

# High levels of endemism and local differentiation in the fungal and algal symbionts of saxicolous lecideoid lichens along a latitudinal gradient in southern South America

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## Abstract

Saxicolous, lecideoid lichenized-fungi have a cosmopolitan distribution but, being mostly cold adapted, are especially abundant in polar and high-mountain regions. To date, little is known of their origin or the extent of their trans-equatorial dispersal. Several mycobiont genera and species are thought to be restricted to either the northern or southern hemisphere, whereas others are thought to be widely distributed and occur in both hemispheres. However, these assumptions often rely on morphological analyses and lack supporting molecular genetic data. Also unknown is the extent of regional differentiation in the southern Polar Regions.

An extensive set of lecideoid lichens (185) was collected along a latitudinal gradient at the southern end of South America, always staying in areas of subantarctic climate by increasing the elevation of the collecting sites with decreasing latitude. The investigated specimens were brought into a global context by including Antarctic and cosmopolitan sequences from other studies. For each symbiont three markers were used to identify intraspecific variation (mycobiont: ITS, mtSSU, RPB1; photobiont: ITS, psbJ-L, COX2). For the mycobiont the saxicolous genera *Lecidea*, *Porpidia*, *Poeltidea* and *Lecidella* and their photobionts *Asterochloris* and *Trebouxia* were phylogenetically revised. The results show for several globally distributed species groups geographically highly differentiated subclades, classified as operational taxonomical units (OTUs), which were assigned to the different regions of southern South America (sSA). Further, for sSA, several small endemic and well supported clades were detected at the species level for both symbionts.

## Keywords

subantarctic subregion, pioneer vegetation on rock, global distribution, local differentiation, endemism, glacial refugia

*Dedicated to Hannes Hertel on his 80<sup>th</sup> birthday in appreciation of his life-long investigation of lecideoid lichens.*

## Introduction

Saxicolous 'lecideoid' lichens (Hertel 1984) comprise genera and species described under the generic name *Lecidea* sensu Zahlbruckner (1925) and comprise crustose species with apothecia lacking a thalline margin and with non-sepate ascospores. As such they are a heterogenous, non-monophyletic group and, although some do belong to the genus *Lecidea* s. str. (Lecideaceae), most belong to other genera and families, such as *Carbonea*, *Lecidella* (Lecanoraceae), *Porpidia*, *Poeltidea* and *Cyclohymeria* (Lecideaceae). In addition to their morphological similarities, lecideoid lichenized fungi are strongly associated with green microalgal photobionts of the cosmopolitan class Trebouxiophyceae (Buschbom and Mueller 2004; Fryday and Hertel 2014; Hertel 1984; 2007; Ruprecht et al. 2012a; Ruprecht et al. 2016; Schmull et al. 2011; Zhao et al. 2015).

The inconspicuous morphology of this group complicates their systematic treatment. Large taxonomic groups are often distinguishable by just a few microscopic traits, such as spore size and septation or ascus-type, but species level identification can be difficult, often relying on cryptic characters like excipulum pigmentation and structure or the secondary metabolites produced. The fundamental taxonomic work on lecideoid lichens (Castello 2003; Fryday 2005; Fryday and Hertel 2014; Gowan 1989; Hafellner 1984; Hertel 1984; 1995; Inoue 1995; Knoph and Leuckert 1994; Knoph et al. 2004) mostly used morphological and chemical characters, but lacked molecular genetic data. Extensive collections, especially from the southern hemisphere are very often older than 50 years, which precludes the use of molecular methods, because of the common problem of DNA degradation in mycobiont specimen older than 20 years. During the last decade, molecular re-evaluations have helped to redefine the species concepts behind these diverse groups but were mostly focused on the northern hemisphere (Buschbom and Mueller 2004; McCune et al. 2017; Orange 2014; Schmull et al. 2011; Zhao et al. 2015; Zhao et al. 2016) and Antarctica (Ruprecht et al. 2010; 2012b), although the links to a better understanding of distribution- and speciation patterns in the group are still largely missing. Meanwhile, intermediate latitudes in the southern hemisphere remain understudied and recently published results (Ruprecht et al. 2016) have emphasized the extent of the knowledge gap in southern South American lecideoid lichens, not only from the mycobiont perspective but also from that of the associated green microalgae.

The use of DNA sequence data and phylogenetic methods has largely contributed to the idea that cosmopolitan genera often show locally differentiated subgroups or cryptic species, which can be influenced by ecological factors and may be restricted to isolated areas (Branco et al. 2015; Kraichak et al. 2015; Leavitt et al. 2011; Lumbsch and Leavitt 2011; Walser et al. 2005). Lichens, as well as non-lichenized fungi, with an arctic-alpine distribution in the northern hemisphere are, however, a notable exception to this pattern, often comprising relatively homogenous genetic entities, mostly at the species level, with widespread distributions. A number of studies, such as those on *Porpidia flavicunda* (Buschbom 2007), *Flavocetraria cucullata* and *F. nivalis* (Geml et al. 2010) as well as for several different types of fungi (Geml 2011), indicate continuing intercontinental gene-flow in species that are present in both the northern and southern hemispheres. However, trans-equatorial dispersal is less frequently shown for other, similar lineages, such as the lichenized-fungal genus *Lichenomphalia* (Geml et al. 2012) or the species *Cetraria aculeata* (Fernandez-Mendoza and Printzen 2013). In contrast, although the distribution of green algal photobionts of the genus *Trebouxia* extends across

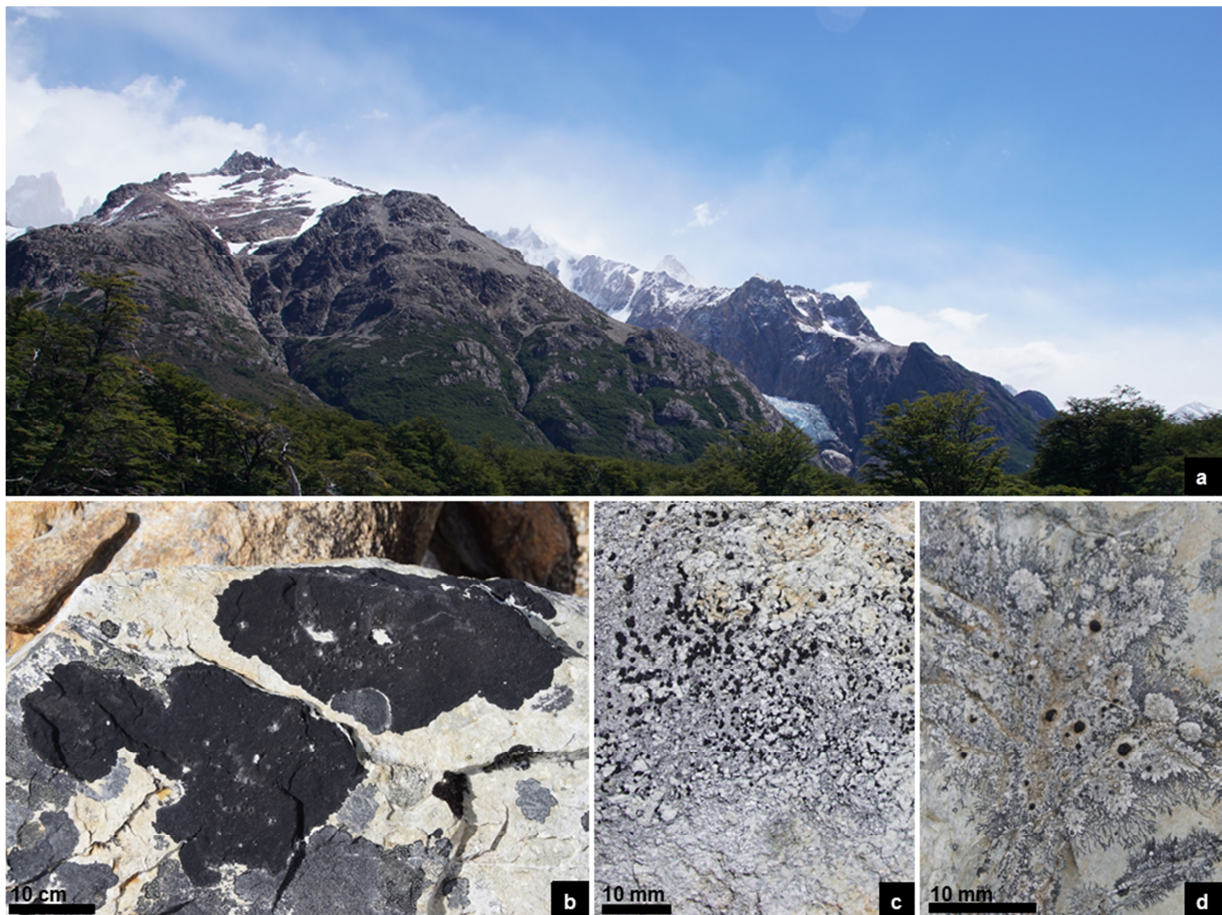
broad intercontinental regions, especially in the northern hemisphere (Leavitt et al. 2015), a pattern of trans-equatorial dispersal with low diversification is common (Muggia et al. 2010; Ruprecht et al. 2012a). However, for the mycobionts, strong diversification and endemism in the southern hemisphere is expected, resulting in the development of several distinct species and genera; for example, *Lecidea aurantia*, *L. cambellensis* (Fryday and Hertel 2014) or *L. cancriformis* (Castello 2003), *Poeltidea* (Hertel 1984), *Gondwania*, *Shackletonia* (Arup et al. 2013) and *Protousnea* (Calvelo et al. 2005). Interestingly, this does not seem to be the case for the cosmopolitan green algal genus *Trebouxia*, although one exception was found in the most extreme areas in continental Antarctica (Ruprecht et al. 2012a).

The most probable scenarios for disjunct distributions is that they can be caused (1) by vicariant history or long distance dispersal, such as for the species *Staurolemma omphalarioides*, which is known from the Mediterranean region and Norway (Bendiksby et al. 2014), (2) by transition from the Arctic to Patagonia in the Pleistocene and resulting in cryptic specialisation as shown in the bipolar lichen *Cetraria aculeata* (Fernandez-Mendoza and Printzen 2013) and (3) by glacial refugia during the last ice ages at the southern end of South America (Paula and Leonardo 2006). A good example of this is the highly differentiated and endemic lichen species *Porpidia navarina*, which is known only from one of the southernmost islands (Isla Navarino) that was ice free during the Last Glacial Maximum (Douglass et al. 2005; Ruprecht et al. 2016). (4) Finally, adaptation and subsequent specialisation to the harsh climate conditions in Antarctic cold deserts (Ruprecht et al. 2012a; Ruprecht et al. 2010; Schroeter et al. 2011) can also lead to the high local differentiation in global species and endemism in the southern Polar regions.

Lichens are ideal model-systems to test these hypotheses, because several genera and species are globally distributed and form locally differentiated subgroups (Fernandez-Mendoza et al. 2011). Additionally, at least double the information is available compared to other organisms because lichens consist of a symbiotic relationship of two or more independently distributed partners. This main symbiotic relationship is formed by a fungus (mycobiont) and green algae and/or cyanobacteria (photobiont). Additionally, a diverse community of associated bacteria (Aschenbrenner et al. 2016; Grube et al. 2015), algae (Moya et al. 2017; Peksa and Skaloud 2011; Ruprecht et al. 2014), endolichenic or lichenicolous fungi and basidiomycete yeasts (Arnold et al. 2009; Lawrey and Diederich 2003; Spribille et al. 2016) are part of the lichen thallus.

This study focuses on the geographically isolated, tapering southern end of the South American continent (southern Patagonia, including the islands around Tierra del Fuego and Cape Horn). Due to climatic conditions equivalent to Maritime Antarctica, the southern subpolar region (or subantarctic subregion), which is characterized by an absence of arboreal vegetation (Brummitt 2001; Morrone 2000) is included as part of the Antarctic floral kingdom (Takhtajan and Cronquist 1986). The subantarctic subregion extends northwards through the continent at increasing elevations along the mountain ranges of the southern Andes (Morrone 2000). To the south, Maritime Antarctica is the closest landmass, separated by about 900 km of ocean and the Antarctic Circumpolar Current (Allison et al. 2010; McCave et al. 2014). These areas are colonized by specialized cold-adapted organisms, which often act as pioneer vegetation (Bilovitz et al. 2015; Caccianiga and Andreis 2004; Hertel 1984). Among other organisms, the globally distributed saxicolous lecideoid lichens are one of the most

frequent vegetation types, forming diverse communities on rocks and boulders, mainly in treeless areas above a temperate rainforest (Fig. 1; Goffinet et al. 2012; Hertel 2007; Ruprecht et al. 2016). In the current study, the generic phylogenetic classification of the two dominant symbionts (myco- and photobiont), along with their distribution and diversification along climate gradients, were re-evaluated with three marker datasets for each symbiont based on several phylogenetic methods (distance, model based and bGMYC). To accomplish this, both symbionts of saxicolous lecideoid lichen specimens from sSA were placed in a global context using sequence information from the first author's project framework, from collaborating partners and from official databases (e.g. GenBank). Additionally, newly generated sequences of species that had previously only been described morphologically were included, as well as sequences of uncertain application in the genera *Lecidea* s. str. (Hertel 1984), *Porpidia*, *Poeltidea*, *Lecidella* (mycobiont) and *Asterochloris* and *Trebouxia* (photobiont).



**Figure 1:** a) Classical subantarctic subregion above tree level: Parque Nacional Los Glaciares, Argentina; (b) saxicolous crustose lichens on siliceous rock: *Lecidea auriculata*, *L. kalbii*, *Poeltidea perusta*, *Rhizocarpon geographicum*; (c) *Lecidea lapicida*; (d) inc. sed. *Poeltidea* sp. 1.

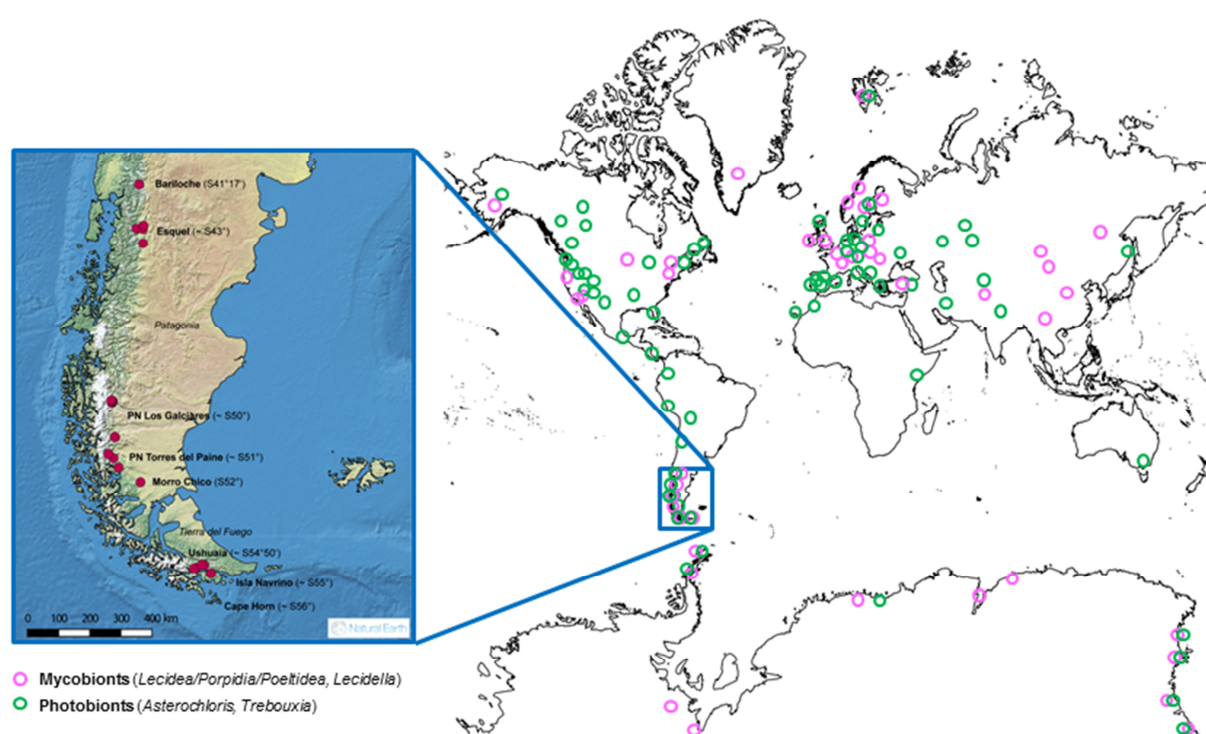
## Material and Methods

### Collecting sites and material

One hundred and eighty five saxicolous lecideoid lichen samples were collected in southern South America along a latitudinal gradient following the subantarctic climatic subregion by increasing elevation from south (Cerro Bandera, Isla Navarino, CL, S55°, 620 m a.s.l.) to north (Cerro Catedral, Bariloche, AR, S41°, 2100 m a.s.l.) and including some areas at a lower elevation in southern Chile.

The specimens were collected from siliceous rock in areas above the treeline that were dominated by subantarctic climatic conditions with an annual mean temperature (BIO<sub>1</sub>) of 0 to 7.8 °C and an annual precipitation (BIO<sub>12</sub>) of 320 to 1640 mm (Karger et al. 2017; Fig. 2, Table S1 & S2).

All our specimens collected from southern South America (sSA) are deposited in the Herbarium of the University of Salzburg (SZU).



**Figure 2:** World map showing the locations of the included accessions obtained from Genbank and our own database. Pink circles show the collecting points of the mycobiont and green circles of the photobiont accessions. The enlarged map in color shows the sampling sites from this study in southern South America.

### DNA amplification and sequencing

Total DNA was extracted from individual thalli by using the DNeasy Plant Mini Kit (Qiagen) according to the manufacturer's instructions. The PCR mix contained 0.5 units of GoTaq DNA polymerase, 0.2 nM of each of the four dNTPs, 0.3 μM of each primer and about 1 ng genomic DNA.

For each symbiont, three markers were amplified and sequenced with the primers presented in Table S3 with conditions as described in Ruprecht et al. (2014) and Ruprecht et al. (2016). Unpurified PCR-products were sent to Eurofins Genomics/Germany for sequencing.

**Mycobiont:** The internal transcribed spacer region of the nuclear ribosomal DNA (ITS) was amplified for all specimens. Furthermore, the mitochondrial small subunit (mtSSU) and the large subunit of DNA-dependent RNA polymerase 2 (RPB1) were amplified for the *Lecidea/Porpidida/Poeltidea* group.

**Photobiont:** To get a first overview of the different taxa at species and/or genus level of the associated green microalgae available to the mycobiont, a broad screening along the internal transcribed spacer region of the nuclear ribosomal DNA (ITS) was performed as described in Ruprecht et al. (2016). Additionally, for *Trebouxia* a chloroplast marker, a variable protein-coding gene including an intergenic spacer region (psbJ-L), and a fragment of the mitochondrial cytochrome oxidase subunit 2 gene (COX2) were chosen. Additionally, all three markers were sequenced from four *Trebouxia* cultures (2×S02/Antarctica, A02/Antarctica and A12/Sweden; Table S2d) provided by S. Ott (Düsseldorf), to calibrate the concatenated dataset.

### **Phylogenetic analyses**

Sequences were assembled and edited using Geneious Pro 6.1.8 ([www.geneious.com](http://www.geneious.com)), and aligned with MAFFT v7.017 (Kato et al. 2002) using preset settings (algorithm: auto select, scoring matrix: 200PAM/k=2 and gap open penalty: 1.34 – 0.123).

Maximum likelihood analyses (ML) were performed using the program IQ-TREE web server (Trifinopoulos et al. 2016) with default settings (Ultrafast bootstrap analyses, 1000 BT alignments, 1000 max. iterations, min correlation coefficient: 0.99, SH-aLRT branch test with 1000 replicates) and presented as a consensus tree. The respective evolutionary models were selected with the implemented model finder (Kalyanamoorthy et al. 2017) of the program IQ-TREE (Table S4).

The Bayesian phylogenies were inferred using the Markov Chain Monte Carlo (MCMC) procedure as implemented in the program MrBayes 3.2. (Ronquist and Huelsenbeck 2003). The analysis was performed assuming the general time reversible model of nucleotide substitution including estimation of invariant sites and a discrete gamma distribution with six rate categories (GTR + I +  $\Gamma$ ; Rodriguez et al. 1990). Two runs with 5 million generations each starting with a random tree and employing 4 simultaneous chains were executed. Every 1,000th tree was saved into a file. Subsequently, the first 25% of trees were deleted as the "burn in" of the chain. A consensus topology with posterior probabilities for each clade was calculated from the remaining 3,751 trees. The phylogenies of the mycobiont of the *Lecidea/Porpidia/Poeltidea* group were rooted with *Farnoldia jurana* subsp. *jurana*, and for *Lecidella* with species of the closely related genera *Lecanora*, *Rhizoplaca* and *Carbonea*, whereas the algal phylogenies were midpoint rooted. All phylogenies were visualized with the program Figtree v1.4.3 (Rambaut 2014).

### **OTU- and cluster delimitation**

For each phylogenetically coherent group (*Lecidea/Porpidia/Poeltidea*, *Lecidella*, *Asterochloris* and *Trebouxia*) the ITS marker was used to generate OTUs using ABGD (Puillandre et al. 2012). The default settings were used, except 'X' (relative gap) at 0.9 and the distance JC69 were chosen. OTUs with a sequence similarity lower than 97.5% were divided to subunits using phylogenetic criteria based on Leavitt et al. (2015) for *Trebouxia* (Table S5).

An alternative cluster delimitation was done by using GMYC models (Reid and Carstens 2012) on the ITS phylogeny *Lecidea/Porpidia/Poeltidea*. Time calibrated phylogenetic reconstructions were carried out in Beast2 (Bouckaert et al. 2014) using the same model settings as for the Bayesian analyses (GTR + I +  $\Gamma$ ; Rodriguez et al. 1990) as starting conditions. The suitability of a molecular clock was

assessed using the tests implemented in MEGA. The bGMYC method was carried out using the most conservative approach, enforcing a strict clock and a constant size single population prior, thus decreasing the chances of introducing spurious clusters caused by an overfitting the phylogenetic reconstructions.

A maximum clade credibility tree was calculated in treeannotator (Bouckaert et al. 2104) using substitute by: most recent common ancestor (mrca) weights. We used a recursive multi-tree approach implemented in the R package bGMYC (Reid & Carstens 2012) to incorporate phylogenetic uncertainty. The GMYC analysis was iteratively run on a subset of 200 randomly chosen trees using a chain length of 50,000 sampling steps, a burn-in of 40000 and a thinning parameter of 100. The results of all GMYC analyses are summarized in a matrix of pairwise co-assignment probabilities for each haplotype. To obtain a consensus partition making use of k-medoids clustering (Kaufman and Rousseeuw 1990) and optimum average silhouette width to estimate the optimum number of clusters as used in (Ortiz-Alvarez et al. 2015). For the latter we used function *pamk* as implemented in R package *fpc* (Henning 2014) on the co-assignment matrix converted into its dissimilarity correlate.

## Results

### **Phylogenetic analyses, OTU and cluster delimitation**

Four overall phylogenies for the saxicolous genera *Lecidea/Porpidia/Poeltidea* (Lecideaceae), *Lecidella* (Lecanoraceae), *Asterochloris* and *Trebouxia* (Trebouxiophyceae) using the marker ITS were calculated (Figs. 3 - 6). Additionally, two multi-marker trees for *Lecidea/Porpidia/Poeltidea* (ITS/mtSSU/RPB1; Fig. S1) and *Trebouxia* (ITS/psbJ-L/COX2; Fig. S2) were also calculated.

In all cases the ML analyses (IQ-TREE web server; Trifinopoulos et al. 2016) of the six phylogenies recovered the same tree topology as the MrBayes analysis (Ronquist & Huelsenbeck 2003). Therefore, we only present here the Bayesian tree with support values of the ML analyses.

For the multi-marker trees no conflict was found with the single marker trees, thus they are not shown. OTU scores with a sequence similarity higher than 97.5 % were calculated for groups with at least three accessions and are summarized in Table S5.

The assignment of uncertain accessions to mycobiont-species or subspecies was also based on morphological data, but these data are not included here.

***Lecidea/Porpidida/Poeltidea* - ITS (Fig. 3):** This molecular phylogeny includes all relevant taxonomically identified sequences of the genera *Lecidea*, *Porpidia*, *Poeltidea* and *Cylcohymania* provided by the project framework of the first author or downloaded from the NCBI database (GenBank) to bring the newly generated sequences of this study into a global context. The final data matrix for the phylogeny comprised 192 single sequences of the marker nrITS with a length of 593 characters and includes sequences of specimens of the genera *Lecidea* (144) *Porpidia* (42), *Poeltidea* (3), *Cylcohymania* (2) and was rooted with *Farnoldia jurana* subsp. *jurana* as outgroup.

The phylogenetically delimited groups revealed were assigned to OTU-, species-, cluster- and genus level.

All three analyses (distance-, model based and bGMYC) showed similar topologies, but at different levels. The groups gained with distance approach (OTUs) were used to show the intraspecific and/or the cryptic speciation; model based approaches were used for the assignment at species level and the clusters based on the bGMYC were used for grouping of closely related species or dividing highly heterogeneous species.

Altogether, 110 (*Lecidea*: 77; *Porpidia*: 31; *Cyclohymeria*: 1; *Poeltidea*: 3) OTUs were classified. These OTUs were assigned to species, including groups of subspecies and clusters (*Lecidea*: 20; *Porpidia*: 7; *Cyclohymeria*: 1; *Poeltidea*: 2).

The backbone of this phylogeny is not supported, but at least four main groups can be recognized. The first group, with low support, is formed solely by species of the genus *Lecidea* s. str. However, it can be considered a consistent group, because it is strongly supported by the three-marker phylogeny (Fig. S1). The southern hemisphere lineage (*P. navarina*) is situated outside the *Lecidea* group and next to the second group, which is an intermixed group of *Lecidea* and *Porpidia* species with two weakly supported accessions of the genus *Cyclohymeria* at the base. The third group is solely formed by species of the genus *Porpidia* and the fourth by the southern hemisphere genus *Poeltidea*.

The *Lecidea* group forms 17 clusters. The well supported, heterogeneous and cosmopolitan species cluster L01 (*L. atrobrunnea* subsp.) is sister to the well supported and diverse cluster L02 (inc. sed. *L.* sp. 1/endemic to sSA, *L. promiscens*/cosmopolitan and *L. swartzioidea*/northern hemisphere). Cluster L03 (inc. sed. *L.* sp. 2) forms a highly supported and very homogenous clade, comprising specimens from Antarctica, the Arctic and sSA. An unidentified specimen from continental Antarctica (T8883b) and an Arctic specimen of *L. protabacina* form clusters L04 and L05.

Cluster L06 includes *L. confluens* and an accession from Genbank (*Porpidia speirea*; Schmull et al. 2011). The placement of this latter accession in the *Lecidea* s. str. group could be caused by an incorrect species assignment (*Lecidea confluens* and *P. speirea* are morphologically quite similar and mainly distinguished by the ascus-type), or an uncertain species concept. The latter seems to not be the case, because two accessions of *P. speirea* from China were included in the phylogeny and are part of cluster P02, which agrees with the findings of Buschbom and Mueller (2004), who described this species as closely related to *P. tuberculosa*, which was confirmed in this phylogeny. Cluster L07 includes species related to *L. laboriosa* (northern hemisphere), such as the Antarctic and Chinese species *L. polypycnidophora* the bipolar *L. andersonii* and the Antarctic *L.* sp. UCR1. The Californian specimen of *Lecidea violascens* and an undetermined specimen from the Austrian Alps (*L.* sp. UR00280) are also part of this cluster.

Several well distinguished species form strongly supported clusters, such as the variable accessions from the northern hemisphere and maritime Antarctica of *L. silacea* subsp. together with an unidentified specimen from sSA (*L.* sp. UR00130) and *L. fuscoatrina* (cluster L08), followed by the northern hemisphere species *L. leucothallina* and *L. obluridata* (cluster L09). *Lecidea plana* (northern hemisphere; cluster L10) and *L. lithophila* (northern hemisphere, maritime Antarctica; cluster L11) form a highly supported clade.

Two recently newly described species, *Lecidea aptrootii* (Khan et al. 2018) and *L. uniformis* (McCune et al. 2017) are molecularly very closely related to the accession of *L. fuscoatra* var. *grisella* (Zhao et al. 2016), a taxon which was recognized by Aptroot & Van Herk (2007) at the species level as *L.*



*grisella*. Together with *L. fuscoatra* they form the strongly supported cluster L12. This cluster is sister to cluster L13, which includes the Antarctic and, so far, endemic species *L. cancriformis* and a closely related, but heterogeneous subspecies group (*L. cancriformis* subsp.) from sSA. Another new and endemic species from sSA (inc. sed. *L. sp. 4*), forms the highly supported cluster L14.

Cluster L15 is formed by the very common, heterogeneous and cosmopolitan species group *L. lapicida* subsp. (including the cosmopolitan *L. lapicida* var. *pantherina*) and is sister to the northern hemisphere cluster L16, which consists of *L. lapicida* var. *lapicida*. These subspecies show no morphological differentiation and are separated only by their different chemotypes, but have according to Hertel (1995) different ecological requirements. The now cosmopolitan species *L. medusula*, previously only reported for the southern hemisphere (Fryday & Hertel 2014) forms cluster L17 with specimen from sSA, the Arctic and the Austrian Alps at the base of this clade. The species included in this group are part all referable to *Lecidea* s. str. (Hertel 1984).

The second group, which contains species of the genera *Lecidea* s. str. and *Porpidia*, is highly supported with the newly described species/genus *Cyclohymania epilthica* (cluster C01) basal to the group, although with weak support. It is formed by two well-known and cosmopolitan species *L. tessellata* and *L. auriculata* (cluster L18 & L19) and the southern hemisphere *L. kalbii* (cluster 20) as well as a well-supported, northern hemisphere group of *Porpidia* species including *P. speirea*, *P. tuberculosa*, *P. melinodes* and *P. flavicunda* (cluster P02, P03) and other closely related species: *P. hydrophila*, *P. rugosa*, *P. degelii* and *P. albocaerulescens* (cluster P04).

However, species of the genus *Porpidia* are clearly distinguishable morphologically from species of *Lecidea*, by their ascus type and additionally by the associated green microalgae of the genus *Asterochloris* (Wirth et al. 2013; Ruprecht et al. 2016).

The third group is formed by three clusters of *Porpidia* species and is divided into two well supported main subgroups. One is formed by cluster P05 including the cosmopolitan species inc. sed. *P. sp. 1* subsp. together with *P. cinereoatra*, *P. contraopenda*, *P. musiva*, *P. irrigua*, inc. sed. *P. sp. 2* and *P. striata*. *Porpidia islandica* forms the highly supported cluster P06. The other strongly supported subgroup is formed by the heterogeneous and cosmopolitan cluster P07, including *P. flavocruenta*, *P. macrocarpa* subsp. and *P. macrocarpa*, the quite differing accessions from Turkey and China that were identified as *P. crustulata* and the inc. sed. *P. sp. 3*.

The genus *Poeltidea*, which occurs only in the southern hemisphere, forms clade IV and consists of two clusters, POE01 (*P. perusta*) and POE02 (inc. sed. *P. sp. 1*).

**Note:** The family *Porpidaceae* was included in the synonymy to *Lecideaceae* (Lecideales) by Lumbsch & Huhndorf (2010), which is still the case in the current issue of *Outline of Ascomycota: 2017* (Wijayawardene et al. 2018). The investigated genera *Lecidea* s. str. (Hertel 1984), *Porpidia*, *Poeltidea* as well as *Cyclohymania* and *Farnoldia* are all assigned to this family, although *Farnoldia* appears to occupy a peripheral position.



***Lecidea/Porpidida/Poeltidea* - ITS/mtSSU/RPB1 (Fig. S1):** The final data matrix of this phylogeny contains 204 concatenated sequences of the markers ITS, mtSSU and RPB1 with a length of 2115 characters and includes sequences of specimens of the genera *Lecidea*, *Porpidia* and *Poeltidea* and was rooted with *Farnoldia jurana* subsp. *jurana* as outgroup. Specimens from the project framework of the first author (Antarctica, Arctic, Austria) with the same three markers were added.

All available sequences of this study were included to show the abundance of the different specimens in the studied areas of sSA. The phylogenetically delimited groups revealed were assigned to OTU-, species-, and genus level. Additionally, the distribution of the OTUs is shown beside the genus information.

This multi-marker phylogeny is not fully comparable to the overall single marker (ITS) phylogeny of *Lecidea/Porpidida/Poeltidea* because of the limited availability of sequences of the chosen markers in GenBank. The topology is, in most cases, similar and it forms the same four groups, but in many cases, they show greater support. The *Lecidea* group, at least, is strongly supported in this phylogeny. Because of the limited availability of *Porpidia* sequences in GenBank, the topology of this group is slightly different with *P. navarina* clustering together with *P. cinereoatra* and *P. macrocarpa*, but with low support.

Finally, the genus *Poeltidea* with two species is still at the base of this phylogeny.

The OTUs obtained from the ITS sequences are still very well supported. Many clades show clearly a local differentiation at OTU level and are endemic to sSA. The two largest clades (OTUs Lcd58 and Lcd62) are part of the cosmopolitan *L. lapicida* cluster and are the most abundant accessions. These are followed by *Porpidia navarina* and inc. sed. *Lecidea* sp. 1 (both species endemic to sSA), *L. promiscens* (cosmopolitan species group) and other smaller groups.

***Lecidella* - ITS (Fig. 4):** To bring the new accessions of *Lecidella* from sSA into a global context, the species concept and most of the published accessions of Zhao et al. (2015) were used. Additionally, to this dataset several sequences from Genbank and from the project framework of the first author were added. The final data matrix of this phylogeny contains 76 sequences of the marker ITS with a length of 538 characters and was rooted with species of the genera *Carbonea*, *Lecanora* and *Rhizoplaca* to obtain well-defined units in the genus *Lecidella*.

The backbone of the phylogeny is unresolved, but four strongly supported main clades are formed; three (*L. enteroleucella*, *L. stigmatea* and *L. elaeochroma*) are the same as those identified by Zhao et al. (2015) plus a fourth clade (*L. sp. nova*) with two species only occurring in Antarctica and sSA. All available sequences for this group were included to show the abundance of the different accessions. The phylogenetically delimited groups revealed were assigned to OTU-, clade-, and genus level. Additionally, the global distribution of the locally differentiated OTUs is shown beside the genus information.

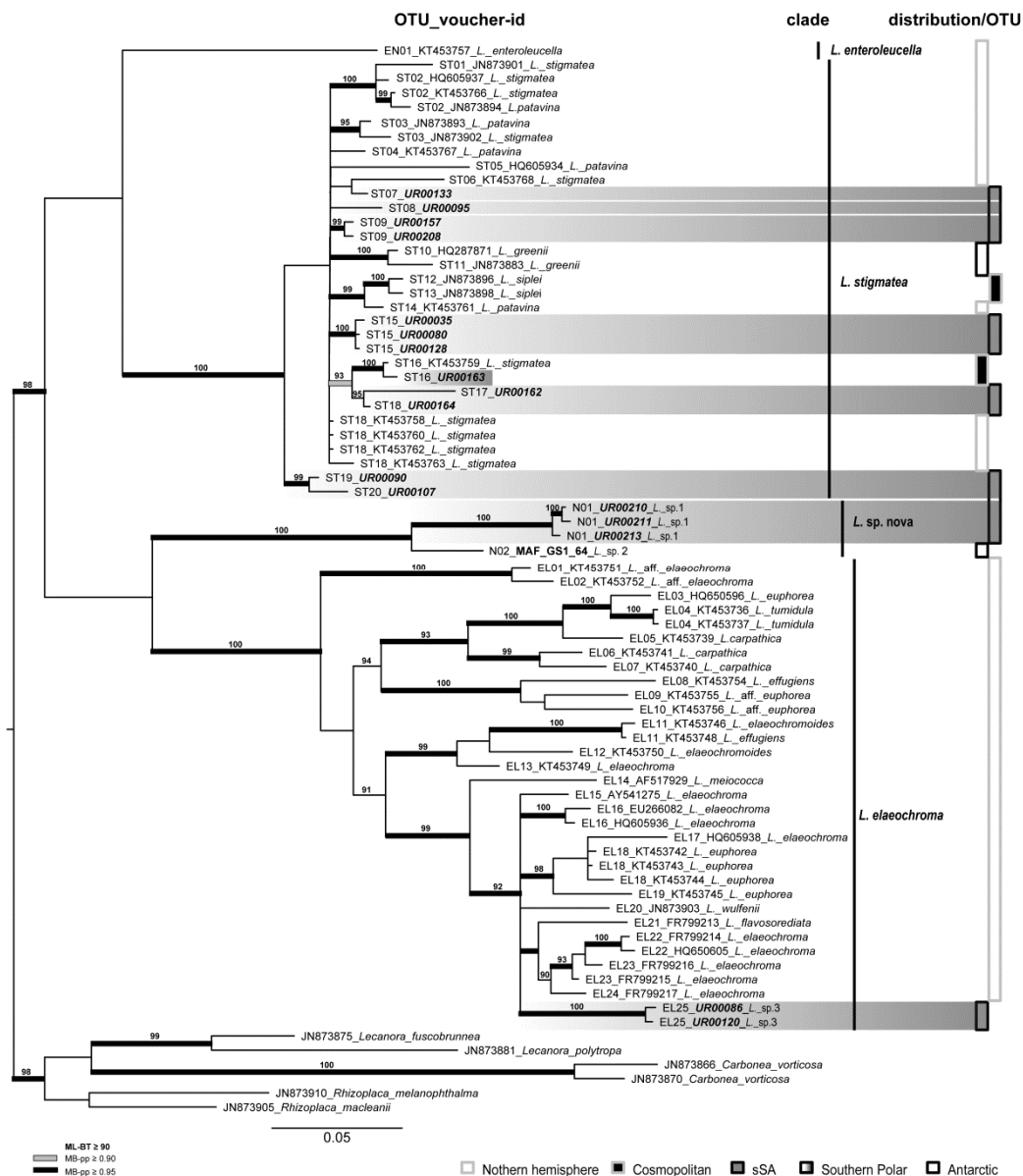
*Lecidella enteroleucella* is still the only member of the first clade.

The second clade (*L. stigmatea*) is completely unresolved. *Lecidella patavina* and *L. stigmatea* are intermixed and not assignable. These two species differ most noticeably in that the hymenium of *L. patavina* is interspersed with oil droplets, whereas that of *L. stigmatea* is not. That the accessions of

these two species are intermixed perhaps indicates that either only one species is involved or that the defining character has been interpreted inconsistently. *Lecidella greenii* and *L. siplei* form well supported lineages and the 12 sequences of the species in this study show a clear local differentiation at OTU level.

A third, new and strongly supported, clade (*L. sp. nova*) shows two new species from sSA (*L. sp. 1*) and continental Antarctica (*L. sp. 2*).

The fourth clade (*L. elaeochroma*) shows a few separated and well supported species (*L. tumidula*, *L. meiococca*, *L. wulfenii*, *L. flavosorediata* and *L. sp. 3*, which is endemic to sSA). *Lecidella elaeochroma*, *L. euphorea*, *L. carpathica*, *L. elaeochromoides* and *L. effugiens* are not assignable because of mingling in different highly supported lineages. None of the investigated specimens were morphologically similar to the southern hemisphere species *Lecidella sublapicida* (Knoph & Leuckert 1994).



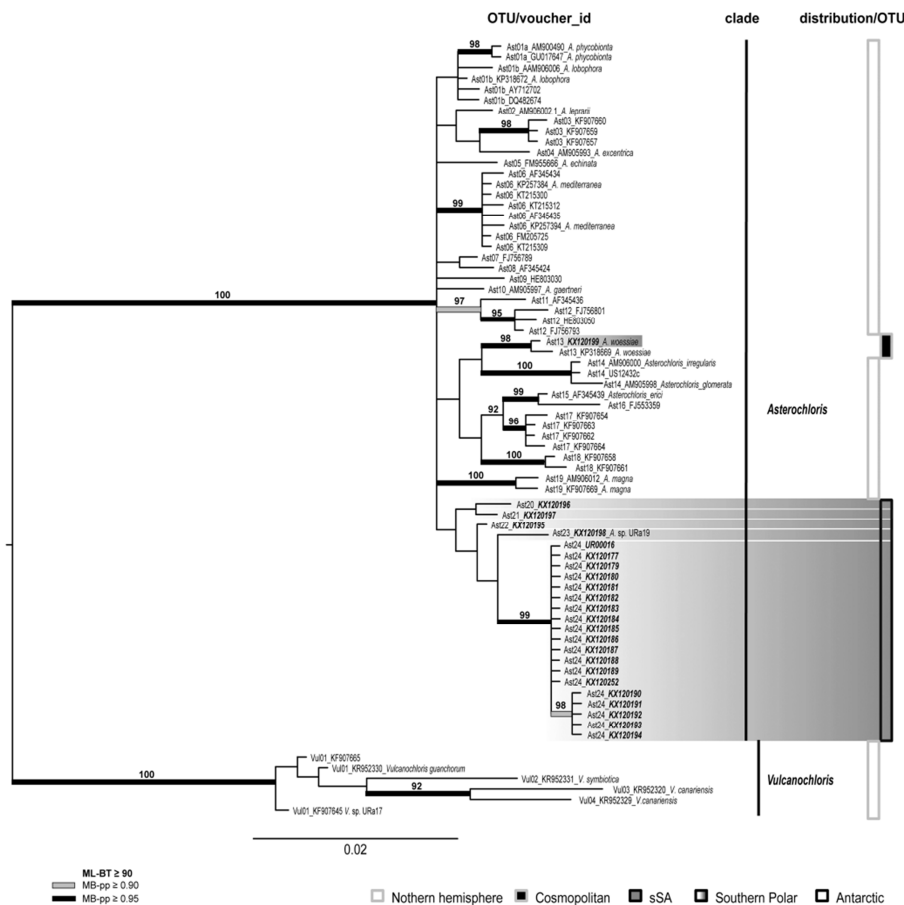
**Figure 4:** Phylogeny of the genus *Lecidella* with accessions from sSA integrated in the species concept and most of the published accessions (Zhao et al. 2015) using the **marker ITS**. Voucher information is preceded by the OTU number. The bars beside the phylogeny show the affiliation to clades and distribution. sSA accessions are highlighted in grey and those restricted to sSA on OTU-level, with a full-length bar. The bootstrap values with  $\geq 95$  support of ML analyses were directly mapped on the Bayesian tree with  $\geq 0.90$  (gray) and  $\geq 0.95$  (black) support posterior probability values (branches in bold).

**Asterochloris** - ITS (Fig 5): All the *Porpidia* species in this study are not only associated with *Trebouxia* as photobiont, but also with a green microalgae of the genus *Asterochloris*. The accessions obtained from sSA were brought into a global context by adding all relevant taxonomically identified sequences from GenBank and from the project framework of the first author. The final data matrix of this phylogeny contains 73 sequences of the marker ITS with a length of 519 characters.

The phylogeny was rooted midpoint and divided into two main clades (genera), *Asterochloris* and *Vulcanochloris*. The accessions from sSA occur only in the *Asterochloris* clade. The backbone of this clade is unresolved. Again, all available sequences for this group are included to show the abundance of the different accessions. The phylogenetically delimited groups revealed were assigned to OTU-, clade-, and genus level. Additionally, the global distribution of the locally differentiated OTUs is shown beside the genus information.

The topology of the species from GenBank show a similar pattern to that already described in Ruprecht et al. (2014).

Only one accession from sSA clusters together with the cosmopolitan species *A. woessiae*. A highly supported and homogeneous clade is formed by 19 specimens (*A. sp.* URa18) only occurring on Isla Navarino and one accession from the other side of the Beagle channel (Tierra del Fuego) in the southernmost part of sSA. Four other accessions (*A. sp.* URa19, *A. sp.* URa20, *A. sp.* UR00027 and *A. sp.* UR00123) are placed in the main group with low support.



**Figure 5:** Phylogeny of the genus *Asterochloris* including all available relevant taxonomically identified sequences using the marker ITS. Voucher information is preceded by the OTU number. The bars beside the phylogeny show the affiliation to genera and distribution. sSA accessions are highlighted in grey and those restricted to sSA on OTU-level, with a full-length bar. The bootstrap values with ≥ 95 support of ML analyses were directly mapped on the Bayesian tree with ≥ 0.90 (gray) and ≥ 0.95 (black) support posterior probability values (branches in bold).

**Trebouxia - ITS (Fig. 6):** To bring the new accessions of *Trebouxia* from sSA into a global context, the species/OTU concept and the dataset reduced to one accession of each OTU of Leavitt et al. (2015) was used. Additionally, several new sequences from GenBank and from the project framework of the first author were added to this dataset. The final data matrix of this phylogeny contains 159 sequences of the marker ITS with a length of 803 characters and was midpoint-rooted.

The phylogenetically delimited groups revealed were assigned to OTU- and clade level as described in Leavitt et al. (2015).

The backbone of the phylogeny is unresolved, but five strongly supported main clades were formed; four clades (I, A, G and S) correspond to those of Leavitt et al. (2015) plus a fifth clade (N) with three specimens only occurring in sSA on Isla Navarino and on the north side of the Beagle channel at Tierra del Fuego.

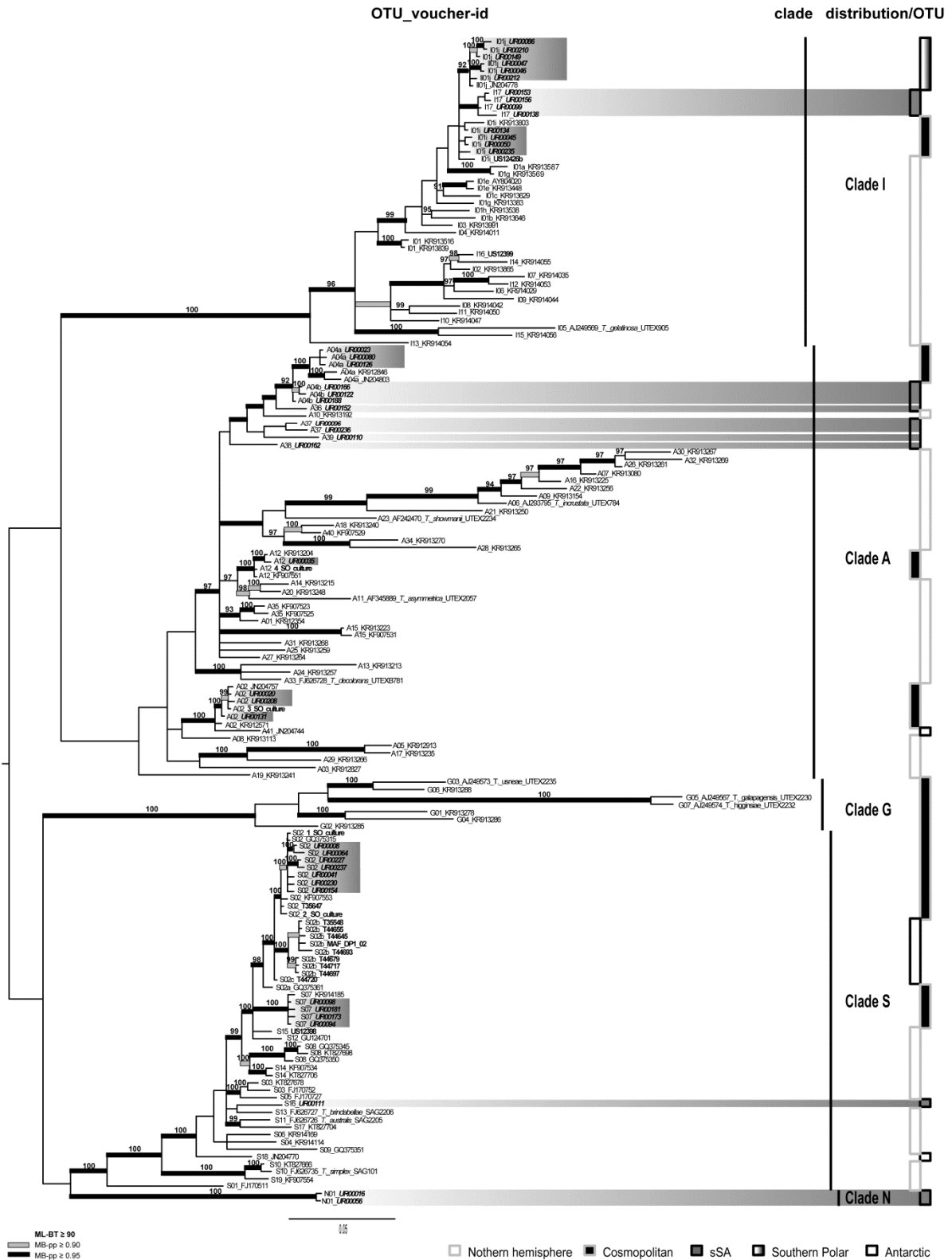
Three different groups were formed by accessions assigned to Clade I. Because of a sequence similarity below the threshold of 97.5 % the subOTU I01i was divided into two subunits (I01i, I01j) with a cosmopolitan and southern Polar distribution, plus an independent OTU I17 solely occurring in sSA. Due to the addition of the diverse accessions from sSA to the existing OTU I01, which already has 10 subOTUs (I01, I01a – i) described by Leavitt et al. (2015), most of them were transferred into distinct OTUs. However, these have not been renamed here, as this is an open system and a regrouping with new accessions is expected in the future.

Altogether, clade A includes 39 OTUs with the specimens of this study forming part of two cosmopolitan (A02, A04) and four locally differentiated (A36 - A39) OTUs. A04 has a sequences similarity of 96.7% and was subdivided in two subunits (A04a, A04b).

Fifty percent of the sSA accessions of this marker are contained in the cosmopolitan OTUs S02 and S07 of clade S. S02 was subdivided into four subunits with the accessions from sSA only being assigned to S02 together with northern hemisphere specimens. S02b is solely formed by specimen from continental Antarctica, a similar finding was described in Ruprecht et al. (2012a; *T. jamesii* subsp. is equivalent to S02b in this study). Another strongly supported OTU (S16) consists only of accessions from sSA.

The new and highly supported clade N appeared with two haplotypes (three accessions), all of which are located at the southernmost part of sSA.

No accession from this study is part of clade G.



**Figure 6:** Phylogeny of the genus *Trebouxia* with accessions from SSA integrated in to the species concept and most of the published accessions of Leavitt et al. 2015 using the marker ITS. Voucher information is preceded by the OTU number. The bars beside the phylogeny show the affiliation to the clades. sSA accessions are highlighted in grey and those restricted to sSA on OTU-level, with a full-length bar. The bootstrap values with  $\geq 95$  support of ML analyses were directly mapped on the Bayesian tree with  $\geq 0.90$  (gray) and  $\geq 0.95$  (black) support posterior probability values (branches in bold).

**Trebouxia - ITS/psbJ-L/COX2 (Fig. S2):** The data matrix of this phylogeny contains 217 concatenated sequences of the markers ITS, psbJ-L and COX2 with a length of 1693 characters. Only sSA specimens are included to demonstrate the intraspecific differentiation. This dataset was calibrated with four cultured *Trebouxia* specimens (Table S2d, 2×S02/Antarctica, A02/Antarctica and A12/Sweden). Interestingly, the psbJ-L sequences of A02 of the cultured specimen from Antarctica are different to the North American specimen from Leavitt et al. (2015).

The dataset still shows the same number of OTUs as the ITS phylogeny (Fig. 6) and the grouping is the same. Clade A shows nine well supported groups at species level (A02, A12, A38, A39, A04a, A04b, A36, A37) with A36 and A04b being closely related. Interestingly, the subOTUs A04a and A04b are more separated with the marker psbJ-L than in the ITS phylogeny.

Clade I is divided into two subOTUs (I01i, I01j) and one newly developed distinct OTU (I17) because of its heterogeneous structure. No COX2 sequences were included, because they were not assignable.

More than half of the sequences are included in the homogenous and cosmopolitan OTUs S02 and a smaller part in S07. These groups are closely related and share similar COX2 sequences. The OTU S16, which occurs only in sSA, is clearly separated at species level from S02 and S07.

The new clade N is still strongly supported in this dataset, but basal to clade S.

### **Distribution of species and OTUs: globally distributed vs. restricted to sSA and/or southern Polar regions**

Altogether, 185 mycobiont specimens forming 54 OTUs assigned to 24 species of the genera *Lecidea*, *Porpidia*, *Poeltidea* and *Lecidella* were identified.

Four species of the genus *Lecidea* (inc. sed. *L. sp. 2*, *L. auriculata*, *L. medusula*, *L. tessellata*) and *Porpidia macrocarpa* are globally distributed at species and OTU level.

By far the most abundant accessions are formed by locally differentiated OTUs (Lcd58, Lcd62; 48 accessions) and belong to the cosmopolitan cluster *Lecidea lapicida* (L15), with the next most frequent groups being *Lecidella stigmatea* (13) and *Lecidea promiscens* (9). Finally, altogether 13 species or single sequences are so far only described and/or known from sSA or the southern Polar regions (Table 1, Figs. 3, S1 & 4).

**Table 1:** Mycobiont distribution of species and OTUs. Species and OTUs with different distributions (globally/sSA) are marked in bold.

species - distribution		n	OTU - distribution	
inc. sed. <i>Lecidea sp. 2</i>	globally	8	LP_Lcd15	globally
<i>Lecidea auriculata</i>	globally	13	LP_Lcd72	globally
<i>Lecidea medusula</i>	globally	3	LP_Lcd70	globally
<i>Lecidea tessellata</i>	globally	3	LP_Lcd71	globally
<i>Porpidia macrocarpa</i>	globally	4	LP_Porp27	globally
<b>Subtotal</b>	<b>5</b>	<b>31</b>		<b>5</b>
<b><i>Lecidea atrobrunnea</i> subsp.</b>	<b>globally</b>	<b>5</b>	<b>LP_Lcd01, 05</b>	<b>southern polar</b>
<b><i>Lecidea lapicida</i> subsp.</b>	<b>globally</b>	<b>48</b>	<b>LP_Lcd58, 62, 68</b>	<b>sSA</b>
<b><i>Lecidea promiscens</i> subsp.</b>	<b>globally</b>	<b>9</b>	<b>LP_Lcd09 - 11</b>	<b>sSA</b>
<b><i>Lecidella stigmatea</i></b>	<b>globally</b>	<b>13</b>	<b>LL_ST07, 08, 09, 15 - 20</b>	<b>sSA</b>
<b>inc. sed. <i>Porpidia sp. 1</i> subsp.</b>	<b>globally</b>	<b>5</b>	<b>LP_Porp11, 12</b>	<b>sSA</b>
<b><i>Porpidia macrocarpa</i> subsp.</b>	<b>globally</b>	<b>2</b>	<b>LP_Porp21, 24</b>	<b>sSA</b>
<b>Subtotal</b>	<b>6</b>	<b>81</b>		<b>21</b>



inc. sed. <i>Lecidea</i> sp. 1	sSA	8	LP_Lcd08a, 08b	sSA
inc. sed. <i>Lecidea</i> sp. 3	sSA	4	LP_Lcd25, 26	sSA
inc. sed. <i>Lecidea</i> sp. 4	sSA	8	LP_Lcd53 - 56	sSA
inc. sed. <i>Lecidella</i> sp. 1	sSA	3	LL_N01	sSA
inc. sed. <i>Lecidella</i> sp. 3	sSA	2	LL_EL25	sSA
inc. sed. <i>Poeltidea</i> sp.1	sSA	3	LP_Poe03	sSA
<i>Lecidea cancriformis</i> subsp.	sSA	19	LP_Lcd44 – 49, 51, 52	sSA
<i>Lecidea kalbii</i>	sSA	4	LP_Lcd76, 77	sSA
<i>Lecidea</i> sp. UR00096	sSA	1	LP_Lcd57	sSA
<i>Lecidea</i> sp. UR00130	sSA	1	LP_Lcd33	sSA
<i>Lecidea</i> sp. UR00141	sSA	1	LP_Lcd75	sSA
<i>Porpidia navarina</i>	sSA	13	LP_Porp01	sSA
<i>Poeltidea perusta</i>	sSA	5	LP_Poe01, 02	sSA
<b>Subtotal</b>	<b>13</b>	<b>73</b>		<b>28</b>
<b>Total:</b>	<b>24</b>	<b>185</b>		<b>54</b>

The photobionts comprise 199 accessions that are assigned to 19 OTUs. Most of the algal specimens (125) belong to globally distributed taxa, especially Tr\_S02a with 84 accessions followed by Tr\_S07, Tr\_A02, Tr\_A12, Tr\_A04a and a single accession of *Asterochloris woessiae* from a lower elevation area close to Esquel, Argentina. The very heterogeneous OTU Tr\_I0i was divided into two sub-OTUs: I01i with a global distribution and I01j that occurs in Antarctica and sSA. OTU I17 occurs solely in sSA. A surprisingly high number of 82 accessions (*Asterochloris* and *Trebouxia*) form 13 clearly separated OTUs and were, so far, only found in sSA (Table 2, Figs. 5, 6 & S2).

**Table 2:** Photobiont distribution of species and OTUs

species	n	OTU - distribution	
<i>A. woessiae</i>	1	Ast13	globally
<i>Trebouxia</i> sp.	7	Tr_A02	globally
<i>Trebouxia</i> sp.	5	Tr_A04a	globally
<i>Trebouxia</i> sp.	6	Tr_A12	globally
<i>Trebouxia</i> sp.	5	Tr_I01i	globally
<i>Trebouxia</i> sp.	84	Tr_S02	globally
<i>Trebouxia</i> sp.	17	Tr_S07	globally
<b>Subtotal</b>	<b>125</b>	<b>7</b>	
<i>A. sp.</i> UR00027	1	Ast22	sSA
<i>A. sp.</i> UR00123	1	Ast21	sSA
<i>A. sp.</i> URa18	19	Ast24	sSA
<i>A. sp.</i> URa19	1	Ast23	sSA
<i>Trebouxia</i> sp.	6	Tr_A04b	sSA
<i>Trebouxia</i> sp.	1	Tr_A36	sSA
<i>Trebouxia</i> sp.	2	Tr_A37	sSA
<i>Trebouxia</i> sp.	4	Tr_A38	sSA
<i>Trebouxia</i> sp.	5	Tr_A39	sSA
<i>Trebouxia</i> sp.	20	Tr_I01j	southern Polar
<i>Trebouxia</i> sp.	11	Tr_I17	sSA
<i>Trebouxia</i> sp.	3	Tr_S16	sSA
<b>Subtotal</b>	<b>74</b>	<b>12</b>	
<b>Total</b>	<b>199</b>	<b>19</b>	

Summarizing, for the mycobiont the percentage distribution of accessions at OTU level shows a high rate of local differentiation and endemism for the sSA specimens vs those that are globally distributed (83:17). In particular, Parque Nacional Torres del Paine and Morro Chico with 100% each, and the southernmost sampling point, Isla Navarino with 90% have the highest amount of specialized

accessions. In contrast, the photobiont OTUs show a higher rate of globally distributed accessions (32:68). However, both symbionts show no significant specialization along the latitudinal gradient in southern South America (Table 3).

**Table 3:** Summary of investigation sites with elevation, climate variables BIO1 (annual mean temperature) and BIO 12 (annual precipitation), using CHELSA (Karger et al. 2017), and information about locally differentiated OTUs and/or endemic species.

location	latitude (°S)	altitude m a.s.l.	climate variables		locally diff. OTUs and/or endemic species to sSA (yes/no - proportional)					
			Bio 1 (°C)	Bio 12 (mm)	mycobiont		photobiont			
					n	yes	no	n	yes	no
Bariloche (AR)	41.2	2001 to 2061	1.7	1642	18	56	44	18	17	83
Esquel (AR)	42.8	1964 to 2122	1.2 to 1.4	1140 to 1180	26	69	31	26	23	77
Tecka-Corcovado (AR)	43.5	797	7.8	685	9	89	11	9	56	44
PN Los Glaciares (AR)	49.2 to 50.5	558 to 1481	0.2 to 4.1	322 to 512	43	81	19	40	32	68
PN Torres del Paine (CL)	51.1 to 51.6	118 to 324	3.9 to 6.5	545 to 818	12	100		13	38	62
Morro Chico (CL)	52	208	6.4	341	10	100		9	44	56
Ushuaia (AR)	54.7 to 54.8	407 to 794	1.6 to 4.0	489 to 756	34	76	24	35	11	89
Isla Navarino (CL)	55	607 to 741	1.9 to 3.3	628 to 739	33	90	10	52	38	62
<b>Total (mean)</b>					<b>185</b>	<b>83</b>	<b>17</b>	<b>202</b>	<b>32</b>	<b>68</b>

## Discussion

For the four re-evaluated groups *Lecidea/Porpidia/Poeltidea*, *Lecidella* (mycobiont), *Asterochloris* and *Trebouxia* (photobiont), the geographical isolated southern end of the South American continent supports a high degree of locally differentiated subclades (OTUs) in globally distributed species as well as endemic lineages at the species and genus level. This was, to some extent, unexpected for these mostly globally distributed genera and can partially be explained by the lack of sequence information for most of the southern hemisphere lecideoid mycobiont species ( Fryday & Hertel 2014; Knoph & Leuckert 1994). This also applies to the photobionts because of the limited availability of molecular studies for the southern Polar Regions (e.g. Fernandez-Mendoza *et al.* 2011; Muggia *et al.* 2010; Ruprecht *et al.* 2012a).

However, local differentiation (cryptic speciation) is quite common in lichen forming fungi (Dal Grande *et al.* 2017; Kraichak *et al.* 2015; Leavitt *et al.* 2011; Lumbsch and Leavitt 2011), but has rarely been described for the most common and widespread lichen photobiont taxa *Trebouxia* (Fernandez-Mendoza *et al.* 2011; Leavitt *et al.* 2015; Ruprecht *et al.* 2012a) and *Asterochloris* (Skaloud *et al.* 2015).

In particular, the lichen cluster (L15, Fig. 3) *Lecidea lapicida*, which occurs in polar and high mountainous regions worldwide (Hafellner and Türk 2016; Hertel 1984; Hertel and Andreev 2003), shows locally differentiated accessions at the OTU level that are endemic to sSA. Austrian and Antarctic accessions are closely related, but they are clearly distinct from the two main OTUs (Lcd58, Lcd62) that comprise 48 of the 185 sSA specimens. The heterogeneous clades of *Porpidia macrocarpa* subsp., which include specimens from Antarctica and the Austrian Alps, show a similar pattern. *Lecidea atrobrunnea* subsp. is the only exception, forming two southern polar OTUs with accessions from both Antarctica and sSA (Fig. 3). The same pattern is also known for *Usnea aurantiacoatra* (Laguna Defior 2016) and *Cetraria aculeata* (Fernandez-Mendoza *et al.* 2011). A different example is *Lecidea cancriformis*, which was, so far, described as endemic to Antarctica and is one of the dominant crustose lichens in the most extreme areas of the continent (Castello 2003;

Hertel 2007; Ruprecht et al. 2010). The Antarctic accessions belong to a single, well supported OTU (Lcd50, Fig. 3), but there are seven closely related OTUs occurring in sampling areas north of Tierra del Fuego. However, the whole cluster L13 including *L. cancriformis* subsp. remains confined to the southern Polar Regions. Several other species, as well as the genus *Poeltidea*, occur solely in the southern Polar Regions. *Lecidea medusula*, which was previously only investigated morphologically and thought to be endemic to the southern hemisphere (Hertel 2009), is shown to be a cosmopolitan species. However, in total, the cosmopolitan species/OTUs (e.g. *L. auriculata*, *L. tessellata*) are outnumbered by those that are endemic to sSA (Table 1).

The *Lecidella* phylogeny, based on the data of Zhao et al. (2015), reveals a new southern polar species-level clade (*L. sp. nova*) with accessions from sSA and continental Antarctica. The specimens are not morphologically assignable to the available species descriptions (e. g. Knoph & Leuckert 1994; Ruprecht et al. 2012b; Wirth et al. 2013). All the other sequences added to Zhao et al.'s phylogeny form well supported and distinguished OTUs endemic to sSA.

Interestingly, several bipolar (incl. high mountainous areas worldwide) and abundant mycobiont species occurring in continental and maritime Antarctica, for example *Lecidea andersonii*, *L. polypycnidophora* (Hertel 2007; Ruprecht et al. 2010, Ruprecht et al. 2016), *Lecidella siplei* (Ruprecht et al. 2012b) were not found in the sSA regions.

In contrast to the mycobiont, the photobiont shows the opposite pattern. In particular, the genus *Trebouxia* is known as globally widely distributed with often low diversification (Muggia et al. 2010; Ruprecht et al. 2012a). These findings are supported in this study with more than half of the accessions assigned to two cosmopolitan OTUs of the genus *Trebouxia* (S02, S07) plus some smaller groups (A02, A04a, A12; Leavitt et al. 2015; Figs. 6, S2, Table 2). The remaining *Trebouxia* and *Asterochloris* accessions form highly diverse and locally differentiated and/or endemic groups, including a new clade from Isla Navarino (*Trebouxia* clade N), which was surprising at this unprecedented scale. The contrasting distribution behavior of the cosmopolitan photobionts could be caused mainly by their wide choice of mycobiont partners (Kroken and Taylor 2000) allowing them access to the different distribution strategies of the various lichens.

The most southern sampling area at Isla Navarino shows, for the mycobiont, not only locally restricted OTUs, but also strongly supported endemic species (e.g. *Porpidia navarina*; Ruprecht et al. 2016), which is also the case for *Asterochloris* (*A. sp.* URa18) and for *Trebouxia* (clade N). As this area was ice-free during the Last Glacial Maximum (Douglass et al. 2005) the likely reason can be explained by the concept of glacial refugia where the cold and glacial phases were the drivers of population divergences and (cryptic) speciation after transition from the northern to the southern hemisphere (Fernandez-Mendoza and Printzen 2013; Paula and Leonardo 2006; Stewart et al. 2010). Furthermore, the two southernmost areas on the South American continent sampled (Parque Nacional Torres del Paine and Morro Chico), which both have 100% locally differentiated OTUs and endemic species for the mycobiont (Table 3), are influenced by the violent westerly gales caused by the split of the Humboldt current to the north and the Antarctic circumpolar current (ACC) to the south (Silva et al. 2009). This further leads to the assumption that mycobiont dispersal is limited through this asymmetrical wind system, which is caused by the undertow of the ACC, driven by westerly winds over the circumpolar streamlines (Allison et al. 2010). Moreover the flow speed of the ACC between

the Last Glacial Maximum and the Holocene has remained almost unchanged (McCave et al. 2014). Nonetheless, several other strongly supported species groups that only occur in sSA in other areas, such as *Lecidella* sp. 1 at 2000 m a.s.l. close to Esquel (S42.8°) or endemic lineages in *Trebouxia* (S16, A38, A39), hint to further, and so far unknown, separation events at the remote and climatically extreme southern end of the American continent.

**Taxonomy:** It is well known that the mycobiont genera *Lecidea* and *Porpidia* (Fig. 3) are not clearly separated and our phylogeny confirms that the species currently included in *Porpidia* do not form a monophyletic group (i.e. Buschbom & Mueller 2004; Schmull et al. 2011; Ruprecht et al. 2016; Fig. 3 & S1). Additionally, the newly described species/genus *Cyclohymania epilithica* with perithecioid apothecia and an apparently *Porpidia* - type ascus (McCune et al. 2017) is situated among these two genera. In general, species of the genera *Lecidea* and *Porpidia* are morphologically differentiated by ascus-type (*Lecidea*/*Porpidia*), larger ascospores with the presence of a perispore in *Porpidia* and different genera of associated green microalgae as photobionts (*Trebouxia* sp. in *Lecidea* sp.; *Asterochloris* sp. and *Trebouxia* sp. in *Porpidia* sp.; Ruprecht et al. 2016). *Chlorella* sp. as described by Li et al. (2013) was not found in the sSA *Porpidia* species. Although, several new sequences were added for previously only morphologically described species e.g. *L. kalbii*, *L. promiscens*, *L. swartzioidea*, *L. lithophila*, *Poeltidea perusta*, and sequences for other *Porpidia* species obtained from Genbank, the re-evaluated phylogeny could not be resolved. Still, three species, morphologically assigned to *Lecidea* s. str. (*L. auriculata*, *L. tessellata*, *L. kalbii*; Fryday and Hertel 2014; Hertel 1984; Wirth et al. 2013) form, together with several *Porpidia* species, a highly supported, but intermixed group. Although clearly defined groups for *Porpidia* are easily recognized and a name at the genus level is available for at least one of them (*Haplocarpon*) it would be premature to formally recognize these groups as genera because of the uncertain systematic position of the type species of the genus, *Porpidia trullisata*, a rare species for which molecular data is not yet available. However, the three other groups are formed solely by species of *Lecidea* s. str., *Porpidia*, and *Poeltidea*, respectively. The unresolved and intermixed topology of several species in the two main clades of the *Lecidella* phylogeny (*L. stigmathea* and *L. elaeochroma*, Fig. 4) could not be improved with the additional specimens from sSA. Only an extended species sampling can help to unravel the inconsistent relationships in both these phylogenies (*Lecidea*/*Porpidida*/*Poeltidea*, Fig. 3; *Lecidella*, Fig. 4).

## Conclusions

The species-rich group of lecideoid lichens found widespread in Alpine and Polar Regions in southern South America comprises highly divergent OTUs of cosmopolitan species as well as several endemic species. Three factors may contribute to the observed differentiation and endemism: a) the geographical isolation of this southernmost landmass north of Antarctica, b) limited dispersal caused by the Antarctic circumpolar current system, and c) the presence of regional glacial refugia.

The diverging patterns of dispersal in the cosmopolitan lecideoid lichen group are still under researched. Gaining larger datasets along the assumed distribution routes of the highest mountain ranges (Garrido-Benavent & Perez-Ortega, 2017) and a consequent sampling for a better global coverage will help to understand colonization events and specialization in this, so far, quite overlooked group of crustose lichens.

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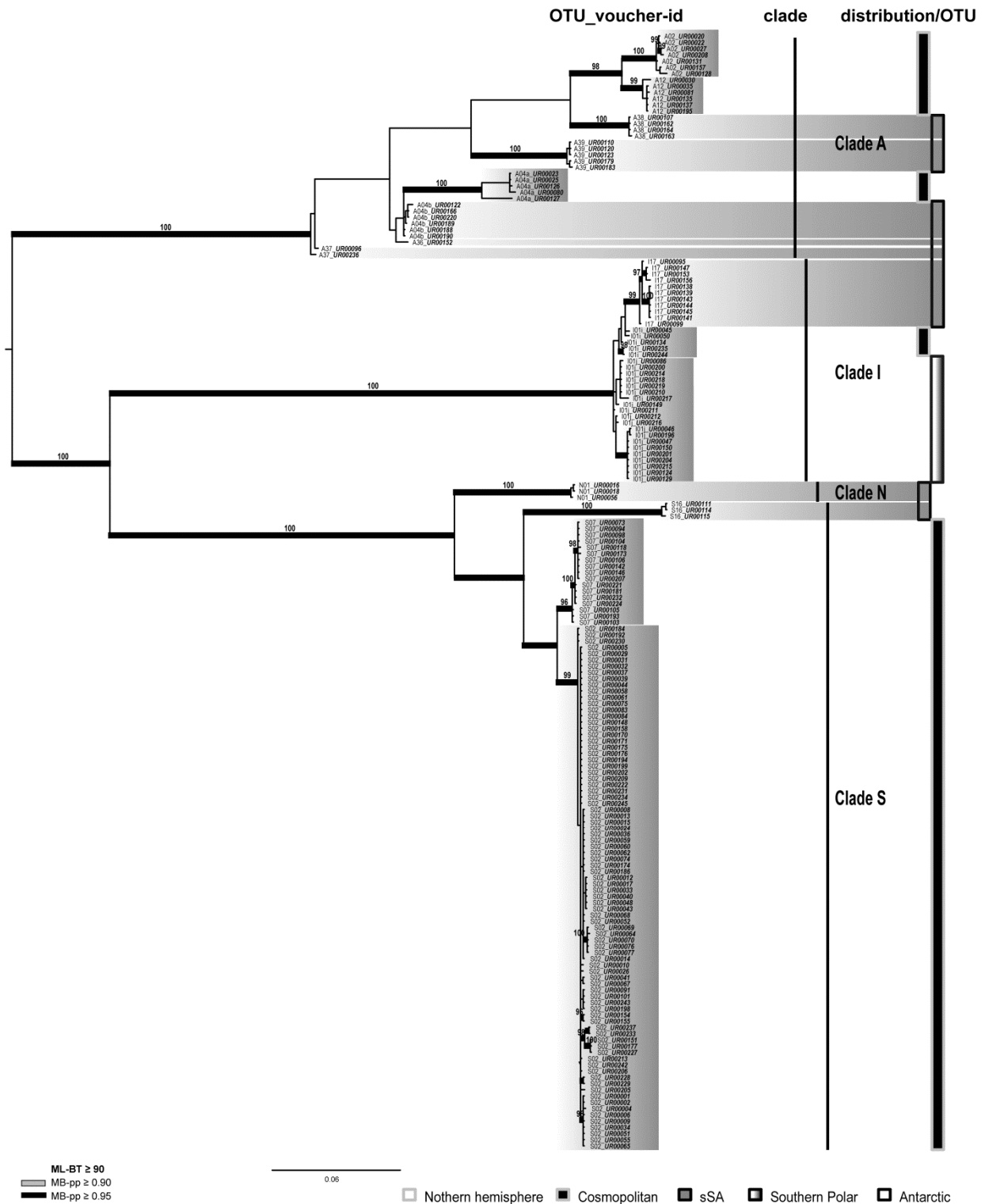
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## Supplementary Information



**Figure S2:** Phylogeny of concatenated ITS, *psbJ-L* and *COX2* sequences showing only the investigated specimens from sSA of the genus *Trebouxia*. Voucher information is preceded by the OTU number. The bars beside the phylogeny show the affiliation to the clades and distribution. sSA accessions are highlighted in grey and those restricted to sSA on OTU-level, with a full-length bar. The bootstrap values with  $\geq 95$  support of ML analyses were directly mapped on the Bayesian tree with  $\geq 0.90$  (gray) and  $\geq 0.95$  (black) support posterior probability values (branches in bold).

## Supplementary Information

**Table S1:** Investigation sites: location\_id, location (country, region, area), altitude, latitude, longitude, CHELSA climate variables BIO1 (annual mean temperature) and BIO12 (annual precipitation; Karger *et al.* 2017).

location_id	country	region	area	altitude m a.s.l.	latitude	longitude	bio1	bio12
TdF_GM_1	Argentina	Tierra del Fuego, Ushuaia	Glaciar Martial	570	-54,78991798	-68,39034302	1,6	489
TdF_GM_2	Argentina	Tierra del Fuego, Ushuaia	Glaciar Martial	587	-54,78952697	-68,39129596	1,6	489
TdF_GM_3	Argentina	Tierra del Fuego, Ushuaia	Glaciar Martial	593	-54,789	-68,39313998	1,8	526
TdF_CB_1	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	607	-54,96288098	-67,634564	2,7	701
TdF_CB_2	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	623	-54,96410097	-67,63851698	2,7	701
TdF_CB_3	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	619	-54,96530604	-67,64167897	2,7	701
TdF_CB_4	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	657	-54,97040299	-67,64538897	2,3	737
TdF_CB_5	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	694	-54,973166	-67,642288	2,3	737
TdF_CB_6	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	702	-54,97335803	-67,64681004	2,3	737
TdF_CB_7	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	688	-54,97366698	-67,65027696	3,3	650
TdF_CB_8	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	680	-54,97164301	-67,632565	2,6	628
TdF_CB_9	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	730	-54,97210502	-67,63245997	2,6	628
TdF_CB_10	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	744	-54,97210301	-67,63207901	2,6	628
TdF_CB_11	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	741	-54,97349499	-67,63205403	2,6	628
TdF_CB_12	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	765	-54,97333699	-67,63534997	1,9	739
TdF_CB_13	Chile	Tierra del Fuego, Región de Magallanes y de la Antártica Chilena, Isla Navarino	Cerro Bandera	741	-54,97261003	-67,63830702	1,9	739

## Supplementary Information

location_id	country	region	area	altitude m a.s.l.	latitude	longitude	bio1	bio12
TdF_CC_1	Argentina	Tierra del Fuego, Ushuaia	Cerro Castor	683	-54,71255503	-68,00119598	2,2	652
TdF_CC_2	Argentina	Tierra del Fuego, Ushuaia	Cerro Castor	682	-54,712507	-67,99986896	2	648
TdF_CC_3	Argentina	Tierra del Fuego, Ushuaia	Cerro Castor	684	-54,71230902	-67,99831504	2	648
TdF_CC_4	Argentina	Tierra del Fuego, Ushuaia	Cerro Castor	686	-54,71235797	-67,997316	2	648
TdF_CC_5	Argentina	Tierra del Fuego, Ushuaia	Cerro Castor	690	-54,71236903	-67,99557298	2	648
TdF_CC_6	Argentina	Tierra del Fuego, Ushuaia	Cerro Castor	794	-54,71009804	-67,99191898	2	648
TdF_VL_1	Argentina	Tierra del Fuego, Ushuaia	Valle de Lobos	365	-54,69848701	-68,13101297	3,7	448
TdF_VL_2	Argentina	Tierra del Fuego, Ushuaia	Valle de Lobos	369	-54,69806196	-68,130846	3,7	448
TdF_TdF_1	Argentina	Tierra del Fuego, Ushuaia	Parque Nacional de T.d. F.	675	-54,81220898	-68,53777701	2,1	756
TdF_TdF_2	Argentina	Tierra del Fuego, Ushuaia	Parque Nacional de T.d. F.	628	-54,81220697	-68,53777399	2,1	756
TdF_TdF_3	Argentina	Tierra del Fuego, Ushuaia	Parque Nacional de T.d. F.	407	-54,81801404	-68,55260703	4	715
RM_MC_1	Chile	Región de Magallanes y de la Antártica Chilena, Laguna Blanca	Morro Chico	208	-52,05869998	-71,41999399	6,4	341
RM_TdP_1	Chile	Región de Magallanes y de la Antártica Chilena, Patagonia chilena	south of P.N. Torres del Paine	143	-51,57855699	-72,60027903	6,5	818
RM_TdP_2	Chile	Región de Magallanes y de la Antártica Chilena, Patagonia chilena	south of P.N. Torres del Paine	118	-51,26429002	-72,86597597	6,4	545
RM_TdP_3	Chile	Región de Magallanes y de la Antártica Chilena, Patagonia chilena	NP Torres del Paine	135	-51,12115997	-73,14255497	5,4	730
RM_TdP_4	Chile	Región de Magallanes y de la Antártica Chilena, Patagonia chilena	NP Torres del Paine	239	-51,123999	-73,142545	5,4	730
RM_TdP_5	Chile	Región de Magallanes y de la Antártica Chilena, Patagonia chilena	NP Torres del Paine	342	-51,12560699	-73,14431098	3,9	770
SC_CC_1	Argentina	Provincia de Santa Cruz, El Calafate	Cerro Cristal	955	-50,55998401	-72,79423401	2	512
SC_CC_2	Argentina	Provincia de Santa Cruz, El Calafate	Cerro Cristal	1054	-50,56179198	-72,78976704	1,3	512
SC_CC_3	Argentina	Provincia de Santa Cruz, El Calafate	Cerro Cristal	1086	-50,564484	-72,78745397	1,3	512
SC_CC_4	Argentina	Provincia de Santa Cruz, El Calafate	Cerro Cristal	1253	-50,56685499	-72,78100502	0,8	492
SC_CC_5	Argentina	Provincia de Santa Cruz, El Calafate	Cerro Cristal	994	-50,56108003	-72,79271403	2	512
SC_LP_1	Argentina	Provincia de Santa Cruz, El Chalten	Lomo del Plague Tumbado	1109	-49,36369599	-72,94175098	1,5	467
SC_LP_2	Argentina	Provincia de Santa Cruz, El Chalten	Lomo del Plague Tumbado	1163	-49,35924604	-72,94870402	0,9	501
SC_LP_3	Argentina	Provincia de Santa Cruz, El Chalten	Lomo del Plague Tumbado	1280	-49,35681302	-72,96007801	0,7	585
SC_LP_4	Argentina	Provincia de Santa Cruz, El Chalten	Lomo del Plague Tumbado	1388	-49,35929197	-72,96415002	0,2	502
SC_LP_5	Argentina	Provincia de Santa Cruz, El Chalten	Lomo del Plague Tumbado	1452	-49,35928803	-72,96619101	0,2	502

Table S1-2

## Supplementary Information

location_id	country	region	area	altitude m a.s.l.	latitude	longitude	bio1	bio12
SC_LP_6	Argentina	Provincia de Santa Cruz, El Chalten	Lomo del Plague Tumbado	1483	-49,359283	-72,96717203	0	473
SC_LT_1	Argentina	Provincia de Santa Cruz, El Chalten	path to Laguna de los Tres	558	-49,315723	-72,900999	4,1	322
SC_LT_2	Argentina	Provincia de Santa Cruz, El Chalten	path to Laguna de los Tres	578	-49,31370498	-72,90347401	4,1	322
SC_LT_3	Argentina	Provincia de Santa Cruz, El Chalten	path to Laguna de los Tres	705	-49,30902997	-72,91458598	3,4	346
SC_LT_4	Argentina	Provincia de Santa Cruz, El Chalten	path to Laguna de los Tres	721	-49,29002903	-72,94508597	3,2	392
SC_LT_5	Argentina	Provincia de Santa Cruz, El Chalten	path to Laguna de los Tres	864	-49,280158	-72,97340297	2,8	368
SC_LT_6	Argentina	Provincia de Santa Cruz, El Chalten	path to Laguna de los Tres	1103	-49,280762	-72,98022601	1,4	389
SC_LT_7	Argentina	Provincia de Santa Cruz, El Chalten	Laguna de los Tres	1182	-49,27974704	-72,98398999	0,9	399
CH_TC_1	Argentina	Provincia de Chubhut, Tecka-Corcovado		797	-43,49470097	-71,28400097	7,8	685
CH_AL_1	Argentina	Provincia de Chubhut, Esquel	P.N. de Alerces	882	-42,90906301	-71,63743003	6,9	1143
CH_LH_1	Argentina	Provincia de Chubhut, Esquel	La Hoya	1964	-42,811456	-71,25711199	1,4	1140
CH_LH_2	Argentina	Provincia de Chubhut, Esquel	La Hoya	2011	-42,81073096	-71,25773703	1,4	1140
CH_LH_3	Argentina	Provincia de Chubhut, Esquel	La Hoya	2089	-42,809372	-71,25885802	1,2	1161
CH_LH_4	Argentina	Provincia de Chubhut, Esquel	La Hoya	2109	-42,80920302	-71,259703	1,2	1161
CH_LH_5	Argentina	Provincia de Chubhut, Esquel	La Hoya	2122	-42,80799503	-71,25616098	1,2	1180
CH_CC_1	Argentina	Provincia de Chubhut, Esquel	Cerro La Cruz	1046	-42,9288889	-71,3016139	7,3	985
RN_CC_1	Argentina	Provincia de Rio Negro, Bariloche	Cerro Catedral	2001	-41,17281304	-71,48415403	1,7	1642
RN_CC_2	Argentina	Provincia de Rio Negro, Bariloche	Cerro Catedral	2075	-41,17067096	-71,48645704	1,7	1642
RN_CC_3	Argentina	Provincia de Rio Negro, Bariloche	Cerro Catedral	2061	-41,16764098	-71,48550603	1,7	1642
RN_CC_4	Argentina	Provincia de Rio Negro, Bariloche	Cerro Catedral	2048	-41,17334202	-71,48629401	1,7	1642

## References

Karger, D.N., Conrad, O., Bohner, J., Kawohl, T., Kreft, H., Soria-Auza, R.W., Zimmermann, N.E., Linder, H.P. & Kessler, M. (2017) Data Descriptor: Climatologies at high resolution for the earth's land surface areas. *Scientific Data* 4.



## Supplementary Information

**Table S2a:** Saxicolous lecideoid lichen specimens from southern South America (sSA) collected by the first author and used in this study. Taxonomic information was taken from the following literature: Ruprecht et al. (2010); Fryday and Hertel (2014); Hafellner and Türk (2016); Ruprecht et al. (2016).

(SZU)		Mycobiont						Associated green micro algae				Asterochloris & Chloroidium			A. N.
Voucher_ID	Location_id	Species	Cluster	OTU_id	Accession numbers			Trebouxia	Accession numbers			Species_name	OTU_id	ITS	
					ITS	mtSSU	RPB1	OTU_id	ITS	psbJ-L	COX2				
UR00001	TdF_GM_1	<i>Lecidea atrobrunnea</i> (Ramond ex Lam. DC.) Schaer. subsp.	L01	LP_Lcd05	MK620100	MK684579	MK684920	Tr_S02	MK619907	MK684744	MK684487				
UR00002	TdF_GM_1	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	KX120200	MK684580	MK684921	Tr_S02	MK619908	MK684745	MK684488				
UR00004	TdF_GM_2	inc. sed. <i>Poeltidea</i> sp. 1	POE02	LP_Poe03	MK620101	MK684581		Tr_S02	MK619909						
UR00005	TdF_GM_2	<i>Lecidea cancriiformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd51	MK659868	MK684582	MK684922	Tr_S02	MK619910	MK684746					
UR00006	TdF_GM_2	<i>Lecidea medusula</i> (Dodge) Hertel	L17	LP_Lcd70	KX120204	MK684583	MK684923	Tr_S02	MK619911	MK684747	MK684489				
UR00008	TdF_GM_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	KX120202	MK684584	MK684924	Tr_S02	MK619912	MK684748	MK684490				
UR00009	TdF_GM_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620103	MK684585	MK684925	Tr_S02	MK619913	MK684749	MK684491				
UR00010	TdF_GM_3	<i>Lecidea auriculata</i> Th.Fr.	L19	LP_Lcd72	KX120212	MK684586	MK684926	Tr_S02	MK619914	MK684750	MK684492				
UR00012	TdF_CB_1	inc. sed. <i>Porpidia</i> sp. 1 subsp.	P06	LP_Porp12	KX120227	MK684587	MK685048	Tr_S02	MK619915	MK684751	MK684493	A. sp. URa18	Ast24	KX120177	
UR00013	TdF_CB_1	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120214	MK684588	MK685038	Tr_S02	KX120242	MK684752		A. sp. URa19	Ast23	KX120198	
UR00014	TdF_CB_1	inc. sed. <i>Porpidia</i> sp. 1 subsp.	P06	LP_Porp11	KX120229	MK684589	MK685049	Tr_S02	KX120245	MK684753		A. sp. URa18	Ast24	KX120183	
UR00015	TdF_CB_1	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120215	MK684590	MK685039	Tr_S02	KX120243	MK684754	MK684494	A. sp. URa18	Ast24	KX120184	
UR00016	TdF_CB_2	inc. sed. <i>Porpidia</i> sp. 1 subsp.	P06	LP_Porp11	KX120230	MK684591	MK685050	Tr_N01	MK619916	MK684755		A. sp. URa18	Ast24	KX120184	
UR00017	TdF_CB_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	KX120201	MK684592	MK684927	Tr_S02	MK619917	MK684756	MK684495				
UR00018	TdF_CB_4	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120216	MK684593	MK685040	Tr_N01	KX120249			A. sp. URa18	Ast24	KX120193	
UR00020	TdF_CB_5	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120217	MK684594	MK685041	Tr_A02	KX120252			A. sp. URa18	Ast24	KX120178	
UR00022	TdF_CB_5	<i>Porpidia macrocarpa</i> (DC.) Hertel & A.J.Schwab	P07	LP_Porp27	KX120232	MK684595	MK685051	Tr_A02	KX120247			A. sp. URa18	Ast24	KX120191	
UR00023	TdF_CB_6	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120226	MK684596	MK685042	Tr_A04a	KX120251	MK684757	MK684496	A. sp. URa18	Ast24	KX120189	
UR00024	TdF_CB_7	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620104	MK684597	MK684928	Tr_S02	MK619918	MK684758	MK684497				
UR00025	TdF_CB_7	inc. sed. <i>Lecidea</i> sp. 4 subsp.	L14	LP_Lcd53	MK620105	MK684598	MK684929	Tr_A04a	MK619919	MK684759					
UR00026	TdF_CB_7	<i>Poeltidea perusta</i> (Nyl.) Hertel & Hafellner	POE01	LP_Poe01	MK620106	MK684599	MK684886	Tr_S02	MK619920	MK684760	MK684498				
UR00027	TdF_CB_7	<i>Porpidia macrocarpa</i> (DC.) Hertel & A.J.Schwab	P07	LP_Porp27	KX120234	MK684600	MK685052	Tr_A02	KX120248			A. sp. UR00027	Ast22	KX120195	
UR00029	TdF_CB_7	inc. sed. <i>Porpidia</i> sp. 1 subsp.	P06	LP_Porp12	KX120228	MK684601	MK685053	Tr_S02	MK619921	MK684761		A. sp. URa18	Ast24	Kx120190	
UR00030	TdF_CB_7	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120218	MK684602		Tr_A12	KX120252			A. sp. URa18	Ast24	KX120185	
UR00031	TdF_CB_7	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120219	MK684603		Tr_S02	MK619922	MK684762		A. sp. URa18	Ast24	KX120179	
UR00032	TdF_CB_8	<i>Porpidia macrocarpa</i> (DC.) Hertel & A.J.Schwab	P07	LP_Porp27	KX120233	MK684604		Tr_S02	MK619923	MK684763		A. sp. URa18	Ast24	KX120188	
UR00033	TdF_CB_8	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620107	MK684605	MK684930	Tr_S02	MK619924	MK684764	MK684499				
UR00034	TdF_CB_9	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620108	MK684606	MK684931	Tr_S02	MK619925	MK684765	MK684500				

Table S2-1

## Supplementary Information

Voucher_ID	Location_id	Species	Cluster	OTU_id	ITS	mtSSU	RPB1	OTU_id	ITS	psbJ-L	COX2	Species	OTU_id	ITS
UR00035	TdF_CB_10	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST15	MK620109			Tr_A12	MK619926	MK684766	MK684501			
UR00036	TdF_CB_11	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620110	MK684607	MK684932	Tr_S02	MK619927	MK684767	MK684502			
UR00037	TdF_CB_11	<i>Poeltidea perusta</i> (Nyl.) Hertel & Hafellner	POE01	LP_Poe02	MK620111	MK684608	MK684887	Tr_S02	MK619928	MK684768	MK684503			
UR00039	TdF_CB_11	<i>Poeltidea perusta</i> (Nyl.) Hertel & Hafellner	POE01	LP_Poe02	MK620112	MK684609	MK684888	Tr_S02	MK619929	MK684769	MK684504			
UR00040	TdF_CB_12	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620113	MK684610	MK684933	Tr_S02	MK619930	MK684770				
UR00041	TdF_CB_12	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620114	MK684611	MK684934	Tr_S02	MK619931	MK684771	MK684505			
UR00043	TdF_CB_12	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120220	MK684612	MK685043	Tr_S02	KX120246	MK684772	MK684506	A. sp. URa18	Ast24	KX120186
UR00044	TdF_CB_12	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120221	MK684613	MK685044	Tr_S02	MK619932			A. sp. URa18	Ast24	KX120180
UR00045	TdF_CB_13	inc. sed. <i>Lecidea</i> sp. 4 subsp.	L14	LP_Lcd53	MK620115	MK684614	MK684935	Tr_I01i	MK619933					
UR00046	TdF_CB_13	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120222	MK684615	MK685045	Tr_I01j	KX120238			A. sp. URa18	Ast24	KX120194
UR00047	TdF_CB_13	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120223	MK684616		Tr_I01j	KX120239	MK684773		A. sp. URa18	Ast24	KX120181
UR00048	TdF_CB_13	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120224	MK684617	MK685046	Tr_S02	KX120244	MK684774	MK684507	A. sp. URa18	Ast24	KX120192
UR00050	TdF_CB_13	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620116	MK684618	MK684936	Tr_I01i	MK619934					
UR00051	TdF_CC_1	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620117	MK684619	MK684937	Tr_S02	MK619935	MK684775	MK684508			
UR00052	TdF_CC_1	inc. sed. <i>Porpidia</i> sp. 1 subsp.	P06	LP_Porp11	KX120231	MK684620	MK685054	Tr_S02	KX120240	MK684776	MK684509	A. sp. URa18	Ast24	KX120182
UR00055	TdF_CC_1	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620118	MK684621	MK684938	Tr_S02	MK619936					
UR00056	TdF_CC_1	<i>Porpidia navarina</i> Ruprecht & Türk	P01	LP_Porp01	KX120225	MK684622	MK685047	Tr_N01	KX120254		MK684510	A. sp. URa18	Ast24	KX120187
UR00057	TdF_CC_2	inc. sed. <i>Poeltidea</i> sp. 1	POE02	LP_Poe03	MK620119	MK684623						Chl. sp. UR00057		MK620073
UR00058	TdF_CC_2	inc. sed. <i>Poeltidea</i> sp. 1	POE02	LP_Poe03	MK620120	MK684624		Tr_S02		MK684777		Chl. sp. UR00058		MK620074
UR00059	TdF_CC_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620121	MK684625	MK684939	Tr_S02	MK619937	MK684778	MK684511			
UR00060	TdF_CC_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620122	MK684626	MK684940	Tr_S02	MK619938	MK684779	MK684512			
UR00061	TdF_CC_4	<i>Lecidea auriculata</i> Th.Fr	L19	LP_Lcd72	MK620123	MK684627	MK684941	Tr_S02	MK619939	MK684780	MK684513			
UR00062	TdF_CC_4	<i>Lecidea auriculata</i> Th.Fr	L19	LP_Lcd72	MK620124	MK684628	MK684942	Tr_S02	MK619940	MK684781	MK684514			
UR00064	TdF_CC_5	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620126	MK684629	MK684943	Tr_S02	MK619941	MK684782	MK684515			
UR00065	TdF_CC_5	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620126	MK684630		Tr_S02	MK619942	MK684783	MK684516			
UR00067	TdF_CC_6	<i>Poeltidea perusta</i> (Nyl.) Hertel & Hafellner	POE01	LP_Poe02	MK620127	MK684631		Tr_S02	MK619943	MK684784	MK684517			
UR00068	TdF_CC_6	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620128	MK684632	MK684944	Tr_S02	MK619944	MK684785				
UR00069	TdF_CC_6	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620129	MK684633	MK684945	Tr_S02	MK619945	MK684786				
UR00070	TdF_CC_6	<i>Lecidea medusula</i> (Dodge) Hertel	L17	LP_Lcd70	MK620130	MK684634	MK684946	Tr_S02	MK619946	MK684787	MK684518			
UR00073	TdF_VL_1	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620131	MK684635	MK684947	Tr_S07	MK619947	MK684788	MK684519			
UR00074	TdF_VL_1	<i>Poeltidea perusta</i> (Nyl.) Hertel & Hafellner	POE01	LP_Poe02	MK620132	MK684636		Tr_S02	MK619948	MK684789	MK684520			
UR00075	TdF_VL_2	<i>Lecidea kalbii</i> Hertel subsp.	L20	LP_Lcd76	MK620133	MK684637	MK684948	Tr_S02	MK619949	MK684790	MK684521			
UR00076	TdF_VL_2	<i>Lecidea auriculata</i> Th.Fr.	L19	LP_Lcd72	MK620134	MK684638		Tr_S02	MK619950	MK684791	MK684522			
UR00077	TdF_VL_2	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620135	MK684639		Tr_S02	MK619951	MK684792	MK684523			

Table S2-2

## Supplementary Information

Voucher_ID	Location_id	Species	Cluster	OTU_id	ITS	mtSSU	RPB1	OTU_id	ITS	psbJ-L	COX2	Species	OTU_id	ITS
UR00079	TdF_TdF_1	<i>Porpidia macrocarpa</i> (DC.) Hertel & A.J.Schwab	P07	LP_Porp27	KX120235	MK684640	MK685055					A. sp. URa20	Ast20	KX120196
UR00080	TdF_TdF_2	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST15	MK620136			Tr_A04a	MK619952	MK684793				
UR00081	TdF_TdF_2	<i>Lecideia promiscens</i> Nyl. subsp.	L02	LP_Lcd10	MK620137			Tr_A12	MK619953	MK684794	MK684524			
UR00083	TdF_TdF_3	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620138	MK684641		Tr_S02	MK619954	MK684795	MK684525			
UR00084	TdF_TdF_3	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620139	MK684642		Tr_S02	MK619955	MK684796	MK684526			
UR00086	RM_MC_1	inc. sed. <i>Lecidella</i> sp. 3		LL_EL25	MK620140			Tr_I01j	MK619956					
UR00090	RM_MC_1	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST19	MK620141									
UR00091	RM_MC_1	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620142	MK684643		Tr_S02	MK619957	MK684797	MK684527			
UR00094	RM_MC_1	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620143	MK684644		Tr_S07	MK619958	MK684798	MK684528			
UR00095	RM_MC_1	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST08	MK620144			Tr_I17	MK619959	MK684799				
UR00096	RM_MC_1	<i>Lecideia</i> sp. UR00096	L14	LP_Lcd57	MK620145			Tr_A37	MK619960	MK684800				
UR00098	RM_MC_1	<i>Lecideia kalbii</i> Hertel subsp.	L20	LP_Lcd76	MK620146	MK684645	MK684949	Tr_S07	MK619961	MK684801	MK684529			
UR00099	RM_MC_1	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd45	MK620147			Tr_I17	MK619962					
UR00101	RM_MC_1	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620148	MK684646	MK684950	Tr_S02	MK619963	MK684802	MK684530			
UR00103	RM_MC_1	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620149	MK684647	MK684951	Tr_S07	MK619964					
UR00104	RM_TdP_1	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	KX120203	MK684648	MK684952	Tr_S07	MK619965	MK684803	MK684531			
UR00105	RM_TdP_1	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620150	MK684649	MK684953	Tr_S07	MK619966	MK684804				
UR00106	RM_TdP_1	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620151	MK684650	MK684954	Tr_S07	MK619967	MK684805	MK684532			
UR00107	RM_TdP_1	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST20	MK620152			Tr_A38	MK619968	MK684806				
UR00110	RM_TdP_2	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd46	MK620153	MK684651	MK684955	Tr_A39	MK619969	MK684807				
UR00111	RM_TdP_2	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620154	MK684652	MK684956	Tr_S16	MK619970	MK684808	MK684533			
UR00114	RM_TdP_2	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620155	MK684653	MK684957	Tr_S16	MK619971	MK684809	MK684534			
UR00115	RM_TdP_2	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620156	MK684654	MK684958	Tr_S16	MK619972		MK684535			
UR00118	RM_TdP_3	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620157	MK684655	MK684959	Tr_S07	MK619973		MK684536			
UR00120	RM_TdP_4	inc. sed. <i>Lecidella</i> sp. 3		LL_EL25	MK620158			Tr_A39	MK619974		MK684537			
UR00122	RM_TdP_4	inc. sed. <i>Lecideia</i> sp. 4 subsp.	L14	LP_Lcd56	MK620159	MK684656	MK684960	Tr_A04b	MK619975	MK684810	MK684538			
UR00123	RM_TdP_5	<i>Porpidia macrocarpa</i> (DC.) Hertel & A.J.Schwab subsp.	P07	LP_Porp21	KX120237	MK684657		Tr_A39	KX120250	MK684811		Ast21	KX120197	
UR00124	SC_CC_1	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd47	MK620160	MK684658	MK684961	Tr_I01j	MK619976	MK684812				
UR00126	SC_CC_1	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd47	MK620161	MK684659	MK684962	Tr_A04a	MK619977	MK684813				
UR00127	SC_CC_1	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd47	MK620162	MK684660	MK684963	Tr_A04a	MK619978		MK684539			
UR00128	SC_CC_2	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST15	MK620163			Tr_A02	MK619979		MK684540			
UR00129	SC_CC_2	<i>Lecideia promiscens</i> Nyl. subsp.	L02	LP_Lcd09	KX120205	MK684661	MK684964	Tr_I01j	MK619980					
UR00130	SC_CC_3	<i>Lecideia</i> sp. UR00130	L08	LP_Lcd33	MK620164	MK684662	MK684965							
UR00131	SC_CC_3	inc. sed. <i>Lecideia</i> sp. 4 subsp.	L14	LP_Lcd54	MK620165	MK684663	MK684966	Tr_A02	MK619981					

Table S2-3

## Supplementary Information

Voucher_ID	Location_id	Species	Cluster	OTU_id	ITS	mtSSU	RPB1	OTU_id	ITS	psbJ-L	COX2	Species	OTU_id	ITS
UR00133	SC_CC_4	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST07	MK620166									
UR00134	SC_CC_4	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd49	MK620167	MK684664	MK684967	Tr_I01i	MK619982					
UR00135	SC_CC_5	inc. sed. <i>Lecideia</i> sp. 3 subsp.	L08	LP_Lcd26	KX120209	MK684665	MK684968	Tr_A12	MK619983	MK684814				
UR00137	SC_LP_1	inc. sed. <i>Lecideia</i> sp. 3 subsp.	L08	LP_Lcd26	MK620168	MK684666	MK684969	Tr_A12	MK619984	MK684815				
UR00138	SC_LP_1	<i>Lecideia tessellata</i> Flörke	L18	LP_Lcd71	KX120213	MK684667	MK684970	Tr_I17	MK619985	MK684816				
UR00139	SC_LP_1	<i>Lecideia tessellata</i> Flörke	L18	LP_Lcd71	MK620169	MK684668	MK684971	Tr_I17	MK619986	MK684817				
UR00141	SC_LP_2	<i>Lecideia</i> sp. UR00141	L19	LP_Lcd75	MK620170	MK684669	MK684972	Tr_I17	MK619987					
UR00142	SC_LP_3	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620171	MK684670	MK684973	Tr_S07	MK619988	MK684818	MK684541			
UR00143	SC_LP_3	inc. sed. <i>Lecideia</i> sp. 4 subsp.	L14	LP_Lcd55	MK620172	MK684671	MK684974	Tr_I17	MK619989	MK684819				
UR00144	SC_LP_3	inc. sed. <i>Lecideia</i> sp. 4 subsp.	L14	LP_Lcd55	MK620173	MK684672	MK684975	Tr_I17	MK619990	MK684820				
UR00145	SC_LP_3	inc. sed. <i>Lecideia</i> sp. 4 subsp.	L14	LP_Lcd54	MK620174	MK684673	MK684976	Tr_I17	MK619991	MK684821				
UR00146	SC_LP_3	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620175	MK684674		Tr_S07	MK619992		MK684542			
UR00147	SC_LP_4	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd49	MK620176	MK684675		Tr_I17	MK619993	MK684822				
UR00148	SC_LP_4	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd52	MK620177			Tr_S02	MK619994					
UR00149	SC_LP_4	<i>Lecideia promiscens</i> Nyl. subsp.	L02	LP_Lcd11	MK620178	MK684676	MK684977	Tr_I01j	MK619995	MK684823				
UR00150	SC_LP_4	<i>Lecideia promiscens</i> Nyl. subsp.	L02	LP_Lcd09	MK620179	MK684677	MK684978	Tr_I01j	MK619996	MK684824				
UR00151	SC_LP_4	<i>Lecideia promiscens</i> Nyl. subsp.	L02	LP_Lcd09	MK620180	MK684678	MK684979	Tr_S02	MK619997	MK684825				
UR00152	SC_LP_5	<i>Lecideia promiscens</i> Nyl. subsp.	L02	LP_Lcd09	MK620181	MK684679	MK684980	Tr_A36	MK619998	MK684826	MK684543			
UR00153	SC_LP_6	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd49	MK620182	MK684680	MK684981	Tr_I17	MK619999					
UR00154	SC_LP_6	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd49	MK620183	MK684681	MK684982	Tr_S02	MK620000	MK684827				
UR00155	SC_LP_6	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd49	MK620184	MK684682		Tr_S02	MK620001	MK684828				
UR00156	SC_LP_6	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd48	MK620185	MK684683	MK684983	Tr_I17	MK620002					
UR00157	SC_LP_6	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST09	MK620186			Tr_A02	MK620003					
UR00158	SC_LP_6	inc. sed. <i>Lecideia</i> sp. 2 (T43427)	L04	LP_Lcd15	MK620187	MK684684	MK684984	Tr_S02	MK620004	MK684829				
UR00162	SC_LT_1	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST17	MK620188			Tr_A38	MK620005	MK684830	MK684544			
UR00163	SC_LT_2	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST16	MK620189			Tr_A38	MK620006	MK684831	MK684545			
UR00164	SC_LT_2	<i>Lecidella stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST18	MK620190			Tr_A38	MK620007	MK684832	MK684546			
UR00166	SC_LT_3	<i>Lecideia cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd46	MK620191	MK684685		Tr_A04b	MK620008	MK684833	MK684547			
UR00170	SC_LT_4	<i>Lecideia auriculata</i> Th.Fr	L19	LP_Lcd72	MK620192	MK684686	MK684985	Tr_S02	MK620009	MK684834				
UR00171	SC_LT_5	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620193	MK684687	MK684986	Tr_S02	MK620010	MK684835				
UR00173	SC_LT_5	<i>Lecideia auriculata</i> Th.Fr	L19	LP_Lcd72	MK620194	MK684688	MK684987	Tr_S07	MK620011	MK684836				
UR00174	SC_LT_6	inc. sed. <i>Lecideia</i> sp. 2 (T43427)	L04	LP_Lcd15	MK620195	MK684689	MK684988	Tr_S02	MK620012	MK684837				
UR00175	SC_LT_7	<i>Lecideia auriculata</i> Th.Fr.	L19	LP_Lcd72	MK620196	MK684690	MK684989	Tr_S02	MK620013	MK684838				
UR00176	SC_LT_7	<i>Lecideia lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620197	MK684691		Tr_S02	MK620014	MK684839				

Table S2-4

## Supplementary Information

Voucher_ID	Location_id	Species	Cluster	OTU_id	ITS	mtSSU	RPB1	OTU_id	ITS	psbJ-L	COX2	Species	OTU_id	ITS
UR00177	SC_LT_7	inc. sed. <i>Lecidea</i> sp. 2 (T43427)	L04	LP_Lcd15	KX120211	MK684692	MK684990	Tr_S02	MK620015	MK684840	MK684548			
UR00179	CH_TC_1	<i>Lecidea cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd44	MK620198	MK684693	MK684991	Tr_A39	MK620016	MK684841				
UR00181	CH_TC_1	<i>Lecidea kalbii</i> Hertel subsp.	L20	LP_Lcd77	MK620199	MK684694	MK684992	Tr_S07	MK620017	MK684842	MK684549			
UR00183	CH_TC_1	<i>Lecidea cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd46	MK620200	MK684695	MK684993	Tr_A39	MK620018	MK684843				
UR00184	CH_TC_1	<i>Lecidea kalbii</i> Hertel subsp.	L20	LP_Lcd77	MK620201	MK684696	MK684994	Tr_S02	MK620019	MK684844				
UR00186	CH_TC_1	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620202	MK684697	MK684995	Tr_S02	MK620020	MK684845				
UR00188	CH_TC_1	<i>Lecidea tessellata</i> Flörke	L18	LP_Lcd71	MK620203	MK684698	MK684996	Tr_A04b	MK620021	MK684846	MK684550			
UR00189	CH_TC_1	<i>Lecidea cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd46	MK620204	MK684699	MK684997	Tr_A04b	MK620022	MK684847				
UR00190	CH_TC_1	<i>Lecidea cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd44	MK620205	MK684700	MK684998	Tr_A04b	MK620023	MK684848	MK684551			
UR00192	CH_TC_1	<i>Lecidea lapicida</i> (ach.) Ach. subsp.	L15	LP_Lcd58	MK620206	MK684701	MK684999	Tr_S02	MK620024	MK684849				
UR00193	CH_AL_1	<i>Porpidia macrocarpa</i> (DC.) Hertel & A.J.Schwab subsp.	P07	LP_Porp24	KX120236	MK684702		Tr_S07	MK620025	MK684850		<i>A. woessiae</i>	Ast13	KX120199
UR00194	CH_LH_1	inc. sed. <i>Lecidea</i> sp. 2 (T43427)	L04	LP_Lcd15	MK620207	MK684703	MK685000	Tr_S02	MK620026	MK684851				
UR00195	CH_LH_1	inc. sed. <i>Lecidea</i> sp. 3 subsp.	L08	LP_Lcd25	KX120210	MK684704	MK685001	Tr_A12	MK620027	MK684852	MK684552			
UR00196	CH_LH_1	inc. sed. <i>Lecidea</i> sp. 1	L02	LP_Lcd08a	KX120208	MK684705	MK685002	Tr_I01j	MK620028	MK684853				
UR00198	CH_LH_2	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620208	MK684706	MK685003	Tr_S02	MK620029	MK684854				
UR00199	CH_LH_2	<i>Lecidea medusula</i> (Dodge) Hertel	L17	LP_Lcd70	MK620209	MK684707	MK685004	Tr_S02	MK620030	MK684855				
UR00200	CH_LH_3	<i>Lecidea atrobrunnea</i> (Ramond ex Lam. DC.) Schaer. subsp.	L01	LP_Lcd01	KX120206	MK684708	MK685005	Tr_I01j	MK620031					
UR00201	CH_LH_3	<i>Lecidea promiscens</i> Nyl. subsp.	L02	LP_Lcd09	MK620210	MK684709	MK685006	Tr_I01j	MK620032					
UR00202	CH_LH_3	inc. sed. <i>Lecidea</i> sp. 1	L02	LP_Lcd08a	MK620211	MK684710	MK685007	Tr_S02	MK620033	MK684856				
UR00204	CH_LH_3	<i>Lecidea promiscens</i> Nyl. subsp.	L02	LP_Lcd09	MK620212	MK684711	MK685008	Tr_I01j	MK620034	MK684857				
UR00205	CH_LH_4	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620213	MK684712	MK685009	Tr_S02	MK620035	MK684858				
UR00206	CH_LH_4	<i>Lecidea auriculata</i> Th.Fr.	L19	LP_Lcd72	MK620214	MK684713	MK685010	Tr_S02	MK620036	MK684859	MK684553			
UR00207	CH_LH_4	<i>Lecidea auriculata</i> Th.Fr.	L19	LP_Lcd72	MK620215	MK684714	MK685011	Tr_S07	MK620037	MK684860				
UR00208	CH_LH_4	<i>Lecidella stigmattea</i> (Ach.) Hertel & Leuckert		LL_ST09	MK620216			Tr_A02	MK620038					
UR00209	CH_LH_4	<i>Lecidea auriculata</i> Th.Fr.	L19	LP_Lcd72	MK620217	MK684715	MK685012	Tr_S02	MK620039	MK684861				
UR00210	CH_LH_5	inc. sed. <i>Lecidella</i> sp. 1		LL_N01	MK620218			Tr_I01j	MK620040	MK684862				
UR00211	CH_LH_5	inc. sed. <i>Lecidella</i> sp. 1		LL_N01	MK620219			Tr_I01j	MK620041	MK684863				
UR00212	CH_LH_5	<i>Lecidea atrobrunnea</i> (Ramond ex Lam. DC.) Schaer. subsp.	L01	LP_Lcd05	KX120207	MK684716	MK685013	Tr_I01j	MK620042	MK684864				
UR00213	CH_LH_5	inc. sed. <i>Lecidella</i> sp. 1		LL_N01	MK620221			Tr_S02	MK620043	MK684865	MK684554			
UR00214	CH_LH_5	<i>Lecidea atrobrunnea</i> (Ramond ex Lam. DC.) Schaer. subsp.	L01	LP_Lcd01	MK620222	MK684717	MK685014	Tr_I01j	MK620044	MK684866				
UR00215	CH_LH_5	<i>Lecidea promiscens</i> Nyl. subsp.	L02	LP_Lcd09	MK620223	MK684718	MK685015	Tr_I01j	MK620045					
UR00216	CH_LH_5	inc. sed. <i>Lecidea</i> sp. 1	L02	LP_Lcd08a	MK620224	MK684719	MK685016	Tr_I01j	MK620046	MK684867				
UR00217	CH_LH_5	inc. sed. <i>Lecidea</i> sp. 1	L02	LP_Lcd08a	MK620225	MK684720	MK685017	Tr_I01j	MK620047	MK684868				
UR00218	CH_LH_5	inc. sed. <i>Lecidea</i> sp. 3 subsp.	L08	LP_Lcd25	MK620226	MK684721	MK685018	Tr_I01j	MK620048	MK684869				

Table S2-5

## Supplementary Information

Voucher_ID	Location_id	Species	Cluster	OTU_id	ITS	mtSSU	RPB1	OTU_id	ITS	psbJ-L	COX2	Species	OTU_id	ITS
UR00219	CH_LH_5	inc. sed. <i>Lecidea</i> sp. 1	L02	LP_Lcd08a	MK620227	MK684722	MK685019	Tr_I01j	MK620049	MK684870				
UR00220	CH_CC_1	<i>Lecidea cancriformis</i> (Dodge & Baker) subsp.	L13	LP_Lcd46	MK620228	MK684723		Tr_A04b	MK620050	MK684871	MK684555			
UR00221	RN_CC_1	inc. sed. <i>Lecidea</i> sp. 2 (T43427)	L04	LP_Lcd15	MK620229	MK684724	MK685020	Tr_S07	MK620051	MK684872				
UR00222	RN_CC_1	inc. sed. <i>Lecidea</i> sp. 1	L02	LP_Lcd08a	MK620230	MK684725	MK685021	Tr_S02	MK620052	MK684873				
UR00224	RN_CC_1	<i>Lecidea auriculata</i> Th.Fr.	L19	LP_Lcd72	MK620231	MK684726		Tr_S07	MK620053	MK684874	MK684556			
UR00227	RN_CC_2	inc. sed. <i>Lecidea</i> sp. 2 (T43427)	L04	LP_Lcd15	MK620232	MK684727	MK685022	Tr_S02	MK620054	MK684875	MK684557			
UR00228	RN_CC_2	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620233	MK684728	MK685023	Tr_S02	MK620055	MK684876	MK684558			
UR00229	RN_CC_2	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd62	MK620234	MK684729	MK685024	Tr_S02	MK620056	MK684877	MK684559			
UR00230	RN_CC_2	<i>Lecidea auriculata</i> Th.Fr.	L19	LP_Lcd72	MK620235	MK684731	MK685025	Tr_S02	MK620057		MK684560			
UR00231	RN_CC_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620236	MK684732	MK685026	Tr_S02	MK620058	MK684878	MK684561			
UR00232	RN_CC_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd68	MK620237	MK684733	MK685027	Tr_S07	MK620059		MK684562			
UR00233	RN_CC_3	inc. sed. <i>Lecidea</i> sp. 1	L02	LP_Lcd08b	MK620238	MK684734	MK685028	Tr_S02	MK620060	MK684879	MK684563			
UR00234	RN_CC_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620239	MK684735	MK685029	Tr_S02	MK620061	MK684880	MK684564			
UR00235	RN_CC_3	<i>Lecidea atrobrunnea</i> (Ramond ex Lam. DC.) Schaer. subsp.	L01	LP_Lcd01	MK620240	MK684736	MK685030	Tr_I01i	MK620062	MK684881				
UR00236	RN_CC_3	inc. sed. <i>Lecidea</i> sp. 1	L02	LP_Lcd08b	MK620241	MK684737	MK685031	Tr_A37	MK620063					
UR00237	RN_CC_3	<i>Lecidea lapicida</i> (Ach.) Ach. subsp.	L15	LP_Lcd58	MK620242	MK684738	MK685032	Tr_S02	MK620064	MK684882	MK684565			
UR00242	RN_CC_4	inc. sed. <i>Lecidea</i> sp. 2 (T43427)	L04	LP_Lcd15	MK620243	MK684739	MK685033	Tr_S02	MK620065	MK684883	MK684566			
UR00243	RN_CC_4	inc. sed. <i>Lecidea</i> sp. 2 (T43427)	L04	LP_Lcd15	MK620244	MK684740	MK685034	Tr_S02	MK620066	MK684884	MK684567			
UR00244	RN_CC_4	<i>Lecidea promiscens</i> Nyl. subsp.	L02	LP_Lcd09	MK620245	MK684741	MK685035	Tr_I01i	MK620067					
UR00245	RN_CC_4	<i>Lecidea auriculata</i> Th.Fr.	L19	LP_Lcd72	MK620246	MK684742	MK685036	Tr_S02	MK620068	MK684885	MK684568			

**Table S2b:** Additional photobiont (*Asterochloris/Vulcanochloris*, *Trebouxia*) sequences: Newly generated accessions (marked in bold) and downloaded from GenBank (NCBI) worldwide. The representative sequences for the *Trebouxia* OTUs, as defined by Leavitt et al. (2015) that were additionally included to the phylogeny (*Trebouxia* - ITS, Figure 6) are not mentioned in the table. Taxonomic information was taken from the following literature: Leavitt et al. (2015); Moya et al. (2015); Skaloud et al. (2015); Vancurova et al. (2015)

Voucher_id	Country	Algal species	OTU_id	Accession number ITS
	Italy	<i>Asterochloris phycobionta</i> Tschermak-Woess	Ast01	AM900490
	Italy, Trento	<i>A. phycobionta</i> Tschermak-Woess	Ast01	GU017647
	Czech Rep., Vltava Mt.	<i>A. lobophora</i> Skaloud & Peksa	Ast01	AM906006
	Slovakia, Povazsky Inovec Mts.	<i>A. lobophora</i> Skaloud & Peksa	Ast01	KP318672
	USA, Florida	<i>A. sp.</i> RY666	Ast01	AY712702
	USA, Arkansas	<i>A. sp.</i> RY1160	Ast01	DQ482674
	Czech Rep., Sumava Mts.	<i>A. leprarii</i> Skaloud & Peksa	Ast02	AM906002

## Supplementary Information

Voucher_id	Country	Algal species	OTU_id	Accession number ITS
T51483 (SZU)	Austria, Salzburg	<i>A. sp.</i> Ura14	Ast03	KF907660
T51478 (SZU)	Austria, Salzburg	<i>A. sp.</i> Ura14	Ast03	KF907659
T51474 (SZU)	Austria, Salzburg	<i>A. sp.</i> Ura14	Ast03	KF907657
	USA, Vermont	<i>A. excentrica</i> UTEX1714 (Archibald) Skaloud & Peksa	Ast04	AM905993
	Czech Rep., Luzicke hory Mts.	<i>A. echinata</i> Skaloud & Peksa	Ast06	FM955666
	USA	<i>A. sp.</i> MN107	Ast06	AF345434
	Spain, Alicante	<i>A. mediterranea</i> E.Barreno, S.Chiva, P.Moya & P.Škaloud	Ast06	KP257384
	Sweden, Öland	<i>A. sp.</i> DrostopA1	Ast06	KT215300
	Sweden, Öland	<i>A. sp.</i> Gynged8b	Ast06	KT215312
	Yugoslavia	<i>A. sp.</i> I03	Ast06	AF345435
	Spain, Lancerote	<i>A. mediterranea</i> E.Barreno, S.Chiva, P.Moya & P.Škaloud	Ast06	KP257394
	Spain, Tarragona	<i>A. sp.</i> MACB 90574	Ast06	FM205725
	Sweden, Oland	<i>A. sp.</i> GyngedA9	Ast06	KT215309
		<i>T. sp.</i> s45553	Ast07	FJ756789
	Australia	<i>A. sp.</i> 7090	Ast08	AF345424
	India, Himachal Pradesh		Ast09	HE803030
	Czech Rep., Snezik Mts.	<i>A. gaertneri</i> Skaloud & Peksa	Ast10	AM905997
	Italy	<i>A. sp.</i> MN03	Ast11	AF345436
		<i>A. sp.</i> K1028	Ast12	FJ756801
	India: Uttarakhand		Ast12	HE803050
		<i>A. sp.</i> K1091	Ast12	FJ756793
	Spain, Somosierra	<i>A. woessiae</i> Skaloud & Peksa	Ast13	KP318669
	Slovakia, Gelnica	<i>A. irregularis</i> (Hildreth & Ahmadijan) Skaloud & Peksa	Ast14	AM906000
US12432c (SZU)	Norway, Svalbard	<i>A. irregularis</i> (Hildreth & Ahmadijan) Skaloud & Peksa	Ast14	MK620072
	Czech Rep., Studenec Mts.	<i>A. glomerata</i> (Warén) Skaloud & Peksa	Ast14	AM905998
	USA, Whitinsville, MA	<i>A. erici</i> UTEX 910 (Ahmadijan) Skaloud & Peksa	Ast15	AF345439
	Canada	-	Ast16	FJ553359
T51469 (SZU)	Sweden, Öland	<i>A. sp.</i> Ura16	Ast17	KF907654
T51494 (SZU)	Germany, Bayern	<i>A. sp.</i> Ura16	Ast17	KF907663
T51493 (SZU)	Germany, Bayern	<i>A. sp.</i> Ura16	Ast17	KF907662
T51495 (SZU)	Germany, Bayern	<i>A. sp.</i> Ura16	Ast17	KF907664
T51477 (SZU)	Austria, Salzburg	<i>A. sp.</i> Ura15	Ast18	KF907658
T51487 (SZU)	Austria, Salzburg	<i>A. sp.</i> Ura15	Ast18	KF907661
	USA, Washington	<i>A. magna</i> (Archibald) Skaloud & Peksa	Ast19	AM906012
T51501 (SZU)	Germany, Bayern	<i>A. magna</i> (Archibald) Skaloud & Peksa	Ast19	KF907669
Ps01/GÖSS-001	Germany, Bayern	<i>Vulcanochloris sp.</i> Ura17	Vul01	KF907645
T51496 (SZU)	Germany, Bayern	<i>V. sp.</i> Ura17	Vul01	KF907665
	Spain, La Plama	<i>V. guanchorum</i> Vancurová, Peksa, Nemcová & Skaloud	Vul01	KR952330
	Spain, La Plama	<i>V. symbiotica</i> Vancurová, Peksa, Nemcová & Skaloud	Vul02	KR952331
	Spain, La Plama	<i>V. canariensis</i> Vancurová, Peksa, Nemcová & Skaloud	Vul03	KR952320
	Spain, La Plama	<i>V. canariensis</i> Vancurová, Peksa, Nemcová & Skaloud	Vul04	KR952329

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Voucher_id	Country	Algal species	OTU_id	Accession number ITS
T35895 (SZU)	Antarctica, S. Victoria Land	<i>Trebouxia</i> sp. Ura2	Tr_A02	JN204757
T44641 (SZU)	Antarctica, Darwin Area	<i>T. sp.</i> Ura3	Tr_A04	JN204803
T51458 (SZU)	Spain, Almeria	<i>T. sp.</i> Ura8	Tr_A15	KF907531
Ps06/ALM-071*	Spain, Almeria	<i>T. sp.</i> Ura16	Tr_A35	KF907523
T51465 (SZU)	Spain, Almeria	<i>T. sp.</i> Ura16	Tr_A35	KF907525
T51457 (SZU)	Spain, Almeria	<i>T. sp.</i> Ura10	Tr_A40	KF907529
T33712 (SZU)	Antarctica, S. Victoria Land	<i>T. sp.</i> Ura2	Tr_A41	JN204744
US12426b (SZU)	Norway, Svalbard		Tr_I01i	MK620071
T43008 (SZU)	Antarctica, S. Victoria Land		Tr_I01j	JN204778
US12399 (SZU)	Norway, Svalbard		Tr_I16	MK620070
T35647 (SZU)	Antarctica, Darwin Area		Tr_S02	JN204751
Ps019/GYN-051*	Sweden, Öland		Tr_S02	KF907553
MAF_DP1_02	Antarctica, Transantarctic Mts.		Tr_S02b	MK226845
T35548 (SZU)	Antarctica, Darwin Area		Tr_S02b	JN204748
T44645 (SZU)	Antarctica, Darwin Area		Tr_S02b	MK226909
T44655 (SZU)	Antarctica, Darwin Area		Tr_S02b	MK226915
T44679 (SZU)	Antarctica, Darwin Area		Tr_S02b	MK226927
T44697 (SZU)	Antarctica, Darwin Area		Tr_S02b	MK226932
T44717 (SZU)	Antarctica, Darwin Area		Tr_S02b	MK226949
T44720 (SZU)	Antarctica, Darwin Area		Tr_S02c	MK226951
	United Kingdom, Scotland		Tr_S03	KT827678
	Ukraine		Tr_S08	KT827698
	Bolivia		Tr_S10	KT827666
Ps012/Hoch-042*	Austria, Salzburg	<i>T. sp.</i> Ura4	Tr_S12	KF907551
	Turkey		Tr_S14	KT827706
Ps013/Hoch-038*	Austria, Salzburg	<i>T. sp.</i> Ura11	Tr_S14	KF907534
US12398 (SZU)	Norway, Svalbard		Tr_S15	MK620069
	Kenya		Tr_S17	KT827704
T42990 (SZU)	Antarctica, Darwin Area	<i>T. sp.</i> Ura1	Tr_S18	JN204770
Ps020/GYN-006*	Sweden, Öland	<i>T. sp.</i> Ura12	Tr_S19	KF907554

Table S2-8



## Supplementary Information

**Table 2c:** Additional Mycobiont (*Lecidella*, *Lecideia*, *Porpidia*) sequences: Own and newly generated (marked in bold) accessions and from Genbank (NCBI) worldwide. Taxonomic information was taken from the following literature: Ruprecht et al. (2010, 2012); Wirth et al. (2013); Orange (2014); Zhao et al. (2015); Hafellner and Türk (2016); McCune et al. (2017).

Voucher_id	Country	Mycobiont species	Cluster	OTU_id	Accession number		
					ITS	mtSSU	RBP1
	China, Xinjiang	<i>Lecidella</i> aff. <i>elaeochroma</i> (Ach.) Choisy		LL_EL01	KT453751		
	China, Xinjiang	<i>L. aff. elaeochroma</i> (Ach.) Choisy		LL_EL02	KT453752		
	Finland	<i>L. euphorea</i> (Flörke) Hertel		LL_EL03	HQ650596		
	China, Xinjiang	<i>L. tumidula</i> (A. Massal.) Knoph & Leuckert		LL_EL15	KT453736		
	China, Xinjiang	<i>L. tumidula</i> (A. Massal.) Knoph & Leuckert		LL_EL15	KT453737		
	China, Inner Mongolia	<i>L. carpathica</i> Körb.		LL_EL04	KT453739		
	China, Xinjiang	<i>L. carpathica</i> Körb.		LL_EL06	KT453741		
	China, Xinjiang	<i>L. carpathica</i> Körb.		LL_EL15	KT453740		
	China, Yunnan	<i>L. effugiens</i> (Nilson) Knoph & Hertel		LL_EL08	KT453754		
	China, Yunnan	<i>L. aff. euphorea</i> (Flörke) Hertel		LL_EL09	KT453755		
	China, Shaanxi	<i>L. aff. euphorea</i> (Flörke) Hertel		LL_EL10	KT453756		
	China, Xinjiang	<i>L. elaeochromoides</i> (Nyl.) Knoph & Hertel		LL_EL08	KT453746		
	China, Xinjiang	<i>L. effugiens</i> (Nilson) Knoph & Hertel		LL_EL08	KT453748		
	China, Xinjiang	<i>L. elaeochromoides</i> (Nyl.) Knoph & Hertel		LL_EL12	KT453750		
	China, Xinjiang	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL13	KT453749		
	Sweden	<i>L. meiococca</i> (Nyl.) Leuckert & Hertel		LL_EL14	AF517929		
		<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL15	AY541275		
	Hungary	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL16	EU266082		
	Turkey, Trabazon	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL16	HQ605936		
	Turkey, Trabazon	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL13	HQ605938		
	United Kingdom	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL13	FR799217		
	China, Xinjiang	<i>L. euphorea</i> (Flörke) Hertel		LL_EL18	KT453742		
	China, Xinjiang	<i>L. euphorea</i> (Flörke) Hertel		LL_EL18	KT453743		
	China, Xinjiang	<i>L. euphorea</i> (Flörke) Hertel		LL_EL18	KT453744		
	China, Xinjiang	<i>L. euphorea</i> (Flörke) Hertel		LL_EL13	KT453745		
T39666 (SZU)	Austria, Salzburg	<i>L. wulfenii</i> (Hepp) Körb		LL_EL13	JN873903		
	United Kingdom	<i>L. flavosorediata</i> (Vězda) Hertel & Leuckert		LL_EL21	FR799213		
	United Kingdom	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL22	FR799214		
	Belgium	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL22	HQ650605		
	United Kingdom	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL19	FR799215		
	United Kingdom	<i>L. elaeochroma</i> (Ach.) Choisy		LL_EL19	FR799216		

## Supplementary Information

Voucher_id	Country	Mycobiont species	Cluster	OTU_id	ITS	mtSSU	RBP1
	China, Shaanxi	<i>L. enteroleucella</i> (Nyl.) Hertel		LL_EN01	KT453757		
<b>MAF_GS1_64</b>	Antarctica, Transantarctic Mts.	inc. sed. <i>Lecidella</i> sp. 2		LL_N02	MK208746		
T38608 (SZU)	Austria	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST01	JN873901		
	Turkey	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST02	HQ605937		
	China	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST02	KT453766		
U.Ruprecht48 (SZU)	Austria	<i>L. patavina</i> (A.Massal.) Knoph & Leuckert		LL_ST02	JN873894		
T39655 (SZU)	Austria	<i>L. patavina</i> (A.Massal.) Knoph & Leuckert		LL_ST03	JN873893		
T39665 (SZU)	Austria	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST03	JN873902		
	China	<i>L. patavina</i> (A.Massal.) Knoph & Leuckert		LL_ST04	KT453767		
	Turkey	<i>L. patavina</i> (A.Massal.) Knoph & Leuckert		LL_ST05	HQ605934		
	China	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST06	KT453768		
T43015 (SZU)	Antarctica, S. Victoria Land	<i>L. greenii</i> Ruprecht & Türk		LL_ST10	HQ287871		
T33586 (SZU)	Antarctica, S. Victoria Land	<i>L. greenii</i> Ruprecht & Türk		LL_ST11	JN873883		
T32991 (SZU)	Antarctica, S. Victoria Land	<i>L. siplei</i> (Dodge & Baker) May. Inoue		LL_ST12	JN873896		
T33457 (SZU)	Antarctica, S. Victoria Land	<i>L. siplei</i> (Dodge & Baker) May. Inoue		LL_ST13	JN873898		
	China	<i>L. patavina</i> (A.Massal.) Knoph & Leuckert		LL_ST14	KT453761		
	China, Xinjiang	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST16	KT453759		
	China	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST18	KT453758		
	China	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST18	KT453760		
	China	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST18	KT453762		
	China	<i>L. stigmatea</i> (Ach.) Hertel & Leuckert		LL_ST18	KT453763		
<b>AAS_Convey00458</b>	Antarctic Peninsula	<i>Lecidea atrobrunnea</i> (Ramond) Schaer.	L01	LP_Lcd01	MK620076	MK684569	MK684891
<b>AAS_Smith12030</b>	Antarctic Peninsula	<i>L. atrobrunnea</i> (Ramond) Schaer.	L01	LP_Lcd01	MK620079	MK684571	MK684893
LE_A060124	Antarctic Peninsula	<i>L. atrobrunnea</i> (Ramond ex Lam. DC.) Schaer.	L01	LP_Lcd01	GU074457	GU074505	MK684899
	Turkey, Trabazon	<i>L. atrobrunnea</i> (Ramond ex Lam. DC.) [ <i>L. syncarpa</i> Zahlbr.]	L01	LP_Lcd02	KF570277		
UCR174803	USA, California	<i>L. atrobrunnea</i> subsp. <i>saxosa</i> Hertel & Leuckert (Ramond) Schaer.	L01	LP_Lcd03	GU074456	GU074507	MK684918
Lund_LG770	Greenland	<i>L. atrobrunnea</i> (Ramond ex Lam. DC.) Schaer.	L01	LP_Lcd04	EU259897	GU074510	MK684906
<b>LE_A060137</b>	Antarctic Peninsula	<i>L. atrobrunnea</i> (Ramond ex Lam. DC.) Schaer.	L01	LP_Lcd05	MK620083	MK684573	MK684900
<b>US12406 (SZU)</b>	Norway, Svalbard	<i>L. atrobrunnea</i> (Ramond ex Lam. DC.) Schaer.	L01	LP_Lcd06	MK620265		
T34435 (SZU)	Austria, Kärnten	<i>L. atrobrunnea</i> subsp. <i>stictica</i> Hertel & Leuckert (Ramond) Schaer.	L01	LP_Lcd07	EU259899	GU074506	MK684908
<b>UR00471 (SZU)</b>	Austria, Salzburg	<i>L. promiscens</i> Nyl. subsp.	L02	LP_Lcd12	MK620263		
<b>MAF_LI_2a (SZU)</b>	Antarctica, Livingston Island	<i>L. promiscens</i> Nyl. subsp.	L02	LP_Lcd13	MK620091		
<b>UR00422 (SZU)</b>	Austria, Salzburg	<i>L. swartzioidea</i> Nyl.	L02	LP_Lcd14	MK620260		
<b>LE_A111504</b>	Antarctica, Enderby Land	inc. sed. <i>L.</i> sp. 2	L03	LP_Lcd15	MK620085	MK684575	MK684902
T43427 (SZU)	Norway, Svalbard	inc. sed. <i>L.</i> sp. 2	L03	LP_Lcd15	GU074426	GU074502	MK684917
<b>T48883b (SZU)</b>	Antarctica, S. Victoria Land	<i>L.</i> sp. T48883b	L04	LP_Lcd16	MK620099		
	USA, Alaska	<i>L. protobacina</i> Nyl.	L05	LP_Lcd17	KY800506		
T39641 (SZU)	Austria	<i>L. confluens</i> (Weber) Ach.	L06	LP_Lcd18	EU263921	GU074492	
	Switzerland	<i>L.</i> sp. ( <i>P. speirea</i> )	L06	LP_Lcd19	HQ650631	DQ986865	DQ986829.1
LOSD #1165	USA, South Dakota	<i>L.</i> sp. JCL0865	L07	LP_Lcd20	EU263929	GU074501	MK684907

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## Supplementary Information

Voucher_id	China Country	<i>L. cf. polypycnidophora</i> Ruprecht & Türk Mycobiont species	L07 Cluster	LP_Lcd20 OTU_id	MH231423 ITS	mtSSU	RBP1
	China	<i>L. cf. polypycnidophora</i> Ruprecht & Türk	L07	LP_Lcd20	MH231446		
LE_A0511701	Antarctica, MacRobertson Land	<i>L. polypycnidophora</i> Ruprecht & Türk	L07	LP_Lcd21	MK620081	MK684572	MK684897
LE_A0515601	Antarctica, Dronning Maud Land	<i>L. andersonii</i> Filson	L07	LP_Lcd22	GU074445	GU074469	MK684898
T43425 (SZU)	Norway, Svalbard	<i>L. andersonii</i> Filson	L07	LP_Lcd22	GU074442	GU074467	MK684915
T43003	Antarctica, S. Victoria Land	<i>L. andersonii</i> Filson	L07	LP_Lcd22	GU074451	GU074461	MK684912
LE_A105701	Antarctica, Dronning Maud Land	<i>L. andersonii</i> Filson	L07	LP_Lcd22	MK620084	MK684574	MK684901
LE_A133003	Antarctica, MacRobertson Land	<i>L. sp.</i> UCR1	L07	LP_Lcd23	MK620086	GU074475	MK684903
UR00280 (SZU)	Austria, Salzburg	<i>L. sp.</i> UR00280	L07	LP_Lcd24	MK620250		
UCR_43266UCR1	USA, California	<i>L. laboriosa</i> Müll. Arg.	L07	LP_Lcd27	EU259902	MK684890	
	USA, California	<i>L. violascens</i> H. Magn.	L07	LP_Lcd28	KY800510		
AAS_Convey00507B	Antarctica, Ellsworth Land	<i>L. silacea</i> Ach.	L08	LP_Lcd29	MK620077		
T42156 (SZU)	Austria, Tirol	<i>L. silacea</i> Ach.	L08	LP_Lcd30	GU074424	GU074496	
UR00271 (SZU)	Austria, Salzburg	<i>L. silacea</i> Ach.	L08	LP_Lcd31	MK620249		
T48781(SZU)	Antarctica, S. Victoria Land	<i>L. sp.</i> T48781	L08	LP_Lcd32	MK620097		
UCR_646Kerry	USA, California	<i>L. fuscoatra</i> Hertel & Leuckert	L08	LP_Lcd34	EU259900		MK684919
	Norway	<i>L. leucothallina</i> Arnold	L09	LP_Lcd35	MG973072		
T42730 (SZU)	Austria, Osttirol	<i>L. obluridata</i> Nyl.	L09	LP_Lcd36	GU074423		
LD L03170	Sweden	<i>L. plana</i> (J. Lahm) Nyl.	L10	LP_Lcd37	EU259903	GU074497	MK684895
LD L03316	Sweden	<i>L. plana</i> (J. Lahm) Nyl.	L10	LP_Lcd38	EU259904	GU074498	MK684896
MAF_LI_1c (SZU)	Antarctica, Livingston Island	<i>L. lithophila</i> (Ach.) Ach.	L11	LP_Lcd39	MK620090		
UR00246 (SZU)	Austria, Oberösterreich	<i>L. lithophila</i> (Ach.) Ach.	L11	LP_Lcd40	MK620054	MK684743	MK685037
	China	<i>L. fuscoatra</i> (L.) Ach. var. <i>grisella</i> (Flörke) Nyl.	L12	LP_Lcd41	KR061350		
	Pakistan	<i>L. aptrootii</i> M. Khan, A.N. Khalid, H.T. Lumbsch	L12	LP_Lcd41	MH618901		
		<i>L. uniformis</i> McCune	L12	LP_Lcd42	KY800507		
T40136 (SZU)	Austria	<i>L. fuscoatra</i> (L.) Ach.	L12	LP_Lcd43	EU263922	GU074490	MK684909
AAS_FFE00012	Antarctica, Ellsworth Land	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	MK620078	MK684570	MK684892
LE_A151501	Antarctica, MacRobertson Land	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	MK620087	MK684576	MK684904
LE_A151902	Antarctica, MacRobertson Land	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	MK620088	MK684577	MK684905
LE_A057501	Antarctica, Princ. Elisabeth Land	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	GU074440	GU074479	
T42988 (SZU)	Antarctica, Darwin Area	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	GU074435	GU074481	MK684912
T35604 (SZU)	Antarctica, Darwin Area	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	EU257671	GU074480	
T43005 (SZU)	Antarctica, S. Victoria Land	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	MK620096	MK684578	MK684913
T43020 (SZU)	Antarctica, S. Victoria Land	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	GU074431	GU074484	MK684914
T43028 (SZU)	Antarctica, S. Victoria Land	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	GU074430		
LE_A040202	Antarctica, Princ. Elisabeth Land	<i>L. cancriformis</i> Doge & Baker	L13	LP_Lcd50	MK620080		
UR00372 (SZU)	Austria, Salzburg	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd59	MK620256		
MAF_LI_2f (SZU)	Antarctica, Livingston Island	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd60	MK620093		
UR00379 (SZU)	Austria, Salzburg	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd60	MK620257		
UR00423 (SZU)	Austria, Salzburg	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd61	MK620261		
MAF_LI_3b (SZU)	Antarctica, Livingston Island	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd63	MK620094		
T48875 (SZU)	Antarctica, S. Victoria Land	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd63	MK620098		

Table S2-11

## Supplementary Information

Voucher_id	Country	Mycobiont species	Cluster	OTU_id	ITS	mtSSU	RBP1
US12426a(SZU)	Norway, Svalbard	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd64	MK620269		
US12398(SZU)	Norway, Svalbard	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd65	MK620264		
H42375 (GZU)	Austria	<i>L. lapicida</i> (Ach.) Ach. var. <i>pantherina</i> Ach.	L15	LP_Lcd66	AF332118		
T42143	Austria, Tirol	<i>L. lapicida</i> (Ach.) Ach. var. <i>pantherina</i> Ach.	L15	LP_Lcd66		GU074494	
US12409(SZU)	Norway, Svalbard	<i>L. lapicida</i> (Ach.)	L15	LP_Lcd67	MK620266		
UR00418 (SZU)	Austria, Salzburg	<i>L. lapicida</i> (Ach.) Ach. var. <i>lapicida</i>	L16	LP_Lcd69	MK620259		
T42745 (SZU)	Austria, Osttirol	<i>L. lapicida</i> (Ach.) Ach. var. <i>lapicida</i>	L16	LP_Lcd69	GU074425	GU074493	MK684910
UR00355 (SZU)	Austria, Salzburg	<i>L. lapicida</i> (Ach.) Ach. var. <i>lapicida</i>	L16	LP_Lcd69	MK620255		
UR00289 (SZU)	Austria, Salzburg	<i>L. medusula</i> (Dodge) Hertel	L17	LP_Lcd70	MK620251		
US12432a(SZU)	Norway, Svalbard	<i>L. medusula</i> (Dodge) Hertel	L17	LP_Lcd70	MK620270		
H49249 (GZU)	Austria, Steiermark	<i>L. tessellata</i> Flörke	L18	LP_Lcd71	EU263926	GU074491	MK684894
T43426	Norway, Svalbard	<i>L. auriculata</i> Th.Fr.	L19	LP_Lcd72	GU074428	GU074499	MK684916
LOS_L04184	Sweden	<i>L. auriculata</i> Th.Fr.	L19	LP_Lcd73	GU074427	GU074500	
US12411(SZU)	Norway, Svalbard	<i>L. auriculata</i> Th.Fr.	L19	LP_Lcd74	MK620267		
	China	<i>P. speirea</i> (Ach.) Kremp	P02	LP_Porp02	KY509522		
	China	<i>P. speirea</i> (Ach.) Kremp	P02	LP_Porp02	KY509523		
	Ireland	<i>Porpidia tuberculosa</i> (Sm.) Hertel & Knoph	P02	LP_Porp03	KJ162322		
	Norway	<i>P. melinodes</i> (Körb.) Gowan & Ahti	P03	LP_Porp04	KJ162326		
	Norway	<i>P. flavicunda</i> (Ach.) Gowan	P03	LP_Porp05	KJ162332		
	Norway, Swalbard	<i>P. flavicunda</i> (Ach.) Gowan	P03	LP_Porp05	KP314488		
US12413(SZU)	Norway, Swalbard	<i>P. flavicunda</i> (Ach.) Gowan	P03	LP_Porp05	MK620268		
US12432c(SZU)	Norway, Swalbard	<i>P. flavicunda</i> (Ach.) Gowan	P03	LP_Porp05	MK620271		
	UK, Wales	<i>P. hydrophila</i> (Fr.) Hertel & A.J.Schwab	P04	LP_Porp06	KJ162319		
	Faroe Islands	<i>P. rugosa</i> (Taylor) Coppins & Fryday	P04	LP_Porp07	KJ162320		
	USA, West Virginia	<i>P. degelii</i> (H. Magnusson) Lendemer	P04	LP_Porp08	KJ653480	KJ653474	
	USA, North Carolina	<i>P. albocaerulescens</i> (Wulfen) Hertel & Knoph	P04	LP_Porp09	KJ653476	KJ653472	DQ986828
MAF_LI_1a (SZU)	Antarctica, Livingston Island	inc. sed. <i>Porpidia</i> sp. 1 subsp.	P05	LP_Porp10	MK620089		
UR00296 (SZU)	Austria, Salzburg	inc. sed. <i>Porpidia</i> sp. 1 subsp.	P05	LP_Porp10	MK620253		
UR00428 (SZU)	Austria, Salzburg	inc. sed. <i>Porpidia</i> sp. 1 subsp.	P05	LP_Porp10	MK620262		
	Austria, Tirol	<i>P. contraponenda</i> (Arnold) Knoph & Hertel	P05	LP_Porp13	KJ162298		
	Ireland	<i>P. cineroatra</i> (Ach.) Hertel & Knoph subsp.	P05	LP_Porp14	KJ162306	KF683104	
	Turkey	<i>P. musiva</i> (Körb.) Hertel & Knoph	P05	LP_Porp15	HQ605939		
	UK, Wales	<i>P. irrigua</i> A. Orange	P05	LP_Porp16	KJ162302		
UR00248 (SZU)	Austria, Oberösterreich	inc. sed. <i>Porpidia</i> sp. 2	P05	LP_Porp17	MK620248		
	UK, Wales	<i>P. striata</i> Fryday	P05	LP_Porp18	KJ162316		
	Faroe Islands	<i>P. islandica</i> Fryday	P06	LP_Porp19	KJ162313		
	Norway	<i>P. flavocruenta</i> Fryday & Buschbom	P07	LP_Porp20	KJ162274		
UR00292 (SZU)	Austria, Salzburg	<i>P. macrocarpa</i> (DC.) Hertel & A.J.Schwab subsp.	P07	LP_Porp22	MK620252		
	UK, Wales	<i>P. macrocarpa</i> (DC.) Hertel & A.J.Schwab subsp.	P07	LP_Porp23	KJ162271		
MAF_LI_4b (SZU)	Antarctica, Livingston Island	<i>P. macrocarpa</i> (DC.) Hertel & A.J.Schwab subsp.	P07	LP_Porp25	MK620095		
T39740 (SZU)	Austria	<i>P. macrocarpa</i> (DC.) Hertel & A.J.Schwab	P07	LP_Porp26	EU263923	GU074511	

## Supplementary Information

Voucher_id	Country	Mycobiont species	Cluster	OTU_id	ITS	mtSSU	RBP1
UR00411(SZU)	Austria, Salzburg	<i>P. macrocarpa</i> (DC.) Hertel & A.J.Schwab subsp.	P07	LP_Porp27	MK620258	MK684730	MK685056
	Turkey, Trabazon	<i>P. crustulata</i> (Ach.) Hertel & Knoph	P07	LP_Porp28	HQ605941		
	China, Guancen Mountain	<i>P. crustulata</i> (Ach.) Hertel & Knoph	P07	LP_Porp29	KF303294		
MAF_LI_2c (SZU)	Antarctica, Livingston Island	inc. sed. <i>Porpidia</i> sp. 3	P07	LP_Porp30	MK620092		
UR00330 (SZU)	Austria, Salzburg	inc. sed. <i>Porpidia</i> sp. 3	P07	LP_Porp30	MK620254		
	USA, Washington	<i>Cyclohymeria epilithica</i> McCune & M.J.Curtis	C01	Cyc01	KY800503		
	USA, Oregon	<i>Cyclohymeria epilithica</i> McCune & M.J.Curtis	C01	Cyc01	KY800505		
T39660 (SZU)	Austria, Salzburg	<i>Farnoldia jurana</i> (Schaer.) Hertel subsp. <i>jurana</i>		F01	EU263920	GU074511	MK684889
T35647 (SZU)	Antarctica, Darwin Area	<i>Carbonea vorticosa</i> (Flörke) Hertel			JN873866		
T43429 (SZU)	Norway, Svalbard	<i>C. vorticosa</i> (Flörke) Hertel			JN873870		
T44628 (SZU)	Antarctica, Darwin Area	<i>Lecanora fuscobrunnea</i> Dodge & Baker			JN873875		
UCR_47815UCR1	USA, California	<i>L. polytropa</i> (Ehrh. ex Hoffm.) Rabenh.			JN873881		
T33597 (SZU)	Antarctica, S. Victoria Land	<i>Rhizoplaca macleanii</i> (Doge) Castello			JN873905		
T38107 (SZU)	Switzerland, Wallis	<i>R. melanophthalma</i> (DC.) Leuckert & Poelt			JN873910		

**Table 2d:** Cultured Trebouxia specimen provided by Sieglinde Ott, Heinrich Heine Universität, Düsseldorf, Germany

Culture	Country	Mycobiont species	Cultured photobiont			Accession number		
			Species	Clade	OTU_id	ITS	psbJ-L	COX2
1_SO	Antarctica, Southern Maritime Antarctica	<i>Umbilicaria antarctica</i> (Frey & I.M.Lamb) Llano	<i>Trebouxia</i> sp.	S	Tr_S02	MH813466	MH818849	MH818853
2_SO	Antarctica, Northern Victoria Land	<i>Pleopsidium chlorophanum</i> (Wahlenb.) Zopf	<i>Trebouxia</i> sp.	S	Tr_S02	MH813467	MH818850	MH818854
3_SO	Antarctica, Northern Victoria Land	<i>Buellia frigida</i> Darb	<i>Trebouxia</i> sp.	A	Tr_A02	MH813468	MH818851	MH818855
4_SO	Sweden	<i>Fulgensia bracteata</i> (Hoffm.) Räsänen	<i>Trebouxia</i> sp.	A	Tr_A12	MH813469	MH818852	MH818856

## Supplementary Information

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## Supplementary Information

**Table S3: Marker and primer used in this study**

Marker	Primer Name	Primer Sequence 5'→3'	Temp C°	Reference
ITS	18S-ITS uni-for	GTG AAC CTG CGG AAG GAT CAT T	60.3	(Ruprecht <i>et al.</i> 2012)
	ITS1	TCC GTA GGT GAA CCT GCG G	61.0	(White <i>et al.</i> 1990)
	ITS1aT	ATC TAT CGT GXM MAC ACC G	54.5	(Ruprecht <i>et al.</i> 2014)
	ITS1F	CTT GGT CAT TTA GAG GAA GTA A	54.7	(Gardes & Bruns 1993)
	ITS1L	GTA GGT GAA CCT GCG GAA	56.0	this study
	ITS1-sense-A	TCC ACA CCG AGM ACA AC	54.0	(Ruprecht <i>et al.</i> 2014)
	ITS1T	GGA AGG ATC ATT GAA TCT ATC GT	57.1	(Kroken & Taylor 2000)
	ITS2-antisense-A	AAG GTT TCC CTG CTT GAC A	54.5	(Ruprecht <i>et al.</i> 2014)
	ITS4	TCC TCC GCT TAT TGA TAT GC	55.3	(White <i>et al.</i> 1990)
	ITS4bT_mod	CCA AAA SGC GTC CTG C A	55.2	(Ruprecht <i>et al.</i> 2014)
	ITS4L	CGA TCC GAG GTC AAC CA	55.2	this study
	ITS4T	GTT CGC TCG CCG CTA CTA	58.2	(Kroken & Taylor 2000)
	LR1850	CCT CAC GGT ACT TGT TC	50.4	(Bhattacharya <i>et al.</i> 1996)
	nr-SSU-1780-5'	TGC GGA AGG ATC ATT GAT TC	55.3	(Piercey-Normore & Depriest 2001)
	NS7m	GGC AAT AAC AGG TCT GT	52.8	(Bhattacharya <i>et al.</i> 1996)
RPB1	fRPB1-C rev	CCX GCD ATX TCR TTR TCC ATR TA	56.8	(Matheny <i>et al.</i> 2002)
	gRPB1-A for	GAK TGT CCK GGW CAT TTT GG	57.3	(Matheny <i>et al.</i> 2002)
	RPB1_for_Lec	CCA GTC TTY CAY GTT GGT AT	55.3	this study
mtSSU	CU6	TGT GGC ACG TCT ATA GCC CA	59.4	( <a href="https://nature.berkeley.edu/brunslab/tour/primers.html">https://nature.berkeley.edu/brunslab/tour/primers.html</a> )
	mrSSU1	AGC AGT GAG GAA TAT TGG TC	55.3	(Zoller <i>et al.</i> 1999)
	mtSSU for2	AAT XGC CTR RCG GCK GAA C	55.3	(Ruprecht <i>et al.</i> 2010)
	mtSSU rev2	AAA ATA AAG TAA GGG YTT RCG TTA ATT	55.9	(Ruprecht <i>et al.</i> 2010)
COX2	COXIIif2	TTA ACG CCT AAC GAG GGA AC	57.3	(Lindgren <i>et al.</i> 2014)
	COXIIr	ATACGAAATCCCGTTCCTGA	55.3	(Lindgren <i>et al.</i> 2014)
	COX sense	AACGCCTAACGAGGGAAC	56.7	this study
psbJ-L	psbF	GTW GTW CCA GTA TTR GAC AT	52.2	(Werth & Sork 2010)
	psbR	AAC CRA ATC CAX AYA AAC AA	50.1	(Werth & Sork 2010)
	psbL-sense	TTA ATT TTC GTT TTA GCT GTT C	50.9	(Ruprecht <i>et al.</i> 2014)
	psbJ-antisense	TTC CTA AAT TTT TTC GTT TCA ATA	50.8	(Ruprecht <i>et al.</i> 2014)

## Supplementary Information

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## Supplementary Information

**Table S4:** Evolutionary models of the Maximum Likelihood analyses.

<b>Phylogeny</b>	<b>Mycobiont</b>	<b>Photobiont</b>
<i>Lecidea/Porpidia/Poeltidea</i> - ITS	TIM2+F+I+G4	
<i>Lecidea/Porpidia/Poeltidea</i> - ITS/mtSSU/RPB1	TIM2e+I+G4	
<i>Lecidella</i> - ITS	TNe+I+G4	
<i>Asterochloris</i> - ITS		TIM2e+I+G4
<i>Trebouxia</i> - ITS		SYM+I+G4
<i>Trebouxia</i> - ITS/psbJ-L/COX2		TPM3u+F+G4

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## Supplementary Information

**Table S5:** Scores of sequence similarity in % of more than 3 accessions per OTU

OTU $\geq$ 3 accessions	sub - OTU	sequence similarity %
LP_Lcd01		99.8
LP_Lcd08 total		97.3
	LP_08a	97.9
	LP_08b	99.8
LP_Lcd09		99.4
LP_Lcd15		98.6
LP_Lcd46		99.1
LP_Lcd49		99.2
LP_Lcd50		98.6
LP_Lcd58		98.7
LP_Lcd62		98.9
LP_Lcd71		98.8
LP_Lcd72		98.9
LP_Porp 27		98.5
LL_N01		99.4
Ast24		99.8
Tr_A02		99.4
Tr_A04 total		96.7
	Tr_A04a	97.7
	Tr_A04b	98.8
Tr_S02 total		94.8
	Tr_S02	98.0
	Tr_S02b	98.4
	Tr_I01i	97.5
	Tr_I01j	98.6
Tr_I17		99.1

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