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Ceratocystis fagacearum Pest Report to support ranking of EU candidate priority pests

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1. Introduction to the report

This document is one of the 28 Pest Reports produced by the EFSA Working Group on EU Priority Pests under task 3 of the mandate M-2017-0136. It supports the corresponding Pest Datasheet published together on Zenodo¹ and applies the methodology described in the Methodology Report published on the EFSA Journal (EFSA, 2019).

This Pest Report has five sections. In addition to this introduction, a conclusion and references, there are two key sections, sections 2 and 3.

Section 2 first summarises the relevant information on the pest related to its biology and taxonomy. The second part of Section 2 provides a review of the host range and the hosts present in the EU in order to select the hosts that will be evaluated in the expert elicitations on yield and quality losses. The third part of Section 2 identifies the area of potential distribution in the EU based on the pest's current distribution and assessments of the area where hosts are present, the climate is suitable for establishment and transient populations may be present. The fourth part of Section 2 assesses the extent to which the presence of the pest in the EU is likely to result in increased treatments of plant protection products. The fifth part of section 2 reviews additional potential effects due to increases in mycotoxin contamination or the transmission of pathogens.

In Section 3, the expert elicitations that assess potential yield losses, quality losses, the spread rate and the time to detection are described in detail. For each elicitation, the general and specific assumptions are outlined, the parameters to be estimated are selected, the question is defined, the evidence is reviewed and uncertainties are identified. The elicited values for the five quantiles are then given and compared to a fitted distribution both in a table and with graphs to show more clearly, for example, the magnitude and distribution of uncertainty. A short conclusion is then provided.

The report has two appendices. Appendix A contains a host list created by amalgamating the host lists in the EPPO Global Database (EPPO, online) and the CABI Crop Protection Compendium (CABI, 2018). Appendix B provides a summary of the evidence used in the expert elicitations.

It should be noted that this report is based on information available up to the last day of the meeting² that the Priority Pests WG dedicated to the assessment of this specific pest. Therefore, more recent information has not been taken into account.

For *Ceratocystis fagacearum*, the following documents were used as key references: pest categorisation by EFSA PLH Panel (2018); pest risk analyses (PRAs) by Norway (VKM, 2013) and UK (Webber, 2015).

¹ Open-access repository developed under the European OpenAIRE program and operated by CERN, <u>https://about.zenodo.org/</u>

² The minutes of the Working Group on EU Priority Pests are available at <u>http://www.efsa.europa.eu/sites/default/files/wgs/plant-health/wg-plh-EU Priority pests.pdf</u>



2. The biology, ecology and distribution of the pest

2.1. Summary of the biology and taxonomy

The fungus *Ceratocystis fagacearum* is a single taxonomic entity. The name *C. fagacearum*, used in Council Directive 2000/29/EC, is substituted in this document by the more recent *Bretziella fagacearum* (de Beer et al., 2017) consistent with the EFSA pest categorisation (EFSA PLH Panel, 2018). *B. fagacearum* is a vascular pathogen and the causal agent of oak wilt. The pathogen is mainly spread through the transportation across root grafts formed between diseased and healthy trees. Above-ground spread is considerably slower and less common (CFIA, 2018). In red oaks, after a tree has been killed, the fungus grows out into the inner bark where mats of mycelium and fruiting structures are produced. The sporulating mats attract fungus-feeding arthropods such as nitidulid beetles (e.g. *Carpophilus sayi* and *Colopterus truncatus*), which act as vectors of the fungus as they move to fresh wounds on healthy trees.

2.2. Host plants

2.2.1. List of hosts

B. fagacearum mainly causes symptoms on *Quercus* spp. and no North American oak species have been found to be immune. Red oaks (subgenus *Erythrobalanus*) are the most susceptible and usually die within a few weeks of infection. American white oaks (subgenus *Lepidobalanus*) are found to be more tolerant. Oak species belonging to this subgenus may take several years to die or recover from the disease.

The susceptibility of European white oaks (*Quercus petraea*, *Quercus pubescens*, *Quercus robur*) was assessed by inoculating hundreds of oaks in West Virginia and South Carolina (EPPO, 2011; MacDonald et al., 2001). All inoculated oaks, regardless of species, appeared to be susceptible and died within a year after inoculation.

Appendix A provides the full list of hosts.

2.2.2. Main hosts in the European Union

Quercus cerris - Turkey oak: its wood tends to crack, and therefore it is frequently used as firewood. It is often planted in urban areas as an ornamental tree. It has a useful role in soil conservation, erosion control and reforestation of bare soils because of its ability to establish and grow quickly in a range of soil types. The acorns and young coppice shoots represent an important source of food for animals in Mediterranean agro-silvopastoral systems (de Rigo et al., 2016).

Quercus frainetto - Hungarian oak: firewood, timber and grazing. Because of the durability of its wood, it has sometimes been used as construction material in civil engineering and mining (Mauri et al., 2016).

Quercus ilex - Holm oak: coppices principally provide firewood, while the more structured high forests have more protective and recreational functions. It is also an ornamental species for gardens and parks. In the Iberian Peninsula the holm oak woodlands (dehesas in Spain and montados in Portugal) provide trees for shading livestock, firewood from pruning and refuge and breeding sites for a large number of vertebrates, whereas the grassland is used by cows and sheep for milk and meat production, and acorns for feeding pigs (de Rigo and Caudullo, 2016).

Quercus palustris - Pin oak: its hard and heavy wood is generally used for fuel wood, wood pulp, and railway sleepers. Ornamental species for urban landscapes. The acorns are an important food source for a number of wild species (Enescu and Durrant, 2016).



Quercus pubescens - Downy oak: pure and mixed stands are very common in France (8 760 km2 of almost pure forests), Italy (8 500 km2 of almost pure forests), Balkan countries. Mainly used as firewood, it is also commonly used for afforestation in southern Europe. It is among the most frequent hosts of all the economically important truffles (Pasta et al., 2016).

Quercus pyrenaica - Pyrenean oak: coppices are used for livestock grazing and firewood. Its wood is ideal for barrel manufacturing. It is also an ornamental species and in the Iberian Peninsula the Pyrenean oak forests have such a high landscape importance that they are protected by European legislation (Nieto Quintano et al., 2016).

Quercus robur and *Quercus petraea* - Pedunculate and sessile oak: oak stands are frequently managed either as high forest or as coppice with standards. Their oak forests are amongst the most economically important deciduous forest trees in Europe, providing high quality hardwood with many uses (including barrels for wines and spirits). Its quality is strongly determined by the forest management, as the most valuable oak wood is produced in high mixed forests on fertile sites with long economic rotations (about 160 years of age for *Q. petraea*, about 130 years for *Q. robur*). Other important uses are firewood, charcoal, and ornamental. They play a crucial ecological role, supporting many insect, bird and mammal species (Eaton et al., 2016).

Quercus suber - Cork oak: This species is grown for its thick corky bark, harvested in late spring or early summer every 9-12 years. Cork is the sixth most important nontimber forest product in the world (Houston Durrant et al., 2016) and 87% of its total production comes from the EU (Cork Quality Council, online). The open structure of cork oak forest landscapes is biologically very diverse and has a high conservation value, providing firewood, pasture, herbs, mushrooms, beekeeping and supporting leisure activities. Many cork oak savannas are protected ecosystems in Europe (Houston Durrant et al., 2016).

In general, oaks, especially old specimens, harbour a remarkable interesting and diverse flora and fauna: the biodiversity in these trees is very high. It is a complex web of factors that contribute to making the oak a habitat for many species. The long life cycle, the different stages of decay etc are probably important reasons for their high biodiversity (Nilsson, 2006).

Other tree species have also been found to be susceptible to infection. Chinese chestnut (*C. mollissima*) is reported to be naturally infected and highly susceptible (Rexrode and Brown, 1983). Inoculation experiments have shown that American chestnut (*Castanea dentata*), European chestnut (*C. sativa*), American chinquapin (*Castanea pumila*), tanoak (*Lithocarpus*) and several varieties of apple (*Malus*) are also susceptible (Bretz and Long, 1950; Rexrode and Brown, 1983).

2.2.3. Hosts selected for the evaluation

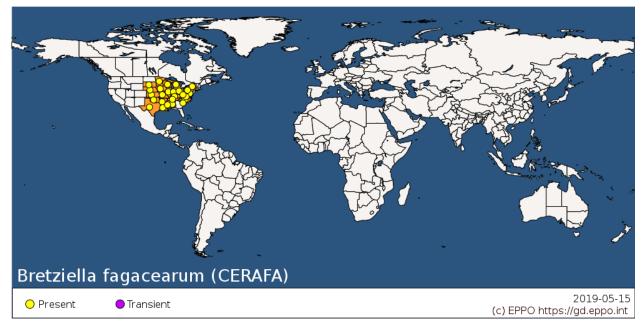
Species other than *Quercus* were not considered in the EKE, as there is very little evidence that they are relevant hosts for *B. fagacearum*. Since only *Quercus* species are considered to be hosts and there is insufficient evidence to show that the *Quercus* species in Europe have different susceptibilities to *B. fagacearum*, the *Quercus* species in the EU were grouped together in the assessments of impact.

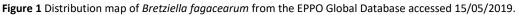


2.3. Area of potential distribution

2.3.1. Area of current distribution

Figure 1 provides an overview of the current area of distribution of the pest. Additional map with details on the US distribution is provided at EDDMapS (online), where the pathogen is reported as present in Texas and the eastern and mid-western states of the US. In the EU no outbreaks have yet been reported.





2.3.2. Area of potential establishment

The main hosts, *Quercus* spp. are widely distributed within the EU territory (see Figure 2 in EFSA PLH Panel, 2018). Three of the oak species native to Europe (*Q. petraea*, *Q. pubescens* and *Q. robur*) have been shown to be highly susceptible to *B. fagacearum* in inoculation trials. The distribution ranges of *Q. robur* and *Q. petraea* overlap to a large extent and cover most of Europe (distribution maps are provided by Eaton et al., 2016). Although the northern limit excludes the most northern parts of Scandinavia (map by Hallanaro and Pylvänäinen, 2001), *Q. robur* seems particularly well adapted to the Northern EU. *Quercus palustris* and *Quercus rubra*, which were introduced from North America into Europe as planted trees, are also susceptible to the disease (Webber, 2015).

According to EFSA (2018) the EU climate does not represent a limiting factor for the establishment of the pathogen in most of the EU, as the climate types suitable to *B. fagacearum* survival overlap to a large extent with the distribution of potential hosts.



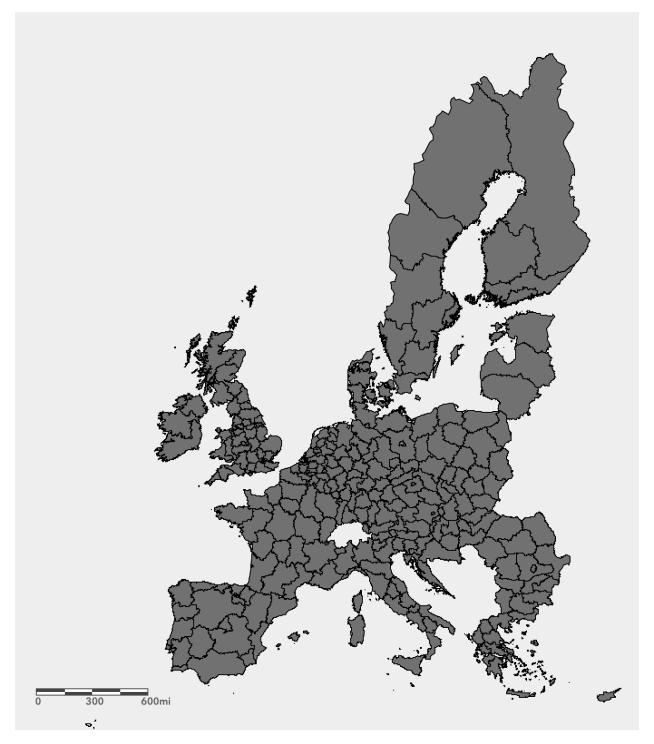


Figure 2 The potential distribution of the pest in the EU NUTS2 regions based on the scenarios established for assessing the impacts of the pest by the EFSA Working Group on EU Priority Pests (EFSA, 2019). This link provides an online interactive version of the map that can be used to explore the data further: <u>https://arcg.is/X0CyO</u>.



2.3.3. Transient populations

Bretziella fagacearum is not expected to form transient populations in the EU (for "transient" see the definition in EFSA, 2019).

2.3.4. Conclusions on the area of potential distribution

The area of potential distribution of *B. fagacearum* is equivalent to the area where the main hosts (i.e. *Quercus* spp.) occur in the EU (compare Figure 2 by EFSA PLH Panel 2018 with Figure 2 of current report).

2.4. Expected change in the use of plant protection products

Control methods and treatment options are reviewed by Harrington (2013) (see EFSA PLH Panel, 2018) and Koch et al. (2010). Propiconazole is a fungistatic compound (approved in the EU) which inhibits *B. fagacearum* growth *in vitro* and is the primary fungicide used for oak wilt control (Koch et al., 2010). Preventive propiconazole treatments are effective against symptom development and mortality in live, white, and red oaks (Blaedow et al., 2010). Therapeutic propiconazole treatments are effective at arresting symptom development in white oaks and can delay wilt in red oaks if applied prior to extensive crown wilt (Koch et al., 2010). However, the use of chemicals in natural habitats and managed forests is not feasible for either therapeutic or preventive objectives. Due to the fact that no effective treatments with plant protection products (PPPs) are currently available, the most suitable PPP indicator is Case "A" and the category is "0" based on Table 2.

Table 1: Expected changes in the use of Plant Protection Products (PPPs) following *Bretziella fagacearum* establishment in the EU in relation to four cases (A-D) and three level score (0-2) for the expected change in the use of PPPs

Expected change in the use of PPPs	Case	PPPs indicator
PPPs effective against the pest are not available/feasible in the EU	Α	0
PPPs applied against other pests in the risk assessment area are also effective against the pest, without increasing the amount/number of treatments	В	0
PPPs applied against other pests in the risk assessment area are also effective against the pest but only if the amount/number of treatments is increased	С	1
A significant increase in the use of PPPs is not sufficient to control the pest: only new integrated strategies combining different tactics are likely to be effective	D	2

2.5. Additional potential effects

2.5.1. Mycotoxins

The species is not known to be related to problems caused by mycotoxins.

2.5.2. Capacity to transmit pathogens

The species is not known to vector any plant pathogens.



3. Expert Knowledge Elicitation report

3.1. Yield and quality losses

3.1.1. Structured expert judgement

3.1.1.1. Generic scenario assumptions

All the generic scenario assumptions common to the assessments of all the priority pests are listed in the section 2.4.1.1 of the Methodology Report (EFSA, 2019).

3.1.1.2. Specific scenario assumptions

- All *Quercus* species in the EU are hosts, even though not all European *Quercus* species have been tested for their susceptibility.
- Only *Quercus* species are considered hosts. *Castanea* spp. (including hybrids) are not considered as hosts in the assessment, even though *C. sativa* has been shown by artificial inoculation to be susceptible and *C. mollissima* is reported to be naturally infected and highly susceptible.
- The area of potential establishment coincides with the area in the EU where the host species are present.
- Trees of all ages are equally susceptible (CFIA, 2018).
- We assume that all *Quercus* species in the EU are equally susceptible. This is based on the results by MacDonald et al. (2001), showing that the susceptibility of European oaks *Q. robur*, *Q. pubescens* and *Q. petraea* is similar to that of red oaks (*Q. rubra*).
- Mechanisms for disease transmission and their role in maintaining the epidemics in the EU include:
 - Natural root graft transmission.
 - Movement of bark beetles. Scolytus intricatus has been suggested as a potential vector of *B. facagearum* (Gibbs, 1981; Doganlar and Schopf, 1984; Yates, 1984).
 S. intricatus is widespread in Europe; it feeds on a large number of Quercus species; and it is known to be a vector of Ophiostoma roboris and Ceratocystis piceae, two pathogens associated to oak decline (Eisenhauer, 1989; Šrůtka 1996; CABI, 2018). For our assessment, S. intricatus is assumed to be a vector.
 - Human-assisted transmission.
 - We consider the mechanisms above as sufficient to sustain the epidemic. Transmission via insects attracted to mats produced by red oaks is not considered.

3.1.1.3. Selection of the parameter(s) estimated

Since tree death by *B. fagacearum* can be so rapid as to occur within four weeks of infection (Sakalidis et al., 2017), the assessment takes into account only the yield losses caused by the pathogen and not quality losses.



The percentage of trees lost (the percentage of dead trees in the whole population) was selected as the yield loss value, and it was calculated as the product of the disease prevalence (percentage of infected trees) and the mortality rate of infected trees.

3.1.1.4. Defined question(s)

What is the percentage yield loss in forest stands under the scenario assumptions in the area of the EU under assessment for *Ceratocystis fagacearum*, as defined in the Pest Report?

3.1.1.5. Evidence selected

The experts reviewed the evidence obtained from the literature (see Table B.1 in Appendix B) selecting the data and references used as the key evidence for the EKE on impact. Two points were made:

- Data on disease prevalence are provided in Haight et al. (2011)
- Data on tree mortality are based on several papers that report a very high mortality rate of infected trees

3.1.1.6. Uncertainties identified

- European oaks are considered to be as susceptible as US red oaks based on artificial inoculation experiments. There are no data on the susceptibility of EU oaks in natural conditions. Uncertainty is higher in Southern Europe where other oak species such as *Q*. *ilex* and *Q*. *suber*, for which we have no data on susceptibility, are more common.
- Prevalence was estimated assuming that *Scolytus intricatus* is the only vector. The uncertainty is related to the fact that we do not have data on the vector capacity and efficiency of *S. intricatus*, and there might be other vectors in the EU.
- There is limited information on disease prevalence (only one paper, Haight et al. 2011)
- Data on prevalence from one location in Minnesota (Haight et al. 2011) had to be extrapolated to the whole EU. There is limited knowledge on the extent to which climate affects disease prevalence.
- Experimental data on tree mortality are from small populations
- There are several reports of high percentages of dead trees but the time period during which the disease had been present in the population is not provided.
- Distribution of some EU *Quercus* species (e.g. *Q. suber*)

3.1.2. Elicited values for yield losses

What is the percentage yield loss in forest stands under the scenario assumptions in the area of the EU under assessment for *C. fagacearum*, as defined in the Pest Report?

The five elicited values on yield loss in *Quercus* plantations on which the group agreed are reported in the table below.



 Table 2: Summary of the 5 elicited values on yield loss (%) on Quercus plantations

Percentile	1%	25%	50%	75%	99%
Expert elicitation	0.05%	1.2%	2%	4%	15%

3.1.2.1. Justification for the elicited values for yield loss on Quercus sp.

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

The upper value is based on a scenario with a 15% disease prevalence and 100% mortality rate of infected trees. The estimate of disease prevalence was based on the 0.6% value calculated for Minnesota (Haight et al., 2011) under the worst-case-scenario assumption that the candidate vector in the EU is more efficient than US vectors and the consideration that environmental conditions in EU are on average more favourable than those in Minnesota. For these reasons, the 0.6% estimate was increased to 15%.

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

The lower value is based on the 0.6% estimate for disease prevalence in Minnesota (Haight et al., 2011). The experts considered that such a value would be found in an area characterised by relatively favourable conditions for hosts and vectors. Hence, in a best-case scenario, the lowest prevalence in the EU would be lower than 0.6%. The experts also considered that in Southern Europe temperatures might be too high for pathogen growth, and vector densities might be very low. For these reasons, the 0.6% estimate was decreased to 0.05 %.

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

The median value is based on the 0.6% estimate for prevalence in Minnesota (Haight et al., 2011). The experts considered a scenario where tree species would be as vulnerable as in Minnesota, while environmental conditions would be variable but on average more favourable: hence, the prevalence in the EU should be higher than in Minnesota.

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

The precision reflects the fact that the experts are more confident in the lower value than in the upper value.



3.1.2.2. Estimation of the uncertainty distribution for yield loss on Quercus sp.

The comparison between the fitted values of the uncertainty distribution and the values agreed by the group of experts is reported in the table below.

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert elicitation	0.05%					1.2%		2%		4%					15%
Fitted distribution	0.3%	0.4%	0.5%	0.7%	0.9%	1.2%	1.4%	2.1%	3.1%	3.8%	5.0%	6.6%	9.2%	12%	17%

Table 3:Fitted values of the uncertainty distribution on the yield loss (%) on *Quercus* sp.

Fitted distribution: Lognorm(0.031423,0.034851), @RISK7.5

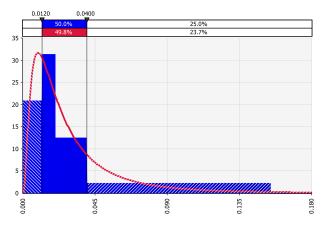


Figure 3 Comparison of judged values (histogram in blue) and fitted distribution (red line) for yield loss on Quercus sp.

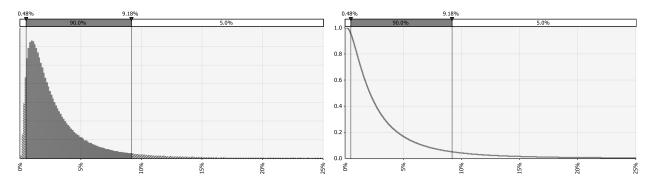


Figure 4 Fitted density function to describe the uncertainties with 90% uncertainty interval (left) and fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded (right) for yield loss on *Quercus* sp.



3.1.3. Conclusions on yield and quality losses

Based on the general and specific scenarios considered in this assessment, the percentage yield loss (here with the meaning of mortality rate) is estimated to be 2.1% (with a 95% uncertainty range of 0.4 - 12%).

3.2. Spread rate

3.2.1. Structured expert judgement

3.2.1.1. Generic scenario assumptions

All the generic scenario assumptions common to the assessments of all the priority pests are listed in the section 2.4.2.1 of the Methodology Report (EFSA, 2019).

3.2.1.2. Specific scenario assumptions

- *S. intricatus* is a vector and is responsible for the spread of the disease. Both active and passive (wind-driven) dispersal mechanisms are considered.
- Root grafting commonly occurs in oak forests in the EU
- Human-assisted dispersal: management activities allowing human assisted spread are related to the development of the tree such as thinning and not to post-harvest movement. As there is little management of oak plantations in the EU, we assume that the role of human-assisted dispersal is limited.
- We assume that transmission via root grafts is only responsible for local dispersal (between neighboring plants); insect transmission is required for longer-distance dispersal and for the formation of new disease foci.
- We assume that, even though mat formation may occur in red oaks in the EU, spread via Nitidulidae species will not occur because Nitidulidae in Europe (see Jelinek et al., 2016, for a tentative list) are not known to be associated with fungal mats.

3.2.1.3. Selection of the parameter(s) estimated

The spread rate has been assessed as the number of meters per year.

3.2.1.4. Defined question(s)

What is the spread rate in 1 year for an isolated focus within this scenario based on average European conditions? (units: m/year)

3.2.1.5. Evidence selected

The experts reviewed the evidence obtained from the literature (see Table B.2 in Appendix B) selecting the data and references used as the key evidence for the EKE on spread rate.



3.2.1.6. Uncertainties identified

- Lack of data to determine how effective European native scolytids would be as vectors.
- The timing of maturation feeding for the candidate vector *S. intricatus* might be a limiting factor for disease spread (it peaks in late summer, while the susceptibility of American oaks is greatest in spring/early summer)
- The potential role in pathogen transmission of other insect species commonly present in the EU is unknown. In general, possible vectors other than scolytids (e.g. birds, other insects) are not considered.
- Nothing is known about the potential for infected European oaks to produce sporulating mats of *B. fagacearum* after infection.

3.2.2. Elicited values for the spread rate

What is the spread rate in 1 year for an isolated focus within this scenario based on average European conditions? (units: m/year)

The five elicited values on spread rate on which the group agreed are reported in the table below.

Table 4: Summary of the 5 elicited values on spread rate (m/y)

Percentile	1%	25%	50%	75%	99%
Expert elicitation	5	65	100	350	2500

3.2.2.1. Justification for the elicited values of the spread rate

Reasoning for a scenario which would lead to wide spread (99th percentile / upper limit)

The upper value was agreed based on a scenario where insect transmission is the most important means of spread. According to Gibbs et al. (1984), the maximum distance of flight of the candidate vector *S. intricatus* is 0.35 km. The experts increased the value to 2.5 km in order to account for the possibility that maximum flight distances are longer (based on knowledge about similar species) and for potential wind-driven dispersal of the insects.

Reasoning for a scenario, which would lead to limited spread (1st percentile / lower limit)

The lower value was agreed based on a scenario where insect transmission does not occur and the disease only spreads by root-to-root pathogen transmission. The spread rates reported for root-graft transmission in the US (10-40 m/year) were corrected to 5 m/year, considering that the oak density in forests in the EU is variable and that oak density would be a limiting factor for disease spread.

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



The median value was agreed based on a scenario where transmission occurs both via root grafts and insect movement, but where the relative contribution of insect transmission is more important than in the US (as *S. intricatus* might be a better vector than those in the US).

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

The precision interval reflects the uncertainty on the relevance of insect transmission: hence, there is low uncertainty around the lower estimate and a higher uncertainty around the upper estimate.



3.2.2.2. Estimation of the uncertainty distribution for the spread rate

The comparison between the fitted values of the uncertainty distribution and the values agreed by the group of experts is reported in the table below.

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert elicitation	5					65		100		350					2,50 0
Fitted distributio n	6	9	14	23	35	51	71	127	227	315	467	712	1,160	1,771	2,898

Table 5:Fitted values of the uncertainty distribution on the spread rate (m/y)

Fitted distribution: Lognorm(313.73,707.48), @RISK7.5

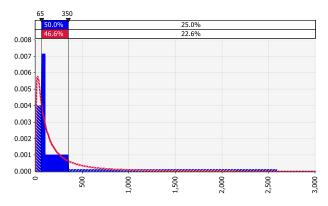


Figure 5 Comparison of judged values (histogram in blue) and fitted distribution (red line) for spread rate.

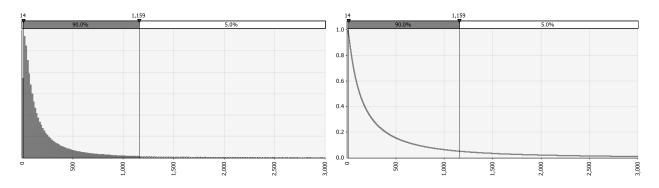


Figure 6 Fitted density function to describe the uncertainties with 90% uncertainty interval (left) and fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded (right) for spread rate.



3.2.3. Conclusions on the spread rate

Based on the general and specific scenarios considered in this assessment, the maximum distance expected to be covered in one year by *B. fagacearum* is 127 m (with a 95% uncertainty range of 9 - 1771 m).

3.3. Time to detection

3.3.1. Structured expert judgement

3.3.1.1. Generic scenario assumptions

All the generic scenario assumptions common to the assessments of all the priority pests are listed in the section 2.4.2.1 of the Methodology Report (EFSA, 2019).

3.3.1.2. Specific scenario assumptions

No specific assumptions are introduced for the assessment of the time to detection.

3.3.1.3. Selection of the parameter(s) estimated

The time for detection has been assessed as the number of months between the first event of pest transfer to a suitable host and its detection.

3.3.1.4. Defined question(s)

What is the time between the event of pest transfer to a suitable host and its first detection within this scenario based on average European conditions? (unit: months)

3.3.1.5. Evidence selected

The experts reviewed the evidence obtained from the literature (see Table B.3 in Appendix B) selecting the data and references used as the key evidence for the EKE on time to detection.

3.3.1.6. Uncertainties identified

- The time to symptom expression is variable: from one month to several years
- The time to detection depends on how frequently the affected area is surveyed

3.3.2. Elicited values for the time to detection

What is the time between the event of pest transfer to a suitable host and its first detection within this scenario based on average European conditions? (unit: months)

The five elicited values on time to detection on which the group agreed are reported in the table below.



Table 6: Summary of the 5 elicited values on time to detection (months)

Percentile	1%	25%	50%	75%	99%
Expert elicitation	8	33	45	70	110

3.3.2.1. Justification for the elicited values of the time to detection

Reasoning for a scenario which would lead to a long time for detection (99th percentile / upper limit)

The upper value represents the time needed for a focus of dead trees (a death pocket) to appear and for the subsequent detection of the death pocket. The value was estimated based on a worst-case scenario where the time to symptom expression is several years long and the disease occurs in areas that are not frequently surveyed, where trees are not very visible and death pockets less easy to detect.

Reasoning for a scenario which would lead to a short time for detection (1st percentile / lower limit)

The lower value is based on the following considerations. Experimental data show that the minimum time to symptom development is 1 month. In an ideal case, a newly symptomatic tree would be identified in the first survey after symptom development, i.e. on average 3 months later, as regular surveys in forest areas usually occur twice a year. After identification, time is needed to isolate the pathogen in the lab and to prepare the report. The experts agreed that in a best-case scenario the disease would not be detected before 8 months.

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

The median value represents the time needed for a death pocket to appear and then to be detected. The experts considered that a death pocket can appear within 1 year. The probability of subsequent detection depends on the pocket size, which increases in time (median estimate of spread rate: 100 m/year), and on survey frequency. Finally, the experts included the time needed for pathogen isolation and confirmation in the lab and for subsequent reporting.

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

The precision reflects the fact that experts are not confident in the lower values (hence, the first quantile supports the median) and that there is uncertainty towards the upper limit.



3.3.2.2. Estimation of the uncertainty distribution for the time to detection

The comparison between the fitted values of the uncertainty distribution and the values agreed by the group of experts is reported in the table below.

Percentile	1%	2.5%	5%	10%	17%	25%	33%	50%	67%	75%	83%	90%	95%	97.5%	99%
Expert elicitation	8					33		45		70					110
Fitted distributio n	9	13	16	21	26	32	37	47	59	67	77	89	104	118	136

Table 7:Fitted values of the uncertainty distribution on the time to detection (months)

Fitted distribution: Gamma(3.5766,14.501), @RISK7.5

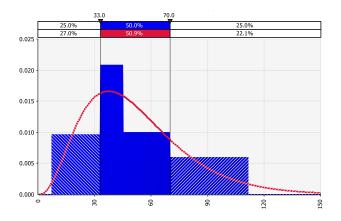


Figure 7 Comparison of judged values (histogram in blue) and fitted distribution (red line) for time to detection.

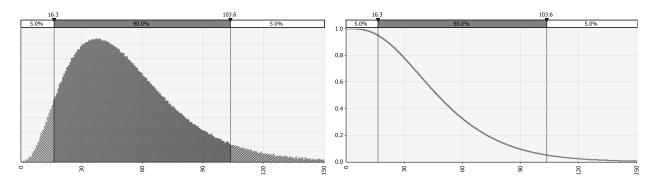


Figure 8 Fitted density function to describe the uncertainties with 90% uncertainty interval (left) and fitted descending distribution function showing the likelihood (y-axis) that a given proportion (x-axis) maybe exceeded (right) for time to detection.



3.3.3. Conclusions on the time to detection

Based on the general and specific scenarios considered in this assessment, the time between the event of pest transfer to a suitable host and its detection is estimated to be 47 months (with a 95% uncertainty range of 13 - 118 months).

4. Conclusions

Hosts selection

Species other than *Quercus* were not considered in the EKE, as there is very little evidence that they are relevant hosts for *B. fagacearum*. Since only *Quercus* species are considered to be hosts and there is insufficient evidence to show that the *Quercus* species in Europe have different susceptibilities to *B. fagacearum*, the *Quercus* species in the EU were grouped together in the assessments of impact.

Area of potential distribution

The area of potential distribution of *B. fagacearum* is equivalent to the area where the main hosts (i.e. *Quercus* spp.) occur in the EU.

Increased number of treatments

Due to the fact that no effective treatments with plant protection products (PPPs) are currently available, the most suitable PPP indicator is Case "A" and the category is "0".

Yield loss and quality losses

Based on the general and specific scenarios considered in this assessment, the percentage yield loss (here with the meaning of mortality rate) is estimated to be 2.1% (with a 95% uncertainty range of 0.4 - 12%).

Spread rate

Based on the general and specific scenarios considered in this assessment, the maximum distance expected to be covered in one year by *B. fagacearum* is 127 m (with a 95% uncertainty range of 9 - 1771 m).

Time for detection after entry

Based on the general and specific scenarios considered in this assessment, the time between the event of pest transfer to a suitable host and its detection is estimated to be 47 months (with a 95% uncertainty range of 13 - 118 months).



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Appendix A – CABI/EPPO host list

The following list, defined in the Methodology Report (EFSA, 2019) as the full list of host plants, is compiled merging the information from the most recent PRAs, the CABI Crop Protection Compendium and the EPPO Global Database. Hosts from the CABI list classified as 'Unknown', as well as hosts from the EPPO list classified as 'Alternate', 'Artificial', or 'Incidental' have been excluded from the list.

Genus	Species epithet
Castanea	
Quercus	
Quercus	alba
Quercus	coccinea
Quercus	ellipsoidalis
Quercus	falcata
Quercus	macrocarpa
Quercus	palustris
Quercus	petraea
Quercus	prinus
Quercus	pubescens
Quercus	robur
Quercus	rubra
Quercus	shumardii
Quercus	stellata
Quercus	velutina
Quercus	virginiana



Appendix B – Evidence tables

B.1 Summary on the evidence supporting the elicitation of yield and quality losses

Susceptibility	Infection	Symptoms	Impact	Additional information	Reference	Limitation/uncertainties
	Incidence	Severity	Losses			
Q. fusiformis			Mortality rate of infected trees (dead crown cover as % affected crown cover): 52-57% (and 81%)	Spread of <i>B. fagacearum</i> from 4 different foci monitored in live oak (Q. fusiformis) with infrared aerial photography, 1982-1987. Data on mortality rate are for 1987. The range 52-57% is min-max of three of the four foci.	Appel et al., 1989	No information on disease prevalence. Removed trees were counted as dead in the analysis. Tree removal is reported for two sites: there is no information on rate of removal, and on whether there was any removal at the other two sites.
Q. fusiformis	Only infected trees were selected	Average crown loss: ~60-100%	Mortality rate of infected trees in different experimental plots: ~40- 100%	Experiment on efficacy of propiconazole, 1987 -1990. Disease development in treated and untreated trees live oaks under natural infection. Nine plots located in urban and rural oak wilt centers, located on the perimeters of disease centers. Plots=groups of trees in yards, or rural stands. Total 100 trees. The ranges reported here for crown loss and mortality rate are for 'untreated' plots and are extracted from Table 2 in the paper. Crown loss reported here is the same as in the table; mortality rate is calculated as 'No. dead'/'No. trees'.	Appel, 1994	Results from a very small population of trees
Q. fusiformis	Density of disease centres in survey area: 800 in			Survey, Fort Hood (Texas), 2001 IKONOS 1-meter satellite imagery used to identify potential oak mortality. Survey area: 119,000 ha.	Appel, 2007	No more information, e.g. no estimate of the size of disease centres



	11.9 km² (1 centre/150 ha)				
Q. macrocarpa Q. rubra		Mortality rate: <i>Q. rubra</i> : 83% <i>Q. macrocarpa</i> : 11%	Area in Sherburne County, Minnesota, 1960- 1971	French and Bergdahl, 1973, cited in Gibbs and French, 1980	
Species present in Anoka County: <i>Q. ellipsoidalis,</i> <i>Q. rubra, Q.</i> <i>macrocarpa</i> (primarily <i>Q.</i> <i>rubra</i>)	0.6% infected oak trees		Anoka County (Minnesota). Area: 1156 km2. Number of oaks: 5.92 million oaks. Estimate: in 2007, Anoka County has a population of 885 oak wilt pockets covering 5.47 km2 and including 33583 infected trees. Number and location of infected trees existing in 2007 were estimated from data on oak wilt pockets discovered in the period 2003-2006, using a disease spread model.	Haight et al., 2011	Estimates of incidence are aggregated for all land cover types (although the model has land-cover- specific parameters). The model does not distinguish between different Quercus species.
Red/ white oak	Red/ white oak ratio in states sustaining epidemics: 1.32-2.58		The severity of oak wilt in a state is positively correlated with red to white oak ratios in oak forest (on a wood volume basis). The calculated ratios for states sustaining epidemics range from 1.32 to 2.58 for Michigan, Minnesota, and Wisconsin.	Juzwik, 2009	Empirical rule-of-thumb, not useful for extrapolation to the EU
	7.7% area affected by oak wilt		Study region: four counties in Texas. Oak wilt area estimated using infrared aerial photography. Of the total area sampled, 7.7% (743 of 9613 ha) was affected by oak wilt.	Stewart et al., 2014	
	Area affected by oak wilt in Texas (2007): >2630 ha		In Texas, oak wilt was estimated to affect a minimum of 6,500 acres in 2007 (Texas Forest Service, 2007).	Webber, 2015	
	Area affected by oak wilt in Minnesota (2001): 6216 ha		Between 1991 and 2001, oak wilt was estimated to affect 15,359 acres in Minnesota.	Webber, 2015	



	Area affected by oak wilt in Texas: 453-5811 ha (1988-2000)		See Table 1 in the paper Area affected: cumulative area affected only within confirmed oak wilt infection centres.	Wilson, 2005	No data on the size of the oak tree population
Q. macrocarpa Q. alba Q. ellipsoidalis Q. rubra		 Mortality rate: <i>Q. macrocarpa</i> (bur oak): 19.9% <i>Q. alba</i> (white oak): 28.3% <i>Q. ellipsoidalis</i> (Hill's yellow oak): 55.4% <i>Q. borealis</i> (syn. <i>Q. rubra</i>) (red oak): 52.9% 	Survey in Pilot Knob State Park, Iowa, 1945	Young, 1949	No information on the survey

B.2 Summary on the evidence supporting the elicitation of the spread rate

Spread	Additional information	Reference
	Means of spread: underground root to root transmission via functional grafts is the slowest but most common means of spread. It is very much dependent on the availability of interconnection and the density of oak: e.g. in the Wisconsin oak savanna, an average distance of less than 30 feet (~9 m) between mature oak trees assures disease transmission.	Appel et al., 1989; Gibbs and French, 1980; Whitford et al., 2007
	Favourable conditions for root-graft transmission exist in the EU, as <i>Quercus</i> -dominated woodlands are found in several EU regions (e.g. ~14% of the total woodland area in Galicia, Spain is covered by pure stands of <i>Q. robur</i> ; ~700,000 ha covered by oak woodland and ~70,000 ha covered by pure stands of Quercus spp. in Italy)	EFSA PLH Panel (2018)
	 Means of spread: above-ground insect transmission. The main insect vectors in the US are: Sap beetles (family <i>Nitidulidae</i>). Those beetles feed on the sporulating mats produced by <i>B. fagacearum</i> between the bark and wood after the tree has died; then they fly to other mats or fresh tree wounds, favouring the infection of new plants. Oak bark (scolytid) beetles making gallery systems in diseased oaks. After emergence, the new generation of beetles will carry <i>B. fagacearum</i> on their bodies and transfer it to the wounds that they make on healthy trees. 	EPPO, 2011; Gibbs et al., 1984; Hayslett et al., 2008; Sakalidis et al., 2017
	The main US vectors are not found in Europe but potential for novel associations cannot be excluded and <i>Scolytus intricatus</i> , an oak bark beetle present in almost all the EU, has already been identified as a potential	EFSA PLH Panel (2018); Webber, 2015



	I.	
	vector of the pathogen. However, a limiting factor for disease spread could be that the phases of maximal insect	
	feeding and optimal tree susceptibility may not coincide closely. The susceptibility of American oaks is greatest in	
	spring/early summer, while feeding by <i>S. intricatus</i> in the UK reaches a peak in the late summer.	
	Means of spread: firewood cut from infected oaks. As sporulating mats develop on dead oak trees, they can also	
	form on wood cut from infected plants.	
Max rate: 40 m/yr	Tree-to-tree spread of B. fagacearum from 4 different foci monitored in live oak (Quercus fusiformis) with	Appel et al. 1989
Average rate: 11-16 m/yr		
(root-graft transmission)	Relative live oak density (area of crown cover divided by total area) in the four foci: 0.17 to 0.3. The focus that	
	expanded most rapidly had the greatest live oak density (0.3). The rapid rates of focus expansion were attributed	
	to a high potential for root grafting and the occurrence of common root systems among clonally propagated live oaks.	
at least 0.35 km	The dispersal behaviour of <i>S. intricatus</i> (potential vector in the UK) is of prime importance in assessing its role as	Gibbs et al., 1984
(potential vector in the UK)	a likely vector of oak wilt and from a field experiment using marked beetles it was estimated that, depending on	01003 et al., 1904
	climatic conditions, adults will fly at least 0.35 km from their emergence site.	
	Comments: relevant for transmission via candidate vector in the EU. However, no information on passive	
	movement and wind-driven dispersal.	Custon 1052
up to 400 m/year	Insect transmissions have been found to cover distances of up to 400 m	Guyton, 1952
(vector transmission in the US)		
7.5 m/yr	Quercus ellipsoidalis stands in Minnesota	Osterbauer, 2011
(root-graft transmission)	(Estimate for root-graft transmission in the US. Original source of information not provided)	
up to 600 m/year	Quercus ellipsoidalis (northern pin oak), Q. rubrus (northern red oak), Q. alba (white oak) and Q. macrocarpa (bur	Shelstad et al. 1991
vector transmission in the US)	oak)	
	Three test sites, in different counties in central Minnesota, 1977-1987. Oak-type forest predominant (see Table 1	
	in the paper).	
	Colour infrared aerial photography covering a ten-year interval. Expansion of oak wilt around existing disease	
	centres attributed to root grafting; occurrence of new disease centres attributed to insect transmission.	
	Bate of new infection contro formation was determined on a ner year basis. For each new infection control the	
	Rate of new infection centre formation was determined on a per year basis. For each new infection centre, the nearest active infection centre was considered as the source of infection.	
	Thearest active infection centre was considered as the source of infection.	



B.3 Summary on the evidence supporting the elicitation of the time to detection

Reference	Case	Aspect	Results
			/ evidence
Detection methods	Ι	T	
EPPO, 2001		Effects on detectability	Cultures of <i>B. fagacearum</i> isolated from infected wood tissue may be identified following the
			EPPO diagnostic protocols
Wilson, 2005		Additional information	Colour infrared remote sensing technology is used extensively in Texas to detect new oak wilt
			infection centres over large areas.
Biology of the pest	1	-	T
Blaedow and Juzwik,	Population dynamics	Effects on symptoms	The length of time between root inoculations and incipient wilt development ranges from several
2010 and references		expression	weeks to several years. The pathogen is capable of surviving undetected in the roots of
therein			apparently healthy trees for many years.
EFSA PLH Panel, 2018	Transfer capacity	Effects on incidence	In the USA the fungus mats are produced on red oaks that are infected in late summer. Mats
			form on these trees usually in spring the following year.
EFSA PLH Panel, 2018	Transfer capacity	Effects on incidence	Fungal mats are typically viable to attract casual insect vectors for only 2-3 weeks. Fungal mats
			deteriorate rapidly with the onset of high summer temperatures.
EFSA PLH Panel, 2018	Transfer capacity	Effects on detectability	B. fagacearum overwinters in diseased or dead trees and insect vectored infection generally
			takes place in the spring when the trees are most susceptible.
Gibbs and French,	Population dynamics	Effects on symptoms	In 40% of the oak trees grafted to an initially infected tree, symptoms were detected only 3 years
1980		expression	after the tree had died.
Gibbs and French,	Population dynamics	Effects on symptoms	When transmission occurs via the root system, above-ground symptom development in newly
1980		expression	infected trees might take several years.
			Time lags of (at least) 4 years were observed between occurrence of symptoms in neighbouring
			trees in northeast Virginia and in the Sinissippi Forest (Illinois).
Gibbs and French,	Transfer capacity	Effects on incidence	Wounds older than three days are not suitable sites for infection.
1980; Webber, 2015			
Juzwik, 2009	Transfer capacity	Effects on detectability	Highest frequency of insect-mediated transmission in the US: mid to late spring
			(Pseudopityopthorus spp.); during spring months (C. truncatus and C. sayi)
Peacock and Fulbright,	Population dynamics	Effects on symptoms	Disease progression in root-infected trees is often delayed in comparison to trees inoculated
2009		expression	above ground. Symptomless trees in naturally-infected stands may already have the pathogen
			within their roots.
Webber, 2015		Effects on detectability	In case oak wilt becomes established in the UK, symptoms could be initially misattributed to
			other disorders already present such as chronic or acute oak decline.
			This could make early detection difficult or impossible.



Webber, 2015	Life cycle	Effects on incidence	Under UK conditions, the behaviour of <i>Scolytus intricatus</i> could be suitable for the transmission of <i>B. fagacearum</i> . However, disease spread could be impeded because the phases of maximal insect feeding and optimal tree susceptibility may not coincide closely. In the US, the susceptibility of oaks to <i>B. fagacearum</i> is greatest during springwood formation in spring and early summer. In the UK, feeding by <i>S. intricatus</i> reaches a peak during late-wood formation, later in the year.
Wilson, 2005		Additional information	Foliar symptoms, patterns of tree mortality and presence of fungal mats can be indicators, but laboratory isolation of the fungus is usually required to confirm the diagnosis.
Host conditions during	the period of potenti	al detection	
Appel, 1995	Host species	Effects on symptoms expression	White oaks typically limit symptom development to a few branches per year
Camilli et al., 2009	Host species	Effects on symptoms expression	Symptom expression in live oaks (above-ground inoculation): symptoms first appeared 31 days after inoculation, 60% of the trees were symptomatic after 12 weeks
Davies, 1992	Host species	Effects on symptoms expression	In Spanish and blackjack red oaks, symptom expression occurs as quickly as 28 days after contagion.
Juzwik, 2011	Host species	Effects on symptoms expression/detectability	Branch dieback (single or several) in highly resistant species may or may not lead to tree death and may be misdiagnosed as oak decline.
Juzwik, 2011	Host species	Effects on symptoms expression	Veinal chlorosis and necrosis are unique leaf symptoms in live oaks that can be diagnostic for the disease. Leaf abscission of the semi-evergreen live oaks, as with the red oaks, also is typical.
Juzwik, 2000, 2011; Webber, 2015	Host species	Effects on symptoms expression	Red oaks typically die within 3 months of first symptom expression. Live oaks in Texas develop symptoms more slowly but usually die within 3 to 8 months of infection. White oaks may take several years to die.
Peacock and Fulbright, 2009	Host species	Effects on symptoms expression	Symptom expression in red oaks (above-ground inoculation): symptoms developed within 6 weeks following inoculation; trees completely wilted within the same year
Wilson, 2005	Host species	Effects on symptoms expression/detectability	Time of occurrence of leaf symptoms. Live oaks (Texas): primarily in the spring and fall. Red oaks: early spring (Texas); late June-early July (northern part of the disease range).