 2. Potential sources of infection have been considered to assess the risk in the wider environment and potential sites for monitoring and control.

The impact of potential infection on the Scottish economy and environment was assessed and mapped by comparing the extent and distribution of the combined high-risk zone to key locations for priority woodland habitat, designated landscapes, agricultural land use and horticultural trade.

4 Mapping the likelihood of *X. fastidiosa* infection

4.1 Climatic suitability for *X. fastidiosa*

4.1.1 The role of climate in controlling the distribution of *Xylella fastidiosa*

Until recently *Xylella* was largely restricted to tropical and sub-tropical regions of the Americas; although one strain is known to affect broadleaf trees in north eastern USA. The bacterium is characterized by genetic diversity, pathogenic plasticity and wide host range. Most strains of *X. fastidiosa* are sensitive to cold and climate is believed to play a key role in limiting the geographic range of *X. fastidiosa* diseases in North America. Most *Xylella* associated disease in USA occurs where winters are mild, such as south eastern US, and published risk models for *X. fastidiosa* are typically based on minimum winter temperature thresholds (Costello *et al*., 2017). The *Xylella* pathogen responsible for Bacterial Leaf Scorch (BLS) in urban Oak trees in the USA is cold-hardy and believed to over winter in trunks and roots of infected trees. BLS is endemic in New Jersey and New York has been reported as far north as southern Ontario (APS, 2018).

Based on the current distribution and extent of *X. fastidiosa* in Europe and climate data from the WorldClim database the apparent temperature threshold for the pathogen is a winter minimum of between 1.1 - 4.5 ºC (Cendoya *et al.,* 2018). However, the spread of disease is currently being controlled by co-ordinated rigorous monitoring and control strategies (White *et al.*, 2017) and it is too soon to be confident of the role of climate in controlling the spread of the disease in Europe (Bosso *et al*., 2016).

In north east USA, BLS is a widespread disease of urban trees infected with *Xylella fastidiosa* subsp. *multiplex*. In the north, infected street trees are reported to be slow to develop symptoms and may even remaining asymptomatic (Henneberger et al 2004). Elsewhere, Pierce's Disease of grape infected with *X. fastidiosa* subsp. *fastidiosa* affects vineyards from Florida to California, in the USA, and Central and South America. Pierce's Disease is less prevalent in areas with severe winters (Purcell, 1977). In northern California infected vineyards were reported to recover after a cold winter (Lieth *et al*., 2012). Purcell and Feil (2201) published a risk map to predict the severity of Pierce’s Disease in grapevines based on minimum winter temperature thresholds (Table 1).

Pierce’s Disease risk to grapevines	Winter minimum
No risk	<-1.1 °C
Low risk	-1.1 – 1.7 °C
High risk	1.7 - 4.5 °C
Severe risk	>4.5 °C

Table 1 Winter minimum temperature risk thresholds to predict the severity of Pierce’s disease in grape vines (Purcell and Feil, 2001).

For the current project, Purcell and Feil’s temperature thresholds have been applied to the UK, to determine the potential risk of disease caused by a *Xylella* pathogen in the UK Figure 3. The Met Office observed climate data, long term monthly mean temperature for December, January and February were used to determine the frequency of effective cold sanitation, when winter minimum temperature reach -1.1 ºC.

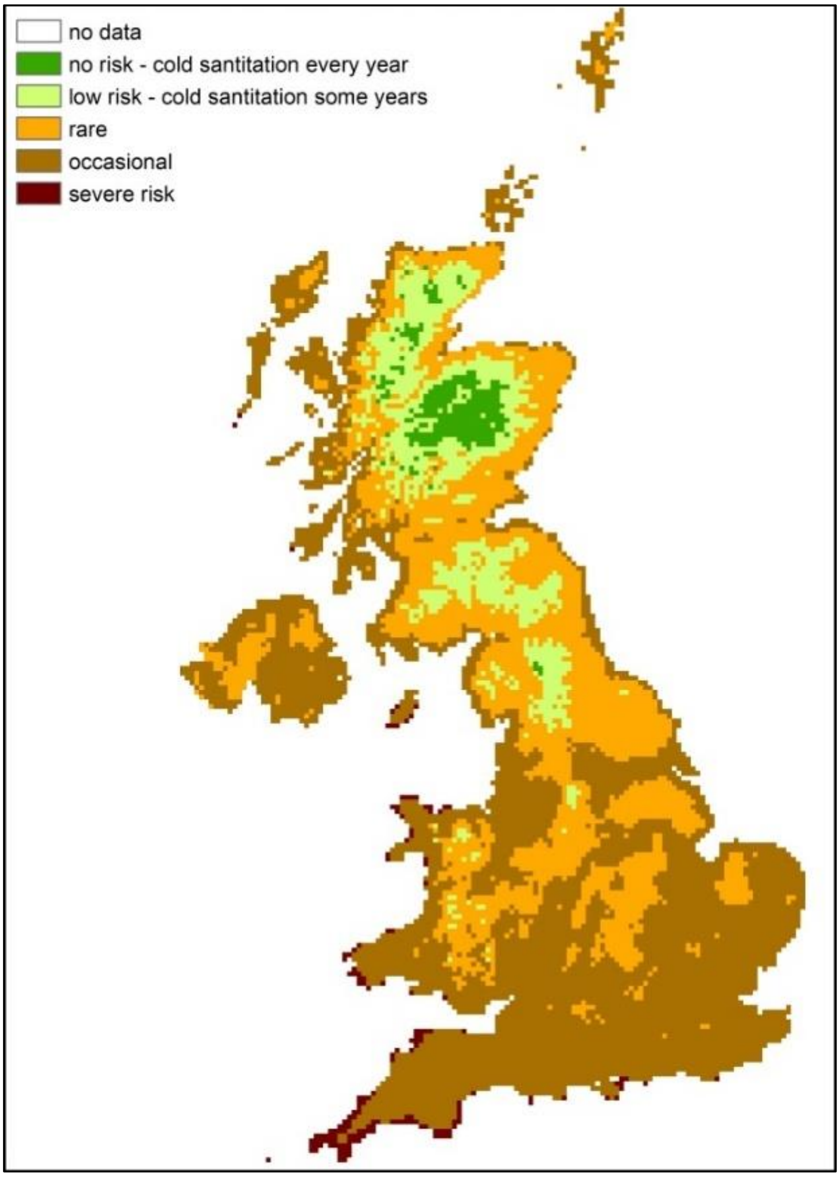

Figure 3 Potential climate risk for the *Xylella fastidiosa* pathogen in Scotland based on 'seasonal sanitation' temperature thresholds for Pierce's disease in grapevines. Source data: UK Met Office winter min temp (1961 - 1990; 1971 – 2000 and 1981 – 2010).

The temperature distribution suggests that the current climate in the Scottish uplands appears to be too cold for *Xylella* to persist through the winter, although it is highly uncertain how relevant the risk thresholds for *X. fastidiosa* subsp. *fastidiosa* in Californian vineyards are for Scotland, where the pathogen strain and host species may be different.

4.1.2 Climate suitability for *Xylella fastidiosa* in Scotland

Defra (2017b) updated the *X. fastidiosa* risk to plant health in the UK by comparing the climate of the northern distribution limit of the pathogen in the USA and the UK using the global Köppen-Geiger climate classification (Kottek *et al*., 2006). *X. fastidiosa* has been reported in areas characterised by a wide range of Köppen-Geiger climate types. Most disease localities have a temperature climate but *X. fastidiosa* has also been reported from sites with a tropical, arid and cold climate. Figure 4 illustrates that the climate of New Jersey and southern Ontario, which form the northern limit of *X. fastidiosa* in the USA, is classed as 'Dfa' which is a Cold climate (seasonal snow) with no dry season and warm summers, whereas the climate is classed as 'Cfb', a Temperate climate with less winter snow, except for upland Scotland which is classed as 'Cfc' due to the cool summers. The European Food Safety Authority (EFSA) Panel on Plant Health conclude that most climate types in the EU, including that of the UK, are suitable for the establishment of *X. fastidiosa* (EFSA, 2019).

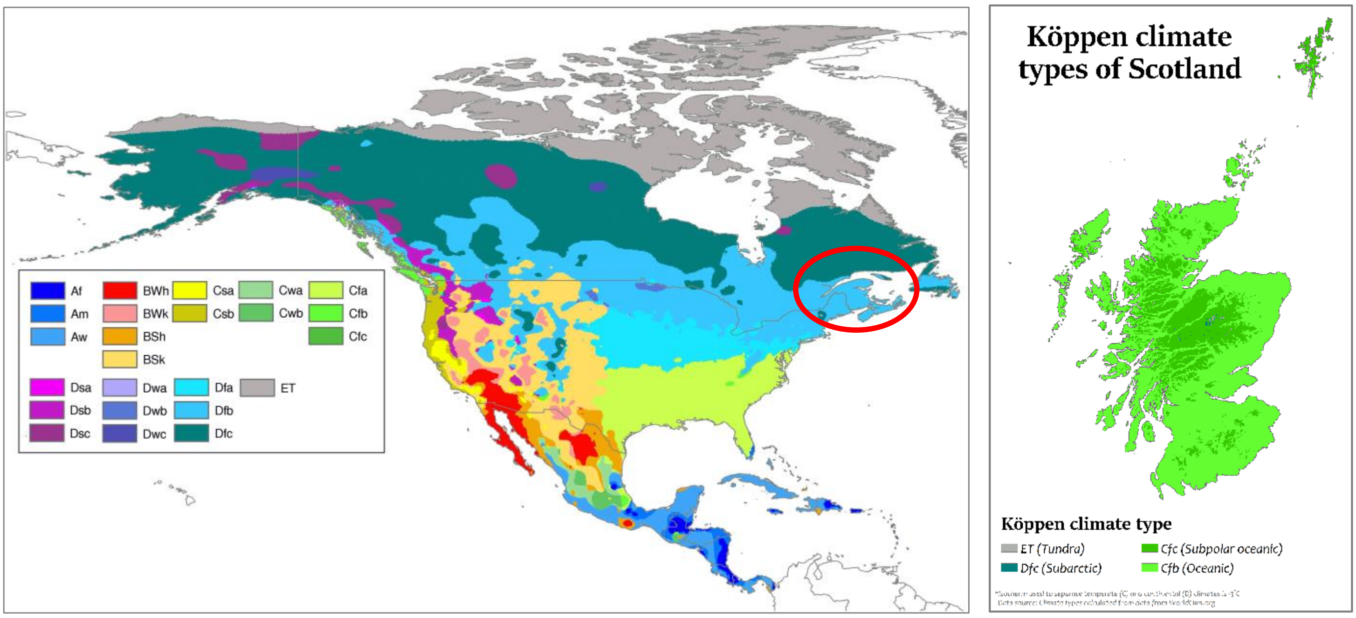

Figure 4 Scottish climate compared to the climate across the USA and Canada as represented by the global Köppen-Geiger climate classification. The Red circle represents the northernmost limit of *Xylella fastidiosa* subspecies *multiplex*. Adam Peterson (CC BY-SA 4.0; https://commons.wikimedia.org/w/index.php?curid=50252806)

In 2017, DEFRA concluded that *X. fastidiosa* subsp. *multiplex* presents the greatest threat to the UK as none of the other subspecies have been found in temperate climates, and the UK has much milder winters and cooler summers than those at the northern-most limits of its distribution in North America, which are characterised by seasonal snow cover. The previous risk assessment, that the pathogen is "unlikely to moderately likely" to become established in the UK, was confirmed as sound and the potential to cause economic, environmental and social impacts remains "small" (DEFRA, 2017b). Recent work, using the species distribution model (SDM) technique, has assessed the effect of climate on the current distribution of *X. fastidiosa* sub-species in the EU (EFSA, 2019). The modelling results suggest the risk is greatest in southern coastal Europe, through southern France and the Atlantic regions of southern Portugal and France. The relative risk that *X. fastidiosa* can establish in the UK is low; however, small areas on the south coast of England are mapped as marginally suitabile in the general *X. fastidiosa* species map. A wider extent of the coastal regions in the UK, including Scotland, are included as marginally suitable for *X. fastidiosa* subsp. *Multiplex,* which had the highest extent of suitable climate in the EU. The modelling suggests that the climate variable having the greatest control on the potential distribution of the *X.f* subspecies *fastidiosa* and *X.f* subspecies *multiplex* was the mean temperature in the coldest quarter of the year, whereas for the *X.f* subspecies *pauca,* it was the minimum temperature of the coldest quarter. This suggests in areas of Scotland where winter temperatures are low the climate may provide an effective check on the speed of spread and ultimate distribution of the disease.

The Köppen-Geiger climate classification is designed for global datasets and masks much of the spatial variation in climate within the UK. Figure 5, below, illustrates a more spatially refined classification of UK climate using national data from the Met Office. The map on the left shows the UK climate zones used in the Forestry Commission, Ecological Site Classification (Pyatt and Suarez, 1997) using two climate variables, accumulated temperature and soil moisture deficit. The ESC climate zone thresholds are presented in Table 2.

ESC Climate Zone	Accumulated temperature (Day degrees >5°C)	Moisture Deficit (mm)
Sub-alpine	<575	<60
Cool wet	575 - 1,200	<20-90
Cool moist		90-160
Warm wet	1,200 - 2,400	<20-90
Warm moist		90-160
Warm dry		160-260
Very warm moist	2,400 - >3,000	90-160
Very warm dry		160-260
Very warm arid		260->320

Table 2 ESC temperature and soil moisture thresholds for the climate zones used to illustrate the current (baseline) climate and UK Met Office climate change predictions (2080 high emission scenario) presented in Figure 5.

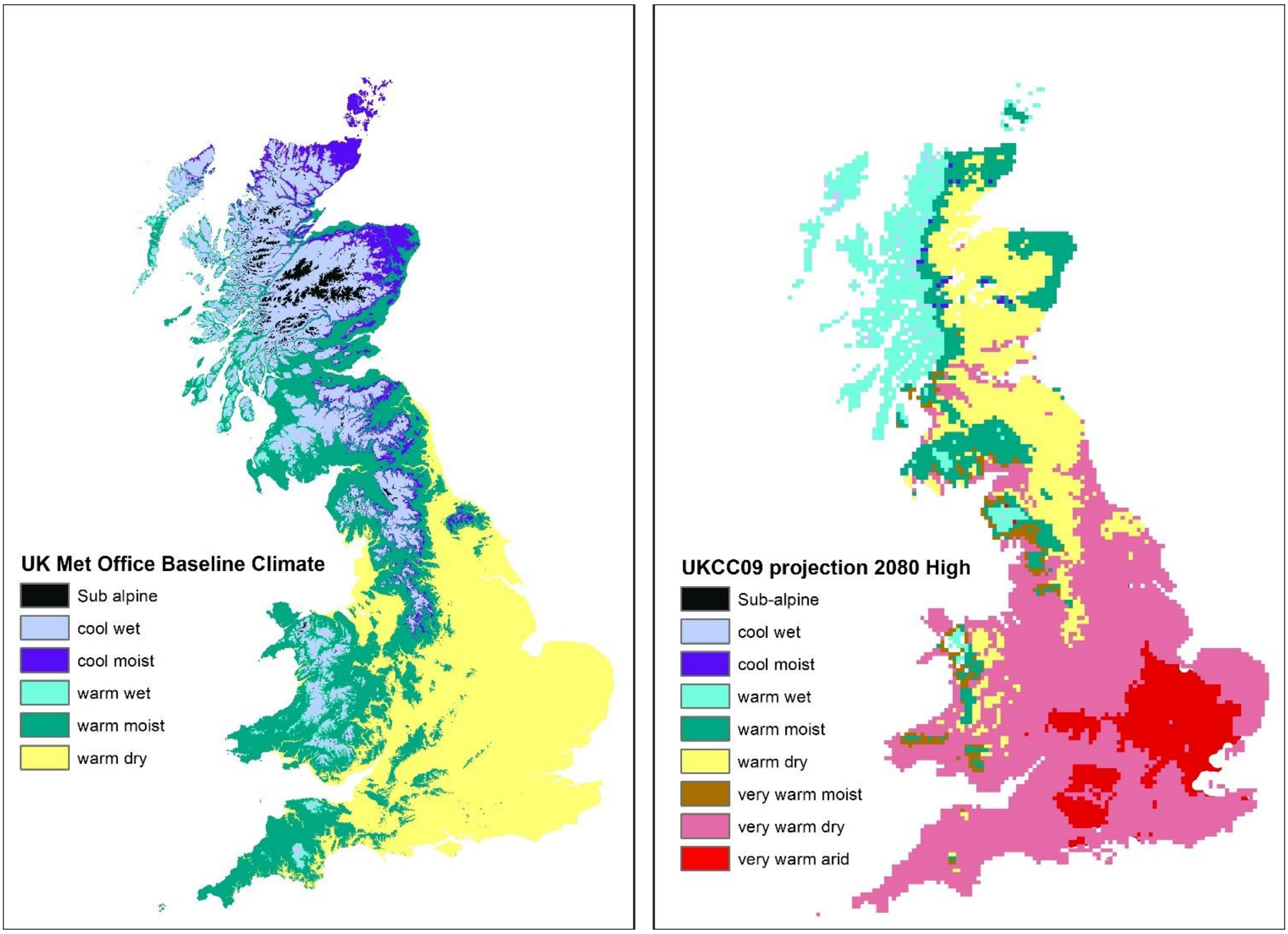

Figure 5. ESC UK climate zones defined using Met Office* observed annual climate mean and predicted climate for 2080. The map on the left illustrates the distribution and extent of current UK climate zones defined by the baseline long term data (1960-1990) and the map on the right shows the distribution and extent of UK climate zones following the impact of predicted climate change by 2080. *The data did not include Shetland, so it is not shown on these maps.

As shown in the baseline map (left) the Scottish climate is cooler than southern England; however, across the coastal margins of southern Scotland the accumulated temperature is similar to south west England and much of Wales. Thus, if the *Xylella* pathogen was to be become established in England it may also survive in the current climate of the coastal region of south and central Scotland.

Many authors report a link between climate (particularly temperature) and disease spread suggesting *Xylella* symptoms are more severe in warm conditions (reviewed in, Daugherty et al, 2017) and can be checked by cold winters (Purcell, 1977; Henneberger et al 2004; Ledbetter et al 2009). The interactions between climate & pathogen and climate & vector behaviour have not been studied in a temperate climate so the consequences of predicted climate change are highly uncertain. As illustrated in Figure 5 the climate of central and eastern Scotland is predicted to become at least as warm and dry as southern England by 2080. Predicted climate change across England, Wales and in to southern Scotland suggests temperatures will rise to become as warm as southern France and northern Italy suggesting the UK is at increasing risk from *Xylella*.

4.2 Potential host plants for *X. fastidiosa* in Scotland

X. fastidiosa infects a wide range of tree, shrub and herb species in the Americas from Argentina to Canada. Several subspecies and strains of *X. fastidiosa* are known to cause disease but the mechanism leading to host plant specificity is poorly understood leaving high uncertainty regarding potential host species in the European flora. EFSA maintains a list of host plants on which *X. fastidiosa* has been observed. The list includes both naturally and experimentally infected host plants and includes 359 species from 204 genera and 75 botanical families. https://ec.europa.eu/food/plant/plant_health_biosecurity/legislation/emergency_measures/X._fastidiosa-fastidiosa/susceptible_en.

Many species native to southern Mediterranean are potential hosts for the pathogen. Most species are not native to the UK and those that are native are typically of warmer climates and restricted to southern Britain. Appendix 1 includes all UK species known to be susceptible to *X. fastidiosa.* Many of the high risk susceptible non-native species (Defra 2018b) such as olives, rosemary, lavender and flowering cherries, are grown widely in gardens and used in landscape planting. There are also important, common and widespread species (genera) found in Scottish woodland (*Acer pseudoplatanus*, *Prunus avium*) and agriculture (*Brassica*, *Daucus carota*) including several grass and grain species (*Avena fatua*) and arable weeds (*Chenopodium album*).

4.3 Disease spread and potential vectors for *X. fastidiosa* in Scotland

Xylella fastidiosa is a rod-shaped bacterium that lacks flagella for motility and dispersal occurs via sap feeding insect vectors. The *X. fastidiosa* bacterium lacks vector specificity, thus all sap feeding species, such as leaf hoppers, sharp shooters and spittlebugs, are potential vectors and many of these are common and are widely distributed. *X. fastidiosa* bacteria persist as a biofilm in the insect foregut (APS, 2018) and can be transmitted to new hosts by both nymphs and adults. A key diagnostic feature of BLS is the random development of disease symptoms within the crowns of infected trees suggesting that the disease is not spread directly from tree-to-tree (APS, 2018). A second potential route of infection is via vegetative propagation; *X. fastidiosa* is known to persist in root grafts of almond, citrus, grape, peach.

Due to the relatively recent emergence of the *X. fastidiosa* threat in Europe, there is no consolidated data on which potential insect vectors are most likely to transmit disease.

Currently two EU funded projects (PONTE and XF-Actors) are working on this. ANSES (the French agency for food, environment and occupational health) identified 50 potential vector species in France, most of which are also known to occur in the UK. Only two of the potential vectors identified by ANSES for *X. fastidiosa* are known to use oak or ash in the UK; they are *Ledra aurita* which is widespread in England and *Cicadetta montana* which is currently restricted to the New Forest. The UK BRIGIT research programme, on vector-borne disease of plants, will investigate the geographic distribution and migration, genetic population structure and host specificity of 20 xylem-feeding insect species which may transmit *X. fastidiosa* in the UK. However, the project only started in 2019 and currently there remains considerable uncertainty as to the behaviour of potential vector species in Scotland [Note - some early insights are provided by the PHC project commissioned at the same time as this study – Park *et al.,* 2019, reference PHC2018_06].

4.3.1 Spittlebug *Philaenus spumarius* (L.) as a model insect vector species in the UK

In Europe, the meadow spittlebug *Philaenus spumarius* is the only epidemiologically relevant vector of *X. fastidiosa* identified as responsible for bacterial transmission. Recent surveys in southern Italy revealed *P. spumarius* migrate seasonally between patches of herbaceous ground cover in olive groves and adjacent pine and oak trees. However, *P. spumarius* has not been recorded in either the OakEcol or AshEcol databases, so there are no records of *P. spumarius* feeding in these tree species in the UK (Mitchell et al., 2014).

In this project, *P. spumarius* has been used as a model vector species because it is a common species across most of Europe and widespread in north Africa, Russia, Afghanistan and Japan. The species can tolerate a wide environmental range and lives in almost all open habitats including meadows, parks & gardens, wayside & arable wasteland, marshland, streambanks and open woodland. They are absent only in very wet and very dry habitat. The species is polyphagous and has been recorded feeding on over 170 host plants including grass and tree species but particularly herbaceous legumes with high amino acid concentrations in the xylem sap (Yurtsever, 2000). Sap feeding insects typically only fly short distances though they may be carried further in windy conditions. Unusually, *P. spumarius* is a strong flier and both male and female can fly >1 km in less than 1 h continuous flight (Yurtsever, 2000).

4.3.1.1 Climate envelope for *Philaenus spumarius* (L.) in the UK

The National Biodiversity Network (NBN) online atlas provides data on species distribution in the UK. It should be noted that the NBN data includes systematic survey data and ad hoc reports and is thus subject to recorder bias as there is likely to be fewer records from areas of low human population density. There are 4,553 records of *Philaenus spumarius* in the NBN database and the distribution of these in Scotland is shown in Figure 6. The distribution of *Philaenus spumarius* in the dataset did not exactly mirror that of the Scottish population (illustrated in Figure 9) and was sufficiently independent to be suitable data source for this project. The NBN database was used to reclass the UK climate data in terms of apparent climate suitability for *P. spumarius;* Table 3 reports the number of *P. spumarius* site records within each UK climate zone.

Accumulated temperature	**Wind exposure**	**Soil Moisture deficit**		
		Dry	**Moist**	**Wet**
Sub Alpine	Severe			
	High			6
	Moderate			14
	Sheltered			1
Cool	Severe			26
	High		13	75
	Moderate		59	139
	Sheltered		78	127
Warm	Severe		7	5
	High		96	14
	Moderate	314	739	25
	Sheltered	1,661	1,134	20

Table 3 Distribution of records for *P. spumarius* in NBN database between UK climate zones

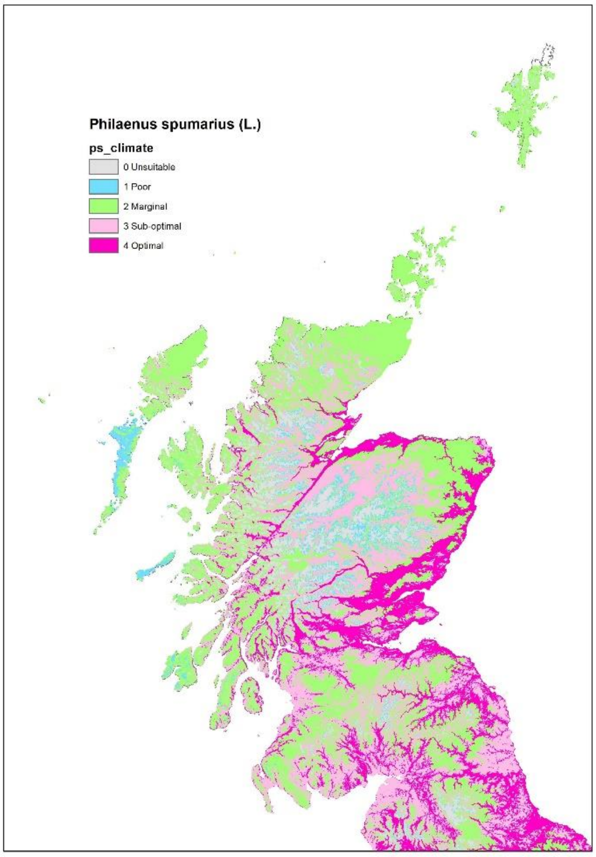

Figure 6 Recorded distribution of *Philaenus spumarius* (NBN Gateway) used to reclass the climate data in terms of apparent climate suitability for the model sap feeding insect vector. National UK datasets were used in the analysis and a subset of the map is displayed to show Scotland more clearly.

The optimal conditions for *Philaenus spumarius* in the UK are:

- Annual accumulated temperature (>5°C) mean 1,600°C ± 294; medium 1,674°C. [Warm].
- Moisture deficit (mm) mean 149 ±43 mm; medium 154 mm. [Dry]
- DAMS score (Detailed Aspect Method of Survey = exposure to wind) mean 12 ±2; medium 12. [Sheltered].

Insect vectors are more commonly found in sites that are warm, sheltered and dry or moist. Records are less common in areas which are cold or exposed. It was assumed such sites are less suitable for sap feeding insects and therefore the risk of disease spread in such areas is also reduced.

4.3.1.2 Landcover preferences of *Philaenus spumarius* (L.) in the UK

An attempt was made to assess the relative risk of disease spread into the Scottish landscape via a polyphagous sap feeding insect vector. The Landcover 2007 data was used to determine the broad habitat type for each NBN record site. The table below illustrates the distribution of NBN records between habitat types (details of the grouping are provided in Appendix 2). Habitat suitability for *P. spumarius* was determined using the ratio between the proportion of NBN records and proportion of UK area for each Habitat. In the NBN database 22.5% of the records for *P. spumarius* are from sites with improved grassland habitat, which is more than any other land cover; however, improved grassland is also the most abundant land cover in the UK, so this is not unexpected. The high incidence of *P. spumarius* records from urban/suburban sites may suggest that parks and gardens provide good habitat for the cuckoo spit and/or its observers.

Habitat type	**% of NBN records**	**% land cover**	**ratio**	**Relative risk**
Suburban and urban	8.9	3.1	2.87	Not included in map
Deciduous woodland	11.5	7.4	1.55	High
Improved grassland	22.5	15.2	1.48	
Arable	17.9	13.7	1.31	
Native grassland	13.1	10.5	1.25	
Conifer	7.8	7.5	1.04	Medium
Heath	6.8	11.2	0.61	
Wetlands and water margin	5.3	13.1	0.41	Low
Sand dune and coastal habitat	3.5	8.6	0.41	
Other – montane, saltmarsh & unvegetated habitats	2.7	9.8	0.28	No risk

Table 4 Distribution of NBN Gateway records for *P. spumarius* between habitat type.

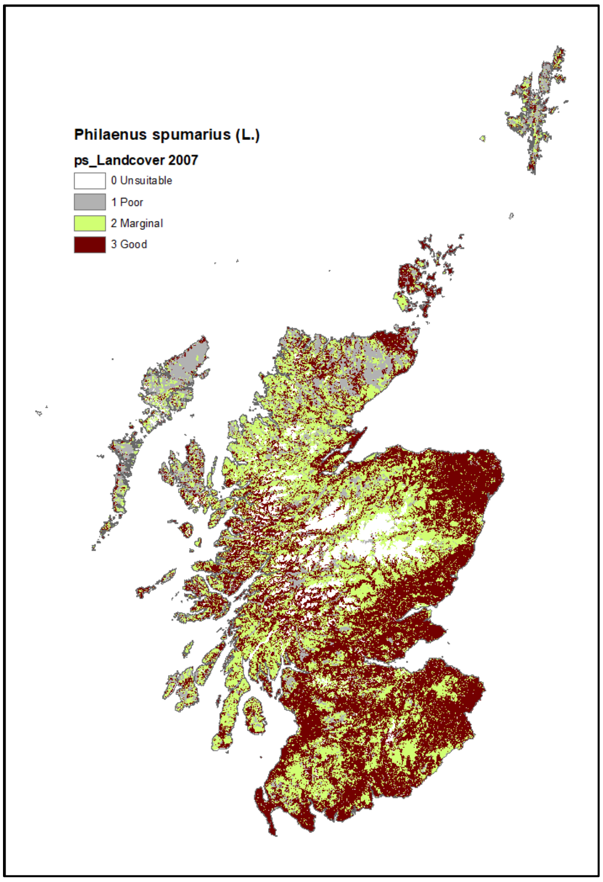

Figure 7 The landcover suitability classification for *Philaenus spumarius*.

It was assumed that the preferred habitat types, such as deciduous woodland and improved grassland, would support large populations of insect vectors and represent the greatest risk of disease spread; conifer forest and heathlands provide good habitat and present a medium risk. Whereas the marginal habitat types, wetlands and sand dunes, present a low risk and montane habitat presents no risk of disease spread by this vector.

The climate and landcover derived risk maps were combined to define the relative risk of disease spread through the landscape via sap feeding insects (Figure 8). The combined high-risk zone (shown in purple in the map on the right) is defined by the area where climate and land cover are both highly suitable for *Philaenus spumarius* and there is no check on the insect vector population and potential spread of disease.

It would have been preferable to refine the combined high-risk zone using a climate suitability map for the pathogen (like that presented in Figure 5). However, there is low confidence that the observed thermal threshold for Pierce's disease in grape are relevant for potential Xylella disease in Scotland, so the combined high-risk zone has been left unmodified as it defines well the environmental space for the most likely insect vector *Philaenus spumarius* in the UK.

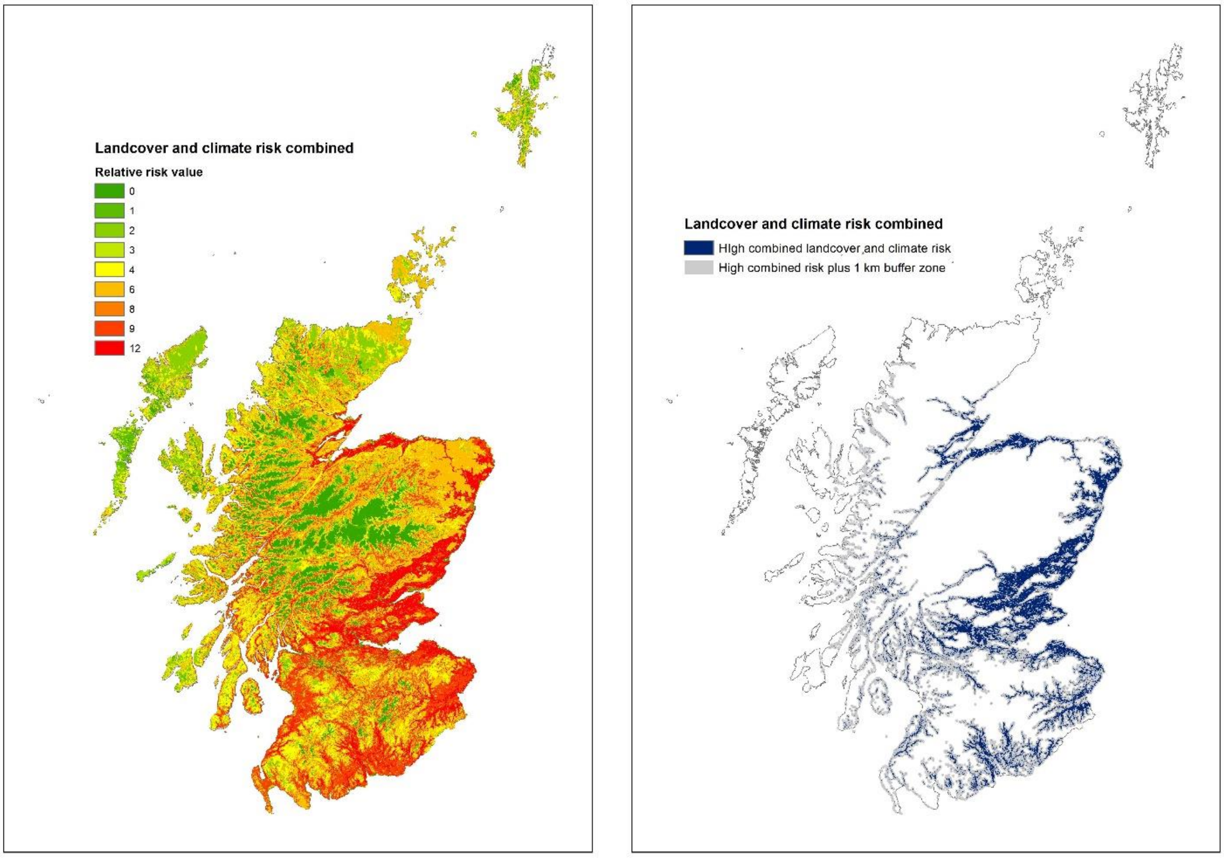

Figure 8 The combined high-risk zone defined by the combined landcover and climate suitability for sap feeding insects (which might act as vectors of *Xylella*) includes 25,618 km^2 and covers 32.4% of Scotland

4.4 Risk of importation

Defra recognise the horticultural trade in plants grown in the EU poses a risk to plant health in the UK and, to minimize the risk of importing pathogens, the trade in host species is now controlled. As of September 2018, plant growers, suppliers and retailers of 76 high risk host species must ensure their stock has been inspected and is accompanied by a plant passport. Defra identified nine host species which present the highest risk from *Xylella* to plant health in the UK: *Polygala myrtifolia*, *Olea europaea*, *Rosmarius officinalis*, *Nerium Oleander*, *Spartium junceum*, Lavenders, *Prunus*, *Hebe* and coffee (Defra, 2017); most of which the RHS (Royal Horticultural Society) advise are hardy in Scotland. The registered nurseries should prevent the diseases spreading, as they have responsibility and expertise to check and report disease symptoms, but a system failure (including shipment of asymptomatic plants) may lead to *X. fastidiosa* being introduced to trade pathways and potential escape into wild habitat.

The quantity and pattern of trade in horticultural garden plants reflects the population density across Scotland as garden centres and nurseries are located close to their customers. Figure 9 illustrates the distribution of retail outlets for potentially infected host species in Scotland.

The forest nursery trade is another potential route. The UK imports considerable numbers of bare root trees, particularly hedging stock of hawthorn, hazel and blackthorn. The demand for new trees from the Scottish forestry sector is estimated to be between 55 – 59 million per year (information provided by Confor Nursery Group Dec 2018). This includes planting material required to restock the managed forest estate (predominantly conifer) and new woodland creation schemes (mixed conifer and broadleaf). Forestry Commission nurseries supply 68% of the trees used in the UK Public Forest Estate, the rest is largely sourced from private UK nurseries and currently <5% are sourced from imported stock. The most commonly imported tree species for use in forestry are beech, birch and alder. There are 10 Forest Reproductive Material suppliers in Scotland registered to import tree seeds and seedlings and 20 Scottish registered forest traders. Imported material may be retained amongst other stock before sale or use. From these sites, predominantly in the east of Scotland, young trees will be transported for sale or use elsewhere in the country.

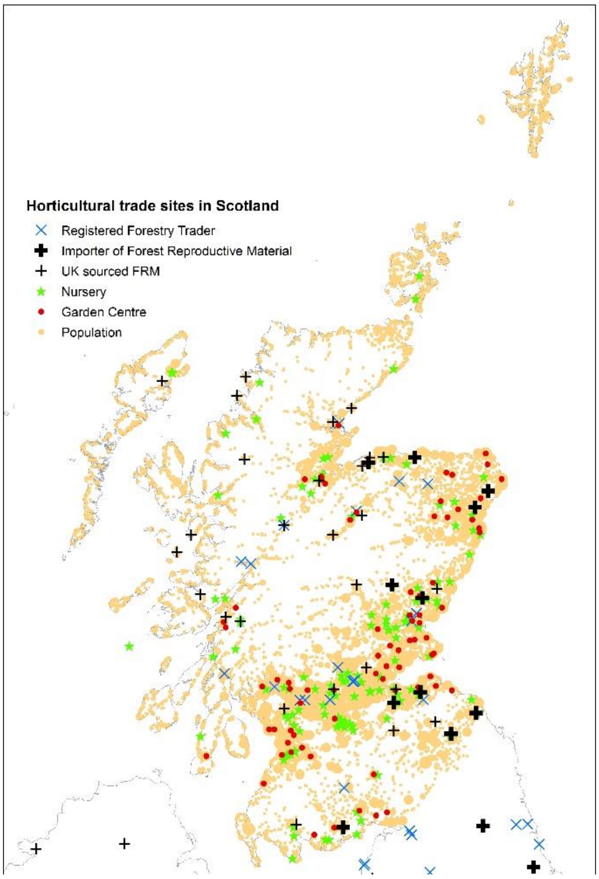

Figure 9 Distribution of horticulture and forestry plant traders in Scotland.

There remain significant evidence gaps in the scale, extent and routes of international trade. The extent of trade from Europe and across the world into Scotland via England and the rest of the UK is not known; this has recently been evidenced by the spread of Oak processionary moth on imported large oak trees from Netherlands and Germany). It is also important to better understand the scale of horticultural export trade from Scotland. There is a risk that asymptomatic *X. fastidiosa* infection in horticultural (herbaceous) plants raised in UK may severely affect export from plants from Scottish nurseries; six Scottish Forest Reproductive Material suppliers are registered as exporters.

5 Mapping the impact of *X. fastidiosa* infection

5.1 Potential impact of *X. fastidiosa* infection to Scottish biodiversity

The EU list of host plant species known to be susceptible to European strains of *Xylella* (Appendix 1) includes native tree species (sycamore - *Acer pseudoplatanus* L., cherry - *Prunus avium* L. and plum - *Prunus domestica* L.) and genera (ash - Fraxinus, oak – Quercus and willow – Salix). The recent Action Oak review (Appendix 4) reports that a phylogenetic clade within subsp. *multiplex* is known to affect a wide range of oak species, including *Quercus robur* (Nunney, *et al*., 2013).

To assess the potential impact of *Xylella* infection on native woodland the current distribution of designated (Figure 10) and priority (Figure 11) woodland habitat was compared with the extent of the combined high-risk zone. The statistics are reported in Table 5; 40.7% of woodland mapped in the National Forest Inventory falls inside the combined high-risk zone. This zone includes 51% of the native woodland in Scotland, of which 23,371 ha is designated native woodland.

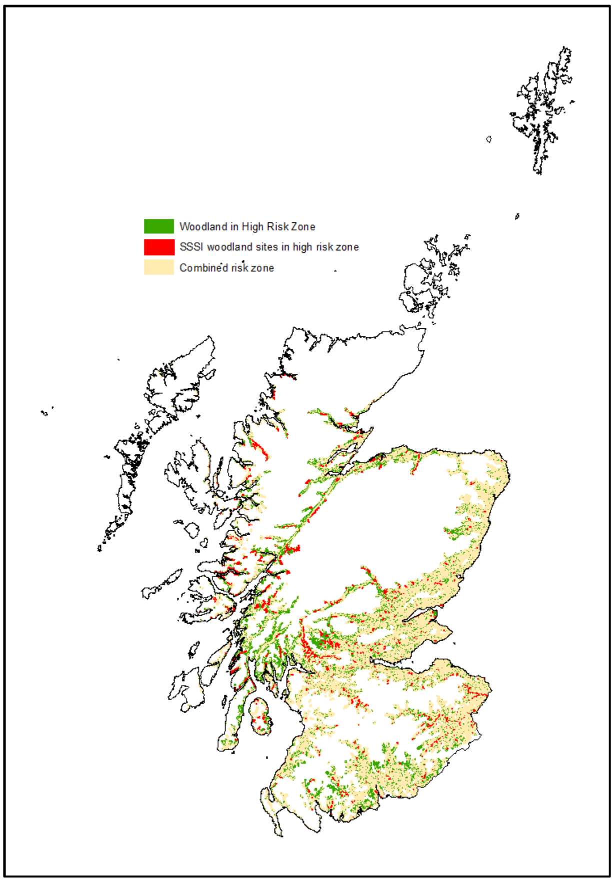

Figure 10 The extent of woodland cover in the combined high-risk zone and the distribution of designated woodland sites, shown in red.

Designation	Area (ha) within combined high-risk zone	% Designation
SAC	54,623	8.4
SSSI	113,269	11.6
NNR	18,090	10.5
National Park	14,533	16.4
National Scenic Area	205,315	14.9
National Forest Inventory	583,849	40.7
Native Woodland	150,866	51.0
Agricultural Land Grade 1 & 2	172,007	96.1

Table 5 The extent of conservation and landscape designations within the combined high-risk zone

Some native woodland stands may contain few species which are susceptible to *Xylella* but several woodland communities have assemblages in which vulnerable species are likely to occur. In lowland mixed ash (NVC W8) and oak (NVC W10) woodland *Rosa canina*, *Prunus avium* and *Acer pseudoplatanus,* which are all potential host species, are likely to be present. Forestry Commission Scotland (now Scottish Forestry) mapped the site suitability for individual NVC communities to target native woodland expansion in the Scottish Rural Development Programme 2014 – 2020. These maps have been used to predict areas of the W8 and W10 woodland in the broadleaf woodland of the National Forest Inventory.

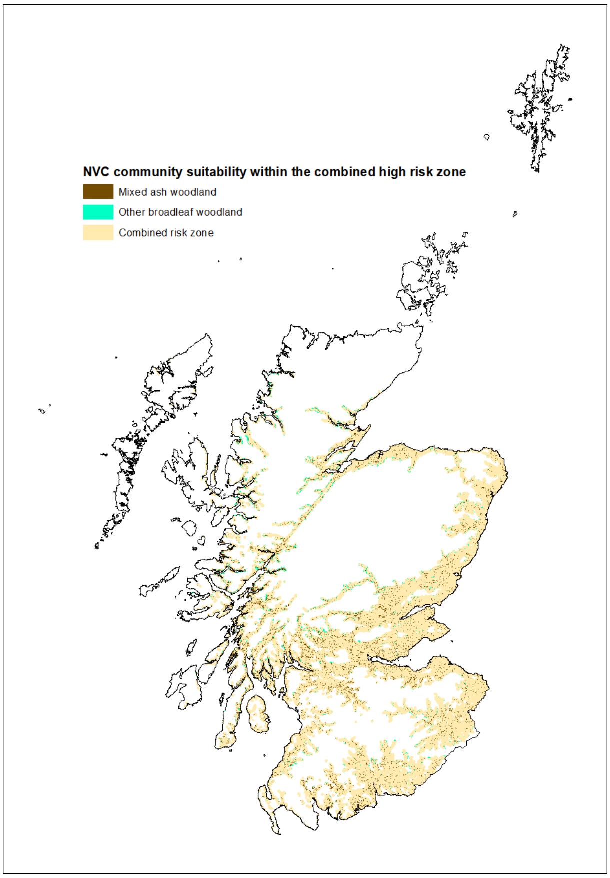

Figure 11 The extent of broadleaf woodland in the combined high-risk zone. Mixed ash woodland (NVC W8), shown in brown in the map, typically includes several species known to be susceptible to *Xylella* infection.

5.2 Potential impact of *X. fastidiosa* infection on Scottish agriculture and economy

About 15% of Scotland, 13,340 km², is forested. The biggest forest areas are in Dumfries and Galloway, Tayside, Argyll and the Scottish Highlands. Scottish forestry is dominated by Sitka spruce, with some Scots Pine, Norway Spruce and Douglas Fir. None of the key conifer species are known to be vulnerable to diseases caused by *Xylella*; however, many broadleaf tree species are known to be susceptible. A potential threat to forestry is the use of sycamore as a nurse crop in stands of oak and beech in broadleaf plantations.

The agricultural value of the land within the combined high risk zone using the Land Capability for Agriculture in Scotland classification (MLURI, 2010) is illustrated in Figure 12. The LCA ranks land on the basis of its soil and climate to indicate the potential productivity and cropping flexibility. There are seven classes in Scotland with Class 1 land has the highest potential flexibility of use whereas Class 7 land is of very limited agricultural value. Less than a quarter of Scotland is suitable for crop cultivation; the combined high-risk zone includes most of the land in Scotland capable of supporting arable agriculture (100% of Class 1; 96% of Class 2 and 70% of Class 3) within the agricultural heartland of the east coastal lowlands of Grampian, Angus, Fife.

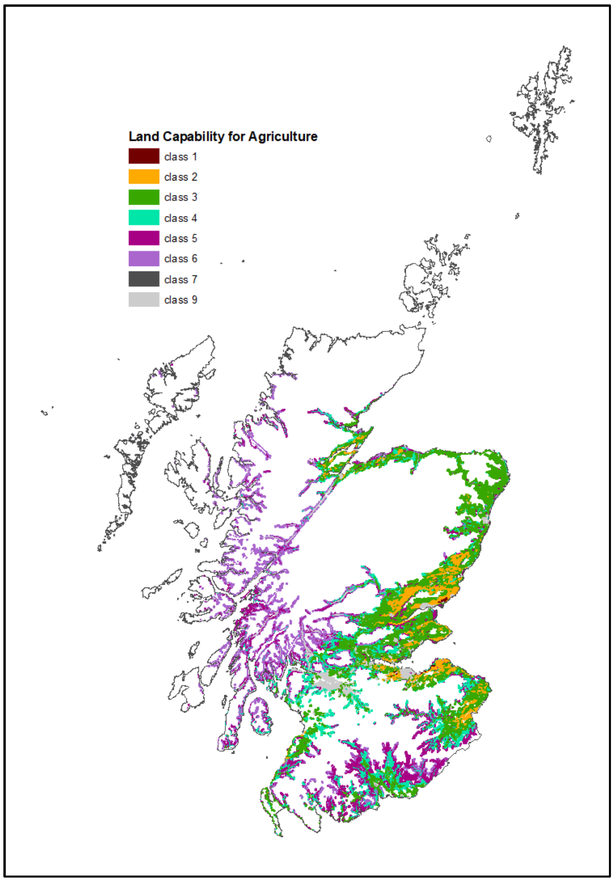

Figure 12 The extent and distribution of the best and most versatile land within the combined high risk zone as illustrated by the Macaulay Land Capability for Agriculture in Scotland classification (MLURI, 2010).

Several of the principal commodity species are thought to be susceptible to *Xylella fastidiosa* including barley, potatoes, carrots, and brassicas (oil seed rape, turnips and sprouts); this suggests almost all arable agriculture and market gardens may be at risk. Within the agricultural heartlands there are also many nurseries raising bulbs, flowers and horticultural plants.

The extent of designated landscape in the combined high-risk zone is illustrated in Figure 13. It is apparent that the relative risk from disease is high in the Loch Lomond and the

Trossachs National Park whereas the protective cooler climate in the uplands of the Cairngorms, means most of that National Park falls outside the high risk zone.

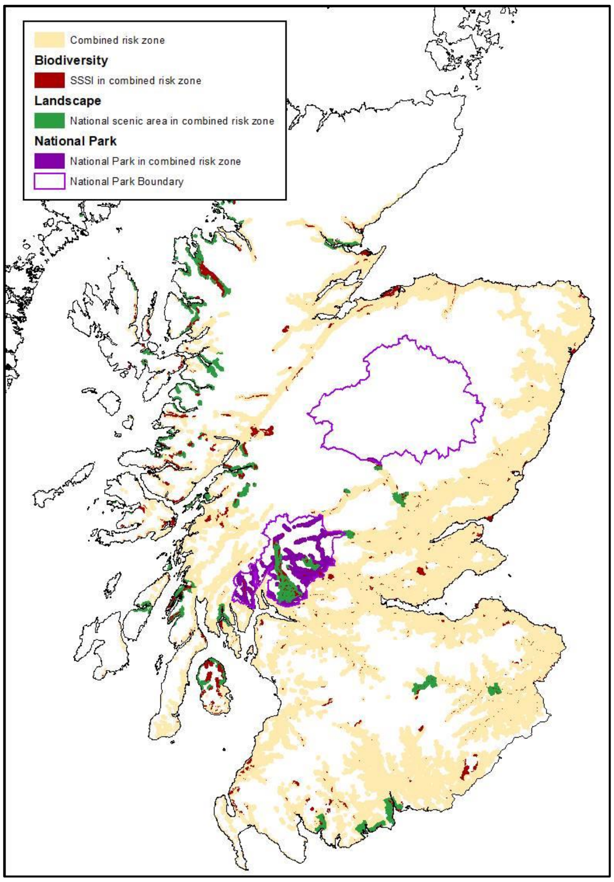

Figure 13 The extent of designated landscape within the combined high-risk zone.

	Proportion of population and plant traders located within the combined high-risk zone
Population	81%
Garden centres	86%
All plant nurseries	79%
Registered plant nursery	86%
Register forest reproductive material supplier	76%

Table 6 the proportion of Scottish population and plant traders within the combined high-risk zone

The statistics in Table 6 reveal the large proportion of Scottish horticulture and plant trading occurs within the combined high-risk zone. It is recommended that surveillance for infection is concentrated within the defined high-risk zone, particularly the 18,566 ha of land within 1 km of a garden centre.

6 Conclusions

The potential severity of disease in Scotland is unknown. It will depend on the combination of ecological, biotic, and abiotic factors that control the infection dynamics of the different *X. fastidiosa* genotypes, their plant-host specificity and the range of potential insect vectors. The epidemiology of *X. fastidiosa*-diseases in Scotland may differ dramatically from elsewhere in Europe if the vector species have different host plant preferences, feeding habits, and dispersal abilities.

The current spread of disease is controlled by rigorous monitoring and co-ordinated control strategies and it is too soon to be confident of a role for climate in the control of disease spread in Europe. However, across the coastal margins of southern Scotland the accumulated temperature is equivalent to south west England and much of Wales. Thus, if the *Xylella* pathogen was to be become established in England it may also survive in the coastal regions of south and central Scotland. Predicted climate change across England, Wales and southern Scotland suggests temperatures will rise to become as warm of southern France and northern Italy suggesting the UK is at increasing risk from *Xylella*.

It is evident that most potential host species are likely to be grown in gardens or used in landscape planting. The results of the project led by Steven White (PHC2018/05), which modelled the effectiveness of surveillance monitoring to detect an outbreak of *Xylella* in Scotland, suggest a mixture of risk-based and national surveillance is the likely to be the best option for detecting potential *X. fastidiosa* outbreaks in Scotland. In the absence of information on the most likely route of *X. fastidiosa* introduction into Scotland it would be prudent to develop a surveillance strategy for the nursery and trade sectors at sites where potential host species are grown, sold and planted within the high risk zone of the densely populated central belt from Clydeside and Stirlingshire in the west to Fife and the Lothians in the East. The most recent EFSA review suggest the relative risk of infection in potential host species in Scottish woodland, grassland, arable margins and agricultural crops remains low.

The ecological conditions in Scotland may limit the virulence and severity of the pathogen. It is highly likely that infected plants will be less stressed than plants in Europe due to reduced water stress in the cooler, moist Scottish climate. It is possible that *X. fastidiosa* infection may become established unseen in Scotland in asymptomatic hosts species, particularly short-lived herbaceous species.

Case studies in the EFSA host plant database reveal that the asymptomatic period of *X. fastidiosa* infection varies significantly for different host and pathogen subspecies combinations. Asymptomatic periods of over a year were reported for shade trees *Ulmus americana* (American Elm) and *Platanus occidentalis (American Sycamore*) infected with *X. fastidiosa* subsp. *multiplex.* The variable and long asymptomatic period present a considerable limitation to successful detection and control, particularly where surveillance is led by visual inspection. The potential asymptomatic period of UK native potential host species in the cooler wetter conditions of the UK climate needs to be determined.

Currently there remains considerable uncertainty as to the behaviour of potential vector species in Scotland, which may be resolved by the findings of the current UK BRIGIT research programme on vector-borne disease of plants. The sap-feeding insects are more commonly found in sites with diverse herbaceous vegetation which are warm and sheltered. Records are less common in areas which are cold or exposed, and insect vectors and the associated risk of disease spread is therefore likely to be reduced in such areas. The combined high-risk zone includes 81% of the population (and their gardens), over half the native woodland and all the best and most versatile agricultural land.

There remain significant evidence gaps in the scale, extent and routes of international trade; however most horticultural trade falls within the combined high-risk zone 86% of the garden centres and 79% of the plant nurseries. The extent of trade from Europe and across the world into Scotland via England and the rest of the UK is not known. It is also important to better understand the scale of horticultural export trade from Scotland. Tree and shrub host species may appear to be resilient to *X. fastidiosa* infection due to the cool Scottish climate.

7 References

America Phytopathological Society (APS) web page: A.B. Gould and J.H. Lashomb. 2007 Bacterial leaf scorch of shade trees. The Plant Health Instructor. DOI: 10.1094/PHI-I-2007-0403-07. https://www.apsnet.org/edcenter/disandpath/prokaryote/pdlessons/Pages/BacterialLeafScorch.aspx (Accessed 8th April 2019)

Bosso, L., Febbraro, MD., Cristinzio, G., Zoina, A., Russo, D., 2016 Shedding light on the effects of climate change on the potential distribution of *X. fastidiosa* in the Mediterranean basin. *Biological Invasions* 18:6 1759-1768. DOI 10.1007/s10530-016-1118-1.

Bosso, L., Russo, D., Febbraro, MD., Zoina, A., Cristinzio, G., 2016 Potential distribution of *X. fastidiosa* in Italy: a maximum entropy model. Poster.

BRIGIT Vector-borne diseases of plants. Project home web page: https://www.jic.ac.uk/brigit/ (Accessed 9th April 2019)

Cendoya, M., Martínez-Minaya, J., Ferrer-Matoses, A., Dalmau, V., Conesa, D., López-Quílez, A., Vicent, A., 2018 Spatial Bayesian modelling applied to the surveys of *Xylella fastidiosa* in the demarked area in Alicante (Spain). European Research on Emerging Plant diseases. H2020 POnTE and XF-Actors projects; presentation to the 2nd Joint Annual Meeting, Valencia Spain 23-26 October 2018.

Chapman, D., White, S., Bullock, J., Prnell, S., Mastin, A., 2018 Estimating the dispersal and spread of *Xylella fastidiosa* in Puglia. European Research on Emerging Plant diseases. H2020 POnTE and XF-Actors projects; presentation to the 2nd Joint Annual Meeting, Valencia Spain 23-26 October 2018.

Costello, MJ., Steinmaus, SJ., Boisseranc, CJ. 2017 Environmental variables influencing the incidence of Pierce's disease. *Australian Journal of Grape and Wine Research* 23:2.

Daugherty, MP., Zeilinger, AR., Almeida, RPP., 2017 Conflicting effects of climate and vector behaviour on the spread of a plant pathogen. *Phytobiomes* 1: 46-53.

Defra 2017 *Xylella fastidiosa*. Plant Pest Factsheet. Helen Anderson (Defra), version 3. July 2017.

Defra, 2017 Updating the UK Rapid Pest Risk Analysis for *X. fastidiosa*. Defra Risk and Horizon Scanning Team. 14th September 2017.

Defra 2017 Xylella high risk hosts. Information Note. https://planthealthportal.defra.gov.uk/assets/factsheets/Xylella-host-info-note.pdf

Defra & APHA 2017 Xylella fastidiosa. Implications for importers and users of trees, shrubs and herbaceous plants. UK Plant Health Guidance Document. 7pp. https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/598470/xylel la-fastidiosa-impl-trade.pdf

Defra 2018 Consolidated EU *X. fastidiosa* host list. 26/02/2018.

Defra 2018 *X. fastidiosa*: Information about controls for importers and users of trees, shrubs and herbaceous plants. UK plant health guidance. Edward Birchall and Dan Munro (APHA) updated September 2018.

EFSA Panel on Plant Health 2015 Scientific opinion on the risks to plant health posed by *Xylella fastidiosa* in the EU territory, with the identification and evaluation of risk reduction options. EFSA Journal 13(1), 3989, 262 pp.

European Commission 2018 Commission database of Host plants found to be susceptible to X. fastidiosa in the Union territory - update 11. Brussels 19/09/2018.

Harris JL., Balci, Y. 2015 Population structure of the bacterial pathogen *Xylella fastidiosa* among street trees in Washington D.C. *PLoS One* 10(3).Henneberger, TSM., Stevenson, KL., Britton, KO., Chang, CJ., 2004 Distribution of *Xylella fastidiosa* in sycamore associated with low temperature and host resistance. *Plant Disease* 88: 951–958.

Kottek M., Grieser, J., Beck, C., Rudolf, R., Rubel, F., 2006 World Map of the Koppen-Geiger climate classification updated. *Meteorologische Zeitschrift* 15(3): 259-263.

Lago, C., Garzo, E., Morena, A., Fereres A. 2018. Flight behaviour and patterns of directional movement on *Philaenus spumarius*. European Research on Emerging Plant diseases. H2020 POnTE and XF-Actors projects; presentation to the 2nd Joint Annual Meeting, Valencia Spain 23-26 October 2018.

Ledbetter, CA., Chen, J., Livingston, S., Groves, RL., 2009 Winter curing of *Prunus dulcis* cv 'Butte,' *P. webbii* and their interspecific hybrid in response to Xylella fastidiosa infections. *Euphytica* 169: 113–122.

Lieth, JH., Meyer, MM., Yeo, K-H., Kirkpatrick, BC., 2012 Modelling cold curing of Pierce's Disease in *Vitis vinifera* 'Pinot Noir' and 'Cabernet Sauvignon' grapevines in California. *The American Phytopathological Society* 101(12): 1492-1500. http://dx.doi.org/10.1094/PHYTO-08-10-0207

Maculay Land Use Research Institute: Land Capability for Agriculture in Scotland June 2010.

Spatial data source (dated Dec 2017): https://data.gov.uk/dataset/72ba06ca-0239-4e99-a9ad-4a48f755a3bd/land-capability-for-agriculture-scotland leaflet: https://www.hutton.ac.uk/learning/exploringscotland/land-capability-agriculture-scotland

Mitchell, RJ., 2014 AshEcol: An excel spreadsheet of Ash-associated biodiversity. April 2014. DOI: 10.13140/RG.2.1.3543.4486. James Hutton Institute.

Nunney, L., Vickerman, D.B., Bromley, R.E., Russell, S.A., Hartman, J.R., Morano, L.D., Stouthamer, R. 2013 Recent evolutionary radiation and host plant specialization in the *X. fastidiosa* a subspecies native to the United States. *Applied and Environmental Microbiology* 79: 2189-2200.

POnTE Pest Organisms Threatening Europe. EU Horizon 2020 project home web page: https://www.ponteproject.eu/ (Accessed 9th April 2019)

Purcell, AH., 1977 Cold therapy of Pierce's Disease of grapevines. *Plant Disease Reporter* 61: 514-518.

Purcell, AH., and Feil, H., 2001 Glassy-winged sharpshooter. *Pesticide Outlook* 12(5): 199-203.

Pyatt, DG., Suarez, JC., 1997. An Ecological Site Classification for Forestry in Great Britain with special reference to Grampian, Scotland. Forestry Commission Technical Paper 20. ISBN 085538347X.

White, SM., Bullock, JM., Hooftman, DAP., DS Chapman, DS., 2017 Modelling the spread and control of *X. fastidiosa* in the early stages of invasion in Apulia, Italy. *Biological Invasions* 19: 1825-1837.

XFActors EU Horizon 2020 project home web page: https://www.xfactorsproject.eu/ (Accessed 9th April 2019).

Yurtsever, S., 2000 On the polymorphic meadow spittlebug, *Philaenus spumarius* (L.) (Homoptera: Cercopidae) *Turk J Zool* 24: 447-459.

8 Appendices

1 Native species known to be susceptible to *X. fastidiosa*

Trees and Shrubs	Herbs		Grasses
Acer platanoides	Bidens	Parthenocissus quinquefolia	Agrostis
Acer pseudoplatanus	Brassica	Pelargonium hortorum	Avena fatua
Aesculus	Capsella bursa - pastoris	Plantago lanceolata	Bromus
Alnus	Chenopodium	Polygala myrtifolia	Festuca
Cornus	Conium maculatum	Polygonum arenastrum	Hordeum murinum
Fagus	Convolvulus arvensis	Polygonum convolvulus	Hordeum vulgare
Fraxinus	Conyza canadensis	Polygonum lapathifolium	Lolium mulliflorum
Fuchsia	Coronopus didymus	Polygonum persicaria	Lolium perenne
Ilex	Daucus carota	Ranunculus repens	Phleum pratense
Juniperus	Epilobium	Rheum rhabarbarum	Poa annua
Ligustrum	Erodium cicutarium	Rosa	Setaria
Populus	Euphorbia	Rosmarinus officinalis	Carex
Prunus avium	Fragaria	Rubus	
Prunus cerasifera	Geranium dissectum	Rumex crispus	
Prunus cerasus	Hedera helix	Salsola	
Prunus domestica	Helianthus	Salvia	
Prunus mahaleb	Lactuca serriola	Senecio vulgaris	
Pinus taeda	Lathyrus	Silybum marianum	
Pyrus	Lavandula dentata	Sisymbrium	
Platanus	Lonicera	Solanum	
Quercus palustris	Lupinus	Solidago virgaurea	
Quercus robur	Malva parviflora	Sonchus asper	
Rhamnus	Marrubium vulgare	Sonchus oleraceus	
Salix	Medicago sativa	Spartium junceum	
Sambucus nigra	Melilotus albus	Stellaria media	
Syringa ulgaris	Melilotus officinalis	Trifolium pratense	
Ulmus	Melissa officinalis	Trifolium repens	
	Mentha	Urtica dioica	
	Montia	Vaccinium	
	Myrtus communis	Verbena	
	Oenanthe	Veronica persica	
	Oenothera	Vicia	
	Origanum majorana	Vinca major	

The underlined species are included in the consolidated list of plants known to be susceptible to *X. fastidiosa* in the EU which consequently require a plant passport for import into the UK Defra (2018). Other species are included in the European Commission database of host plants found to be susceptible to *X. fastidiosa* in the union territory (EC 2018).

2 Reclassification of Landcover 2007 in terms of (a) habitat suitability for sap feeding insects and (b) risk of disease spread

Habitat group	**Landcover 2007 Broad Habitat**	**Suitability for sap feeding insects**	**Risk of disease spread**
Built up area	Suburban, Urban, Despoiled land; Industrial; Bare	High	Not included in mapping
Native woodland	Deciduous woodland, Orchard, Woodland scrub	High	High
Improved grass	Improved grassland including hay		
Arable	Arable – bare; barley; unknown; wheat		
Native grassland	Acid grassland; Bracken dominated grassland		
	Calcareous grassland		
	Neutral grassland		
	Rough and low-productivity grassland		
Conifer forest	Coniferous woodland, Recent planting, Mixed, Felled	Good	Medium
Heathland	Dwarf shrub heath – Gorse; Heather; Heather and grass, Burnt heather		
Wetlands	Freshwater – River; Lake	Poor	Low
	Bog; Bog - Grass dominated; Heather dominated		
	Fen, marsh and swamp		
Other	Montane habitats	Not suitable	No risk
	Supra-littoral sediment – Sand dune; Sand dune with shrubs		
	Littoral sediment - saltmarsh		
	Inland rock, Littoral rock, Supra-littoral rock		

3 Spatial data sources

Spatial data	IPR owners
Climate zones - derived from UKCC09 Met Data	Forest Research – Paul Taylor
Mean monthly minimum temperature	https://www.metoffice.gov.uk/climate
UK distribution of tree-phloem feeding insect vector species: *Philaenus spumarius*, *Ledra aurita*, *Cicadetta montana*	https://nbnatlas.org/ >80 data providers to the NBN Atlas for these species
Extent and distribution of preferred habitat for phloem feeding vector species - derived from landcover map 2015	CEH
Registered nurseries	Plant Health Centre
Registered forest trader	Forestry Commission
Registered forest reproductive material supplier	Forestry Commission
Settlements - combination of Ordnance Survey 250k point data for villages, towns and cities	Strategi features: contains Ordnance Survey data © Crown copyright and database right 2012
Plant retailers in Scotland listed on the internet – represented by selected settlements	Includes small independent businesses, regional and national chains. http://www.thegardeningwebsite.co.uk/garden-centres-in-scotland-c439.html
Population (2001) - represents the distribution of people, gardens, urban areas with amenity planting across Scotland	General Register Office for Scotland (since 2011, National Records of Scotland https://www.nrscotland.gov.uk/)

4 Information on Xylella from the Action Oak review

Name	***X. fastidiosa* ssp. *multiformis***
Symptoms and damage	Similar to those associated with water deficiency: leaf scorching and stunting in leaves, fruit & plant height
Epidemiology and distribution	Obligately insect vectored from saproxylic insects, especially sharp shooters/leafhoppers (Cicadellidae, subfamily Cicadellinae) and spittle bugs (family Cercopidae) Forms a biofilm-like layer within vascular system Completely blocks water transport in affected vessels Not yet present in the UK, but present in France Numerous alternate horticultural hosts UK climate and insects could support the pathogen
Control	Monitoring and eradication of symptomatic plants to prevent pathogen entry into the UK
Risk: Impact	High – Catastrophic (uncertain)
Risk: Spread	High – Medium dependent on site(s) of introduction and environment suitable for pathogen and vector
Assessment of knowledge	Incomplete

X. fastidiosa: is a high priority threat to native oak. It is considered one of the most dangerous plant bacterial species worldwide, causing a variety of diseases, with substantial economic impact for agriculture, public gardens and the environment. It is an insect vectored vascular wilt disease that forms a biofilm-like layer within xylem cells and tracheary elements blocking water transport in susceptible hosts (Chatterjee, et al., 2008). This leads to symptoms similar to water deficiency including leaf scorch, stunting of leaves, fruit, and eventually death.

X. fastidiosa has four subspecies that show some host specialization. These are subsp. *fastidiosa,* subsp. *multiplex,* subsp. *pauca,* and subsp. *sandyi* (www.cabi.org). Four phylogenetic clades within subsp. *multiplex* are identified; 'almond', 'peach', 'oak' and 'other types' (Nunney, et al., 2013). The oak group included isolates from periwinkle, pin (*Q. palustris*), red (*Q. rubra*) and turkey oaks (*Q. cerris*), as well as scarlet (*Q. coccinea*), English (*Q, robur*) and shumard (*Q. shumardii*) oaks. *Platanus*, *Ulmus*, *Alnus* and *Acer* were also represented in this group.

Xyllela fastidiosa is largely restricted to the Americas and it is regulated in the EU as quarantine organism under Council Directive 2000/29/EC. However, a European case was recently reported in the Apulia region of southern Italy where it was associated with 'rapid decline of olives' (Saponari, et al., 2013). Sequence information identified the bacterium detected as *X. fastidiosa* subsp. *pauca*. Other suspected hosts associated with the Apulia outbreak include species of *Malva*, *Portulaca* (purslane), *Quercus*, *Sorghum* and periwinkle.

The diagnosis of *X. fastidiosa* in *Quercus* has not been confirmed. Most diseases caused by *X. fastidosa* have been limited to hot climates, except for scorch of hardwood trees caused by *X. fastidiosa* subsp. *multiplex* which was found as far North as Southern Ontario (Goodwin & Zhang 1997). It is also associated with Oak Declines in North America.

X. fastidiosa is obligately insect transmitted by xylem-feeding insects, but the bacteria can be transmitted via vegetative propagation such as grafting. Xylem feeding insects, especially sharp shooters/leafhoppers (Cicadellidae), and spittle bugs (Cercopidae) are the most important known vectors of *X. fastidiosa* and these taxa are common in the UK (Pest Risk Analysis). The bacterium is not egg transmitted, and is maintained in the adult foregut through the production of a bacterial biofilm (Almeida & Purcell 2006). In order to determine whether insects are possibly *X. fastidiosa* vectors in the UK, traps should be routinely set up, and the catch assessed for *X. fastidiosa*. The UK is towards the northern limit of where *X. fastidiosa* is expected to establish. As this is a quarantine pathogen, laboratory research is difficult but the UK needs to be equipped to carry out molecular assays for the different subspecies. Research priorities are pathways of introduction, methods of eradication and control.

Chatterjee, S., Almeida, R.P. and Lindow, S. 2008. Living in two worlds: the plant and insect lifestyles of *X. fastidiosa*. Annual Review of Phytopathology 46, 243-271.

Saponari, M., Boscia, F., Nigro, F., Martelli GP. 2013. Identification of DNA sequences related to *X. fastidiosa* in oleander, almond and olive trees exhibiting leaf scorch symptoms in Apulia (Southern Italy). Journal of Plant Pathology 95, 659-668.

Goodwin PH, Zhang S. 1997. Distribution of *X. fastidiosa* in southern Ontario as determined by the polymerase chain reaction. Canadian Journal of Plant Pathology 19, 13-18.

Nunney, L., Vickerman, D.B., Bromley, R.E., Russell, S.A., Hartman, J.R., Morano, L.D., Stouthamer, R. 2013. Recent evolutionary radiation and host plant specialization in the X. fastidiosa a subspecies native to the United States. Applied and Environmental Microbiology 79, 2189-2200.

Almeida, R.P.P., Purcell, A.H. 2006. Patterns of *X. fastidiosa* colonization on the precibarium of sharpshooter vectors relative to transmission to plants. Annals of the Entomological Society of America 99, 884-890.