Journal of Plant Diseases and Protection (2026) 133:172
https://doi.org/10.1007/s41348-026-01366-4

ORIGINAL ARTICLE

Biscogniauxia rosacearum, first evidence in Germany and pest risk analysis for the potentially quarantine relevant charcoal canker fungus

Gritta Schrader[1] · Steffen Bien[2] · Clovis Douanla-Meli[1] · Björn Hoppe[1] · Gitta Jutta Langer[2]

Received: 30 September 2025 / Accepted: 7 October 2026
© The Author(s) 2026

Abstract
Since *Biscogniauxia rosacearum* has been detected in Germany for the first time, a pest risk analysis (PRA) for this wood-decaying fungus with potential quarantine relevance is presented. This species which is known to be distributed throughout the Mediterranean region and presumably native to the Middle East, is usually found on Rosaceae and other deciduous trees. Two new host tree species were identified, *Abies grandis* and *Pseudotsuga menziesii*. Furthermore, this ascomycete was compared to *Biscogniauxia mediterranea*, which is prevalent in Germany, and was distinguished in a multigene phylogeny based on ITS, *TUB*, and *ACT* sequence alignment. In addition, a qPCR-assay using a previously published species-specific primer combination for the detection of B. mediterranea was applied on a selection of isolated B. mediterranea and B. rosacearum strains, which revealed that this primer combination is unsuitable for identifying *B. mediterranea*, since it specifically amplifies DNA of *B. rosacearum*.

Keywords Graphostromataceae · Wood-decay fungus · Pest risk analysis · Multigene phylogeny · Tree pathogen

Introduction

The genus *Biscogniauxia* Kuntze comprises approximately 90 species names (as of September 2025; www.indexfungorum.org, www.mycobank.org) and belongs to the family Graphostromataceae M.E. Barr, J.D. Rogers & Y.M. Ju, order Xylariales Nannf. within the phylum Ascomycota (Senanayake et al. 2015; Daranagama et al. 2018; Hyde et al. 2020). The family furthermore includes the genera *Camillea* Fr., *Cryptostroma* P.H. Greg. & S. Waller, *Graphostroma* Piroz., *Obolarina* Pouzar, and *Vivantia* J.D. Rogers, Y.M. Ju & Cand. (Hyde et al. 2020; Li et al. 2021) (Hyde et al. 2020; Li et al. 2021). The genus *Biscogniauxia* was named by Carl Ernst Otto Kuntze in 1891 to honour the Belgian botanist Célestin Alfred Cogniaux (1841–1916) (Kuntze 1891). Species of *Biscogniauxia* have a worldwide distribution and have been recorded on a wide range of woody host plants (Bahmani et al. 2021). *Biscogniauxia* species comprise pathogens and endophytes of angiosperms (Hyde et al. 2020; Tropf et al. 2025). However, they are also known as endophytes of the woody and foliar tissues of conifers. For instance, *B. mediterranea* (De Not.) (Fig. 1a-c) and the type species *B. nummularia* (Bull.) Kuntze (Fig. 1d-g) have recently been found in association with Scots pine (*Pinus sylvestris* L.) and giant sequoia (*Sequoiadendron giganteum* (Lindl.) J. Buchholz) (Bußkamp et al. 2020; Langer et al. 2024). As plant pathogens, *Biscogniauxia* species are able to cause severe wood-decay and such events frequently occur in trees which are already significantly weakened for example by abiotic factors, such as intense drought (Ju et al. 1998). According to the phylogenetic analysis by Koukol et al. (2014), the anamorphic fungus *Cryptostroma corticale* (Ellis & Everh.) P. H. Greg. & H. Waller, which is the causal agent of Sooty bark disease (SBD), is closely related to *B. bartholomei* (Peck) Lar. N. Vassiljeva and *G. platystomum* (Schwein.) Piroz. According to Daranagama et al. (2018), the genus *Biscogniauxia* seems to be paraphyletic within the Graphostromataceae. As indicated by Ju et al. (1998), *Biscogniauxia* species are well adapted to dry habitats, or at least, to habitats that are dry for part of the year. The mycelial development occurs inside the bark of the host

✉ Gritta Schrader
gritta.schrader@julius-kuehn.de

[1] Julius Kühn Institute (JKI) – Federal Research Centre for Cultivated Plants, Institute for National and International Plant Health, Braunschweig, Germany

[2] Department of Forest Protection, Northwest German Forest Research Institute (NW-FVA), Göttingen, Germany

Published online: 29 October 2026



Fig. 1 *Biscogniauxia* spp. and infected host tissues. a-c) Fructification of *Biscogniauxia mediterranea* (a-b = 2025-72, c = 2023-33), d-g) Symptoms of damage due to *B. nummularia*, h-l) the studied host tissue from which *Biscogniauxia rosacearum* was isolated, h-j) *Abies grandis* (2021-69), k-l) *Pseudotsuga menziesii* (2024-73)

plants and the fructifications, both anamorphic and teleomorphic, are produced superficially on the twigs, branches, and trunks of angiosperm plants (Hyde et al. 2020). In addition to teleomorphs, several species exhibit a periconiella- or nodulisporium-like anamorph (Hyde et al. 2020).

According to the USDA database (Farr and Rossman 2022), 13 *Biscogniauxia* species are known to occur in Europe. These include *B. anceps* (Sacc.) J.D. Rogers, Y.M. Ju & Cand. (Rogers et al. 1996), *B. capnodes* (Berk.) Y.M. Ju & J.D. Rogers. (https://www.gbif.org/species/3461055), *B. cinereolilacina* (J.H. Mill.) Pouzar (Pouzar 1979, 1986), *B. communapertura* Y.M. Ju & J.D. Rogers (Ju et al. 1998), *B. dennisii* (Pouzar) Pouzar (Pouzar 1979), *B. granmoi* Lar.N. Vassiljeva (Læssøe et al. 1999; Zíbarová and Kout 2017),

B. marginata (Fr.) Pouzar (Pouzar 1979, 1986; Chlebicki and Bujakiewicz 1994), *B. mediterranea* (Ju et al. 1998; Zíbarová and Kout 2017), *B. nummularia* (Pouzar 1979, 1986; Læssøe et al. 1999), *B. querna* Pouzar (Pouzar 1986), *B. repanda* (Fr.) Kuntze (Pouzar 1979, 1986; Chlebicki and Bujakiewicz 1994), *B. rosacearum* M.L. Raimondo & Carlucci, and *B. simplicior* Pouzar (Pouzar 1986).

Until recently, only four *Biscogniauxia* species were known to occur in Germany, namely *B. capnodes* on a non-native *Latania* sp., (Ju et al. 1998), *B. mediterranea* on oak (Ju et al. 1998; Bußkamp et al. 2020, 2024; Langer and Bußkamp 2021, 2023) and Scots pine (Bußkamp et al. 2020), *B. nummularia* on *Fagus sylvatica* (Ju et al. 1998; Læssøe et al. 1999; Tropf et al. 2025), and *B. repanda* on the Betulaceae *Alnus glutinosa* (L.) Gaertn. and *Betula pendula* Roth (Schmid-Heckel 1988; Chlebicki and Bujakiewicz 1994). According to own observations as well as the relevant literature, *B. nummularia*, *B. mediterranea*, and *B. rosacearum* can induce strip-cankers on their host trees, also referred to as charcoal canker or tarcrust (Hendry et al. 1998; Granata and Sidoti 2004; Nugent et al. 2005; Ragazzi et al. 2007; Henriques et al. 2015; Luchi et al. 2015; Raimondo et al. 2016; Yangui et al. 2019). First visible signs of infection or parasitic growth are often bark blisters on the host tree (Fig. 1e), later on blackish, elongated bark lesions (strip cankers) on the trunks (Fig. 1d) and branches appear and teleomorphs (Fig. 1a-d, g) and/or anamorphs (Fig. 1e-f) are produced. The parasitic growth of the three *Biscogniauxia* species lead to wood decay often followed by green wood and brittle fracture (Fig. 1g).

The occurrence of *B. mediterranea* has been reported in Africa, Europe, North and Central America (Ju et al. 1998). It is widely distributed in Europe, where it is associated with oak (Ju et al. 1998) and the causal agent of charcoal canker on *Quercus suber* L. (Fagaceae) in the Mediterranean basin (Hyde et al. 2020). It has been hypothesized that *B. mediterranea* enters the host tree initially through the trunk and leaves (Gharbi et al. 2020), where it can be recognised as an endophyte in apparently healthy plants (Tropf et al. 2025). However, it can switch to its pathogenic lifestyle in water-stressed host plants (Edwards et al. 2003). *Biscogniauxia mediterranea* has been detected frequently in various tree species (Ju et al. 1998; Langer and Bußkamp 2021; Bußkamp et al. 2024).

The latent pathogen *B. nummularia* is considered to be one of the most frequently detected fungal endophytes in European beech (*Fagus sylvatica* L., Fagaceae) (Chapela and Boddy 1988; Nugent et al. 2005; Langer et al. 2021; Langer and Bußkamp 2021; Tropf et al. 2025). When its host is stressed by drought and heat, the fungus can transit from an endophytic to a pathogenic lifestyle, causing various symptoms such as bark necrosis, bark blistering, bark ruptures, strip-cankers, and brittle fractures (Granata and Whalley 1994; Hendry et al. 1998; Nugent et al. 2005). *Biscogniauxia nummularia* is the causal agent of beech bark tar crust disease and charcoal canker in *F. orientalis* and *F. sylvatica* (Vujanovic et al. 2020; Patejuk et al. 2022; Zamani et al. 2024). Additionally, it is one of the key fungal agents in beech decline (Granata and Whalley 1994; Granata and Sidoti 2004) and vitality loss of beech (Langer and Bußkamp 2021, 2023). *Biscogniauxia nummularia* can form periconiella-like anamorphs in vitro and in planta, which produce powdery, light-coloured, globose conidia (Petrini and Petrini 1985; Langer 2024). Although *B. nummularia* has been detected in many different angiosperms and gymnosperms (Petrini and Petrini 1985), to date, fruiting bodies and damage to trees have only been documented in *F. orientalis* Lipsky and *F. sylvatica* (Petrini and Petrini 1985; Nugent et al. 2005; Langer and Bußkamp 2023; Zamani et al. 2024).

Biscogniauxia rosacearum is presumably native to the Middle East, and has already been reported in the EU. For instance, it is the causal agent of the charcoal canker on species in the family Rosaceae Juss., including *Pyrus communis* L. (pear), *Prunus domestica* L. (plum), and *Cydonia oblonga* Mill. (quince), first observed in Italy (Raimondo et al. 2016). Despite the fact that *B. rosacearum* is of phytosanitary significance (EFSA 2022; JKI 2025), it is not currently listed as a quarantine pest or a regulated non-quarantine pest in the annexes to Regulation (EU) 2019/2072. Furthermore, it is not listed by the European and Mediterranean Plant Protection Organization (EPPO). Generally, *B. rosacearum* infects a broad range of host plants, including almond (*Prunus dulcis* (Mill.) D.A.Webb, Rosaceae), grapevine (*Vitis vinifera* L., Vitaceae), pear, plum, quince, strawberry tree (*Arbutus unedo* L., Ericaceae) and various oak species in the Mediterranean region, Middle East, and Africa (Raimondo et al. 2016; Bahmani et al. 2021; Sohrabi et al. 2022; Bashiri et al. 2022; Yangui et al. 2024). Recently, *B. rosacearum* has been found for the first time in Germany on *Abies grandis* (Douglas ex D.Don) Lindl. (Pinaceae) and on *Pseudotsuga menziesii* (Mirbel) Franco (Pinaceae). Therefore, an express pest risk analysis (Express-PRA) on *Biscogniauxia rosacearum* was conducted and disseminated (JKI 2025).

Both, *B. rosacearum* and the closely related species *B. mediterranea* are thought to have a high degree of intraspecific diversity (Henriques et al. 2016; Bashiri et al. 2022). Regarding *B. mediterranea*, it is assumed that the epidemiology of the disease caused by this species may have changed. Its high genetic variability, even in small populations, is attributed to its heterothallic mating system, its high sexual reproduction rate, and the production of large quantities of ascospores (Vannini et al. 2008; Henriques

et al. 2016). The same likely applies to *B. rosacearum*. A previously unpublished phylogenetic analysis based on ITS sequences (JKI 2025) indicates that *B. rosacearum* has a much broader host range and a more extensive geographical distribution than is currently recognised. This is largely related to the fact that in the past, some sequences belonging to *B. rosacearum* have been incorrectly assigned to *B. mediterranea* and deposited in sequence databases as such, due to inadequate taxonomical identification. Therefore, comparison of current sequence data with older entries can easily lead to confusion.

Therefore, the aims of this study were to:

1) present additional information on *B. mediterranea*, *B. nummularia*, and *B. rosacearum,*
2) identify *B. rosacearum* strains that may not have been identified initially and that were assigned to *Biscogniauxia* in the strain collection of the Northwest German Forest Research Institute (NW-FVA),
3) identify potential *B. rosacearum* entries in the NCBI GenBank database that may not have been identified previously,
4) test and evaluate the species-specific primers for *B. mediterranea* published by Luchi et al. (2005),
5) evaluate the host and distribution range of *B. rosacearum* so far as known, *and,*
6) assess the phytosanitary risk of *B. rosacearum* by conducting a pest risk analysis (PRA) according to the standards of the International Plant Protection Convention (IPPC) and the European and Mediterranean Plant Protection Organization (EPPO).

Materials and methods

Cases of disease and fungal isolation

The forest sites and cases of diseases associated with the incidences of *B. rosacearum* in Germany were studied in 2021 and 2024 as part of routine forest protection consulting and causal analysis of forest damage by the Northwest German Forest Research Institute (NW-FVA). Two specimens of *B. rosacearum* were isolated and identified according to the methods described in Langer and Bußkamp (2023) and Langer et al. (2024) and stored in the NW-FVA strain collection.

The *Biscogniauxia rosacearum*-strain NW-FVA 6753 (=isolate 2021-69-SB-Z1-112, NCBI Genbank Accession No. PX239669) was isolated from twigs (Fig. 1i-j) of a diseased, 48-year-old grand fir (*A. grandis*) sampled on 16 June 2021 in a private forest close to Kirchlinteln, Lower Saxony, Germany. The affected tree, suffering from Fir bark disease (Langer and Rohde 2018), was also infected among others with *B. nummularia*, *Diplodia mutila* (Fr.) Fr., *D. sapinea* (Fr.) P. Karst., *Fusarium lateritium* Nees, *Nemania serpens* (Pers.) Gray, *Neonectria neomacrospora* (C. Booth & Samuels) Mantiri & Samuels, *Phomopsis* sp., and *Xylaria* sp. Furthermore, *Heterobasidion annosum* (Fr.) Bref. and *Armillaria* root rot were detected.

The *Biscogniauxia rosacearum*-strain NW-FVA 13169=isolate 2024-73-Ü1–2, Accession No. PX239675) was retrieved from a shoot from Douglas fir (*P. menziesii*) aged 30 years, sampled on 27 August 2024 in a forest close to Genthin, Saxony-Anhalt, Germany. The studied tree suffered from Swiss needle cast (causal agent: *Nothophaeocryptopus gaeumannii* (T. Rohde) Videira, C. Nakash., U. Braun & Crous), *H. annosum* root rot and infestation with Cooley spruce gall adelgid (*Adelges cooleyi* (Gillette)) and weevils of the Curculionidae family. Beside a few other fungi, *B. nummularia* and *Peniophora cinerea* (Pers.) Cooke were additionally isolated from the studied Douglas fir tissue. In both cases of disease, there was no obvious evidence that *B. rosacearum* was the primary causal agent, and no pathogenicity tests have yet been carried out on Douglas firs and grand firs. To date, Koch's postulate for *B. rosacearum* has not been met in either of the two tree species.

In order to compare the cultural characteristics of the German *B. rosacearum* strains with other similar species, strains of *B. mediterranea* (NW-FVA 9136=Dgl-2022-2-Z2-68, Accession No. PX239670) isolated from *P. menziesii* sampled on 9 June 2022 in Baden-Wuerttemberg close to Iffezheim (Langer et al. 2025), and NW-FVA 11840=2023-110-1-Ü3-37b, Accession No. PX239672) isolated from *Quercus petraea* (Mattuschka) Liebl., sampled on 11 October 2023 in Hesse) were inoculated onto PDA agar, observed and documented with culture photos after 7, 14, 21, and 28 days (Fig. 2). The *B. mediterranea* teleomorph of the specimen 2025-72 (strain NW-FVA 13980, isolate: 2025-72-3, Accession No. PX239676, Fig. 1a-b) was isolated from *F. sylvatica* sampled by J. Bußkamp on 21 May 2025 in Germany, in the Harz mountains close to Wernigerode.

Molecular Identification and phylogenetic analysis

Extraction of genomic DNA from all isolated strains was conducted following the method described in Tropf et al. (2025).

The 5.8 S nuclear ribosomal gene with the two flanking internal transcribed spacers ITS-1 and ITS-2 (ITS) was amplified using the primer pair ITS-1 F+ITS4 (White et al. 1990). Additionally, partial sequences of the β-tubulin gene (*TUB*) and the actin gene (*ACT*) were generated using the primer pairs T1+T2 (O'Donnell and Cigelnik 1997)

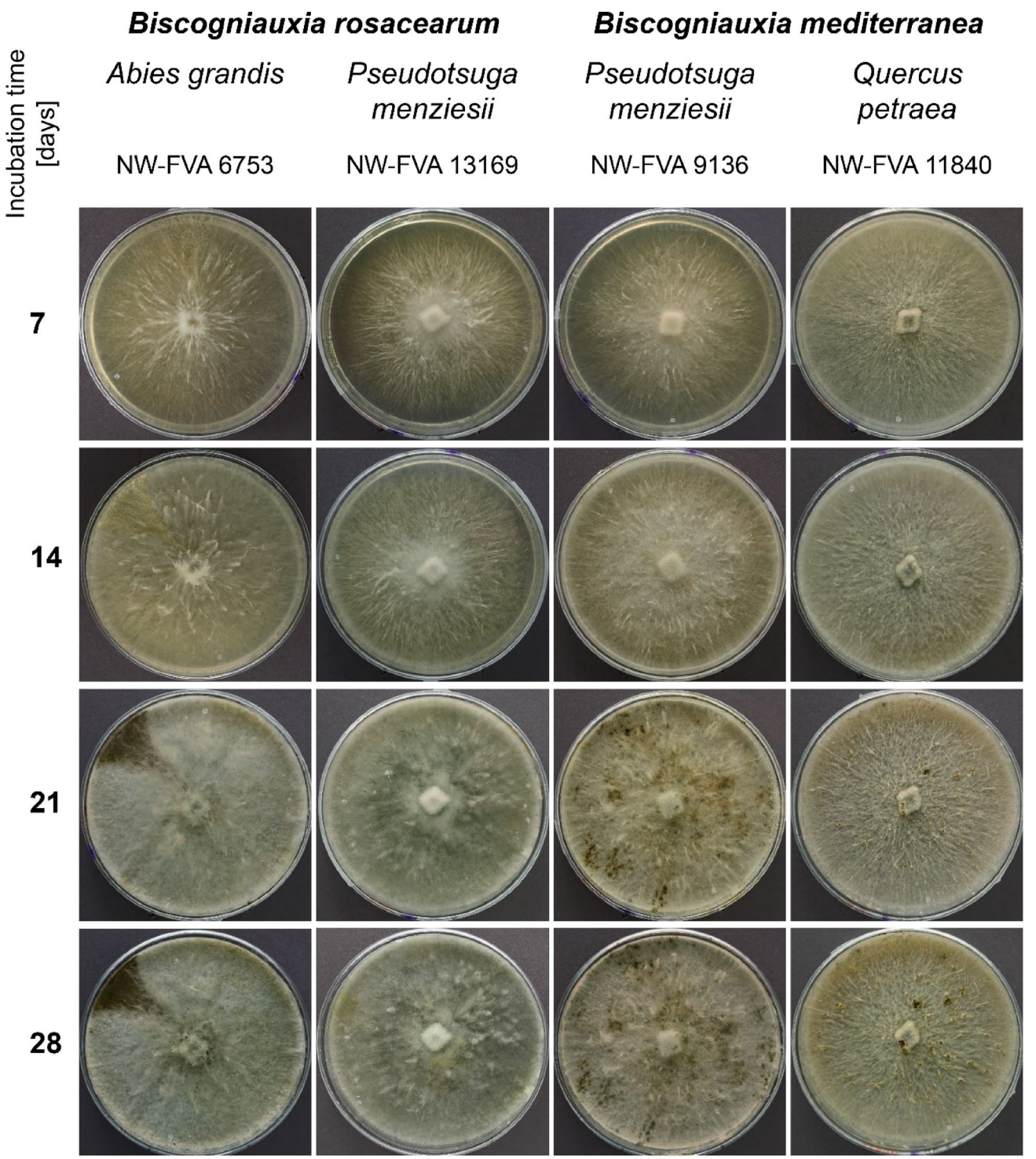


Fig. 2 Cultural characteristics of *B. rosacearum* and *B. mediterranea* isolated from different host species (*Abies grandis*, *Pseudotsuga menziesii*, *Quercus petraea*) on PDA medium

and *ACT*-512 F+*ACT*-783R (Carbone and Kohn 1999), respectively. The mixture for all PCR reactions consisted of 2.5 µl 10×PCR reaction buffer (with 20 mmol/l $MgCl_2$, Carl Roth, Karlsruhe, Germany), 1 µl of each primer (10 mmol/l), 2.5 µl $MgCl_2$ (25 mmol/l), 0.1 µl Roti®-Pol Taq HY Taq polymerase (Carl Roth, Karlsruhe, Germany), 2.5 µl of 2 mmol/l dNTPs (Biozym Scientific GmbH, Hessisch Oldendorf, Germany), and 1 µl of extracted DNA solution. Each reaction was topped up to a volume of 20 µl by adding HPLC grade water (Carl Roth, Karlsruhe, Germany).

A GeneExplorer 96 (Hangzhou BIOER Technology, Hangzhou, China) was used to carry out the DNA amplifications. PCR conditions for ITS and *ACT* followed Bien et al. (2020) and Raimondo et al. (2016), respectively. The PCR conditions for the *TUB* region were as follows: initial denaturation at 95 °C for 5 min, followed by 35 cycles of 95 °C for 30 s, 58 °C for 30 s and 72 °C for 60 s, with a 10 min extension at 72 °C on the final cycle. PCR products were visualised in 1% agarose gel, and sent to Eurofins Scientific Laboratory (Ebersberg, Germany) for sequencing. Consensus sequences were generated from all the resulting sequences, which were then visually checked and edited as necessary using the BioEdit Sequence Alignment Editor (v. 7.2.5; Hall (1999). Sequences were submitted to GenBank (Sayers et al. 2022), see also Online Resource 1.

For the phylogenetic analysis, two datasets were compiled. Dataset 1 consists of sequence data from three loci (ITS, *TUB*, *ACT*; if available) from strains of *Biscogniauxia* isolated in this study and further sequences retrieved from the NCBI GenBank including those of ex-type strains, following the data composition used in the phylogenetic analyses of Raimondo et al. (2016) and Qiao et al. (2024). For dataset 2, ITS sequence of *B. rosacearum* ex-type strain CBS 141,046 (GenBank Accession No. KT253493) was used for a Blastn search on NCBI GenBank on April 11, 2025. Of the higher-matching sequences identified, those with a percentage identity value > 98% were used together with ITS sequences from *B. mediterranea* and *B. rosacearum* strains isolated in this study and the ones reported in the study by Luchi et al. (2005) and Raimondo et al. (2016). Sequence data from both datasets and from all single loci were aligned automatically using MAFFT v. 7.490 (Katoh et al. 2002; Katoh and Standley 2013) as implemented in Geneious R11 (Kearse et al. 2012), and manually adjusted if necessary.

The multilocus (ML) analyses for dataset 1 (separately for all single loci and the concatenated dataset) and dataset 2 were performed by RAxML v. 8.2.11 (Stamatakis 2006, 2014) as implemented in Geneious Prime® 2025.0.3 (Kearse et al. 2012) using the GTRGAMMA model with the rapid bootstrapping and search for best scoring ML tree algorithm including 1000 bootstrap replicates.

qPCR analysis

DNA extracts from *B. rosacearum* strains NW-FVA 6753 and NW-FVA 13,169 as well as from *B. mediterranea* strains NW-FVA 6717, NW-FVA 9136, NW-FVA 10,508, NW-FVA 11,840, NW-FVA 12,572, and NW-FVA 13,121 were used for qPCR following Luchi et al. (2005) using the primer and probe combination presented therein. This primer and probe combination was originally intended in the aforementioned study for the specific detection of *B. mediterranea*. DNA extracts from all samples were brought to final DNA concentration of 80 ng/µl. qPCR was performed in a StepOnePlus™ PCR System (Applied Biosystems, Waltham, MA, USA). The reaction was performed in a final volume of 20 µl. qPCR mixture contained 300 nmol/l each forward primer and reverse primer, 200 nmol/l fluorogenic probe, 1x qPCR Blue Probe Mix and 50 µM ROX Additive (Biozym Scientific GmbH, Hessisch-Oldendorf, Germany), and 1 µl template DNA. Each DNA sample was assayed in four replicates. Four wells contained 1 µl HPLC grade water each instead of DNA sample as 'no-template control'. The PCR protocol according to Luchi et al. (2005) was followed.

Express pest risk analysis (PRA)

To identify the risk of introducing the fungus into new areas, i.e. the potential of its entry and establishment, as well as its risk of spread and the potential impacts, an Express-PRA for the PRA area, i.e. EU member states, in particular Germany, was conducted as described in Schrader et al. (2024). In case the outcome of the PRA indicates that the pest is a potential quarantine pest, phytosanitary measures have to be applied (Schrader et al. 2024). The PRA followed the steps according to the standards of the IPPC (IPPC 2001) and the European and Mediterranean Plant Protection Organization (EPPO) (EPPO 2024). PRA and the different aspects to be assessed are also regulated by the European Union (EU) (EU 2016), in line with IPPC and EPPO. The PRA describes the biology of the fungus, as well as its geographical distribution and areas infested. It further assesses its host plants and their presence in the PRA area, i.e. Germany and the EU. In addition, the PRA includes information about the symptoms of the pathogen, a discussion, whether climate in its area of distribution is comparable to the PRA area, and identifies potential pathways of introduction and spread. An important aspect is the assessment of known impacts in infested areas and in areas potentially being infested. Detection and diagnostics are briefly described as well. Finally, it is discussed, whether an infestation could easily be eradicated.

Results

Additional information on *B. mediterranea*, *B. nummularia*, and *B. rosacearum*

Typical habitus of a *Biscogniauxia* teleomorph (Fig. 1a-d) and anamorph (Fig. 1e-f) and some of the typically caused symptoms (e.g. strip-canker Fig. 1d), as well as the studied material of the first evidences from *B. rosacearum* are presented in Fig. 1h-l. Stroma of *B. nummularia* (Fig. 1e) were produced as a cushion-like fungal mass under the bark (Fig.

1f), visible as bark blisters. The pressure from the stroma causes the bark to peel or strip off in patches or strips (Fig. 1e-g). Wood-decay by *Biscogniauxia* species leads to brittle fracture (Fig. 1g).

A comparison of the growth patterns exhibited by *B. mediterranea* and *B. rosacearum* on PDA medium did not reveal any discernible distinguishing characteristics with regard to their cultural characteristics (see Fig. 2). Nevertheless, both species demonstrate a certain degree of variability in their cultural appearance, such as colouration of aerial mycelium, degree of pigmentation and pigmented spots within culture medium or degree of mycelial tufts formation.

Molecular identification and phylogenetic analysis

Except from two strains isolated and identified in the study, no other *Biscogniauxia* of the strain NW-FVA-collection could be assigned to *B. rosacearum.* The combined sequence dataset over all DNA loci analyzed (dataset 1) using ML consisted of 76 isolates including the outgroup and comprised 2139 characters. The gene boundaries in the concatenated multi-locus alignment were as follows: ITS: 1–878, *TUB*: 879–1829, *ACT*: 1830–2139. The analyses of all single loci datasets (not shown) as well as the concatenated dataset revealed phylogenetic trees of highly similar topology. The ML phylogeny of the multi locus dataset including ML bootstrap values is shown in Fig. 3. Strains of *B. mediterranea* and *B. rosacearum* form well-supported, closely related but distinctly separate monophyletic clades, respectively. Six of the German *Biscogniauxia* isolates (NW-FVA 10508, NW-FVA 9136, NW-FVA 12572, NW-FVA 6717, NW-FVA 13121, and NW-FVA 11840) have been shown to cluster in the *B. mediterranea* clade, and two isolates (NW-FVA 6753 and NW-FVA 13169) cluster in the *B. rosacearum* clade.

The sequence dataset 2 of ITS sequences primarily retrieved from GenBank after Blast search with *B. rosacearum* consisted of 129 isolates including the outgroup and comprised 517 characters. The ML phylogeny of dataset including ML bootstrap values is shown in Fig. 4. Apart from the strains used as outgroup and strains used as reference strains of *Biscogniauxia mediterranea* all strains retrieved from GenBank cluster in a well-supported clade together with strains of *B. rosacearum* analyzed in depth in Raimondo et al. (2016) and Sohrabi et al. (2022) and strains isolated in this study. The majority of strains retrieved from GenBank which should be assigned to *B. rosacearum* according to our analysis were designated as *B. mediterranea*.

qPCR analysis

qPCR revealed positive amplification curves for all tested *B. rosacearum* strains (NW-FVA 6753: Ct mean ± SD = 17,92 ± 0,06, ΔRn mean = 5,119; NW-FVA 13169: Ct mean ± SD = 17,34 ± 0,03, ΔRn mean = 5,222). No signal was observed for wells containing sample DNA of *B. mediterranea* strains and NTCs. An amplification plot is displayed in Fig. 5.

Express pest risk analysis

Based on the findings of this study and the literature review on *Biscogniauxia*, in accordance with the procedure described in Material and Methods, the following results have been obtained:

Biology of the organism

Fungi from the genus *Biscogniauxia* are generally considered opportunistic pathogens that occur endophytically in the sapwood and bark of healthy trees without causing any obvious disease symptoms. However, they can cause significant damage to severely weakened or damaged trees. Drought conditions in the Mediterranean region have been found to influence the aggressiveness of *B. rosacearum* and can lead to the outbreak of the disease (van Dyk et al. 2021). The fungus forms a hard mycelial mat (stroma) to multiply and spread to new host plants. *Biscogniauxia rosacearum* has a high reproduction rate and is heterothallic, i.e. the mycelia are self-incompatible or self-sterile. Initially, powdery, light-coloured, asexual spores (conidia) are produced. A specific vector is not mentioned in the literature. According to Raimondo et al. (2016), the fungus is primarily dispersed by wind or insects; occasionally also by other animals or by water. In a later stage, the fungus produces black sexual spores (ascospores), which are also transported by wind, water, or animals. While conidia are typically formed in spring or early summer, sexual spores are found in summer and fall. Both spore types can cause infections (Raimondo et al. 2016; Crocker et al. 2018).

Geographical distribution of the fungus and areas infested

Apart from the two findings in Germany, the fungus has been detected in Iran, Italy, Portugal, Spain, South Africa, and Tunisia (Raimondo et al. 2016; Pinna et al. 2019; Spies et al. 2020; Bahmani et al. 2021; van Dyk et al. 2021; Sohrabi et al. 2022; Bashiri et al. 2022; Yangui et al. 2024). However, the phylogenetic analysis based on ITS sequences retrieved from GenBank presented here suggests a much

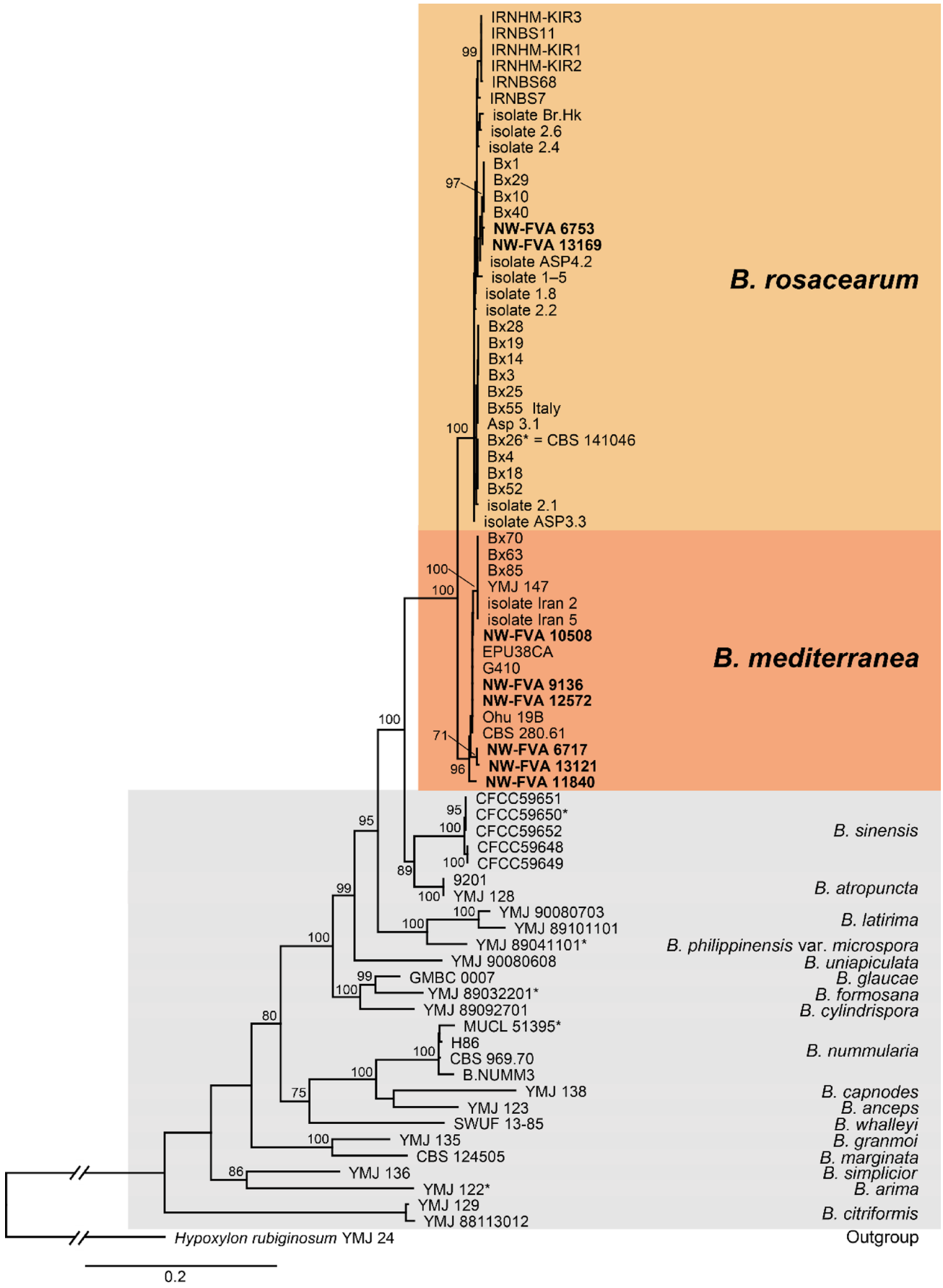

IRNHM-KIR3
IRNBS11
IRNHM-KIR1
IRNHM-KIR2
IRNBS68
IRNBS7
isolate Br.Hk
isolate 2.6
isolate 2.4
Bx1
Bx29
Bx10
Bx40
NW-FVA 6753
NW-FVA 13169
isolate ASP4.2
isolate 1–5
isolate 1.8
isolate 2.2
Bx28
Bx19
Bx14
Bx3
Bx25
Bx55 Italy
Asp 3.1
Bx26* = CBS 141046
Bx4
Bx18
Bx52
isolate 2.1
isolate ASP3.3
B. rosacearum
Bx70
Bx63
Bx85
YMJ 147
isolate Iran 2
isolate Iran 5
NW-FVA 10508
EPU38CA
G410
NW-FVA 9136
NW-FVA 12572
Ohu 19B
CBS 280.61
NW-FVA 6717
NW-FVA 13121
NW-FVA 11840
B. mediterranea
CFCC59651
CFCC59650*
CFCC59652
CFCC59648
CFCC59649
B. sinensis
9201
YMJ 128
B. atropuncta
YMJ 90080703
YMJ 89101101
B. latirima
YMJ 89041101*
B. philippinensis var. microspora
YMJ 90080608
B. uniapiculata
GMBC 0007
YMJ 89032201*
B. glaucae
B. formosana
YMJ 89092701
B. cylindrispora
MUCL 51395*
H86
CBS 969.70
B.NUMM3
B. nummularia
YMJ 138
YMJ 123
SWUF 13-85
B. capnodes
B. anceps
B. whalleyi
YMJ 135
CBS 124505
B. granmoi
B. marginata
YMJ 136
YMJ 122*
B. simplicior
B. arima
YMJ 129
YMJ 88113012
B. citriformis
Hypoxylon rubiginosum YMJ 24
Outgroup
0.2

Fig. 3 Phylogeny obtained by maximum likelihood analysis of the combined ITS, *TUB*, and *ACT* sequence alignment of *Biscogniauxia* strains (dataset 1). ML bootstrap support values above 70% are shown at the nodes. *Hypoxylon rubiginosum* strain YMJ 24 is used as outgroup. Strain numbers of ex-type strains are emphasised with an asterisk (*). Strains analysed in this study are emphasised in bold. Branches that are crossed by diagonal lines are shortened by 50%

larger distribution area (North Africa, Middle East, Southern to Central Europe, China, USA, see Fig. 4). So far, occurrences in the EU have been confirmed only sporadically. Surveys would be necessary to determine the actual distribution status Table 1.

Host plants and their presence in the PRA area

To date, several host plants are known. *Biscogniauxia rosacearum* was found to be endophytic, parasitic, saprobic, and also associated with woody tissues damaged by other pathogens:

In Italy, *B. rosacearum* was found on 13- to 20-year-old pear trees (*Pyrus communis*), plum (*Prunus domestica*), quince (*Cydonia oblonga*), and downy oak (*Quercus pubescens* Willd.) in Apulia (Raimondo et al. 2016). Additionally, it has also been isolated from insect boreholes in oak trees in Sardinia (Pinna et al. 2019). In Iran, the fungus has been detected on *Vitis vinifera* (confirmed by greenhouse pathogenicity tests), as well as on *Quercus castaneifolia* C.A.Mey., *Q. infectoria* Oliv., *Q. libani* Oliv., *Q. brantii* Lindl., and *Prunus dulcis* (Bahmani et al. 2021; Sohrabi et al. 2022; Bashiri et al. 2022). Studies of oak dieback in the Iranian forests of the Zagros Mountains (Bashiri and Abdollahzadeh 2024) revealed that *B. rosacearum* was one of the most frequently detected fungi associated with oak dieback, alongside *Obolarina persica* Mirab., Y.M. Ju, H.M. Hsieh & J.D. Rogers (wrongly addressed as *Biscogniauxia persica*), *Cytospora hedjaroudei* Bashiri & Abdollahz., *C. zagrosensis* Bashiri & Abdollahz., *Neocosmospora metavorans* (Al-Hatmi, S.A. Ahmed & de Hoog) Sand.-Den. & Crous, and *Neocosmospora* sp. In Tunisia, *B. rosacearum* was detected on *Arbutus unedo* in 2020 (Yangui et al. 2024) and on *Myrtus communis* L. in co-infection with *Diaporthe foeniculina* (Sacc.) Udayanga & Castl. (Khadraoui et al. 2025). In South Africa, *B. rosacearum* was associated with olive (*Olea europaea* L.) trunk disease symptoms (Spies et al. 2020; van Dyk et al. 2021).

Results of phylogenetic studies conducted by Raimondo et al. (2016) also included *Platypus cylindrus* (Fabricius, J.C., 1792), arthropods (Portugal), *Holcus lanatus* L., *Quercus ilex* L., and *Pinus sylvestris* (Spain) as hosts. The European Food Safety Authority (EFSA) (EFSA 2022) also mentions *P. sylvestris* as a host plant, but no further evidence is found for this.

In Germany, *B. rosacearum* was detected in two diseased trees in two federal states, Lower Saxony and Saxony-Anhalt. In 2021, a strain of *B. rosacearum* was isolated from the shoot tissue of a 48-year-old grand fir (*Abies grandis*) suffering from fir bark necrosis, which was also infected with *Diplodia sapinea*, *D. mutila*, and *Neonectria neomacrospora*. In 2024, another strain was isolated together with a *Coniochaeta* sp. from dying shoots of a 30-year-old Douglas fir (*Pseudotsuga menziesii*). The affected Douglas fir also exhibited Swiss needle cast caused by the pathogen *Nothophaeocryptopus gaeumannii*, root rot caused by *Heterobasidion annosum*, shoot dieback, nicking, and mealybug infestation (this study).

Fruiting bodies (teleomorphs) and charcoal cankers have so far only been recorded on the following plant species: pears, plums and quinces (Raimondo et al. 2016), almond trees (Sohrabi et al. 2022), grapevine (Bahmani et al. 2021), and oaks (Bashiri et al. 2022).

Again, phylogenetic analysis of ITS Blast results suggests an even broader host range, including several additional *Quercus* (*Q. cerris* L., *Q. faginea* Lam., *Q. ilex*, *Q. robur* L., *Q. suber* L.) and *Pinus* (*P. mugo* Turra, *P. nigra* J.F.Arnold, *P. pinaster* Ait.) species, and further woody and herbaceous plants. Most of the host plants, including pear, plum, quince, grapevine, Douglas fir, grand fir and various oak and pine species are economically and ecologically important plants used for agriculture and forestry in Germany, as well as in the EU.

Symptoms

In pathogenicity tests on *Vitis vinifera*, disease symptoms such as yellowing and necrosis of the leaves were observed two weeks after inoculation under greenhouse conditions. Brown lesions spread on the stems above and below the inoculation site. Stem cross-sections showed wedge-shaped necrosis of the vascular tissue (Bahmani et al. 2021). Charcoal-like cankers in the bark were observed on stems of pears, plums, and quinces (Raimondo et al. 2016).

Climate in distribution area and PRA area

So far, the fungus has been reliably detected in Mediterranean regions and in South Africa, but also on two individual plants (grand fir and Douglas fir) in Lower Saxony and Saxony-Anhalt, showing that at least in Mediterranean EU member states, climate is matching, but possibly also in Central Europe due to the confirmed occurrence in Germany. In addition, analysis of the ITS sequence data of *Biscogniauxia* strains provided in the NCBI GenBank also suggests a large distribution area based on unverified evidence from China and the USA (see ITS phylogram, Fig. 4).

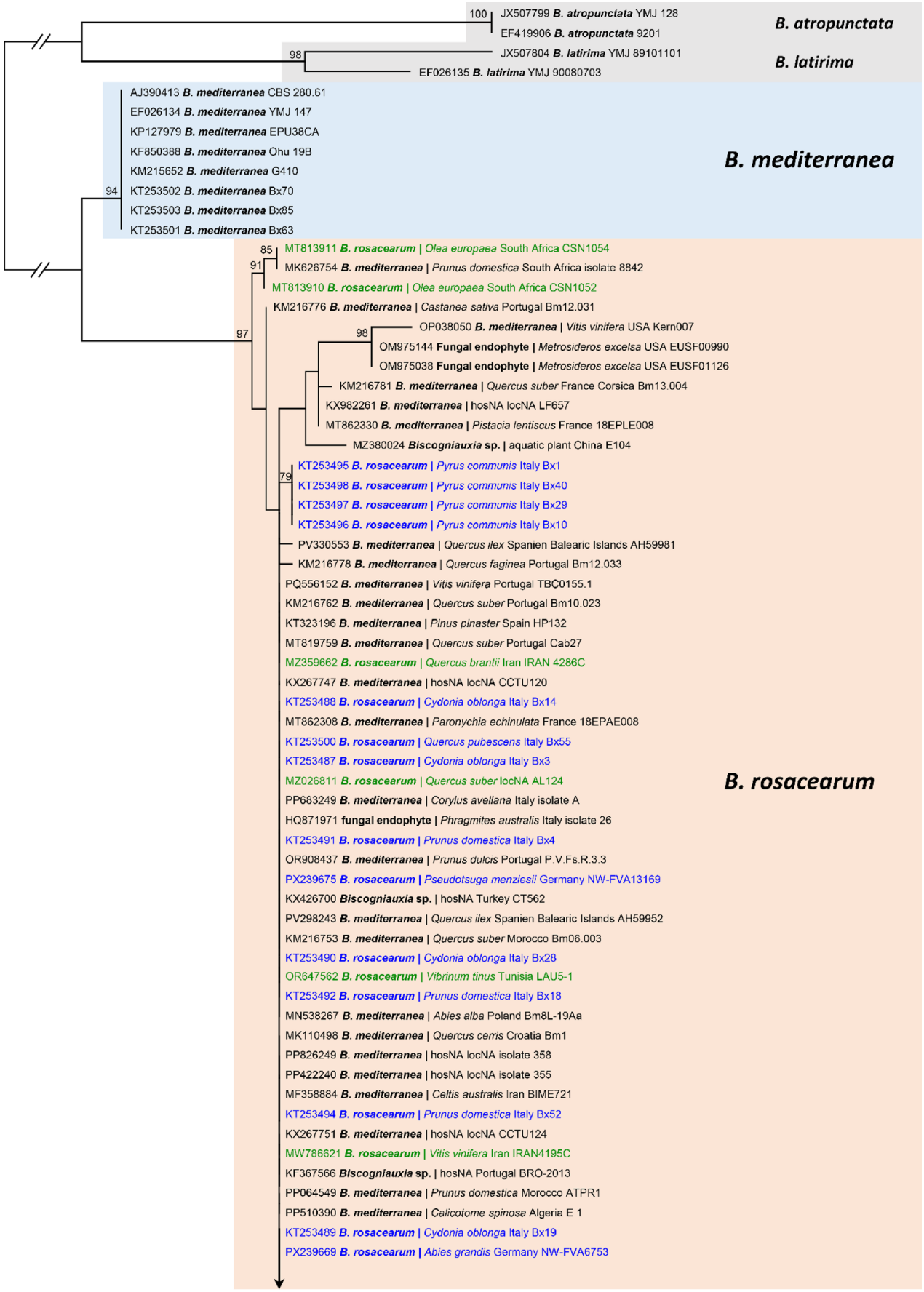

100
JX507799 B. atropunctata YMJ 128
EF419906 B. atropunctata 9201
B. atropunctata
98
JX507804 B. latirima YMJ 89101101
EF026135 B. latirima YMJ 90080703
B. latirima
AJ390413 B. mediterranea CBS 280.61
EF026134 B. mediterranea YMJ 147
KP127979 B. mediterranea EPU38CA
KF850388 B. mediterranea Ohu 19B
KM215652 B. mediterranea G410
94
KT253502 B. mediterranea Bx70
KT253503 B. mediterranea Bx85
KT253501 B. mediterranea Bx63
B. mediterranea
85
MT813911 B. rosacearum | Olea europaea South Africa CSN1054
91
MK626754 B. mediterranea | Prunus domestica South Africa isolate 8842
MT813910 B. rosacearum | Olea europaea South Africa CSN1052
KM216776 B. mediterranea | Castanea sativa Portugal Bm12.031
97
98
OP038050 B. mediterranea | Vitis vinifera USA Kern007
OM975144 Fungal endophyte | Metrosideros excelsa USA EUSF00990
OM975038 Fungal endophyte | Metrosideros excelsa USA EUSF01126
KM216781 B. mediterranea | Quercus suber France Corsica Bm13.004
KX982261 B. mediterranea | hosNA locNA LF657
MT862330 B. mediterranea | Pistacia lentiscus France 18EPLE008
MZ380024 Biscogniauxia sp. | aquatic plant China E104
79
KT253495 B. rosacearum | Pyrus communis Italy Bx1
KT253498 B. rosacearum | Pyrus communis Italy Bx40
KT253497 B. rosacearum | Pyrus communis Italy Bx29
KT253496 B. rosacearum | Pyrus communis Italy Bx10
PV330553 B. mediterranea | Quercus ilex Spanien Balearic Islands AH59981
KM216778 B. mediterranea | Quercus faginea Portugal Bm12.033
PQ556152 B. mediterranea | Vitis vinifera Portugal TBC0155.1
KM216762 B. mediterranea | Quercus suber Portugal Bm10.023
KT323196 B. mediterranea | Pinus pinaster Spain HP132
MT819759 B. mediterranea | Quercus suber Portugal Cab27
MZ359662 B. rosacearum | Quercus brantii Iran IRAN 4286C
KX267747 B. mediterranea | hosNA locNA CCTU120
KT253488 B. rosacearum | Cydonia oblonga Italy Bx14
MT862308 B. mediterranea | Paronychia echinulata France 18EPAE008
KT253500 B. rosacearum | Quercus pubescens Italy Bx55
KT253487 B. rosacearum | Cydonia oblonga Italy Bx3
MZ026811 B. rosacearum | Quercus suber locNA AL124
PP683249 B. mediterranea | Corylus avellana Italy isolate A
HQ871971 fungal endophyte | Phragmites australis Italy isolate 26
KT253491 B. rosacearum | Prunus domestica Italy Bx4
OR908437 B. mediterranea | Prunus dulcis Portugal P.V.Fs.R.3.3
PX239675 B. rosacearum | Pseudotsuga menziesii Germany NW-FVA13169
KX426700 Biscogniauxia sp. | hosNA Turkey CT562
PV298243 B. mediterranea | Quercus ilex Spanien Balearic Islands AH59952
KM216753 B. mediterranea | Quercus suber Morocco Bm06.003
KT253490 B. rosacearum | Cydonia oblonga Italy Bx28
OR647562 B. rosacearum | Vibrinum tinus Tunisia LAU5-1
KT253492 B. rosacearum | Prunus domestica Italy Bx18
MN538267 B. mediterranea | Abies alba Poland Bm8L-19Aa
MK110498 B. mediterranea | Quercus cerris Croatia Bm1
PP826249 B. mediterranea | hosNA locNA isolate 358
PP422240 B. mediterranea | hosNA locNA isolate 355
MF358884 B. mediterranea | Celtis australis Iran BIME721
KT253494 B. rosacearum | Prunus domestica Italy Bx52
KX267751 B. mediterranea | hosNA locNA CCTU124
MW786621 B. rosacearum | Vitis vinifera Iran IRAN4195C
KF367566 Biscogniauxia sp. | hosNA Portugal BRO-2013
PP064549 B. mediterranea | Prunus domestica Morocco ATPR1
PP510390 B. mediterranea | Calicotome spinosa Algeria E 1
KT253489 B. rosacearum | Cydonia oblonga Italy Bx19
PX239669 B. rosacearum | Abies grandis Germany NW-FVA6753
B. rosacearum

Fig. 4 Phylogeny obtained by maximum likelihood analysis of ITS sequence alignment of *Biscogniauxia* strains (dataset 2). ML bootstrap support values above 70% are shown at the nodes. Strains of *B. atropunctata* and *B. latirima* Y.M. Ju & J.D. Rogers are used as outgroup. For every strain clustered in the *B. rosacearum* clade GenBank accession number, taxon designation as listed in GenBank (in bold), host or substrate (if available), country of isolation (if available), and strain number are given. Strain numbers of ex-type strains are emphasised with an asterisk (*). Branches that are crossed by diagonal lines are shortened by 50%. Blue = strains of *B. rosacearum* analysed intensively in Raimondo et al. (2016) and Sohrabi et al. (2022), and this study, respectively. Green = strains designated as *B. rosacearum* in GenBank. hosNA = no host or substrate available, locNA = no country of isolation available

Pathways and natural spread

Plants for planting are considered the main pathway. According to Raimondo et al. (2016), the fungus is naturally spread by wind or insects.

Known impacts in infested areas

Biscogniauxia species are primarily known as endophytes, secondary pathogens and facultative saprophytes. They can infect old and weakened host plants and persist as endophytes in the aboveground parts of oaks and other tree species. Furthermore, they may remain latent and only develop symptoms when the trees are stressed, for example by drought. *Biscogniauxia* species are able to rapidly colonize xylem and bark tissues, and can cause necrosis and canker formation, in severe cases even leading to tree death. Also younger and healthier trees are increasingly being infected (Henriques et al. 2016; Raimondo et al. 2016). In the case of *B. rosacearum* Bahmani et al. (2021) and Masi et al. (2021) have demonstrated that phytotoxins play a considerable role in the disease process.

Expected (further) establishment and spread in Germany and the EU

Based on the detection of *B. rosacearum* in Lower Saxony and Saxony-Anhalt, further establishment of the fungus in Germany is to be expected, also because of its high reproduction rate and spread potential by wind and insects. Since *B. rosacearum* occurs endophytically and has not been originally associated with damage in Germany (and thus does not attract attention), it may already be more widespread than previously thought.

There is evidence (see ITS phylogram, Fig. 4) that *B. rosacearum* already occurs in some, primarily southern, EU Member States. Further establishment is expected as well in these areas, out of the reasons mentioned above.

Expected impacts caused by the fungus in Germany and the EU

In climatically suitable areas, significant damage to the host plants is to be expected, especially if they are already weakened by drought or infestation with other pests. However, *B. rosacearum* was probably not the cause of the observed damage in the two trees infected in Germany.

Detection and diagnosis

Morphological identification is particularly challenging. As shown in Fig. 2, the synopsis of *B. mediterranea* and *B. rosacearum* pure cultures cultivated for 7, 14, 21, and 28 days on PDA do not provide salient distinguishing features. *Biscogniauxia rosacearum* can be unambiguously identified using the ITS DNA region. This result was confirmed by multi-locus sequence analysis (MLSA). In the past, especially before its initial description by Raimondo et al. (2016), the fungus was generally referred to as the closely related species *B. mediterranea* and deposited accordingly in databases. Therefore, confusion can easily arise when comparing new sequence data with existing ITS database entries. Until recently, findings on genetic diversity or host range, for example, were assigned erroneously to *B. mediterranea* based on incorrect species delimitation presumably due to these mentioned Blast inconsistencies (Yangui et al. 2022; Zamani et al. 2025). Furthermore, in addition to species assignment based on ITS database comparisons, rapid detection using qPCR and the specific primer/probe combination presented by Luchi et al. (2005) can currently lead to misinterpretation of test results. The qPCR was used to verify the results derived from the phylogenetic analysis of the German isolates. It confirmed that the isolates were correctly identified as to *B. mediterranea* and *B. rosacearum*. However, the amplification of the *B. mediterranea* isolates (target) was not observed, while the *B. rosacearum* isolates (non-target) were amplified. It is noteworthy that the ITS sequence (from isolate Bm1 = Bm4) employed by Luchi et al. (2005) and previously by Mazzaglia et al. (2001) for primer designing to target *B. mediterranea* grouped to *B. rosacearum* in the phylogeny, thereby corroborating the qPCR findings. Raimondo et al. (2016) provides specific identification guidelines but detection is difficult in asymptomatic but latently infected host plants.

Eradication of an infestation

There is no known way to control the fungus by fungicides. To date, the only effective control method is felling and destroying (burning) the infected host plants. However, this would only be useful if *B. rosacearum* was not yet

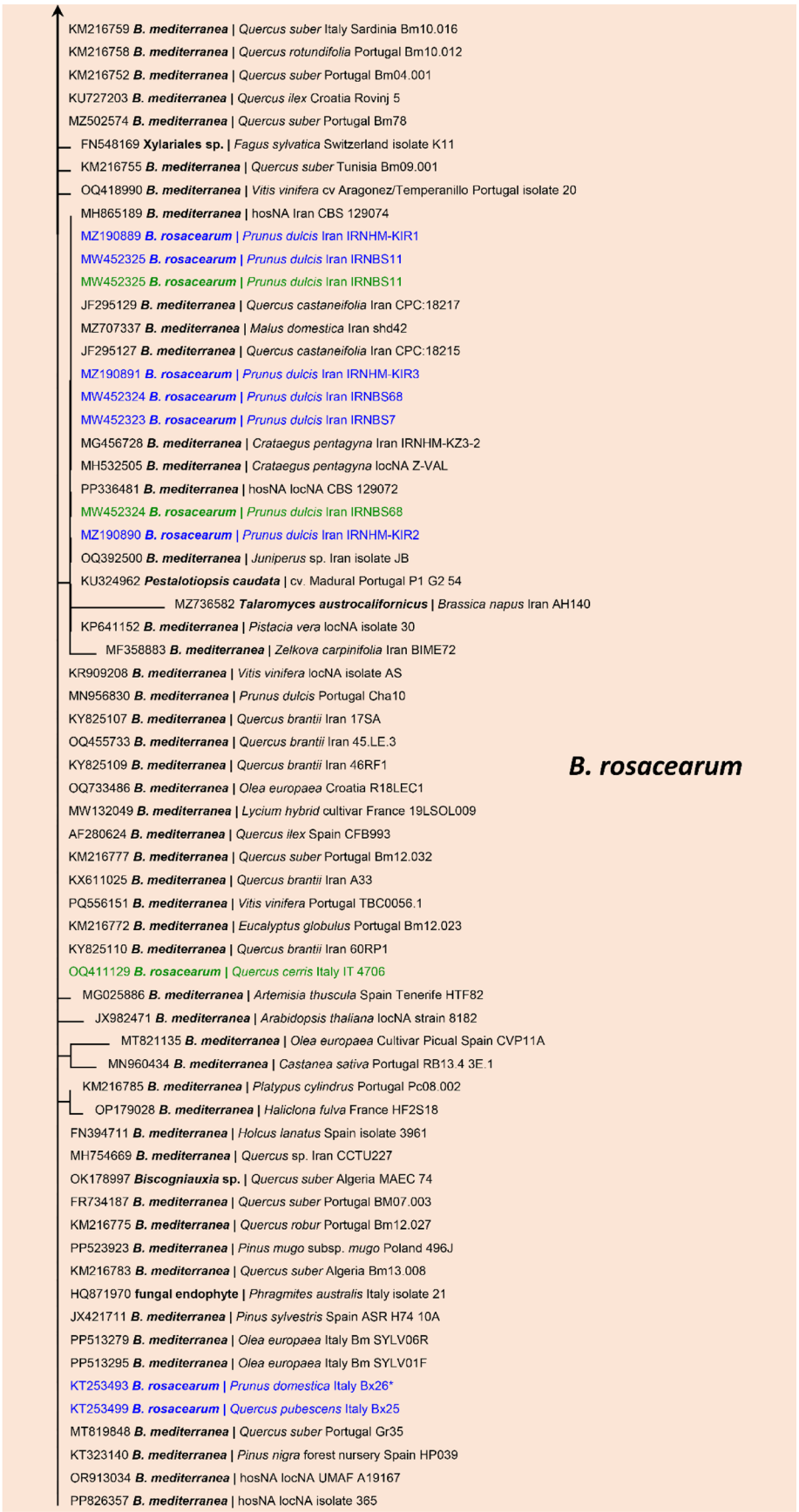


Fig. 4 (continued)

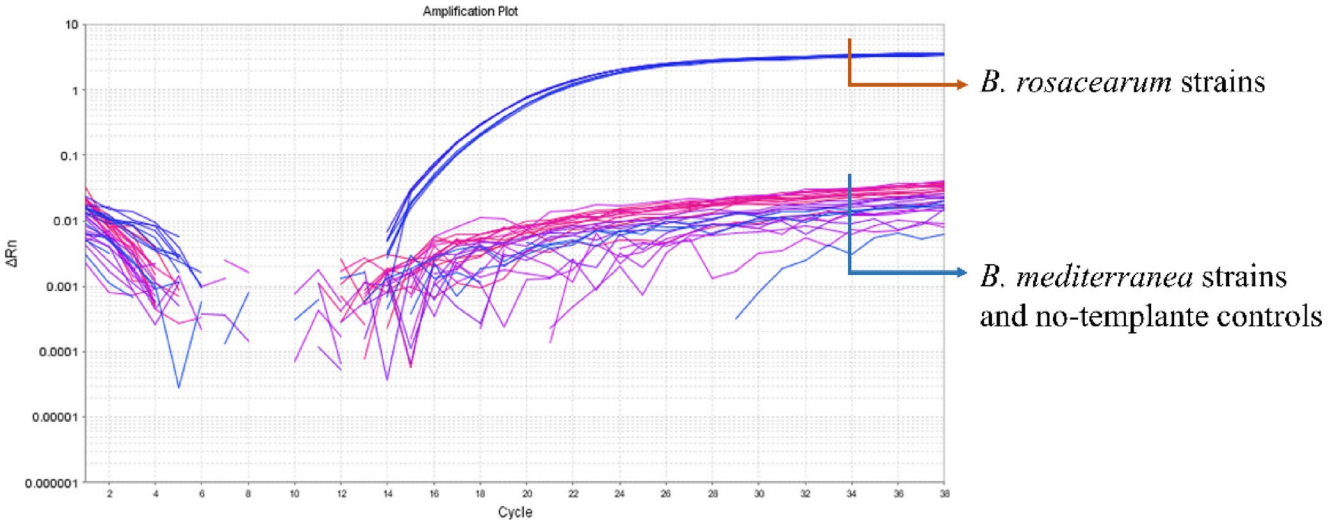


Fig. 5 Amplification plot from qPCR analysis for *Biscogniauxia mediterranea* with specific primer/probe combination. Analysis adapted from Luchi et al. (2005) including strains of *B. mediterranea* and *B. rosacearum*

Table 1 Summary of important findings in the Express Pest Risk Analysis for *Biscogniauxia rosacearum*

Taxonomy	Fungi, Ascomycota, Xylariales, Graphostromataceae, *Biscogniauxia, Biscogniauxia rosacearum* M.L. Raimondo & Carlucci EPPO Code: BISCRO High intraspecific diversity
Summary	• likely native to the Middle East, • already present in the EU, • not regulated in the EU, • broad range of host plants, including pear, plum, quince, grapevine, and various oak species, • probably significantly broader host range, • probably wide geographical distribution, • could most probably become established in Germany, • further establishment in Southern EU member states expected, • high potential to cause damage to certain Rosales and oaks (charcoal canker, strip canker), • endophytic or opportunistic occurrence in numerous tree species, • insufficient information regarding the phylogenetic diversity and the pathogenicity of different *B. rosacearum* strains towards various tree species, • more information needed to determine phytosanitary risk of the fungus; certainty of assessment low.
Geographical distribution	Germany, Iran, Italy, Portugal, Spain, South-Africa, Tunisia. Most probably also North Africa, Middle East, Southern Europe to Central Europe, China, USA.
Host plants	Almond (*Prunus dulcis*), common myrtle (*Myrtus communis*), Douglas fir (*Pseudotsuga menziesii*), grand fir (*Abies grandis*), grapevine (*Vitis vinifera*), oak species (*Quercus brantii*, *Q. castaneifolia*, *Q. infectoria*, *Q. libani*, *Q. pubescens*), olive tree (*Olea europaea*), pear (*Pyrus communis*), plum (*Prunus domestica*), quince (*Cydonia oblinga*), strawberry tree (*Arbutus unedo*). Phylogenetical investigations: *Holcus lanatus*, *Quercus ilex*, *Pinus sylvestris*
Symptoms	leaf yellowing, necrosis, brown lesions, charcoal-like bark alterations
Pathways	Plants for planting
Natural spread	Wind, insects
Known impacts	primarily known as secondary or opportunistic pathogens and facultative saprophytes, necrosis and canker formation, potentially leading to tree death, younger and healthier trees increasingly being affected
Control	Felling and burning of infested plants. Improving tree health

References to the findings can be found in the main text

widespread. In principle, it would be necessary to identify infestation-free areas, including determining whether and to what extent the fungus occurs endophytically without symptoms. Depending on the results, preventative measures could then be taken to avoid or mitigate further spread of the fungus. If possible, in urban agricultural areas measures to improve tree health, such as reducing compaction, mulching, irrigation, and fertilization, should be taken. Visibly

infected branches should be removed, both to reduce the amount of inoculum present and to prevent potentially dangerous tree breaks (Crocker et al. 2018).

Since occurrences of *B. rosacearum* in the EU have so far only been confirmed sporadically, and there are only two isolated cases in Germany, further surveys would be necessary to determine the actual distribution status.

Discussion

Raimondo et al. (2016) were able to show that the two species *B. mediterranea* and *B. rosacearum* can be distinguished by their micromorphological characteristics. As described by the latter authors, the species differ in the size of their asci and ascospores, however, the distinction between the two anamorphic types remains rather vague. So far as known, *B. mediterranea* forms a periconiella-like anamorph form (Ju and Rogers 1996), while *B. rosacearum* forms a nodulisporium-like form (Raimondo et al. 2016). A comprehensive comparative morphological study, in particularly of anamorphic structures, would be required, including a significant number of isolates from both fungal species, preferably from a wide variety of localities and host species. Henriques et al. (2015) compared previously published data on anamorphic structures of *B. mediterranea* with their own isolates identified as this species and found considerable variability. However, based on current knowledge, at least some of the isolates examined by the authors belong to *B. rosacearum* and can be found within the respective clade in the ITS-phylogeny presented here. Teleomorph structures, however, are usually produced on the substrate rather than in culture. Hence, if it is not possible to examine these micromorphological characteristics and only pure cultures are available, it will not be possible to distinguish between the two species on the basis of their culture-based characteristics alone. Therefore, the addition of molecular information (ITS sequence data according to this study is sufficient) is essential for an unambiguous identification.

The multi-locus sequence analysis (MLSA) using three target genes allowed to designate the two newly isolated cultures as *B. rosacearum* and to identify false GenBank database entries that require an updated species annotation. Rapid advancements in (meta)barcoding of organisms in various environments not only require the application of modern molecular techniques, but also high-quality database entries containing reference sequence material to identify species accordingly. This of course has been under debate for various reasons and is not restricted to false entries due to lacking morphological identification but also due to duplicates, redundancies and errors in species determination algorithms (Chen et al. 2017; Stein and Gailing 2025). Therefore, it is necessary to carefully interpret the obtained information and, preferably, verify the results with additional information and expertise beyond DNA sequences. Reliable species-level assignments require both, curated reference material and an accurate phylogeny based on molecular analyses, as described in this article.

In conclusion, the study successfully achieved the aims outlined in the introduction. It was demonstrated that the fungal strains that could initially only be assigned to the *Biscogniauxia* genus in reference to the NW-FVA strain collection could be identified as *B. rosacearum*. It was shown that the species-specific primers for *B. mediterranea* published by Luchi et al. (2005) can lead to misinterpretation of test results, since the specific primer/probe combination used amplified *B. rosacearum* instead of *B. mediterranea*. As a result of this, it is now possible to identify *B. rosacearum* entries in the NCBI GenBank database not having been identified previously.

In the PRA, it could be shown that - with these new results for the identification and distinction of the two *Biscogniauxia* species – the distribution range of *B. rosacearum* is much larger than previously known. Furthermore, in the PRA it is assumed that *B. rosacearum* can establish in Germany due to suitable climatic conditions and the availability of potential host plants; (further) establishment in southern European and Mediterranean EU member states is to be expected. A more detailed assessment of climatic conditions required by the fungus to establish and spread, in combination with modelling its spread potential would therefore be useful to better estimate the risks for its host plants present in Europe.

Biscogniauxia rosacearum poses a high damage potential for some Rosales and oaks, causing “charcoal canker”. The development of “charcoal canker” in other host plants has not been observed to date, so that it would be important to investigate whether the Koch’s postulates could be fulfilled for these species. In addition, insufficient information exists on the phylogenetic diversity and pathogenicity of different *B. rosacearum* strains towards different host species. In other tree species, the fungus seems not to cause any damage, but only occurs endophytically or opportunistically. The confusion regarding the two species *B. rosacearum* and *B. mediterranea* further complicates matters, as there may be errors with regard to the assignments of host plants and impacts of the two different species and their current distribution. Due to these uncertainties, it was not possible to conclusively assess the phytosanitary risk of *B. rosacearum* at this stage of the study. Therefore, there is an urgent need for further research, also to finally determine whether the fungus qualifies as a potential quarantine pest for the EU.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s41348-0

26-01366-4.

Author contributions All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Gitta Langer, Steffen Bien and Gritta Schrader. The molecular analyses were performed by Steffen Bien. The first draft of the manuscript was written by Gritta Schrader, Steffen Bien, and Gitta Langer and all authors commented on previous versions of the manuscript. Clovis Douanla-Meli and Björn Hoppe made substantial contributions to the manuscript. All authors read and approved the final manuscript. Funding acquisition: Gitta Langer.

Funding Open Access funding enabled and organized by Projekt DEAL. The study was conducted as part of the TroWaK project ("Trockenheitsrisiken im Wald unter Klimawandel", "Drought risks in forests under climate change") which receives funding via the Waldklimafonds ("Forest climate fund", WKF) funded by the German Federal Ministry of Agriculture, Food and Regional Identity (BMLEH), formerly Federal Ministry of Food and Agriculture (BMEL) and the Federal Ministry for the Environment, Climate Action, Nature Conservation and Nuclear Safety (BMUKN), formerly Federal Ministry for the Environment, Nature Conservation, Nuclear Safety and Consumer Protection (BMUV) administrated by the Agency for Renewable Resources (FNR) under grant agreement No 2220WK92D4. Additional funding was provided by the Julius Kuehn Institute (JKI) – Federal Research Centre for Cultivated Plants, Institute for National and International Plant Health.

Declarations

Conflict of interest The author(s) declare that they do not have any conflicts of interest.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/licenses/by/4.0/.

References

Bahmani Z, Abdollahzadeh J, Amini J, Evidente A (2021) *Biscogniauxia rosacearum* the charcoal canker agent as a pathogen associated with grapevine trunk diseases in Zagros region of Iran. Sci Rep. https://doi.org/10.1038/s41598-021-93630-w

Bashiri S, Abdollahzadeh J (2024) Taxonomy and pathogenicity of fungi associated with oak decline in northern and central Zagros forests of Iran with emphasis on coelomycetous species. Front Plant Sci 15:20yay. https://doi.org/10.3389/fpls.2024.1377441

Bashiri S, Abdollahzadeh J, Evidente A (2022) Diagnosing and pathogenicity of *Biscogniauxia* species, the causal agents of oak charcoal canker and decline in Zagros forests of Iran. J Plant Pathol 104(3):1011–1025. https://doi.org/10.1007/s42161-022-01124-z

Bien S, Kraus C, Damm U (2020) Novel collophorina-like genera and species from *Prunus* trees and vineyards in Germany. Persoonia 45(1):46–67. https://doi.org/10.3767/persoonia.2020.45.02

Bußkamp J, Langer GJ, Langer EJ (2020) *Sphaeropsis sapinea* and fungal endophyte diversity in twigs of Scots pine (*Pinus sylvestris*) in Germany. Mycol Progress 19(9):985–999. https://doi.org/10.1007/s11557-020-01617-0

Bußkamp J, Bien S, Neumann L, Blumenstein K, Terhonen E, Langer GJ (2024) Endophytic community in juvenile *Acer pseudoplatanus* and pathogenicity of *Cryptostroma corticale* and other associated fungi under controlled conditions. J Plant Pathol 106(2):565–577. https://doi.org/10.1007/s42161-023-01575-y

Carbone I, Kohn LM (1999) A method for designing primer sets for speciation studies in filamentous ascomycetes. Mycologia 91(3):553–556. https://doi.org/10.1080/00275514.1999.12061051

Chapela IH, Boddy L (1988) Fungal colonization of attached beech branches II. Spatial and temporal organization of communities arising from latent invaders in bark and functional sapwood, under different moisture regimes. New Phytol 110(1):47–57. https://doi.org/10.1111/j.1469-8137.1988.tb00236.x

Chen Q, Zobel J, Verspoor K (2017) Duplicates, redundancies and inconsistencies in the primary nucleotide databases: a descriptive study. Database (Oxford) baw163. https://doi.org/10.1093/database/baw163

Chlebicki A, Bujakiewicz A (1994) *Biscogniauxia repanda*, *B. marginata* and *Camarops polysperma* (Pyrenomycetes) in Poland and Lithuania. Acta Mycol 29:53–58. https://doi.org/10.5586/am.1994.006

Crocker E, Bordas A, Coyle D (2018) Biology, Ecology, and Management of *Biscogniauxia* (*Hypoxylon*) Canker in the Southeastern U.S. SREF. Forest Health Research and Education Center, Department of Forestry and Natural Resources, University of Kentucky, Lexington, USA, Factsheet, SREF-FH- 009

Daranagama D, Hyde K, Sir E, Thambugala K, Tian Q, Samarakoon MC, Mckenzie E, Jayasiri S, Tibpromma S, Bhat DJ, Liu X, Stadler M (2018) Towards a natural classification and backbone tree for Graphostromataceae, Hypoxylaceae, Lopadostomataceae and Xylariaceae. Fungal Divers 88:1–165. https://doi.org/10.1007/s13225-017-0388-y

Edwards J, Kshirsagar, Maitland, Mekkamol, Nugent, Phosri C, Rodtong S, Ruchikachorn, Sangvichien E, George S, Sihanonth P, Suwannasai N, Thienhirun, Whalley A, Whalley MA (2003) The Xylariaceae as phytopathogens. Recent Res Developments Plant Sci 1:1–19

EFSA (European Food Safety) (2022) Plant Health Newsletter on Horizon Scanning EN-7282. EFSA Supporting Publications 19(4, March 2022):31. https://doi.org/10.2903/sp.efsa.2022.EN-7282

EPPO (2024) EPPO Standards – PM 5 Pest Risk Analysis

EU (2016) Regulation (EU) 2016/2031 of the European Parliament of the Council of 26 October 2016 on protective measures against pests of plants, amending Regulations (EU) 228/2013, (EU) 652/2014 and (EU) 1143/2014 of the European Parliament and of the Council and repealing Council Directives 69/464/EEC, 74/647/EEC, 93/85/EEC, 98/57/EC, 2000/29/EC, 2006/91/EC and 2007/33/EC. Official Journal of the European Union, L 317/4 , 101 pp. http://data.europa.eu/eli/reg/2016/2031/oj

Farr DF, Rossman AY (2022) Fungal databases - fungus-host distributions. In: U.S. National Fungus Collections Fungal Database. https://nt.ars-grin.gov/fungaldatabases/fungushost/fungushost.cfm . Accessed 4 May 2022

Gharbi Y, Ennouri K, Bouazizi E, Cheffi M, Triki M (2020) First report of charcoal disease caused by *Biscogniauxia mediterranea* on *Olea europaea* in Tunisia. J Plant Pathol. https://doi.org/10.1007/s42161-020-00531-4

Granata G, Whalley AJS (1994) Decline of beech associated with *Biscogniauxia nummularia* in Italy. Petria 4(2):111–115

Granata G, Sidoti A (2004) *Biscogniauxia nummularia*: pathogenic agent of a beech decline. For Pathol 34(6):363–367. https://doi.org/10.1111/j.1439-0329.2004.00377.x

Hall T (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser 41:95–98. https://doi.org/10.14601/Phytopathol_Mediterr-14998u1.29

Hendry SJ, Lonsdale D, Boddy L (1998) Strip-cankering of beech (*Fagus sylvatica*): Pathology and distribution of symptomatic trees. New Phytol 140(3):549–565. https://doi.org/10.1111/j.1469-8137.1998.00282.x

Henriques J, Nóbrega F, Sousa E, Lima A (2015) Morphological and genetic diversity of *Biscogniauxia mediterranea* associated to *Quercus suber* in the Mediterranean Basin. Revista de Ciências Agrárias

Henriques J, Nóbrega F, Sousa E, Lima A (2016) Analysis of the genetic diversity and phylogenetic relationships of *Biscogniauxia mediterranea* isolates associated with cork oak. Phytoparasitica. https://doi.org/10.1007/s12600-015-0503-0

Hyde K, Norphanphoun C, Maharachchikumbura S, Bhat DJ, Jones E, Bundhun D, Chen YJ, Bao D-F, Boonmee S, Calabon M, Chaiwan N, Kandawatte T, Dai D-Q, Dayarathne M, Devadatha B, Dissanayake A, Dissanayake L, Doilom M, Dong W, Zhang S (2020) Refined families of Sordariomycetes. Mycosphere 11:1058. https://doi.org/10.5943/mycosphere/11/1/7

IPPC (2001) International Standard on Phytosanitary Measures (ISPM) 11. Pest Risk Analysis for Quarantine Pests. IPPC, FAO, Rome. International Plant Protection Convention, Rome

JKI (2025) Express-PRA zu *Biscogniauxia rosacearum* – Auftreten – Julius Kühn-Institut, Institut für nationale und internationale Angelegenheiten der Pflanzengesundheit, am: 24.06.2025. Zuständige Mitarbeiter: Dr. Gritta Schrader, Dr. Björn Hoppe, Dr. Clovis Douanla-Meli; unter Mitwirkung von Dr. Steffen Bien und Dr. Gitta Langer, Nordwestdeutsche Forstliche Versuchsanstalt, Göttingen

Ju Y-M, Rogers JD (1996) A revision of the genus Hypoxylon. APS Press, the American Phytopathological Society, St. Paul, Minn.

Ju Y, Rogers J, Martín F, Granmo A (1998) The genus Biscogniauxia. Mycotaxon 66:1–98

Katoh K, Misawa K, Kuma K, Miyata T (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res 30(14):3059–3066. https://doi.org/10.1093/nar/gkf436

Katoh K, Standley DM (2013) MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Mol Biol Evol 30(4):772–780. https://doi.org/10.1093/molbev/mst010

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A (2012) Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28(12):1647–1649. https://doi.org/10.1093/bioinformatics/bts199

Khadraoui H, Hlaiem S, Yangui I, Hmissi S, Messaoud C, Ezzine O, Mohamed Lahbib BJ (2025) Co-infection of Diaporthe foeniculina and Biscogniauxia rosacearum in Myrtus communis in Tunisia: influence of temperature and rainfall. Eur J Plant Pathol. https://doi.org/10.1007/s10658-024-02990-2

Koukol O, Kelnarová I, Černý K (2014) Recent observations of sooty bark disease of sycamore maple in Prague (Czech Republic) and the phylogenetic placement of *Cryptostroma corticale*. Forest Pathol. https://doi.org/10.1111/efp.12129

Kuntze O (1891) Revisio generum plantarum: vascularium omnium atque cellularium multarum secundum leges nomenclaturae internationales cum enumeratione plantarum exoticarum in itinere mundi collectarum ... A. Felix [etc.], Leipzig

Læssøe T, Granmo A, Scheuer C (1999) *Biscogniauxia granmoi* (Xylariaceae) in Europe. Österrreichische Z für Pilzkunde 8:139–147

Langer GJ (2024) Einfluss des Klimawandels auf pilzliche und komplexe Erkrankung von Waldbäumen. Sachverständigenbüro Baum 4 GmbH (ed) Fachtagung der Baumkontrolleure, 13.-14. Mai 2024 in Wiesbaden -. Patzer-, Berlin, Hannover, pp 34–52

Langer GJ, Rohde M (2018) Tannen - Rindennekrose; Waldschutzinfo Nr. 12 / 2018. https://doi.org/10.5281/zenodo.8005524

Langer GJ, Bußkamp J (2021) Fungi associated with woody tissues of European beech and their impact on tree health. Front Microbiol 12:702476. https://doi.org/10.3389/fmicb.2021.702467

Langer GJ, Bußkamp J (2023) Vitality loss of beech: a serious threat to *Fagus sylvatica* in Germany in the context of global warming. J Plant Dis Prot 130:1101–1115. https://doi.org/10.1007/s41348-023-00743-7

Langer GJ, Bußkamp J, Blumenstein K, Terhonen E, Elsevier, Cambridge UK (2021) Oxford, UK, 175–205

Langer GJ, Bien S, Bußkamp J (2024) Filamentous fungi associated with disease symptoms in non-native giant sequoia (*Sequoiadendron giganteum*) in Germany—a gateway for alien fungal pathogens? Pathogens 13(9):715. https://doi.org/10.3390/pathogens13090715

Langer GJ, Bußkamp J, Peters S, Wietschorke J, Grüner J, Faust J, Wonsack D (2025) Pests and fungal pathogens associated with Douglas fir stands showing crown defoliation and vitality loss. J für Kulturpflanzen 77(02):70–80. https://doi.org/10.5073/JfK.2025.02.06

Li Q, Gong X, Zhang X, Pi Y, Long S, Wu Y, Shen X, Kang Y, Kang J (2021) Phylogeny of Graphostromatacea with two new species (*Biscogniauxia glaucae* sp. nov. and *Graphostroma guizhouensis* sp. nov.) and new record of *Camillea broomeana* isolated in China. Arch Microbiol. https://doi.org/10.1007/s00203-021-02574-2

Luchi N, Capretti P, Pinzani P, Orlando C, Pazzagli M (2005) Real-time PCR detection of *Biscogniauxia mediterranea* in symptomless oak tissue. Lett Appl Microbiol 41:61–8. https://doi.org/10.1111/j.1472-765X.2005.01701.x

Luchi N, Capretti P, Feducci M, Vannini A, Ceccarelli B, Vettraino AM (2015) Latent infection of *Biscogniauxia nummularia* in *Fagus sylvatica*: a possible bioindicator of beech health conditions. iForest - Biogeosciences For. https://doi.org/10.3832/ifor1436-008

Masi M, Bashiri S, Cimmino A, Bahmani Z, Abdollahzadeh J, Evidente A (2021) Phytotoxins Produced by two *Biscogniauxia rosacearum* strains, causal agents of grapevine trunk diseases, and charcoal canker of oak tlurees in Iran. Toxins (Basel) 13(11):812. https://doi.org/10.3390/toxins13110812

Mazzaglia A, Anselmi N, Gasbarri A, Vannini A (2001) Development of a polymerase chain reaction (PCR) assay for the specific detection of Biscogniauxia mediterranea living as an endophyte in oak tissues. Mycol Res 105(8):952–956.https://doi.org/10.1017/S0953756201004403

Nugent LK, Sihanonth P, Thienhirun S, Whalley AJS (2005) *Biscogniauxia*: a genus of latent invaders. Mycologist 19(1):40–43. https://doi.org/10.1017/S0269915X05001060

O'Donnell K, Cigelnik E (1997) Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. Mol Phylogenet Evol 7(1):103–116. https://doi.org/10.1006/mpev.1996.0376

Patejuk K, Baturo-Cieśniewska A, Pusz W, Kaczmarek-Pieńczewska A (2022) Biscogniauxia charcoal canker—a new potential threat for mid-European forests as an effect of climate change. Forests 13(1):89. https://doi.org/10.3390/f13010089

Petrini L, Petrini O (1985) Xylariaceous Fungi as Endophytes. Sydowia 28:216–234

Pinna C, Linaldeddu BT, Deiana V, Maddau L, Montecchio L, Lentini A (2019) Plant Pathogenic Fungi Associated with *Coraebus florentinus* (Coleoptera: Buprestidae) Attacks in Declining Oak Forests. Forests 10(6):488. https://doi.org/10.3390/f10060488

Pouzar Z (1979) Notes on taxonomy and nomenclature of Nummularia (Pyrenomycetes). Cesk Mykol 33(4):207–219

Pouzar Z (1986) A key and conspectus of Central European species of *Biscogniauxia* and *Obolarina* (Pyrenomycetes). Cesk Mykol 40(1):1–10

Qiao C, Zhao R, Li D, Ding X (2024) A new species of *Biscogniauxia* associated with pine needle blight on *Pinus thunbergii* in China. Forests (Basel) 15(6):956. https://doi.org/10.3390/f15060956

Ragazzi A, Fedi I, Mesturino L (2007) The oak decline: A new problem in Italy. Eur J For Pathol 19:105–110. https://doi.org/10.1111/j.1439-0329.1989.tb00240.x

Raimondo M, Lops F, Carlucci A (2016) Charcoal Canker of Pear, Plum, and Quince Trees Caused by *Biscogniauxia rosacearum* sp. nov. in Southern Italy. Plant Dis. https://doi.org/10.1094/PDIS-09-15-1037-RE

Rogers JD, Ju Y-M, Candoussau F (1996) *Biscogniauxia anceps* comb. nov. and *Vivantia guadalupensis* gen. et sp. nov. Mycol Res 100(6):669–674. https://doi.org/10.1016/S0953-7562(96)80196-1

Sayers EW, Cavanaugh M, Clark K, Pruitt KD, Schoch CL, Sherry ST, Karsch-Mizrachi I (2022) GenBank. Nucleic Acids Res 50(D1):D161–D164. https://doi.org/10.1093/nar/gkab1135

Schmid-Heckel H (1988) Pilze in den Berchtesgadener Alpen, 2. Aufl. 1990. Nationalparkverwaltung, Berchtesgaden

Schrader G, Kehlenbeck H, Wilstermann A, Kaminski K (2024) Pest Risk Analysis in Germany over the course of time. Themenheft: Pflanzengesundheit 76(02):15–23. https://doi.org/10.5073/JfK.2024.02.03

Senanayake I, Maharachchikumbura S, Hyde K, Bhat DJ, Jones E, Mckenzie E, Dai D-Q, Daranagama D, Dayarathne M, Goonasekara I, Konta S, Li W, Shang Q-J, Stadler M, Wijayawardene N, Xiao Y-P, Norphanphoun C, Li Q, Liu X, Erio C (2015) Towards unraveling relationships in Xylariomycetidae (Sordariomycetes). Fungal Divers 73:73–144. https://doi.org/10.1007/s13225-015-0340-y

Sohrabi M, Mohammadi H, Armengol Fortí J, León Santana M (2022) New report of *Biscogniauxia rosacearum* as a pathogen on almond trees in Iran. J Plant Dis Prot 129(2):411–417. https://doi.org/10.1007/s41348-022-00582-y

Spies CFJ, Mostert L, Carlucci A, Moyo P, van Jaarsveldwald WJ, du Plessis IL, van Dyk M, Halleen F (2020) Dieback and decline pathogens of olive trees in South Africa. Persoonia - Mol Phylogeny Evol Fungi. https://doi.org/10.3767/persoonia.2020.45.08

Stamatakis A (2006) RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics 22(21):2688–2690. https://doi.org/10.1093/bioinformatics/btl446

Stamatakis A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30(9):1312–1313. https://doi.org/10.1093/bioinformatics/btu033

Stein F, Gailing O (2025) Identification of BOLD engine deficiencies and suggestions for improvement based on a curated *Tachina* (Diptera) record set. PLoS One 20(8):e0331216. https://doi.org/10.1371/journal.pone.0331216

Tropf J, Bien S, Bußkamp J, Langer GJ, Langer EJ (2025) Fungi associated with Vitality loss of European beech in central Germany. Mycol Progress 24(1):53. https://doi.org/10.1007/s11557-025-02041-y

van Dyk M, Spies CFJ, Mostert L, van der Rijst M, du Plessis IL, Moyo P, van Jaarsveld WJ, Halleen F (2021) Pathogenicity Testing of Fungal Isolates Associated with Olive Trunk Diseases in South Africa. Plant Dis 105(12):4060–4073. https://doi.org/10.1094/PDIS-08-20-1837-RE

Vannini A, Lucero G, Anselmi N, Vettraino AM (2008) Response of endophytic *Biscogniauxia mediterranea* to variation in leaf water potential of *Quercus cerris*. For Pathol 39:8–14. https://doi.org/10.1111/j.1439-0329.2008.00554.x

Vujanovic V, Kim SH, Latinovic J, Latinovic N (2020) Natural fungicolous regulators of *Biscogniauxia destructiva* sp. nov. that causes beech bark tarcrust in southern European (*Fagus sylvatica*) forests. Microorganisms 8(12):1999. https://doi.org/10.3390/microorganisms8121999

White TJ, Bruns T, Lee SJWT, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: guide methods Appl 18(1):315–322

Yangui I, Zouaoui Boutiti M, Vettraino AM, Bruni N, Vannini A, Ben Jamaâ ML, Boussaid M, Messaoud C (2019) *Biscogniauxia mediterranea* associated with cork oak (*Quercus suber*) in Tunisia: relationships between phenotypic variation, genetic diversity and ecological factors. Fungal Ecol 41:224–233. https://doi.org/10.1016/j.funeco.2019.07.001

Yangui I, Hlaiem S, Ben Jamâa ML, Vannini A, Vettraino AM, Messaoud C (2022) Difference in pathogenicity and genetic variability among isolates of *Biscogniauxia mediterranea* from *Quercus suber* in Tunisia. Biologia (Bratisl) 77(7):1713–1721. https://doi.org/10.1007/s11756-021-01003-5

Yangui I, Hlaiem S, Khadraoui H, Messaoud C, Ben Jamâa ML, Ezzine O (2024) *Biscogniauxia rosacearum*: A newly identified pathogen of strawberry tree (*Arbutus unedo* L.) in North Africa. Forest Pathol 54(2):e12862. https://doi.org/10.1111/efp.12862

Zamani SM, Sepasi N, Afarin S, Ahangaran Y, Gholami Ghavam Abad R, Askary H (2024) Report of *Biscogniauxia nummularia* as pathogenic agent of charcoal canker disease of beech (*Fagus orientalis*) from Iran. Iran J For Range Prot Res 21(2):350–358. https://doi.org/10.22092/ijfrpr.2024.364708.1611

Zamani SM, Mojerlou S, Alizadeh M, Ghanaei S (2025) First report of charcoal disease caused by *Biscogniauxia mediterranea* (De Not.) Kuntze on *Juniperus excelsa* M. Bieb. in Iran. Trees 39(1):17. https://doi.org/10.1007/s00468-024-02585-8

Zíbarová L, Kout J (2017) Xylariaceous pyrenomycetes from Bohemia: Species of *Biscogniauxia* and *Hypoxylon* new to the Czech Republic, and notes on other rare species. Czech Mycol 69:77–108. https://doi.org/10.33585/cmy.69106

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.