

Fungi ahoy! Diversity on marine wooden substrates in the high North

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Abstract

Marine fungi are severely understudied in the polar regions. We used molecularly identified cultures to study fungi inhabiting 50 intertidal and sea-floor logs along the North Norwegian coast. The aim was to explore the taxonomic and ecological diversity and to examine factors shaping the marine wood-inhabiting fungal communities. The 577 pure cultures analysed clustered into 147 operational taxonomic units (OTUs) based on 97% *ITS* sequence similarity. Ascomycota was dominating, but OTUs belonging to Basidiomycota, Mucoromycotina and Chytridiomycota were also isolated. Nine OTUs could not be assigned to any fungal phylum. Almost half of the OTUs were considered non-marine. The western and eastern part of the Norwegian Barents Sea coast hosted different communities. Geography and substrate and site level variables contributed to shaping these communities. We characterized a previously overlooked fungal community in a poorly studied area, discovered high diversity and report many taxa for the first time from marine environment.

Key words: Ascomycota; culturing; community ecology; *ITS*; marine fungi; taxonomy; phylogeny; Norway

Introduction

Marine fungi form an ecologically heterogeneous assembly of species growing and sporulating in marine, intertidal or estuarine habitats (Kohlmeyer and Kohlmeyer, 1979). They appear as parasites on algae and animals, as mutualistic symbionts, and as saprotrophs, and play functional roles in nutrient recycling, biogeochemical processes and food web dynamics of the oceans. Most studies of marine fungi to date have been based on morphological characterization of fruit bodies, other structures and isolated cultures. More recently, Sanger sequencing, DNA fingerprinting and high throughput sequencing have provided new insights into the diversity and systematics of marine fungi (Stoeck and Epstein, 2003; Zuccaro et al., 2008; Amend et al., 2012). Recently, a high diversity of poorly known fungal lineages were recovered in analyses of rDNA SSU sequences from the marine environment (Richards et al., 2012). The majority of the unexplored diversity was among the early diverging lineages of Kingdom Fungi (Chytridiomycota and Zygomycota) and the Basidiomycota yeasts. When it comes to better studied marine fungi, the vast majority of them are Ascomycota, primarily belonging to Halosphaeriaceae (Microascales, Sordariomycetes,) and Lulworthiales (Sordariomycetes), which are both derived from terrestrial ancestors (Spatafora et al., 1998).

Some terrestrial or freshwater taxa are frequently encountered in marine environments, and to the ones that can grow there the term facultative marine fungi has been applied (Kohlmeyer, 1974). The ecological role of facultative marine species in marine habitats has been debated since the beginning of their discovery (Sparrow, 1937; Johnson, 1967; Shearer, 1972; Raghukumar and Raghukumar, 1999). In spite of an abundance of terrestrial species in marine studies (e.g. Johnson, 1967), mycologists have tended to focus on obligate marine fungi, overlooking isolates of non-obligate species which have often been considered contaminants

or originating from resting structures. This conservative study tradition in marine mycology contradicts the idea that extensive fungal plasticity and metabolic versatility enables fungi to adapt to different ecological niches (Slepecky and Starmer, 2009; Wittenberg et al., 2009). Indeed, as Richards et al. (2012) show, terrestrial to marine transitions and vice-versa have occurred frequently and apparently are small evolutionary steps for fungi.

Few surveys of marine wood-inhabiting fungi have been conducted in northern waters, and these report species typical for temperate oceans (Jones et al., 1972; Schaumann, 1975; Pang et al., 2011). A study from the arctic waters of Svalbard documented a relatively high number of new and unidentified species, and indicated the occurrence of a distinctive wood-inhabiting arctic mycota (Pang et al., 2011). In two studies from other arctic seas focusing on algae and sediment fungi, respectively, several culture isolates could not be identified to species level, suggesting these might represent new taxa (Bubnova and Kireev, 2009; Bubnova, 2010).

Water temperature and salinity are the two main ecological drivers affecting the distribution of marine wood-inhabiting fungi at a global scale (Booth and Kenkel, 1986; Hughes, 1986). At a local and substrate scale, environmental parameters having an influence on the occurrence of marine fungi include, among others, habitat, zonation in relation to water level and its fluctuations, substrate type and cover of marine organisms which indicates the duration of presence in the marine environment (Kohlmeyer and Kohlmeyer, 1979). However, the importance of some characteristics of the wooden substrates such as diameter and decay stage barely has been studied in marine mycology, even though these factors are important for terrestrial fungi (Juutilainen et al., 2011; Nordén et al., 2013). The geographic source of drift wood may play a role in structuring wood-inhabiting marine fungal communities, but is difficult to control for in surveys based on natural substrates. The main source of shore-cast

wood in the North Norwegian coast is Siberia (Johansen and Hytteborn, 2001), from which the wood is transported by the great Siberian rivers and polar ocean currents. During parts of the journey the wood drifts fixed in sea ice before it is released due to melting of the ice as it travels south. A large part of the wooden material ends up on the coast of Svalbard, but some drifts further south and comes ashore on the North Norwegian coast (Johansen and Hytteborn, 2001; Hellmann et al., 2013).

The aims of our study were (i) to explore the taxonomic, phylogenetic and ecological diversity of wood-inhabiting marine fungi in northern waters focusing on Ascomycota and Basidiomycota, and (ii) to study the environmental factors shaping the fungal communities along the long coastline of Northern Norway. Due to different large and small scale environmental factors, we expect differences in the marine wood-inhabiting mycota between the eastern and western part of the study area. We selected a culture-based approach in order to obtain proper study material from which we could sequence multiple genetic markers (*ITS* and *LSU*). Moreover, the fungal cultures provide opportunities for later, more in-depth taxonomic studies.

Material and methods

Study area

We surveyed wooden substrate units, i.e. logs and pieces of wood (hereafter referred to as logs), along the North Norwegian coast between May and October 2010. Of the 50 logs studied at 23 sites (Fig 1), 47 represented shore-cast intertidal and 3 represented sea bottom units (Table S1 in Supplementary data). One shore-cast, oily substrate unit was excluded from data analyses, since no isolates were recovered from it. The sites were located along the approximately 1 000 km long coastline between Bodø (67°14'82"N 015°06'12"E) in the south

and Vadsø (70°04'06"N 30°06'25"E) in the northeast. The western part of the study area is slightly warmer than the eastern one (annual sea surface temperature 7°C and 6°C, respectively) (Locarnini et al., 2010). Salinity is 34 practical salinity units in both parts (Antonov et al., 2010). In the western part of the North Norwegian coast there is less shore-cast wood and a bigger proportion of it is broadleaved and of local origin, whereas the eastern part is rich in debris from (Siberian) coniferous tree species that do not or scarcely grow in the area (Table S1, personal observations).

Sampling and culturing

We chose the sampled logs randomly among those showing signs of recent and long lasting presence in the sea (indicated among other features by cover of marine algae and animals). We included logs from the breaker zone only if they had recently been in the sea and if there were no intertidal units available. Shore-cast logs were sampled at low tide. Sea bottom units were caught with an Agassiz trawl. We recorded or measured ecological variables including habitat type (rocky, stony, gravelly, sandy or muddy shore), zone of sampling (tide, breaker, sublittoral or sea bottom), log attachment type (loose or fixed), tree species (broadleaved tree or conifer), log quality (whole trunk, broken trunk, cut trunk (including pieces of boards and planks), branch or unknown (for logs that could not be characterized)), position (vertical or horizontal), compass orientation, basal and apical diameter, length, decay class based on knife penetration according to Hottola and Siitonen (2008) and ranging from 1=hard to 5=very soft, percent of marine organisms covering the log (=epiphyte cover) and percent of remaining bark cover (Table S1).

We flame sterilized a knife and forceps and used them to obtain the samples. We cut off a thin slice of the surface wood (approximately 1 mm) on the sampling point, cut out a wooden cube

and placed it in a clean plastic bag which was closed air-tight. We collected 12 wooden cubes, 5 x 5 x 2 mm in dimensions, on each side (upper, lower and both flanks) of the log in the basal, middle and apical part. Basal and apical cubes were taken 10 cm from each end, respectively, and middle cubes at the midpoint of the unit. When the sampling point was covered by tree bark, an additional bark cube was taken in order to capture those fungi specialized in bark on marine substrates (Kohlmeyer and Kohlmeyer, 1979). We kept the samples among ice bricks in a cold bag until plating them the same day, usually within 10 hours of sampling. Each cube was placed on a 1/5 malt extract agar plate that was prepared with filtered autoclaved seawater and amended with the antibiotics streptomycin (25 mg/L) and tetracycline (10 mg/L).

Isolation plates were incubated in the dark at 15°C, checked once a week until the dish was fully covered and fungi growing out of the cubes were isolated in axenic cultures. Cubes of agar with fresh mycelium from the growing edges of the fungal colonies were cut out and frozen at -25°C in 2% CTAB Buffer. We positioned control dishes in the laminar flow hood and in unused plastic bags similar to the ones used in sampling in order to detect possible aerial contaminants. The controls either did not have any growing cultures or included fungi not detected on the focal dishes.

DNA extraction, amplification and sequencing

We extracted the DNA of pure culture isolates using a modified cetyltrimethyl ammonium bromide (CTAB) extraction protocol (Murray and Thompson, 1980) and amplified the target loci according to Mysterud et al. (2007). PCR amplification was performed on a PTC-0200 DNA engine (MJ Research, Waltham, Massachusetts, USA) using the primer pairs ITS5-ITS4 (White et al., 1990) and LR0R-LR5 (Vilgalys and Hester, 1990; Rehner and Samuels, 1994)

in 0.5 μ M concentration and the Illustra PuReTaq Ready-To-Go PCR beads (GE Healthcare, Buckinghamshire, UK) in a reaction volume of 25 μ l.

We cleaned the PCR products using 0.25 units of ExoSAP-IT (Affymetrix, Santa Clara, CA, USA) for 6 μ l of PCR product. Sequencing reactions were performed on an Applied Biosystems 3730 DNA analyzer in BigDye Terminator sequencing buffer using PCR primers as sequencing primers and the BigDye Cycle Sequencing kit v3.1 (Applied Biosystems, Foster City, California, USA). The samples were subjected to capillary electrophoresis on an Applied Biosystems 3730 DNA analyser (Foster City, CA, USA).

Bioinformatics and statistical analyses

We automatically assembled forward and reverse sequences and manually edited assemblies in Geneious version 5.6.2. We clustered the *ITS* sequences using Blastclust (available at: <http://toolkit.tuebingen.mpg.de/blastclust>) with 97% sequence similarity cut-off value. For each *ITS* cluster, hereafter referred to as an operational taxonomic unit (OTU), we chose a full length high quality *ITS* sequence (i.e. no ambiguous sites) as representative sequence and sequenced the corresponding isolate for the *LSU* region. BLASTn searches of *ITS* and *LSU* sequences against NCBI's nr nucleotide database were used to assign taxonomy to each of the OTUs.

We used EstimateS version 8.2.0 (Colwell, 2009) to calculate expected species accumulation curves based on the Mao Tau estimator (Colwell et al., 2004) and total species richness (γ -diversity) (Whittaker, 1960) estimate based on the Michaelis-Menten richness estimator MMMeans (Raaijmakers, 1987; Colwell et al., 2004).

We ran maximum likelihood phylogenetic analyses in RAxML version 7.2.6 (Stamatakis, 2006) and Bayesian inferences in MrBayes version 3.2.1 (Ronquist et al., 2012). We extracted and concatenated the 5.8S region from the representative *ITS* sequences with the *LSU* sequence data. This combined 5.8S/*LSU* data set was aligned with default options using the MUSCLE algorithm (Edgar, 2004) embedded in Geneious and corrected by eye. The alignment matrix measured 126 taxa by 1389 characters having 750 unique site patterns and 28.9% gaps. We created data subsets of *ITS* sequences for the different fungal orders and made alignments using either MUSCLE (Edgar, 2004) or MAFFT (Kato and Standley, 2013) algorithms with default settings. The alignments were improved by eye and analyses run in RAxML. All alignments are available from: <http://doi.org/10.5061/dryad.qg82k>

We based the ecological annotation of detected OTUs on top *LSU* BLAST matches, existing literature and the WoRMS database (Appeltans et al., 2012). In addition to key taxonomic literature of marine fungi (Kohlmeyer and Kohlmeyer, 1979; Jones et al., 2009), information from reference studies of marine fungi (Henningsson, 1974; Rees et al., 1979; Petersen and Koch, 1997; Tchesunov et al., 2008; Bubnova and Kireev, 2009; Bubnova, 2010; Azevedo et al., 2011; Pang et al., 2011) and other marine fungal literature were utilized. We considered an OTU to be obligate or facultative marine if the taxon (identified using BLAST matches) was known to be a marine one or was at least reported from the sea. The term ‘non-marine’ is used in this paper to refer to taxa previously only reported from terrestrial or freshwater habitats.

For community ecology analyses we used a community matrix where outliers, three sea-bottom logs and an additional two logs from a separate area in the south were excluded. This was done in order to focus the analyses on communities inhabiting logs in one type of main habitat (shore) in two geographical areas comparable in size: the western area, covering sites 4–14 in

Fig 1 and the eastern area, covering sites 16–23. First, we performed a geographic comparison of OTU frequency and abundance in Qiime version 1.5.0 (Caporaso et al., 2010). G-tests and ANOVAs run with default settings were used to study whether OTUs occurred more abundantly or more frequently in the western or eastern part. Thirteen OTUs were analysed, all of which occurred at least five times in the dataset.

We ran a non-metric multidimensional scaling (NMDS) ordination analysis in R with packages *vegan* and *MASS* (Venables and Ripley, 2002; Oksanen et al., 2013; R Core Team, 2013). Variables fitted to the ordination diagram as factors and vectors included geography (western or eastern area), county and site, latitude and longitude (UTM coordinates for northern latitude and eastern longitude), sampling month and ecological variables (see Sampling). In addition, we included diversity parameters derived from the community matrix: α -diversity (=OTU richness on each log) (Whittaker, 1960), the number of OTUs in each phylum and order and Faith's (1992) index of phylogenetic diversity (PD) of each log to account for any effect on the dispersion in the ordination space. We calculated a distance matrix from the community data matrix using Kulczynski dissimilarity index as implemented in *vegan* (Oksanen et al., 2013). In addition to the NMDS, separate Mantel tests were performed to compare the community matrix with Euclidean distance matrices of vectors and numerical factors.

We considered the two areas to be separate habitats within the landscape and calculated a β -diversity (Whittaker, 1960) measure, the classic Sørensen index, using the full data set in EstimateS (Colwell, 2009). To reveal whether fungal communities are phylogenetically clustered we calculated phylogenetic community measures, PD, net relatedness index (NRI) and nearest taxon index (NTI), in Phylocom version 4.2 (Webb, 2000; Webb et al., 2002;

Webb et al., 2008) . The latter two indices count phylogenetic distances of species communities and compare them with computationally created null communities. We excluded two single-isolate logs and used logs and samples. Phylocom was run using A 5.8S tree including one study isolate per OTU per log as a phylogenetic backbone (Fig S1, alignment available from: <http://doi.org/10.5061/dryad.qg82k>) and null community option -m 1 which maintains the species richness in each sample, but randomizes their identities. The number of generations used in calculations was 9999.

Further details of the methods and analyses can be found in Supplement 1.

Results

Fungal diversity

ITS sequences were obtained from 577 pure cultures and clustered into 147 OTUs (Table 1, Table S2). More than half of the OTUs were singletons (Table 1). More OTUs were found in the western than eastern area, but the average α -diversity was similar (on average 6.55 for the western, 6.81 for the eastern part and 6.66 for the whole dataset). OTU accumulation curves show that sampling was insufficient in both parts, as well as the whole study area, since the curves do not reach an asymptote (Fig 2). The Michaelis-Menten richness estimate suggests 254 OTUs to exist on coastal marine wood in the whole study area, which is almost twice as high as the observed γ -diversity. A representative partial *LSU* sequence was successfully generated for 125 (85%) of the *ITS* based OTUs.

Taxonomy and phylogeny

Ascomycota clearly dominated the recovered community with 122 (83%) of the OTUs assigned to the phylum (Fig 3, Table S2). Only ten OTUs belonged to Basidiomycota, five to

subphylum Mucoromycotina and one to Chytridiomycota. Nine OTUs only represented by *ITS* sequences could not be assigned to any fungal phylum. The five most frequent orders were Hypocreales, Helotiales, Pleosporales, Lulworthiales and Eurotiales, and altogether Ascomycota was represented by 15 orders. At the taxonomic level of order, the communities recovered in the two sea areas were similar, although some orders were more abundant in the western part, and some were missing in one of the sea areas (Fig. 4). In Basidiomycota, Agaricales and Cantharellales occurred most frequently with four and two OTUs, respectively (Table S2). At the genus level the most frequent OTUs had affinities to ascomycete anamorphs such as *Cadophora*, *Cladosporium* and *Penicillium* (Fig 3). Five OTUs fruiting in culture were identified morphologically as *Asteromyces cruciatus*, *Amylocarpus encephaloides*, *Digitatispora marina*, *Lulworthia sp.* and cf. *Phialophorophoma litoralis*. Only the first mentioned was likely represented by *ITS* or *LSU* sequence data in GenBank.

The phylogenetic diversity of the fungal communities based on *5.8S* sequences was similar in both sea areas (Table 1). No phylogenetic clustering of fungal assemblages was detected when comparing phylogenetic distances of observed and null communities using NRI and NTI, as indicated by negative or close to zero values (Table 1). Separate order-level phylogenies using *ITS* data from all the 577 isolates, revealed that several of the OTUs putatively included more than one species, as indicated by well-supported sub-clades (Figs 5 and S2).

Ecology

Marine taxa are present in every phylum throughout the *5.8S/LSU* tree (Fig 3). Sixty-seven of the 125 OTUs having *LSU* sequences were classified as marine based on *LSU* BLAST match and literature, whereas 58 OTUs (46%) were judged as non-marine. The primarily marine taxa Lulworthiales and Halosphaeriaceae (Microascales) included ten and seven OTUs,

respectively. Numerous OTUs classified as marine were also present in Eurotiales (6 out of 8 OTUs marine), Hypocreales (14/25), Helotiales (10/22) and Pleosporales (7/19). Xylariales included four OTUs, all of which were categorized as non-marine. In Basidiomycota three out of nine OTUs were classified as marine. Two of these are yeasts and one a filamentous fungus, *Digitatispora marina*. In Mucoromycotina three out of five OTUs were categorized as marine. Six out of the 19 most frequent OTUs were obligate marine, namely Lulworthiaceae sp., *Emericellopsis maritima*, *Asteromyces cruciatus*, Halosphaeriaceae sp., *Lulworthia* sp. and *Amylocarpus encephaloides* (Table S3). The primarily marine taxa Lulworthiales and Halosphaeriaceae (Microascales) had fewer and poorer (=low sequence similarity) BLAST matches than primarily non-marine orders, although their phylogenetic diversities were higher (Figs 3, 5 and S2, Table S2). Among the ten OTUs (encompassing 53 isolates) recovered from the marine order Lulworthiales, a majority had low sequence similarity BLAST matches and were not considered conspecific with any GenBank reference sequence (Fig 5). The trend observed across all orders was that BLAST hits of marine OTUs had lower sequence similarity than terrestrial ones (Figs S3 and S4).

Fungal communities

The fungal community composition differed between the sea areas. The number of shared OTUs found in both areas was 30 out of 147 and the β -diversity between the western and eastern area was 0.339 which means the two communities were more different from than similar with each other. The logs in the western part were slightly more heterogeneous in fungal community composition compared to the eastern part as indicated by mean and median Sørensen index values closer to zero (Table 1). None of the most frequent OTUs were associated with a particular sea area according to ANOVA and g-tests.

The NMDS ordination demonstrates a compositional difference in the fungal communities in the western and eastern part of our study area (Fig 6). Logs from a particular site were often far apart in the ordination space (result not shown), indicating high local heterogeneity. Several factors had strong relationships to the compositional variation in the ordination space. Taxonomic parameters that explained most of the dispersion in the ordination space were the number of OTUs in Helotiales, Capnodiales, Pleosporales, Ascomycota, Lulworthiales, Hypocreales, Mytilinidiales, Agaricales, and α -diversity (Table 2, Fig 6c). Variables that co-varied with the compositional variation were latitude, epiphyte cover, month, log attachment, habitat type, orientation, county, zone of sampling, geography, log position and tree type (Table 2, Fig 6b). The ordination shows that geography divides the communities (Fig 6a), and logs having different attachment (fixed or loose) and tree type host distinct communities (Fig 6b). Loose coniferous logs and logs in the breaker zone are associated with higher α -diversity, whereas broadleaved logs that have more epiphytes are associated with decreased α -diversity and increased number of Agaricales and Lulworthiales OTUs (Figs 6b and 6c). Mantel tests, where differences in community composition and geographic distances were related, indicated significant relationship between fungal community composition and geographic distance (Table 2). In addition, month, epiphyte cover and decay stage correlated with community composition.

Discussion

Taxonomy and phylogeny

Wood-inhabiting species are the most studied among marine fungi (Barghoorn and Linder, 1944; Jones, 2011b). Nevertheless, this study, based on almost 600 axenic cultures provided new information about their taxonomic diversity, highlighting that this group of fungi is still poorly known at regional and global scales. It was estimated that the logs would host up to

250 OTUs. However, we think the true diversity is likely to be even higher, considering that i) we studied only a small fraction of the surface wood of the 50 logs, ii) not all fungi grow in culture, and iii) several of the OTUs consisted of two or more well-supported sub-groups that might represent different species. The majority of the OTUs were members of Ascomycota representing a total of fifteen orders that were relatively evenly distributed between the two geographic regions. Some less diverse orders were absent in one or the other area, e.g. Xylariales and Sordariales, which is most likely a sampling effect, not a real distribution pattern, given the unsaturated species accumulation curves for the data set.

Out of the 19 most frequent taxa discovered in this study, eight have been recovered in four other culturing based reference studies made in West-Eurasian temperate and arctic seas, whereas only two were found in non-culture reference studies (Table S3). The higher taxonomic overlap between culturing based plating surveys (Henningsson, 1974; Rees et al., 1979; Bubnova and Kireev, 2009; Bubnova, 2010) compared to fruit body based ones (Petersen and Koch, 1997; Azevedo et al., 2011; Pang et al., 2011) was expected, since it is well known that different study methods favor the discovery of certain taxa at the expense of others. Only two cosmopolitan taxa of obligate marine fungi were isolated in this study, namely *Ceriosporopsis halima* and *Lulwoana uniseptata* (= *Zalerion maritimum*) (Hughes, 1986; Jones, 1993). The surprising absence of cosmopolitan taxa in our study, such as the genus *Corollospora* or the species *Humicola alopallonella*, can partly be explained by our sampling method. Mycelia of marine fungi, known to prefer the surface layers of the wood (Kohlmeyer and Kohlmeyer, 1979), may have been excluded in the mechanical surface sterilization of the sampling points. Secondly, the cool incubation temperature used is not optimal for the growth of several cosmopolitans (Panbianco, 1994), and hence they might have been outcompeted by faster growing fungi. And finally, the lack of publicly available

reference sequences for marine fungi (discussed below) must have contributed to the apparent absence of some cosmopolitan marine fungi.

Facultative marine fungi

In this first larger scale culturing study on wood-inhabiting marine fungi in the northern seas we detected many taxa that have not been considered obligately marine. Only about 30 (20%) of the taxa detected in this study are reported in key taxonomic literature of marine fungi (Kohlmeyer and Kohlmeyer, 1979; Jones et al., 2009) and considered obligately marine. However, many of the OTUs have affinities to taxa reported from marine environments, which underlines the need to explore the marine wood-inhabiting mycota outside the framework set by traditional taxonomic literature of marine mycology. For example, *Tolypocladium cylindrosporum* (TR169) was the eleventh most common OTU in this study and identified with 100% *ITS* and *LSU* sequence similarity. It has been found in culturing studies from arctic waters (Bubnova and Kireev, 2009; Bubnova, 2010), but is not found in key taxonomic literature of marine fungi.

Cadophora (Leotiomycetes) was frequently isolated and it seems to represent a previously overlooked dominant component of the marine wood-inhabiting mycota. Five OTUs had close affinity to this genus and these include the most, second and fifth most frequent OTU detected in this study. The genus has been found in the marine environment only recently (Gunde-Cimerman et al., 2005; Burgaud et al., 2009; Almeida et al., 2010), however, older records of the genus *Phialophora* might be considered to represent *Cadophora* due to nomenclatural recombinations (Gams, 2000; Harrington and McNew, 2003). *Cadophora* is an anamorphic genus in Helotiales, morphologically similar to *Phialophora* but molecularly distinct from this genus (Harrington and McNew, 2003). *Phialophora* is considered a plant

symbiont that has also been found inhabiting marine wooden substrates with medium and low frequency of occurrence in the North Sea and the Baltic Sea (Henningsson, 1974; Rees et al., 1979). However, Kohlmeyer and Kohlmeyer (1979) did not mention either genera and in Jones et al. (2009) *Phialophora* is mentioned as an anamorph genus to *Gaeumannomyces* (Sordariomycetes). Contamination is unlikely to explain the high frequency of *Cadophora*, especially since contamination controls were either negative or included taxa phylogenetically distinct from *Cadophora*. What roles the species of *Cadophora* play in marine ecosystems remains unknown.

The occurrence of terrestrial species in marine environments is not a new discovery (Elliott, 1930; Sparrow, 1937), but the great number of them found in this and other studies underlines our limited knowledge of these fungi and their ecology. One bottleneck in molecular surveys of fungi, as in this study as well, is often too low resolution in species identification. In this study the primarily marine taxa, Halosphaeriaceae (Microascales) and Lulworthiales included most of the OTUs having poor BLAST matches across the *ITS* region. Furthermore, only one morphologically identified culture had >97% similar *ITS* BLAST match. The *ITS* region has barely been used in marine mycology and the recent barcoding effort of marine fungi is therefore of significant importance (Velmurugan et al., 2013). Since the barcoding efforts of marine fungi are still in their infancy, there is obvious uncertainty in the taxonomic assignments of the detected OTUs. Thus, we cannot conclude whether putative terrestrial taxa found in this study represent facultative marine fungi or new lineages that are specializing to a marine habitat.

Community ecology

The fungal communities were different between the western and eastern part of the North

Norwegian coast, and this was due to geography and several site and substrate level variables. The most important variable affecting community composition was the latitude. The logs included in the analysis were within a 150 km latitudinal and 500 km longitudinal range. It is peculiar why latitude was significant rather than longitude. The importance of the latitude might, in addition to geographical variation, reflect the distribution of the sites in inner parts of the fjords and by the open sea. Sites by the open sea were more in the northern parts of the studied area. If latitude reflected the distribution of sites, different fungal communities would dwell in logs in the inner parts vs. by the open sea, which is an interesting topic to address in the future research of marine wood-inhabiting fungi.

Epiphyte cover was the most important substrate level variable influencing the communities. This suggests that fungal communities on driftwood change along the duration of presence in marine habitat, which is in line with an earlier finding by Tan et al. (1989). The α -diversity decreased with epiphyte cover. This result likely reflects the vast difference in the numbers of marine and non-marine fungi (Blackwell, 2011; Jones, 2011a); a small fraction of all fungal species is able to exist in wood which has been long in the marine realm. In contrast to α -diversity, the number of Agaricales and Lulworthiales OTUs increased with epiphyte cover. This is to be expected considering that Lulworthiales is a marine order and the only Agaricales included in the ordination was the obligate marine *Digitatispora marina* (TR666).

Attachment and tree type were important and reflected the geographic distribution of the communities. More OTUs were isolated from loose than fixed logs (on average 7.70 vs. 6.30, respectively). One might think that the increased α -diversity in loose logs is due to recolonization of the logs in the breaker zone by airborne fungi. However, this was not the case, since higher α -diversity was detected in loose logs also in the intertidal zone (on average

7.47 vs. 6.30). Coniferous logs hosted more culturable fungal species than broadleaved logs, but the difference was minimal (on average 4.85 vs. 4.76 respectively) and unlikely to explain the increase in α -diversity. Habitat type and zone of sampling were of importance in shaping the communities which is in line with previous studies (e.g. Hyde, 1989; Petersen and Koch, 1997). However, their confidence ellipsoids were largely overlapping in the ordination space (results not shown). Sampling month seemed to have a major impact on the fungal communities, but sampling was biased on a temporal scale as the western part was sampled during May-July and the eastern mostly from August to September. Marine fungal communities on wood are not known to change drastically during the summer (cf. Tan et al., 1989), and this result likely represents an artifact in our study caused by biased sampling. Other insufficiently sampled variables include orientation and position, and thus their importance cannot be justified.

Some ecological variables difficult to measure representatively were not taken into account in this study, including site water temperature, salinity and origin of the shore-cast wood.

Differences in temperature and salinity are known to be important on a global scale (Booth and Kenkel, 1986; Hughes, 1986). In this study in a limited geographic area with overlapping seasonal fluctuations, differences in mean surface water temperature and salinity are small (Sælen, 1950; Eilertsen and Skarðhamar, 2006) and unlikely to explain the different communities between the western and eastern part of Norwegian Barents Sea coast. At site level differences in these variables are likely notable due to local hydrographic variation, but this information could not have been caught at sufficient resolution with field measurements, especially when sampling in different localities at different times of the season. The origin of logs might be one of the key factors shaping the fungal communities, and explaining the differences in community composition and diversity. The logs originating from Siberia found

in the east may be initially inoculated with a different fungal community than logs of (mostly) local origin in the western part of the study area.

Conclusions

Northern marine wooden substrates host species-rich fungal communities consisting of both obligate and facultative marine species. Diverse communities with previously unknown dominant taxa can be revealed with culturing methods, but additional and more effective sampling and identification methods (i.e. high throughput sequencing) are needed to reveal the true diversity and ecological preferences of marine-wood inhabiting fungi in the northern seas. Geography and ecological factors such as length of submersion and log attachment type shape the fungal communities on drift wood. Many of the taxa we report for the first time from marine wooden material could not be identified to species because of lack of barcode sequences. It is therefore not known whether these taxa represent facultative marine fungi or new lineages that are specializing to a marine habitat. For more than a half century has marine mycological research explored the morphological diversity of obligate marine fungi on driftwood. It is time to move beyond fruit bodies towards an integrated approach to gain a more holistic view of the fungal communities drifting around the world's oceans.

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Tables

Table 1. Comparison of the wood-inhabiting fungal assemblages in the western and eastern part of the study area

	Western part	Eastern part	Whole data set
Number of isolates	322	255	577
Number of OTUs	105	72	147
Number of singletons (of all OTUs)	71 (68%)	49 (68%)	99 (67%)
Number of OTU occurrences	190	143	333
Sørensen index ^{a,c}	0.07 ± 0.105	0.16 ± 0.151	0.10 ± 0.121
Sørensen index ^{b,c}	0.00	0.15	0.00
PD ^{a,d}	0.46 ± 0.137	0.47 ± 0.109	0.46 ± 0.124
PD ^{b,d}	0.45	0.47	0.46
NRI ^{a,e}	-0.07 ± 1.156	-0.02 ± 1.161	-0.05 ± 1.146
NRI ^{b,e}	0.22	0.08	0.21
NTI ^{a,f}	-0.03 ± 1.267	-0.00 ± 1.060	-0.02 ± 1.167
NTI ^{b,f}	0.39	-0.03	0.34

^a Means (±SD).

^b Medians.

^c The classic Sørensen index is used here to evaluate the β -diversity between the logs in each geographical area.

^d Faith's index of phylogenetic diversity.

^e Net Relatedness Index.

^f Nearest Taxon Index.

Table 2. Results of the three-dimensional NMDS ordination and the Mantel tests: statistically significant parameters ($P \leq 0.05$) are in bold

NMDS ordination					
Diversity	r^2	P	Variable	r^2	P
Helotiales	0.510	0.001	Latitude	0.272	0.007
Capnodiales	0.481	0.001	Epiphyte	0.182	0.031
Pleosporales	0.425	0.001	Month	0.180	0.003
Ascomycota	0.302	0.004	Attachment	0.154	0.001
Lulworthiales	0.281	0.001	Orientation	0.149	0.002
α-diversity	0.275	0.001	Habitat type	0.131	0.043
Hypocreales	0.201	0.027	County	0.130	0.001
Mytilinidiales	0.188	0.024	Zone	0.100	0.032
Agaricales	0.171	0.036	Geography	0.086	0.007
Microascales	0.168	0.064	Position	0.081	0.004
Ascomycota IS ^a	0.083	0.351	Tree type	0.077	0.018
Leucosporidiales	0.075	0.358	Site	0.452	0.283
PD	0.072	0.407	Longitude	0.179	0.057
Xylariales	0.061	0.547	Bark	0.116	0.171
Basidiomycota	0.059	0.524	Substrate type	0.103	0.362
Chaetothyriales	0.055	0.520	Length	0.101	0.229
Eurotiales	0.053	0.522	Decay	0.097	0.154
			Apical diameter	0.086	0.294
			Basal diameter	0.073	0.367
Mantel test					
Variable	r^b	P			
Latitude	0.153	0.004			
Month	0.135	0.008			
Epiphyte	0.117	0.049			
Decay	0.113	0.048			
Latitude &	0.108	0.006			
Longitude	0.090	0.015			
Bark	0.032	0.314			
Length	0.023	0.341			
Basal diameter	0.003	0.475			

^a IS = Incertae sedis.

^b Spearman correlation coefficient

Figure legends

Fig 1. Location of the study area and sampling sites on the North Norwegian coast. Diamonds represent fungal communities inhabiting logs in the western part and triangles in the eastern part of the study area. Site names are followed by numbers of logs sampled.

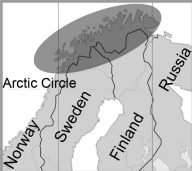
Fig 2. OTU accumulation and estimated richness. Solid lines show rarefaction curves based on Mao Tau estimator, dotted line shows 95% confidence limits and dashed line Michaelis-Menten estimate of γ -diversity. WP=Western part, EP=Eastern Part, WD=Whole data set.

Fig 3. Phylogenetic and ecological diversity of the 125 wood-inhabiting OTUs based on a combined *5.8S/LSU* data set. Maximum likelihood bootstrap support values >80 and Bayesian posterior probabilities >0.90 are shown on branches. Marine OTUs are in italics and in blue. Best *LSU* BLAST matches are shown in brackets and matches with $<80\%$ sequence similarity are marked with an asterisk (*). Number of logs/sites each OTU occurred in is given after BLAST match identities. Scale bar shows nucleotide substitutions per site. Maximum likelihood and Bayesian analyses produced highly similar trees, and the topology of the latter is shown here. Differences were related to some low supported nodes of the Bayesian tree shown as polytomies in the maximum likelihood tree.

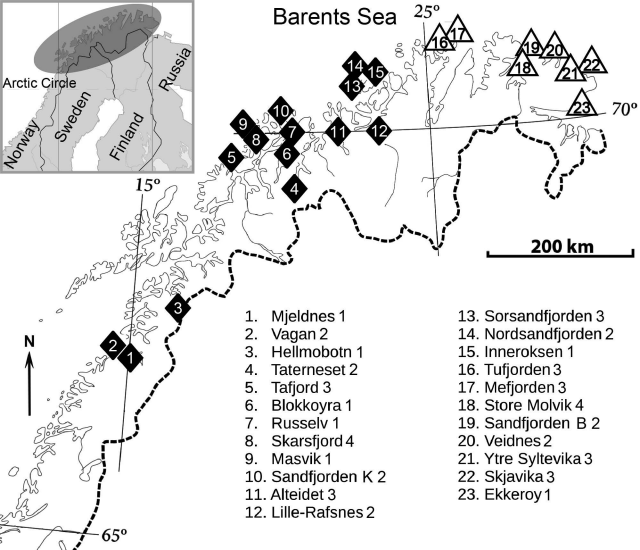
Fig 4. Ascomycetous OTUs detected based on *LSU* and *ITS* top hits in the two sea areas. Taxonomic annotation is followed by the total number of OTUs in parentheses. Number of ascomycetous OTUs in the western part was 88, in the eastern part 63 and in the whole data set 122.

Fig 5. *ITS* phylogeny among Lulworthiales isolates found in this study. Grey boxes represent OTUs and their representative isolates are in bold. Taxa labeled with GenBank accession numbers represent best BLAST matches of the study isolates. RAxML standard bootstrap values are shown above branches or at nodes. Scale bar shows nucleotide substitutions per site.

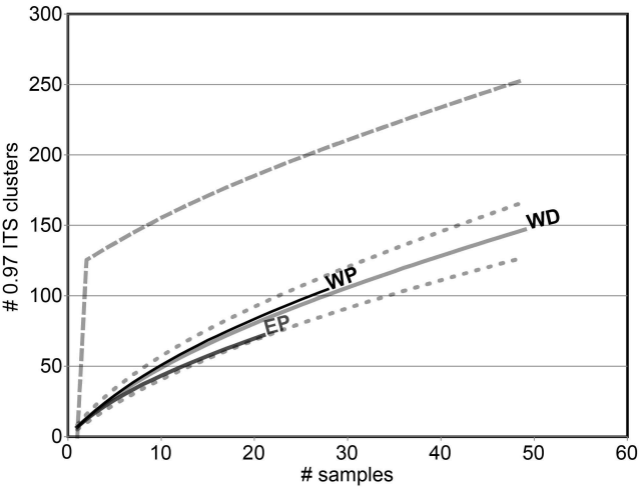
Fig 6. The NMDS ordination of fungal communities inhabiting 44 logs and important ecological and taxonomic parameters influencing the dispersion of OTUs in the ordination space: a) geography, b) attachment type, tree type, epiphyte cover and latitude, and c) taxonomic parameters. Diamonds represent fungal communities inhabiting logs in the western part and triangles in the eastern part of the study area. Circled diamonds are sublittoral logs by the shore and filled triangles logs in the breaker zone. The 95% confidence ellipsoids are drawn based on standard errors of the averages of the points for attachment (filled ellipsoids) and tree type (dashed for broadleaved and dotted for coniferous logs). Agar=Agaricales, Asco=Ascomycota, Capn=Capnodiales, Helo=Helotiales, Hypo=Hypocreales, Lulw=Lulworthiales, Myti=Mytilinidiales, Pleo=Pleosporales and α = α -diversity. The two first dimensions of the three studied are plotted. Four of the statistically significant parameters (zone, habitat type, orientation and log position) are not shown, since these included parameter categories with only few observations making it difficult to evaluate their importance.



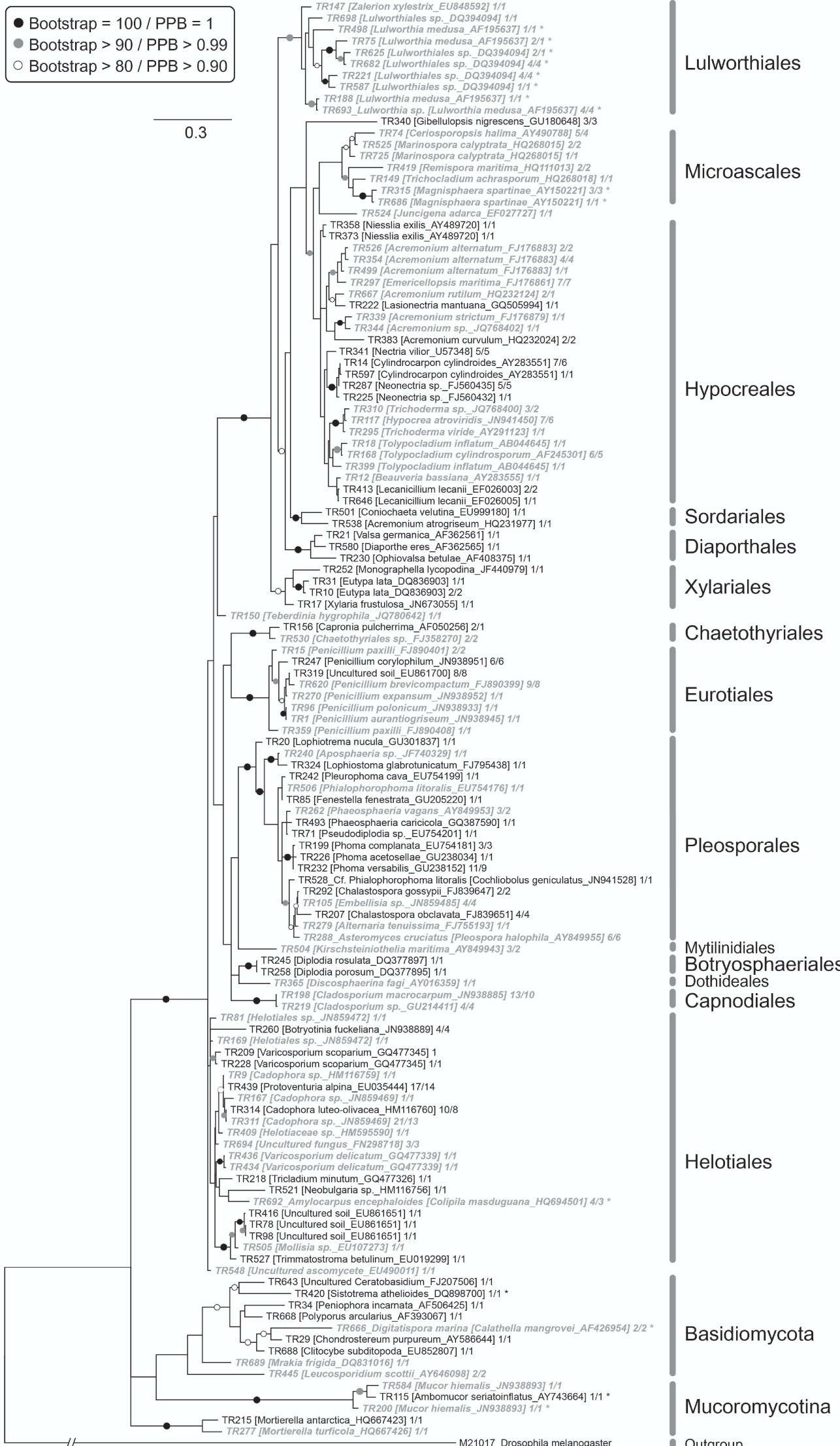
Barents Sea

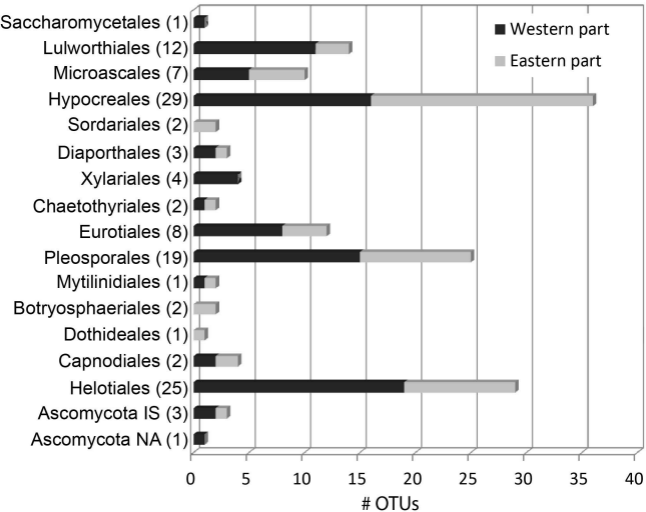


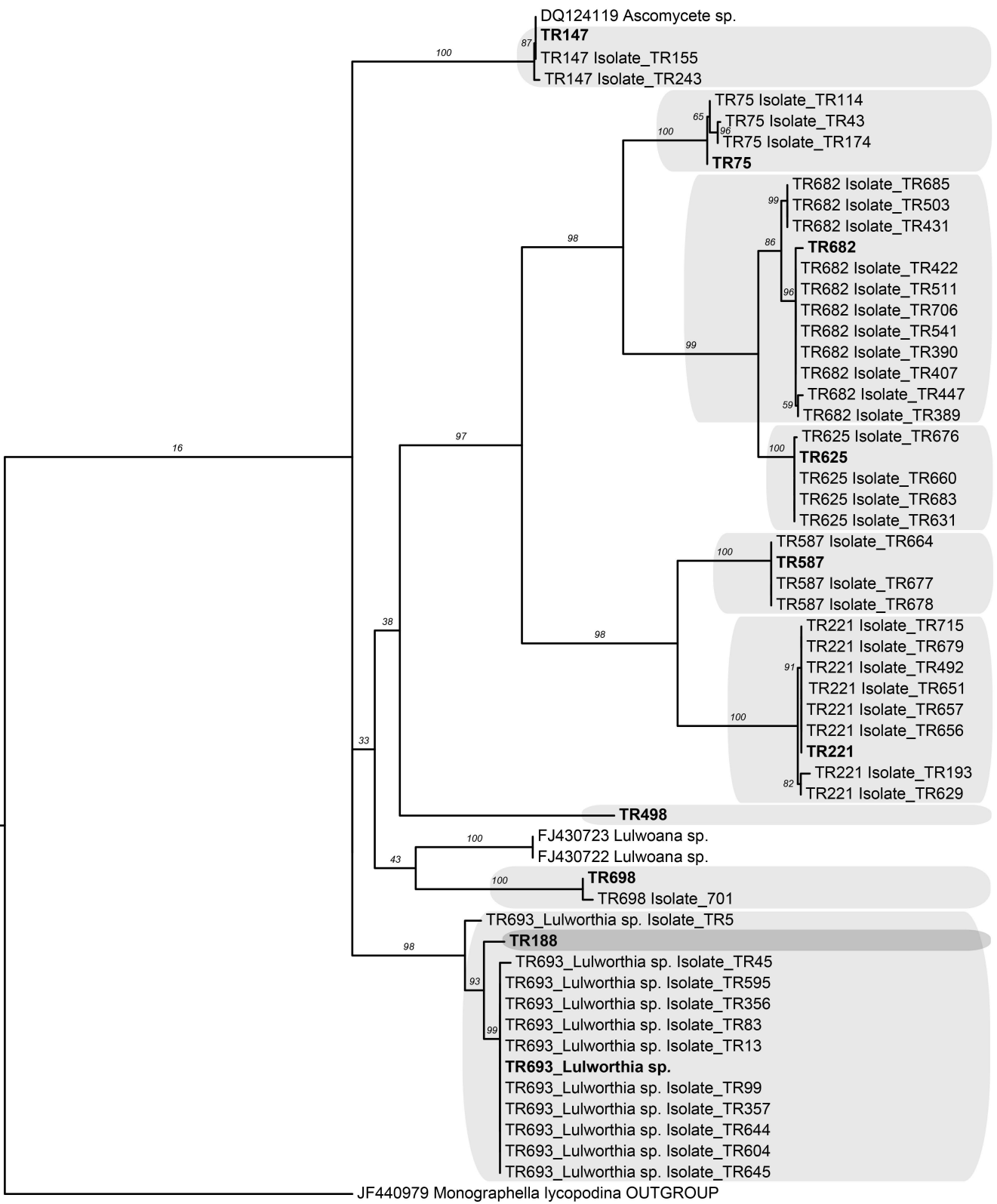
- | | |
|---------------------|-----------------------|
| 1. Mjeldnes 1 | 13. Sorsandfjorden 3 |
| 2. Vagan 2 | 14. Nordsandfjorden 2 |
| 3. Hellmobotn 1 | 15. Inneroksen 1 |
| 4. Taterneset 2 | 16. Tufjorden 3 |
| 5. Tafjord 3 | 17. Mefjorden 3 |
| 6. Blokkoyra 1 | 18. Store Molvik 4 |
| 7. Russelv 1 | 19. Sandfjorden B 2 |
| 8. Skarsfjord 4 | 20. Veidnes 2 |
| 9. Masvik 1 | 21. Ytre Syltevika 3 |
| 10. Sandfjorden K 2 | 22. Skjavika 3 |
| 11. Alteidet 3 | 23. Ekkeroy 1 |
| 12. Lille-Rafsnes 2 | |

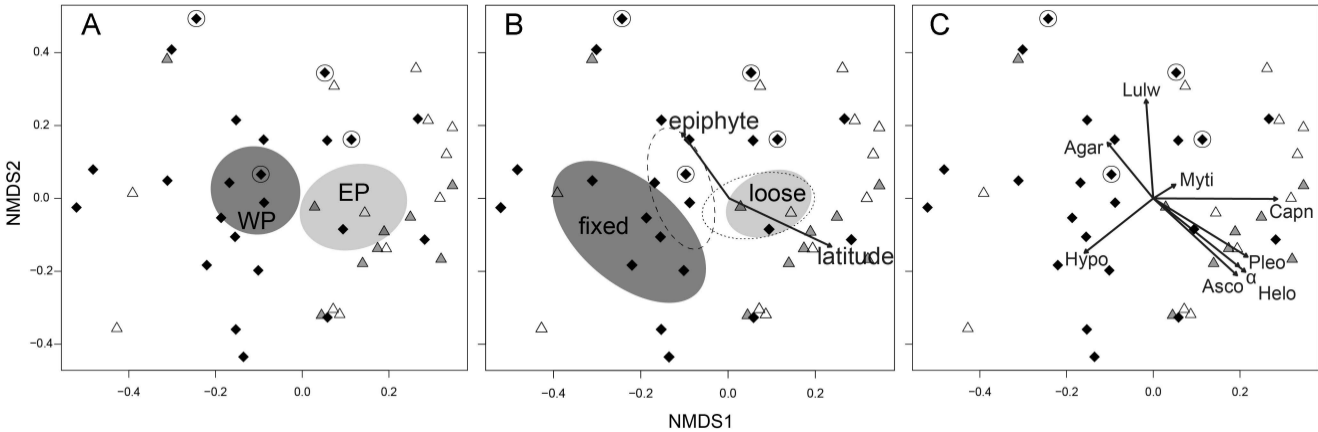


- Bootstrap = 100 / PPB = 1
- Bootstrap > 90 / PPB > 0.99
- Bootstrap > 80 / PPB > 0.90









Supplementary Material

The supplementary material in this file includes details of the methods and analyses, titles and legends to four supplementary figures and two supplementary tables. The supplementary tables and figures focus on OTU annotation and phylogeny, and a comparison of taxa found in this study and reference studies.

Supplementary Methods

DNA amplification

The PCR reactions consisted of 20 μ l reaction mix (15 μ l Milli-Q water, 2.5 μ l forward primer and 2.5 μ l reverse primer) and 5 μ l of template DNA diluted 1:50. The cyclic PCR program consisted of an initial 3 min denaturation step at 94°C, followed by 40 cycles of 30 s at 94°C, 30 s at 52°C (annealing) and 1 min at 72°C (synthesis), and termination with a 10 min elongation step at 72°C.

We prepared negative controls in order to detect and exclude possible contaminations. Successful PCR reactions resulted in single bands observed on 1% agarose gel stained with GelGreen Nucleic Acid Gel Stain (Biotum, Hayward, California, USA), using Superladder-Low 100 bp Ladder (Thermo Fisher Scientific, Surrey, UK) as a standard size marker. The gels were photographed under an UV-trans-illuminator. The thermal program used to clean PCR products was: 30 min incubation at 37°C for degrading remaining primers and nucleotides followed by 15 min incubation at 80°C to inactivate ExoSAP-IT.

Phylogenetic and ordination analyses

The maximum likelihood analyses of the 5.8S/LSU data set was ran in RAxML version 7.2.6 (Stamatakis, 2006) using the rapid hill climbing algorithm (Stamatakis et al., 2007) with two data partitions and joint branch length optimization, combined with standard bootstrapping. General time reversible nucleotide substitution model under Γ model of rate distribution (GTR+GAMMA) was applied with maximum likelihood estimate of the alpha-parameter. The bootstrap probabilities were calculated on the resulting single best tree using 100 bootstrap replicates.

We chose the nucleotide substitution model for the Bayesian analysis using MrModeltest version 2.3 (Nylander, 2004). Symmetric (SYM) nucleotide substitution model with proportion of invariable sites (I) and GAMMA was used for the 5.8S and GTR+I+GAMMA for the LSU partition of the data set. The Markov Chain Monte Carlo (MCMC) analysis was called from random starting tree with 4 chains and 5 runs. A sample frequency of 500 and diagnosing frequency of 5 000 generations was used, and the nucleotide substitution model parameters were unlinked across partitions. After 3 000 000 generations, the average standard deviation of split frequencies had reached stationary at 0.008 and chain swopping frequency was acceptable. We used a relative burn-in of 25% resulting in 150 005 trees sampled from which the consensus tree and posterior probabilities were calculated.

We ran maximum likelihood analyses of the order level ITS data sets using rapid hill climbing algorithm with random or parsimony starting tree, GTR+GAMMA substitution model and standard bootstrapping with 100 replicates.

The starting point for the non-metric multidimensional scaling ordination was an untransformed presence/absence data matrix with OTUs and substrate units hosting them. Three sea bottom logs and two separate logs from the south were removed from the analyses as outliers, as well as singletons. We tested different dissimilarity indices using the rankindex function in vegan (Oksanen et al., 2013). Chao and Kulczynski indices performed best in separating communities along gradients in our data (results not shown), and since Kulczynski is good in detecting underlying ecological gradients (Faith et al., 1987), we used it to calculate the distance matrix. Environmental variable fitting was done separately for attachment type, since this had missing observations which were excluded prior to fitting the variable. In Mantel tests geographic distance matrices were tested separately with north (latitude) and east (longitude) coordinates and both together. In addition, following vectors and numerical factors could be included in the analysis: month, epiphyte cover, decay stage, bark cover, length and base diameter. The two lowest stress values for the ordination were 20.00609, procrustes

sum of squares based on 999 permutations=2.194e-06, correlation in a symmetric procrustes rotation=1 and significance=0.001.

Titles and legends to Supplementary Tables:

Table S1. Sampled logs and variables. The outlier logs excluded from the NMDS ordination, Mantel tests and Qiime analyses are in italics. The single-OTU logs excluded from the Phylocom analyses are in bold and the oily log, supporting no fungal growth and excluded from all analyses, is in grey font.

Table S2. GenBank top BLAST matches of the OTUs and their accession numbers.

Table S3. Most frequent taxa found in this and other studies of marine fungi in the western-Eurasian temperate and arctic sea areas. Numbers represent frequency of occurrence on substrate units (and sites). *Cadophora* spp., *Penicillium* spp., *Cladosporium* spp. *Nectria* s. lato and Lulworthiaceae spp. include data from several OTUs. The vertical line separates plating method based culturing studies and studies based on direct observation combined with incubation of substrates.

Titles and legends to Supplementary Figures:

Fig S1. 5.8S phylogenetic tree among isolates used in phylogenetic community analyses. One isolate per OTU per substrate unit was included in the analyses, and the tree was constructed using the rapid hill algorithm in RAxML.

Fig S2. Ordinal ITS trees among all isolates and their GenBank top BLAST matches.

Fig S3. Box-plot diagram showing the sequence similarity of GenBank top BLAST matches for 89 marine and non-marine OTUs detected in this study. Environmental sequences were filtered out of this graph, and only hits with genus or species level identification were included.

Fig S4. Distribution of LSU and ITS GenBank BLAST matches for marine vs. non-marine OTUs. Marine OTUs in solid black line, non-marine in dashed grey line. Unidentified and environmental sequences were excluded from this graph and only hits with genus or species level identification were included.

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Log	Geography	County	Site	Longitude	Latitude	Month	Habitat type	Zone	Attachment	Tree type	Substrate type	Position	Diam_base (cm)
SU007	Western part	Troms	Sandfjorden K	676738.62	7798101.18	5	sandy	tide	loose	broadleaved	broken trunk	horizontal	20
SU008	Western part	Troms	Sandfjorden K	676588.4	7798176.79	5	sandy	tide	loose	broadleaved	cut trunk	horizontal	8
SU009	Western part	Troms	Taterneset	694950.3	7692764.39	5	sandy	tide	loose	broadleaved	branch	horizontal	5
SU010	Western part	Troms	Taterneset	694939.18	7692724.09	5	sandy	tide	loose	broadleaved	unknown	horizontal	7
SU011	Western part	Troms	Blokkoyra	692015.4	7749370.98	5	sandy	tide	loose	broadleaved	branch	horizontal	5
SU012	Western part	Troms	Russelv	700561.82	7771172.08	5	rocky	tide	loose	broadleaved	cut trunk	horizontal	15
SU013	Western part	Troms	Tafjord	621798.03	7731704.72	5	rocky	tide	loose	broadleaved	cut trunk	horizontal	8
SU014	Western part	Troms	Tafjord	621811.77	7731708.09	5	rocky	tide	loose	broadleaved	cut trunk	horizontal	11
SU015	Western part	Troms	Tafjord	621864.43	7731724.33	5	sandy	tide	fixed	broadleaved	whole trunk	horizontal	14
SU017	Western part	Troms	Skarsfjord	649289.18	7766613.91	6	gravel	tide	fixed	broadleaved	broken trunk	horizontal	8
SU018	Western part	Troms	Skarsfjord	649287.09	7766614.7	6	gravel	sublittoral	NA	broadleaved	cut trunk	horizontal	5
SU019	Western part	Troms	Skarsfjord	649257.4	7766589.66	6	gravel	sublittoral	NA	conifer	cut trunk	horizontal	8
SU020	Western part	Troms	Skarsfjord	649257.4	7766589.66	6	gravel	sublittoral	NA	conifer	cut trunk	horizontal	8
SU025	Western part	Troms	Masvik	640945.18	7768835.43	6	sandy	tide	fixed	conifer	cut trunk	horizontal	52
SU026	Western part	Finnmark	Inneroksen	781029.74	7861419.7	5	sea-bottom	sea_bottom	NA	conifer	cut trunk	horizontal	4
SU041	Western part	Troms	Alteidet	769175.48	7784280.94	8	stony	tide	fixed	conifer	cut trunk	vertical	20
SU042	Western part	Troms	Alteidet	769172.37	7784261.52	8	stony	tide	fixed	conifer	cut trunk	vertical	19
SU043	Western part	Troms	Alteidet	769175.39	7784291.99	8	stony	tide	loose	conifer	cut trunk	horizontal	12
SU048	Western part	Finnmark	Sorsandfjorden	0764152.26	7851988.00	8	sandy	tide	fixed	conifer	cut trunk	horizontal	22
SU049	Western part	Finnmark	Sorsandfjorden	764155.75	7851993.38	8	sandy	tide	fixed	conifer	unknown	vertical	11
SU050	Western part	Finnmark	Sorsandfjorden	763019.55	7852213.58	8	sandy	tide	loose	conifer	cut trunk	horizontal	14
SU051	Western part	Finnmark	Nordsandfjorden	767049.08	7853749.77	8	rocky	tide	fixed	broadleaved	whole trunk	horizontal	4
SU052	Western part	Finnmark	Nordsandfjorden	766986.12	7853096.82	8	sandy	tide	fixed	broadleaved	broken trunk	horizontal	5
SU065	Western part	Finnmark	Lille-Rafsnes	823676.39	7789415.6	8	gravel	sublittoral	NA	broadleaved	unknown	horizontal	5
SU066	Western part	Finnmark	Lille-Rafsnes	823676.39	7789497.3	8	gravel	tide	NA	broadleaved	unknown	horizontal	15
<i>SU091</i>	<i>Western part</i>	<i>Nordland</i>	<i>Hellmobotn</i>	<i>562100.00</i>	<i>7524063.00</i>	<i>10</i>	<i>sea-bottom</i>	<i>sea_bottom</i>	<i>NA</i>	<i>broadleaved</i>	<i>unknown</i>	<i>horizontal</i>	<i>5</i>
<i>SU107</i>	<i>Western part</i>	<i>Nordland</i>	<i>Vagan</i>	<i>494000.00</i>	<i>7464000.00</i>	<i>10</i>	<i>NA</i>	<i>tide</i>	<i>NA</i>	<i>broadleaved</i>	<i>broken trunk</i>	<i>horizontal</i>	<i>5</i>
<i>SU108</i>	<i>Western part</i>	<i>Nordland</i>	<i>Vagan</i>	<i>494000.00</i>	<i>7464000.00</i>	<i>10</i>	<i>NA</i>	<i>tide</i>	<i>NA</i>	<i>broadleaved</i>	<i>broken trunk</i>	<i>horizontal</i>	<i>4</i>
<i>SU109</i>	<i>Western part</i>	<i>Nordland</i>	<i>Mjeldnes</i>	<i>505000.00</i>	<i>7459000.00</i>	<i>10</i>	<i>sea-bottom</i>	<i>sea_bottom</i>	<i>NA</i>	<i>broadleaved</i>	<i>cut trunk</i>	<i>horizontal</i>	<i>12</i>
SU054	Eastern part	Finnmark	Mefjorden	887985.43	7924138.69	8	stony	breaker	loose	conifer	cut trunk	horizontal	29
SU055	Eastern part	Finnmark	Mefjorden	887996.63	7924128.68	8	stony	breaker	loose	broadleaved	broken trunk	horizontal	5
SU058	Eastern part	Finnmark	Tufjorden	886884.36	7919881.07	8	stony	tide	loose	conifer	cut trunk	horizontal	30
SU059	Eastern part	Finnmark	Tufjorden	886762.43	7919582.72	8	stony	tide	fixed	conifer	cut trunk	horizontal	24
SU060	Eastern part	Finnmark	Tufjorden	886842.69	7919686.73	8	stony	tide	loose	conifer	cut trunk	horizontal	25
SU061	Eastern part	Finnmark	Mefjorden	888206.48	7924320.06	8	stony	tide	NA	conifer	cut trunk	horizontal	36
SU067	Eastern part	Finnmark	Veidnes	1026050.21	7910345.54	9	stony	tide	loose	conifer	cut trunk	horizontal	28
SU068	Eastern part	Finnmark	Veidnes	1026384.74	7910539.64	9	stony	breaker	loose	conifer	unknown	horizontal	36
SU069	Eastern part	Finnmark	Store Molvik	997783.34	7908723.45	9	stony	breaker	loose	conifer	cut trunk	horizontal	5
SU070	Eastern part	Finnmark	Store Molvik	997833.08	7908761.06	9	stony	tide	loose	conifer	cut trunk	horizontal	10
SU073	Eastern part	Finnmark	Store Molvik	998194.5	7909136.47	9	stony	breaker	NA	conifer	cut trunk	horizontal	10
SU074	Eastern part	Finnmark	Store Molvik	998198.43	7909147.49	9	stony	breaker	NA	broadleaved	broken trunk	horizontal	5
SU076	Eastern part	Finnmark	Sandfjorden B	1020016.72	7915933.2	9	rocky	tide	fixed	conifer	cut trunk	horizontal	3
SU077	Eastern part	Finnmark	Sandfjorden B	1020004.72	7915926.69	9	rocky	breaker	loose	conifer	cut trunk	horizontal	7
SU078	Eastern part	Finnmark	Ytre Syltevika	1067176.98	7899436.32	9	gravel	tide	loose	conifer	cut trunk	horizontal	7
SU079	Eastern part	Finnmark	Ytre Syltevika	1067190.8	7899494.09	9	stony	breaker	loose	conifer	cut trunk	horizontal	17
SU080	Eastern part	Finnmark	Ytre Syltevika	1067247.5	7899693.04	9	stony	breaker	loose	conifer	cut trunk	horizontal	26
SU085	Eastern part	Finnmark	Skjavika	1073986.18	7900557.99	9	sandy	tide	loose	conifer	cut trunk	horizontal	31
SU086	Eastern part	Finnmark	Skjavika	1073981.85	7900524.12	9	sandy	tide	loose	conifer	unknown	horizontal	13
SU088	Eastern part	Finnmark	Skjavika	1073981.84	7900561.91	9	stony	tide	loose	conifer	broken trunk	horizontal	9
SU090	Eastern part	Finnmark	Ekkeroy	1069801.11	7844794.14	9	stony	tide	loose	conifer	cut trunk	horizontal	40

Log	Diam_apex (cm)	Length (m)	Decay	Epiphyte (%)	Bark (%)	Orientation	PD	α -diversity	Chytridiomycota	Mucoromycotina	Basidiomycota	Ascomycota	Fungi_NA	Agaricales
SU007	18	2.5	1	0	0	S-N-S	0.531	9	0	0	0	9	0	0
SU008	5	0.6	1	10	40	W-E-W	0.677	5	0	0	1	4	0	1
SU009	3	1	2	0	10	S-N-S	0.485	12	0	0	0	11	1	0
SU010	7	0.6	3	0	0	W-E-W	0.623	9	0	1	0	7	1	0
SU011	3	0.9	2	0.5	90	S-N-S	0.439	11	0	0	0	10	1	0
SU012	6	1.8	1	0.5	80	W-E-W	0.338	5	0	0	0	5	0	0
SU013	7	0.9	2	0.5	0	S-N-S	0.53	10	0	0	1	9	0	1
SU014	9	1.9	2	0.5	0	S-N-S	0.449	9	0	0	1	5	3	0
SU015	10	1.3	2	0.5	0.5	W-E-W	0.394	5	0	0	0	5	0	0
SU017	7	1.4	2	80	0	W-E-W	0.568	4	0	0	1	3	0	1
SU018	4	1	1	20	5	W-E-W	0.188	1	0	0	0	1	0	0
SU019	8	1.8	3	0.5	0	W-E-W	0.598	8	0	0	0	8	0	0
SU020	8	1.8	3	0.5	0	W-E-W	0.33	4	0	0	0	4	0	0
SU025	39	8	2	15	0	S-N-S	0.267	3	0	0	0	3	0	0
SU026	4	0.1	4	5	0	NA	0.24	1	0	0	0	1	0	0
SU041	17	0.4	2	5	0	up-down	0.357	4	0	0	0	4	0	0
SU042	19	0.6	2	20	0	up-down	0.486	8	0	1	0	7	0	0
SU043	12	3	2	0.5	0	S-N-S	0.364	7	0	0	2	5	0	0
SU048	18	3.9	2	5	0	E-W-E	NA	0	0	0	0	0	0	0
SU049	9	2.2	2	0.5	0	up-down	0.491	5	0	0	0	5	0	0
SU050	13	1.2	2	0.5	0	S-N-S	0.566	10	0	0	1	9	0	0
SU051	1	2.2	2	1	95	S-N-S	0.414	11	0	0	0	11	0	0
SU052	1	2	1	0	70	S-N-S	0.445	8	0	0	0	8	0	0
SU065	2	2.7	1	0.5	5	W-E-W	0.375	6	0	0	0	6	0	0
SU066	10	2.2	4	0	5	S-N-S	0.742	11	0	1	0	10	0	0
SU091	2	0.2	4	0.5	0	NA	0.432	6	0	0	0	6	0	0
SU107	5	0.2	2	0.5	0	NA	0.385	6	0	0	0	6	0	0
SU108	3	0.3	2	0.5	0	NA	0.476	8	0	0	0	8	0	0
SU109	12	0.7	5	0.5	0	NA	0.712	4	1	0	0	3	0	0
SU054	24	4.2	2	1	0	S-N-S	0.471	4	0	0	0	4	0	0
SU055	4	1.7	2	1	80	S-N-S	0.453	15	0	0	0	15	0	0
SU058	26	1.8	2	0.5	0	S-N-S	0.364	5	0	0	0	5	0	0
SU059	10	2.4	2	0.5	0	S-N-S	0.486	9	0	1	0	8	0	0
SU060	24	1.9	2	0.5	0	S-N-S	0.632	6	0	1	0	5	0	0
SU061	19	5.5	2	0	0	W-E-W	0.344	6	0	0	0	6	0	0
SU067	28	3.3	2	1	0	W-E-W	0.62	7	0	0	0	7	0	0
SU068	30	2.5	2	0	0	S-N-S	0.496	8	0	0	0	8	0	0
SU069	5	0.4	2	0	0	W-E-W	0.328	6	0	0	1	5	0	0
SU070	6	0.8	2	0	0	W-E-W	0.59	8	0	0	1	6	1	0
SU073	10	1.2	2	0.5	0	W-E-W	0.441	7	0	0	0	6	1	0
SU074	5	0.5	1	0.5	0	S-N-S	0.467	2	0	0	1	1	0	1
SU076	3	0.5	1	0	0	W-E-W	0.568	6	0	0	0	6	0	0
SU077	7	0.9	1	0	0	S-N-S	0.324	8	0	0	0	8	0	0
SU078	6	1.6	1	20	0	S-N-S	0.247	3	0	0	0	3	0	0
SU079	14	5.1	1	0	0	S-N-S	0.607	10	0	0	0	10	0	0
SU080	24	3.1	2	0	0	S-N-S	0.595	7	0	0	1	6	0	0
SU085	25	3.2	2	40	0	S-N-S	0.503	6	0	0	1	4	1	1
SU086	12	0.7	2	0	0	W-E-W	0.414	8	0	0	0	8	0	0
SU088	4	1.3	1	0.5	0	S-N-S	0.459	6	0	0	0	6	0	0
SU090	31	6.6	2	0.5	0	W-E-W	0.402	6	0	0	0	5	1	0

Log	Cantharellales	Polyporales	Russulales	Cystofilobasidiales	Leucosporidiales	Saccharomycetales	Lulworthiales	Microascales	Hypocreales	Diaporthales	Xylariales	Chaetothyriales
SU007	0	0	0	0	0	0	1	2	2	0	0	0
SU008	0	0	0	0	0	0	1	1	0	0	1	0
SU009	0	0	0	0	0	0	0	0	3	1	1	1
SU010	0	0	0	0	0	0	0	0	3	0	0	1
SU011	0	0	0	0	0	0	1	1	2	0	0	0
SU012	0	0	0	0	0	0	0	0	1	0	0	0
SU013	0	0	0	0	0	1	0	0	1	0	1	0
SU014	0	0	1	0	0	0	0	0	2	0	0	0
SU015	0	0	0	0	0	0	0	0	1	0	1	0
SU017	0	0	0	0	0	0	1	0	0	0	0	0
SU018	0	0	0	0	0	0	0	0	0	0	0	0
SU019	0	0	0	0	0	0	4	1	0	0	0	0
SU020	0	0	0	0	0	0	1	0	0	0	0	0
SU025	0	0	0	0	0	0	1	0	1	0	0	0
SU026	0	0	0	0	0	0	0	1	0	0	0	0
SU041	0	0	0	0	0	0	0	1	3	0	0	0
SU042	0	0	0	0	0	0	0	0	3	0	0	0
SU043	1	1	0	0	0	0	0	0	2	0	0	0
SU048	0	0	0	0	0	0	0	0	0	0	0	0
SU049	0	0	0	0	0	0	0	2	1	0	0	0
SU050	1	0	0	0	0	0	0	0	1	0	1	0
SU051	0	0	0	0	0	0	0	0	1	0	0	0
SU052	0	0	0	0	0	0	0	0	2	1	0	0
SU065	0	0	0	0	0	0	2	0	0	0	0	0
SU066	0	0	0	0	0	0	0	0	4	0	0	0
SU091	0	0	0	0	0	0	2	0	0	0	0	0
SU107	0	0	0	0	0	0	3	0	1	0	0	0
SU108	0	0	0	0	0	0	1	0	3	0	0	0
SU109	0	0	0	0	0	0	1	1	0	0	0	0
SU054	0	0	0	0	0	0	0	0	0	0	0	0
SU055	0	0	0	0	0	0	1	0	7	1	0	0
SU058	0	0	0	0	0	0	0	0	1	0	0	0
SU059	0	0	0	0	0	0	0	0	1	0	0	0
SU060	0	0	0	0	0	0	0	0	1	0	0	0
SU061	0	0	0	0	0	0	0	0	3	0	0	0
SU067	0	0	0	0	0	0	2	1	0	0	0	1
SU068	0	0	0	0	0	0	0	0	1	0	0	0
SU069	0	0	0	0	1	0	0	0	0	0	0	0
SU070	0	0	0	1	0	0	0	1	3	0	0	0
SU073	0	0	0	0	0	0	0	0	1	0	0	0
SU074	0	0	0	0	0	0	1	0	0	0	0	0
SU076	0	0	0	0	0	0	0	2	3	0	0	0
SU077	0	0	0	0	0	0	0	0	0	0	0	0
SU078	0	0	0	0	0	0	0	0	1	0	0	0
SU079	0	0	0	0	0	0	0	1	3	0	0	0
SU080	0	0	0	0	1	0	0	0	1	0	0	0
SU085	0	0	0	0	0	0	0	0	1	0	0	0
SU086	0	0	0	0	0	0	0	0	2	0	0	0
SU088	0	0	0	0	0	0	0	0	4	0	0	0
SU090	0	0	0	0	0	0	1	0	2	0	0	1

Log	Eurotiales	Pleosporales	Mytilinidiales	Botryosphaeriales	Capnodiales	Dothideales	Helotiales	Sordariales	Ascomycota_incertae_sedis
SU007	3	0	0	0	0	0	1	0	0
SU008	0	1	0	0	0	0	0	0	0
SU009	0	2	0	0	0	0	3	0	0
SU010	1	1	0	0	0	0	1	0	0
SU011	0	0	0	0	0	0	5	0	1
SU012	2	0	0	0	0	0	2	0	0
SU013	2	2	0	0	1	0	1	0	0
SU014	0	1	0	0	1	0	1	0	0
SU015	1	1	0	0	0	0	1	0	0
SU017	1	0	0	0	0	0	1	0	0
SU018	0	0	0	0	0	0	1	0	0
SU019	0	0	1	0	0	0	2	0	0
SU020	0	0	1	0	0	0	2	0	0
SU025	0	0	0	0	0	0	1	0	0
SU026	0	0	0	0	0	0	0	0	0
SU041	0	0	0	0	0	0	0	0	0
SU042	1	1	0	0	0	0	1	0	1
SU043	1	0	0	0	1	0	1	0	0
SU048	0	0	0	0	0	0	0	0	0
SU049	0	0	0	0	0	0	2	0	0
SU050	1	3	0	0	1	0	2	0	0
SU051	1	5	0	0	1	0	3	0	0
SU052	0	2	0	0	0	0	3	0	0
SU065	0	1	0	0	1	0	2	0	0
SU066	3	1	0	0	1	0	1	0	0
SU091	2	0	0	0	1	0	1	0	0
SU107	0	1	0	0	0	0	1	0	0
SU108	0	1	0	0	0	0	3	0	0
SU109	1	0	0	0	0	0	0	0	0
SU054	0	1	0	0	1	0	1	0	1
SU055	0	1	0	2	1	0	2	0	0
SU058	0	1	0	0	1	0	1	1	0
SU059	1	2	0	0	1	0	3	0	0
SU060	1	2	0	0	0	0	1	0	0
SU061	0	1	0	0	1	0	1	0	0
SU067	2	0	0	0	0	0	1	0	0
SU068	2	0	0	0	1	0	4	0	0
SU069	0	1	1	0	1	0	2	0	0
SU070	0	1	0	0	0	0	1	0	0
SU073	1	1	0	0	0	0	3	0	0
SU074	0	0	0	0	0	0	0	0	0
SU076	0	1	0	0	0	0	0	0	0
SU077	1	4	0	0	0	1	2	0	0
SU078	0	0	0	0	0	0	2	0	0
SU079	1	1	0	0	0	0	4	0	0
SU080	0	2	0	0	1	0	1	0	1
SU085	0	1	0	0	0	0	2	0	0
SU086	1	1	0	0	0	0	4	0	0
SU088	0	1	0	0	0	0	1	0	0
SU090	0	0	0	0	1	0	0	0	0

Query	LSU hit				ITS hit									
OTU (morphological identification)	Organism	Phylum	Order	Accession number	Pairwise Identity	Bit-Score	Coverage	Organism	Phylum	Order	Accession number	Pairwise Identity	Bit-Score	Coverage
TR311	Cadophora sp.	Ascomycota	Helotiales	JN859469	100.0%	1494.48	100.00%	Cadophora sp.	Ascomycota	Helotiales	GU212389	99.8%	1115.77	99.52%
TR439	Protoventuria alpina	Ascomycota	Pleosporales	EU035444	100.0%	1494.48	100.00%	Helotiales sp.	Ascomycota	Helotiales	GU212426	99.8%	1023.8	98.79%
TR198	Cladosporium macrocarpum	Ascomycota	Capnodiales	JN938885	100.0%	1478.25	100.00%	Cladosporium sp.	Ascomycota	Capnodiales	HQ829067	100.0%	922.808	100.00%
TR692 (Amylocarpus encephaloides)	Colipila masdugwana	Ascomycota	Helotiales	HQ694501	94.3%	1272.66	100.00%	Ascomycota sp.	Ascomycota	na	FJ896405	90.8%	753.291	100.00%
TR314	Cadophora luteo-olivacea	Ascomycota	Helotiales	HM116760	100.0%	1494.48	100.00%	Phialocephala sp.	Ascomycota	Helotiales	FM999988	99.8%	1092.32	100.00%
TR297	Emericellopsis maritima	Ascomycota	Hypocreales	FJ176861	100.0%	1465.62	100.00%	Emericellopsis sp.	Ascomycota	Hypocreales	JQ796759	99.1%	1003.96	98.62%
TR232	Phoma versabilis	Ascomycota	Pleosporales	GU238152	100.0%	1492.67	100.00%	Pleosporales sp.	Ascomycota	Pleosporales	JF773593	99.8%	953.465	100.00%
TR117	Hypocrea atroviridis	Ascomycota	Hypocreales	JN941450	99.9%	1465.62	100.00%	H.rufa rRNA	Ascomycota	Hypocreales	X93987	100.0%	1083.31	100.00%
TR14	Cylindrocarpon cylindroides	Ascomycota	Hypocreales	AY283551	100.0%	1467.43	100.00%	Uncultured Nectria	Ascomycota	Hypocreales	HQ211747	99.6%	964.285	100.00%
TR620	Penicillium brevicompactum	Ascomycota	Eurotiales	FJ890399	100.0%	1492.67	99.88%	Uncultured fungus	na	na	GQ999382	99.8%	1047.24	100.00%
TR682	Lulworthiales sp.	Ascomycota	Lulworthiales	DQ394094	92.6%	1182.49	100.00%	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	82.3%	322.286	57.64%
TR693 (Lulworthia sp.)	Lulworthia medusa	Ascomycota	Lulworthiales	AF195637	95.7%	1305.12	100.00%	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	83.3%	491.803	88.57%
TR168	Tolypocladium cylindrosporium	Ascomycota	Hypocreales	AF245301	100.0%	1469.23	100.00%	Tolypocladium cylindrosporium	Ascomycota	Hypocreales	AB208110	100.0%	1003.96	100.00%
TR666 (Digitatispora marina)	Calathella mangrovei	Basidiomycota	Agaricales	AF426954	96.4%	1379.06	100.00%	Flagelloscypha sp.	Basidiomycota	Agaricales	AY571041	79.3%	450.325	70.17%
TR319	Uncultured soil	na	na	EU861700	99.5%	1478.25	100.00%	Penicillium virgatum	Ascomycota	Eurotiales	JF439503	97.8%	984.122	100.00%
TR247	Penicillium corylophilum	Ascomycota	Eurotiales	JN938951	99.5%	1474.64	100.00%	Penicillium melinii	Ascomycota	Eurotiales	AY373923	99.8%	1027.4	98.62%
TR221	Lulworthiales sp.	Ascomycota	Lulworthiales	DQ394094	93.4%	1222.17	100.00%	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	80.4%	352.943	74.09%
TR341	Nectria vilior	Ascomycota	Hypocreales	U57348	100.0%	1467.43	100.00%	Nectria flavoviridis	Ascomycota	Hypocreales	HQ897791	99.1%	980.516	100.00%
TR260	Botryotinia fuckeliana	Ascomycota	Helotiales	JN938889	100.0%	1494.48	100.00%	Botryotinia fuckeliana	Ascomycota	Helotiales	HQ171053	99.1%	921.004	100.00%
TR288 (Asteromyces cruciatus)	Pleospora halophila	Ascomycota	Pleosporales	AY849955	99.5%	1474.64	100.00%	Pleospora sp.	Ascomycota	Pleosporales	GQ120976	97.9%	973.302	99.65%
TR219	Cladosporium sp.	Ascomycota	Capnodiales	GU214411	100.0%	1478.25	100.00%	Cladosporium perangustum	Ascomycota	Capnodiales	JF499836	100.0%	987.729	100.00%
TR74	Ceriosporopsis halima	Ascomycota	Microascales	AY490788	100.0%	1463.82	100.00%	Ceriosporopsis halima	Ascomycota	Microascales	EU557364	87.8%	699.19	100.00%
TR667	Acremonium rutilum	Ascomycota	Hypocreales	HQ232124	99.6%	1445.78	100.00%	Acremonium rutilum	Ascomycota	Hypocreales	AB540580	95.8%	951.662	100.00%
TR625	Lulworthiales sp.	Ascomycota	Lulworthiales	DQ394094	92.1%	1160.85	100.00%	Acremonium sp.	Ascomycota	Hypocreales	FJ571421	79.4%	316.876	70.58%
TR207	Chalastospora obclavata	Ascomycota	Pleosporales	FJ839651	99.9%	1487.26	100.00%	Uncultured fungus	na	na	GU054232	99.7%	1059.86	100.00%
TR10	Eutypa lata	Ascomycota	Xylariales	DQ836903	98.5%	1429.55	100.00%	Diatrypella favacea	Ascomycota	Xylariales	JN689955	99.3%	1007.57	98.11%
TR31	Eutypa lata	Ascomycota	Xylariales	DQ836903	99.8%	1472.84	100.00%	Eutypa lata	Ascomycota	Xylariales	AY462541	97.1%	978.712	100.00%
TR354	Acremonium alternatum	Ascomycota	Hypocreales	FJ176883	99.0%	1429.55	100.00%	Acremonium sp.	Ascomycota	Hypocreales	JN207340	92.4%	821.819	100.00%
TR287	Neonectria sp.	Ascomycota	Hypocreales	FJ560435	99.9%	1462.02	100.00%	Neonectria lungdunensis	Ascomycota	Hypocreales	FJ430736	99.8%	904.774	98.44%
TR340	Gibellulopsis nigrescens	Ascomycota	Ascomycota Incertae sedi	GU180648	99.4%	1431.36	98.17%	Uncultured fungus	na	na	GU054046	94.1%	843.46	100.00%
TR504	Kirschsteiniotelia maritima	Ascomycota	Mytilinidiales	AY849943	100.0%	1499.89	100.00%	Uncultured fungus	na	na	FJ475767	82.2%	630.662	100.00%
TR310	Trichoderma sp.	Ascomycota	Hypocreales	JQ768400	99.6%	1458.41	100.00%	Uncultured Hypocrea	Ascomycota	Hypocreales	HQ211656	99.8%	1097.73	100.00%
TR530	Chaetothyriales sp.	Ascomycota	Chaetothyriales	FJ358270	99.9%	1496.28	100.00%	Uncultured eukaryote	na	na	GU941426	98.7%	931.825	52.90%
TR315	Magnisphaera spartinae	Ascomycota	Microascales	AY150221	95.1%	1263.64	98.89%	Nectria rubropeziza	Ascomycota	Hypocreales	HQ897797	76.2%	399.831	100.00%
TR105	Embellisia sp.	Ascomycota	Pleosporales	JN859485	99.6%	1478.25	100.00%	Embellisia sp.	Ascomycota	Pleosporales	JQ796753	99.8%	1065.27	100.00%
TR15	Penicillium paxilli	Ascomycota	Eurotiales	FJ890401	98.9%	1451.19	100.00%	Penicillium aurantiacobrunneum	Ascomycota	Eurotiales	JN617670	99.7%	1038.22	100.00%
TR587	Lulworthiales sp.	Ascomycota	Lulworthiales	DQ394094	93.7%	1231.18	100.00%	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	78.5%	349.336	76.66%
TR75	Lulworthia medusa	Ascomycota	Lulworthiales	AF195637	91.3%	1141.02	100.00%	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	78.3%	376.387	79.68%
TR694	Uncultured fungus	na	na	FN298718	98.7%	1443.98	100.00%	Uncultured Helotiales	Ascomycota	Helotiales	JF449882	98.6%	892.15	94.48%
TR445	Leucosporidium scottii	Basidiomycota	Leucosporidiales	AY646098	100.0%	1521.53	100.00%	Leucosporidium scottii	Basidiomycota	Leucosporidiales	AF444496	100.0%	1072.49	98.67%
TR262	Phaeosphaeria vagans	Ascomycota	Pleosporales	AY849953	99.9%	1487.26	100.00%	Entrophospora sp.	Glomeromycota	Diversisporales	AY035665	99.7%	1034.62	98.80%
TR71	Pseudodiplodia sp.	Ascomycota	Ascomycota Incertae sedi	EU754201	99.9%	1485.46	100.00%	Uncultured ascomycete	Ascomycota	na	AM901853	99.0%	1021.99	98.64%
TR147	Zalerion xylestrix	Ascomycota	Lulworthiales	EU848592	100.0%	1472.84	100.00%	Ascomycete sp.	Ascomycota	na	DQ124119	100.0%	948.055	94.59%
TR526	Acremonium alternatum	Ascomycota	Hypocreales	FJ176883	99.4%	1442.18	100.00%	Uncultured fungus	na	na	FJ235861	92.2%	794.769	100.00%
TR538	Acremonium atrogriseum	Ascomycota	Sordariales	HQ231977	100.0%	1469.23	100.00%	Uncultured compost	na	na	FM177651	99.6%	985.926	100.00%
TR150	Teberdinia hygrophila	Ascomycota	Ascomycota Incertae sedi	JQ780642	99.5%	1469.23	100.00%	Pseudeurotium bakeri	Ascomycota	incertae sedis	GU934582	98.9%	962.482	100.00%
TR199	Phoma complanata	Ascomycota	Pleosporales	EU754181	100.0%	1492.67	100.00%	Uncultured Phoma	Ascomycota	Pleosporales	JX010732	96.4%	803.785	100.00%
TR98	Uncultured soil	na	na	EU861651	98.9%	1427.75	99.51%	Phialocephala sp.	Ascomycota	Helotiales	FJ903362	99.3%	1418.73	90.10%
TR29	Chondrostereum purpureum	Basidiomycota	Agaricales	AY586644	99.9%	1544.97	100.00%	Chondrostereum purpureum	Basidiomycota	Agaricales	GQ411519	99.8%	1139.21	100.00%
TR725	Marinospora calyptata	Ascomycota	Microascales	HQ268015	99.3%	1436.77	100.00%	Ceriosporopsis halima	Ascomycota	Microascales	EU557364	84.0%	428.685	62.39%
TR527	Trimmatostroma betulinum	Ascomycota	Helotiales	EU019299	99.8%	1467.43	100.00%	Mollisia sp.	Ascomycota	Helotiales	AY354269	99.3%	957.072	62.17%
TR34	Peniophora incarnata	Basidiomycota	Russulales	AF506425	99.4%	1449.39	100.00%	Uncultured basidiomycete	Basidiomycota	na	AM902071	99.1%	994.943	100.00%
TR156	Capronia pulcherrima	Ascomycota	Chaetothyriales	AF050256	99.5%	1474.64	100.00%	Capronia pilosella	Ascomycota	Chaetothyriales	DQ826737	95.6%	1059.86	100.00%
TR525	Marinospora calyptata	Ascomycota	Microascales	HQ268015	97.1%	1352.01	100.00%	Ceriosporopsis halima	Ascomycota	Microascales	EU557364	84.8%	652.302	100.00%
TR292	Chalastospora gossypii	Ascomycota	Pleosporales	FJ839647	99.6%	1478.25	100.00%	Alternaria sp.	Ascomycota	Pleosporales	JQ775551	96.1%	966.089	100.00%
TR85	Pyrenochaeta unguis-hominis	Ascomycota	Pleosporales	GQ387622	99.5%	1471.03	99.88%	Phoma sp.	Ascomycota	Pleosporales	AY293797	88.5%	1184.3	90.98%
TR419	Remispora maritima	Ascomycota	Microascales	HQ111013	99.5%	1434.96	99.88%	Uncultured Ascomycota	Ascomycota	na	HQ433116	87.6%	425.078	57.95%
TR413	Lecanicillium lecanii	Ascomycota	Ascomycota Incertae sedi	EF026003	100.0%	1467.43	100.00%	Cordyceps confragosa	Ascomycota	Hypocreales	AB079127	100.0%	1058.06	100.00%
TR222	Lasionectria mantuana	Ascomycota	Hypocreales	GQ505994	99.9%	1458.41	100.00%	Acremonium cereale	Ascomycota	Hypocreales	AB540571	100.0%	1045.44	100.00%

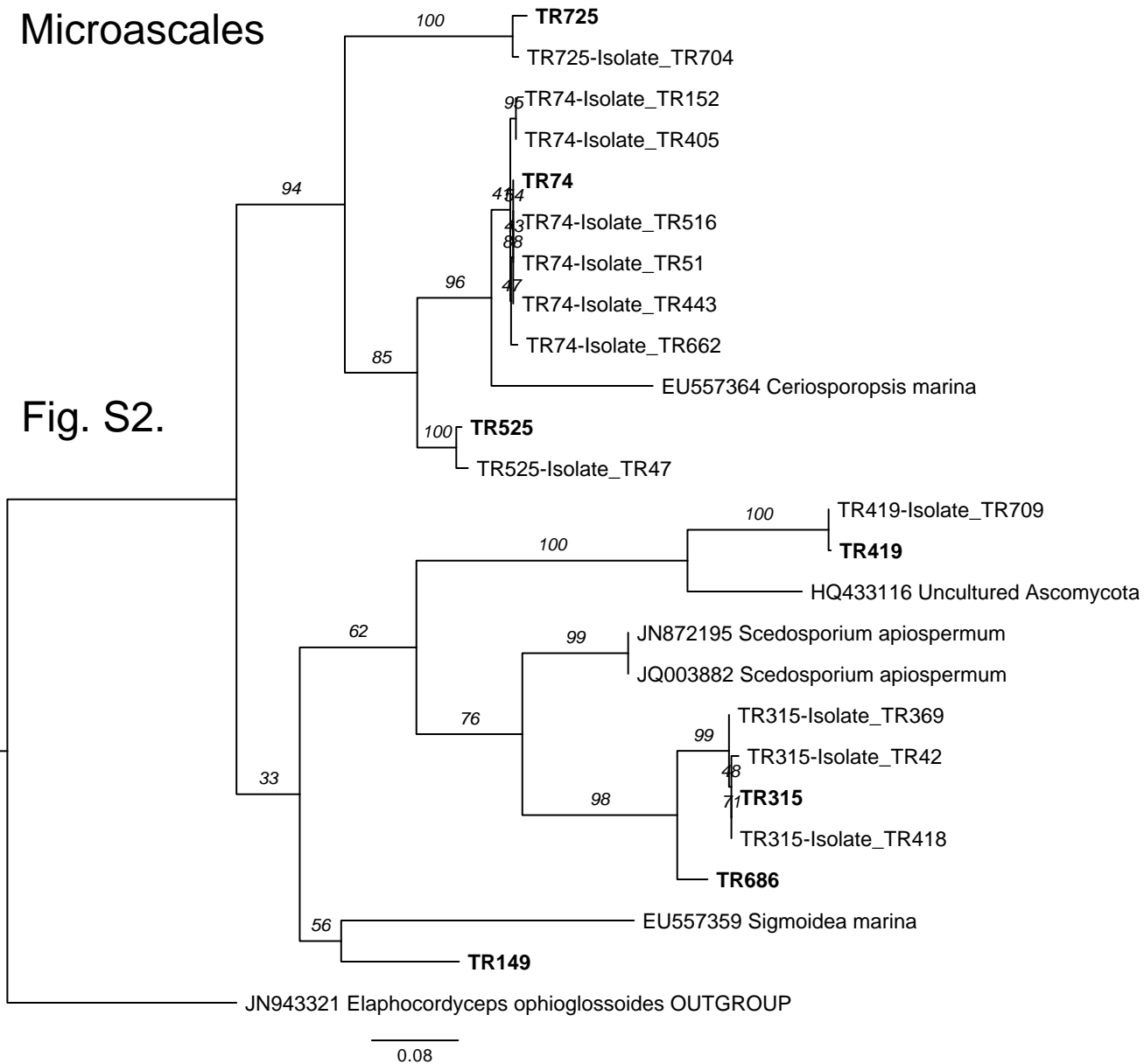
Query	LSU hit					ITS hit								
OTU (morphological identification)	Organism	Phylum	Order	Accession number	Pairwise Identity	Bit-Score	Coverage	Organism	Phylum	Order	Accession number	Pairwise Identity	Bit-Score	Coverage
TR252	Monographella lycopodina	Ascomycota	Xylariales	JF440979	100.0%	1476.44	100.00%	Monographella lycopodina	Ascomycota	Xylariales	JF440979	99.8%	969.695	100.00%
TR209	Varicosporium scoparium	Ascomycota	Helotiales	GQ477345	98.9%	1453.0	100.00%	Helotiales sp.	Ascomycota	Helotiales	HQ649856	97.6%	897.561	98.52%
TR228	Varicosporium scoparium	Ascomycota	Helotiales	GQ477345	99.8%	1485.46	100.00%	Uncultured Helotiales	Ascomycota	Helotiales	GU327459	87.9%	1016.58	97.33%
TR383	Acremonium curvulum	Ascomycota	Hypocreales	HQ232024	96.5%	1332.17	99.39%	Uncultured fungus	na	na	HQ260252	97.1%	865.1	100.00%
TR242	Pleurophoma cava	Ascomycota	Ascomycota Incertae sedi	EU754199	100.0%	1494.48	100.00%	Ascomycota sp.	Ascomycota	na	JN120373	99.1%	928.218	100.00%
TR240	Aposphaeria sp.	Ascomycota	Pleosporales	JF740329	99.4%	1467.43	100.00%	Uncultured Pleosporales	Ascomycota	Pleosporales	JF449873	98.8%	868.707	95.02%
TR698	Lulworthiales sp.	Ascomycota	Lulworthiales	DQ394094	99.4%	1438.57	100.00%	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	85.6%	545.904	93.93%
TR524	Juncigena adarca	Ascomycota	Ascomycota Incertae sedi	EF027727	97.4%	1361.03	100.00%	Marine ascomycete	Ascomycota	na	AF422992	90.3%	845.263	100.00%
TR20	Lophiotrema nucula	Ascomycota	Pleosporales	GU301837	98.8%	1447.59	100.00%	Lophiostoma cynaroidis	Ascomycota	Pleosporales	EU552138	90.6%	1375.45	99.47%
TR78	Uncultured soil	na	na	EU861651	98.9%	1427.75	99.51%	Phialocephala sp.	Ascomycota	Helotiales	FJ903362	99.4%	1406.11	93.95%
TR167	Cadophora sp.	Ascomycota	Helotiales	JN859469	100.0%	1494.48	100.00%	Uncultured fungus	na	na	JQ910888	99.2%	1296.11	100.00%
TR115	Ambomucor seriatoinflatus	Mucoromycotina	Mucorales	AY743664	96.5%	1546.77	100.00%	Helicostylum pulchrum	Mucoromycotina	Mucorales	AB614353	99.4%	1193.31	99.26%
TR689	Mrakia frigida	Basidiomycota	Cystofilobasidiales	DQ831016	100.0%	1546.77	100.00%	Uncultured compost	na	na	FM177664	100.0%	1142.82	100.00%
TR688	Clitocybe subditopoda	Basidiomycota	Agaricales	EU852807	100.0%	1557.59	100.00%	Clitocybe subditopoda	Basidiomycota	Agaricales	EU852800	99.7%	1178.89	97.20%
TR277	Mortierella turficola	Mucoromycotina	Mortierellales	HQ667426	97.9%	1653.17	98.27%	Uncultured fungus	na	na	EF434039	96.4%	1045.44	100.00%
TR668	Polyporus arcularius	Basidiomycota	Polyporales	AF393067	98.8%	1503.49	100.00%	Uncultured fungus	na	na	FJ820589	99.8%	1173.48	100.00%
TR643	Uncultured Ceratobasidium	Basidiomycota	Cantharellales	FJ207506	98.1%	1440.37	100.00%	Uncultured soil	na	na	GU083284	97.8%	1074.29	98.75%
TR200	Mucor hiemalis	Mucoromycotina	Mucorales	JN938893	95.1%	1480.05	100.00%	Mucor hiemalis	Mucoromycotina	Mucorales	EU484251	92.3%	839.853	99.31%
TR584	Mucor hiemalis	Mucoromycotina	Mucorales	JN938893	99.6%	1667.6	100.00%	Mucor hiemalis	Mucoromycotina	Mucorales	HM172810	99.5%	976.909	100.00%
TR528 (cf. Phialophorophoma litoralis)	Cochliobolus geniculatus	Ascomycota	Pleosporales	JN941528	97.5%	1397.09	100.00%	Dendryphion penicillatum	Ascomycota	Pleosporales	DQ865101	90.0%	771.325	96.87%
TR21	Valsa germanica	Ascomycota	Diaporthales	AF362561	100.0%	1467.43	99.88%	Valsa germanica	Ascomycota	Diaporthales	JQ086564	99.8%	964.285	99.44%
TR295	Trichoderma viride	Ascomycota	Hypocreales	AY291123	99.5%	1454.8	100.00%	Hypocreaceae sp.	Ascomycota	Hypocreales	JF773606	99.0%	1056.26	99.35%
TR686	Magnisphaera spartinae	Ascomycota	Microascales	AY150221	94.6%	1245.61	98.76%	Scedosporium apiospermum	Ascomycota	Microascales	JN872195	90.0%	331.303	46.18%
TR434	Varicosporium delicatum	Ascomycota	Helotiales	GQ477339	99.0%	1458.41	100.00%	Uncultured fungus	na	na	EU516850	96.7%	791.162	50.58%
TR149	Trichocladium achrasporum	Ascomycota	Microascales	HQ268018	99.0%	1418.73	100.00%	Sigmoidea marina	Ascomycota	Microascales	EU557359	78.4%	452.129	95.11%
TR420	Sistotrema athelioides	Basidiomycota	Cantharellales	DQ898700	95.4%	1326.76	99.64%	Uncultured Cantharellaceae	Basidiomycota	Cantharellales	DQ273369	82.2%	587.381	100.00%
TR499	Acremonium alternatum	Ascomycota	Hypocreales	FJ176883	98.8%	1418.73	100.00%	Uncultured fungus	na	na	FJ235864	84.6%	636.072	100.00%
TR230	Ophiovalsa betulae	Ascomycota	Diaporthales	AF408375	100.0%	1469.23	100.00%	Fungal endophyte	na	na	FJ025237	98.2%	969.695	95.94%
TR521	Neobulgaria sp.	Ascomycota	Hypocreales	HM116756	97.2%	1393.49	100.00%	Helotiales sp.	Ascomycota	Helotiales	GU934595	99.7%	1043.63	100.00%
TR373	Niesslia exilis	Ascomycota	Hypocreales	AY489720	100.0%	1467.43	100.00%	Eucasphaeria capensis	Ascomycota	incertae sedis	EU272516	99.7%	1054.45	100.00%
TR17	Xylaria frustulosa	Ascomycota	Xylariales	JN673055	98.3%	1418.73	100.00%	Nemania serpens	Ascomycota	Xylariales	EF155504	99.5%	1021.99	100.00%
TR339	Acremonium strictum	Ascomycota	Hypocreales	FJ176879	99.8%	1463.82	100.00%	Uncultured Hypocreales	Ascomycota	Hypocreales	JF449611	99.7%	1045.44	100.00%
TR96	Penicillium polonicum	Ascomycota	Eurotiales	JN938933	99.3%	1462.02	100.00%	Penicillium concentricum	Ascomycota	Eurotiales	EU833217	99.3%	1016.58	100.00%
TR493	Phaeosphaeria caricicola	Ascomycota	Pleosporales	GQ387590	99.2%	1458.41	100.00%	Uncultured soil	na	na	EU479972	90.9%	794.769	100.00%
TR270	Penicillium expansum	Ascomycota	Eurotiales	JN938952	100.0%	1492.67	100.00%	Penicillium sp.	Ascomycota	Eurotiales	FR799498	99.2%	911.988	100.00%
TR1	Penicillium aurantiogriseum	Ascomycota	Eurotiales	JN938945	99.3%	1462.02	100.00%	Penicillium concentricum	Ascomycota	Eurotiales	EU551180	98.9%	948.055	100.00%
TR365	Discosphaerina fagi	Ascomycota	Dothideales	AY016359	100.0%	1492.67	100.00%	Uncultured fungus	na	na	GQ851743	99.8%	1040.03	100.00%
TR258	Diplodia porosum	Ascomycota	Botryosphaerales	DQ377895	100.0%	1492.67	100.00%	Diplodia mutila	Ascomycota	Botryosphaerales	JQ659284	99.3%	1011.17	99.83%
TR344	Acremonium sp.	Ascomycota	Hypocreales	JQ768402	100.0%	1472.84	100.00%	Acremonium sp.	Ascomycota	Hypocreales	AM262392	98.8%	857.886	91.30%
TR358	Niesslia exilis	Ascomycota	Hypocreales	AY489720	98.6%	1416.93	100.00%	Eucasphaeria capensis	Ascomycota	incertae sedis	EU272516	93.0%	872.313	100.00%
TR501	Coniochaeta velutina	Ascomycota	Sordariales	EU999180	98.9%	1420.54	100.00%	Lecythophora sp.	Ascomycota	Sordariales	AY219880	96.5%	942.645	100.00%
TR580	Diaporthe eres	Ascomycota	Diaporthales	AF362565	100.0%	1467.43	100.00%	Phomopsis sp.	Ascomycota	Diaporthales	EU571102	100.0%	1036.42	100.00%
TR646	Lecanicillium lecanii	Ascomycota	Ascomycota Incertae sedi	EF026005	100.0%	1467.43	100.00%	Torrubiella cf.	Ascomycota	Hypocreales	EU009974	99.8%	939.038	99.81%
TR12	Beauveria bassiana	Ascomycota	Hypocreales	AY283555	99.9%	1462.02	100.00%	Phialocephala sp.	Ascomycota	Helotiales	JN379801	99.6%	998.549	100.00%
TR279	Alternaria tenuissima	Ascomycota	Pleosporales	FJ755193	100.0%	1492.67	100.00%	Alternaria sp.	Ascomycota	Pleosporales	GU584947	100.0%	1020.19	100.00%
TR416	Uncultured soil	na	na	EU861651	99.0%	1433.16	99.51%	Phialocephala sp.	Ascomycota	Helotiales	FJ903362	98.7%	1380.86	93.73%
TR399	Tolypocladium inflatum	Ascomycota	Hypocreales	AB044645	96.3%	1333.98	100.00%	Uncultured fungus	na	na	FJ820809	91.6%	801.982	100.00%
TR548	Uncultured ascomycete	Ascomycota	na	EU490011	98.4%	1431.36	99.88%	Uncultured fungus	na	na	EF434152	99.8%	1000.35	100.00%
TR505	Mollisia sp.	Ascomycota	Helotiales	EU107273	99.5%	1458.41	100.00%	Uncultured fungus	na	na	HQ611331	96.9%	1388.08	99.76%
TR498	Lulworthia medusa	Ascomycota	Lulworthiales	AF195637	93.5%	1229.38	100.00%	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	84.1%	477.376	81.16%
TR9	Cadophora sp.	Ascomycota	Helotiales	HM116759	99.8%	1485.46	100.00%	Cadophora malorum	Ascomycota	Helotiales	DQ404350	98.5%	944.448	100.00%
TR409	Helotiaceae sp.	Ascomycota	Helotiales	HM595590	98.6%	1440.37	100.00%	Uncultured Helotiales	Ascomycota	Helotiales	DQ182441	89.7%	1011.17	94.46%
TR506	Pyrenochaeta corni	Ascomycota	Pleosporales	GQ387609	99.5%	1474.64	100.00%	Fungal sp.	na	na	HQ392612	96.4%	877.724	100.00%
TR169	Helotiales sp.	Ascomycota	Helotiales	JN859472	98.8%	1445.78	100.00%	Uncultured fungus	na	na	FJ554282	98.5%	933.628	99.63%
TR359	Penicillium paxilli	Ascomycota	Eurotiales	FJ890408	97.0%	1379.06	100.00%	Penicillium charlesii	Ascomycota	Eurotiales	FJ430769	98.9%	913.791	100.00%
TR81	Helotiales sp.	Ascomycota	Helotiales	JN859472	98.2%	1422.34	100.00%	Uncultured soil	na	na	JQ666493	100.0%	969.695	100.00%
TR436	Varicosporium delicatum	Ascomycota	Helotiales	GQ477339	99.0%	1453.0	99.88%	Uncultured Clathrophaerina	Ascomycota	Helotiales	HQ211784	97.1%	904.774	100.00%
TR225	Neonectria sp.	Ascomycota	Hypocreales	FJ560432	100.0%	1467.43	100.00%	Neonectria faginata	Ascomycota	Hypocreales	JQ868432	99.2%	904.774	100.00%
TR226	Phoma acetosellae	Ascomycota	Pleosporales	GU238034	99.6%	1474.64	100.00%	Didymella sp.	Ascomycota	Pleosporales	HM068373	98.7%	940.841	100.00%

Query	LSU hit				ITS hit									
OTU (morphological identification)	Organism	Phylum	Order	Accession number	Pairwise Identity	Bit-Score	Coverage	Organism	Phylum	Order	Accession number	Pairwise Identity	Bit-Score	Coverage
TR218	Tricladium minutum	Ascomycota	Helotiales	GQ477326	97.7%	1404.31	100.00%	Uncultured Pezizomycotina	Ascomycota	na	FJ378725	97.4%	881.33	98.32%
TR324	Lophiostoma glabrotunicatum	Ascomycota	Pleosporales	FJ795438	100.0%	1489.07	99.88%	Tumularia aquatica	Ascomycota	incertae sedis	AY265337	99.2%	915.594	97.92%
TR597	Cylindrocarpon cylindroides	Ascomycota	Hypocreales	AY283551	99.8%	1458.41	100.00%	Neonectria lungdunensis	Ascomycota	Hypocreales	FJ430736	98.8%	883.134	100.00%
TR18	Tolypocladium inflatum	Ascomycota	Hypocreales	AB044645	100.0%	1469.23	100.00%	Tolypocladium inflatum	Ascomycota	Hypocreales	AB114224	100.0%	984.122	100.00%
TR245	Diplodia rosulata	Ascomycota	Botryosphaerales	DQ377897	100.0%	1492.67	100.00%	Diplodia mutila	Ascomycota	Botryosphaerales	JQ659284	99.3%	991.336	99.65%
TR188	Lulworthia medusa	Ascomycota	Lulworthiales	AF195637	95.7%	1305.12	100.00%	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	85.4%	486.393	88.59%
TR215	Mortierella antarctica	Mucoromycotina	Mortierellales	HQ667423	100.0%	1743.34	98.27%	Uncultured Mortierellaceae	Mucoromycotina	Mortierellales	GQ219843	99.2%	1132.0	100.00%
TR576	-	-	-	-	-	-	-	Fusarium sp.	Ascomycota	Hypocreales	GQ505464	99.8%	1011.17	100.00%
TR52	-	-	-	-	-	-	-	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430722	89.1%	306.056	39.73%
TR109	-	-	-	-	-	-	-	Uncultured fungus	na	na	GU065525	99.2%	861.493	55.27%
TR697	-	-	-	-	-	-	-	Nowakowskiella elegans	Chytridiomycota	Chytridiales	AY353257	95.8%	269.988	24.96%
TR69	-	-	-	-	-	-	-	Phialocephala sp.	Ascomycota	Helotiales	FJ903362	99.1%	1409.72	90.91%
TR718	-	-	-	-	-	-	-	Rhizamoeba saxonica	na	na	GU001159	89.1%	169.0	18.42%
TR458	-	-	-	-	-	-	-	Flagelloscypha sp.	Basidiomycota	Agaricales	AY571041	86.0 %	389.011	53.28%
TR535	-	-	-	-	-	-	-	Uncultured compost	na	na	FM177664	99.8%	1115.77	99.84%
TR82	-	-	-	-	-	-	-	Uncultured fungus	na	na	FN812819	100.0%	1077.9	100.00%
TR531	-	-	-	-	-	-	-	Rhizamoeba saxonica	na	na	GU001159	88.8%	174.41	22.79%
TR65	-	-	-	-	-	-	-	Uncultured fungus	na	na	FJ820718	99.7%	1045.44	100.00%
TR108	-	-	-	-	-	-	-	Fungal sp.	na	na	HQ026492	92.3%	803.785	100.00%
TR716	-	-	-	-	-	-	-	Nectria lugdunensis	Ascomycota	Hypocreales	DQ247777	99.8%	737.061	71.35%
TR72	-	-	-	-	-	-	-	Uncultured fungus	na	na	FN298760	94.6%	747.881	100.00%
TR57	-	-	-	-	-	-	-	Pezicula sp.	Ascomycota	Helotiales	JN225939	96.1%	789.358	100.00%
TR131	-	-	-	-	-	-	-	Lulwoana sp.	Ascomycota	Lulworthiales	FJ430721	83.7%	459.342	91.63%
TR56	-	-	-	-	-	-	-	Uncultured Helotiales	Ascomycota	Helotiales	JF449882	99.8%	845.263	99.58%
TR248	-	-	-	-	-	-	-	Neonectria galligena	Ascomycota	Hypocreales	JQ434582	98.9%	820.016	99.36%
TR283	-	-	-	-	-	-	-	Neonectria sp.	Ascomycota	Hypocreales	FJ560437	99.4%	827.229	99.36%
TR62	-	-	-	-	-	-	-	Uncultured saccharomyceta	Ascomycota	Saccharomycetales	HQ211601	97.6%	767.718	100.00%
TR55	-	-	-	-	-	-	-	Lophiostoma cynaroidis	Ascomycota	Pleosporales	EU552138	96.1%	695.583	100.00%
TR724	-	-	-	-	-	-	-	Fungal sp.	na	na	FJ612956	95.4%	313.269	46.89%

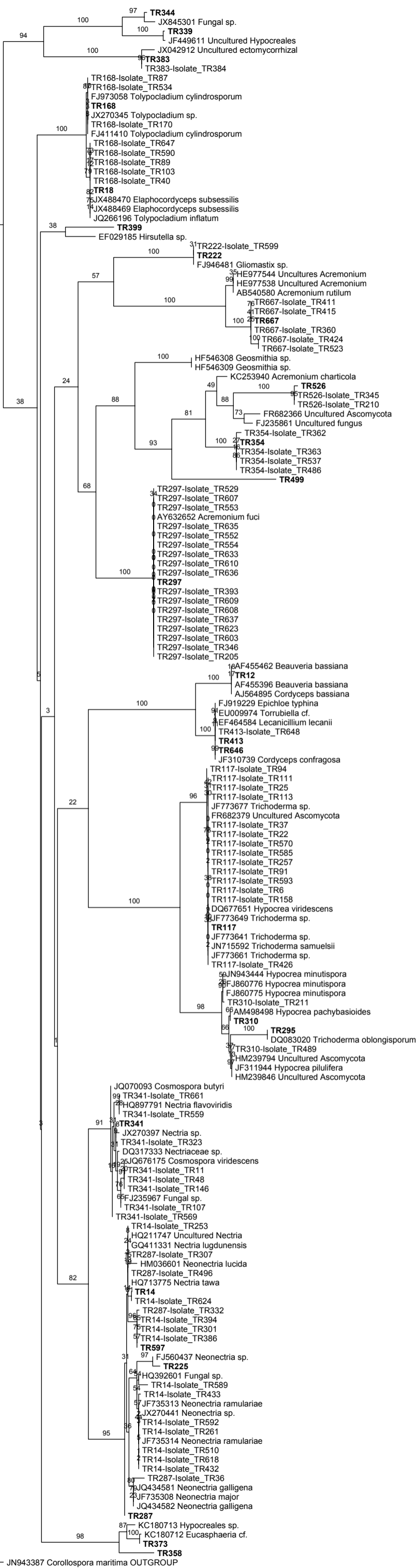
Taxon [OTUs]	Observation method	plating	plating	plating	plating	Field inventory & incubation	Field inventory & incubation	Field inventory & incubation	Field inventory & incubation
	Identification method	morphological	morphological	morphological	morphological	molecular & morphological	morphological	morphological	morphological
	Substrate	wood	wood	wood	sediment	wood	wood	wood	wood
	Location	Reference	Reference	Reference	Reference	Reference	Reference	Reference	Reference
	Barents and Norwegian Sea	North Sea	North Sea, Baltic	Kara Sea	White Sea	North Atlantic	Norwegian & Greenland Sea	Western Baltic Sea	Western Baltic Sea
	this study	Rees & al 1979	Henningson 1974	Bubnova 2010	Bubnova 2009	Azevedo et al. 2011	Pang et al. 2011	Petersen & Koch 1996, larch	Petersen & Koch 1996, oak
Cadophora spp. [TR311 , TR314]	0.48 (0.65)								
Penicillium spp. [TR620, TR319, TR247]	0.40 (0.74)	0.56	(0.33)						
Helotiales sp. [TR439]	0.34 (0.61)								
Cladosporium spp. [TR198, TR219]	0.34 (0.52)	0.60	(0.50)						
Nectria s. lato [TR14, TR341, TR287]	0.26 (0.39)								
Pleosporales sp. [TR232]	0.22 (0.39)								
Lulworthiaceae spp. [TR682, TR221]	0.16 (0.30)								
Emericellopsis maritima [TR297]	0.14 (0.30)								
Hypocrea atroviridis [TR117]	0.14 (0.26)				+				
Asteromyces cruciatus [TR288]	0.12 (0.26)	0.19							
Tolypocladium cylindrosporium [TR168]	0.12 (0.22)			0.39	0.02				
Halosphaeriaceae sp. [TR74]	0.10 (0.17)								
Lulworthia sp. [TR693]	0.08 (0.17)					0.72	0.06	0.30	0.80
Botryotinia fuckeliana [TR260]	0.08 (0.17)								
Embellisia sp. [TR105]	0.08 (0.13)		(0.17)						
Amylocarpus encephaloides [TR692]	0.08 (0.13)						0.06		0.33
Fusarium sp. [TR576]	0.08 (0.04)	0.23	(0.67)						
Acremonium sp. [TR354]	0.08 (0.04)		(0.33)		+				
Chalastospora sp. [TR207]	0.08 (0.04)								
Lulwoana uniseptata (incl. Zalerion maritimum) [TR147]	+	0.13	(0.50)			0.37		0.20	0.55
Trichoderma [TR310]	+	0.06	(0.17)						
Trichoderma viride [TR295]	+		(0.17)						
Halosphaeria mediosetigera (incl. anamorph Culcitalna achraspora) [TR149]	+		(0.17)			0.17		0.40	0.60
Tolypocladium inflatum [TR18]	+			0.61	0.07				
Penicillium expansum [TR270]	+				0.10				
Acremonium rutilum [TR667]	+				0.01				
Acremonium strictum [TR339]	+				0.01				
Ceriosporopsis halima [TR74]	+					0.33		0.10	
Marinospora calyptata [TR725]	+								0.80
Digitatispora marina [TR666]	+								0.38
Cirrenalia macrocephala		+				0.46		0.80	
Dictyosporium pelagicum		+						1.00	
Alternaria maritima		0.15							
Cephalosporium sp.		0.15							
Doratomyces stemonitis		0.15							
Stachybotrys lobulata		0.15							
Monodictys pelagica		0.13						0.40	0.60
Phialophora sp.		0.08	(1.00)						
Humicola grisea		0.08							
Emericellopsis stolckiae		0.06							
Scopulariopsis sp.		0.04	(0.17)						
Rhinoclaadiella sp.		0.04	(0.33)						
Humicola alopallonella		0.04						0.25	0.38
Epicoccum nigrum		0.04							
Stemphylium maritimum		0.04							
Gliomastix sp.		0.04							
Dendryphiella salina		0.02	(0.17)		0.02				
Pseudeurotium zonatum			(0.17)	0.67	0.01				
Pseudogymnoascus roseus (incl. anamorph Geomyces pannorum)			(0.17)	0.56	0.06				
Penicillium thomii			(0.17)		0.01				
Phoma sp.			(1.00)		+		0.02		
anamorphic Pseudeurotium				0.56					
Penicillium chrysogenum				0.33	+				
Penicillium nalgiovense				0.33	0.04				
Penicillium spinulosum				0.33	0.01				
Cladosporium cladosporioides				0.28	+				
Trichoderma koningii				0.28	0.01				
Penicillium glabrum				0.28					
Penicillium lanosum				0.22	0.01				
Tolypocladium geodes				0.22					
Penicillium miczynskii				0.22					
Penicillium purpureescens				0.22					
Penicillium citrinum					0.15				
Penicillium variable					0.06				
Penicillium italicum					0.05				
Penicillium chermesinum					0.03				
Penicillium cyclopium					0.03				
Acremonium tubakii					0.02				
Cladosporium herbarum					0.02				
Acremonium chrysogenum					0.02				
Penicillium steckii					0.02				
Gliomastix mucorum					0.01				
Penicillium frequentans					0.01				
Penicillium janthinellum					0.01				
Penicillium palitans					0.01				
Penicillium vinaceum					0.01				
Phoma herbarum					0.01				
Acremonium furcatum					0.01				
Acremonium kiliense					0.01				
Fusarium moniliforme					0.01				
Dendryphiella arenaria					0.01				

Microascales

Fig. S2.



Hypocreales



JN943387 *Corollospora maritima* OUTGROUP

Sordariales

GU566297 Ascomycota sp.

13

41 AB190399 Phialophora intermedia

FM177651 Uncultured compost

69

TR538

69

TR538_Isolate_TR687

37

97

HM589238 Ascomycota sp.

TR501

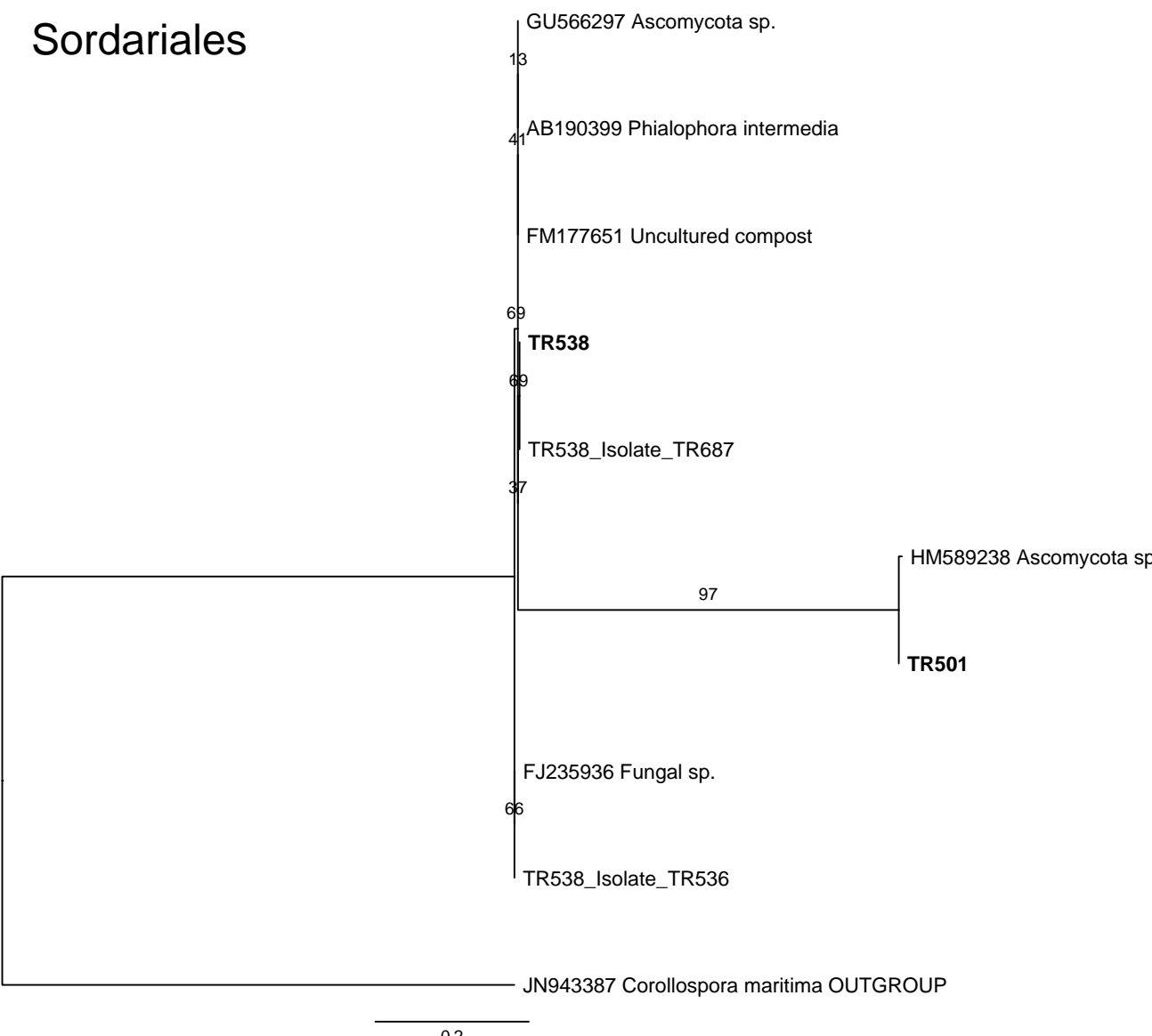
FJ235936 Fungal sp.

66

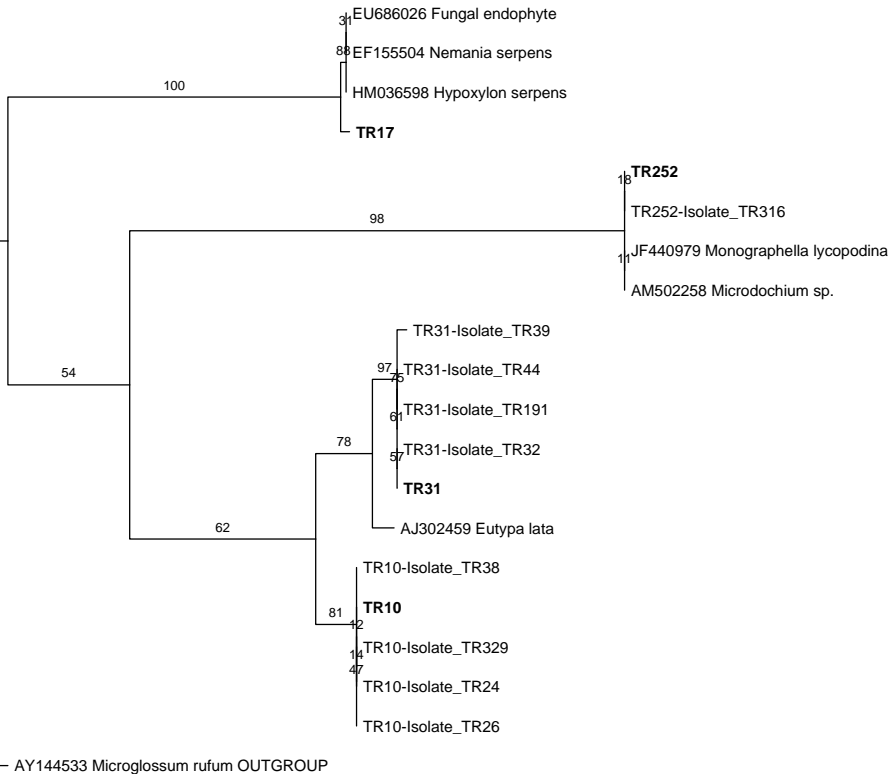
TR538_Isolate_TR536

JN943387 Corollospora maritima OUTGROUP

0.2

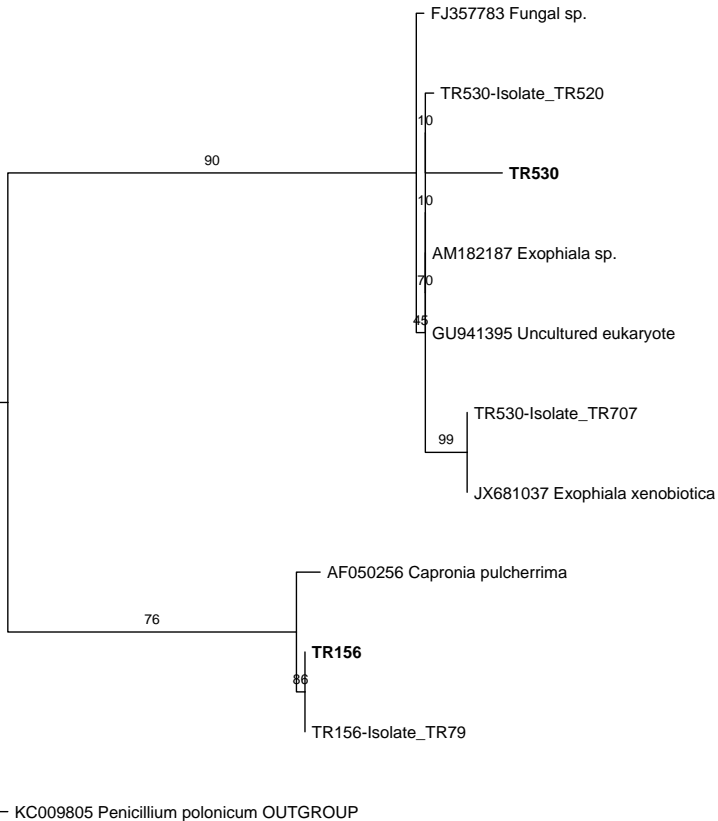


Xylariales



0.05

Chaetothyriales



0.03

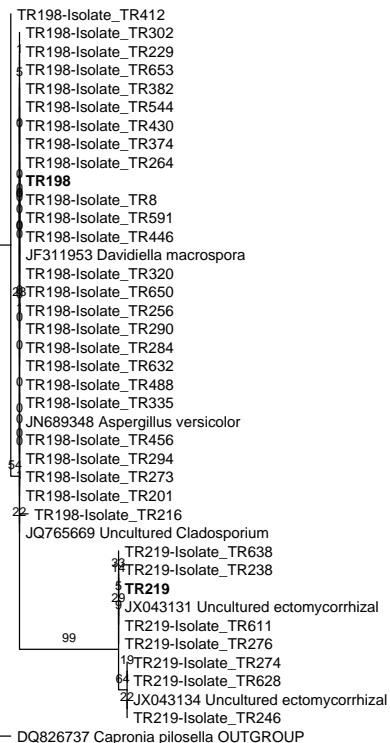
Eurotiales



Pleosporales

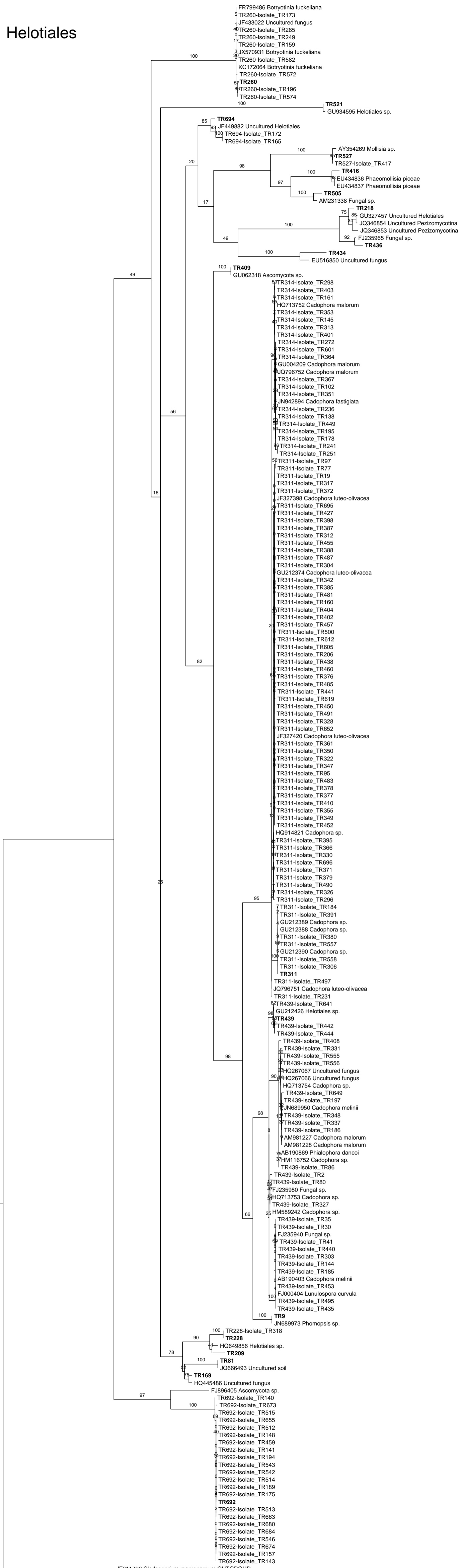


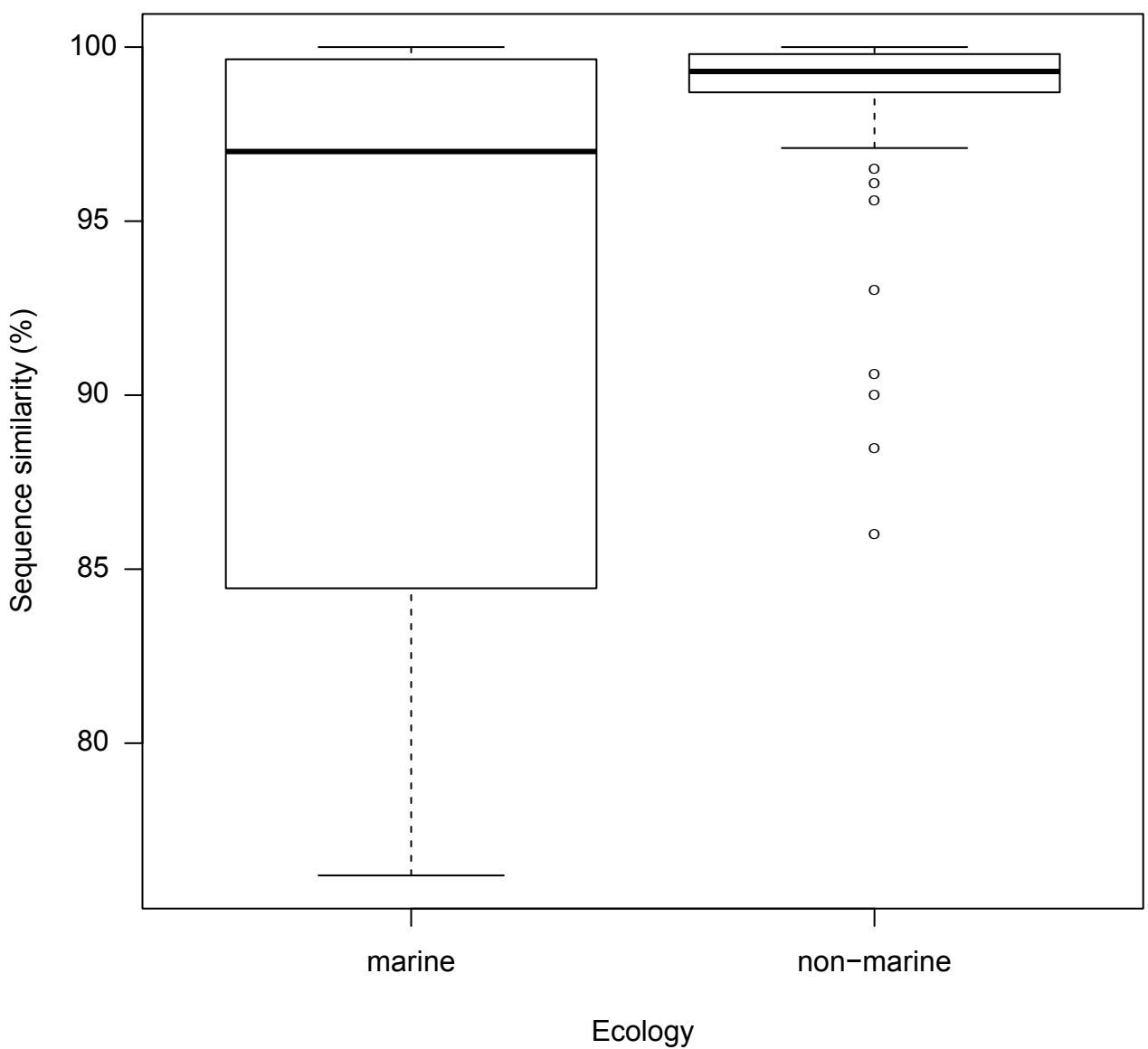
Capnodiales

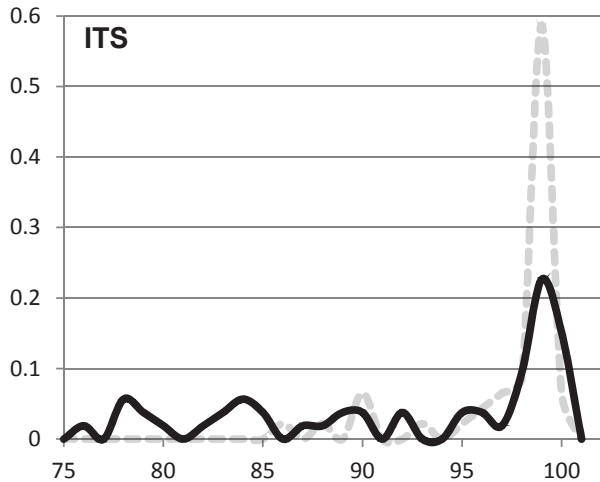
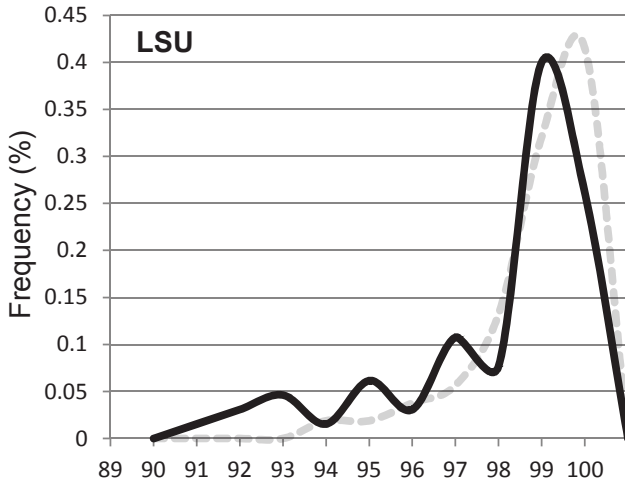


0.05

Helotiales







Sequence similarity (%)