

Worldwide review of bacterial diseases of oaks (*Quercus* sp.) and their potential threat to trees in Central Europe

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The phenomenon of hhh Europe has been observed for over 100 years. In this time, many attempts have been made to describe this phenomenon considering biotic, abiotic and anthropogenic factors. Recently, an increasing intensity of bacterial tree diseases has been observed both in Europe and around the world. Moreover, climate change is contributing to an increase in the range of pathogens. The aim of this publication was to highlight the most important bacterial diseases occurring on oaks around the world, and to discuss the potential threat to native oaks occurring in Central Europe: English oak (*Quercus robur* L.) and sessile oak (*Quercus petraea* (Matt.) Liebl.). The main focus was on three diseases caused by different bacteria: bacterial leaf streak (caused by *Xylella fastidiosa*), acute oak decline (caused by *Gibbsiella quercinecans*, *Rahnella victoriana* and *Brenneria goodwinii*) and drippy nut disease (caused by *Brenneria quercina*—formerly *Erwinia quercina*). At present, these are the only known bacterial diseases that cause damage to oak stands. Information on each of the above-mentioned diseases is given in the review, ranging from their origin, importance, list of host plants and their potential threat to native oaks of Central Europe.

Introduction

The native species of oaks occurring in Central European forests include English oak (*Quercus robur* L.) and sessile oak (*Quercus petraea* (Matt.) Liebl.). These native species are important both from an economic and environmental point of view (Andrzejczyk, 2009; Stavi et al., 2022). In the 1980s and 1990s, the phenomenon of mass dieback of oak stands was observed across Europe. These events were caused by many abiotic factors, e.g. drought (Sohar et al., 2014; Colangelo et al., 2018), biotic factors, e.g. insects, fungi and oomycetes (Oszako et al., 2009; Denman and Webber, 2009; McConnell and Balci, 2014; Solla et al., 2021) and anthropogenic factors (Schütt et al. 1985).

Many factors that directly or indirectly contribute to the tree dieback phenomenon have been discussed in the literature (Oszako, 2007; Marçais and Desprez-Loustau, 2014). Earlier studies focused on damage of acorns (Stocka, 1997; Kowalski, 1999), leaves (Mańka, 1998), shoots and trunks (Kowalski, 1991), the roots of oaks (Przybył, 1999) and seedlings (Grzywacz, 1990; Mańka, 1998). Among the biotic factors responsible for the weakening and dieback of oak stands, bacterial pathogens are particularly important. Several bacteria can cause diseases in oaks. The most common are *Gibbsiella quercinecans*, *Brenneria goodwinii*, *B. roseae* subsp. *roseae*, *B. roseae* subsp. *americana*, *Lonsdalea quercina*, *G. greigii*, *Rahnella* spp., *Xylella fastidiosa* and *Pantoea agglomerans* (Brady et al., 2010; Denman et al., 2012; Scortichini et al., 1993; Nones et al., 2022). These bacteria

form part of a group of organisms that have so far been associated with the phenomenon of weakened oak stands. Some pathogenic bacteria have a wide host range and can be found in several niches. For example, *Pantoea agglomerans* (formerly *Erwinia herbicola*/*Enterobacter agglomerans*) is known as an epiphyte or pathogen of plants but can also be found as an opportunistic pathogen in humans. *Serratia* sp. is also an opportunistic human pathogen found in plants (Grimont et al., 1977; Grimont and Grimont, 1984). Nevertheless, some of these organisms can cause serious damage to oak stands and contribute to their diseases in the short and long term. Currently, knowledge about bacterial diseases of oaks is limited. This study therefore aimed to compile detailed information on the risks, symptoms and occurrence of bacterial diseases that may pose a serious threat to oak stands. Important issues related to the occurrence of bacterial oak diseases and their threat to native oak species (*Q. robur* and *Q. petraea*) occurring in Central Europe are discussed. At the same time, the present overview aimed to identify research questions that should be investigated in order to identify threats from bacteria in forestry and new research that increases the knowledge about these threats.

Methods

For a comprehensive approach to the phenomenon of oak bacterial diseases, various published studies related to this topic

were reviewed. The Web of Science database was queried in January 2022 to collect the relevant literature. To exclude irrelevant literature items, a filter confining the search to issues related to forestry and biology was imposed. Various keywords were used starting with the more general ones, e.g. 'bacteria', which resulted in a search of 14 495 records. However, when the search was narrowed down to 'bacterial diseases', no results were obtained with the filters turned on. Finally, the following keywords were used: 'bacteria', 'pathogen' and 'tree', which resulted in a database of 83 records appropriate for this topic, which were the basis for further searching. A dash was used when searching for an exact phrase and keywords were entered in TOPIC (TS) to search within titles, abstracts and author keywords in the records.

After initial database queries, the search was further narrowed down to include three diseases and their causative agents related to the dieback of oaks. The final search used the following keywords: 'bacterial leaf streak', '*X. fastidiosa*', 'acute oak decline', '*Gibbsiella quercinecans*', '*Rahnella victoriana*', '*Brenneria goodwinii*', 'drippy nut disease' and '*Brenneria quercina*'. A total of 123 articles from 1991 to January 2022 were obtained. This review is based on a selection of articles from these results plus some works that were cited within the selected articles. Articles not used in the author's assessment did not contain any relevant information.

The findings of our review are presented in three sections focused on the overarching diseases bacterial leaf streak, acute oak decline and drippy nut disease, followed by a synthesis of the most important findings in a summary section.

Bacterial leaf streak

Bacterial leaf streak (BLS) in forest trees is a complex disease caused by, abiotic and biotic factors. This disease is especially important today because water stress has a significant influence on the development of symptoms (McElrone et al., 2001; Choi et al., 2013). Among the biotic factors, one of the most important is the bacterium *X. fastidiosa*, which manifests as brown or orange discoloration on leaves (Desprez-Loustau et al., 2021). This disease is primarily transmitted by the insects *Philaenus spumarius* and *Neophilaenus campestris* (Godefroid and Durán, 2022) and occurs mainly in the eastern part of the USA (Lashomb et al., 2002). When plants are infected, the bacteria live in the xylem vessels, limiting sap flow and causing the appearance of leaf wilting.

Initially, *X. fastidiosa* was primarily associated with diseases of arable crops and citrus trees. However, further research has shown that the organism lives as an endophyte in many other plant species (Gambetta et al., 2007; Chatterjee et al., 2008; Purcell, 2013; Roper et al., 2019). The full extent of host species was originally overlooked, as many plants living within areas overlapping with the natural distribution of *X. fastidiosa* have evolved appropriate defence mechanisms that protect them against severe bacterial infections for example *Vitis rotundifolia* (Ruel and Walker, 2006). *X. fastidiosa* is a relatively well-known organism and was the first non-viral plant pathogen to have its full genome sequenced (Simpson et al., 2000). Extensive research over the past decades has shown that *X. fastidiosa* is a genetically

diverse species with several subspecies (Denancé et al., 2019). Most diseases of *X. fastidiosa* have been reported in regions with Mediterranean, tropical and subtropical climates (EFSA, 2018a, 2018b; 2019; 2022).

In forestry, BLS was mainly reported in native American oak, elm and sycamore species such as *Quercus rubra*, *Ulmus americana* and *Platanus occidentalis* (Wells et al., 1987; Lashomb et al., 2002; Sinclair and Lyon, 2005; Sherald, 2007; Harris and Balci, 2015). Oaks have been shown to be particularly susceptible. Eighteen species have been reported as natural hosts of *X. fastidiosa*, mainly in the *Quercus* sections *Lapidobalanus* and *Lobatae* (Gould and Lashomb, 2007). Of the latter group, pedunculate oak and northern red oak are most often infected by bacteria (Sherald, 2007; McElrone et al., 2008; Harris and Balci, 2015). BLS predominantly affects trees on the east coast of the USA, primarily in Florida, South and North Carolina, Tennessee, Oklahoma, Kentucky, Missouri, Indiana, Pennsylvania, New Jersey, New York and Washington DC (Sherald and Kotska, 1992; Hartman et al., 1995; Sinclair and Lyon, 2005; Sherald, 2007; Nunney et al., 2013; Harris et al., 2014). It should be noted that research conducted by local scientists mainly concerns native species, but Nunney et al. (2013) also confirmed the presence of *X. fastidiosa* in English oak (of European origin) planted in the USA. The complete list of *X. fastidiosa* natural hosts (not only tree species) can be found in the EFSA database (EFSA, 2018a; Delbianco et al., 2019).

Despite these reports from North American, in Europe *X. fastidiosa* has thus far been reported primarily as a threat to agriculture and horticulture (EFSA, 2015, 2019; Lashomb et al., 2002; Baldi and Porta, 2017). In forest areas, this bacterium did not seem to cause any serious damage. However, the situation has recently changed when the causative agent of olive tree dieback in southern Italy (OQDS or CoDiRO) was identified as *X. fastidiosa* (Wells et al., 1987; Saponari et al., 2013; Almeida, 2016). This report has led to the mass testing of trees in other parts of Italy and the rest of the Mediterranean countries in Europe. These large-scale studies confirmed the presence of *X. fastidiosa* in various plant species in Italy (Tuscany), Spain and the Balearic Islands, Portugal, Germany and France (EFSA, 2019). After significant consequences were observed due to the presence of *X. fastidiosa* in Italy, extensive research was also carried out in France (Denancé et al., 2017). A total of 45 000 samples of a variety of plant species were collected and analyzed. The presence of the bacterium was confirmed in only 3 per cent of the samples, including some forest tree species such as *Acer pseudoplatanus*, *Quercus ilex* and *Quercus suber* (Denancé et al., 2017). According to various epidemiological models, this pathogen may have appeared in Corsica as early as in 1985 (Soubeyrand et al., 2018), and since then has established, inter alia, in southern Italy (Strona et al., 2017) and in the Balearic Islands (Moralejo et al., 2019).

It is difficult to predict the impact of introduced strains of *X. fastidiosa* in new areas. Some reports from Italy indicated that this bacterium can potentially pose a high risk to olive trees, while in California its importance on this host was negligible (Krugner et al., 2014). So far, nearly a hundred forest tree species have been studied to identify possible hosts for *X. fastidiosa* in Europe (Mauri et al., 2017). According to the EFSA database, 15 species have been classified as potential host plants globally (Table 1), including several species of oak, e.g. *Q. ilex* or *Q. suber* (EFSA 2015, 2018b, 2019). To date, only nine species of trees have

been recorded as host plants in Europe. Interestingly, the species affected by BLS in the USA, such as *Q. rubra*, were not included in this list. This may be because *X. fastidiosa* has been observed mainly in the Mediterranean basin, where it is not very common.

It is also worth mentioning that different subspecies of *X. fastidiosa* may pose greater or lesser threats to various host plants. The greatest threat to oaks and other forest trees is *X. fastidiosa* subsp. *multiplex*, mainly due to the overlap in the distribution range of the pathogen and the host species (Desprez-Loustau et al., 2021) (Table 1). This subspecies evolved over 15 000 years ago and is specialized in temperate climate zones. Thanks to this, it is well adapted to infect host plants, including oaks, found in these climate zones (Nunney et al., 2013). Another feature related to the adaptation of this subspecies is its ability to survive in cooler conditions in comparison with the other subspecies (Sicard et al., 2018). However, climate change in recent years has led to a shift in the geographic ranges of various organisms. It cannot be ruled out that the warmer summers and milder winters recently observed in the temperate zone may soon lead to the emergence of threats from other subspecies such as *X. fastidiosa* subsp. *fastidiosa* and *X. fastidiosa* subsp. *sandyi*, which are currently responsible for the infestation of almonds and oleanders in USA (Nunney et al., 2013). Recent research shows that that western European countries have the highest risk for appearance of *X. fastidiosa*, but that the Mediterranean basin runs the highest risk for establishment and spread of *X. fastidiosa* (Frem et al. 2020).

The above information shows that oak species found in Central Europe, in particular *Q. robur*, could be under threat from *X. fastidiosa*. Pedunculate oak infection has already occurred in France (Denancé et al., 2017) and, large-scale studies in Europe have also confirmed the presence of *X. fastidiosa* in Germany (EFSA, 2019). Moreover, in the light of climate change, much warmer summers and milder winters may lead to the spread of BLS to forest trees of Central Europe. Such infestations may become a serious problem in future.

Acute oak decline

The disease defined as Acute Oak Decline (AOD) is not a new phenomenon. The name stems from the rapid and dynamic course of the disease, which can lead to mortality of trees in 5–6 years (Denman et al., 2010). The first reports of this disease were recorded at the beginning of the 20th century in Great Britain. At that time, the cause of the disease was assumed to be a combination of two pathogens: *Tortrix viridana* responsible for early spring defoliation of trees and *Erysiphe alphitoides* appearing as powdery mildew on second-flush leaves in summer (Day, 1927; Osmaston, 1927; Robinson, 1927; Robin 1992). This combination of pathogens over the long term has led to rapid weakening and, consequently, dieback of trees.

In Great Britain, the AOD phenomenon has been observed again in recent years. The course of the disease (rapid deterioration of tree health and a high level of tree mortality) is consistent with the description of AOD from the beginning of the 20th century, although bacteria are now considered to be the causative factors (Denman and Webber, 2009). Trees affected by AOD show profuse exudates from between the cracks in the bark



Figure 1 Symptoms of Acute Oak Decline on *Quercus robur* observed on a weakening tree (photo by Alejandro Solla, Staffordshire, UK).

(Figure 1). Initially, necrotic spots are present from just below the bark, and these transform into fluid-filled cavities that flow from underneath the bark in spring (Denman and Webber, 2009). Over time, the exudates dry out to form shiny, sticky drops on the bark's surface.

Recent studies have identified *Gibbsiella quercinecans*, *Rahnella victoriana* and *Brenneria goodwinii* to be the main causative agents of AOD in Great Britain (Denman et al., 2017; 2014; Bakhshi ganje et al., 2020; Brady et al., 2022). All three bacterial species play a role in lesion formation in the current outbreak of AOD in Britain, although *B. goodwinii* is the most dominant. Additionally, as reported by Brady et al. (2022), *B. goodwinii* develops the fastest even when tissues were infected with all three bacteria. All three pathogens are gram-negative bacteria that have been described relatively recently. The first reports of *G. quercinecans* originate from 2010, when the bacterium was described by Brady et al. (2010) as one of the agents responsible for the mass dieback of *Q. robur* and *Q. petraea* oaks in Great Britain. Another AOD-related bacterium is *R. victoriana* isolated in visibly weakened oak stands (Brady et al., 2014). *B. goodwinii* was only described in 2012 (Denman et al., 2012). Multiple pathogenicity tests showed that *B. goodwinii* was the most detrimental pathogen (Bakhshi ganje et al., 2020). However, most studies indicate the other two bacteria are most often isolated from exudates on weakened oaks (Brown et al., 2014; Denman et al., 2017; 2014; Broberg et al., 2018). Some bacteria may spread in rainy and windy weather when the exudates are smeared by water, or through the impact of droplets that cause bacterial cells to 'burst' over long distances. Infection also takes place through natural openings in the trees (stomata, spiracles), uncovered cuticles and, most importantly, through various types of damage (Király et al., 1977). However, the most common way of spreading bacteria is through insects. Dark exudates were often observed in the larval galleries of *Agrilus biguttatus* (Denman and Webber, 2009; Denman et al., 2014, 2017). The presence of bacteria in these galleries, as well as the presence of the characteristic outlet openings (D-shaped), may indicate a relationship between the organisms (Denman et al., 2014).

Table 1 Forest tree species, presence of natural infection and the subspecies of *X. fastidiosa*. Subspecies responsible for infections according to the EFSA database (EFSA 2022).

Species	Natural infection	<i>Xylella fastidiosa</i> subspecies
<i>Acer griseum</i>	USA	Multiplex
<i>A. rubrum</i>	USA	Multiplex
<i>A. platanoides</i>	USA, Canada	Multiplex
<i>A. pseudoplatanus</i>	France	Multiplex
<i>Aesculus hippocastanum</i>	Canada	Unknown
<i>Alnus rhombifolia</i>	USA	Multiplex
<i>Ficus carica</i>	USA, France, Spain	Multiplex
<i>Fraxinus americana</i>	USA	Multiplex
<i>F. angustifolia</i>	Spain	Multiplex
<i>Juglans regia</i>	Spain	Fastidiosa
<i>Liquidambar styraciflua</i>	USA	Multiplex
<i>Olea europaea</i>	USA, Argentina, Brazil, Italy, Spain, France	Multiplex, Pauca
<i>Prunus avium</i>	USA, Italy, Spain, France	Fastidiosa, Multiplex, Pauca
<i>P. cerasifera</i>	USA, France	Multiplex
<i>Quercus agrifolia</i>	USA	Xf subsp. Unknown
<i>Q. alba</i>	USA	Xf subsp. Unknown
<i>Q. coccinea</i>	USA	Multiplex
<i>Q. falcata</i>	USA	Multiplex
<i>Q. ilex</i>	France	Pauca
<i>Q. imbricaria</i>	USA	Unknown
<i>Q. incana</i>	USA	Unknown
<i>Q. laevis</i>	USA	Multiplex
<i>Q. laurifolia</i>	USA	Unknown
<i>Q. macrocarpa</i>	USA	Multiplex
<i>Q. nigra</i>	USA	Multiplex
<i>Q. palustris</i>	USA	Multiplex
<i>Q. petraea</i>	USA	Multiplex
<i>Q. phellos</i>	USA	Multiplex
<i>Q. pubescens</i>	USA	Multiplex
<i>Q. robur</i>	Portugal	Multiplex
<i>Q. rubra</i>	USA	Multiplex
<i>Q. shumardii</i>	USA	Multiplex
<i>Q. suber</i>	France, USA	Multiplex
<i>Q. velutina</i>	USA	Unknown
<i>Q. virginiana</i>	USA	Unknown
<i>Ulmus americana</i>	USA	Fastidiosa, Multiplex
<i>U. crassifolia</i>	USA	Multiplex
<i>U. glabra</i>	USA	Unknown

AOD caused by bacteria has been described relatively recently in the UK and similar symptoms had already been observed in oaks in Spain (Biosca et al., 2003; Poza-Carrión et al., 2008). It was mostly thought that the effusions visible on oak trunks (*Q. robur*) were caused by the presence of *B. quercina* and *Serratia* spp. bacteria. Only in 2020, was the presence of the bacteria *G. quercinecans* and *B. goodwinii* confirmed in the exudate of weakened oaks in the northern part of Spain (González and Córdia, 2020). Recently, the negative influence of *B. goodwinii* on *Q. suber* in Portugal (Fernandes et al., 2022) and on *Q. brantii* in Iran (Zolfaghari et al., 2022) has also been confirmed. Additionally, Zolfaghari et al. (2022) emphasized the negative impact of drought in combination with the presence of the pathogen, which led to significantly faster death of host plants. Very high

temperatures and lack of water cause plant stress, which makes them more susceptible to various types of infection. Such long-term phenomena can spread the disease much faster.

AOD caused by bacteria may pose a very serious threat to native oak species in Central Europe. Literature reports indicate a growing problem as well as an ever-increasing area of damage caused by these microorganisms. In 2021, Tkaczyk et al. (2021) confirmed the presence of *G. quercinecans* and *B. goodwinii* in exudates on declining pedunculate oaks in Poland. Along with the bacteria on these trees, there were also visible exit holes characteristic of *A. biguttatus*. It is difficult to determine whether the phenomenon of AOD is really present in Poland and if the presence of bacteria was clearly related to the health condition of the studied trees. As described by Tkaczyk et al. (2021), it



Figure 2

is necessary to conduct further detailed studies to confirm or rule out the hypothesis of the AOD phenomenon in Poland. In 2020, the presence of AOD was also reported in Switzerland (Ruffner et al., 2020) and similar observations have been made in other parts of Central Europe. Zalkalns and Celma (2021) reported the occurrence of *G. quercinecans* and *B. goodwinii* in oak (*Q. robur*) stands in Latvia. These findings indicate that AOD is more widespread in Central Europe than previously thought. It is likely not new either, and the lack of information on this topic is because the effusions on oak trunks are often caused by other factors, e.g. *Armillaria* stem bleeding, *Phytophthora* stem bleeding, *Agrilus* stem bleeding or frost and drought cracks (Denman et al., 2014). Consequently, the contribution of known and previously described factors to these exudates has not been investigated sufficiently. In addition, AOD is included in very few reports on forest tree bacterial diseases, which is why they are often overlooked at the diagnostic stage. An increase in new information about AOD has caused greater interest in this phenomenon, which in turn translated to more reports about the occurrence of this phenomenon in various parts of Europe. Such reports do not necessarily mean that AOD is new for a given region.

Drippy nut disease

Drippy nut disease is a bacterial disease that affects oak acorns. This phenomenon was first described in 1967 (Hildebrand and Schroth, 1967) in the USA (California). Drippy nut disease was mainly observed on native species such as *Quercus agrifolia* and *Quercus wislizenii*. A typical symptom of this phenomenon is the appearance of clear, brown or sometimes foaming discharge from the acorn (Figure 2). This phenomenon intensifies in the spring and autumn period and both older and mature acorns as well as younger, not yet fully developed ones are infected (Hildebrand and Schroth, 1967). The bacterium was originally described by Hildebrand and Schroth (1967) as *Erwinia quercina* but was later classified, along with several other pathogenic bacteria, under the genus *Brenneria* by Hauben et al. (1998). Since then, this species has been described as *B. quercina*. This bacterial infection most likely occurs because of damage to the acorn by insects from the *Curculionidae* family (Hildebrand and Schroth, 1967). In the mid-twentieth century in California, these bacteria were isolated only from acorns with characteristic symptoms, despite attempts to isolate *B. quercina* from leaves or other tree tissues (Hildebrand and Schroth, 1967).

Since the first report of drippy nut disease caused by *B. quercina*, there has not been much new information about the

disease, and little is known about its course and significance (Wright et al., 1989; Raabe, 1990). The drippy nut disease phenomenon resurfaced at the end of the 20th century when typical symptoms, i.e. profuse exudation of acorn juices and their rotting, were observed in the area of Madrid in Spain (Soria et al., 1997). Research at the time showed that *B. quercina* was responsible for damage to as much as 30–40 per cent of the acorns in this region. This problem turned out to be very important economically because acorns are harvested in Spain for the feeding of Iberian pigs (Soria et al., 1997).

In the following years, the weakening of native oaks in Spain had begun to intensify. Abundant exudates and bleeding cankers were observed on the tree trunks (Biosca et al., 2003). The symptoms were very similar, with longitudinal cracks extending through the affected areas and mucus oozing from the crevices over time and running down the bark surface. Bacteria isolated from attacked oaks (*Q. ilex* and *Q. pyrenaica*) in Spain was identified as *B. quercina* based on biochemical characterisation, fatty acid profiling, rep-PCR and 16S rRNA gene sequencing. These isolates have been found to induce symptoms of cortical cancer during pathogenicity tests (Biosca et al., 2003; Poza-Carrión et al., 2008). Nowadays, drippy nut disease is not an important disease in *Quercus* spp. in Iberia, although in some years and areas it could impair natural regeneration and the success of restoration plans.

Even though the bacterium *B. quercina* does not currently infect native oak species found in the region of Central Europe, its description was included as a potential threat in the future. Climate change will affect many organisms both hosts and pathogens (Ramsfield et al., 2016). For *X. fastidiosa* and *B. goodwinii*, climate change is of great importance when considering the potential spread of the disease. In the case of *X. fastidiosa*, there are differences in pathogenicity between subspecies. Presently, the greatest threat to oak stands is *X. fastidiosa* subsp. *multiplex* mainly due to its adaptation to the climate prevailing in central Europe (Nunney et al. 2013). Climate warming will naturally lead to the shifting of geographic limits and ranges of organisms, enabling other subspecies such as *X. fastidiosa* subsp. *fastidiosa* to find a suitable ecological niche. On the other hand, there is the situation in Iran described by Zolfaghari et al. (2022) where a significant weakening of plants was observed. This was due to high temperatures and water scarcity, which led to the increased death of *Q. brantii* due to infection by *B. goodwinii*. These climate conditions increase the exposure of trees to pathogens, which can easily infect weakened plants. This can lead to the exacerbation of the dieback phenomenon. The examples shown above show that although the bacterium *B. quercina* only damaged acorns in the USA, it contributed to much more serious damage by causing cankers under different conditions and on other host plants. Perhaps the emergence of this bacterium in Central Europe and the infestation of species native to this area (*Q. robur* and *Q. petraea*) will lead to an even greater threat than that observed at the beginning of the 21st century in Spain.

Summary

Bacteria associated with plants can have both beneficial and negative effects on the development of their hosts. Epiphytic bacteria may be present on the entire surface of the plant and not affect its growth in any way. Other organisms considered

endobionts live inside plants. Some of them are residents (endophytes), which means they may be present in the plants all the time, and some may only be in their hosts periodically. Such bacteria can be pathogens or only become pathogens under certain conditions (Newton et al. 2010; Stengel et al. 2022). However, so far, knowledge about bacterial pathogens of oaks in Central Europe is limited. Until now, exudates on trunks have been associated mainly with mechanical damage (due to the action of insects or other biotic agents) or infections by pathogens of the genus *Phytophthora* (Jung et al., 1996; Oszako, 2007; Oszako et al., 2009). However, mainly due to reports about the presence of Acute Oak Decline in Great Britain (Denman et al., 2010), more and more attention has been paid to the threats from bacterial pathogens recently.

The first reports oaks native to Central Europe (*Q. robur* and *Q. petraea*) suffering from bacterial diseases date back to the beginning of the 1920s (Falck, 1918; Klimesch, 1924; Yossifovitch, 1926; Day, 1927; Osmaston, 1927; Robinson, 1927). The emergence of new threats from bacteria may intensify this process of oak decline. The presence of *G. quercinecans* and *B. goodwinii* has been confirmed in Poland, Latvia and Switzerland (Ruffner et al., 2020; Tkaczyk et al., 2021; Zalkalns and Celma, 2021). It is true that further research is necessary to confirm the negative impact of such bacteria, but examples from the literature show how different organisms in different environments may contribute to the decline of native oak stands in Central Europe. As mentioned earlier, the presence of stem exudates can often be mistakenly associated with the influence of other biotic and abiotic factors. Therefore, it is necessary to conduct basic research aimed at understanding the scale of the problem related to bacterial diseases on oaks and testing them for pathogenicity. In addition, paying attention to the importance of bacterial diseases in forestry may contribute to the development of phytopathology, which will contribute to the improvement of forest trees health. More importantly, drawing diagnostic service's attention to this problem may also help to limit the spread of these diseases. Therefore, it is necessary to continue research in this field and to react early to emerging threats from biological factors, including pathogenic bacteria.

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Conflict of interest statement

None declared.

Data Availability

No new data were generated or analysed in support of this research.

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