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ORIGINAL PAPER

Fungal community diversity in soils under pedunculate oak *Quercus robur* L. and European beech *Fagus sylvatica* L. saplings produced with different technologies

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ABSTRACT

Fungi constitute a vital element of forest biological diversity. A deeper understanding of their role in the forest crops can impact the modification of forest management. Hence the need to understand the role of fungal in community of forest crops better.

The aim of this study was to investigate fungal communities associated with soil under asymptomatic and dead two-year-old saplings of *Quercus robur* and *Fagus sylvatica* that were produced as bare-root and containerized seedlings.

The fungal communities in soil were analysed by next-generation sequencing (Illumina SBS technology) of internal transcribed spacer (ITS) region.

In all the samples, a total of 1293 taxa were identified (including 1137 fungi taxa) and a total of 63,321 sequences were obtained. The relative abundance of Ascomycota (58.08%) was the highest, followed by, Basidiomycota (16.79%), Glomeromycota (0.17%), Mucoromycota (0.1%), and Oomycota (0.06%). Fungi dominated in the community associated with asymptomatic saplings, while saprotrophs dominated in the soil of dead saplings. Fungal biodiversity was associated with tree species. No differences were observed between the pathogen fungi frequency in the fungal community of dead and living trees. *Fusarium oxysporum* was statistically significantly (p=0.019) associated with the containerized seedling group. The results showed that the fungal community of the soil samples under saplings from containerised production were more diverse than the ones produced in the traditional technology, hence it is advisable to use the planting stock with container-grown seedlings.

KEY WORDS

Common beech, Common oak, crops, diversity of fungal community, *Fusarium oxysporum*, mycorrhizal fungi, saprotrophs

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Introduction

Fungi and Oomycota which colonise tree roots and soil, are a vital element of forest ecosystems and constitute an important element of forest biodiversity (Behnke-Borowczyk and Kwaśna, 2010; Prada-Salcedo *et al*., 2021). Soil mycobiota can have a profound effect on plant growth and health (Frąc *et al*., 2018). However, the knowledge about the qualitative and quantitative diversity of fungal communities in soil under forest trees is still insufficient. A deeper comprehension of the role the fungi serve, particularly in the early stages of plant succession (Kwaśna *et al*., 2008), can influence and lead to modifying forest crops regeneration, *e.g.,* use of container seedlings, introduction of mycorrhization of seedlings.

Previous studies of root-associated fungi have mainly focused on mycorrhizal fungi (Basidiomycota) (Horton and Bruns, 2001; Allen *et al*., 2003; Bruns and Shefferson, 2004; Menkis *et al*., 2005). However, many saprotrophic microbes live on or near the root systems of trees. Common examples include Ascomycete genera as: *Acremonium*, *Alternaria*, *Aspergillus*, *Botrytis*, *Chaetomium*, *Cladosporium*, *Fusarium*, *Ilyonectria*, *Penicillium*, and *Trichoderma* (Behnke-Borowczyk and Kwaśna, 2010; Frąc *et al*., 2018). Other soil-born fungi can be pathogenic for plants. For example, fungal pathogens associated with roots of mature *Fraxinus* (Przybył, 2002) and *Quercus* (Halmschlager and Kowalski, 2004) trees as well as diseased *Pinus sylvestris* (L.), *Picea abies* (L.) H. Karst. (Menkis *et al*., 2006), and *Quercus robur* (L.) (Jankowiak *et al*., 2022) seedlings were investigated. In addition, soil preparation and slash management (Kwaśna *et al*., 2008, 2015), technology in nursery production (Behnke-Borowczyk *et al*., 2020), and stand development (Kwaśna *et al*., 2015, 2019) may influence soil fungal communities. According to Pietras *et al*. (2015) seedlings produced in forest nurseries are characterized by a relatively high diversity and species richness of ectomycorrhizal fungal communities, but edaphic factors do not directly participate in the formation of mycorrhizal communities in forest nurseries. Each tree is characterized by specific fungal symbionts (Rudawska and Leski, 2009). One of the conditions for high success of forest cultivation is the use of seedlings with abundant and diverse mycorrhiza (Aleksandrowicz-Trzcińska, 2004). The use of seedlings to crops renewal with a covered root system reduces damage to the root system during the production of planting material, and the planting process, and keeps the roots in a state of natural freshness, while protecting the developing mycorrhizae (Glura and Korzeniewicz, 2013). Therefore, it was assumed that the fungal communities associated with this method of seedling production at the stage of forest cultivation should be more diverse and dominated by mycorrhizal fungi. It is crucial to understand the role of the fungal community, particularly among the most valuable European forest tree species, *i.e.,* the common oak *Q. robur* and the common beech *Fagus sylvatica* L. Hence, the aim was to study the soil mycobiota from under the live (L) and dead (D) roots of the common beech (F) and the common oak (Q) coming from the cultivation established from the seedlings of various production technologies (container – K, and traditional N). The study will allow a better understanding of the impact of the tree seedling production technology on the occurrence of taxa, and the role and the function of taxa in the soil. It was assumed that (1) saprotrophs and pathogens will dominate in the soil fungal community under the roots of dead trees; (2) mycorrhizal fungi will dominate in the soil fungal communities under the live tree roots; (3) the fungal community associated with containerized cuttings will be dominated by mycorrhizal fungi, and the community will be more diverse than in the case of bare-root cuttings.

Materials and methods

The research material consisted of the soil coming from under the live and dead common beeches and common oaks. The samplings came from a year-long cultivation located in Wielisławice Forest Subdistrict (Forest Experimental Station Siemianice (51°14'46.0"N 18°06'15.6"E), which is part of a long-term experiment titled 'Comparing the growth of the chosen tree species in cultivations set up with the seedlings produced in various technologies'. The crop was set up on a clearing where Scots pine used to grow (March 2017). The cultivation was established on a site of fresh mixed coniferous forest, on rusty podzolic soil. The average annual temperature for this area in 2017 is 9.2°C, and the total rainfall was 635 mm. The field experiment is being conducted in a completely randomised block design with five repetitions. After clearing the debris, the ground was ploughed into trenches using furrow plough with cultivator. The distance between the rows was 1.5 m. Each experimentational field (block) covered the area of 450 m^2. The planting spacing was 1.5×0.8 m. One-year-old planting material with bare-root system and containerized seedlings, which were used for establishing the cultivation, came from Dobrygość nursery. On the established crop, each of the trees was positioned. In September 2017, in the year in which the plantation was established, the tree survival rate was assessed. Survival was the ratio of the number of trees that survived on the crop to that that was planted. 15 soil samples (0.5 kg each) were collected from the following variants: KQL – live asymptomatic oak seedlings from container nursery; KQD – dead oak seedlings from container nursery; NQL – live asymptomatic oak seedlings with bare-root system; NQD – dead oak seedlings with bare-root system; KFL – live asymptomatic beech seedlings from container nursery; KFD – dead beech seedlings from container nursery; NFL – live asymptomatic beech seedlings with bare-root system; NFD – dead beech seedlings with a bare-root system. In total, 120 samples were collected. The soil was collected directly under the seedlings in October 2017. The samples from each variant were combined, precisely mixed, and submitted to further analysis (identification of fungal community). A sample weighing 1 g was intended for other stages of the analysis.

Fungal community structure analysis. The DNA extraction was conducted using DNeasy PowerSoil Kit (QIAGEN, Hilden, Germany) in compliance with the producer's protocol. The identification of the fungal species was conducted using rDNA ITS1, 5.8S sequence region. The analysis was conducted using ITS1FI2 – 5 ' GAA CCW GCG GAR GGA TCA 3 ' (Schmidt *et al.*, 2013) and 5.8S – 5 ` CGC TGC GTT CTT CAT CG 3 ` primers (Vilgalys *et al.*, 1990). The amplification reaction was conducted in the final volume of 25.0 µl which contained 2 µl of DNA, 0.2 µl of each primer, 12.5 µl 2X PCR MIX (A&A Biotechnology, Gdynia, Poland) and filled up to the final volume with deionised water. Next, 35 cycles took place which included: double-stranded DNA denaturation of 30 s in 94°C, adding starters at 56°C for 30 s, the synthesis of the strands at 72°C for 30 s and the final prolongation at 72°C for 7 min. The PCR product was checked on 1% agarose gel tinted with Midori Green Advance DNA (Genetics). The obtained PCR products were purified and sequenced using Illumina SBS technology (Genomed S.A. Warszawa, Poland). The results were subjected to the bioinformatical, and statistical analysis as described thoroughly by Behnke-Borowczyk *et al.* (2019). The sequences were compared with the referential sequences deposited in the National Centre for Biotechnology Information database (GenBank) (Benson *et al.*, 2018) using BLAST algorithm. Sequences are clustered into bins called 'Operational Taxonomic Units' (OTUs) based upon similarity. For the purpose of identification, the percentage of similarity of the analysed sequence with the reference sequence

was assumed at the level of 98-100% for species, 94-97% for the genus level and 80-94% for the order corresponding to at least 90% overlap with the reference sequence. Diversity was defined as a number of species in the sample. The Latin names of the identified fungi were adopted according to Index Fungorum (http://www.indexfungorum.org). The taxa frequency was determined on the basis of the percentage value in the fungal community. The function of fungi in the community was determined based on literature data and the DEEMY information system for characterization and determination of ectomycorrhizae (Agerer and Rambold, 2004-2014; Rudawska *et al*., 2016).

The statistical analysis of biodiversity was conducted using five indexes: Margalef index (Mg), Shannon diversity index (H) which is used to determine the species richness of the community. Moreover, Shannon evenness index (E) and Berger-Parker index (d) were also used. The dominance of a single taxon was analysed with Simpson index (D) (Magurran, 1988). The number of obtained sequences in the studied sample was treated as the abundance of organisms. Furthermore, the assessment of the tree survival rate during cultivation was conducted as well.

To visualize the composition of fungal communities, we used non-metric multidimensional scaling (NMDS) with the Bray-Curtis dissimilarity index (Rożek *et al*., 2023). To find differences between fungal communities by seedling production type, we conducted a similarity analysis, which is a non-parametric statistical test. We used the anosim function implemented in the vegan package (R Core Team, 2021). The test statistic R=0 indicates an even distribution of high and low ranks within and between groups, while R=1 suggests dissimilarity between groups. We will reject the null hypothesis of no statistically significant differences at the α=0.05. In order to identify, which fungi species could be considered as indicator species associated with a certain group of seedlings on the base of seedling production type, we applied *multipatt* function in *indicspecies* package (R Core Team, 2021). Another element of the study was the chemical analysis of the soil (treated as a research background). The soil samples were collected randomly in a distance of 20 m from each other and at the depth of 25 cm. The samples were taken in accordance with the Polish standard PN-R-04031:1997. At first, the samples were poured into a container, mixed thoroughly, and combined into 2 general samples weighing about 1 kg – Siemianice I and Siemianice II. In the soil samples, the following elements were marked: –pH in KCl with electrochemical technique; the content of phosphorous and potassium following Egner-Riehm method of atomic emission spectrometry with inductively coupled plasma mass spectrometry; the magnesium content following Schachtschabel method of atomic emission spectrometry with inductively coupled plasma mass spectrometry; the nitrogen content with the direct method using TruSpec CNS analyser; the Corg content with a modified Tiurin method; $N\text{-}NO_3$, $N\text{-}NH_4$ content with electrochemical method after the extraction in 0.03 N acetic acid.

Results

Fungal community structure analysis. In all the analysed samples a total of 1293 taxa were identified (including 1137 fungal taxa) and a total of 63,321 sequences were obtained. A total number of Ascomycota phylum sequences reached 36,778 (58.08%), of non-cultivated fungi 11,356 (17.93%), of Basidiomycota it was 10,631 (16.79%), the organisms without a sequence found in NCBI database 4,031 (6.37%), of Glomeromycota it was 107 (0.17%), Mucoromycota 63 (0,10%), Oomycota 37 (0,06%) and other organisms 317 (0,50%; Figs. 1, 2).

In all the analysed samples, due to the ecological role played by each taxon in the community, mycorrhizal fungi were highest in numbers of reads (58.43%), next were saprotrophs

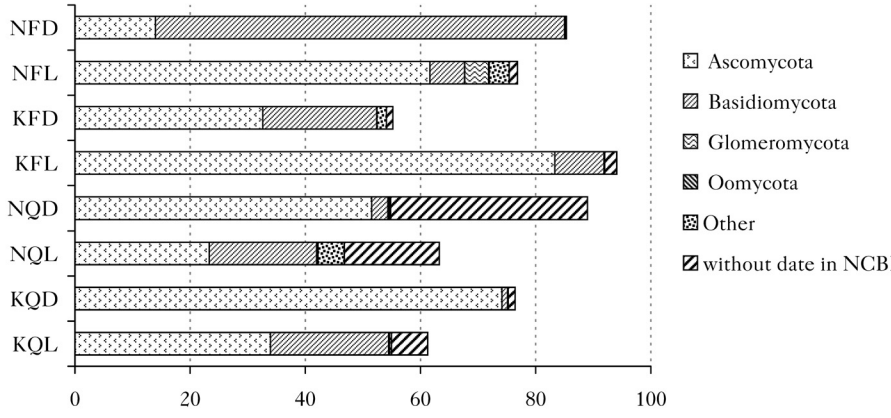

Fig. 1.

Relative abundance [%] of fungi at phylum level, non-cultivated fungi, and organisms whose sequences are not in the NCBI database and in the samples

KQL – live asymptomatic oak seedlings from container nursery; KQD – dead oak seedlings from container nursery; NQL – live asymptomatic oak seedlings with bare-root system; NQD – dead oak seedlings with bare-root system; KFL – live asymptomatic beech seedlings from container nursery; KFD – dead beech seedlings from container nursery; NFL – live asymptomatic beech seedlings with bare-root system; NFD – dead beech seedlings with a bare-root system

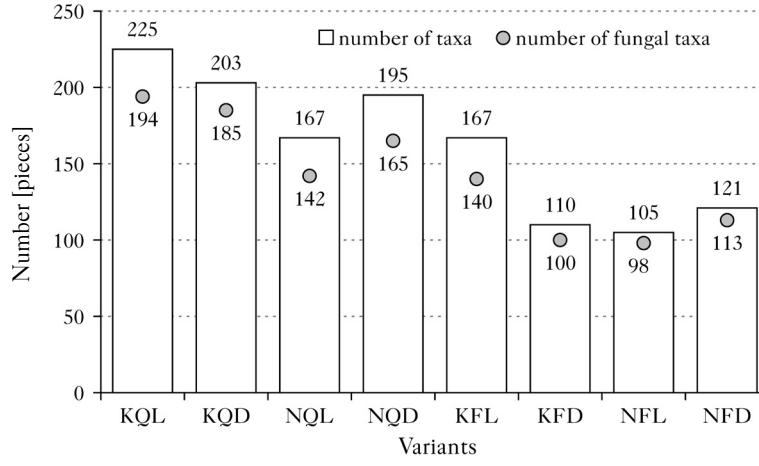

Fig. 2.

Number of total taxa and number of fungal taxa in the analysed samples

KQL – live asymptomatic oak seedlings from container nursery; KQD – dead oak seedlings from container nursery; NQL – live asymptomatic oak seedlings with bare-root system; NQD – dead oak seedlings with bare-root system; KFL – live asymptomatic beech seedlings from container nursery; KFD – dead beech seedlings from container nursery; NFL – live asymptomatic beech seedlings with bare-root system; NFD – dead beech seedlings with a bare-root system

(20.96%) and pathogens (19.70%). The antagonists constituted 0.06%. Among all the samples, only one a lichenivorous fungus, namely *Tremella anaptychiae* (J.C. Zamora & Diederich) was identified. Mycorrhizal fungi dominated in the soil collected from live trees in the samples: KFL (79.65%), NFL (43.67%) and NQL (17.68%). Saprotrophs dominated in the soil connected with dead trees, *i.e.*, in the NFD (63.02%), NQD (40.89%), KFD (19.85%) samples. The percentages of the fungi with the unknown function, or a function which was ambiguous to define, were the greatest in the KQD (41.57%) and KQL (22.19%) samples. The greatest share of pathogenic fungi was observed in the NQD (6.1%), KQD (5.50%) and the KQL (5.17%) samples as shown in Figure 3.

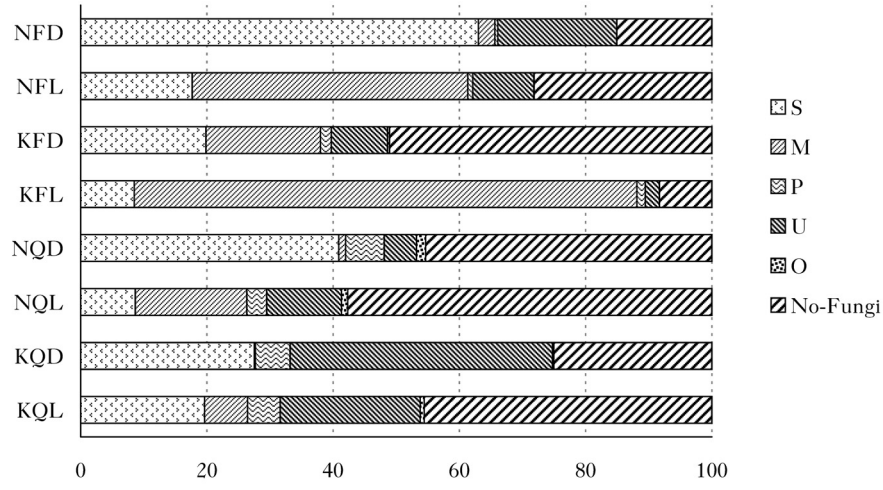

Fig. 3.

Relative abundance [%] of the saprotroph (S), mycorrhizal fungi (M), pathogens (P), unknown function (U), other (O) in the samples. Percentage [%] of function groups of fungi in the analysed samples

KQL – live asymptomatic oak seedlings from container nursery; KQD – dead oak seedlings from container nursery; NQL – live oak seedlings with bare-root system; NQD – dead oak seedlings with bare-root system; KFL – live beech seedlings from container nursery; KFD – dead beech seedlings from container nursery; NFL – live beech seedlings with bare-root system; NFD – dead beech seedlings with a bare-root system

Phialocephala sp. (8.09%, ecological status unknown), *Hyaloscypha variabilis* (Hambl. & Sigler) Vohník, Fehrer & Réblová (3.53%, saprotroph), *Phialemonium* sp. (3.53%, unknown), and *Scleroderma verrucosum* (Bull.) Pers. (2.44% mycorrhizal fungus) dominated in the KQL. The dominant fungi in the rhizosphere soil samples in the KQD were *Phialemonium* sp. (34.44%), *H. variabilis* (16.93%), *Dictyochaeta* sp. (7.51%, saprotroph), and *Diaporthe* sp. (3.65%). For the NQL samples, *Hydnotrya* sp. (6.35%, mycorrhizal fungus), *Phialocephala* sp. (3.24%), *Laccaria proxima* (Boud.) Pat. (7.71%, mycorrhizal fungus), and *Mycena sanguinolenta* (Alb. & Schwein.) P. Kumm. (2.87%, saprotroph) were the most abundant, while for the NQD samples it was *Hyaloscypha* sp. (34.81%, saprotroph). In the KFL, KFD, NFL samples *Hydnotrya* sp. genus dominated (respectively: 76.69%, 17.56%, 35.17%, mycorrhizal fungi). Moreover, saprotroph *Pseudogymnoascus* sp. (8.51%) and *Pseudogymnoascus roseus* Raillo (7.03%) dominated in the NFL and *Deconica phyllogena* (Sacc.) Noordel. (30.23%, saprotroph), *Mycena epipterygia* (Scop.) Gray (20.74%, saprotroph) dominated in the NFD samples (Appendix).

Only eight taxa common for all analysed samples were found. Eleven taxa were recovered in soil samples under oak (Q), whereas five taxa were found in soil samples under beech (F; Table 1). Moreover, eight taxa were found in soil samples under container production (K) saplings, whereas five taxa were recovered in soil samples under bare-root system (N) saplings. Three taxa were detected from soil samples originating from live (L) saplings, whereas five taxa occurred in soil samples under dead saplings (D) (Table 1, 2; Supplement).

The D-Mg indices were higher in oak (12.121-15.684) than in those beech saplings (5.988--8.634). The community of the KQL samples (15.684) had the highest value of D-Mg index, whereas the NFL variant showed the lowest value (5.988). The Shannon diversity index was highest in KQL (3.548) and lowest in KFL (0.881). Shannon's evenness index-E achieved the highest in the case of KQL community (0.742), and the lowest values were for KFL (0.198) and KQD (0.417). The Simpson's index was highest in KFL (0.699) and lowest in NQD (0.407).

Table 1.

Taxa common for all analysed samples (transparent/white background), for the oak (light grey background) for the beech (dark grey background). KQL – live asymptomatic oak seedlings from container nursery; KQD – dead oak seedlings from container nursery; NQL – live asymptomatic oak seedlings with bare-root system; NQD – dead oak seedlings with bare-root system; KFL – live asymptomatic beech seedlings from container nursery; KFD – dead beech seedlings from container nursery; NFL – live asymptomatic beech seedlings with bare-root system; NFD – dead beech seedlings with a bare-root system

KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
			Hyaloscypha variabilis				
			Hydnotrya sp.				
			Phialocephala sp.				
			Mycena sp.				
	Ciliolarina pinicola *Diaporthe* sp.				*Dictyochaeta* sp.		
	Leotiomycetes *Oidiodendron maius*				*Pseudogymnoascus* sp.		
	Paraphaeosphaeria neglecta *Sporothrix dentifunda*				Agaricales		
	Sporothrix sp. *Trichoderma* sp.				*Sebacina* sp.		
	Xenopolyscytalum sp. *Mortierella* sp. *Pythium volutum*				*Trechisporales* sp.		

The Berger-Parker Dominance Index assumed the highest values for the fungal root community in KFL (0.834), whereas the lowest for the KQL sample (0.146; Table 3).

Seedling survival. The mean survival rate of the trees in the experiment (all tree species and technology type) after the first vegetation season was 88.48%. The rate was most statistically significant (F=15.337; p=0.00021) in the KQ variant. The lowest results, below the average for the experiment, were achieved for the beech regardless of the manner of seedling production used in the experiment as shown in Figure 4.

Soil parameters. The pHKCl values in the analysed samples was lower. The content of total nitrogen (Ntotal) as well as potassium and magnesium in both samples was low. The ratio C:N on the surface from which sample I was collected was high whereas in sample II it was low. When the ratio of potassium to magnesium (K: Mg) is above 3.5:1, the consumption of magnesium from the soil is hindered. On both surfaces the ratio K:Mg was high. The results of the soil analysis are collected in Table 4.

Analysis of similarity indicated that fungal communities showed statistically significant differences (R=0.406, p=0.019) between seedlings of different tree species and different production technologies (Fig. 5).

Moreover, we found that out of the total number of species (77), only one of them, namely *Fusarium oxysporum* Schltdl., was statistically significantly (p=0.019) associated with containerized seedling group.

Discussion

So far most of the studies on the comparison of survival of traditional and container seedlings focused mainly on Scots pine (for example Barzdajn, 2010; Glura and Korzeniewicz, 2013; Barzdajn

Table 2.

Taxa common for the containerised seedlings (white background), bare-root seedlings (light grey background), live seedlings (black background) and dead seedlings (background)

KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Cadophora sp. *Dictyochaeta* sp.		*Lachnum* sp.		*Cadophora* sp. *Dictyochaeta* sp.		*Lachnum* sp.	
Exophiala sp. *Penicillium* sp.		Leotiomycetes		*Exophiala* sp. *Penicillium* sp.		Leotiomycetes	
Rhizoscyphus sp. *Sporothrix* sp.		*Rhizoscyphus ericae*		*Rhizoscyphus* sp. *Sporothrix* sp.		*Rhizoscyphus ericae*	
Agaricales		*Luellia* sp.		Agaricales		*Luellia* sp.	
Trechisporales		*Pythium volutum*		Trechisporales		*Pythium volutum*	
Dictyochaeta sp.	*Fusarium* sp.	*Dictyochaeta* sp.	*Fusarium* sp.	*Dictyochaeta* sp.	*Fusarium* sp.	*Dictyochaeta* sp.	*Fusarium* sp.
Leotiomycetes	*Lambertella tubulosa*	Leotiomycetes	*Lambertella tubulosa*	Leotiomycetes	*Lambertella tubulosa*	Leotiomycetes	*Lambertella tubulosa*
Trechisporales	*Sporothrix* sp.	Trechisporales	*Sporothrix* sp.	Trechisporales	*Sporothrix* sp.	Trechisporales	*Sporothrix* sp.
	Mortierella sp.		*Mortierella* sp.		*Mortierella* sp.		*Mortierella* sp.
	Pythium volutum		*Pythium volutum*		*Pythium volutum*		*Pythium volutum*

KQL – live asymptomatic oak seedlings from container nursery; KQD – dead oak seedlings from container nursery; NQL – live asymptomatic oak seedlings with bare-root system; NQD – dead oak seedlings with bare-root system; KFL – live asymptomatic beech seedlings from container nursery; KFD – dead beech seedlings from container nursery; NFL – live asymptomatic beech seedlings with bare-root system; NFD – dead beech seedlings with a bare-root system

Table 3.

The biodiversity indices of total taxa in the samples

Index	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Index D-Mg	15.684	10.023	12.888	12.121	8.634	6.680	5.988	7.228
Shannon`s diversity index H	3.548	1.900	3.289	1.979	0.881	2.594	2.095	1.919
Shannon`s evenness index E	0.742	0.417	0.731	0.427	0.198	0.656	0.547	0.458
Simpson Index	0.052	0.274	0.067	0.407	0.699	0.137	0.248	0.223
Berger-Parker Dominance	0.146	0.458	0.164	0.250	0.834	0.322	0.466	0.354

KQL – live asymptomatic oak seedlings from container nursery; KQD – dead oak seedlings from container nursery; NQL – live asymptomatic oak seedlings with bare-root system; NQD – dead oak seedlings with bare-root system; KFL – live asymptomatic beech seedlings from container nursery; KFD – dead beech seedlings from container nursery; NFL – live asymptomatic beech seedlings with bare-root system; NFD – dead beech seedlings with a bare-root system

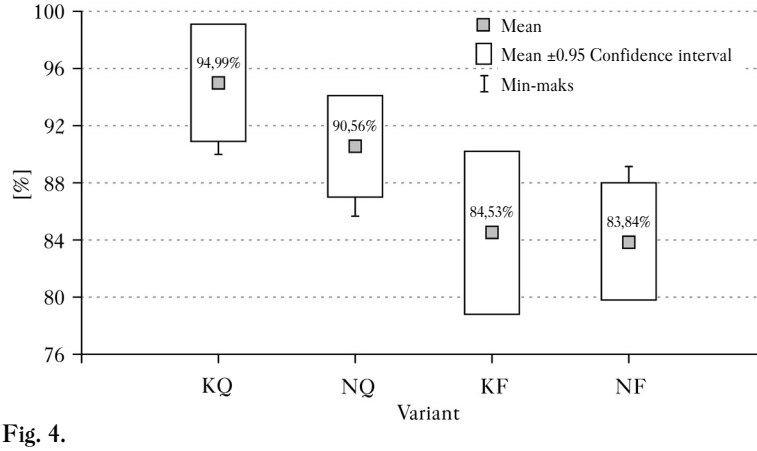

Fig. 4.

Survival rate of samplings KQ – the oaks from containerised production, NQ – the oaks with bare-root system, KF – the beeches from containerised production, NF – the beeches with bare-root system

Table 4.

The concentration of macronutrients, pH and organic matter content calculated as average of the five samples taken from each variant of the experiment in the soil samples[1]

Parameter	Siemianice I	Siemianice II
P [mg/100g soil]	3.72	3.13
K [mg/100g soil]	3.25	2.42
Mg [mg/100g soil]	0.41	0.17
N_{total} [% air-dried soil]	0.04	0.03
pH_{KCl}	3.90	4.20
C [% air-dried soil]	0.67	0.19
Organic matter [% air-dried soil]	1.20	0.30
N-NO_3 [mg/kg air-dried soil]	9.69	5.51
N-NH_4 [mg/kg air-dried soil]	7.48	7.12
P_2O_5 [mg/100g soil]	8.52	7.17
K_2O [mg/100g soil]	3.91	2.91
MgO [mg/100g soil]	0.68	0.28
C:N ratio	17.00	6.00
K:Mg ratio	7.93	14.24

[1]optimal values: 20 mg/100 g soil of jointly N-NO_3 and NNH_4, 18 mg/100 g of K_2O, 5 mg/100 g of P_2O_5 and 7 mg/100 g of MgO

and Kowalkowski, 2016). Survival of container seedlings in each case was higher than that of seedlings with a bare root system. The high survival rate of Scots pine container seedlings in the first year of life of trees on cultivation is confirmed by Glura and Korzeniewcz (2013). This technology helps overcome repotting shock and the effects of growing season differences between the nursery and the crop (Barzdajn and Kowalkowski, 2016). These are the factors that probably influenced the higher survival rate of oak and beech in one-year cultivation.

The lowest survival rate in our experiment was characteristic of European beech seedlings. Szyguła *et al.* (2012), indicate the relationship between deformation of root systems and tree survival. Szewczyk (2014) states that mistakes made during the planting of Scots pine are responsible for its dieback on crops. In our research, similarly to Korzeniewicz *et al.* (2018) the experiment was set up by a team of experienced workers under the supervision of the authors

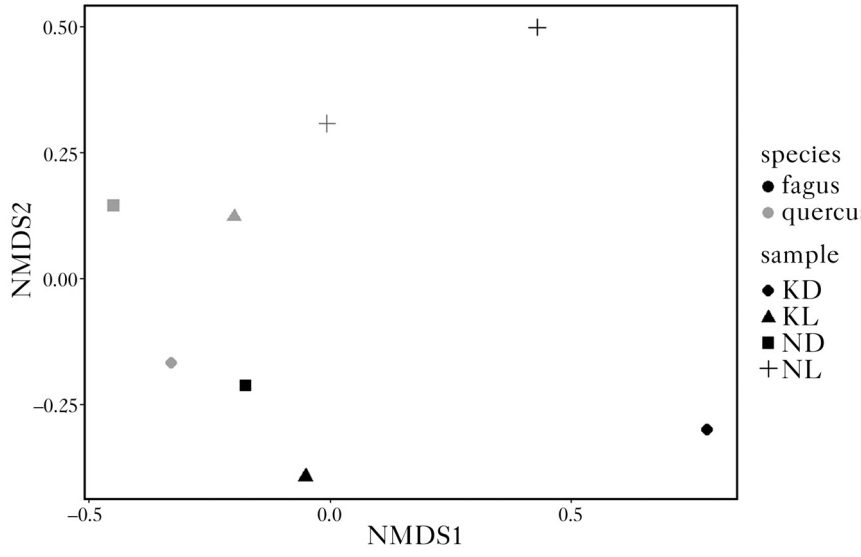

Fig. 5.

NMDS ordination of fungal community composition

KD – dead seedlings from container nursery; KL – live asymptomatic seedlings from container nursery; NL – live asymptomatic seedlings with bare-root system; ND – dead seedlings with a bare-root system

of the experiment, therefore the influence of the factor related to the quality of planting is rather doubtful. It seems more probable that the insufficient amount of nutrients stored in the root systems, especially those with a bare root system, was a key factor affecting beeches survival (Korzeniewicz *et al*., 2018). This probability is confirmed by the results of the soil analysis, in which there were no optimal values of macroelements for the development of the young forest generation. It should be emphasized that the seedlings used in the experiment were not mycorrhized. Perhaps the use of artificial mycorrhization would increase the survival rate of beech. As indicated by Szabla (2009) and Kuc and Aleksandrowicz-Trzcińska (2012), controlled mycorrhization affects both the growth parameters and the vitality of seedlings in crops, especially Scots pine, pedunculate oak and common beech.

Our understanding of the roles soil-born fungi in surviving the artificial regeneration of oak and beech is still limited. This is especially true seedlings derived from different seedling production technologies. The fungal soil communities connected with the oak and the beech seedlings differed. The fungi of Ascomycota division constituted the greatest share in the communities. The exponential share of Ascomycota stems from, among other, the abundance, widespread and intensive production of easily dispersed spores (Kwaśna *et al*., 2016). It is also the result of their role (saprotroph) which they serve in the soil environment, which also explains their dominating share over Basidiomycota in the studied communities.

The Oomycota in the studied communities were represented by members of the genus *Pythium* that are well-known agents of damping-off (Bełka *et al*., 2019). The share of these taxa in the analysed community did not exceed 0.1%.

Many fungal species, depending on the environmental conditions, adopt various life-history strategies, from parasites to endophytes (Unuk *et al*., 2019). Members of the genus *Phialemonium*, which abundantly occurred in the KQD (over 34%) and in the KQL (over 3%) samples are a good example. Thus far, they were isolated from the dead tissues of young *Q. robur* (Kowalski,

1996). They are also well-known as human's opportunistic pathogens (Proia *et al.*, 2004), endophytes (Manzotti *et al.*, 2020). *Exophiala* species, which also dominated in the KQD community are considered cosmopolitan and adjusted to living in various environments. They have been viewed as human and animal pathogens, they exist in soil, air, water, and plant tissues (De Hoog *et al.*, 2011; Maciá-Vicente *et al.*, 2016). The function of the fungi belonging to *Phialemonium* and *Exophiala* genus has not been fully identified and the studies of these fungi should be continued, particularly the studies concerned with their function in the fungal community connected with forest trees. Due to discrepant information found in literature, the functions were not attributed to the fungi belonging to these genera in the study. According to Unuk *et al.* (2019) the fungi from *Mycena* genus, which dominated in the NFD sample, are saprotroph. Kowalski (2008), however, classified *Mycena galopus* (Pers.) P. Kumm. As an ectomycorrhizal species. Considering the specificity of the analysed samples, the dominance of the fungi of the *Mycena* genus in the communities connected with the dead trees, they have been categorised as saprotroph.

In An Information System for Characterization and Determination of EctoMYcorrhizae (DEEMY) 54 species of ectomycorrhizal fungi (ECM) connected with the genus *Fagus* and 75 species connected with the genus *Quercus* were described. In the soil from under the beeches, the fungi of *Russula* genus were identified. Moreover, in the soil connected with the genus *Fagus*, and *Quercus* other species of ECM fungi from DEEMY database were found, such as: *Acephala macrosclerotiorum,* Münzenb. & Bubner *Laccaria proxima*, *Laccaria tortilis* (Bolton) Cooke, which create mycorrhiza with *Pinus* genus. The mycorrhizal species of *Hydnotrya* dominated the fungal community in the KFL (over 75% frequency), in the KFD (17%) and in the NFL samples (35%). *Hydnotrya* sp. Together with the identified *Hydnotrya Tulasnei* (Berk.) Berk. & Broome constitute ectomycorrhizal associations with *P. abies* and *F. sylvatica* (Stielow *et al.*, 2010), which has been confirmed by the study findings. *Laccaria proxima* reached over 7% frequency and *Laccaria* genus over 2% in the NQL samples. Both species are classified among the most important ectomycorrhizal fungi in the temperate, tropical and alpine zones (Cho *et al.*, 2018). Among the mycorrhizal fungi in the KQL samples (over 5%), *Scleroderma areolatum* Ehrenb., *Scleroderma verrucosum* (Bull.) Pers. And *Scleroderma* sp. Were identified. *Scleroderma areolatum* is associated with ectomycorrhizal root systems of beech (Mrak *et al.*, 2017), whereas *S. verrucosum* lives mycorrhizal associations with oak in the forest nurseries (Pietras *et al.*, 2015). Our findings confirmed that *S. verrucosum* has a high affinity to *Q. robur*.

The most common fungal pathogens were species belonged to the *Chalara*, *Malassezia* and *Fusarium* genera. These fungi represent typically soil-borne pathogens (Theelen *et al.*, 2018). Their share in all communities is a minor one. *Malassezia* is a fungus classified to animal pathogens (mammals) (Theelen *et al.*, 2018), and its negative impact on plants has not been confirmed. *Fusarium* spp. Which is a representative of the most numerously occurring plant pathogens causes, among others, damping-off and leaf spot (Lamichhane *et al.*, 2017). Members of the genus *Fusarium* were common for all the analysed communities of the dead saplings, and *F. oxysporum* was statistically significantly associated with the containerized seedling group.

Antagonistic interactions in reference to the fungi from *Fusarium* genus are manifested by the fungi from *Trichoderma* genus, among others (Świerczyńska *et al.*, 2011). They were identified in the fungal communities connected with the oak. The low frequency of pathogens and relatively high share of the mycorrhizal fungi improve the chances of producing a healthy and good quality planting stock (Behnke-Borowczyk *et al.*, 2020). It has been confirmed by a high survival rate of the oaks from the container production. *Dictyochaeta* species dominated in the KQD fungi community (7.51%). These fungi were isolated from asymptomatic and dead stems of *Q. robur* seedlings in Poland (Jankowiak *et al.*, 2022). Members of this genus were isolated in

the decomposing leaves, wood, bark, branches in the beech and the oak (Whitton *et al*., 2000), hence they were classified here as saprotroph. Among the saprotrophs that were most frequently found in the fungal communities were *Hyaloscypha* spp. (in NQD over 34%), including *H. variabilis* (in KQD over 16% and in KQL over 3%). *Hyaloscypha* species are typically cosmopolitan fungi (GBIF), and are also classified as mycorrhizal fungi (*e.g.*, *Hyaloscypha finlandica* (C.J.K. Wang & H.E. Wilcox) Vohník, Fehrer & Réblová), although not is association with forest trees (Mrnka *et al*., 2020). *Deconica phyllogena* deserves a special mention among the identified taxa. It occurs in some regions of Canada and Europe (Discover Life Maps, 2021). It is classified as a saprotroph and its share in the NFD sample exceeded 30%.

Phialocephala species had relatively high levels of abundance in soil samples in this study. *Phialocephala fortinii* C.J.K. Wang & H.E. Wilcox dominated in the KQD samples (over 34%), and *Phialocephala* sp. was considerably present in the KQL samples (over 8%). In addition to these both species, *Phialocephala glacialis* Grünig & T.N. Sieber was also identified. *Phialocephala* species are generally reported as root- and branch colonising dark septate endophytic fungi (Kowalski and Kehr, 1995; Grünig *et al*., 2008, 2009). Species of the *Ph. fortinii* sensu lato (s.l.) – *Acephala applanata* Gru¨nig & T.N. Sieber, species complex were also isolated from diseased *Abies alba* Mill. seedling roots (Jankowiak *et al*., 2016) and from roots of dead and asymptomatic *Q. robur* seedlings (Jankowiak *et al*., 2022).

In conclusion, we found that the fungal diversity was mainly depended on the tree species. The fungal community of oak was much more diverse than the fungal community of beech. Among saprotrophs the most common fungi were *Hyaloscypha* spp., *Deconica phyllogena, Mycena* spp., *Dictyochaeta* spp., *Paraphaeosphaeria neglecta* Verkley, Riccioni & Stielow. In addition, the fungal community of trees from container production (K) were more diverse than those produced following the traditional technology (N). Hence, it is advisable to use planting stock with covered root system, *i.e*., 'containerised seedlings'.

Authors' contributions

Conceptualization and design of the study – M.B. and R.K.; methodology, R.K., M.B. and J.B.B.; implementation of the study – M.B., J.B.B., N.K. and R.K.; analysis of the data – R.K., J.S. and M.B.; writing-original draft preparation – M.B., J.B.B., N.K. and R.K.; writing-review and editing – R.K. and M.B.

Conflicts of interest

The authors declare no conflict of interest.

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Supplement

Share [%] of individual species of fungi in communities. Similarity – similarity to a reference sequence in the database NCBI [%]. Variants: KQL – live oak seedlings from container nursery; KQD – dead oak seedlings from container nursery; NQL – live oak seedlings with bare-root system; NQD – dead oak seedlings with bare-root system; KFL – live beech seedlings from container nursery; KFD – dead beech seedlings from container nursery; NFL – live beech seedlings with bare-root system; NFD – dead beech seedlings with a bare-root system.

Taxa	Trophic group	Similarity [%]	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Acephala macrosclerotiorum Münzenb. & Bubner	mycorrhiza	100.00.	0.030	0.006	0.094	0.000	0.011	0.000	0.000	0.000
Acephala sp.	mycorrhiza	99.48	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Acremonium sordidulum W. Gams & D. Hawksw.	saprotroph	100.00	0.000	0.000	0.000	0.012	0.000	3.564	0.000	0.000
Acremonium sp.	saprotroph	100.00	0.000	0.013	0.000	1.584	0.022	0.000	0.000	0.000
Alatospora acuminata Ingold	pathogen	98.98	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000
Alternaria sp.	saprotroph	99.50	0.000	0.006	0.000	0.012	0.011	0.106	0.000	0.000

Supplement continued (2)

Taxa	Trophic group	Similarity [%]	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Alternaria triticina Prasada & Prabhu	saprotroph	100.00	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Ampelomyces quisqualis Ces.	pathogen	100.00	0.089	0.006	0.000	0.000	0.000	0.000	0.000	0.000
Angustimassarina sp.	pathogen	100.00	0.000	0.000	0.000	0.037	0.000	0.000	0.000	0.000
Archaeorhizomyces borealis Menkis. T.Y. James & Rosling	mycorrhiza	97.74	0.059	0.000	0.000	0.012	0.000	0.000	0.164	0.000
Articulospora tetracladia Ingold	entomopathogen	97.46	0.000	0.000	0.752	1.146	0.000	0.000	0.000	0.000
Basidiomycota										
Beauveria pseudobassiana S.A. Rehner & Humber	entomopathogen	100.00	0.089	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Blumeria graminis (DC.) Speer	pathogen	100.00	0.000	0.000	0.000	0.012	0.153	0.026	0.000	0.000
Boreoplaca ultrafrigida Timdal	pathogen	97.37	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000
Cadophora finlandica (C.J.K. Wang & H.E. Wilcox) T.C. Harr. & McNew	pathogen	98.50	0.119	0.000	0.047	0.000	0.000	0.000	0.164	0.000
Cadophora sp.	pathogen	98.95	0.089	0.305	0.000	0.000	0.022	0.026	0.000	0.074
Cadophora spadicis Travadon. D.P. Lawr.. Roon. Lath.. Gubler. W.F. Wilcox. Rolsh. & K. Baumgartner	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
Candelabrum spinulosum Beverw.	saprotroph	100.00	0.000	0.312	0.000	0.000	0.000	0.000	0.000	0.000
Candida oregonensis Phaff & Carmo Souza	pathogen	99.03	0.000	0.000	0.000	0.085	0.000	0.000	0.000	0.000
Cenococcum geophilum Fr.	mycorrhiza	98.86	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000
Ceratobasidium sp.	saprotroph	98.20	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
Chaetosphaeria ciliata Réblová & Seifert	saprotroph	99.47	0.000	0.000	0.094	0.012	0.005	0.000	0.000	0.011
Chalara dualis Aramb. & Gamundí	pathogen	97.97	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Chloridium virescens (Pers.) W. Gams & Hol. Jech.	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
Ciliolarina pinicola (Henn. & Plöttn.) Huhtinen	saprotroph	100.00	0.030	0.013	0.047	0.012	0.000	0.000	0.000	0.000
Clonostachys sp.	pathogen	97.93	0.000	0.000	0.000	0.000	0.027	0.211	0.000	0.000
Colletotrichum sp.	pathogen	100.00	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Colpoma quercinum (Pers.) Wallr.	saprotroph	99.45	0.386	0.019	0.047	0.000	0.000	0.000	0.000	0.000
Colpoma sp.	saprotroph	97.80	0.327	0.006	0.094	0.000	0.005	0.000	0.000	0.000
Colpoma sp.	saprotroph	99.45	0.535	0.045	0.047	0.000	0.000	0.026	0.000	0.000
Cryptosporiopsis sp.	pathogen	100.00	0.119	0.013	0.000	0.000	0.000	0.000	0.000	0.000
Cyphellophora reptans (de Hoog) Réblová & Unter.	pathogen	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Dendrophoma cytisporoides Sacc.	pathogen	100.00	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Devriesia sp.	pathogen	100.00	0.208	0.025	0.0000	0.183	0.038	0.000	0.000	0.000
Diaporthe eres Nitschke	pathogen	99.53	0.000	0.076	0.000	0.000	0.000	0.000	0.000	0.000
Diaporthe sp.	pathogen	99.12	0.238	3.652	0.094	0.024	0.027	0.000	0.000	0.000
Dictyochaeta sp.	saprotroph	99.49	1.158	7.508	0.141	0.000	0.005	0.026	0.041	0.201
Didymella macrostoma (Mont.) Qian Chen & L. Cai	pathogen	99.42	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Didymella sp.	pathogen	100.00	0.000	0.000	0.047	0.000	0.005	0.000	0.000	0.000
Didymellaceae sp.	pathogen	98.85	0.119	0.013	0.000	0.037	0.016	0.000	0.000	0.000
Diplodia seriata De Not.	pathogen	99.05	0.000	0.000	0.000	0.000	0.016	0.053	0.000	0.000
Disaeta arbuti Bonar	pathogen	100.00	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000
Dothideomycetes sp.	pathogen	100.00	0.059	0.000	0.000	0.000	0.016	0.026	0.000	0.000
Exophiala psychrophila O.A. Pedersen & Langvad	unknown	99.13	0.000	0.325	0.000	0.000	0.000	0.000	0.000	0.000
Exophiala sp.	unknown	99.56	0.178	1.349	0.047	0.000	0.005	0.026	0.000	0.011

Supplement continued (3)

Taxa	Trophic group	Similarity [%]	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Filosporella sp.	pathogen	98.53	0.000	0.000	0.000	0.061	0.000	0.000	0.000	0.021
Fusarium merismoides Corda	pathogen	100.00	0.030	0.006	0.000	0.061	0.011	0.000	0.000	0.021
Fusarium oxysporum Schltdl.	pathogen	100.00	0.030	0.013	0.000	0.000	0.000	0.000	0.000	0.011
Fusarium solani (Mart.) Sacc.	pathogen	100.00	0.000	0.000	0.000	0.000	0.323	0.000	0.000	0.000
Fusarium sp.	pathogen	99.46	0.000	0.006	0.047	0.122	0.005	0.053	0.000	0.011
Fusarium tricinctum (Corda) Sacc.	pathogen	100.00	0.000	0.000	0.000	0.037	0.005	0.000	0.000	0.000
Fusicladium sp.	pathogen	98.98	0.030	0.006	0.000	0.037	0.000	0.000	0.000	0.000
Geomyces auratus Traaen	mycorrhiza	100.00	0.030	0.000	0.000	0.061	0.000	0.000	0.000	0.011
Glarea sp.	pathogen	99.49	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Gorgomyces honrubiae A. Roldán	unknown	100.00	0.000	0.000	0.000	0.024	0.000	0.000	0.000	0.000
Gyoerffyella sp.	saprotroph	99.48	0.030	0.000	0.188	0.232	0.000	0.000	0.000	0.021
Helotiaceae sp.	saprotroph	97.76	1.544	0.980	1.128	0.293	1.024	3.933	1.520	0.583
Helotiales sp.	saprotroph	99.55	4.693	2.182	2.022	2.949	0.405	0.211	1.561	1.686
Heterotruncatella spartii (Senan. Camporesi & K.D. Hyde) F. Liu. L. Cai & Crous	pathogen	98.52	0.000	0.000	0.000	0.012	0.005	0.000	0.000	0.000
Hyaloscypha melinii Vohník. Fehrer & Réblová	saprotroph	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Hyaloscypha sp.	saprotroph	99.05	0.089	0.000	0.564	34.808	0.000	0.000	0.041	0.011
Hyaloscypha variabilis (Hambl. & Sigler) Vohník. Fehrer & Réblová	saprotroph	99.53	3.534	16.930	1.363	0.463	0.356	2.693	0.945	1.834
Hyaloscyphaceae sp.	saprotroph	99.10	0.000	0.000	0.047	0.037	0.000	0.000	0.000	0.000
Hydnotrya sp.	mycorrhiza	100.00	0.743	0.127	6.347	0.073	76.689	17.555	35.168	1.294
Hydnotrya tulasnei (Berk.) Berk. & Broome	mycorrhiza	100.00	0.000	0.000	0.141	0.012	2.904	0.449	1.397	0.042
Ilyonectria mors-panacis (A.A. Hildebr.) A. Cabral & Crous	pathogen	99.44	0.030	0.000	0.000	0.414	0.000	0.000	0.000	0.011
Ilyonectria robusta (A.A. Hildebr.) A. Cabral & Crous	pathogen	98.26	0.000	0.000	0.000	0.829	0.000	0.000	0.000	0.000
Ilyonectria sp.	pathogen	100.00	0.000	0.000	0.000	0.232	0.000	0.000	0.041	0.011
Infundichalara microchona (W. Gams) Réblová & W. Gams	saprotroph	100.00	0.000	0.000	0.094	0.000	0.000	0.000	0.000	0.000
Jattaea sp.	saprotroph	99.00	0.000	0.000	0.000	0.000	0.016	0.000	0.000	0.000
Lachnellula subtilissima (Cooke) Dennis	pathogen	97.50	0.059	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Lachnum sp.	saprotroph	99.50	0.000	0.000	0.235	0.012	0.000	0.000	0.288	0.021
Lambertella tubulosa Abdullah & J. Webster	saprotroph	99.51	0.000	0.356	0.047	1.487	0.000	0.026	0.000	0.223
Lapidomyces hispanicus de Hoog & Stielow	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
Lecanicillium muscarium (Petch) Zare & W. Gams	pathogen	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Lemonniera sp.	pathogen	100.00	0.119	0.006	0.000	0.000	0.011	0.000	0.000	0.000
Leotiomycetes		99.49	0.297	1.075	0.987	0.049	0.016	0.000	0.123	0.032
Leptodontidium sp.	pathogen	100.00	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.021
Leptosphaeria rubefaciens (Togliani) Gruyter. Aveskamp & Verkley	pathogen	100.00	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000
Magnohelicospora fuscospora (Linder) R.F. Castaneda. Hern.0Restr. & Gené	unknown	98.47	0.000	0.000	0.047	0.000	0.000	0.000	0.041	0.000
Mariannaea elegans G. Arnaud	saprotroph	100.00	0.119	1.075	0.000	0.000	0.000	0.000	0.000	0.000
Melanodiplodia sp.	pathogen	100.00	0	0.006	0.000	0.000	0.000	0.000	0.000	0.011
Metapochonia bulbillosa (W. Gams & Malla) Kepler. S.A. Rehner & Humber	unknown	100.00	0.000	0.000	0.094	0.000	0.000	0.000	0.000	0.000

Supplement continued (4)

Taxa	Trophic group	Similarity [%]	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Microsphaeropsis olivacea (Bonord.) Höhn.	pathogen	97.7	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000
Mollisia sp.	saprotroph	97.96	0.059	0.102	0.000	0.012	0.000	0.000	0.000	0.000
Monilinia laxa (Aderh. & Ruhland) Honey	pathogen	98.91	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Monodictys arctica M.J. Day & Currah	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.123	0.000
Nectria sp.	saprotroph	99.03	0.119	0.401	0.000	0.037	0.000	0.000	0.000	0.000
Nectriaceae sp.	saprotroph	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000
Neobulgaria sp.	saprotroph	99.16	0.000	0.000	0.094	0.049	0.000	0.000	0.000	0.000
Neocatenulostroma sp.	pathogen	100.00	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
Neocucurbitaria acerina Wanas. Camporesi. E.B.G. Jones & K.D. Hyde	pathogen	100.00	0.000	0.000	0.094	0.000	0.000	0.000	0.000	0.000
Oidiodendron eucalypti Crous	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.082	0.000
Oidiodendron maius G.L. Barron	pathogen	98.54	0.356	0.006	0.094	0.012	0.000	0.000	0.000	0.000
Oidiodendron periconioides Morrall	pathogen	99.03	0.000	0.006	0.000	0.000	0.000	0.026	0.000	0.000
Oidiodendron sp.	pathogen	99.51	0.267	0.000	0.047	0.000	0.000	0.158	0.000	0.000
Ophiosphaerella sp.	pathogen	100.00	0.059	0.000	0.000	0.037	0.000	0.000	0.000	0.011
Ophiostomataceae sp.	saprotroph	100.00	0.386	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Orbilia aristata (Velen.) Velen.	saprotroph	99.56	0.000	0.000	0.094	0.000	0.000	0.000	0.000	0.000
Paraphaeosphaeria neglecta Verkley. Riccioni & Stielow	saprotroph	99.58	0.505	0.032	0.188	0.634	0.000	0.000	0.000	5.652
Paraphaeosphaeria sporulosa (W. Gams & Domsch) Verkley. Göker & Stielow	saprotroph	100.00	0.000	0.000	0.423	0.232	0.000	0.000	0.000	0.021
Paraphaeosphaeria verruculosa Verkley. Göker & Stielow	saprotroph	100.00	0.178	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Penicillium miczynskii K.W. Zaleski	saprotroph	100.00	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Penicillium sp.	saprotroph	100.00	0.386	0.153	0.047	0.000	0.011	0.317	0.000	0.011
Periconia sp.	pathogen	100.00	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000
Petriella sp.	pathogen	100.00	0.059	0.000	0.000	0.037	0.000	0.000	0.000	0.000
Peyronellaea sp.	pathogen	99.41	0.059	0.000	0.141	0.000	0.000	0.000	0.000	0.000
Pezicula cinnamomea (DC.) Sacc.	pathogen	97.04	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
Phaeoisaria loranthacearum Crous & R.K. Schumach.	pathogen	100.00	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Phaeosphaeria sp.	pathogen	100.00	0.000	0.000	0.000	0.061	0.000	0.000	0.000	0.000
Phialemonium sp.	unknown	100.00	3.534	34.436	0.846	0.000	0.027	0.000	0.000	0.032
Phialocephala fortinii C.J.K. Wang & H.E. Wilcox	unknown	98.10	0.030	0.000	0.000	0.024	0.000	0.000	0.000	0.032
Phialocephala glacialis Grünig & T.N. Sieber	unknown	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Phialocephala sp.	unknown	99.48	8.019	0.331	3.244	0.488	0.126	2.033	2.383	1.198
Phialophora	saprotroph	98.97	0.000	0.083	0.000	0.000	0.000	0.000	0.000	0.000
Phlyctema vagabunda Desm.	pathogen	100.00	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000
Phoma sp.	pathogen	100.00	0.000	0.000	0.000	0.707	0.000	0.000	0.000	0.000
Pleosporales sp.	pathogen	100.00	0.000	0.006	0.047	0.000	0.005	0.000	0.000	0.000
Pleurophoma ossicol Crous. Krawczynski & H.0G. Wagner	pathogen	99.15	0.000	0.000	0.047	0.049	0.471	0.000	0.000	0.000
Polylobatispora sp.	unknown	100.00	0.000	0.000	0.047	0.000	0.033	0.000	1.356	0.000
Proliferodiscus sp.	saprotroph	99.51	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.011
Pseudoanguillospora stricta S.H. Iqbal	unknown	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Pseudocamaropycnis pini Crous	pathogen	98.60	0.000	0.006	0.000	0.000	0.005	0.000	0.000	0.042
Pseudocamarosporium piceae Wijayaw. Camporesi & K.D. Hyde	pathogen	100.00	0.030	0.000	0.047	0.000	0.000	0.000	0.000	0.000

Supplement continued (5)

Taxa	Trophic group	Similarity [%]	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Pseudogymnoascus roseus Raillo	saprotroph	100.00	0.000	0.000	0.000	0.000	0.000	0.026	7.025	0.000
Pseudogymnoascus sp.	saprotroph	100.00	0.238	0.000	0.000	0.000	0.011	0.026	8.505	0.053
Pyrenochaeta cava (Schulzer) Gruyter. Aveskamp & Verkley	pathogen	100.00	0.059	0.0130	0.188	0.000	0.000	0.053	0.000	0.000
Pyrenochaeta sp.	pathogen	100.00	0.030	0.006	0.047	0.000	0.000	0.000	0.000	0.000
Pyrenochaetopsis leptospora (Sacc. & Briard) Gruyter. Aveskamp & Verkley	pathogen	99.47	0.000	0.000	0.000	0.146	0.000	0.000	0.000	0.000
Pyrenochaetopsis sp.	pathogen	100.00	0.030	0.006	0.000	0.000	0.000	0.000	0.000	0.000
Rhizoscyphus ericae (D.J. Read) W.Y. Zhuang & Korf	mycorrhiza	99.49	0.030	0.000	0.047	0.024	0.000	0.000	0.123	0.011
Rhizoscyphus sp.	mycorrhiza	98.48	0.089	0.191	0.000	0.000	0.137	0.026	0.000	0.265
Rhizosphaera sp.	pathogen	99.55	0.000	0.000	0.000	0.122	0.000	0.000	0.000	0.000
Rhytismatales sp.	pathogen	100.00	0.089	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sarea resinae (Fr.) Kuntze	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000
Scolecobasidium fusiforme Matsush.	pathogen	100.00	0.356	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Setomelanomma holmii M. Morelet	pathogen	99.51	0.000	0.000	0.000	0.049	0.000	0.000	0.000	0.011
Simplicillium lamellicola (F.E.V. Sm.) Zare & W. Gams	antagonist	99.54	0.059	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sordariomycetes sp.	pathogen	99.04	0.000	0.006	0.047	0.012	0.000	0.000	0.000	0.000
Sporocadus microcyclus F. Liu. L. Cai & Crous	unknown	100.00	0.000	0.025	0.000	0.000	0.000	0.000	0.000	0.000
Sporothrix dentifunda (Aghayeva & M.J. Wingf.) Z.W. de Beer. T.A. Duong & M.J. Wingf.	pathogen	100.00	0.089	0.083	0.470	0.219	0.000	0.000	0.000	0.000
Sporothrix inflata de Hoog	pathogen	100.00	0.000	0.000	0.000	0.512	0.000	0.000	0.000	0.000
Sporothrix sp.	pathogen	99.54	0.743	0.496	0.893	0.756	0.016	0.106	0.000	0.011
Talaromyces diversus (Raper & Fennell) Samson. N. Yilmaz & Frisvad	pathogen	100.00	0.059	0.108	0.000	0.000	0.000	0.000	0.000	0.000
Talaromyces funiculosus (Thom) Samson. N. Yilmaz. Frisvad & Seifert	pathogen	99.53	0.743	0.694	0.000	0.000	0.005	0.000	0.000	0.000
Tetracladium maxilliforme (Rostr.) Ingold	saprotroph	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Tetracladium sp.	saprotroph	100.00	0.089	0.000	0.047	0.085	0.005	0.000	0.000	0.000
Tolypocladium sp.	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
Trichoderma asperellum Samuels. Lieckf. & Nirenberg	antagonista	100.00	0.000	0.019	0.000	0.000	0.000	0.000	0.000	0.000
Trichoderma sp.	antagonista	100.00	0.059	0.045	0.094	0.122	0.000	0.000	0.000	0.000
Trichomonascus sp.	pathogen	98.40	0.000	0.000	0.047	0.000	0.022	0.079	0.000	0.011
Venturia sp.	pathogen	100.00	0.030	0.000	0.000	0.061	0.005	0.000	0.041	0.000
Verticillium sp.	saprotroph	100.00	0.119	0.000	0.094	0.500	0.000	0.000	0.041	0.000
Wickerhamomyces silvicola (Wick.) Kurtzman. Robnett & Bas.0Powers	pathogen	99.52	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Xenochalara juniperi M.J. Wingf. & Crous	unknown	99.53	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Xenopolyscytalum pinea Crous	pathogen	98.46	0.030	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Xenopolyscytalum sp.	pathogen	99.49	0.416	0.089	0.047	0.122	0.071	0.000	0.000	0.106
Yarrowia lipolytica (Wick. Kurtzman & Herman) Van der Walt & Arx	saprotroph	100.00	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
Zalerion sp.	saprotroph	99.02	0.000	0.006	0.000	0.110	0.005	0.000	0.000	0.095
Agaricales sp.	mycorrhizal fungus	99.52	0.208	0.013	0.000	0.000	0.016	0.106	0.082	1.251
Apiotrichum porosum Stautz	pathogen	100.00	0.238	0.000	0.000	0.000	0.005	0.264	0.000	0.000
Bannozyma sp.	unknown	100.00	0.030	0.000	0.000	0.000	0.000	0.026	0.000	0.000

Supplement continued (6)

Taxa	Trophic group	Similarity [%]	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Bannozyma yamatoana (Nakase. M. Suzuki & Itoh) Q.M. Wang. F.Y. Bai. M. Groenew. & Boekhout	unknown	99.05	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Basidiomycota		97.93	2.643	0.407	2.821	0.475	0.427	1.505	2.383	15.12
Burgoa anomala (H.H. Hotson) Goid.	saprotroph	98.16	0.000	0.000	0.000	0.061	0.000	0.000	0.000	0.000
Ceratobasidiaceae sp.	saprotroph	97.76	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
Ceratobasidium sp.	saprotroph	99.12	0.000	0.000	0.000	0.012	0.005	0.026	0.000	0.000
Corticiales sp.	saprotroph	100.00	0.327	0.000	0.094	0.085	0.000	0.000	0.000	0.000
Cryptococcus sp.	pathogen	100.00	0.000	0.006	0.000	0.098	0.000	0.000	0.000	0.000
Curvibasidium cygneicollum J.P. Samp.	saprotroph	100.00	0.000	0.006	0.047	0.000	0.000	0.000	0.041	0.000
Cystobasidiales sp.	pathogen	100.00	0.000	0.025	0.000	0.000	0.000	0.000	0.000	0.000
Cystobasidium pinicola (F.Y. Bai. L.D. Guo & J.H. Zhao) Yurkov. Kachalkin. H.M. Daniel. M. Groenew. Libkind. V. de García. Zalar. Gouliam. Boekhout & Begerow	pathogen	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Cystofilobasidium infirmominiatum (Fell. I.L. Hunter & Tallman) Hamam. Sugiy. & Komag.	unknown	100.00	0.000	0.000	0.000	0.000	0.000	0.026	0.000	0.000
Deconica phyllogena (Sacc.) Noordel.	saprotroph	100.00	1.337	0.146	0.564	0.085	0.011	0.000	0.000	30.230
Delicatula integrella (Pers.) Fayod	saprotroph	98.94	0.267	0.000	0.000	0.024	0.000	0.000	0.000	0.000
Dioszegia fristingensis Á. Fonseca. J. Inácio & J.P. Samp.	unknown	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Fellomyces sp.	unknown	99.35	0.059	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Fellozyma inositophila (Nakase & M. Suzuki) Q.M. Wang. F.Y. Bai. M. Groenew. & Boekhout	unknown	100.00	0.000	0.006	0.000	0.000	0.005	0.000	0.000	0.000
Filobasidium wieringae (Á. Fonseca. Scorzetti & Fell) Xin Zhan Liu. F.Y. Bai. M. Groenew. & Boekhout	unknown	99.39	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Flammulina velutipes (Curtis) Singer	saprotroph	100.00	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Galerina allospora A.H. Sm. & Singer	saprotroph	99.25	0.000	0.000	0.000	0.000	0.077	0.000	0.000	0.000
Galerina pseudocamerina Singer	saprotroph	98.91	0.059	0.000	0.094	0.000	0.531	0.000	0.000	0.000
Ganoderma applanatum (Pers.) Pat.	saprotroph	100.00	0.000	0.006	0.000	0.000	0.000	2.376	0.000	0.000
Genolevuria sp.	pathogen	98.77	0.089	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Hamamotoa singularis (Phaff & Carmo Souza) Q.M. Wang. F.Y. Bai. M. Groenew. & Boekhout	unknown	98.13	0.000	0.165	0.000	0.000	0.005	0.396	0.000	0.000
Heterobasidion annosum (Fr.) Bref.	pathogen	100.00	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Hypholoma fasciculare (Huds.) P. Kumm.	saprotroph	98.57	0.000	0.000	0.000	0.012	0.000	3.775	0.000	0.011
Hypholoma sp.	saprotroph	98.18	0.000	0.000	0.000	0.073	0.000	0.211	0.000	0.011
Inocybe sp.	mycorrhiza	100.00	0.000	0.000	0.000	0.561	0.000	0.000	0.000	0.000
Itersonilia pannonica (Niwata. Tornai0Leh. T. Deák & Nakase) Xin Zhan Liu. F.Y. Bai. M. Groenew. & Boekhout	pathogen	98.42	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000
Itersonilia pastinacae Channon	pathogen	100.00	0.000	0.019	0.000	0.000	0.000	0.000	0.000	0.000
Kwoniella betulae K. Sylvester. Q.M. Wang & Hittinger	pathogen	100.00	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
Kwoniella pini (Golubev & I. Pfeiff.) Xin Zhan Liu. F.Y. Bai. M. Groenew. & Boekhout	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.053	0.000	0.000

Supplement continued (7)

Taxa	Trophic group	Similarity [%]	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Laccaria proxima (Boud.) Pat.	mycorrhiza	100.00	0.000	0.000	7.710	0.012	0.005	0.000	0.000	0.000
Laccaria sp.	mycorrhiza	99.64	0.059	0.000	2.022	0.000	0.000	0.000	0.000	0.000
Laccaria tortilis (Bolton) Cooke	mycorrhiza	100.00	0.000	0.000	0.564	0.000	0.000	0.000	0.000	0.000
Laetiporus sp.	pathogen	99.51	0.000	0.013	0.000	0.024	0.000	0.000	0.000	0.000
Leucosporidium creatinivorum (Golubev) V. de García. M.A. Coelho. T. Maia. L.H. Rosa. A.B.M. Vaz. C.A. Rosa. J.P. Samp. P. Gonç. M.R. Van Broock & Libkind0	unknown	100.00	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.00
Leucosporidium drummii Yurkov. A.M. Schäfer & Begerow	unknown	100.00	0.000	0.013	0.000	0.073	0.000	0.026	0.000	0.000
Leucosporidium krtinense Mašínová. A. Pontes. J.P. Samp. & Baldrian	unknown	100.00	0.030	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Luellia sp.	unknown	98.27	0.356	0.000	0.094	0.134	0.000	0.000	0.123	2.449
Malassezia globosa Midgley. E. Guého & J. Guillot	pathogen	100.00	0.000	0.000	0.000	0.037	0.000	0.792	0.000	0.000
Microstroma sp.	pathogen	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.041	0.021
Mycena amicta (Fr.) Quél.	saprotroph	99.61	0.149	0.000	0.000	0.000	0.751	0.000	0.000	0.000
Mycena epipterygia (Scop.) Gray	saprotroph	100.00	1.158	0.045	0.235	0.000	3.638	0.000	0.000	20.740
Mycena galopus (Pers.) P. Kumm.	saprotroph	99.63	0.178	0.000	0.000	0.012	0.011	3.458	0.082	0.000
Mycena megaspora Kauffman	saprotroph	98.91	0.059	0.000	0.141	0.000	0.000	0.000	0.000	0.000
Mycena pruinatipes Robich	saprotroph	98.42	0.564	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Mycena sanguinolenta (Alb. & Schwein.) P. Kumm.	saprotroph	100.00	3.208	0.000	2.868	0.000	2.482	0.000	0.000	0.021
Mycena sp.	saprotroph	98.46	2.287	0.006	0.329	0.012	0.186	4.303	0.082	0.170
Nolanea conferenda (Britzelm.) Sacc.	saprotroph	99.23	0.653	0.000	0.141	0.037	0.164	0.449	0.000	0.011
Papiliotrema flavescens (Saito) Xin Zhan Liu. F.Y. Bai. M. Groenew. & Boekhout	pathogen	100.00	0.000	0.000	0.000	0.146	0.000	0.000	0.000	0.000
Peniophora pini (Schleich. ex DC.) Boidin	saprotroph	99.57	0.000	0.000	0.000	0.098	0.000	0.000	0.000	0.000
Phaeotremella sp.	saprotroph	100.00	0.000	0.000	0.000	0.037	0.000	0.000	0.000	0.000
Piskurozyma sp.	unknown	97.93	0.000	0.006	0.000	0.000	0.011	0.000	0.000	0.000
Pseudotomentella sp.	mycorrhiza	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.260	0.000
Rhodotorula sp.	pathogen	100.00	0.000	0.000	0.000	0.012	0.000	0.079	0.000	0.000
Russula sp.	mycorrhiza	99.56	0.000	0.006	0.000	0.353	0.000	0.000	0.041	0.000
Saitozyma paraflava Xin Zhan Liu. F.Y. Bai. M. Groenew. & Boekhout	unknown	100.00	0.000	0.000	0.000	0.146	0.000	0.000	0.000	0.000
Scleroderma areolatum Ehrenb.	mycorrhiza	98.61	1.544	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Scleroderma sp.	mycorrhiza	98.63	1.634	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Scleroderma verrucosum (Bull.) Pers.	mycorrhiza	100.00	2.435	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sebacina sp.	saprotroph	98.74	0.624	0.000	0.000	0.122	0.044	0.158	0.164	0.032
Serpula himantioides (Fr.) P. Karst.	saprotroph	100.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Sistotrema sp.	mycorrhiza	100.00	0.030	0.006	0.000	0.012	0.000	0.000	0.000	0.011
Slooffia sp.	pathogen	100.00	0.000	0.057	0.000	0.000	0.000	0.000	0.000	0.000
Solicoccozyma terreus (Di Menna) Yurkov	unknown	100.00	0.030	0.000	0.000	0.037	0.011	0.000	0.000	0.000
Sterigmatosporidium polymorphum G. Kraep. & U. Schulze	unknown	100.00	0.000	0.000	0.000	0.000	0.000	0.026	0.000	0.000
Suillus luteus (L.) Roussel	mycorrhiza	100.00	0.030	0.000	0.799	0.000	0.005	0.000	0.000	0.000
Tausonia pullulans (Lindner) Xin Zhan Liu. F.Y. Bai. M. Groenew. & Boekhout	pathogen	100.00	0.000	0.006	0.000	0.000	0.000	0.000	0.000	0.000

Supplement continued (8)

Taxa	Trophic group	Similarity [%]	KQL	KQD	NQL	NQD	KFL	KFD	NFL	NFD
Thelephora terrestris Ehrh.	saprotroph	98.25	0.089	0.000	0.000	0.000	0.016	0.000	0.000	0.000
Trechisporales sp.	unknown	99.16	0.030	0.025	0.047	0.000	0.093	1.742	0.247	0.965
Tremella anaptychiae J.C. Zamora & Diederich	lichenicolous	98.68	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000
Tulasnella sp.	mycorrhiza	97.27	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000
Tyromyces fissilis (Berk. & M.A. Curtis) Donk	saprotroph	99.21	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.000
Xerocomellus cisalpinus (Simonini. H. Ladurner & Peintner) Klofac	mycorrhiza	98.48	0.000	0.000	0.000	0.000	0.000	0.000	0.370	0.000
Glomeromycota										
Acaulospora lacunosa J.B. Morton	mycorrhiza	99.26	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000
Archaeosporales sp.	mycorrhiza	100.00	0.000	0.000	0.000	0.000	0.000	0.000	3.944	0.000
Glomerales sp.	mycorrhiza	98.63	0.000	0.006	0.000	0.000	0.000	0.026	0.000	0.000
Glomeromycota		100.00	0.000	0.000	0.000	0.000	0.011	0.000	0.205	0.000
Mucoromycota										
Absidia cylindrospora Hagem	pathogen	99.60	0.000	0.000	0.000	0.037	0.005	0.000	0.000	0.000
Mortierella sp.	saprotroph	100.00	0.030	0.019	0.141	0.171	0.000	0.502	0.041	0.201
Umbelopsis isabellina (Oudem.) W. Gams	pathogen	100.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011
Oomycota										
Chaetopsis canovae Rambelli	pathogen	97.03	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Pythium attrantheridium Allain Boulé & Lévesque	pathogen	100.00	0.000	0.000	0.141	0.000	0.000	0.000	0.000	0.000
Pythium macrosporum Vaartaja & Plaäts Nit.	pathogen	99.08	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
Pythium sylvaticum W.A. Campb. & F.F. Hendrix	pathogen	100.00	0.030	0.000	0.047	0.024	0.005	0.000	0.000	0.000
Pythium volutum Vanterp. & Truscott	pathogen	97.74	0.089	0.013	0.047	0.183	0.000	0.026	0.123	0.021
Uncultivated fungi			38.729	23.562	36.577	10.798	5.922	44.298	23.131	14.452
No sequence in the NCBI database			6.296	1.190	16.502	34.186	2.082	1.109	1.438	0.201

STRESZCZENIE

Różnorodność zbiorowisk grzybów gleby spod sadzonek dębu szypułkowego *Quercus robur* L. i buka zwyczajnego *Fagus sylvatica* L. wyprodukowanych różnymi technologiami

Grzyby i organizmy grzybopodobne są istotnymi elementami ekosystemów leśnych. Wpływają one na zdrowotność, wzrost i produktywność roślin. Istotne jest zrozumienie roli zbiorowisk grzybów związanych z gatunkami lasotwórczymi. Celem badań było porównanie struktury zbiorowisk grzybów w glebie spod żywych i martwych korzeni buka zwyczajnego i dębu szypułkowego pochodzących z rocznej uprawy założonej z sadzonek wyprodukowanych różnymi technologiami. Przyjęto, że saprotrofy i patogeny będą dominować w zbiorowiskach grzybów glebowych pod korzeniami martwych drzew, grzyby mykoryzowe będą dominować w zbiorowiskach grzybów glebowych pod żywymi korzeniami drzew oraz że zbiorowisko grzybów związane z sadzonkami kontenerowymi będzie zdominowane przez grzyby mykoryzowe i będzie bardziej zróżnicowane niż w przypadku sadzonek z gołym korzeniem.

Próby pochodziły z rocznej uprawy z leśnictwa Wielisławice (51°14'46,0"N 18°06'15,6"E). Materiał sadzeniowy pochodził ze szkółki Dobrygość. Pobrano 15 próbek gleby (po 0,5 kg każda) z wariantów: KQL – żywe dęby ze szkółki kontenerowej; KQD – martwe dęby ze szkółki kontenerowej; NQL – żywe dęby z nagim systemem korzeniowym; NQD – martwe dęby z nagim systemem korzeniowym; KFL – żywe buki ze szkółki kontenerowej; KFD – martwe buki ze szkółki kontenerowej; NFL – żywe buki z nagim systemem korzeniowym; NFD – martwe buki z nagim systemem korzeniowym. Łącznie pobrano 120 próbek.

Ekstrakcję DNA przeprowadzono przy pomocy zestawu DNeasy PowerSoil Kit. Identyfikację gatunków grzybów wykonano przy użyciu regionu rDNA ITS1, 5.8S. Analizę przeprowadzono z użyciem starterów ITS1FI2 – 5' GAA CCW GCG GAR GGA TCA 3' oraz 5.8S – 5' CGC TGC GTT CTT CAT CG 3'. Otrzymane produkty PCR zsekwencjonowano, stosując technologię Illumina SBS. Wyniki poddano analizie bioinformatycznej i statystycznej. Sekwencje porównano z sekwencjami referencyjnymi zdeponowanymi w bazie danych NCBI przy użyciu algorytmu BLAST. Różnorodność definiowano jako liczbę gatunków w próbce. Przeprowadzono analizę statystyczną różnorodności biologicznej oraz dokonano oceny przeżywalności drzew w okresie uprawy.

Do wizualizacji składu zbiorowisk grzybów wykorzystano niemetryczne skalowanie wielowymiarowe (NMDS) ze wskaźnikiem odmienności Braya-Curtisa. Przeprowadzono analizę podobieństwa funkcją anosim w pakiecie wegańskim (R Core Team 2021). W celu określenia, które gatunki grzybów można uznać za gatunki wskaźnikowe związane z określoną grupą sadzonek na podstawie typu produkcji, zastosowano funkcję multipatt w pakiecie indicspecies (R Core Team 2021). Kolejnym etapem badań była analiza chemiczna gleby (tło badawcze) (tab. 4).

We wszystkich analizowanych próbach zidentyfikowano 1293 taksony i uzyskano łącznie 63 321 sekwencji. W zbiorowiskach grzybów dominowały taksony z typów Ascomycota i Basidiomycota (ryc. 1 i 2). W analizowanych próbach najwięcej było grzybów mykoryzowych (58,43%), saprotrofów (20,96%) i patogenów (19,70%) (ryc. 3). W zbiorowiskach związanych z żywymi drzewami dominowały grzyby mykoryzowe. Saprotrofy dominowały w glebie związanej z martwymi drzewami (ryc. 3). Zbiorowisko grzybów związane z dębem było znacznie bardziej zróżnicowane i liczniejsze niż zbiorowisko związane z bukiem. W zbiorowisku grzybów związanych z martwymi drzewami dominowały grzyby rozkładające drewno (saprotrofy), natomiast w przypadku sadzonek żywych dominowały grzyby mykoryzowe. Wśród saprotrofów najczęściej izolowanymi grzybami były *Hyaloscypha* spp., *Deconica phyllogena*, *Mycena* spp., *Dictyochaeta* sp. i *Paraphaeosphaeria neglecta*. Nie stwierdzono różnicy między udziałem patogenów w zbiorowisku drzew żywych i martwych. Różnorodność taksonomiczna grzybów zależała głównie od gatunków sadzonek drzew (tab. 1-3, suplement). Zbiorowiska grzybów drzew z produkcji kontenerowej były bardziej zróżnicowane niż produkowane w technologii tradycyjnej.

Średnia przeżywalność drzew w doświadczeniu po pierwszym sezonie wegetacyjnym wyniosła 88,48% (ryc. 4). Analiza podobieństw wykazała, że zbiorowiska grzybów wykazywały istotne statystycznie różnice ($R=0,406$, $p=0,019$) pomiędzy sadzonkami różnych gatunków drzew i różnymi technologiami produkcji (ryc. 5). *Fusarium oxysporum* był istotnie statystycznie związany z sadzonkami kontenerowymi.

Wyniki badań wskazują, że należy rozważyć szersze wykorzystanie sadzonek kontenerowych dębu szypułkowego do odnowień i zalesień ze względu na ich większą przeżywalność niż sadzonek z nagim systemem korzeniowym.