

# Patterns of fungal diversity in needles, rootlets and soil of endemic *Pinus peuce*

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## Abstract

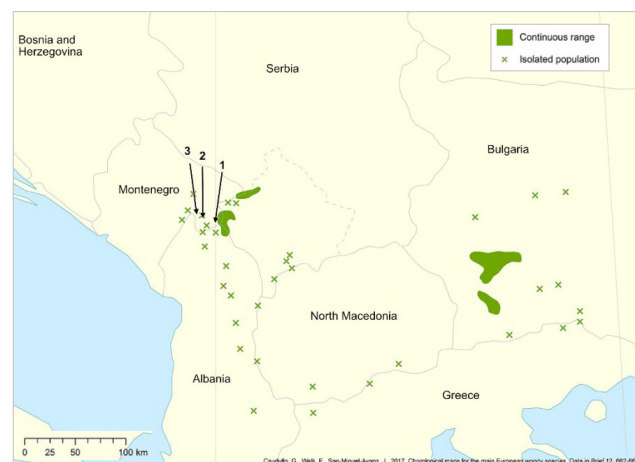
*Pinus peuce* is a five-needle pine native to high-elevation montane habitats of the Balkans. This study aimed to assess the diversity and composition of fungal communities associated with soil, rootlets and living needles of *P. peuce* at three high-altitude forest sites with different edaphic conditions and stand characteristics in south-eastern Montenegro. In total, 90 samples of each substrate (needles, rootlets and soil) were sampled. DNA amplification using ITS2 rDNA as a marker and high-throughput sequencing resulted in 23,394 high-quality reads, representing 825 fungal taxa. There were 52.5% Basidiomycota, 43.9% Ascomycota and 3.6% Mucoromycotina. There were 118 unique fungal taxa in the rootlets, 230 in soil and 113 in the needles, and only 8 taxa were shared. The most common fungi in rootlets were *Rhizopogon mohelensis* (11.0%), *Suillus americanus* (8.4%), and *R. fallax* (6.9%), in soil – *Phlebiopsis gigantea* (5.1%), *Tylospora asterophora* (2.9%), and *Sollicocossima terricola* (2.7%), and in the needles – *Dothideomyces* sp. (17.6%), *Dothideomyces* sp. (10.7%), and *Leotiomyces* sp. (6.5%). The results showed that functional tissues and the rhizosphere soil of *P. peuce* were inhabited by a high diversity of fungi. Fungal communities in the rootlets and soil were largely determined by the site conditions such as soil properties and forest stand composition.

**Keywords:** *Pinus peuce*, five needle pine, high-altitude forests, ectomycorrhiza, pathogens, saprotrophs, Montenegro

## Introduction

*Pinus peuce* Griseb. is one of the two European pine species from the subgenus *Strobus*. It is a tertiary relict and endemic to the Balkans, where it is rare and has limited distribution between the latitudes 41° and 43° N (Figure 1), i.e. in the areas that include parts of Montenegro, Serbia, Albania, North Macedonia, Greece and Bulgaria (Jovanović 2007, Alexandrov and Andonovski 2011). *Pinus peuce* is adapted to high elevations and grows between 1,200 m and 2,300 m a.s.l. BSE, i.e. in areas characterised by cold and high-humidity mountain climate. It is predominantly found on silicate soils with a varying soil depth and fertility. On carbonate soils, it is usually present on deeper and more humid soils of northern expositions (Janković et al. 1987). *Pinus peuce* characteristically forms dense and pure forest stands, but at the upper tree line it often grows in small and scattered stands (Jovanović 2007) (Figure 2). It can also grow in admixture with *Picea abies*, *Abies alba*, and at lower altitudes with *Fagus sylvatica*. At the upper tree line, it can form mixed forest stands with *Pinus heldreichii*. Nowadays the total area occupied by *P. peuce*

is only about 20,500 ha (Alexandrov and Andonovski 2011).



**Figure 1.** The map of the Balkan region showing the distribution of *Pinus peuce* (Caudullo et al. 2017)

The sampling sites are arrowed and numbered: 1 – Bogičevica, 2 – Visitor, and 3 – Zeletin.



**Figure 2.** *Pinus peuce* forest stands at the Bogičevica site in southeastern Montenegro

*Pinus peuce* is one of the most valuable conifer tree species in the Balkans (Stevanović et al. 1995, Jovanović 2007, Alexandrov and Andonovski 2011) due to its high ecological adaptability, the provision of ecosystem services such as protection of soil and water as well as biodiversity conservation. In Montenegro, at the optimum growth conditions, *P. peuce* reaches up to 30 m in height and up to 1 m in diameter. Commonly, stems have branches down to the ground, while root systems have a characteristic central root with large lateral roots, which penetrate deep into the soil. In preserved forests, trees can reach the age of ca. 200 years, and individual specimens over 300 years. Even at high altitudes, *P. peuce* produces high yields of wood (Jovanović 2007) while its resin provides high quality derivatives (Alexandrov and Andonovski 2011), but nowadays it is not harvested due to protection.

In the last 50 years, only limited natural regeneration was reported for *P. peuce* forests, though recent observations show more extensive regeneration in the abandoned mountain areas (Figure 2). *Pinus peuce* is classified as nearly threatened by the International Union for Conservation of Nature Red List of Threatened Species (IUCN) and it is protected in the Balkan countries. It is expected to adapt well to the climate change and can be a promising tree species for forestry and nature conservation in high-elevation mountain areas (Jovanović 2007, Alexandrov and Andonovski 2011). Hence, it requires special attention, i.e. the development and application of conservation measures (Janković et al. 1987, Stevanović et al. 1995).

Fungi play key roles in montane forest ecosystems and represent an important part of biodiversity (Baldrian 2017, Bowman and Arnold 2018, Nilsson et al. 2019). They directly influence several physiological processes in trees and contribute to carbon, nutrient and water cycling (Nemergut et al. 2013, Stewart et al. 2018). Despite their importance and possible impact on tree health, information on fungi associated with *P. peuce* is scarce.

Moreover, the knowledge about fungal communities associated with pines from subgenus *Strobus* is also limited. Among different fungi associated with trees, ectomycorrhizal (ECM) fungi directly influencing the uptake of nutrients and water in pine forests affect soil characteristics and overall plant vitality (Nemergut et al. 2013, Bowman and Arnold 2018, Mello and Balestrini 2018, Stewart et al. 2018, Nilsson et al. 2019). They can be essential for successful regeneration, i.e. the establishment and growth of tree seedlings, in particular on marginal habitats under harsh environmental conditions (Brundrett 2008, Menkis et al. 2012). Saprotrophic fungi that are decomposers of dead organic matter, drive nutrient cycling in forest ecosystems (Lindahl et al. 2007, Baldrian 2017, Terhonen et al. 2019). Fungal pathogens can affect health and growth of forest trees (Stenlid et al. 2016, Elvira-Recuenco et al. 2020), while fungal endophytes and epiphytes can support ecological adaptation of host trees (Paszowski 2006, Schulz and Boyle 2015, Stewart et al. 2019).

Our aim was to study fungal communities associated with the soil, rootlets and living needles of *P. peuce* in order to fill knowledge gaps about fungal communities associated with five needle pines growing in high-elevation habitats. By using high-throughput sequencing (Lynikienė et al. 2020), we examined fungal communities at three different forest sites. As the local-scale heterogeneity of soil microhabitats and vegetation type has been identified as one of the most important drivers of fungal diversity (Geml 2019, Yamauchi et al. 2021), we further hypothesized that edaphic conditions and stand characteristics at each site may influence both the diversity and composition of fungal communities, thereby revealing the site-specific effects on associated fungi.

## Materials and methods

### Study sites

The study sites were at Bogičevica, Visitor and Zeletin (a detailed description of each site is below) in south-eastern Montenegro (Figure 1, Table 1). These sites represented characteristic *P. peuce* forest stands growing at ca. 1,600–2,100 m altitudes. The geographical distance between the Bogičevica site and two other sites (Visitor and Zeletin) was about 12–15 km. The distance between Visitor and Zeletin sites was about 5 km. All three sites differed from each other in terms of forest stand composition and age, soil characteristics and elevation (Table 1). Climatic conditions were similar for all three sites.

The climate at the study sites, according to the Köppen climate classification, is a humid cold temperate boreal climate with cool summer and cold winter (Dfc, Dfwcx) (Burić et al. 2014). The winter minimum is below  $-30^{\circ}\text{C}$  and the summer maximum is above  $10^{\circ}\text{C}$ . The arid period is absent. However, the primary precipitation maximum is in the late autumn or winter. The secondary precipitation maximum occurs in the late spring or early summer.

**Table 1.** The study sites, where the soil, rootlets and needles of *P. peuce* were sampled

Site	Position	Alt. (m)	Soil type *	Forest stand
Bogičevica (Mt. Prokletije)	N 42.5650422 E 20.0332079	1,970–2,100	Rendzina to brown acid soil on quartz sandstone	Pure <i>Pinus peuce</i> stand (90–200-year-old)
Visitor (Mt. Visitor)	N 42.6146217 E 19.8821091	1,880–2,000	Brown soil on basic igneous rock	Pure <i>Pinus peuce</i> stand (10–60-year-old)
Zeletin (Mt. Visitor)	N 42.6330433 E 19.8359449	1,600–1,800	Brown soil on cherts	Mixed <i>Pinus peuce</i> , <i>Abies alba</i> and <i>Fagus sylvatica</i> stand (100–120-year-old)

\* based on Fušić and Đuretić 2000.

The winters are usually cold and snowy, while summers are usually cool. In summer, at the elevations above 1,500–1,600 m the average air temperature can be above 10°C for up to four months.

At the Bogičevica site *P. peuce* is growing in admixture with *P. abies* and *A. alba* at the elevation of ca 1,700 m (at lower elevations *Abieti-Picenion* forest type is situated). At the elevation of ca. 1,800 m, it is growing in admixture with *P. abies*. Above, *P. peuce* forms pure forest stands, which extends up to the uppermost mountain ridges. The sampling site was in pure, old-growth *P. peuce* forest stand with the majority of trees aged between 100 and 200 years. Trees were 25–30 m in height and 50–60 cm in diameter. The sampling site was located on the slope and between altitudes 1,970 m and 2,100 m, i.e. from the mountain plateau with glacial lake Ridsko up to the top of the mountain. The slope has north and northeast-facing exposition. The forest site is characterised as a *Pinetum peucis montenegrinum* Bleč. et Tat. type. The site at Bogičevica has the silicate geological structure: quaternary conglomerates composed of quartz and calcite. It is brown acid soil type on quartz sandstone (Fušić and Đuretić 2000), which is variable in depth due to the intense soil erosion on the mountain slopes and ridges, which makes it very shallow and skeletal (more than 50% of the skeleton). Transient A (B) and (B) C soil horizon present. The humus layer is thin, dark and densely colonised by the roots of grasses, shrubs and forest trees. The A horizon is brown or dark brown and is 8–12 cm deep.

At the Visitor site, *P. peuce* is growing from the elevation of ca. 1,600 m, where it is mixed with *P. abies* and *A. alba* (at lower elevations *Abieti-Picenion* forest type is situated). Pure *P. peuce* forest stand, which is dominated by 100–200-year-old trees, is growing above the elevation of ca. 1,800 m and extends up to the uppermost mountain ridges (alt. 2,210 m). The sampling site was on the exposed mountain slope (alt. 1,900–2,000 m), on an abandoned mountain pasture, where forest of *P. peuce* has regenerated. The site has north and northwest-facing exposition and is dominated by 10–60-year-old trees of *P. peuce*. On the south-facing slope, an old forest stand of *P. heldreichii* is situated, which has also regenerated and is mixed with *P. peuce* on the sampling site. The Visitor site is dominated by silicate geological soil structure, where the keratophyres, quartz keratophyres, andensitis, dacities and diabases are the most common eruptive rocks, but the highest

mountain peaks are composed of Triassic limestone. On the sampling site, the soil is dystric camisoles on igneous rock (Fušić and Đuretić 2000). As primary eruptive rocks are compact and resistant to weathering, the soil stays in initial stage for a very long time and its development is very slow. It is mainly shallow and skeletal (with large fragments of stones) and acidic. The characteristic soil profile is A (B) C. The A and B horizons are poorly differentiated in terms of colour and mechanical composition. The topsoil layer is dark. Mineralization of humus is very slow, resulting in its accumulation. The B horizon has fragments of brown, yellow or orange colour, which is due to the release of iron.

At the Zeletin site, the forest vegetation is differing compared to vegetation on near neighbouring areas. At the elevation of 1,200–1,600 m, *Fagus sylvatica* forest or mixed *F. sylvatica* and *A. alba* forest is situated (forest types *Fagetum moesiaca* Bleč. et. Lakš, and Ass. *Abieti-Fagetum*). The sampling was carried out at the elevation of 1,600–1,800 m, where *P. peuce* is mixed with *F. sylvatica* and *A. alba* in a dense, old-growth forest stand (100–150 yr.) on the mountain slope of east and south-east-facing exposition and was characterised by the well-developed soil. Pure *P. peuce* forest stands occur at the elevation of ca. 2,060 m and up to the top of the mountain, where these stands alternate with mountain pastures. At the sampling site, the soil is dystric cambisol on chert (Fušić and Đuretić 2000). In the dense, old-growth and mixed coniferous and deciduous forest, the soil is well developed, and it has a A (B) C profile. The A horizon is dark brown, and with a high humus content, loose, and with a crumbly structure; sand-loam or loamy. The B horizon is brown or dark brown, with orange-grey shades and loamy.

### Experimental design and sampling

At each study site, stands of *P. peuce* were healthy-looking, i.e. showed no signs of damage or decline. The sampling was carried out in autumn 2015 and at each site included needles, rootlets and the rhizosphere soil of *P. peuce*. The rootlets and samples of surrounding fine fraction soil were randomly collected under 5–15-year-old trees of *P. peuce* growing at ca. 50 m from each other. These trees were used for sampling as roots of old-growth trees were not accessible. Besides, it was shown that roots of smaller trees are often connected to older trees via the common ECM (ectomycorrhizal) fungal network and may

share the same fungal taxa (Simard et al. 1997). The soil samples with rootlets were taken down to 20 cm depth and included lateral rootlets with attached fine roots. Twigs with the current and previous year living needles were randomly collected up to 2 m from the ground. Samples were individually packed into plastic bags, transported to the laboratory, and kept at 4°C for a maximum period of one week before processing. For each sample, rootlets were separated from the soil, soaked in cold water for 12 h and gently washed in tap water to remove any of the remaining soil. Fine roots were separated from lateral rootlets, placed in 1.5 ml centrifugation tubes, and stored at -20°C before used for DNA extraction. Individual samples of fine fraction soil, which was sieved using a sieve (mesh size 2 mm × 2 mm), were placed in plastic bags, and stored at -20°C before used for DNA extraction. At each site, 30 root, 30 needle and 30 soil samples were taken.

Sampled materials, i.e. twigs with needles, soil and roots, were taken in a close vicinity. Taken together, the sampling resulted in 90 needle, 90 rootlet and 90 soil samples of *P. peuce*.

### **Soil chemical analyses and texture**

At least 100 g of soil from each sample was dried at room temperature (ca. 21°C) for 24 h. Soil pH was determined using a combined glass-electrode in 1 M KCl of soil suspension 1:2.5 (w/v). The humus content was determined by wet oxidation with 0.02 M KMnO<sub>4</sub>. Total nitrogen was determined by the Kjeldahl method (Topalović et al. 2018). The available phosphorus and potassium (extraction with ammonium-acetate-lactate solution at pH = 3.7) were determined according to the Egner-Riehm-Domingo method using the spectrophotometry and flame photometry, respectively. Total carbonates were determined by the volumetric method (Topalović et al. 2018). The available Fe, Mn, Zn and Cu (extraction with 0.005 M DTPA) as well as exchangeable Ca and Mg (extraction with 1 M CH<sub>3</sub>COONH<sub>4</sub>) were determined using flame atomic absorption spectrometry (AA-6800, Shimadzu). The values of the above-mentioned soil parameters were expressed on air-dried basis. Particle size distribution was analysed using the sieve and the pipette method (Topalović et al. 2018).

### **Molecular analysis**

DNA extractions were done from individual needle, rootlet and soil samples, which were previously freeze-dried at -60°C for 48 h (Alpha 1-4 LD, Martin Christ, Germany). Samples were placed in separate 2 ml tubes with screw cap and homogenised in a Fastprep machine (Precellys, Montigny-le-Bretonneux, France). About 100 mg of freeze-dried soil per sample was used for DNA extraction, which was done using Zymo Soil Kit (Zymo Research, Irvine, USA). For isolation of genomic DNA from the rootlets and needles, 200 mg of material was taken from each respective sample and the extraction was completed using

the CTAB protocol (Menkis et al. 2014). The DNA isolated from the rootlets was directly used in PCR reactions, while DNA isolated from the needles was additionally purified using JetQuick DNA Purification Kit (Genomed GmbH, Leinfelden, Germany). The DNA concentration of each sample was determined using a NanoDrop™ One spectrophotometer (Thermo Scientific, Rodchester, NY, USA) and adjusted to 10 ng/μL. Amplification by PCR of the ITS2 rDNA region was done using barcoded fungal-specific primer gITS7 (Ihrmark et al. 2012) and barcoded universal primer ITS4 (White et al. 1990). All samples of the same substrate (needles, rootlets or soil) and site were amplified using primers with the same barcode, resulting in 9 different barcodes (3 substrates × 3 sites). Amplification of multiple samples with the same barcode was done owing to get a broader representation of fungal communities per each substrate and site. PCR controls were also included. Amplifications were performed using the Applied Biosystems 2720 thermal cycler (Foster City, CA, USA). An initial denaturation step started at 95°C for 2 min, followed by 27 amplification cycles of denaturation at 95°C for 30 s, annealing at 55°C for 30 s, and extension at 72°C for 60 s. The thermal cycling was ended by a final extension step at 72°C for 7 min (Lazarević and Menkis 2020). The PCR products were analysed using gel electrophoresis on 1% agarose gels stained with Nancy-520 (Sigma-Aldrich, Sweden). PCA products were purified using a sodium acetate protocol (Menkis et al. 2015). Purified PCR products were quantified using a Qubit fluorometer 4.0 (Thermo Fisher Scientific, Waltham, MA, USA), and an equimolar mix of all PCA products was used as a part of a larger sample for high-throughput sequencing using a Pacific Biosciences RS II platform (Menlo Park, CA, USA) and one SMRT cell at the SciLifeLab (Uppsala, Sweden).

### **Bioinformatics**

Principles of bioinformatics followed Lynikienė et al. (2020). The sequences obtained were subjected to quality control and clustering in the SCATA NGS sequencing pipeline available at <http://scata.mykopat.slu.se>. The initial procedure started with quality filtering of the sequences that included the removal of sequences shorter than 200 bases, sequences with low read quality, primer dimers and homopolymers, which were collapsed to 3 bases before clustering. Only sequences containing a barcode and primer were retained. Then, the primer and sample barcodes were removed from the sequence, but information on the sample and sequence association was stored as meta-data. A single-linkage clustering based on 98% similarity was used to cluster sequences into different taxa. For each cluster, the sequence of the most common genotype was used for taxonomic identification. For clusters containing only two sequences, a consensus sequence was produced. The taxa were taxonomically identified using the GenBank database and the BLASTn algorithm (Altschul et al. 1997). The reliability of each reference sequence was manually checked for each

taxon. If available, the sequence of a type species was used as a reference. The following criteria were used for species identification: sequence coverage > 80%; 94–97% similarity to genus level and  $\geq 98\%$  similarity to species level. Sequences deviating from these criteria were identified only to a high taxonomic rank and were given unique names (Lynikienė et al. 2020, Lazarević and Menkis 2020). Representative sequences of fungal non-singletons are available from GenBank under accession numbers MZ441403–MZ442202.

### Statistical analyses

The statistical analysis of the soil data was performed using IBM SPSS Statistics 23.0 software package (IBM 2015). The significant differences between the means were determined using the one-way ANOVA and Duncan's test at  $p < 0.05$ . Rarefaction analysis was performed to evaluate the relationship between the cumulative number of fungal taxa and the number of generated high-quality fungal sequences using Analytical Rarefaction v.1.3 (Raup 1975, Tipper 1979, Holland 2003). Differences in richness of fungal taxa in study sites of *P. peuce* were compared by non-parametric chi-square testing (Magurran 1988). As each of the datasets was subjected to multiple comparisons, confidence limits for  $p$ -values of the chi-square test were reduced using the Bonferroni correction. The Shannon diversity index, qualitative Sørensen similarity index and principal coordinate analysis (PCA) in CANOCO 5 (CANOCO 2012) were used to characterise the diversity and composition of fungal communities (Shannon 1948, ter Braak et al. 1998, Sokal and Rohlf 2005). For PCA, log-transformed data and Canoco default parameters were used. The nonparametric Mann-Whitney test in Minitab v. 18.1 (Minitab 2017) was used to test if the Shannon diversity index among different substrates was statistically similar or not.

### Results

Although the soils of the study sites differed according to the geological structure and type (Table 1), the soil texture in different study sites was similar as it was sandy loam. At the Bogičevica site, sand percentage ( $68.5 \pm 2.58$ , mean  $\pm$  SD) was significantly higher than it was at the Visitor ( $65.9 \pm 4.72$ ) or Zeletin ( $65.8 \pm 5.46$ ) sites ( $p < 0.05$ ). The percentage of clay was significantly higher at the Zeletin site ( $10.8 \pm 1.06$ ) compared to the Bogičevica ( $8.6 \pm 0.54$ ) or Visitor ( $8.5 \pm 1.23$ ) sites ( $p < 0.05$ ). At all three sites, soils were well drained.

Soil analyses showed that *P. peuce* forests were growing on very acidic to acidic soils, which were rich in humus and nitrogen (Table 2). Furthermore, soils were poor in available P, had moderate availability of K, high content of Fe and Mn, optimal content of Zn and low to optimal content of Cu. Values for electrolytic conductivity (EC) covers the range from infertile to very fertile soils. The exchangeable Ca and Mg were in a range from the low to optimal level. Among the three sites, the most favourable growth

conditions were found to be at the Visitor site due to higher soil pH, the highest level of humus as well as of nutrients such as N, P, K, Ca, Mg and Zn (Table 2).

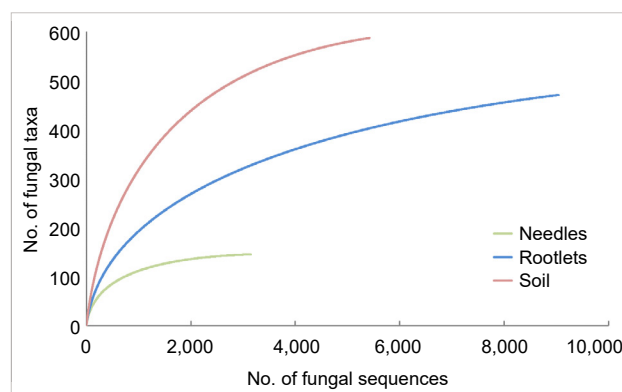
The soil at the Zeletin site had the lowest pH value, significantly higher level of available Fe and EC value, but significantly lower content of available P and Mn (Table 2). The soil at the Bogičevica site had the lowest content of humus, N and the EC value, but the highest level of Mn and Cu (Table 2).

**Table 2.** Soil chemical characteristics of *Pinus peuce* stands at the Bogičevica, Visitor and Zeletin sites

Soil parameter	Bogičevica	Visitor	Zeletin
pH (KCl)	4.26 $\pm$ 0.09 b	4.78 $\pm$ 0.96 a	4.04 $\pm$ 0.07 b
Humus (%)	5.50 $\pm$ 0.56 c	14.0 $\pm$ 6.80 a	8.30 $\pm$ 1.29 b
N (%)	0.20 $\pm$ 0.02 c	0.61 $\pm$ 0.20 a	0.33 $\pm$ 0.15 b
P <sub>2</sub> O <sub>5</sub> (mg/100g)	2.1 $\pm$ 0.73 b	2.5 $\pm$ 0.47 a	1.6 $\pm$ 0.54 c
K <sub>2</sub> O (mg/100g)	9.5 $\pm$ 0.26 b	16.7 $\pm$ 2.92 a	16.7 $\pm$ 4.88 a
Ca (mg/100g)	44.5 $\pm$ 4.59 b	255 $\pm$ 255 a	108 $\pm$ 30.2 b
Mg (mg/100g)	7.59 $\pm$ 0.85 b	20.8 $\pm$ 20.1 a	11.3 $\pm$ 1.89 b
Fe (mg/kg)	68.5 $\pm$ 15.2 b	68.1 $\pm$ 15.7 b	97.0 $\pm$ 39.0 a
Mn (mg/kg)	64.3 $\pm$ 5.78 a	40.7 $\pm$ 11.7 b	32.7 $\pm$ 19.5 c
Zn (mg/kg)	1.58 $\pm$ 0.34 b	3.23 $\pm$ 1.50 a	1.59 $\pm$ 0.96 b
Cu (mg/kg)	0.99 $\pm$ 0.13 a	0.58 $\pm$ 0.27 b	0.50 $\pm$ 0.22 b
EC ( $\mu$ S/cm)	43.7 $\pm$ 20.7 c	145 $\pm$ 88.0 b	252 $\pm$ 173 a

Note: Values show the mean  $\pm$  standard deviation. Within each row, values followed by the same letter do not differ significantly at  $p > 0.05$ .

Amplification and PacBio sequencing of fungal ITS2 rDNA from 90 samples of each rootlet, soil and needles resulted in 72,505 sequence reads. Quality filtering showed that 23,394 (32.3%) reads were of high-quality and were retained, while 49,111 (67.3%) low-quality reads were excluded. Clustering of high-quality reads showed the presence of 978 non-singleton taxa and 1,464 singletons, which were excluded. Rarefaction analysis showed that species accumulation curves have either reached (needles) or were approaching the asymptote (rootlets and soil), showing that the sequencing method used was sufficient for the detection of all or nearly all fungal community in each particular substrate (Figure 3).



**Figure 3.** Rarefaction curves showing the relationship between the cumulative number of fungal taxa and the number of ITS2 rDNA sequences from needles, rootlets, and soil from the forest stands of *Pinus peuce*

Taxonomic classification showed that among all taxa 825 (84.4%) were fungal (Supplementary Table S1) and 153 (15.6%) were non-fungal, which were excluded. The detected fungi were 52.5% Basidiomycota, 43.9% Ascomycota and 3.6% Mucoromycotina. Identification at least to genus level was successful for 469 (56.6%) fungal taxa (Supplementary Table 1), representing 67.9% of all high-quality fungal sequences. The number of fungal taxa detected at each site and substrate (the soil, rootlets or needles) is shown in Table 3.

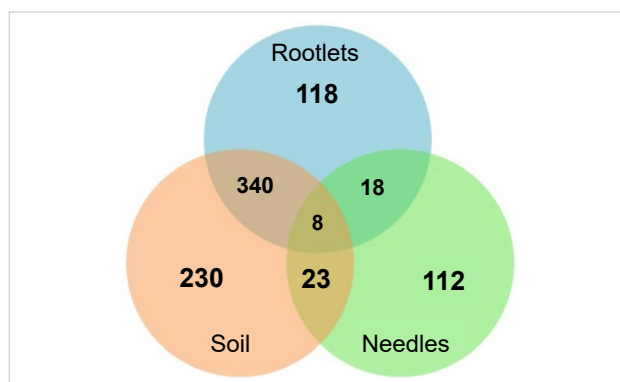
In rootlets, the richness of fungal taxa was significantly higher at the Zeletin site than at the Visitor site ( $p < 0.05$ ), but in this respect, both sites did not differ significantly from the Bogičevica site ( $p > 0.05$ ) (Table 3). In the soil, the richness of fungal taxa was similar between the Zeletin and Visitor sites ( $p > 0.05$ ) but differed significantly from those at the Bogičevica site ( $p < 0.05$ ) (Table 3).

**Table 3.** Generated high-quality ITS2 rDNA fungal sequences and detected diversity of fungal taxa at different sampling sites of *Pinus peuce*

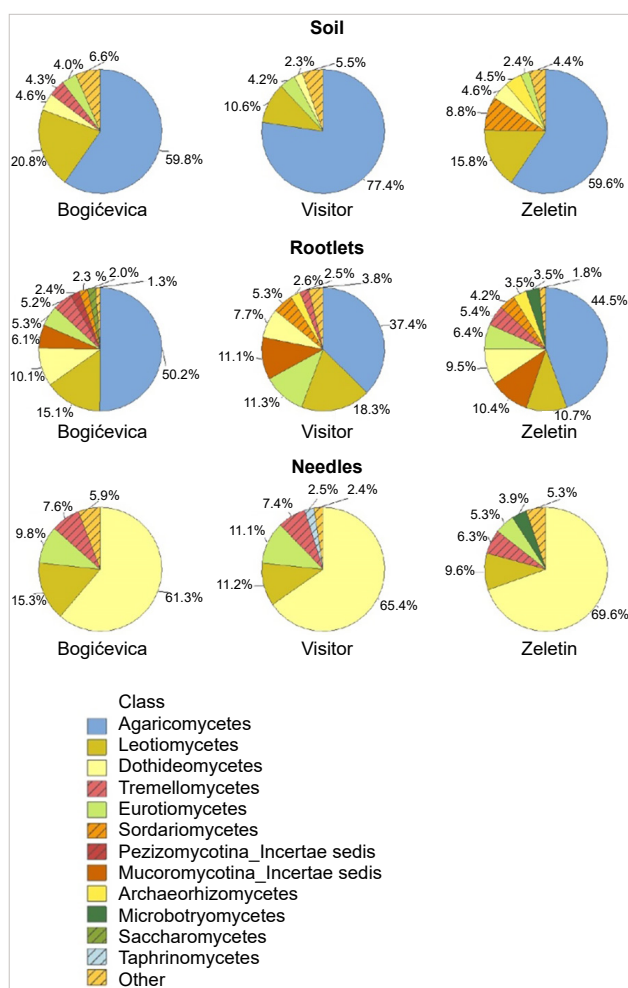
Study site	Substrate	No. of fungal sequences	No. of fungal taxa	Shannon diversity index
Bogičevica	Rootlets	3,060	228 ab	4.0
	Soil	1,850	227 a	3.5
	Needles	1,219	119 a	4.1
All Bogičevica		6,129	448	
Visitor	Rootlets	3,424	202 a	3.1
	Soil	1,960	293 b	4.8
	Needles	837	79 b	3.3
All Visitor		6,221	441	
Zeletin	Rootlets	2,331	212 b	4.1
	Soil	2,219	311 b	4.8
	Needles	457	76 c	3.4
All Zeletin		5,007	435	
All sites		17,357	825	

Note: Within the column "No. of fungal taxa", values followed by the same letter in chi-square test (compared among samples of the same substrate) do not differ significantly at  $p > 0.05$ .

In needles, the richness of fungal taxa was significantly higher at the Zeletin site compared to the Visitor site ( $p < 0.05$ ), and both showed a significantly higher richness of fungal taxa than at the Bogičevica site ( $p < 0.05$ ) (Table 3). The number of unique fungal taxa differed among different substrates (roots, soil or needles) as shown in Figure 4. When all sites were taken together, there were 118 unique fungal taxa in the rootlets, 230 in the soil and 112 in the needles (Figure 4). There were 340 fungal taxa that were shared between the rootlet and soil samples, but only 18 taxa were shared between the rootlet and needle samples, and 23 between the soil and needle samples. Overall, only 8 fungal taxa were common to all substrates (rootlets, soil and needles) (Figure 4).



**Figure 4.** A Venn diagram showing the diversity of unique fungal taxa found in rootlets, soil and needles of *Pinus peuce*, and the number of fungal taxa shared between different substrates. Samples from different sites are combined.



**Figure 5.** Relative abundance of fungal classes in the soil, rootlets and needles at the Bogičevica, Visitor and Zeletin sampling sites of *Pinus peuce* in Montenegro. "Other" represent fungal classes with a relative abundance of less than 2%.

Within each substrate (soil, rootlets or needles), the composition of fungal classes was similar among different sites (Figure 5). Consequently, at different proportions Agaricomycetes (37.4%–50.2% and 59.8%–77.4%, respectively) dominated fungal communities in the soil and rootlets, while Dothideomycetes (61.3%–69.6%) dominated in the needles (Figure 5).

The most common fungi in rootlets were *Rhizopogon mohelensis* (11.3%), *Suillus americanus* (8.7%), *Rhizopogon fallax* (7.1%), *Suillus graulatus* (6.8%), *Thelephora*

*terrestris* (3.8%), *Phialocephala fortinii* (3.3%), *Suillus luteus* (2.9%) and *Meliniomyces bicolor* (2.3%) (Table 4). In the soil, these were *Phlebiopsis gigantea* (5.2%), *Tylospora asterophora* (2.9%), *Sollicoccozyma terricola* (2.8%), *Hygrocybe intermedia* (2.4%) and *Russula vesca* (2.3%) (Table 5). In needles, these were *Dothideomycetes* sp. 3360\_7 (17.6%), *Dothideomycetes* sp. 3360\_10 (10.7%), *Leotiomyces* sp. 3360\_16 (6.5%), *Sydowia polyspora* (5.9%), *Coleosporium larxicola* (5.1%), *Dothideomycetes* sp. 3360\_34 (4.6%) and *Lophodermium pinastri* (4.4%) (Table 6).

**Table 4.** Relative abundance (%) of the 20 most common fungal taxa associated with the rootlets of *Pinus peuce* in Montenegro

Fungal taxon	P*	GenBank reference	SeqL, bp	Sequence identity, %	Study sites			All
					Bo	Vi	Ze	
<i>Rhizopogon mohelensis</i>	B	KX610702	341	339/341 (99)	11.8	17.3	1.8	11.3
<i>Suillus americanus</i>	B	KM882918	330	328/330 (99)	2.7	19.9	-	8.7
<i>Rhizopogon fallax</i>	B	KC152199	345	344/345 (99)	6.7	7.2	7.4	7.1
<i>Suillus granulatus</i>	B	KX230633	331	331/331 (100)	0.0	17.5	-	6.8
<i>Thelephora terrestris</i>	B	KT447173	313	313/313 (100)	10.3	0.5	-	3.8
<i>Phialocephala fortinii</i>	A	LC131028	236	236/238 (99)	5.8	0.9	3.3	3.3
<i>Suillus luteus</i>	B	KX230614	331	331/331 (100)	1.7	5.9	-	2.9
<i>Meliniomyces bicolor</i>	A	HQ157926	238	238/238 (100)	0.8	0.6	6.9	2.3
<i>Mycena leptcephala</i>	B	HQ604773	310	310/311 (99)	2.0	0.6	3.4	1.9
<i>Tomentella stuposus</i>	B	KP753365	314	313/314 (99)	-	-	6.6	1.7
<i>Agaricomycetes</i> sp. 3360_15	B	JX042709	277	241/284 (85)	1.4	-	4.1	1.6
<i>Suillus variegatus</i>	B	MG597425	329	329/329 (100)	-	-	5.6	1.5
<i>Archaeorhizomyces borealis</i>	A	NR_126144	215	215/215 (100)	0.8	-	4.5	1.5
<i>Tylospora asterophora</i>	B	AF052558	288	288/288 (100)	0.4	-	5.0	1.4
<i>Trechispora</i> sp. 3360_33	B	JX392812	320	318/320 (99)	0.5	2.9	-	1.3
<i>Agaricomycetes</i> sp. 3360_18	B	KJ595006	338	318/341 (93)	1.3	1.1	1.5	1.3
<i>Tremellomyces</i> sp. 3360_44	B	KR265945	253	247/253 (98)	3.4	-	-	1.2
<i>Gyoerffyella</i> sp. 3360_31	A	KU516480	242	242/242 (100)	0.5	1.7	0.6	1.0
<i>Inocybe rufoalba</i>	B	KX602273	274	274/274 (100)	2.6	-	-	0.9
<i>Agaricomycetes</i> sp. 3360_35	B	JF519610	305	305/305 (100)	0.0	0.3	2.8	0.9
All of 20 taxa					52.7	76.4	53.5	62.4

Note: P – Phylum, SeqL – Sequence Length, Bo – Bogićevica, Vi – Visitor, Ze – Zeletin; \* A – Ascomycota, B – Basidiomycota.

**Table 5.** Relative abundance (%) of the 20 most common fungal taxa associated with the soil of *Pinus peuce* in Montenegro

Fungal taxon	P*	GenBank reference	SeqL, bp	Sequence identity, %	Study sites			All
					Bo	Vi	Ze	
<i>Phlebiopsis gigantea</i>	B	KX426965	302	302/302 (100)	22.9	-	-	5.2
<i>Tylospora asterophora</i>	B	AF052558	288	288/288 (100)	5.3	-	4.1	2.9
<i>Sollicoccozyma terricola</i>	B	KY558367	329	329/329 (100)	3.1	0.6	4.5	2.8
<i>Hygrocybe ingrata</i>	B	KF291225	269	268/270 (99)	4.1	4.5	-	2.6
<i>Hygrocybe intermedia</i>	B	EU784321	344	294/295 (99)	-	6.7	-	2.4
<i>Russula vesca</i>	B	DQ422018	321	321/321 (100)	-	-	5.5	2.3
<i>Inocybe whitei</i>	B	JF908146	286	286/287 (99)	0.1	-	4.7	2.0
<i>Mortierella humilis</i>	M	MG052956	333	333/333 (100)	0.9	3.1	1.2	1.8
<i>Dothideomycetes</i> sp. 3360_46	A	FJ554252	241	241/241 (100)	3.9	0.3	1.8	1.7
<i>Archaeorhizomyces</i> sp. 3360_50	A	KR266833	211	210/211 (99)	-	1.3	3.0	1.7
<i>Clavulina coralloides</i>	B	EU862223	333	332/333 (99)	1.0	-	3.5	1.7
<i>Mucoromycotina</i> sp. 3360_37	M	KR265910	297	290/298 (97)	2.1	2.6	0.4	1.6
<i>Hygrocybe singeri</i>	B	KC581351	318	313/319 (98)	0.1	3.9	0.1	1.5
<i>Microbotryomycetes</i> sp. 3360_57	B	KC818329	303	303/303 (100)	0.3	1.2	2.0	1.3
<i>Pseudotrachelium metapodium</i>	B	KJ417308	308	307/309 (99)	-	3.6	-	1.3
<i>Leotiomyces</i> sp. 3360_63	A	HQ021989	242	242/242 (100)	0.6	2.2	0.8	1.3
<i>Agaricomycetes</i> sp. 3360_49	B	KM402954	292	292/293 (99)	-	-	2.7	1.1
<i>Leohumicola minima</i>	A	HQ691252	241	241/241 (100)	0.2	2.4	0.0	0.9
<i>Laccaria laccata</i>	B	KM067834	300	300/300 (100)	-	-	2.3	0.9
<i>Cenococcum geophilum</i>	A	HM189723	242	242/242 (100)	0.1	-	2.1	0.9
All of 20 taxa					44.7	32.4	38.7	37.9

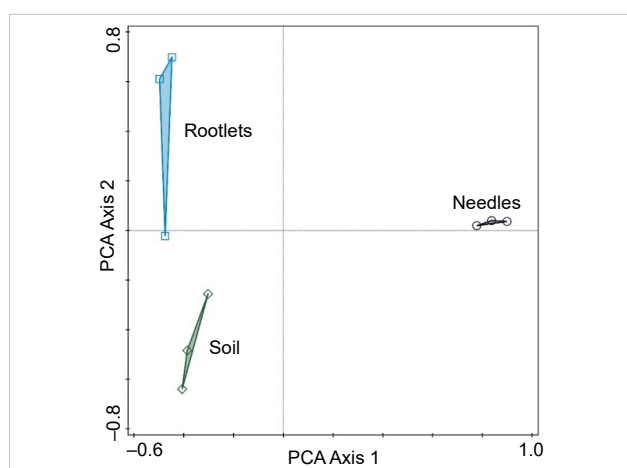
Note: P – Phylum, SeqL – Sequence Length, Bo – Bogićevica, Vi – Visitor, Ze – Zeletin; \* A – Ascomycota, B – Basidiomycota.

**Table 6.** Relative abundance (%) of the 20 most common fungal taxa associated with the needles of *Pinus peuce* in Montenegro

Fungal taxon	P*	GenBank reference	SeqL, bp	Sequence identity, %	Study sites			All
					Bo	Vi	Ze	
<i>Dothideomycetes</i> sp. 3360_7	A	KP897336	257	251/257 (98)	20.2	10.2	20.8	17.6
<i>Dothideomycetes</i> sp. 3360_10	A	NR_145090	238	216/246 (88)	11.5	14.2	1.3	10.7
<i>Leotiomyces</i> sp. 3360_16	A	KR267039	242	242/243 (99)	4.2	12.1	5.3	6.5
<i>Sydowia polyspora</i>	A	KU516591	256	256/256 (100)	5.8	6.6	5.0	5.9
<i>Celosporium laricicola</i>	A	FJ997287	255	249/253 (98)	4.6	8.1	1.5	5.1
<i>Dothideomycetes</i> sp. 3360_34	A	KP891395	241	239/241 (99)	3.9	6.8	3.1	4.6
<i>Lophodermium pinastri</i>	A	HM060657	239	239/239 (100)	6.8	0.1	2.2	4.4
<i>Dothideomycetes</i> sp. 3360_36	A	KP897893	250	230/253 (91)	2.2	1.6	11.4	3.3
<i>Leotiomyces</i> sp. 3360_51	A	FR846479	237	237/237 (100)	3.2	0.5	1.8	2.3
<i>Helotiales</i> sp. 3360_53	A	HQ845750	242	242/242 (100)	2.2	3.2	0.7	2.2
<i>Leotiomyces</i> sp. 3360_77	A	JF449635	241	241/241 (100)	1.8	2.5	1.3	1.9
<i>Dothideomycetes</i> sp. 3360_96	A	FR682183	242	240/242 (99)	0.4	2.5	7.0	1.9
<i>Cryptococcus</i> sp. 3360_109	B	KM216339	317	298/299 (99)	1.5	1.2	1.3	1.4
<i>Cladosporium macrocarpum</i>	A	MF077231	242	242/243 (99)	1.5	0.8	2.0	1.4
<i>Sarcinomyces crustaceus</i>	A	NR_121503	267	265/267 (99)	1.7	0.8	-	1.2
<i>Phaffia</i> sp. 3360_92	B	HF558647	351	309/355 (87)	1.1	1.9	0.4	1.2
<i>Eurotiomyces</i> sp. 3360_126	A	FR682181	248	248/248 (100)	1.2	0.6	0.7	1.0
<i>Lachnellula calyciformis</i>	A	KC464636	239	239/239 (100)	1.6	-	-	1.0
<i>Dothideomycetes</i> sp. 3360_115	A	AM901716	239	221/242 (91)	0.9	1.7	-	1.0
<i>Epithamnolia xanthoriae</i>	A	KY814539	237	233/238 (98)	1.3	0.6	0.2	1.0
All of 20 taxa					77.6	76.0	65.9	75.5

Note: P – Phylum, SeqL – Sequence Length, Bo – Bogičevica, Vi – Visitor, Ze – Zeletin; \* A – Ascomycota, B – Basidiomycota.

Principal coordinates analysis (PCA) of fungal communities explained 35.5% variation on axis 1 and 17.4% on axis 2. PCA showed that fungal communities from the same substrate (samples representing different sites) clustered together (Figure 6). PCA also showed that fungal communities in different substrates (needles, rootlets and soil) were separated from each other (Figure 6), showing that fungal communities in each of these substrates were largely different. In needles, the Shannon diversity index was between 3.3 and 3.5, in rootlets between 3.1 and 4.1, and in the soil between 4.1 and 4.8 (Table 3). The Mann-Whitney test showed that the Shannon diversity in-



**Figure 6.** Ordination diagram based on principal coordinates analysis (PCA) of fungal communities from needles, rootlets and soils of *Pinus peuce* in Montenegro

Each point in the diagram represents a single sample. Samples of the same substrate (needles, rootlets or soil) are enveloped.

dex among different substrates did not differ significantly ( $p > 0.05$ ). The Sørensen similarity index of fungal communities was the following: needles vs. rootlets – 0.06, needles vs. soil – 0.06, and rootlets vs. soil – 0.6.

## Discussion

Five-needle pines, which belong to the subgenus *Strobus* (section *Quinquefoliae*), are unique in their ecology and distribution. There are 24 *Pinus* spp. in this subgenus, which are native to Europe, North and Central America and Asia (Gernandt et al. 2005). Most of these species are characterized by a narrow distribution and high-elevation habitats, i.e. growing under harsh environmental conditions. Information about fungal diversity associated with those *Pinus* species is still limited, while the available knowledge is mainly on the above ground sporocarps or on ECM fungi. For example, ECM communities of *P. cembra* were described from the European Alps (Bacher et al. 2010, Reiner et al. 2015), of *P. albicaulis* (Mohatt et al. 2008, Cripps and Antibus 2011, Jenkins et al. 2018), *P. flexilis* (Cripps and Antibus 2010) and *P. monticola* from North America, of *P. walchiniana* from the Himalayas (Sagar and Lakhnupal 2005, Tyub et al. 2018) and of *P. amamiana* from Japan (Murata et al. 2017). These studies emphasise the importance of ECM fungi for natural regeneration and survival of those tree species, all of which have limited distribution and represent important tree species in montane ecosystems. Apart from ECM fungi, the data on fungi associated with the soil (Merges et al. 2018) and needles of five-needle pines is scarce but could provide important knowledge on potential pathogens and endophytic fungi.



The survey of fungal fruitbodies in native forests of North Macedonia and Bulgaria have showed that *P. peuce* is associated with nearly 400 fungal species (Kalucka et al. 2013), while only six fungal species have been recorded in Montenegro (Perić and Perić 2004, Kasom and Karadelev 2012). *Heterobasidion annosum* and *Phaeolus schweinitzii* were reported as decay fungi of mature *P. peuce* trees (Papazov 1969, Rossnev 1985, Tomanić et al. 1998). *Cenangium feruginosum*, *Cenangium abietis* and *Ungulina marginata* were frequently recorded on weakened trees (Papazov 1969, Tomanić et al. 1998). Previous studies on needle pathogens that were carried out in native forests have revealed the presence of a potentially invasive species *Dothistroma septosporum* in Montenegro (Lazarević et al. 2017) and *Cytospora pinastri* in Bulgaria (Georgieva and Marković 2018). *Lophodermium* fungi were shown to be present in forests and in forest plantations (Tomanić et al. 1998, Georgieva and Marković 2018).

The results of the present study have expanded the available knowledge on endemic *P. peuce*, demonstrating that needles, rootlets and the rhizosphere soil are inhabited by taxa-rich communities of fungi (Table 3). The detected fungal communities were largely specific to each particular substrate (Figures 4–6), showing their adaptation and substrate preferences. In support, the qualitative Sørensen similarity index was very low when compared between the aboveground (needles) and belowground (rootlets or soil) substrates, repeatedly demonstrating the potential importance and functional preferences of associated fungi. Interestingly, the site conditions had only a limited effect on associated fungal communities as in different sites these were similar (Figures 5–6).

Among the principal fungi identified in the soil and rootlets, there were taxa from genera *Suillus* and *Rhizopogon*, which are closely related and almost exclusively restricted to Pinaceae (Bruns et al. 2002). Moreover, a limited number of *Suillus* fungi appear to be specific to five-needle pines (Klofac 2013), and this symbiosis can be essential for tree survival under harsh environmental conditions. For example, *Suillus* fungi could be regarded as the most important and widespread symbionts of *P. cembra* in the Alps (Reiner et al. 2015) and of *P. albicaulis* in North America (Mohatt et al. 2008). *Suillus americanus* (*S. sibiricus*) readily forms ECM symbiosis with five-needle pines (Liao et al. 2016), which are found in different regions worldwide (Mohatt et al. 2008, Reiner et al. 2015). It is a protected fungus in many European countries, including North Macedonia (Karadelev 1998), Bulgaria (Boev 2011) and Montenegro (Kasom and Karadelev 2012), where it was recorded in native forest stands of *P. peuce*. In agreement, the results of the present study provided evidence that *S. americanus* is a common and an important symbiont of *P. peuce* as it was detected in both rootlets and soil (Table 4, Supplementary Table 1). Surveys on the aboveground sporocarp production and analyses of fine roots have shown that *Suillus granulatus* is the dominant fungus

in *P. heldreichii* forests in Montenegro (Lazarević et al. 2011, Lazarević and Menkis 2018). In the present study, *S. granulatus* occurred only at the Visitor site, where *P. heldreichii* forest is in close proximity (see above). Liao et al. (2016) showed that *S. granulatus* can also readily form ECMs with pines from the subgenus *Strobus*. *Suillus luteus* and *S. variegatus* were also detected in rootlet and soil samples (Table 4, Supplementary Table 1), showing that *P. peuce* is associated with different suilloid fungi, which can colonise tree roots in high-elevation habitats. Fungi from the genus *Rhizopogon* are also primarily associated with Pinaceae but are not strictly host specific (Bruns et al. 2002) and are also known to form ECM symbioses with trees in high-elevation coniferous forests (Kjøller and Bruns 2003, Mohatt et al. 2008, Lazarević and Menkis 2018). Contrary to *Suillus* spp., *Rhizopogon* species produce hypogeous sporocarps and their spores are mainly dispersed by animals (Grubisha et al. 2007, Mohatt et al. 2008). This makes the gene flow of *Rhizopogon* species more restricted (Grubisha et al. 2007), leading to genetic differentiation among isolated populations (Grubisha et al. 2007, Murata et al. 2017) and eventually to the evolution of different *Rhizopogon* species. *Rhizopogon mohelensis* was one of the most detected fungi in this study, particularly in pure *P. peuce* forests, but less abundantly found in mixed forests. By contrast, *R. fallax* was commonly detected in all study sites (Table 4). *Rhizopogon fallax* belongs to *R. salebrosus* group (Dowie et al. 2017), which is associated with both native *P. cembra* and introduced *P. strobus*, as five-needle pines in Europe (Kohout et al. 2011, Merges et al. 2018). *R. mohelensis* was reported from many countries in Europe (Holec et al. 2013). It belongs to *R. roseolus* group and sometimes can be misidentified as *R. rubescens*.

It appears that both *Suillus* and *Rhizopogon* possess specific ecological adaptations important for the establishment of *Pinus* spp. on marginal habitats and after the forest disturbance (Kjøller and Bruns 2003, Mohatt et al. 2008). Such host specialists may often represent the dominant ECM species in high-elevation habitats characterised by extreme conditions (Bruns et al. 2002, Antibus et al. 2010, Merges et al. 2018). Certain suilloid fungi can be of special importance to five-needle pines due to host specialisation, high efficiency of the nutrient and water uptake and transfer between the symbiosis partners, and an exclusion of mycoheterotrophy (Jenkins et al. 2018). The common occurrence of suilloid fungi was particularly notable at the Visitor site containing newly regenerated *P. peuce* trees, but their abundance was lower in old-growth stands (Table 1 and 3).

Among other fungi commonly detected in rootlets, there were *Thelephora terrestris* and *Phialocephala fortinii* (Table 4). *Thelephora terrestris* is ECM fungus of medium-distance smooth exploration type with rhizomorphs (Veselá et al. 2021), which allows efficient transportation of nutrients and water over long distances. This property appears to be especially suitable for undisturbed, but very

stony habitats with high soil heterogeneity (Reiner et al. 2015). *Phialocephala fortinii* belongs to a complex of dark septate endophytes, which forms non-specific associations with many plant hosts (Tedersoo et al. 2008). Interestingly, *P. fortinii* was also commonly detected in rootlets of old-growth endemic *P. heldreichii* in high-elevation habitats and under similar ecological conditions. (Lazarević and Menkis 2018).

*Tomentella stuposa* and *Tylospora asterophora* were the other two ECM fungi found in common association with *P. peuce* rootlets (Table 4). *Tomentella* are among dominant species in older coniferous forests worldwide (Lilleskov and Bruns 2005, Mrak et al. 2020). *Tylospora asterophora* is known as one of the most consistent and abundant ECM fungus associated with *P. abies* (Eberhardt et al. 1999). *Meliniomyces bicolor* (*Piceirhiza bicolorata*) colonise roots of *Pinus*, *Picea* and *Betula* trees, but also to form ericoid mycorrhiza with shrubs from the Ericaceae family (Grelet et al. 2009). A high presence of *M. bicolor* in the present study could be influenced by the occurrence of *Vaccinium myrtillus* in the ground vegetation. According to Horton et al. (1999), the sharing of ECM fungi between coniferous trees and plants from Ericaceae may play a major role in plant community dynamics. Ericaceous plants were shown to play an important role in the formation of ECM communities associated with *P. strobus* (Kohout et al. 2011).

Although a number of fungi were shared between the rootlet and soil samples as indicated by a high value of the Sørensen similarity index, soil samples were characterised by a higher abundance of saprotrophic fungi as compared to rootlet samples (dominated by ECM fungi) (Table 4 and 5), which led to the differentiation of fungal communities in these two substrates (Figure 5). Among the dominant fungi in the soil, there was *P. gigantea*, which is known as a common saprophytic fungus that causes white rot in conifer logs and stumps (Copenhaver et al. 2014), thereby playing an important role in the decomposition of conifer wood debris. It was common at the Bogićevica site, likely due to the vast availability of dead wood, which was absent at the other two sites. *Phlebiopsis gigantea* was shown to have the ability to colonise soil and interact with tree roots (Vasiliauskas et al. 2007), but in soil it is unlikely to interact with *Heterobasidion* root-rot fungi, which were also found in the present study, as these are not able to freely grow in soil (Gaitnieks et al. 2016). *Solicoccozyma terricola* was another commonly detected saprotrophic fungus known from the soils of temperate forests (Mašínová et al. 2017). *Hygrocybe intermedia* and *Hygrocybe ingrata* were also among dominant fungi, which are known to be common in montane grasslands in Montenegro. These fungi, while being red-listed, are often associated with habitats of *P. heldreichii* (Perić and Perić 2004), which are nutrient-poor, but support high diversity of fungi (Lazarević and Menkis 2018). Interestingly, recently described ubiquitous soil fungi of the genus *Archaeorhizomyces* (Rosling et al.

2011) were also detected (Table 5). Although functional properties, reproduction structures and dispersal strategy of these fungi are largely unknown, the current observation expands available knowledge on the host tree species and geographical distribution.

A number of ECM fungi were also commonly detected in the soil, including *Tylospora asterophora*, *Russula vesca*, *Inocybe whitei*, *Laccaria laccata* and *Cenococcum geophilum* (Table 5), showing that these may be important symbionts of forest trees grown in high-elevation habitats. However, as these ECM fungi were mainly detected at the Zeletin site (Table 5), the possibility should not be excluded that their occurrence was also affected by the other tree species (*A. alba* or *F. sylvatica*) present there.

Living needles are known to be associated with diverse trophic groups of fungi, including endophytes, epiphytes and pathogens. Many of these can be functionally important and metabolically active taxa, which respond to changes in the environment (Nguyen et al. 2016). They appear to be able to colonise different tree species, but factors driving their distribution remains largely unclear (Terhonen et al. 2019). Among the dominant fungi associated with the needles of *P. peuce*, there were *Dothideomyces* sp. 3360\_7, *Dothideomyces* sp. 3360\_10 and *Leotiomyces* sp. 3360\_16 (Table 6), which could not be identified to the species or genus level, thereby not only posing a challenge to fungal taxonomists, but also limiting the identification of their ecology and functional roles. Further, *Sydowia polyspora* was detected in *P. peuce* needles (Table 6), which is the fungus with a wide geographical distribution and common occurrence in Europe (Botella and Diez 2010). The pathogenic behaviour of *S. polyspora* to young conifers (genera *Thuja*, *Abies*, *Tsuga*, *Larix*, *Picea* and *Pinus*) was previously reported (Talgo et al. 2010). Besides, it has been recently reported as one of the most abundant needle pathogens in high-altitude *P. heldreichii* forests in Montenegro (Lazarević and Menkis 2020), showing that it is not restricted by harsh environmental conditions prevailing in these habitats. *Sydowia* symptoms include needle discoloration, necrosis and shoot dieback. However, the fungus is favoured by a warm climate, especially if the host is stressed by drought or insect attack (Muñoz-Adalia et al. 2017). *Celosporium laricicola* was another commonly detected fungus (Table 6), which was recently described from needles of *Larix lyallii* in Canada (Tsuneda et al. 2010) and needles of *P. abies* in Sweden (Nguyen et al. 2016). Fungi from the genus *Celosporium* are commonly recovered from alpine habitats and may be biotrophic or necrotrophic (Brown et al. 2015). *Lophodermium pinastri* was also common in needles of *P. peuce* (Table 6). It has global distribution and is commonly associated with pines (Reignoux et al. 2014, Millberg et al. 2015). *L. pinastri* colonises healthy needles latently as an endophyte, initiates active growth at the beginning of needle senescence and sporulates after the needle fall. It is a dominant coloniser of dying needles and a saprotroph

contributing to their decomposition (Reignoux et al. 2014). Besides, *L. pinastri* was one of the most detected fungi on *P. heldreichii* needles in Montenegro (Lazarević and Menkis 2020) and frequently reported from *P. nigra* and *P. sylvestris* growing in forests, forest nurseries and plantations in the Balkan region (Karadžić and Milijašević 2008, Dobrev et al. 2016).

In summary, *P. peuce* in high-elevation mountain habitats harbour diverse communities of fungi, composition of which in different geographical locations appeared to be very similar.

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## Supplements

**Table S1.** Relative abundance (%) of fungal taxa associated with the rootlets, soil and needles of *Pinus peuce* in Montenegro

Taxon	P *	GenBank reference	SeqL, bp	Compared, bp	Similarity, %	Bogičevića				Visitor				Zeletin				Total	
						Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All		
<i>Rhizopogon mohelnensis</i>	B	KX610702	341	339/341	99	11.83	0.08	-	5.92	17.26	0.46	-	9.64	1.84	0.27	-	0.98	5.83	
<i>Suillus sibiricus</i>	B	KM882918	330	328/330	99	2.75	0.08	-	1.39	19.86	2.30	-	11.65	-	-	-	-	4.67	
<i>Rhizopogon fallax</i>	B	KC152199	345	344/345	99	6.67	0.41	-	3.41	7.21	0.10	-	4.00	7.42	0.32	-	3.59	3.68	
<i>Suillus granulatus</i>	B	KX230633	331	331/331	100	0.03	0.08	-	0.03	17.52	0.31	-	9.74	-	-	-	-	3.50	
<i>Dothideomyces</i> sp. 3360_7	A	KP897336	257	251/257	98	-	-20.22	6.10	-	-10.16	1.37	-	-20.79	1.90	3.19	-	-	-	
<i>Tylospora asterophora</i>	B	AF052558	288	288/288	100	0.36	5.25	-	1.22	-	-	-	4.98	4.10	-	-	4.13	1.62	
<i>Thelephora terrestris</i>	B	KT447173	313	313/313	100	10.29	0.41	-	5.22	0.47	0.31	-	0.35	-	-	-	-	1.97	
<i>Russula vesca</i>	B	DQ422018	321	321/321	100	-	-	-	-	-	-	-	-	2.15	5.50	-	3.44	0.99	
<i>Dothideomyces</i> sp. 3360_10	A	NR_145090	238	216/246	88	-	-11.46	3.46	-	0.05	14.22	1.93	-	-	1.31	0.12	1.95		
<i>Phialocephala fortinii</i>	A	LC131028	236	236/238	99	5.82	0.33	-	2.97	0.93	0.05	-	0.53	3.35	0.05	-	1.58	1.69	
<i>Phlebiopsis gigantea</i>	B	KX426965	302	302/302	100	-	-22.89	-	4.55	-	-	-	-	-	-	-	-	1.61	
<i>Meliniomyces bicolor</i>	A	HQ157926	238	238/238	100	0.75	0.25	-	0.42	0.55	0.05	-	0.32	6.86	1.80	-	3.99	1.42	
<i>Suillus luteus</i>	B	KX230614	331	331/331	100	1.73	0.08	-	0.88	5.90	-	-	3.25	-	-	-	-	1.47	
<i>Leotiomycetes</i> sp. 3360_16	A	KR267039	242	242/243	99	-	-	4.22	1.27	-	-	-	12.07	1.62	-	-	5.25	0.48	1.17
<i>Cenococcum geophilum</i>	A	HM189723	242	242/242	100	0.10	0.08	-	0.07	-	-	-	2.02	2.07	-	-	1.86	0.56	
<i>Sydowia polyspora</i>	A	KU516591	256	256/256	100	-	0.08	5.78	1.76	-	-	-	6.57	0.88	-	-	5.03	0.46	1.07
<i>Mycena leptoccephala</i>	B	HQ604773	310	310/311	99	2.03	0.66	-	1.14	0.64	0.20	-	0.42	3.43	0.18	-	1.68	1.04	
<i>Solicoccozyma terricola</i>	B	KY558367	329	329/329	100	0.46	3.12	-	0.85	0.18	0.61	-	0.29	0.21	4.46	-	2.08	1.00	
<i>Celosporium larixicola</i>	A	FJ997287	255	249/253	98	-	-	4.65	1.40	-	-	-	8.12	1.09	-	-	1.53	0.14	0.93
<i>Tomentella bresadolae</i>	B	KP753365	314	313/314	99	-	-	-	-	-	-	-	-	6.61	0.18	-	3.16	0.91	
<i>Agaricomycetes</i> sp. 3360_18	B	KJ595006	338	318/341	93	1.34	2.54	-	1.17	1.08	0.10	0.12	0.64	1.46	0.41	-	0.86	0.89	
<i>Hygrocybe intermedia</i>	B	EU784321	344	294/295	99	-	-	-	-	0.53	6.68	-	2.40	-	-	-	-	0.86	
<i>Dothideomyces</i> sp. 3360_34	A	KP891395	241	239/241	99	0.03	-	3.95	1.21	-	-	-	6.81	0.92	-	-	3.06	0.28	0.84
<i>Gyosphyella</i> sp. 3360_31	A	KU516480	242	242/242	100	0.49	0.33	-	0.31	1.66	0.10	-	0.95	0.56	0.68	-	0.56	0.61	
<i>Agaricomycetes</i> sp. 3360_15	A	JX042709	277	241/284	85	1.44	-	-	0.72	-	-	-	-	4.12	-	-	1.92	0.81	
<i>Neohygrocybe ingrata</i>	B	KF291225	269	268/270	99	0.03	4.10	-	0.83	-	4.54	-	1.43	-	-	-	-	0.81	
<i>Lophodermium pinastri</i>	A	HM060657	239	239/239	100	-	-	6.81	2.06	-	-	-	0.12	0.02	-	-	2.19	0.20	0.79
<i>Archaeorhizomyces borealis</i>	A	NR_126144	215	215/215	100	0.78	-	-	0.39	-	-	-	-	4.55	0.14	-	2.18	0.77	
<i>Suillus variegatus</i>	B	MG597425	329	329/329	100	-	-	-	-	-	0.05	-	0.02	5.62	0.09	-	2.66	0.77	

Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total	
						Root-lets	Soil	Nee-dles	All	Root-lets	Soil	Nee-dles	All	Root-lets	Soil	Nee-dles	All		
<i>Russula laurocerasi</i>	B	KF245533	321	321/321	100	-	-	-	-	-	-	-	-	0.73	1.71	-	1.10	0.32	
<i>Agaricomycetes</i> sp. 3360_28	B	HQ154222	294	294/294	100	-	0.16	-	0.03	-	-	-	-	-	1.72	0.36	-	0.96	0.29
<i>Inocybe whitei</i>	B	JF908146	286	286/287	99	-	0.08	-	0.02	-	-	-	-	-	0.51	4.73	-	2.34	0.68
<i>Trechispora</i> sp. 3360_33	B	JX392812	320	318/320	99	0.49	-	-	0.24	2.89	0.10	-	1.62	-	-	-	-	-	0.67
<i>Clavulina cristata</i>	B	EU862223	333	332/333	99	0.07	0.98	-	0.23	-	-	-	-	-	0.43	3.52	-	1.76	0.59
<i>Mortierella humilis</i>	M	MG052956	333	333/333	100	0.03	0.90	-	0.20	0.12	3.11	-	1.04	0.21	1.22	-	0.64	0.63	
<i>Dothideomycetes</i> sp. 3360_36	A	KP897893	250	230/253	91	-	-	2.16	0.65	-	-	1.55	0.21	-	-	11.38	1.04	0.60	
<i>Tremellomycetes</i> sp. 3360_44	B	KR265945	253	247/253	98	3.37	-	-	1.68	-	-	-	-	-	-	-	-	0.59	
<i>Dothideomycetes</i> sp. 3360_46	A	FJ554252	241	241/241	100	0.03	3.94	-	0.80	0.09	0.31	-	0.14	0.04	1.80	-	0.82	0.57	
<i>Hygrocybe singeri</i>	B	KC581351	318	313/319	98	-	0.08	-	0.02	0.50	3.93	-	1.51	-	0.09	-	0.04	0.56	
<i>Mucoromycotina</i> sp. 3360_37	M	KR265910	297	290/298	97	0.10	2.13	-	0.47	0.12	2.60	-	0.88	-	0.36	-	0.16	0.53	
<i>Archaeorhizomycetes</i> sp. 3360_50	A	KR266833	211	210/211	99	-	-	-	-	-	1.33	-	0.42	0.04	2.97	-	1.34	0.54	
<i>Inocybe rufoalba</i>	B	KX602273	274	274/274	100	2.65	0.66	-	1.45	-	-	-	-	-	0.05	-	0.02	0.52	
<i>Leohumicola minima</i>	A	HQ691252	241	241/241	100	0.46	0.25	-	0.28	0.67	2.40	-	1.13	-	0.05	-	0.02	0.51	
<i>Agaricomycetes</i> sp. 3360_47	B	HF565071	304	274/274	100	-	-	-	-	-	-	-	-	1.24	0.23	-	0.68	0.20	
<i>Microbotryomycetes</i> sp. 3360_57	B	KC818329	303	303/303	100	0.10	0.33	-	0.11	0.06	1.17	-	0.40	0.09	2.03	-	0.94	0.46	
<i>Agaricomycetes</i> sp. 3360_35	B	JF519610	305	305/305	100	0.03	-	-	0.02	0.29	-	-	0.16	2.83	0.09	-	1.36	0.46	
<i>Leotiomycetes</i> sp. 3360_63	A	HQ021989	242	242/242	100	0.07	0.57	-	0.15	0.20	2.24	-	0.82	0.04	0.81	-	0.38	0.46	
<i>Dothideomycetes</i> sp. 3360_72	A	KR266782	235	235/235	100	0.29	0.33	-	0.21	1.20	0.36	-	0.77	0.69	-	-	0.32	0.44	
<i>Pezizomycotina</i> sp. 3360_156	A	HM488471	239	238/239	99	0.78	0.90	-	0.57	0.09	0.05	-	0.06	1.03	0.32	-	0.62	0.40	
<i>Laccaria laccata</i>	B	KM067834	300	300/300	100	-	-	0.05	0.02	-	-	-	-	0.94	2.25	-	1.44	0.42	
<i>Leotiomycetes</i> sp. 3360_51	A	FR846479	237	237/237	100	-	0.25	3.19	1.01	-	-	0.48	0.06	-	0.05	1.75	0.18	0.43	
<i>Eurotiomycetes</i> sp. 3360_54	A	KF617857	257	257/257	100	0.56	0.82	-	0.44	0.38	1.48	-	0.68	0.13	0.09	-	0.10	0.43	
<i>Dothideomycetes</i> sp. 3360_55	A	KC876287	239	236/240	98	1.76	-	-	0.88	0.20	-	-	0.11	0.56	-	-	0.26	0.43	
<i>Agaricomycetes</i> sp. 3360_49	B	KM402954	292	292/293	99	-	-	-	-	-	-	-	-	0.56	2.66	-	1.44	0.41	
<i>Pseudotrachelomyces metapodium</i>	B	KJ417308	308	307/309	99	-	-	-	-	0.06	3.62	-	1.17	-	-	-	-	0.42	
<i>Helotiales</i> sp. 3360_53	A	HQ845750	242	242/242	100	-	-	2.16	0.65	-	-	3.23	0.43	-	-	0.66	0.06	0.40	
<i>Cladosporium macrocarpum</i>	A	MF077231	242	242/243	99	0.03	0.49	1.46	0.55	-	0.87	0.84	0.39	0.04	0.09	1.97	0.24	0.40	
<i>Eurotiomycetes</i> sp. 3360_45	A	FJ475710	258	244/258	95	0.92	-	-	0.46	0.96	0.36	-	0.64	-	-	-	-	0.39	
<i>Agaricomycetes</i> sp. 3360_79	B	FJ475683	320	317/320	99	2.19	-	-	1.09	-	-	-	-	-	-	-	-	0.39	
<i>Leotiomycetes</i> sp. 3360_77	A	JF449635	241	241/241	100	-	-	1.84	0.55	-	-	2.51	0.34	0.04	0.14	1.31	0.20	0.37	
<i>Rhizoscyphus ericae</i>	A	JQ711893	240	235/240	98	1.21	0.08	-	0.62	-	-	-	-	0.56	0.14	-	0.32	0.31	
<i>Chroogomphus helveticus</i>	B	GU187514	344	339/344	99	0.82	-	-	0.41	0.88	-	-	0.48	0.13	-	-	0.06	0.33	
<i>Dothideomycetes</i> sp. 3360_96	A	FR682183	242	240/242	99	-	-	0.43	0.13	-	-	2.51	0.34	-	-	7.00	0.64	0.35	
<i>Agaricomycetes</i> sp. 3360_65	B	HF674653	314	314/314	100	-	-	-	-	-	-	-	-	0.39	1.04	-	0.64	0.18	
<i>Colpoma</i> sp. 3360_87	A	KP276572	243	240/245	98	1.70	-	-	0.85	-	-	-	-	-	-	-	-	0.30	
<i>Lachnum cf. pygmaeum</i>	A	KY200575	237	237/238	99	0.36	0.57	-	0.29	0.85	-	-	0.47	0.17	0.18	-	0.16	0.32	
<i>Amphinema</i> sp. 3360_88	B	KP753294	288	288/288	100	1.67	0.25	-	0.88	-	-	-	-	-	-	-	-	0.31	
<i>Agaricomycetes</i> sp. 3360_61	B	HM488497	286	281/286	98	0.95	1.48	-	0.77	0.18	-	-	0.10	-	-	-	-	0.31	
<i>Agaricomycetes</i> sp. 3360_82	B	KX115677	312	310/312	99	1.54	0.25	-	0.82	0.06	-	-	0.03	-	-	-	-	0.30	
<i>Rhytismatales</i> sp. 3360_73	A	KC480046	240	240/241	99	1.70	-	-	0.85	-	-	-	-	-	-	-	-	0.30	
<i>Resinicium bicolor</i>	B	MF319079	292	291/292	99	-	-	-	-	-	-	-	-	1.97	0.23	-	1.02	0.29	
<i>Agaricomycetes</i> sp. 3360_60	B	HF675445	303	303/304	99	1.44	-	-	0.72	-	-	-	-	0.21	0.05	-	0.12	0.29	
<i>Lactarius deterrimus</i>	B	AF249286	358	358/358	100	1.63	-	-	0.82	-	-	-	-	-	-	-	-	0.29	
<i>Solicozozyma aerea</i>	B	KX359612	325	325/325	100	0.23	0.90	-	0.29	0.29	1.02	-	0.48	-	0.05	-	0.02	0.28	
<i>Leotiomycetes</i> sp. 3360_80	A	JN655656	242	241/242	99	0.56	0.08	-	0.29	0.06	0.15	-	0.08	0.64	0.41	-	0.48	0.27	
<i>Cryptococcus podzolicus</i>	B	KJ701018	255	255/255	100	0.13	1.07	-	0.28	0.03	0.41	-	0.14	0.09	0.77	-	0.38	0.26	
<i>Hydnum ellipsoidesporium</i>	B	KX388666	309	309/309	100	-	-	-	-	-	-	-	-	-	0.63	-	0.28	0.08	
<i>Mucoromycotina</i> sp. 3360_91	M	EU690137	344	333/336	99	0.03	0.08	-	0.03	-	0.10	-	0.03	-	1.89	-	0.84	0.27	
<i>Trechisporales</i> sp. 3360_105	B	KU973892	298	298/298	100	0.42	-	-	0.21	0.12	-	-	0.06	0.69	0.59	-	0.58	0.27	
<i>Russula integra</i>	B	KM085365	350	350/350	100	-	-	-	-	-	-	-	-	1.76	0.14	-	0.88	0.25	
<i>Cryptococcus</i> sp. 3360_109	B	KM216339	317	298/299	99	-	-	1.51	0.46	-	-	1.19	0.16	-	-	1.31	0.12	0.25	
<i>Pyronemataceae</i> sp. 3360_56	A	KR019795	256	256/256	100	0.52	0.41	-	0.34	0.64	-	-	0.35	-	-	-	-	0.25	
<i>Agaricomycetes</i> sp. 3360_62	B	HM234147	293	283/294	96	-	-	-	-	-	-	-	-	1.63	0.18	-	0.84	0.24	
<i>Sordariomycetes</i> sp. 3360_100	A	FJ553102	256	256/256	100	1.08	0.08	-	0.55	-	-	-	-	0.30	-	-	0.14	0.24	
<i>Eurotiomycetes</i> sp. 3360_159	A	HQ022171	259	253/259	98	0.49	0.16	-	0.28	0.53	0.20	-	0.35	0.04	0.05	-	0.04	0.24	
<i>Mortierella camargensis</i>	M	MF001324	346	346/346	100	0.20	0.08	-	0.11	-	0.36	-	0.11	0.04	1.08	-	0.50	0.22	
<i>Umbelopsis</i> sp. 3360_89	M	MF101398	293	293/293	100	-	-	-	-	0.03	0.31	-	0.11	0.04	1.40	-	0.64	0.22	
<i>Inocybe</i> sp. 3360_84	B	FN669215	301	300/302	99	-	-	-	-	-	-	-	-	0.60	1.08	-	0.76	0.22	
<i>Amphinema byssoides</i>	B	KT692928	271	271/272	99	1.01	0.08	-	0.52	-	-	-	-	0.26	-	-	0.12	0.22	
<i>Sarcinomyces crustaceus</i>	A	NR_121503	267	265/267	99	-	-	1.68	0.51	-	-	0.84	0.11	-	-	-	-	0.22	
<i>Phaffia</i> sp. 3360_92	B	HF558647	351	309/355	87	-	-	1.08	0.33	-	-	-	1.91	0.26	-	0.44	0.04	0.22	
<i>Inocybe nitidiuscula</i>	B	HQ604214	292	283/293	97	-	-	-	-	-	-	-	-	0.13	1.58	-	0.76	0.22	
<i>Amanita submembranacea</i>	B	KX882673	253	253/253	100	0.03	1.80	-	0.38	-	-	-	-	0.56	0.05	-	0.28	0.21	
<i>Dothideomycetes</i> sp. 3360_182	A	FJ554156	233	233/233	100	0.82	0.33	-	0.47	-	0.05	-	0.02	-	0.36	-	0.16	0.22	
<i>Paraphaeosphaeria sporulosa</i>	A	KX664338	245	245/245	100	-	-	-	-	-	1.79	-	0.56	-	-	-	-	0.20	
<i>Leotiomycetes</i> sp. 3360_83	A	KJ827884	238	237/238	99	-	-	-	-	-	1.79	-	0.56	-	-	-	-	0.20	
<i>Cuphophyllus colemannianus</i>	B	KM248879	307	301/310	97	-	-	-	-	-	1.79	-	0.56	-	-	-	-	0.20	
<i>Cadophora orchidicola</i>	A	LT821468	241	241/242	99	0.03	0.08	-	0.03	0.61	0.31	-	0.43	0.17	0.09	-	0.12	0.20	

Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total
						Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All	
<i>Leotiomyces</i> sp. 3360_114	A	KR267017	240	240/241	99	0.10	-	-	0.05	0.23	1.17	-	0.50	-	-	-	-	0.20
<i>Didymella macrostoma</i>	A	MH203391	249	249/249	100	-	0.08	0.65	0.21	0.03	0.36	0.84	0.24	-	0.14	0.66	0.12	0.20
<i>Tarzetia</i> sp. 3360_152	A	AJ969614	274	274/274	100	-	-	-	-	-	-	-	-	0.04	1.49	-	0.68	0.20
<i>Leotiomyces</i> sp. 3360_123	A	JQ346970	243	243/243	100	0.65	-	-	0.33	0.03	-	-	0.02	0.04	0.05	-	0.04	0.13
<i>Saccharomyces</i> sp. 3360_137	B	MF483204	322	320/325	98	0.13	1.89	-	0.44	-	0.26	-	0.08	-	0.05	-	0.02	0.19
<i>Russula puellaris</i>	B	HM189943	352	352/352	100	-	-	-	-	-	-	-	-	-	1.35	-	0.60	0.17
<i>Piloderma bicolor</i>	B	KP814514	283	283/283	100	1.05	-	-	0.52	-	-	-	-	-	-	-	-	0.18
<i>Eurotiomyces</i> sp. 3360_126	A	FR682181	248	248/248	100	-	-	1.24	0.38	-	-	0.60	0.08	-	-	0.66	0.06	0.18
<i>Inocybe subcarpta</i>	B	HQ604208	287	285/287	99	0.98	0.08	-	0.51	-	-	-	-	-	-	-	-	0.18
<i>Lachnellula calyciformis</i>	A	KC464636	239	239/239	100	-	-	1.62	0.49	-	-	-	-	-	-	-	-	0.17
<i>Dothideomyces</i> sp. 3360_115	A	AM901716	239	221/242	91	-	-	0.86	0.26	-	-	1.67	0.23	-	-	-	-	0.17
<i>Epithamnia xanthoriae</i>	A	KY814539	237	233/238	98	-	-	1.30	0.39	-	-	0.60	0.08	-	-	0.22	0.02	0.17
<i>Microbotryomyces</i> sp. 3360_104	B	HQ021788	320	315/322	98	-	-	-	-	-	-	-	-	0.04	1.26	-	0.58	0.17
<i>Pleotrichocladium opacum</i>	A	NR_155696	244	244/244	100	0.23	0.16	-	0.15	0.06	0.31	-	0.13	0.04	0.41	-	0.20	0.16
<i>Agaricomycetes</i> sp. 3360_128	B	JF519253	236	292/294	99	-	-	-	-	-	-	-	-	1.24	-	-	0.58	0.17
<i>Russula cyanoxantha</i>	B	KR364093	316	316/316	100	-	-	-	-	-	-	-	-	0.47	0.81	-	0.58	0.17
<i>Chroogomphus rutilus</i>	B	DQ367894	324	315/325	97	0.95	-	-	0.47	-	-	-	-	-	-	-	-	0.17
<i>Hygrocybe persistens</i> var. <i>konradii</i>	B	FM208893	333	299/306	98	-	0.08	-	0.02	0.18	1.07	-	0.43	-	-	-	-	0.16
<i>Tremellomyces</i> sp. 3360_93	B	KR265960	251	251/251	100	-	-	1.08	0.33	-	-	0.36	0.05	-	-	0.88	0.08	0.16
<i>Sordariomyces</i> sp. 3360_119	A	LN910167	309	213/216	99	-	-	-	-	-	1.28	-	0.40	-	0.09	-	0.04	0.16
<i>Leotiomyces</i> sp. 3360_146	A	FJ827178	238	238/239	99	0.10	-	-	0.05	0.06	-	-	0.03	0.21	0.09	-	0.14	0.07
<i>Leotiomyces</i> sp. 3360_162	A	FJ378856	237	237/238	99	0.59	0.25	-	0.34	-	0.05	-	0.02	0.13	0.09	-	0.10	0.16
<i>Hymenogaster pruinaus</i>	B	GU479240	306	292/294	99	-	-	-	-	-	-	-	-	0.30	0.90	-	0.54	0.16
<i>Heterocephalacria</i> sp. 3360_118	B	MG909556	309	300/309	97	-	-	0.59	0.18	-	-	1.31	0.18	-	-	0.88	0.08	0.15
<i>Agaricomycetes</i> sp. 3360_134	B	KX115896	305	303/305	99	0.07	0.49	-	0.13	0.18	0.46	-	0.24	0.09	0.05	-	0.06	0.15
<i>Tuber</i> sp. 3360_155	A	MF352808	290	290/290	100	-	-	-	-	-	-	-	-	1.03	0.09	-	0.52	0.15
<i>Eurotiomyces</i> sp. 3360_183	A	MF571440	250	236/253	93	-	-	-	-	-	1.33	-	0.42	-	-	-	-	0.15
<i>Clavulinopsis laeticolor</i>	B	EU118618	302	300/302	99	0.03	1.97	-	0.41	-	-	-	-	-	-	-	-	0.14
<i>Hygrocybe punicea</i>	B	KF291133	305	302/302	100	-	-	-	-	-	1.28	-	0.40	-	-	-	-	0.14
<i>Leotiomyces</i> sp. 3360_196	A	KU871238	242	242/242	100	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Leotiomyces</i> sp. 3360_207	A	HG513095	243	243/244	99	0.16	-	-	0.08	0.47	0.20	-	0.32	-	-	-	-	0.14
<i>Clavulina rugosa</i>	B	EU862224	338	338/338	100	-	-	-	-	-	-	-	-	0.43	0.59	-	0.46	0.13
<i>Hygrocybe</i> sp. 3360_129	B	KF291176	322	315/327	96	-	-	-	-	0.03	1.17	-	0.39	-	-	-	-	0.14
<i>Eurotiomyces</i> sp. 3360_143	A	HM230883	264	248/264	94	0.49	-	-	0.24	0.23	0.05	-	0.14	-	-	-	-	0.14
<i>Hyaloscypha leuconica</i> var. <i>bulbopilosa</i>	A	JN033451	236	235/236	99	0.03	-	-	0.02	0.09	-	-	0.05	0.34	0.09	-	0.20	0.08
<i>Oidiodendron chlamydosporicum</i>	A	MG597466	234	234/235	99	-	0.25	-	0.05	-	0.20	-	0.06	0.26	0.50	-	0.34	0.14
<i>Dothideomyces</i> sp. 3360_170	A	FJ554038	249	246/247	99	0.03	-	0.76	0.24	-	-	0.96	0.13	-	-	0.22	0.02	0.14
<i>Pezizomycotina</i> sp. 3360_230	A	FJ553817	240	238/240	99	0.29	0.41	-	0.23	0.15	-	-	0.08	0.13	-	-	0.06	0.13
<i>Eurotiomyces</i> sp. 3360_172	A	MF571008	256	240/258	93	-	-	0.97	0.29	-	-	0.60	0.08	-	-	-	-	0.13
<i>Eurotiomyces</i> sp. 3360_223	A	FN565212	248	239/248	96	-	-	-	-	-	-	-	-	0.73	0.27	-	0.46	0.13
<i>Marasmius scorodonius</i>	B	JN943593	396	396/396	100	-	-	-	-	0.03	-	-	0.02	0.90	-	-	0.42	0.13
<i>Bulleromyces</i> sp. 3360_141	B	LC272845	268	254/270	94	-	-	0.54	0.16	-	-	1.19	0.16	-	-	0.44	0.04	0.13
<i>Rhizoscyphus ericae</i>	A	LC131030	238	236/238	99	0.03	0.25	-	0.07	0.20	0.56	-	0.29	-	-	-	-	0.13
<i>Clavaria flavipes</i>	B	KP257119	307	307/307	100	0.10	0.82	-	0.21	0.03	0.41	-	0.14	-	-	-	-	0.13
<i>Leotiomyces</i> sp. 3360_218	A	KJ828161	243	236/243	97	0.72	-	-	0.36	-	-	-	-	-	-	-	-	0.13
<i>Helotiales</i> sp. 3360_300	A	KX610429	240	240/240	100	-	-	-	-	0.53	0.20	-	0.35	-	-	-	-	0.13
<i>Dothideomyces</i> sp. 3360_306	A	JN033400	239	216/241	90	-	-	-	-	0.06	1.02	-	0.35	-	-	-	-	0.13
<i>Umbelopsis</i> sp. 3360_133	M	KF313131	291	291/291	100	-	0.16	-	0.03	0.06	0.66	-	0.24	0.04	0.14	-	0.08	0.12
<i>Humicolopsis cephalosporioides</i>	A	KY065165	242	242/242	100	-	-	-	-	-	-	-	-	0.04	0.90	-	0.42	0.12
<i>Leotiomyces</i> sp. 3360_169	A	KC876167	248	246/248	99	0.03	1.64	-	0.34	-	-	-	-	-	-	-	-	0.12
<i>Herpotrichia</i> sp. 3360_181	A	KT270203	242	240/242	99	0.29	0.41	0.11	0.26	-	-	-	-	0.04	0.18	-	0.10	0.12
<i>Hyaloscyphaceae</i> sp. 3360_203	A	AB986451	238	225/238	95	0.07	0.08	-	0.05	0.06	0.82	-	0.29	-	-	-	-	0.12
<i>Tylospora</i> sp. 3360_307	B	MG597440	279	279/279	100	0.07	0.16	-	0.07	0.29	0.05	-	0.18	0.17	0.09	-	0.12	0.12
<i>Leotiomyces</i> sp. 3360_132	A	HQ022057	242	242/242	100	0.13	0.25	-	0.11	-	0.51	-	0.16	-	0.14	-	0.06	0.12
<i>Umbelopsis vinacea</i>	M	KC489486	293	293/294	99	-	0.16	-	0.03	0.15	0.10	-	0.11	-	0.50	-	0.22	0.12
<i>Leotiomyces</i> sp. 3360_211	A	KM246498	240	240/241	99	-	0.74	-	0.15	-	-	-	-	0.04	0.45	-	0.22	0.12
<i>Phacidopycnis washingtonensis</i>	A	KP759280	235	235/239	98	-	-	-	-	-	-	2.27	0.31	-	-	0.22	0.02	0.12
<i>Infundichalara microchona</i>	A	NR_154074	240	235/240	98	0.10	0.41	-	0.13	-	-	-	-	0.47	-	-	0.22	0.11
<i>Lecanoromycetes</i> sp. 3360_184	A	KJ008842	240	240/240	100	0.07	-	-	0.03	0.15	-	-	0.08	0.34	0.14	-	0.22	0.10
<i>Inocybe auricoma</i>	B	HQ604526	259	257/260	99	-	-	-	-	-	-	-	-	0.34	0.50	-	0.38	0.11
<i>Mucoromycotina</i> sp. 3360_243	M	KU208027	299	290/300	97	-	0.90	-	0.18	-	-	-	-	-	0.36	-	0.16	0.11
<i>Mycena amicta</i>	B	MH145355	310	310/310	100	0.49	-	-	0.24	-	-	-	-	0.17	-	-	0.08	0.11
<i>Eurotiomyces</i> sp. 3360_148	A	KT219248	255	239/255	94	-	-	-	-	-	0.92	-	0.29	-	-	-	-	0.10
<i>Cortinarius rubrobrunneus</i>	B	NR_131851	299	296/301	98	0.46	0.08	-	0.24	-	0.05	-	0.02	-	-	-	-	0.09
<i>Mollisia minutella</i>	A	KU325451	239	238/239	99	-	-	-	-	-	-	-	-	0.73	0.05	-	0.36	0.10
<i>Leotiomyces</i> sp. 3360_236	A	KJ827004	243	234/235	99	0.07	0.66	-	0.16	-	0.31	-	0.10	-	0.09	-	0.04	0.10
<i>Rhodospordiobolus colostri</i>	B	NR_155730	301	301/301	100	0.13	-	0.27	0.15	-	-	0.24	0.03	-	-	1.31	0.12	0.10
<i>Rutstroemia</i> sp. 3360_280	A	KT269323	245	245/246	99	-	1.39	-	0.28	-	0.05	-	0.02	-	-	-	-	0.10
<i>Genolevuria amylytica</i>	B	NR_137810	273	265/271	98	-	-	0.59	0.18	-	-	0.12	0.02	-	-	1.09	0.10	0.10



Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevića				Visitor				Zeletin				Total	
						Root-lets	Soil	Nee-dies	All	Root-lets	Soil	Nee-dies	All	Root-lets	Soil	Nee-dies	All		
<i>Hygrocybe punicea</i>	B	KM248892	296	291/303	96	0.03	0.33	-	0.08	-	0.61	-	0.19	-	-	-	-	0.10	
<i>Rhizoscyphus ericae</i>	A	LC131030	238	234/238	98	-	0.08	-	0.02	0.26	0.36	-	0.26	-	-	-	-	0.10	
<i>Oidiodendron griseum</i>	A	AF062797	235	235/235	100	0.03	0.16	-	0.05	0.03	0.31	-	0.11	-	0.32	-	0.14	0.10	
<i>Lophodermium conigenum</i>	A	HM060651	245	245/245	100	-	-	0.05	0.02	-	0.05	-	0.02	-	-	3.28	0.30	0.10	
<i>Dothideomyces</i> sp. 3360_247	A	KP892073	246	239/250	96	-	-	0.38	0.11	-	-	1.08	0.14	-	-	0.22	0.02	0.10	
<i>Dothideomyces</i> sp. 3360_267	A	KP897917	245	238/250	95	-	-	0.27	0.08	-	-	0.48	0.06	-	-	1.75	0.16	0.10	
<i>Leotiomyces</i> sp. 3360_326	A	KC753434	238	237/239	99	0.20	-	-	0.10	0.32	-	-	0.18	-	-	-	-	0.10	
<i>Inocybe petiginosa</i>	B	AM882708	275	275/275	100	-	-	-	-	-	-	-	-	0.39	0.32	-	0.32	0.09	
<i>Eurotiomyces</i> sp. 3360_204	A	KJ188554	283	283/284	99	-	0.08	-	0.02	-	0.15	-	0.05	0.09	0.45	-	0.24	0.09	
<i>Sebacina epigaea</i>	B	JQ665490	290	290/290	100	-	-	-	-	-	-	-	-	0.09	0.63	-	0.32	0.09	
<i>Eurotiomyces</i> sp. 3360_219	A	KX116038	250	256/253	94	-	0.49	-	0.10	-	0.51	-	0.16	-	-	-	-	0.09	
<i>Microglossum olivaceum</i>	A	KC595251	240	213/216	99	-	-	-	-	0.03	0.77	-	0.26	-	-	-	-	0.09	
<i>Mucor hiemalis</i>	M	MF326610	268	268/269	99	0.23	0.08	-	0.13	0.03	0.20	-	0.08	-	0.14	-	0.06	0.09	
<i>Pseudogymnoascus pannorum</i>	A	MG597475	240	240/241	99	0.10	0.25	-	0.10	0.06	0.15	-	0.08	0.04	0.18	-	0.10	0.09	
<i>Ilyonectria mors-panacis</i>	B	LT821473	256	256/257	99	0.10	0.41	-	0.13	0.12	0.05	-	0.08	0.09	0.05	-	0.06	0.09	
<i>Hyaloscyphaeaceae</i> sp. 3360_333	A	AB986448	239	226/241	94	0.52	-	-	0.26	-	-	-	-	-	-	-	-	0.09	
<i>Dothideomyces</i> sp. 3360_167	A	KU063812	247	214/256	84	-	-	0.38	0.11	-	-	0.48	0.06	-	-	0.88	0.08	0.09	
<i>Clavulina cf. amethystina</i>	B	EU862208	335	333/335	99	-	-	-	-	-	-	-	-	0.09	0.59	-	0.30	0.09	
<i>Taphrina americana</i>	A	NR_155874	294	293/294	99	-	-	0.38	0.11	-	-	0.96	0.13	-	-	-	-	0.09	
<i>Eurotiomyces</i> sp. 3360_228	A	KJ827128	249	239/249	96	-	-	-	-	-	0.77	-	0.24	-	-	-	-	0.09	
<i>Leotiomyces</i> sp. 3360_261	A	MF568920	236	236/236	100	-	-	-	-	0.20	0.26	-	0.19	0.04	0.09	-	0.06	0.09	
<i>Sordariomyces</i> sp. 3360_475	A	EF635769	261	261/261	100	-	-	-	-	0.41	0.05	-	0.24	-	-	-	-	0.09	
<i>Taphrina vestergrenii</i>	A	NR_155886	315	312/315	99	-	-	0.43	0.13	-	-	0.24	0.03	-	-	0.88	0.08	0.08	
<i>Leotiomyces</i> sp. 3360_142	A	KR266870	237	236/237	99	-	-	-	-	0.03	0.66	-	0.23	-	-	-	-	0.08	
<i>Hygrophorus eburneus</i>	B	AY463485	293	293/293	100	-	-	-	-	-	-	-	-	0.56	0.05	-	0.28	0.08	
<i>Penicillium jensenii</i>	A	MH063657	257	257/258	99	0.07	0.16	-	0.07	0.15	0.20	-	0.14	-	0.05	-	0.02	0.08	
<i>Mortierella verticillata</i>	M	MH304896	333	332/333	99	-	-	-	-	0.03	0.66	-	0.23	-	-	-	-	0.08	
<i>Leotiomyces</i> sp. 3360_195	A	HF674577	242	242/242	100	-	-	-	-	-	-	-	-	0.21	-	-	0.10	0.03	
<i>Agaricomycetes</i> sp. 3360_269	B	JN032542	304	239/257	93	-	-	-	-	0.03	0.61	-	0.21	-	-	-	-	0.07	
<i>Eurotiomyces</i> sp. 3360_281	A	FJ553681	256	241/241	100	-	-	0.38	0.11	-	-	0.84	0.11	-	-	-	-	0.08	
<i>Sebacina</i> sp. 3360_322	B	KM576578	241	294/294	100	0.46	-	-	0.23	-	-	-	-	-	-	-	-	0.08	
<i>Sebacina</i> sp. 3360_355	B	KM576578	294	294/294	100	-	-	-	-	-	-	-	-	0.13	0.50	-	0.28	0.08	
<i>Penicillium spinulosum</i>	A	KX302054	250	250/251	99	-	0.33	-	0.07	-	0.10	-	0.03	0.17	0.18	-	0.16	0.08	
<i>Leotiomyces</i> sp. 3360_362	A	KU587020	239	235/237	99	0.03	0.08	-	0.03	-	-	-	-	0.47	0.05	-	0.24	0.08	
<i>Trichoderma paraviridescens</i>	A	MH347308	268	268/268	100	0.23	-	-	0.11	0.03	0.05	-	0.03	0.17	0.05	-	0.10	0.08	
<i>Boletus pruinatus</i>	B	KX168647	395	395/395	100	-	-	-	-	-	-	-	-	0.43	0.14	-	0.26	0.07	
<i>Flagellospora leucorhynchus</i>	A	KC834049	233	230/240	96	-	-	-	-	0.38	-	-	0.21	-	-	-	-	0.07	
<i>Taphrina carpini</i>	A	MF927666	292	290/293	99	-	-	0.43	0.13	-	-	0.48	0.06	-	-	0.22	0.02	0.07	
<i>Inocybe</i> sp. 3360_199	B	KM409417	293	293/293	100	-	-	-	-	-	-	-	-	-	0.59	-	0.26	0.07	
<i>Tremellomyces</i> sp. 3360_213	B	KP897453	273	268/273	98	-	-	0.54	0.16	-	-	0.24	0.03	-	-	0.22	0.02	0.07	
<i>Leotiomyces</i> sp. 3360_222	A	KX116007	241	235/241	98	-	0.49	-	0.10	0.06	-	-	0.03	-	0.23	-	0.10	0.07	
<i>Dothideomyces</i> sp. 3360_273	A	KC876203	239	237/239	99	-	-	-	-	-	-	-	-	0.17	0.05	-	0.10	0.03	
<i>Halenospora varia</i>	A	KR091829	239	239/239	100	-	-	-	-	-	-	-	-	0.09	0.50	-	0.26	0.07	
<i>Leotiomyces</i> sp. 3360_278	A	KJ827376	241	240/242	99	0.07	0.16	-	0.07	-	-	-	-	-	0.41	-	0.18	0.07	
<i>Eurotiomyces</i> sp. 3360_285	A	KJ827128	249	240/249	96	0.39	0.08	-	0.21	-	-	-	-	-	-	-	-	0.07	
<i>Mucoromycotina</i> sp. 3360_319	M	HQ022209	299	298/299	99	-	-	-	-	-	-	-	-	-	0.59	-	0.26	0.07	
<i>Eurotiomyces</i> sp. 3360_377	A	MF486314	249	248/250	99	-	-	-	-	-	-	-	-	-	0.59	-	0.26	0.07	
<i>Tremellomyces</i> sp. 3360_468	B	KP897203	259	238/259	92	-	-	0.38	0.11	-	-	0.36	0.05	-	-	0.66	0.06	0.07	
<i>Trichoderma hunanense</i>	A	NR_154571	261	261/261	100	-	-	-	-	0.03	0.05	-	0.03	0.09	0.36	-	0.20	0.07	
<i>Penicillium inflatum</i>	A	AJ608959	262	252/262	96	-	-	-	-	-	0.61	-	0.19	-	-	-	-	0.07	
<i>Eurotiomyces</i> sp. 3360_192	A	KC876149	271	270/271	99	-	0.08	-	0.02	-	-	-	-	0.21	0.18	-	0.18	0.06	
<i>Sordariomyces</i> sp. 3360_198	A	KM492988	294	270/311	87	-	-	-	-	-	0.61	-	0.19	-	-	-	-	0.07	
<i>Dothideomyces</i> sp. 3360_202	A	KR266735	229	220/239	92	0.26	0.33	-	0.20	-	-	-	-	-	-	-	-	0.07	
<i>Inocybe cf. subnudipes</i>	B	AM882983	297	259/259	100	-	-	-	-	-	-	-	-	0.17	0.36	-	0.24	0.07	
<i>Mycena strobilinoidea</i>	B	MG654744	312	312/312	100	-	0.08	-	0.02	-	0.05	-	0.02	-	-	-	-	0.01	
<i>Mucoromycotina</i> sp. 3360_233	M	KX115766	333	333/333	100	-	0.08	-	0.02	-	0.05	-	0.02	0.04	0.41	-	0.20	0.07	
<i>Cryptococcus</i> sp. 3360_256	B	KU057816	248	247/248	99	-	-	0.49	0.15	-	-	0.36	0.05	-	-	-	-	0.07	
<i>Alternaria alternata</i>	A	MF497381	253	253/253	100	-	-	0.27	0.08	-	0.10	0.24	0.06	-	0.05	0.44	0.06	0.07	
<i>Helotiales</i> sp. 3360_303	A	KY228609	241	230/244	94	0.07	0.25	-	0.08	-	0.26	-	0.08	-	0.09	-	0.04	0.07	
<i>Rhizmatales</i> sp. 3360_314	A	KJ406976	241	223/223	100	-	-	-	-	-	-	-	1.31	0.18	-	-	0.22	0.02	0.07
<i>Sordariomyces</i> sp. 3360_317	A	KT195220	233	233/237	98	0.03	-	-	0.02	0.12	0.36	-	0.18	-	-	-	-	0.07	
<i>Dothideomyces</i> sp. 3360_330	A	KP892073	246	237/251	94	-	-	0.49	0.15	-	-	0.24	0.03	-	-	0.22	0.02	0.07	
<i>Ascomycota</i> sp. 3360_369	A	FJ008678	255	254/255	99	-	-	0.32	0.10	-	-	-	-	-	-	1.31	0.12	0.07	
<i>Spirosphaera beverwijkiana</i>	A	EF029215	239	227/240	95	0.07	-	-	0.03	0.09	0.36	-	0.16	-	-	-	-	0.07	
<i>Leotiomyces</i> sp. 3360_389	A	FJ554032	237	231/242	95	0.33	0.16	-	0.20	-	-	-	-	-	-	-	-	0.07	
<i>Dothideomyces</i> sp. 3360_448	A	KJ827513	242	242/242	100	-	-	0.22	0.07	-	-	0.84	0.11	-	-	0.22	0.02	0.07	
<i>Chaetothiales</i> sp. 3360_450	A	KY228801	257	245/259	95	-	0.25	-	0.05	0.20	0.10	-	0.14	-	-	-	-	0.07	
<i>Agaricomycetes</i> sp. 3360_161	B	HF675636	316	314/317	99	-	-	-	-	-	-	-	-	0.09	0.09	-	0.08	0.02	
<i>Agaricomycetes</i> sp. 3360_175	B	MF484818	293	283/296	96	0.36	-	-	0.18	-	-	-	-	-	-	-	-	0.06	

Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total	
						Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All		
<i>Tomentella</i> sp. 3360_208	B	AB848642	315	315/315	100	-	-	-	-	-	-	-	-	0.17	0.32	-	0.22	0.06	
<i>Mortierella</i> sp. 3360_227	M	JX975932	336	330/335	99	-	0.33	-	0.07	-	0.05	-	0.02	-	0.23	-	0.10	0.06	
<i>Agaricomycetes</i> sp. 3360_231	M	MF484108	304	303/305	99	0.36	-	-	0.18	-	-	-	-	-	-	-	-	0.06	
<i>Lachnum</i> sp. 3360_286	A	KJ542305	237	235/238	99	-	-	-	-	0.32	-	-	0.18	-	-	-	-	0.06	
<i>Rhizoscyphus</i> sp. 3360_292	A	AB847069	236	223/236	94	0.36	-	-	0.18	-	-	-	-	-	-	-	-	0.06	
<i>Lecanoromycetes</i> sp. 3360_293	A	KM494215	245	236/246	96	-	-	0.59	0.18	-	-	-	-	-	-	-	-	0.06	
<i>Wilcoxina rehmii</i>	A	MF926519	254	253/254	99	-	-	-	-	-	-	-	-	0.39	0.09	-	0.22	0.06	
<i>Agaricomycetes</i> sp. 3360_320	B	AY097046	301	301/303	99	0.10	-	-	0.05	-	-	-	-	0.30	0.05	-	0.16	0.06	
<i>Sordariomycetes</i> sp. 3360_324	A	KT219230	295	248/257	96	-	0.08	-	0.02	0.03	0.41	-	0.14	-	0.05	-	0.02	0.06	
<i>Leotiomycetes</i> sp. 3360_395	A	KX776920	237	235/237	99	0.16	-	-	0.08	0.15	-	-	0.08	0.04	-	-	0.02	0.06	
<i>Mycocentrospora cantuariensis</i>	A	NR_154144	251	241/251	97	-	-	0.38	0.11	-	-	-	-	-	-	0.88	0.08	0.06	
<i>Dothideomycetes</i> sp. 3360_474	A	FJ554069	244	243/246	99	-	-	0.27	0.08	-	-	0.36	0.05	-	-	0.66	0.06	0.06	
<i>Archaeorhizomycetes</i> sp. 3360_571	A	KT219753	214	213/214	99	-	-	-	-	-	0.41	-	0.13	-	0.14	-	0.06	0.06	
<i>Sordariomycetes</i> sp. 3360_214	A	MF486092	253	252/254	99	-	-	-	-	-	0.51	-	0.16	-	-	-	-	0.06	
<i>Eurotiomycetes</i> sp. 3360_217	A	KU839262	285	283/285	100	-	-	-	-	0.23	0.10	-	0.16	-	-	-	-	0.06	
<i>Hygrocybe cf. cantharellus</i>	B	HM020689	334	332/336	99	-	-	-	-	-	0.51	-	0.16	-	-	-	-	0.06	
<i>Lecanoromycetes</i> sp. 3360_252	A	KX776599	239	230/238	97	0.03	-	-	0.02	0.12	0.26	-	0.14	-	-	-	-	0.06	
<i>Tetracladium</i> sp. 3360_254	A	KJ735010	240	240/241	99	0.03	0.16	-	0.05	-	-	-	-	0.09	0.14	-	0.10	0.05	
<i>Neonectria lugdunensis</i>	A	KM231762	248	248/256	97	-	0.08	-	0.02	-	-	0.10	-	0.03	0.09	0.23	-	0.14	0.06
<i>Hygrocybe persistens</i>	B	JF908062	309	305/309	99	-	-	-	-	-	0.51	-	0.16	-	-	-	-	0.06	
<i>Aureobasidium pullulans</i>	B	KP131644	249	249/249	100	-	-	0.11	0.03	-	-	0.72	0.10	-	-	0.44	0.04	0.06	
<i>Hyaloscyphaceae</i> sp. 3360_309	A	GU393951	242	238/242	98	0.03	0.33	-	0.08	0.03	-	-	0.02	0.09	0.09	-	0.08	0.06	
<i>Cladophialophora</i> sp. 3360_328	A	MG597448	253	241/254	95	-	0.08	-	0.02	-	-	-	-	0.04	0.36	-	0.18	0.06	
<i>Oidiodendron echinulatum</i>	A	MG597467	236	229/236	97	0.10	-	-	0.05	0.09	-	-	0.05	0.13	0.05	-	0.08	0.06	
<i>Mucoromycotina</i> sp. 3360_357	M	HQ021782	365	364/372	98	0.03	0.08	-	0.03	0.03	0.10	-	0.05	0.04	0.18	-	0.10	0.06	
<i>Phialocephala fortinii</i>	A	AY078132	237	237/238	98	0.03	-	-	0.02	0.18	-	-	0.10	0.04	-	-	0.02	0.05	
<i>Hodophilus micaceus</i>	B	KU882871	305	305/305	100	-	-	-	-	-	0.51	-	0.16	-	-	-	-	0.06	
<i>Entoloma ochreoprunuloides</i>	B	KC710092	288	288/288	100	-	0.82	-	0.16	-	-	-	-	-	-	-	-	0.06	
<i>Sordariomycetes</i> sp. 3360_518	A	KJ827417	249	245/249	98	-	-	-	-	-	-	-	-	-	0.45	-	0.20	0.06	
<i>Helotiales</i> sp. 3360_186	A	KX611542	240	239/241	99	0.03	0.41	-	0.10	0.03	-	-	0.02	0.04	0.05	-	0.04	0.05	
<i>Eurotiomycetes</i> sp. 3360_235	A	KJ008739	232	224/242	93	-	-	-	-	-	-	-	-	0.13	0.23	-	0.16	0.05	
<i>Leotiomycetes</i> sp. 3360_238	A	KJ826721	243	241/244	99	-	0.41	-	0.08	0.06	-	-	0.03	-	0.09	-	0.04	0.05	
<i>Tremellomycetes</i> sp. 3360_242	B	KY558349	311	259/323	80	-	-	0.38	0.11	-	-	0.24	0.03	-	-	-	-	0.05	
<i>Penicillium miczynskii</i>	A	KU727794	255	255/256	99	0.03	0.16	-	0.05	0.03	0.05	-	0.03	-	0.18	-	0.08	0.05	
<i>Dicranophora</i> sp. 3360_289	M	KT736107	272	246/261	94	-	-	-	-	-	0.46	-	0.14	-	-	-	-	0.05	
<i>Mortierella alpina</i>	M	KC018216	344	344/344	100	0.03	0.25	-	0.07	0.06	0.05	-	0.05	-	0.09	-	0.04	0.05	
<i>Fusarium</i> sp. 3360_315	A	KT347168	260	260/260	100	-	0.25	-	0.05	0.03	0.15	-	0.06	0.04	-	-	0.02	0.05	
<i>Mortierella gamsii</i>	M	JX975968	344	341/344	99	0.03	0.33	-	0.08	-	0.05	-	0.02	0.04	0.09	-	0.06	0.05	
<i>Symmetrospora gracilis</i>	B	EU002876	299	293/302	97	-	-	0.32	0.10	-	-	0.12	0.02	-	-	0.44	0.04	0.05	
<i>Phaeothecoidea melaleuca</i>	A	KC008881	236	213/216	99	-	0.16	-	0.03	0.03	-	-	0.02	0.21	0.05	-	0.12	0.05	
<i>Leotiomycetes</i> sp. 3360_429	A	KJ826841	234	227/235	97	0.20	0.16	-	0.13	-	0.05	-	0.02	-	-	-	-	0.05	
<i>Leotiomycetes</i> sp. 3360_439	A	HQ021922	237	231/240	96	-	-	-	-	-	0.46	-	0.14	-	-	-	-	0.05	
<i>Agaricomycetes</i> sp. 3360_452	B	EU624338	308	289/296	98	-	-	-	-	0.26	-	-	0.14	-	-	-	-	0.05	
<i>Hyaloscyphaceae</i> sp. 3360_455	A	JX852344	240	232/240	97	0.29	-	-	0.15	-	-	-	-	-	-	-	-	0.05	
<i>Eurotiomycetes</i> sp. 3360_461	A	KJ826912	250	245/250	98	-	-	-	-	-	0.31	-	0.10	-	0.14	-	0.06	0.05	
<i>Dothideomycetes</i> sp. 3360_820	A	FR682186	251	231/251	92	-	-	0.05	0.02	-	-	-	-	-	-	1.75	0.16	0.05	
<i>Oidiodendron</i> sp. 3360_165	A	AB986458	234	229/234	98	-	0.08	-	0.02	-	-	-	-	0.04	0.27	-	0.14	0.05	
<i>Entoloma conferendum</i>	B	MF977971	296	296/296	100	-	-	-	-	0.23	-	-	0.13	-	-	-	-	0.05	
<i>Scopuloides hydroides</i>	B	LN611118	293	292/293	99	-	-	-	-	-	-	-	-	0.30	0.05	-	0.16	0.05	
<i>Typhula intermedia</i>	B	AB267394	296	294/298	99	0.07	0.16	0.22	0.13	-	-	-	-	-	-	-	-	0.05	
<i>Hygrocybe lepida</i>	B	KF306331	328	327/328	99	-	-	-	-	-	0.41	-	0.13	-	-	-	-	0.05	
<i>Eurotiomycetes</i> sp. 3360_253	A	JQ346927	262	244/262	93	-	0.08	-	0.02	0.15	0.10	-	0.11	-	-	-	-	0.05	
<i>Dothideomycetes</i> sp. 3360_257	A	HF947037	246	227/252	90	-	-	0.11	0.03	-	-	0.48	0.06	-	-	0.44	0.04	0.05	
<i>Mortierella</i> sp. 3360_260	M	JX270424	340	328/340	96	-	-	-	-	-	-	-	-	-	0.36	-	0.16	0.05	
<i>Agaricomycetes</i> sp. 3360_265	B	FR750601	318	316/318	99	-	-	-	-	-	0.41	-	0.13	-	-	-	-	0.05	
<i>Tetracladium globosum</i>	A	JX029133	240	239/241	99	-	0.16	-	0.03	-	0.10	-	0.03	0.09	0.09	-	0.08	0.05	
<i>Dothideomycetes</i> sp. 3360_351	A	KP898201	240	228/240	95	-	-	-	-	-	0.41	-	0.13	-	-	-	-	0.05	
<i>Sagenomella griseoviridis</i>	A	LC177648	244	244/249	98	-	-	-	-	-	0.10	-	0.03	-	0.27	-	0.12	0.05	
<i>Eurotiomycetes</i> sp. 3360_361	A	MH451802	256	244/256	95	-	-	-	-	0.12	0.20	-	0.13	-	-	-	-	0.05	
<i>Eurotiomycetes</i> sp. 3360_385	A	HQ022171	260	250/260	96	-	-	-	-	0.23	-	-	0.13	-	-	-	-	0.05	
<i>Russula olivacea</i>	B	AF418634	377	372/378	98	-	-	-	-	-	-	-	-	0.26	0.09	-	0.16	0.05	
<i>Leotiomycetes</i> sp. 3360_441	A	MF665262	238	199/200	99	-	-	-	-	-	0.20	0.24	0.10	-	-	0.44	0.04	0.05	
<i>Sagenomella verticillata</i>	A	LC177652	260	260/262	99	-	-	-	-	-	-	-	-	-	0.36	-	0.16	0.05	
<i>Sphaerobolus iowensis</i>	B	AY650256	310	309/310	99	0.03	0.08	-	0.03	0.15	0.05	-	0.10	-	-	-	-	0.05	
<i>Dothideomycetes</i> sp. 3360_653	A	FJ554220	240	236/241	98	-	-	0.38	0.11	-	-	-	-	0.04	-	-	0.02	0.05	
<i>Mucoromycotina</i> sp. 3360_768	M	HQ022261	326	315/326	97	-	-	-	-	0.03	0.36	-	0.13	-	-	-	-	0.05	
<i>Taphrina sacchari</i>	A	AF492117	295	289/295	98	-	-	0.22	0.07	-	-	0.36	0.05	-	-	-	-	0.04	
<i>Hydnotrya michaelis</i>	A	EU784275	299	283/244	98	0.23	-	-	0.11	-	-	-	-	-	-	-	-	0.04	
<i>Amphinema diadema</i>	B	GQ162811	288	286/290	99	-	-	-	-	-	-	-	-	0.09	0.23	-	0.14	0.04	

Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total	
						Root-lets	Soil	Nee-dles	All	Root-lets	Soil	Nee-dles	All	Root-lets	Soil	Nee-dles	All		
<i>Cladophialophora</i> sp. 3360_263	A	KF636403	252	248/253	98	-	0.49	-	0.10	-	-	-	-	0.04	-	-	-	0.02	0.04
<i>Leotiomyces</i> sp. 3360_264	A	KJ826695	235	233/237	98	-	-	-	-	0.06	0.26	-	0.11	-	-	-	-	-	0.04
<i>Vishniacozyma victoriae</i>	B	MF062235	234	234/234	100	0.07	0.08	-	0.05	-	0.15	0.12	0.06	-	-	-	-	-	0.04
<i>Sordariomyces</i> sp. 3360_287	A	KC243967	228	219/233	94	-	-	-	-	0.15	0.10	-	0.11	-	-	-	-	-	0.04
<i>Agaricomycetes</i> sp. 3360_295	B	JQ890252	269	267/270	99	0.16	-	-	0.08	-	-	-	-	0.09	-	-	-	0.04	0.04
<i>Exobasidiomyces</i> sp. 3360_296	B	KR262419	288	268/288	93	-	-	0.32	0.10	-	-	0.12	0.02	-	-	-	-	-	0.04
<i>Leotiomyces</i> sp. 3360_299	A	HQ022246	241	236/242	98	-	0.08	-	0.02	0.06	0.15	-	0.08	-	0.05	-	-	0.02	0.04
<i>Eurotiomyces</i> sp. 3360_302	A	KJ826851	248	248/251	99	0.03	-	-	0.02	-	0.05	-	0.02	0.09	0.14	-	-	0.10	0.04
<i>Eurotiomyces</i> sp. 3360_329	A	MF568997	252	246/252	98	-	0.16	-	0.03	-	0.26	-	0.08	-	-	-	-	-	0.04
<i>Leotiomyces</i> sp. 3360_339	A	KR267040	234	232/235	99	-	-	-	-	-	0.36	-	0.11	-	-	-	-	-	0.04
<i>Agaricomycetes</i> sp. 3360_348	B	JQ420999	302	302/302	100	0.03	-	-	0.02	0.06	0.20	-	0.10	-	-	-	-	-	0.04
<i>Leotiomyces</i> sp. 3360_372	A	EF029215	240	225/241	93	0.13	0.08	-	0.08	0.06	-	-	0.03	-	-	-	-	-	0.04
<i>Tomentella</i> sp. 3360_373	B	KM576662	315	314/317	99	-	-	-	-	-	-	-	-	-	0.32	-	-	0.14	0.04
<i>Leotiomyces</i> sp. 3360_392	A	KJ826793	239	235/240	98	-	-	-	-	-	0.31	-	0.10	-	-	-	-	-	0.03
<i>Mortierella cystojenkii</i>	M	JX976030	330	326/328	100	-	0.08	-	0.02	0.03	-	-	0.02	-	0.23	-	-	0.10	0.04
<i>Agaricomycetes</i> sp. 3360_420	B	KJ705174	276	236/296	80	-	-	-	-	-	0.36	-	0.11	-	-	-	-	-	0.04
<i>Laccaria laccata</i>	B	KM067889	299	296/301	98	0.03	-	-	0.02	-	-	-	-	0.09	0.18	-	-	0.12	0.04
<i>Leotiomyces</i> sp. 3360_433	A	FJ475754	239	231/239	97	0.07	-	-	0.03	-	-	-	-	0.21	-	-	-	0.10	0.04
<i>Leotiomyces</i> sp. 3360_442	A	EU690593	256	245/248	99	-	-	-	-	-	0.36	-	0.11	-	-	-	-	-	0.04
<i>Eurotiomyces</i> sp. 3360_490	A	KJ827879	270	259/271	96	-	-	-	-	-	-	-	-	-	0.32	-	-	0.14	0.04
<i>Agaricomycetes</i> sp. 3360_540	B	KC759480	312	312/313	99	-	-	-	-	-	-	-	-	0.17	0.14	-	-	0.14	0.04
<i>Lecanoromycetes</i> sp. 3360_550	A	HQ022121	241	238/241	99	-	-	-	-	-	-	-	-	0.21	0.09	-	-	0.14	0.04
<i>Coniochaeta</i> sp. 3360_584	A	MH473956	249	249/249	100	-	-	-	-	0.20	-	0.11	-	-	-	-	-	-	0.04
<i>Melanohalea elegantula</i>	A	KX457702	242	238/243	98	-	-	-	-	-	-	-	-	-	-	-	1.53	0.14	0.04
<i>Dothiora</i> sp. 3360_855	A	NR_155059	259	249/260	96	-	-	0.27	0.08	-	-	0.24	0.03	-	-	-	-	-	0.04
<i>Agaricostilbomyces</i> sp. 3360_237	B	KX195103	289	235/307	77	-	-	0.22	0.07	-	-	0.24	0.03	-	-	-	-	-	0.03
<i>Mortierella</i> sp. 3360_241	M	MF423576	327	324/330	98	0.07	-	-	0.03	0.03	0.05	-	0.03	-	0.09	-	-	0.04	0.03
<i>Agaricomycetes</i> sp. 3360_248	B	KM402927	288	279/292	96	-	-	-	-	-	-	-	-	0.26	-	-	-	0.12	0.03
<i>Cystodendron</i> sp. 3360_276	A	KX611556	239	237/241	98	-	-	-	-	-	-	-	-	-	0.27	-	-	0.12	0.03
<i>Gymnostellatospora japonica</i>	A	AF062818	241	239/241	99	-	-	-	-	-	-	-	-	0.17	0.09	-	-	0.12	0.03
<i>Agaricomycetes</i> sp. 3360_284	B	KX115620	325	314/329	95	-	-	-	-	-	0.31	-	0.10	-	-	-	-	-	0.03
<i>Sordariomyces</i> sp. 3360_304	A	MF976656	243	237/243	98	-	-	-	-	-	-	0.12	0.02	-	-	-	1.09	0.10	0.03
<i>Armillaria ostoyae</i>	B	JN657460	478	478/478	100	-	-	-	-	-	-	-	-	0.21	0.05	-	-	0.12	0.03
<i>Agaricomycetes</i> sp. 3360_323	B	KC176356	315	241/329	73	-	-	-	-	-	0.31	-	0.10	-	-	-	-	-	0.03
<i>Mortierella antarctica</i>	M	MH304899	337	336/337	99	-	-	-	-	-	0.31	-	0.10	-	-	-	-	-	0.03
<i>Pseudogymnoascus pannorum</i>	A	LN714595	239	236/241	98	0.03	-	-	0.02	-	-	-	-	-	0.18	-	-	0.08	0.03
<i>Ganoderma applanatum</i>	B	MH160077	288	288/288	100	-	-	-	-	-	0.05	-	0.02	-	0.23	-	-	0.10	0.03
<i>Eurotiomyces</i> sp. 3360_345	A	KX116037	253	251/253	99	-	-	-	-	-	0.31	-	0.10	-	-	-	-	-	0.03
<i>Eurotiomyces</i> sp. 3360_359	A	MH450451	256	244/257	95	0.07	0.08	-	0.05	-	0.15	-	0.05	-	-	-	-	-	0.03
<i>Mucor hiemalis</i>	M	MH266219	271	271/272	99	-	0.08	-	0.02	-	0.15	-	0.05	0.04	0.05	-	-	0.04	0.03
<i>Sordariomyces</i> sp. 3360_370	A	MH450805	245	245/246	99	-	-	-	-	-	0.10	-	0.03	-	0.09	-	-	0.04	0.02
<i>Agaricomycetes</i> sp. 3360_375	B	KX115577	294	291/302	96	0.03	-	-	0.02	0.03	0.20	-	0.08	-	-	-	-	-	0.03
<i>Leotiomyces</i> sp. 3360_381	A	KJ826793	237	236/240	98	-	0.08	-	0.02	-	0.20	-	0.06	-	0.05	-	-	0.02	0.03
<i>Archaeorhizomyces</i> sp. 3360_386	A	JQ347010	215	202/215	94	-	0.08	-	0.02	0.03	0.20	-	0.08	-	-	-	-	-	0.03
<i>Agaricomycetes</i> sp. 3360_391	B	KX222980	299	297/300	99	-	-	-	-	0.18	-	-	0.10	-	-	-	-	-	0.03
<i>Agaricomycetes</i> sp. 3360_397	B	KX115947	311	303/311	97	0.07	0.33	-	0.10	-	-	-	-	-	-	-	-	-	0.03
<i>Gorgomyces</i> sp. 3360_398	A	NR_154062	242	231/243	95	-	-	-	-	-	-	-	-	-	0.23	-	-	0.10	0.03
<i>Xerocomus ferrugineus</i>	B	DQ066398	360	360/361	99	-	-	-	-	-	-	-	-	0.09	0.18	-	-	0.12	0.03
<i>Dothiora</i> sp. 3360_412	A	NR_155059	259	245/260	94	-	-	0.16	0.05	-	-	0.36	0.05	-	-	-	-	-	0.03
<i>Helotiales</i> sp. 3360_418	A	JX852359	244	244/244	100	0.16	0.08	-	0.10	-	-	-	-	-	-	-	-	-	0.03
<i>Phaeohelotium epiphyllum</i>	A	KT876976	240	234/240	98	-	-	-	-	0.12	-	-	0.06	-	0.05	-	-	0.02	0.03
<i>Mortierella parvispora</i>	M	KU516633	331	331/331	100	0.07	-	-	0.03	-	0.15	-	0.05	-	0.05	-	-	0.02	0.03
<i>Glomeromyces</i> sp. 3360_453	M	FR772327	289	288/289	99	0.10	-	-	0.05	0.09	-	-	0.05	-	-	-	-	-	0.03
<i>Helotiales</i> sp. 3360_458	A	KY228788	240	227/241	94	-	0.08	-	0.02	-	0.26	-	0.08	-	-	-	-	-	0.03
<i>Rhytismataceae</i> sp. 3360_460	A	FR837916	239	228/241	95	-	-	0.27	0.08	-	-	0.12	0.02	-	-	-	-	-	0.03
<i>Agaricomycetes</i> sp. 3360_492	B	KX115615	320	319/320	99	-	-	-	-	-	0.31	-	0.10	-	-	-	-	-	0.03
<i>Cladophialophora chaetospora</i>	A	LC077702	265	264/266	99	0.03	-	-	0.02	-	-	-	-	0.04	0.09	-	-	0.06	0.02
<i>Eurotiomyces</i> sp. 3360_496	A	KP897537	238	234/242	97	-	-	0.32	0.10	-	-	-	-	-	-	-	-	-	0.03
<i>Sordariomyces</i> sp. 3360_497	A	MH452656	256	248/266	93	-	-	-	-	-	0.31	-	0.10	-	-	-	-	-	0.03
<i>Calycina marina</i>	A	KT185677	241	232/241	96	-	-	0.22	0.07	-	-	0.12	0.02	-	-	-	0.22	0.02	0.03
<i>Helotiales</i> sp. 3360_555	A	KT270126	236	234/238	98	-	-	-	-	0.09	0.05	-	0.06	-	0.05	-	-	0.02	0.03
<i>Eurotiomyces</i> sp. 3360_633	A	KJ827128	249	226/250	90	0.03	0.16	-	0.05	0.03	0.10	-	0.05	-	-	-	-	-	0.03
<i>Archaeorhizomyces</i> sp. 3360_686	A	KT196257	215	209/216	97	-	-	-	-	-	0.10	-	0.03	0.09	0.09	-	-	0.08	0.03
<i>Oidiodendron pilicola</i>	A	MG597470	235	232/235	97	0.07	0.08	-	0.05	0.03	-	-	0.02	0.04	0.05	-	-	0.04	0.03
<i>Dothideomyces</i> sp. 3360_715	A	FR682198	242	223/242	92	-	-	0.22	0.07	-	-	0.12	0.02	-	-	-	0.22	0.02	0.03
<i>Tetracladium maxilliforme</i>	A	KU519119	239	237/239	99	-	-	0.22	0.07	-	-	0.24	0.03	-	-	-	-	-	0.03
<i>Leotiomyces</i> sp. 3360_754	A	KU062190	239	220/242	91	-	-	-	-	0.12	0.10	-	0.10	-	-	-	-	-	0.03
<i>Eurotiomyces</i> sp. 3360_773	A	MF486314	253	243/253	96	-	-	-	-	-	-	-	-	-	0.27	-	-	0.12	0.03
<i>Lycoperdon perlatum</i>	B	KY950489	307	307/308	99	-	0.08	-	0.02	-	0.05	-	0.02	-	0.14	0.22	0.08	0.03	0.03

Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total	
						Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All		
<i>Eurotiomycetes</i> sp. 3360_801	A	MF486314	254	232/254	91	-	-	-	-	-	-	-	-	0.27	-	0.12	0.03		
<i>Meliniomyces variabilis</i>	A	EF093173	240	240/241	99	0.13	-	-	0.07	-	-	-	-	-	-	-	0.02		
<i>Botrytis cinerea</i>	A	MH329278	239	239/240	99	-	-	-	-	-	0.26	0.12	0.10	-	-	-	0.03		
<i>Leotiomyces</i> sp. 3360_1421	A	KJ827842	241	239/244	98	0.03	-	-	0.02	-	-	-	-	0.04	0.18	-	0.10	0.03	
<i>Beauveria bassiana</i>	A	MH483769	254	253/255	99	-	0.33	-	0.07	-	-	-	-	-	0.05	-	0.02	0.03	
<i>Eurotiomycetes</i> sp. 3360_290	A	HQ022024	248	246/248	99	-	0.08	-	0.02	-	-	-	-	0.04	0.14	-	0.08	0.03	
<i>Agaricomycetes</i> sp. 3360_310	B	HE687089	355	333/360	93	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01	
<i>Heterobasidion abietinum</i>	B	KT355028	295	295/295	100	-	0.33	0.05	0.08	-	-	-	-	-	-	-	-	0.03	
<i>Cortinarius hinnuleus</i>	B	AY669665	288	288/288	100	-	-	-	-	-	-	-	-	-	0.23	-	0.10	0.03	
<i>Dactylonectria hordeicola</i>	A	MF440368	254	254/255	99	-	-	-	-	0.09	0.10	-	0.08	-	-	-	-	0.03	
<i>Torula herbarum</i>	A	MH225772	247	246/247	99	-	-	-	-	-	0.05	-	0.02	-	0.18	-	0.08	0.03	
<i>Agaricomycetes</i> sp. 3360_350	B	JN652992	342	307/310	99	-	-	-	-	-	-	-	-	0.13	0.09	-	0.10	0.03	
<i>Agaricomycetes</i> sp. 3360_376	B	GU189680	299	293/299	98	-	-	-	-	-	-	-	-	-	0.23	-	0.10	0.03	
<i>Helotiales</i> sp. 3360_378	A	JX852359	244	238/244	98	-	-	-	-	-	-	-	-	0.13	0.09	-	0.10	0.03	
<i>Agaricomycetes</i> sp. 3360_383	B	KM023223	302	295/302	98	-	-	-	-	0.15	-	-	0.08	-	-	-	-	0.03	
<i>Leotiomyces</i> sp. 3360_401	A	HQ021837	239	231/239	97	-	-	-	-	-	0.26	-	0.08	-	-	-	-	0.03	
<i>Eurotiomycetes</i> sp. 3360_407	A	JQ346925	262	252/263	96	-	-	-	-	-	0.26	-	0.08	-	-	-	-	0.03	
<i>Cladophialophora</i> sp. 3360_408	A	KF636403	251	248/253	98	0.07	0.16	-	0.07	-	-	-	-	-	0.05	-	0.02	0.03	
<i>Eurotiomycetes</i> sp. 3360_413	A	HG936562	281	275/285	96	-	-	-	-	0.03	0.20	-	0.08	-	-	-	-	0.03	
<i>Chaetothyriales</i> sp. 3360_416	A	KY228666	275	251/276	91	-	-	-	-	0.15	-	-	0.08	-	-	-	-	0.03	
<i>Naganishia onofrii</i>	B	MH634709	316	316/316	100	-	-	-	-	-	0.26	-	0.08	-	-	-	-	0.03	
<i>Trichoderma asperellum</i>	A	MH608367	267	267/267	100	-	0.08	-	0.02	0.06	0.05	-	0.05	-	0.05	-	0.02	0.03	
<i>Dothideomycetes</i> sp. 3360_428	A	KJ188587	233	228/234	100	-	-	-	-	-	-	-	-	-	0.23	-	0.10	0.03	
<i>Leotiomyces</i> sp. 3360_432	A	GU327457	238	238/238	100	0.10	0.08	-	0.07	0.03	-	-	0.02	-	-	-	-	0.03	
<i>Hygrocybe chlorophana</i>	B	JF908052	309	304/309	98	-	-	-	-	-	0.26	-	0.08	-	-	-	-	0.03	
<i>Hyalodendriella betulae</i>	A	NR_156207	239	234/242	97	-	-	-	-	-	-	-	-	0.21	-	-	0.10	0.03	
<i>Eurotiomycetes</i> sp. 3360_440	A	MF486235	248	235/250	94	-	-	-	-	-	0.15	-	0.05	-	0.09	-	0.04	0.03	
<i>Helotiales</i> sp. 3360_445	A	LC131017	242	242/242	100	0.03	0.08	-	0.03	-	0.05	-	0.02	-	0.09	-	0.04	0.03	
<i>Cryptococcus</i> sp. 3360_446	B	HG324303	322	309/324	95	-	-	0.16	0.05	0.03	-	-	0.02	-	-	0.22	0.02	0.03	
<i>Phaeotheca fissurella</i>	A	KM216356	237	218/220	99	-	-	0.27	0.08	-	-	-	-	-	-	-	-	0.03	
<i>Lactarius blennius</i>	B	AY606944	359	359/359	100	-	-	-	-	-	-	-	-	-	0.17	0.05	-	0.10	0.03
<i>Umbelopsis ramanniana</i>	M	EU715662	304	302/314	96	-	0.16	-	0.03	-	-	-	-	-	0.14	-	0.06	0.03	
<i>Tomentellopsis</i> sp. 3360_469	B	HQ533015	312	305/314	97	-	-	-	-	-	-	-	-	0.13	0.09	-	0.10	0.03	
<i>Pezizomycotina</i> sp. 3360_470	A	KJ827304	240	240/240	100	-	0.25	-	0.05	-	-	-	-	0.04	0.05	-	0.04	0.03	
<i>Leotiomyces</i> sp. 3360_471	A	KF359573	248	243/249	98	-	-	-	-	-	-	-	-	0.04	0.18	-	0.10	0.03	
<i>Pezizomycotina</i> sp. 3360_479	A	MF486235	250	243/251	97	-	0.08	-	0.02	0.09	0.05	-	0.06	-	-	-	-	0.03	
<i>Leotiomyces</i> sp. 3360_481	A	JQ346977	232	232/239	97	-	-	-	-	-	-	-	-	0.13	-	-	0.06	0.02	
<i>Inocybe</i> sp. 3360_483	B	FJ904135	287	273/291	94	-	-	-	-	-	-	-	-	-	0.23	-	0.10	0.03	
<i>Leotiomyces</i> sp. 3360_491	A	KU208067	245	216/247	97	0.10	0.16	-	0.08	-	-	-	-	-	-	-	-	0.03	
<i>Lophodermium</i> sp. 3360_500	A	LM654180	240	238/243	98	-	-	0.11	0.03	-	-	0.24	0.03	-	0.05	-	0.02	0.03	
<i>Tarsetta catinus</i>	A	DQ200833	273	273/275	99	-	-	-	-	-	-	-	-	-	0.23	-	0.10	0.03	
<i>Thelephora terrestris</i>	B	KY693686	312	310/314	99	-	-	-	-	0.03	0.05	-	0.03	-	0.14	-	0.06	0.03	
<i>Leotiomyces</i> sp. 3360_514	A	KJ826609	249	237/251	94	0.16	-	-	0.08	-	-	-	-	-	-	-	-	0.03	
<i>Curvibasidium rogersii</i>	B	JX188232	309	309/309	100	-	0.16	0.05	0.05	-	-	-	-	-	-	0.44	0.04	0.03	
<i>Tomentella cinerascens</i>	B	AF272915	316	315/316	99	-	-	-	-	-	-	-	-	0.17	0.05	-	0.10	0.03	
<i>Rickenella fibula</i>	B	MG982530	307	305/307	99	0.16	-	-	0.08	-	-	-	-	-	-	-	-	0.03	
<i>Leotiomyces</i> sp. 3360_541	A	HM488471	239	235/239	98	-	0.25	-	0.05	0.03	-	-	0.02	-	0.05	-	0.02	0.03	
<i>Cladophialophora</i> sp. 3360_551	A	AB986416	266	265/268	99	-	-	-	-	0.09	0.10	-	0.08	-	-	-	-	0.03	
<i>Leotiomyces</i> sp. 3360_569	A	HQ022246	242	240/242	99	0.10	-	-	0.05	-	0.10	-	0.03	-	-	-	-	0.03	
<i>Archaeorhizomyces</i> sp. 3360_587	A	KJ826637	218	205/218	94	-	-	-	-	-	0.26	-	0.08	-	-	-	-	0.03	
<i>Leotiomyces</i> sp. 3360_593	A	MF486833	240	239/242	99	-	0.33	-	0.07	-	0.05	-	0.02	-	-	-	-	0.03	
<i>Leotiomyces</i> sp. 3360_596	A	FJ554360	241	241/242	99	-	0.25	-	0.05	-	-	-	-	0.04	0.05	-	0.04	0.03	
<i>Tetracladium</i> sp. 3360_599	A	KX343162	237	237/238	99	-	-	-	-	0.09	0.10	-	0.08	-	-	-	-	0.03	
<i>Mycena galopus</i>	B	HM240534	305	304/305	99	-	0.08	-	0.02	0.09	0.05	-	0.06	-	-	-	-	0.03	
<i>Sordariomycetes</i> sp. 3360_614	A	KP891859	284	231/300	77	-	-	0.16	0.05	-	-	0.12	0.02	-	-	0.22	0.02	0.03	
<i>Penicillium simplicissimum</i>	A	KM396382	257	257/260	99	0.10	0.08	-	0.07	-	-	-	-	-	0.05	-	0.02	0.03	
<i>Leohumicola minima</i>	A	KY228486	241	235/241	98	-	0.16	-	0.03	-	0.15	-	0.05	-	-	-	-	0.03	
<i>Dothideomycetes</i> sp. 3360_637	A	KJ826807	241	240/241	99	-	0.08	-	0.02	-	0.05	-	0.02	0.04	0.09	-	0.06	0.03	
<i>Eurotiomycetes</i> sp. 3360_645	A	MH451264	251	248/253	98	-	-	-	-	-	0.20	-	0.06	-	0.05	-	0.02	0.03	
<i>Helotiales</i> sp. 3360_709	A	KY228609	240	228/243	94	0.10	0.16	-	0.08	-	-	-	-	-	-	-	-	0.03	
<i>Trechispora invisitata</i>	B	KP814425	303	295/304	97	-	-	-	-	-	-	-	-	0.09	0.14	-	0.10	0.03	
<i>Neonectria candida</i>	A	MH063618	254	254/256	99	-	-	-	-	-	0.10	-	0.03	-	0.14	-	0.06	0.03	
<i>Leotiomyces</i> sp. 3360_761	A	JQ272351	248	236/248	95	0.03	0.16	-	0.05	-	0.10	-	0.03	-	-	-	-	0.03	
<i>Dothideomycetes</i> sp. 3360_826	A	KP891693	240	230/241	95	-	-	0.22	0.07	-	-	-	-	-	-	0.22	0.02	0.03	
<i>Dothideomycetes</i> sp. 3360_841	A	AM901764	242	218/246	89	-	-	0.22	0.07	-	-	-	-	-	-	0.22	0.02	0.03	
<i>Capronia</i> sp. 3360_1656	A	AY112917	258	256/258	99	-	0.16	-	0.03	-	0.15	-	0.05	-	-	-	-	0.03	
<i>Lemonniera</i> sp. 3360_288	A	KX096679	241	233/241	97	-	-	0.22	0.07	-	-	-	-	-	-	-	-	0.02	
<i>Entrophospora</i> sp. 3360_325	M	KJ542310	245	245/249	98	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01	
<i>Leptodontidium trabinellum</i>	A	KY853449	238	236/240	98	-	-	-	-	-	0.15	-	0.05	-	0.05	-	0.02	0.02	

Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total
						Root-lets	Soil	Nee-dies	All	Root-lets	Soil	Nee-dies	All	Root-lets	Soil	Nee-dies	All	
<i>Lecythophora</i> sp. 3360_340	A	KJ735003	245	243/248	98	-	0.08	-	0.02	-	-	-	-	-	0.14	-	0.06	0.02
<i>Mucoromycotina</i> sp. 3360_341	M	HQ022261	314	310/322	96	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Peizomycotina</i> sp. 3360_349	A	MH451826	260	259/260	99	-	0.08	-	0.02	0.03	0.10	-	0.05	-	-	-	-	0.02
<i>Leotiomyces</i> sp. 3360_352	A	MF405784	242	244/283	86	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02
<i>Peizomyces</i> sp. 3360_354	A	KY687549	279	368/375	98	-	-	-	-	-	-	-	-	0.17	-	-	0.08	0.02
<i>Sebacina epigaea</i>	B	KF000427	294	294/294	100	-	-	-	-	0.06	0.10	-	0.06	-	-	-	-	0.02
<i>Peizomycotina</i> sp. 3360_368	A	MH450646	238	232/241	96	-	0.08	-	0.02	-	-	-	-	-	0.14	-	0.06	0.02
<i>Eurotiomyces</i> sp. 3360_371	A	HQ022301	254	243/262	93	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Galerina sideroides</i>	B	KT008365	297	293/306	96	-	0.33	-	0.07	-	-	-	-	-	-	-	-	0.02
<i>Mucoromycotina</i> sp. 3360_402	M	KX222765	288	273/314	87	-	-	-	-	-	0.10	-	0.03	-	0.09	-	0.04	0.02
<i>Eurotiomyces</i> sp. 3360_403	A	HQ022171	256	248/259	96	0.13	-	-	0.07	-	-	-	-	-	-	-	-	0.02
<i>Penicillium alogum</i>	A	KT887869	257	254/260	98	0.03	-	-	0.02	-	0.15	-	0.05	-	-	-	-	0.02
<i>Mortierella fluviat</i>	M	KX227756	341	339/342	99	-	-	-	-	0.06	0.10	-	0.06	-	-	-	-	0.02
<i>Entoloma sericeum</i>	B	KY706153	299	299/301	99	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Agaricomycetes</i> sp. 3360_431	B	HQ154277	298	289/298	97	0.13	-	-	0.07	-	-	-	-	-	-	-	-	0.02
<i>Agaricomycetes</i> sp. 3360_443	B	KX115853	316	294/326	90	-	0.33	-	0.07	-	-	-	-	-	-	-	-	0.02
<i>Mucoromycotina</i> sp. 3360_456	M	JX316327	343	342/343	99	0.03	-	-	0.02	-	-	-	-	-	0.14	-	0.06	0.02
<i>Dothideomyces</i> sp. 3360_463	A	EF434104	240	232/242	96	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Mucoromycotina</i> sp. 3360_465	M	KX193024	352	348/352	99	-	-	-	-	-	-	-	-	-	0.18	-	0.08	0.02
<i>Agaricomycetes</i> sp. 3360_480	B	HQ154278	304	280/306	92	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Tomentella</i> sp. 3360_482	B	KT275628	312	304/314	97	-	-	-	-	0.09	0.05	-	0.06	-	-	-	-	0.02
<i>Hygrocybe spadicea</i>	B	KF291201	323	321/326	98	-	-	-	-	0.03	0.15	-	0.06	-	-	-	-	0.02
<i>Ascomycota</i> sp. 3360_487	A	FN435802	272	236/243	97	-	-	0.22	0.07	-	-	-	-	-	-	-	-	0.02
<i>Leotiomyces</i> sp. 3360_489	A	MF486962	237	235/240	98	-	0.08	-	0.02	-	-	-	-	-	0.14	-	0.06	0.02
<i>Pleosporales</i> sp. 3360_493	A	KR187108	222	209/233	90	-	-	-	-	-	-	0.48	0.06	-	-	-	-	0.02
<i>Leotiomyces</i> sp. 3360_501	A	HQ021922	240	231/242	95	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Coprinellus micaceus</i>	B	MH562051	296	295/298	99	-	-	-	-	-	-	-	-	-	0.18	-	0.08	0.02
<i>Tomentella</i> sp. 3360_506	B	KT275628	314	300/316	95	-	-	-	-	0.12	-	-	0.06	-	-	-	-	0.02
<i>Agaricomycetes</i> sp. 3360_517	B	KT273808	281	280/281	99	-	-	-	-	0.09	0.05	-	0.06	-	-	-	-	0.02
<i>Sepedonium chrysospermum</i>	A	KT946851	262	261/266	98	-	-	-	-	-	-	-	-	-	0.18	-	0.08	0.02
<i>Lecythophora</i> sp. 3360_527	A	MF062193	251	250/251	99	-	-	-	-	0.03	0.15	-	0.06	-	-	-	-	0.02
<i>Archaeospora leptoticha</i>	M	AJ567807	288	283/295	96	-	-	-	-	-	-	-	-	-	0.18	-	0.08	0.02
<i>Dothideomyces</i> sp. 3360_535	A	FR682198	240	225/243	93	-	-	0.22	0.07	-	-	-	-	-	-	-	-	0.02
<i>Eurotiomyces</i> sp. 3360_542	A	KJ828664	255	250/258	97	-	-	-	-	-	0.15	-	0.05	-	0.05	-	0.02	0.02
<i>Eurotiomyces</i> sp. 3360_561	A	MH452116	261	248/261	95	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Pezizula ericae</i>	A	KY979197	239	239/241	99	0.03	-	-	0.02	0.03	0.10	-	0.05	-	-	-	-	0.02
<i>Eurotiomyces</i> sp. 3360_572	A	KJ826709	253	252/255	99	-	-	-	-	-	-	-	-	0.04	0.14	-	0.08	0.02
<i>Infundichalara microchona</i>	A	NR_154074	239	234/241	99	0.07	-	-	0.03	-	-	-	-	0.09	-	-	0.04	0.02
<i>Archaeorhizomyces</i> sp. 3360_578	A	KU064046	211	211/211	100	-	-	-	-	-	-	-	-	0.17	-	-	0.08	0.02
<i>Eurotiomyces</i> sp. 3360_579	A	MH451155	258	255/258	99	-	-	-	-	0.12	-	-	0.06	-	-	-	-	0.02
<i>Sarcinomyces</i> sp. 3360_600	A	KU057815	251	251/255	98	0.13	-	-	0.07	-	-	-	-	-	-	-	-	0.02
<i>Helotiales</i> sp. 3360_603	A	KY228554	240	230/241	95	-	-	-	-	-	0.12	-	0.06	-	-	-	-	0.02
<i>Dothideomyces</i> sp. 3360_609	A	KR266735	237	230/239	96	-	-	0.11	0.03	-	-	0.12	0.02	-	-	0.22	0.02	0.02
<i>Leotiomyces</i> sp. 3360_611	A	FJ827174	243	243/243	100	0.07	-	-	0.03	0.06	-	-	0.03	-	-	-	-	0.02
<i>Mortierella macrocystis</i>	M	JQ272448	330	329/330	99	-	-	-	-	0.06	-	-	0.03	-	0.09	-	0.04	0.02
<i>Dothideomyces</i> sp. 3360_615	A	HM488599	235	231/236	98	-	0.25	-	0.05	-	-	-	-	0.04	-	-	-	0.02
<i>Dothideomyces</i> sp. 3360_625	A	MF486985	236	231/239	97	-	-	-	-	-	-	-	-	-	0.18	-	0.08	0.02
<i>Hyaloscypha aureliella</i>	A	AB546942	237	228/237	96	0.10	0.08	-	0.07	-	-	-	-	-	-	-	-	0.02
<i>Rhizopogon cf. salebrosus</i>	B	KJ595008	345	337/345	98	0.10	-	-	0.05	0.03	-	-	0.02	-	-	-	-	0.02
<i>Scytalidium album</i>	A	MF992676	231	229/241	95	-	-	-	-	-	-	-	-	-	0.18	-	0.08	0.02
<i>Leotiomyces</i> sp. 3360_638	A	KF617439	233	227/237	96	-	-	-	-	-	-	-	-	0.13	0.05	-	0.08	0.02
<i>Eurotiomyces</i> sp. 3360_643	A	MH450344	281	281/281	100	-	-	-	-	0.12	-	-	0.06	-	-	-	-	0.02
<i>Dothideomyces</i> sp. 3360_655	A	KJ827642	232	224/241	93	-	0.33	-	0.07	-	-	-	-	-	-	-	-	0.02
<i>Eurotiomyces</i> sp. 3360_660	A	KJ827128	249	245/249	98	-	0.33	-	0.07	-	-	-	-	-	-	-	-	0.02
<i>Cladophialophora</i> sp. 3360_662	A	KY228825	265	264/266	99	0.03	0.08	-	0.03	-	-	-	-	0.04	0.05	-	0.04	0.02
<i>Helotiales</i> sp. 3360_664	A	EF093149	239	236/241	98	-	0.08	-	0.02	-	-	-	-	-	0.14	-	0.06	0.02
<i>Exobasidiomyces</i> sp. 3360_680	B	EU784219	271	269/294	91	-	-	0.22	0.07	-	-	-	-	-	-	-	-	0.02
<i>Archaeorhizomyces</i> sp. 3360_689	A	FJ440863	214	207/214	97	-	-	-	-	0.03	0.15	-	0.06	-	-	-	-	0.02
<i>Mycena cinerella</i>	B	KT900146	298	298/308	97	0.10	-	-	0.05	-	0.05	-	0.02	-	-	-	-	0.02
<i>Mucoromycotina</i> sp. 3360_724	M	MF482006	347	341/350	97	-	-	-	-	0.03	0.10	-	0.05	-	0.05	-	0.02	0.02
<i>Aureobasidium subglaciale</i>	A	MF001328	242	242/250	97	0.03	-	-	0.02	0.06	0.05	-	0.05	-	-	-	-	0.02
<i>Hodophilus</i> sp. 3360_734	B	KP257170	306	294/307	96	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Phomopsis columnaris</i>	A	KX610405	247	246/250	98	-	0.25	-	0.05	0.03	-	-	0.02	-	-	-	-	0.02
<i>Dothideomyces</i> sp. 3360_774	A	KC243967	232	220/233	94	-	-	-	-	0.12	-	-	0.06	-	-	-	-	0.02
<i>Leotiomyces</i> sp. 3360_791	A	KR266546	235	220/239	92	-	-	-	-	-	-	-	-	-	0.18	-	0.08	0.02
<i>Dothideomyces</i> sp. 3360_793	A	KJ827863	248	234/250	94	-	-	-	-	-	-	-	-	-	0.88	0.08	0.02	0.02
<i>Hygrocybe konradii</i> var. <i>konradii</i>	B	JF908058	313	308/313	98	-	-	-	-	-	0.20	-	0.06	-	-	-	-	0.02
<i>Mortierella amoebaoides</i>	M	GU559984	339	339/339	100	-	-	-	-	-	-	-	-	-	0.18	-	0.08	0.02
<i>Dothideomyces</i> sp. 3360_797	A	KJ827292	239	229/242	95	-	-	0.16	0.05	-	-	0.12	0.02	-	-	-	-	0.02

Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total	
						Root-lets	Soil	Nee-dles	All	Root-lets	Soil	Nee-dles	All	Root-lets	Soil	Nee-dles	All		
<i>Mortierella gamsii</i>	M	AJ878508	330	324/332	98	0.07	-	-	0.03	0.03	0.05	-	0.03	-	-	-	-	0.02	
<i>Mucoromycotina</i> sp. 3360_817	M	KR265941	327	307/319	96	-	-	-	-	-	0.15	-	0.05	-	-	-	-	0.02	
<i>Herpotrichiellaceae</i> sp. 3360_827	A	AB847033	261	233/271	86	-	-	-	-	0.09	0.05	-	0.06	-	-	-	-	0.02	
<i>Trichoderma harzianum</i>	A	MF408543	271	271/271	100	0.10	-	-	0.05	0.03	-	-	0.02	-	-	-	-	0.02	
<i>Bannozya</i> sp. 3360_834	B	KY558343	301	301/302	99	-	-	0.22	0.07	-	-	-	-	-	-	-	-	0.02	
<i>Penicillium nothofagi</i>	A	KY558626	260	260/260	100	0.03	0.16	-	0.05	-	0.05	-	0.02	-	-	-	-	0.02	
<i>Helotiales</i> sp. 3360_863	A	JX001635	240	233/240	97	-	-	-	-	-	0.05	-	0.02	-	0.14	-	0.06	0.02	
<i>Hyaloscyphaceae</i> sp. 3360_875	A	JX852344	238	231/240	96	-	-	-	-	-	-	-	-	0.17	-	-	0.08	0.02	
<i>Metapochonia bulbillosa</i>	A	MH483845	277	277/279	99	0.13	-	-	0.07	-	-	-	-	-	-	-	-	0.02	
<i>Dothideomycetes</i> sp. 3360_895	A	MF487022	238	226/238	95	0.03	0.25	-	0.07	-	-	-	-	-	-	-	-	0.02	
<i>Eurotiomycetes</i> sp. 3360_2200	A	EU624333	265	263/270	97	-	-	-	-	-	-	-	-	0.13	0.05	-	0.08	0.02	
<i>Spirosphaera</i> sp. 3360_2353	A	EF029215	241	232/242	96	0.03	-	-	0.02	-	-	-	-	0.13	-	-	0.06	0.02	
<i>Alatospora</i> sp. 3360_343	A	KF730798	232	231/240	96	-	0.08	-	0.02	-	0.10	-	0.03	-	-	-	-	0.02	
<i>Microbotryomycetes</i> sp. 3360_346	B	HG936309	300	261/311	84	-	-	0.11	0.03	-	-	-	-	-	-	0.22	0.02	0.02	
<i>Endoconidioma populii</i>	A	KX611029	257	253/257	98	-	-	0.05	0.02	-	-	0.24	0.03	-	-	-	-	0.02	
<i>Chaetothyriales</i> sp. 3360_365	A	KY228796	263	259/264	98	-	-	-	-	0.03	-	-	0.02	0.04	0.05	-	0.04	0.02	
<i>Eurotiomycetes</i> sp. 3360_374	A	KJ826974	248	241/248	97	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Agaricomycetes</i> sp. 3360_384	B	HM044549	311	310/315	98	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Helotiales</i> sp. 3360_393	A	KT268583	239	234/239	98	0.03	-	-	0.02	-	-	-	-	-	-	0.05	-	0.02	0.01
<i>Chaetothyriales</i> sp. 3360_405	A	KY228527	253	242/257	94	0.03	-	-	0.02	0.06	-	-	0.03	-	-	-	-	0.02	
<i>Leotiomyces</i> sp. 3360_409	A	FR846475	238	227/242	94	0.03	0.08	-	0.03	-	-	-	-	0.04	-	-	0.02	0.02	
<i>Flagellospora leucorhynchus</i>	A	KC834049	239	233/241	97	-	-	-	-	0.09	-	-	0.05	-	-	-	-	0.02	
<i>Leotiomyces</i> sp. 3360_426	A	MH447081	240	227/241	94	-	-	-	-	-	-	-	-	-	-	0.66	0.06	0.02	
<i>Lecanoromycetes</i> sp. 3360_430	A	KR266636	245	228/248	92	0.07	-	-	0.03	-	0.05	-	0.02	-	-	-	-	0.02	
<i>Oidiodendron</i> sp. 3360_444	A	KX640642	234	227/235	97	-	-	-	-	0.03	0.10	-	0.05	-	-	-	-	0.02	
<i>Helotiales</i> sp. E3360_451	A	LC131010	242	241/242	99	-	0.16	-	0.03	-	-	-	-	-	0.05	-	0.02	0.02	
<i>Ramularia vizellae</i>	A	NR_154914	236	236/237	99	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Leotiomyces</i> sp. 3360_457	A	JF449786	234	233/237	98	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Umbelopsis</i> sp. 3360_462	M	KT354998	294	279/294	95	-	-	-	-	0.03	0.10	-	0.05	-	-	-	-	0.02	
<i>Curvibasidium</i> sp. 3360_473	B	JX188232	308	298/309	96	-	-	-	-	-	-	-	-	-	-	0.66	0.06	0.02	
<i>Lachnum</i> sp. 3360_476	A	MH633930	237	231/238	97	0.03	0.16	-	0.05	-	-	-	-	-	-	-	-	0.02	
<i>Agaricomycetes</i> sp. 3360_499	B	JF440568	327	282/290	97	-	-	0.05	0.02	-	-	0.24	0.03	-	-	-	-	0.02	
<i>Cordyceps confragosa</i>	A	MH400797	255	255/255	100	0.07	-	-	0.03	-	-	-	-	0.04	-	-	0.02	0.02	
<i>Agaricomycetes</i> sp. 3360_510	B	HQ154242	310	302/313	96	-	-	-	-	-	0.05	-	0.02	-	0.09	-	0.04	0.02	
<i>Agaricomycetes</i> sp. 3360_511	B	FR750673	297	287/298	96	-	0.08	-	0.02	-	0.10	-	0.03	-	-	-	-	0.02	
<i>Agaricomycetes</i> sp. 3360_516	B	JF519107	301	299/304	98	-	-	-	-	-	0.15	-	0.05	-	-	-	-	0.02	
<i>Lecanoromycetes</i> sp. 3360_525	A	MH450782	250	249/256	97	0.03	-	-	0.02	0.03	0.05	-	0.03	-	-	-	-	0.02	
<i>Umbelopsis ramanniana</i>	M	AB193542	314	313/315	99	0.03	0.16	-	0.05	-	-	-	-	-	-	-	-	0.02	
<i>Alternaria infectoria</i>	A	MG978343	253	252/253	99	-	-	-	-	-	0.15	-	0.05	-	-	-	-	0.02	
<i>Eurotiomycetes</i> sp. 3360_536	A	MF485821	258	246/262	94	-	-	-	-	0.09	-	-	0.05	-	-	-	-	0.02	
<i>Capronia</i> sp. 3360_545	A	EU139148	255	239/256	91	-	-	-	-	-	-	-	-	-	-	0.66	0.06	0.02	
<i>Dothideomycetes</i> sp. 3360_548	A	MF569914	243	226/243	93	-	0.08	-	0.02	-	0.10	-	0.03	-	-	-	-	0.02	
<i>Dothideomycetes</i> sp. 3360_549	A	KP897537	243	227/244	93	-	-	0.11	0.03	-	-	-	-	-	-	0.22	0.02	0.02	
<i>Humicola fuscoatra</i>	A	KX976675	246	245/246	99	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Bannozya yamatoana</i>	B	AF444634	301	297/301	99	-	-	0.05	0.02	-	-	0.24	0.03	-	-	-	-	0.02	
<i>Leotiomyces</i> sp. 3360_568	A	KX403772	239	198/200	99	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Leotiomyces</i> sp. 3360_580	A	JQ256424	249	230/251	92	-	0.25	-	0.05	-	-	-	-	-	-	-	-	0.02	
<i>Microbotryomycetes</i> sp. 3360_583	B	LT608083	319	316/324	98	-	-	-	-	-	0.05	-	0.02	-	0.09	-	0.04	0.02	
<i>Pezizaceae</i> sp. 3360_589	A	KM576471	278	278/279	99	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Leotiomyces</i> sp. 3360_591	A	MF486932	239	232/239	97	-	0.25	-	0.05	-	-	-	-	-	-	-	-	0.02	
<i>Agaricomycetes</i> sp. 3360_592	B	GU180308	300	290/301	96	-	-	-	-	0.06	0.05	-	0.05	-	-	-	-	0.02	
<i>Leotiomyces</i> sp. 3360_597	A	KU062752	239	229/240	95	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Lepista sordida</i>	B	JQ293096	298	297/300	99	-	-	-	-	-	0.15	-	0.05	-	-	-	-	0.02	
<i>Leotiomyces</i> sp. 3360_606	A	KC966259	228	227/240	95	-	0.08	-	0.02	-	-	-	-	-	0.09	-	0.04	0.02	
<i>Peniophora</i> sp. 3360_608	A	HQ608100	238	234/243	96	0.07	0.08	-	0.05	-	-	-	-	-	-	-	-	0.02	
<i>Taphrina</i> sp. 3360_610	A	LT602860	295	293/295	99	-	-	-	-	-	0.05	0.24	0.05	-	-	-	-	0.02	
<i>Mycosphaerellaceae</i> sp. 3360_616	A	JF764806	238	227/248	92	-	-	0.11	0.03	-	-	0.12	0.02	-	-	-	-	0.02	
<i>Mortierella</i> sp. 3360_618	M	KM357302	289	282/295	96	-	-	-	-	-	-	-	-	0.04	0.09	-	0.06	0.02	
<i>Cyphellophora</i> sp. 3360_621	A	KY987519	261	259/262	99	-	-	-	-	0.03	0.10	-	0.05	-	-	-	-	0.02	
<i>Infundichalara microchona</i>	A	NR_154074	239	231/239	97	-	-	0.05	0.02	-	-	0.24	0.03	-	-	-	-	0.02	
<i>Agaricomycetes</i> sp. 3360_636	A	KU975468	299	273/301	91	-	-	-	-	0.03	0.10	-	0.05	-	-	-	-	0.02	
<i>Inocybe subnudipes</i>	B	AM882983	297	254/259	98	-	-	-	-	-	-	-	-	-	0.14	-	0.06	0.02	
<i>Leotiomyces</i> sp. 3360_650	A	FR682186	248	239/250	96	-	-	0.11	0.03	-	-	0.12	0.02	-	-	-	-	0.02	
<i>Agaricomycetes</i> sp. 3360_651	B	FJ440936	295	289/297	97	-	-	-	-	-	-	-	-	0.04	0.09	-	0.06	0.02	
<i>Stereaceae</i> sp. 3360_663	B	FR846481	301	297/301	99	-	-	-	-	-	-	-	-	0.13	-	-	0.06	0.02	
<i>Dothideomycetes</i> sp. 3360_667	A	KX909214	251	251/251	100	0.03	-	0.05	0.03	-	-	-	-	0.04	-	-	0.02	0.02	
<i>Dothideomycetes</i> sp. 3360_669	A	MH450823	229	228/230	99	-	-	-	-	0.09	-	-	0.05	-	-	-	-	0.02	
<i>Microbotryomycetes</i> sp. 3360_672	B	HQ022074	303	292/303	96	0.03	-	-	0.02	0.03	0.05	-	0.03	-	-	-	-	0.02	
<i>Helotiales</i> sp. 3360_687	A	JN655578	238	237/239	99	0.03	0.16	-	0.05	-	-	-	-	-	-	-	-	0.02	



Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total
						Root-lets	Soil	Nee-dies	All	Root-lets	Soil	Nee-dies	All	Root-lets	Soil	Nee-dies	All	
<i>Agaricomycetes</i> sp. 3360_590	B	EU784310	303	251/286	88	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Dothideomycetes</i> sp. 3360_595	A	MH452221	249	245/249	98	-	-	-	-	0.03	0.05	-	0.03	-	-	-	-	0.01
<i>Leotiomyces</i> sp. 3360_598	A	KJ542232	241	210/245	86	-	0.16	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Leotiomyces</i> sp. 3360_605	A	KF359573	248	245/249	98	-	-	-	-	-	-	-	-	0.04	-	-	0.02	0.01
<i>Eurotiomyces</i> sp. 3360_612	A	KJ827879	269	259/270	96	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Rhizoscyphus ericae</i>	A	LC131030	236	231/237	97	-	-	-	-	0.03	0.05	-	0.03	-	-	-	-	0.01
<i>Pseudotomentella tristis</i>	B	AF274771	299	299/304	98	-	-	-	-	-	-	-	-	-	0.09	-	-	0.01
<i>Candida santamariae</i>	A	LT548269	280	279/281	99	-	0.08	-	0.02	0.03	-	-	0.02	-	-	-	-	0.01
<i>Eurotiomyces</i> sp. 3360_630	A	FJ553478	232	223/234	95	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Agaricomycetes</i> sp. 3360_631	B	KP329587	286	246/267	92	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Leotiomyces</i> sp. 3360_640	A	KC019893	243	230/243	95	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Arcangeliella borziana</i>	B	AF373599	359	349/353	99	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Lophodermium autumnale</i>	A	HQ902158	238	218/240	91	-	-	0.11	0.03	-	-	-	-	-	-	-	-	0.01
<i>Sordariomyces</i> sp. 3360_649	A	KT219458	252	248/255	97	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Magnaportheales</i> sp. 3360_652	A	GQ923979	264	253/266	95	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Leotiomyces</i> sp. 3360_654	A	JF519582	239	238/241	99	-	-	-	-	-	-	-	-	0.04	0.05	-	0.04	0.01
<i>Eurotiomyces</i> sp. 3360_657	A	MF485974	250	238/257	93	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Eurotiomyces</i> sp. 3360_659	A	JQ346926	260	246/263	94	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Leotiomyces</i> sp. 3360_661	A	JN655617	238	214/239	90	-	-	-	-	0.06	-	0.03	-	-	-	-	-	0.01
<i>Mortierella</i> sp. 3360_665	M	MF077647	341	341/342	99	-	-	-	-	0.03	0.05	-	0.03	-	-	-	-	0.01
<i>Sporobolomyces symmetricus</i>	B	KJ701207	299	299/300	99	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Hygrocybe konradii</i> var. <i>konradii</i>	B	JF908058	312	310/313	99	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Chaetothriomycetidae</i> sp. 3360_670	A	KP202997	261	246/266	92	-	-	0.05	0.02	-	-	0.12	0.02	-	-	-	-	0.01
<i>Septoria taraxaci</i>	A	EF535662	239	238/239	99	-	0.16	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Paraphoma chrysanthemicola</i>	A	MH063752	235	234/235	99	-	-	-	-	0.06	-	0.03	-	-	-	-	-	0.01
<i>Saccharomyces</i> sp. 3360_675	A	KX222722	269	246/269	91	-	0.08	-	0.02	-	-	-	-	0.04	-	-	0.02	0.01
<i>Tomentolopsis</i> sp. 3360_677	B	KX168655	323	307/323	95	-	-	-	-	-	-	-	-	0.04	0.05	-	0.04	0.01
<i>Dothideomycetes</i> sp. 3360_679	A	MF486801	242	237/242	98	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Dothideomycetes</i> sp. 3360_681	A	AM901716	237	231/239	97	0.03	-	0.05	0.03	-	-	-	-	-	-	-	-	0.01
<i>Cistella</i> sp. 3360_682	A	MF494618	240	239/240	99	0.07	-	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Cladophialophora</i> sp. 3360_683	A	EU139143	255	249/257	97	0.07	-	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Leotiomyces</i> sp. 3360_684	A	FR682170	244	225/247	91	-	-	0.11	0.03	-	-	-	-	-	-	-	-	0.01
<i>Mortierella pseudozygospora</i>	M	JX975880	330	324/331	98	-	-	-	-	0.03	0.05	-	0.03	-	-	-	-	0.01
<i>Alatospora pulchella</i>	A	KF730803	239	228/243	94	0.07	-	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Archaeorhizomyces</i> sp. 3360_690	A	KJ826784	213	209/213	98	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Eurotiomyces</i> sp. 3360_691	A	MH451542	251	245/260	94	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Archaeorhizomyces</i> sp. 3360_692	A	MF569783	214	210/214	98	0.07	-	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Phaeohelotium epiphyllum</i>	A	KT876976	235	231/239	97	-	0.16	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Sordariomyces</i> sp. 3360_696	A	FJ552924	258	257/268	96	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Dothideomycetes</i> sp. 3360_697	A	FR682198	243	211/245	86	-	-	0.11	0.03	-	-	-	-	-	-	-	-	0.01
<i>Mortierella</i> sp. 3360_700	M	KF588530	331	322/332	97	0.03	0.08	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Cystofilobasidium capitatum</i>	B	KY103156	321	319/321	99	0.03	-	-	0.02	-	-	-	-	-	-	0.22	0.02	0.01
<i>Leotia lubrica</i>	A	KF836615	254	253/255	99	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Galerina</i> sp. 3360_704	B	AF251180	310	293/313	94	0.03	0.08	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Mortierella</i> sp. 3360_706	M	MF423510	351	349/351	99	-	-	-	-	0.05	-	0.02	-	0.05	-	0.02	-	0.01
<i>Agaricomycetes</i> sp. 3360_712	B	KJ026754	308	298/314	95	-	0.16	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Agaricostilbomyces</i> sp. 3360_713	B	GU327508	346	299/349	86	-	-	0.05	0.02	-	-	0.12	0.02	-	-	-	-	0.01
<i>Mortierella globulifera</i>	M	NR_077211	329	327/329	99	-	-	-	-	0.03	0.05	-	0.03	-	-	-	-	0.01
<i>Leotiomyces</i> sp. 3360_717	A	KR267062	235	222/236	94	-	0.08	-	0.02	0.03	-	-	0.02	-	-	-	-	0.01
<i>Agaricomycetes</i> sp. 3360_718	M	MF484953	287	284/288	99	-	-	-	-	0.06	-	0.03	-	-	-	-	-	0.01
<i>Devriesia</i> sp. 3360_725	A	AY251068	237	215/223	96	-	0.08	-	0.02	-	0.05	-	0.02	-	-	-	-	0.01
<i>Dothideomycetes</i> sp. 3360_726	A	LC085195	240	224/244	92	-	-	-	-	0.03	0.05	-	0.03	-	-	-	-	0.01
<i>Agaricomycetes</i> sp. 3360_729	B	MH424913	284	260/290	90	-	-	-	-	-	-	-	-	-	0.05	0.22	0.04	0.01
<i>Hypogymnia tubulosa</i>	A	MH536014	241	240/244	98	-	-	-	-	-	-	-	-	-	-	0.44	0.04	0.01
<i>Tremellomyces</i> sp. 3360_731	B	HM240826	252	245/253	97	-	-	0.11	0.03	-	-	-	-	-	-	-	-	0.01
<i>Cadophora luteo-olivacea</i>	A	MF467888	240	233/243	96	-	-	-	-	-	-	-	-	-	0.09	-	0.04	0.01
<i>Agaricomycetes</i> sp. 3360_733	B	KX115662	315	253/320	79	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Malassezia restricta</i>	B	CP030254	367	367/369	99	-	0.16	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Agaricomycetes</i> sp. 3360_738	B	KY706174	317	289/322	90	-	0.16	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Agaricomycetes</i> sp. 3360_740	B	KP257119	306	288/309	93	-	0.16	-	0.03	-	-	-	-	-	-	-	-	0.01
<i>Dothideomycetes</i> sp. 3360_744	A	FR682170	244	222/247	90	-	-	0.05	0.02	-	-	-	-	-	-	0.22	0.02	0.01
<i>Leotiomyces</i> sp. 3360_748	A	KR267045	238	231/238	97	0.03	-	-	0.02	-	0.05	-	0.02	-	-	-	-	0.01
<i>Gyromitra esculenta</i>	A	GU373505	293	291/293	99	-	-	-	-	-	-	-	-	0.04	0.05	-	0.04	0.01
<i>Arthoniomycetes</i> sp. 3360_751	A	KF617635	290	292/299	77	-	-	0.11	0.03	-	-	-	-	-	-	-	-	0.01
<i>Candida boidinii</i>	A	KP055797	279	277/279	99	-	-	-	-	0.05	-	0.02	-	0.05	-	0.02	-	0.01
<i>Dothideomycetes</i> sp. 3360_756	A	KJ826706	236	224/237	95	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Penicillium chabudae</i>	A	NR_144845	257	256/257	99	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Ramalina</i> sp. 3360_758	A	JN084059	250	239/250	96	-	-	-	-	-	-	-	-	-	-	0.44	0.04	0.01
<i>Exobasidium arescens</i>	B	FJ896135	294	291/295	99	0.03	0.08	-	0.03	-	-	-	-	-	-	-	-	0.01



Table S1 (continued)

Taxon	P *	GenBank reference	Seq. bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total	
						Root-lets	Soil	Nee-dles	All	Root-lets	Soil	Nee-dles	All	Root-lets	Soil	Nee-dles	All		
<i>Phaeosphaeria</i> sp. 3360_762	A	KJ529006	247	246/249	99	-	-	0.11	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Dothideomyces</i> sp. 3360_763	A	MF486423	248	242/249	97	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Agaricomycetes</i> sp. 3360_764	B	MF483501	316	312/318	98	0.07	-	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Cladophialophora</i> sp. 3360_766	A	MG597449	277	277/278	99	-	-	-	-	-	-	-	-	0.04	0.05	-	-	0.04	0.01
<i>Cyphellophora</i> sp. 3360_770	A	KC191577	253	242/260	93	-	-	-	-	-	-	-	-	-	-	-	0.44	0.04	0.01
<i>Leotia lubrica</i>	A	EU784369	249	249/254	98	-	-	-	-	-	-	-	-	0.04	0.05	-	-	0.04	0.01
<i>Dothideomyces</i> sp. 3360_775	A	KJ827253	241	241/244	99	0.03	-	0.05	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Leotiomycetes</i> sp. 3360_778	A	KC834048	244	229/245	93	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Tetracladium</i> sp. 3360_783	A	KT270284	240	236/240	98	-	-	-	-	0.03	0.05	-	0.03	-	-	-	-	-	0.01
<i>Pseudeurotium</i> sp. 3360_785	A	KY432737	235	232/241	96	-	0.08	-	0.02	-	0.05	-	0.02	-	-	-	-	-	0.01
<i>Diodendron</i> sp. 3360_786	A	AB986456	235	234/235	99	-	-	-	-	-	-	-	-	0.09	-	-	-	0.04	0.01
<i>Glomus</i> sp. 3360_792	M	KF836948	284	281/284	99	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Sordariomycetes</i> sp. 3360_799	A	HG936858	248	247/249	99	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Sordariomycetes</i> sp. 3360_805	A	KJ828097	230	226/234	97	-	0.08	-	0.02	0.03	-	-	0.02	-	-	-	-	-	0.01
<i>Phialocephala</i> sp. 3360_811	A	KJ817289	236	232/240	97	0.07	-	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Penicillium</i> sp. 3360_812	A	HM036609	252	240/254	94	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Helotiales</i> sp. 3360_815	A	KY228719	237	217/239	91	-	0.08	-	0.02	0.03	-	-	0.02	-	-	-	-	-	0.01
<i>Dothideomyces</i> sp. 3360_818	A	MF487115	229	225/234	96	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Hygrocybe spadicea</i>	B	KF291201	324	316/326	97	-	-	-	-	0.03	0.05	-	0.03	-	-	-	-	-	0.01
<i>Dothideomyces</i> sp. 3360_822	A	KJ827275	240	231/245	94	0.07	-	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Leotiomycetes</i> sp. 3360_824	A	KJ827591	241	238/242	98	-	-	-	-	0.03	-	-	0.02	-	0.05	-	-	0.02	0.01
<i>Leotiomycetes</i> sp. 3360_828	A	NR_156543	236	217/240	90	-	-	0.11	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Eurotiomycetes</i> sp. 3360_833	A	MH451802	256	251/256	98	0.03	-	-	0.02	-	0.05	-	0.02	-	-	-	-	-	0.01
<i>Agaricomycetes</i> sp. 3360_835	B	KT351650	313	279/314	89	-	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Slooffia cresolica</i>	B	KY105427	307	302/308	98	-	-	-	-	-	-	-	-	0.04	0.05	-	-	0.04	0.01
<i>Dothideomyces</i> sp. 3360_837	A	LN714003	237	224/239	94	-	-	-	-	-	-	0.24	0.03	-	-	-	-	-	0.01
<i>Ascomycota</i> sp. 3360_839	A	KX815494	256	247/260	95	-	-	0.11	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Agaricomycetes</i> sp. 3360_840	B	MH270630	320	291/329	88	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Thelephora</i> sp. 3360_842	B	LC029037	309	304/309	98	-	-	-	-	-	-	-	-	0.04	0.05	-	-	0.04	0.01
<i>Dothideomyces</i> sp. 3360_843	A	KJ827604	239	236/241	98	-	0.16	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Aquapoterium</i> sp. 3360_844	A	NR_111345	235	224/238	94	0.03	-	-	0.02	-	-	-	0.04	-	-	-	-	-	0.01
<i>Dimorphospora</i> sp. 3360_845	A	KY038042	237	224/237	95	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Solicoccozyma aerea</i>	B	KY105431	320	320/323	99	-	-	-	-	-	0.05	-	0.02	-	0.05	-	-	0.02	0.01
<i>Mortierella alpina</i>	M	KX343159	340	340/344	99	-	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Leptosphaeria biglobosa</i>	A	MF687677	249	246/250	98	-	0.08	-	0.02	-	0.05	-	0.02	-	-	-	-	-	0.01
<i>Dothideomyces</i> sp. 3360_854	A	MF486220	250	250/251	99	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Leotiomycetes</i> sp. 3360_856	A	HQ022246	241	236/242	98	-	0.16	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Leotiomycetes</i> sp. 3360_857	A	FJ378856	237	232/238	97	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Russula amoenoides</i>	B	KU205283	370	363/373	97	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Leotiomycetes</i> sp. 3360_864	A	KR266584	237	217/238	91	0.03	-	-	0.02	-	-	-	0.04	-	-	-	-	-	0.01
<i>Eurotiomycetes</i> sp. 3360_865	A	KX776979	257	246/250	98	-	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Agaricomycetes</i> sp. 3360_867	B	KP889587	281	273/291	94	0.03	-	-	0.02	0.03	-	-	0.02	-	-	-	-	-	0.01
<i>Myxotrichum cancellatum</i>	A	AF062811	235	234/235	99	0.03	-	-	0.02	-	-	-	-	0.04	-	-	-	-	0.01
<i>Dothideomyces</i> sp. 3360_877	A	MF486382	247	239/249	96	-	0.08	-	0.02	-	0.05	-	0.02	-	-	-	-	-	0.01
<i>Tremella</i> sp. 3360_878	B	NR_155908	258	250/260	96	-	-	0.11	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Penicillium</i> sp. 3360_879	A	AJ608959	248	247/257	96	-	-	-	-	-	-	-	-	0.04	0.05	-	-	0.04	0.01
<i>Tremellomycetes</i> sp. 3360_881	B	KU062911	322	287/333	86	-	-	0.11	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Monocillium griseo-ochraceum</i>	A	NR_156406	267	266/268	99	-	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Leotiomycetes</i> sp. 3360_883	A	JQ313102	242	241/243	99	-	-	-	-	-	-	-	-	0.04	0.05	-	-	0.04	0.01
<i>Agaricomycetes</i> sp. 3360_885	B	KX115682	289	274/289	95	-	-	-	-	0.06	-	-	0.03	-	-	-	-	-	0.01
<i>Capnobotryella</i> sp. 3360_887	A	AJ972856	236	236/237	99	-	0.08	-	0.02	-	-	0.12	0.02	-	-	-	-	-	0.01
<i>Leohumicola minima</i>	A	KY228692	238	233/240	97	-	-	-	-	0.06	-	-	0.03	-	-	-	-	-	0.01
<i>Tausonia pullulans</i>	B	LC202045	312	311/314	99	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Meliniumyces</i> sp. 3360_890	A	EF093175	236	235/237	99	0.07	-	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Dothideomyces</i> sp. 3360_893	A	KJ827863	248	247/249	99	-	-	0.05	0.02	-	-	-	-	-	-	-	0.22	0.02	0.01
<i>Metapochonia suchlasporia</i>	A	MG813181	291	290/291	99	-	0.08	-	0.02	-	-	-	-	-	0.05	-	-	0.02	0.01
<i>Sordariomycetes</i> sp. 3360_897	A	KJ826970	319	315/322	98	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Pochonia cordycepsociata</i>	A	KM263567	276	267/269	99	-	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Chaetosphaeria</i> sp. 3360_899	A	JN559404	240	235/242	97	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Leotiomycetes</i> sp. 3360_902	A	KJ826609	241	239/244	98	-	-	-	-	0.06	-	-	0.03	-	-	-	-	-	0.01
<i>Amphinema</i> sp. 33360_907	B	JN943898	281	267/290	92	0.07	-	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Agaricomycetes</i> sp. 3360_909	B	FJ553628	275	272/277	98	0.07	-	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Mycena epipterygia</i> var. <i>lignicola</i>	B	KP454034	307	306/310	99	0.07	-	-	0.03	-	-	-	-	-	-	-	-	-	0.01
<i>Tolypocladium sinense</i>	A	KX082969	244	243/246	99	-	0.08	-	0.02	-	-	-	-	-	0.05	-	-	0.02	0.01
<i>Leotiomycetes</i> sp. 3360_916	A	HQ021922	239	224/242	93	-	-	-	-	-	0.10	-	0.03	-	-	-	-	-	0.01
<i>Eurotiomycetes</i> sp. 3360_917	A	KY484990	293	270/294	92	-	-	-	-	-	-	-	-	0.04	0.05	-	-	0.04	0.01
<i>Leotiomycetes</i> sp. 3360_918	A	KJ827050	238	220/240	92	-	0.08	-	0.02	-	0.05	-	0.02	-	-	-	-	-	0.01
<i>Verticillium leptobactrum</i>	A	KC810999	282	277/282	98	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01
<i>Agaricomycetes</i> sp. 3360_921	B	AB854709	287	285/288	99	-	-	-	-	-	-	-	-	-	0.09	-	-	0.04	0.01

Table S1 (continued)

Taxon	P *	GenBank reference	SeqL, bp	Compared, bp	Similarity, %	Bogičevica				Visitor				Zeletin				Total
						Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All	Root-lets	Soil	Needles	All	
<i>Archaeorhizomyces</i> sp. 3360_922	A	JQ347010	218	201/218	92	-	-	-	-	0.05	-	0.02	0.04	-	-	0.02	0.01	
<i>Leotiomyces</i> sp. 3360_925	A	MF486962	240	237/240	99	-	0.08	-	0.02	-	-	-	-	-	0.05	-	0.02	
<i>Pseudotomentella</i> sp. 3360_938	B	AB848561	286	232/254	91	-	-	-	-	-	-	-	-	0.09	-	-	0.04	
<i>Eurotiomyces</i> sp. 3360_1003	A	NR_121503	269	248/270	92	-	-	0.11	0.03	-	-	-	-	-	-	-	-	
<i>Leotiomyces</i> sp. 3360_1041	A	FJ554315	235	233/236	99	-	0.16	-	0.03	-	-	-	-	-	-	-	-	
<i>Hyaloscypha</i> sp. 3360_1045	A	JN033434	239	239/239	100	-	0.16	-	0.03	-	-	-	-	-	-	-	-	
<i>Mollisia</i> sp. 3360_1050	A	MG195461	238	220/239	92	-	-	-	-	-	-	-	-	0.09	-	-	0.04	
<i>Agaricomycetes</i> sp. 3360_1065	B	HQ021825	302	271/316	86	-	-	-	-	0.10	-	0.03	-	-	-	-	-	
<i>Archaeorhizomyces</i> sp. 3360_1076	A	KT196163	217	215/221	97	-	-	-	-	0.10	-	0.03	-	-	-	-	-	
<i>Mycoarthritis</i> sp. 3360_1120	A	KJ735002	236	233/239	97	-	0.16	-	0.03	-	-	-	-	-	-	-	-	
<i>Dothideomyces</i> sp. 3360_1207	A	KP897314	250	228/252	90	-	-	-	-	-	-	-	-	-	-	0.44	0.04	
<i>Leotiomyces</i> sp. 3360_1276	A	KJ828491	239	226/240	94	-	-	-	-	-	-	-	-	0.04	0.05	-	0.04	
<i>Sordariomyces</i> sp. 3360_1340	A	MG160372	247	199/200	99	-	-	-	0.06	-	-	0.03	-	-	-	-	-	
<i>Leotiomyces</i> sp. 3360_1412	A	FJ553913	239	237/241	98	-	0.08	-	0.02	0.03	-	0.02	-	-	-	-	-	
<i>Leotiomyces</i> sp. 3360_1500	A	HQ021922	237	226/240	94	-	-	-	-	0.10	-	0.03	-	-	-	-	-	
<i>Lecanoromyces</i> sp. 3360_1530	A	KJ828461	237	226/239	95	-	-	-	-	-	-	-	-	0.09	-	-	0.04	
<i>Pseudogymnoascus</i> sp. 3360_1580	A	MG001401	241	241/241	100	-	-	-	-	0.10	-	0.03	-	-	-	-	-	
<i>Hymenoscyphus</i> sp. 3360_1704	A	EU700265	236	227/235	97	0.07	-	-	0.03	-	-	-	-	-	-	-	-	
<i>Helotiales</i> sp. 3360_1705	A	MF043976	241	232/241	96	-	-	0.11	0.03	-	-	-	-	-	-	-	-	
<i>Microbotryomyces</i> sp. 3360_1758	B	KP891320	316	293/324	90	-	-	-	-	-	-	-	-	-	-	0.44	0.04	
<i>Microbotryomyces</i> sp. 3360_1792	B	FM997952	302	301/303	99	-	-	-	-	-	-	-	-	0.09	-	-	0.04	
<i>Leotiomyces</i> sp. 3360_1801	A	FJ553147	250	226/252	90	0.03	-	-	0.02	-	0.05	-	0.02	-	-	-	-	
<i>Eurotiomyces</i> sp. 3360_1819	A	MF485821	262	245/264	93	-	-	-	-	0.10	-	0.03	-	-	-	-	-	
<i>Dothideomyces</i> sp. 3360_1835	A	FR682251	242	222/245	91	-	-	0.05	0.02	-	-	0.12	0.02	-	-	-	-	
<i>Articulospora tetracladia</i>	A	LC131005	240	240/240	100	0.07	-	-	0.03	-	-	-	-	-	-	-	-	
<i>Alternaria cheiranthi</i>	A	AF229457	250	248/249	99	-	-	0.05	0.02	-	0.05	-	0.02	-	-	-	-	
<i>Eurotiomyces</i> sp. 3360_1939	A	HQ022099	256	244/257	95	-	-	-	-	0.06	-	0.03	-	-	-	-	-	
<i>Agaricomycetes</i> sp. 3360_1958	B	KC753430	317	311/318	98	0.03	0.08	-	0.03	-	-	-	-	-	-	-	-	
<i>Glutinoglossum peregrinans</i>	A	KX694173	263	260/269	97	-	-	-	-	0.10	-	0.03	-	-	-	-	-	
<i>Eurotiomyces</i> sp. 3360_1998	A	KM023206	269	255/273	93	-	-	-	-	0.06	-	0.03	-	-	-	-	-	
<i>Dothideomyces</i> sp. 3360_1999	A	KF983522	247	228/250	91	-	-	-	-	-	-	-	-	-	-	0.44	0.04	
<i>Hypholoma sublateralium</i>	B	KX449453	304	304/305	99	-	-	-	-	-	-	-	-	0.09	-	-	0.04	
<i>Hygrocybe</i> sp. 3360_2205	B	KF291176	318	310/326	95	-	-	-	-	0.10	-	0.03	-	-	-	-	-	
<i>Cladophialophora</i> sp. 3360_2221	A	GU446638	267	263/268	98	0.07	-	-	0.03	-	-	-	-	-	-	-	-	
<i>Agaricomycetes</i> sp. 3360_2245	B	MF569455	306	303/314	96	-	0.08	-	0.02	0.03	-	0.02	-	-	-	-	-	
<i>Paraleptosphaeria</i> sp. 3360_2390	A	KY554203	247	247/247	100	-	-	-	-	-	-	-	-	0.04	-	-	0.02	
<i>Sordariomyces</i> sp. 3360_2437	A	KU061960	260	97/105	92	-	-	0.11	0.03	-	-	-	-	-	-	-	-	

Note: P – Phylum, SeqL – Sequence Length; \* A – Ascomycota, B – Basidiomycota, M – Mucoromycotina.