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3 **Basidiomycota isolated from the Mediterranean Sea – phylogeny and putative ecological roles**
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24 Running Head: Basidiomycota in marine environment
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63 **Abstract**
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65 Basidiomycota are an **ecologically and taxonomically** diverse fungal phylum, colonizing all terrestrial
66 ecosystems, with 30,000 described species. **By contrast, in marine habitats Basidiomycota are under-**
67 **represented when compared to the more abundant Ascomycota.** Recently, we investigated the marine
68 mycobiota mainly in the Mediterranean Sea, confirming the scarcity of Basidiomycota. **However, a**
69 **low rank taxonomic identification based on morphological features, proved impossible, since most**
70 **of the strains remained sterile in axenic culture.** Nevertheless, considering the great potential and
71 biotechnological value of Basidiomycota, it would be useful to define their precise taxonomic
72 placement. To this end, 34 marine Basidiomycota isolated from different **marine** substrates underwent
73 **molecular analyses and 123 newly generated sequences were obtained and deposited in GenBank.**
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75 Sequencing of the Internal Transcribed Spacer (nrITS) regions allowed us to **affiliate** the 34 strains
76 **with** six classes, but **a lower** taxonomic **identification was** reached with a multi-locus phylogenetic
77 analysis.
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Keywords: Marine fungi; Algae; Sponges; Phylogeny; Bioremediation; Biotechnological potential

1. Introduction

The marine environment, commonly divided into coastal regions (influenced by land), pelagic and deep-sea habitats (recognised as extreme), is home to a huge variety of microorganisms, among which fungi are often dominant (Richards et al., 2012). Marine fungi are classified as obligate that grow and reproduce exclusively in the sea, or facultative, terrestrial species able to grow and reproduce in marine environments. Those fungi whose obligate or facultative marine nature is undefined are called marine-derived. Marine fungi have been retrieved worldwide from a broad range of biotic and abiotic substrates such as algae, sponges, corals, sediments etc. (Jones and Pang, 2012; Raghukumar, 2017). Living as mutualists (ecto- and endosymbionts), parasites, pathogens and saprobes, these organisms play an important role as primary degraders, thus contributing to nutrient recycling (Raghukumar, 2017; Richards et al., 2012). Even if the total number of marine fungi has been estimated to exceed 10,000 taxa, a recent update on accepted classification described only 1,112 species, mostly affiliated to Ascomycota (Jones et al., 2015). Basidiomycota are under-represented, with only 74 species (12 obligate and 62 facultative) contributing to marine fungal diversity (Jones et al., 2015; Jones and Pang, 2012; Raghukumar, 2017).

Basidiomycota living in marine habitats are an ecologically and taxonomically diverse group morphologically categorised as filamentous species, able to grow on several substrates such as seagrasses and mangrove wood, and single-celled yeasts, found in association with algae, seagrasses and dead animals or free-floating in the sea. In addition, some fungi (e.g. Cystobasidiales) can exhibit true dimorphism (Jones and Pang, 2012). Most of the Basidiomycota retrieved from the above mentioned unique environments belong to the following classes: Agaricomycetes (e.g. *Nia vibrissa* and *Schizophyllum commune*, *Grammothele fuligo*, *Peniophora* sp.), Microbotryomycetes (e.g. *Rhodosporidium diobovantum* and *R. babjeave*), Tremellomycetes (e.g. *Cryptococcus* spp.), Ustilaginomycetes (e.g. *Pseudozyma aphidis*), and Wallemiomycetes (e.g. *Wallemia sebi*) (Jones et al., 2015). Yet, a significant number of taxa remain undescribed or identified only at genus level. This

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183 is mainly due to the following reasons: i) several isolates in axenic cultures do not develop the
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185 reproductive structures necessary for morphological identification (sterile mycelia) (Bovio et al.,
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187 2017; Gnavi et al., 2017; Panno et al., 2013); ii) molecular approaches relying on the internal
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189 transcribed spacers (nrITS), small or large ribosomal subunits (nrSSU and nrLSU) are not always
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191 exhaustive (Binder et al., 2013; Hibbett et al., 2014; Hibbett et al., 2007; Jancic et al., 2015).
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194 **Among marine fungi**, the understudied Basidiomycota may be an untapped source of potentially
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196 novel enzymes and bioactive compounds due to the extreme environmental conditions they adapt to
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198 (high salinity and pressure, pH, oxidative stress, low temperature, chemicals and metals) (Bodke et
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200 al., 2012; Dalmaso et al., 2015). For instance, the production of ligninolytic enzymes, such as
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202 peroxidases and laccases, is well documented in the sponge derived strain *Peniophora* sp. CBMAI
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204 1063 (Bonugli-Santos et al., 2012; Bonugli-Santos et al., 2016), in the mangrove associated *Phlebia*
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206 sp. MG-60 (Luo et al., 2005; Raghukumar et al., 2008) and in *Flavodon flavus* isolated from the
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208 seagrass *Thalassia hemprichii* (Mtui and Nakamura, 2008). This could signal the great potential of
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210 salt-tolerant Basidiomycota in treating coloured industrial effluents and in degrading aromatic
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212 recalcitrant pollutants (Bonugli-Santos et al., 2012).
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216 Recently, the cultivable mycobiota associated to macro-algae, **seagrasses**, sponges and a crude oil
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218 contaminated site were investigated in the Mediterranean Sea and in the Atlantic Ocean, confirming
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220 the scarcity of Basidiomycota in comparison to their terrestrial counterpart and to the most dominant
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222 Ascomycota (Bovio et al., 2017; Garzoli et al., 2015; Gnavi et al., 2017; Panno et al., 2013). **In this**
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224 **paper, by means of a combined multi-locus phylogenetic analysis, the authors provide a better**
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226 **phylogenetic placement of 34 Basidiomycota (Bovio et al., 2017; Gnavi et al., 2017; Panno et al.,**
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228 **2013), thus increasing our understanding of fungal diversity in the marine environment.**
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243 **2. Materials and Methods**
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246 **2.1. Fungal isolates and DNA extraction.**
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249 Fungal isolates used in this study were previously retrieved from different substrates in the
250 Mediterranean Sea and in the Atlantic Ocean (Table 1) and are preserved at the *Mycoteca*
251 *Universitatis Taurinensis* (MUT). The organisms were originally isolated on Corn Meal Agar
252 SeaWater (CMASW; SW, 3.4% w/v Sea Salt mix – Sigma-Aldrich, Saint Louis, USA – in ddH₂O)
253 medium.
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260 Genomic DNA was extracted from about 100 mg of mycelium, which was carefully scraped from
261 Malt Extract Agar (MEA) plates, transferred to a 2 mL Eppendorf tubes and disrupted in a MM400
262 tissue lyzer (Retsch GmbH, Haan, Germany). A NucleoSpin kit (Macherey Nagel GmbH, Duren, DE,
263 USA) was used and extraction proceeded according to the manufacturer's instructions. The quality
264 and quantity of DNA samples were measured spectrophotometrically with Infinite 200 PRO
265 NanoQuant (TECAN, Switzerland). DNA was stored at -20° C.
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273 **2.2. PCR amplification and data assembling**
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276 Depending on the order/family of affiliation and on the availability of sequences in GenBank, specific
277 markers were amplified in a T100 Thermal Cycler (Bio-Rad, Hercules, CA, USA) (Hibbett et al.,
278 2007).
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283 The nrITS rDNA region was amplified for all strains using the universal primers ITS1/ITS4 (White
284 et al., 1990). Partial nrLSU rDNA was amplified for Polyporales, Psathyrellaceae and
285 Schizophyllaceae using the universal primers LROR/LR7 (Vilgalys and Hester, 1990); partial nrSSU
286 rDNA for Ustilaginaceae, Cistobasidiomycetes, Microbotriomycetes and Holtermanniales using
287 primers PNS1/NS41 (Hibbett, 1996); D1/D2 region of nrLSU rDNA for Ustilaginaceae,
288 Cistobasidiomycetes, Microbotriomycetes and Holtermanniales using primers NL1/NL4 (Kurtzman
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301 and Robnett, 1998). The thermocycler was programmed as previously described (Gnavi et al., 2017;
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305 Kurtzman and Robnett, 1998).

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308 **For Wallemiaceae**, partial sequences of the protein coding genes RNA polymerase II subunits *rpb1*
309 and *rpb2* were obtained by using primers RPB1WF/RPB1WR and RPB2WF/RPB2WR, **respectively**
310 (Nguyen et al., 2015); RPB1-Af/RPB1-Cr were used to amplify *rpb1* in Polyporales and
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312 Psathyrellaceae (Carlson et al., 2014; Matheny, 2005). Translation elongation factor *ef-1 α* was
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314 amplified by using primers EFdf/EF1-2218R (Matheny et al., 2007) for Cistobasidiomycetes,
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316 Microbotriomycetes, Schizophyllaceae, Holtermanniales, Psathyrellaceae and Polyporales. Finally,
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318 partial sequences of the pre-rRNA processing protein encoding gene *tsr1* were amplified for the
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320 Wallemiaceae with the specific primer pair TSR1WF/TSR1WR (Nguyen et al., 2015). PCR
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322 parameters for *rpb1* were: initial denaturation at 95 °C for 3 min; 36 cycles at 95 °C for 30 s, 50 °C
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324 for 1 min and 72 °C for 1 min; final extension of 8 min at 72 °C. A touchdown PCR protocol was set
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326 for *ef-1 α* gene: initial denaturation at 94 °C for 2 min; 9 cycles at 94 °C for 40 s, 60 °C for 40 s (minus
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328 1°C per cycle), 72 °C for 2 min; 36 cycles at 94 °C for 45 s, annealing at 53 °C for 1 min 30 s,
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330 extension at 72 °C for 2 min; final extension at 72 °C for 10 min. The PCR profile for *rpb1W*, *rpb2W*
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332 and *tsr1W* was as described in Nguyen et al. (2015).
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338 Reaction mixture consisted of 20 ng genomic DNA, 10x PCR Buffer (15 mM MgCl₂, 500 mM KCl,
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340 100 mM Tris-HCl, pH 8.3), 200 μ M each dNTP, 1 μ M each primer, 2.5 U Taq DNA Polymerase
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342 (Qiagen, Chatsworth, CA, USA), in 50 μ L final volume. **For problematic cases**, additional MgCl₂
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344 and/or 2.5% DMSO facilitated the reaction.
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347 Amplicons were visualized on a 1.5 % agarose gel stained with 5 mL 100 mL⁻¹ ethidium bromide and
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349 a GelPilot 1 kb plus DNA Ladder was used; PCR products were purified and sequenced at MacroGen
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351 Europe Laboratory (Amsterdam, The Netherlands). The resulting ABI chromatograms were
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353 processed and assembled to obtain consensus sequences using Sequencer 5.0 (GeneCodes, Ann
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363 Arbor, Michigan, USA <http://www.genecodes.com>). Newly generated sequences were deposited in
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365 GenBank (Table 1).
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367 368 **2.3. Sequence alignment and phylogenetic analysis** 369

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371 Eleven datasets were assembled on the basis of BLASTn results and of recent phylogenetic studies
372 that included allied taxa, as follows: Psathyrellaceae (Nagy et al., 2013; Orstadius et al., 2015),
373 Peniophoraceae (Hallenberg et al., 1996), Ustilaginaceae (Wang et al., 2015a), Sporidiobolaceae
374 (Wang et al., 2015b), Schizophyllaceae (Siqueira et al., 2016), Polyporales (Phleboid clade and
375 *Trametes*) (Binder et al., 2013; Justo and Hibbett, 2011; Miettinen et al., 2016), Holtermanniales (Liu
376 et al., 2015; Wuczkowski et al., 2011) and Wallemiales (Jancic et al., 2015) (Table 2; Table S1-S9).
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378 Sequences were retrieved from GenBank.
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386 Alignments for each gene were generated using MUSCLE (default conditions for gap openings and
387 gap extension penalties), implemented in MEGA v. 7.0 (Molecular Evolutionary Genetics Analysis),
388 visually inspected and trimmed by TrimAl v. 1.2 (<http://trimal.cgenomics.org>) to delimit and discard
389 ambiguously aligned regions. Since preliminary analyses suggested no incongruence among single-
390 loci phylogenetic trees, alignments were concatenated into a single data matrix with SequenceMatrix
391 v. 1.8 (Vaidya et al., 2011). The appropriate evolutionary model under the Akaike Information
392 Criterion (AIC) was determined for each partition with jModelTest 2 (Darriba et al., 2012).
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394 Phylogenetic inferences were calculated using two approaches. First, Bayesian Inference (BI) was
395 performed with MrBayes 3.2.2 (Ronquist et al., 2012) under GTR + I + G evolutionary model (best
396 model). The alignment was run for 10 million generations with two independent runs each containing
397 four Markov Chains Monte Carlo (MCMC) and sampling every 1000 iterations. The first 2,500 trees
398 were discarded as “burn-in” (25 %). Using the Sumt function of MrBayes a consensus tree was
399 generated and Bayesian posterior probabilities (BPP) were estimated. In a second approach,
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401 Maximum Likelihood (ML) estimate was performed using RAxML v. 8.1.2 (Stamatakis, 2014) with
402 the same substitution model (GTR + G + I) and 1,000 bootstrap replicates. Support values from
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421 bootstrapping runs (MLB) were mapped on the globally best tree using the “-f a” option of RAxML
422 and “-x 12345” as a random seed to invoke the novel rapid bootstrapping algorithm.
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428 Consensus trees were imported and visualized in FigTree v. 1.4.2
429 (<http://tree.bio.ed.ac.uk/software/figtree>). Due to the topological similarity similarity of the two
430 resulting trees, only Bayesian analysis with BPP values are reported (Figures 1-9).
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434 3. Results and Discussion

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438 Thirty-four Basidiomycota retrieved from a range of marine substrates were previously identified at
439 genus, family, order and sometimes at class level, on the basis of a single ribosomal gene (nrITS or
440 26S) (Bovio et al., 2017; Gnavi et al., 2017; Panno et al., 2013). However, the nrITS marker is not
441 sufficient for a thorough phylogenetic analyses, due to intraspecies (across a population of
442 individuals) and intra-genomic (due to multiple copies of the ribosomal region distributed over one
443 or more chromosomal locations) variations (Lindner and Banik, 2011). Protein-coding genes such as
444 *ef-1 α* , *rpb1* and *rpb2* are more suitable for a deep phylogeny, since a high variability in the intronic
445 regions is combined with more conserved exons (Raja et al., 2017; Stielow et al., 2015). To identify
446 the strains under investigation (Table 2) at lower taxonomic levels, appropriate molecular markers
447 were amplified. Unfortunately, due to the lack of sequences in public databases, it was not always
448 possible to build complete datasets. The family Peniophoraceae (Russulales) was an extreme case
449 and only an nrITS - based dataset was created (Table S.3). Amplification of *rpb1* and *rpb2* was often
450 problematic, and valid sequences were obtained only for the order Wallemiales by using specific non-
451 degenerated primers. In total, 123 newly generated sequences were obtained: 29 nrITS, 31 nrLSU, 8
452 nrSSU, 6 D1/D2, 33 *ef-1 α* , 13 *rpb1*, 2 *rpb2* and 2 *tsr1* (Table1).
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470 By applying a multi-locus approach, species identification was achieved for twenty Agaricomycetes
471 (Fig. 1, 2, 3, 4, 5, S.1, S.2), one Cystobasiodiomycetes (Fig. 6), five Microbotriomycetes (Fig. 6),
472 one Tremellomycetes (Fig. S.3), one Ustilaginomycetes (Fig. S.4), and two Wallemiomycetes (Fig.
473 7). Four strains were identified only at genus level (Fig. 1).
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3.1. Agaricomycetes

Agaricomycetes are widely distributed in the marine environment and have been commonly recovered from mangroves (Jones and Pang, 2012), sponges (Gao et al., 2008; Naim et al., 2017) and deep-sea sediments (Zhang et al., 2016). According to nrITS similarity, 24 Agaricomycetes were classified as Agaricales (14), Polyporales (8) and Russulales (2).

3.1.1. Agaricales

Within this order, six strains belonged to Psathyrellaceae and eight to Schizophyllaceae. For both families, consensus phylogenetic trees were based on nrITS, nrLSU and *ef-1 α* (Fig. 1, 2). The strain MUT 4775 was identified as *Coprinellus radians* and MUT 2331 as *Psathyrella candolleana*. The species *C. radians* is not new to the marine environment and was found in association with the marine sponge *Dragmacidon reticulatum* (Passarini et al., 2015) and with the zoanthid *Palythoa haddoni* (Qin et al., 2015). Species of *Psathyrella* occur mainly in terrestrial habitats, even though the ability to occupy uncommon niches is not rare for this genus (e.g. *P. aquatica* produces basidiomes underwater in the Rogue River in Oregon) (Frank et al., 2010). For MUT 2232, MUT 2282, MUT 4897 and MUT 5171 it was not possible to go below genus level (Fig.1), but a focus on the genus *Coprinellus* placed MUT 4897 and MUT 5171 within the “bisporus” group of the core Setulosi clade, and MUT 2232 and MUT 2282 in the Micacei clade (Fig. S.1). Although the presence of new lineages cannot be excluded, it would be risky to claim a novel species, since the lack of *ef-1 α* reference sequences in GenBank is an issue that must be taken into account.

With respect to Schizophyllaceae, two clades of *Schizophyllum commune* were recognised (Fig. 2), and the strains of marine origin fell into clade 1. To ensure the validity of our findings, three strains of terrestrial *S. commune* (MUT 1037, MUT 3331 and MUT 3335) were included in the analysis. The isolates under investigation were confirmed to be *S. commune* (Fig. 2), an organism that has been often found in marine environments (Gnavi et al., 2017; Liu et al., 2017; Zhang et al., 2016; Joel and Bhimba, 2013; Panno et al., 2013; Gao et al., 2008). With the exception of MUT 3019, all the strains

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543 were isolated from algae and seagrass, whose colonization may be facilitated by the secretion of the
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545 hemicellulose degrading xylanases (Kolenova et al., 2005; Rytioja et al., 2014). In fact, MUT 4875
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547 and MUT 5240 were seen to use xylan as the sole source of carbon in the presence of salt (personal
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549 communication by Drs Spina and Garzoli).
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551 552 3.1.2. Russulales 553

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555 Due to the lack of sequences in public databases, the phylogenetic tree relative to the order Russulales
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557 (family Peniophoraceae) was based only on nrITS. Regardless of this, MUT 4993 and MUT 5203
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559 were recognised as *Peniophora cinerea* and *P. incarnata*, respectively. Unidentified strains of
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561 *Peniophora* were isolated from the tropical seagrass *Enhalus acoroides* (Sakayaroj et al., 2010),
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563 sediments (González-Martínez et al., 2017) and from the Brazilian sponge *Amphimedon viridis*
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565 (Menezes et al., 2010).
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568 Lee et al. (2014) accepted *P. cinerea* and *P. incarnata* as highly efficient degraders of polycyclic
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570 hydrocarbons. Intriguingly, two strains of *Peniophora* sp. were retrieved from an oil polluted marine
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572 site in the Mediterranean sea (Bovio et al., 2017).
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574 575 3.1.3 Polyporales 576

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578 Eight isolates belonged to four families of the order Polyporales, namely Bjerkanderaceae (MUT
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580 2492 and MUT 5195), Irpicaceae (MUT 2288, MUT 2370 and MUT 2966), Meruliaceae (MUT 1939)
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582 and Polyporaceae (MUT 2444 and MUT 3263). Bjerkanderaceae, Irpicaceae and Meruliaceae were
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584 part of the Phleboid clade (plus *Tyromyces* clade) of Polyporales (Binder et al., 2013). A three loci
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586 dataset (nrITS, nrLSU and *ef-1 α*) was created to build a consensus phylogenetic tree (Fig. 4). MUT
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588 2370 and MUT 2966 formed a strongly supported cluster with *Irpex lacteus*, while MUT 2288
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590 grouped with *Ceriporia lacerata*, two species that have recently been detected in deep-sea sediments
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592 (Liu et al., 2017; Zhang et al., 2016).
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603 MUT 5195 clustered together with *Bjerkandera adusta*. MUT 2492 appeared related to *Lopharia*
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605 *spadicea*, although affiliation to other species could not be excluded. To further knowledge of this
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607 issue, herbarium specimens of *Porostereum fulvum* were obtained from the Université Claude
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609 Bernard, Lyon (LY18491 and LY18496; Table 1) and a focus on the Bjerkanderaceae was based on
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611 a two-loci dataset (nrITS and nrLSU) (Fig S.2). As a result, MUT 2492 was identified as *L. spadicea*.
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613 This organism may play an important role in the marine ecosystem: beside the ability to reduce
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615 wastewater toxicity (Tigini et al., 2013), *L. spadicea* exhibits algicidal properties (Jia et al., 2013).
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617 Finally, MUT 1939, isolated from polluted seawater in the Mediterranean Sea (Bovio et al., 2017),
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619 was identified as *Tyromyces fissilis*, found for the first time in the marine habitat.
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623 As for Polyporaceae, MUT 2444 and MUT 3263 were at first recognised as *Trametes* sp. Following
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625 a phylogenetic analysis focused on the genus *Trametes* and based on a five-loci dataset (nrITS,
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627 nrLSU, *rpb1*, *rpb2*, *ef-1 α*), the two isolates were identified as *T. gibbosa* (Lenzites clade) (Fig. 5), a
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629 species that had never been found in any marine habitats until now. The ability of species of *Trametes*
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631 to degrade PAH, and pentachlorophenols (PCP) through lignocellulolytic enzymes is widely accepted
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633 (Treu and Falandysz, 2017). Moreover, Knezevic et al. (2015) assessed the protective activity of *T.*
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635 *gibbosa* extracts against H₂O₂-induced DNA damage in human peripheral blood leukocytes. Finally,
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637 methanol extracts of *T. gibbosa* showed a broad spectrum of activity against a number of pathogens
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639 such as *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* etc. (Appiah et al., 2017).
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641 Beside a degradative function, these evidences may indicate a protective role against pathogens
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643 and/or damage caused to the sponges by potential mutagenic compounds.
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647 3.2. Cystobasidiomycetes and Microbotryomycetes

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649 According to the D1/D2 region of nrLSU, one strain was associated to Cystobasidiomycetes (order
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651 *incertae sedis*) and five to Microbotryomycetes (order Sporidiobolales). A four-loci (nrSSU, nrITS,
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653 D1/D2, *ef-1 α*) dataset was created and identification at species level was reached for all isolates
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655 (Table S.6, Fig. 6).
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663 3.2.1. Cystobasidiomycetes *incertae sedis*
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666 Among Cystobasidiomycetes (Fig. 6), MUT 5471 isolated from *P. pavonica*, fell into the Aurantiaca
667 clade of the Buckleyzymaceae family proposed by Wang et al. (2015b) and was identified as
668 *Buckleyzyma aurantiaca*, a psychrophilic yeast frequently found in cold habitats and in deep-sea
669 sediments (Nagahama et al., 2001; Sabri et al., 2001). Noteworthy is the ability of this organism to
670 produce antioxidant and photoprotective carotenoids (Zoz et al., 2015) that, besides being of
671 biotechnological importance, could guarantee adaptation advantages in the sea.
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679 3.2.2. Sporidiobolales
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682 The order Sporidiobolales consists of three separate clades: *Rhodosporidium*, *Sporidiobolus* and
683 mixed *Rhodosporidium/Sporidiobolus* (Wang et al., 2015b). These basidiomycetous yeasts are
684 common inhabitants of the marine habitats and have been frequently found in deep-sea waters
685 (Raghukumar, 2017). MUT 73, MUT 2266, MUT 2415 and MUT 2669 belonged to the
686 *Rhodosporidium* clade, whereas MUT 4384 fell into the *Sporidiobolus* group (Fig. 6). Specifically,
687 MUT 2266 and MUT 73 were recognised as *Rhodotorula graminis* while MUT 2669 was identified
688 as *R. diobovata*. MUT 2415 formed a mixed cluster together with *R. mucilaginosa*, *R. pacifica*, *R.*
689 *sphaerocarpa* and *R. taiwanensis*; however, Blastn analysis of two markers (nrITS and D1/D2)
690 showed a 100% similarity with strains of *R. mucilaginosa*. Finally, MUT 4384 was identified as
691 *Sporobolomyces roseus*. The role of yeast cells in the sea is still unclear although a positive correlation
692 between their density and water pollution has been demonstrated long ago (Hagler and Mendonça-
693 Hagler, 1981). Strains of *R. diobovata* and *R. mucilaginosa* have been found in the sea surface
694 microlayer, where levels of UV and concentrations of pollutants are particularly high (Chang et al.,
695 2016). Moreover, Wang et al. (2016), showed the ability of a marine strain of *R. mucilaginosa* (Mar-
696 Y3) to degrade dimethyl phthalate esters (DMPE), used in plastic products, cosmetics and
697 insecticides. A recent investigation reported high concentrations of phthalate esters in coastal areas
698 near Marseilles indicating an excess of these compounds throughout the Mediterranean (Paluselli et
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723 al., 2017), which would justify the presence of *R. mucilaginosa* MUT 2415 on the sponge *G.*
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725 *compressa*.
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727 728 **3.3. Tremellomycetes and Ustilagomycetes** 729

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731 Only two strains (MUT 2943 and MUT 2264), isolated from two Atlantic sponges, were affiliated
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733 with Tremellomycetes and Ustilagomycetes.
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735 736 3.3.1 Holtermanniales 737

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739 MUT 2943 belonged to the Holtermanniales, a small order of the class Tremellomycetes that includes
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741 extremophilic yeasts commonly found in the Arctic, Antarctic, Alpine environments and salty lakes
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743 (Turchetti et al., 2013; Wuczkowski et al., 2011; Zhang et al., 2017). Taxonomic assignment was
744
745 inferred by building a four-loci (nrITS, nrSSU, D1/D2, *ef-1 α*) phylogenetic tree (Fig. 7). MUT 2943
746
747 grouped into the *Holtermanniella festucosa* clade, a species found in association with the Arctic
748
749 sponge *Halichondria panicea* (Kachalkin, 2014), but never in seawater in temperate regions. By
750
751 investigating a strain of *H. festucosa* isolated from an oligotrophic lake in Patagonia, Brandao et al.
752
753 (2011) observed pectinolytic and esterase activities and production of mycosporine, a UV-absorbing
754
755 metabolite. This makes MUT 2943 fascinating from at least two points of view: beside a potential
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757 application in cosmeceutical, it might shield its host from microbial biofilm formation (Masak et al.,
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759 2014; Orgaz et al., 2006).
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762 763 3.4.2. Ustilaginales 764

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766 Ustilaginales and Urocystales are the two orders recognised in the class Ustilaginomycetes (Wang et
767
768 al., 2015a). MUT 2264 fell into the Moesziomyces group of the Ustilaginaceae (Ustilaginales),
769
770 together with *Pseudozyma aphidis* (currently *Moesziomyces aphidis*) and *P. rugulosa* (Fig. 8).
771
772 Considering the high similarity (99%) of nrITS, nrSSU and D1/D2 with sequences available in
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774 GenBank, this strain was identified as *P. aphidis*, which has been recently hypothesised to be
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776 conspecific with *P. rugulosa* (Kruse et al., 2017). In 2003, Gadanho et al. isolated this yeast from
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783 water samples collected in the Atlantic Ocean (south Portugal). Furthermore, two excellent squalene
784 producers, *Pseudozyma* sp. JCC207 and *Pseudozyma* sp. SD301, were found in seawater (100 m
785 below the surface) (Chang et al., 2008) and in the mangrove ecosystem (seawater and soil) (Song et
786 al., 2015). The synthesis of squalene, sought for pharmaceutical applications due to its antimicrobial,
787 antitumor and antioxidant properties, increases significantly in *Pseudozyma* sp. SD301 at 1.5% and
788 3% sea salt concentrations (Song et al., 2015). Last, but not the least, *P. aphidis* is a great producer
789 of biosurfactants (Goossens et al., 2016), molecules important in the degradation of hydrophobic
790 contaminants. Considering the salinity of the Atlantic Ocean (around 3%) and the great volumes of
791 seawater filtered daily by sponges, *P. aphidis* MUT 2264 may protect its host from both biotic and
792 abiotic dangers.
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804 805 **3.4. Wallemiomycetes**

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807 Wallemiomycetes, consists of the single order Wallemiales and the single monogeneric family
808 Wallemiaceae. On the basis of nrITS region, MUT 103 and MUT 4935 were highly similar (>98%)
809 to members of the *Wallemia sebi* species complex (WSSC), which includes *W. canadiensis*, *W.*
810 *mellicola*, *W. sebi* and *W. tropicalis* (Jancic et al., 2015). Specific primers developed by Nguyen et
811 al. (2015) were used to amplify the protein coding genes *tsr1*, *rpb1* and *rpb2*; the consensus
812 phylogenetic tree (Fig. 7) allowed to identify the two organisms as *W. sebi sensu strictu*. Living in
813 harsh environments such as hypersaline water (Zalar et al., 2005), *W. sebi* is recognised as xerophilic
814 and halotolerant. MUT 103 and MUT 4935 were isolated from *P. pavonica* and *P. oceanica*,
815 respectively in the Mediterranean Sea (on average 3% salts). Interestingly, Jancic et al. (2015)
816 detected β -glucosidase activity in six strains of *W. sebi* at concentration of NaCl up to 17%, that in
817 this case might explain the ability to colonize these substrates.
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831 832 **4. Hypothetical ecological role**

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834 Although Ascomycota are dominant in the marine environment, the importance of Basidiomycota
835 should not be neglected, considering the key role they play in the ecosystem and the large number of
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843 potentially active metabolites produced in this unique habitat (Raghukumar, 2017). For instance, the
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845 degradation of recalcitrant molecules such as lignin and tannins by white rot fungi (e.g. *F. flavus*)
846
847 increases the availability of cellulose or “ready to use” substances for other marine organisms. Hence,
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849 marine Basidiomycota are active in the cycle of nutrients and allow large quantities of biomass to
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851 return in the food chain of the ecosystem (Raghukumar, 2017).
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853
854 The occurrence of these fungi in the sea is not accidental: most likely, they are metabolically active
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856 and live as saprobes, symbionts or parasites of plants and/or animals. It must be considered that in
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858 the sea, Basidiomycota rarely develop specialised reproductive structures (e.g. basidiomes), thus
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860 relegating their dispersion to hyphal fragments that would not freely survive in such a hostile
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862 environment unless they find a supporting substrate (biotic or abiotic). This indicates that marine
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864 Basidiomycota are not merely terrestrial contaminants; indeed, they may be the result of a selective
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866 pressure that has enabled them to live in unusual niches. Furthermore, marine Basidiomycota are
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868 often retrieved in their yeast form (Jones et al., 2015). This is not surprising, since yeasts are
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870 particularly adapted to aquatic environments (Libkind et al., 2017).
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874 In 1972, Park classified aquatic micro-organisms as highly adapted “Indwellers”, “Immigrants”,
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876 whose main habitat is extra-aquatic or “Transients”, that start to die and decrease their activities as
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878 soon as they reach a new environment and as a result, have no ecological significance. The
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880 Basidiomycota investigated in this work, were isolated on CMASW (3.4% Sea Salt) and the majority
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882 of them were not growing in the absence of salts, indicating the development of adaptation
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884 mechanisms.
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887 In general, the ecological role of marine fungi is still largely unknown and, for the Basidiomycota
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889 here identified, we can only draw hypotheses based on evidences available in literature. For example,
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891 considering the anti-fungal properties of strains of *Coprinellus* sp. isolated from the Mediterranean
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893 sponge *Psammocinia* sp. (Paz et al. 2010) it can be speculated that the secretion of metabolites with
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895 antimicrobials in the marine environment may knock out other competitors and/or protect the host
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903 from pathogens. Similar consideration can have the production of melanin (with antimicrobial and
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905 antitumor effects) by *S. commune*, a species commonly found in marine environments (Arun et al.,
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907 2015; Joel and Bhimba, 2013). Zhao et al. (2013), investigated a strain of *C. lacerata* recovered from
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909 the star fish *Acanthaster planci* and isolated compounds with antimicrobial activities (Ríos and
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911 Andújar, 2017).

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914 Certainly, one could argue that spores of terrestrial fungi are washed into the Sea. However, the
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916 sporadic presence of an “Immigrant” fungus in the aquatic habitat, does not necessarily mean the it
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918 has no ecological significance (Park et al. 1972).

921 **5. Conclusions**

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923 Basidiomycota are poorly represented in the marine environment and a definite estimate of the species
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925 inhabiting this ecosystem is still incomplete. This work demonstrates that i) many basidiomycetous
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927 fungi populate the coastal and oceanic marine ecosystems and that ii) accurate multi-locus molecular
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929 approaches are necessary for a correct taxonomic placement and identification. The last point is
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931 extremely important and could be a starting point for future studies aimed at shedding light on the
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933 ecological role of marine Basidiomycota, with a view to exploiting their great biotechnological
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935 potential.

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1600 1601 1602 CAPTIONS TO ILLUSTRATIONS

1603
1604 **Figure 1.** Bayesian phylogram of Psathyrellaceae (Agaricales) based on a combined nrITS, nrLSU
1605 and *ef-1 α* dataset. The tree is rooted to *Agrocybe praecox*. Branch numbers indicate BPP values; Bar
1606 = expected changes per site (0.03).

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1612 **Figure 2.** Bayesian phylogram of Schizophyllaceae (Agaricales) based on a combined nrITS, nrLSU
1613 and *ef-1 α* The tree is midpoint rooted. Branch numbers indicate BPP values; Bar = expected changes
1614 per site (0.007).

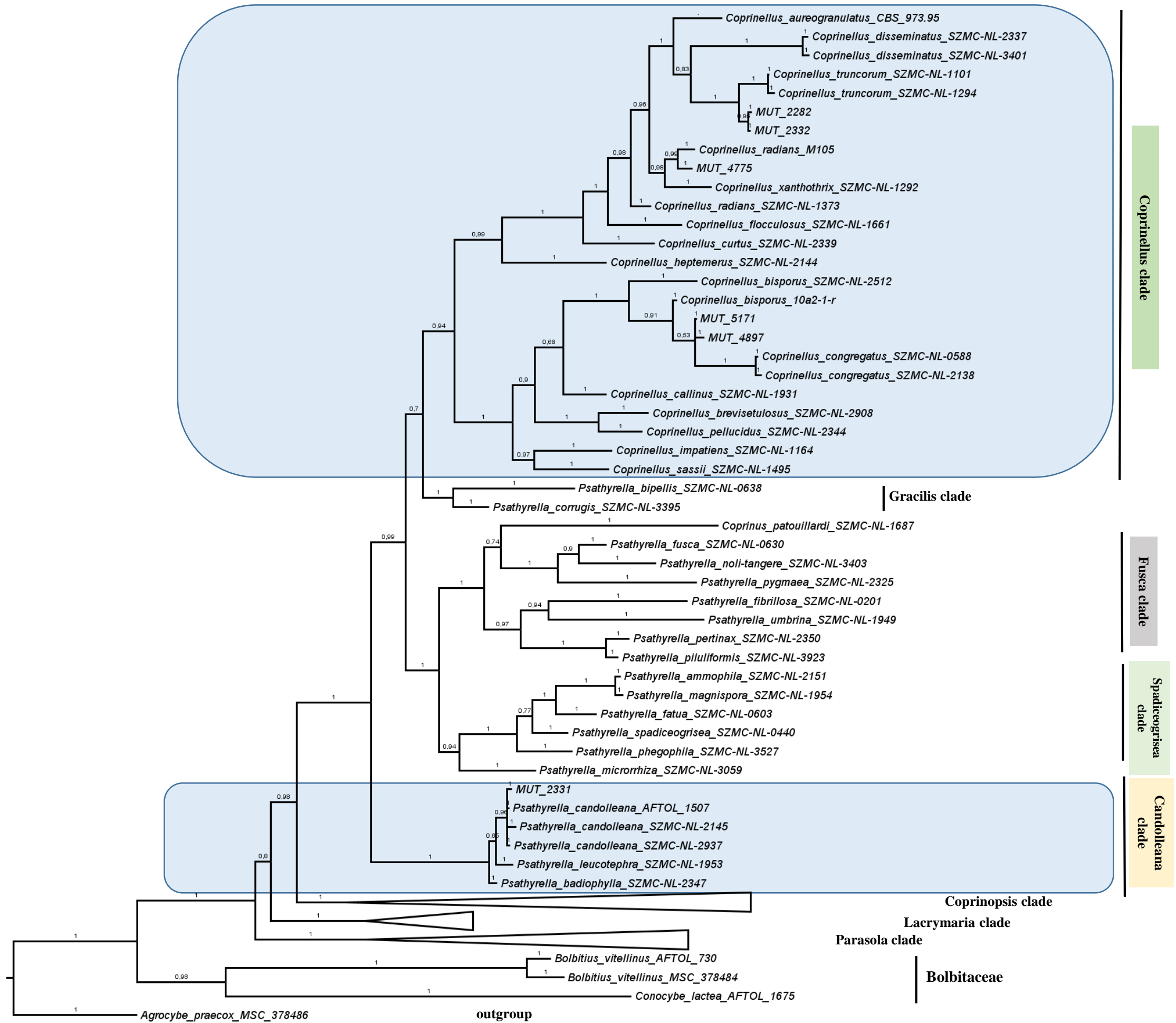
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1623 **Figure 3.** Bayesian phylogram of Peniophoraceae (Russulales) based on nrITS. The tree is rooted to
1624 the section *Validae* of *Amanita*, Agaricales (*Amanita rubescens* and *A. citrina*). Branch numbers
1625 indicate BPP values; Bar = expected changes per site (0.05).
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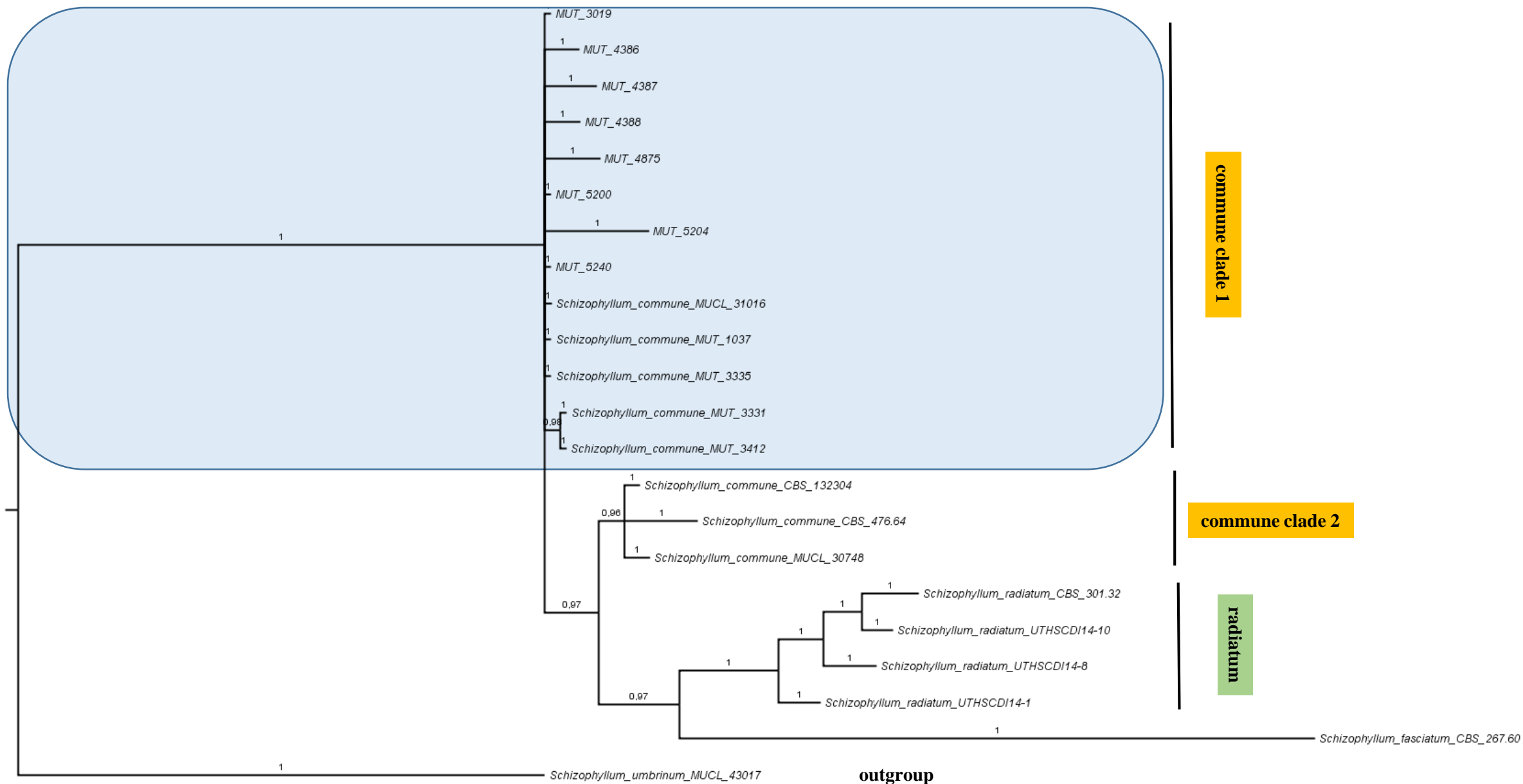
1630 **Figure 4.** Bayesian phylogram of the Phleboid clade of Polyporales based on a combined nrITS,
1631 nrLSU and *ef-1 α* dataset. The tree is rooted to *Heterobasidion annosum*. Branch numbers indicate
1632 BPP values; Bar = expected changes per site (0.04).
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1638 **Figure 5.** Bayesian phylogram of the genus *Trametes* (Polyporaceae) based on a combined nrITS,
1639 nrLSU, *ef-1 α* , *rpb1* and *rpb2* dataset. The tree is rooted to *Lopharia cinerascens*. Branch numbers
1640 indicate BPP values; Bar = expected changes per site (0.04).
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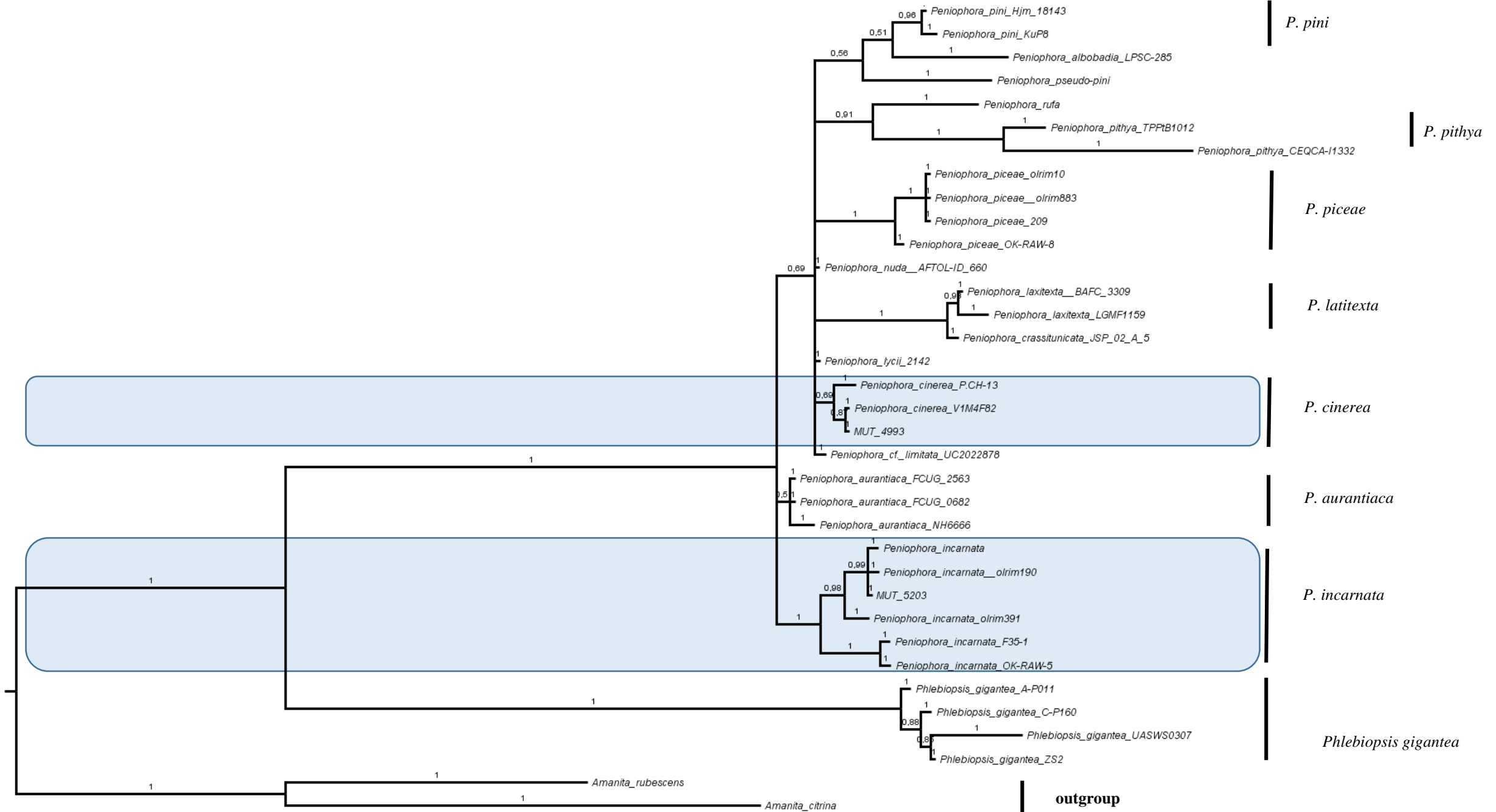
1645 **Figure 6.** Bayesian phylogram of Cystobasidiomycetes/Microboryomycetes based on a combined
1646 nrITS, nrSSU, D1/D2 and *ef-1 α* dataset. The tree is rooted to Ustilagomycotina (*Microstroma*
1647 *phylloplanum*). Branch numbers indicate BPP values; Bar = expected changes per site (0.08).
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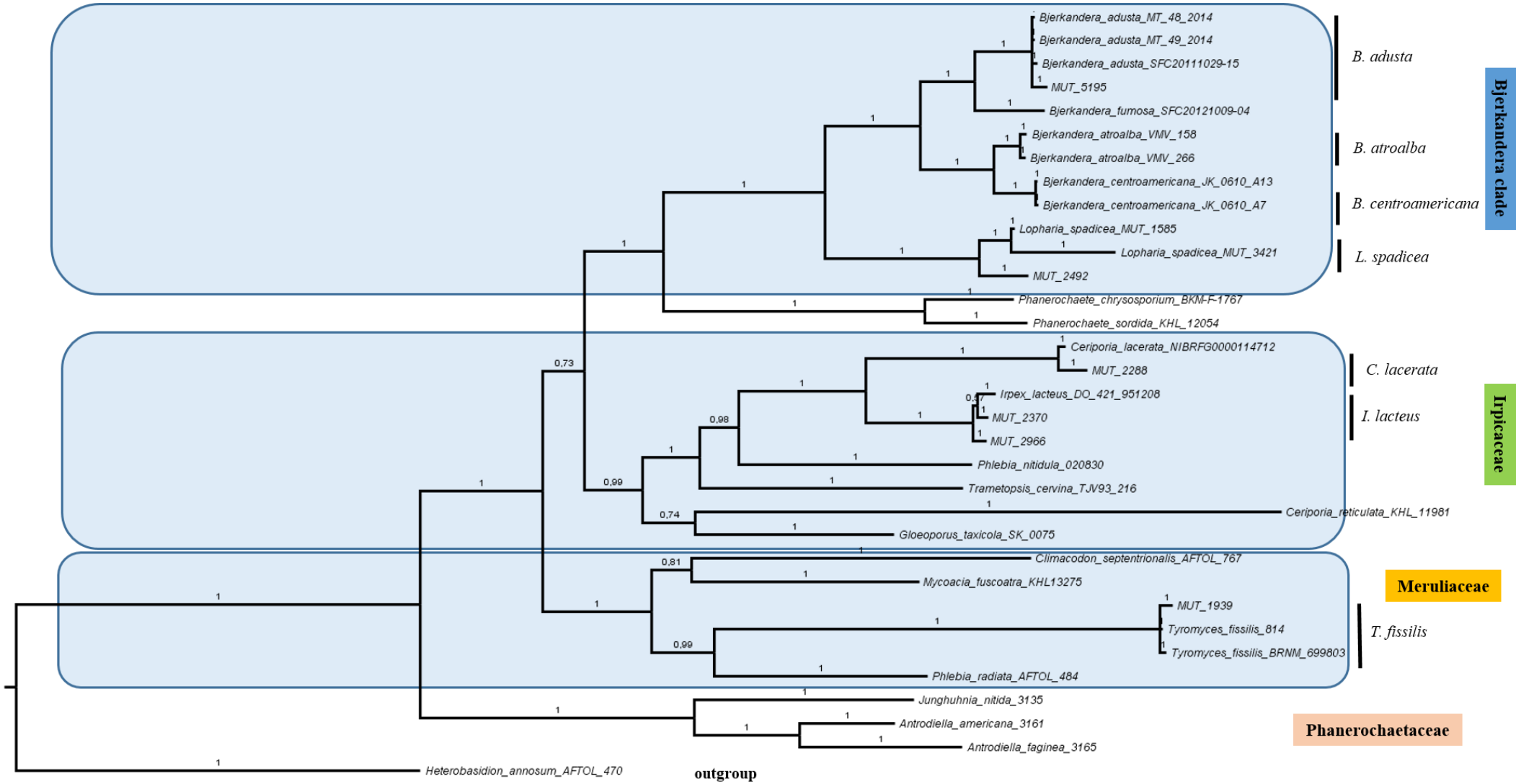
1652 **Figure 7.** Bayesian phylogram of Wallemiales based on a combined nrITS, *rpb1*, *rpb2* and *tsr1*
1653 dataset. The midpoint rooted. Branch numbers indicate BPP values; Bar = expected changes per site
1654 (0.004).
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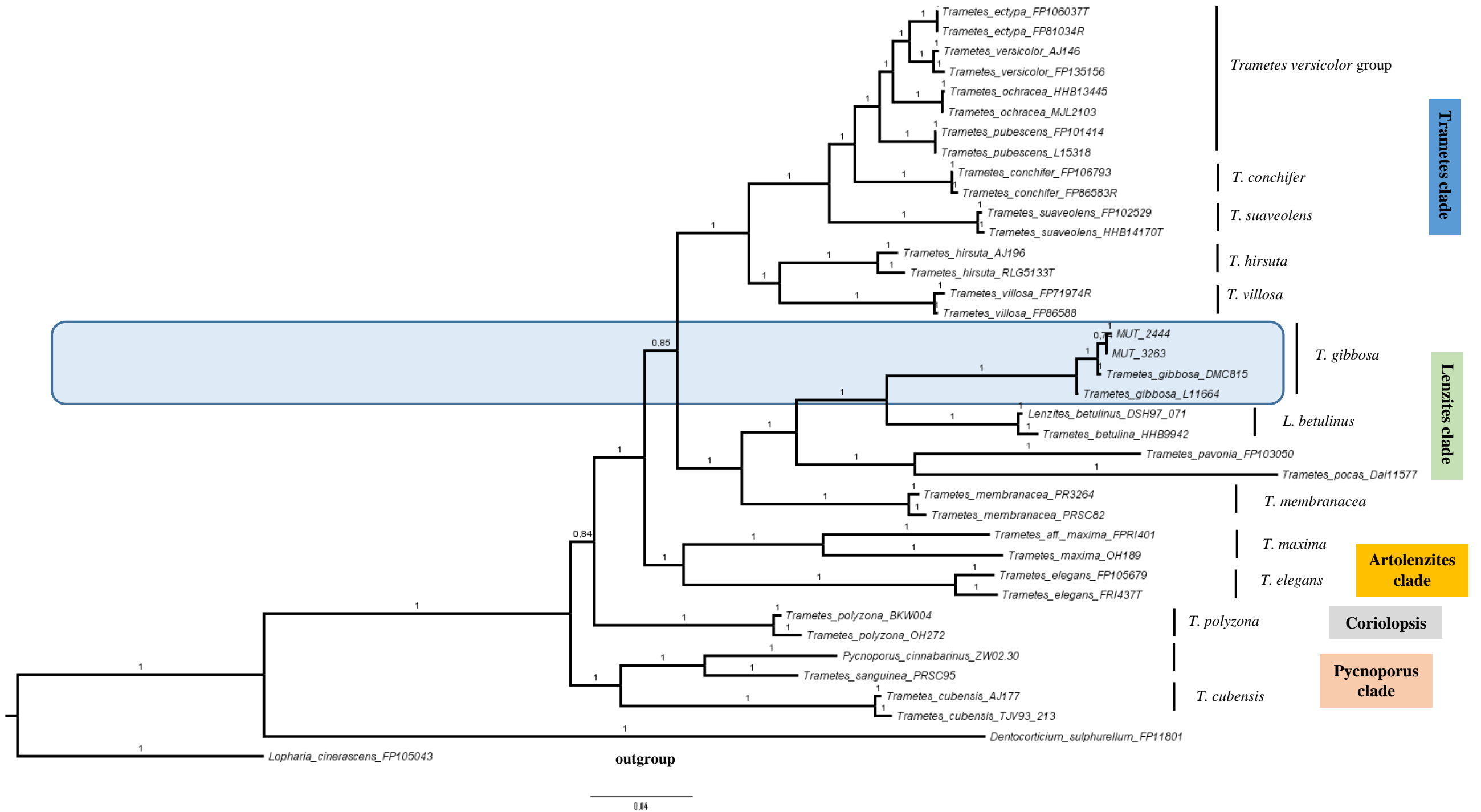


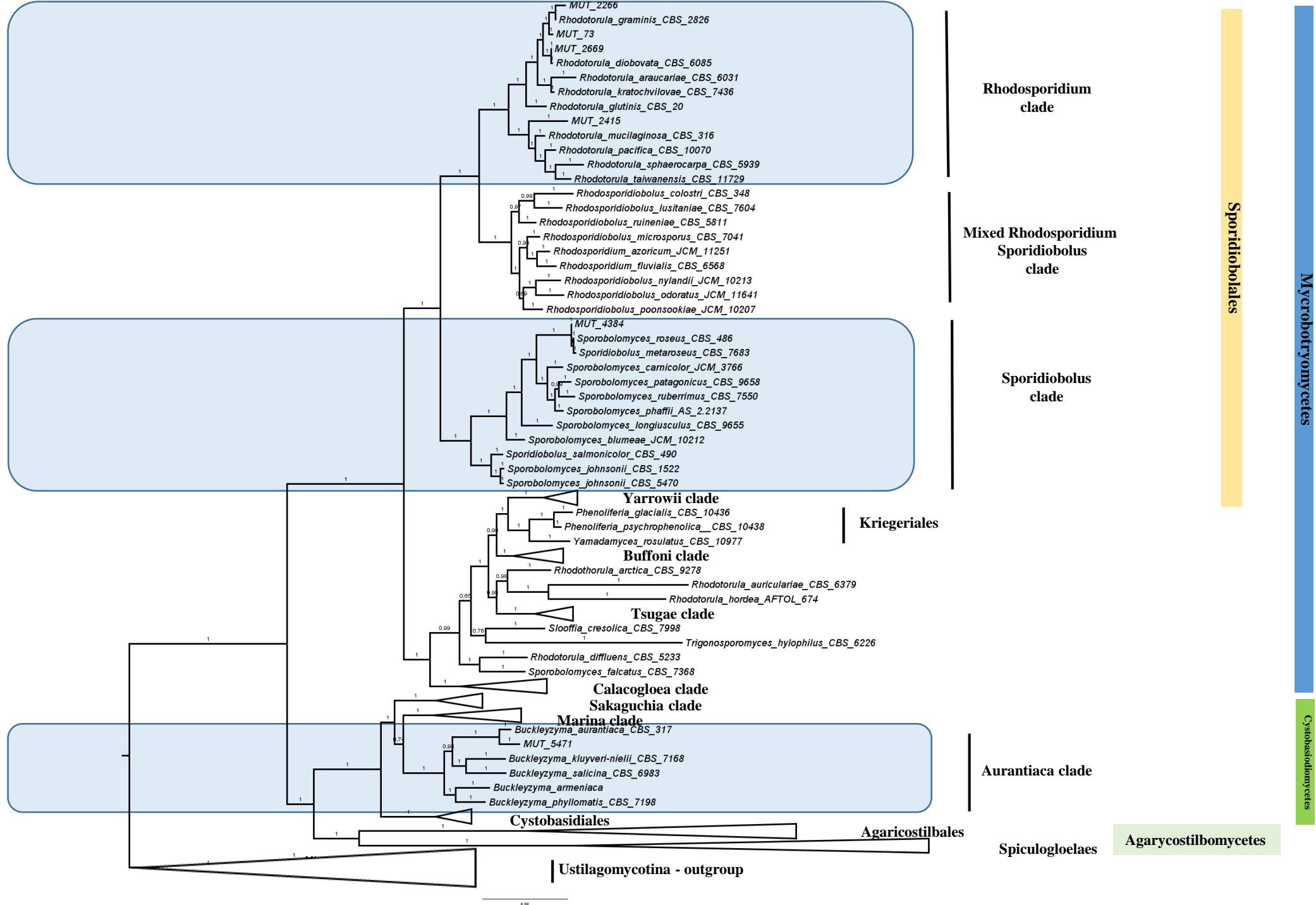


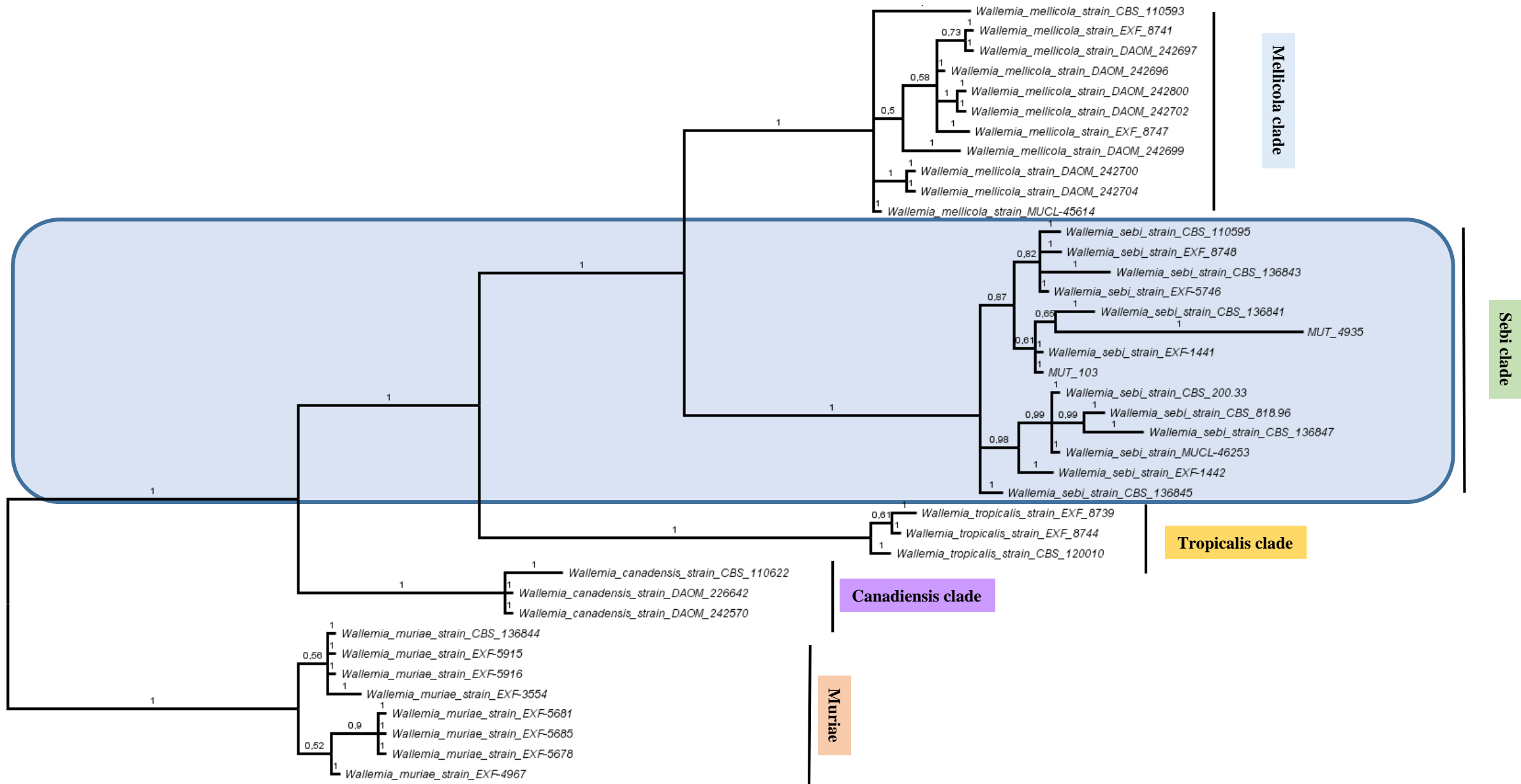
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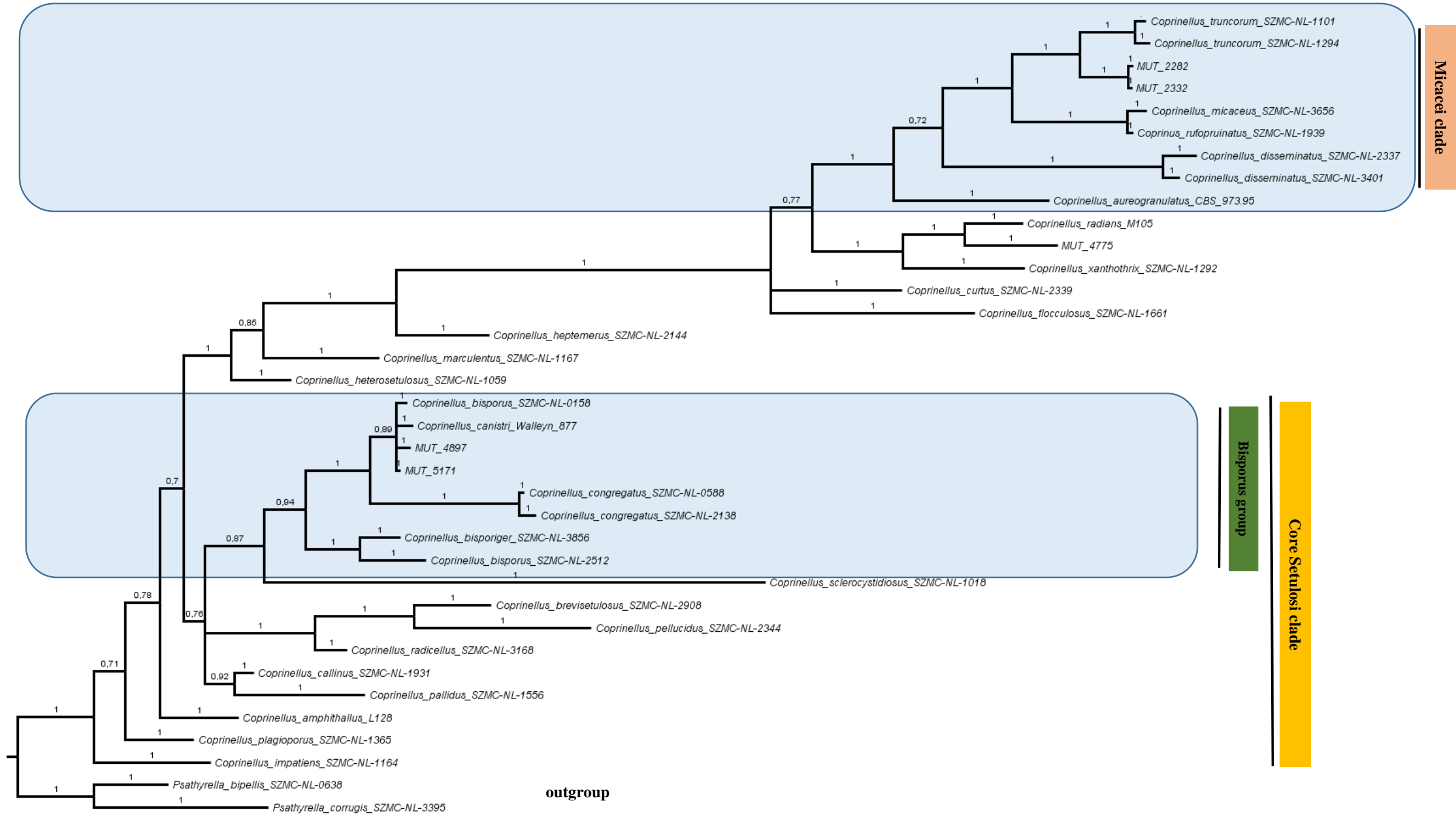


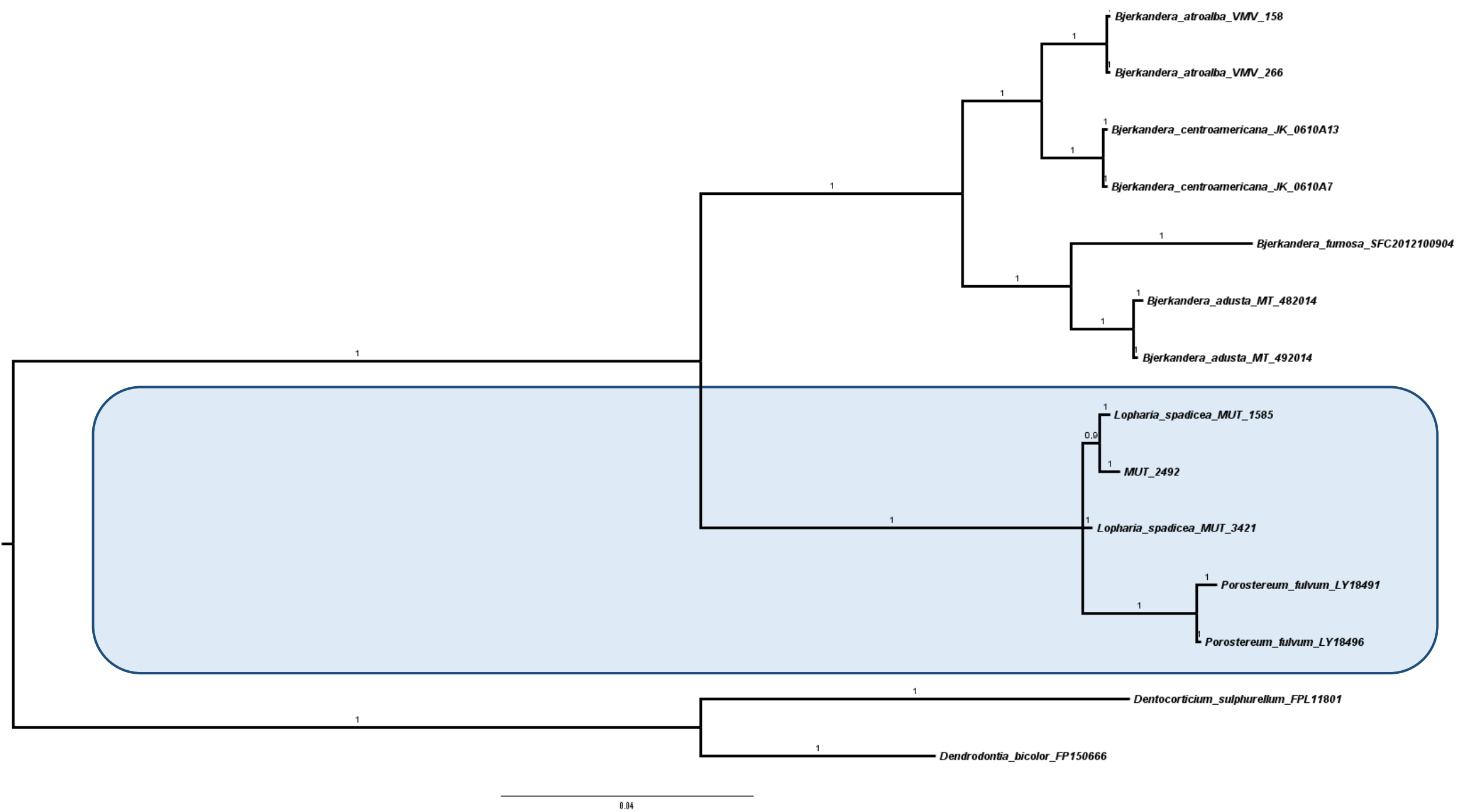


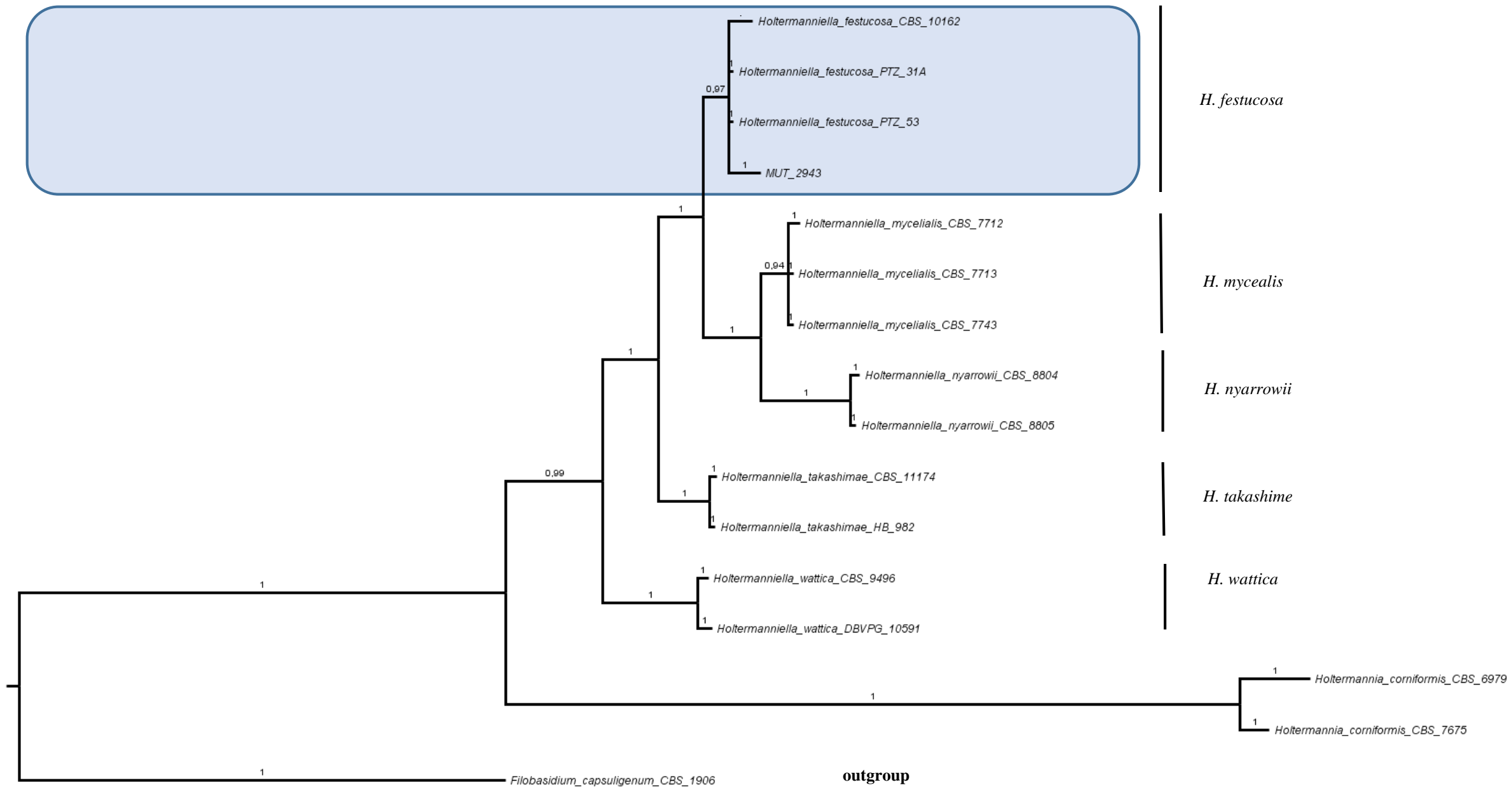












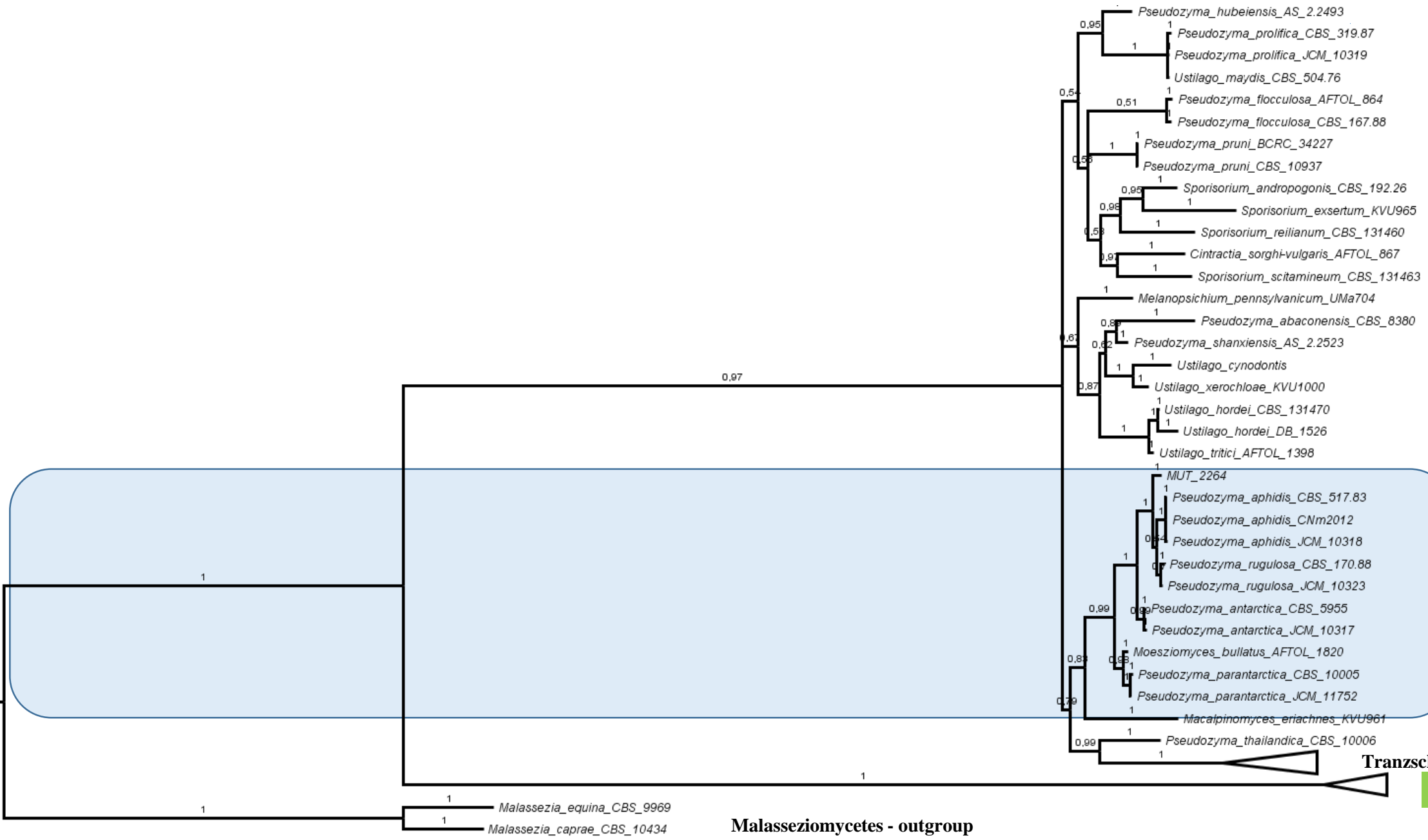
Ustilaginales

Sporisorium clade

Ustilago clade

Moesziomyces clade

Tranzscheliella
Urocystales



Malasseziomycetes - outgroup

0.08

Table 1. List of strains analysed. Source of isolation, final identification and GenBank accession numbers relative to the markers amplified and sequenced.

STRAIN	SUBSTRATE	IDENTIFICATION	<i>nrITS</i>	<i>nrLSU</i>	<i>nrSSU</i>	<i>D1/D2</i> (<i>nrLSU</i>)	<i>ef-1a</i>	<i>rpb1</i>	<i>rpb2</i>	<i>tsr1</i>
<i>Agaricomycetes</i>										
<i>Agaricales</i>										
<i>Psathyrellaceae</i>										
MUT 2331	<i>Grantia compressa</i>	<i>Psathyrella candolleana</i>	MF125293	MF125290	--	--	--	--	--	--
MUT 2332	<i>Grantia compressa</i>	<i>Coprinellus</i> sp.	MF140469	MF140461	--	--	--	MF282006	--	--
MUT 2282	<i>Grantia compressa</i>	<i>Coprinellus</i> sp.	MF140467	MF140459	--	--	MF150864	MF282004	--	--
MUT 4775	<i>Flabellia petiolata</i>	<i>Coprinellus radians</i>	KR014370 [§]	KP671736 [§]	--	--	MF150868	--	--	--
MUT 4897	<i>Padina pavonica</i>	<i>Coprinellus</i> sp.	KM355983	MF140457	KM355995	--	MF150860	MF282001	--	--
MUT 5171	<i>Padina pavonica</i>	<i>Coprinellus</i> sp.	KT699134	MF140458	--	--	MF150861	MF282002	--	--
<i>Schizophyllaceae</i>										
MUT 3019	<i>Aplysina cavernicola</i>	<i>Schizophyllum commune</i>	MF098694	MF115836	--	--	MF136466	--	--	--
MUT 4386	<i>Posidonia oceanica</i>	<i>Schizophyllum commune</i>	MF098692	MF115835	--	--	MF136459	MF282007	--	--
MUT 4387	<i>Posidonia oceanica</i>	<i>Schizophyllum commune</i>	MF098693	MF115834	--	--	MF136460	--	--	--
MUT 4388	<i>Posidonia oceanica</i>	<i>Schizophyllum commune</i>	KC339233	MF115833	--	--	MF136461	--	--	--
MUT 4875	<i>Flabellia petiolata</i>	<i>Schizophyllum commune</i>	KX988018 [§]	MF115832	--	--	MF136462	--	--	--
MUT 5200	<i>Padina pavonica</i>	<i>Schizophyllum commune</i>	KT715697	MF115831	--	--	MF136463	--	--	--
MUT 5204	<i>Padina pavonica</i>	<i>Schizophyllum commune</i>	KT715698	MF115830	--	--	MF136464	--	--	--
MUT 5240	<i>Padina pavonica</i>	<i>Schizophyllum commune</i>	KM355991	MF115829	--	--	MF136465	--	--	--
<i>Polyporales</i>										
<i>Bjerkanderaceae</i>										
MUT 2492	<i>Dysidea fragilis</i>	<i>Lopharia spadicea</i>	MF140468	MF140460	--	--	MF150871	--	--	--
MUT 5195	<i>Padina pavonica</i>	<i>Bjerkandera adusta</i>	KM355986	MF115840	--	--	MF150867	--	--	--
<i>Irpicaceae</i>										
MUT 2288	<i>Grantia compressa</i>	<i>Ceriporia lacerata</i>	MF125292	MF125289	--	--	MF150865	MF282005	--	--
MUT 2370	<i>Dysidea fragilis</i>	<i>Irpex lacteus</i>	MF098696	MF115838	--	--	MF150863	MF282003	--	--
MUT 2966	<i>Aplysina cavernicola</i>	<i>Irpex lacteus</i>	MF098695	MF115837	--	--	MF136434	--	--	--
<i>Meruliaceae</i>										
MUT 1939	<i>Oil splil water</i>	<i>Tyromyces fissilis</i>	KU935697 [*]	MF115839	--	--	MF150866	--	--	--
<i>Polyporaceae</i>										
MUT 2444	<i>Dysidea fragilis</i>	<i>Trametes gibbosa</i>	MF098690	MF115827	--	--	--	--	--	--
MUT 3263	<i>Dysidea fragilis</i>	<i>Trametes gibbosa</i>	MF098691	MF115828	--	--	MF136433	MF136440	--	--
<i>Russulales</i>										
<i>Peniophoraceae</i>										
MUT 4993	<i>Flabellia petiolata</i>	<i>Peniophora cinerea</i>	KR014375 [§]	KP671738 [§]	KT587326 [§]	--	MF150870	--	--	--
MUT 5203	<i>Padina pavonica</i>	<i>Peniophora incarnata</i>	KM355987	MF125291	--	--	MF150862	--	--	--
<i>Cystobasidiomycetes</i>										
<i>Cystobasidiomycetes</i>										
<i>incertae sedis</i>										
<i>Buckleyzymaceae</i>										
MUT 5471	<i>Padina pavonica</i>	<i>Buckleyzyma aurantiaca</i>	MF102877	--	MF112029	KU314991 [§]	MF136428	MF136437	--	--

Microbotryomycetes										
<i>Sporidiobolales</i>										
<i>Sporidiobolaceae</i>										
MUT 73	<i>Padina pavonica</i>	<i>Rhodotorula graminis</i>	<u>MF102880</u>	--	<u>MF112032</u>	<u>KU158181</u> [§]	<u>MF136431</u>	--	--	--
MUT 2266	<i>Pachymatisma johnstonia</i>	<i>Rhodotorula graminis</i>	<u>MF102881</u>	--	<u>MF112033</u>	<u>MF112036</u>	<u>MF136432</u>	--	--	--
MUT 2415	<i>Grantia compressa</i>	<i>Rhodotorula mucilaginoso</i>	<u>MF423718</u>	--	<u>MF521972</u>	<u>MF521975</u>	--	--	--	--
MUT 2669	<i>Posidonia oceanica</i>	<i>Rhodotorula diobovata</i>	<u>MF102878</u>	--	<u>MF112030</u>	<u>MF112034</u>	<u>MF136429</u>	<u>MF136438</u>	--	--
MUT 4384	<i>Posidonia oceanica</i>	<i>Sporobolomyces roseus</i>	<u>MF102879</u>	--	<u>MF112031</u>	<u>MF112035</u>	<u>MF136430</u>	<u>MF136439</u>	--	--
Tremellomycetes										
<i>Holtermanniales</i>										
MUT 2943	<i>Sycon ciliatum</i>	<i>Holtermanniella festucosa</i>	<u>MF125294</u>	--	<u>MF164047</u>	<u>MF196244</u>	<u>MF150869</u>	--	--	--
Ustilaginomycetes										
<i>Ustilaginales</i>										
<i>Ustilaginaceae</i>										
MUT 2264	<i>Pachymatisma johnstonia</i>	<i>Pseudozyma aphidis</i>	<u>MF423717</u>	--	<u>MF521971</u>	<u>MF521974</u>	--	--	--	--
Wallemiomycetes										
<i>Wallemiales</i>										
<i>Wallemiaceae</i>										
MUT 103	<i>Padina pavonica</i>	<i>Wallemia sebi</i>	<u>KT699119</u>	--	--	--	--	<u>MF136441</u>	<u>MF136443</u>	<u>MF136445</u>
MUT 4935	<i>Padina pavonica</i>	<i>Wallemia sebi</i>	<u>MF098689</u>	--	--	--	--	<u>MF136442</u>	<u>MF136444</u>	<u>MF136446</u>
Additional non marine strains										
MUT 1037	basidiome	<i>Schizophyllum commune</i>	<u>MF423708</u>	<u>MF423698</u>	--	--	<u>MF977550</u>	--	--	--
MUT 3331	basidiome	<i>Schizophyllum commune</i>	<u>MF423710</u>	<u>MF423700</u>	--	--	<u>MF977551</u>	--	--	--
MUT 3335	basidiome	<i>Schizophyllum commune</i>	<u>MF423711</u>	<u>MF423701</u>	--	--	<u>MF977552</u>	--	--	--
MUT 3412	<i>Carpinus</i> trunk	<i>Schizophyllum commune</i>	<u>MF423715</u>	<u>MF423705</u>	--	--	<u>MF977553</u>	--	--	--
MUT 1585	basidiome	<i>Lopharia spadicea</i>	<u>MF919666</u>	<u>MF919668</u>	--	--	<u>MF948006</u>	--	--	--
MUT 3421	dead branch	<i>Lopharia spadicea</i>	<u>MF919667</u>	<u>MF919669</u>	--	--	<u>MF948007</u>	--	--	--
LY18491	<i>Ulex europaeus</i>	<i>Porostereum fulvum</i>	<u>MG649452</u>	<u>MG649454</u>	--	--	--	--	--	--
LY18496	decaying branch	<i>Porostereum fulvum</i>	<u>MG649453</u>	<u>MG649455</u>	--	--	--	--	--	--

§ sequences obtained by Gnani et al (2017); * sequence obtained by Bovio et al (2017).

Table 2. Type of datasets used for phylogenetic analyses with number of taxa included, characters of the alignment and support of the resulting phylogram

Family/Order/Class	Dataset	Ingroup taxa	Characters	Number of supported nodes in Bayesian analysis (BPP > 0.70)	Number of supported nodes in ML analysis (BS > 0.5)
Psathyrellaceae	nrITS+nrLSU+ <i>ef-1α</i>	86	1696 bp	67 (80%)	67 (80%)
Psathyrellaceae (<i>Coprinellus</i>)	nrITS+nrLSU	34	1284 bp	29 (85%)	25 (73%)
Schizophyllaceae	nrITS+nrLSU+ <i>ef-1α</i>	22	1671 bp	8 (36%)	9 (41%)
Phleboid clade of Polyporales	nrITS+nrLSU+ <i>ef-1α</i>	32	1991 bp	26 (81%)	29 (90%)
Bjerkanderaeae	nrITS+nrLSU	13	1054 bp	11 (85%)	13 (100%)
Polyporaceae	nrITS+nrLSU+ <i>ef-1α+rpb1+rpb2</i>	37	3820 bp	35 (95%)	34 (92%)
Russulales (Peniophoraceae)	nrITS	33	480 bp	18 (55%)	21 (63%)
Holtermanniales	nrITS+nrSSU+D1/D2+ <i>ef-1α</i>	15	2663 bp	10 (67%)	14 (93%)
Ustilaginales	nrITS+nrSSU+D1/D2	40	2231 bp	30 (75%)	26 (65%)
Cystobasidiomycetes-Microbotryomycetes	nrITS+nrSSU+D1/D2+ <i>ef-1α</i>	86	2743 bp	66 (77%)	71 (83%)
Wallemiaceae	nrITS+ <i>rpb1+rpb2+tsr1</i>	39	1733 bp	16 (41%)	25 (64%)

1 **SUPPLEMENTARY MATERIALS**

2 **Supplementary Figure S.1.** Bayesian phylogram of the genus *Coprinellus* based on a nrITS and
 3 nrLSU dataset. The tree is rooted to the gracilis clade of Psathyrellaceae (*Psathyrella bipellis* and *P.*
 4 *corrugis*). Branch numbers indicate BPP values; Bar = expected changes per site (0.02).

5 **Supplementary Figure S.2.** Bayesian phylogram of Bjerkanderaceae based on a nrITS and nrLSU
 6 dataset. The tree is rooted to Polyporaceae (*Dendrodontia bicolor* and *Dentocorticium sulphurellum*).
 7 Branch numbers indicate BPP values; Bar = expected changes per site (0.04).

8 **Supplementary Figure S.3.** Bayesian phylogram of Holtermanniales based on a combined nrITS,
 9 nrSSU, D1/D2 and *ef-1a* dataset. The tree is rooted to *Filobasidium capsuligenum*. Branch numbers
 10 indicate BPP values; Bar = expected changes per site (0.02).

11 **Supplementary Figure S.4.** Bayesian phylogram of Ustilaginales based on a combined nrITS,
 12 nrSSU and D1/D2 dataset. The tree is rooted to Malasseziomycetes (*Malassezia equina* and *M.*
 13 *caprae*). Branch numbers indicate BPP values; Bar = expected changes per site (0.08).

14 **Supplementary Table S.1. Genbank sequences used for the multilocus phylogenetic analysis of**
 15 **Psathyrellaceae.**

TAXON	STRAIN	SUBSTRATE	nrITS	nrLSU	<i>ef-1a</i>
<i>Agrocybe praecox</i>	MSC 378486	unknown	AY194531	AY207140	DQ061276
<i>Bolbitius vitellinus</i>	MSC 378484	unknown	AY194519	AY207147	DQ408148
<i>Bolbitius vitellinus</i>	AFTOL 730	grass	DQ200920	AY691807	DQ408148
<i>Conocybe lactea</i>	AFTOL 1675	lawn	DQ486693	DQ457660	--
<i>Coprinellus aureogranulatus</i>	CBS 973.95	soil	GQ249274	GQ249283	GQ249267
<i>Co. bisporus</i>	SZMC-NL-2512	unknown	FN396107	FN396159	FN396215
	10a2-1-r	<i>Populus cathayana</i>	KT192303	--	--
<i>Co. brevisetulosus</i>	SZMC-NL-2908	unknown	GU227711	JN159585	--
<i>Co. callinus</i>	SZMC-NL-1931	unknown	FN396105	FN396158	FN396213
<i>Co. congregatus</i>	SZMC-NL-2138	unknown	FM878013	FM876270	--
	SZMC-NL-0588	unknown	JN943129	JQ045866	--
<i>Co. curtus</i>	SZMC-NL-2339	unknown	FM878016	FM876273	FM897246
<i>Co. disseminatus</i>	SZMC-NL-2337	unknown	FM878017	FM876274	--
	SZMC-NL-3401	unknown	JN159561	JN159587	--
<i>Co. radians</i>	M105	unknown	HM595561	HM595607	--
	SZMC-NL-1373	unknown	JN943118	JN159596	--
<i>Co. flocculosus</i>	SZMC-NL-1661	unknown	FN396138	FN396208	--
<i>Co. heptemerus</i>	SZMC-NL-2144	unknown	FM163178	FM160731	FM897243
<i>Co. impatiens</i>	SZMC-NL-1164	unknown	FM163177	FM160732	FM897261
<i>Co. pellucidus</i>	SZMC-NL-2344	unknown	FM878023	FM876280	-
<i>Co. sassii</i>	SZMC-NL-1495	unknown	FN396101	FN396155	FN396210

<i>Co. truncorum</i>	SZMC-NL-1294	unknown	<u>FM878007</u>	<u>FM876263</u>	<u>FM897228</u>
	SZMC-NL-1101	unknown	<u>FM878006</u>	<u>FM876262</u>	<u>FM897225</u>
<i>Co. xanthothrix</i>	SZMC-NL-1292	unknown	<u>FM878008</u>	<u>FM876264</u>	<u>FM897229</u>
<i>Coprinopsis atramentaria</i>	SZMC-NL-4245	unknown	<u>FN396123</u>	<u>FN396172</u>	<u>FN396225</u>
<i>Cop. calospora</i>	CBS 612.91	soil	<u>GQ249275</u>	<u>GQ249284</u>	<u>GQ249268</u>
<i>Cop. candidolanata</i>	SZMC-NL-2338	unknown	<u>FM878002</u>	<u>FM876257</u>	<u>FM897251</u>
<i>Cop. cinerea</i>	SZMC-NL-2141	unknown	<u>FN396149</u>	<u>FN396190</u>	--
<i>Cop. episcopalisis</i>	SZMC-NL-3032	unknown	<u>FN396118</u>	<u>FN396200</u>	<u>FN396222</u>
<i>Cop. erythrocephala</i>	SZMC-NL-4153	unknown	<u>FN396125</u>	<u>FN396174</u>	<u>FN396227</u>
<i>Cop. gonophylla</i>	SZMC-NL-0378	unknown	<u>FN396147</u>	--	<u>FN396242</u>
<i>Cop. insignis</i>	SZMC-NL-4244	unknown	<u>FN396124</u>	<u>FN396173</u>	<u>FN396226</u>
<i>Cop. krieglsteinerii</i>	SZMC-NL-2345	unknown	<u>FM878019</u>	<u>FM876276</u>	--
<i>Cop. laanii</i>	CBS 476.70	unknown	<u>GQ249276</u>	<u>GQ249285</u>	--
<i>Cop. lagopus</i>	SZMC-NL-2532	unknown	<u>FM878031</u>	<u>FM876289</u>	<u>FM897248</u>
<i>Cop. macrocephala</i>	SZMC-NL-1376	unknown	<u>FN396126</u>	<u>FN396175</u>	--
<i>Cop. marscibilis</i>	SZMC-NL-2140	unknown	<u>FM878020</u>	<u>FM876277</u>	<u>FM897257</u>
<i>Cop. spelaiophila</i>	SZMC-NL-3031	unknown	<u>FN396117</u>	<u>FN396167</u>	<u>FN396221</u>
<i>Cop. narcotica</i>	SZMC-NL-2342	unknown	<u>FM163180</u>	<u>FM160729</u>	<u>FN396244</u>
<i>Cop. pannucioides</i>	SZMC-NL-3528	unknown	<u>FN396143</u>	<u>FN396202</u>	<u>FN396238</u>
<i>Cop. poliomallus</i>	SZMC-NL-2336	unknown	<u>FM163182</u>	<u>FM160727</u>	<u>FM897244</u>
<i>Cop. pseudonivea</i>	SZMC-NL-2340	unknown	<u>FM163181</u>	<u>FM160728</u>	<u>FN430698</u>
<i>Cop. sclerotiger</i>	CBS 596.80	soil	<u>GQ249277</u>	<u>GQ249286</u>	<u>GQ249269</u>
<i>Cop. semitalis</i>	CBS 291.77	unknown	<u>GQ249278</u>	<u>GQ249287</u>	<u>GQ249270</u>
<i>Coprinus bellulus</i>	SZMC-NL-2341	unknown	<u>FM163176</u>	<u>FM160680</u>	--
<i>Coprinus cortinatus</i>	SZMC-NL-1621	unknown	<u>FN396121</u>	<u>FN396171</u>	<u>FN396224</u>
<i>Coprinus coniothorus</i>	SZMC-NL-3414	unknown	<u>FN396122</u>	<u>FN396207</u>	--
<i>Coprinus patouillardii</i>	SZMC-NL-1687	unknown	<u>FM878009</u>	<u>FM876265</u>	<u>FM897238</u>
<i>Coprinus utrifer</i>	SZMC-NL-0591	unknown	<u>FN396140</u>	<u>FN396209</u>	--
<i>Lacrymaria glareosa</i>	WU 16293	unknown	<u>HQ872015</u>	<u>HQ847134</u>	<u>HQ847208</u>
<i>L. lacrymabunda</i>	SZMC-NL-2140	unknown	<u>FM163184</u>	<u>FM160725</u>	<u>FN430688</u>
<i>L. pyrotricha</i>	CBS 573.79	unknown	<u>GQ249280</u>	<u>GQ249289</u>	<u>GQ249272</u>
<i>L. velutina</i>	AFTOL 478	unknown	<u>DQ490639</u>	<u>AY700198</u>	--
<i>Parasola auricoma</i>	SZMC-NL-0087	unknown	<u>FM163185</u>	<u>FM160724</u>	<u>FM897236</u>
<i>Pa. conopilus</i>	SZMC-NL-0285	unknown	<u>FM163225</u>	<u>FM160684</u>	<u>FM897237</u>
<i>Pa. leioccephala</i>	SZMC-NL-0466	unknown	<u>FM163192</u>	<u>FM160717</u>	<u>FM897241</u>
<i>Pa. lilatincta</i>	SZMC-NL-0660	unknown	<u>FM163195</u>	<u>FM160714</u>	<u>FM897230</u>
<i>Pa. megasperma</i>	SZMC-NL-1924	unknown	<u>FM163208</u>	<u>FM160701</u>	<u>FM897232</u>
<i>Pa. misera</i>	SZMC-NL-0667	unknown	<u>FM163211</u>	<u>FM160698</u>	<u>FM897240</u>
<i>Pa. plicatilis</i>	SZMC-NL-0287	unknown	<u>FM163212</u>	<u>FM160697</u>	--
<i>Psathyrella ammophila</i>	SZMC-NL-2151	unknown	<u>FM163220</u>	<u>FM160689</u>	<u>FM897260</u>
<i>Ps. badiophylla</i>	SZMC-NL-2347	unknown	<u>FN430699</u>	<u>FM876268</u>	<u>FM897252</u>
<i>Ps. bipellis</i>	SZMC-NL-0638	unknown	<u>FN430700</u>	<u>FN396160</u>	<u>FN396216</u>
<i>Ps. candolleana</i>	AFTOL 1507	unknown	<u>DQ494689</u>	<u>DQ110874</u>	--
<i>Ps. candolleana</i>	SZMC-NL-2145	unknown	<u>FM878001</u>	<u>FM876256</u>	--
<i>Ps. candolleana</i>	SZMC-NL-2937	unknown	<u>FN396114</u>	<u>FN396165</u>	<u>FN396220</u>
<i>Ps. corrugis</i>	SZMC-NL-3395	unknown	<u>FN430692</u>	<u>FN396205</u>	<u>FN396240</u>
<i>Ps. fatua</i>	SZMC-NL-0603	unknown	<u>FN396142</u>	<u>FN396201</u>	<u>FN396237</u>
<i>Ps. fibrillosa</i>	SZMC-NL-0201	unknown	<u>FN396137</u>	<u>FN396181</u>	<u>FN396232</u>
<i>Ps. fusca</i>	SZMC-NL-0630	unknown	<u>FM878021</u>	<u>FM876278</u>	<u>FM897256</u>
<i>Ps. leucotephra</i>	SZMC-NL-1953	unknown	<u>FM163226</u>	<u>FM160683</u>	<u>FM897219</u>
<i>Ps. magnispora</i>	SZMC-NL-1954	unknown	<u>FM163227</u>	<u>FM160682</u>	<u>FM897218</u>
<i>Ps. microrhiza</i>	SZMC-NL-3059	unknown	<u>FN396130</u>	<u>FN396178</u>	<u>FN396230</u>
<i>Ps. noli-tangere</i>	SZMC-NL-3403	unknown	<u>FN396144</u>	<u>FN396203</u>	<u>FN396239</u>
<i>Ps. pertinax</i>	SZMC-NL-2350	unknown	<u>FM878012</u>	<u>FM876269</u>	<u>FM897259</u>
<i>Ps. phegophila</i>	SZMC-NL-3527	unknown	<u>FN396129</u>	<u>FN396198</u>	<u>FN396229</u>
<i>Ps. piluliformis</i>	SZMC-NL-3923	unknown	<u>FN396136</u>	<u>FN396185</u>	<u>FN396235</u>
<i>Ps. pygmaea</i>	SZMC-NL-2325	unknown	<u>FM878011</u>	<u>FM876267</u>	<u>FM897224</u>
<i>Ps. spadicea</i>	SZMC-NL-3450	unknown	<u>FN396134</u>	<u>FN396183</u>	<u>FN396180</u>
<i>Ps. spadiceogrisea</i>	SZMC-NL-0440	unknown	<u>FM878024</u>	<u>FM876282</u>	<u>FM897223</u>
<i>Ps. umbrina</i>	SZMC-NL-1949	unknown	<u>FM878004</u>	<u>FM876260</u>	<u>FM897226</u>
<u>Additional taxa for Coprinellus</u>					
<i>Co. amphitallus</i>	L128	unknown	<u>HQ846978</u>	<u>HQ847065</u>	--
<i>Co. bisporiger</i>	SZMC-NL-3856	unknown	<u>HQ846976</u>	<u>HQ847063</u>	--
<i>Co. bisporus</i>	SZMC-NL-0158	unknown	<u>GU227705</u>	<u>HQ847062</u>	--
<i>Co. canistri</i>	Walley 877	unknown	<u>HQ846985</u>	--	--

<i>Co. heterosetulosus</i>	SZMC-NL-1059	unknown	<u>GU227708</u>	<u>HQ847075</u>	--
<i>Co. marculentus</i>	SZMC-NL-1167	unknown	<u>GU227706</u>	<u>HQ847089</u>	--
<i>Co. micaceus</i>	SZMC-NL-3656	unknown	<u>JN159567</u>	<u>JN159588</u>	--
<i>Co. pallidus</i>	SZMC-NL-1556	unknown	<u>HQ846989</u>	<u>HQ846989</u>	--
<i>Co. plagiosporus</i>	SZMC-NL-1365	unknown	<u>HQ846981</u>	<u>HQ847068</u>	--
<i>Co. radicellus</i>	SZMC-NL-3168	unknown	<u>GU227719</u>	<u>HQ847077</u>	--
<i>Co. sclerocystidiosus</i>	SZMC-NL-1018	unknown	<u>HQ846991</u>	<u>HQ847079</u>	--
<i>Co. rufopruinatus</i>	SZMC-NL-1939	unknown	<u>FN396104</u>	<u>FN396157</u>	--

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17 **Supplementary Table S.2. Genbank sequences used for the multilocus phylogenetic analysis of**
18 **Schizophyllaceae.**

TAXON	STRAIN	SUBSTRATE	nrITS	nrLSU	<i>ef-1a</i>
<i>S. commune</i>	CBS 132304	clinical patient	<u>LT217530</u>	<u>LT217561</u>	<u>LT217595</u>
	CBS 476.64	unknown	<u>LT217531</u>	<u>LT217562</u>	<u>LT217596</u>
	MUCL 30748	<i>Saccharum officinarum</i>	<u>LT217534</u>	<u>LT217566</u>	<u>LT217600</u>
	MUCL 31016	Hay	<u>LT217535</u>	<u>LT217567</u>	<u>LT217601</u>
<i>S. radiatum</i>	CBS 301.32	unknown	<u>LT217537</u>	<u>LT217569</u>	<u>LT217603</u>
	UTHSCSA DI14-1	unknown	<u>LT217539</u>	<u>LT217571</u>	<u>LT217605</u>
	UTHSCSA DI14-8	unknown	<u>LT217543</u>	<u>LT217577</u>	<u>LT217611</u>
	UTHSCSA DI14-10	unknown	<u>LT217545</u>	<u>LT217579</u>	<u>LT217613</u>
<i>S. fasciatum</i>	CBS 267.60	unknown	<u>LT217559</u>	<u>LT217593</u>	<u>LT217627</u>
<i>S. umbrinum</i>	MUCL 43017	unknown	<u>LT217560</u>	<u>LT217594</u>	<u>LT217628</u>

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21 **Supplementary Table S.3. Genbank nrITSsequences used for the phylogenetic analysis of**
22 **Peniophoraceae.**

TAXON	STRAIN	SUBSTRATE	nrITS
<i>Amanita citrina</i>	TENN61704	unknown	<u>FJ596867</u>
<i>Amanita rubescens</i>	MC01-556	sporocarp	<u>AJ889922</u>
<i>Peniophora albobadia</i>	LPSC-285	unknown	<u>KU530154</u>
<i>Peniophora aurantiaca</i>	FCUG 2563	unknown	<u>AF210825</u>
<i>Peniophora aurantiaca</i>	FCUG 0682	unknown	<u>AF210827</u>
<i>Peniophora aurantiaca</i>	NH6666	unknown	<u>AF210829</u>
<i>Peniophora cf. limitata</i>	UC2022878	litter	<u>KP814438</u>
<i>Peniophora cinerea</i>	V1M4F82	wheat plant	<u>KT692548</u>
<i>Peniophora cinerea</i>	P.CH-13	wood	<u>KF562015</u>
<i>Peniophora crassitunicata</i>	JSP 02 A 5	nest of <i>Atta capiguara</i>	<u>KR093906</u>
<i>Peniophora incarnata</i>	NH10271	unknown	<u>AF506425</u>
<i>Peniophora incarnata</i>	olrim391	<i>Picea abies</i>	<u>AY781263</u>
<i>Peniophora incarnata</i>	F35-1		<u>JF439504</u>
<i>Peniophora incarnata</i>	OK-RAW-5	wood pellets	<u>KX766174</u>
<i>Peniophora incarnata</i>	olrim190	<i>Picea abies</i>	<u>AY805616</u>
<i>Peniophora laxitexta</i>	LGMF1159	Leaves of <i>Vochysia divergens</i>	<u>JX559580</u>
<i>Peniophora laxitexta</i>	BAFC 3309	unknown	<u>FJ882040</u>
<i>Peniophora lycii</i>	2142	unknown	<u>JX046435</u>
<i>Peniophora nuda</i>	AFTOL-ID 660	unknown	<u>DQ411533</u>
<i>Peniophora piceae</i>	209	bottom sediment of bog	<u>JX507718</u>
<i>Peniophora piceae</i>	olrim10	<i>Picea abies</i>	<u>AY781264</u>
<i>Peniophora piceae</i>	OK-RAW-8	wood pellets	<u>KX766177</u>
<i>Peniophora piceae</i>	olrim883	<i>Picea abies</i>	<u>AY805634</u>

<i>Peniophora pini</i>	KuP8	<i>Pinus contorta</i> var. <i>latifolia</i>	<u>KP698183</u>
<i>Peniophora pini</i>	Hjm 18143	unknown	<u>EU118651</u>
<i>Peniophora pithya</i>	TPPtB1012	unknown	<u>AF119520</u>
<i>Peniophora pithya</i>	CEQCA-I1332	<i>Siphocampylus</i> sp. Pohl	<u>KC771449</u>
<i>Peniophora pseudo-pini</i>	TPPpB1007	unknown	<u>AF119514</u>
<i>Peniophora rufa</i>	TPRuB1014	unknown	<u>AF119516</u>
<i>Phlebiopsis gigantea</i>	A-P011	unknown	<u>AF087487</u>
<i>Phlebiopsis gigantea</i>	C-P160	unknown	<u>AF087488</u>
<i>Phlebiopsis gigantea</i>	UASWS0307	forest soil	<u>EF174446</u>
<i>Phlebiopsis gigantea</i>	ZS2	unknown	<u>JX946673</u>

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24 **Supplementary Table S.4. Genbank sequences used for the multilocus phylogenetic analysis of**
 25 **the Phleboid clade of Polyporales.**

TAXON	STRAIN	SUBSTRATE	nrITS	nrLSU	<i>ef-1a</i>
<i>Antrodia americana</i>	3161	unknown	<u>JN710509</u>	<u>JN710509</u>	<u>JN710711</u>
<i>A. faginea</i>	3165	unknown	<u>JN710514</u>	<u>JN710514</u>	<u>JN710712</u>
<i>Bjerkandera adusta</i>	MT 49214	unknown	<u>KT305935</u>	<u>KT305935</u>	<u>KT305938</u>
	MT 482014	unknown	<u>KT305936</u>	<u>KT305936</u>	--
	SFC20111029-15	unknown	<u>KJ704813</u>	<u>KJ704828</u>	--
<i>B. atroalba</i>	VMV 216	unknown	<u>KT305931</u>	<u>KT305931</u>	<u>KT305939</u>
	VMV 158	unknown	<u>KT305932</u>	<u>KT305932</u>	<u>KT305940</u>
<i>B. centroamericana</i>	JK0610/A7	unknown	<u>KT305933</u>	<u>KT305933</u>	<u>KT305941</u>
	JK9610/A13	unknown	<u>KT305934</u>	<u>KT305934</u>	<u>KT305942</u>
<i>Bjerkandera fumosa</i>	SFC20121009-04	unknown	<u>KJ704824</u>	<u>KJ704839</u>	--
<i>Ceriporia lacerata</i>	NIBRFG0000114712	unknown	<u>JN641761</u>	<u>JN641759</u>	--
<i>C. reticulata</i>	KHL 11981	unknown	<u>JX109845</u>	<u>EU118614</u>	<u>JX109899</u>
<i>Climacodon septentrionalis</i>	AFTOL 767	acer	<u>AY854082</u>	<u>AY684165</u>	<u>AY885151</u>
<i>Gleoporus taxicola</i>	SK 0075	unknown	<u>JX109847</u>	<u>JX109847</u>	<u>JX109901</u>
<i>Heterobasidion annosum</i>	AFTOL 470	xylem	<u>JF440572</u>	--	<u>DQ028583</u>
<i>Junghuhnia nitida</i>	3135	unknown	<u>JN710560</u>	<u>JN710560</u>	<u>JN710721</u>
<i>Ischnoderma resinosum</i>	CIRM-BRFM 955	unknown	<u>GU731564</u>	<u>AJ487927</u>	--
	DO 421/951208	unknown	<u>JX109852</u>	<u>JX109852</u>	<u>JX109911</u>
<i>Mycocacia fuscoatra</i>	KHL13275	unknown	<u>JN649352</u>	<u>JN649352</u>	<u>JX109908</u>
<i>Phanerochaete chrysosporium</i>	BKM-F-1767	unknown	<u>HQ188436</u>	<u>GQ470643</u>	<u>HQ188379</u>
<i>Ph. sordida</i>	KHL 12054	unknown	<u>EU118653</u>	<u>EU118653</u>	--
<i>Phlebia nitidula</i>	20830	unknown	<u>EU118655</u>	<u>EU118655</u>	--
<i>P. radiata</i>	AFTOL 484	unknown	<u>AY854087</u>	<u>AF287885</u>	<u>AY885156</u>
<i>Trametopsis cervina</i>	TJV 93 216	unknown	<u>JN165020</u>	<u>JN164796</u>	<u>JN164882</u>
<i>Tyromyces fissilis</i>	814	acer campestre	<u>HQ728291</u>	<u>HQ729001</u>	--
	BRNM 699803	populus tremula	<u>HQ728292</u>	<u>HQ729002</u>	--

26

27 **Supplementary Table S.5. Genbank sequences used for the multilocus phylogenetic analysis of**
 28 **Polyporaceae.**

TAXON	STRAIN	SUBSTRATE	nrITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>ef-1a</i>
<i>Coriolopsis polyzona</i>	BKW-004	unknown	<u>JN164978</u>	<u>JN164790</u>	<u>JN164844</u>	<u>JN164856</u>	<u>JN164881</u>
	OH272sp	unknown	<u>JN164979</u>	--	--	--	--
<i>Lenzites betulinus</i>	HHB-9942-Sp	unknown	<u>JN164983</u>	<u>JN164794</u>	<u>JN164822</u>	<u>JN164860</u>	<u>JN164895</u>
	DSH97	unknown	<u>KF573021</u>	--	--	<u>KF573147</u>	<u>KF573092</u>
<i>Lopharia cinerascens</i>	FP-105043-sp	unknown	<u>JN165019</u>	<u>JN164813</u>	<u>JN164840</u>	<u>JN164874</u>	<u>JN164900</u>
<i>Pycnoporus cinnabarinus</i>	ZW 02-30	unknown	<u>DQ411525</u>	<u>AY684160</u>	<u>JN164843</u>	<u>DQ408121</u>	<u>DQ02860</u>

	PR-SC-95	unknown	<u>JN164982</u>	<u>JN164795</u>	<u>JN164842</u>	<u>JN164858</u>	<u>JN164897</u>
<i>Trametes aff. maxima</i>	FPRI-401	unknown	<u>JN164933</u>	<u>JN164802</u>	<u>JN164836</u>	<u>JN164863</u>	<u>JN164884</u>
<i>Trametes conchifer</i>	FP-106793	unknown	<u>JN164924</u>	<u>JN164797</u>	<u>JN164823</u>	<u>JN164849</u>	<u>JN164887</u>
	FP-86583-R	unknown	<u>JN164939</u>	--	--	<u>KF573095</u>	<u>KF573038</u>
<i>Trametes cubensis</i>	AJ177	unknown	<u>JN164905</u>	<u>JN164787</u>	--	--	--
	TJV-93-213	unknown	<u>JN164923</u>	<u>JN164798</u>	<u>JN164834</u>	<u>JN164865</u>	<u>JN164883</u>
<i>Trametes ectypa</i>	FP-81034-R	unknown	<u>JN164930</u>	--	<u>KF573149</u>	<u>KF573094</u>	<u>KF573041</u>
	FP-106037-T	unknown	<u>JN164929</u>	<u>JN164803</u>	<u>JN164824</u>	<u>JN164848</u>	<u>JN164888</u>
<i>Trametes elegans</i>	FRI-437-T	unknown	<u>JN164985</u>	--	<u>KF573177</u>	<u>KF573142</u>	<u>KF573080</u>
	FP-105679-Sp	unknown	<u>JN164944</u>	<u>JN164799</u>	<u>JN164833</u>	<u>JN164861</u>	<u>JN164899</u>
<i>Trametes gibbosa</i>	L-11664-Sp	unknown	<u>JN164943</u>	<u>JN164800</u>	<u>JN164831</u>	<u>JN164859</u>	<u>JN164896</u>
	DMC815	unknown	<u>KC589144</u>	<u>KC589164</u>	--	--	--
<i>Trametes hirsuta</i>	AJ196	unknown	<u>JN164916</u>	--	--	<u>KF573125</u>	<u>KF573071</u>
	RLG-5133-T	unknown	<u>JN164941</u>	<u>JN164801</u>	<u>JN164829</u>	<u>JN164854</u>	<u>JN164891</u>
<i>Trametes maxima</i>	OH-189-Sp	unknown	<u>JN164957</u>	<u>JN164804</u>	<u>JN164816</u>	<u>JN164864</u>	<u>JN164885</u>
<i>Trametes membranacea</i>	PR-3264	unknown	<u>JN164946</u>	--	<u>KF573169</u>	<u>KF573132</u>	<u>KF573084</u>
	PR-SC-82	unknown	<u>JN164945</u>	<u>JN164805</u>	<u>JN164832</u>	<u>JN164857</u>	<u>JN164893</u>
<i>Trametes ochracea</i>	MJL-2103	unknown	<u>JN164948</u>	--	<u>KF573158</u>	<u>KF573121</u>	<u>KF573056</u>
	HHB-13445-Sp	unknown	<u>JN164954</u>	<u>JN164812</u>	<u>JN164826</u>	<u>JN164852</u>	<u>JN164904</u>
<i>Trametes pavonia</i>	FP-103050-Sp	unknown	<u>JN164958</u>	<u>JN164806</u>	<u>JN164835</u>	<u>JN164862</u>	<u>JN164886</u>
<i>Trametes pocas</i>	Dai11577	unknown	<u>KC848253</u>	<u>KC848340</u>	--	--	--
<i>Trametes pubescens</i>	L-15318-Sp	unknown	<u>JN164949</u>	--	<u>KF573162</u>	<u>KF573113</u>	<u>KF573064</u>
	FP-101414-Sp	unknown	<u>JN164963</u>	<u>JN164811</u>	<u>JN164827</u>	<u>JN164851</u>	<u>JN164889</u>
<i>Trametes suaveolens</i>	HHB-14170-T	unknown	<u>JN164968</u>	--	<u>KF573167</u>	<u>KF573128</u>	<u>KF573066</u>
	FP-102529-Sp	unknown	<u>JN164966</u>	<u>JN164807</u>	<u>JN164828</u>	<u>JN164853</u>	<u>JN164890</u>
<i>Trametes versicolor</i>	AJ146	unknown	<u>JN164912</u>	--	<u>KF573152</u>	<u>KF573107</u>	<u>KF573048</u>
	FP-135156-Sp	unknown	<u>JN164919</u>	<u>JN164809</u>	<u>JN164825</u>	<u>JN164850</u>	<u>JN164878</u>
<i>Trametes villosa</i>	FP-86588-Sp	unknown	<u>JN164970</u>	--	--	<u>KF573127</u>	<u>KF573073</u>
	FP-71974-R	unknown	<u>JN164969</u>	<u>JN164810</u>	<u>JN164830</u>	<u>JN164855</u>	<u>JN164892</u>
<i>Dentocorticium sulphurellum</i>	FP-11801	unknown	<u>JN165018</u>	--	<u>JN164841</u>	<u>JN164876</u>	<u>JN164903</u>

29

30 **Supplementary Table S.6. Genbank sequences used for the multilocus phylogenetic analysis of**
31 **Microbotryomycetes and Cystobasidiomycetes.**

TAXON	STRAIN	SUBSTRATE	nrITS	D1/D2 (nrLSU)	nrSSU	<i>ef-1a</i>
Agaricostilbomycetes						
Agaricostilbales						
<i>S. clavatus</i>	AS 2.2318	<i>Sorbus pohuashanensis</i>	<u>AY364839</u>	<u>AY364839</u>	<u>KJ708406</u>	<u>KJ707894</u>
<i>S. diospyroris</i>	JCM 12157	leaf of <i>Diospyros morristiana</i>	<u>AB126047</u>	--	<u>AB124560</u>	<u>KJ707904</u>
<i>S. lactophilus</i>	CBS 7527	dead branch of <i>Abies firma</i>	<u>AF444545</u>	<u>AF177411</u>	<u>AB021675</u>	<u>KJ707889</u>
<i>S. pyrrosiae</i>	JCM 12159	leaf of <i>Pyrrosia lingua</i>	<u>AB126045</u>	<u>AB124562</u>	<u>AB126045</u>	<u>KJ707903</u>
<i>S. sasicola</i>	CBS 7285	dead leaf of <i>Sasa</i> sp.	<u>AF444548</u>	<u>AF177412</u>	<u>AB021688</u>	<u>KJ707900</u>
<i>S. taupoensis</i>	CBS 7898	dead leaf of <i>Nothofagus fusca</i>	<u>AF444592</u>	<u>AF177413</u>	<u>D66886</u>	<u>KJ707901</u>
<i>S. xanthus</i>	CBS 7513	dead leaf of <i>Acer rufinerve</i>	<u>AF444547</u>	<u>AF177414</u>	<u>D64118</u>	<u>KJ707902</u>
Spiculogloelae						
<i>S. coprosmicola</i>	JCM 8767	leaf of <i>Coprosma tenuifolia</i>	<u>AF444576</u>	<u>AF189981</u>	<u>D66879</u>	<u>KJ707908</u>
<i>S. dimmenae</i>	JCM 8762	leaf of <i>Pseudowintera colorata</i>	<u>AB038046</u>	<u>AB644404</u>	<u>D66881</u>	<u>KJ707907</u>
<i>S. linderiae</i>	CBS 7893	dead leaf of <i>Lindera obtusiloba</i>	<u>AF444582</u>	<u>AF189989</u>	<u>D66885</u>	<u>KJ707906</u>
<i>S. novozealandicus</i>	JCM 8756	leaf of <i>Pseudowintera colonata</i>	<u>AB038048</u>	<u>KJ708467</u>	<u>KJ708443</u>	<u>KJ707851</u>
<i>S. subbrunneus</i>	CBS 7196	dead leaf of <i>Oryza sativa</i>	<u>AF444549</u>	<u>AF189997</u>	<u>AB021691</u>	<u>KJ707909</u>
Cystobasidiomycetes						
Cystobasidiales						
<i>R. minuta</i>	CBS 319	air	<u>AF190011</u>	<u>AF189945</u>	<u>D45367</u>	<u>KJ707825</u>
<i>R. slooffiae</i>	CBS 5706	throat swab	<u>AF444627</u>	<u>AF444722</u>	<u>AB126653</u>	<u>KJ707828</u>
Aurantiaca clade <i>i.s.</i>						
<i>R. armeniaca</i>	JCM 8977	leaf of <i>Callistemon viminalis</i>	<u>AF444523</u>	<u>AF189920</u>	<u>AB126644</u>	<u>KJ707762</u>
<i>R. aurantiaca</i>	CBS 317	air	<u>AF444538</u>	<u>AF189921</u>	<u>KJ708436</u>	<u>AF444538</u>

<i>S. kluyveri-nielii</i>	CBS 7168	leaf of <i>Dombeya rotundifolia</i>	AF444544	AF189988	AB021674	KJ707760
<i>S. phyllomatis</i>	CBS 7198	leaf of <i>Dombeya rotundifolia</i>	AF444515	AF189991	AB021685	KJ707761
<i>S. salicinus</i>	CBS 6983	leaf of <i>Salix</i> sp.	AF444511	AF189995	AB021687	KJ707758
<i>S. gracilis</i>	CBS 71	decaying leaves	AF444578	AF189985	KJ708433	KJ707799
<i>R. marina</i>	CBS 2365	shrimp	AF444504	AF189944	AB126645	KJ707795
<i>S. symmetricus</i>	CBS 9727	Siberian silver birch	AY364836	AY364836	KJ708350	KJ707800
<i>S. vermiculatus</i>	JCM 10224	Leaf of <i>Pennisetum pedicellatum</i>	AB030335	AF460176	AB030322	KJ707801
Sakaguchia clade i.s.						
<i>R. cladiensis</i>	CBS 10878	headwaters	FJ008055	FJ008049	KJ708354	KJ707847
<i>R. oryzicola</i>	AS 2.2363	unknown	AY335160	AY335161	KJ708352	KJ707853
<i>R. oryzicola</i>	AS 2.3289	unknown	KP216523	KJ708451	KJ708353	KJ707848
Microbotryomycetes						
<i>R. arctica</i>	CBS 9278	soil	AB478857	AB478858	KJ708371	KJ707856
<i>R. auriculariae</i>	CBS 6379	basidiome of <i>Auricularia auricula-judae</i>	AF444507	AF189922	KJ708429	KJ707935
<i>R. cresolica</i>	CBS 7998	soil contaminated with orthocresol	AF444570	AF189926	KJ708365	KJ707942
<i>R. diffluens</i>	CBS 5233	leaf of <i>Tillandsia usneoides</i>	AF444533	AF075485	KJ708380	KJ707939
<i>S. falcatus</i>	CBS 7368	dead leaf of <i>Miscanthus sinensis</i>	AF444543	AF075490	AB021670	KJ707943
<i>R. hordea</i>	AFTOL 674	leaf of <i>Hordeum hexastichon</i>	AF444524	AF189933	AY657013	KJ707802
<i>R. hylophila</i>	CBS 6226	tunnel of <i>Xyleborus aemulus</i>	AF444622	AF363645	KJ708431	KJ708236
Kriegeriales						
<i>R. glacialis</i>	CBS 10436	glacier cryoconite	EF151249	EF151258	KJ708381	KJ707831
<i>R. psychrophenolica</i>	CBS 10438	mud at the glacier foot	EF151246	EF151255	KJ708382	KJ707859
<i>R. rosulata</i>	CBS 10977	dead pine needles	EU872492	EU872490	KJ708384	KJ707854
Buffoni clade i.s.						
<i>R. buffonii</i>	CBS 2838	<i>Boletus edulis</i> var. <i>albus</i>	AF444526	AF189924	KJ708362	KJ707946
<i>R. bogoriensis</i>	CBS 4101	leaf of <i>Randia malleifera</i>	AF444536	AF189923	KJ708363	KJ707949
<i>R. pustula</i>	CBS 6527	fruit of <i>Ribes nigrum</i>	AF444531	AF189964	KJ708361	KJ707937
Calacogloea clade i.s.						
<i>R. cycloclastica</i>	CBS 8448	soil	AF444732	AF444631	KJ708376	KJ707775
<i>R. eucalyptica</i>	CBS 8499	unknown	EU075185	EU075183	KJ708377	--
<i>R. philyla</i>	CBS 6272	tunnel of <i>Xyleborus ferrugineus</i>	AF444506	AF075471	KJ708438	KJ707772
<i>R. retinophila</i>	CBS 8446	soil	AF444624	AF444730	KJ708373	KJ707771
<i>R. terpenoidalis</i>	CBS 8445	soil	AF444623	AF444729	KJ708374	KJ707774
Tsugae clade i.s.						
<i>R. pilati</i>	CBS 7039	litter of <i>Abies alba</i>	AF444598	AF189963	KJ708364	KJ707947
<i>S. tsugae</i>	CBS 5038	<i>Tsuga heterophylla</i>	AF444580	AF189998	AB021692	KJ707945
Yarrowii clade i.s.						
<i>R. silvestris</i>	CBS 11420	dead needles of <i>Picea abies</i>	GQ121045	GQ121044	KJ708366	KJ707849
<i>R. straminea</i>	CBS 10976	dead pine needles	EU872491	EU872489	KJ708367	KJ707844
<i>R. yarrowii</i>	CBS 7417	decaying mushroom	AF444628	AF189971	AB032658	KJ707938
Sporidiobolales						
<i>R. araucariae</i>	CBS 6031	rotting bark of <i>Araucaria araucana</i>	AF444510	AF070427	KJ708435	KJ707862
<i>R. diobovata</i>	CBS 6085	sea water	AF444502	AF070421	AB073271	KJ707865
<i>R. glutinis</i>	CBS 20	air	AF444539	AF070429	X69853	KJ707869
<i>R. graminis</i>	CBS 2826	grass	AF444505	AF070431	X83827	KJ707868
<i>R. kratochvilovae</i>	CBS 7436	unknown	AF444520	AF071436	AB073273	KJ707863
<i>R. mucilaginoso</i>	JCM 8115T	unknown	AF444541	AF070432	AB021668	KJ707861
<i>R. pacifica</i>	CBS 10070	deep-sea sediment	AB026006	AB026006	KJ708397	KJ707860
<i>R. sphaerocarpa</i>	CBS 5939	Antarctic sea	AF444499	AF070425	AB073275	KJ707867
<i>R. taiwanensis</i>	CBS 11729	<i>Artemisia princeps</i>	GU646862	GU646863	KJ708409	KJ707838
<i>R. azoricum</i>	JCM 11251	soil	AB073229	AF321977	AB073269	KJ707813
<i>R. colostri</i>	CBS 348	Human colostrum	JN246563	AY372177	KJ708399	KJ707818
<i>R. fluviale</i>	CBS 6568	brackish water	AY015432	AF189915	AB073272	KJ707816
<i>R. lusitaniae</i>	CBS 7604	soil of woodland	AY015430	AF070423	AB073274	KJ707812
<i>S. microsporus</i>	CBS 7041	herbaceous culm	AF444535	AF070436	KJ708441	KJ707817
<i>S. nylandii</i>	JCM 10213	leaf of <i>Oryza sativa</i>	AB030323	AF387123	AB030319	KJ707822
<i>S. odoratus</i>	JCM 11641	basidiome of <i>Myxarium nucleatum</i>	KJ778638	AF387125	KJ708427	KJ707819
<i>S. poonsookiae</i>	JCM 10207	leaf of <i>Mangifera indica</i>	AB030327	AF387124	AB030320	KJ707821
<i>S. ruineniae</i>	CBS 5811	dung of goat	AF444491	AF070434	AB021693	KJ707820

<i>S. blumeae</i>	JCM 10212	leaf of <i>Blumea</i> sp.	AB030331	AY213010	AB030321	KJ707926
<i>S. carnicolor</i>	JCM 3766	unknown	AY069991	AY070008	KJ708434	KJ707912
<i>S. johnsonii</i>	CBS 5470	leaf of <i>Rubus</i>	AY015431	AF070435	L22261	KJ707914
<i>S. johnsonii</i>	CBS 1522	fodder yeast	AF444509	AF189975	--	KJ707916
<i>S. longiusculus</i>	CBS 9655	subsurface water	JN246566	KJ708464	KJ708400	KJ707929
<i>S. metaroseus</i>	CBS 7683	plant	EU003482	EU003461	KJ708415	KJ707841
<i>S. patagonicus</i>	CBS 9658	subsurface water	AY552329	AY158656	KP216518	KJ707930
<i>S. phaffii</i>	AS 2.2137	dead leaf of <i>Nerium indicum</i>	AY069995	AY070011	KJ708404	KJ707918
<i>S. roseus</i>	CBS 486	unknown	AY015438	AF070441	X60181	KJ707917
<i>S. ruberrimus</i>	CBS 7550	soil	AY015439	AF070442	KJ708402	KJ707915
<i>S. salmonicolor</i>	CBS 490	unknown	AY015434	AF070439	AB021697	KJ707923
Ustilagomycotina						
<i>M. phylloplanum</i>	CBS 8073	leaf of <i>Banksia collina</i>	AF190004	AB038131	AJ496258	KP323116
<i>M. phylloplanum</i>	JCM 9035	leaf of <i>Banksia collina</i>	AB038131	AF190004	AJ496258	--

32

33 **Supplementary Table S.7. Genbank sequences used for the multilocus phylogenetic analysis of**
34 **Holtermanniales.**

TAXON	STRAIN	SUBSTRATE	nrITS	D1D2 (nrLSU)	nrSSU	<i>ef-1a</i>
<i>Holtermanniella festucosa</i>	CBS 10162	<i>Festuca valesiaca</i>	KY102693	KY107040	KF036633	KF037052
	PTZ 53	unknown	AY633979	AY661812	--	--
	PTZ 31A	unknown	AY633978	AY661811	--	--
<i>H. mycelialis</i>	CBS 7712	soil-Antartica	AF408417	AJ311450	KF036641	KF037073
	CBS 7713	soil-Antartica	AF408418	AJ311451	--	--
	CBS 7743	plant-Antartica	AF408419	AJ311452	--	--
<i>H. nyarrowii</i>	CBS 8804	bird-Antartica	KY103594	AY006480	KF036643	KF037075
	CBS 8805	soil-Antartica	KY103593	KY107872	--	--
<i>H. wattica</i>	CBS 9496	soil-Antartica	NR_138371	KY107874	KF036662	KF037099
	DBVPG 10591	forest soil	KU745362	KU745305	--	--
<i>H. takashimae</i>	CBS 11174	litter	NR_137721	FM242574	KF036679	KF037163
	HB 982	litter	FM246501	FN430735	--	--
<i>Holtermannia corniformis</i>	CBS 6979	unknown	AF410472	AF189843	AF053718	KF037162
	CBS 7675	dead wood	GU937756	GU937761	--	--
	CBS 1906	sake-moto	AF444381	AF363642	AB075544	KF037152

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36 **Supplementary Table S.8. Genbank sequences used for the multilocus phylogenetic analysis of**
37 **Ustilaginales.**

TAXON	STRAIN	SUBSTRATE	nrITS	D1/D2 (nrLSU)	nrSSU
Malasseziomycetes					
<i>Malassezia caprae</i>	CBS 10434	goat	AY743656	KF706456	AY743656
<i>Malassezia equina</i>	CBS 9969	horse	KF706439	AY743621	KF706454
Urocystales					
<i>Urocystis colchici</i>	AFTOL 1647	unknown	DQ839596	DQ838576	DQ839595
<i>Urocystis eranthidis</i>	HMK 292	unknown	JN367299	JN367324	JN367352
Ustilaginales					
<i>Macalpinomyces eriachnes</i>	CBS 131454	<i>Eriachne sulcate</i>	JN367287	JN367312	JN367340
<i>Melanopsichium pennsylvanicum</i>	UMa7041	unknown	JN367288	JN367313	JN367341
<i>Moesziomyces bullatus</i>	AFTOL 1820	<i>Pennisetum typhoideum</i>	DQ831013	DQ831011	DQ831012
<i>Pseudozyma abaconensis</i>	CBS 8380	sea water	FJ008053	FJ008047	KP322956
<i>Pseudozyma antarctica</i>	JCM 10317	lake sediment - Antarctica	JN942668	JN940521	JN940463
<i>Pseudozyma antarctica</i>	CBS 5955	soil - Antarctica	AB089358	AJ235302	KP322960
<i>Pseudozyma aphidis</i>	JCM 10318	aphid secretion	AB089362	AB089363	JN940465
<i>Pseudozyma aphidis</i>	CBS 517.83	aphid secretion	AF294699	AJ235303	--
<i>Pseudozyma aphidis</i>	CNm2012	unknown	KF443199	KF443201	KF443200
<i>Pseudozyma flocculosa</i>	AFTOL 864	<i>Secale cereale</i>	DQ411535	AY745712	DQ092923
<i>Pseudozyma flocculosa</i>	CBS 167.88	unknown	AF294690	AJ235299	AF294717
<i>Pseudozyma hubeiensis</i>	CGMCC 2.2493	wastewater	DQ008954	DQ008953	KP322957

<i>Pseudozyma prolifica</i>	JCM 10319	<i>Scirpus microcarpus</i>	<u>AB089368</u>	<u>AB089369</u>	--
<i>Pseudozyma prolifica</i>	CBS 319.87	<i>Scirpus microcarpus</i>	<u>AF294700</u>	<u>AJ235298</u>	<u>AF294724</u>
<i>Pseudozyma pruni</i>	BCRC 34227	<i>Prunus mume</i>	<u>NR 137557</u>	<u>EU379943</u>	--
<i>Pseudozyma pruni</i>	CBS 10937	<i>Prunus mume</i>	<u>EU379942</u>	<u>EU379943</u>	<u>KP322958</u>
<i>Pseudozyma parantarctica</i>	JCM 11752	human blood	<u>JN942671</u>	--	<u>JN940457</u>
<i>Pseudozyma parantarctica</i>	CBS 10005	human blood	<u>AB089356</u>	<u>AB089357</u>	<u>JN940457</u>
<i>Pseudozyma rugulosa</i>	CBS 170.88	mouldy leaf	<u>AF294697</u>	<u>AJ235300</u>	--
<i>Pseudozyma rugulosa</i>	JCM 10323	<i>Zea mays</i>	<u>JN942670</u>	<u>JN940523</u>	<u>JN940458</u>
<i>Pseudozyma shanxiensis</i>	AS 2.2523	<i>Quercus mongolica</i>	<u>DQ008956</u>	<u>DQ008955</u>	<u>KP866247</u>
<i>Pseudozyma thailandica</i>	CBS 10006	human blood	<u>AB089354</u>	<u>AB089355</u>	<u>KP322959</u>
<i>Sporisorium andropogonis</i>	CBS 192.26	<i>Psidium guajava</i>	<u>AY740042</u>	<u>AY740095</u>	<u>KP322962</u>
<i>Sporisorium exsertum</i>	KVU 9651	unknown	<u>JN367293</u>	<u>JN367318</u>	<u>JN367347</u>
<i>Sporisorium reilianum</i>	CBS 131460	<i>Zea mays</i>	<u>KF706438</u>	<u>KF706430</u>	<u>KF706441</u>
<i>Sporisorium scitamineum</i>	CBS 131463	<i>Saccharum sp.</i>	<u>JN367296</u>	<u>JN367321</u>	<u>KP322965</u>
<i>Cintractia sorghi-vulgaris</i>	AFTOL 867	unknown	<u>DQ200931</u>	<u>AY745726</u>	<u>DQ234548</u>
<i>Tranzscheliella hypodytes</i>	RK0741	unknown	<u>JN367298</u>	<u>JN367323</u>	<u>JN367351</u>
<i>Tranzscheliella williamsii</i>	CBS 131475	unknown	<u>JN367310</u>	<u>JN367338</u>	<u>KP322974</u>
<i>Ustilago cynodontis</i>	MS 1	<i>Cynodon dactylon</i>	<u>AY740168</u>	<u>AY740168</u>	<u>JN367355</u>
<i>Ustilago hordei</i>	CBS 131470	<i>Hordeum vulgare</i>	<u>KF706437</u>	<u>KF706429</u>	<u>KP322978</u>
<i>Ustilago hordei</i>	DB 1526	unknown	<u>JN367303</u>	<u>JN367329</u>	<u>JN367357</u>
<i>Ustilago tritici</i>	AFTOL 1398	unknown	<u>DQ846894</u>	<u>DQ094784</u>	<u>DQ846895</u>
<i>Ustilago maydis</i>	CBS 504.76	<i>Zea mays</i>	<u>AY854090</u>	<u>AF453938</u>	<u>KP322979</u>
<i>Ustilago xerochloae</i>	KVU 10001	unknown	<u>JN367311</u>	<u>JN367339</u>	<u>JN367362</u>

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39 **Supplementary Table S.9. Genbank sequences used for the multilocus phylogenetic analysis of**
40 **Walleiales.**

TAXON	STRAIN	SUBSTRATE	nrITS	<i>tsr1</i>	<i>rbp1</i>	<i>rbp2</i>
<i>W. sebi</i>	CBS 818.96NT	Sunflower seed	<u>AY328915</u>	<u>KM035026</u>	<u>KM035115</u>	<u>KM035204</u>
	CBS 110595	Domestic interior, dormitory	<u>AY302511</u>	<u>KM035073</u>	<u>KM035162</u>	<u>KM035250</u>
	CBS 200.33	Unknown	<u>AY302519</u>	<u>KM196459</u>	<u>KM196359</u>	<u>KM196408</u>
	EXF-1441	Unknown	<u>KJ494640</u>	<u>KM196417</u>	<u>KM196323</u>	<u>KM196369</u>
	EXF-1442	Unknown	<u>KJ494643</u>	<u>KM196418</u>	<u>KM196324</u>	<u>KM196370</u>
	MUCL 46253d	Flavoured mineral water	<u>KJ494638</u>	<u>KM196443</u>	<u>KM196344</u>	<u>KM196397</u>
	CBS 136843	Archive	<u>KJ409909</u>	<u>KM035063</u>	<u>KM035152</u>	<u>KM035240</u>
	CBS 136845	Office building	<u>KJ409911</u>	<u>KM035065</u>	<u>KM035154</u>	<u>KM035242</u>
	CBS 136847	Boiled eggs plant	<u>KJ409913</u>	<u>KM035067</u>	<u>KM035156</u>	<u>KM035244</u>
	EXF-8748	Office dust	<u>KJ409896</u>	<u>KM035045</u>	<u>KM035134</u>	<u>KM035223</u>
	EXF-5746	Hypersaline water of saltern	<u>KJ494642</u>	<u>KM196429</u>	<u>KM196335</u>	<u>KM196382</u>
	CBS 110582a	Hypersaline water of saltern	<u>AY302499</u>	<u>KM196448</u>	<u>KM196319</u>	<u>KM196401</u>
	CBS 110600	Hypersaline water of Dead Sea	<u>AY302513</u>	<u>KM196454</u>	<u>KM196354</u>	<u>KM196405</u>
	CBS 202.33	Sea salt	<u>AY328912</u>	<u>KM196453</u>	<u>KM196353</u>	<u>KM196404</u>
	EXF-5860	Hypersaline water of solar saltern	<u>KJ494636</u>	<u>KM196435</u>	--	<u>KM196387</u>
	<i>W. mellicola</i>	CBS 110593	Straw hat	<u>AY302509</u>	<u>KM196464</u>	<u>KM196318</u>
EXF-8741		Dust in house	<u>KJ409883</u>	<u>KM035030</u>	<u>KM035119</u>	<u>KM035208</u>
EXF-8747		House dust	<u>KJ409895</u>	<u>KM035044</u>	<u>KM035133</u>	<u>KM035222</u>
DAOM 242696		Dust in house	<u>KJ409884</u>	<u>KM035031</u>	<u>KM035120</u>	<u>KM035209</u>
DAOM 242697		Dust in house	<u>KJ409886</u>	<u>KM035033</u>	<u>KM035122</u>	<u>KM035211</u>
DAOM 242699		House dust	<u>KJ409890</u>	<u>KM035039</u>	<u>KM035128</u>	<u>KM035217</u>
DAOM 242700		House dust	<u>KJ409892</u>	<u>KM035041</u>	<u>KM035130</u>	<u>KM035219</u>
DAOM 242702		Dust in house	<u>KJ409887</u>	<u>KM035034</u>	<u>KM035123</u>	<u>KM035212</u>
DAOM 242704		House dust	<u>KJ409894</u>	<u>KM035043</u>	<u>KM035132</u>	<u>KM035221</u>
DAOM 242800		Dust in house	<u>KJ409885</u>	<u>KM035032</u>	<u>KM035121</u>	<u>KM035210</u>
MUCL 45614	Flower of unidentified angiosperm	<u>KJ494626</u>	<u>KM196442</u>	<u>KM196343</u>	<u>KM196396</u>	
<i>W. canadensis</i>	DAOM 226642	Indoor of residence	<u>KJ409879</u>	<u>KM035025</u>	<u>KM035114</u>	<u>KM035203</u>
	DAOM 242570	Indoor environment	<u>KJ409918</u>	<u>KM035080</u>	<u>KM035169</u>	<u>KM035257</u>
	CBS 110622	Catwalk in silos	<u>AY302517</u>	<u>KM196457</u>	<u>KM196357</u>	<u>KM196407</u>
<i>W. Tropicalis</i>	EXF-8739 T	House dust	<u>KJ409878</u>	<u>KM035023</u>	<u>KM035112</u>	<u>KM035201</u>
	EXF-8744	House dust	<u>KJ409891</u>	<u>KM035040</u>	<u>KM035129</u>	<u>KM035218</u>
	CBS 120010	Soil	<u>KM217176</u>	<u>KM196470</u>	<u>KM196317</u>	<u>KM196415</u>

<i>W. muriae</i>	CBS 136844	Office building	<u>KJ409910</u>	<u>KM035064</u>	<u>KM035153</u>	<u>KM035241</u>
	EXF-3554	Saturated sugar solution	<u>KJ494605</u>	<u>KM196422</u>	<u>KM196328</u>	<u>KM196374</u>
	EXF-4967	Hypersaline water of Dead Sea	<u>KJ494610</u>	<u>KM196423</u>	<u>KM196329</u>	<u>KM196375</u>
	EXF-5678	Halophyte	<u>KJ494603</u>	<u>KM196426</u>	<u>KM196332</u>	<u>KM196379</u>
	EXF-5681	Halophyte	<u>KJ494600</u>	<u>KM196427</u>	<u>KM196333</u>	<u>KM196380</u>
	EXF-5685	Halophyte	<u>KJ494601</u>	<u>KM196428</u>	<u>KM196334</u>	<u>KM196381</u>
	EXF-5915	Living room wall	<u>KJ494593</u>	<u>KM035091</u>	<u>KM035180</u>	<u>KM035266</u>
	EXF-5916	Kitchen wall	<u>KJ494594</u>	<u>KM035090</u>	<u>KM035179</u>	<u>KM035265</u>

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