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Endophytic and endolichenic fungal diversity in maritime Antarctica based on cultured material and their evolutionary position among *Dikarya*

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Abstract: Fungal endophytes comprise one of the most ubiquitous groups of plant symbionts. They live asymptotically within vascular plants, bryophytes and also in close association with algal photobionts inside lichen thalli. While endophytic diversity in land plants has been well studied, their diversity in lichens and bryophytes are poorly understood. Here, we compare the endolichenic and endophytic fungal communities isolated from lichens and bryophytes in the Barton Peninsula, King George Island, Antarctica. A total of 93 fungal isolates were collected from lichens and bryophytes. In order to determine their identities and evolutionary relationships, DNA sequences of the nuclear internal transcribed spacer (ITS), nuclear ribosomal small subunit (nuSSU), nuclear large subunit (nuLSU), and mitochondrial SSU (mtSSU) rDNA were obtained and protein coding markers of the two largest subunit of RNA polymerase II (*RPB1* and *RPB2*) were generated. Multilocus phylogenetic analyses revealed that most of the fungal isolates were distributed in the following six classes in the phylum *Ascomycota*: *Dothideomycetes*, *Eurotiomycetes*, *Lecanoromycetes*, *Leotiomycetes*, *Pezizomycetes* and *Sordariomycetes*. For the first time we report the presence of subphylum *Mortierellomycotina* that may belong to an undescribed order in endophytic fungi. Taken together, our results imply that lichens and bryophytes provide similar niches and harbour a selection of these fungi, indicating generalists within the framework of evolutionary adaptation.

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INTRODUCTION

The kingdom *Fungi* is comprised of a diverse range of organisms engaged in parasitic, saprophytic, symbiotic, endoparasitic and endophytic lifestyles (Mueller *et al.* 2004, Crespo *et al.* 2014). Current estimates for the global number of fungal species have risen from 2.2 million to as many as 3.8 million species (Hawksworth & Lucking 2017). Fungal endophytes are an ecologically diverse group, residing within plant tissues without causing any apparent symptoms of infection (Petrini 1991, Wilson 1995, Zhang *et al.* 2013). While most studies of fungal endophytes have focused on those species that live in vascular plants, endophytes also live in nonvascular plants including bryophytes (*i.e.*, mosses, liverworts, and hornworts), which are functionally important (Upson *et al.* 2007, Hoshino *et al.* 2009, U'Ren *et al.*, 2010, Siciński *et al.* 2011, Zhang *et al.* 2013). These fungi affect the host in diverse ways: promoting greater tolerance to extreme pH, vegetative growth and resistance to pathogens

(Narisawa *et al.* 2002, Davey and Currah, 2006). The habitat range of these fungi is also broad; they have been isolated from many different land plants from all terrestrial ecosystems ranging from the tropics to the Polar Regions (Arnold *et al.* 2009, Zhang *et al.* 2013, Yu *et al.* 2014). Lichen thalli can also harbour endolichenic fungi that are typically found as endophytes in plants (Girlanda *et al.* 1997, Li *et al.* 2007, Arnold *et al.* 2009, Kannangara *et al.* 2009, U'Ren *et al.* 2010). These fungi also live in close association with algal photobionts inside apparently healthy lichen thalli, forming persistent and symptomless infections.

The importance of these endolichenic fungi remains unknown. However, abundant endolichenic fungi are present within lichen thalli, and their presence is presumed to play an important ecological role, such as assisting lichen formation, growth and protecting against insect herbivores by producing bioactive substances (Li *et al.* 2007, Paranagama *et al.* 2007). In addition, fungal endophytes are a phylogenetically diverse group. The vast majority of known endophytic and endolichenic fungi belong to the phylum *Ascomycota*,

distributed among the *Arthoniomycetes*, *Sordariomycetes*, *Dothideomycetes*, *Lecanoromycetes*, *Leotiomyces*, *Pezizomycetes*, and *Eurotiomycetes* (Arnold *et al.* 2009, Park *et al.* 2015).

King George Island is the largest island in the South Shetland Islands belonging to the maritime Antarctic zone where the climate is milder due to oceanic influences (Kanda & Komárková 1997, Sancho & Pintado 2004, Li *et al.* 2007). While invasive plant species have increased recently (Chown *et al.* 2012), only two native species of flowering plants, Antarctic hair grass (*Deschampsia antarctica*) and Antarctic pearlwort (*Colobanthus quitensis*), are found so far. Vegetation is predominantly made up of lichens and bryophytes, which are specially adapted to survive in this area. Furthermore, several performance indicators show that this region is an excellent habitat for lichens and bryophytes (Øvstedal & Lewis-Smith 2001, Kim *et al.* 2006, Green *et al.* 2012). In addition, several black meristematic fungi were reported in Antarctic lichens (Selbmann *et al.* 2013). Thus, we selected King George Island as a model to explore the diversity of endophytic and endolichenic fungal communities associated with lichens and bryophytes. Since they lack visible reproductive structures and other distinctive phenotypic traits for classification, DNA sequence-based sample identification is prerequisite for objective exploration of the species diversity. We gathered DNA sequences of the nuclear internal transcribed region (ITS), nuclear ribosomal short subunit (nuSSU) and large subunit (nuLSU), mitochondrial ribosomal short subunit (mtSSU) rDNA, and the two largest subunits of RNA polymerase II (*RPB1* and *RPB2*). Endolichenic fungi resemble fungal endophytes of plants in taxonomy, mode of transmission procedure, and evolutionary history (U'Ren *et al.* 2010). Then we pose the

question: are endolichenic and endophytic fungal communities in Barton Peninsula, King George Island different from each other or overlapping, forming flexible symbiotic relationships in both bryophytes and lichens? And lastly, do these fungal communities flourish through a host-specific evolutionary process?

Here we compare the endolichenic fungi with endophytic fungal communities isolated from lichens and bryophytes at the same location on the Barton Peninsula, King George Island. Furthermore, in order to resolve the evolutionary relationships, we prepared a five-locus dataset (nuSSU, nuLSU, mtSSU, *RPB1* and *RPB2*) of selected taxa in phylum *Ascomycota*.

MATERIALS AND METHODS

Study site and lichen sample collection

Sixty-one lichen samples growing on soil, rock and moss were collected from the Barton Peninsula, King George Island located in the Antarctic (Fig. 1) and preserved at -20°C in sterile polyethylene tubes to prevent contamination from airborne fungal species (Supplementary Table S1). Lichen samples were identified by macro- and micro-morphological characteristics and chemical contents according to the species definition as described by Øvstedal & Lewis-Smith (2001).

Isolation of endolichenic fungi

Isolation of the internal fungi was performed as previously described by Li *et al.* (2007). The surface of the lichen thalli was

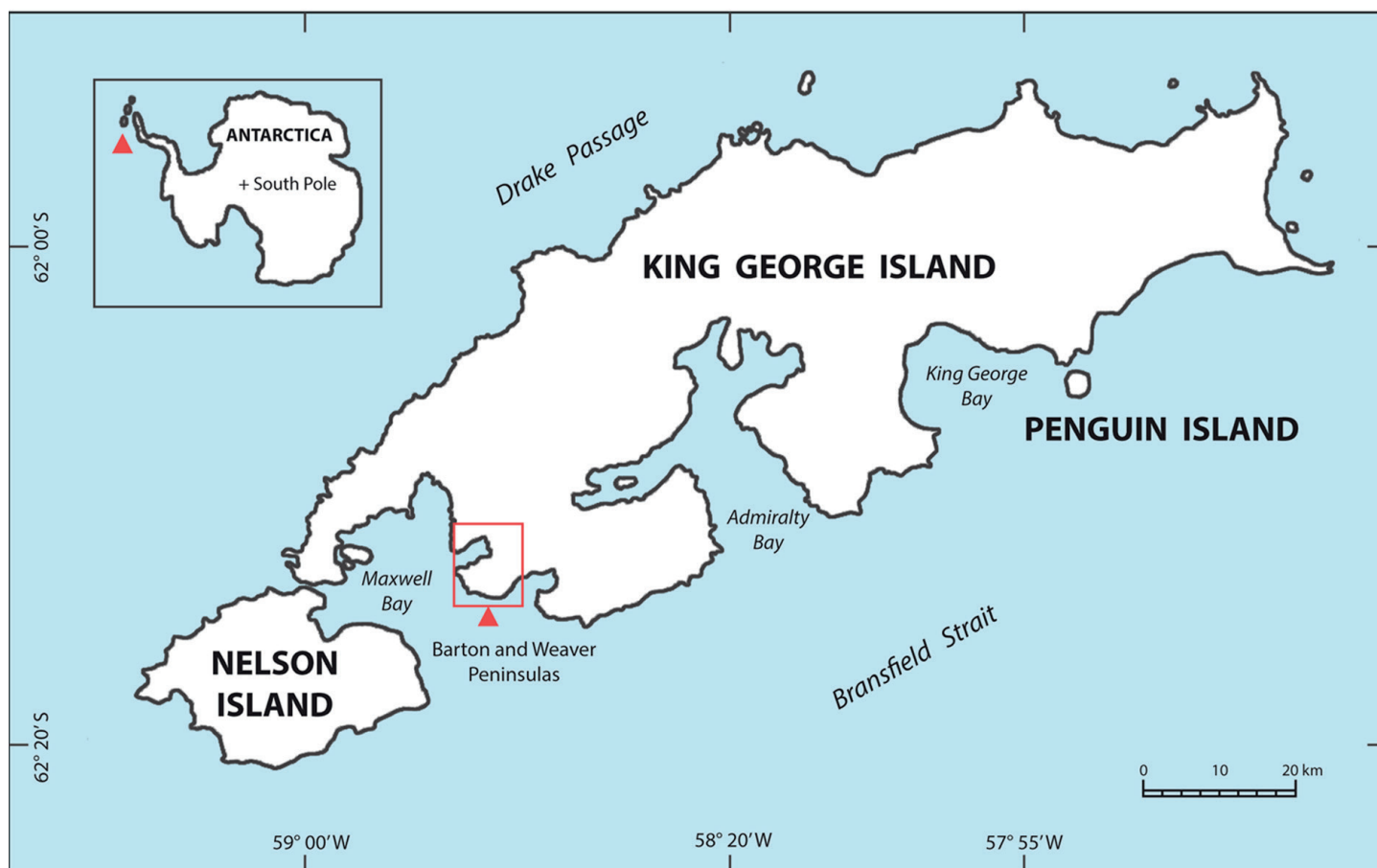


Fig. 1. Study area on Barton and Weaver Peninsula, King George Island in Antarctica (marked by red arrow).

cut into 0.5 cm² and the lichen thalli fragments were washed for 3 h in streaming water, then immersed in 75 % ethanol for 1 min, in 2 % sodium hypochlorite for 3 min and then in 75 % ethanol for 30 s. Finally, each fragment was gently rinsed with sterilised distilled water and the water was subsequently analysed by PCR to check for fungal contamination of the thalli surface. Sterilised samples were then dried with sterile paper towels and then plated on PDA with 0.01 % streptomycin and incubated at 15 °C. Fungi growing from each fragment were isolated into pure cultures on 2 % malt extract broth (ME, Difco, Sparks, USA) solid medium. All endolichenic fungi were grouped into different morphotypes based on the following culture phenotypic characteristics: colony colour, texture, growth rates and cell shape on ME solid medium. This is because endolichenic fungi rarely produce spores, therefore morphological features for identification is very limited (Choi *et al.* 1999). All fungal isolates were deposited at the Korea Lichen and Allied Bioresources Center (KOLABIC) at the Korea Lichen Research Institute (KoLRI) of Sunchon National University.

DNA extraction, amplification and sequencing

Fungal DNA extraction was performed using a DNeasy Plant Mini Kit according to the manufacturer's protocols (Qiagen, Hilden, Germany). We amplified and sequenced the following six markers: nuSSU using primers NS1 (White *et al.* 1990) and NS24 (Gargas & Taylor 1992), nuLSU using primers LROR (Rehner & Samuels 1994) and LR7 (Vilgalys & Hester 1990), mtSSU using mrSSU1 and mrSSU3R (Zoller *et al.* 1999), *RPB1* using RPB1-AFasc and RPB1-6R1asc2 (Hofstetter *et al.* 2007), *RPB2* using fRPB2-7cF and fRPB2-11aR (Liu *et al.* 1999), and ITS using ITS4 and ITS5 (White *et al.* 1990). In the case of endophytic fungal isolates from bryophytes living in King George Island, ITS sequences were used for analysis as described by Yu *et al.* (2014).

Sequence assembly and multiple sequence alignments

Sequences were assembled and edited using the software CodonCode Aligner (CodonCode Corp., Dedham, MA, USA). Sequence identity was assessed using the mega-BLAST search function in GenBank (Sayers *et al.* 2011). We used the program MAFFT v. 7 (Kato & Toh 2008) to align DNA sequences of 418 samples (Supplementary Table S1 and S3) for each gene region. For all six loci, we applied the G-INS-I alignment algorithm (recommended for sequences with global homology), '200PAM/K = 2' scoring matrix, and offset value = 0.0, with the remaining parameters set to default values. To improve the accuracy of the ITS and *RPB2* alignments for downstream OTU (operational taxonomic units) delimitation, only the newly generated sequences of endophytic and endolichenic fungi isolated from bryophytes and lichens on the King George Island were included. Multiple sequence alignments were performed in MAFFT using the same parameters as described above. The program Gblocks v. 0.91b (Talavera & Castresana 2007) was used to remove ambiguously aligned regions, using options for a "less stringent" selection on the Gblocks web server (http://molevol.cmima.csic.es/castresana/Gblocks_server.html) for subsequent phylogenetic analyses.

OTU delimitation analyses

Since endophytic and endolichenic fungi lack visible reproductive structures and other distinctive phenotypic traits, and moreover,

because morphology-based species circumscriptions have been shown to be inadequate for characterisation of species-level diversity (Arnold *et al.* 2009), we used the Automatic Barcode Gap Discovery method (ABGD; Puillandre *et al.* 2012) to circumscribe OTUs representing candidate species. ABGD employs a genetic distance-based approach to detect a 'barcode gap', separating OTUs based on non-overlapping values of intra- and interspecific genetic distances and is independent of any topology (Hebert *et al.* 2003, Puillandre *et al.* 2012). This method infers a model-based confidence limit for intraspecific divergence and then detects the barcode gap as a first significant gap beyond this limit to infer primary partitions. The primary data partitions are then recursively split to obtain finer partitions using the same approach until no further gaps can be detected (Puillandre *et al.* 2012). We used the ABGD web server (<http://www.wabi.snv.jussieu.fr/public/abgd/abgdweb.html>) to identify barcode gaps in the ITS of endophytic and endolichenic fungi as well as the *RPB1* data matrix. Puillandre *et al.* (2012) suggested that implementing a P_{max} value of 0.01 provides the most accurate estimate for the number of groups based on empirical comparisons of groupings inferred using ABGD with data from previous studies where species groups are well-characterised. Genetic distances were calculated using the JC69 model (default parameter), and other model parameters were set using default parameter values as follows, with the exception of the P_{max} value: $P_{min} = 0.001$, $P_{max} = 0.01$, steps = 10 and Nb bins = 20. We implemented a range of values for the gap width (X) between 0.1 and 1.5, to assess the consistency of the inferred groups under varying gap width values.

Phylogenetic analyses

Individual gene topologies were reconstructed using the program RAxML v. 8.1.11 (Stamatakis 2006, Stamatakis *et al.* 2008), as implemented on the CIPRES Web Portal, with the GTR-GAMMA model as described below. Support values were assessed using the "rapid bootstrapping" option with 1 000 replicates. We compared individual gene topologies to identify conflicting nodes, statistically supported (*i.e.* ≥ 70 % bootstrap). Incongruence among clades with bootstrap values < 70 % was considered statistically insignificant (Divakar *et al.* 2012, Wiens 1998). Without evidence of conflicting evolutionary histories, independent markers were combined to achieve maximum phylogenetic resolution and support. Two concatenated datasets were prepared: a two-gene (nuSSU and nuLSU) dataset of 362 samples representing *Dikarya* and member of *Mortierellales*, and a five-gene (nuSSU, nuLSU, mtSSU, *RPB1* and *RPB2*) dataset of 150 samples representing major groups of *Ascomycota*. As ITS data were impossible to align across *Dikarya* and *Zygomycota*, this locus was excluded from the concatenated dataset. In order to evaluate the phylogenetic relation of two samples (EFOMIA09 and EFOMIA10) grouping with *Mortierellomycotina* an additional two gene larger dataset published in Wagner *et al.* (2013) was used.

The ML analyses of all the three concatenated data sets were performed in RAxML with the GTR-GAMMA model, a parameter (Γ) for rate heterogeneity among sites and without a parameter for estimating the proportion of invariable sites. We used locus-specific model partitions treating all loci as separate partitions, and evaluated nodal support using 1 000 bootstrap pseudoreplicates. An alternative partition strategy was inferred via PartitionFinder v. 1.1.1 (Lanfear *et al.* 2012). The best-



Fig. 2. A total of 32 representative endophytic fungal cultures from 32 OTUs based on the *RBP2* gene sequences. The OTU number is in the upper left corner and the name of the fungus is on the bottom centre of the photographs. The endophytic fungi were cultured on potato dextrose agar media or malt-yeast extract media. The three endophytic fungi, EFOMIA09, EFOMIA10, and EFOMIA16, were cultured on PDA supplemented with 30 µg/mL of Rose Bengal to prohibit bacterial contamination.

fitting partition scheme was selected from a total of 16 initial pre-defined partitions, corresponding to the complete nuSSU region, the complete nuLSU region, the complete mtSSU region, the first, second and third codon positions of two coding region in the *RPB1*, two introns in the *RPB1*, two intronic regions in the *RPB1*, the first, second and third codon positions of the coding region in the *RPB2*, and an intron in the *RPB2*.

In order to validate the ability of ABGD to infer evolutionarily independent species-level lineages from ITS and *RPB2* sequences, we analysed sequence data from the nuclear and mitochondrial genomes within a phylogenetic framework to identify OTUs that exhibited genealogical exclusivity across independent loci (Avisé & Ball 1990).

RESULTS

Endolichenic fungal isolation and OTU delimitation

A total of 61 endolichenic fungal isolates were collected from 45 Antarctic lichen samples. Among these, 21 lichen species were identified, belonging to 10 families: *Candelariaceae*, *Cladoniaceae*, *Lecanoraceae*, *Parmeliaceae*, *Physciaceae*, *Pilocarpaceae*, *Ramalinaceae*, *Sphaerophoraceae*, *Stereocaulaceae*, and *Teloschistaceae* (Supplementary Table S1). In addition, 32 endophytic fungal isolates were obtained, including 16 that have been previously described (Yu *et al.* 2014), were isolated from 13 bryophytes (Supplementary Table S1). Representatives of endolichenic and endophytic fungal isolates are shown in Fig. 2. The sample identities were confirmed by analyses of the ITS1-5.8S and ITS2 rDNA region (ITS region) sequences.

Sequences: Endolichenic and endophytic isolates were grouped into 33 OTU in ABGD analyses of the ITS region and 34 OTUs from analysing a single copy gene *RPB2* (Fig. 3 and Supplementary Table S1). Since results of both datasets were similar, only the cluster of the *RPB2* marker is shown in Fig. 3. Of these, only seven OTUs were closely related to known fungal species with higher than 97 % sequence similarity. They were identified as *Anthostomella leucospermi*, *Chaetomium globosum*, *Peziza varia*, *Phoma herbarum*, and *Phoma violacea* with 98% sequence similarity cut-off (Supplementary Table S2), ABGD clustering and monophyletic relationship. For OTU validation, nuSSU, nuLSU and mtSSU loci exhibited significantly less variability than the ITS region, and the two protein coding markers *RPB1* and *RPB2*. The comparison between OTUs inferred from the ITS and *RPB2* sequences revealed high levels of genealogical concordance between the ITS and the protein coding markers. Relationships among OTUs are shown in maximum likelihood (ML) topology in Fig. 4 and Supplementary Fig. S1.

Molecular phylogeny

A total of 508 sequences were newly generated for this study, including 73 ITS, 92 nuSSU, 92 nuLSU, 91 mtSSU, 72 *RPB1* and 88 *RPB2* sequences (Supplementary Table S1). The two gene (nuSSU and nuLSU) data matrix contained 362 taxa with 2 185 unambiguously aligned nucleotide positions (Supplementary Table S1 and S3). The five gene data matrix contained 150 taxa with 4 643 unambiguously aligned nucleotide positions (Supplementary Table S3). Topologies of single-locus analyses did not conflict and hence combined analyses were performed.

The ML phylogeny estimated from the concatenated two-gene and five-gene data matrixes are depicted as a cartoon tree in Fig. 4 (full tree in Supplementary Fig. S1) and Fig. 5, respectively. Of the 93 isolates from the studied area, almost all were in phylum *Ascomycota*, two were in *Basidiomycota* and another two belonged to *Mortierellales* (*Mortierellomycotina*). In *Basidiomycota*, isolates clustered only in the order *Boletales* of *Agaricomycetes*. However, in *Ascomycota* they were spread throughout the tree. Within *Ascomycota*, the largest number of isolates grouped with *Leotiomycetes*, followed by *Sordariomycetes* and *Dothideomycetes*. Three isolates belonged to *Eurotiomycetes* whereas one isolate each were assigned to *Lecanoromycetes* and *Pezizomycetes*. All the OTUs discovered in ABGD analysis were found to be monophyletic in multilocus phylogenies.

DISCUSSION

Lichens and bryophytes are important components of current ecosystems, particularly in the Antarctic King George Island. Many genera of fungi commonly found as endophytes also occur within asymptomatic lichens and bryophytes (Kannangara *et al.* 2009, U'Ren *et al.* 2010, U'Ren *et al.* 2012, Zhang *et al.* 2013, Yu *et al.* 2014). Endophytic fungi largely lack reproductive structures and other visible phenotypic features, therefore traditional morphology-based species circumscriptions have shown to be inadequate to objectively characterise species-level diversity in this group of fungi (Arnold *et al.* 2009, Wagner *et al.* 2013, Oono *et al.* 2014, Chen *et al.* 2015). Here we used multilocus DNA sequence data for accurate sample identification and applied the barcode gap detection approach (Puillandre *et al.* 2012) to objectively circumscribe candidate species of endophytic fungi.

In this study, we reveal the endolichenic and endophytic fungal diversity in dominant lichen and bryophyte species in the Barton Peninsula of King George Island. Sixty-one endolichenic fungal isolates (numbered ELXXXXXX) were successfully obtained from 44 lichen samples belonging to 21 lichen species. The isolation frequency and diversity of 61 endolichenic fungi were compared with their host lichen family. Interestingly, endolichenic fungal isolation frequency was not related with the diversity of host lichen species. Namely, the number of lichen species in *Parmeliaceae* and *Stereocaulaceae* was higher than in other families but the isolation frequency of endolichenic fungi was not significantly different among the families.

In ABGD analyses, we circumscribed 34 candidate species (OTUs) for the 93 samples isolated from common lichen and bryophytes species of Antarctic King George Island. The results of endophytic fungi isolated from bryophytes species have been published in our previous study and here we focus on the endolichenic fungi (Yu *et al.* 2014). Since the obtained sequences are from axenic cultures of isolated fungi, these could be used as reference sequences for identification of environmental and soil fungi and also for detection of cryptic species. The species-level OTUs detected in this study were numbered OTU1 to OTU34 (Fig. 3). It is interesting to note that most of the OTUs from the isolates of Antarctic King George Island represent undescribed species. Candidate species level OTU9 was the most common taxon in Antarctic King George Island, followed by OTU26 and OTU29 (Fig. 3).

Moreover, the candidate species-level OTUs numbers 1, 2, 15 and 19 were present in both lichen and bryophyte samples

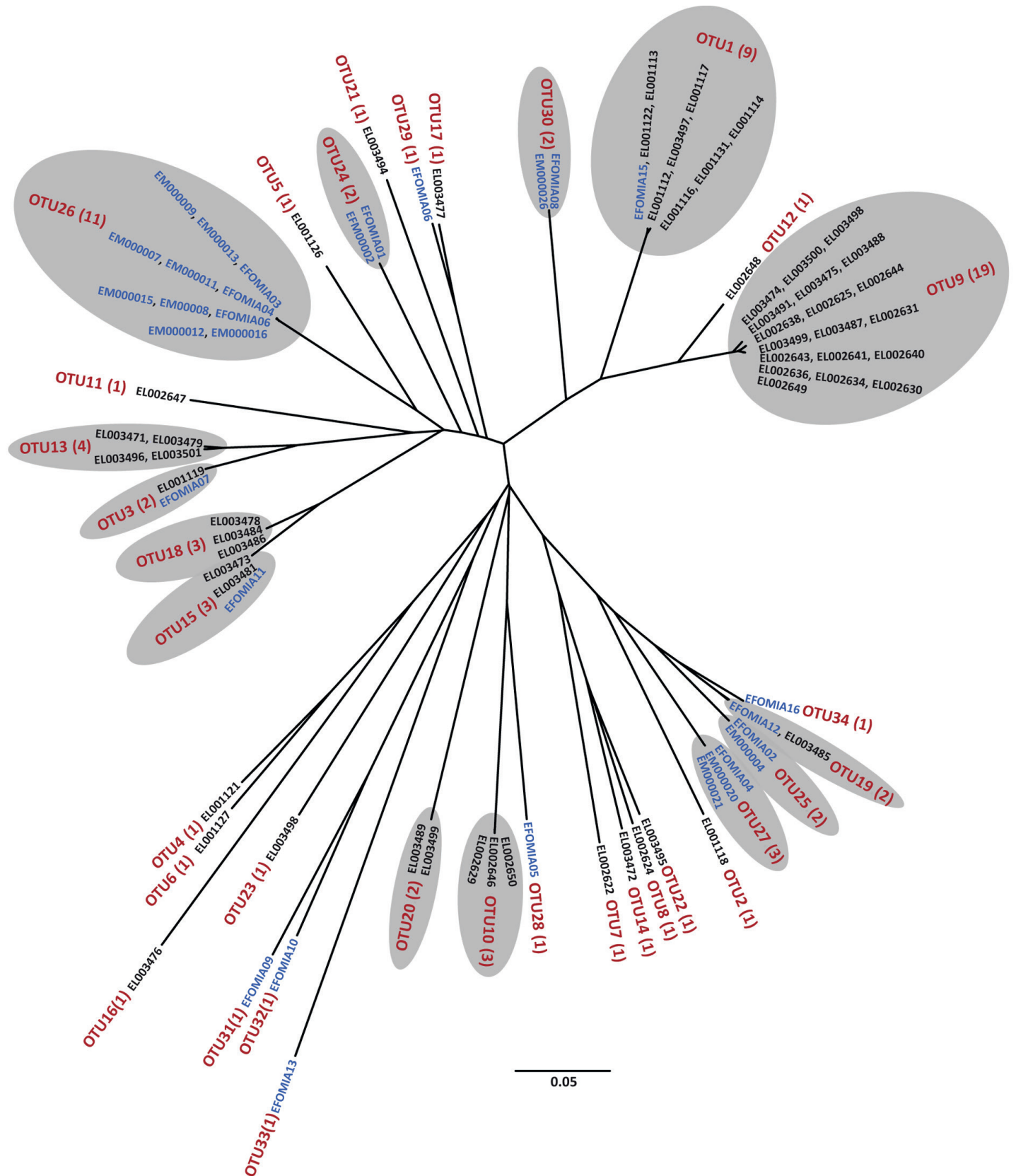


Fig. 3. Candidate species-level OTUs inferred from Automatic Barcode Gap Discovery (ABGD) analysis of the *RPB2* dataset. OTUs are numbered from 1 to 34 and the numbers in parentheses represents isolates clustered in each OTU. Endolichenic fungi isolated from lichen thalli are indicated in black, and endophytic fungi isolated from bryophytes are marked in blue.

collected from the same area, indicating generalists in the same ecological niches. Judging from the estimated total of 1.5 million (Hawksworth 1991) to as many as 5.1 million fungal species (Blackwell 2011, Rosling *et al.* 2011), our results

demonstrate that also in the Antarctic, a high percentage of endophytic (endolichenic) fungal species remain undescribed. Similar results have been reported in tropical endophytes (Arnold & Lutzoni 2007). A detailed morphological study of the



Fig. 4. Maximum Likelihood analysis based on concatenated five-locus dataset of small and large subunit (nuSSU and nuLSU) rDNA, mitochondrial small subunit (mtSSU) rDNA, and protein coding *RPB1* and *RPB2* markers of 62 taxa representing major lineages of *Ascomycota*. Two taxa of *Saccharomycetes* are used as outgroup. Node support $\geq 70\%$ is given on the branches. Taxon labels starting with “EL” in red represents endolichenic fungal isolates from lichen, and endophytic fungal isolates from bryophytes are labelled starting with “EF” or “EM” in blue.

cultures may aid in the formal description of these taxa in an integrative framework. However, developing robust hypotheses of species identification continues to be a 'work-in-progress' for examining species diversity in an unexplored area. Here, we assessed evolutionary independence of OTUs inferred from the ITS and *RPB2* markers, using mitochondrial and protein coding loci. Results from independent and concatenated datasets supported to large extent monophyly of OTUs inferred from ITS and *RPB2* sequences (Fig. 4 and Supplementary Fig. S1). This validation approach suggests that species level diversity assessed in the ABGD program likely provides a reasonable estimate of species diversity in the studied area. Moreover, the method implemented in our study for discovering species-level diversity based on OTUs is routinely used for organisms where morphological features are scarce or absent, such as bacteria (reviewed in Yarza *et al.* 2014). Similar to the previous studies (Arnold *et al.* 2009, U'Ren *et al.* 2012, Chen *et al.* 2015), our results demonstrate that most of the endophytic and endolichenic fungal isolates from the Antarctic King George Island belonged to classes *Dothideomycetes*, *Eurotiomycetes*, *Lecanoromycetes*, *Leotiomycetes*, *Pezizomycetes* and *Sordariomycetes* of *Ascomycota*. Only two samples belonged to *Basidiomycota* and another two to *Mortierellomycotina* (Fig. 4 and Supplementary Fig. S1). A detailed analysis of *Mortierellomycotina* including a larger dataset revealed that the two isolates EFOMIA09 and EFOMIA10, belong to a sister clade of *Mortierellales* (Supplementary Fig. S1, 2). This relationship was strongly supported (bootstrap 90 %). Currently with six genera belonging to the *Mortierellaceae* family, they are accepted members of *Mortierellomycotina*, and these fungi are commonly found as soil inhabiting saprobic organisms on decaying organic matter (Wagner *et al.* 2013). This is the first report of endophytic fungi in *Mortierellomycotina* and the sister relation of our two isolates to the order *Mortierellales* suggest that these samples may belong to an undescribed order within this group. A detailed morphological study of the cultures is needed to formally describe this lineage as a new order within *Mortierellomycotina*.

Using a five-locus dataset phylogeny, we establish the evolutionary relation of 89 Ascomycete endophytic and endolichenic fungi isolated from common bryophytes and lichen species of Antarctic King George Island. Our results demonstrate that these fungi were distributed in 10 orders in *Pezizomycotina* (Fig. 4). In accordance with previous studies, endophytic fungi isolated from different hosts and geographic regions such as arctic, boreal, temperate and tropical, were mostly grouped with *Pezizomycotina* (Arnold *et al.* 2009, Gazis *et al.* 2012, U'Ren *et al.* 2012, Chen *et al.* 2015). While *Leotiomycetes* and *Sordariomycetes* predominated the studied area, the *Pezizomycetes* and *Lecanoromycetes* were the least common, with only a single isolate each. Although, Antarctic endophyte (including endolichenic) assemblages were especially dominated by species belonging to the order *Helotiales* (*Leotiomycetes*), orders *Sordariales* and *Xylariales* (*Sordariomycetes*), these were least common in tropical and temperate areas (see *e.g.* Arnold & Lutzoni 2007). Indeed, *Lecanoromycetes* included the major lineages of lichen forming fungi (Miadlikowska *et al.* 2014, Jaklitsch *et al.* 2016). Our results demonstrate that of the 61 endolichenic fungal isolates from lichen thalli just one was grouped as *Umbilicariales* (*Lecanoromycetes*), suggesting no host specificity. These data are in agreement with a recent metabarcoding study, in

which authors showed low specificity of endolichenic fungi segregated from lichen taxa growing in an alpine habitat (Fernández-Mendoza *et al.* 2017). While we establish the phylogenetic relations of most of the isolates in different orders of *Pezizomycotina*, the relationship of the isolates EL001127 and EL001121 in *Eurotiomycetes*, and EL003489 and EL003490 in *Dothideomycetes* remains unclear. These may belong to undescribed orders and a detailed study focusing especially on these two classes is needed in order to fix their systematic positions.

The host lichens are *Usnia antarctica*, *Cladonia borealis*, and *Psilolechia lucida*, mainly growing on moss mats in the island. Therefore, it is highly possible that some endophytes can facultatively select their hosts between lichens and bryophytes at a given location. This result is consistent with a previous study (Furbino *et al.* 2014). If it is true, we might rule out the hypothesis that in Antarctica, these endophytes colonise lichen thalli to obtain their carbon sources from photobionts (symbiotic algae). Rather, lichens could be serving a more important function as a shelter for the endophytes in extreme environmental conditions.

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Table S1. Endolichenic and endophytic fungal isolated from the Antarctic lichen and moss samples.

Table S2. Blast search results from endolichenic fungal isolates using ITS region sequences.

Table S3. A total 324 taxa and the retrieved nuSSU, nuLSU, mtSSU, RPB1, and RPB2 sequences from GenBank.

Figure S1. Maximum Likelihood analysis based on concatenated two-locus dataset of small and large subunit (nuSSU and nuLSU) rDNA of 272 taxa (2 and 10 ingroup taxa of *Dikarya* and *Mortierellomycotina*, respectively) and 1 outgroup taxon *Umbelopsis* as member of the *Mucorales*); representing major lineages. Node support equal and or above 70 % is given on the branches. Taxon labels starting with “EL” in red represents endolichenic fungal isolates from lichen thalli, while labels starting with “EF” or “EM” in blue indicate endophytic fungal isolates of bryophytes.

Figures S2. Maximum Likelihood analysis of the *Mortierellomycotina* dataset published in [HYPERLINK \l "Wagner et al. \(2013\)](#), showing phylogenetic relation of the isolates EFOMIA09 and EFOMIA10. Node support equal and or above 70 % is given on the branches.

Table S1. Endolichenic and endophytic fungal isolated from the Antarctic lichen and moss samples.

Voucher	Isolated lichen or moss	Lichen family	Substratum	Area, GPS	Altitude (m)	GenBank accession number					
						ITS	nuSSU	nuLSU	mtSSU	RPB1	RPB2
Endolichenic fungi											
EL001112	<i>Cladonia</i> sp.	Cladoniaceae	on Moss	62°13'21.5"S,58°46'50.9"W	16	KU354797	KU354705	KU354613	KU354521	n/d	KU354945
EL001113	<i>Sphaerophorus globosus</i>	Sphaerophoraceae	on Moss	62°14'27.5"S,58°44'59.6"W	5	KU354798	KU354706	KU354614	KU354522	n/d	KU354946
EL001114	<i>Sphaerophorus globosus</i>	Sphaerophoraceae	on Moss	62°14'27.5"S,58°44'59.6"W	5	KU354799	KU354707	KU354615	KU354523	n/d	KU354947
EL001116	<i>Stereocaulon alpinum</i>	Stereocaulaceae	on Moss	62°14'27.8"S,58°44'42.1"W	5	KU354800	KU354708	KU354616	KU354524	n/d	KU354948
EL001117	<i>Stereocaulon alpinum</i>	Stereocaulaceae	on Moss	62°14'27.8"S,58°44'42.1"W	5	KU354801	KU354709	KU354617	KU354525	n/d	KU354949
EL001118	<i>Stereocaulon alpinum</i>	Stereocaulaceae	on Rock	62°13'29.9"S,58°47'21.0"W	10	KU354802	KU354710	KU354618	KU354526	KU354873	KU354950
EL001119	<i>Usnea antarctica</i>	Parmeliaceae	on Moss	62°13'30.9"S,58°46'41.4"W	88	KU354803	KU354711	KU354619	KU354527	n/d	KU354951
EL001121	<i>Cladonia borealis</i>	Cladoniaceae	on Moss	62°13'30.9"S,58°46'41.4"W	88	KU354804	KU354712	KU354620	KU354528	KU354874	KU354952
EL001122	<i>Cladonia borealis</i>	Cladoniaceae	on Moss	62°13'21.5"S,58°46'50.9"W	16	KU354805	KU354713	KU354621	KU354529	n/d	KU354953
EL001126	<i>Physcia</i> sp.	Physciaceae	on Rock	62°14'23.9"S,58°45'33.2"W	5	KU354808	KU354714	KU354622	KU354530	KU354875	KU354954
EL001127	<i>Pseudophebe pubescens</i>	Parmeliaceae	on Rock	62°13'45.2"S,58°40'55.3"W	70	KU354809	KU354715	KU354623	KU354531	KU354876	KU354955
EL001131	<i>Usnea aurantiacoatra</i>	Parmeliaceae	on Moss	62°14'27.3"S,58°44'36.3"W	5	KU354810	KU354716	KU354624	KU354532	n/d	KU354956
EL002622	<i>Ramalina</i> sp.	Ramalinaceae	on bark	HagleyparkinChristChurch	96	n/d ^b	KU354717	KU354625	n/d	KU354877	KU354957
EL002624	<i>Candelaria</i> sp.	Candelariaceae	on Rock	Hagleypark	96	KU354812	KU354718	KU354626	KU354533	KU354878	KU354958
EL002625	<i>Psilolechia lucida</i>	Pilocarpaceae	on Rock	74°37'21.1"S,164°13'55.4"E	96	KU354813	KU354719	KU354627	KU354534	KU354879	KU354959
EL002628	<i>Ramalina</i> sp.	Ramalinaceae	on bark	HagleyparkinChristChurch	96	KU354814	KU354720	KU354628	KU354535	KU354880	n/d
EL002629	<i>Candelariella</i> sp.	Candelariaceae	on Moss	74°37'28.0"S,164°13'52.9"E	96	KU354815	KU354721	KU354629	KU354536	KU354881	KU354960
EL002630	<i>Psilolechia lucida</i>	Pilocarpaceae	on Rock	74°37'28.9"S,164°13'53.1"E	96	KU354816	KU354722	KU354630	KU354537	KU354882	KU354961
EL002631	<i>Psilolechia lucida</i>	Pilocarpaceae	on Rock	74°37'28.9"S,164°13'53.1"E	96	KU354817	KU354723	KU354631	KU354538	KU354883	KU354962
EL002634	<i>Caloplaca</i> sp.	Teloschistaceae	on Moss	74°37'28.9"S,164°13'53.1"E	96	KU354818	KU354724	KU354632	KU354539	KU354884	KU354963
EL002636	<i>Caloplaca</i> sp.	Teloschistaceae	on Moss	74°37'28.9"S,164°13'53.1"E	96	KU354819	KU354725	KU354633	KU354540	KU354885	KU354964
EL002638	<i>Lecanora</i> sp.	Ramalinaceae	on Moss	74°37'28.9"S,164°13'53.1"E	96	KU354820	KU354726	KU354634	KU354541	KU354886	KU354965
EL002640	<i>Lecidella</i> sp.	Lecanoraceae	on Moss	74°37'22.9"S,164°13'38.6"E	96	KU354821	KU354727	KU354635	KU354542	KU354887	KU354966
EL002641	<i>Lecidella</i> sp.	Lecanoraceae	on Moss	74°37'22.9"S,164°13'38.6"E	96	KU354822	KU354728	KU354636	KU354543	KU354888	KU354967
EL002643	<i>Lecidella</i> sp.	Lecanoraceae	on Moss	74°37'22.9"S,164°13'38.6"E	96	KU354823	KU354729	KU354637	KU354544	KU354889	KU354968
EL002644	<i>Caloplaca</i> sp.	Teloschistaceae	on Moss	74°36'49.5"S,164°13'03.5"E	96	KU354824	KU354730	KU354638	KU354545	KU354890	KU354969
EL002646	<i>Psilolechia lucida</i>	Pilocarpaceae	on Rock	74°37'19.1"S,164°13'48.9"E	96	KU354825	KU354731	KU354639	KU354546	KU354891	KU354970
EL002647	<i>Psilolechia lucida</i>	Pilocarpaceae	on Rock	74°37'19.1"S,164°13'48.9"E	96	KU354826	KU354732	KU354640	KU354547	KU354892	KU354971
EL002648	<i>Psilolechia lucida</i>	Pilocarpaceae	on Moss	74°37'19.1"S,164°13'48.9"E	96	KU354827	KU354733	KU354641	KU354548	KU354893	KU354972
EL002649	<i>Buellia pycnogonoides</i>	Physciaceae	on Moss	74°37'24.6"S,164°13'46.2"E	96	KU354828	KU354734	KU354642	KU354549	KU354894	KU354973
EL002650	<i>Lepraria</i> sp.	Stereocaulaceae	on Moss	74°37'24.6"S,164°13'46.2"E	96	KU354829	KU354735	KU354643	KU354550	KU354895	KU354974
EL003471	<i>Usnea antarctica</i>	Parmeliaceae	on Moss	62°13'29.48"S,58°47'04.98"W	58	KU354830	KU354736	KU354644	KU354551	KU354896	KU354975
EL003472	<i>Usnea antarctica</i>	Parmeliaceae	on Moss	62°13'29.48"S,58°47'04.98"W	58	KU354831	KU354737	KU354645	KU354552	KU354897	KU354976
EL003473	<i>Usnea antarctica</i>	Parmeliaceae	on Moss	62°13'29.48"S,58°47'04.98"W	58	KU354832	KU354738	KU354646	KU354553	KU354898	KU354977
EL003474	<i>Usnea antarctica</i>	Parmeliaceae	on Rock	62°13'30.62"S,58°46'53.67"W	70	KU354833	KU354739	KU354647	KU354554	KU354899	KU354978
EL003475	<i>Sphaerophorus globosus</i>	Sphaerophoraceae	on Rock	62°13'30.62"S,58°46'53.67"W	70	KU354834	KU354740	KU354648	KU354555	KU354900	KU354979
EL003476	<i>Usnea antarctica</i>	Parmeliaceae	on Moss	62°13'30.85"S,58°46'43.22"W	108.9	KU354835	KU354741	KU354649	KU354556	KU354901	KU354980
EL003477	<i>Usnea antarctica</i>	Parmeliaceae	on Moss	62°13'30.85"S,58°46'43.22"W	108.9	KU354836	KU354742	KU354650	KU354557	n/d	KU354981
EL003478	<i>Sphaerophorus globosus</i>	Sphaerophoraceae	on Moss	62°13'30.85"S,58°46'43.22"W	108.9	KU354837	KU354743	KU354651	KU354558	KU354902	KU354982
EL003479	<i>Cladonia borealis</i>	Cladoniaceae	on Moss	62°13'30.85"S,58°46'43.22"W	108.9	KU354838	KU354744	KU354652	KU354559	KU354903	KU354983
EL003480	<i>Cladonia borealis</i>	Cladoniaceae	on Moss	62°13'30.85"S,58°46'43.22"W	108.9	KU354839	KU354745	KU354653	KU354560	n/d	n/d
EL003481	<i>Umbilicaria antarctica</i>	Parmeliaceae	on Rock	62°13'30.85"S,58°46'43.22"W	108.9	KU354840	KU354746	KU354654	KU354561	KU354904	KU354984
EL003484	<i>Umbilicaria antarctica</i>	Parmeliaceae	on Rock	62°13'30.85"S,58°46'43.22"W	108.9	KU354841	KU354747	KU354655	KU354562	KU354905	KU354985
EL003485	<i>Usnea antarctica</i>	Parmeliaceae	on Rock	62°13'30.85"S,58°46'43.22"W	109	KU354842	KU354748	KU354656	KU354563	KU354906	KU354986
EL003486	<i>Pseudophebe pubescens</i>	Parmeliaceae	on Rock	62°13'30.85"S,58°46'43.22"W	109	KU354843	KU354749	KU354657	KU354564	KU354907	KU354987

EL003487	<i>Himantormia lugubris</i>	<i>Parmeliaceae</i>	on Moss	62°14'03.83"S,58°46'21.42"W	102	KU354844	KU354750	KU354658	KU354565	KU354908	KU354988
EL003488	<i>Sphaerophorus globosus</i>	<i>Sphaerophoraceae</i>	on Moss	62°14'03.83"S,58°46'21.42"W	102	KU354845	KU354751	KU354659	KU354566	KU354909	KU354989
EL003489	<i>Cladonia furcata</i>	<i>Cladoniaceae</i>	on Moss	62°14'03.83"S,58°46'21.42"W	102	KU354846	KU354752	KU354660	KU354567	n/d	KU354990
EL003490	<i>Umbilicaria antarctica</i>	<i>Parmeliaceae</i>	on Moss	62°14'03.83"S,58°46'21.42"W	102	KU354847	KU354753	KU354661	KU354568	n/d	KU354991
EL003491	<i>Cladonia borealis</i>	<i>Cladoniaceae</i>	on Moss	62°14'17.22"S,58°45'56.39"W	26	KU354848	KU354754	KU354662	KU354569	KU354910	KU354992
EL003493	<i>Usnea antarctica</i>	<i>Parmeliaceae</i>	on Rock	62°12'11.31"S,58°47'08.38"W	135	KU354849	KU354755	KU354663	KU354570	KU354911	KU354993
EL003494	<i>Stenea aurantiacoatra</i>	<i>Parmeliaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	KU354850	KU354756	KU354664	KU354571	n/d	KU354994
EL003495	<i>Stereocaulon alpinum</i>	<i>Stereocaulaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	KU354851	KU354757	KU354665	KU354572	KU354912	KU354995
EL003496	<i>Stereocaulon alpinum</i>	<i>Stereocaulaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	KU354852	KU354758	KU354666	KU354573	KU354913	KU354996
EL003497	<i>Stereocaulon alpinum</i>	<i>Stereocaulaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	KU354853	KU354759	KU354667	KU354574	n/d	KU354997
EL003498	<i>Stereocaulon alpinum</i>	<i>Stereocaulaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	n/d	KU354760	KU354668	KU354575	KU354914	KU354998
EL003498-2	<i>Stereocaulon alpinum</i>	<i>Stereocaulaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	KU354854	KU354761	KU354669	KU354576	KU354915	KU354999
EL003499	<i>Stereocaulon alpinum</i>	<i>Stereocaulaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	n/d	KU354762	KU354670	KU354579	KU354916	KU355000
EL003499-2	<i>Stereocaulon alpinum</i>	<i>Stereocaulaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	n/d	n/d	n/d	KU354578	n/d	n/d
EL003500	<i>Cladonia gracilis</i>	<i>Cladoniaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	KU354855	KU354763	KU354671	KU354580	KU354917	KU355001
EL003501	<i>Cladonia gracilis</i>	<i>Cladoniaceae</i>	on Rock	62°13'22.85"S,58°46'57.15"W	31	KU354856	KU354764	KU354672	KU354581	KU354918	KU355002
Endophytic fungi											
EFOMIA01	<i>Andreaea</i> sp.	n/a ^a	n/a	62°14'11.1"S,58°46'16.6"W	48	HQ335293*	KU354765	KU354673	KU354582	KU354919	KU355003
EM000002	<i>Andreaea</i> sp.	n/a	n/a	62°14'11.1"S,58°46'16.6"W	48	KU354857	KU354766	KU354674	KU354583	KU354920	KU355004
EFOMIA02	<i>Andreaea</i> sp.	n/a	n/a	62°14'11.1"S,58°46'16.6"W	48	HQ335294*	KU354767	KU354675	KU354584	KU354921	KU355005
EM000004	<i>Warnstorfia sarmentosa</i>	n/a	n/a	62°14'11.1"S,58°46'16.6"W	48	KU354858	KU354768	KU354676	KU354585	KU354922	KU355006
EFOMIA03	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335295*	KU354769	KU354677	KU354586	KU354923	KU355007
EM000006	<i>Polytrichastrum alpinum</i>	n/a	n/a	62°14'31.3"S,58°43'42.3"W	5	KU354859	KU354770	KU354678	KU354587	KU354924	KU355008
EM000007	<i>Polytrichastrum alpinum</i>	n/a	n/a	62°14'31.3"S,58°43'42.3"W	5	KU354860	KU354771	KU354679	KU354588	KU354925	KU355009
EM000008	<i>Polytrichastrum alpinum</i>	n/a	n/a	62°14'31.3"S,58°43'42.3"W	5	KU354861	KU354772	KU354680	KU354589	KU354926	KU355010
EM000009	<i>Polytrichastrum alpinum</i>	n/a	n/a	62°14'31.3"S,58°43'42.3"W	5	KU354862	KU354773	KU354681	KU354590	KU354927	KU355011
EM000011	<i>Polytrichastrum alpinum</i>	n/a	n/a	62°14'31.3"S,58°43'42.3"W	5	KU354863	KU354774	KU354682	KU354591	KU354928	KU355012
EM000012	<i>Polytrichastrum alpinum</i>	n/a	n/a	62°14'31.3"S,58°43'42.3"W	5	KU354864	KU354775	KU354683	KU354592	KU354929	KU355013
EM000013	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	KU354865	KU354776	KU354684	KU354593	KU354930	KU355014
EM000014	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	KU354866	KU354777	KU354685	KU354594	KU354931	KU355015
EM000015	<i>Polytrichastrum alpinum</i>	n/a	n/a	62°14'31.3"S,58°43'42.3"W	5	KU354867	KU354778	KU354686	KU354595	KU354932	KU355016
EM000016	<i>Sanionia uncinata</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	KU354868	KU354779	KU354687	KU354596	KU354933	KU355017
EFOMIA04	<i>Barbiophozia hatcheri</i>	n/a	n/a	62°14'27.3"S,58°44'36.2"W	6	HQ335296*	KU354780	KU354688	KU354597	KU354934	KU355018
EM000020	<i>Barbiophozia hatcheri</i>	n/a	n/a	62°14'27.3"S,58°44'36.2"W	6	KU354869	KU354781	KU354689	KU354598	KU354935	KU355019
EM000021	<i>Barbiophozia hatcheri</i>	n/a	n/a	62°14'27.3"S,58°44'36.2"W	6	KU354870	KU354782	KU354690	KU354599	KU354936	KU355020
EFOMIA05	<i>Chorisodontium aciphyllum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335297*	KU354783	KU354691	KU354600	n/d	KU355021
EFOMIA06	<i>Chorisodontium aciphyllum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335298*	KU354784	KU354692	KU354601	KU354937	KU355022
EFOMIA07	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335299*	KU354785	KU354693	KU354602	KU354938	KU355023
EFOMIA08	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335300*	KU354786	KU354694	KU354603	KU354939	KU355024
EM000026	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	KU354871	KU354787	KU354695	KU354604	KU354940	KU355025
EFOMIA09	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335301*	KU354788	KU354696	KU354605	n/d	KU355026
EFOMIA10	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335302*	KU354789	KU354697	n/d	n/d	KU355027
EFOMIA11	<i>Polytrichum strictum</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335303*	KU354790	KU354698	KU354606	KU354941	KU355028
EFOMIA12	<i>Andreaea</i> sp.	n/a	n/a	62°14'27.3"S,58°44'36.2"W	6	HQ335304*	KU354791	KU354699	KU354607	KU354942	KU355029
EFOMIA13	<i>Polytrichastrum alpinum</i>	n/a	n/a	62°14'31.3"S,58°43'42.3"W	5	HQ335305*	KU354792	KU354700	KU354608	KU354943	KU355030
EFOMIA14	<i>Sanionia uncinata</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	HQ335306*	KU354793	KU354701	KU354609	n/d	n/d
EM000033	<i>Sanionia uncinata</i>	n/a	n/a	62°13'31.0"S,58°46'41.4"W	88	KU354872	KU354794	KU354702	KU354610	n/d	n/d
EFOMIA15	<i>Polytrichum strictum</i>	n/a	n/a	62°14'11.1"S,58°46'16.6"W	48	HQ335307*	KU354795	KU354703	KU354611	n/d	KU355031
EFOMIA16	<i>Chorisodontium aciphyllum</i>	n/a	n/a	62°14'11.1"S,58°46'16.6"W	48	HQ335308*	KU354796	KU354704	KU354612	KU354944	KU355032

^a n/a=not available.

^b n/d=not determined.

* GenBank accession nos. were retrieved fro Yu *et al.* (2014).

Table S2. Blast search results from endolichenic fungal isolates using ITS region sequences.

Endolichenic fungal isolates	Most closely related fungi (GenBank Accession No.)	Similarity (%)
EL002649	<i>Leotiomyces</i> sp. (AB752274)	100
EL002634	<i>Leotiomyces</i> sp. (AB752274)	100
EL002644	<i>Leotiomyces</i> sp. (AB752274)	100
EL003480	<i>Leotiomyces</i> sp. (AB752274)	100
EL002640	<i>Leotiomyces</i> sp. (AB752274)	100
EL002641	<i>Leotiomyces</i> sp. (AB752274)	100
EL002625	<i>Leotiomyces</i> sp. (AB752274)	100
EL002630	<i>Leotiomyces</i> sp. (AB752274)	100
EL003475	<i>Leotiomyces</i> sp. (AB752274)	100
EL003496	<i>Leotiomyces</i> sp. (AB752274)	100
EL003497	<i>Leotiomyces</i> sp. (AB752274)	100
EL003498-2	<i>Leotiomyces</i> sp. (AB752274)	100
EL003499	<i>Leotiomyces</i> sp. (AB752274)	100
EL001131	<i>Leotiomyces</i> sp. (AB752274)	100
EL001113	Fungal sp. (JN053084)	99
EL003472	Fungal sp. (JN053084)	99
EL003476	<i>Capronia</i> sp. (EU139148)	94
EL003477	Ascomycota sp. (FJ008686)	97
EL003490	Ascomycota sp. (FJ008686)	97
EL001118	<i>Chaetomium globosum</i> (KM268672)	100
EL002646	<i>Phoma herbarum</i> (KT876698)	100
EL001119	Fungal endophyte voucher EFOMIA 07 (HQ335299)	100
EL003479	Fungal endophyte EFOMIA11 (HQ335303)	100
EL003481	Fungal endophyte EFOMIA11 (HQ335303)	100
EL003488	Fungal endophyte EFOMIA11 (HQ335303)	100
EL001112	Fungal endophyte EFOMIA15 (HQ335307)	100
EL001114	Fungal endophyte EFOMIA15 (HQ335307)	100
EL001116	Fungal endophyte EFOMIA15 (HQ335307)	99
EL001117	Fungal endophyte EFOMIA15 (HQ335307)	100
EL001122	Fungal endophyte EFOMIA15 (HQ335307)	100
EL003491	Fungal endophyte EFOMIA15 (HQ335307)	100
EL002631	Uncultured soil fungus clone D139 (JX489808)	100
EL002636	Uncultured soil fungus clone D139 (JX489808)	100
EL002643	Uncultured soil fungus clone D139 (JX489808)	100
EL003471	Uncultured endophytic fungus clone 375S-67 (KC456734)	100
EL003473	Uncultured endophytic fungus clone 375S-67 (KC456734)	100
EL003474	Uncultured endophytic fungus clone 375S-67 (KC456734)	100
EL002638	<i>Thelebolus</i> sp. (KT223586)	100
EL002648	<i>Thelebolus</i> sp. (KT223586)	100
EL002629	<i>Phoma violacea</i> (LN833555)	100
EL002650	<i>Phoma violacea</i> (LN833555)	100
EL001121	Uncultured fungus clone 3232D7 (KF618001)	99
EL001126	Uncultured fungus clone 3232D7 (KF618001)	99
EL003487	Fungal endophyte isolate SNP418 (KP335594)	100
EL003489	Fungal endophyte isolate SNP418 (KP335594)	100

EL003495	<i>Anthostomella leucospermi</i> (EU552100)	98
EL002628	<i>Peziza varia</i> (AF491556)	99
EL003501	<i>Barrmaelia macrospora</i> (KC774566)	93
EL003500	<i>Coniochaetales</i> sp. (JX188111)	97
EL003499-2	<i>Sordariomycetes</i> sp. (JQ760905)	98
EL003498	<i>Leotiomyces</i> sp. (AB752274)	100
EL003494	<i>Helotiales</i> sp. (KM503089)	96
EL003493	<i>Umbilicaria lyngei</i> (JQ739996)	92
EL003486	<i>Xylariales</i> cf. JP60-5 (GQ906952)	96
EL003485	<i>Coniochaetales</i> sp. (JX188111)	97
EL003484	Uncultured fungus clone 3203N2 (KF617233)	99
EL003478	<i>Hyalodendriella betulae</i> (EU040232)	96
EL002647	<i>Cephalosporium</i> sp. (KF367533)	98
EL002624	<i>Xylaria</i> sp. (JN225909)	100
EL002622	<i>Biscogniauxia</i> sp. (JN225898)	98
EL001127	Uncultured fungus (KF297156)	93

Table S3. A total 324 taxa and the retrieved nuSSU, nuLSU, mtSSU, *RPB1*, and *RPB2* sequences from GenBank.

Taxa	nuSSU	nuLSU	mtSSU	<i>RPB2</i>	<i>RPB1</i>
<i>Acarospora bullata</i>	AY640980	AY640939	-	-	-
<i>Acarospora canadensis</i>	AY640981	AY640940	-	-	-
<i>Acarospora cervina</i>	AY640982	AY640941	-	-	-
<i>Acarospora clauzadeana</i>	-	AY640946	-	-	-
<i>Acarospora complanata</i>	AF356653	AF356654	-	-	-
<i>Acarospora hilaris</i>	AY640983	AY640942	-	-	-
<i>Acarospora laqueata</i>	AY640984	AY640943	DQ991757	AY641024	DQ782860
<i>Acarospora macrospora</i> subsp. <i>macrospora</i>	AY640985	AY640944	-	-	-
<i>Acarospora schleicheri</i>	AY640986	AY640945	AY584694	AY641026	DQ782859
<i>Acarosporina microspora</i>	AY584667	AY584643	AY584612	AY584682	DQ782818
<i>Agaricostilbum hyphaenes</i>	AY665775	NG_042408	-	AY788845	AY780933
<i>Agonimia</i> sp.	DQ782885	DQ782913	-	DQ782874	DQ782853
<i>Aleuria aurantia</i>	AY544698	AY544654	-	DQ247785	DQ471120
<i>Ampelomyces quisqualis</i>	AY293782	AY293795	-	-	-
<i>Anisomeridium polypori</i>	-	-	-	-	DQ782822
<i>Aphanoascus fulvescens</i>	AJ315172	AY176708	-	-	-
<i>Apiospora sinensis</i>	AY083815	AY083831	-	-	-
<i>Arachniotus ruber</i>	AJ315166	AY176746	-	-	-
<i>Arthrinium phaeospermum</i>	AY083816	AY083832	-	-	-
<i>Arthroderma curreyi</i>	AJ315165	AY176726	-	-	-
<i>Ascobolus carbonarius</i>	AY544720	AY544677	-	-	-
<i>Ascobolus crenulatus</i>	AY544721	AY544678	FJ713607	DQ470893	DQ471132
<i>Ascosphaera apis</i>	X69849	AY004344	-	-	-
<i>Ascosacculus heteroguttulatus</i>	-	AY227122	-	-	-
<i>Ascosalsum cincinnatulum</i>	-	AY227120	-	-	-
<i>Aspergillus fumigatus</i>	-	AY660917	-	XM_741647	XM_747744
<i>Aspergillus nidulans</i>	-	AF454167	-	-	-
<i>Astrocystis cocoes</i>	AY083804	AY083823	-	-	-
<i>Auxarthron zuffianum</i>	L28062	AY176712	-	-	-
<i>Bacidia schweinitzii</i>	-	DQ782911	DQ972998	DQ782872	DQ782830
<i>Baeomyces placophyllus</i>	AF356657	AF356658	-	-	-
<i>Barssia oregonensis</i>	AY544696	AY544652	-	-	-
<i>Biatoridium monasteriense</i>	AY640988	AY640947	-	-	-
<i>Bimuria novae-zelandiae</i>	AY016338	AY016356	-	-	-
<i>Botryosphaeria ribis</i>	AF271129	AY004336	-	-	-
<i>Botryotinia fuckeliana</i>	AY544695	AY544651	AY544732	DQ247786	DQ471116
<i>Byssochlamys nivea</i>	M83256	AY176750	-	-	-
<i>Byssothecium circinans</i>	AY016339	AY016357	-	-	-
<i>Cainia graminis</i>	AY083801	AF431949	-	-	-
<i>Caloscypha fulgens</i>	DQ247807	DQ247799	-	DQ247787	DQ471126
<i>Camarops microspora</i>	AY083800	AY083821	-	-	-
<i>Candida albicans</i>	X53497	X70659	-	-	-
<i>Candida glabrata</i>	AY198398	-	AF442299	-	-
<i>Candida lusitaniae</i>	M55526	-	-	-	-
<i>Candida tropicalis</i>	M55527	-	-	AY485615	-
<i>Canoparmelia caroliniana</i>	AY584658	AY584634	AY584613	AY584683	DQ782817
<i>Capnodium coffeae</i>	DQ247808	DQ247800	FJ190609	-	DQ471162
<i>Capronia mansonii</i>	-	AY004338	-	-	-
<i>Capronia pilosella</i>	DQ823106	AF279378	FJ225725	DQ840561	DQ840554
<i>Capronia pilosella</i>	U42473	DQ823099	-	-	DQ471123
<i>carospora clauzadeana</i>	AY640987	-	-	-	-
<i>Carpoligna pleurothecii</i>	AY544689	AY544685	-	-	-
<i>Cephalotheca sulfurea</i>	AF096173	AF431950	-	-	-
<i>Ceramothyrium carniolicum</i>	AF346418	AY004339	-	-	-
<i>Chaetomella acutiseta</i>	AY544728	AY544679	AY544734	DQ470886	DQ471125
<i>Chaetomium globosum</i>	AY545725	AY545729	-	-	-
<i>Cheilymenia stercorea</i>	AY544705	AY544661	-	-	-
<i>Chlorociboria</i> cf. <i>aeruginosa</i>	AY544713	AY544669	-	-	-
<i>Chrysoportha cubensis</i>	-	AF408338	-	-	-

<i>Cladonia caroliniana</i>	AY584664	AY584640	AY584614	AY584684	-
<i>Coccidioides immitis</i>	-	-	L14536	-	-
<i>Coccomyces dentatus</i>	AY544701	AY544657	AY544736	DQ247789	-
<i>Coccotrema cucurbitula</i>	AF274114	AF274092	-	-	-
<i>Coccotrema pocillarium</i>	AF274113	AF274093	-	-	-
<i>Cochliobolus heterostrophus</i>	AY544727	AY544645	AY544737	DQ247790	DQ518183
<i>Coenogonium leprieurii</i>	AF465457	AF465442	-	-	-
<i>Coltricia perennis</i>	AF026583	KJ000223	U27028	AY864867	AY218526.2
<i>Cordyceps crassisporea</i>	AB067697	AB067706	-	-	-
<i>Cordyceps cylindrica</i>	AF327400	AF327382	-	-	-
<i>Cordyceps irangiensis</i>	AF327396	AF327389	-	-	-
<i>Cordyceps khaoyaiensis</i>	AF327393	AF327375	-	-	-
<i>Cordyceps militaris</i>	AF049146	AF327374	-	-	-
<i>Cordyceps pseudomilitaris</i>	AF327394	AF327376	-	-	-
<i>Cordyceps sinensis</i>	AB067736	AB067738	-	-	-
<i>Cordyceps tuberculata</i>	AF327401	AF327384	-	-	-
<i>Corollospora maritima</i>	U46871	AF491260	-	-	-
<i>Crinula caliciiformis</i>	AY544729	AY544680	-	-	-
<i>Cryphonectria cubensis</i>	L42439	-	-	-	-
<i>Cryphonectria havanensis</i>	L42440	AF408339	-	-	-
<i>Cryptodiaporthe corni</i>	AF277119	AF408343	-	-	-
<i>Cryptosphaeria eunomia</i> var <i>eunomia</i>	AY083807	AY083826	-	-	-
<i>Cudonia circinans</i>	AF107343	AF279379	-	-	-
<i>Cudoniella clavus</i>	DQ470992	DQ470944	FJ713604	DQ470888	DQ471128
<i>Curvularia brachyspora</i>	L36995	AF279380	-	-	-
<i>Debaryomyces hansenii</i>	-	AF485980	-	-	-
<i>Delphinella strobiligena</i>	AY016341	AY016358	-	-	-
<i>Dendrographa leucophaea</i> f. <i>minor</i>	AF279381	AF279382	GU561843	AY641034	-
<i>Dermatocarpon luridum</i>	AY640989	AY640948	-	-	-
<i>Dermatocarpon minutum</i>	AY584668	AY584644	-	DQ782863	DQ782821
<i>Dermea acerina</i>	DQ247809	DQ247801	DQ976373	DQ247791	DQ471164
<i>Diaporthe eres</i>	DQ471015	AF408350	FJ190607	DQ470919	-
<i>Diaporthe phaseolorum</i>	L36985	DPU47830	-	-	-
<i>Dibaeis baeomyces</i>	AF113712	AF279385	AY584704	AY641037	DQ842011
<i>Dimerella lutea</i>	AF279386	AF279387	-	-	-
<i>Diploschistes ocellatus</i>	AF038877	AY605077	-	-	DQ366252
<i>Diploschistes scruposus</i>	AF279388	AF279389	-	-	-
<i>Disciotis venosa</i>	AY544711	AY544667	FJ713606	DQ470892	DQ471131
<i>Discosphaerina fagi</i>	AY016342	AY016359	-	-	-
<i>Discula destructiva</i>	AF429719	AF408359	-	-	-
<i>Discula fraxinea</i>	AF277106	-	-	-	-
<i>Dissophora decumbens</i>	HQ667440	HQ667355	-	-	-
<i>Dissophora ornata</i>	HQ667441	NG_042537	-	-	-
<i>Dothidea insculpta</i>	DQ247810	AY640949	FJ190602	DQ247792	DQ471154
<i>Dothidea insculpta</i>	U42474	-	-	-	-
<i>Dothidea ribesia</i>	AY016343	AY016360	-	-	-
<i>Dothidea sambuci</i>	AY544722	AY544681	AY544739	DQ522854	-
<i>Emericellopsis terricola</i>	X80705	-	-	-	-
<i>Emericellopsis terricola</i>	U44112	ETU57082	-	-	-
<i>Endocarpon pallidulum</i>	DQ823104	DQ823097	FJ225674	DQ840559	DQ840552
<i>Eremascus albus</i>	M83258	AY004345	AF442353	-	-
<i>Eremothecium gossypii</i>	AF113137	-	FJ225740	-	DQ840555
<i>Erysiphe friesii</i> var <i>dahurica</i>	AB033478	AB022382	-	-	-
<i>Erysiphe mori</i>	AB033484	AB022418	-	-	-
<i>Exophiala dermatitidis</i>	DQ823107	DQ823100	-	-	-
<i>Exophiala jeanselmei</i>	-	AF050271	-	-	-
<i>Exophiala pisciphila</i>	DQ823108	DQ823101	FJ225744	DQ840563	DQ840556
<i>Farrowia longicollea</i>	AF207685	AF286408	-	-	-
<i>Farrowia seminuda</i>	AF207686	AF286410	-	-	-
<i>Fasciatispora petrakii</i>	AY083809	AY083828	-	-	-
<i>Fuscidea lygaea</i>	AY640990	AY640950	-	-	-

<i>Gaeumannomyces graminis</i> var <i>graminis</i>	AF277125	AF362557	-	-	-
<i>Gamsiella multivaricata</i>	JQ040248	NG_042550	-	-	-
<i>Geoglossum nigrinum</i>	AY544694	AY544650	AY544740	DQ470879	DQ471115
<i>Gibberella zeae</i>	-	AY188924	GZU34520	-	-
<i>Glyphium elatum</i>	AF346419	AF346420	-	-	-
<i>Glypholecia scabra</i>	AY640991	AY640951	-	-	-
<i>Gnomonia gnomon</i>	DQ471019	AF408361	FJ190615	DQ470922	DQ471167
<i>Gnomonia setacea</i>	AF277121	AF362563	-	-	-
<i>Gnomoniella fraxini</i>	-	AF362552	-	-	-
<i>Golovinomyces orontii</i>	AB033483	AB077697	-	-	-
<i>Graphina poitiae</i>	AF465459	AF465447	-	-	-
<i>Gyalecta hypoleuca</i>	AF465460	AF465453	-	-	-
<i>Gyalecta jenensis</i>	AF279390	AF279391	-	-	-
<i>Gyalecta ulmi</i>	AF465464	AF465463	-	-	-
<i>Gyromitra californica</i>	AY544717	AY544673	AY544741	DQ470891	DQ471130
<i>Gyromitra</i> cf. <i>melaleucoides</i>	AY544707	AY544663	-	-	-
<i>Gyromitra esculenta</i>	U42648	AY640952	-	-	-
<i>Halorosellinia oceanica</i>	AY083803	AY083822	-	-	-
<i>Halosarpheia cincinnatula</i>	AF352077	-	-	-	-
<i>Halosarpheia heteroguttulata</i>	AF352085	-	-	-	-
<i>Halosarpheia lotica</i>	AF352081	-	-	-	-
<i>Halosarpheia marina</i>	AF352082	AY227125	-	-	-
<i>Hamigera avellanea</i>	D14406	AB000620	-	-	-
<i>Helvella</i> cf. <i>compressa</i>	AY544699	AY544655	-	-	-
<i>Hydropisphaera erubescens</i>	AY545722	AY545726	AY545730	-	DQ518182
<i>Hymenelia lacustris</i>	AY640992	AY640953	-	-	-
<i>Hypocenyce scalaris</i>	DQ782886	DQ782914	DQ912274	DQ782875	DQ782854
<i>Hypocrea americana</i>	AY544693	AY544649	AY544743	-	DQ522853
<i>Hypomyces polyporinus</i>	AF543771	AJ459301	-	-	-
<i>Hyponectria buxi</i>	AF130976	AY083834	-	-	-
<i>Hypoxyton fragiforme</i>	AY083810	AY083829	-	-	-
<i>Kluyveromyces waltii</i>	-	-	AF442341	-	-
<i>Lachnum bicolor</i>	AY544690	AY544674	-	-	-
<i>Lachnum virgineum</i>	AY544688	AY544646	AY544745	DQ470877	-
<i>Lasallia pennsylvanica</i>	AF356664	AF356665	-	-	-
<i>Lecanactis abietina</i>	AY548805	AY548812	-	-	-
<i>Lecanora aticoncolor</i>	AY640993	AY640954	-	-	-
<i>Lecanora hybocarpa</i>	DQ782883	DQ782910	DQ912273	DQ782871	DQ782829
<i>Lempholemma polyanthes</i>	AF356690	AF356691	-	-	-
<i>Leotia lubrica</i>	AY544687	AY544644	AY544746	DQ470876	DQ471113
<i>Lepolichen coccophorus</i>	AF274110	AF274096	-	-	-
<i>Leptogium cyanescens</i>	AF356671	AF356672	-	-	-
<i>Letendraea helminthicola</i>	-	AY016362	-	-	-
<i>Leveillula taurica</i>	AB033479	AB022387	-	-	-
<i>Lichinella iodopulchra</i>	-	-	-	DQ832328	DQ782857
<i>Lindra thalassiae</i>	DQ470994	DQ470947	FJ190593	-	-
<i>Littispora abonnis</i>	AY227137	-	-	-	-
<i>Lobaria quercizans</i>	AF279396	AF279397	-	-	-
<i>Lobosporangium transversale</i>	HQ667488	HQ667404	-	-	-
<i>Lojkania enalia</i>	AY016346	AY016363	-	-	-
<i>Lulworthia fucicola</i>	AF050481	AF491270	-	-	-
<i>Lulworthia grandispora</i>	AF047582	AF491271	FJ190595	-	-
<i>Lulworthia grandispora</i>	DQ522855	DQ522856	-	-	-
<i>Magnaporthe grisea</i>	AB026819	-	AF056626	-	-
<i>Magnisphaera stevemossago</i>	AY227140	AY227135	-	-	-
<i>Maronea chilensis</i>	AY640994	AY640955	-	-	-
<i>Maronea constans</i>	AY640995	AY640956	-	-	-
<i>Melanconis marginalis</i>	AF277122	AF408373	-	-	-
<i>Menispora tortuosa</i>	AY544723	AY544682	-	-	-
<i>Microascus trigonosporus</i>	DQ471006	DQ470958	FJ190600	DQ470908	DQ471150
<i>Microascus trigonosporus</i>	L36987	MTU47835	-	-	-

<i>Microdochium nivale</i>	AF548077	AF024596	-	-	-
<i>Microxyphium citri</i>	AY016340	AY004337	-	-	-
<i>Modicella malleola</i>	KF053133	KF053131	-	-	-
<i>Modicella reniformis</i>	KF053134	KF053132	-	-	-
<i>Mollisia cinerea</i>	DQ470990	DQ470942	DQ976372	DQ470883	DQ471122
<i>Monascus purpureus</i>	DQ782881	DQ782908	-	-	-
<i>Monascus purpureus</i>	-	-	FJ225780	-	DQ842012
<i>Monilinia fructicola</i>	AY544724	AY544683	-	-	-
<i>Monilinia laxa</i>	AY544714	AY544670	-	DQ470889	-
<i>Morchella cf. elata</i>	AY544709	AY544665	-	-	-
<i>Morchella cf. esculenta</i>	AY544708	AY544664	AY544750	DQ470880	DQ471117
<i>Mortierella antarctica</i>	HQ667503	-	-	-	-
<i>Mortierella cogitans</i>	-	HQ667360	-	-	-
<i>Mortierella elongatula</i>	HQ667505	NG_042565	-	-	-
<i>Mortierella kuhlmanii</i>	HQ667457	NG_042544	-	-	-
<i>Mortierella rishiksha</i>	HQ667469	HQ667385	-	-	-
<i>Mycoblastus sanguinari</i>	DQ782879	DQ782915	DQ912276	DQ782867	DQ782827
<i>Myriangium duriae</i>	AY016347	AY016365	-	-	-
<i>Natantispora lotica</i>	-	AY227124	-	-	-
<i>Nectria cinnabarina</i>	U32412	U00748	-	-	AY489666
<i>Nectria haematococca</i>	-	-	FJ713623	-	-
<i>Neofabraea malicorticis</i>	AY544706	AY544662	-	-	-
<i>Neolecta vitellina</i>	AY640996	AF279401	-	-	-
<i>Neurospora crassa</i>	X04971	AF286411	AF442356	XM_952013	XM_959004
<i>Ochrolechia juvenalis</i>	AY640997	AY640957	-	-	-
<i>Ochrolechia parella</i>	AF274109	AF274097	-	-	-
<i>Ochrolechia szatalaensis</i>	AF274108	AF274102	-	-	-
<i>Orbilia auricolor</i>	DQ471001	DQ470953	-	DQ470903	-
<i>Orbilia vinosa</i>	DQ471000	DQ470952	-	-	DQ471145
<i>Orceolina kerguelensis</i>	DQ366257	AY212830	AF381561	DQ366256	-
<i>Otiidea onotica</i>	AF006308	AF335121	-	-	-
<i>Oxydothis frondicola</i>	AY083818	AY083835	-	-	-
<i>Paracoccidioides brasiliensis</i>	AF238302	PBU81263	-	-	-
<i>Peltigera canina</i>	AF356681	AF286822	-	-	-
<i>Peltigera degenii</i>	AY584681	AY584657	AY584628	AY584688	DQ782826
<i>Peltula auriculata</i>	DQ832332	DQ832330	DQ922953	DQ832331	DQ782856
<i>Peltula obscurans</i>	AF356692	AF356693	-	-	-
<i>Peltula umbilicata</i>	AF356688	AF356689	DQ922954	DQ832335	DQ782855
<i>Peltula umbilicata</i>	DQ782887	DQ832334	-	-	-
<i>Penicillium freii</i>	AY640998	AY640958	-	-	-
<i>Pertusaria amara</i>	AF274104	AF274101	-	-	-
<i>Pertusaria dactylina</i>	DQ782880	DQ782907	DQ972973	DQ782868	DQ782828
<i>Pertusaria erythrella</i>	AF274106	AF274100	-	-	-
<i>Pertusaria scaberula</i>	AF274105	AF274099	-	-	-
<i>Petractis luetkemuelleri</i>	AF465461	AF465454	-	-	-
<i>Peziza proteana f. sparassoides</i>	AY544703	AY544659	-	-	DQ518184
<i>Peziza quelepidotia</i>	AY640999	AY640959	-	-	-
<i>Peziza succosa</i>	U53383	AF335166	-	-	-
<i>Peziza vesiculosa</i>	DQ470995	DQ470948	AF431960	-	-
<i>Phaeosphaeria avenaria</i>	AY544725	AY544684	-	-	-
<i>Phaeotrichum benjaminii</i>	AY016348	AY004340	-	-	-
<i>Phoma glomerata</i>	AY293783	AY293796	-	-	-
<i>Phyllactinia moricola</i>	AB033481	AB02240	-	-	-
<i>Physcia aipolia</i>	-	-	DQ912290	-	-
<i>Pichia guilliermondii</i>	AB013587	-	-	-	-
<i>Pichia guilliermondii</i>	-	-	-	AY485613	-
<i>Piedraia hortae</i>	AY016349	AY016366	-	-	-
<i>Placopsis perrugosa</i>	AF356659	AF356660	-	-	-
<i>Placynthium nigrum</i>	AF356673	AF356674	-	-	-
<i>Plagiostoma euphorbiae</i>	AF277114	AF408382	-	-	-
<i>Pleopsidium chlorophanum</i>	AY316151	AY640960	DQ991756	DQ525442	DQ782858

<i>Pleopsidium chlorophanum</i>	DQ525541	DQ842017	-	-	-
<i>Pleospora herbarum</i>	DQ247812	DQ247804	FJ190610	DQ247794	DQ471163
<i>Podosphaera xanthii</i>	AB033482	AB022410	-	-	-
<i>Polysporina simplex</i>	AY641000	AY640961	-	-	-
<i>Porpidia albocaerulescens</i>	AF356675	AF356676	-	-	-
<i>Potebniamyces pyri</i>	DQ470997	DQ470949	-	DQ470900	-
<i>Preussia terricola</i>	AY544726	AY544686	-	-	-
<i>Protomyces inouyei</i>	AY548295	NG_042406	-	DQ471135	AY548299
<i>Pyrenophora phaeocomes</i>	DQ499595	DQ499596	FJ190591	DQ497614	-
<i>Pyrenophora tritici-repentis</i>	AY544716	AY544672	-	-	-
<i>Pyrenula cruenta</i>	AF279406	AF279407	-	-	-
<i>Pyrenula pseudobufonia</i>	AY641001	AY640962	AY584720	AY641068	DQ840558
<i>Pyrgillus javanicus</i>	DQ823110	DQ823103	FJ225774	DQ842009	DQ842010
<i>Pyronema domesticum</i>	DQ247813	DQ247805	FJ190613	DQ247795	DQ471166
<i>Raciborskiomyces longisetosum</i>	AY016351	AY016367	-	-	-
<i>Ramichloridium anceps</i>	DQ823109	DQ823102	FJ225752	DQ840564	DQ840557
<i>Rhizocarpon disporum</i>	AF356677	AF356678	-	-	-
<i>Rhytisma acerinum</i>	AF356695	AF356696	-	-	-
<i>Rocella boergesenii</i>	AY548807	AY548814	-	-	-
<i>Rocella fuciformis</i>	AY584678	AY584654	EU704082	DQ782866	DQ782825
<i>Rosellinia necatrix</i>	AY083805	AY083824	-	-	-
<i>Saccharomyces castellii</i>	Z75577	-	AF442313	-	-
<i>Saccharomyces cerevisiae</i>	J01353	J01355	-	-	-
<i>Saccharomyces cerevisiae</i>	Z75578	-	-	-	-
<i>Sagaaromyces abonnis</i>	-	AY227118	-	-	-
<i>Saitoella complicata</i>	AY548297	NG_027621	AY548290	DQ471133	AY548300
<i>Sarcogyne regularis</i> var <i>regularis</i>	AY641003	AY640964	-	-	-
<i>Sarcogyne similis</i>	AY641005	AY640966	-	-	-
<i>Sarcosagium campestre</i>	AY641002	AY640963	-	-	-
<i>Sarcoscypha coccinea</i>	AY544691	AY544647	AY544755	DQ497612	-
<i>Sarcosphaera crassa</i>	AY544712	AY544668	-	-	-
<i>Sarea resiniae</i>	AY641004	AY640965	-	-	-
<i>Schismatomma decolorans</i>	AY548809	AY548815	-	-	-
<i>Schizosaccharomyces pombe</i>	X54866	Z19136	-	-	-
<i>Schizosaccharomyces pombe</i>	JN938992	JN938920	-	JN985155	-
<i>Scoliciosporum umbrinum</i>	AY641006	AY640967	-	-	-
<i>Scutellinia scutellata</i>	DQ247814	DQ247806	FJ190587	DQ247796	-
<i>Setomelanomma holmii</i>	AY161121	AF525678	-	-	-
<i>Setosphaeria monoceras</i>	AY016352	AY016368	-	-	-
<i>Seynesia erumpens</i>	AF279409	AF279410	-	-	-
<i>Simonyella variegata</i>	AY584669	AY584645	AY584631	DQ782861	DQ782819
<i>Sordaria fimicola</i>	AY545724	AY545728	-	-	-
<i>Sordaria macrospora</i>	AY641007	AY346301	-	-	-
<i>Spathularia flavida</i>	Z30239	AF433146	-	-	-
<i>Sphaerophorus globosus</i>	L37532	AF356680	-	-	-
<i>Spiromastix warcupii</i>	DQ782882	DQ782909	FJ225794	-	-
<i>Sporastatia polyspora</i>	AY641008	AY640968	-	-	-
<i>Sporastatia testudinea</i>	AY641009	AY640969	-	-	-
<i>Staurothele frustulenta</i>	DQ823105	DQ823098	-	DQ840560	DQ840553
<i>Stereocaulon paschale</i>	AF279412	AF279413	-	-	-
<i>Stictis radiata</i>	U20610	AF356663	AY584727	AY641079	-
<i>Strangospora pinicola</i>	AY641011	AY640971	-	-	-
<i>Strobilomyces floccopus</i>	AY662661	AY612824	-	AY858964	AY786065
<i>Stylodothis puccinioides</i>	AY016353	AY004342	-	-	-
<i>Sydowia polyspora</i>	AY544718	AY544675	-	-	-
<i>Taphrina communis</i>	AY641012	AY640972	-	-	-
<i>Thamnia subuliformis</i>	AF113714	AF356679	-	-	-
<i>Thelocarpella gordensis</i>	AY641014	AY640974	-	-	-
<i>Thelocarpon laureri</i>	AY641015	AY640975	-	-	-
<i>Thyridium vestitum</i>	AY544715	AY544671	-	-	-
<i>Torrubiella luteorostrata</i>	AF327398	AF327388	-	-	-

<i>Trapelia involuta</i>	AF119499	AF274098	-	-	-
<i>Trapelia placodioides</i>	AF119500	AF274103	AF431962	DQ366260	DQ366259
<i>Trematosphaeria heterospora</i>	AY016354	AY016369	AF346429	DQ497615	-
<i>Trichoglossum hirsutum</i>	AY544697	AY544653	-	DQ470881	DQ471119
<i>Tryblidiopsis pinastri</i>	AF106013	AY004335	-	-	-
<i>Trypethelium</i> sp.	AY584676	AY584652	AY584632	AY584690	DQ782824
<i>Umbelopsis changbaiensis</i>	KM017674	KF727448	-	-	-
<i>Umbelopsis ramanniana</i>	NG_017189	-	-	-	-
<i>Umbelopsis westeae</i>	KM017690	-	-	-	-
<i>Umbilicaria mammulata</i>	AY648114	DQ782912	DQ912305	DQ782873	DQ782831
<i>Umbilicaria muehlenbergii</i>	AY641016	AY640977	-	-	-
<i>Valsa ambiens</i> subsp. <i>leucostomoides</i>	AF277120	AF362564	-	-	-
<i>Varicosporina ramulosa</i>	U43846	AF491276	-	-	-
<i>Verpa conica</i>	AY544710	AY544666	-	-	-
<i>Verrucaria pachyderma</i>	AF356667	AF356668	-	-	-
<i>Verticillium</i> cf. <i>epiphytum</i>	AY180327	AF213032	-	-	-
<i>Westerdykella cylindrica</i>	AY016355	AY004343	AF346430	DQ470925	DQ471168
<i>Xanthomendoza fallax</i>	AY641018	AY640979	-	-	-
<i>Xanthoria elegans</i>	AY641017	AY640978	-	-	-
<i>Xylaria acuta</i>	AY544719	AY544676	-	DQ247797	DQ471118
<i>Xylaria hypoxylon</i>	AY544692	AY544648	-	DQ470878	DQ471114

Figure S1. Maximum Likelihood analysis based on concatenated two-locus dataset of small and large subunit (nuSSU and nuLSU) rDNA of 272 taxa (2 and 10 ingroup taxa of *Dikarya* and *Mortierellomycotina*, respectively) and 1 outgroup taxon *Umbelopsis* as member of the *Mucorales*); representing major lineages. Node support equal and or above 70 % is given on the branches. Taxon labels starting with “EL” in red represents endolichenic fungal isolates from lichen thalli, while labels starting with “EF” or “EM” in blue indicate endophytic fungal isolates of bryophytes.

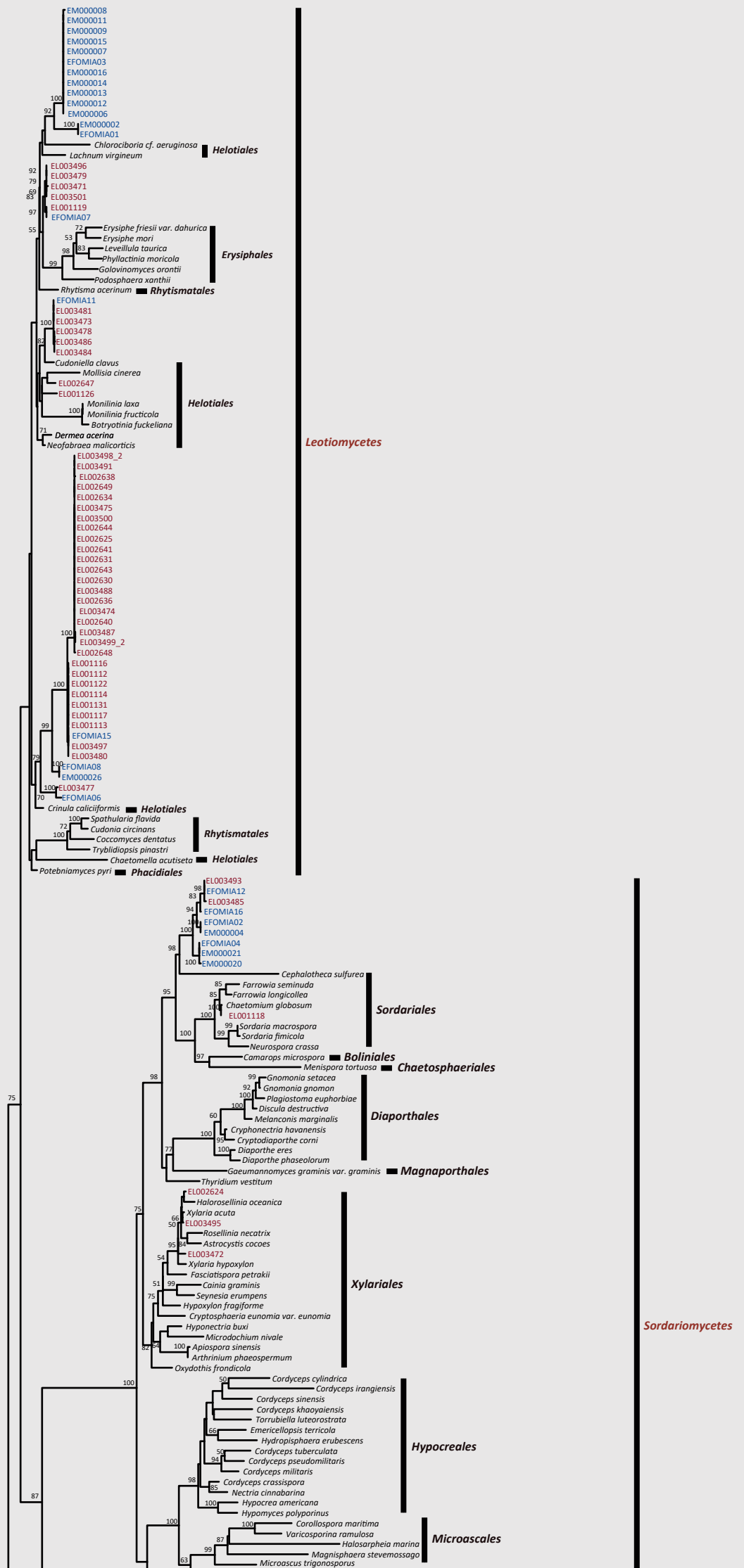
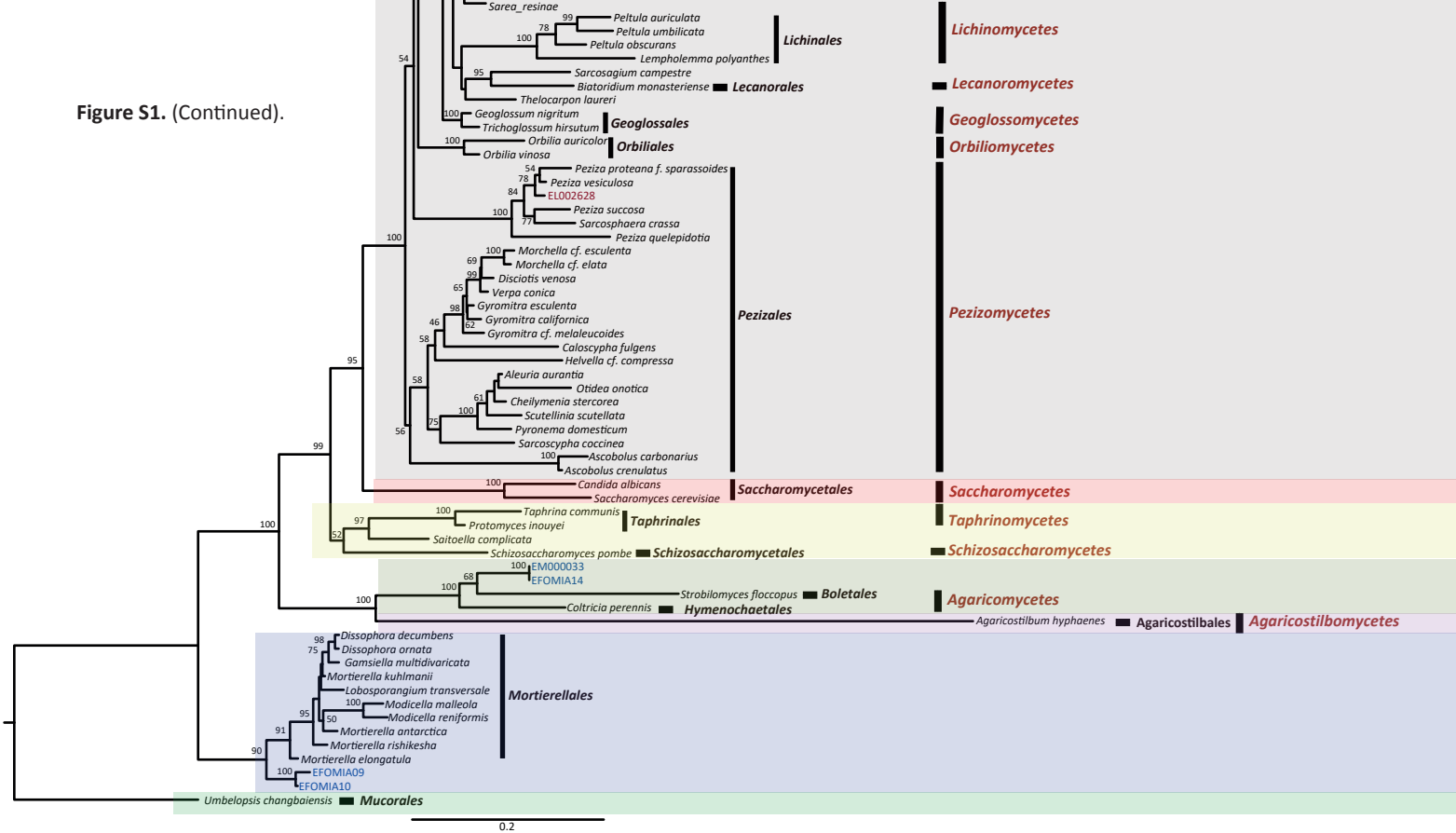


Figure S1. (Continued).



Figure S1. (Continued).



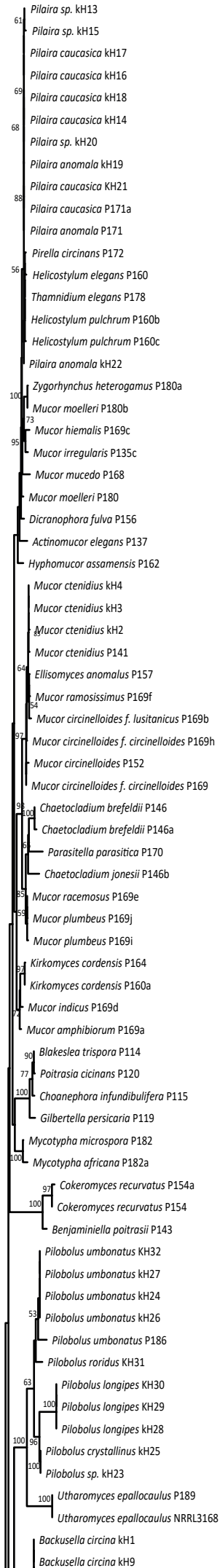


Figure S2. Maximum Likelihood analysis of the *Mortierellomycotina* dataset published in HYPERLINK \l "Wagner *et al.* (2013), showing phylogenetic relation of the isolates EFOMIA09 and EFOMIA10. Node support equal and or above 70 % is given on the branches.

Figure S2. (Continued).

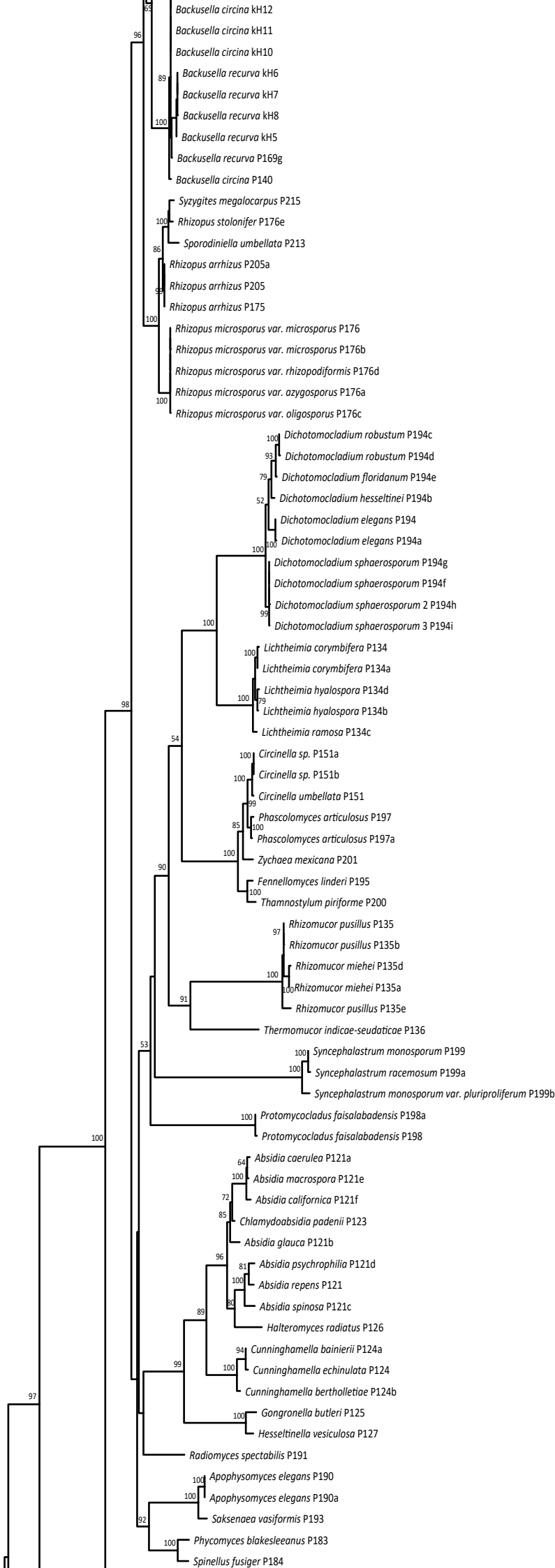


Figure S2. (Continued).

