Flora of Lichenicolous Fungi

Volume 1 · Basidiomycota

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SUPPLEMENTARY MATERIAL

National Museum of Natural History

Luxembourg · 2022

Class *Agaricomycetes*, order *Agaricales*

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Supplementary document S1. Methods used to determine the placement of lichenicolous species in the phylogeny of the tribe *Arrheniae* (*Agaricales*) (page 33).

Taxon sampling

To place the lichenicolous *Arrhenia peltigerina* and the lichenicolous specimen of *A.* aff. *subglobisemen* in the tribe *Arrheniae* (*Agaricales*), a molecular phylogeny of the tribe was constructed using sequences of the ITS1, 5.8S and ITS2, and approximately 1300 bases of the 5′ end of the LSU nuclear rDNA, the most common sequences found for these species in GenBank. Alignments from two previous molecular phylogenetic studies of the tribe (Lawrey et al. 2009, Dal Forno et al. 2013) used to investigate the *Dictyonema* s. l. clade (now referred to as subtribe *Dictyonemateae*; Dal Forno et al. 2020) were used as a basis for constructing the database, which was supplemented by sequences obtained by BLAST searches with the new sequences. The final database of ITS + nuLSU sequences represented 39 sequences, 20 in the *Dictyonemateae* (*Acantholichen*, *Cora*, *Cyphellostereum*, *Dictyonema*), *Eonema pyriforme*, 15 (including the new sequences) in *Arrhenia* and three sequences of *Lichenomphalia* (of the tribe *Lichenomphalieae*) used as an outgroup (see Supplementary document S2).

Molecular data obtained from *Arrhenia* specimens

For the new sequences of *Arrhenia peltigerina* and *A.* aff. *subglobisemen*, DNA extractions, amplifications and sequencing procedures follow Ertz et al. (2009, 2011). A fragment of c. 1.2 kb at the 5’ end of the nuLSU rDNA was amplified using primers LIC15R (Miadlikowska et al. 2002) and LR7 (Vilgalys & Hester 1990). For *A. peltigerina*, the yield of the PCR was weak and therefore a fragment of c. 0.9 kb was reamplified using primers LIC15R and LR5 (Vilgalys & Hester 1990). A fragment of c. 0.6 kb of the nuITS rDNA (ITS1 + 5.8 S + ITS4) was amplified using primers ITS1F and ITS4 (White et al. 1990) for *A.* aff. *subglobisemen* (failed for *A. peltigerina*). Both strands were sequenced by Macrogen® using the amplification primers, and with the additional primers LR3 and LR3R (Vilgalys & Hester 1990) for the nuLSU. Sequence fragments were assembled with Sequencher version 4.6 (Gene Codes Corporation, Ann Arbor, Michigan).

Phylogenetic analysis

The newly generated ITS + nuLSU sequences were edited in Geneious 7.1.7 (Kearse et al. 2012). After removing primer binding sites for all sequences, each sample was automatically aligned with MAFFT using the --auto option (Katoh & Toh 2005). Ambiguously aligned sites in the ITS1 and ITS2 region were not excluded from the analysis. This resulted in a total alignment length of 2139, 803 bases for ITS and 1336 for nuLSU. Data sets for each locus were initially analysed separately and evaluated for potential conflict by comparing the non-parametric bootstrap values obtained for each resolved clade in each tree. Strongly supported clades (BS higher than 70%) that are in disagreement are an indication of significant conflict that precludes combination of the data sets (Mason-Gamer & Kellogg 1996). Since no conflict was detected in our data sets, we combined them (nuLSU + ITS) and subjected the combined dataset to maximum likelihood (ML) searches using RAxML 7.2.6 (Stamatakis 2006, Stamatakis et al. 2005), with non-parametric bootstrapping using 500 replicates under the universal GTRGAMMA model.

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Supplementary document S2. Species, GenBank accession numbers (nuLSU + ITS) and specimen information (only for lichenicolous taxa) of fungi used in the phylogenetic analysis of the tribe *Arrheniae*, *Agaricales* (page 33). Newly produced sequences in bold font.

Species	**GenBank (ITS+nuLSU)**	**Country**	**Host**	**Specimen**
Acantholichen galapagoensis	EU825953			
Arrhenia acerosa	KP965784			
Arrhenia cf. *acerosa*	MK277598			
Arrhenia auriscalpium	AAU66428			
Arrhenia chlorocyanea	OVU66456			
Arrhenia epichysium	OEU66442			
Arrhenia griseopallida	PGU66436			
Arrhenia lobata	ALU66429			
Arrhenia obscurata	OOU66448			
Arrhenia peltigerina	**MW882126**	Luxembourg	*Peltigera rufescens*	Diederich 16735 (BR)
Arrhenia philonotis	OPU66449			
Arrhenia retirugis	EU118604			
Arrhenia rustica	MK278422			
Arrhenia sphagnicola	OSU66453			
Arrhenia aff. *subglobisemen*	**MW882127/MW882125**	Canada	*Peltigera chionophila*	Björk 19420 (BR)
Arrhenia velutipes	OVU66455			
Cora asperoides	EU825960			
Cora cryptoarachnoidea	EU825957			
Cora hymenocarpa	EU825959			
Cora imi	EU825958			
Cora minor	EU825969			
Cora terrestris	EU825963			
Cora viliewoa	EU825956			
Cora wilsoniorum	EU825961			
Cyphellostereum nitidum	EU825970			
Cyphellostereum pusiolum	EU825976			
Cyphellostereum sp.	EU825971			
Dictyonema aeruginosulum	EU825955			

Supplementary document S2. (Continued)

Species	GenBank (ITS+nuLSU)	Country	Host	Specimen
Dictyonema hernandezii 1	EU825977			
Dictyonema hernandezii 2	EU825966			
Dictyonema schenkianum	EU825972			
Dictyonema sp. 1	EU825974			
Dictyonema sp. 2	EU825973			
Dictyonema sp. 3	EU825975			
Dictyonema sp. 4	EU825978			
Eonema pyriforme	EU118605			
Lichenomphalia grisella	OGU66443			
Lichenomphalia hudsoniana	OHU66446			
Lichenomphalia velutina	OVU66454			

Class *Agaricomycetes*, order *Cantharellales*

by P. Diederich, M. Sikaroodi & J. D. Lawrey

Supplementary document S3. Methods used to determine the placement of lichenicolous species in the phylogeny of the order *Cantharellales* (pages 51 and 67).

Taxon sampling

To place the known lichenicolous and the new lichenicolous species collected from *Parmelia* spp. in the *Cantharellales*, a molecular phylogeny of the order was constructed using sequences of the ITS1, 5.8S and ITS2, and approximately 1300 bases of the 5′ end of the LSU nuclear rDNA, the most common sequences found for these species in GenBank. Alignments from previous molecular phylogenetic studies of the order (Diederich et al. 2014, Lawrey et al. 2007, 2016, 2020) were used as a basis for constructing the database, which was supplemented by sequences obtained by BLAST searches with the new sequences. The final database of ITS + nuLSU sequences represented 107 sequences, including the two new sequences and five sequences (three for nuLSU and two for ITS) used as an outgroup (Supplementary Table S4).

Molecular data obtained from *Parmeliicida pandemica*

Genomic DNA was extracted from samples (Berger 35564 and Diederich 18144) containing ca. 20 bulbils excised from the specimens and washed in 70% ethanol using the Fast DNA Spin Kit from MP Biomedicals (Santa Ana, CA) according to the manufacturer’s protocol. About 10 ng of extracted DNA were subjected to a standard PCR in a 20 μL reaction volume using Taq Gold polymerase (Applied Biosystems, Foster City, CA), also according to manufacturer’s protocols, with the objective of amplifying the internal transcribed spacer (ITS) and nuclear large subunit (nuLSU) regions of rDNA. The products were purified with Ampure magnetic beads (Agencourt Bioscience, Beverly, MA) and the purified PCR products were used in standard sequencing reactions with BigDye Terminator Ready Reaction Mix v3.1 (Applied Biosystems). The sequencing reactions were purified using Sephadex G-50 (Sigma-Aldrich, St. Louis, MO), dried in a speedvac, denatured in HiDi Formamide (Applied Biosystems) and run on an ABI3130-xl capillary sequencer (Applied Biosystems). The data collected were analysed using ABI software, and the sequences were then assembled together with the software Sequencher version 5.0 (Gene Codes, Ann Arbor, MI) for manual corrections in base calling and to make contiguous alignments of overlapping fragments. The primers used for both amplification and sequencing were LR0R, LR3R, LR5, LR7, LR16 (http://www.biology.duke.edu/fungi/mycolab/primers.htm) for nuLSU, and ITS1F, ITS2, ITS3, ITS4 and ITS5 (Gardes & Bruns 1993; White et al, 1990) for ITS.

Phylogenetic analysis

In addition to our newly generated sequences of *Parmeliicida pandemica* (GenBank accessions MZ509446 and MZ509450), we included sequences used in earlier analyses of lichenicolous *Cantharellales* (Diederich et al. 2014, Lawrey et al. 2007, 2016, 2020) and those from a broad range of taxa representing recognized orders and families within the *Cantharellales* (Binder et al. 2005, Dunham et al. 2003, Hibbett et al. 2007, 2014, Matheny et al. 2007, Masumoto & Degawa 2020, Moncalvo et al. 2006, Wilson et al. 2006) and sequences with high (>95%) similarity from GenBank. The final data sets (all GenBank accession numbers included in Supplementary Table S4) contained 52 (nuLSU) and 57 (ITS) ingroup terminals. Sequences from *Cerinomyces crustulinus* (Bourdot & Galzin) G. W. Martin, *Tilletiaria anomala* Bandoni & B. N. John and *Platygloea disciformis* (Fr.) Neuhoff were used as outgroups for the nuLSU dataset; *Tremellodendron ocreatum* (Berk.) P. Roberts and *Sebacina vermifera* Oberw. were used as outgroups for ITS.

The newly generated nuLSU and ITS sequences were edited in Geneious v.8.1.6 (http://www.geneious.com/) and automatically aligned with MAFFT using the --auto option (Katoh & Toh 2005). The alignments were trimmed and subjected to analysis of ambiguously aligned regions using the GUIDANCE webserver (Penn et al. 2010a,b); regions aligned with low confidence (below 0.93) were removed. The final nuLSU dataset had 1152 characters, 483 of which were variable. The ITS data set had an alignment length of 1055 characters, 760 of which were variable. The GUIDANCE score for the nuLSU alignment was 0.964227; the score for ITS was 0.700920. Sequences of *Cantharellus* spp. are known to exhibit high levels of rate heterogeneity in nuDNA and long branch lengths in phylogenies (Moncalvo et al. 2006, Matheny et al. 2007), and the ITS sequences in our data set proved especially difficult to align. These were therefore dropped from both data sets. Also, since the two data sets contained sequences representing different species and specimens, they were analysed separately. Maximum likelihood (ML) searches were done using RAxML 7.2.6 (Stamatakis 2006, Stamatakis et al. 2005) with non-parametric bootstrapping of 1000 replicates under the universal GTRGAMMA model. A Bayesian analysis was also performed for the same data sets using Markov chain Monte Carlo sampling (Larget & Simon 1999) in MrBayes 3.1.2 (Huelsenbeck & Ronquist 2001). Substitution models for each data set were selected in jModelTest 0.1.1 (Posada 2008), which employs PhyML 3.0 (Guindon & Gascuel 2003) to estimate the likelihood of the data under 24 models of evolution using a fixed topology. The AICc values under each model were compared and the model with the lowest AICc value (TrN+I+G for nuLSU and TIM2+I+G for ITS) was selected. Two parallel analyses were then run in MrBayes for 10,000,000 generations, with 4 chains each, sampling every 100 generations. Burn-in trees (initial 25%) were discarded for each run and posterior probabilities (PP) of the nuLSU and ITS matrices were determined by calculating a majority-rule consensus tree generated from the post-burn-in trees by the MCMCMC runs using the sumt option of MrBayes. RAxML and MrBayes analyses were performed using the CIPRES Web Portal 3.1 (Miller et al. 2010) and the University of Oslo Bioportal (http://www.bioportal.uio.no). The most likely trees were then produced (–lnL=13014.4750 for the nuLSU tree; –lnL=16048.4590 for the ITS tree). Relationships were considered supported if they had ML-BS values of 70 or greater and Bayesian posterior probabilities (PP) of 0.95 or greater. Phylogenetic trees were visualized using FigTree v. 1.4.2 (Rambaut 2012).

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Supplementary document S4. Species, GenBank accession numbers (nuLSU + ITS) and specimen information (only for lichenicolous taxa) of fungi used in the phylogenetic analysis of the order *Cantharellales* (pages 51 and 67). Newly produced sequences in bold font. Type material of lichenicolous species is indicated with (T).

Species	GenBank ITS/nuLSU	Country	Host	Specimen
Bergerella atrofusca (T)	MN902070 both	Austria	*Physcia aipolia*	Berger 34240 (BR)
Botryobasidium botryosum	DQ267124/–			
Botryobasidium candicans	–/AJ406440			
Botryobasidium isabellinum	–/AF393047			
Botryobasidium subcoronatum 1	–/AF287850			
Botryobasidium subcoronatum 2	DQ200924/–			
Botryobasidium vagum	–/AJ406439			
Botryobasidium sp. 1	–/AJ406444			
Botryobasidium sp. 2	–/AJ406445			
Botryobasidium sp. 3	KP814226/–			
Bryoclavula phycophila	–/LC508118			
Bulbilla applanata 1	KC336079/–	Bolivia	*Lobariella crenulata*	Flakus 16424 (KRAM)
Bulbilla applanata 2 (T)	KC336078/–	Bolivia	*Pseudocyphellaria* sp.	Flakus 16422 (KRAM)
Burgella flavoparmeliae	–/DQ915469	USA	*Flavoparmelia baltimorensis*	Buck 38682 (NY)
Burgella lutea (T)	KC336076/KC336075	Bolivia	corticolous lichens	Etayo 27623 (BR)
Burgellopsis nivea (T)	–/KC336077	Scotland	saxicolous lichens	Coppins 21845 (E)
Burgoa angulosa (T)	–/DQ915471	Spain	*Physcia aipolia*	Etayo 16256 (MA)
Burgoa anomala	AB972800/–			
Burgoa moriformis (T)	–/DQ915477	Ireland	dead lichen thalli	Coppins 15829 & O'Dare (E)
Burgoa verzuoliana 1	–/DQ915475			
Burgoa verzuoliana 2	–/AB972758			
uncultured *Cantharellales*	DQ368717 both			
Ceratobasidium bulbillifaciens (T)	–/KC336073	Germany	bark of *Acer platanoides*	Cezanne-Eichler 8193 (BR)
Ceratobasidium cereale	JF429709/–			
Ceratobasidium sp. 1	–/AF354095			
Ceratobasidium sp. 2	–/DQ097889			
Ceratobasidium sp. 3	KC336072/–			
Ceratobasidium sp. 4	GQ850447/–			
Ceratobasidium sp. 5	DQ102430/–			
uncultured *Ceratobasidium* sp. 6	FM866376/–			
uncultured *Ceratobasidium* clone 7	JF912463/–			
Cerinomyces crustulinus	–/AY586643			

Supplementary document S4. (Continued)

Species	**GenBank ITS/nuLSU**	**Country**	**Host**	**Specimen**
Clavulina caespitosa	–/DQ056370			
Clavulina cinerea	–/AJ406433			
Clavulina craterelloides	–/AY391718			
Clavulina cristata	–/AY586648			
Clavulina humicola	–/D7Q056367			
Clavulina nigricans	–/AY391719			
Clavulina sp. 1	FN669173/–			
Clavulina sp. 2	DQ202266/–			
uncultured *Clavulina* voucher 3	JN168693/–			
uncultured *Clavulina* voucher 4	JN168698/–			
Clavulinaceae sp.	AJ534708/–			
Gloeotulasnella cystidiophora	–/AY585831			
Hydnum albidum	AY817135/–			
Hydnum albomagnum	DQ218305/–			
Hydnum albidum	–/AY293186			
Hydnum albomagnum	–/AY700199			
Hydnum ellipsosporum	AY817138/–			
Hydnum magnorufescens	KC293545/–			
Hydnum ovoideisporum f. *depauperatum*	KC293544/–			
Hydnum aff. *repandum*	DQ218306/–			
Hydnum rufescens 1	–/AJ406427			
Hydnum rufescens 2	AY817137/–			
Hydnum umbilicatum 1	–/AY041170			
Hydnum umbilicatum 2	AJ534973/–			
Hydnum vesterholtii	HE611085/–			
Minimedusa obcoronata 1	–/GQ303309			
Minimedusa obcoronata 2	GQ303278/–			
Minimedusa polyspora 1	–/AB972779			
Minimedusa polyspora 2	–/DQ915476			
Minimedusa polyspora 3	KF182184/–			
Minimedusa polyspora 4	AB972802/–			
Minimedusa pubescens (T)	–/DQ915473	Belgium	*Scoliciosporum chlorococcum*	Heylen L03/117 (BR)
uncultured *Minimedusa* clone	GU055556/–			
Multiclavula corynoides	MCU66440/–			
Multiclavula mucida 1	EU909345 both			
Multiclavula mucida 2	–/AF287875			
Multiclavula mucida 3	DQ521417/–			
Neoburgoa freyi 1 (T)	KX423756 both	Switzerland	*Cladonia rangiferina*	Zimmermann LF1256 (G)
Neoburgoa freyi 2	KX423755 both	Switzerland	*Cladonia rangiferina*	id., culture JL596-16
Parmeliicida pandemica 1 (T)	**MZ509450 both**	France	*Parmelia saxatilis*	Diederich 18144 (BR)

Supplementary document S4. (Continued)

Species	GenBank ITS/nuLSU	Country	Host	Specimen
Parmeliicida pandemica 2	**MZ509446 both**	Austria	*Parmelia sulcata*	Berger 35564 (GMUF)
Platygloea disciformis	–/AY629314			
Sebacina vermifera	DQ983816/–			
Sistotrema alboluteum	–/AJ606042			
Sistotrema brinkmannii 1	–/AJ406430			
Sistotrema brinkmannii 2	HM535376/–			
Sistotrema confluens	–/AY647214			
Sistotrema coroniferum	–/AM259215			
Sistotrema coronilla	DQ397337/–			
Sistotrema eximum 1	–/AF393076			
Sistotrema eximum 2	AM259218/–			
Sistotrema oblongisporum 1	–/AY647210			
Sistotrema oblongisporum 2	GQ162819/–			
Sistotrema raduloides 1	–/AY647213			
Sistotrema raduloides 2	KP739873/–			
Sistotrema sernanderi	AF506476 both			
Sistotremastrum niveocremeum	–/AJ406429			
Thanatephorus cucumeris 1	–/AF354068			
Thanatephorus cucumeris 2	JQ692292/–			
Thanatephorus cucumeris 3	EU244845/–			
Thanatephorus theobromae	HQ424252/–			
uncultured *Thanatephorus* clone	FJ688116/–			
Tilletiaria anomala	–/AY745715			
Tremellodendron ocreatum	KT339265/–			
uncultured *Tulasnella* isolate GA2b	EF374113 both			
Uthatobasidium fusisporum	DQ398957/–			
uncultured basidiomycete	AM902055/–			
uncultured *Basidiomycota*	GU328620 both			
uncultured fungus	KF617752 both			
uncultured mycorrhiza	AY634130 both			
fungal sp.	JN104552/–			

Class *Agaricomycetes*, order *Corticiales*

by P. Diederich, M. Ghobad-Nejhad & J. D. Lawrey

Supplementary document S5. Methods used to determine the placement of lichenicolous and endolichenic species in the phylogeny of the family *Corticiaceae* (*Corticiales*) (page 71).

Species for the phylogenetic analyses were sampled from the four families in the order *Corticiales* with more focus on the family *Corticiaceae* (Ghobad-Nejhad et al. 2021). Generic types were included and for each species, only one specimen was selected, preferably from the type specimens. A concatenated dataset was constructed from the sequences of nuLSU and ITS regions. The alignments were computed in MUSCLE (Madeira et al. 2019) and optimised using Gblocks v. 0.91b (Castresana 2000). The combined dataset was analysed using MrBayes v. 3.2.7a (Ronquist et al. 2012), implementing the GTR + G model of nucleotide evolution for ITS and GTR + I + G for nuLSU, as inferred from MrModeltest 2.3 (Nylander 2004). *Leptocorticium tenellum* from *Russulales* was selected as an outgroup following He et al. (2019). The dataset was analysed using two independent runs for 20M generations. The trees and parameters were sampled every 5000 generations. Burn-in was set to discard 50 % of samples. The majority-rule consensus tree was assembled from post-burn-in trees. The Bayesian analyses were run at the CIPRES Science Gateway (Miller et al. 2010).

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Supplementary document S6. Species, GenBank accession numbers (nuLSU + ITS) and specimen information (only for lichenicolous taxa) of fungi used in the phylogenetic analysis of the family *Corticiaceae*, *Corticiales* (page 71). Type material of lichenicolous species is indicated with (T).

Species	GenBank ITS/nuLSU	Country	Host	Specimen
Australovuilleminia coccinea	HM046875/HM046930			
Basidiodesertica hydei	MW077150/MW077159			
Bernardia incrustans	MH855759/MH867272			
Corticium boreoroseum	MW805845/HM046919			
Corticium malagasoroseum	MW805856/MW805822			
Corticium roseum	MH856944/MH868469			
Corticium silviae (T)	MH520061/MH520061	Switzerland	*Thamnolia*	Feusi (G)
Corticium thailandicum	MW805868/MW805831			
Cytidia salicina	GU590881/HM046921			
Dendrocorticium polygonioides	MH857528/MH869064			
Dendrocorticium roseocarneum	MH858810/MH870449			

Supplementary document S6. (Continued)

Species	GenBank ITS/nuLSU	Country	Host	Specimen
Dendrominia dryina	JX892936/JX892937			
Dendrominia ericae	JX892938/JX892939			
Dendrominia maculata	–/AY586652			
Disporotrichum dimorphosporum	MH859776/MH871538			
Erythricium atropatanum	GU590876/GU590880			
Erythricium aurantiacum	HQ168397/HQ168397	Luxembourg	*Physcia tenella*	Diederich 16901 (BR)
Erythricium hypnophilum	MW805859/MW805824			
Erythricium laetum	GU590875/GU590878			
Erythricium salmonicolor	KF029722/KF029722			
Erythricium vernum	MW805865/MW805828			
Giulia tenuis	–/EF589739			
Laetisaria agaves	MW805851/–			
Laetisaria buckii (T)	–/DQ915472	USA	*Bacidia heterochroa*	Buck 43835 (NY)
Laetisaria culmigena	EU622849/EU622848			
Laetisaria endoxylon	MW805854/–			
Laetisaria fuciformis	MH856485/MH868023			
Laetisaria lichenicola (T)	NR_121484/HQ168400	Luxembourg	*Physcia tenella*	Diederich 16900 (BR)
Laetisaria marsonii	NR_164214/EU622839			
Laetisaria nothofagicola	DQ915474/DQ915474			
Laetisaria roseipellis	EU622846/EU622844			
Lawreymyces bogotensis	MF070062/–	Colombia	*Normandina* sp.	Lücking & Moncada 41028a (B)
Lawreymyces columbiensis	MF070060/–	Colombia	*N. columbiensis*	Moncada 10521 (B)
Lawreymyces confusus	MF070057/–	Colombia	*N.* aff. *columbiensis*	Moncada 10567 (B)
Lawreymyces foliaceae	MF070054/–	Colombia	*Agonimia foliacea*	Lücking & Moncada 33368 (B)
Lawreymyces palicei	AY542865/AY542865	Ecuador	*A. foliacea*	Palice & Soldán 4369 (F)
Lawreymyces pulchellae	MF070063/–	Colombia	*N. pulchella*	Moncada 10624 (B)
Lawreymyces spiribillei	MF070056/–	Colombia	*A. foliacea*	Moncada 5410 (B)
Leptocorticium tenellum	KU183719/KU183720			
Marchandiomyces allantosporus	MW805877/–			
Marchandiomyces aurantioroseus	KP864659/HM046929			
Marchandiomyces corallinus	AY583327/AY583331	Scotland	*Parmelia sulcata*	Diederich 15630 (BR)
Marchandiomyces lignicola	AY583328/–			
Marchandiomyces sp.	KU213580/–			
Punctularia strigosozonata	MH855559/MH867064			
Punctulariopsis obducens	HM046918/HM046933			
Punctulariopsis subglobispora	HM046917/HM046932			
Vuilleminia comedens	HM046882/HM046922			
Vuilleminia cystidiata	HM046909/HM046923			
Vuilleminia pseudocystidiata	HM046888/HM046928			
Waitea arvalis	NR_119689/EU622842			
Waitea circinata	MH855962/MH867457			
Waitea guianensis	MW449090/MW449101			

Class *Tremellomycetes*, order *Filobasidiales*

by P. Diederich, A. M. Millanes, A. Flakus, P. Rodriguez-Flakus, J. Etayo & M. Wedin

Supplementary document S7. Methods used to determine the phylogenetic relationships of the lichenicolous taxa of the order *Filobasidiales* (pages 83 and 84).

Molecular data obtained from *Zyzygomyces* specimens

DNA from lichenicolous specimens was extracted using the Qiagen DNeasy Plant Mini Kit (Qiagen, Venlo, the Netherlands), according to the manufacturer's instructions. Specific primers suitable for species in the *Tremellomycetes*, viz. ITS1F (Gardes and Bruns, 1993), LR5 (Vilgalys and Hester, 1990), BasidLSU3-3, BasidLSU1-3, BasidLSU1-5 and BasidLSU3-5 (Millanes et al. 2011) were used to amplify the internal transcribed spacer (ITS) and a fragment of ca. 1000 nucleotides in the nuLSU.

PCR amplifications were performed using Illustra™ Hot Start PCR beads, according to the manufacturer's instructions, following Millanes et al. (2011). For the primer pairs ITS1F/BasidLSU3-3 and BasidLSU3-5/LR5, the PCR settings consisted of initial denaturing at 95 ºC for 3 min, four cycles (95 ºC for 40 s, 53 ºC for 40 s and 72 ºC for 90 s), four cycles (95 ºC for 30 s, 50 ºC for 30 s and 72 ºC for 90 s), and finally 32 cycles (95 ºC for 30 s, 47 ºC for 30 s and 72 ºC for 90 s) with a final extension at 72 ºC for 480 s. For the primer pair ITS1F/BasidLSU1- 3, BasidLSU1-5/LR5 and LR0R/LR5 we used initial denaturing at 95 ºC for 3 min, four cycles (95 ºC for 40 s, 56 ºC for 40 s and 72 ºC for 90 s), four cycles (95 ºC for 30 s, 53 ºC for 30 s and 72 ºC for 90 s) and finally 32 cycles (95 ºC for 30 s, 50 ºC for 30 s and 72 ºC for 90 s) with a final extension at 72 ºC for 420 s. Before sequencing, the PCR products were purified with Exo-sap-ITTM (USB Corporation, Cleveland, Ohio, USA). The purified samples were sequenced by Macrogen (Madrid, Spain). Sequence fragments were assembled and edited using Geneious Prime ®2021.0.3. (https://www.geneious.com).

Taxon sampling and phylogenetic analyses

We produced two data matrices for subsequent phylogenetic analyses, using sequences of the ITS1, 5.8S, ITS2, and LSU nuclear rDNA. The first (dataset 1) included only 9 taxa in *Zyzygomyces*, as a fair representation of the diversity in the group, and representatives of the seven accepted genera in the *Filobasidiales* (i.e., *Goffeauzyma*, *Filobasidium*, '*Heterocephalacria*', *Naganishia*, *Piskurozyma*, *Solicoccozyma* and *Syzygospora*; Liu et al. 2015). *Holtermannia corniformis* was used as outgroup, based on Liu et al. (2015). We assembled this dataset to test the monophyly of *Zyzygomyces* within the *Filobasidiales*. In dataset 1, large parts of the ITS could not be aligned and were therefore excluded from the matrix. The second (dataset 2) included all sequenced *Zyzygomyces* specimens, and a sequence of '*Heterocephalacria*' *sinensis* was used as outgroup, based on the trees obtained using dataset 1. In this dataset, larger parts of the ITS1 and ITS2 were used, which allowed to better test species delimitation in the genus. Dataset 1 consisted of 33 terminals with 1225 characters – 316 of which were parsimony-informative and 757, constant. Dataset 2 consisted of 55 terminals with 1552 characters – 126 of which were parsimony-informative and 1234, constant.

For phylogenetic analyses, sequences were aligned using MAFFT version 7 (Katoh et al. 2019) with the Q-INS-i algorithm. The alignments were trimmed to exclude ambiguously aligned regions using GBlocks (Castresana 2000), following the relaxed conditions described by Talavera & Castresana (2007), and manually checked, before and after trimming, using Mesquite 3.7 (Maddison & Maddison 2021). We considered two independent partitions, ITS (1-553) and nuLSU (554-1225), in analyses of dataset 1, and four independent partitions, ITS1 (1-202), 5.8S (203-358), ITS2 (359-592) and nuLSU (593-1552), in analyses of dataset 2. Each partition was analysed individually by maximum likelihood ultrafast bootstrap in IQTree to assess for conflicts. Strongly supported clades (IQTree UF-BS higher than 95 %) in disagreement were considered an indication of significant conflict (Mason - Gamer & Kellogg 1996, Hoang et al. 2018). Since no conflict was detected in our data sets, we combined them and analysed them using maximum likelihood (ML) and Bayesian approaches. Maximum likelihood analyses were carried out in IQTree (Nguyen et al. 2015). Model selection for each partition was achieved using ModelFinder in IQTree (Kalyaanamoorthy et al. 2017), with the corrected Akaike information criterion (AICc). For dataset 1, the TIM2e + Γ4 was selected for both the ITS and the nuclear LSU. For dataset 2, the K2P was selected for the ITS1, the K3P for the 5.8S, the K2P + Γ for the ITS2, and the TN + F + Γ4 for the nuclear LSU. We assessed node support by standard bootstrap using 1000 bootstrap pseudoreplicates. Bayesian analyses were performed by Markov chain Monte Carlo (MCMC) sampling as implemented in the software MrBayes 3.2.7a (Ronquist et al. 2012) As not all models tested by ModelFinder in IQTree can be directly implemented in MrBayes, for the Bayesian analyses we selected among a subsample of substitution models using the corrected Akaike information criterion (AICc) as implemented in jModelTest 2 (Darriba et al. 2012), allowing only 3 substitution schemes, using full likelihood optimization and four discrete gamma categories. For dataset 1, the GTR + I+ Γ was selected for both the ITS and nuclear LSU rDNA. For dataset 2, the K80 + Γ was selected for the ITS1, the GTR + Γ for the 5.8S, the HKY + Γ for the ITS2, and the GTR + Γ for the nuclear LSU rDNA. The combined analyses treated the different regions as separate partitions with topology linked across partitions but separate model parameter values and proportional rates across partitions. For each combined dataset, two parallel runs were performed, each with four chains, three of which were incrementally heated with a temperature of 0.15. The analyses were diagnosed for convergence every 100 000 generations and were set to halt automatically when the average standard deviation of splits across runs in the last half of the analysis descended below 0.01. Every 100th tree was saved. The first 50% of each run was discarded as burn-in. Both ML and Bayesian analyses were performed on the CIPRES Web Portal (Miller et al. 2015).

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Supplementary document S8. Species, GenBank accession numbers (ITS + nuLSU) and specimen information (only for lichenicolous taxa) of fungi used in the phylogenetic analyses of the order *Filobasidiales* (pages 83 and 84). Newly produced sequences in bold font. Type material of lichenicolous species is indicated with (T).

Species	GenBank ITS/nuLSU	Country	Host	Specimen
Filobasidium floriforme	AF190007/AF075498			
Filobasidium globosporum	AF444336/AF075495			
Goffeauzyma aciditolerans	KF036583/AY731790			
'*Heterocephalacria*' *arrabidensis*	AF444362/KY107865			
'*Heterocephalacria*' *fruticeti*	MK307720/KT314192			
'*Heterocephalacria*' *gelida*	KC455903/KC433839			
'*Heterocephalacria*' *hypogea*	MK307721/KT253539			
'*Heterocephalacria*' *lusitanica*	MK307716/EU002809			

Supplementary document S8. (Continued)

Species	GenBank ITS/nuLSU	Country	Host	Specimen
‘*Heterocephalacria*’ *mucosa*	LC270816/LC270814			
‘*Heterocephalacria*’ *septentrionalis* 1	MN128411/MN449978			
‘*Heterocephalacria*’ *septentrionalis* 2	MN066369/MN066371			
‘*Heterocephalacria*’ *septentrionalis* 3	MN449980/–			
‘*Heterocephalacria*’ *sinensis*	MG909556/KY614524			
‘*Heterocephalacria*’ sp. 1	MH697742/FN824500			
‘*Heterocephalacria*’ sp. 2	MK307714/–			
‘*Heterocephalacria*’ sp. 3	MK307718/FN428974			
Holtermannia corniformis (outgroup)	AF410472/AF189843			
Naganishia antarctica	AF145326/AF075488			
Naganishia globosa	AF444372/AF181539			
Piskurozyma sorana	EU541305/–			
Solicoccozyma aeria 1	AF145324/AF145324			
Solicoccozyma aeria 2	AF444351/AF181523			
Syzygospora alba	JN053509/JN043616			
Syzygospora pallida	JN053508/JN043615			
Zyzygomyces aipoliae 1 (T)	**ON921473/ON922573**	Sweden	*Physcia aipolia*	Millanes & Olsson 726 (S)
Zyzygomyces aipoliae 2	**ON921474/ON922574**	Sweden	*Physcia aipolia*	Millanes & Olsson 726 (S)
Zyzygomyces aipoliae 3	**ON921475/ON922575**	Austria	*Physcia aipolia*	Berger 31521 (herb. Berger)
Zyzygomyces aipoliae 4	**ON921476/ON922576**	Luxembourg	*Physcia aipolia*	Diederich 18185 (BR)
Zyzygomyces bachmannii 1	**ON921477/ON922577**	USA, Alaska	*Cladonia coccifera*	Pérez-Ortega 1070 (MAF-Lich)
Zyzygomyces bachmannii 2	**ON921478/ON922578**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 1080 (MAF-Lich)
Zyzygomyces bachmannii 3	**ON921479/ON922579**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 2368 (MAF-Lich)
Zyzygomyces bachmannii 4	**ON921480/ON922580**	Spain	*Cladonia* sp.	Merinero s.n. (MAF-Lich)
Zyzygomyces bachmannii 5	**ON921481/ON922581**	USA, Alaska	*Cladonia gracilis* ssp. *elongata*	Pérez-Ortega 1732 (MAF-Lich)
Zyzygomyces bachmannii 6	**ON921482/ON922582**	France	*Cladonia furcata*	Sérusiaux s.n. (BR)
Zyzygomyces bachmannii 7	**ON921483/ON922583**	USA, Alaska	*Cladonia gracilis* ssp. *turbinata*	Pérez-Ortega 1737 (MAF-Lich)
Zyzygomyces bachmannii 8	**ON921484/ON922584**	Sweden	*Cladonia macroceras*	Wedin 6802 (UPS)
Zyzygomyces bachmannii 9	**ON921485/ON922585**	Canary Islands	*Cladonia* sp.	Diederich 16685 (BR)
Zyzygomyces bachmannii 10	**ON921486/ON922586**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 1730 (MAF-Lich)
Zyzygomyces bachmannii 11	**ON921487/ON922587**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 2359 (MAF-Lich)
Zyzygomyces bachmannii 12	**ON921488/ON922588**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 2180 (MAF-Lich)
Zyzygomyces bachmannii 13	**ON921489/ON922589**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 2149 (MAF-Lich)
Zyzygomyces bachmannii 14	**ON921490/ON922590**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 2402 (MAF-Lich)
Zyzygomyces bachmannii 15	**ON921491/ON922591**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 2108 (MAF-Lich)
Zyzygomyces bachmannii 16	**ON921492/ON922592**	USA, Alaska	*Cladonia* sp.	Pérez-Ortega 2244 (MAF-Lich)
Zyzygomyces bachmannii 17	**ON921493/ON922593**	USA, Alaska	*Cladonia stellaris*	Pérez-Ortega 1067 (MAF-Lich)
Zyzygomyces leucodermiae	**ON921494/ON922594**	Mauritius	*Leucodermia* sp.	Ertz 23499 (BR)
Zyzygomyces mobergii (T)	**–/ON922595**	Australia	*Polyblastidium* cf. *japonicum*	Moberg A74:11 & B. Owe-Larsson (UPS L-124437)
Zyzygomyces physciacearum 1	**ON921495/ON922596**	Sweden	*Physcia adscendens*	Odelvik 07604 (S F81516)
Zyzygomyces physciacearum 2	**ON921496/ON922597**	Sweden	*Physcia tenella*	Odelvik 10522 (S F178918)

Supplementary document S8. (Continued)

Species	GenBank ITS/nuLSU	Country	Host	Specimen
Zyzygomyces physciacearum 3	**ON921497/ON922598**	Austria	*Physcia dubia* var. *teretiuscula*	Berger 28744 (herb. Berger)
Zyzygomyces physciacearum 4	**ON921498/ON922599**	Italy	*Physcia biziana*	Brackel 5663 (herb. Brackel)
Zyzygomyces physciacearum 5	**ON921499/ON922600**	Spain	*Physcia tenella*	Etayo 24300 (herb. Etayo)
Zyzygomyces physciacearum 6	**ON921500/ON922601**	Spain	*Physcia* sp.	Millanes s. n. (S)
Zyzygomyces physciacearum 7	**ON921501/ON922602**	Spain	*Physcia* sp.	Millanes 1572 (S)
Zyzygomyces physciacearum 8	**ON921502/ON922603**	Italy	*Physcia biziana*	Brackel 6830 (herb. Brackel)
Zyzygomyces physciacearum 9	**ON921503/ON922604**	Italy	*Physcia stellaris*	Kukwa 21560 (UGDA)
Zyzygomyces physciacearum 10	**ON921504/ON922605**	Spain	*Physcia tenella*	Millanes 1571 (S)
Zyzygomyces physciacearum 11	**ON921505/ON922606**	Spain	*Physcia* sp.	Millanes 1588 (S)
Zyzygomyces physciacearum 12	**ON921506/ON922607**	Sweden	*Physcia tenella*	Odelvik 11481 (S F206798)
Zyzygomyces physciacearum 13	**–/ON922608**	Austria	*Physcia dubia* var. *teretiuscula*	Berger 7409 (BR)
Zyzygomyces physconiae 1	**ON921507/ON922609**	Italy	*Physconia grisea*	Brackel 6882 (herb. Brackel)
Zyzygomyces physconiae 2	**ON921508/ON922610**	France	*Physconia grisea*	Poumarat 2013-336 (BR)
Zyzygomyces physconiae 3 (T)	**ON921509/ON922611**	France	*Physconia grisea*	Pinault s. n. (BR) (10 May 2020)
Zyzygomyces physconiae 4	**ON921510/ON922612**	Italy	*Physconia grisea*	Brackel 6579 (herb. Brackel)
Zyzygomyces physconiae 5	**ON921511/ON922613**	Italy	*Physconia grisea*	Diederich 19579 (BR)
Zyzygomyces physconiae 6	**ON921512/ON922614**	France	*Physconia grisea*	Pinault s. n. (BR) (23 March 2020)
Zyzygomyces physconiae 7	**ON921513/ON922615**	Italy	*Physconia grisea*	Brackel 8062 (herb. Brackel)
Zyzygomyces physconiae 8	**ON921514/ON922616**	Italy	*Physconia grisea*	Brackel 8100 (herb. Brackel)
Zyzygomyces polyblastidii 1	**ON921515/ON922617**	Bolivia	*Polyblastidium japonicum*	Etayo 30678 (herb. Etayo)
Zyzygomyces polyblastidii 2	**ON921516/ON922618**	Bolivia	*Polyblastidium* cf. *japonicum*	Etayo 30521 (herb. Etayo)
Zyzygomyces polyblastidii 3 (T)	**ON921517/ON922619**	Bolivia	*Polyblastidium japonicum*	Flakus 27763 (KRAM)
Zyzygomyces polyblastidii s. l. 1	**–/ON922620**	Bolivia	*Polyblastidium* sp.	Etayo 28780 (herb. Etayo)
Zyzygomyces polyblastidii s. l. 2	**–/ON922621**	Bolivia	*Polyblastidium japonicum*	Etayo 29935 (herb. Etayo)
Zyzygomyces polyblastidii s. l. 3	**–/ON922622**	Bolivia	*Polyblastidium* cf. *japonicum*	Flakus 25681 (KRAM)
Zyzygomyces polyblastidii s. l. 4	**–/ON922623**	Bolivia	*Polyblastidium* sp.	Etayo 27414 (herb. Etayo)
Zyzygomyces polyblastidii s. l. 5	**ON921518/ON922624**	USA, North Carolina	*Polyblastidium* sp.	Lendemer 46912 (NY)
Zyzygomyces polyblastidii s. l. 6	**ON921519/ON922625**	USA, North Carolina	*Polyblastidium* sp.	Lendemer 23503 (NY)
Zyzygomyces sp. 1	**–/ON922626**	Japan	*Heterodermia isidiophora*	Ertz 24665 (BR)

Class *Tremellomycetes*, order *Tremellales*

by P. Diederich, A. M. Millanes & M. Wedin

Supplementary document S9. Methods used to determine the phylogenetic relationships of the lichenicolous taxa of the order *Tremellales* (pages 106–109).

Molecular data obtained from *Tremellales* specimens

DNA from lichenicolous specimens was extracted using the Qiagen DNeasy Plant Mini Kit (Qiagen, Venlo, the Netherlands), according to the manufacturer's instructions. Specific primers suitable for species in the *Tremellomycetes*, viz. ITS1F (Gardes & Bruns 1993), LR5 (Vilgalys & Hester 1990), BasidLSU3-3, BasidLSU1-3, BasidLSU1-5 and BasidLSU3-5 (Millanes et al. 2011) were used to amplify the internal transcribed spacer (ITS) and a fragment of ca. 1000 nucleotides in the nuLSU.

PCR amplifications were performed using Illustra™ Hot Start PCR beads, according to the manufacturer's instructions, following Millanes et al. (2011). For the primer pairs ITS1F/BasidLSU3-3 and BasidLSU3-5/LR5, the PCR settings consisted of initial denaturing at 95 ºC for 3 min, four cycles (95 ºC for 40 s, 53 ºC for 40 s and 72 ºC for 90 s), four cycles (95 ºC for 30 s, 50 ºC for 30 s and 72 ºC for 90 s), and finally 32 cycles (95 ºC for 30 s, 47 ºC for 30 s and 72 ºC for 90 s) with a final extension at 72 ºC for 480 s. For the primer pair ITS1F/BasidLSU1-3, BasidLSU1-5/LR5 and LR0R/LR5, we used initial denaturing at 95 ºC for 3 min, four cycles (95 ºC for 40 s, 56 ºC for 40 s and 72 ºC for 90 s), four cycles (95 ºC for 30 s, 53 ºC for 30 s and 72 ºC for 90 s) and finally 32 cycles (95 ºC for 30 s, 50 ºC for 30 s and 72 ºC for 90 s) with a final extension at 72 ºC for 420 s. Before sequencing, the PCR products were purified with Exo-sap-ITTM (USB Corporation, Cleveland, Ohio, USA). The purified samples were sequenced by Macrogen (Madrid, Spain). Sequence fragments were assembled and edited using Geneious Prime ®2021.0.3. (https://www.geneious.com).

Taxon sampling and phylogenetic analyses

We produced two data matrices for subsequent phylogenetic analyses, using sequences of the ITS1, 5.8S, ITS2, and LSU nuclear rDNA. The first (dataset 1) included representatives of the eleven currently accepted families in the group (i. e., *Bulleraceae*, *Bulleribasidiaceae*, *Carcinomycetaceae*, *Cryptococcaceae*, *Cuniculitremaceae*, *Naemateliaceae*, *Phaeotremellaceae*, *Rhynchogastremaceae*, *Sirobasidiaceae*, *Tremellaceae* and *Trimorphomycetaceae*; Liu et al. 2015). In addition, we included one representative of each sequenced and previously described lichenicolous species, plus all sequenced specimens for the species newly described in this Flora. *Trichosporon ovoides* was used as outgroup, based on Liu et al. (2015). In dataset 1, large parts of the ITS could not be aligned and were therefore excluded from the matrix. The second (dataset 2) included a larger number of *Biatoropsis* specimens, and *Tremella macrobasidiata* was used as outgroup, based on previous phylogenies. In this dataset, larger parts of the ITS1 and ITS2 were used, which allowed to better test species delimitation in this genus (Supplementary Table S10). Dataset 1 consisted of 132 terminals with 1085 characters – 343 of which were parsimony-informative and 590, constant. Dataset 2 consisted of 84 terminals with 1325 characters – 214 of which were parsimony-informative and 1025, constant.

For phylogenetic analyses, sequences were aligned using MAFFT version 7 (Katoh et al. 2019) with the Q-INS-i algorithm. The alignments were trimmed to exclude ambiguously aligned regions using GBlocks (Castresana 2000), following the relaxed conditions described by Talavera & Castresana (2007), and manually checked, before and after trimming, using Mesquite 3.7 (Maddison & Maddison 2021). We considered four partitions, ITS1 (1-15), 5.8S (16-123), ITS2 (124-191) and nuLSU (192-1085), in analyses of dataset 1 and ITS1 (1-88), 5.8S (89-247), ITS2 (248-384) and nuLSU (385-1325), in analyses of dataset 2. Each partition was analysed individually by maximum likelihood ultrafast bootstrap in IQTree to assess for conflicts. Strongly supported clades (IQTree UF-BS higher than 95 %) in disagreement were considered an indication of significant conflict (Mason-Gamer & Kellogg 1996, Hoang et al. 2018). Since no conflict was detected in our data sets, we combined them and analysed them using maximum likelihood (ML) and Bayesian approaches. Maximum likelihood analyses were carried out in IQTree (Nguyen et al. 2015). Model selection for each partition was achieved using ModelFinder in IQTree (Kalyaanamoorthy et al. 2017), with the corrected Akaike information criterion (AICc). For dataset 1, TIM3e + I + Γ4 was selected for all partitions, which were merged in a single partition in the ML analyses. For dataset 2, the TNe+I+Γ4 was selected for all partitions, which were merged in a single partition in the ML analyses. We assessed node support by standard bootstrap using 1000 bootstrap pseudoreplicates. Bayesian analyses were performed by Markov chain Monte Carlo (MCMC) sampling as implemented in the software MrBayes 3.2.7a (Ronquist et al. 2012) As not all models tested by ModelFinder in IQTree can be directly implemented in MrBayes, for the Bayesian analyses we selected among a subsample of substitution models using the corrected Akaike information criterion (AICc) as implemented in jModelTest 2 (Darriba et al. 2012), allowing only 3 substitution schemes, using full likelihood optimization and four discrete gamma categories. For dataset 1, the GTR + Γ was selected for the ITS1, the GTR + I for the 5.8S, the GTR + I + Γ for the ITS2, and the SYM + I + Γ for the nuclear LSU rDNA. For dataset 2, the HKI + I was selected for the ITS1, the JC for the 5.8S, the K80 + Γ for the ITS2, and the GTR + I + Γ for the nuclear LSU rDNA. The combined analyses treated the different regions as separate partitions with topology linked across partitions, but separate model parameter values and proportional rates across partitions. For each combined dataset, two parallel runs were performed, each with four chains, three of which were incrementally heated with a temperature of 0.15. The analyses were diagnosed for convergence every 100 000 generations and were set to halt automatically when the average standard deviation of splits across runs in the last half of the analysis descended below 0.01. Every 100th tree was saved. The first 50% of each run was discarded as burn-in. Both ML and Bayesian analyses were performed on the CIPRES Web Portal (Miller et al. 2015).

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Supplementary document S10. Species, GenBank accession numbers (ITS + nuLSU) and specimen information (only for lichenicolous taxa or for newly sequenced specimens) of fungi used in the phylogenetic analyses of the order *Tremellales* (pages 106–109). Newly produced sequences in bold font. Type material of lichenicolous species is indicated with (T).

Species	GenBank (ITS+nuLSU)	Country	Host	Specimen
Biatoropsis angulatae (T)	**ON873035/ON930037**	USA, Minnesota	*Usnea angulata*	Henderson 59 (BR)
Biatoropsis antarcticae 1 (T)	**ON873036/ON930038**	Antarctica	*Usnea antarctica*	Etayo 31265 (MAF-Lich)
Biatoropsis antarcticae 2	**–/ON930039**	Antarctica	*Usnea antarctica*	Etayo 31457 (herb. Etayo)
Biatoropsis hafellneri 1	KX687745/**ON930040**	Canary Islands	*Usnea cornuta*	Wagner 16-14 (BR)
Biatoropsis hafellneri 2	KX687728/**ON930041**	Norway	*Usnea cornuta*	Haugan 7969, young basidioma (O L157359)
Biatoropsis hafellneri 3	**ON873037/ON930042**	Norway	*Usnea cornuta*	Haugan 7969, old basidioma (O L157359)

Supplementary document S10. (Continued)

Species	**GenBank (ITS+nuLSU)**	**Country**	**Host**	**Specimen**
Biatoropsis hafellneri 4	KJ404880/KJ437226	Azores	*Usnea cornuta*	Diederich 17087b (S F264687)
Biatoropsis hafellneri 5	KJ404881/–	UK	*Usnea cornuta*	Wedin 7306 (S F92121)
Biatoropsis hafellneri 6	KX687729/**ON930043**	UK	*Usnea cornuta*	Millanes (S F291458)
Biatoropsis hafellneri 7	KX687725/**ON930044**	Madeira	*Usnea fragilescens* aggr.	Diederich 17796, pale (S F291456)
Biatoropsis hafellneri 8	KX687726/**ON930045**	Madeira	*Usnea fragilescens* aggr.	Diederich 17796, dark (S F291456)
Biatoropsis hafellneri 9	KX687723/**ON930046**	Madeira	*Usnea fragilescens* aggr.	Diederich 17791 (S F291448)
Biatoropsis hafellneri 10	KX687722/**ON930047**	Madeira	*Usnea fragilescens* aggr.	Diederich 17788 (BR)
Biatoropsis hafellneri 11	KX687727/**ON930048**	Madeira	*Usnea fragilescens* aggr.	Diederich 17800 (BR)
Biatoropsis hafellneri 12	**ON873038/ON930049**	Canary Islands	*Usnea cornuta*	Wagner 16-13 (BR)
Biatoropsis hafellneri 13 (T)	KJ406274/KJ406304	UK	*Usnea cornuta*	Wedin 7308 (F102403)
Biatoropsis hafellneri 14	KX687724/**ON930050**	Madeira	*Usnea fragilescens* aggr.	Diederich 17793 (BR)
Biatoropsis hirtae	**ON873039/ON930051**	USA, Arizona	*Usnea hirta*	Thayer 34 (BR)
Biatoropsis macaronesica 1	KX687743/**ON930052**	Madeira	*Usnea esperantiana*	Diederich 17774 (BR)
Biatoropsis macaronesica 2	KX687741/**ON930053**	Madeira	*Usnea esperantiana*	Diederich 17772 (BR)
Biatoropsis macaronesica 3	**ON873040/ON930054**	Canary Islands	*Usnea macaronesica*	Wagner 16-9 (BR)
Biatoropsis macaronesica 4	KX687742/**ON930055**	Madeira	*Usnea esperantiana*	Diederich 17773 (S F291464)
Biatoropsis macaronesica 5	KJ406281/KJ406311	Spain	*Usnea glabrata*	Pérez-Ortega b (MAF-Lich)
Biatoropsis macaronesica 6	KX687745/**ON930056**	Madeira	*Usnea esperantiana*	Diederich 17780 (BR)
Biatoropsis macaronesica 7	KJ404859/KJ437204	New Zealand	*Usnea flavocardia*	Myles (S F186043)
Biatoropsis macaronesica 8	KX687746/**ON930057**	Madeira	*Usnea flavocardia*	Diederich 17782 (S)
Biatoropsis macaronesica 9	KX687740/**ON930058**	Madeira	*Usnea flavocardia*	Diederich 17770 (BR)
Biatoropsis macaronesica 10	KX687747/**ON930059**	Madeira	*Usnea flavocardia*	Diederich 17797 (BR)
Biatoropsis macaronesica 11	KX687744/**ON930060**	Madeira	*Usnea flavocardia*	Diederich 17779 (BR)
Biatoropsis macaronesica 12	KJ404857/KJ437202	Spain	*Usnea glabrata*	Pérez-Ortega a (MAF-Lich)
Biatoropsis macaronesica 13 (T)	**ON873041/ON930061**	Canary Islands	*Usnea esperantiana*	Wagner 16-10 (BR)
Biatoropsis macaronesica 14	KJ406276/KJ406306	New Zealand	*Usnea* sp. (gr. *cornuta*)	Wedin 9033 (S F180874)
Biatoropsis millanesiana 1 (T)	MN973671/MN973663	Mauritius	*Usnea exasperata* s. l.	Diederich 18524 (MAU)
Biatoropsis millanesiana 2	MN973667/MN973659	Mauritius	*Usnea exasperata*	Diederich 19029 (MAU)
Biatoropsis millanesiana 3	MN973666/MN973658	Mauritius	*Usnea exasperata*	Diederich 18979 (MAU)
Biatoropsis millanesiana 4	MN973668/MN973660	Mauritius	*Usnea exasperata*	Diederich 18997 (MAU)
Biatoropsis millanesiana 5	MN973669/MN973661	Mauritius	*Usnea exasperata*	Diederich 18921 (MAU)
Biatoropsis millanesiana 6	KX687750/MN973656	Mauritius	*Usnea exasperata*	Diederich 18087 (SEY)
Biatoropsis millanesiana 7	MN973670/MN973662	Mauritius	*Usnea exasperata*	Diederich 18291 (MAU)
Biatoropsis minuta 1 (T)	KJ404869/KJ437214	Spain	*Usnea barbata*	Aragón (S F102398)
Biatoropsis minuta 2	KJ406265/KJ406295	Sweden	*Usnea lapponica*	Hagner (S F92134)
Biatoropsis minuta 3	KJ404866/KJ437211	Canada	*Usnea* cf. *barbata*	Diederich 17269 (BR)
Biatoropsis minuta 4	KJ404870/KJ437215	Spain	*Usnea lapponica*	Burgaz (MA-Fungi 48236)
Biatoropsis minuta 5	KJ404871/KJ437216	Spain	*Usnea* cf. *barbata*	Merinero (S F264683)
Biatoropsis minuta 6	JN053487/JN043593	Sweden	*Usnea lapponica*	Wedin 7903 (S F102401)
Biatoropsis minuta 7	KJ406264/KJ406294	Sweden	*Usnea lapponica*	Hagner (UPS 355785)

Supplementary document S10. (Continued)

Species	GenBank (ITS+nuLSU)	Country	Host	Specimen
Biatoropsis minuta 8	KJ406266/KJ406296	India	*Usnea lapponica*	Divakar (MAF-Lich)
Biatoropsis minuta 9	KX687730/**ON930062**	Sweden	*Usnea lapponica*	Westberg (S F291459)
Biatoropsis nigrescens 1 (T)	**ON873042/ON930063**	Australia	*Usnea capillacea*	Berger 32655 (BR)
Biatoropsis nigrescens 2	**ON873043/ON930064**	New Zealand	*Usnea* sp.	Berger 31714 (herb. Berger)
Biatoropsis protousneae 1 (T)	KJ406287/KJ406317	Chile	*Protousnea dusenii*	Pérez-Ortega 207 (S F291460)
Biatoropsis protousneae 2 (T)	KJ406291/KJ406321	Chile	*Protousnea dusenii*	Pérez-Ortega 207 (MAF-Lich)
Biatoropsis protousneae 3	KJ404861/KJ437206	Argentina	*Protousnea dusenii*	Wedin 8601 (S F264822)
Biatoropsis protousneae 4	KJ406289/KJ406319	Chile	*Protousnea dusenii*	Pérez-Ortega 257 (MAF-Lich)
Biatoropsis protousneae 5	KJ404860/KJ437205	Chile	*Protousnea dusenii*	Pérez-Ortega 216 (MAF-Lich)
Biatoropsis protousneae 6	KJ404865/KJ437210	Argentina	*Protousnea dusenii*	Wedin 8615 (S F264823)
Biatoropsis rubicundae 1 (T)	KX687749/MN973657	France	*Usnea rubicunda*	Diederich 18149 (BR)
Biatoropsis rubicundae 2	KJ404885/KJ437230	USA, California	*Usnea ceratina*	Kocourková (S F264679)
Biatoropsis rubicundae 3	KJ404884/KJ437229	New Zealand	*Usnea* sp.	Berger 16609 (S F92784)
Biatoropsis rubicundae 4	MN973672/MN973664	New Zealand	*Usnea rubicunda*	Berger 31715 (S)
Biatoropsis rubicundae 5	KJ404883/KJ437228	New Zealand	*Usnea rubicunda*	Wedin 9429 (S F181399)
Biatoropsis usnearum 1	**ON873044/ON930065**	USA, Minnesota	*Usnea cavernosa*	Gockman 5796 (BR)
Biatoropsis usnearum 2	**ON873045/ON930066**	USA, Minnesota	*Usnea cavernosa*	Gockman 5556 (BR)
Biatoropsis usnearum 3	**ON873046/ON930067**	USA, Minnesota	*Usnea subfloridana*	Gockman 5547 (BR)
Biatoropsis usnearum 4	KJ404875/KJ437220	Sweden	*Usnea florida*	Westberg 09-675 (S F264682)
Biatoropsis usnearum 5	**ON873047/ON930068**	USA, Minnesota	*Usnea* cf. *subfloridana*	Gockman 5554b
Biatoropsis usnearum 6	**ON873048/ON930069**	USA, Minnesota	*Usnea* cf. *subfloridana*	Gockman 5600 (BR)
Biatoropsis usnearum 7	KX687738/**ON930070**	UK	*Usnea* cf. *florida*	Millanes 507 (S F291462)
Biatoropsis usnearum 8	KJ404877/KJ437222	Sweden	*Usnea subfloridana*	Westberg 09-674 (S F264680)
Biatoropsis usnearum 9	KX687734/**ON930072**	Canada	*Usnea* sp.	Björk 14689 (UBC)
Biatoropsis usnearum 10	KX687733/**ON930073**	Canada	*Usnea glabrescens*	Goward (UBC)
Biatoropsis usnearum 11	–/**ON930074**	USA, Minnesota	*Usnea cavernosa*	Gockman 5797 (BR)
Biatoropsis usnearum 12	KX687732/**ON930075**	Canada	*Usnea glabrescens*	Goward s.n, brown galls (UBC)
Biatoropsis usnearum 13	KX687731/**ON930076**	Canada	*Usnea glabrescens*	Goward s.n, pale galls (UBC)
Biatoropsis usnearum 14	–/**ON930077**	Canada	*Usnea glabrescens*	Björk 22523 (UBC)
Biatoropsis usnearum 15	**ON873049/ON930078**	Canada	*Usnea barbata*	Bjork 22569 (UBC)
Biatoropsis usnearum 16	**ON873050/ON930079**	Sweden	*Usnea* sp.	Millanes 005 (S-F102399)
Biatoropsis usnearum 17	KJ404876/KJ437221	Sweden	*Usnea subfloridana*	Westberg 09-676 (S F264681)
Biatoropsis usnearum 18	KJ404878/KJ437224	Austria	*Usnea* cf. *florida*	Hafellner 49578 (GZU 02-99)
Biatoropsis usnearum 19	KJ404879/KJ437225	UK	*Usnea subfloridana*	Coppins (S F102407)
Biatoropsis sp. E	KJ404882/KJ437227	Argentina	*Protousnea magellanica*	Wedin 8742 (S F264824)
Bullera alba	AF444368/AF075500			
Bulleribasidium oberjochense	GU327541/AF416646			
Carcinomyces effibulatus	JN053499/JN043605			
Carlosrosaea vrieseae	JX268526/JX280388			
Cryptococcus neoformans	AF444326/AF075484			

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Species	GenBank (ITS+nuLSU)	Country	Host	Specimen
Derxomyces mrakii	AB022932/AB118871			
Dimennazyma cistialbidi	KF036589/AY562135			
Dioszegia hungarica	AB049614/AF075503			
Fellomyces polyborus	AF444411/AF189859			
Fibulobasidium inconspicuum	AF444318/AF363641			
Fonsecazyma mujuensis	KF036595/DQ333884			
Gelidatrema spencermartinsiae	EU249514/DQ513279			
Genolevuria amylolytica	KF036585/AY562134			
Hannaella sinensis	AF444468/AF189884			
Heterocephalacria solida	**ON873051/ON930080**	Denmark	*Marasmiellus ramealis*	Eriksen (C F-125449)
Kockovaella thailandica	AB054095/AF075516			
Kwoniella mangroviensis	AF444646/AF444742			
Naematelia encephala	AF042402/AF042220			
Nielozyma melastomae	AB118872/AB119464			
Papiliotrema bandonii	GU327539/AF416642			
Phaeotremella foliacea	JN053502/JN043609			
Pseudotremella moriformis	AF444331/AF075493			
Rhynchogastrema coronatum	MH168095/KJ170152			
Saitozyma flava	AF444338/AF075497			
Sirobasidium brefeldianum	–/ON930081	UK	Unidentified pyrenomycete	
Sirobasidium magnum	JN053497/JN043603			
Sterigmatosporidium polymorphum	KF036596/AY032662			
Sugitazyma miyagiana	AF444409/AF189858			
Tremella anaptychiae (T)	KY950297 KY950300	Spain	*Anaptychia ciliaris*	Zamora (MAF-Lich 21306)
Tremella brodoae (T)	–/**ON930082**	France	*Brodoa intestiniformis*	Pinault (BR)
Tremella caloplacae	**ON873052/ON930083**	Crete	*Variospora dolomiticola*	Diederich 18575 (BR)
Tremella candelariellae (T)	**ON873053/ON930084**	Luxembourg	*Candelariella vitellina*	Diederich 4836 (BR)
Tremella celata (T)	KT334577/KT334589	Spain	*Ramalina fraxinea*	Zamora (MAF-Lich 19726)
Tremella cetraculeata (T)	**ON873054/ON930085**	Canada	*Cetraria aculeata*	Hollinger 14274 (UBC)
Tremella cetrariae 1	**ON873055/ON930086**	Spain	*Cetraria islandica*	Zamora (G)
Tremella cetrariae 2 (T)	**ON873056/ON930087**	Austria,	*Cetraria islandica*	Zimmermann, old basidioma (BR)
Tremella cetrariae 3 (T)	**ON873057/ON930088**	Austria,	*Cetraria islandica*	Zimmermann, young basidioma (BR)
Tremella cetrariae 4	**ON873058/ON930089**	Spain	*Cetraria islandica*	Etayo (MA-Fungi)
Tremella cetrariellae (T)	KT334562/KT334572	Norway	*Cetrariella delisei*	Millanes 1130 (S F264653)
Tremella cetrariicola	JN053490/JN043596	Finland	*Tuckermanopsis chlorophylla*	Suija (S F102413)
Tremella christiansenii	**ON873059/ON930090**	France	*Physcia adscendens*	Pinault (BR)
Tremella cladoniae	**ON873060/ON930091**	Sweden	*Cladonia coniocraea*	Millanes 696 (S F255323)
Tremella conidioparmotrema (T)	**ON873061/ON930092**	Ecuador	*Parmotrema* sp.	Etayo 19911 (BR)
Tremella conidiopunctelia 1 (T)	**ON873062/ON930093**	USA, New Jersey	*Punctelia caseana*	Waters 5448 (NY)

Supplementary document S10. (Continued)

Species	GenBank (ITS+nuLSU)	Country	Host	Specimen
Tremella conidiopunctelia 2	**ON873063/ON930094**	USA, New Jersey	*Punctelia caseana*	Lendemer 17452 (NY)
Tremella conidiopunctelia subsp. *parmelinellae* (T)	**ON873064/ON930095**	USA, Florida	*Parmelinella amazonica*	Common 9239A (BR)
Tremella coppinsii	JN053496/JN043602	Estonia	*Platismatia galuca*	Suija 38a (TU)
Tremella diederichiana	KT334580/KT334592	Spain	*Lecidea* aff. *erythrophaea*	Zamora (MAF-Lich 19739)
Tremella diploschistina (T)	JN790586/JN790588	Sweden	*Diploschistes scruposus*	Westberg 09-400 (S F211875)
Tremella endosporogena (T)	KT334579/KT334591	Spain	*Lecanora carpinea*	Zamora (MAF-Lich 19742)
Tremella everniae	JN053493/JN043599	USA, Maine	*Evernia mesomorpha*	Kneiper (S)
Tremella flakusii 1 (T)	**ON873065/ON930096**	Bolivia	*Crocodia clathrata*	Flakus 25804 (KRAM)
Tremella flakusii 2	**ON873066/ON930097**	Brazil	*Crocodia aurata*	Aptroot 84597 (BR)
Tremella flavoparmeliae 1	–/**ON930098**	USA, Minnesota	*Flavoparmelia caperata*	Gockman 5667 (BR)
Tremella flavoparmeliae 2 (T)	–/**ON930099**	USA, North Carolina	*Flavoparmelia caperata*	Hodkinson 11027 (NY)
Tremella flavoparmeliae 3	–/**ON930100**	USA, North Carolina	*Flavoparmelia caperata*	Lendemer 43694 (NY)
Tremella fuciformis	AF444316/AF075476			
Tremella globispora	AF444432/AF189869			
Tremella graphidis (T)	KR058781/KR058786	USA, Florida	*Graphis assimilis*	Common 9434B (BR)
Tremella haematommatis	JN053510/JN043617	USA, Florida	*Haematomma persoonii*	Sérusiaux 1750 (BR)
Tremella herpothalli (T)	**ON873067/ON930101**	Bolivia	*Herpothallon* sp.	Flakus 26854 (LPB)
Tremella hypogymniae	**ON873068/ON930102**	Sweden	*Hypogymnia physodes*	Millanes, Westberg & Klopfstein (S)
Tremella huuskonenii (T)	KR857031/KR857095	Canada	*Bryoria pikey*	T. Goward 11–50 (UBC)
Tremella imshaugiae (T)	MW115411/MW115393	UK	*Imshaugia aleurites*	Paul (E 00722344)
Tremella leptogii	JN053476/JN043582	Brazil	*Leptogium* cf. *cyanescens*	Vital & Buck 19510 (S-F102417)
Tremella lethariae	**ON873069/ON930103**	USA, California	*Letharia vulpina*	Miller (E)
Tremella leucodermiae 1 (T)	**ON873070/ON930104**	Bolivia	*Leucodermia leucomelos*	Etayo 28197 (LPB)
Tremella leucodermiae 2	**ON873071/ON930105**	Bolivia	*Leucodermia vulgaris*	Etayo 27974 (LPB)
Tremella lichenicola	JN053504/JN043611	Germany	*Violella fucata*	Diederich (UPS-256878)
Tremella lobariacearum (T)	JN053473/JN043579	Madeira	*Lobaria macaronesica*	Diederich 4935 (BR)
Tremella macrobasidiata 1 (T)	KT334582/KT334594	Spain	*Lecanora chlarotera*	Zamora (MA-Fungi 80867)
Tremella macrobasidiata 2	KT334583/KT334595	Portugal	*Lecanora chlarotera*	Zamora (MAF-Lich 19755)
Tremella mayrhoferi (T)	MH168093/MH168097	Sweden	*Lecanora allophana*	Zamora (UPS L-877384)
Tremella mesenterica	JN053463/JN043568			
Tremella nashii 1	**ON873072/ON930106**	USA, Arizona	*Usnea hirta*	Thayer 39j (BR)
Tremella nashii 2	**ON873073/ON930107**	USA, Arizona	*Usnea hirta*	Thayer 39c (BR)
Tremella nephromatis (T)	JN053475/JN043581	Canada	*Nephroma parile*	Goward 92–350 (BR)
Tremella parmeliarum	JN053511/JN043618	Canary Islands	*Parmotrema reticulatum*	Diederich 16574 (BR)
Tremella parmohypotropi 1	–/**ON930108**	USA, Texas	*Parmotrema hypotropum*	Walden 0031 (BR)
Tremella parmohypotropi 2 (T)	–/**ON930109**	USA, Texas	*Parmotrema hypotropum*	Gockman 5784 (BR
Tremella pertuceracea (T)	**ON873074/ON930110**	Bolivia	*Pertusaria sp.*	Flakus 25096 (KRAM)
Tremella pertusae 1	**ON873075/ON930111**	Spain	*Pertusaria pertusa*	Etayo 31421 (herb. Etayo)
Tremella pertusae 2	**ON873076/ON930112**	Spain	*Pertusaria pertusa*	Etayo 31241 (herb. Etayo)

Supplementary document S10. (Continued)

Species	**GenBank (ITS+nuLSU)**	**Country**	**Host**	**Specimen**
Tremella pertusae 3	**ON873077/ON930113**	Spain	*Pertusaria pertusa*	Etayo 31720 (herb. Etayo)
Tremella pertusae 4 (T)	**ON873078/ON930114**	Italy	*Pertusaria pertusa*	Brackel 7593 (BR)
Tremella pertusariae	JN053494/JN043600	France	*Pertusaria hymenea*	Diederich 16331 (S-F102502)
Tremella pertusariicola 1	**ON873079/ON930115**	Bolivia	*Pertusaria* sp.	Etayo 30665 (herb. Etayo)
Tremella pertusariicola 2 (T)	**ON873080/ON930116**	Bolivia	*Pertusaria* cf. *rigida*	Flakus 27677 (KRAM)
Tremella pertutexanae	**ON873081/ON930117**	USA, Florida	*Pertusaria texana*	Common 10165C (BR)
Tremella phaeographinae	KR058782/KR058787	USA, Florida	*Phaeographis* sp.	Common 9481B (BR)
Tremella phaeophysciae	JN053480/JN043586	Estonia	*Phaeophyscia orbicularis*	Suija (TU-55041)
Tremella pseudocyphellariae (T)	**ON873082/ON930118**	Mauritius	*Pseudocyphellaria desfontainii*	Diederich 18851 (MAU)
Tremella puncteliae (T)	**ON873083/ON930119**	Mexico	*Punctelia borreri*	Etayo 25013 (MEXU)
Tremella puncteliotegens (T)	**ON873084/ON930120**	New Zealand	*Punctelia borreri* s. lat.	Galloway (MAF-Lich)
Tremella purpurascentis 1	**ON873085/ON930121**	USA, Florida	*Dirinaria purpurascens*	Common 10066B (BR)
Tremella purpurascentis 2	**ON873086/ON930122**	USA, Florida	*Dirinaria purpurascens*	Common 9917C (BR)
Tremella purpurascentis 3	**ON873087/ON930123**	USA, Florida	*Dirinaria purpurascens*	Common 9621B (BR)
Tremella purpurascentis 4 (T)	**ON873088/ON930124**	USA, Florida	*Dirinaria purpurascens*	Common 9891C (BR)
Tremella pyrenulae (T)	KR058784/KR058789	USA, Florida	*Pyrenula ochraceoflavens*	Common 9170B (BR)
Tremella ramalinae	JN053513/JN043620	Spain	*Ramalina fraxinea*	Etayo (UPS 158799)
Tremella rhabdodisci 1	**ON873089/ON930125**	Japan	*Rhabdodiscus inalbescens*	Ertz 24561 (BR)
Tremella rhabdodisci 2 (T)	**ON873090/ON930126**	Japan	*Rhabdodiscus inalbescens*	Thor 35584 (UPS)
Tremella rhabdodisci 3	**ON873091/ON930127**	Japan	*Rhabdodiscus inalbescens*	Ertz 24603 (BR)
Tremella robusta (T)	**ON873092/ON930128**	USA, California	*Dendrographa franciscana*	Ertz 12420 (BR)
Tremella stictae	–/**ON930129**	Vietnam	*Sticta* sp.	Zhurbenko 199 (BR)
Tremella teloschistis 1	–/**ON930130**	USA, Texas	*Teloschistes exilis*	Walden 0014 (BR)
Tremella teloschistis 2	**ON873093/ON930131**	USA, Texas	*Teloschistes exilis*	Walden 0018 (BR)
Tremella teloschistis 3	**ON873094/ON930132**	USA, Texas	*Teloschistes exilis*	Walden 0027 (BR)
Tremella teloschistis 4	**ON873095/ON930133**	USA, Texas	*Teloschistes exilis*	Walden 0019 (BR)
Tremella tornabeae 1	**ON873096/ON930134**	Canary Islands	*Tornabea scutellifera*	Pérez-Ortega 8024 (MAF-Lich)
Tremella tornabeae 2	**ON873097/ON930135**	Canary Islands	*Tornabea scutellifera*	Diederich 18204 (BR)
Tremella tubulosae	MW115408/MW115390	Spain	*Hypogymnia tubulosa*	Zamora (S)
Tremella tuckerae (T)	JN053482/JN043588	Mexico	*Ramalina sinensis*	Tucker 37335 (SBBG)
Tremella umbilicariae (T)	KM507564/–	Peru	*Umbilicaria* sp.	Santesson P62:55 (UPS L687273)
Tremella variae (T)	KT334587/KT334599	Spain	*Lecanora varia*	Pérez-Ortega 1748 (MAF-Lich 19748)
Tremella wedinii (T)	MN258555/MN243150	USA, Florida	*Glyphis scyphulifera*	Common 10067B (BR)
Tremella wirthii	JN053492/JN043598	The Netherlands	*Protoparmelia hypotremella*	Herk (BR)
Trichosporon ovoides (outgroup)	AF444439/AF075523			
Trimorphomyces papilionaceus	AF444483/AF075491			
Vishniacozyma carnescens	KF036588/AB035054			

Class *Agaricostilbomycetes*, order *Agaricostilbales*

by P. Diederich, A. M. Millanes, J. Etayo, P. P. G. van den Boom & M. Wedin

Supplementary document S11. Species, GenBank accession numbers (ITS + nuLSU) and specimen information of fungi used in the phylogenetic analyses of the family *Crittendeniaceae* (page 283). Type material is indicated with (T). See Diederich et al. (2022) for more details.

Species	**GenBank ITS/nuLSU**	**Country**	**Host**	**Specimen**
Crittendenia absistentis 1	OM521987/OM521967	U. K.	*Bacidia absistens*	Palice 25624 (PRA)
Crittendenia absistentis 2 (T)	OM521988/OM521968	U. K.	*Bacidia absistens*	Coppins 25367 (E 01002244)
Crittendenia bacidinae (T)	MT520701/MT482333	Azores	*Bacidina apiahica*	van den Boom 56783 (BR)
Crittendenia byssolomatis (T)	OM521989/OM521969	Azores	*Byssoloma maderense*	van den Boom 60700 (BR)
Crittendenia coppinsii 1 (T)	MT520689/MT482329	U. K.	*Melanelixia glabratula*	Coppins 16400 (K(M)-39188)
Crittendenia coppinsii 2	MT520690/–	Norway	*Melanelixia glabratula*	Westberg & Olsson (UPS)
Crittendenia coppinsii 3	OM521990/OM521970	France	*Melanelixia subaurifera*	Pinault (BR)
Crittendenia coppinsii 4	MT520692/MT482331	Belgium	*Melanohalea exasperatula*	van den Boom 54983 (herb. van den Boom)
Crittendenia coppinsii 5	MT520693/–	Sweden	*Melanohalea exasperatula*	Westberg (S, UPS F-805352)
Crittendenia coppinsii 6	MT520694/–	Sweden	*Melanohalea exasperatula*	Westberg (S, UPS F-805353)
Crittendenia coppinsii 7	MT520696/–	Sweden	*Melanohalea exasperatula*	Odelvik 11471 (S F-206720)
Crittendenia coppinsii 8	MT520691/MT482330	Sweden	*Melanohalea exasperatula*	Westberg et al. (UPS F-796396)
Crittendenia heterodermiae (T)	OM521991/OM521971	Bolivia	*Heterodermia comosa*	Etayo 32711 (LPB)
Crittendenia hypotrachynae 1 (T)	MT520702/MT482334	Azores	*Hypotrachyna endochlora*	Etayo 31093 (PO)
Crittendenia hypotrachynae 2	MT520703/MT482335	Azores	*Hypotrachyna* sp.	Etayo 30945 (herb. Etayo)
Crittendenia kakouettae 1	OM521992/OM521972	Azores	*Byssoloma kakouettae*	van den Boom 58880 (BR)
Crittendenia kakouettae 2 (T)	OM521993/OM521973	Azores	*Byssoloma kakouettae*	van den Boom 58956 (BR)
Crittendenia kakouettae 3	MT520700/MT482332	Canary Islands	*Byssoloma kakouettae*	Diederich 16490 (BR)
Crittendenia lecidellae 1 (T)	MT520705/MT482337	Canada	*Lecidella elaeochroma*	Björk 17999 (UBC)
Crittendenia lecidellae 2	MT520704/MT482336	Spain	*Lecidella elaeochroma*	Zamora (G)
Crittendenia lichenicola 1 (T)	–/OM521985	Norway	*Micarea prasina*	Tønsberg 12000 (BG L-73887)
Crittendenia lichenicola 2	OM521994/OM521974	U. K.	*Micarea micrococca*	Coppins 21517 (E)
Crittendenia parvispora 1 (T)	OM521996/OM521976	France	*Bacidia laurocerasi*	Quelen (BR)
Crittendenia parvispora 2	OM521995/OM521975	Cape Verde	*Bacidia polychroa*	van den Boom 36943 (BR)
Crittendenia physciiphila 1 (T)	OM522000/OM521980	France	*Physcia adscendens*	Pinault (BR)
Crittendenia physciiphila 2	OM522001/OM521981	France	*Physcia adscendens*	Pinault (BR)
Crittendenia physciiphila 3	OM521997/OM521977	Spain	*Physciella chloantha*	Etayo 18287 (herb. Etayo)
Crittendenia physciiphila 4	OM521998/OM521978	France	*Phaeophyscia orbicularis*	Pinault (BR)
Crittendenia physciiphila 5	–/OM521986	USA	*Phaeophyscia rubropulchra*	Buck 27763 (NY)
Crittendenia physciiphila 6	OM521999/OM521979	Spain	*Phaeophyscia orbicularis*	Etayo 25106 (herb. Etayo)
Crittendenia physconiae (T)	MT520706/MT482338	Spain	*Physconia distorta*	Zamora (G)
Crittendenia stictae (T)	OM522002/OM521982	Bolivia	*Sticta fuliginosa* s. lat.	Etayo 26611 et al. (LPB)
Crittendenia teloschistis 1 (T)	OM522004/OM521984	Canary Islands	*Teloschistes flavicans*	Koller (BR [ex herb. Berger 26836])
Crittendenia teloschistis 2	OM522003/OM521983	Bolivia	*Teloschistes exilis*	Etayo 32788 (LPB)

Class *Cystobasidiomycetes*, order *Cyphobasidiales*

by P. Diederich, A. M. Millanes, A. Flakus, P. Rodriguez-Flakus, J. Etayo & M. Wedin

Supplementary document S12. Methods used to determine the phylogenetic relationships of the lichenicolous taxa of the class *Cystobasidiomycetes* (page 305).

Molecular data obtained from *Cyphobasidium* specimens

DNA from lichenicolous specimens was extracted using the Qiagen DNeasy Plant Mini Kit (Qiagen, Venlo, the Netherlands) or QIAamp DNA Investigator Kit (Qiagen, Hilden, Germany), according to the manufacturer's instructions. General fungal primers, i. e., ITS1F (Gardes & Bruns 1993), LR5 (Vilgalys & Hester 1990), NS1 and ITS2 (White et al. 1990), specific primers suitable for basidiomycetes, i. e., nuSSU1088Rb, BasidLSU3-3, BasidLSU1-5 (Millanes et al. 2011), and specific primers targeting *Cyphobasidium*, i. e., CnLSU- 70F, CnLSU-589R, CITS2-837R (Millanes et al. 2016), ITS_symrho_1F and LR0_symrho_R (Spribille et al. 2016) were combined to amplify the nSSU, the ITS, and a fragment with length between 600–1000 bp of the nLSU in the nuclear ribosomal DNA. PCR amplifications were performed using Illustra™ Hot Start PCR beads or AmpliTaq™ 360 DNA Polymerase, according to the manufacturer's instructions, following Flakus et al. (2019), Millanes et al. (2011, 2016) and Spribille et al. (2016). For the primer pair ITS1F/BasidLSU3-3 the PCR settings consisted of initial denaturing at 95 ºC for 3 min, four cycles (95 ºC for 40 s, 53 ºC for 40 s and 72 ºC for 90 s), four cycles (95 ºC for 30 s, 50 ºC for 30 s and 72 ºC for 90 s), and finally 32 cycles (95 ºC for 30 s, 47 ºC for 30 s and 72 ºC for 90 s) with a final extension at 72 ºC for 480 s. For the primer pair BasidLSU1-5/LR5, we used initial denaturing at 95 ºC for 3 min, four cycles (95 ºC for 40 s, 56 ºC for 40 s and 72 ºC for 90 s), four cycles (95 ºC for 30 s, 53 ºC for 30 s and 72 ºC for 90 s), and finally 32 cycles (95 ºC for 30 s, 50 ºC for 30 s and 72 3ºC for 90 s) with a final extension at 72 ºC for 420 s. For the primer pair ITS_symrho_1F/LR0_symrho_R we used 35 cycles of 95°C denaturation for 60 s, 50°C for 60 s, and 72°C for 60 s. For the primer pairs ITS1F/CnLSU-589R and CnLSU- 70F/LR5, we used initial denaturation at 95 ºC for 5 min, four cycles (95 ºC for 40 s, 56 ºC for 40 s, and 72 ºC for 90 s), four cycles (95 ºC for 30 s, 53 ºC for 30 s, and 72 ºC for 90 s), and finally 32 cycles (95 ºC for 30 s, 50 ºC for 30 s, and 72 ºC for 90 s) with a final extension at 72 ºC for 420 s. Finally, for the primer pair NS1/CITS2-837R or tnuSSU2-3 and nssu1088Rb/ITS2, we used initial denaturation at 95 ºC for 5 min, followed by 35 cycles (95 ºC for 30 s, 50 ºC for 30 s, and 72 ºC for 90 s) with a final extension at 72 ºC for 420 s.

Before sequencing, the PCR products were purified with Exo-sap-ITTM (USB Corporation, Cleveland, Ohio, USA). The purified samples were sequenced by Macrogen (Madrid, Spain, or Amsterdam, the Netherlands). Sequence fragments were assembled and edited using Geneious Prime ®2021.0.3. (https://www.geneious.com).

Taxon sampling and phylogenetic analyses

To place *Cyphobasidium* in the class *Cystobasidiomycetes*, a molecular phylogeny of the group was constructed using sequences of the SSU, ITS1, 5.8S, ITS2 and LSU nuclear rDNA. Sequences were selected from previous molecular phylogenetic studies of the class (Millanes et al. 2016, Wang et al. 2015) and additionally obtained from fresh material collected in Bolivia (specimens deposited at LPB and KRAM). Species for the phylogenetic analyses were sampled to represent *Cyphobasidium*, all orders in the *Cystobasidiomycetes* (viz. *Buckleyzymales*, *Cyphobasidiales*, *Cystobasidiales*, *Erythrobasidiales*, *Naohideales* and *Sakaguchiales*) and two families incertae sedis in the *Cystobasidiomycetes* (viz. *Microsporomycetaceae* and *Symmetrosporaceae*). *Rhodotorula mucilaginosa* (*Microbotryomycetes*) was used as an outgroup. The final database of nuLSU + ITS + nuLSU consisted of 34 terminals with 2743 characters – 444 of which were parsimony-informative and 2002, constant.

For phylogenetic analyses, sequences were aligned using MAFFT version 7 (Katoh et al. 2019) with the Q-INS-i algorithm. The alignments were trimmed to exclude ambiguously aligned regions using GBlocks (Castresana 2000), following the relaxed conditions described by Talavera & Castresana (2007), and manually checked, before and after trimming, using Mesquite 3.7 (Maddison & Maddison 2021). We considered five partitions, nuSSU (1-1696), ITS1 (1697-1818), 5.8S (1819-1971), ITS2 (1972-2164) and nuLSU (2165-2743), in our analyses. Each partition was analysed individually by maximum likelihood ultrafast bootstrap in IQTree to assess for conflicts. Strongly supported clades (IQTree UF-BS higher than 95 %) in disagreement were considered an indication of significant conflict (Mason - Gamer & Kellogg 1996, Hoang et al. 2018). Since no conflict was detected in our data sets, we combined them and analysed them using maximum likelihood (ML) and Bayesian approaches. Maximum likelihood analyses were carried out in IQTree (Nguyen et al. 2015). Model selection for each partition was achieved using ModelFinder in IQTree (Kalyaanamoorthy et al. 2017), with the corrected Akaike information criterion (AICc). The TIM2+F+I+ Γ4 was selected for both the nuclear SSU and the 5.8S, and the GTR+F+I+ Γ4 was selected for the ITS1, the ITS2 and the nuLSU. We assessed node support by standard bootstrap using 1000 bootstrap pseudoreplicates. Bayesian analyses were performed by Markov chain Monte Carlo (MCMC) sampling as implemented in the software MrBayes 3.2.7a (Ronquist et al. 2012) As not all models tested by ModelFinder in IQTree can be directly implemented in MrBayes, for the Bayesian analyses we selected among a subsample of substitution models using the corrected Akaike information criterion (AICc) as implemented in jModelTest 2 (Darriba et al. 2012), allowing only 3 substitution schemes, using full likelihood optimization and four discrete gamma categories. The GTR + I+ Γ was selected for both the nuclear SSU and the 5.8S, and the GTR + Γ was selected for the ITS1, the ITS2 and the nuLSU. The combined analyses treated the different regions as separate partitions with topology linked across partitions but separate model parameter values and proportional rates across partitions. For each combined dataset, two parallel runs were performed, each with four chains, three of which were incrementally heated with a temperature of 0.15. The analyses were diagnosed for convergence every 100 000 generations and were set to halt automatically when the average standard deviation of splits across runs in the last half of the analysis descended below 0.01. Every 100th tree was saved. The first 50% of each run was discarded as burn-in. Both ML and Bayesian analyses were performed on the CIPRES Web Portal (Miller et al. 2015).

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Supplementary document S13. Species, GenBank accession numbers (nuSSU + ITS + nuLSU) and specimen information (only for lichenicolous taxa) of fungi used in the phylogenetic analyses of the class *Cystobasidiomycetes* (page 305). Newly produced sequences in bold font. Type material of lichenicolous species is indicated with (T).

Species	GenBank nuSSU/ITS/nuLSU	Country	Host	Specimen
Buckleyzyma armeniaca	AB126644/AB038112/AF189920			
Buckleyzyma phyllomatis	AB021685/AB030350/AF189991			
Cyrenella elegans	KJ708360/KJ778626/KJ708454			
Cyphobasidium enterographicola (T)	**–/ON922982/ON922967**	Réunion	*Enterographa pallidella*	Ertz 17902 (BR)
Cyphobasidium hypogymniicola 1	KU587705/KU587700/KU587694	USA, Maine	*Hypogymnia krogiae*	Hawksworth (S-F264671)
Cyphobasidium hypogymniicola 2	–/–/KU587693	USA, Maine	*Hypogymnia physodes*	Mann & Cole 9092 (WIS)
Cyphobasidium hypogymniicola 3	**–/ON922983/–**	USA, Minnesota	*Hypogymnia physodes*	Gockman 5673 (BR)
Cyphobasidium hypotrachynicola (T)	**ON922958/–/ON922968**	Bolivia	*Hypotrachyna* sp.	Etayo 33322 (LPB)
Cyphobasidium aff. *hypotrachynicola* 1	**ON922959/ON922984/ON922969**	Bolivia	*Hypotrachyna* sp.	Flakus 25637 (KRAM)
Cyphobasidium aff. *hypotrachynicola* 2	**ON922960/–/ON922970**	Bolivia	*Hypotrachyna* sp.	Etayo 34397 (LPB)
Cyphobasidium aff. *hypotrachynicola* 3	**–/ON922985/ON922971**	Bolivia	*Parmotrema reticulatum*	Flakus 25091 (KRAM)
Cyphobasidium lecaniicola (T)	**ON922961/ON922986/ON922972**	Belgium	*Lecania naegelii*	Ertz 25890 (BR)
Cyphobasidium puncteliicola (T)	**–/ON922987/–**	USA, Missouri	*Punctelia graminicola*	Harris 50901 (NY)
Cyphobasidium usneicola 1	**ON922962/–/ON922973**	Bolivia	*Usnea* sp.	Flakus 25336 (KRAM)
Cyphobasidium usneicola 2	**ON922963/–/ON922974**	Bolivia	*Usnea* sp.	Etayo 34294 (LPB)
Cyphobasidium usneicola 3	**ON922964/–/ON922975**	Bolivia	*Usnea* sp.	Etayo 32934 (LPB)
Cyphobasidium usneicola 4	KU587706/KU587704/KU587699	USA, California	*Usnea subscabrosa*	Muggia (S-F264675)
Cyphobasidium usneicola 5	**ON922965/–/ON922976**	Bolivia	*Usnea* sp.	Etayo 30606 (LPB)
Cyphobasidium usneicola 6	–/KU587702/KU587697	Galapagos	*Usnea galapagona*	Clerc 08/334 (S-F264673)
Cyphobasidium usneicola 7	**ON922966/–/–**	Bolivia	*Usnea* sp.	Etayo 29850 (LPB)
Cyphobasidium usneicola 8	–/KU587703/KU587698	Ecuador	*Usnea praetervisa*	Truong 279 (S-F264672)
Cystobasidium fimetarium	AY124479/–/AY512843			
Erythrobasidium hasegawianum	D12803/AB030352/AF189899			
Erythrobasidium yunnanense	AF229176/AB030353/AB127358			
Hasegawazyma lactosa	D45366/AF444540/AF189936			
Microsporomyces bloemfonteinensis	KJ708359/EU075189/EU075187			
Microsporomyces magnisporus	KJ708428/AB112078/AB111954			
Naohidea sebacea	KP216515/DQ911616/DQ831020			
Occultifur externus	AB055193/AB055202/AF189909			
Rhodotorula mucilaginosa (outgroup)	X84326/AB026017/AF070432			
Sakaguchia dacryoidea	D13459/AB049027/AF189972			
Sakaguchia lamellibrachiae	AB126646/AB025999/AB025999			
Symmetrospora marina	AB126645/AB038116/AF189944			
Symmetrospora vermiculata	AB030322/AB030335/AF460176			

Class *Microbotryomycetes*

by P. Diederich, A. M. Millanes, J. Etayo & M. Wedin

Supplementary document S14. Methods used to determine the placement of lichenicolous species in the phylogeny of the class *Microbotromycetes* (page 325).

Molecular data obtained from *Kriegeriopsis* specimens

DNA from lichenicolous specimens was extracted using the Qiagen DNeasy Plant Mini Kit (Qiagen, Venlo, the Netherlands), according to the manufacturer's instructions. Specific primers suitable for species in *Pucciniomycotina*, viz. ITS_symrho_1F and LR0_symrho_R (Spribille et al. 2016) were used to amplify the internal transcribed spacer (ITS). Primers BasidLSU1-5 (Millanes et al. 2011) and LR5 (Vilgalys & Hester 1990) were used to amplify a fragment of ca. 600 nucleotides in the nuLSU.

For the primer pairs ITS_symrho_1F/LR0_symrho_R, we used initial denaturing at 95°C for 3 min, four cycles of 95°C for 40 s, 53°C for 40 s and 72°C for 90 s, four cycles of 95°C for 30 s, 50°C for 30 s and 72°C for 90 s, and finally 32 cycles of 95°C for 30 s, 47°C for 30 s and 72°C for 90 s, with a final extension at 72°C for 420 s. For the primer pair Basid LSU1-5/LR5, we followed Millanes et al. (2015).

Before sequencing, the PCR products were purified with Exo-sap-ITTM (USB Corporation, Cleveland, Ohio, USA). The purified samples were sequenced by Macrogen (Madrid, Spain). Sequence fragments were assembled and edited using Geneious Prime ®2021.0.3. (https://www.geneious.com).

Taxon sampling

To place the lichenicolous *Kriegeriopsis livingstonensis* in the class *Microbotryomycetes*, a molecular phylogeny of the group was constructed using sequences of the ITS1, 5.8S, ITS2, and LSU nuclear rDNA. Sequences were selected from previous molecular phylogenetic studies of the class (Wang et al. 2016, Li et al. 2020, Pontes et al. 2020, Perini et al. 2021). Species for the phylogenetic analyses were sampled from 9 families (and 11 genera considered as incertae sedis), representing all orders in the *Microbotryomycetes* (viz. *Heterogastridiales*, *Kriegeriales*, *Leucosporidiales*, *Microbotryales*, and *Sporidiobolales*/*Heitmaniales*) with more focus on the families *Camptobasidiaceae* and *Kriegeriaceae* (*Kriegeriales*), according to our preliminary BLAST searches. *Phyllozyma dimennae* (*Spiculogroeomycetes*) was used as an outgroup). The final database of nuLSU + ITS + nuLSU consisted of 37 terminals with 1057 characters – 303 of which were parsimony-informative and 533, constant.

Phylogenetic analysis

For phylogenetic analyses, sequences were aligned using MAFFT version 7 (Katoh et al. 2019) with the Q-INS-i algorithm. The alignments were trimmed to exclude ambiguously aligned regions using GBlocks (Castresana 2000), following the relaxed conditions described by Talavera & Castresana (2007), and manually checked, before and after trimming, using Mesquite 3.7 (Maddison & Maddison 2021). We considered four independent partitions, ITS1 (1-110), 5.8S (111-216), ITS2 (217-417) and nuLSU (418-1057), in our analyses. Each partition was analysed individually by maximum likelihood ultrafast bootstrap in IQTree to assess for conflicts. Strongly supported clades (IQTree UF-BS higher than 95 %) in disagreement were considered an indication of significant conflict (Mason- Gamer & Kellogg 1996, Hoang et al. 2018). Since no conflict was detected in our data sets, we combined them (nuLSU + ITS) and analysed them using maximum likelihood (ML) and Bayesian approaches. Maximum likelihood analyses were carried out in IQTree (Nguyen et al. 2015). Model selection for each partition was achieved using ModelFinder in IQTree (Kalyaanamoorthy et al. 2017), with the corrected Akaike information criterion (AICc). The GTR+F+ Γ4 was selected for the ITS1, the TNe+ Γ4 for the 5.8S, the TVM + F+ Γ4 for the ITS2, and the GTR+F+I+ Γ4 for the nuclear LSU. We assessed node support by standard bootstrap using 1000 bootstrap pseudoreplicates. Bayesian analyses were performed by Markov chain Monte Carlo (MCMC) sampling as implemented in the software MrBayes 3.2.7a (Ronquist et al. 2012) on the CIPRES Web Portal (Miller et al. 2015). As not all models tested by ModelFinder in IQTree can be directly implemented in MrBayes, for the Bayesian analyses we selected among a subsample of substitution models using the corrected Akaike information criterion (AICc) as implemented in jModelTest 2 (Darriba et al. 2012), allowing only 3 substitution schemes, using full likelihood optimization and four discrete gamma categories. Following this scheme, the F81 + Γ was selected for the ITS1, the JC for the 5.8S, the SYM + I + Γ for the ITS2, and the GTR + Γ for the nuclear LSU rDNA. The combined analyses treated the different regions as separate partitions with topology linked across partitions but separate model parameter values and proportional rates across partitions. For each combined dataset, two parallel runs were performed, each with four chains, three of which were incrementally heated with a temperature of 0.15. The analyses were diagnosed for convergence every 100 000 generations and were set to halt automatically when the average standard deviation of splits across runs in the last half of the analysis descended below 0.01. Every 100th tree was saved. The first 50% of each run was discarded as burn-in.

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Supplementary document S15. Species, GenBank accession numbers (nuLSU + ITS) and specimen information (only for lichenicolous taxa) of fungi used in the phylogenetic analyses of the class *Microbotryomycetes* (page 325). Newly produced sequences in bold font. Type material of the lichenicolous species is indicated with (T).

Species	GenBank ITS/nuLSU	Country	Host	Specimen
Camptobasidium arcticum	MN983248/MK454798			
Camptobasidium hydrophilum	MN626358/AY212991			
Chrysozyma griseoflava	AF444557/AF189986			
Colacogloea peniophorae	DQ202270/AY629313			
Cryolevonia giraudoae	MN622687/MN626546			
Cryolevonia schafbergensis	MN058074/MN058075			
Curvibasidium cygneicollum	AF444490/AF189928			
Glaciozyma antarctica	AF444529/AF189906			
Glaciozyma martinii	EU149807/KY107753			
Heterogastridium pycnidioideum	GU291276/GU291290			
Kriegeria eriophori	AF444602/NR_119455			
Kriegeriopsis livingstonensis 1	**ON922977/–**	Antarctica	*Tetramelas* aff. *graminicola*	Etayo 31529 (herb. Etayo)
Kriegeriopsis livingstonensis 2	**ON922978/–**	Antarctica	*Tetramelas* aff. *graminicola*	Etayo 31456 (herb. Etayo)
Kriegeriopsis livingstonensis 3	**ON922979/–**	Antarctica	*Tetramelas* aff. *graminicola*	Etayo 31633 (herb. Etayo)
Kriegeriopsis livingstonensis 4 (T)	**ON922980/ON926889**	Antarctica	*Tetramelas* aff. *graminicola*	Etayo 31519 (MAF-Lich)
Kriegeriopsis livingstonensis 5	**ON922981/ON926890**	Antarctica	*Tetramelas* aff. *graminicola*	Etayo 31469 (MAF-Lich)
Leucosporidium scottii	AF444495/AF070419			
Meredithblackwellia eburnea	JX508799/JX508798			
Microbotryum scabiosae	KJ778632/KJ708459			
Oberwinklerozyma yarrowii	AF444628/AF189971			
Phenoliferia psychrophenolica	EF151246/EF151255			
Phenoliferia psychrophila	EF151243/EF151252			
Phyllozyma dimennae (outgroup)	AB038046/AB644404			
Pseudohyphozyma buffonii	AF444526/AF189924			
Pseudoleucosporidium fasciculatum	KJ778628/AY212993			
Psychromyces glacialis 1	MK671633/MT301949			
Psychromyces glacialis 2	MK460401/MK454861			
Reniforma strues	AF444573/AF189912			
Rhodosporidiobolus nylandii	AB030323/AF387123			
Rosettozyma petaloides	NR_174037/–			
Sampaiozyma ingeniosa	AF444534/AF189934			
Slooffia tsugae	AF444580/AF189998			
Spencerozyma crocea	FM957565/AY372179			
Trigonosporomyces hylophilus	AF444622/AF363645			
Vonarxula javanica	AF444532/AF189935			
Yamadamyces rosulatus	EU872492/EU872490			
Yunzhangia auriculariae	AF444507/AF189922			