OCCURRENCE OF SEVERAL NEEDLE PATHOGENS IN YOUNG FOREST STANDS OF SCOTS PINE IN LATVIA

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Abstract
This study aimed to investigate the spread of several needle pathogens from the genera *Dothistroma*, *Diplodia*, and *Lecanosticta* that have been introduced to Latvia in recent decades. The occurrence of these pathogens was assessed in 165 forest stands of Scots pine (*Pinus sylvestris* L.). Stands were selected across Latvia based on stand composition (pine monocultures), stand age (up to 20-year-old pines), and an approximate area of one or more hectares. Stands were surveyed during either the spring or autumn of 2021. The needle cast rate was determined in each stand by inspecting 10 random trees and collecting one representative sample from three symptomatic pines. Needle pathogens were identified based on morphological characteristics and molecular analysis with species-specific primers for four pathogens: *Dothistroma septosporum*, *Dothistroma pini*, *Diplodia sapinea*, and *Lecanosticta acicola*. The analysis revealed that *Dothistroma septosporum* and *Diplodia sapinea* were the most common pathogens found in 30% and 18% of stands, respectively. *L. acicola* was not detected in any of the analysed samples. Since all tested pathogens are recently established in Latvia, monitoring their spread and impact to local forests is important.
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Keywords: *Dothistroma septosporum, Dothistroma pini, Diplodia sapinea*, needle cast, *Pinus sylvestris*.

Introduction

Scots pine *Pinus sylvestris* is an abundant and economically important tree species in Baltic Sea region, hosting many pathogenic organisms (Ruotsalainen & Persson, 2013; Raitelaitytė et al., 2017). The main invasive fungal species causing pine needle and shoot diseases in the Baltic region are *Dothistroma septosporum*, *Dothistroma pini*, *Diplodia sapinea*, and *Lecanosticta acicola* (Drenkhan & Hanso, 2009; Adamson et al., 2015a, 2015b).

Dothistroma needle blight (DNB), or red band needle blight, is a major global pine disease (Mullett et al., 2021). It affects over 80 conifer species, with pines being the most common host (Raitelaitytė et al., 2017). Symptoms begin as yellow or light brown bands on needles that turn brick red before the needles die. Fruiting bodies develop within these bands, aiding disease spread, progressing from the lower crown upward and inner branches outward (Gonthier & Nicolotti, 2013).

First identified in Africa and North America in the 1950s–1960s, *Dothistroma* primarily affected *Pinus contorta, P. nigra*, and *P. radiata* (Gibson et al., 1974). Today, it has been reported on 109 *Pinaceae* species, including 95 pine species, some *Picea* spp., and *Larix decidua* (Drenkhan et al., 2016). While early outbreaks were mild, the disease has intensified in plantations (Harrington & Wingfield, 1998). Since the 1990s, outbreaks have increased across the Northern Hemisphere, affecting more species and regions, including the Baltic countries (Villebonne & Maugard, 1999; Hanso & Drenkhan, 2008). Severe infections reduce biomass growth, and tree mortality occurs when needle loss exceeds 85% (Gonthier & Nicolotti, 2013). Although *Dothistroma* alone rarely kills trees, it increases susceptibility to secondary infections, such as *Armillaria* spp. in young pine stands (Gonthier & Nicolotti, 2013). Two *Dothistroma* species cause needle blight: *D. septosporum* and *D. pini* (Barnes et al., 2004). *D. septosporum* is on the European and Mediterranean Plant Protection Organization (EPPO) quarantine list (EPPO, 2005). Both species occur in Latvia, with *D. septosporum* widespread and *D. pini* found in isolated western stands (Ķiesnere, 2014).

Diplodia sapinea is increasingly spreading across the Northern Hemisphere due to climate change, though initially, it was found only in southern regions. The first recorded cases of *D. sapinea* infection in Estonia date back to 2007, followed by reports in Sweden and Finland (Brodde et al., 2023). *D. sapinea* has a broad host range, but it primarily affects conifers. *Diplodia sapinea* induces various disease symptoms in conifers, such as needle browning, shoot blight, twig and branch dieback, crown wilt, and bark cankers in mature trees. It can also cause collar rot, root disease, seedling damping-off, and blue stain in sapwood. *Diplodia sapinea* is thought to be native to pine forests in the Northern Hemisphere, where it exists as an endophyte in pine shoots, becoming an opportunistic pathogen when the tree is under stress conditions, such as drought, insect damage, or frost (Adamson et al., 2021).

Lecanosticta acicola (Thüm.) Syd. (syn. *Mycosphaerella dearnessii* M. E. Barr) causes brown-spot needle blight, a major pine disease first identified in North America in 1876 (Tainter & Baker, 1996). It was first reported in Europe in 1942 in Spain, likely arriving through two historical infection routes: from the Mississippi region to Spain and from northeastern North America to Italy, then Northern Europe (Janoušek et al., 2014). Symptoms appear as small, irregular circular spots with well-defined margins, initially yellow or light gray green, later turning brown with a yellow halo (Van Der Nest et al., 2019). The disease has spread rapidly across Europe in recent decades (Drenkhan & Hanso, 2009; Jankovský et al., 2009; Markovskaja et al., 2011; Hintsteiner et al., 2012; Adamson et al., 2015a; Adamčíková et al., 2021) and is listed as a quarantine organism by EPPO (EPPO, 2008). Initially *L. acicola* was found on ornamental pines in urban areas (Adamson et al., 2015a; Adamčíková et al., 2021), but it has since been observed in some *P. sylvestris* forest stands (Adamson et al., 2018). The disease spreads upward, driven by moisture, with spore dispersal starting at 2–3 °C (Tainter & Baker, 1996). In Latvia, *L. acicola* has been found only on ornamental pines, first reported in 2012 at the National Botanic Garden in Salaspils, with subsequent findings in 2016, and later near Daugavpils (Mullett et al., 2018; EPPO, 2021).

A better understanding of the distribution, impact, and contributing factors of these invasive pathogens is essential for developing effective management strategies. Therefore, this study aims to assess the occurrence and spread of pine needle and shoot diseases in Latvian pine forests, focusing on their potential impact on forest ecosystems.

Materials and Methods

The occurrence of needle diseases was assessed in young stands of Scots pine (*P. sylvestris*). In total, 165 survey sites were randomly selected across Latvia from the database of ʻLatvia's State Forests' based on specific criteria: age up to 20 years, stand composition classified as pine monocultures, various forest types (Bušs, 1997), and an approximate area of one or more hectares. The selected stands were located near roads for easier accessibility. Stands were surveyed in 2021 (155 in spring and 10 in autumn).

Fieldwork methodology was adapted from previous studies of needle pathogens (e.g. Drenkhan & Hanso, 2009; Adamson et al., 2018). Each stand or planting site was visually assessed to evaluate overall vitality, presence of animal-caused damage, dead trees, and anthropogenic impacts. In each surveyed stand, 10 pines were randomly selected, and symptoms were recorded. Symptoms mainly included necrotic spots of varying shapes and colours. In symptomatic areas of needles, shoots, or cones, fungal reproductive structures (acervuli, pycnidia, or fruiting bodies) were examined.

In each surveyed stand, samples were collected from 2–3 symptomatic trees. If needles were already desiccated, they were collected along with a twig fragment. Samples were placed in labelled sterile bags and transported in a cooler box to the laboratory. Microscopic examination was conducted immediately or after storage at -20 °C.

For fungal identification, each needle sample was examined under a microscope for assessment of morphological characteristics of pathogenic fungi. In addition, fragments from symptomatic needles were analysed using molecular methods in collaboration with the Estonian University of Life Sciences (Prof. R. Drenkhan). Total DNA was extracted using the Thermo Fisher Scientific GeneJET Genomic DNA Purification Kit. Pathogens were identified through polymerase chain reaction (PCR) using species-specific primers for *D. septosporum*, *D. pini*, *L. acicola*, and *D. sapinea* (see Table 1).

The PCR cycling protocol (Adamson et al., 2015a) included an initial denaturation at 95 °C for 15 minutes, followed by 40 cycles of denaturation (95 °C for 30 s), annealing (for primers DStub2-F and R DPtef-F and R at 66 °C, but Latef-F and R DiSapiF and DiploR at 62 °C for 30 s), and extension (72 °C for 1 min), with a final extension at 72 °C for 10 minutes. PCR products (5 µl) were analysed on 1% agarose gel to confirm pathogen presence.

The relative proportion of symptomatic pines was calculated based on the total number of analysed trees in each forest type and compared among forest groups (dry, wet or over wet and drained (Table 2)) using the Chi-square test.

Results and Discussion

In total, 165 pine sapling stands were surveyed in 2021, covering an area of 382 hectares (Table 2). The tree ages ranged from 3 to 19 years. The majority of analysed stands (160 or 97%) showed some needle cast symptoms. The proportion of healthy and symptomatic pines in dry and drained forest types was close to predicted values of Chi-square test, but in wet or over wet forest sites more symptomatic pines than predicted were observed ($p<0.05$). Previous studies have suggested that selecting the right forest type for pine cultivation can help reduce the risk of needle blight in pines (Boateng & Lewis, 2015; Bulmann et al., 2016). Our findings support this, showing that pine saplings might experience more needle blight damage in wet or over wet forest types.

Invasive needle pathogens were detected in 50% of analysed stands in total. ***Dothistroma*** was identified as the dominant genus in collected needle samples based on microscopic characteristics, including characteristic red discoloration on needles, acervuli, and conidia. The disease was detected in 68 out of 165 pine stands surveyed. Infected stands varied in age and forest type. Crown damage was mostly minor and localized, affecting 0–50% of surveyed trees (on average, 0.3% per stand). Despite mild symptoms, some authors suggest that *Dothistroma* infections can still reduce biomass production in conifers (Gonthier & Nicolotti, 2013). While tree mortality in such cases is rare (2% of severe needle loss), the risk increases when *Dothistroma* co-occurs with other pathogens like *Armillaria* spp. or *Diplodia* spp. (Gonthier & Nicolotti, 2013).

The distribution map ʻFigure 1' of molecularly identified *Dothistroma septosporum* indicates that it is widespread across Latvia (49 records). Molecular analyses confirmed that symptoms were primarily caused by *D. septosporum*, aligning with previous studies showing its dominance in Latvia (Ķiesnere, 2014). Although both *D. septosporum* and *D. pini* have been identified on Scots pine in Latvia (Ķiesnere, 2014), only *D. septosporum* was found in this study. The pathogen's adaptation and virulence are linked to its genetic diversity, influenced by sexual reproduction potential. Both mating types of *D. septosporum* exist in Latvia, but some stands may possess only one, limiting the sexual reproduction (Ķiesnere, 2014).

Table 1
Primers used for Dothistroma septosporum, Dothistroma pini, Lecanosticta acicola, and Diplodia sapinea identification

Target Organism	*Primers (Forward & Reverse)*	*Reaction Components*
Dothistroma septosporum	DStub2-F (5' – CGAACATGGACTGAGCAAAAC – 3') DStub2-R (5' – GCACGGCTCTTTCAAATGAC – 3') (Ioos et al., 2010)	4 µl HOT FIREPol® Blend Master Mix RTL With 10 mM $MgCl_2$ (Solis BioDyne) 0.5 µl of each primer 14 µl ddH_2O 1 µl DNA sample (50 ng/µl)
Dothistroma pini	DPtef-F (5' – ATTTTTCGCTGCTCG – 3') DPtef-R (5' – CAATGTGAGATG – 3') (Ioos et al., 2010)	0.2 µl HOT FIREPol® polymerase 2 µl HOT FIREPol® 10x Buffer B2 1.6 µl 25 mM $MgCl_2$ 0.5 µl of each primer 13.2 µl ddH_2O 2 µl DNA sample (50 ng/µl)
Lecanosticta acicola	Latef-F (5' – GCAAATTTTCGCCGTTTATC – 3') Latef-R (5' – TGTGTTCCAAGAGTGCTTGC – 3') (Ioos et al., 2010)	4 µl HOT FIREPol® Blend Master Mix RTL With 10 mM $MgCl_2$ (Solis BioDyne) 0.5 µl of each primer 14 µl ddH_2O 1 µl DNA sample (50 ng/µl)
Diplodia sapinea	DiSapiF (5' – CCCTTATATATCAAACTATGCTTTGT – 3') DiploR (5' – TTACATAGAGGATTGCCTTCG – 3') (Riit, 2014)	4 µl HOT FIREPol® Blend Master Mix RTL With 10 mM $MgCl_2$ (Solis BioDyne) 0.5 µl of each primer 14 µl ddH_2O 1 µl DNA sample (50 ng/µl)

Table 2
Characteristics of the surveyed pine stands in 2021 grouped by forest type (area, number, average age, and vitality)

Forest type according Bušs 1997 (D – dry, W – wet or over wet and Dr – drained)	***Total area, ha***	***Number of stands***	***Average age, years***	***Proportion of healthy trees, %***	***Proportion of trees with needle damage, %***
Hylocomiosa (D)	112.3	44	9.7	45%	55%
Myrtillosa (D)	132.8	53	9.2	39%	61%
Vacciniosa (D)	55.2	23	9.5	29%	71%
Cladinoso-callunosa (D)	1.6	1	8.0	40%	60%
Myrtilloso-sphagnosa (W)	9.7	5	10.4	34%	66%
Vaccinioso-sphagnosa (W)	13.8	8	10.1	16%	84%
Myrtillosa mel. (Dr)	31.8	14	9.1	51%	49%
Vacciniosa mel. (Dr)	14.5	9	10.6	27%	73%
Myrtillosa turf. mel. (Dr)	3.8	3	9.0	20%	80%
Vacciniosa turf. mel. (Dr)	1.8	1	13.0	0%	100%
Callunosa turf. mel. (Dr)	1.0	2	6.5	65%	35%
Caricoso-phragmitosa (W)	4.0	2	10.0	35%	65%

Several factors may explain the recent increase of *Dothistroma* needle blight incidence in the Northern Hemisphere, including climate change and expanding plantation forestry with susceptible tree species. In British Columbia, outbreaks have been linked to warm, wet weather patterns in the mid-to-late 1990s (Woods et al., 2005). Similarly, in Europe, prolonged rainfall has been associated with disease outbreaks (Kirisits & Cech, 2006; Hanso & Drenkhan, 2008; Drenkhan & Hanso, 2009; Welsh et al., 2014; Woods et al., 2016; Markovskaja et al., 2020). High humidity and excessive precipitation escalate *D. septosporum* spore germination and needle infection (Brown et al., 2003; Boateng & Lewis, 2015). In regions without distinct seasonal variations, infections persist and spread year-round (Rodas & Wingfield, 2020).

As a disease management strategies, copper-based fungicides are effective but are mainly used in managed forests in Australia and New Zealand (Bulmann et al., 2016). Other approaches focus on silvicultural interventions, such as thinning young pine stands and pruning. *Dothistroma* spores primarily disperse within a two-meter radius (Boateng & Lewis, 2015), so thinning young pine stands can reduce disease spread. Pruning young pine stands and selecting appropriate site conditions can help reduce disease incidence (Boateng & Lewis, 2015; Bulmann et al., 2016). In Europe, the most widely adopted strategy involves breeding resistant pine species and restricting the movement of infected planting material (Bulmann et al., 2016; Markovskaja et al., 2020).

Diplodia sapinea was detected in 29 of 165 or 18% of surveyed stands 'Figure 2'. In four of those stands, all trees appeared healthy, with no visible needle damage, and only one tree showed minor, localised crown damage. This could be due to the endophytic nature of the fungus, which is often found in pine branches, buds, and needles, becoming pathogenic only under stress conditions (Stanosz et al., 2001; Bußkamp et al., 2020; Oliva et al., 2020).

Our data indicated that the characteristic soil properties of different forest types have probably influenced the contrasting patterns of *D. sapinea* presence. Sites where *D. sapinea* was absent had soils with higher water-holding capacities, while affected sites were located on bedrock, possibly making them more vulnerable to drought stress. The previous study suggested that *D. sapinea* may contributed to the crown dieback, impacting trees' ability to recover after severe drought, but the predictions of future drought-fungus caused dieback varies by region, season, and emission scenario (Brodde et al., 2023).

The ecology and pathogenicity of this species is also related to its origin. A study on the genetic diversity of *D. sapinea* in Europe found that its origin in the Baltics could be attributed to its long history as an endophyte or asymptomatic organism (Adamson et al., 2021). The European *D. sapinea* population is dominated by a single haplotype and high genetic similarity across different regions, indicating significant gene flow between countries, except for Italy and Georgia. *Diplodia sapinea* in Latvia are genetically similar to Estonia's samples, suggesting that the infection may have originated from Germany (Adamson et al., 2021).

Removing infected trees showing symptoms is recommended to prevent further spread (Brodde et al., 2019; Rodas & Wingfield, 2020).

There were no records of ***Lecanosticta acicola*** in pine stands in this study. Based on these data, we conclude that in Latvia, as in other European countries, the disease is mainly or initially found in populated areas on ornamental pine plantings (Adamson et al., 2015a; Adamčíková et al., 2021). However, in Estonia, the infection of Scots pine and the spread of the disease in forest stands were already reported in 2016 (Adamson et al., 2018).

Currently, *Lecanosticta acicola* has been reported in 24 European countries, and its distribution is expected to increase (Tubby et al., 2023). *Lecanosticta acicola* is not typically a pathogen of *P. sylvestris*; it generally prefers other *Pinus* species. However, since *P. sylvestris* is an important species in Europe, monitoring the occurrence of *L. acicola* remains critical. To prevent widespread outbreaks, precautionary measures should include avoiding planting new trees near infected ones, developing resistant varieties, and applying fungicides (Van Der Nest et al., 2019).

Figure 1

Distribution of Dothistroma septosporum needle blight in surveyed forest stands: ● – forest stands, where the symptoms were caused by the fungus Dothistroma septosporum, ● – forest stands in which Dothistroma septosporum was not found

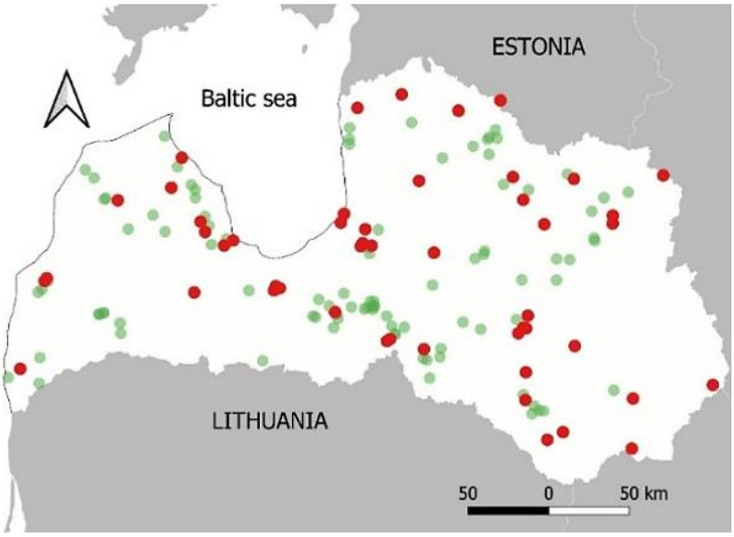
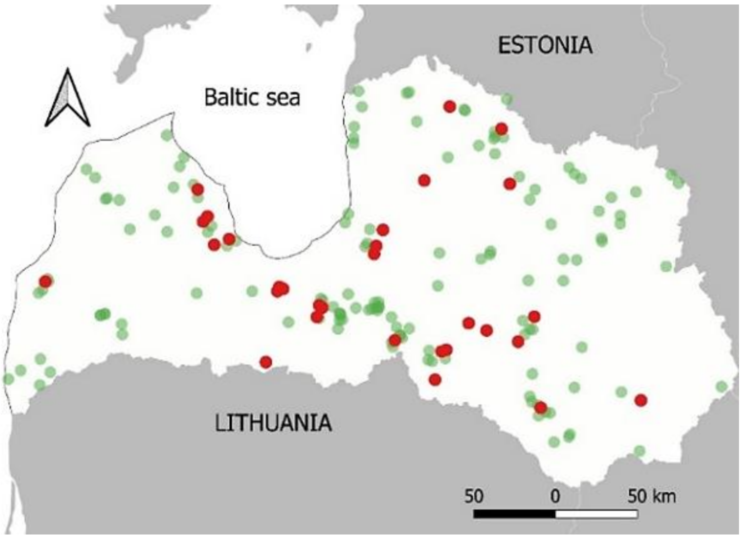


Figure 2

Distribution of Diplodia sapinea needle blight in surveyed forest stands: ● – forest stands, where the symptoms were caused by the fungus D. sapinea, ● – surveys where D. sapinea was not found



A recent genome-wide analysis of *Lecanosticta acicola* revealed genetic introgression between the southern and northern lineages, indicating active mating between them. Additionally, phenotypic differences were identified based on enzymatic activity, with introgressed strains resembling the southern lineage (Marcet-Houben et al., 2024). These results highlight ongoing genetic admixture in a recently expanded population, which could lead to the emergence of new traits in this fungal pathogen affecting conifers.

Conclusions

1. Based on surveys conducted in 2021, nearly all young pine stands analysed around Latvia showed some needle cast symptoms, and in 50% of the stands analysed the presence of invasive fungal pathogens was detected. The dominant invasive needle blight causing species was *Dothistroma septosporum*, which was found to be widespread across the country.
2. *Diplodia sapinea* was also frequently encountered, particularly in nutrient-poor and drought-prone sites. As this species is causing blue stain, its presence in the young plantings should also be considered in the relation to the further wood quality.
3. To reduce the impact of these pathogens, it is recommended to implement silvicultural practices, such as thinning or twig removal in infected areas, consider appropriate forest types and genetically resistant pine clones for planting.
4. Future research should focus on understanding the dynamics, virulence, spread and impact of these pathogens to local forest ecosystems as well as economic losses and further perspectives for infected stands.

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