Fine-scale spatial diversity of saproxylic fungi in coarse woody debris revealed by DNA sequencing.

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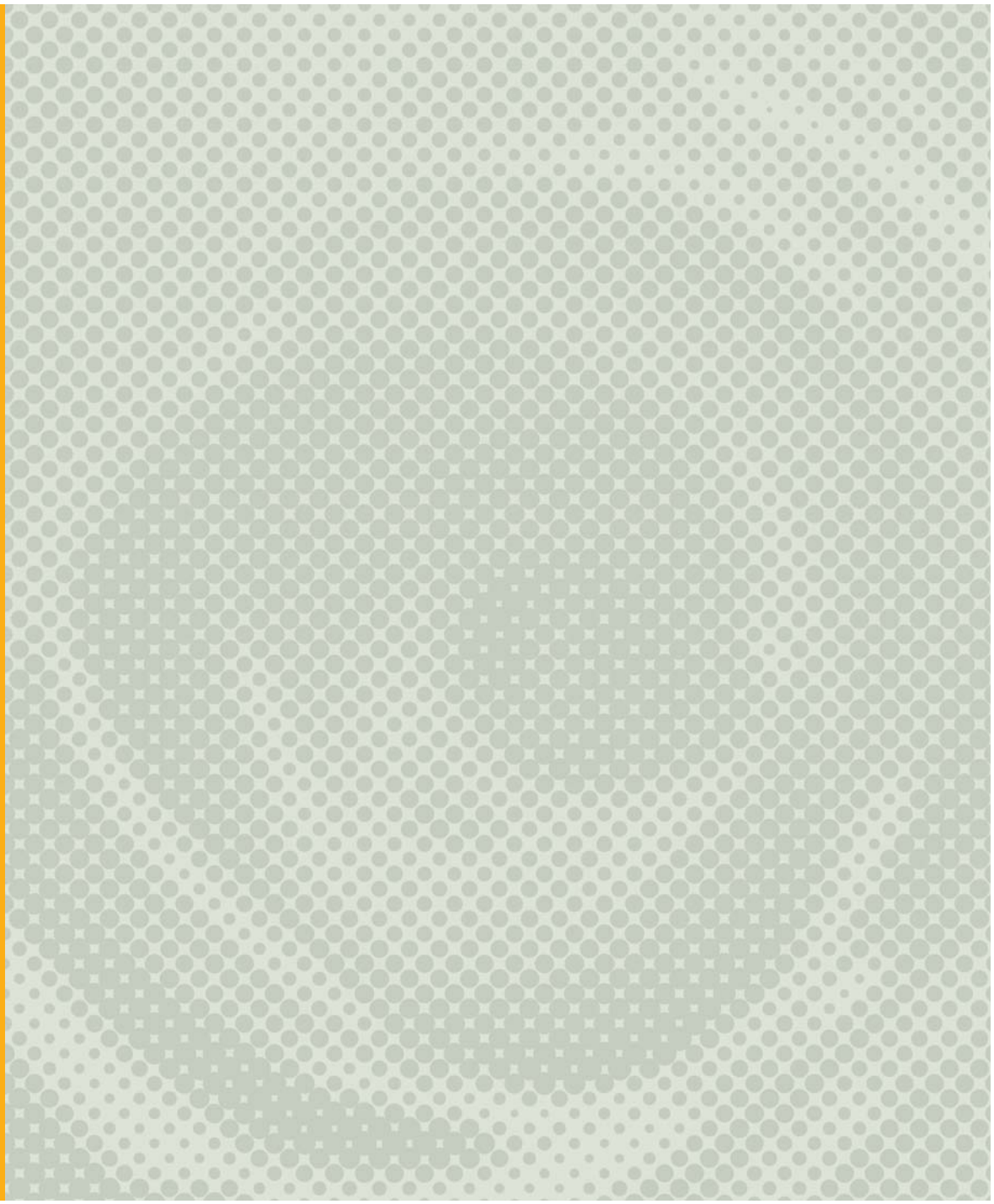

Foreword

With this thesis I am ending my master degree in General Ecology at the Department of Ecology and Natural Resource Management, Norwegian University of Life Sciences (UMB).

From the first semester at UMB I knew that I was going to specialize within forest ecology. At a field trip to Østmarka forest reserve with Vidar Selås and Sigmund Håvard the fall 2003 I was introduced to the concept coarse woody debris for the first time, and found it very interesting. A couple of days later I watched a nature program on the television in this program they interviewed a forest ecologist. That day I decided to become a forest ecologist my self.

I would like to thank my main supervisor professor Mikael Ohlson for professional assistance with the thesis, for coming up with the approach to the problem in this thesis and for quick and constructive feed back on the drafts. I would also like to thank you for always having time to a small talk about forest ecology. Great thanks should also be given to my co supervisor associated professor Håvard Kauserud (UIO) for professional assistance with the thesis and for introducing me to the interesting world of saproxylic fungi and genetics.

Tor Erik Brandrud was a tremendous help in the field where he helped me locate the logs examined in this study. He also helped me classify the different species of fungi, thank you. I would also like to thank Cecilie Mathiesen for assisting me at the laboratories in Oslo, Katrine Eldegard for helping me out with the statistical analyses and Marie L. Davey, Johan Asplund and Anders Røynstrand for reading through the manuscript and coming with important suggestions to corrections in the text.

But most of all I would like to thank my wife Anita for her patience the past six years.

Finally a little message to my self: remember to relax in the evenings now when you have no more homework. Go swim in all the small forest lakes, sit quietly in the forest and look for moose or simply go fishing in the evening sun.

Ås. 8. may 2009.

John Wirkola Dirksen
Forest Ecologist

Abstract

Two different methods: fruiting body registration and DNA sequencing were compared to see which one detected most species of saproxylic fungi from four logs of *Picea abies* in southern Norway. DNA sequencing was superior detecting 89 different OTU's (species) while the fruiting body registration detected only 29 species. The differences were most pronounced within ascomycetes where 39 OTU's were detected from DNA sequencing, while only one species was found as fruiting body. Many different groups of fungi were registered within the logs (wood decaying fungi, plant pathogens, mycoparasites, entomopathogens, mycorrhizal fungi, and sugar fungi). The diversity of fungi differed between the logs but also within individual wood discs from a single log. Due to a predetermined sampling method I was able to do statistical interference about the distribution of the detected OTU's. *Antrodia serialis* showed statistically differences in the distribution within and between logs. *Phellinus nigrolimitatus* showed no significant differences in its distribution. Species accumulation curves for all four logs showed no sign of leveling off. Three red-listed species *P. nigrolimitatus, Phlebia firma* and *Oligoporus placentus* were all detected with DNA sequencing from logs where no fruiting bodies from these species were recorded. The bottom line is that DNA sequencing gives scientists an opportunity to study saproxylic fungi communities that are other wise hidden from the naked eye.

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1.0. Introduction

Coarse woody debris (CWD) is one of the most important ecological structures in boreal forest ecosystems (Harmon et al. 1986; Jonsson et al. 2005; Samuelsson et al. 1994; Siitonen 2001). For example, 4000–5000 saproxylic (dead wood dependent) species are registered in Finland, which represents about 20-25% of all the species living in Finnish forests (Siitonen (2001). In Sweden the number of saproxylic species registered is 6000–7000 (Dahlberg & Stokland 2004). Insects and fungi are the two groups of organism having most species known to be associated with dead wood. In Sweden 3000 insect species and 2500 fungi species are saproxylic (Dahlberg & Stokland 2004).

Saproxylic fungi occurring on CWD (mostly downed logs) have been studied extensively (Bader et al. 1995; Berglund et al. 2005; Høiland & Bendiksen 1996; Lindblad 1998; Penttila et al. 2004; Renvall 1995; Sippola et al. 2001) and see Lonsdale et al. (2008) for a recent review. Most studies have been based on the registration of fruiting bodies from saproxylic fungi represented on CWD. When using this method fruiting bodies of saproxylic fungi found on individual logs in an area are registered. The advantages with this method are that it is possible to survey considerable amounts of CWD, i.e. many logs, in a relatively short time over a large area and because the method is not destructive, it is possible to use it in forest reserves. Sippola et al. (2004) compared fruiting bodies of saproxylic fungi from sites with different logging regimes and found that the total species number did not differ between these sites. However, species indicative of old-growth forests and species considered as threatened (red-listed) were not found in sites with more than 150 stumps/ha. The communities of wood decaying fungi found in old-growth forest versus managed forest have been compared by Penttila et al. (2004) and they found that stands with old-growth forests (age 129-198 years, no or only few cut stumps) on average had 80% more species than mature forest stands (<120 years, cut stumps abundant) and 38% more species than over-mature forest stands (age >120 years, cut stumps abundant). Decay class (Sippola et al. 2004), diameter (Renvall 1995) and age class (Penttila et al. 2004) also affect the fungal communities in CWD. The amount of CWD in an area is important for saproxylic fungi; more species are found in close vicinity to CWD rich areas (Edman et al. 2004; Sippola & Renvall 1999). Ohlson et al. (1997) has shown that the amount of CWD *per se* is more important for saproxylic fungi than long-term forest stand continuity. Furthermore, the community of saproxylic fungi differs between CWD and fine woody debris (FWD). Norden et al. (2004)

and Kruys & Jonsson (1999) found that if the same volume of CWD and FWD were compared, the number of species was highest for FWD. However, when fruiting bodies are used to describe the diversity of saproxylic fungi, some species will always be overlooked since many fungi produce short-lived ephemeral fruiting bodies, typically only lasting for a few days to weeks. Most fungal mycelia might also need considerable time until a fruiting potential is obtained. Furthermore, many fungi produce only microscopic fruiting structures (e.g. conidia) and, hence, are not possible to observe by eye.

Different DNA analysis techniques have made it possible to detect fungi in their microbial stage inside their substrates, e.g. endophytic fungi in plants (Rodriguez et al. 2009) or decaying logs (Allmér et al. 2006). Among the different techniques, DNA sequencing is much used to characterize the composition of fungal communities (e.g. O'Brien et al. 2005). When a DNA sequence has been obtained directly from the environment (i.e. environmental sequencing) or from cultured fungal mycelia with unknown taxonomic affinity, this sequence can be compared to sequences available in public databases such as GenBank. Based on the sequence similarity to sequences with known taxonomic affiliation in GenBank it is possible, though with a certain degree of uncertainty, to indicate which species or genus the unknown sequence belongs to. In this context, the term Operational Taxonomic Unit (OTU) are used as an approximation for species due to the uncertain taxonomic belonging.

DNA sequencing has been used in many studies of saproxylic fungi in both living and dead wood. Vasiliauskas et al. (1996) and Vasiliauskas & Stenlid (1998) used DNA sequencing to identify saproxylic fungi in bark peeling wounds on Norway spruce (*Picea abies*) stems. In two other studies, Vasiliauskas et al. (2004) and Vasiliauskas et al. (2005a) analyzed which effects the biological control agent (Rotstop) had on the diversity of saproxylic fungi in Norway spruce stumps and found that after four and six years treatment the species richness of fungi were lower in treated stumps. The fungal colonization pattern on exposed wood discs was investigated by Vasiliauskas et al. (2005b), they concluded that freshly cut CWD are important for the fungi communities in managed stands.

Two studies have compared the ability of a fruiting body registration versus DNA sequencing in detecting species of saproxylic fungi in Norway spruce. Allmér et al. (2006) looked at the fungal communities in branches and tops from slash piles from twenty trees. A total of 31 species were found as fruiting bodies and only three of these were detected using DNA sequencing. On the contrary, they found 25 species only as mycelia. Hence, a very small overlap in fungal diversity was detected with the two alternative methods. Similarly, Gustafsson (2002) compared the two methods in detecting fungal species richness in logs

from two different forest sites in Sweden. In one site 100 wood discs from a single log were investigated and 16 species were detected using DNA sequencing, while only three of these species were found as fruiting bodies. In another site, 10 different logs were examined using less intensive sampling of wood discs, and here, 25 species were detected using DNA sequencing and 14 species as fruiting bodies with an overlap of ten species.

In this study I wanted to compare the two different methods for investigating saproxylic fungal communities in CWD, i.e. fruiting body registration versus DNA sequencing. My study is based on a detailed approach to reveal spatial variation in fungal community composition on the scale of single logs. A total of 637 wood samples, originating from 49 wood discs that were cut in intervals of one meter from four separate logs in an old-growth Norway spruce forest landscape, were analyzed. The sampling method I used differs from earlier studies using DNA sequencing (Allmér et al. 2006; Gustafsson 2002; Vasiliauskas et al. 2005b) by having a predetermined pattern for selection of the wood samples. With this method the sampling becomes independent of visible fungal colonization on the wood discs, meaning that apparently non-colonized wood is also sampled. Because the samples were taken from the same location on each wood disc it is possible to make statistical inferences about the individual OTU's distribution within the logs. More specific, the aims of this study were to reveal; 1) whether a higher diversity of saproxylic fungi is detected using DNA sequencing compared to registration of fruiting bodies; 2) to what extent the methods are able to detect the overall fungal diversity in the logs, and; 3) the spatial distribution of the most frequent OTUs within logs.

2.0. Methods

2.1. Study area

The study area is located in south eastern Norway in the municipality of Siljan (UTM 32 v 0542141 6581154) in a large private-owned property (Fritzøe skoger). The area is dominated by Norway spruce forests, but Scots pine (*Pinus sylvestris*) forests are found on the dryer hills and along mires. The study area, half a hectare, is a small spruce forest of moderate productivity. No clear cuttings are found in the surrounding forest landscape but traces of selective logging are found. However, the last selective logging occurred a century ago and the study site has a multi layered stand structure with characteristics of an old-growth forest with intermediate amounts of CWD, i.e. 9.5 m^3/ha. The area is part of a forest landscape that

has been used in a research project on land-use history and ecosystem function (Bach et al. 2008; Nielsen et al. 2007; Totland et al. 2006).

2.2. Field work

Four logs of Norway spruce (hereafter named log A, B, C and D) with varying lengths and base diameters of approximately 40 cm were chosen for this study (Table 1). All logs belonged to decay class two (in average) according to the classification proposed by Renvall (1995): "*Wood fairly hard; knife penetrates ca. 1-2 cm into the wood. Bark on spruce starting to break up and small patches of epixylic cryptogams may already be found"*. All macroscopic fruiting bodies present on the four logs were registered multiple times during the period August to October 2008. The location of all fruiting bodies was registered from the base of the log as well as wood decay class (according to Renvall 1995) above each fruiting body. Agarics were collected from logs twice during the autumn period while the other fruiting bodies were collected at the end of the season before the logs were sliced (see below). All fruiting bodies were classified to species or genera (four collections of Agarics were not determined to species since they were destroyed during transport to the laboratory).

Table 1. Characteristics of the four investigated logs.

Log number	Total length (m)[1]	Diameter "base" (cm)[2]	Diameter top (cm)	Number of wood discs	Number of DNA isolates	Number of DNA sequences	Number of OTU's[3]	Number of unique OTU's
A	12.6	35	16.4	11	153	105	36	15
B	7.8	34.4	25.5	6	82	47	16	5
C	20.6	36	16	19	281	201	53	29
D	14.1	31.3	10.3	13	199	129	33	12

[1] The entire length of the log including the base where no samples were taken.
[2] Diameter where first disc was cut, in average 170 cm above the base.
[3] OTU is an abbreviation for operational taxonomic unit that again is an approximation for species.

A total of 49 wood discs were cut from the four logs with a chain saw in intervals of one meter (Table 1) and the wood discs transported to laboratory within 24 hours. No wood discs from the bases were obtained, since the bases were highly decayed compared to the other parts. The wood discs were stored in a cooler holding 4^{o}C for maximum three days until further analyses. From each wood disc thirteen wood samples (approximately 6 x 6 x 2mmn in size) were obtained from the interior of the discs to avoid contamination from the surface (Fig. 1). The sampling position of the individual wood samples from the discs was predetermined and being independent of the size of the discs (Table 2). To avoid

contamination between the different samples the wood chisel, used to cut out the samples, were sterilized over a flame between each sampling.

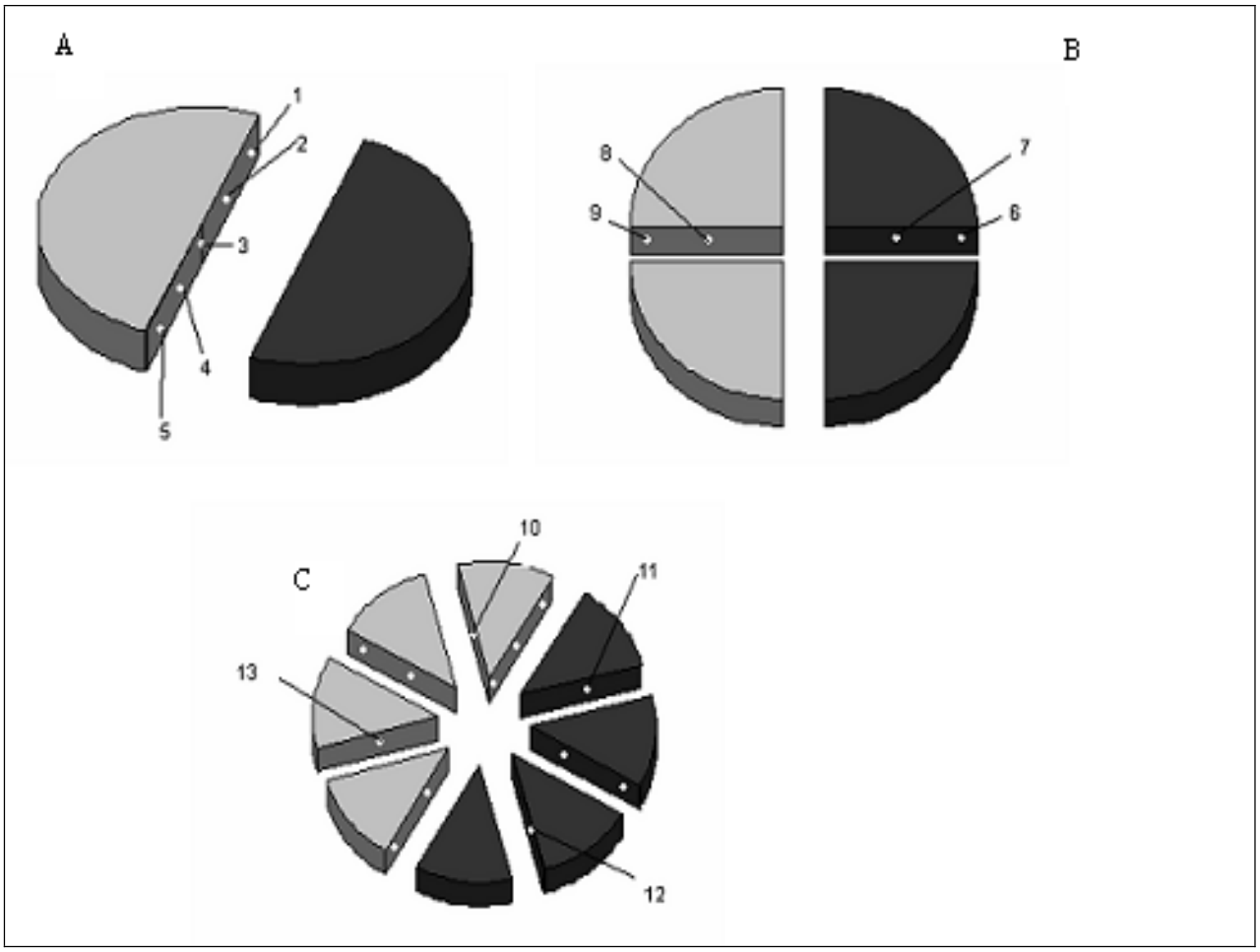

Figure. 1. All wood samples were taken from the interior of the wood discs. Samples one to five were taken along a vertical line. B) Samples six to nine was taken along a horizontal line. C) Samples ten to 13 was taken in between the horizontal and the vertical lines. Samples no. 1, 6, 5, 9 constitute circle 1. Sample no. 10, 11, 12, 13 constitute circle 2, sample no. 2, 7, 4, 8 constitute circle 3 and sample no. 3 was from the core.

Table 2. Location of the 13 wood samples.

Sample number	Wood samples location on the disc
1	Two centimeters from the edge
2	Between the middle and sample no. 1
3	In the middle of the disc
4	Between the middle and sample no. 5
5	Two centimeters from the edge
6	Two centimeters from the edge
7	Between the middle and sample no. 6
8	Between the middle and sample no. 9
9	Two centimeters from the edge
10	Between the middle and the edge of the disc
11	Between the middle and the edge of the disc
12	Between the middle and the edge of the disc
13	Between the middle and the edge of the disc

Each wood sample was placed in a Petri dish containing malt extract agar (MEA) and the antibiotics tetracycline and streptomycin to prevent bacterial growth. The Petri dishes were placed in room temperature (approximately 25ºC) until mycelial growth. In some cases only one type of mycelium grew out from the wood samples, in others several types of mycelia, and in some cases there was a mixture of bacteria and possibly yeasts, as well. In those cases with more than one type of mycelia, each of the different types was transferred to new Petri dishes. In those cases where a mixture of typically basidiomycete mycelia and sporulating ascomycetes (e.g. *Penicillium* spp.) appeared, only the basidiomycete mycelia were transferred to new petri dishes and included in further analyses. Since multiple mycelia grew out from some wood samples, the total number of DNA isolates is higher than the total number of wood samples (Table 1). When each Petri dish contained only one type of mycelia (monocultures) a piece of the mycelium (5 square mm) was put into an Eppendorf tube containing 600 mL 2% CTAB. Each tube was kept at -80^{o}C before DNA extraction.

2.3. DNA analyses

DNA extraction followed largely a 2 % CTAB protocol (Murray & Thompson 1980). The Eppendorf tubes were first placed in a heating bench holding approximately 60ºC between 30 and 45 min. After heating, 600 µl of chloroform was added and the tubes were vortexed to mix the contents, and the tubes were placed in a centrifuge and run maximum speed 13.000 rpm for 15 min. After spinning 400 µl of the upper aqueous phase was transferred to another tube containing 400 µl cold isopropanol (-18ºC) and inverted. DNA was allowed to precipitate for at least ten minutes before the tubes were centrifuged for 10 minutes at 13.000 rpm. Further, the isopropanol were poured out and 300 µl cold 70% ethanol (-18ºC) was put into the tubes, the tubes were then centrifuged for two minutes before the ethanol were poured out and the tubes were placed in a heating bench until all remaining ethanol had evaporated. Finally 60 µl of MilliQ-water was added and the tubes were stored at -20ºC before further analyses.

Primers ITS5 and ITS4 (White et al. 1990) were used for amplifying the internal transcribed spacer (ITS) region from all DNA isolates. PCR was performed in 20 µL reactions containing 12 µL 100 x diluted template DNA and 8 µL reaction mix (final concentrations: 4 X 250 mM dNTPs, 0.625 mM of each primer, 2 mM $MgCl_2$ and 1 unit DyNazymeTM II DNA polymerase [Finnzymes Oy, Espoo, Finland] on an Eppendorf thermocycler. In those cases where no amplicon was observed on the gel, an alternative PCR was performed using

PuReTaq™Ready-To-Go™ PCR beads with 5 µL of 100X diluted DNA, 2.5 µL of each 5 µM primer and 15 µM sterilized H_2O. All amplicons were run through agarose gels for a quality check before sequencing. All PCR products were sequenced using the ABI BigDye Terminator sequencing buffer and v3.1 Cycle Sequencing kit (Applied Biosystems) and visualized on an ABI PRISM 3730 Genetic Analyzer (Applied Biosystems).

All sequence chromatograms were controlled manually in BioEdit Sequence Alignment Editor version 5.0.9 (Hall 1999) and in some cases the automatic base calling corrected. All the corrected sequences were submitted to Blastn searches at NCBI to detect the closest matches in GenBank.

2.4. Statistics

To avoid overestimation of the fungal diversity, a conservative 97% similarity cut-off was used for grouping sequences into OTUs using the program Sequencher v.4.1.4 (GeneCodes, Ann Arber, Michigan, USA). Such a cut-off level may account for intraspecific variation, as well as errors (artificial mutations) generated during PCR and has commonly been used in other fungal studies for grouping ITS sequences into OTUs, as a proxy for species (e.g. O'Brien et al. 2005). For OTU's with sequence similarity higher than 97% (at least one of the sequences in the OTU), the species name of the most similar sequence in GenBank was adopted.

Three of the most frequent fungal OTU's were selected for more detailed analyses concerning their distribution within and across logs; *Antrodia serialis, Phellinus nigrolimitatus* and *Ascocoryne cylichnium. Antrodia serialis* was chosen because it is one of the most common species of wood decaying fungi in Norway. *Phellinus nigrolimitatus* is a red-listed species and information about its distributions is relevant for its conservation biology. *Ascocoryne cylichnium* was chosen because it was the only ascomycete found with fruiting bodies.

Data were analysed using SAS/STAT® 9.2 (SAS Institute, Inc., Cary, NC, USA) statistical software. The DNA sequences were count data and were not normally distributed. I fitted log-linear models, assuming a Poisson distribution and log link function. I used the scaled Pearson statistic as a measure of how well the statistical model fitted my data; a χ^2/df value close to one indicates good overall fit, and scale parameter values <0.05 or >2 where considered acceptable. To see if a single of the three OTU's were equally distributed between the logs and wood discs I ran a PROC GLIMMIX analysis in SAS.

I used the program Estimate S (http://viceroy.eeb.uconn.edu/estimates) to calculate species accumulation curves for the four different logs, with 1000 bootstrap replicates. In addition I used the program to make some extrapolation to see if it was possible to get an estimate on the total number of OTU's within the logs.

3.0. Results

From the 637 wood samples a total of 715 DNA isolates were obtained and reliable DNA sequences was obtained from sixty-seven percent (482) of the isolates. A high number of sequences (233) were discarded due to bad quality, to a large extent probably caused by the presence of yeasts that might have overgrown the mycelia, causing mixed templates in the PCR reactions. Forty-three percent of the sequences showed 99 or 100% similarity to various GenBank accessions. When the sequences were grouped into OTU's, based on a 97% similarity criterion, 89 different OTU's were detected (Appendix 1).

3.1. Fruiting body registration versus DNA sequencing

More diverse fungal communities were found in the different logs when using DNA sequencing compared to traditional fruiting body registration. A total of 89 different OTU's were registered from the four logs when using DNA sequencing while only 29 species were found as fruiting bodies (four of these fruits were classified as *Botryobasidium* spp. and two as *Hypholoma* spp., meaning that some of these actually could be the same species). In Appendix 2, all sequences detected using DNA sequencing are presented and in Appendix 3 species registered by fruiting bodies.

From log A, 36 different OTU's were registered using DNA sequencing while only eleven species were found with fruiting bodies (three collects were not identified to species). For log B 16 OTU's were registered from DNA sequencing and 10 different species were found as fruiting bodies. For the longest of the logs, log C, the number of OTU's from DNA sequencing was 53 and the number of species found as fruiting bodies was 14 (five collects were not identified to species). Thirty three different OTU's were registered from DNA sequencing from log D along with eight species registered as fruiting bodies (two collects were not identified to species).

The number of detected polypore species also differed between the two methods. *Phellinus nigrolimitatus* and *A. serialis* were detected both as fruiting bodies and as DNA sequences in log A, while *Fuscoparia viticola* was registered from DNA sequencing only.

Four different polypore species were recorded as fruiting bodies on log B: *Phellinus nigrolimitatus, Antrodia sinuosa, F. viticola* and *Skeletocutis amorphous*. *Phellinus nigrolimitatus* was the only one out of these that was also registered with DNA sequencing. In log C only one polypore (*Oligoporus placentus)* were found by DNA sequencing, while five species were found with both methods: *Antrodia sinuosa, A. serialis, Fomitopsis pinicola, F. viticola* and *Postia caesia*. In log D the only polypore species detected only as fruiting body was *F. viticola*. While the three OTU's *A. serialis, Phellinus* sp.1 and *P. nigrolimitatus* were found only with DNA sequencing. *Postia caesia* were detected with both methods.

The difference between the two methods was even more pronounced when looking at the ascomycetes. As many as 39 different OTU's obtained from DNA sequencing were ascomycetes while only one ascomycete was found as fruiting body on the four logs.

When looking at the corticoid fungi, there was a clear difference in the species found with the two methods. None of the species found as fruiting bodies were found with DNA sequencing and the other way around. The species found as fruiting bodies were *Botryobasidium spp., Hyphodontia spp., Hymenoscyphus improvisius, Hyphoderma argillaceum, Hyphoderma cf. puberum, Tubulicrinis subulatus* and *Sistotrema sernanderi.* the species registered with DNA sequencing were: *Sistotrema brinkmannii, Hypochnicium geogenium, Hypochnicium albostramineum, Hypochnicium sp. Hyphoderma praetermissum, Phlebia firma* and *Zygomycete* sp.

The two agarics *Gymnopilus picreus* and *Pholiota spumosa* were found only as fruiting bodies while a *Hypholoma* species was found with both methods. *Xeromphalina campanella,* were only found using DNA sequencing.

3.2. The distribution of sequences and OTU's within the logs

The total number of obtained sequences and OTU's varied across logs, ranging from 16 to 53 OTU's (Table 1). The number of unique OTU's (i.e. those only found in one of the four logs) also differed between the logs, from 5 to 29 (Table 1). The number of sequences obtained from the different OTU's varied. The most frequently detected OTU included 52 sequences while as many as 47 OTU's were detected with only one sequence (Fig. 2).

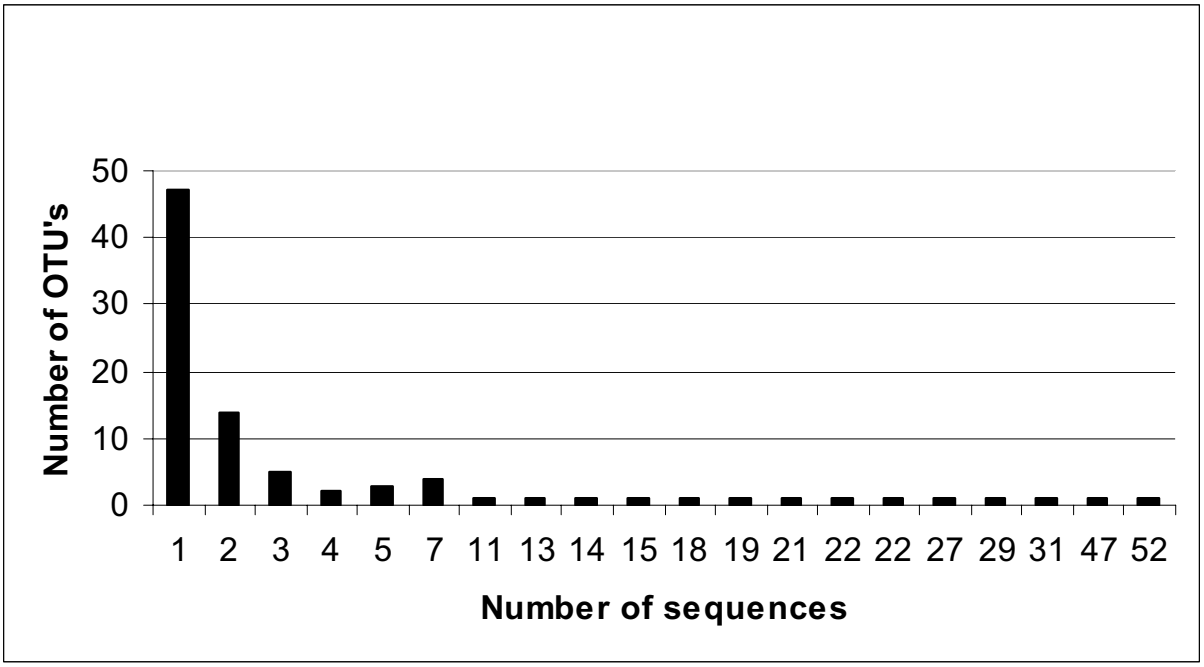

Figure 2. Number of sequences within the 89 different OTU's

Table 3. The proportion of sequences from the 14 most frequent OTU's in the different logs and wood discs (circles) varied. Highlighted OTU's (bold) were found within all four logs. The similarity between my sequences and the ones from the GenBank varies within the different OTU's e.g. some sequences had 99% similarity while other only had 97% in *Antrodia serialis*.

Name of OTU's	Number of sequences	Log A	Log B	Log C	Log D	Circle 1	Circle 2	Circle 3	Core	Similarity
Antrodia serialis	47	0.11	0.02	0.26	0.02	0.06	0.12	0.22	0.16	97-99%
***Ascocoryne cylichnium* 1**	27	0.01	0.02	0.06	0.19	0.04	0.10	0.09	0.09	92-97%
***Ascocoryne cylichnium* 2**	22	0.03	0.02	0.06	0.12	0.01	0.10	0.07	0.03	95-97%
Fomitopsis pinicola	21	-	-	0.15	-	0.03	0.05	0.10	0.06	98-99%
Hypocrea minutispora	31	0.11	-	0.09	0.13	0.13	0.08	0.09	0.03	96-100%
Leptodontidium elatius	19	0.07	-	0.05	0.08	0.06	0.07	0.05	0.03	97-99%
Mortierella sp.	13	0.15	-	0.01	-	0.03	0.03	0.04	0.09	89-91%
Penicillium spinulosum	14	0.03	0.10	0.03	0.05	0.08	0.04	0.01	0.03	97-100%
Phellinus nigrolimitatus	11	0.01	0.10	-	0.07	0.02	0.03	0.05	0.03	98-99%
Phialophora lagerbergii	15	0.04	0.02	0.02	0.09	0.04	0.03	0.05	0.09	91-100%
Talaromyces purpureus	18	-	0.07	0.11	-	0.01	0.06	0.06	0.13	97-100%
Trichoderma viride	46	0.23	0.59	0.06	0.02	0.26	0.15	0.06	0.16	96-100%
***Tulasnella* sp.**	22	0.19	0.02	0.04	0.02	0.04	0.11	0.06	-	83-85%
***Zygomycete sp.* Artz 73**	29	0.04	0.02	0.06	0.20	0.17	0.04	0.06	0.06	96-100%

For definitions to the different circles see Figure 1.

The distribution of the 14 most frequently detected OTU's differed across logs and across the defined circles within the wood discs (Table 3). For example, 11% of the sequences obtained from log A represented an OTU with taxonomic affinity to *A. serialis* while only 2% of all the sequences in log D belonged to this OTU (Table 3).

Seventy percent of the OTU's (62) were only registered in a single log. Eight OTU's were obtained from all four logs. These were among the 14 most frequent OTU's (Table 3) and belonged to seven different orders (Table 4).

Antrodia serialis showed significant differences both in the distribution across logs and within discs (Pearson χ^2/df = 1.87, Log: $F_{3,9} = 5.62$, $P = 0.02$, Circle: $F_{3,9} = 12.6$, $P = 0.001$). One of the OTU's with taxonomic affinity to *A. cylichnium* showed an uneven distribution across logs (Pearson χ^2/df = 1.46, $F_{3,12} = 4.70$, $P = 0.02$). No significant differences in the distribution of *P. nigrolimitatus* were found across logs or circles.

There was a large variation in the number of detected OTU's per sequence along the four logs (Fig. 3). The calculated species accumulation curves for the four logs did not level off, indicating that even more samples and sequences are necessary to reveal the total fungal diversity within the logs.

Of the 482 sequences, 402 could be related to a specific order (80 sequences were not defined to order, these are grouped in: Ascomycota, Zygomycetes and unknown in Table 4). The 402 sequences were grouped into 73 OTU's distributed between 18 different orders. The number of sequences obtained from the different orders differed from a single sequence in Aphyllophorales and Filobasidiales to 96 sequences in Hypocreales (Table 4). The number of OTU's found in each order varied from one OTU in several orders to 15 OTU's in Helotiales (Table 4). The order with most sequences is Hypocreales containing 96 of the 482 sequences while the order with most OTU's is Helotiales containing 15 of the 89 OTU's. Ten of the orders belonged to Basidiomycota while seven belonged to Ascomycota (Table 4).

3.4. Red-listed species

Three species from the Norwegian red-list (Kålås et al. 2006) were found in this study. *Phellinus nigrolimitatus* (near threatened) was found both as mycelia and as fruiting bodies on log A and B. In addition it was found as mycelia in log D where it was not recorded as fruiting body. *Phlebia firma* (Data deficient) was found twice as mycelia in log C but not as fruiting body. *Oligoporus placentus* (endangered) was detected once as mycelia in log C but not as fruiting body.

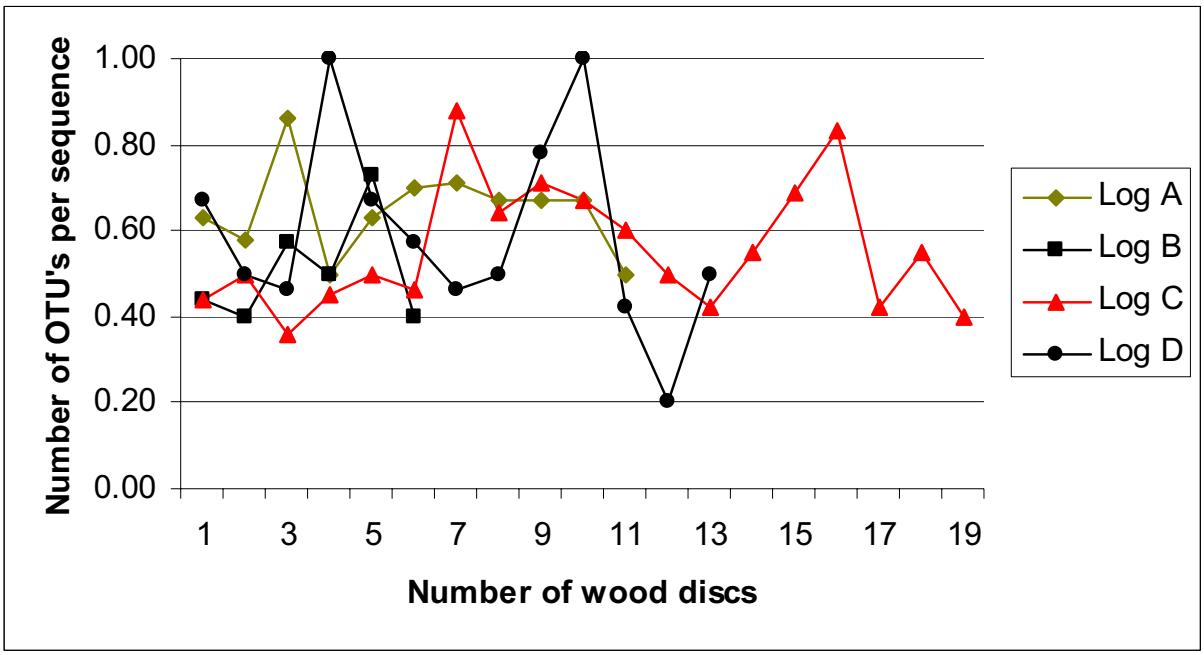

Figure 3. Number of OTU's per sequence in the different wood discs obtained for each meter along the four logs.

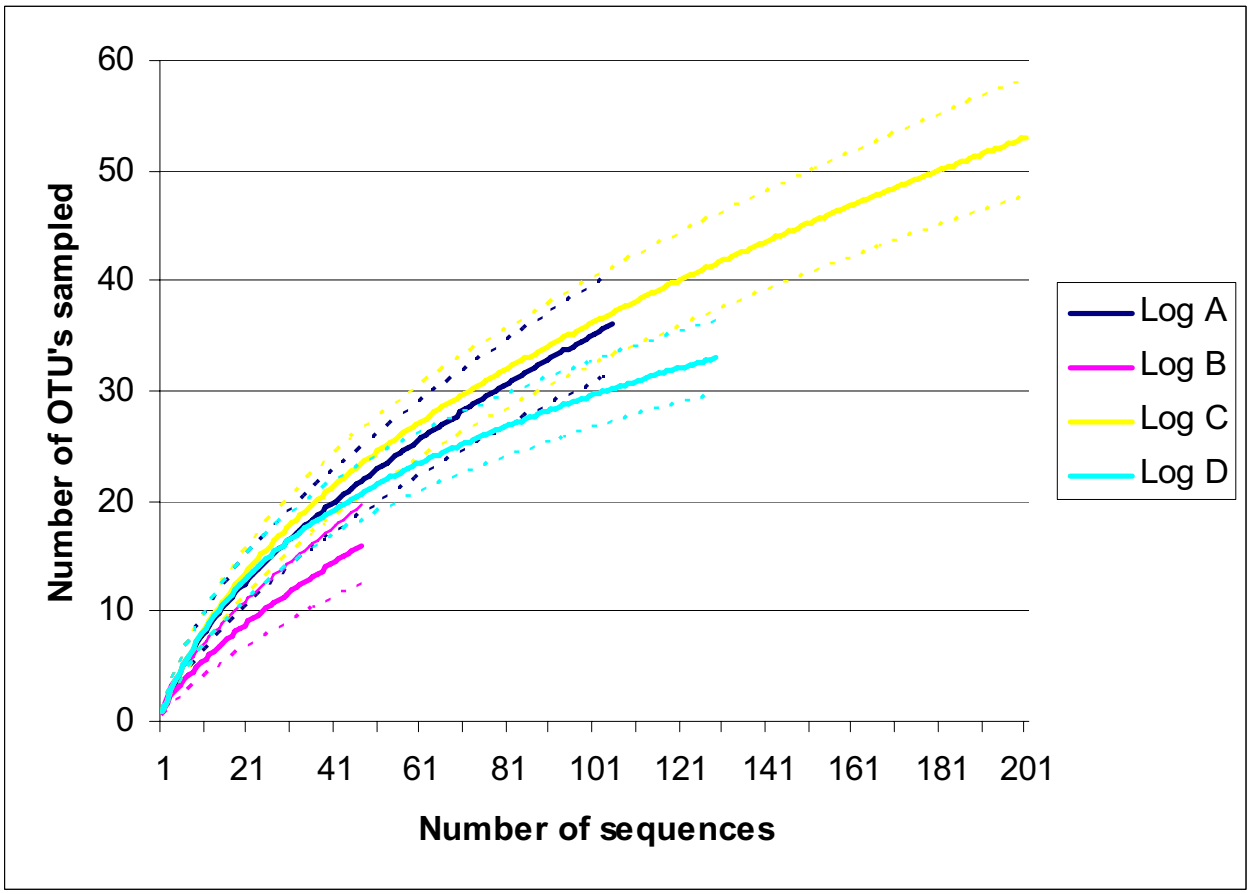

Figure 5. Species accumulation curves for all four logs, where number of OTU's are plotted against sampling intensity. Standard deviation obtained from the 1000 replicate runs are indicatged by dashed lines.

Table 4. The distribution of sequences and OTU's on taxonomic groups (orders) .The 89 OTU's belonged to 15 different orders. Highlighted orders indicates that one OTU from this order was obtained in all four logs.

Name of orders	Number of sequences in each order	Number of OTU's in each order
Agaricales (B)	2	2
Aphyllophorales (B)	1	1
Atheliales (B)	8	3
Cantharellales (B)	27	4
Chaetosphaeriales (A)	2	1
Chaetothyriales (A)	3	1
Corticiales (B)	25	6
Eurotiales (A)	46	7
Filobasidiales (B)	1	1
Helotiales (A)	76	15
Hymenochaetales (B)	13	3
Hypocreales (A)	96	11
Mortierellales (B)	12	3
Mucorales (?)	4	3
Ophiostomatales (A)	3	2
Polyporales (B)	79	8
Russulales (B)	2	1
Saccharomycetales (A)	2	1
Ascomycota (A)	39	6
Zygomecetes (Z)	29	2
Unknown (?)	12	8

B = basidiomycet. A= ascomycet. Z = zygomycete.

4.0. Discussion

Although only four logs of *Picea abies* have been investigated in this study, new information about the complex communities of fungi found within CWD is provided. Wood decaying species and plant pathogens were the two most abundant groups of fungi detected, but also mycoparasites (fungi parasitizing on other fungi), entomopathogens (species that live on insects), mycorrhizal fungi, and sugar fungi (species living of the easily accessible sugars that are released when other fungi break down cellulose and lignin within the wood) were found within the communities. A high diversity of fungal taxa was registered at a fine-scale both across and within single logs.

4.1. Fruiting body registration versus DNA sequencing

For all four logs more species were found when using DNA sequencing (89 OTU's) compared to the fruiting body registration (29 OTU's). Seven of the species found as fruiting bodies were also registered with DNA sequences. Twenty two species were only found as

fruiting bodies and not with DNA sequencing. The figures for OTU's/species detected from the individual logs were 36/11, 16/11, 53/14 and 33/8 for log A, B, C and D, respectively. The difference between the two methods was most pronounced when looking at ascomycetes, where 39 OTU's were found from DNA sequencing while only one species was found as fruiting body. Many ascomycetes produce only microscopic fruiting structures and, hence, are difficult to detect by eye. The difference between the two methods was not so pronounced when it comes to polypores, which could be because this group of fungi produces macroscopic fruiting bodies that normally are enduring for a long time. More red-listed species were found with DNA sequencing compared to fruiting bodies (see section 4.3). In the group corticoid fungi there was a clear difference between the species detected with the two methods. Seven species were found only as fruiting bodies and seven species were found only with DNA sequencing. It is likely that the species found only as fruiting bodies were growing either on the bark or in the outermost two centimetres of the logs above my samples and therefore not detected as DNA sequences. Two species of Agaricales were found as fruiting bodies and not detected as DNA sequences, these two species were growing on pieces of bark and most likely no mycelia from these species are presented within the wood.

The study by Allmér et al. (2006) also showed large variation between the two methods. From dead wood originating from both branches and tree tops Allmér et al. (2006) recorded 31 species of wood-inhabiting fungi when using fruiting body registration and only three of these were also recorded with the use of DNA sequencing. Moreover, with DNA sequencing, Allmér et al. (2006) detected 25 species that were not detected using fruiting body registration. Gustafsson (2002) registered three species as fruiting bodies and 16 species using DNA sequencing (including the three species found as fruiting bodies) from one log. When Gustafsson inspected 10 logs, a total of 38 species were detected, five species only as fruiting bodies, 23 only as mycelia and ten species were detected with both methods.

It is important, as stated by Allmér et al. (2006), to remember that fitness of saproxylic fungi differs with different classes of decay within the dead wood. The degree and location of decay within the log determines what fungi can be expected to be found in a certain area of the wood and with what frequency they are found. A registration of fruiting bodies will cover all qualities of wood (e.g. different classes of decay, and moisture) represented in a surveyed log while detection of fungi from the interior of the log using DNA sequencing depends critically on the sampling method. Some types of Ascomycota can only be detected by using DNA sequencing, since they reproduce with asexual microscopic conidia and do not produce fruiting bodies (Allmér et al. 2006). There is a seasonal variation in fruiting time for the

different lineages of fungi; Ascomycota mostly produce fruiting bodies in the spring while Basidiomycota produce fruiting bodie in the fall (Norden et al. 2004). Since I only searched the logs for fruiting bodies three times during the fall (2008) there will be a bias in my results concerning the number of ascomycetes found as fruiting bodies. Two small examples can illustrate how important it is to search for fungi during different times of the growth season: 1) *Postia caesius* was not recorded in the beginning of August and only as very small individuals the first of September and as medium sized individuals late in September; 2) No Agaricales were recorded at all in August. Environmental factors can also influence the production of fruiting bodies in fungi. Further, the spring in 2008 was dry, which may have had a negative effect on the species with an annual fruiting body, resulting in no fruit production this year.

4.2. The distribution of sequences and OTU's within the logs

I expected to see a distribution pattern where most OTU's would be most abundant in the exterior of the discs and then decrease towards the interior. However, among the 14 largest OTU's this distribution was only found for *Trichoderma viride* and *Penicillium spinulosum* two common ascomycetes. Many of the 14 largest OTU's had more registrations in the innermost circle than in the outermost circle and all of these 14 OTU's except *Tulasnella* sp. was registered in the core (Table 3). This is interesting and indicates that many of the fungi from this study might be pioneers that were presented already when the tree started to senesce, and when the tree died they started to colonise the wood from the interior.

Significant differences both in the distribution between logs and within discs were only detected for *A. serialis* (log $P = 0.02$, circle $P = 0.001$).

It is interesting that the species accumulation curves showed no signs of levelling off this indicates that the saproxylic communities are even more complex than what have been shown in this study. When performing an extrapolation of the species accumulation curves it was possible to estimate the total number of OTU's within the logs. In log A 36 OTU's was registered, according to the extrapolation 52 OTU's could be expected to be found within this log, meaning that I might have missed as many as 16 OTU's. For the three other logs the figures were: 16/24; 53/69 and 33/42 for log B, C and D, respectively. Future studies needs either more samples from individual logs or sequences of a higher quality to detect the total biodiversity of saproxylic fungi within logs.

Other studies have also had a hard time gathering enough samples to reach the accumulation level. For example, Vasiliauskas et al. (2005b) made a very accurate

examination of one wood disc. Twenty four slices each 1.5mm thick were sliced from the disc. From these 24 slices, 39 wood samples were taken, revealing 18 species 14 that were new for that wood disc (samples had already been taken from the top of the disc) nine out of the 14 species were new for the whole community. When so many new species are found in so little wood volume it becomes very difficult to give a precise estimation of the number of samples needed to get the total number of OTU's in a single log and it becomes insuperable to do estimates for forest types and even forests stands. Vasiliauskas et al. (2005a) took more than 250 samples from 30 discs and were not able to show any decrease in the species accumulation curve either. For the number of sequences obtained from each of the four logs my results is in correspondence with the species-area curve (MacArthur & Wilson 1967). A higher amount of different sequences were found as the length of the logs increased (Table 1), this is due to more niches and less competition as the volume increases. When looking at the number of OTU's from each log this trend is not so clear. Most OTU's were found in log C and fewest in log B as could be expected, but for log A and D that are respectively 12.6 and 14.1m long, more OTU's were found within log A.

To detect 18 different orders from four logs is quite stunning. It is doubtful that a fruiting body registration of four logs could register as many as 15 different species from four logs even in a species rich area. Six of the 18 different orders cover over the majority of the sequences (349) and OTU's (51) (Table 4). That many different OTU's are found within an order does not automatically mean that all of these OTU's are obtained from many sequences. For example nine of the 18 OTU's found in Helotiales have only one sequence, and from Hypocreales four of the 11 OTU's have only one sequence. Eight of the 18 orders have three or less sequences (Table 4). The two largest orders Hypocreales and Helotiales are known plant phatogens, wood degraders and mycoparasites

Forty seven of the 89 OTU's were obtained from only one sequence (Fig. 2) and 75 of the OTU's were obtained from seven or less sequences. One explanation for why so many OTU's were obtained from so few sequences could be that they are genuine rare in dead wood. Another explanation could be that I have taken to few samples to intercept their real frequency within the logs (see section 4.4). Some of the OTU's with only one sequence have taxonomic affinity to species also found in larger OTU's for example two OTU's with *A. cylichnium* and four OTU's with *A. serialis* has only one registration. For all four logs more than a third of the OTU's are unique indicating that the communities of saproxylic fungi in Norway spruce logs differs drastically between logs positioned close to each other.

4.3. Red-listed species

I found fruiting bodies from *P. nigrolimitatus* on two logs (A and B), but the results from the DNA sequencing revealed mycelia from *P. nigrolimitatus* in three of the four logs (A, B and D). Six sequences were obtained from log D while only one and four sequences were obtained from log A and B, respectively. As mentioned all the logs in this study had an average decay class of two (Renvall 1995), according to many different studies, *P. nigrolimitatus* fruiting bodies is almost entirely found on logs in a late class of decay (Bader et al. 1995; Kauserud & Schumacher 2002; Sippola et al. 2001; Stokland & Kauserud 2004; Sverdrup-Thygeson & Lindenmayer 2003). Stokland & Kauserud (2004) searched for *P. nigrolimitatus* on 4146 logs, found it on 93 logs and only once on a log that was weakly decayed (corresponding to decay class two in this study). There might be several explanations for not finding *P. nigrolimitatus* as fruiting body on log D: 1) No fruiting bodies was produced in 2008 due to abiotic factors (the spring in 2008 was very dry in the study area) but since *P. nigrolimitatus* has a perennial fruiting body and no old fruiting bodies from previously years were presented either it is doubtful that this is the right explanation; 2) The mycelia living within the log has not yet occupied enough resources or space to produce fruiting bodies; 3) The log has not yet reached a decay class suitable for *P. nigrolimitatus* to produce fruiting bodies; 4) Different genets of *P. nigrolimitatus* might produce fruiting bodies under different circumstances, it is likely that there could be different genets within the three logs. It has been documented by Kauserud & Schumacher (2002) that no less than 10 different genets can be presented in three different logs. To my knowledge it is the first time ever that mycelia from *P. nigrolimitatus* has been registered in a log without fruiting bodies, it could be very interesting to do further studies on this by examining logs in early decay classes without fruiting bodies of *P. nigrolimitatus* found in areas that are "rich" in *P. nigrolimitatus* to see if this species is actually rare or if it is only rare that it produces fruiting bodies. I guess most readers with some knowledge of saproxylic fungi will conclude that I have misjudged the decay class and that my logs are actually in decay class three, but this is not the case. When checking the decay class above each fruiting body on the individual logs and averaging this, the average was decay class two for all logs (results from the decay class investigation are shown in appendix 3). The reason for not detecting *P. nigrolimitatus* in log C might have to do with the presence of *F. pinicola* in this log. *Fomitopsis pinicola* is an aggressive pathogen pioneer wood decaying fungi that might out compete *P. nigrolimitatus*. Accordingly to Brandrud (pers. com.) *P. nigrolimitatus* is very seldom if at all found together with *F. pinicola* (at least

in Norway). It is interesting that *F. Pinicola* one of the most common wood decaying fungi in Norway only was obtained from one of the logs.

According to the Norwegian Mycological Database (NMD) the red-listed fungi *P. firma* has only been recorded 12 times before in Norway and the red-listed species *O. placentus* only five times. Both sequences that were matched to *P. firma* in the GenBank had a similarity of 99%. *Oligoporus. placentus* had a similarity of 98%. The high similarity for both of these species together with the registration of *P. nigrolimitatus* in a log without fruiting bodies makes these findings very interesting and may encourage for further work on red-listed species with the use of DNA sequencing.

4.4. Is the sampling method useful?

The method for collection of the wood samples used in this study differs from other studies using DNA sequencing (Allmér et al. 2006; Gustafsson 2002; Vasiliauskas et al. 2005b). I chose to use a predetermined pattern (Fig. 1) for the collection of wood samples independent of the proportion of area colonized by fungi as a consequence of this some samples were taken from apparently fresh wood. As a comparison Vasiliauskas et al (2005b), Allmér et al. (2006) and Gustafsson (2002) all took samples in wood that were obviously colonized by fungi. The number of wood samples (13) from my study and these other three studies also differed. Gustafsson (2002) looked for areas colonized by fungi and took three samples from within each of the colonized areas, unfortunately he did not mention how many samples this was in total for the whole log(s). Allmér et al. (2006) also collected samples within colonized areas but did not mention how many samples were taken from each disc, but they did a very interesting calculation over how large (or in reality small) fraction of the wood volume they had actually examined and found that less than 0.1% of the wood volume had been examined. Vasiliauskas et al (2005b) gathered at least six samples from each disc (in central, intermediate and outer part of the discs) if there were a high degree of fungi colonisation in some parts of the disc they gathered additional samples from these areas. My study show that samples from what assumingly looked like fresh wood resulted in fungal growth, which indicates that it gives an underestimation of OTU's if samples are only taken in areas where fungi are obviously presented. On the other hand, there is no doubt that I too have got an underestimation of fungi because I did not take additional samples in areas obviously colonized by fungi. Both methods have their advantages and disadvantages, but if it is

important to say something about the exact distribution of the species within the wood a predetermined pattern for sampling has to be made.

Normally one would exclude the fungal cultures that are obviously contaminated by yeast before isolating DNA. For example Vasiliauskas et al. (2005a) had 947 samples but only 612 (64.4%) yielded fungal cultures without contaminants and therefore only these 64,4% were used further out in their study. In a study by Lygis et al. (2004) only 52.3% of the samples resulted in fungal growth. In my study mycelia from all wood samples (also those that might have been contaminated) had to be isolated because yeast also can be saproxylic and therefore of interest in this study where we want to study all kind of fungi in the community. When using DNA from mycelia that are overgrown by a thin membrane of yeast it is often difficult to get an acceptable DNA sequence as the sequences will often have many double tops, and therefore these sequences can not be matched to sequences from the GenBank. This is the reason for why so many sequences (233) were excluded from my study. Comparisons to the above studies show that if the Petri dishes from this study that looked contaminated (dishes containing sporulating ascomycete species and yeast) had been excluded already before the DNA isolation the proportion of acceptable sequences in this study (67%) is satisfactory. Another thing that can influence how many sequences that are actually obtained from the wood samples is the growth media used, not all types of fungi can grow on artificial growth media. In this study I only used one type of growth media MEA, most likely resulting in the exclusion of some species.

5.0. Conclusion

The comparison between the two different methods shows a clear difference in the number of detected species. More species were found with DNA sequencing (89 OTU's) than what was found when searching for fruiting bodies (29 species). In one single log no less than 53 different OTU's were found and the species accumulation curves for the individual logs showed no sign of leveling off, which indicate a truly high diversity of fungi in CWD on the scale of a forest stand or a forest landscape. It is raised above any doubt that DNA sequencing gives a clearer and more precise picture of the saproxylic fungi communities within CWD compared to fruiting body inventions. The disadvantages is that DNA sequencing is very time consuming as compared to a fruiting body registration, but if we are interested in the fine scale distribution of fungi within CWD, this method is unsurpassed.

6.0. References

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Appendix 1

OTU no.	Genbank Acc. No^	Species name suggested from Genbank	Cove-rage	Simi-larity	Taxonomy
1	AF486121.1	Phialocephala sp.	94%	92%	Helotiales
2	U18957.1	Beauveriasp.	67%	82%	Hypocreales
3	AY606309.1	Phialocephala sp.	52%	88%	Helotiales
4	AB128005.1	Sporothrix sp.	100%	85%	Ophiostomatales
5	AJ878782.1	Mortierella sp.	97%	96%	Mortierellales
6	DQ093703.1	Scytalidium lignicola	97%	99%	Ascomycota
7	DQ317333.1	Nectriaceae sp.	100%	95%	Hypocreales
8	DQ276871.1	Fibulorhizoctonia sp.	100%	98%	Atheliales
9	DQ457642.1	Tulasnella sp.	99%	87%	Cantharellales
10	AF486121.1	Phialocephala dimorphospora	100%	97%	Helotiales
11	AY268211.1	Epacris root fungus	95%	89%	???
12	EU280105.1	Trichoderma hamatum	100%	100%	Hypocreales
13	AF429421.1	Hypochnicium sp.	87%	82%	Corticiales
14	AB255606.1	Tolypocladium inflatum	100%	100%	Hypocreales
15	EU139250.1	Ascomycete sp.	96%	94%	Ascomycota
16	AJ249267.1	Oligoporus placentus	100%	98%	Polyporales
17	EF152547.1	Zygomycetes sp. WD11b	94%	99%	unidentified
18	AJ344139.2	Antrodia sp.	96%	85%	Polyporales
19	EF031099.1	Mortierellales sp. WD7C	100%	100%	Mortierellales
20	FJ235953.1	Fungal sp. AB20	99%	99%	???
21	AY789395.1	Ascocoryne sp.	99%	88%	Helotiales
22	AY781215.1	Ascocoryne sp.	56%	95%	Helotiales
23	DQ270010.1	Cryptocaryon sp.	32%	88%	????
24	DQ494702.1	Xeromphalina sp.	92%	95%	Agaricales
25	AF444382.1	Filobasidium sp.	77%	83%	Filobasidiales
26	AF486121.1	Phialocephala sp.	63%	92%	Helotiales
27	AJ344139.2	Antrodia sp.	99%	91%	Polyporales
28	DQ491417.1	Antrodia sp.	99%	94%	Polyporales
29	AJ344139.2	Antrodia sp.	100%	86%	Polyporales
30	AY606307.1	Phialocephala sp.	35%	95%	Helotiales
31	EF093149.1	Helotiales sp.	100%	96%	Helotiales
32	DQ317330.1	Cadophora sp.	99%	87%	Helotiales
33	AY243948.1	Mucor sp.	100%	94%	Mucorales
34	AY243950.1	Mucor hiemalis f. corticola	100%	99%	Mucorales

35	AF441193.1	Epacrid root endophyte	98%	96%	???
36	DQ248313.1	Symbiotaphrina sp.	76%	95%	Ascomycota
37	AF125942.1	Penicillium sp.	97%	85%	Eurotiales
38	AY558618.1	Phellinus sp.	99%	95%	Hymenochaetales
39	AY532419.1	Talaromyces sp.	81%	85%	Eurotiales
40	U85797.1	Athelia sp.	98%	92%	Atheliales
41	EU294196.1	Hypocrea sp. IMI 206039			Hypocreales
42	AY781230.1	Leptodontidium elatius	96%	99%	????
43	EU871036.1	Trichoderma viride			Hypocreales
44	EU240039.1	Mortierella sp.	100%	91%	Mortierellales
45	AY373294.1	Tulasnella sp.	99%	95%	Cantharellales
46	AM292200.1	Zygomycete sp. Artz 73	99%	98%	unidentified
47	AY373315.1	Tulasnella sp.	59%	85%	Cantharellales
48	AY373934.1	Penicillium thomii	100%	99%	Eurotiales
49	AJ289619.1	Phellinus nigrolimitatus	92%	99%	Hymenochaetales
50	AJ344139.2	Antrodia serialis	99%	97%	Polyporales
51	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
52	AY854081.1	Hyphoderma praetermissum	100%	99%	Corticiales
53	L14527.1	Talaromyces sp.	100%	91%	Eurotiales
54	AF335450.1	Hypholoma sp. F14056	100%	99%	Agaricales
55	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
56	AY558653.1	Fuscoporia viticola	99%	99%	Hymenochaetales
57	EU118654.1	Phlebia firma	100%	99%	Corticiales
58	U85797.1	Athelia decipiens	99%	98%	Atheliales
59	EU128641.1	Penicillium citreonigrum	100%	100%	Eurotiales
60	AY966450.1	Antrodia sinuosa	100%	98%	Polyporales
61	AY599579.1	Postia caesia	98%	98%	Aphyllophorales
62	AF083197.1	Phialophora lagerbergii	99%	98%	Ascomycota
63	DQ317330.1	Cadophora sp. 5R24-1	100%	100%	Helotiales
64	EU139250.1	Ascomycete sp. Uf-2007a	97%	99%	Ascomycota
65	AY373924.1	Penicillium miczynskii	100%	100%	Eurotiales
66	AY789395.1	Ascocoryne sp.	99%	92%	Helotiales
67	DQ093737.1	Sistotrema brinkmannii	100%	99%	Corticiales
68	EU249343.1	Amylostereum areolatum	99%	97%	Russulales
69	AY627835.1	Epacris root fungus	99%	95%	???
70	AF429426.1	Hypochnicium geogenium	94%	98%	Corticiales
71	AY373315.1	Tulasnella sp.	98%	96%	Cantharellales
72	AM945189.1	Cylindrocladium sp.	72%	86%	Hypocreales
73	EU343826.1	Candida ergastensis	100%	100%	Saccharomycetales
74	AF033463.1	Penicillium namyslowskii	100%	100%	Eurotiales

75	DQ069046.1	Phialophora sp.	94%	96%	Ascomycota
76	AY219041.1	Fungal endophyte	99%	99%	???
77	AY268211.1	Epacris root fungus	96%	97%	???
78	AF493247.1	Ophiostoma sp.	100%	94%	Ophiostomatales
79	AY743664.1	Ambomucor sp.	94%	89%	Mucorales
80	EU240133.1	Mortierella sp. WD2G	99%	99%	Hypocreales
81	AB091215.1	Rhinocladiella sp.	99%	95%	Chaetothyriales
82	AF429421.1	Hypochnicium albostramineum	93%	99%	Corticiales
83	AY606309.1	Phialocephala dimorphospora	61%	98%	Helotiales
84	AY606303.1	Phialocephala dimorphospora	61%	98%	Helotiales
85	DQ227264.1	Hyphodiscus hymeniophilus	100%	97%	Hypocreales
86	EU139244.1	Porosphaerella cordanophora	96%	100%	Chaetosphaeriales
87	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
88	AY561210.1	Mollisia minutella	76%	99%	Helotiales
89	EF488112.1	Hypocrea koningii	99%	97%	Hypocreales

Appendix 2

OTU no.	Sample Location*	Genbank Acc. No^	Species names suggested from the GenBank	Cove-rage	Simi-larity	Taxonomy
1	1,8,1	AF486121.1	Phialocephala sp.	94%	92%	Helotiales
2	1,10,6	U18957.1	Beauveria sp.	67%	82%	Hypocreales
3	3,17,7	AY606309.1	Phialocephala sp.	52%	88%	Helotiales
4	4,0,10 A	AB128005.1	Sporothrix sp.	100%	85%	Ophiostomatales
5	1,0,3	AJ878782.1	Mortierella sp.	97%	96%	Hypocreales
6	1,1,4	DQ093703.1	Scytalidium lignicola	97%	99%	Ascomycota
7	1,2,5	DQ317333.1	Nectriaceae sp.	100%	95%	Hypocreales
8	1,4,5	DQ276871.1	Fibulorhizoctonia sp.	100%	98%	Atheliales
9	1,4,8 A	DQ457642.1	Tulasnella sp.	99%	87%	Cantharellales
10	1,7,4	AF486121.1	Phialocephala dimorphospora	100%	97%	Helotiales
11	1,8,9	AY268211.1	Epacris microphylla root	95%	89%	???
12	2,1,5	EU280105.1	Trichoderma hamatum	100%	100%	Hypocreales
13	2,3,2	AF429421.1	Hypochnicium sp.	87%	82%	Corticiales
14	2,5,8	AB255606.1	Tolypocladium inflatum	100%	100%	Hypocreales
15	3,0,3 A	EU139250.1	Ascomycete sp.	96%	94%	Helotiales
16	3,1,4	AJ249267.1	Oligoporus placentus	100%	98%	Polyporales
17	3,4,9	EF152547.1	Zygomycetes sp.	94%	99%	Zygomycete
18	3,6,3	AJ344139.2	Antrodia sp.	96%	85%	Polyporales
19	3,7,5	EF031099.1	Mortierellales sp.	100%	100%	Mortierellales
20	4,0,1 A	FJ235953.1	Fungal sp.	99%	99%	???
21	4,2,6 A	AY789395.1	Ascocoryne sp.	99%	88%	Helotiales
22	1,10,5	AY781215.1	Ascocoryne sp.	56%	95%	Helotiales
23	1,3,10 A	DQ270010.1	Cryptocaryon sp.	32%	88%	????
24	1,5,11	DQ494702.1	Xeromphalina sp.	92%	95%	Agaricales
25	1,6,11 B	AF444382.1	Filobasidium sp.	77%	83%	Filobasidiales
26	3,11,9	AF486121.1	Phialocephala sp.	63%	92%	Helotiales
27	3,12,7	AJ344139.2	Antrodia sp.	99%	91%	Polyporales
28	3,13,3	DQ491417.1	Antrodia sp.	99%	94%	Polyporales
29	3,14,3	AJ344139.2	Antrodia sp.	100%	86%	Polyporales
30	3,15,1	AY606307.1	Phialocephala sp.	35%	95%	Helotiales
31	3,15,3 A	EF093149.1	Helotiales sp.	100%	96%	Helotiales
32	3,15,7	DQ317330.1	Cadophora sp.	99%	87%	Helotiales
33	3,18,6	AY243948.1	Mucor sp.	100%	94%	Mucorales
34	3,7,10	AY243950.1	Mucor hiemalis f. corticola	100%	99%	Mucorales
35	4,10,4	AF441193.1	Epacrid root endophyte	98%	96%	???
36	4,12,2	DQ248313.1	Symbiotaphrina sp.	76%	95%	Ascomycota
37	4,5,12	AF125942.1	Penicillium sp.	97%	85%	Eurotiales

38	4,9,12	AY558618.1	Phellinus sp.	99%	95%	Hymenochaetales
39	3,11,13	AY532419.1	Talaromyces sp.	81%	85%	Eurotiales
40	3,14,11	U85797.1	Athelia sp.	98%	92%	Atheliales
41	1,0,1	DQ083015.1	Hypocrea minutispora	98%	99%	Hypocreales
41	1,0,11	DQ083015.1	Hypocrea minutispora	98%	98%	Hypocreales
41	1,0,7	DQ083015.1	Hypocrea minutispora	98%	98%	Hypocreales
41	1,1,11	DQ083015.1	Hypocrea minutispora	99%	99%	Hypocreales
41	1,3,8	DQ083015.1	Hypocrea minutispora	98%	96%	Hypocreales
41	1,4,2	EU294196.1	Hypocrea sp. IMI 206039			Hypocreales
41	1,7,5	DQ083015.1	Hypocrea minutispora	98%	99%	Hypocreales
41	1,8,5	DQ083015.1	Hypocrea minutispora	98%	99%	Hypocreales
41	3,10,5	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	3,14,9	EU294196.1	Hypocrea sp.	100%	97%	Hypocreales
41	3,15,13	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	3,17,10	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	3,17,6	EU294196.1	Hypocrea sp. IMI 206039	99%	98%	Hypocreales
41	3,18,13	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	3,18,5	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	3,18,8	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	3,3,10	EU294196.1	Hypocrea sp. IMI 206039	100%	99%	Hypocreales
41	3,3,9	EU280104.1	Hypocrea viridescens	99%	100%	Hypocreales
41	3,7,7	EU294196.1	Hypocrea sp. IMI 206039	100%	99%	Hypocreales
41	3,8,9 B	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	4,1,8	AY789395.1	Ascocoryne sp.	99%	96%	Helotiales
41	4,4,4	EU294196.1	Hypocrea sp. IMI 206039	99%	100%	Corticiales
41	4,5,7	EU294196.1	Hypocrea sp. IMI 206039	100%	99%	Hypocreales
41	4,6,11	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	4,6,6	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	4,6,8	DQ083015.1	Hypocrea sp.	98%	99%	Hypocreales
41	4,7,11	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	4,7,6	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
41	4,8,3	EU294196.1	Hypocrea sp. IMI 206039	100%	99%	Hypocreales
41	4,8,7	Z48813.1	Hypocrea pilulifera	100%	99%	Hypocreales
41	4,9,6	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
42	1,0,9	AY781230.1	Leptodontidium elatius	96%	99%	Ascomycota
42	1,1,12	AY781230.1	Leptodontidium elatius	95%	98%	Ascomycota
42	1,1,5	AY781230.1	Leptodontidium elatius	96%	99%	Ascomycota
42	1,1,8	AF475152.1	Leptodontidium elatius	94%	99%	Ascomycota
42	1,2,10	AY781230.1	Leptodontidium elatius	96%	99%	Ascomycota
42	3,10,1	AF475152.1	Leptodontidium elatius	99%	97%	Ascomycota
42	3,3,12	AY781230.1	Leptodontidium elatius	96%	99%	Ascomycota

42	3,4,6 A	AY781230.1	Leptodontidium elatius	96%	98%	Ascomycota
42	3,5,2	AY781230.1	Leptodontidium elatius	96%	99%	Ascomycota
42	3,6,10	AY781230.1	Leptodontidium elatius	84%	99%	Ascomycota
42	3,8,13	AY781230.1	Leptodontidium elatius	96%	99%	Ascomycota
42	3,8,8 A	AY781230.1	Leptodontidium elatius	96%	99%	Ascomycota
42	4,0,6	AY781230.1	Leptodontidium elatius	95%	99%	Ascomycota
42	4,1,2	AY781230.1	Leptodontidium elatius	95%	99%	Ascomycota
42	4,2,13	AY781230.1	Leptodontidium elatius	97%	99%	Ascomycota
42	4,2,6B	AY787713.2	Leptodontidium elatius	93%	99%	Ascomycota
42	4,3,12	AY781230.1	Leptodontidium elatius	96%	99%	Ascomycota
42	4,3,7	AF475152.1	Leptodontidium elatius	99%	99%	Ascomycota
42	4,4,3	AF475152.1	Leptodontidium elatius	94%	98%	Ascomycota
43	1,1,10	DQ846665.1	Trichoderma viride	100%	98%	Hypocreales
43	1,1,13	EU280104.1	Hypocrea viridescens	100%	100%	Hypocreales
43	1,10,10	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	1,2,13	AF218788.1	Trichoderma viride	99%	99%	Hypocreales
43	1,3,1	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	1,3,3	DQ846665.1	Trichoderma viride	100%	98%	Hypocreales
43	1,3,6	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	1,4,13	AF218788.1	Trichoderma viride	99%	99%	Hypocreales
43	1,4,6	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	1,4,7 A	EU263995.1	Trichoderma sp.	100%	96%	Hypocreales
43	1,4,9	EU871036.1	Trichoderma viride			Hypocreales
43	1,5,13	DQ846665.1	Trichoderma viride	100%	99%	Hypocreales
43	1,6,1	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	1,6,10	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	1,7,1	DQ846665.1	Trichoderma viride	100%	99%	Hypocreales
43	1,7,6	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	1,7,9	DQ846665.1	Trichoderma viride	100%	99%	Hypocreales
43	1,9,10	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	2,0,1	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,0,11	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,0,2	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,1,13	FJ481123.1	Trichoderma viride	100%	100	Hypocreales
43	2,1,2	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,1,6	FJ481123.1	Trichoderma viride	100%	98%	Hypocreales
43	2,1,9	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,2,1	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,2,3	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,2,5	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,2,6	FJ481123.1	Trichoderma viride	100%	99%	Hypocreales

43	2,3,1	FJ481123.1	Trichoderma viride	99%	100%	Hypocreales
43	2,3,10	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,3,3	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,3,9	FJ481123.1	Trichoderma viride	100%	99%	Hypocreales
43	2,4,3	FJ481123.1	Trichoderma viride	100%	99%	Hypocreales
43	2,4,5	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	2,4,6	DQ846665.1	Trichoderma viride	100%	100%	Hypocreales
43	2,5,11	FJ481123.1	Trichoderma viride	99%	99%	Hypocreales
43	2,5,12	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,5,2	FJ481123.1	Trichoderma viride	99%	100%	Hypocreales
43	2,5,3	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	2,5,4	FJ481123.1	Trichoderma viride	99%	99%	Hypocreales
43	2,5,7	FJ430783.1	Hypocrea koningii	100%	100%	Hypocreales
43	3,1,10	EU280104.1	Hypocrea viridescens	99%	100%	Hypocreales
43	3,15,5	FJ481123.1	Trichoderma viride	99%	100%	Hypocreales
43	3,2,9	EU280104.1	Hypocrea viridescens	100%	100%	Hypocreales
43	3,3,2	EU280104.1	Hypocrea viridescens	100%	100%	Hypocreales
43	3,3,5	FJ481123.1	Trichoderma viride	100%	100%	Hypocreales
43	3,3,6	FJ481123.1	Trichoderma viride	100%	99%	Hypocreales
43	3,3,9	EU280104.1	Hypocrea viridescens	99%	100%	Hypocreales
43	3,7,9	FJ481123.1	Trichoderma viride	100%	99%	Hypocreales
43	4,10,5	EU871036.1	Trichoderma viride	100%	100%	Hypocreales
43	4,5,10	EU871036.1	Trichoderma sp.	100%	99%	Hypocreales
44	1,10,12	EU240039.1	Mortierella sp.	100%	91%	Mortierellales
44	1,10,13	EU240039.1	Mortierella sp.	100%	91%	Mortierellales
44	1,10,2 A	EU240039.1	Mortierella sp.	100%	91%	Mortierellales
44	1,10,3	EU240039.1	Mortierella sp.	100%	91%	Mortierellales
44	1,10,4	EU240039.1	Mortierella sp.	100%	89%	Mortierellales
44	1,10,7	EU240039.1	Mortierella sp.	99%	90%	Mortierellales
44	1,2,1	EU240039.1	Mortierella sp.	100%	91%	Mortierellales
44	1,6,3	EU240039.1	Mortierella sp.	100%	91%	Hypocreales
44	1,7,3	EU240039.1	Mortierella sp.	100%	91%	Hypocreales
44	1,9,5	EU240039.1	Mortierella sp.	100%	91%	Mortierellales
44	1,9,8	EU240039.1	Mortierella sp.	100%	91%	Mortierellales
44	3,0,13	EU240039.1	Mortierella sp.	100%	91%	Hypocreales
44	3,1,5 A	EU240039.1	Mortierella sp.	99%	91%	Mortierellales
45	1,1,7	AY373294.1	Tulasnella sp.	99%	95%	Cantharellales
45	1,1,9	AY373294.1	Tulasnella sp.	99%	95%	Cantharellales
46	1,2,2	AM292200.1	Zygomycete sp. Artz 73	99%	98%	Zygomycete
46	1,2,3	AM292200.1	Zygomycete sp. Artz 73	99%	98%	Zygomycete
46	1,6,6	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete

46	2,4,7	AM292200.1	Zygomycete sp.	100%	96%	Zygomycete
46	3,14,1	AY805544.1	Zygomycete sp. olrim456	88%	99%	Zygomycete
46	3,14,8	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	3,16,1	AY805544.1	Zygomycete sp. olrim456	91%	100%	Zygomycete
46	3,2,5 A	AY805544.1	Zygomycete sp. olrim456	90%	100%	Zygomycete
46	3,5,1	AY805544.1	Zygomycete sp. olrim456	90%	100%	Zygomycete
46	3,6,1	AY805544.1	Zygomycete sp. olrim456	90%	100%	Zygomycete
46	3,7,6	AM292200.1	Zygomycete sp. Artz 73	100%	97%	Zygomycete
46	3,8,1	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	4,10,10	AY805544.1	Zygomycete sp. olrim456	90%	100%	Zygomycete
46	4,10,13	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	4,10,2	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	4,10,3	AY805544.1	Zygomycete sp. olrim456	90%	100%	Zygomycete
46	4,10,6	AM292200.1	Zygomycete sp. Artz 73	99%	98%	Zygomycete
46	4,10,9	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	4,11,12	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	4,11,2	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	4,11,6	AM292200.1	Zygomycete sp. Artz 73	98%	98%	Zygomycete
46	4,11,8	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	4,11,9	AM292200.1	Zygomycete sp. Artz 73	99%	98%	Zygomycete
46	4,12,10 B	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
46	4,12,9 B	AY805544.1	Zygomycete sp. olrim456	91%	97%	Zygomycete
46	4,4,1	EU294196.1	Zygomycete sp.	99%	100%	Corticiales
46	4,5,9	AM292200.1	Zygomycete sp.	99%	96%	Zygomycete
46	4,6,9 B	AY805544.1	Zygomycete sp. olrim456	90%	100%	Zygomycete
46	4,8,2	AM292200.1	Zygomycete sp. Artz 73	100%	98%	Zygomycete
47	1,3,2	AY373315.1	Tulasnella sp.	59%	85%	Cantharellales
47	1,3,7 A	AY373315.1	Tulasnella sp.	59%	85%	Cantharellales
47	1,3,9	AY373315.1	Tulasnella sp.	59%	85%	Cantharellales
47	1,5,10	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	1,5,7	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	1,5,9	AY373315.1	Tulasnella sp.	59%	85%	Cantharellales
47	1,6,11 A	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	1,6,13	AY373315.1	Tulasnella sp.	64%	83%	Cantharellales
47	1,8,12	AY373315.1	Tulasnella sp.	59%	85%	Cantharellales
47	1,8,4	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	1,8,7	AY373315.1	Tulasnella sp.	61%	85%	Cantharellales
47	1,9,11	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	1,9,12	AY373315.1	Tulasnella sp.	61%	85%	Cantharellales
47	1,9,13	AY373315.1	Tulasnella sp.	59%	85%	Cantharellales
47	2,4,12	AY373315.1	Tulasnella sp.	61%	85%	Cantharellales
47	3,11,4	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	3,11,6	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales

47	3,12,2	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	3,7,13	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	3,9,6	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	4,6,10	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
47	4,6,12	AY373315.1	Tulasnella sp.	60%	85%	Cantharellales
48	1,4,1	AY373934.1	Penicillium thomii	100%	99%	Eurotiales
48	1,5,3	FJ430767.1	Penicillium spinulosum	99%	99%	Eurotiales
48	2,2,9	FJ430767.1	Penicillium spinulosum	99%	99%	Eurotiales
48	2,4,9	FJ430767.1	Penicillium spinulosum	99%	99%	Eurotiales
48	2,5,13	FJ481123.1	Penicillium spinulosum	100%	100%	Eurotiales
48	2,5,6	FJ430767.1	Penicillium spinulosum	99%	98%	Eurotiales
48	3,18,2	FJ430767.1	Penicillium spinulosum	99%	99%	Eurotiales
48	3,5,13	AY373933.1	Penicillium spinulosum	100%	99%	Eurotiales
48	3,5,5	AY373933.1	Penicillium spinulosum	100%	99%	Eurotiales
48	3,6,5	AY373933.1	Penicillium spinulosum	100%	99%	Eurotiales
48	4,0,11	AY373933.1	Penicillium spinulosum	100%	99%	Eurotiales
48	4,12,10 A	AY373934.1	Penicillium thomii	100%	99%	Eurotiales
48	4,12,9 A	FJ430767.1	Penicillium spinulosum	99%	100%	Eurotiales
48	4,8,1	AY373934.1	Penicillium thomii	100%	97%	Eurotiales
49	1,5,4	AJ289619.1	Phellinus nigrolimitatus	92%	99%	Hymenochaetales
49	2,0,12	AJ289619.1	Phellinus nigrolimitatus	93%	99%	Hymenochaetales
49	2,0,5	AJ289619.1	Phellinus nigrolimitatus	91%	99%	Hymenochaetales
49	2,0,8 A	AJ289619.1	Phellinus nigrolimitatus	92%	99%	Hymenochaetales
49	2,4,8	AJ289619.1	Phellinus nigrolimitatus	95%	98%	Hymenochaetales
49	4,0,8	AJ289619.1	Phellinus nigrolimitatus	92%	99%	Hymenochaetales
49	4,6,13 A	AJ289619.1	Phellinus nigrolimitatus	99%	99%	Hymenochaetales
49	4,6,3	AJ289619.1	Phellinus nigrolimitatus	99%	99%	Hymenochaetales
49	4,6,4	AJ289619.1	Phellinus nigrolimitatus	97%	99%	Hymenochaetales
49	4,6,5	AJ289619.1	Phellinus nigrolimitatus	98%	99%	Hymenochaetales
49	4,8,12	AJ289619.1	Phellinus nigrolimitatus	99%	99%	Hymenochaetales
50	1,3,4	AJ344139.2	Antrodia serialis	99%	97%	Polyporales
50	1,5,12	AJ344139.2	Antrodia serialis	100%	99%	Polyporales
50	1,5,5	AJ344139.2	Antrodia serialis	100%	97%	Polyporales
50	1,7,10	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	1,8,11 A	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	1,8,2	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	1,8,8	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	1,9,2	AJ344139.2	Antrodia serialis	99%	98%	Polyporales
50	2,4,4	AJ345010.1	Antrodia serialis	100%	99%	Polyporales

50	3,10,4 A	AJ345010.1	Antrodia serialis	100%	98%	Polyporales
50	3,10,6	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,10,8	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,11,11	DQ491417.1	Antrodia serialis	98%	98%	Polyporales
50	3,11,2	DQ491417.1	Antrodia serialis	98%	98%	Polyporales
50	3,11,3 B	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,11,7	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,11,8	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,12,12 A	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,12,3	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,12,4	AJ344139.2	Antrodia serialis	99%	97%	Polyporales
50	3,12,9	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,13,13	AJ344139.2	Antrodia serialis	99%	98%	Polyporales
50	3,13,2 B	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,13,4	AJ344139.2	Antrodia serialis	100%	97%	Polyporales
50	3,13,8	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,14,2	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,14,4	AJ345010.1	Antrodia serialis	100%	98%	Polyporales
50	3,15,11	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,15,2	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,16,2	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,16,3	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
50	3,4,13	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,4,3 A	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,4,8	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,5,12	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,5,3 A	AJ345010.1	Antrodia serialis	100%	98%	Polyporales
50	3,5,4	AJ345010.1	Antrodia serialis	100%	98%	Polyporales
50	3,5,7	AJ345010.1	Antrodia serialis	100%	98%	Polyporales
50	3,5,8	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,5,9	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,6,12	DQ491417.1	Antrodia serialis	98%	99%	Polyporales
50	3,7,12	AJ345010.1	Antrodia serialis	100%	97%	Polyporales
50	3,8,7 A	DQ491417.1	Antrodia serialis	98%	98%	Polyporales
50	3,9,12	AJ345010.1	Antrodia serialis	100%	98%	Polyporales
50	3,9,7	AJ345010.1	Antrodia serialis	100%	99%	Polyporales
50	4,4,5	DQ491417.1	Antrodia serialis	97%	99%	Polyporales
50	4,5,5	AJ344139.2	Antrodia serialis	100%	98%	Polyporales
51	1,8,3 B	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
51	2,0,9	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
51	3,13,11	AY789395.1	Ascocoryne cylichnium	100%	96%	Helotiales
51	3,13,12	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
51	3,15,10	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
51	3,15,12	AY789395.1	Ascocoryne cylichnium	98%	95%	Helotiales

51	3,3,8	AY789395.1	Ascocoryne cylichnium	100%	96%	Helotiales
51	3,6,2	AY789395.1	Ascocoryne cylichnium	100%	96%	Helotiales
51	3,8,10	AY789395.1	Ascocoryne cylichnium	99%	96%	Helotiales
51	3,9,3	AY789395.1	Ascocoryne cylichnium	100%	96%	Helotiales
51	3,9,8	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
51	4,0,13 A	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
51	4,0,5	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
51	4,1,13	AY789395.1	Ascocoryne cylichnium	98%	97%	Helotiales
51	4,1,3B	AY789395.1	Ascocoryne cylichnium	97%	95%	Helotiales
51	4,1,4	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
51	4,1,7	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
51	4,1,8	AY789395.1	Ascocoryne cylichnium	99%	96%	Helotiales
51	4,2,10	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
51	4,2,12	AY789395.1	Ascocoryne cylichnium	97%	97%	Helotiales
51	4,2,2	AY789395.1	Ascocoryne cylichnium	97%	97%	Helotiales
51	4,2,7	AY789395.1	Ascocoryne cylichnium	100%	96%	Helotiales
51	4,2,9	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
51	4,3,8	AY789395.1	Ascocoryne cylichnium	97%	96%	Helotiales
51	4,4,10	AY789395.1	Ascocoryne cylichnium	97%	95%	Helotiales
51	4,4,6	AY789395.1	Ascocoryne cylichnium	97%	97%	Helotiales
51	4,4,7	AY789395.1	Ascocoryne cylichnium	100%	96%	Helotiales
52	1,7,11	AY854081.1	Hyphoderma praetermissum	100%	99%	Corticiales
52	1,7,2	AY854081.1	Hyphoderma praetermissum	100%	99%	Corticiales
52	1,9,3 B	AY854081.1	Hyphoderma praetermissum	99%	99%	Corticiales
52	3,16,8	AY854081.1	Hyphoderma praetermissum	100%	99%	Corticiales
52	4,0,7	AY854081.1	Hyphoderma praetermissum	100%	99%	Corticiales
53	2,0,7	L14527.1	Talaromyces sp.	100%	91%	Eurotiales
53	2,0,8 B	L14527.1	Talaromyces sp.	99%	91%	Eurotiales
53	2,4,13 B	L14527.1	Talaromyces sp.	100%	91%	Eurotiales
53	3,0,10	L14527.1	Talaromyces sp.	99%	90%	Eurotiales
53	3,0,2 B	L14527.1	Talaromyces sp.	100%	90%	Eurotiales
53	3,0,4 B	L14527.1	Talaromyces sp.	100%	89%	Eurotiales
53	3,0,7 B	L14527.1	Talaromyces sp.	100%	91%	Eurotiales
53	3,11,3 A	L14527.1	Talaromyces sp.	100%	90%	Eurotiales
53	3,13,10	L14527.1	Talaromyces sp.	97%	92%	Eurotiales
53	3,15,3 B	L14527.1	Talaromyces sp.	99%	90%	Eurotiales
53	3,2,11 B	L14527.1	Talaromyces sp.	100%	91%	Eurotiales
53	3,2,13 B	L14527.1	Talaromyces sp.	100%	91%	Eurotiales
53	3,2,5 C	L14527.1	Talaromyces sp.	99%	89%	Eurotiales
53	3,4,10	L14527.1	Talaromyces sp.	100%	91%	Eurotiales

53	3,4,3 B	L14527.1	Talaromyces sp.	100%	90%	Eurotiales
53	3,4,4	L14527.1	Talaromyces sp.	100%	87%	Eurotiales
53	3,5,3 B	L14527.1	Talaromyces sp.	97%	91%	Eurotiales
53	3,6,4	L14527.1	Talaromyces sp.	100%	90%	Eurotiales
54	2,2,4	AF335450.1	Hypholoma sp. F14056	100%	99%	Agaricales
55	3,0,2 A	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,0,4 A	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,0,6	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,0,7 A	AJ560638.1	Fomitopsis pinicola	99%	98%	Polyporales
55	3,0,8	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,1,12	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,1,13	AJ560638.1	Fomitopsis pinicola	100%	99%	Polyporales
55	3,1,3	AJ560638.1	Fomitopsis pinicola	99%	98%	Polyporales
55	3,1,6	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,1,7	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,1,8	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,2,10	AJ560638.1	Fomitopsis pinicola	100%	99%	Polyporales
55	3,2,12	AJ560638.1	Fomitopsis pinicola	100%	99%	Polyporales
55	3,2,3	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,2,6	AJ560638.1	Fomitopsis pinicola	100%	99%	Polyporales
55	3,2,7	AJ560638.1	Fomitopsis pinicola	100%	99%	Polyporales
55	3,2,8	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,3,4	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
55	3,3,7	AJ560638.1	Fomitopsis pinicola	100%	99%	Polyporales
55	3,4,11	AJ560638.1	Fomitopsis pinicola	100%	99%	Polyporales
55	3,4,7	AJ560638.1	Fomitopsis pinicola	100%	98%	Polyporales
56	3,0,9 B	AY558653.1	Fuscoporia viticola	99%	99%	Hymenochaetales
57	3,1,1	EU118654.1	Phlebia firma	100%	99%	Corticiales
57	3,1,5 B	EU118654.1	Phlebia firma	99%	99%	Corticiales
58	3,12,12	U85797.1	Athelia decipiens	99%	98%	Atheliales
58	3,12,5 B	U85797.1	Athelia decipiens	99%	98%	Atheliales
58	3,12,8	U85797.1	Athelia decipiens	98%	94%	Atheliales
58	3,14,12	U85797.1	Athelia decipiens	100%	98%	Atheliales
58	3,14,6	U85797.1	Athelia decipiens	99%	98%	Atheliales
58	3,14,7	U85797.1	Athelia decipiens	99%	98%	Atheliales
58	4,12,4	U85797.1	Athelia sp.	99%	98%	Eurotiales
59	3,1,2	EU128641.1	Penicillium citreonigrum	100%	100%	Eurotiales
59	4,0,13 B	EU128641.1	Penicillium citreonigrum	100%	100%	Eurotiales
59	4,0,1B	EU128641.1	Penicillium citreonigrum	100%	100%	Eurotiales

59	4,12,12 A	AF125942.1	Penicillium sp. NRRL 28148	100%	99%	Eurotiales
59	4,12,3	AF125942.1	Penicillium sp. NRRL 28148	100%	100%	Eurotiales
59	4,12,5 A	AF125942.1	Penicillium sp. NRRL 28148	100%	100%	Eurotiales
59	4,4,12	EU128641.1	Penicillium citreonigrum	100%	100%	Eurotiales
60	3,18,1 A	AY966450.1	Antrodia sinuosa	100%	98%	Polyporales
60	3,18,12	AY966450.1	Antrodia sinuosa	100%	98%	Polyporales
60	3,18,3	AY966450.1	Antrodia sinuosa	99%	98%	Polyporales
60	3,18,4	AY966450.1	Antrodia sinuosa	100%	98	Polyporales
60	3,18,9	AJ416068.1	Antrodia sinuosa	100%	98%	Polyporales
61	4,3,3	AY599579.1	Postia caesia	98%	98%	Aphyllophorales
62	1,0,2	AF083197.1	Phialophora lagerbergii	99%	98%	Ascomycota
62	1,9,3 A	AF083197.1	Phialophora lagerbergii	100%	98%	Ascomycota
62	1,9,4	AF083197.1	Phialophora lagerbergii	99%	99%	Ascomycota
62	2,3,8	AF083197.1	Phialophora lagerbergii	100%	99%	Ascomycota
62	3,8,12	AF083197.1	Phialophora lagerbergii	100%	99%	Ascomycota
62	3,8,3	AF083197.1	Phialophora lagerbergii	100%	99%	Ascomycota
62	3,8,6	AF083197.1	Phialophora lagerbergii	100%	98%	Ascomycota
62	4,1,5 B	AF083197.1	Phialophora lagerbergii	100%	99%	Ascomycota
62	4,5,1	AF083197.1	Phialophora lagerbergii	99%	99%	Ascomycota
62	4,5,11	AF083197.1	Phialophora lagerbergii	100%	98%	Ascomycota
62	4,5,3	AF083197.1	Phialophora lagerbergii	100%	99%	Ascomycota
62	4,5,6	AF083197.1	Phialophora lagerbergii	100%	98%	Ascomycota
62	4,5,8	AF083197.1	Phialophora lagerbergii	100%	98%	Ascomycota
62	4,7,4	AF083197.1	Phialophora lagerbergii	91%	99%	Ascomycota
62	4,9,10	AF083197.1	Phialophora lagerbergii	100%	98%	Ascomycota
63	3,8,8 B	DQ317330.1	Cadophora sp. 5R24-4	100%	100%	Helotiales
63	3,9,2	DQ317330.1	Cadophora sp. 5R24-1	100%	99%	Helotiales
63	3,9,4	DQ317330.1	Cadophora sp. 5R24-5	100%	100%	Helotiales
63	4,2,8	DQ317330.1	Cadophora sp. 5R24-2	100%	99%	Helotiales
63	4,6,2	DQ317330.1	Cadophora sp. 5R24-3	100%	99%	Helotiales
64	4,10,1	EU139250.1	Ascomycete sp. Uf-2007a	97%	99%	Helotiales
64	4,10,11	EU139250.1	Ascomycete sp. Uf-2007a	96%	99%	Helotiales
64	4,10,7	EU139250.1	Ascomycete sp. Uf-2007a	96%	99%	Helotiales
65	4,12,12 B	AY373924.1	Penicillium miczynskii	100%	100%	Eurotiales
65	4,12,6 A	AY373924.1	Penicillium miczynskii	100%	100%	Eurotiales
65	4,12,8	AY373924.1	Penicillium miczynskii	100%	100%	Eurotiales
66	1,2,8	AY789395.1	Ascocoryne cylichnium	99%	92%	Helotiales
66	1,9,6	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
66	2,4,10 B	AY789395.1	Ascocoryne cylichnium	99%	95%	Helotiales
66	3,13,7	AY789395.1	Ascocoryne cylichnium	97%	96%	Helotiales
66	3,15,4	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
66	3,16,12	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
66	3,16,13 B	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales

66	3,16,4	AY789395.1	Ascocoryne cylichnium	100%	95%	Helotiales
66	3,17,3	AY789395.1	Ascocoryne cylichnium	100%	96%	Helotiales
66	3,5,10	AY789395.1	Ascocoryne cylichnium	99%	96%	Helotiales
66	3,5,11	AY789395.1	Ascocoryne cylichnium	100%	93	Helotiales
66	3,9,13	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
66	4,0,9	AY789395.1	Ascocoryne cylichnium	100%	95%	Helotiales
66	4,1,12C	AY789395.1	Ascocoryne cylichnium	97%	94%	Helotiales
66	4,1,5	AY789395.1	Ascocoryne cylichnium	97%	95%	Helotiales
66	4,1,7	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
66	4,2,11	AY789395.1	Ascocoryne cylichnium	99%	97%	Helotiales
66	4,4,11	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
66	4,4,2	AY789395.1	Ascocoryne cylichnium	97%	95%	Helotiales
66	4,4,8	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
66	4,7,10	AY789395.1	Ascocoryne cylichnium	100%	95%	Helotiales
66	4,9,2	AY789395.1	Ascocoryne cylichnium	100%	97%	Helotiales
67	1,0,6	DQ093737.1	Sistotrema brinkmannii	100%	99%	Corticiales
67	4,7,1	DQ093737.1	Sistotrema brinkmannii	99%	99%	Corticiales
67	4,7,12 A	AY089729.1	Sistotrema brinkmannii	100%	99%	Corticiales
67	4,7,8	DQ093737.1	Sistotrema brinkmannii	99%	99%	Corticiales
67	4,7,9	DQ093737.1	Sistotrema brinkmannii	100%	99%	Corticiales
67	4,8,10	DQ093737.1	Sistotrema brinkmannii	100%	99%	Corticiales
67	4,9,1	DQ093737.1	Sistotrema brinkmannii	99%	99%	Corticiales
68	1,1,1	EU249343.1	Amylostereum areolatum	99%	97%	Russulales
68	1,1,2	AY672918.1	Amylostereum chailletii	100%	99%	Russulales
69	1,5,1	AY627835.1	Epacris pulchella root	99%	95%	???
69	4,3,9	AY627835.1	Epacris pulchella root	98%	95%	???
70	3,10,9	AF429426.1	Hypochnicium geogenium	94%	98%	Corticiales
70	4,0,12 A	AF429426.1	Hypochnicium geogenium	95%	98%	Corticiales
70	4,0,1C	AF429426.1	Hypochnicium geogenium	92%	97%	Corticiales
70	4,1,1	AF429426.1	Hypochnicium geogenium	93%	94%	Corticiales
70	4,2,1B	AF429426.1	Hypochnicium geogenium	92%	98%	Corticiales
70	4,2,4	AF429426.1	Hypochnicium geogenium	93%	98%	Corticiales
70	4,2,5	AF429426.1	Hypochnicium sp.	93%	98%	Corticiales
71	1,10,11	AY373315.1	Tulasnella sp.	98%	96%	Cantharellales
71	3,14,10 A	AY373315.1	Tulasnella sp.	99%	96%	Cantharellales
72	1,3,10 B	AM945189.1	Cylindrocladium sp.	72%	86%	Hypocreales
72	1,3,11	EU687024.1	Fungal endophyte isolate	74%	87%	???
72	3,14,13	AM945188.1	Calonectria scoparia	72%	86%	Hypocreales
72	4,5,13 B	AM945188.1	Calonectria sp.	50%	98%	Hypocreales
73	3,0,11	EU343826.1	Candida ergastensis	100%	100%	Saccharomycetales

73	3,0,3 B	AJ606466.1	Candida sp.	99%	95%	Saccharomycetales
74	3,14,10 B	AF033463.1	Penicillium namyslowskii	100%	100%	Eurotiales
75	1,9,1	DQ069046.1	Phialophora sp.	94%	96%	Ascomycota
75	3,7,11	DQ069046.1	Phialophora sp.	91%	95%	Ascomycota
75	3,7,8	DQ069046.1	Phialophora sp.	96%	96%	Ascomycota
76	3,10,10	AY219041.1	Fungal endophyte	99%	99%	???
76	3,10,2	AY219041.1	Fungal endophyte	100%	98%	???
77	3,10,7	AY268211.1	Epacris microphylla root fungi	96%	97%	???
77	3,8,11	AY268211.1	Epacris microphylla root fungi	95%	94%	???
77	3,8,4	AY268211.1	Epacris microphylla root fungi	97%	97%	???
78	3,8,2 B	AF493247.1	Ophiostoma sp.	100%	94%	Ophiostomatales
78	3,9,10	AB200425.1	Ophiostoma subalpinum	100%	99%	Ophiostomatales
79	1,1,6	AY743664.1	Ambomucor sp.	94%	89%	Mucorales
79	3,8,5	AY743664.1	Ambomucor sp.	93%	89%	Mucorales
80	1,8,6	EU240133.1	Mortierella sp. WD2G	99%	99%	Hypocreales
80	3,12,1	EU240133.1	Mortierella sp. WD2G	100%	97%	Mortierellales
81	3,7,1	AB091215.1	Rhinocladiella sp.	99%	95%	Chaetothyriales
81	4,5,4 B	AB091215.1	Rhinocladiella sp.	100%	99%	Chaetothyriales
81	4,8,9	AB091215.1	Rhinocladiella atrovirens	99%	92%	Chaetothyriales
82	2,2,2	AF429421.1	Hypochnicium albostramineum	94%	99%	Corticiales
82	4,4,9	AF429421.1	Hypochnicium albostramineum	93%	99%	Corticiales
83	3,13,5	AY606309.1	Phialocephala dimorphospora	61%	98%	Helotiales
83	3,17,2	AY606308.1	Phialocephala sp.	61%	94%	Helotiales
84	3,15,8	AY606303.1	Phialocephala sp.	61%	98%	Helotiales
84	3,16,10	AY606303.1	Phialocephala dimorphospora	96%	96%	Helotiales
84	3,16,5	AF486121.1	Phialocephala sp.	99%	94%	Helotiales
84	3,17,13	AY606303.1	Phialocephala dimorphospora	96%	97%	Helotiales
85	4,8,8	DQ227264.1	Hyphodiscus hymeniophilus	100%	97%	Hypocreales
86	4,10,12	EU139244.1	Porosphaerella cordanophora	96%	100%	Chaetosphaeriales
86	4,6,9 A	EU139244.1	Porosphaerella cordanophora	95%	98%	Chaetosphaeriales
87	3,0,9 A	EU294196.1	Hypocrea sp. IMI 206039	100%	100%	Hypocreales
88	1,8,10	AY561210.1	Mollisia minutella	76%	99%	Helotiales
88	3,17,9	AJ430223.1	Mollisia minutella	91%	100%	Helotiales
89	2,5,9	EF488112.1	Hypocrea koningii	99%	97%	Hypocreales

Appendix 3

Log and Species number	Name of species	distance from base (m)	diameter next to fruit (cm)	decay class over fruit
1.1	Unknown agaricales	0.7	34.5	3
1.2	Ascocoryne cylichnium	0.85	31.5	3
1.3	Botryobasidum sp.	1.4	31	2
1.4	Ascocoryne cylichnium	1.55	33	3
1.5	Phellinus nigrolimitatus	2.35	30.4	
1.6	Fuscoporia viticola	2.8	29	2
1.7	Unknown corticiales	2,9 - 3,1	29	3
1.8	Fuscoporia viticola	2,9 - 3,6	28.2	2
1.9	Phellinus nigrolimitatus	3.2	28.5	2
1.10	Antrodia serialis	3,2 - 3,45	28	2
1.11	Hyphoderma argillaceum	3.2	28.2	2
1.12	Antrodia serialis	3.65	27.6	2
1.13	Fuscoporia viticola	4,3 - 5,0	26.3	2
1.14	aff Hyphodontia	4,6 - 6,3	26,1 - 23,7	3
1.15	Antrodia serialis	4,85 - 5,10	26.5	2
1.16	Unknown corticiales	5 - 5,5		2
1.17	Antrodia serialis	6,3 - 6,8	23	2
1.18	Antrodia serialis	6,3 - 6,8	23	2
1.19	Antrodia serialis	6.4	23.8	2
1.20	Hymenoscyphus improvisius	7.3	22	3
1.21	Antrodia serialis	7.4	21.4	
1.22	Gymnopilus picreus	7,8 - 8,20	20.6	2
1.23	Mycena cf. Galopoda	7.9	20.6	2
1.24	Pholiota spumosa	8.15	20.6	2
1.25	Antrodia serialis	8.45	20	2
1.26	Hyphoderma argillaceum	9,5 - 9,9	18	4
1.27	Hyphoderma argillaceum	9,8 - 10,1	17.8	3
2.1	Skeletocutis amorphus	0 - 0,6	34.2	2
2.2	Phellinus nigrolimitatus	0.2	34.5	2
2.3	Fuscoporia viticola	0,3 - 0,75	34	2
2.4	Phellinus nigrolimitatus	0.55	34	2
2.5	Fuscoporia viticola	0.65	33.3	2
2.6	Phellinus nigrolimitatus	0.9	33	2
2.7	Fuscoporia viticola	0.95	33.2	3
2.8	Tubulicrinis subulatus	1.2	31.7	3
2.9	Hymenoscyphus improvisius	1.6	31.2	2
2.10	Hyphoderma cf. puberum	1,7 -2,4	31	2

2.11	Fuscoporia viticola	2.1	31	2
2.12	Phellinus nigrolimitatus	2.8	30.2	3
2.13	Skeletocutis amorphus	3.05	30	2
2.14	Fuscoporia viticola	3.3		
2.15	Phellinus nigrolimitatus	3,3 - 3,6	30	2
2.16	Hyphoderma argillaceum	3.6	28.7	2
2.17	Hyphoderma argillaceum	3.65	29	3
2.18	Ascocoryne cylichnium	3.8	28.2	3
2.19	Hypholoma sp.	4.2	27.6	2
2.20	Hypholoma sp.	5.15	28.3	4
2.21	Hypholoma sp.	5.4	28	4
3.1	Fomitopsis pinicola	0.25	35	2
3.2	Dacrymyces stillatus	0,45	34.6	2
3.3	Fuscoporia viticola	0.5	34.6	2
3.4	Fomitopsis pinicola	0.7	34.5	2
3.5	Fomitopsis pinicola	0.7	34.2	1
3.6	Fuscoporia viticola	1	33.1	3
3.7	Fomitopsis pinicola	1.2	33.1	4
3.8	Unknown corticiales	1.2	33.1	2
3.9	Fomitopsis pinicola	1.3	32.2	2
3.10	Fuscoporia viticola	1.4	32.2	2
3.11	Fuscoporia viticola	1.55	33.6	2
3.12	Unknown agaricales	1.7	32.5	2
3.13	Fomitopsis pinicola	1.7	33.5	2
3.14	Botryobasidium sp.	1,7 - 2,2	33.5	2
3.15	Fuscoporia viticola	1.8	33.5	2
3.16	Fomitopsis pinicola	1.8	33.5	2
3.17	Fomitopsis pinicola	1.9	32.1	2
3.18	Fuscoporia viticola		32.1	
3.19	Fomitopsis pinicola	2.05	32.1	2
3.20	Fuscoporia viticola	2.15	33	2
3.21	Mycena epipterygia	2.2	32.1	2
3.22	Fomitopsis pinicola	2.25	32.1	2
3.23	Fomitopsis pinicola	2.25	32.1	2
3.24	Unknown agaricales	2.3	32	2
3.25	Fuscoporia viticola	2.35	32.1	2
3.26	Unknown agaricales	3.15	31	2
3.27	Dacrymyces stillatus	3,8 - 5,2	31 - 28,5	2
3.28	Fomitopsis pinicola	4.1	29	2
3.29	Antrodia serialis	4.9	29	2
3.30	Dacrymyces stillatus	4.95		
3.31	Antrodia serialis	5,30 - 5,45	28	2
3.32	Tubulicrinis subulatus	5,45 - 5,65	27	2
3.33	Antrodia serialis	6.25	26.7	3

3.34	Antrodia serialis	6.35	26.6	2
3.35	Antrodia serialis	6,4 - 6,9	26.7	2
3.36	Sistotrema sernanderi	6,5 - 8,0	25	2
3.37	Antrodia serialis	7.4	25	2
3.38	Postia caesia	7.7	25	2
3.39	Postia caesia	7.9	25.5	2
3.40	Ascocoryne cylichnium	8,5 - 9,0		
3.41	Unknown corticiales	8.55	23.8	2
3.42	Hypholoma sp.	8.8	25.5	2
3.43	Hypholoma sp.		24.5	2
3.44	Hypholoma sp.	9.35	24.5	2
3.45	Botryobasidium intertextum	10 - 10,7	21.5	2
3.46	Antrodia serialis	10.6	22.2	2
3.47	Mycena epipterygia	10.6	22.2	2
3.48	Unknown agaricales		19.2	2
3.49	Botryobasidium cf. botryosum	13,8 - 14,5	16.1	3
3.50	Ascocoryne cylichnium	13	16.5	2
3.51	Antrodia sinuosa	13.8	16	2
4.1	Ascocoryne cylichnium	0	31.3	2
4.10	Botryobasidium sp.	4,8 - 6,1	23.8	2
4.11	Postia caesia	6 - 6,2		2
4.12	Postia caesia	6 - 6,2		2
4.13	Postia caesia	6.2 - 6,5		2
4.14	Postia caesia	6,5 - 6,7		2
4.15	Unknown polypore	6 - 6,7		
4.16	Postia caesius	7.4	18.8	2
4.17	Fuscoparia viticola	8,2 - 9,5	16.3	2
4.18	Postia caesius	8.5	16.3	2
4.19	Fuscoparia viticola	10.2	14.5	2
4.2	Unknown corticiales	2,0 - 2,6	28.3	2
4.3	Hymenoscyphus improvisius	2.1	28.2	2
4.4	Mycena epipterygia	2.6	28	2
4.5	Botryobasidium sp.	3,3 - 4,1	26	2
4.6	Postia caesia	3.4	27	2
4.7	Botryobasidium cf. candicans	3.95	25.3	2
4.8	Postia caesius	4.1	26	2
4.9	Postia caesius	4.6	24.6	2