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SHORT COMMUNICATION

First record of brown spot needle blight (BSNB) caused by *Lecanosticta acicola* on *Pinus mugo* in Finland

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Abstract

Climate change has already been acknowledged to have destabilizing effects on tree health. In addition to increased abiotic disturbances, trees are increasingly negatively impacted by the emergence of fungal pathogens. *Lecanosticta acicola*, the causal agent of brown spot needle blight (BSNB), affects pines and is considered invasive in Europe. In October 2025, typical symptoms of *L. acicola*, brown circumferential lesions with a yellow halo, were observed on an urban tree, *Pinus mugo*. The pathogen was isolated from surface-sterilized needles, and morphological and molecular identification confirmed it as *L. acicola*. Here, we report the first observation of the invasive pathogen *L. acicola* on the non-native host *P. mugo* in Finland. *Lecanosticta acicola* is classified as a Quality Plant Pest by the Finnish Food Authority and as no suitable plant protection methods are currently available in Finland, this finding is of particular significance. The detection of this pathogen highlights a potential threat to forestry and emphasizes the need for preventive strategies to limit its spread, including eradication, breeding and improved integrated pest management (IPM) practices in nurseries.

Keywords Climate change · Emerging · Invasive pathogen · *Mycosphaerella dearnessii* · Scots pine

Introduction

Recent evidence indicates that current environmental trends are increasing the risk of large-scale climate system instability (Ripple et al. 2024). Climate change is a key driver of emerging and invasive forest disturbances, particularly by favouring fungal pathogens. Rising temperatures facilitate the expansion of pathogen geographic ranges, allowing species previously restricted by cold climates to establish in new regions (Dudney et al. 2021; Li et al. 2023; Singh et al. 2023; Terhonen et al. 2025a). This process promotes the introduction of novel disease agents into forest ecosystems, where native host species often lack effective resistance (Barnes et al. 2018; George et al. 2022). In addition, warmer conditions, such as milder winters, enhance pathogen overwintering success and increase infection pressure (Hanso and Drenkhan 2013; Ma et al. 2015; Caballol et al. 2022). Climatic variables, particularly temperature and precipitation, are therefore major determinants of the global distribution of phytopathogenic fungi (Větrovský et al. 2019; Li et al. 2023), and their diversity and invasion potential are expected to increase in forest ecosystems under future climate scenarios.

Lecanosticta acicola is the causal agent of brown spot needle blight (BSNB). Symptoms appear as brown spots surrounded by a yellow halo that encircles the needle (Skilling and Nicholls 1974; van der Nest et al. 2019; Fig. 1a), eventually leading to distal necrosis (Fig. 1b). In the necrotic tissue the fungus forms black stromata (Wolf and Barbour 1941). Finally, *L. acicola* produces oval, black fruiting bodies (acervuli-like) bearing conidia that emerge through the epidermis (Wolf and Barbour 1941; van der Nest et al. 2019). The conidia are subhyaline to dark olive-green and thick-walled (Evans 1984; Siggers 1944; van der Nest et al. 2019; Fig. 1c). They have a rounded tip and a truncated base, and they vary in shape from fusiform to cylindrical, ranging from straight to slightly curved (van der Nest et al. 2019; EPPO 2024; Fig. 1c). Heavily infected pine

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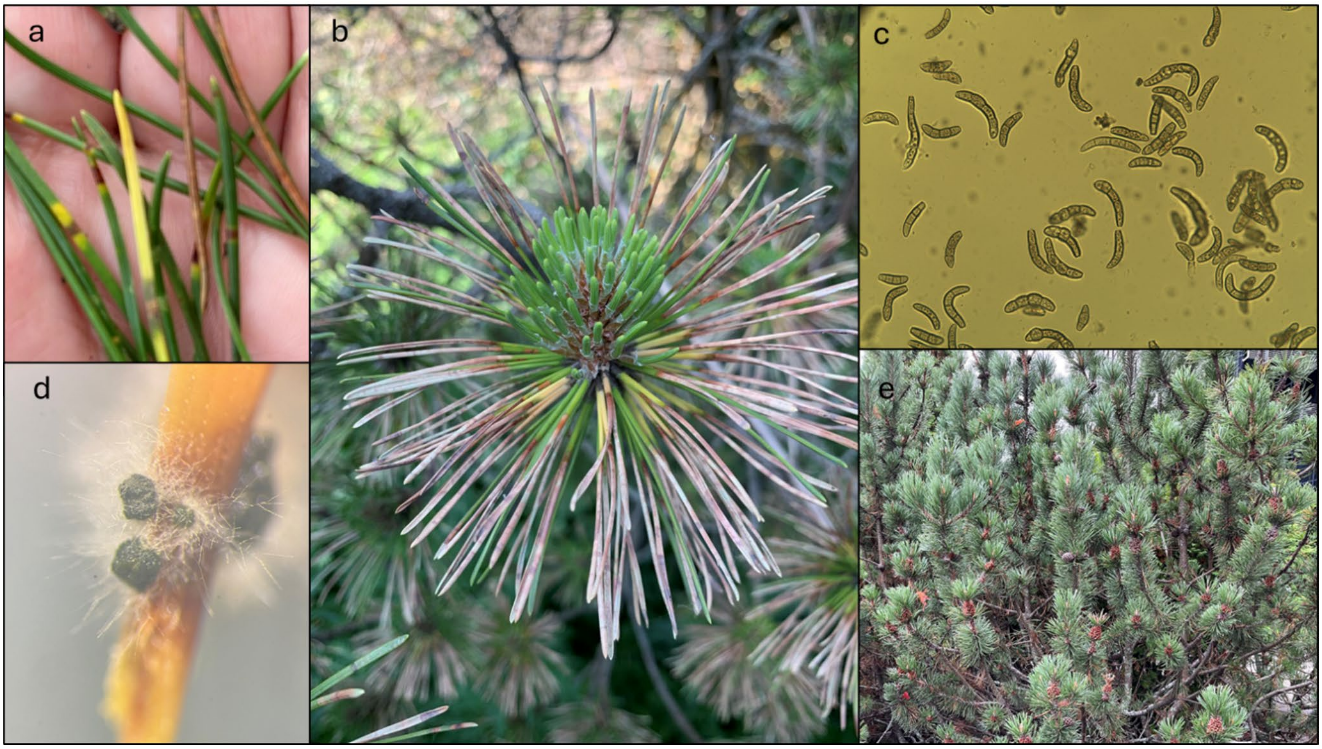

Fig. 1 (**a**) Typical symptoms of brown spot needle blight (BSNB) caused by *Lecanosticta acicola*, documented in Finland in October 2025. Characteristic brown spots with a yellow halo encircle the needle. (**b**) As the disease progresses, needles die from the lesion outward toward the tip, while the current year's needles remain alive, creating the characteristic "lion's tail" appearance. *Pinus mugo* with BSNB symptoms in Tartu, Estonia (June 2023). (**c**) Conidia of *L. acicola* observed under the microscope (60×), displaying the characteristic curved, 1–5-septate morphology. (**d**) *Lecanosticta acicola* conidial mass growing from a brown spot on the needle (10×) From this mass, the conidiospores can be easily observed under the microscope. (**e**) *Pinus mugo* growing as a city tree in Southwest Finland showing needle cast on older needles and typical BSNB symptoms on part of the current-year needles

trees often retain only the current year's needles on twigs, while repeated infections can lead to extensive needle shedding and, in severe cases, tree mortality (van der Nest et al. 2019).*Lecanosticta acicola* was first isolated in 1876 from needles of *Pinus caribaea* in the USA (de Thümen 1878). The disease, BSNB, became widely recognized in the early 1900 s after it caused severe damage to longleaf pine (*P. palustris*) forests in the southeastern United States (Siggers 1944; Sinclair and Lyon 2005). In Europe the first records of the disease were made in 1942 (Spain; Martinez 1942) and 1976 (Croatia; Milatovic 1976). The number of newly reported cases of BSNB has increased markedly in Europe (van der Nest et al. 2019; Laas et al. 2022; Tubby et al. 2023). The pathogen has been recorded on several pine species (such as *P. nigra*, *P. uncinata*, *P. ponderosa*, *P. pumila*, and *P. halepensis*) in 24 European countries (Tubby et al. 2023). In Europe, *L. acicola* is considered an invasive species, with evidence of multiple independent introduction events (Janoušek et al. 2016; Laas et al. 2022; Tubby et al. 2023). Human activity has likely played a major role in its spread across the continent (Janoušek et al. 2016; van der Nest et al. 2019). and the most severe and repeated outbreaks have occurred on *P. mugo* and its variants (van der Nest et al. 2019; Tubby et al. 2023).

Lecanosticta acicola has also been confirmed on Scots pine (*P. sylvestris*) (Adamson et al. 2018; Klaviņa et al. 2025). Distribution modelling suggests that *L. acicola* is likely to become increasingly established in Europe (including Finland) under future climate scenarios (Ogris et al., 2023). Given the economic, cultural, and ecological importance of Scots pine, *L. acicola* should be considered a potential and emerging threat to Finnish pine-dominated forests. Young stands and nurseries are particularly vulnerable (van der Nest et al. 2019), which would affect forest regeneration success and facilitate the spread of the disease into new areas (Tubby et al. 2023).

Attempts to detect *L. acicola* in Finland have been made previously, but without success (Tubby et al. 2023). In October 2025 *L. acicola* was detected for the first time in Finland in symptomatic non-native *P. mugo*.

Materials and methods

In October 2025, needle cast of older needles and brown needle spots were observed on *P. mugo* in southwest Finland (60°22'59.16''N, 23°7'59.16''E). The sampled tree was growing as urban ornamental in front of a building (Fig. 1e). Needles with brown spots and yellow halo were collected for analysis (Fig. 1a). The needles were surface-sterilized with 70% EtOH, air-dried, and then surface-sterilized for 1 min in 2.4% NaOCl, followed by three rinses in sterile deionized water Ten needles with symptoms and one green needle were cut into ~ 1 cm pieces, placed on 2% MEA, and incubated at + 15 °C in darkness for 3 weeks. All fast-growing fungi were discarded. Slowly growing black hyphae surrounded by white hyphae emerging from the brown spots (Fig. 1e) were subcultured, and the conidia were examined microscopically (Fig. 1c). Representative strains are stored on MEA slants at 4 °C at the Natural Resources Institute Finland (Luke).

Molecular identification based on the ITS region was performed following Terhonen (2023). Briefly, DNA was isolated using the PrepMan™ Ultra Sample Preparation Reagent (Applied Biosystems, Foster City, CA, USA) according to Linnakoski et al. (2016). The ITS1–5.8 S–ITS2 region of rDNA was amplified using the primer pair ITS1-F (White et al. 1990) and ITS4 (Gardes and Bruns 1993). The PCR mixture contained DreamTaq Green Mix (2×) (Thermo Scientific™), 200 µM dNTPs, 0.5 µM of each primer, and 1 µl of crude template DNA; the reaction volume was adjusted to 15 µl with autoclaved Milli-Q H_2O. PCR conditions were: 94 °C for 3 min; 30 cycles of 94 °C for 30 s, 55 °C for 1 min, 72 °C for 1 min; and a final extension at 72 °C for 10 min. PCR products were visualised under UV light on 1.5% agarose gel (Ethidium Bromide staining) and purified using the EXO-SAP protocol (Exonuclease I and Shrimp Alkaline Phosphatase; Thermo Fisher Scientific, Waltham, MA, USA) (Linnakoski et al. 2016) and Sanger sequenced using the ITS1 primer at Macrogen (Germany).

The β-tubulin region was amplified using the primer pairs Btub2Fd and Btub4Rd (Woudenberg et al. 2009). Polymerase chain reaction (PCR) was performed using the Phire Plant Direct PCR Master Mix (F160S, Thermo Scientific®, Thermo Fisher Scientific), following the manufacturer's instructions. PCR cycling conditions were as follows: initial denaturation at 98 °C for 30 s; 30 cycles of 98 °C for 5 s, 60 °C for 5 s, and 72 °C for 5 s; followed by a final extension at 72 °C for 1 min. PCR products were visualised under UV light on a 1–1.2% agarose gel stained with DNA Stain G (SERVA Electrophoresis GmbH, Heidelberg, Germany). PCR products were purified using the Monarch® PCR & DNA Cleanup Kit (5 µg) (New England Biolabs, Ipswich, MA, USA) according to the manufacturer's instructions and sent to Eurofins Genomics (Germany) for Sanger sequencing in both directions with primer pair Btub2Fd and Btub4Rd.

ITS and β-tubulin sequences were analysed using MEGA12 (Kumar et al. 2024). Sequence identity was verified by aligning the obtained sequences with reference sequences in the GenBank database via NCBI BLAST (Altschul et al. 1990; Sayers et al. 2025). The ITS (550 b) and β-tubulin (445 b) sequences were deposited in the European Nucleotide Archive (ENA) under accessions OZ373024 and OZ387206, respectively. The ITS and β-tubulin sequences, along with the corresponding BLAST results, are available at Zenodo (DOI: https://doi.org/10.5281/zenodo.17951324).

Phylogenetic analysis

Sequences were aligned using the MUSCLE algorithm (Edgar 2004) implemented in Unipro UGENE v53.0 (Okonechnikov et al. 2012). The resulting alignment was inspected and manually refined where necessary. Phylogenetic placement of the fungal isolates was inferred using maximum likelihood (ML) analysis in raxmlGUI v2.0 (Edler et al. 2021), implementing RAxML with a GTR+Gamma + I nucleotide substitution model. ML analyses were performed in 10 independent runs, and branch support was assessed using thorough bootstrap analysis with 1,000 replicates. The resulting phylogenetic tree was visualised in FigTree v1.4.4 and subsequently edited using graphical softwares. Phylogenetic trees were constructed using a combination of the ITS and β-tubulin regions, as well as the ITS region alone. GenBank accession numbers for the strains used are provided in the Supplementary File.

Results

Four strains of *L. acicola* were isolated from brown spots on still-living, surface-sterilized needles. Morphological identification was performed based on conidial characteristics (Fig. 1d; EPPO Bulletin 2015), and species identity was confirmed for all four strains using ITS rDNA sequencing and β-tubulin (DOI: https://doi.org/10.5281/zenodo.17951324). The ITS region showed a 100% identity (537/537 bp; 100% query coverage) with TYPE strain of *L. acicola* CBS 133,791 (GenBank accession NR_120239.1), while the β-tubulin gene sequence exhibited a 100% identity (326/326 bp; 71% query coverage) with TYPE strain of *L. acicola* WPF13.12 (GenBank accession KC013008.1). The ITS and β-tubulin sequences were submitted to GenBank, and these were identical among all isolates. The phylogenetic analysis further confirmed the species as *L. acicola* (Figs. 2 and 3).

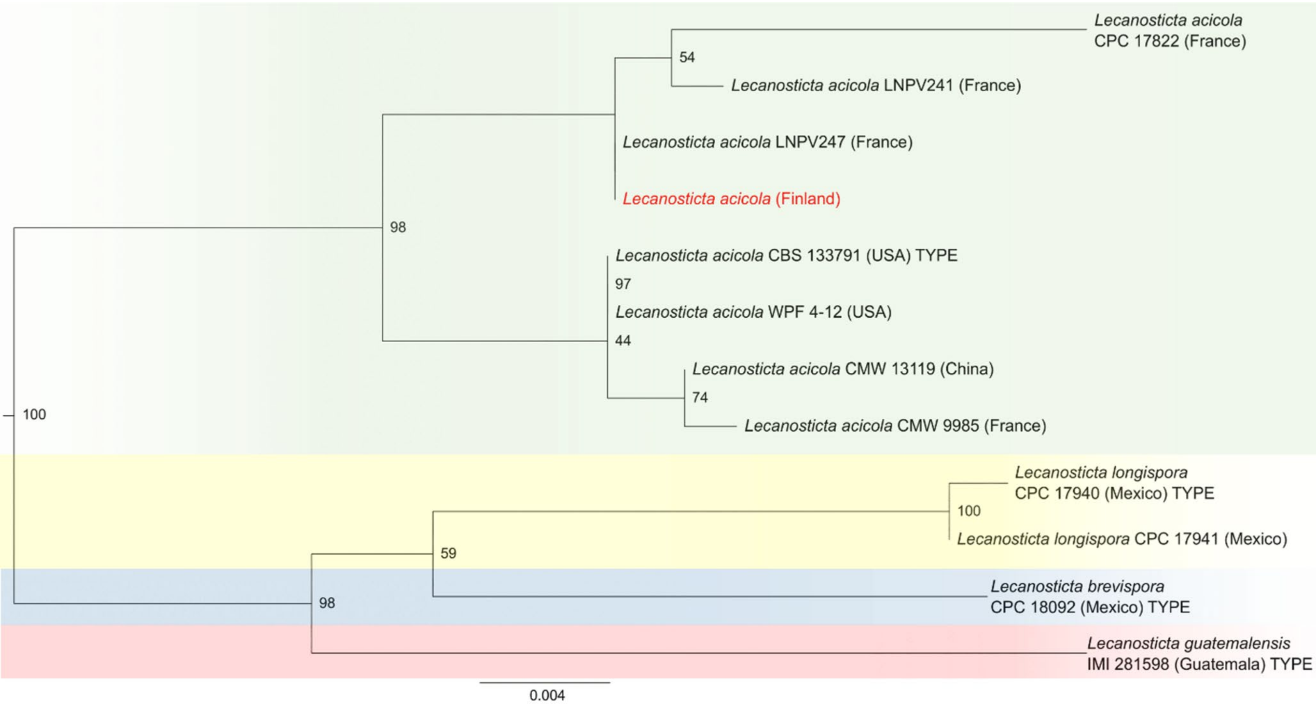

Fig. 2 Phylogram based on maximum likelihood analysis of ITS and β-tubulin sequence data from *Lecanosticta acicola* and closely related species available in GenBank. ML bootstrap values (≥40%) are indicated. The Finnish strain reported in this study is indicated in red. The scale bar indicates 0.004 expected changes per site per branch. The figure presents strain identifications and country of origin based on NCBI GenBank records. Accession numbers for all strains used in the analyses are provided in the Supplementary Files. The Finnish strains were 100% identical so no strain ID were used for the figure. The ENA accession numbers for the Finnish strains are OZ373024 and OZ387206

Discussion

This study reports the first occurrence of brown spot needle blight (BSNB) in Finland. The causal agent, *L. acicola*, has not previously been recorded in the country. Recent findings show that the pathogen can shift from exotic to native hosts, including Scots pine, and may establish in local pine populations (Adamson et al. 2018; Klaviņa et al., 2025). Although the present detection concerns a non-native *P. mugo*, the establishment of *L. acicola* suggests that Finnish conditions may permit its survival and potential spread to native Scots pine (Adamson et al. 2018; Ogris et al. 2023; Klavina et al. 2025).

Scots pine accounts for approximately 50% of the total growing stock volume in Finland (1,250 million m³; Korhonen et al. 2024). Beyond its economic role in the forest industry, Scots pine is also a culturally important species, forming an iconic element of Finland's forest landscapes. Ecologically, its importance is considerable: Finland hosts only around 30 native tree species (Rikkinen 2010), and Scots pine contributes substantially to forest structure, biodiversity, and ecosystem functioning.

In Europe, several eradication attempts have been implemented to prevent the establishment and spread of *L. acicola* (see case studies in Tubby et al. 2023). Despite eradication efforts, *L. acicola* has spread from non-native pine hosts (Adamson et al. 2015) to native Scots pine eight years after its initial detection (Adamson et al. 2018).

EPPO lists *L. acicola* as an A2 pest (EPPO code SCIRAC), indicating that it is present in the EPPO region, but is recommended for regulation as a quarantine pest in member countries to limit its further spread (see PM1/002(34). *Lecanosticta acicola* is classified as a Quality Plant Pest by the Finnish Food Authority so this pathogen must not be present in any plants sold in Finland, making *L. acicola* a new concern for seedling production and trade (see case study 3 in Tubby et al. (2023). At the same time, future availability and effectiveness of control methods are uncertain. In Finland, three fungicidal active substances—azoxystrobin (authorised until 02 August 2026), benzovindiflupyr (authorised until 2 August 2026), and prothioconazole (authorised until 15 August 2026), are currently approved for use in forest nurseries against needle cast diseases. However, first, it is unknown whether these substances are effective against *L. acicola*; second, fungicidal active substances are continuously evaluated in the EU, and some may be withdrawn if they are not reapproved. Additionally, no compensation is provided for discarded seedlings for nursery producers (see case study 3 in Tubby et al. 2023).

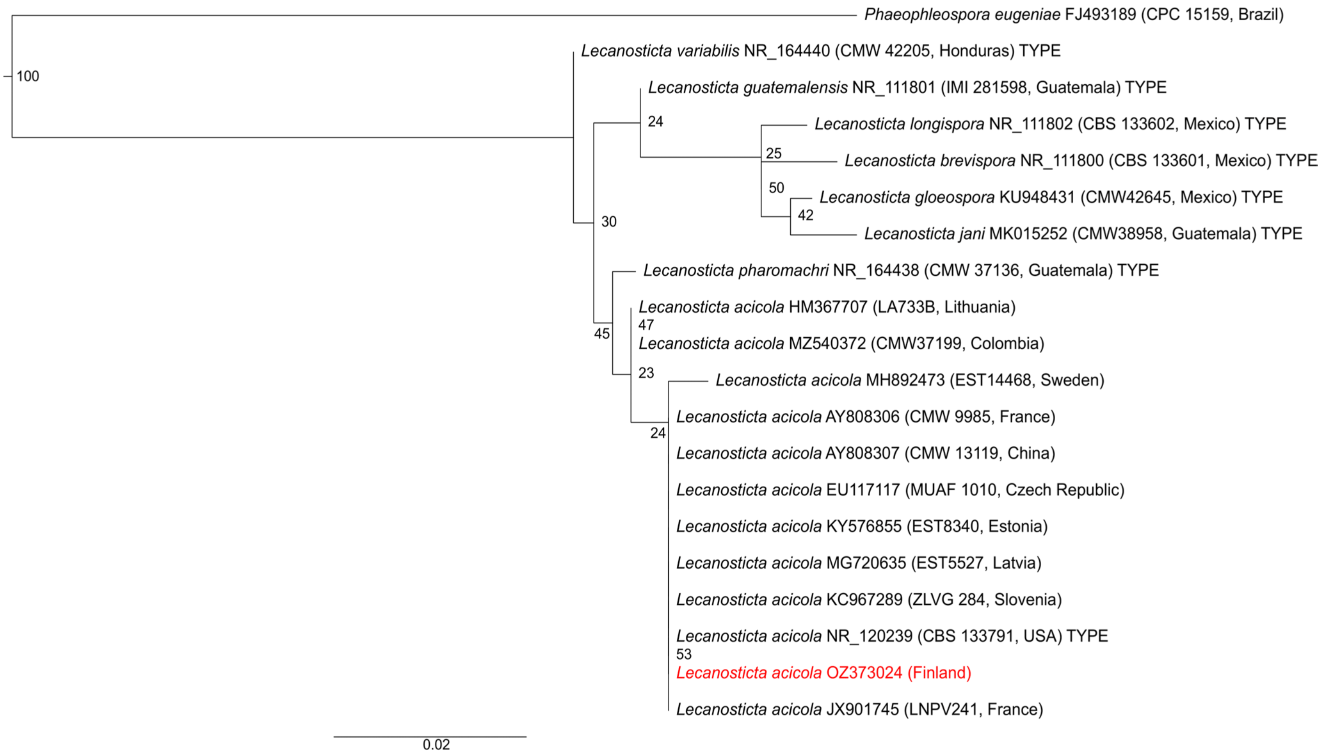

Fig. 3 Phylogenetic tree inferred using maximum likelihood analysis of an ITS dataset from *Lecanosticta acicola* and closely related species. *Phaeophleospora eugeniae* was used as the outgroup. Maximum likelihood bootstrap values (≥20%) are shown. The Finnish strain reported in this study is indicated in red. The scale bar represents 0.02 expected substitutions per site. The NCBI accession numbers of the strains used in the analyses are listed in the Supplementary Files

There is an urgent need for research to ensure preparedness for the potential spread of *L. acicola*, particularly to evaluate how effective integrated pest management (IPM) strategies in forest nurseries could prevent infections. When combined with tree breeding, such approaches may provide viable solutions to improve tree resilience. Scots pine exhibits substantial genetic variation, with heritable traits differing among regions, enabling populations to adapt to local environmental conditions (Kujala et al. 2017; Savolainen et al. 2007; Pyhäjärvi et al. 2019). Following the principle of "the right tree to the right site" and of promoting forest structures that are diverse in both species' composition and genetic variation within species represents an opportunity to reduce disease impacts. Such multi-diversity reduces the risk that any single pathogen or stressor will cause widespread damage.

Identifying the possible genetic basis and heritability of *L. acicola* resistance represents an important step forward, as it could enable the integration of this trait into broader, multi-trait breeding strategies that also consider growth, adaptability, and resistance to other biotic needle and shoot threats (Fraser et al. 2015; Terhonen et al. 2025b). Together with eradication measures, nursery-based IPM, and diversified forest management, these strategies could provide effective means to restrict the spread of the invasive pathogen *L. acicola* in Finland.Overall, tree health should be communicated more effectively to citizens, who can play a valuable role in helping researchers detect new threats (Terhonen et al. 2025a). Keeping trees healthy requires combined efforts from forest owners, policymakers, researchers, government, and the public.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s41348-026-01293-4.

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Declarations

Conflict of interest The authors declare that there is no conflict of interest.

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