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, resistance breeding and improved integrated pest management (IPM) practices in nurseries.

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 & 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 name indicates, brown spots with a yellow halo that encircle the needle (Fig. 1a), that can lead to necrosis at the distal end (Fig. 1b). In the necrotic tissue the fungus forms black stromata. Finally, *L. acicola* produces oval, black fruiting bodies (acervuli-like) bearing conidia that emerge through the epidermis. The conidia are subhyaline to dark olive-green and thick-walled (Fig. 1c). They have a rounded tip and a truncated base, vary in shape from fusiform to cylindrical, and range from straight to slightly curved (Fig. 1c). Heavily infected pine trees often retain only the current year’s needles on twigs (Fig. 1d). Repeated infections can cause extensive needle shedding and, in severe cases, the death of pine trees (van der Nest et al., 2019).

The disease, BSNB, became widely recognized in the early 1900s after it caused severe damage to longleaf pine (*Pinus palustris*) forests in the southeastern United States (de Thümen, 1878; Siggers, 1944; Sinclair & Lyon, 2005). Beginning in the 1990s, BSNB also emerged in many European countries (van der Nest et al., 2019; Laas et al. 2022; 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 significant role in its spread across the continent (Janoušek et al., 2016; van der Nest et al., 2019). The pathogen has been recorded since the 2000s 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). However, the most severe and repeated outbreaks have occurred on *Pinus mugo* (van der Nest et al., 2019; Tubby et al., 2023).

Lecanosticta acicola has also been confirmed on Scots pine (*Pinus 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, which would affect forest regeneration success and facilitate the spread of the disease into new areas.

Attempts to detect *L. acicola* in Finland have been made previously (Tubby et al., 2023), but without success. Symptomatic needles of *Pinus* spp. have been tested at the Natural Resources Institute Finland, and in October 2025 *L. acicola* was detected for the first time in Finland in symptomatic non-native *P. mugo*.

Material 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 tree was growing as urban ornamental in front of a building (Fig. 1d). 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 DDW. Needles 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 ITS1–5.8S–ITS2 region of rDNA was amplified using the primer pair ITS1-F (White et al., 1990) and ITS4 (Gardes & 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 MQ 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 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.

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: 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: 10.5281/zenodo.17951324). The ITS region showed a 100% identity (537/537 bp; 100% query coverage) with TYPE strain of *L. acicola* (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* (GenBank accession KC013008.1). Only reliable regions of 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* (Fig. 2, 3).

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), and by the end of October 2025, the average stumpage price for pine logs was €155 (Natural Resources Institute Finland, statistical database). Beyond its economic role in the forest industry, Scots pine is also a culturally significant species, forming an iconic element of Finland's forest landscapes. Ecologically, its importance is considerable: Finland hosts only around 30 native tree species, 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 significant 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).

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 control and limit pathogen spread. 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). Harnessing this genetic diversity in targeted breeding programs represents an opportunity to reduce any disease impacts. Accordingly, future research should focus on identifying the genetics and heritability underlying possible resistance, thereby enabling effective resistance breeding programs in pines (Fraser et al. 2015, Terhonen et al. 2025b). Together with eradication measures and nursery-based IPM, 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 policymakers, researchers, government, and the public.

Declarations

The authors declare that there is no conflict of interest.

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Figures

Figure 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) *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. e) Hyphae growing from a brown spot on the needle (10×).

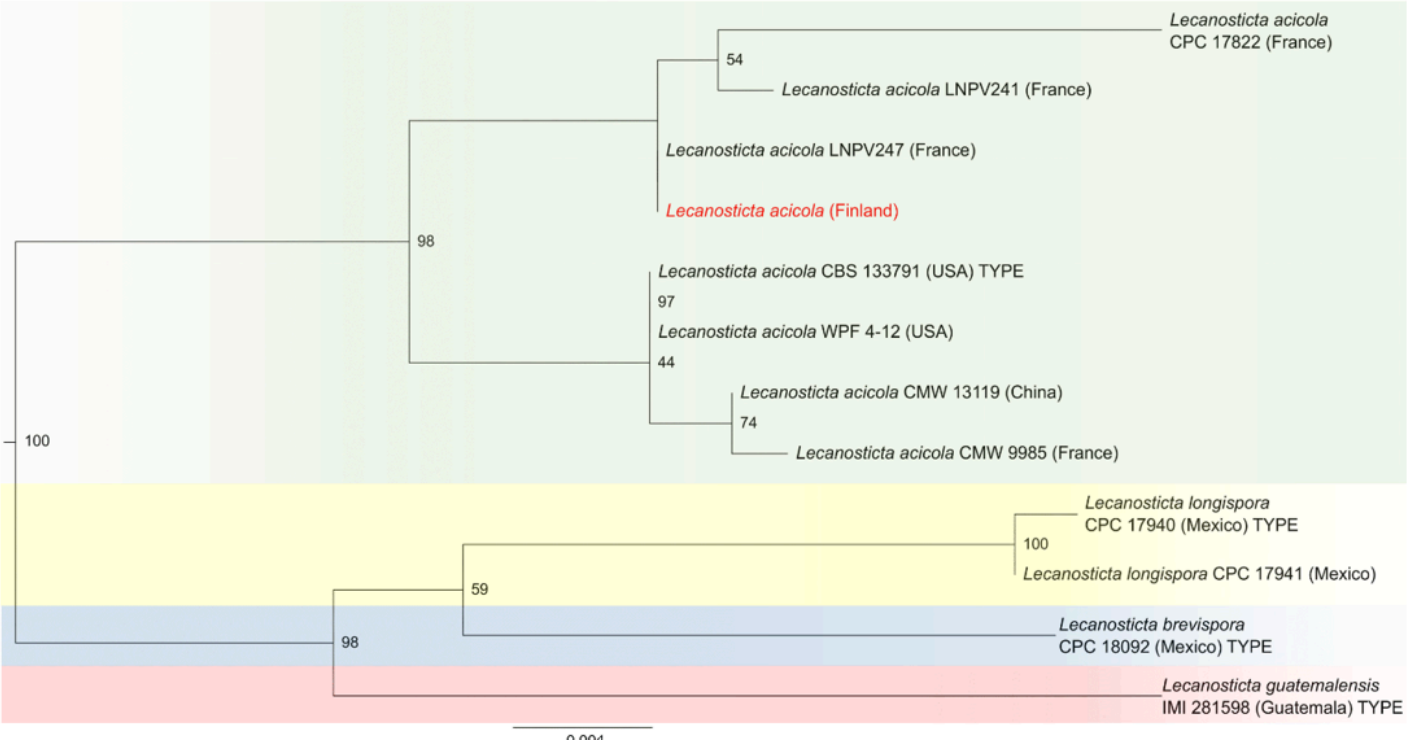

Figure 2

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 0.005 expected changes per site per branch. The NCBI accession numbers of the strains used in the analyses are listed in the Supplementary Files.

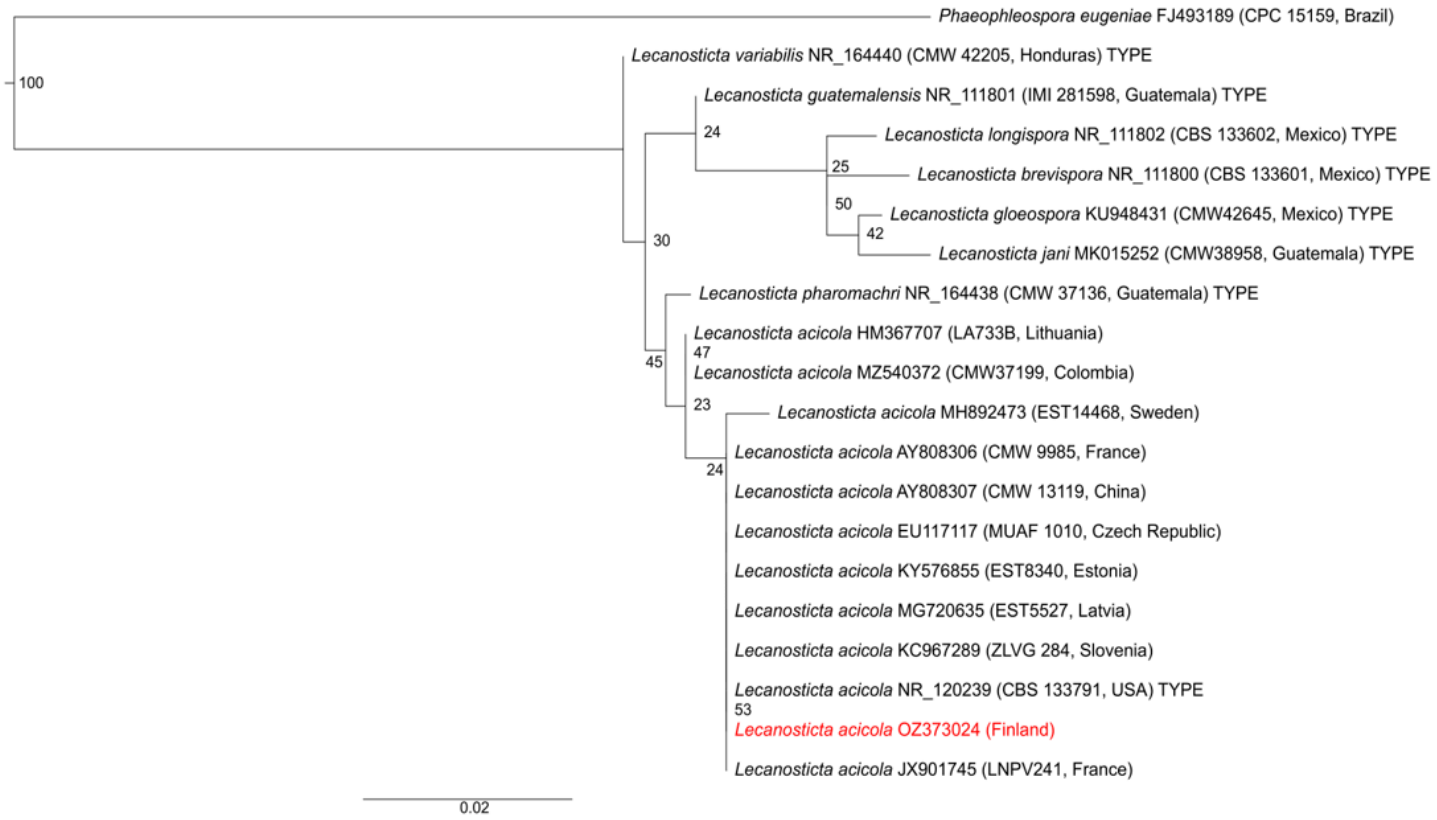

Figure 3

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.

Supplementary Files

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