

Mycosphere Notes 572-624: Exploring the hidden diversity of fungi and fungi-like taxa in different terrestrial microhabitats

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Abstract

This is the 14th in a series of Mycosphere notes where we provide entries on new species and higher taxa, including new host records, and geographical (country) records of fungi and fungi-like species. In this study, we introduce 51 new taxa including one new genus, viz. *Roseosporodochia* and eight new species in *Ascomycota*, viz. *Occultibambusa guizhouensis*, *Periconia baotouensis*, *Teichospora pini* (*Dothideomycetes*), *Basingstokeomyces cryptomeriae* (*Leotiomycetes*), *Apiospora dongruensis*, *Pseudolachnella chinensis*, *Roseosporodochia magnoliae*, *Trichoderma zhuangii* (*Sordariomycetes*); two new genera, viz. *Grandicium*, *Membranothymenium*, and 39 new species in *Basidiomycota*, viz. *Agaricus wadidarbaticus*, *Amyloxenasma cremeum*, *Am. tenuissimum*, *Athelopsis albofarinaceus*, *Burgella yunnanensis*, *Byssocorticium yunnanense*, *Ceriporus nigromarginatus*, *Crepidotus pusillus*, *Cylindrobasidium subbifidum*, *Grammothele albobadia*, *Grandicium tenuissimum*, *Gymnopus linzhiensis*, *Hymenochaete malaysiana*, *Hyphoderma fragilissimum*, *Hyp. punctatum*, *Hyp. yingjiangense*, *Inocybe griseum*, *Lopharia fissurata*, *Mariorajchenbergia yunnanensis*, *Membranothymenium grandinioides*, *Microporellus oblongosporus*, *Phanerochaete yingjiangensis*, *Phlegmacium sinovaricolor*, *Physisporinus pingbianensis*, *Punctularia fragilis*, *Scleroderma roseobrunneum*, *Sebacina yunnanensis*, *Sistotrema albofarinaceum*, *Si. fissuratum*, *Skeletocutis fissurata*, *Sk. wumenshanensis*, *Thelephora tropica*, *Trechispora alborhizomorpha*, *Tre. mangensis*, *Tubulicium yunnanense*, *Vuilleminia bambusicola*, *V. punctata* (*Agaricomycetes*), *Solicoccozyma humicola* (*Tremellomycetes*); one new species in *Mucoromycota*, *Cunninghamella variabilis* (*Mucoromycetes*); and one new species of fungi-like organisms in *Amoebozoa*, *Dictyostelium gracilidiscobasis* (*Dictyosteliomycetes*). We further discussed two new records of *Solicoccozyma aerea* (*Agaricomycetes*) and *Ophiocordyceps vespulae* (*Sordariomycetes*) by expanding their ecology and geographic relationships. The

taxonomic boundaries of these 53 taxa of fungi and fungi-like organisms, which belong to 42 genera, were confirmed using detailed morphology combined with molecular genetics. They were associated with plants, insects, and soil microhabitats with high substrate diversity, e.g., on plants (dead or decaying wood, roots, living infected leaves, leaf litter-associated insects), even in desert habitats, on basidiomata, on soil (in, on), even in frozen soil from Chinese, Omani, and Malaysian collecting sites. This study encourages mycologists, especially taxonomists to explore the undocumented fungal diversity across under-surveyed geographical sites, habitats, hosts, and substrates worldwide.

Keywords – 2 new records – 3 new genera – 48 new species – *Amoebozoa* – *Ascomycota* – *Basidiomycota* – *Mucoromycota* – Phylogeny – Taxonomy

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INTRODUCTION

Fungi are distributed across diverse ecosystems worldwide and play a key role in shaping global biodiversity (Bahram et al. 2022, Wanasinghe et al. 2022, Niskanen et al. 2023). Exploring various fungal communities, such as yeasts, molds, microfungi, and mushrooms, in different ecological niches across terrestrial and aquatic habitats, as well as in harsh environments, has emerged as a prominent trend in mycological research. Fungal taxonomy is the foundation of mycology and it enhances the fungal taxonomic framework, as well as biology, ecology, and diversity. Using polyphasic approaches integrated with morphological, biological, and phylogenetic species concepts is important for narrowing the complexity of fungal taxonomic placements and achieving their accurate classification (Maharachchikumbura et al. 2021, Pem et al. 2021, Thiagaraja et al. 2025). Over the past decade, mycologists have made significant contributions to describing novel fungal species, reassessing morphological species using molecular data, and refining problematic taxonomic placements of certain taxa, leading to a more accurate estimation of global fungal diversity via different “notes series”. Fungal Diversity Notes (2016 taxa), Fungal Planet description sheets (1866 taxa), Mycosphere Notes (571 taxa), AJOM Notes (>200 taxa), CREAM Notes (30 taxa), and New and Interesting Fungi series (7th series) (Chethana et al. 2023, Crous et al. 2023a, 2025, Hyde et al. 2024a, b, Manawasinghe et al. 2024, Visagie et al. 2024, Cao et al. 2025, Hongsanan et al. 2025) can be considered as the most prominent taxonomic note series in modern mycology. Mycosphere Notes, initiated in 2017, serves as a key outlet for fungal taxonomists to share novel discoveries and records in hidden fungal diversity. This is the 14th contribution to the ongoing note series.

Fungi are primarily associated with plant communities (both living and dead) by fulfilling their carbon requirements in terrestrial habitats (Pöhlme et al. 2020, Wanasinghe et al. 2022, Wijesinghe et al. 2023). Both plant and fungal lineages have successfully evolved through interactions between them in different life modes, such as parasitism, mutualism, and saprotrophy (Lutzoni 2018, Kim & Park 2021, Wijesinghe et al. 2023, Wanasinghe et al. 2025). Therefore, it is assumed that plants have either co-evolved with host-specific microorganisms or facilitated the origin and diversification of major fungal lineages (Lutzoni 2018, Cordovez et al. 2019, Kim & Park 2021). Hawksworth’s ratio for estimating global fungal numbers estimated that the species richness of fungi in a given area is about six times ($\times 6$) the species richness of vascular plants (Hawksworth 1991, 2001). Beyond plants, fungal communities are well-established in soils and can be identified as pathogens, saprobes, and mutualists (Zhong et al. 2022, Yasanthika et al. 2025). They exhibit high sensitivity to both biotic (soil microorganisms) and abiotic (drought, heat, and land cover) changes in soil ecosystems (Habib et al. 2025, Yasanthika et al. 2025). Soil fungi play a crucial role in maintaining ecosystem balance by breaking down organic matter and producing

extracellular enzymes that aid in the cycling of carbon and nutrients (Xu et al. 2017, Zhong et al. 2022, Yasanthika et al. 2025). Some soil fungal groups, such as mycorrhizal and endophytic fungi are capable of penetrating plant tissues through the roots, thus forming symbiotic relationships with plants (Fernandes et al. 2015). They are assumed to be the agents of improving the fitness of host plants; e.g., mycorrhizal fungi support plant growth and productivity by increasing nutrient uptake and protecting the plants from pathogenic attacks (Frac et al. 2018, Zhong et al. 2022, Chen et al. 2025).

The global number of fungal species was estimated to be around 12 (11.7–13.2) million by Wu et al. (2019a), and this was later re-evaluated by Baldrian et al. (2023), who estimated it to be around 6.3 million species. However, Niskanen et al. (2023) proposed a revised estimate with a “best estimate” of 2.5 million, based on its ranging of 1.5 to 3.2 million, and the recent authors have followed this estimation (Hyde et al. 2024c). Additionally, among the 10,685 accepted fungal genera (as of 2024), 39.5% were identified as monotypic, raising questions on unnecessary generic splitting or limited research studies worldwide (Hyde et al. 2024d). Therefore, we hypothesize that a substantial portion of the missing fungal diversity is linked to plant communities and soil habitats around the world.

This study focuses on the taxonomic novelties and new records of fungi and fungi-like species, covering plant-associated, wood-decaying, entomopathogenic, and soil-inhabiting taxa. These novel reports belong to four phyla, viz. *Ascomycota*, *Basidiomycota*, *Mucoromycota* and *Amoebozoa* (fungi-like species) found in China, Oman, and Malaysia. The described taxa consist of three new genera, 48 new species, and two new records including ten taxa from *Ascomycota* (three new species of *Dothideomycetes*, one new species in *Leotiomycetes*, one new genus, four new species and one new record in *Sordariomycetes*), 41 taxa from *Basidiomycota* (two new genera and 37 new species in *Agaricomycetes*, one new species and one new record in *Tremellomycetes*), one species from *Mucoromycota* (one new species in *Mucoromycetes*), and one species from *Amoebozoa* (one new species in *Dictyosteliomycetes*). Taxonomic boundaries for all 53 taxa were confirmed with morphology and molecular phylogeny. Detailed descriptions and morphological photo plates were provided, and line drawings were included where necessary. This study presents new documentation on the taxonomy, phylogeny, and ecology of fungi and fungi-like species associated with insects, plants, and soil microhabitats, highlighting the necessity of ongoing research on this largely unexplored realm. The Mycosphere Notes platform enables worldwide mycologists to actively contribute to this ongoing mycological journey.

MATERIALS AND METHODS

Macro and microfungal specimens including some miscellaneous taxa were collected randomly from the woody, soil and insect microhabitats in China, Oman, and Malaysia, 2017–2025. The metadata related to each sample were recorded (Rathnayaka et al. 2024). Morphological studies including macro and micro photographs and fungal isolation for microfungi were carried out following the methodologies described by Hyde et al. (2016) and Senanayake et al. (2020). Some sections of basidiomycetous taxa were mounted in 5% potassium hydroxide, stained with 2% phloxine B dye or cotton blue and Melzer’s reagent for clear visualization of micromorphological structures. The following abbreviations were used: KOH = 5% potassium hydroxide aqueous solution, CB = Cotton Blue, CB– = acyanophilous, CB+ = cyanophilous, IKI+ = Melzer’s reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied), Q_m = mean Q of observed spores $\pm$ standard deviation, in the fungal descriptions. Fungal samples including the holotype and other type materials were deposited at the relevant fungaria, while the isolates of microfungal taxa including the ex-type and other living cultures were deposited at the relevant culture collections. Some dried specimens (mostly basidiomycetes) and the cultures of pure fungal colonies (ascomycetes) were used for DNA extraction. DNA extraction, PCR, gel electrophoresis, and sequencing for fungi were performed following the methods discussed in Dissanayake et al. (2020) and Dong et al. (2024). The newly

generated fungal sequences in this study were deposited in GenBank. Species boundaries were identified with collective analyses of Maximum Likelihood (ML), Bayesian Posterior Probability (BYPP or BI), and Maximum Parsimony (MP). The ML analyses were performed using the CIPRES Science Gateway portal (Miller et al. 2012) or the IQ-Tree web server (<http://iqtree.cibiv.univie.ac.at/>, Nguyen et al. 2014, Chernomor et al. 2016), while BI analyses were processed on the CIPRES Science Gateway portal or MrBayes version 3.2.6 (Ronquist et al. 2012), and MP analyses by PAUP v.4.0b10 (Swofford & Sullivan 2003). The major criteria for defining species boundaries provided by Chethana et al. (2021) and Pem et al. (2021) were followed to identify new fungal species. Newly discovered species were registered in Index Fungorum (2025) and Faces of Fungi database (Jayasiri et al. 2015).

RESULTS

Taxonomy

The classification follows Hyde et al. (2024d), and is updated with recent publications where necessary.

Phylum *Ascomycota*

Class *Dothideomycetes* O.E. Erikss. & Winka

Pleosporales Luttr. ex M.E. Barr

Occultibambusaceae D.Q. Dai & K.D. Hyde

Occultibambusa D.Q. Dai & K.D. Hyde

Index Fungorum number: IF 552013; Facesoffungi number: FoF 01974

Notes – *Occultibambusa* was introduced in *Occultibambusaceae* to accommodate three species, *O. bambusae* (type species), *O. fusispora*, and *O. pustula* (Dai et al. 2017). The establishment was based on morphological characteristics and multi-locus phylogenetic analyses of combined SSU, LSU, *tef1-α* and *rpb2* sequence data (Dai et al. 2017, Pem et al. 2024). *Occultibambusa* is characterized by producing immersed to erumpent, subglobose ascomata with a central ostiole, cylindrical to clavate asci with an ocular chamber, and fusiform, 1–3-septate ascospores with or without a sheath (Dai et al. 2017). The asexual morph is characterized by enteroblastic, phialidic conidiogenous cells, oblong, hyaline to pale brown, aseptate conidia (Dai et al. 2017). *Occultibambusa* species have been reported as saprophytes, mainly found on bamboo substrates in terrestrial habitats (Hyde et al. 2016, Dai et al. 2017, Zhang et al. 2017, Jiang et al. 2021, Yu et al. 2022), or submerged woody debris in freshwater habitats (Hyde et al. 2016, Dong et al. 2020, Wang et al. 2024a). In this study, we described *O. guizhouensis* sp. nov. found on decaying bamboo culms in China, based on molecular phylogenetic analysis (Fig. 1) and morphological characteristics (Fig. 2).

Occultibambusa guizhouensis H.J. Zhao, W. Dong & K.D. Hyde, sp. nov.

Fig. 2

Index Fungorum number: IF 903986; Facesoffungi number: FoF 17898

Etymology – Referring to the region “Guizhou Province”, where the holotype was collected.

Saprobic on dead culms of bamboo. Sexual morph: *Ascostromata* 120–205 µm high, 190–300 µm diam., scattered, immersed to semi-immersed, lenticular to conical, black, lageniform in section, uni- to bi-loculate, coriaceous, with a central ostiole. *Peridium* 15–25 µm wide, composed of several layers of brown to dark brown cells of *textura angularis*. *Hamathecium* 2–3.5 µm wide, comprising dense, subcylindrical, distinctly septate, hyaline, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 65–95 × 13–15.5 µm ($\bar{x}$ = 75.5 × 14.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, apically rounded with an indistinct ocular chamber, short pedicellate. *Ascospores* (16–)19–27 × 4.5–6.5 µm ($\bar{x}$ = 23 × 5.7 µm, n = 30), bi-seriate to overlapped tri-seriate, fusiform with acute ends, hyaline when immature, becoming subhyaline to pale-brown at maturity, 1(–2–3)-septate, not constricted at the septa, slightly curved, smooth-walled, thin-walled, with a thin, irregular-shaped, mucilaginous sheath, guttulate. Asexual morph: Undetermined.

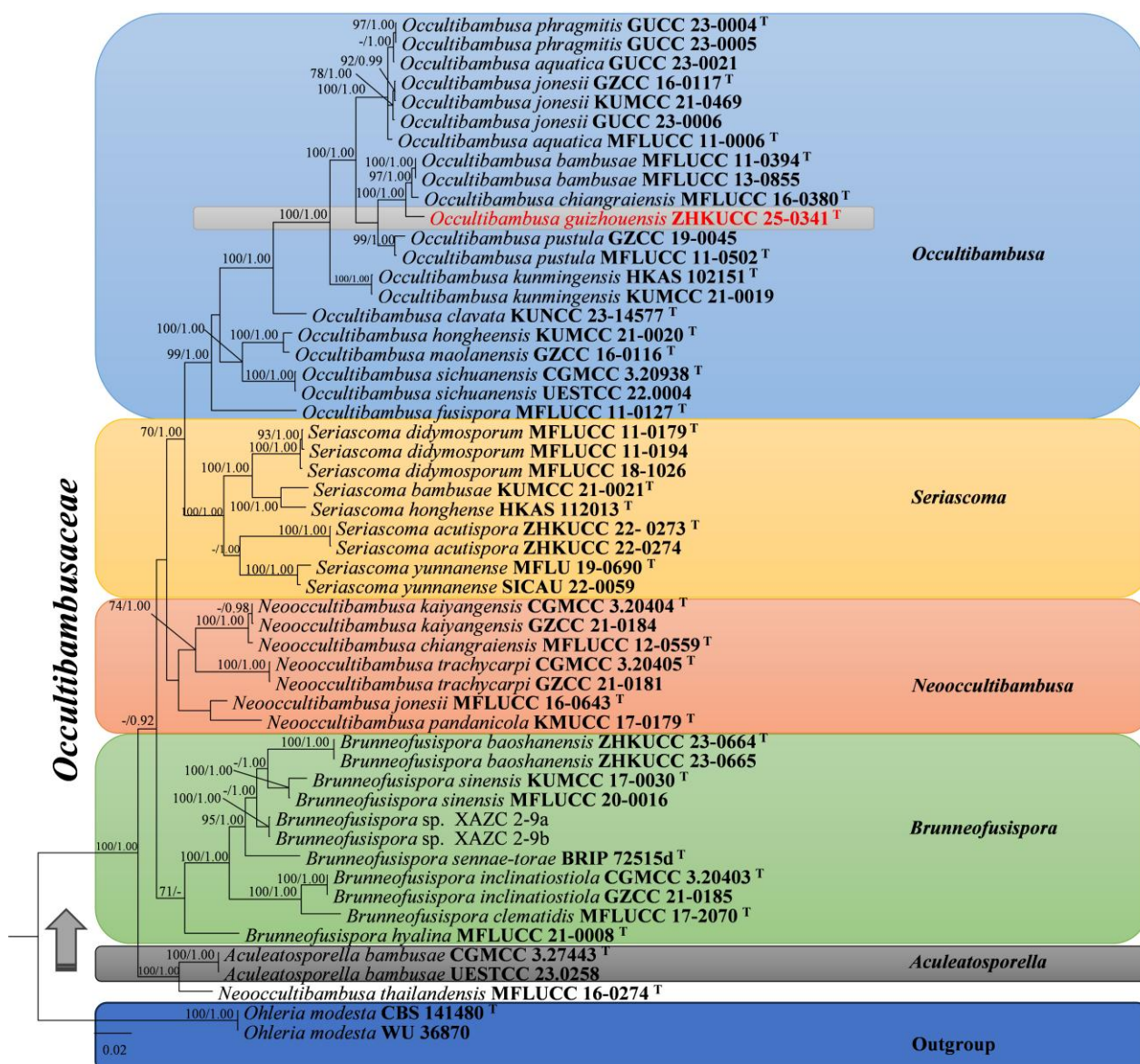


Figure 1 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, *tef1*- α and *rpb2* sequence data. Fifty-three strains were included in the combined sequence analyses, which comprised 6525 characters with gaps (LSU = 937, SSU = 1633, ITS = 1778, *tef1*- α = 1046, *rpb2* = 1129). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. *Ohleria modesta* (CBS 141480 and WU 36870) strains were used as the outgroup taxa. The final ML optimization likelihood is -31157.038025. The matrix included 2300 distinct alignment patterns, with 42.86% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.95 are given above or below the nodes. The newly isolated strains are indicated in red-bold, and the type strains are indicated with ^T.

Culture characteristics – Ascospores germinating on PDA within 24 hours. Colonies on PDA reaching 40–50 mm after 14 days (day–night cycle) at 25°C, circular, raised, aerial mycelium sparse to moderate, with entire margin, pale brown to olivaceous-grey, reverse dark brown to blackish.

Material examined – China, Guizhou Province, Tongren City, on dead culms of bamboo (*Poaceae*), 15 February 2023, Hai-Jun Zhao, GZ016 (MHZU 25-0276, holotype); ex-type ZHKUCC 25-0341.

GenBank accession numbers – LSU: PV771003, ITS: PV771000, *tef1*- α : PV779475.

Notes – In the multi-locus phylogeny, *Occultibambusa guizhouensis* (ZHKUCC 25-0341) grouped with other species of *Occultibambusa* and formed a distinct lineage closely related to *O. bambusae* (MFLUCC 11-0394, 13-0855) and *O. chiangraiensis* (MFLUCC 16-0380) with 100% ML and 1.00 BYPP bootstrap support (Fig. 1). *Occultibambusa guizhouensis* can be distinguished from *O. chiangraiensis* as the latter possesses mostly 3-septate ascospores and lack a sheath (Hyde et al. 2016). In contrast, the ascospores of *O. guizhouensis* are mostly 1-septate and equipped with a thin, irregular-shaped mucilaginous sheath. *Occultibambusa guizhouensis* can be easily distinguished from *O. bambusae* in having subhyaline to mid-brown ascospores, whereas *O. bambusae* has olivaceous ascospores (Dai et al. 2017). Nucleotide comparison between *O. guizhouensis* (ZHKUCC 25-0341) and *O. bambusae* (MFLUCC 11-0394) reveals 1/846 (0.12%), 7/682 (1.03%), and 6/930 (0.65%) base pair (bp) differences in LSU, ITS, and *tef1-α*, respectively. *Occultibambusa guizhouensis* (ZHKUCC 25-0341) and *O. chiangraiensis* (MFLUCC 16-0380) have 14/646 (2.17%) and 11/925 (1.19%) bp differences in ITS and *tef1-α*, respectively. LSU sequence is unavailable for *O. chiangraiensis*. Based on distinct ascospore characteristics and its well-supported placement in the phylogenetic analysis, *O. guizhouensis* is introduced as a new species.

***Teichosporaceae* M.E. Barr**

***Teichospora* Fuckel**

Index Fungorum number: IF 5360; Facesoffungi number: FoF 08367

Notes – Fuckel (1870) introduced *Teichospora* and typified it by *Te. trabicola*. Initially, Von Arx & Müller (1975) classified *Teichospora* in *Pleosporaceae* and typified by *Te. obducens*. Then, Hawksworth et al. (1995) placed it under *Dothideales incertae sedis*, while Barr (2002) erected *Teichosporaceae* and typified the family by *Teichospora* based on morphological characteristics. Later, Jaklitsch et al. (2016) treated in detail *Teichospora* and included several generic synonyms. The key morphological characteristics of *Teichospora* are having broadly ellipsoid to fusiform or broadly ellipsoid to oblong, symmetrical to slightly asymmetrical, muriform ascospores with 3(–4–5) thick, dark transverse septa, 1–3 longitudinal septa, and 1 or 2 V- or Y-septa in terminal cells (Barr 2002, Hyde et al. 2013, Hongsanan et al. 2020, Pem et al. 2024). The asexual morph of the genus is coelomycetous with pycnidial conidiomata, conidiophores reduced to conidiogenous cells and brown unicellular (coniothyrium-like), rarely hyaline unicellular conidia (apospheeria-like) or several-celled brown conidia (Zhang et al. 2012, Hyde et al. 2013, Wijayawardene et al. 2017, Hongsanan et al. 2020). *Teichospora* species have been found as saprotrophs, mostly living on bark and wood of trees and shrubs (Jaklitsch et al. 2016). However, *Te. acaciae* and *Te. grandicipis* are leaf-inhabiting before they are placed in *Curreya* (Marincowitz et al. 2008). Also, *Teichospora striata* was found on senescent leaves and inflorescences, and *Te. viticola* was found on branches before they are placed in *Floricola* (Ariyawansa et al. 2015). In this study, we introduce a saprobic *Teichospora pini* sp. nov. found on *Pinus massoniana* stems from China, based on the multi-gene phylogenetic evidence (Fig. 3) and morphological characteristics (Fig. 4). This finding expands the taxonomic framework of the genus.

***Teichospora pini* Y.H. Yang, Manawasinghe, K.D. Hyde & C.F. Liao sp. nov.**

Fig. 4

Index Fungorum number: IF904302; Facesoffungi number: FoF 18360

Etymology – Referring to the host genus “*Pinus*” that the fungus was found.

Saprobic on dead branches of *Pinus massoniana*. Sexual morph: *Ascomata* 174–300 × 192–376 µm ($\bar{x}$ = 250 × 282 µm, n = 20), scattered or aggregated, black, semi-immersed, neck exposed above the surface of the host, subglobose to pyriform, unilocular, with a distinct ostiole neck. *Ostiole* 129–195 µm ($\bar{x}$ = 153 µm, n = 10), central, papillate, circular in outline, with rounded or flat, periphysate. *Peridium* 13–79 µm wide ($\bar{x}$ = 36 µm, n = 29), composed of two types of layers, inner layer comprising small, flattened, hyaline, thin-walled *textura angularis* cells, outer layer comprising several big, pale brown to brown, thick-walled *textura prismatica* cells. *Hamathecium* comprises 2–4 µm ($\bar{x}$ = 2.5 µm, n = 28) wide, numerous, septate, unbranched, filamentous, hyaline

pseudoparaphyses embedded in a gelatinous matrix. *Asci* 62–117 × 11–16 µm ($\bar{x}$ = 91 × 13 µm, n = 27), 8-spored, bitunicate, fissitunicate, cylindric to clavate, short pedicellate, apically rounded, with a distinct ocular chamber. *Ascospores* 14–20 × 6–8 µm ($\bar{x}$ = 17 × 7 µm, n = 30), uniseriate, overlapping, broadly ellipsoid to fusiform, muriform, straight to slightly curved, hyaline to yellowish when young, becoming pale brown to dark brown at the maturity, 1–6-transversely septate, non-constricted to slightly constricted at the septa, symmetrical to slightly asymmetrical, obtuse at both of ends, 2–4 septa, sometimes pointed and pale brown at the base, a longitudinal septum in a variable number of cells, terminal cells without septa or with a Y-shaped pair of septa, smooth-walled with guttules. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA at 25°C. Colonies on PDA reaching 13 mm diam. after 18 days. Above: colonize white, surface rough, dense, circular, convex with papillate at center, brown around the papillate, entire, floccose, felted, well defined. Reverse: pale brown to brown, entire edge, well defined.

Material examined – China, Yunnan Province, Yuanmou city, on dead stem of *Pinus massoniana* (*Pinaceae*), 19 January 2023, Y.H. Yang, SS01 (MHZU 25-0517, holotype); ex-type ZHKUCC 24-2221, *ibid.*, living culture ZHKUCC 24-2222.

GenBank accession numbers – ZHKUCC 24-2221: ITS = PX392494, *rpb2* = PX398766, SSU = PX392492; ZHKUCC 24-2222: ITS = PX392495, *rpb2* = PX398767, SSU = PX392493.

Notes – The multi-gene phylogenetic analysis revealed that the strains of our species, *Teichospora pini* (ZHKUCC 24-2221 and ZHKUCC 24-2222) clustered within *Teichospora* and formed a separate lineage sister to *Te. pusilla* (C 140, holotype) with 96% ML bootstrap support (Fig. 3, Clade A). Morphologically, *Te. pini* fits with *Teichospora* by having subglobose to pyriform ascomata with ostiolar neck, cylindric, bitunicate asci, and ellipsoid, hyaline to brown ascospores with transversely septate and longitudinal septum and Y-septa in terminal cells (Barr 2002, Hyde et al. 2013, Hongsanan et al. 2020). *Teichospora pini* resembles *Te. pusilla* in having globose to pyriform ascomata with papillate ostiolar, cylindrical to clavate or subclavate, 8-spored asci, and broadly ellipsoid ascospores (Jaklitsch et al. 2016). However, it differs from *Te. pusilla* by having semi-immersed ascomata, a thicker peridium (13–79 µm vs. 13–30 µm) and no surrounded by hyphae, circular and bigger ostiole (129–195 µm vs. (62)75–110(125) µm), longer asci (62–117 µm vs. (86)88–94(95) µm), and longer ascospores (14–20 µm vs. (11.7)13–15(16.2) µm), which are hyaline to brown, 1–6-transversely septate and sometimes pointed at the base (Fig 4). In addition, a single gene comparison between *Te. pini* and *Te. pusilla* shows that there are 2.9% (16/547) bp differences in ITS region. Based on morphological characteristics and molecular phylogenetic evidence, we introduce *Te. pini* as a novel species collected from Yunnan Province, China.

***Periconiaceae* Nann.**

***Periconia* Tode**

Index Fungorum number: IF9263, Facesoffungi Number: FoF 06658

Notes – *Periconia* was introduced by Tode (1791), with *Pe. lichenoides* as the type species. The asexual morph is characterized by macronematous conidiophores, branched or unbranched, pale to dark brown, conidia are globose or ellipsoidal, aseptate, smooth or verruculose and pale brown to brown (Bunning & Griffiths 1984, Tanaka et al. 2015, Su et al. 2023, Pem et al. 2024). The sexual morph is characterized by globose ascomata, immersed or erumpent on host surface, with central periphysate ostiole and neck, 8-spored asci, bitunicate, fissitunicate, oblong, and fusiform ascospores with a septum (Tanaka et al. 2015, Yang et al. 2022, Su et al. 2023). *Periconia* is widely distributed on various hosts in many countries (Liu et al. 2017, Yang et al. 2022, Sun et al. 2025), serving as saprobic fungi on dead branches and leaves (Liu et al. 2017, Samarakoon et al. 2021, Yang et al. 2022, Sun et al. 2025), endophytic fungi on plants (Li et al. 1998, Silva et al. 2024), and pathogenic fungi on plants and humans (Leukel et al. 1948, Kolomiets et al. 2008, Gunasekaran et al. 2021). There are currently more than 200 epithets in Index Fungorum (2025). In this study, we introduce a saprobic *Periconia baotouensis* sp. nov., living on *Hippophae*

rhamnoides from a Chinese desert habitat, based on multi-locus phylogenetic analysis (Fig. 5) and morphological characteristics (Fig. 6).

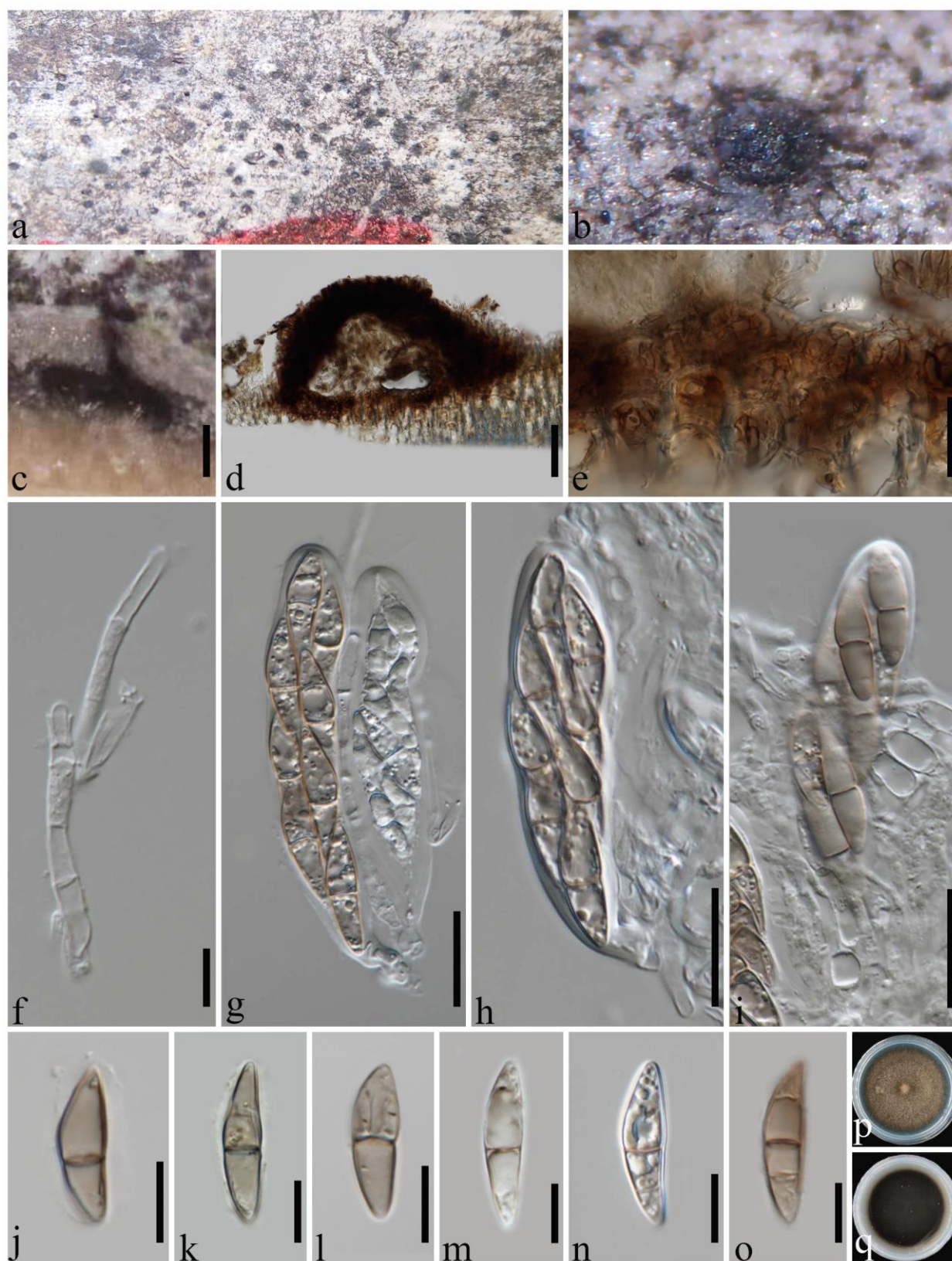


Figure 2 – *Occultibambusa guizhouensis* (MHZU 25-0276, holotype). a, b Ascostromata on dead bamboo culms. c, d Vertical section of an ascostroma. e Peridium. f Pseudoparaphyses. g–i Asci. j–o Ascospores. p, q Views of colony on PDA, surface (p) and reverse (q) side. Scale bars: c, d = 100 μ m, e, g–i = 20 μ m, f = 5 μ m, j–o = 10 μ m.

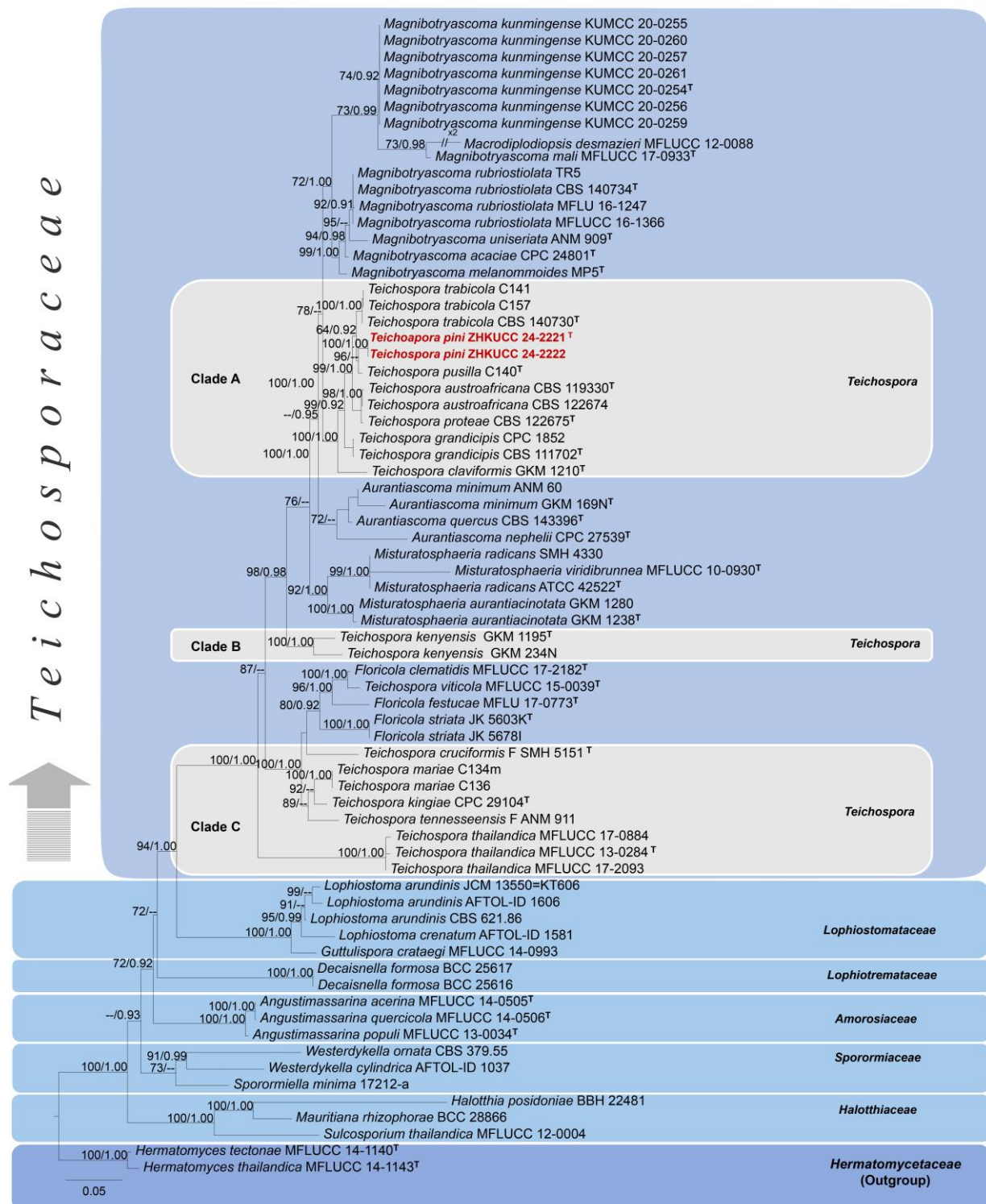


Figure 3 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU, *tef1-α*, and *rpb2* sequence data. Seventy strains were included in the combined sequence analyses, which comprised 4621 characters with gaps (LSU = 913, ITS = 654, SSU = 1049, *tef1-α* = 927, *rpb2* = 1078). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. The final ML optimization likelihood is -25910.301633. The matrix included 1826 distinct alignment patterns, with 46.37% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.90 are given above or below the nodes. *Hermatomyces tectonae* (MFLUCC 14-1140) and *H. thailandica* (MFLUCC 14-1143) were used as the outgroup taxa. The newly isolated strains are indicated in red-bold, and the type strains are indicated with ^T.

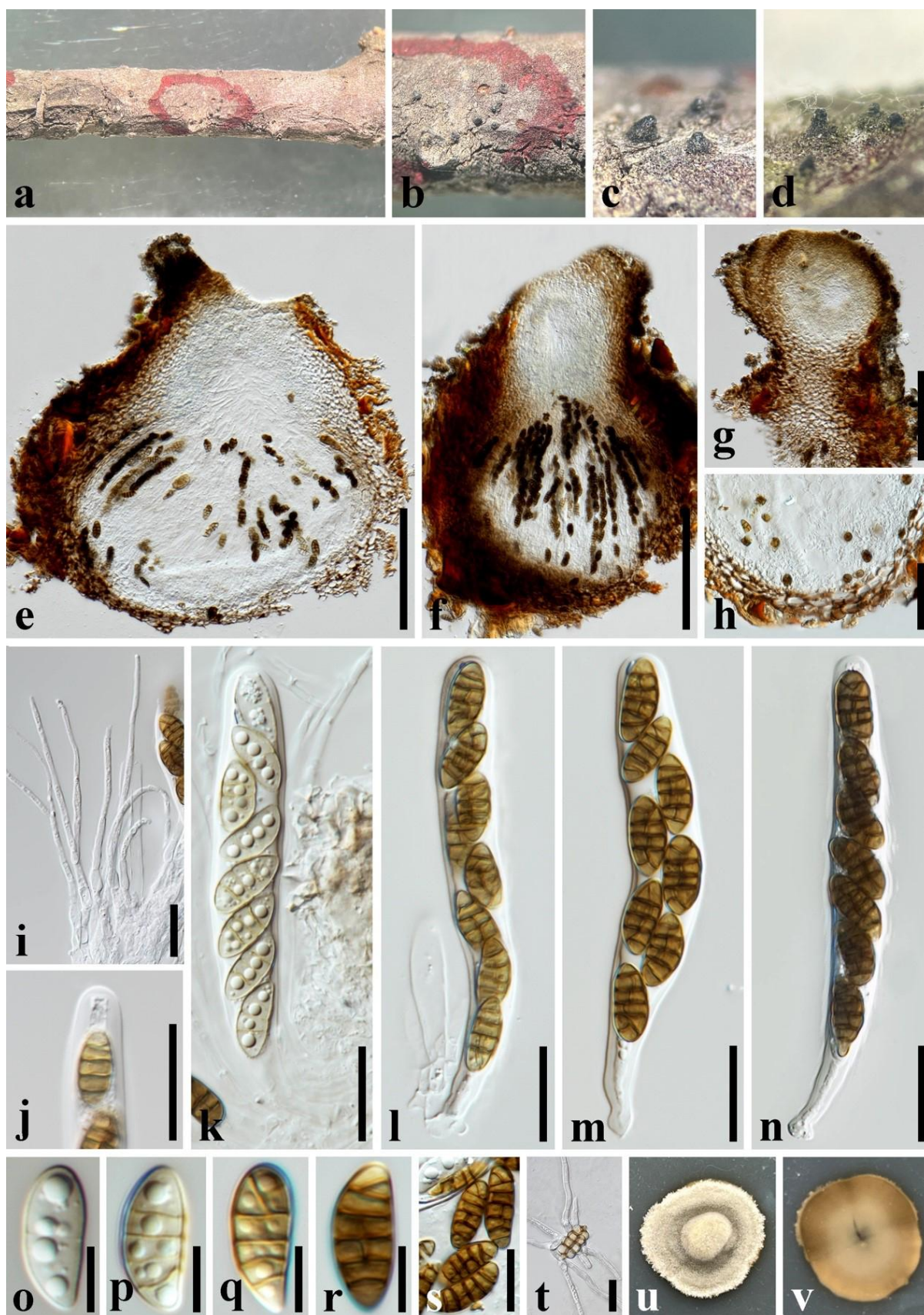


Figure 4 – *Teichospora pini* (MHZU 25-0517, holotype). a–d Ascomata on the dead host surface of *Pinus massoniana*. e, f Longitudinal sections of ascoma. g Longitudinal section of an ostiolar neck. h Peridium. i Pseudoparaphyses. j Apex of the ascus. k–n Asci. o–s Ascospores. t Germinating ascospore. u, v View of culture grown on PDA, upper (u) and lower (v) side. Scale bars: e, f = 100 μ m, g = 100 μ m, h = 40 μ m, i = 10 μ m, j = 20 μ m, k–n = 20 μ m, o–r = 5 μ m, s–t = 10 μ m.

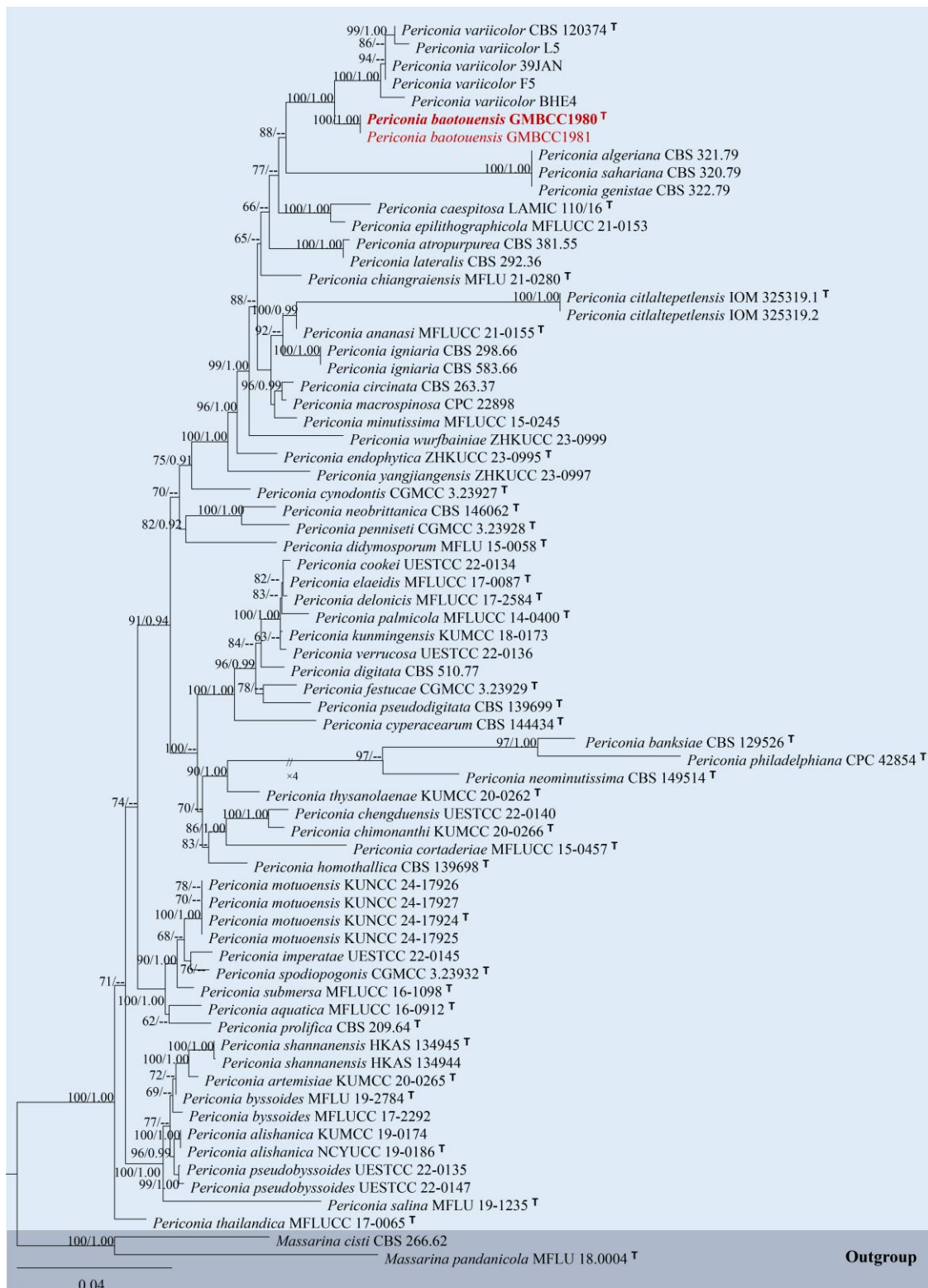


Figure 5 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *rpb2*, SSU, and *tef1-α* sequence data of 70 strains, which comprised 2930 characters (ITS = 1–428, LSU = 429–1191, SSU = 1192–2211, *tef1-α* = 2212–2930). The best scoring RAXML tree with a final likelihood value of -15217.651601 is presented. The matrix had 849 distinct alignment patterns, with 27.20% of undetermined characters or gaps. Bootstrap support values for ML equal to or greater than 60% and clade credibility values equal to or greater than 0.90 from Bayesian inference analysis are labelled at each node. The tree is rooted with *Massarina cisti* (CBS 266.62) and *M. pandanicola* (MFLU 18-0004, ex-type). The new isolates are indicated in red-bold, and the type strains are indicated with T.

Periconia baotouensis T.Y. Du, Tibpromma & Karun. sp. nov.

Fig. 6.

Index Fungorum number: MB 860727; Facesoffungi number: FoF 18272

Etymology – Named after the location “the desert region of Baotou City, China,” from where the holotype was collected.

Saprobic on dead branches of *Hippophae rhamnoides*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substratum effuse, numerous on substrate, dark brown to black, hairy. *Conidiophores* 120–250 $\mu\text{m} \times 4\text{--}7\ \mu\text{m}$ ($\bar{x} = 160 \times 6\ \mu\text{m}$, $n = 20$), macronematous, synnematous, aggregated, erect, straight or flexuous, pale brown, septate, smooth, thick-walled. *Conidiogenous cells* polyblastic, integrated, terminal or lateral on the conidiophore, smooth to verruculose, pale brown, produce dense clusters of conidia. *Conidia* 7.5–12 μm ($\bar{x} = 9.5\ \mu\text{m}$, $n = 50$), one-celled, globose, prickly, verrucose, thick- and rough-walled, pale brown to brown.

Culture characteristics – Conidia germinated on PDA within 24 hours, and germ tubes formed around the conidium. After two weeks at 23–28°C, the colony diam. reached about 2 cm, appearing grayish-green, circular, flat, the aerial mycelium in the middle rises, and with a sparsely hairy edge; dark grayish-green from below, while the edge is white.

Material examined – China, Neimenggu Region, Baotou City, Xiangshawan, on dead branches of *Hippophae rhamnoides* (*Elaeagnaceae*) in the desert, 01 October 2023, T.Y. Du, BTD10 (GMB-W1515, holotype); ex-type GMBCC1980=GMBCC1981.

GenBank accession numbers – GMBCC1980: ITS = PX314711, LSU = PX314709, SSU = PX314707, *tef1*- α = PX310458; GMBCC1981: ITS = PX314712, LSU = PX314710, SSU = PX314708, *tef1*- α = PX310459.

Notes – The multiple-gene phylogenetic analysis revealed that the strains of our species, *Periconia baotouensis* (GMBCC1980, 1981) separately clustered with the strains of *Pe. variicolor* (CBS 120374, L5, 39JAN, F5, and BHE4) with 100% in ML and 1.00 in BYPP statistical support (Fig. 5). Based on the nucleotide bp differences (without gaps) between our new strain (GMBCC1980, ex-type) and *Pe. variicolor* in ITS, the result showed 4.67% (20/428 bp) difference with *Pe. variicolor* (CBS 120374, ex-type), 5.14% (22/428 bp) difference with *Pe. variicolor* (BHE4), 5.37% (23/428 bp) difference with *Pe. variicolor* (L5), 4.20% (18/428 bp) difference with *Pe. variicolor* (39JAN), and 5.06% (12/237 bp) difference with *Pe. variicolor* (F5), while only ITS sequence is available for strains of *Pe. variicolor* in NCBI. Morphologically, the conidia of *Pe. baotouensis* are similar to *Pe. variicolor* (CBS 120374, holotype) in having one-celled, globose, and verrucose conidia (Cantrell et al. 2007). However, the conidiophores of *Pe. variicolor* (CBS 120374, holotype) are mononematous and conidia are dark brown (Cantrell et al. 2007), while synnematous, aggregated conidiophores and prickly, pale brown to brown conidia appear in *Pe. baotouensis*. Based on molecular phylogenetic evidence and morphological characteristics, we introduce *Pe. baotouensis* as a new species from China. As some species of *Periconia* (e.g., *Pe. macrospinoso*) have been reported from desert environments (Sterflinger et al. 2012, Hosseini Moghaddam et al. 2022), our new fungal collection was found on a deciduous shrub in a Chinese desert habitat. Therefore, it is interesting to further investigate their ecological and biological adaptations in stress tolerance and survival of extreme and harsh environmental conditions in desert ecosystems worldwide.

Class *Leotiomyces* O.E. Erikss. & Winka

Helotiales Nannf.

Vandijkellaceae Sand.-Den.

Basingstokeomyces Crous & Denman

Index Fungorum number: IF 848070; Facesoffungi number: FoF 15325

Notes – *Basingstokeomyces* is a monotypic genus established by Crous et al. (2023b) based on phylogenetic and morphological characteristics, with *Ba. allii* collected from *Allium schoenoprasum* in the UK as the type species. The genus is identified as hyphomycetous, characterized by clustered, subcylindrical conidiophores bearing several flat-tipped conidiogenous loci at their apices, producing aseptate, hyaline conidial chains (Crous et al. 2023b). This study

introduces the second species of this genus *Basingstokeomyces cryptomeriae* sp. nov., living on *Cryptomeria japonica* from China, based on multi-gene phylogenetic evidence (Fig. 7) and morphological characteristics (Fig. 8).

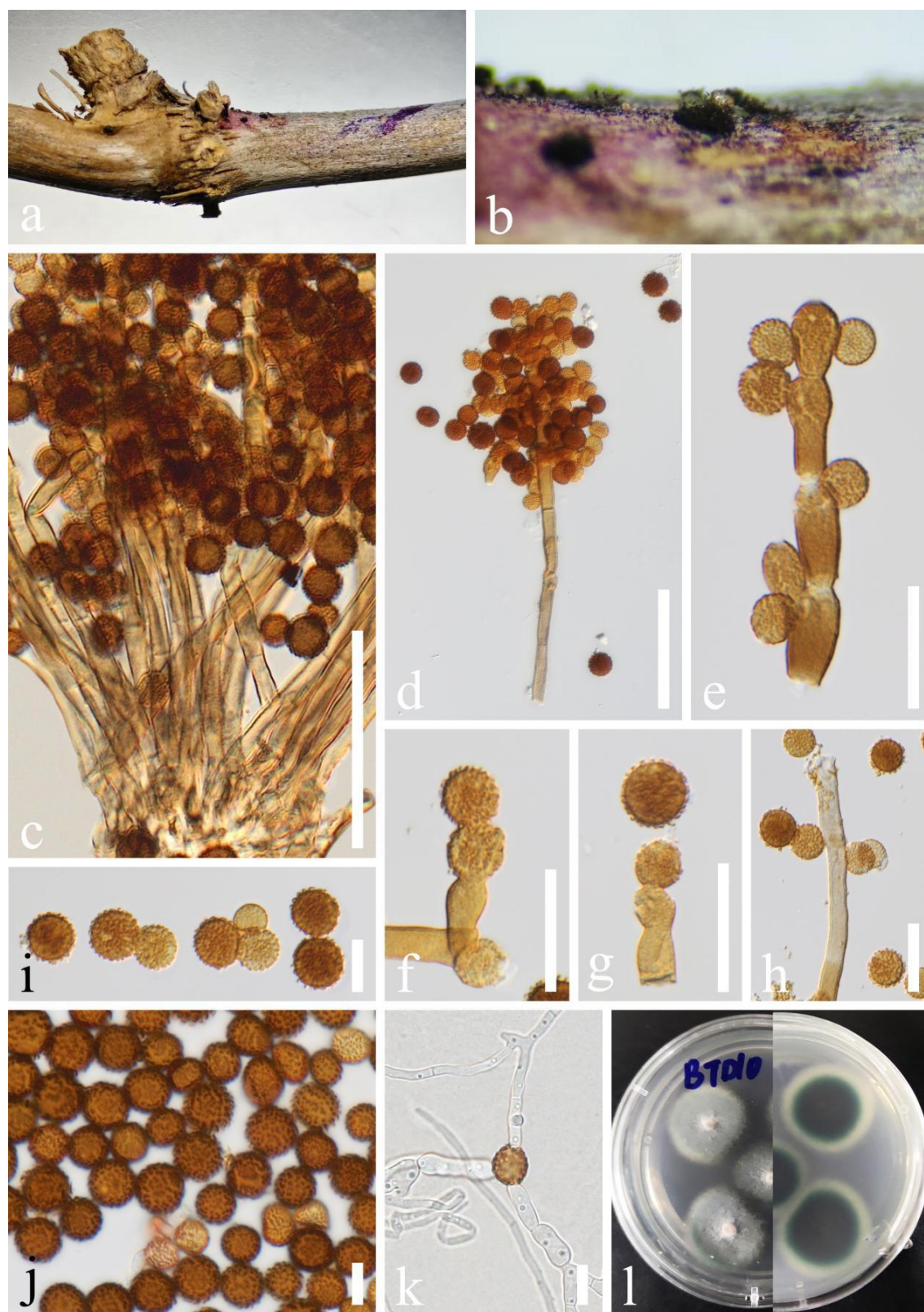


Figure 6 – *Periconia baotouensis* (GMB-W1515, holotype). a Host substrate. b Colonies on the natural substrate. c–h Conidiophores bearing conidiogenous cells and conidia. i, j Conidia. k A germinating conidium. l Colonies grown on PDA for two weeks from (left) above and (right) below. Scale bars: c, d = 50 µm, e–h = 20 µm, i–k = 10 µm.

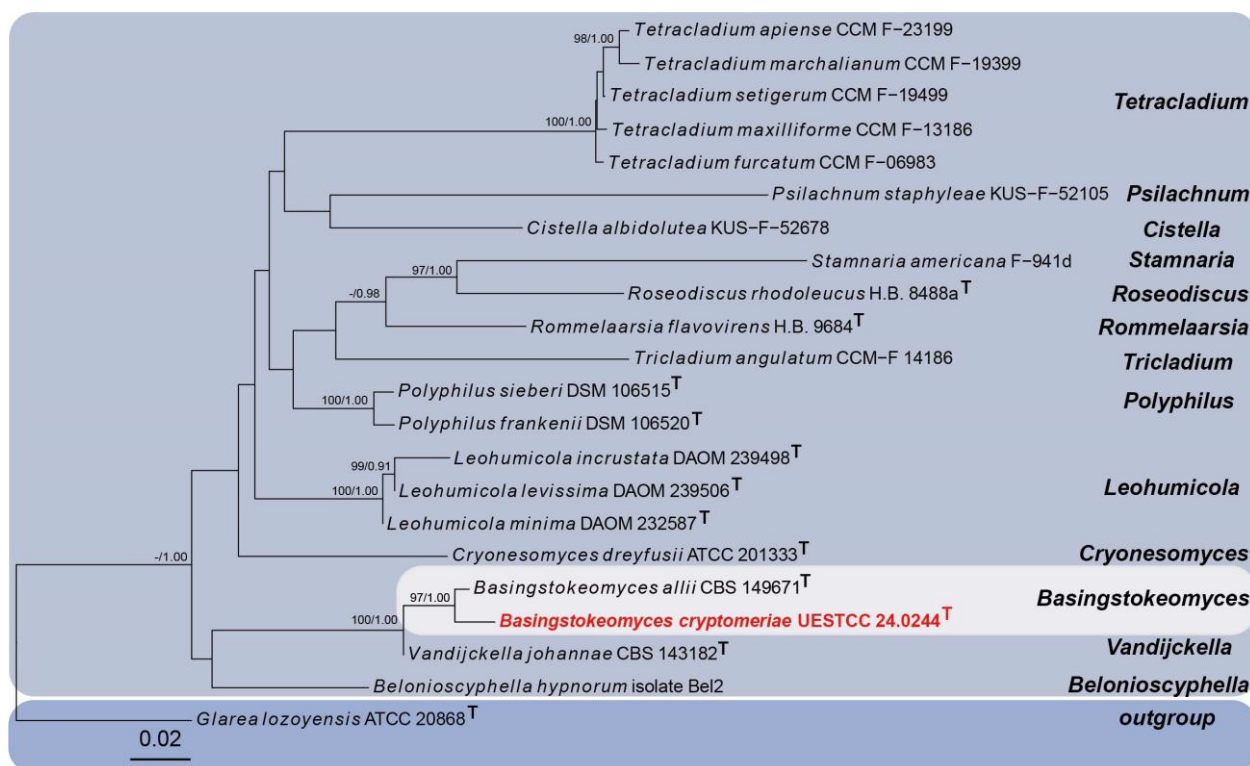


Figure 7 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *rpb2* sequence data. Twenty-two strains were included in the combined sequence analyses, which comprised 4136 characters with gaps (ITS = 589, LSU = 878, SSU = 959, *rpb2* = 1710). Single-gene analyses were also performed, and the topology and clade stability were compared with those from the combined gene analyses. *Glarea lozoyensis* (ATCC 20868) was used as the outgroup. The final ML optimization likelihood is -13511.894. The alignment dataset includes 888 distinct patterns, 457 singleton sites and 3194 constant sites. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.95 are given above or below the nodes. The strain from the current study is in red-bold, and the type strains are indicated with ^T.

***Basingstokeomyces cryptomeriae* W.H. Tian & Maharachch., sp. nov.**

Fig. 8

Index Fungorum number: IF 900089; Facesoffungi number: FoF 18597

Etymology – Referring to the host genus “*cryptomeria*” of the fungus was found.

Saprobic on dead bark of *Cryptomeria japonica*. Asexual morph: Colonies effuse, velvety, white, gregarious, superficial, glistening. Mycelium hyaline, smooth, branched. Conidiophores 50–65 × 1.5–2.5 μm ($\bar{x}$ = 59 × 1.8 μm, n = 20), erect, penicillate, flamelike, hyaline, clusters, subcylindrical, 1–4-septate, with root of 1–3 cylindrical, smooth, hyaline, 0–1-septate primary branches with apical loci that give rise to secondary and tertiary cylindrical branches. Conidiogenous cells 4–11 μm × 1.5–2.5 μm ($\bar{x}$ = 6.6 × 1.7 μm, n = 20), terminal, subcylindrical, hyaline, with one flat-tipped apical loci, unthickened and not darkened. Conidia 11.5–19 × 1.2–2 μm ($\bar{x}$ = 14.8 × 1.7 μm, n = 30), occurring in chains or branched chains, aseptate, subcylindrical, smooth, white or hyaline, ends obtuse. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 24 hours at 25°C, Colonies on PDA, reaching 17 mm diam. after 14 days, circular, white, uniformly textured surface with a distinct, entire margin, reverse white, and sometimes pale yellow.

Material examined – China, Sichuan Province, Ya'an City, Zhougong Mountain, on dead bark of *Cryptomeria japonica* (Cupressaceae), 16 November 2022, Wenhui Tian, ZGS52 (HUEST 24.0256, holotype); ex-type UESTCC 24.0244.

GenBank accession numbers – ITS: PV138485, LSU: PV138412, SSU: PV138374.

Notes – Multigene phylogenetic analysis revealed that our new strain UESTCC 24.0244 clustered with *Basingstokeomyces allii* (CBS 149671) and formed a sister lineage with 97% in ML and 1.00 in BYPP statistical support (Fig. 7). Morphologically, UESTCC 24.0244 is having longer conidiophores ($50\text{--}65 \times 1.5\text{--}2.5$ vs. $30\text{--}50 \times 3\text{--}3.5$ μm) and conidia ($(4\text{--})5\text{--}6(8) \times 1.5\text{--}2$ vs. $11.5\text{--}19 \times 1.2\text{--}2$ μm) when compared to *Ba. allii* CBS 149671 (Crous et al. 2023b). Based on these distinct phylogenetic and morphological characters, we identify *Basingstokeomyces cryptomeriae* as a new species from Sichuan Province, China and this is the second species of the genus.

Class Sordariomycetes O.E. Erikss. & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss.

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr

Apiospora Sacc.

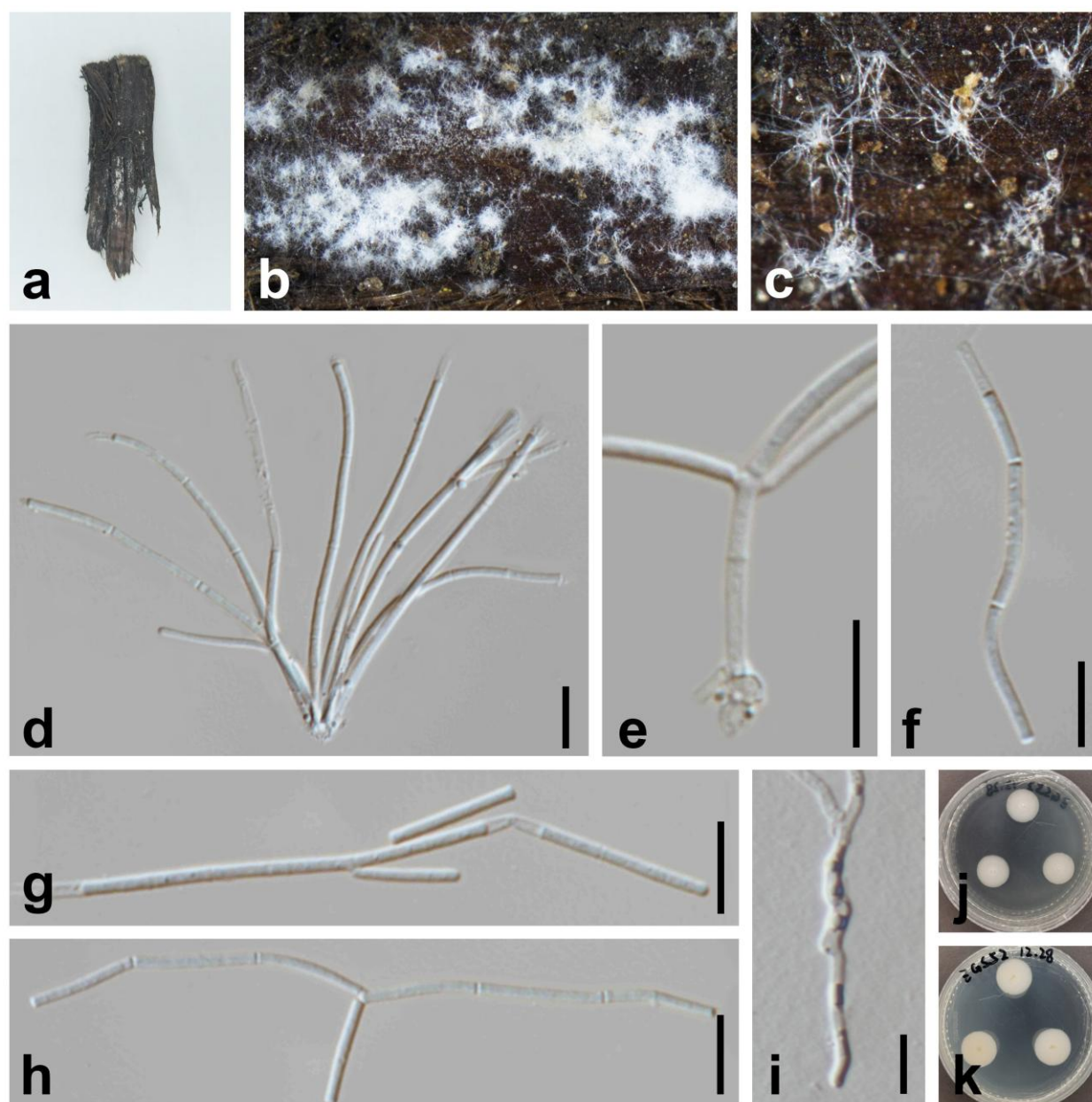


Figure 8 – *Basingstokeomyces cryptomeriae* (HUEST 24.0256, holotype). a Colonies on the dead bark of *Cryptomeria japonica*. b, c Colonies on natural substrate. d, e Conidiophores and conidiogenous cells. f–h Catenate conidia. i A germinating conidium. j, k View of culture grown on PDA, upper (j) and lower (k) side. Scale bars: d–i = 10 μm .

Index Fungorum number: IF 264; Facesoffungi number: FoF 18598

Notes – *Apiospora* was established by Saccardo (1875) without any type indication. Later, Clements & Shear (1931) designated *Ap. montagnei* as the type species of this genus. Crous & Groenewald (2013) confirmed *Arthrinium* belonging to *Apiosporaceae* (*Xylariales*) using combined ITS, *tef1-α* and *tub2* sequence data, and reduced the sexual genus *Apiospora* as a synonym of *Arthrinium* since *Arthrinium* was an older and more frequently used name. *Apiosporaceae* was reclassified in *Amphisphaeriales*, which was reinstated (Senanayake et al. 2015) and exhibited significantly different divergence times from *Xylariales* (Samarakoon et al. 2016, 2022). Pintos & Alvarado (2021) circumscribed *Arthrinium s. str.* by conducting the multi-locus phylogenetic analysis based on ITS, LSU, *tef1-α* and *tub2*, combined with the morphological and ecological data, while the other 55 *Arthrinium* species which clustered in another independent lineage were transferred to *Apiospora*. The holomorphic *Apiospora* is characterized by multi-locular stromata and 1-septate (near the lower cell) ascospores for the sexual morph; by dark brown conidia, with a longitudinal and transparent slit for the coelomycetous asexual stage and by hyaline conidiophores, basauxic conidiogenous cells, globose to subglobose, and pale brown to brown conidia for the hyphomycetous asexual morph (Dai et al. 2016, Wang et al. 2018, Pintos & Alvarado 2021, Tian et al. 2021, Bhunjun et al. 2022, Zhao et al. 2023a, Han et al. 2024). Up to now, 211 epithets are listed under *Apiospora* in Index Fungorum (2025), among which the sequence data of 181 species were available for molecular analyses. The members of *Apiospora* are distributed worldwide, including the tropical, subtropical, Mediterranean, and temperate regions (Pintos & Alvarado 2021, Kwon et al. 2022). This genus comprises saprobes, endophytes and pathogens of a wide range of hosts and substrates (Samuels et al. 1981, Liao et al. 2023, Wei et al. 2024), such as humans, plants, as well as air, lichens, soil and seaweeds (Liao et al. 2023). In this study, we introduce *Apiospora dongruensis* sp. nov. found on infected leaves from China, based on the multi-locus phylogenetic analysis (Fig. 9) and morphological characters (Fig. 10).

Apiospora dongruensis SL Li & Qian Chen, sp. nov.

Fig. 10

Index Fungorum number: IF 904359; Facesoffungi number: FoF 18344

Etymology – Referring to the collecting site “Dongru Village,” where the holotype was collected.

Parasitic on diseased leaves of *Berberis aristata*. Sexual morph: undetermined. Asexual morph: sporulated on PDA after two weeks, forming black spore masses aggregated on white colonies. *Hyphae* 1.4–3 μm in diam. ($\bar{x}$ = 2 μm, n = 30), branched, hyaline to light brown, septate, smooth-walled, forming hyphal coils. *Conidiophores* reduced to *conidiogenous cells*. *Conidiogenous cells* 5–10 × 0.5–2 μm ($\bar{x}$ = 8 × 1 μm, n = 20), aggregated in clusters or discrete, terminal, hyaline, smooth-walled, cylindrical, sometimes slightly inflated, occasionally ovoid. *Conidia* 5–19(–23) × 5–8.5 μm ($\bar{x}$ = 12 × 7 μm, n = 30), ovoid, ellipsoidal to fusiform, lenticular, with a longitudinal and transparent slit when mature, initially hyaline, becoming pale brown to dark brown, aseptate, thin- and smooth-walled.

Culture characteristics – Colonies on PDA reaching 4 cm in one week at 26±2°C, floccose, sparse, concentrically spreading, forming aerial mycelia, margin regular, felt, pale brown in the center, white at the edge, with punctate or patchy black spores, reverse primrose yellow (1A6) to pale, yellow pigment diffusion.

Material examined – China, Xizang Autonomous Region, Nyingchi City, Bayi District, Dongru Village, geographical coordinates 29°38'8"N, 94°20'9"E, on infected leaves of *Berberis aristata* (*Berberidaceae*), 27 August 2024, Q. Chen, (HMAS 354100, holotype); ex-type CGMCC 3.28990, CQ 1830.

GenBank accession numbers – ITS: PV938614, LSU: PV938312, *tub2*: PV945490, *tef1-α*: PV945489.

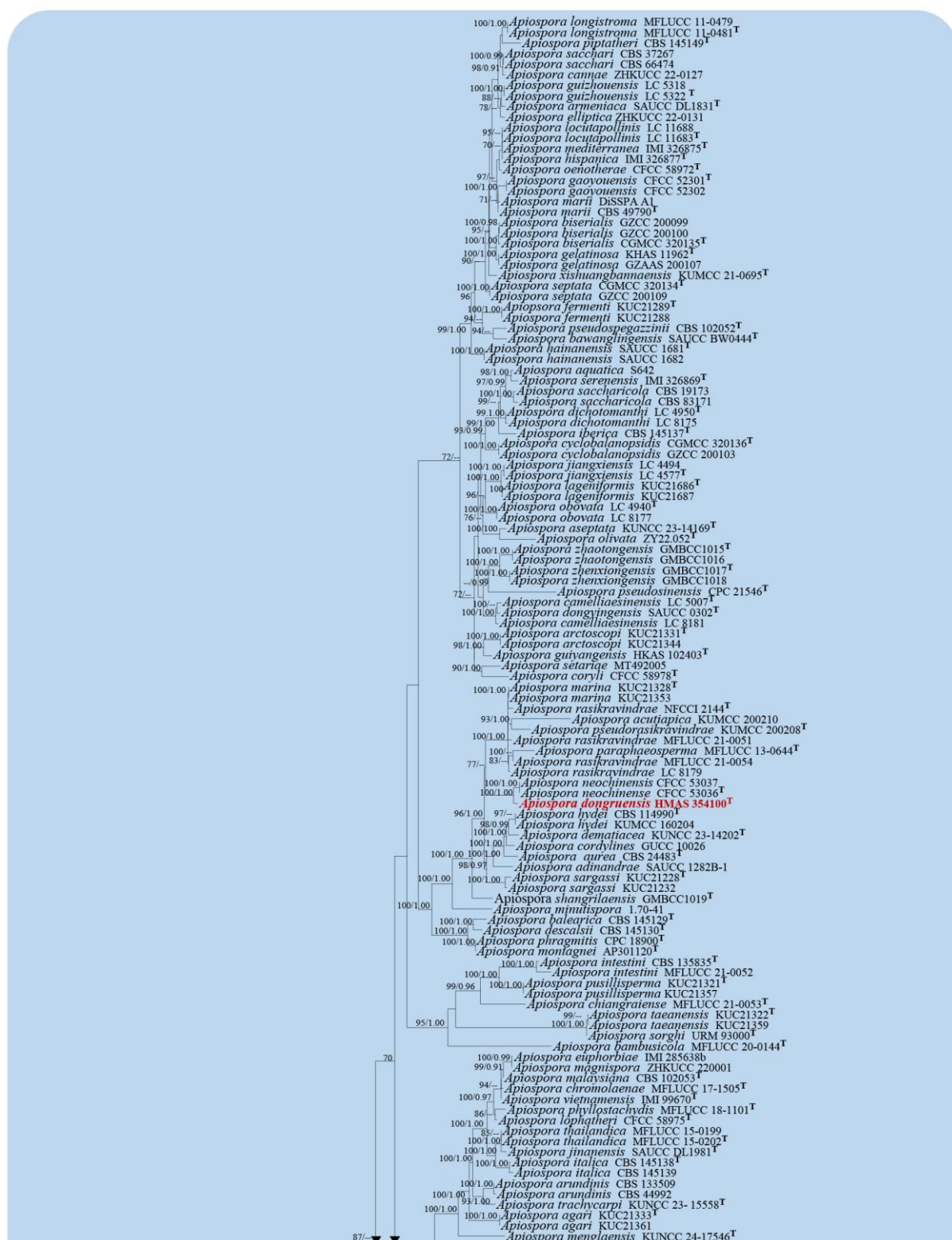


Figure 9 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1*- α , and *tub2* sequence data. One hundred and seventeen strains were included in the combined sequence analyses, which comprised 2954 characters with gaps (ITS = 859, LSU = 881, *tef1*- α = 673, *tub2* = 528). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. *Neoarthrinium urticae* (IMI 326344) was used as the outgroup taxon. The final ML optimization likelihood is -28221.830. The matrix included 1489 distinct alignment patterns, with 49.75% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 70% were given above or below the nodes. The strain from the current study is in red-bold, and the type strains are indicated with ^T.

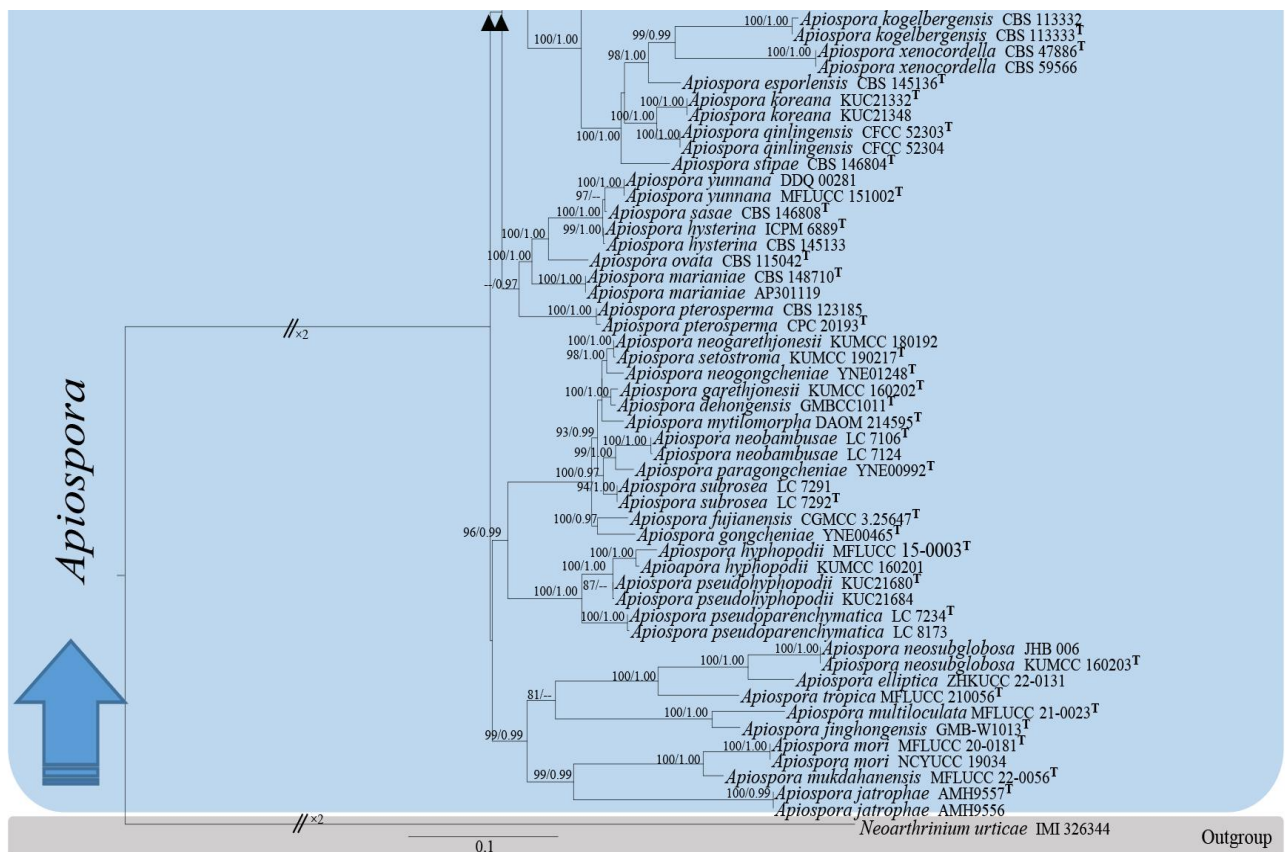


Figure 9 – Continue

Notes – The multigene phylogenetic analysis revealed that the strain of our species, *Apiospora dongruensis* (HMAS 354100) grouped with the other strains of *Apiospora* and formed a separate lineage sister to *Ap. neochinensis* (CFCC 53037, CFCC 53036; type strain) with 100% ML bootstrap support (Fig. 9). Additionally, the nucleotide sequences of *Ap. dongruensis* and *Ap. neochinense* show 0.2% (1/531 bp) difference in ITS, 2.3% (10/434 bp) in *tef1-α*, and 0.5% (2/427 bp) in *tub2*, respectively. Morphologically, *Ap. dongruensis* can be distinguished from *Ap. neochinensis* in having larger conidiogenous cells (5–10 × 0.5–2 μm in *Ap. dongruensis* vs. 1.5–6.5 × 1–3.5 μm in *Ap. neochinensis*) and larger conidia [5–19(–23) × 5–5.5 μm in *Ap. dongruensis* vs. 8.5–11 × 6.5–8 μm in *Ap. neochinensis*, Jiang et al. 2020]. Hence, we introduce *Apiospora dongruensis* as a new member of *Apiospora*. The morphological characters and multi-locus phylogenetic evidence confirm *Ap. dongruensis* is a new species collected from the infected leaves in China.

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Pseudolachnella Teng

Index Fungorum number: IF 9588; Facesoffungi number: FoF 07542

Notes – *Pseudolachnella* was established by Teng (1936) to accommodate *Ps. scolecospora* as the type species. *Pseudolachnella* species are characterized by having stromatic, acervular, setose conidiomata with marginal setae, phialidic conidiogenous cells, and conidia with single to multiple appendages at each end (Hashimoto et al. 2015, Li et al. 2020). Species of this genus have been reported mostly on dead bamboo substrates from China, India and Japan (Li et al. 2020, Huanraluek et al. 2021). Currently, there are 21 accepted *Pseudolachnella* species listed in Species Fungorum (2025). In this study, we introduce *Pseudolachnella chinensis* sp. nov. living on *Hedychium coronarium* leaves from China, based on multi-locus phylogeny (Fig. 11) and morphological comparison (Fig. 12).

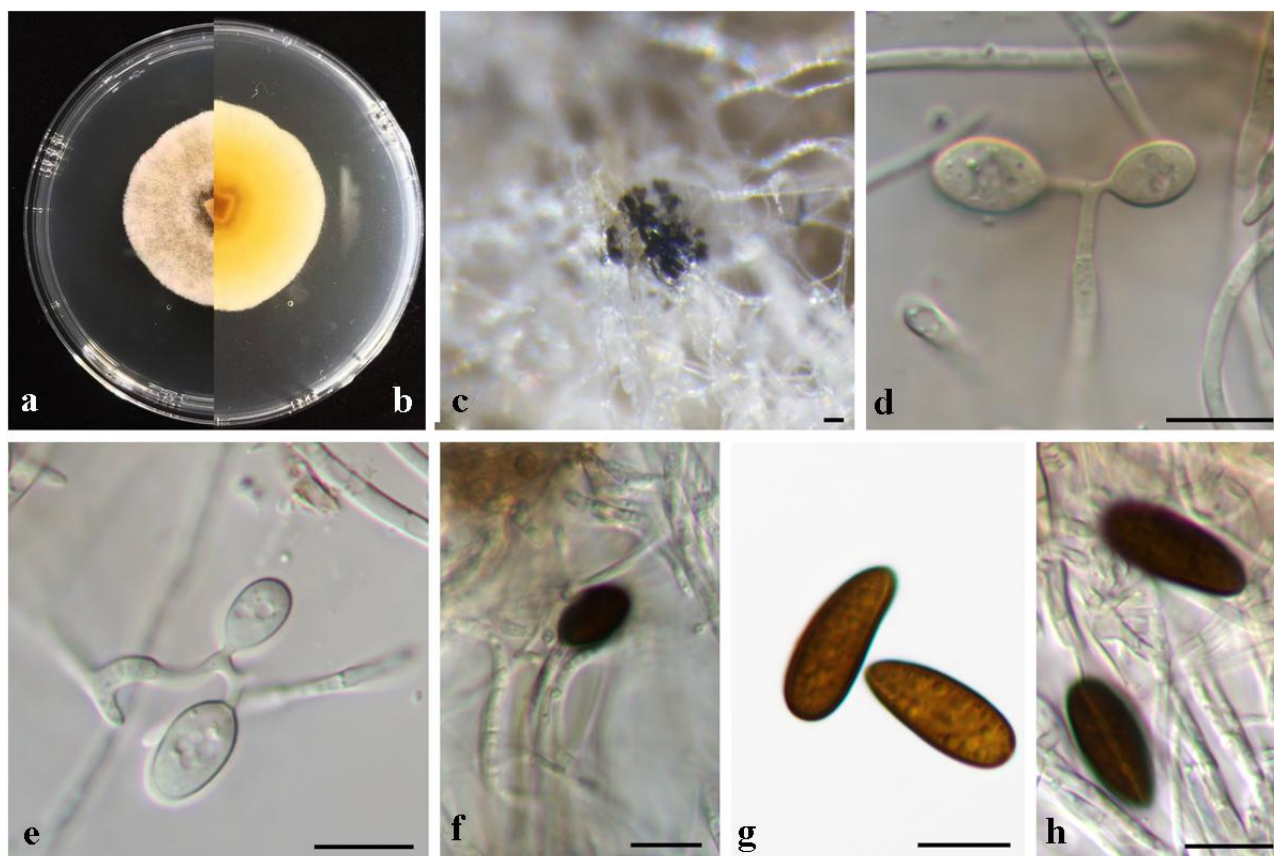


Figure 10 – *Apiospora dongruensis* (HMAS 354100, holotype). a, b The front (left) and reverse (right) views of the colonies on PDA. c Sporulated conidia on aerial mycelia. d, e Conidiogenous cells. f, g Conidia. h Conidia with a longitudinal and transparent slit. Scale bars: c-h = 10 µm.

Pseudolachnella chinensis Tennakoon & S. Hongsanan, sp. nov.

Fig. 12

Index Fungorum number: IF 904363; Facesoffungi number: FoF 17790

Etymology – Named after the country (China) where this fungus was collected.

Saprobic on dead leaf of *Hedychium coronarium*. Sexual morph: Undermined. Asexual morph: Coelomycetous. *Conidiomata* 150–200 µm diam. × 95–130 µm high ($\bar{x}$ = 175 × 114 µm, n = 5), stromatic, acervular, scattered or clustered, superficial to subcuticular, dark brown to black, setose. *Setae* 50–80 µm long, 3–5 µm wide, arising from basal stroma, straight or curved, pale brown at the apex, dark brown at the base, acute, thick-walled, smooth, unbranched. *Conidiophores* absent. *Conidiogenous cells* 10–15 × 4–5 µm, phialidic, subcylindrical to obclavate, usually integrated, indeterminate, hyaline, smooth-walled. *Conidia* 27–33 × 2.5–3.7 µm ($\bar{x}$ = 28 × 2.7 µm, n = 35), subcylindrical to fusiform, acute at the apex, aseptate, hyaline, bearing a single appendage at each end (3–3.5 µm long, 0.5–1 µm wide), smooth-walled.

Material examined – China, Yunnan Province, Kunming, on dead leaf of *Hedychium coronarium* (Zingiberaceae), 26 December 2018, D.S. Tennakoon, DPC030 (SZU25-024, holotype); *ibid.*, 28 December 2018, DPC035 (SZU25-025, paratype).

GenBank accession numbers – SZU25-024: ITS: PV845191, LSU: PV845186, *tef1-α*: PV853876; SZU25-025: ITS: PV845192, LSU: PV845187, *tef1-α*: PV853877.

Notes – The combined gene (LSU, ITS and *tef1-α*) phylogenetic analysis revealed that the two strains of our collection formed a monophyletic clade sister to *Ps. lancangensis* (KUMCC 21-0565) with 84% ML and 1.00 BYPP statistical support (Fig. 11). Morphology of our collection (SZU25-024 and SZU25-025) tallies well with the generic concept of *Pseudolachnella* in having stromatic, acervular conidiomata with marginal setae, phialidic conidiogenous cells, and conidia with single to multiple appendages at each end (Hashimoto et al. 2015). *Pseudolachnella lancangensis* was introduced by Ren et al. (2024) as a sexual morphic species, thus we are unable

to compare their morphologies. Therefore, we compared the base pair differences of ITS (+5.8S) and *tef1-α* gene regions between our collection (SZU25-024) and *Ps. lancangensis* (KUMCC 21-0565). Results revealed that there were 12 bp differences across 505 nucleotides (2.37%) of ITS (+5.8S) gene region and 18 base pair differences across 850 nucleotides of *tef1-α* gene region (2.1%). Thus, we introduce our collection as a new species, *Ps. chinensis* from Yunnan Province, China.

Figure 11 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS and *tef1-α* sequence data. Twenty-two strains were included in the combined sequence analyses, which comprised 2714 characters with gaps (LSU = 1296, ITS = 513, *tef1-α* = 905). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. *Pseudolachnea hispidula* (MFLUCC 15-0583) was used as the outgroup taxon. The final ML optimization likelihood is -6524.976583. The matrix included 295 distinct alignment patterns, with 7.31% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.95 are given above or below the nodes. The strain from the current study is in red-bold, and the type strains are indicated with ^T.

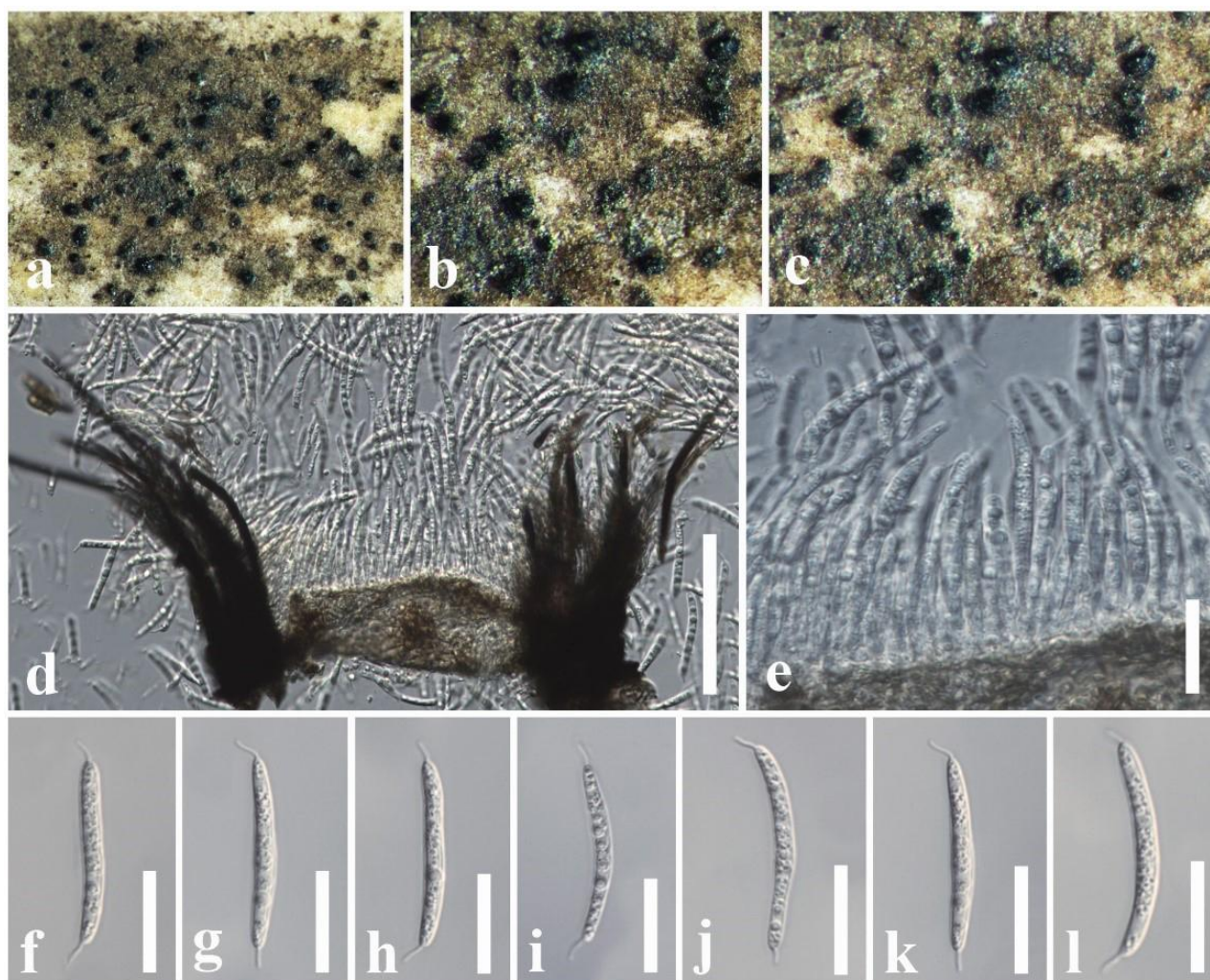


Figure 12 – *Pseudolachnella chinensis* (SZU25-024, holotype). a–c Conidiomata on the dead host surface of *Hedychium coronarium* (Zingiberaceae). d Longitudinal section of a conidioma. e Conidiogenous cells with conidia. f–l Conidia. Scale bars: d = 100 μ m, e–l = 15 μ m.

Hypocreales Lindau

Bionectriaceae Samuels & Rossman

Index Fungorum number: IF 82088; Facesoffungi number: FoF 01367

Bionectriaceae was introduced by Rossman et al. (1999). It is one of the largest fungal families in *Hypocreales* (Rossman et al. 1999, Trovão et al. 2022), and these species have a cosmopolitan distribution mainly in terrestrial and freshwater habitats, with less dominant in marine environments (Zhao et al. 2025a). Species of this family are characterized by having uniloculate, perithecial, rarely cleistothecial ascomata that are white, orange or brown, not changing color in KOH (Rossman et al. 1999, Hou et al. 2023). Some species exhibit acremonium-like or verticillium-like anamorphic characters (Zare & Gams 2016). Multiple gene markers of LSU, ITS, *rpb2* and *tef1- α* sequence data have been used to provide phylogenetic analyses of *Bionectriaceae* (Hou et al. 2023, Zhao et al. 2025a). Based on phylogeny, Zhao et al. (2025a) accepted 50 genera in this family. In this study, a novel genus *Roseosporodochia* was introduced based on morphology and multigene phylogenetic analysis.

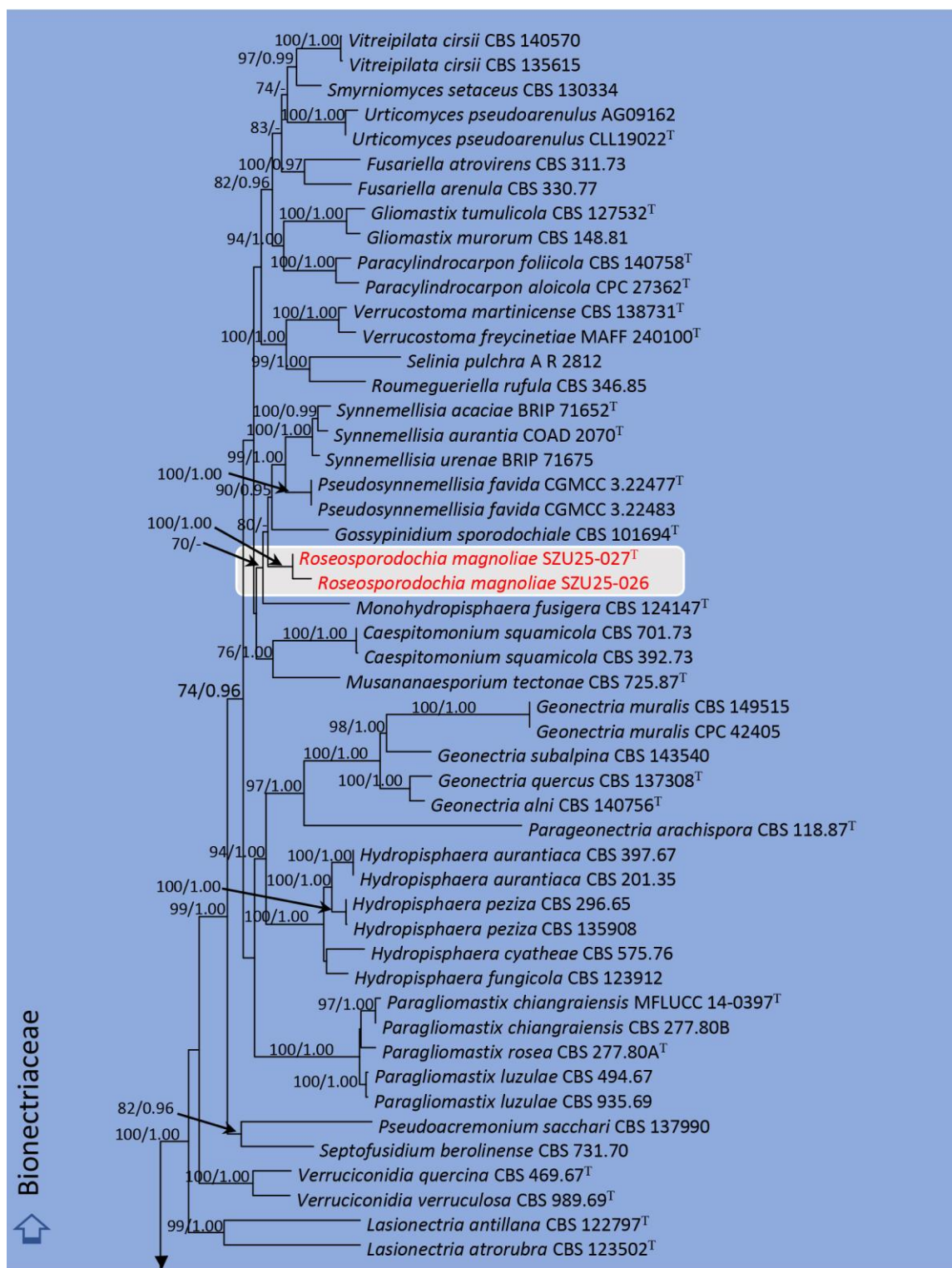


Figure 13 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *rpb2* and *tef1-α* sequenced data. Ninety-seven strains were included in the combined sequence analyses, which comprised 3090 characters with gaps (LSU = 950, ITS= 510, *rpb2*= 810, *tef1-α* = 820). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. *Flammocladiella aceris* (CBS 138906), *F. anomiae* (CLL16017), *F. decora* (CLL16020), and *Bullanoackia australis* (CPC 28976) strains were used as the outgroup taxa. The final ML optimization likelihood is -54154.792. The matrix included 1684 distinct alignment patterns, with 24.75% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.95 are given at the nodes. The strain from the current study is in red bold, and the type strains are indicated with ^T.

Roseosporodochia N.I. de Silva & Hongsanan, gen. nov.

Index Fungorum number: IF 904398, Facesoffungi number: FoF 18599

Etymology – Referring to the presence of pink colored conidiomata (sporodochia).

Saprobic on dead plant twigs. Sexual morph: Undetermined. Asexual morph: *Sporodochia* oval to sub-globose, determinate, conspicuous, superficial, erect, ending in orangish-pink, cushion-like, convex apex containing conidiogenous cells and mucilaginous conidial mass, with a short stem attached to host plant tissue. *Conidiophores* hyaline to pale brown, cylindrical, aggregated, straight to slightly curved, unbranched, smooth. *Conidiogenous cells* hyaline, phialidic. *Conidia* hyaline, ellipsoid to obovoid, aseptate, guttulate, smooth, apex subacute, base obtuse to subtruncate.

Type species – *Roseosporodochia magnoliae* N.I. de Silva & Hongsanan

Notes – Based on the phylogenetic analysis, our two new collections (SZU 25-026 and SZU 25-027) clade with a group consisting of three *Synnemellisia* species, *Pseudosynnemellisia favida* (CGMCC 3.22477), *Gossypinidium sporodochiale* (CBS 101694), and *Monohdropisphaera fusigera* (CBS 124147) with 70% ML bootstrap support (Fig. 13). Further, SZU 25-026 and SZU 25-027 formed a distinct clade within this group. *Synnemellisia* species have conspicuous, superficial, erect, obclavate to obconical, elongated synnemata with a convex apex and golden brown textura intricata stem (Crous et al. 2016a). *Pseudosynnemellisia* species can be differentiated from our collections in having branched conidiophores, ampulliform conidiogenous cells and ellipsoidal, ovoid to clavate conidia (Li et al. 2023). Also, *Monohdropisphaera* species have macronematous, mononematous, unbranched, elongate, erect conidiophores, integrated, monophialidic, terminal conidiogenous cells, obpyriform to fusiform, hyaline to brown, aseptate, solitary or catenulate in short chains conidia (Lechat et al. 2010). These morphological characters indicate that our collections are distinct from *Monohdropisphaera*, *Pseudosynnemellisia*, and *Synnemellisia*. However, our collections and *Gossypinidium sporodochiale* (CBS 101694) show some similarities. *Gossypinidium sporodochiale* sporulated on culture media and produced pink or orange, cottony sporodochia (Hou et al. 2023). Our collections have oval to sub-globose, superficial, erect sporodochia ending in orangish-pink, cushion-like convex apex conidial mass, short stem attached to host plant tissue. However, conidiophores of *Go. sporodochiale* are mostly branched, bearing multiple levels with 1–3 phialides per node (Hou et al. 2023), whereas conidiophores of our collections are solitary, hyaline to pale brown, cylindrical, aggregated, straight to slightly curved, unbranched. Therefore, we identified our collection as a new genus, *Roseosporodochia* in *Bionectriaceae*.

Roseosporodochia magnoliae N.I. de Silva & Hongsanan, sp. nov.

Fig. 14

Index Fungorum number: IF 904399, Facesoffungi number: FoF 18600

Etymology – Referring to the host, *Magnolia*, from which the type species was collected.

Saprobic on dead twigs of *Magnolia grandiflora*. Sexual morph: Undetermined. Asexual morph: *Sporodochia* 70–150 µm high, 200–300 µm diam., oval to sub-globose, determinate, conspicuous, superficial, erect, ending in orangish-pink, cushion-like convex apex containing conidiogenous cells and mucilaginous conidial mass, short stem attached to host plant tissue. *Conidiophores* 6–12 µm long × 1–2.3 µm, ($\bar{x}$ = 7.6 × 1.7 µm, n = 20), solitary, hyaline to pale brown, cylindrical, aggregated, straight to slightly curved, unbranched, smooth. *Conidiogenous cells* 3–4 µm long × 1–2 µm, ($\bar{x}$ = 3.2 × 1.6 µm, n = 20), hyaline, phialidic. *Conidia* 4–6 × 1.3–2.4 µm, ($\bar{x}$ = 5.2 × 1.8 µm, n = 30), hyaline, ellipsoid to obovoid, aseptate, guttulate, smooth, apex subacute, base obtuse to subtruncate.

Material examined – China, Yunnan Province, Kunming, dead twigs of *Magnolia grandiflora* (*Magnoliaceae*), 26 April 2017, N. I. de Silva, MGT44 (SZU25-027, holotype), *ibid.*, MGG12 (SZU25-026, isotype).

GenBank accession numbers – SZU25-027: ITS = PX418405; SZU25-026: ITS = PX418406.

Notes – In the phylogenetic analysis of combined LSU, ITS, *rpb2* and *tefl-α* sequence data, *Roseosporodochia magnoliae* formed an independent clade closely related to *Gossypinidium sporodochiale* (CBS 101694) and *Monohdropisphaera fusigera* (CBS 124147) (Fig. 13).

Morphologically, they have distinct characteristics from each other. *Gossypinidium sporodochiale* sporulated on culture media and produced pink or orange, cottony sporodochia (Hou et al. 2023). Also, *Go. sporodochiale* has straight, slightly curved conidiophores in aerial mycelium that are repeatedly verticillate towards the apex, bearing septate, hyaline, smooth-walled, 1–3(–4) whorls of 1–3 phialides (Hou et al. 2023). Further, conidia of *Go. sporodochiale* are $3\text{--}4.6 \times 2\text{--}2.8 \mu\text{m}$, aseptate, short ellipsoid, hyaline, thin-, smooth-walled, arranged in chains (Hou et al. 2023). However, *Roseosporodochia magnoliae* has oval to sub-globose, superficial, erect, ending in orangish-pink sporodochia with cushion-like convex apex, containing phialidic conidiogenous cells and mucilaginous conidial mass. Also, *R. magnoliae* has cylindrical, aggregated, straight to slightly curved, unbranched, smooth conidiophores, while conidia are $4\text{--}6 \times 1.3\text{--}2.4 \mu\text{m}$, hyaline, ellipsoid to obovoid, aseptate, guttulate, smooth, with a subacute apex and obtuse to subtruncate base. These morphological differences indicated that *Go. sporodochiale* and *R. magnoliae* are distinct species. In addition, considering the base pair differences between *Go. sporodochiale* and *R. magnoliae*, there are 7.69% differences (40/520 bp) in the ITS region. Thus, based on morphological evidence and multigene phylogeny, we introduced *R. magnoliae* as a new species under the new genus *Roseosporodochia*.

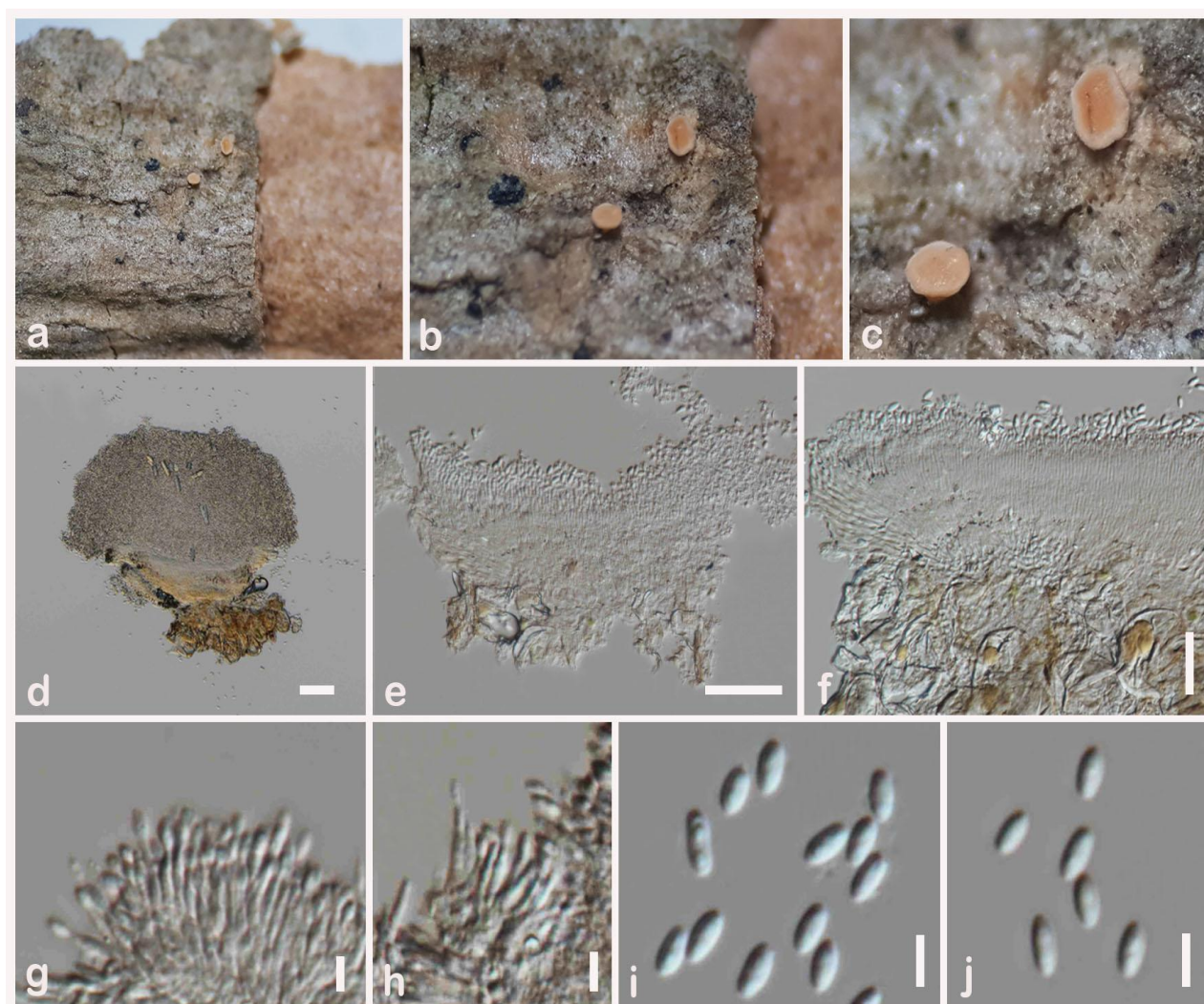


Figure 14 – *Roseosporodochia magnoliae* (SZU 25-027, holotype). a Sporodochia on the dead host surface of *Magnolia grandiflora*. b, c Enlarged views of sporodochia on the dead host surface. d Squash mount of a sporodochium. e Longitudinal section of sporodochium. f Longitudinal section of sporodochium including peridium. g, h Conidiophores and conidia. i, j. Conidia. Scale bars: d, e = 50 μm , f = 20 μm , g–j = 5 μm .

Hypocreaceae De Not.

Trichoderma Pers.

Index Fungorum number: IF 10282; Facesoffungi number: FoF 02075

Notes – *Trichoderma* was established by Persoon (1794) with *Tri. viride* as its type species. This genus is ubiquitous on various substrates and widely distributed throughout the world. It is characterized by perithecia immersed in fleshy stromata of different colors, cylindrical asci with hyaline or green ascospores which disarticulate at the septum, conidiophores forming several types of branch patterns, and hyaline or green conidia (Zhang & Zhuang 2017). ITS, *rpb2* and *tef1-α* were the required markers to identify a *Trichoderma* species and the sequence similarities of *rpb2* (99%) and *tef1-α* (97%) were deemed as species boundaries in the genus (Cai & Druzhinina 2021). More than 560 species are recorded in Index Fungorum (2025), and nearly 120 of which were introduced in the recent five years. China is rich in species diversity of the genus, and many taxa have been reported here (Chen & Zhuang 2017, Zheng et al. 2021, Zhao et al. 2025b). In this study, we introduce *Trichoderma zhuangii* sp. nov., isolated from basidiomata of *Trametes* sp., from China, based on the multi-gene phylogenetic evidence (Fig. 15) and morphological characteristics (Fig. 16).

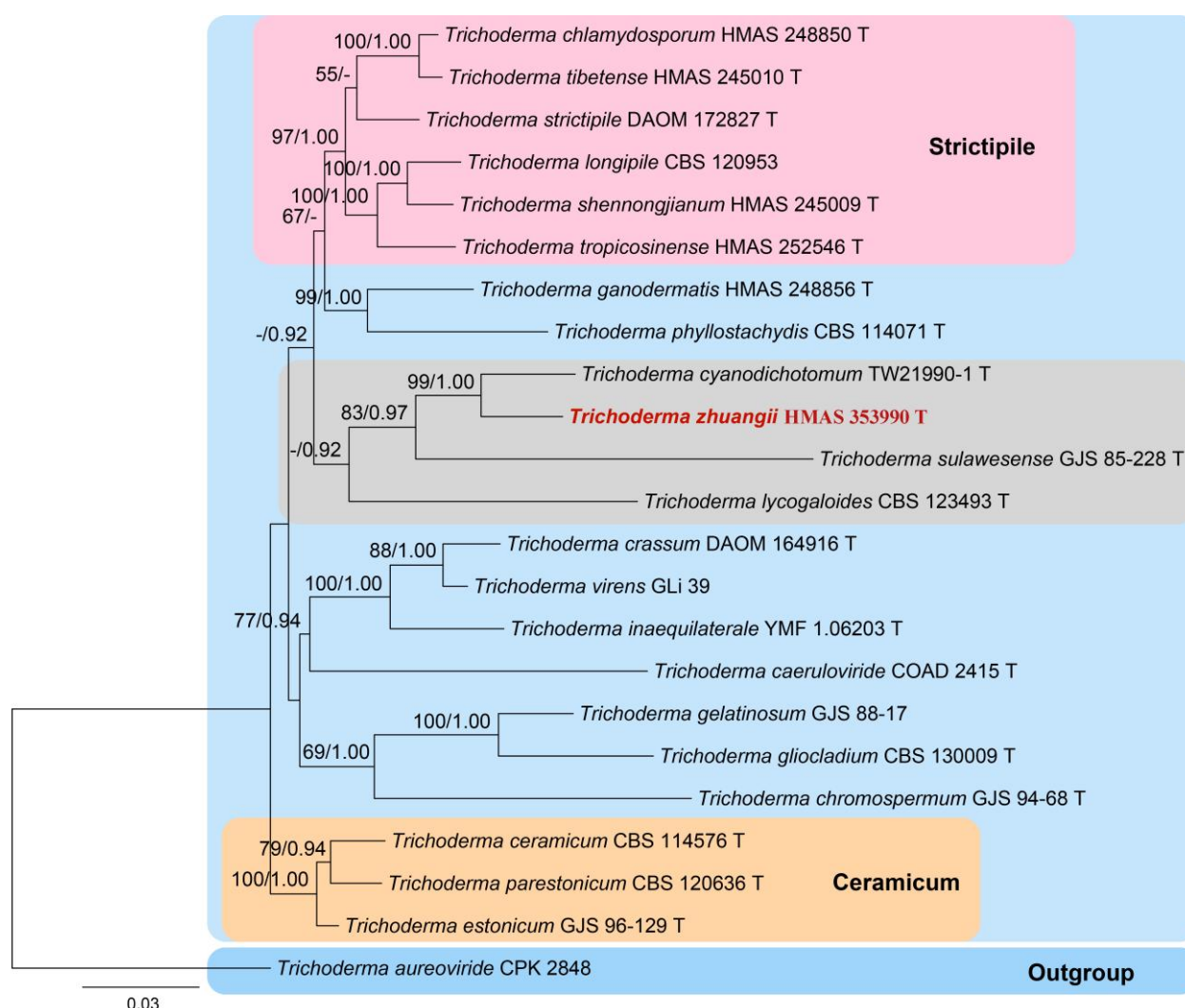


Figure 15 – Phylogram generated from maximum likelihood analysis based on combined *rpb2*, *tef1-α* and ITS sequence data of the more closely related *Trichoderma* species to the new species. Twenty-three strains are included in the combined sequence analyses, which comprised 3064 characters with gaps (*rpb2* = 1091, *tef1-α* = 1326, ITS = 647). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. The best RAxML tree with a final likelihood value of -13545.142 is presented. The evolutionary model

TrN+I+G is applied for all the genes. The matrix had 896 distinct alignment patterns, with 17.72% of undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 50%, BYPP equal to or greater than 0.90 are given above the nodes. *Trichoderma aureoviride* (CPK 2848) was used as the outgroup taxon. The newly generated sequence is in red-bold, and the type strains are indicated with ^T.

Trichoderma zhuangii X.C. Wang & L.Y. Peng, sp. nov.

Fig. 16

Index Fungorum number: FN 572720; Facesoffungi number: FoF 18601

Etymology – The specific epithet is in honor of the Chinese mycologist Professor Wen-Ying Zhuang, Member of the Chinese Academy of Sciences (CAS), who has made contributions to the taxonomy of hypocrealean and cup fungi.

Colonies lethal at 35°C, with similar growth rates on PDA, MEA, CMD and SNA. Colony radius on PDA at 25°C after 72 h: 42–56 mm, covering the plate after 4 days; colony not well zonate; mycelium hyaline to pale white; aerial hyphae hairy to floccose; conidiation green, moderately dense at central area; pale green to the margin; chlamydospores absent; diffusing pigment absent; odor fruity. Colony radius on MEA at 25°C after 72 h: 50–56 mm, covering the plate after 4 days; colony zonate; mycelium hyaline to pale white; aerial hyphae hairy to floccose; conidiation dark green at the center, sparse; green at the middle area, moderately dense; pale green to the margin; chlamydospores absent; diffusing pigment absent; odor fruity. Colony radius on CMD at 25°C after 72 h: 54–60 mm, covering the plate after 4 days; colony flat, translucent; mycelium hyaline; aerial hyphae inconspicuous; conidiation sparse; chlamydospores absent; diffusing pigment absent; odor winey. Colony radius on SNA at 25°C after 72 h: 48–50 mm, covering the plate after 4 days; colony flat, translucent; mycelium hyaline to pale white; aerial hyphae inconspicuous; conidiation sparse; chlamydospores absent; diffusing pigment absent; odor winey. *Conidiophores* somewhat symmetrical or dendriform; main axis recognizable, smooth, 4.5–5.5 µm in diam.; branches paired or unilateral, arising at an angle of less than 90° or nearly to 90°; phialides in whorl of 2–5, lageniform and bowling pin shaped, 7.5–15 × 3–4 µm; conidia ovoid to broad ellipsoidal, green, smooth, 4–6.5 × 3–4 µm.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden of CAS, on basidiomata of *Trametes* sp. (*Polyporaceae*), 29 May 2024, Xin-Cun Wang, culture, Lu-Yao Peng, XCW_SN547 (HMAS 353990, holotype); ex-type CGMCC 3.28903.

GenBank accession numbers – ITS: PV650642; *rpb2* = PV664059, *tef1-α* = PV664060.

Notes – The multi-locus phylogeny revealed that the strain of our species, *Trichoderma zhuangii* (HMAS 353990) formed a separate lineage sister to *Tri. cyanodichotomum* (TW21990-1) with 99% ML and 1.00 BYPP bootstrap supports (Fig. 15). *Trichoderma lycogaloides* and *Tri. sulawesense* forms close lineages to the above species. Sequence similarities between *Tri. zhuangii* and *Tri. cyanodichotomum* are 97.63% for ITS with 14 bp nucleotide differences (including gap), 95.90% for *rpb2* with 44 bp, and 95.34% for *tef1-α* with 59 bp. The key morphological differences distinguishing the new species from *Tri. cyanodichotomum* are the absence of blue–green pigment on PDA reverse, the lacking of chlamydospores on PDA, the presence of a recognizable odor and much longer phialides (7.5–15 vs. 3.7–5.5 µm, Li et al. 2018). The multi-locus phylogenetic analysis in combination with the morphological comparison confirms the novelty of our strain. We introduce *Trichoderma zhuangii* as a new species collected from Yunnan Province, China.

Ophiocordycipitaceae G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora

Ophiocordyceps Petch

Index Fungorum number: IF 3598; Facesoffungi number: FoF 01318

Notes – *Ophiocordyceps*, initially established as a separate genus and *Op. blattae* as the type species. It was later reclassified as a subgenus of *Cordyceps*, mainly based on perithecia arrangement and the size of asci and ascospores (Petch 1931, Kobayasi 1941, Mains 1958). Sung

et al. (2007) provided strong support for the establishment of three families, leading to their proposal to divide them into *Ophiocordycipitaceae*, *Clavicipitaceae*, and *Cordycipitaceae*. *Ophiocordyceps* was suggested as the type genus of *Ophiocordycipitaceae* (Sung et al. 2007). *Ophiocordyceps* differs from other adjacent genera due to its fibrous, hard, flexible, pigmented stromata with perithecia that are superficial or immersed, and the production of whole ascospores that do not disarticulate into part-spores (Ban et al. 2015, Xiao et al. 2019, Yang et al. 2024a). This genus demonstrates an extensive diversity of hosts, infecting various insect orders, including Blattaria, Coleoptera, Dermaptera, Diptera, Hemiptera, Hymenoptera, Isoptera, Lepidoptera, Megaloptera, Mantodea, Odonata, and Orthoptera. Moreover, *Ophiocordyceps* targets insects at multiple life stages, parasitizing larvae, pupae, nymphs, and adults (Sung et al. 2007, Quandt et al. 2014, Ban et al. 2015, Xiao et al. 2019). With over 300 accepted species, it stands as the largest genus in *Ophiocordycipitaceae*, particularly abundant in tropical and subtropical regions, with Asia serving as a hotspot of species diversity (Mongkolsamrit et al. 2019, Xiao et al. 2019, Thanakitpipattana et al. 2020, Yang et al. 2021, 2024a, 2025a, Hyde et al. 2024d, Guan et al. 2025). In this study, we introduce a new host record of the entomopathogenic fungus, *Ophiocordyceps vespulae* on an insect from China (Figs 17, 18).

***Ophiocordyceps vespulae* F.Y. Long, Y.P. Xiao & T.C. Wen**

Fig. 18

Index Fungorum number: IF 556626; Facesoffungi number: FoF 13970

Parasitic on the underside of the leaf litter of *Vespula affinis*, 1.8–2.2 × 0.2–0.5 cm, black, abdominal segments 1 to 2 with yellow-orange. Sexual morph: *Stromata* 6–7 cm long, 0.5–2 mm diam., single, stipitate, unbranched, arising from neck of the host. *Stipe* 4–5 cm long, 0.5–1 mm diam., yellow, fibrous, cylindrical, often flexuous, with a fertile apex. *Fertile head* 1.5–2 cm long, 0.5–1 mm diam., single, cylindrical, or elliptical, yellow. *Perithecia* 540–730 × 200–280 µm ($\bar{x}$ = 635 × 240 µm, n = 40), obliquely immersed, yellowish, narrow flask-shaped to elongated obpyriform. *Asci* 360–600 × 5.6–6.8 µm ($\bar{x}$ = 480 × 6.2 µm, n = 50), narrow cylindrical, apex thickened, hyaline; apical cap 6.3–7.5 diam., hyaline. *Ascospores* almost as long as asci, filiform, hyaline, easily breaking into part-spores. *Partspores* 7.7–11.8 × 1.6–2.8 µm ($\bar{x}$ = 9.8 × 2.2 µm, n = 50), fusiform, hyaline, smooth. Asexual morph: Undetermined.

Material examined – China, Liaoning Province, Tieling City, Xifeng County, at 356 m, 42.663 N; 124.482 E, parasitic on *Vespula affinis* (Hymenoptera), collected from the underside of leaves litter, 10 August 2022, Yuanpin Xiao, TL43, (GZAAS 22-2051).

Known distribution (based on molecular data) – China (Long et al. 2021, Wei et al. 2022)

Known hosts (based on molecular data) – *Vespula* sp. (Long et al. 2021), wasp (Wei et al. 2022)

GenBank accession numbers – ITS: PP761434, LSU: PP758199, *tef1-α*: PP775906, *rpb2*: PP775905.

Notes – Based on the multigene phylogeny of this study, the strain of our new collection (GZAAS 22-2051) clustered together with the strains of *Ophiocordyceps vespulae* (GACP2017064, GZU2017079) with 100% ML and 1.00 BYPP bootstrap support (Fig. 17). Long et al. (2021) introduced *Op. vespulae* as an entomopathogenic fungus parasitic on *Vespula* sp., collected from the underside of leaf litter in Jilin province of China. In comparison of the same gene regions between our collections and GACP2017079 strain there were no bp differences in the ITS, LSU, 4 bp (0.43%) of difference from 920 bp in the *tef1-α* and 6 bp (0.61%) of difference from 981 bp in the *rpb2*. Morphological characters of our species are similar to *Op. vespulae* description provided by Long et al. (2021). Wei et al. (2022) identified a wasp species as a host for *Op. vespulae* in Yunnan Province, China. However, our new collection parasitizes *Vespula affinis* and infects different *Vespula* hosts compared to the type specimen of *Op. vespulae* (Long et al. 2021). According to morpho-molecular analyses we conclude that *Ophiocordyceps vespulae* is a new host record on *Vespula affinis* in China.

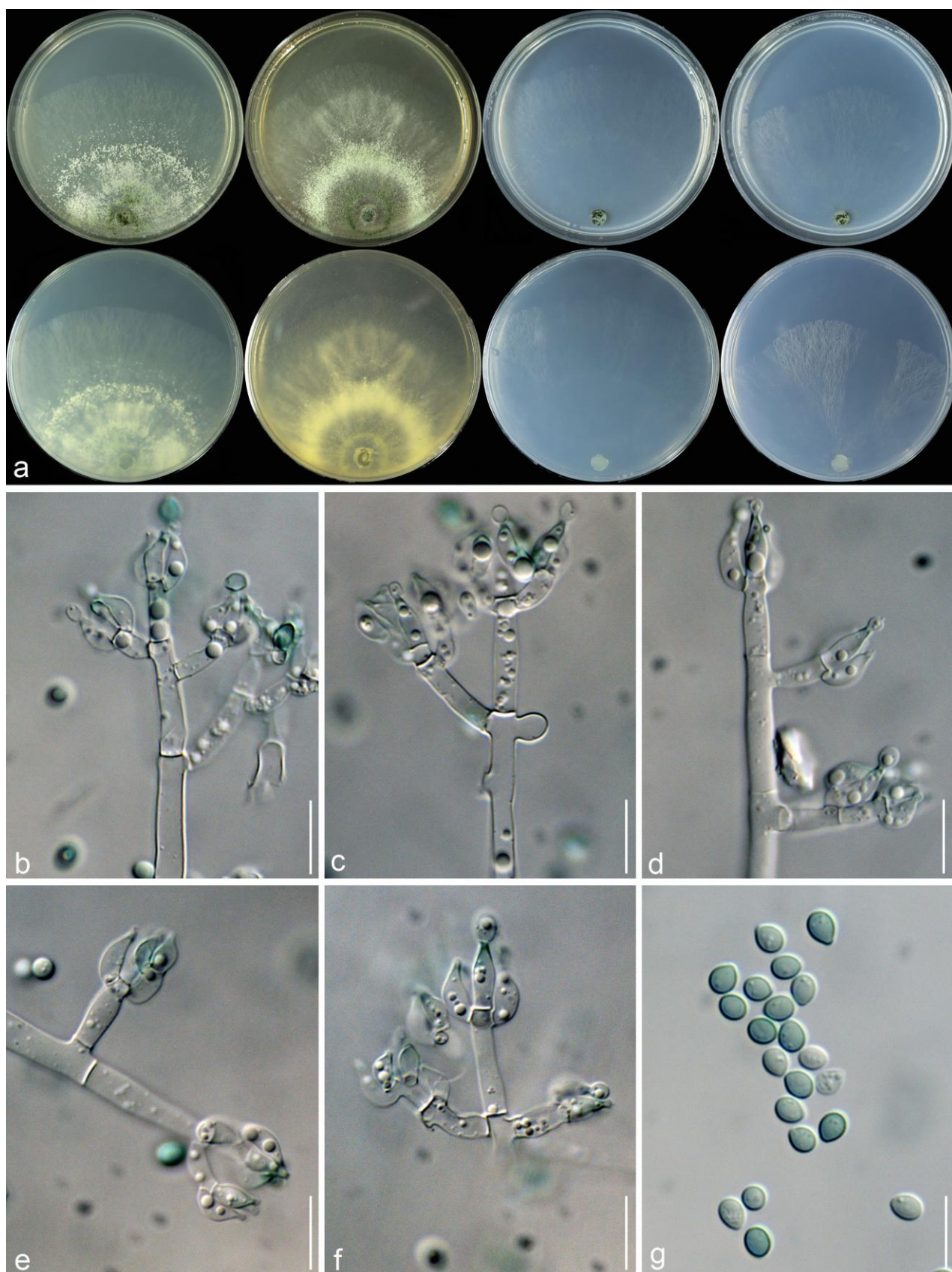


Figure 16 – *Trichoderma zhuangii* (HMAS 353990, holotype). a Colonies: top row left to right, obverse PDA, MEA, CMD, and SNA; bottom row left to right, reverse PDA, MEA, CMD, and SNA. b–f Conidiophores. g Conidia. Scale bars: b–f = 12.5 μ m, g = 10 μ m.



Figure 17 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, *tef1*- α , and *rpb2* sequence data. Sixty-nine strains were included in the combined sequence analyses, which comprised 3111 characters with gaps (ITS = 534, LSU = 811, *tef1*- α = 896, *rpb2* = 870). Single gene analyses were also performed, and topology and clade stability were compared from combined gene analyses. *Tolypocladium inflatum* (OSC 71235) and *Tolypocladium ophioglossoides* (NBRC 106332) strains were used as the outgroup taxa. The RAxML analysis was performed using ultrafast bootstrap approximation (Hoang et al. 2018) with 1000 replicates. The final log-likelihood of the consensus tree is -38628.612624. The consensus tree was summarized based on the extended majority-rule. Bootstrap support values for ML (first set) equal to or greater than 75%, BYPP equal to or greater than 0.90 are given above or below the nodes. The strains from the current study are in red and the type strains are indicated with ^T.

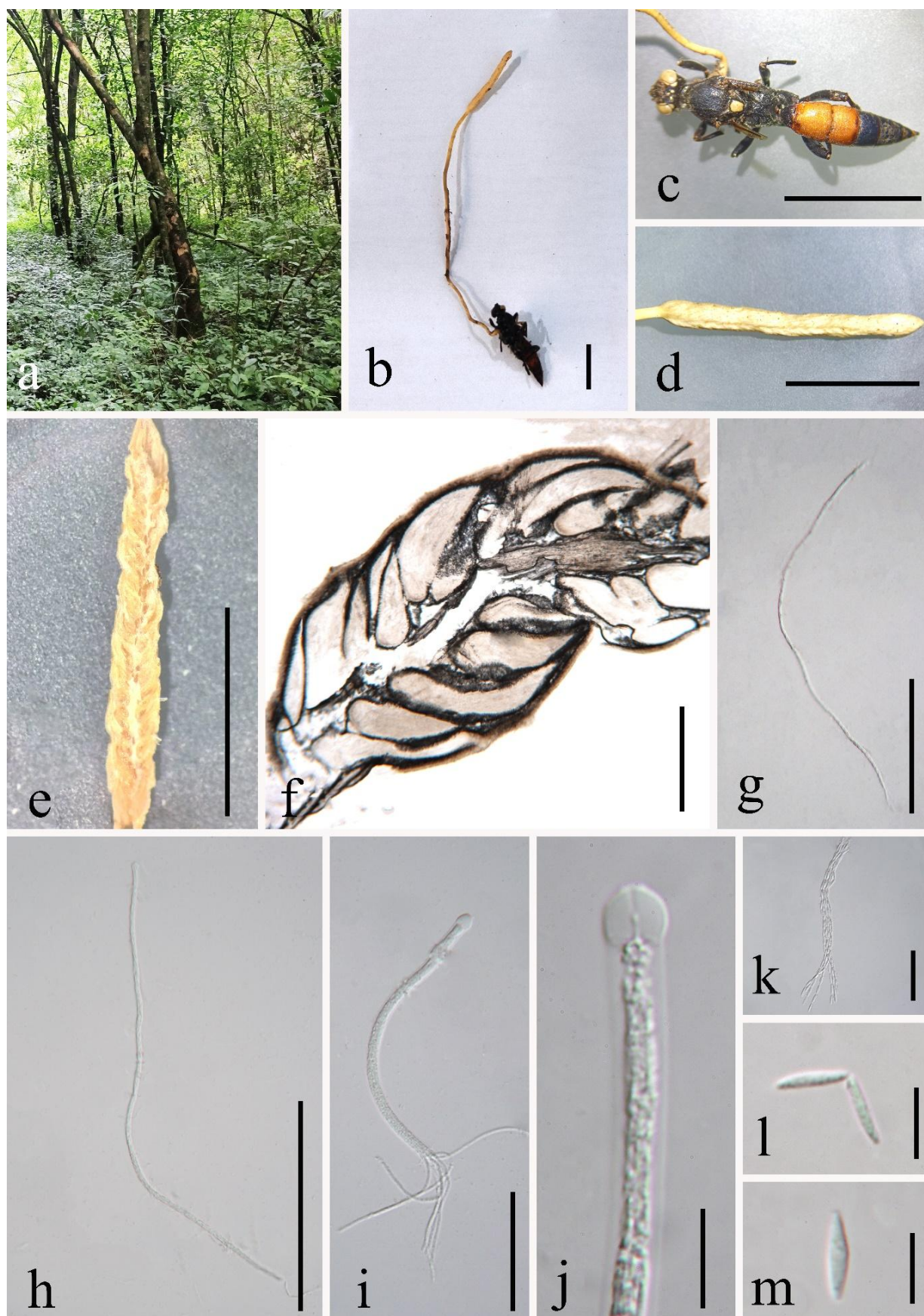


Figure 18 – *Ophiocordyceps vespulae* (GZAAS 22-2051, a new host record). a Habitat where the fungus was collected. b Surface view of *Ophiocordyceps vespulae*. c The host (insect). d Stroma. e Vertical section of a stroma. f Perithecia. g–i Asci. j Apical cap. k Part of ascospores. l–m Part-spores. Scale bars: b–e = 1 cm, f = 500 µm, g–h = 200 µm, i, k = 50 µm, j, l–m = 10 µm.

Phylum Basidiomycota

Class Agaricomycetes Doweld

Agaricales Underw.

Agaricaceae Chevall.

Agaricus L.

Index Fungorum number: IF 17030; Facesoffungi number: FoF 01165

Notes – *Agaricus* is an important saprotrophic mushroom genus in *Agaricaceae*. Species of this genus are mainly distributed in tropical and subtropical regions (Parra 2008, Kerrigan 2016, Zhao et al. 2016, Bhunjun et al. 2024). *Agaricus* is characterized by small to large-sized basidiomata with different colored caps, free lamellae with pinkish to brownish spore-print, an annulate stipe, smooth basidiospores without germ-pore (Zhao et al. 2016). Taxonomically, the known species of *Agaricus* are classified into six subgenera and 27 sections (Zhao et al. 2016, He et al. 2017, Chen et al. 2017, Bashir et al. 2018, 2024, Callac & Chen 2018, Ortiz-Santana et al. 2021, Hussain et al. 2022, Nawaz et al. 2024a). Among these subgenera, *Agaricus* subg. *Minores* consisted of three sections, namely, *Ag.* sect. *Leucocarpi*, *Ag.* sect. *Minores*, and *Ag.* sect. *Pantropicales* (Zhao et al. 2016, Chen et al. 2017, Parra et al. 2018). *Agaricus* sect. *Minores* is considered the largest section in the genus in regard to species with more than 100 named species (Bashir et al. 2024, Nawaz et al. 2024b). With small and delicate basidiomata and very few morphological variations among the species, it is estimated that the section *Minores* contained more cryptic species in tropical and subtropical regions than the documented number (He et al. 2017, 2019). The mountains of Dhofar in summer (July–September) turn into a tropical region with plenty of rainfall, influencing the emergence of various mushrooms including *Agaricus* (Hussain et al. 2022). There are more than 500 known species in the genus, including the most cultivated mushroom in the world, the button mushroom, *A. bisporus* (Zhao et al. 2016, Bashir et al. 2024). In this study, we introduce *Agaricus wadidarbaticus* sp. nov., presumably belongs to section *Minores* collected from Dhofar region, southern Oman, based on the multi-gene phylogenetic evidence (Fig. 19) and morphological characteristics (Figs 20, 21).

Agaricus wadidarbaticus Al-Kharousi, Al-Sadi, Al-Yahya'ei & S. Hussain, sp. nov. Figs 20, 21

Index Fungorum number: IF 904402; Facesoffungi number: FoF 18602

Diagnosis – For diagnosis, compare only with *Agaricus megalosporus*

Etymology – Refers to the holotype location Wadi Darbat, located in the Dhofar Governorate, Salalah, south of the Sultanate of Oman.

Basidiomata medium-sized. *Pileus* 4–6 cm in diam., parabolic to cylindrical at young stage (button stage when the cap is not yet opened), at maturity becoming convex to hemispheric, finally becoming plane with a slightly depressed center; surface fragile, dull and dry, squamulose, squamules light reddish-brown (2.5YR 6/4–10R 4/6) to moderate yellowish-pink (2.5YR 7/4–7.5R 6/6) over a whitish background, at the young stage squamules covered the entire cap, at mature stage squamules disrupted into small patches, concentrated at the center; center slightly depressed at old stage; margins entire, slightly exceeding the lamellae. *Lamellae* free, creamy white at young stage, becoming pinkish to light brown 7.5YR 5/4–7.5YR 3/4) at maturity, with an even edge, close to slightly crowded, intercalated with 0–4 series of lamellulae. *Stipe* 3.5–4 × 1–2.5 cm, central, cylindrical to rounded and slightly bulbous at the base to ventricose from center, clavate towards base, solid with compact interior, smooth, whitish to pale yellowish (2.5Y 9/4–5Y 9/4) below the annulus, light pinkish (2.5R 9/6–2.5R 9/4) above the annulus, the base of the stipe becoming yellow on bruising. *Annulus* descending, medial to slightly superius, single edged, white, fragile, smooth, membranous, thin with floccose texture. Odor and taste are not recorded. *Basidiospores* 5.9 × 3.6 µm, ellipsoid to cylindrical or oblong, light to dark brown in KOH, smooth to slightly finely verrucose, with a prominent apiculus, without apical pore. *Basidia* 14.4–16.4 × 5.9–6.4 µm, frequently bisporic to tetrasporic in all specimens, no monosporic basidia observed, clavate with slightly truncated apex, without granular content observed, hyaline in KOH. *Cheilocystidia* 18.5–23.3 × 8.6–10.7 µm, broadly clavate to broadly cylindrical, long, simple, few septate at the base,

moderate yellow, with terminal elements, terminal elements mostly broadly clavate to broadly cylindrical, with abundant olivaceous granular content, hyaline in KOH. *Pileipellis* is a hymeniderm to epithelium, constituted by interwoven hyphae $27.5\text{--}39.9 \times 6.6\text{--}8.6 \mu\text{m}$, frequently septate, sometimes branched, constricted at septa, hyaline in KOH, terminal elements with rounded ends measuring $30.3\text{--}42 \times 5.4\text{--}7 \mu\text{m}$. *Stipitipellis* constituted by hyphae, measuring $38.4\text{--}55.6 \times 7.4\text{--}11.4 \mu\text{m}$ in diam., frequently septate, rarely branched, constriction at septa, hyaline in KOH, constricted at septa, with terminal elements $47 \times 9.4 \mu\text{m}$ having rounded ends, cylindro-clavate structure. Annulus consisted of cylindrical to elongated cells, septate, slightly constricted at septa, with terminal elements having rounded ends, terminal elements $2.1\text{--}45.2 \times 3.5\text{--}4.8 \mu\text{m}$.

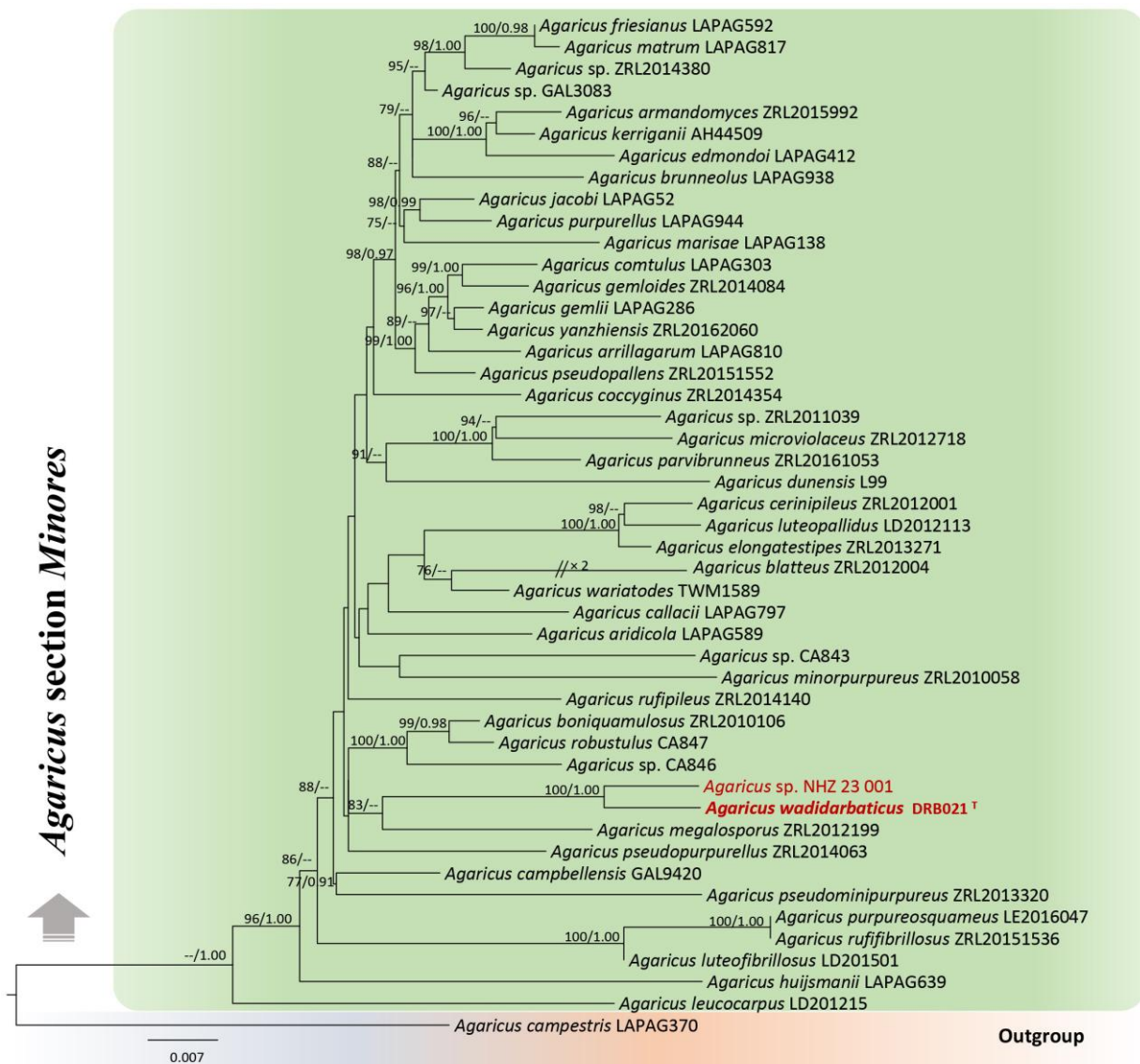


Figure 19. Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *tef1- α* sequence data of *Agaricus* section *Minores*. Forty-seven specimens are included in the combined sequence analyses, which comprised 2306 characters with gaps (ITS = 669, LSU = 942, *tef1- α* = 595). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. The best RAXML tree with a final likelihood value of -10802.111 is presented. The evolutionary model TIM2+F+R3 is applied for all the genes. The matrix had 756 distinct alignment patterns, with 17% of undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.90 are given above the nodes. *Agaricus campestris* (LAPAG370) was used as the outgroup taxon. The newly generated sequences are in red-bold, and the type specimen is indicated with ^T.

Habitat and distribution – Fruiting body formation occurs from early August to early September. Growing solitary and in small groups on humus-rich soil with dead leaves and wood, snails are observed near the basidiomata, saprotrophic. Current distribution is only known from Dhofar region, southern Oman.

Material examined – Oman, Dhofar, Salalah, Darbat, 17° 8'20.54"N, 54°31'33.15"E, on humus-rich soil, 26 August 2023, S. Hussain & Mohammed Al-Jahwari, DRB-23-021 (SQUH DRB-23-021, holotype).

GenBank accession numbers – ITS: PV088617, LSU: PV471051, *tef1*- α : PV477845.

Notes – The combined ITS+nLSU+*tef1*- α phylogenetic analyses (Fig. 19) revealed that our specimens of *Agaricus wadidarbaticus* (DRB-23-021) and potential new species (NHZ-23-001) grouped within the *Agaricus* section *Minores*, forming a monophyletic clade sister to *Ag. megalosporus* (ZRL2012199) with 83% ML bootstrap support. *Agaricus wadidarbaticus* resembles our potential new species (NHZ-23-001) by having a medium-sized pileus covered with reddish-brown squamules, concentrated at the center at mature stage. Both specimens are superous, single edged, white, fragile, smooth, membranous annulus. However, *Ag. wadidarbaticus* can be distinguished from this species by its light reddish-brown to moderate yellowish pink over a whitish background pileus, with slightly bulbous at the base to ventricose from center stipe. Even though both specimens are morphologically looking similar, however, both are distinct species based on their ITS sequences. For example, the BLAST results showed that the proposed new species (DRB-23-021) has 97% sequence similarity with NHZ-23-001. Furthermore, we compared the ITS histograms of these isolates where 18 polymorphic positions were found (Table 1).

Morphologically, the proposed new species *Agaricus wadidarbaticus* differs from its closest similar species *Ag. megalosporus*. *Agaricus megalosporus* was originally described from Thailand, and it has a middle to large sized basidiomem, with pileus (3.5–11 cm), convex to plano-convex, flat or slightly depressed at the disc pileus and larger basidiospores ($5.5\text{--}7.5 \times 3\text{--}4 \mu\text{m}$) compared with other species of section *Minores*, with heavily fibrillose squamulose stipe and relatively large basidiospores and hyaline, broadly clavate, pyriform with cylindrical base cheilocystidia ($20\text{--}43 \times 10\text{--}15 \mu\text{m}$, Chen et al. 2012).

Based on multigene phylogeny, *Agaricus wadidarbaticus* is a distinct species from *Ag. megalosporus*. The other similar species to *Ag. wadidarbaticus* are *Ag. pseudopurpurellus*, *Ag. boniquamulosus*, and *Ag. robustulus*, and undescribed *Agaricus* sp. (CA846), have small-medium basidiomes (pileus diam. between 3–6 cm), and a pileus covered by purple to reddish brown fibrils scales at disc, and scattered towards the margin, appressed in, as compared to medium-sized basidiomata with pileus covered with brownish squamules, and a depressed cap center in *A. wadidarbaticus*. The cheilocystidia of *Ag. pseudopurpurellus* are absent and the pileipellis is cutis, smooth, cylindrical, hyaline or light brown, slightly constricted at septa, as compared to broadly clavate to broadly cylindrical cheilocystidia and interwoven hyphae frequently septate, sometimes branched pileipellis in *Ag. wadidarbaticus*. The *Ag. boniquamulosus* is distinguished by its distinct fibrillose, brown, mess, appressed, denser at disc squamules on the surface of pileus. The odor of this species is strongly of almonds. The *Ag. robustulus* has fleshy sporocarps, with reddish brown or dark golden brown, fibrillose or squamose pileus and the basidiospores size is $5.8 \times 3.7 \mu\text{m}$, with simple, ovoid, pyriform or broadly clavate, with yellowish pigmented cheilocystidia. Thus, based on comprehensive morphological comparison and multigene phylogeny, we conclude one of our collections *Ag. wadidarbaticus* is a new species collected from Oman and other one (NHZ-23-001) is a possible new species in the genus. However, based on the limited information for a completed fungal description, we did not describe NHZ 23 001 as a new species in this study.

Cortinariaceae Singer

Phlegmacium (Fr.) Wünsche

Index Fungorum number: IF 18258; Facesoffungi number: FoF 18603

Notes – *Phlegmacium* was initially circumscribed by Fries (1821) as a tribe of *Agaricus*. In 1836, Fries transferred it to *Cortinarius* as a tribe. Then, Trog (1844) subsequently elevated it to the rank of subgenus within *Cortinarius*. Kummer (1871) proposed *Phlegmacium* as an independent genus; however, this taxonomic treatment remained controversial and was not widely adopted, with most researchers continuing to recognize it as a subgenus of *Cortinarius* (Orton 1955, Singer 1962, Bidaud 1994). Notably, a study by Liimatainen et al. (2022), based on phylogenetic analyses of multi-locus and whole-genome data, re-established *Phlegmacium* at the generic level. *Phlegmacium* is one of the largest genera of *Cortinariaceae* with more than 200 species worldwide (Liimatainen et al. 2022). Most species of *Phlegmacium* are characterized by their viscid to glutinous pileus and dry stipes, if the pileus is dry, the KOH reaction in the context of the pileus is usually yellow, the basidiospores usually amygdaloid to ellipsoid or citriform. In morphology, this genus can be easily confused with the species of *Thaxterogaster* and *Calonarius*. In this study, we introduce *Phlegmacium sinovariecolor* sp. nov. from China, based on the phylogenetic analysis of ITS sequence data (Fig. 22) and morphological characteristics (Fig. 23).

Phlegmacium sinovariecolor M.L. Xie, C.T. Li & Y. Li, sp. nov.

Fig. 23

Index Fungorum number: IF 572728; Facesoffungi number: FoF 18604

Diagnosis – Similar to *Phlegmacium variecolor*, but differs in its smaller basidiomata, smaller and wider basidiospores, as well as the subtropical distribution in China. The ITS sequences of the new species are distinct from other members of the sect. *Phlegmacioida* and deviate from them by at least 10 substitutions and indel positions.



Figure 20 – Macromorphological characters of *Ag. wadidarbaticus* (DRB-23-021) collected from humus-rich soil. a–f Basidiomata in the field. Ruler used as a scale bar = 1 cm.

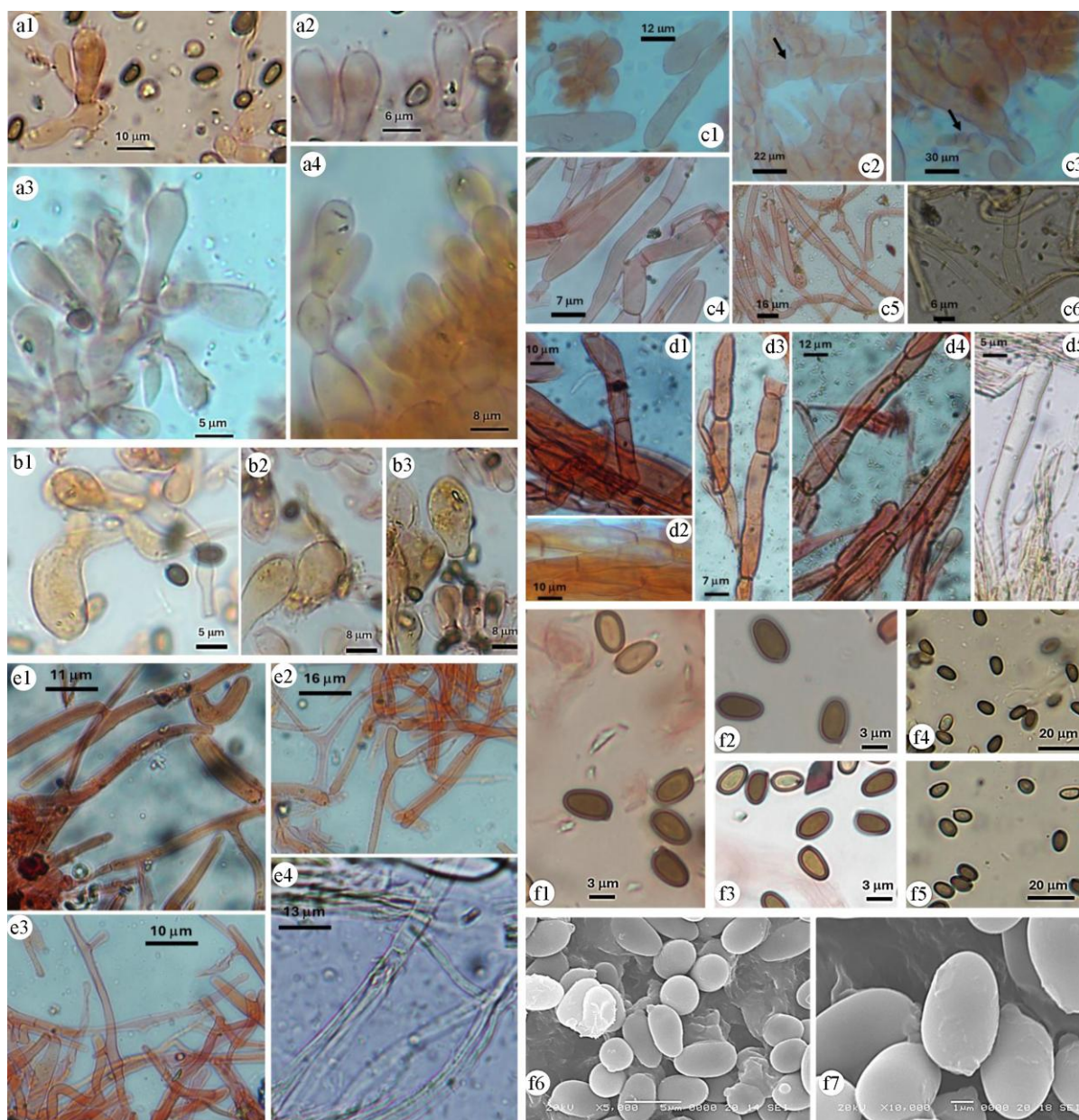


Figure 21 – Light microscopic characteristics of *Ag. wadidarbaticus* (DRB-23-021: a1–d5 at 40× magnification). a1–a4 Basidia. b1–b3 Cheilocystidia. c1–c5 Pileipellis in Congo red, c2–c3 Hymeniderm to epithelium structure represented by arrows, c6 Hyaline in KOH. d1–d5 Stipeipellis anatomical characters, d5 Hyaline in KOH. e1–e4 Annulus hyphae anatomical characters, e4 Hyaline in KOH. f1–f5 Light and scanning electron microscopy of basidiospores. f1–f3 Light microscopy 100× magnification in Congo red, f4–f5 Hyaline in KOH in 40× magnification, f6–f7 Scanning Electron Microscopy magnification, with 5000 × and 10000 × magnification, respectively.

Table 1 Comparison of ITS sequences of *Ag. wadidarbaticus* and undescribed novel species (NHZ-23-001), 18 polymorphic positions were found in the ITS sequences of these taxa

Collections	Variable Positions																		Species
Position	63	74	93	155	194	207	209	253	258	261	268	401	533	600	698	700	707	711	—
BRB-23-021	G	G	G	C	A	T	A	G	T	C	C	C	A	A	T	T	A	G	<i>Ag. wadidarbaticus</i>
NHZ-23-001	A	A	T	T	G	G	G	T	C	T	T	T	G	G	C	C	G	A	Undescribed <i>Ag. species</i>

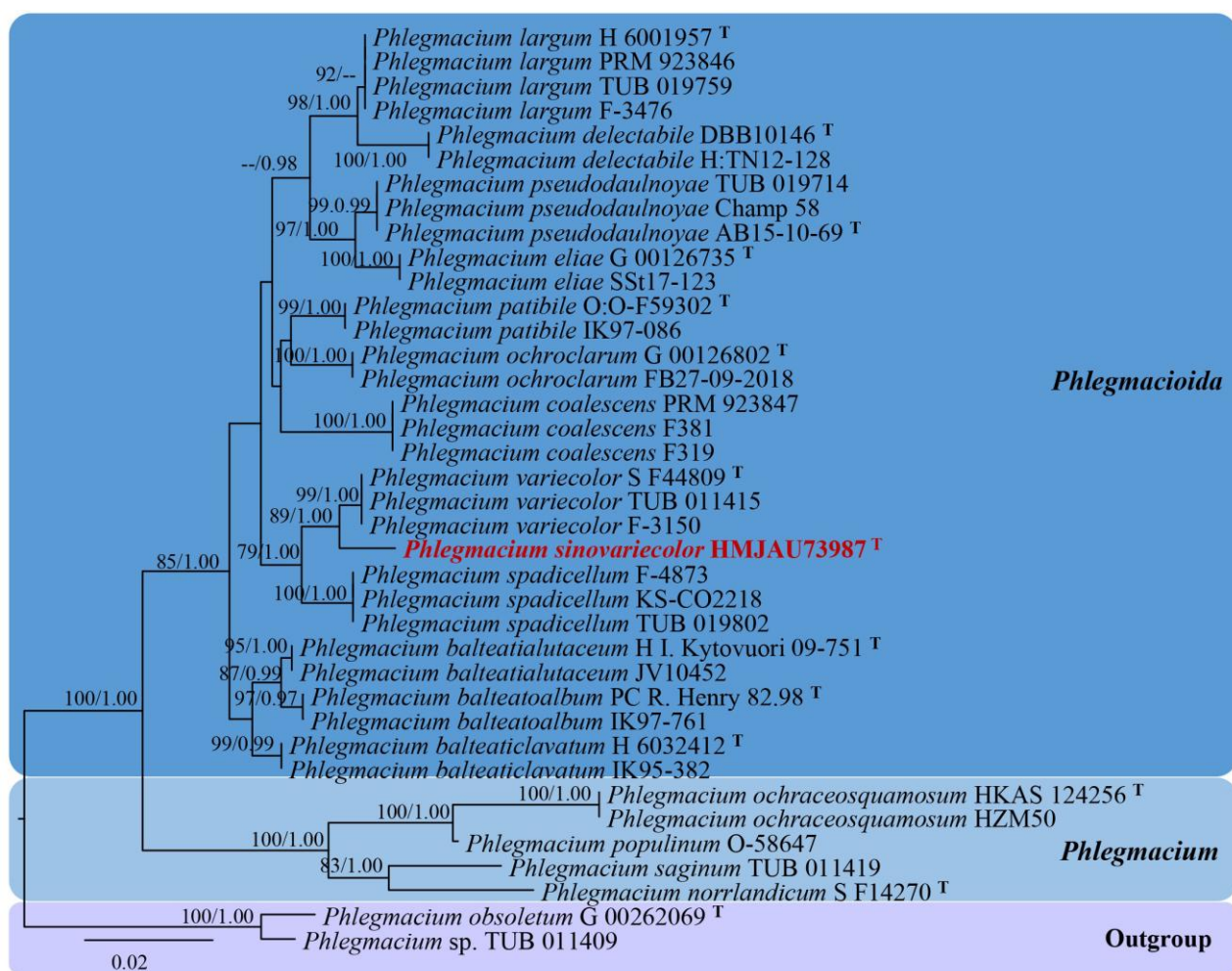


Figure 22 – Phylogram generated from maximum likelihood analysis based on ITS sequence data. Thirty-eight specimens were included in the sequence analyses, which comprised 643 characters with gaps. Single gene analysis was performed. *Phlegmacium obsoletum* (NR130313) and *Phlegmacium* sp. (AY174791) of section *Obsoleta* were used as the outgroup taxa. The final ML optimization likelihood is -1898.841. The matrix included 186 distinct alignment patterns, with 8.67% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 75%, BYPP equal to or greater than 0.95 are given above or below the nodes. The specimen from the current study is in red-bold, and the type specimens are indicated with ^T.

Etymology – The name refers to the affinity of new species to *Phl. variecolor* and the type location, China.

Pileus 1.9–4.8 cm in diam., hemispherical at first, then convex to expanded, margin involuted at first, bluish to somewhat violet at first, later light brown to brown, viscid, very finely innately fibrillose. **Lamellae** emarginate, moderately crowded, bluish grey at first, turns light brown with age, edge even. **Stipe** 2.5–4 cm long, 0.4–0.8 cm thick at apex, slightly expanded at the base, bluish, surface cover with white fibrillose, later yellowish brown, basal mycelium white. **Context** white with bluish tinge, up to 8 mm at the center of the pileus. **Basidiospores** 9.2–10.6 × 4.9–6.1 μm, Q = 1.59–2.12, X_{av.} = 9.9 × 5.4 μm, Q_{av.} = 1.83, amygdaloid, moderately to fairly strongly and densely verrucose. **Cystidia** absent. **Pileipellis** epicutis 90–110 μm thick, with a weak gelatinous layer, 70–90 μm thick, hyphae 2.8–8.8 μm wide, yellowish brown to brown in 5% KOH, at surface with distinctly zebra-striped encrusted. **Hypodermium** present, hyphae 6.3–23 μm wide, somewhat isodiametric to more or less subcellular, pale yellowish to almost colorless in 5% KOH. **Clamp connections** present.

Ecology and distribution – In mixed forests with *Quercus* and *Pinus* trees of subtropical China.

Material examined – China, Anhui Province, Jinzhai County, Dabie Mountains, in mixed forest with *Quercus* and *Pinus* trees, 22 September 2023, Meng-Le Xie, (HMJAU73987, holotype).

GenBank accession numbers – ITS: PV682771.

Notes – The phylogenetic analysis revealed that our specimen, *Phl. sinovariicolor* (HMJAU73987) grouped within section *Phlegmacioida*, forming a separate lineage sister to *Phl. varicolor* (S F44809, TUB011415, F-3150), with 89% ML and 1.00 BYPP bootstrap support (Fig. 22). Nucleotide differences (excluding gaps) between our specimen and *Phl. varicolor* (type collection) revealed that the ITS region has 11/607 bp difference (1.81%). *Phlegmacium sinovariicolor* shares similar morphologies to *Phl. varicolor*. *Phlegmacium varicolor*, however, with a bigger basidiomata, usually > 5.0 cm in diam., and the stipe usually >1.0 cm thick, the basidiospores usually bigger and narrower, $X_{av.} = 10.6 \times 6.0 \mu\text{m}$, $Q_{av.} = 1.77$, and this species is commonly found in boreal and montane regions (Bidaud et al. 1996, Saar 2010, Saar et al. 2022). Based on morphology and molecular phylogenetic evidence, we conclude that *Phl. sinovariicolor* is a new species collected from Anhui Province, China.

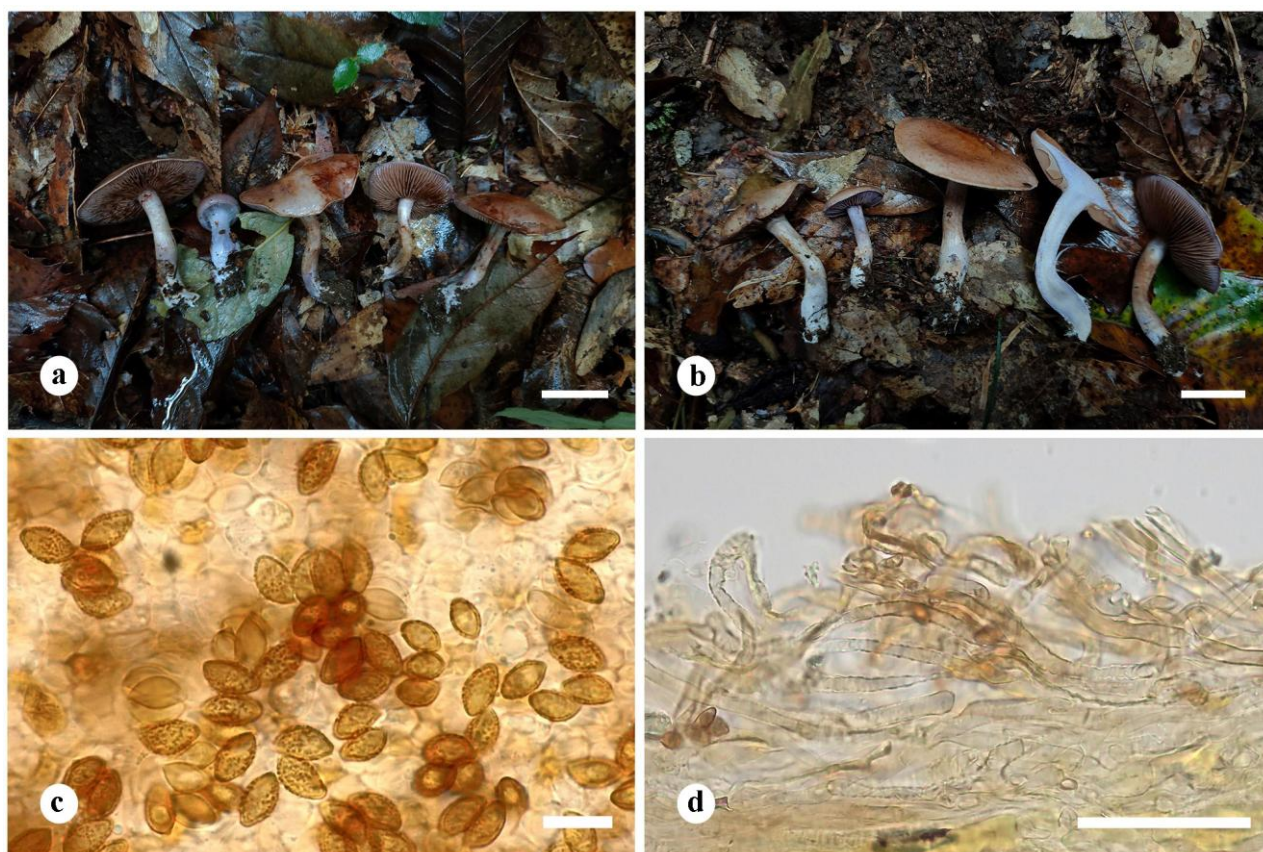


Figure 23 – *Phlegmacium sinovariicolor* (HMJAU73987, holotype). a, b Basidiomata. c Basidiospores. d Epicutis of the pileipellis. Scale bars: a, b = 2 cm, c = 10 μm , d = 50 μm .

Crepidotaceae (S. Imai) Singer

Crepidotus (Fr.) Staude

Index Fungorum number: IF 17403; Facesoffungi number: FoF 17770

Notes – *Crepidotus* was initially introduced under *Agaricus* by Fries (1821), and later Staude (1857) raised it to the generic level with the type species *Cr. mollis* (Donk 1949, Consiglio et al. 2008, He et al. 2019, Na et al. 2022). *Crepidotus* has a worldwide distribution, mostly on decaying wood. The genus is characterized by pleurotoid, semicircular, flabelliform, reniform, or spathuliform basidiomata with an underdeveloped stipe and dark-colored basidiospores, which are

categorized into smooth and ornamented, the presence of cheilocystidia but lack pleurocystidia (Kumar et al. 2020, Na et al. 2022). Recently, advances in molecular techniques, combined with intensified fieldwork by taxonomists and researchers, have led to the discovery of numerous new species commonly characterized through morphological and phylogenetic analyses. A total of 591 epithets are listed under *Crepidotus* in Index Fungorum (2025), approximately 400 species are accepted (<https://indexfungorum.org/Names/Names.asp>, accessed on 16 June 2025), and more than 1,000 sequences of *Crepidotus* are deposited in GenBank (<https://ncbi.nlm.nih.gov/genbank/>, accessed on 16 June 2025), containing 106 identified species. In this study, we introduce *Crepidotus pusillus* sp. nov. found on decaying wood from China, based on the multi-gene phylogenetic evidence (Fig. 24) and morphological characteristics (Fig. 25).

Crepidotus pusillus W.H. Lu & Karun., sp. nov.

Fig. 25

Index Fungorum number: IF 859343; Facesoffungi number: FoF 18605

Diagnosis – The new species differs from the close relative *C. herrerae* by having smaller basidiospores and clavate cheilocystidia.

Etymology – The specific epithet *pusillus* is a Latin adjective, meaning “very small” or “minute”. The name refers to the holotype's notably tiny basidiomata.

Pileus 4–7 mm broad, in young stage spatuliform, rounded reniform to suborbicular, light yellow (4A4-5) to greyish yellow (4C5), when matured fan-shaped, shell-shaped, reniform to suborbicular, pale yellow (4A4) to greyish yellow (4C5), margin wavy or involute, dry, attached laterally or dorsally to the substratum, absence of villi near the point of attachment. *Lamellae* less than 1 mm broad, L = 14–19, l = 1–4, dense, decurrent from a lateral point of attachment. *Stipe* absents or rudimentary lateral. *Context* thin (<3 mm thick), pale yellow (4A3). Odor and taste not distinctive. *Basidiospores*, 5.8–8.0(8.5) × (4)4.5–5.9 µm, [$\bar{x}$ = 7.3 × 5.1, Q = 1.18–1.78, Q_m = 1.45], broadly ellipsoid to ellipsoid, ovoid, smooth, greyish yellow to olive brown in 5% KOH aqueous solution, slightly thick-walled. *Basidia* 18.5–23.5 × 8.0–11.1 µm, clavate, guttiform, hyaline, thin-walled, four-spored, rarely two-spored, sterigmata up to 4 µm long. *Pleurocystidia* absent. *Cheilocystidia* 14.8–22.2 × 10.4–13.6 µm, broadly turbinate to pyriform, rarely vesiculate, hyaline, thin-walled (<0.5 µm). *Pileipellis* a rectocutis composed of cylindric, parallel hyphae, occasionally interwoven, with terminal cells in some areas semierect and bundled. *Lamellar trama* subcylindrical to slightly inflated hyphae. *Clamp connections* present in all tissues. Colors are indicated based on the Kornerup color scale (Kornerup & Wanscher 1967).

Material examined – China, Yunnan Province, Honghe Hani and Yi Autonomous Prefecture, on decaying wood, 17 July 2024, Wenhua Lu, LWH055 (GMB-W1422, holotype); *ibid.*, LWH055b (GMB-W1423, isotype).

GenBank accession numbers – GMB-W1422: ITS = PV659481, GMB-W1423: ITS = PV659482.

Notes – In the multi-locus phylogeny, our species (GMB-W1422 and GMB-W1423) grouped within *Crepidotus*, forming a separate clade sister to *Cr. clavocystidiatus* (FFAAS1316 (holotype), FFAAS1317, FFAAS1318, FFAAS1319), with 89% ML and 0.95 BYPP bootstrap support (Fig. 24, section *Dochmiopus*). Nucleotide differences (excluding gaps) between our collection (GMB-W1422) and *Cr. clavocystidiatus* (FFAAS1316) revealed that the ITS region has a 39/677 bp difference (5.76%), while the LSU is not available for our specimen. Also, our collections share similar morphologies to *Cr. herrerae*, which lacks molecular data. It differs in the size of basidiomata (5–32 µm vs. 4–7 mm), spores (8.5–10.5 × 5–6 µm vs. 5.8–8.0 × 4–5.9 µm), and cheilocystidia with clavate to subclavate in *Cr. herrerae*. *Crepidotus clavocystidiatus*, *Cr. subfulviceps*, and *Cr. iqbalii* are closely related to the new species phylogenetically; however, these three species are presence of stipe and verrucose spores, and clavate cheilocystidia, which can be readily distinguished. Morphological comparison combined with the multi-locus phylogenetic analysis, allows us to establish our collection *Crepidotus pusillus* as a new species collected from Yunnan Province, China.

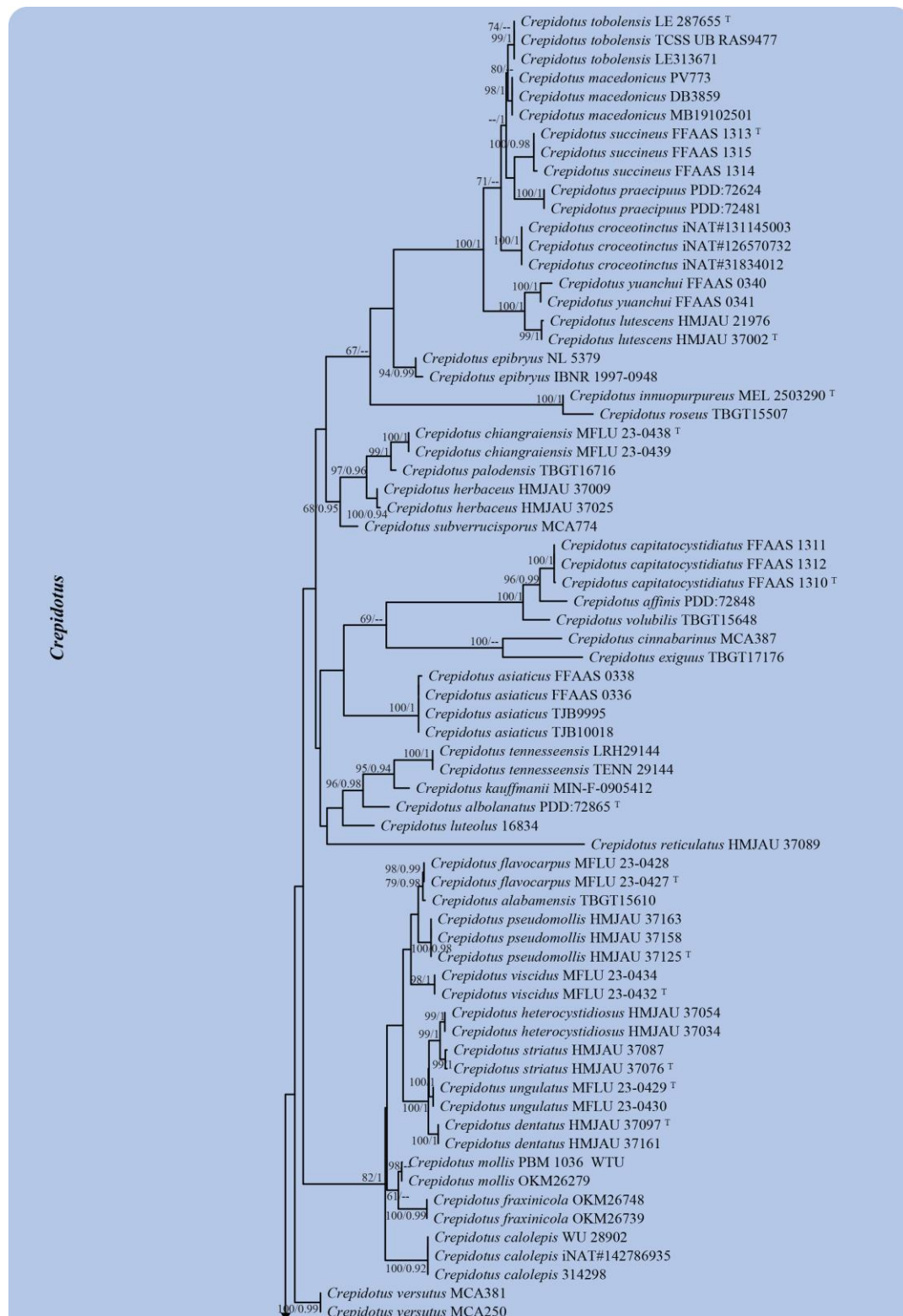


Figure 24 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. One hundred and forty specimens were included in the combined sequence analyses, which comprised 1,601 characters with gaps (ITS = 726, LSU = 875). *Neopaxillus echinospermus* (AH45884 and MPM 2886) and *N. dominicanus* (MCVE 26928) specimens were used as the outgroup taxa. The final ML optimization likelihood is -15304.471259. The matrix included 783 distinct alignment patterns, with 34.06% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 60%, BYPP equal to or greater than 0.90, are given above or below the nodes. The collections from the current study are in red-bold, and the type specimens are indicated with ^T.

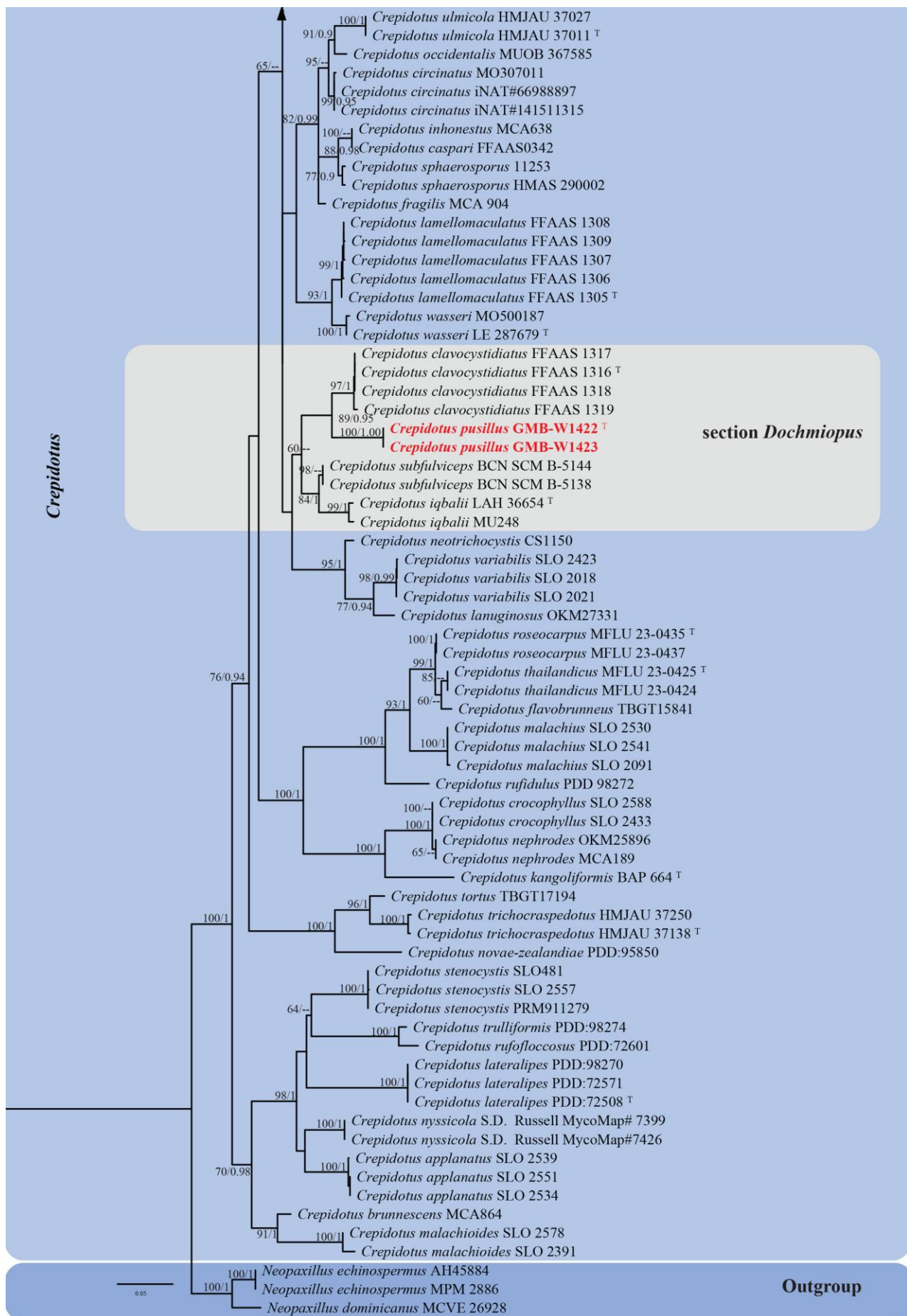


Figure 24 – Continue.

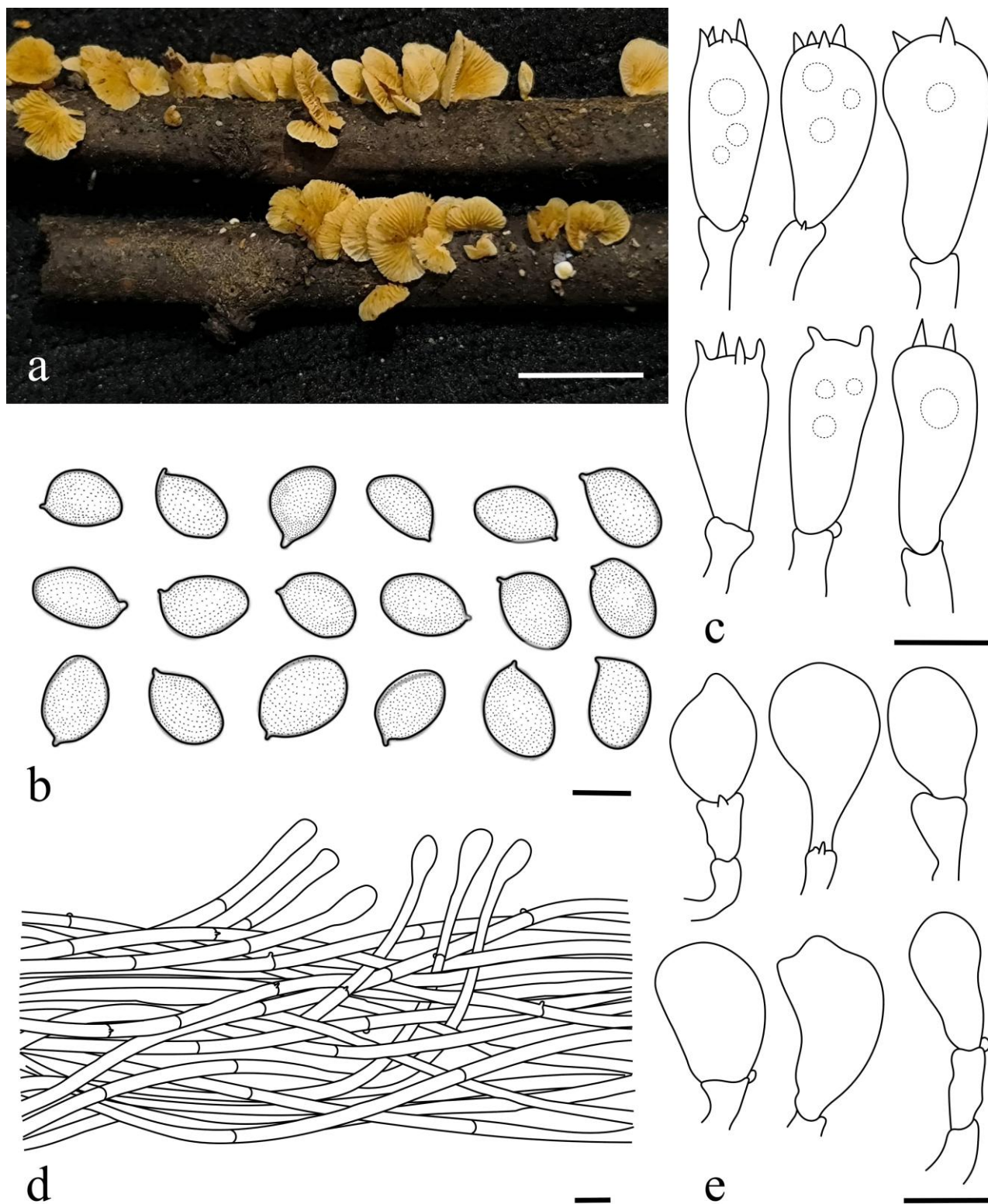


Figure 25 – Morphological features of *Crepidotus pusillus* (GMB-W1422, holotype). a Basidiomata. b Basidiospores. c Basidia. d. Pileipellis. e Cheilocystidia. Scale bars: a = 1 cm, b = 5 µm, c–e = 10 µm.

Inocybaceae Jülich

Inocybe (Fr.) Fr.

Index Fungorum number: IF 17848; Facesoffungi number: FoF 18606

Notes – *Inocybe* was introduced by Fries (1863) to accommodate *Inocybe relicina*. *Inocybe* is well-known for their ectomycorrhizal ecology (Matheny & Moreau 2009). The genus is

distinguished by the occurrence of cheilocystidia and typically also pleurocystidia, which often possess somewhat thickened walls; basidiomata are generally small and commonly brownish, featuring a pileus surface that can range from smooth to rimose, fibrillose, squamulose, or even squarrose in texture; lamellae gradually take on a brownish hue as they mature; a notable odor is frequently present; basidiospores smooth or nodulose in form, and pleurocystidia are usually thick-walled; cheilocystidia are consistently observed across the genus. (Kuyper 1985, Matheny & Swenie 2018, Bandini et al. 2022). *Inocybe* is a species-rich genus of *Agaricales* and more than 850 species have been described worldwide (Matheny & Swenie 2018). In this study, we introduce *Inocybe griseum* sp. nov., living on soil from China (Figs 26, 27).

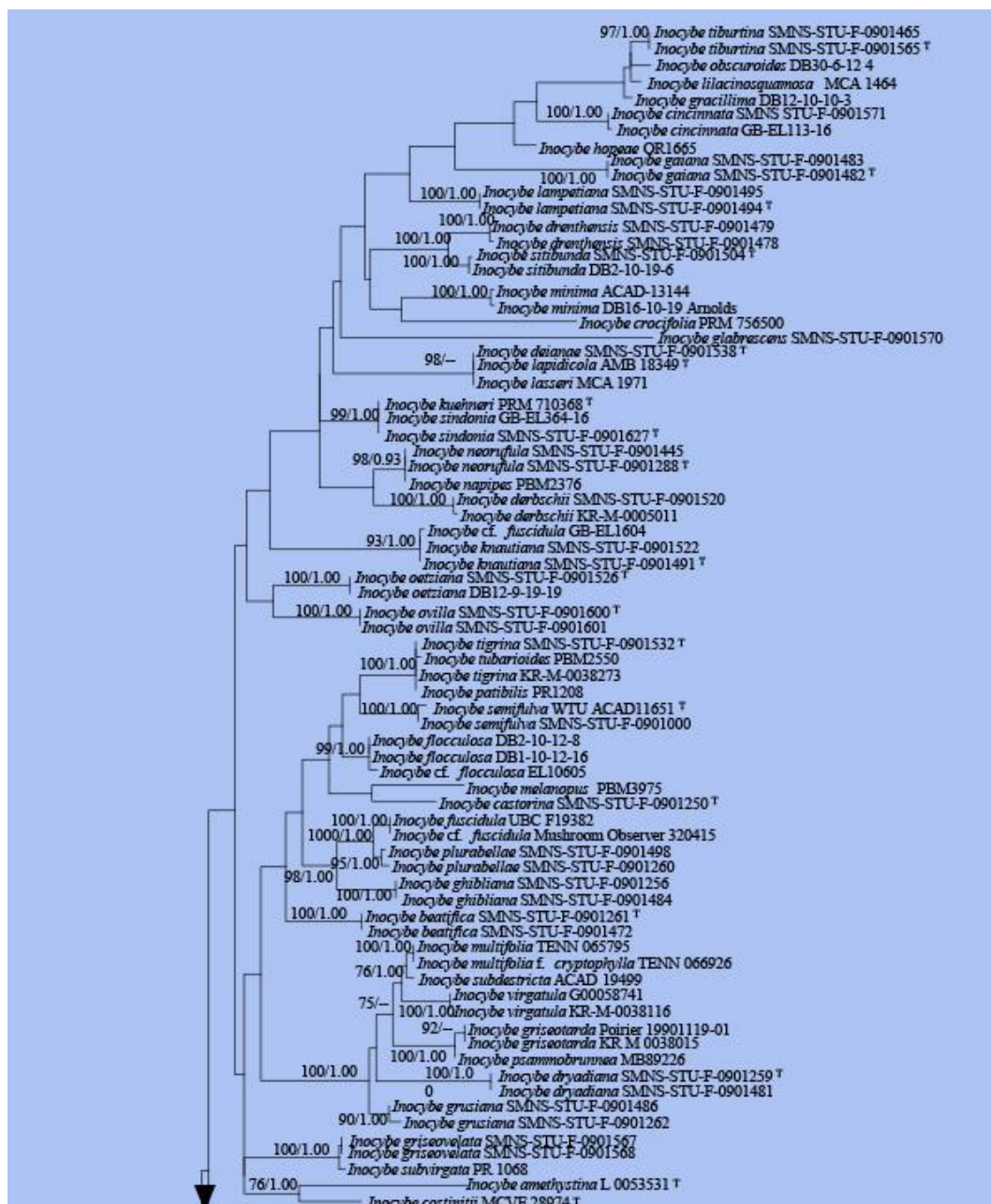


Figure 26 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Three hundred and twenty-nine specimens were included in the combined sequence analyses, which comprised 1637 characters with gaps (LSU = 922, ITS = 715). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. *Pseudosperma spurium* (UTC BK18089723) and (CBSJ 92017) specimens were used as the outgroup taxa. The final ML optimization likelihood is -43558.792575.

The matrix included 1046 distinct alignment patterns, with 42.97% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.90 are given above or below the nodes. The newly introduced sequences are indicated in red-bold, and the type collections are indicated with ^T.

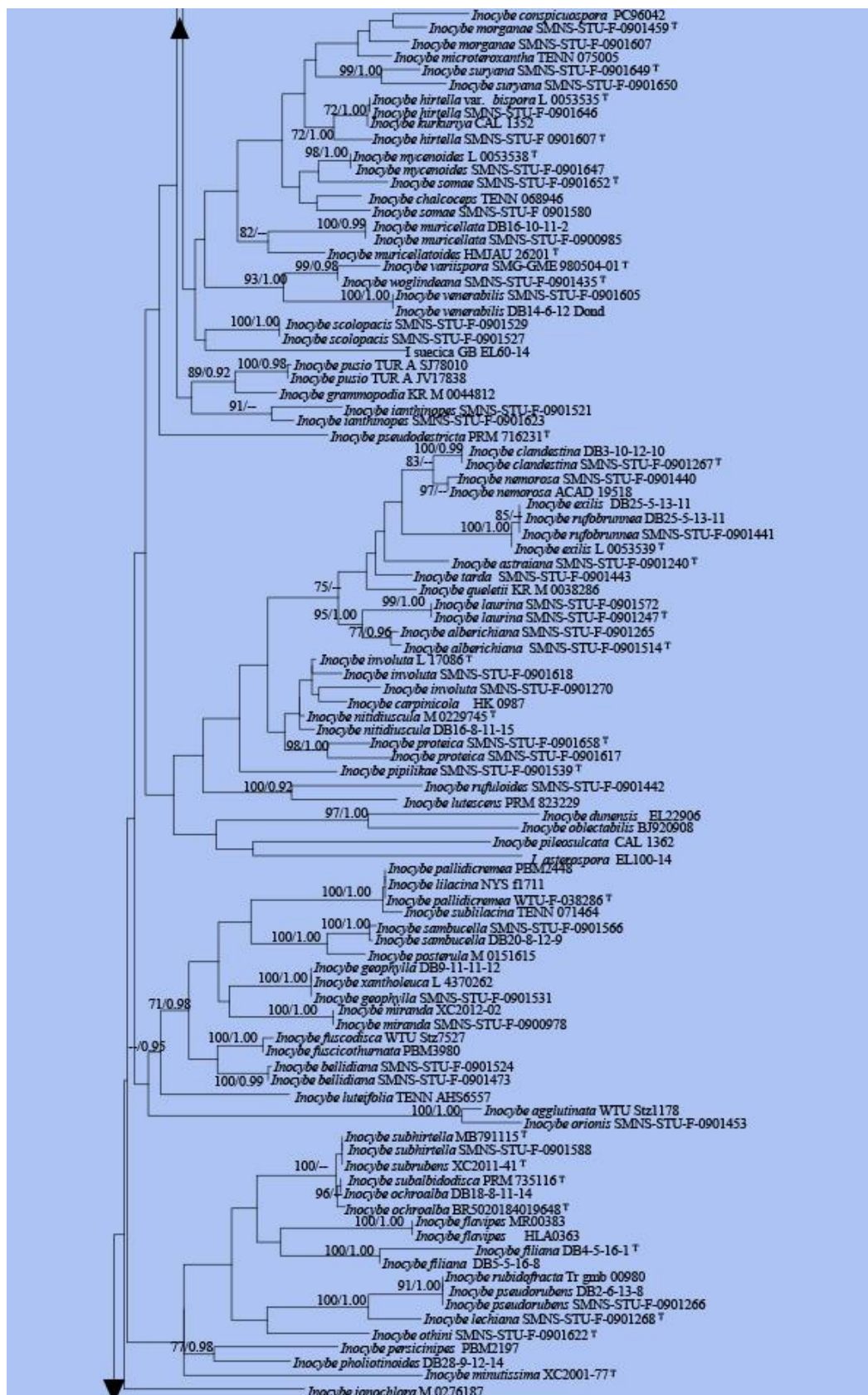


Figure 26 – Continue.



Figure 26 – Continue.



Figure 26 – Continue.

***Inocybe griseum* S.M. Tang & Z.L. Luo sp. nov.**

Fig. 27

Index Fungorum number: IF 903951; Facesoffungi number: FoF 18607

Diagnosis – Differs from other *Inocybe* species by the dark desaturated orange basidiomata, and abundant dark desaturated orange squama on the pileus and stipe surface, with a weakly angular to irregular with several obtuse nodules, apiculus small and indistinct basidiospores.

Etymology – The name “griseum” refers to this species pileus and stipe color are dark desaturated orange.

Basidiomata solitary. *Pileus* 10–20 mm wide, hemispherical, umbonate at centre, dark desaturated orange (#5d4030), abundant dark desaturated orange squama on the surface; inflexed, abundant filamentous of margin; pileus context whitish (#####) in the pileus when young, becoming dark desaturated orange with age. *Lamellae* crowded, 3–5 mm wide, desaturated dark red (#775c53), broadly ventricose, attachment adnexed, lamella edge even or entire. *Stipe* 20–35 × 3–5 mm, cylindrical or curved, solid, slightly widening towards the base, base even to slightly thickened, dark desaturated orange (#5d4030), floccules on the surface; pileus context whitish (#####) in the pileus when young, becoming dark desaturated red (#412220) with age. Color scales are based on <https://colorhexa.com/>). *Basidiospores* 7.9–12.4 × 5.9–9.7 μm av. 10.5 ± 1.1 × 7.3 ± 1.4 μm, Q = 1.5–2.1, av. 1.47 ± 0.21, smooth, thick-walled, weakly angular to irregular with several obtuse nodules, apiculus small and indistinct, yellow in 5% KOH solution. *Basidia* 40–48 × 10–14 μm, av. 45.3 ± 4.2 × 12.5 ± 1.0 μm, mostly 4-spored, rarely 2-spored, present clamp connections, colorless in 5% KOH solution. *Lamellae* edges composed of cheilocystidia and numerous colorless, 100–110 × 12–17 (–28) μm, av. 105 ± 4.1 × 15 ± 2.5 μm, mostly narrowly

utriform, rarely narrowly clavate or narrowly cylindrical, thin-walled, apex mostly obtuse, rarely capitate. *Pleurocystidia* 59–94 × 10–19 µm, av. 73 ± 13.1 × 15 ± 3.0 µm, mostly narrowly utriform, rarely narrowly clavate or narrowly cylindrical, thin-walled, apex mostly obtuse, rarely capitate, present clamp connections, colorless in 5% KOH solution. *Pileipellis* constituted by an epicutis made up of parallel hyphae 4–11 µm wide, thin-walled, with not or only faintly encrusting and parietal yellowish pigment. *Stipitipellis* a cutis of cylindrical, parallel, 5–7 µm wide, thin-walled, with not or only faintly encrusting and parietal yellowish pigment. *Caulocystidia* absent. *Clamp connections* abundant in all tissues.

Material examined – China, Yunnan Province, Dali Autonomous Prefecture, on soil, 23 July 2021, KaiYang Niu, Sjl825 (HKAS 148691, holotype); *ibid.*, 24 July 2021, ZhengQuan Zhang, Sjl831 (HKAS 148692, paratype).

GenBank accession numbers – HKAS 148691: ITS = PV746148, LSU = PV744525; HKAS 148692: ITS = PV746149, LSU = PV744526.

Notes – The initial BLAST results indicate that the sequences derived from the two specimens belong to the family *Inocybaceae*. Through BLAST searches using the ITS region, the closest species identified were *Inocybe* sp. (130822MFBPL0312, with a percentage identification of 94.82% and query cover of 100%) and *Inocybe perlucida* (DB20-8-16-33, with a percentage identification of 94.81% and query cover of 100%).

The multi-locus phylogeny revealed that our collections of *Inocybe griseum* (HKAS 148691 and HKAS 148692) grouped within *Inocybe* separately and formed a sister clade with *I. perlucida* (DB20.8.16.33) with 80% ML statistical support (Fig. 26). However, *I. perlucida* originally described from Switzerland as *I. pseudoasterospora* var. *mycenoides*, later, Bandini ascended *I. pseudoasterospora* var. *mycenoides* to a separate species based on ITS base difference (Bandini et al. 2020), morphologically, *I. perlucida* has thin piles context, thicker and longer stipe (Bandini et al. 2020). The distinct morphological characters, coupled with the significant genetic divergence observed within the clade, provide strong evidence that *I. griseum* represents a novel species collected from Yunnan Province, China.

***Omphalotaceae* Bresinsky**

***Gymnopus* (Pers.) Gray**

Index Fungorum number: IF 17703; Facesoffungi number: FoF 18608

Notes – *Gymnopus* was classified into *Omphalotaceae* with the type species *Gy. fusipes* (He et al. 2019, Feng et al. 2025). Morphologically, the basidiomata of this genus are typically marasmioid, occasionally collybioid, small in size, and often gregarious. The pileus is hemispherical to convex, eventually becoming applanate, sometimes depressed, or umbilicate; it may be smooth, striate, sulcate-striate, or occasionally furfuraceous. Lamellae are adnate to free, distant, occasionally with cross-veins, and sometimes form a pseudocollarium; their color ranges from white to brown. The stipe is filiform, cylindrical to occasionally fusiform, central or sometimes eccentric, and may be smooth, glabrous, tomentose, or pruinose; it can be insititious or not. Currently, there are four sections, namely, *Gy.* sect. *Androsacei*, *Gy.* sect. *Gymnopus*, *Gy.* sect. *Impudicae*, and *Gy.* sect. *Levipedes* were accepted within *Gymnopus* (Oliveira et al. 2019, Petersen & Hughes 2021). This genus comprises more than 300 known species distributed worldwide (He et al. 2019) and holds significant economic and ecological importance (Wilson & Desjardin 2005). In this study, we introduce *Gymnopus linzhiensis* sp. nov., found associated with fallen pine-needles from China, belonging to sect. *Impudicae*, based on multi-gene phylogenetic evidence (Fig. 28) and morphological characteristics (Fig. 29).

***Gymnopus linzhiensis* R.L. Zhao, B. Cao & X.X. Han, sp. nov.**

Fig. 29

Index Fungorum: IF 572834; Facesoffungi number: FoF 17938

Diagnosis – Similar to *Gy. similis*, but differs by the slightly shorter spores (5.82–7.47 µm in length, $Q_m = 2.07$) and smaller cheilocystidia (25.1–33.2 × 4.2–6.0 µm).



Figure 27 – *Inocybe griseum* (HKAS 148691, holotype). a Front view. b Side view of context. c Cheilocystidia. d. Pleurocystidia. e Basidia. f Basidiospores. g Stipitipellis. h Pileipellis. Scale bars: a, b = 1 cm, c–h = 10 µm.

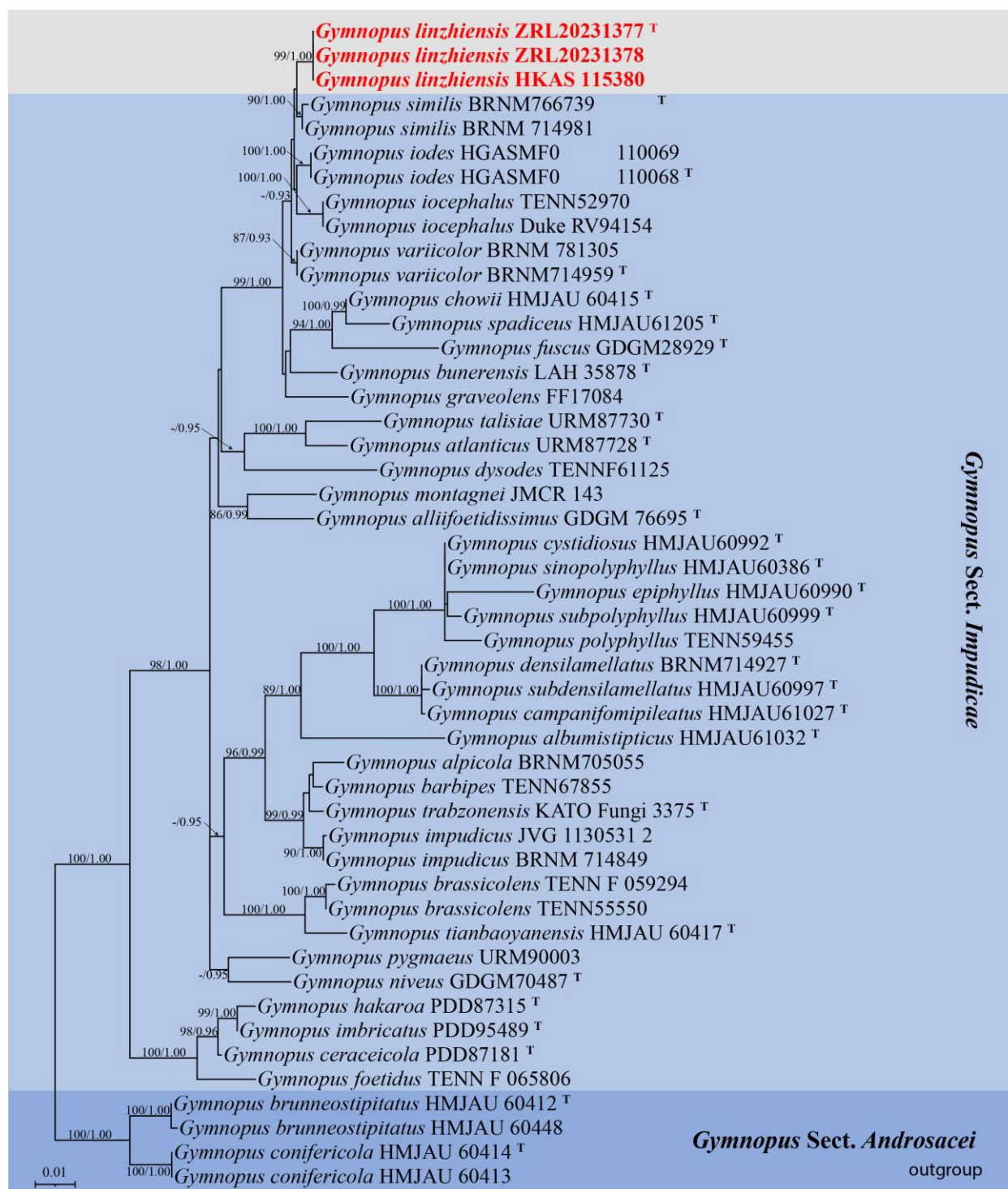


Figure 28 – Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Forty-eight specimens were included in the combined sequence analyses, which comprised 1808 characters with gaps (LSU = 996, ITS= 812). *Gymnopus brunneostipitatus* (HMJAU 60412 and HMJAU 60448) and *Gy. conifericola* (HMJAU 60413 and HMJAU 60414) specimens were used as the outgroup taxa. The final ML optimization likelihood is -6714.537682. The matrix included 536 distinct alignment patterns, with 26.98% of undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 80%, BYPP equal to or greater than 0.90 are given above or below the nodes. The specimens obtained from the current study are in red-bold, and the type specimens are indicated with ^T. Sample labels of the new species and its phylogenetically related species are provided in the order of county name followed by herbarium no./ collection no.

Etymology – Referring to the city “Linzi”, where the holotype was collected.

Basidiomata in pairs or scattered in coniferous forest. *Pileus* 9–45 mm diam., convex to conico-convex when young, plano-convex to applanate when mature, usually with a slightly depressed center, not hygrophanous, sulcate-striate up to 2/3 from margin at maturity, with an involute, irregularly crenulate margin, greyish yellow (4C5) to olive brown (4D8) at the center, yellowish grey (4B2) to blond (4C4) at the edge, usually becomes paler towards the margin. *Context* thin and slightly fragile. *Lamellae* moderately distant, narrowly adnate to adnexed, pale yellow (4A3) to greyish yellow (4C7). *Stipe* 2.7–6.5 × 0.2–0.6 cm, cylindrical, hollow, slightly tapering towards the base, with a surface covered with entirely dirty white tomentose when young, usually tomentose when old, pale orange (5A3) to yellowish brown (5E8). *Odor* and taste are undocumented. *Basidiospores* [n = 30] (5.20)5.82–7.47(8.34) × (2.50)2.86–3.53(3.70) µm, average 6.65 × 3.19 µm, Q = 1.87–2.28, Q_m = 2.07 (±0.21), narrowly ellipsoid to oblong, sometimes sublacrimoid, smooth, thin-walled. *Basidia* [n = 25] (20.5)21.7–27.2(34.1) × (5.6)5.8–6.6(6.9) µm, clavate, hyaline, 2 or 4-spored. *Cheilocystidia* [n = 50] (20.0)25.1–33.2(39.7) × (2.9)4.2–6.0(7.2) µm, numerous, cylindrical, narrowly clavate, irregular, forked, rostrate, or coralloid at the apex, thin-walled. *Pleurocystidia* absent. *Pileipellis* a cutis composed of cylindrical, thin to slightly thick-walled, smooth, or occasionally slightly incrusted hyphae; terminal cells cylindrical, fusoid to subclavate, often irregular, with projections or branched. *Stipitipellis* a cutis composed of cylindrical, parallelly arranged, hyaline, thin-walled hyphae. *Caulocystidia* not observed. *Clamp connections* present but not in all hyphae.

Material examined – China, Xizang Autonomous Region, Linzi City, Zayu County, Zhuwagan Town, N 28°34'52" E 97°6'53", 1622 m asl, on the ground associated with pine-needles (*Pinaceae*), 10 August 2023, Xi-Xi Han, Yan-Yan Zheng, ZRL20231377 (HMAS 288012, holotype); *ibid.*, ZRL20231378 (HMAS 288013, isotype).

GenBank accession numbers – ZRL20231377: ITS = PV815626, LSU = PV815628; ZRL20231378: ITS = PV815625, LSU = PV815629.

Notes – The combined phylogenetic analyses of ITS+nrLSU (Fig. 28) revealed that the samples of our species *Gymnopus linzhiensis* (ZRL20231377, ZRL20231378, HKAS11580) grouped within *Gymnopus*, forming a separate clade sister to *Gy. similis* (BRNM766739, BRNM714981). Additionally, our specimens are phylogenetically closely related to *Gy. iodes* and *Gy. iocephalus*. However, *Gy. similis* from Korea, differs by the ochraceous-gray, brownish orange or brownish red pileus, garlic-like smell, slightly longer spores (6.5–8.0 × 2.7–4.0 µm) and larger cheilocystidia (20–65 × 5–9 µm) (Ryoo et al. 2016). While *Gy. iodes* from China is characterized by its garlicky basidiomata, violet-like pileus and slightly wider spores (5.5–7.5 × 3–4.0 µm) (Li et al. 2022), and *Gy. iocephalus* from the USA differs by the pileipellis hyphae turning blue in KOH and the hymenium lacking cheilocystidia (Halling 1983). The sequence divergence between *Gy. linzhiensis* and *Gy. similis* (BRNM766739) further supports their distinct species, with a variation of 1.59% (10/629 bp, gaps included) in the ITS sequence.

***Physalacriaceae* Corner**

***Cylindrobasidium* Jülich**

Index Fungorum number: IF 17430; Facesoffungi number: FoF 18346

Notes – *Cylindrobasidium* is a corticioid genus, was introduced by Jülich et al. (1974) to accommodate *Cylindrobasidium laeve* (= *Cy. evolvens*) as its type (Burt 1926, Chamuris 1984). *Cylindrobasidium* was identified as a genus containing a white rot species (Ginns & Lefebvre 1993, Kinnunen et al. 2017), however some species have been reported as saprophytic on dead wood (Sonjak et al. 2007, Lin et al. 2021). However, Floudas et al. (2015) revealed that some species of this genus belong to a new type of rot, have been reported as the associates of the Eurasian spruce bark beetle (Harrington et al. 2021). *Cylindrobasidium* is characterized by having cream or pinkish-buff, effused to effused-reflexed basidiomata, a monomitric hyphal system with clamped generative hyphae, presence of subicular and/or hymenial cystidia that are usually cylindrical or fusiform, clavate to narrowly clavate basidia, and pyriform-like basidiospores usually gluing together.

Besides, the hyphae, cystidia, basidia, basidiospores, or at least some of them, are often cyanophilous. In this study, we introduce *Cylindrobasidium subbifidum* sp. nov. found on wood from China, based on the ITS sequence data (Fig. 30) and morphological characteristics (Fig. 31).

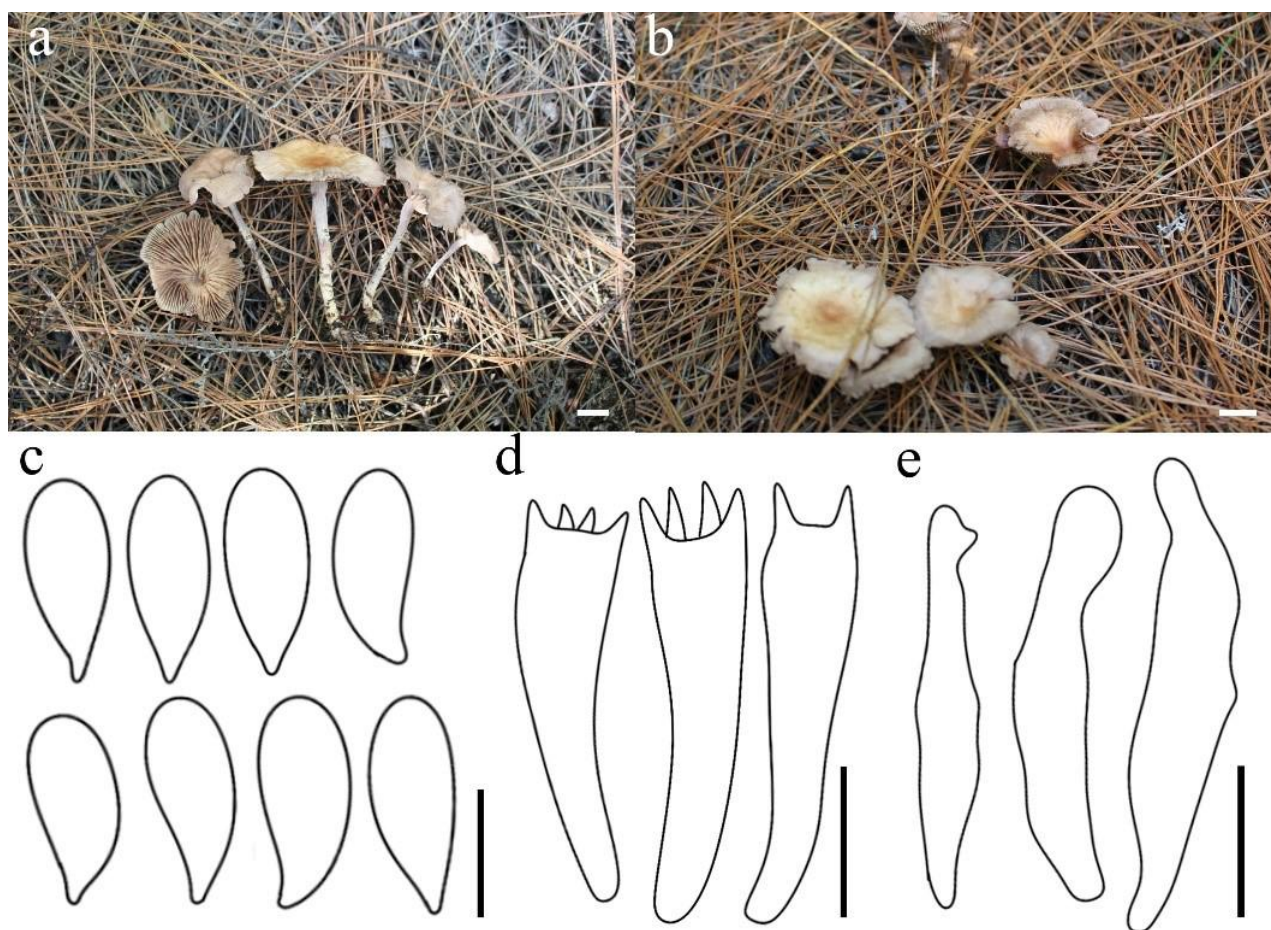


Figure 29 – *Gymnopus linzhiensis* (ZRL20231377, holotype). a, b Basidiomata. c Basidiospores. d Basidia. e Cheilocystidia. Scale bars: a–b = 10 mm, c = 5 µm, d–e = 10 µm.

Cylindrobasidium subbifidum Y.T. Yang & H.M. Zhou, sp. nov.

Fig. 31

Index Fungorum number: IF 904403; Facesoffungi number: FoF 18347

Diagnosis – Differs from other species by the resupinate basidiomata with white to cream hymenial surface, a hyphal system monomitic with clamped generative hyphae, cylindrical to ellipsoid basidiospores measuring $(4.6\text{--}5.0\text{--}5.4\text{--}5.5) \times (2.8\text{--}3.0\text{--}3.2\text{--}3.5)$ µm.

Etymology – *subbifidum* (Lat.): referring to the new species being similar to *Cylindrobasidium bifidum*.

Basidiomata annual, resupinate, adnate, membranous, firstly punctate, later fusing together, without odor and taste when fresh, up to 8 cm long, 1.5 cm wide, 150 µm thick. **Hymenial surface** tuberculate, white to cream when fresh, becoming cream upon drying; Sterile margin white, thinning out, up to 1 mm wide. **Hyphal system** monomitic; generative hyphae with clamp connections. **Subiculum** with dense texture, 70–150 µm thick; generative hyphae, branched, interwoven, gradually vertical toward hymenial layer, thin- to slightly thick-walled, colorless, 2–4 µm in diam., usually covered by crystals in subiculum, IKI–, lightly CB+; tissues unchanged in KOH. **Hymenial layer** 25–45 µm thick, subiculum hyphae more or less vertical, colorless, flexuous, 1.5–3 µm in diam., thin-walled. **Cystidia** of two kinds: (1) hymenial cystidia occasional, with bifurcate apices, thin-walled, $18\text{--}22 \times 4\text{--}6$ µm, CB+; (2) metuloid cystidia numerous, fusiform, thin-walled, $17\text{--}30 \times 6.5\text{--}9$ µm, slightly CB+. **Basidia** narrowly clavate, 4-sterigmate, $15\text{--}20 \times 4\text{--}5.5$ µm. **Basidiospores** cylindrical to ellipsoid, smooth, thin-walled, colorless, with homogenous

contents, IKI–, slightly CB+, (4.6–)5.0–5.4(–5.5) × (2.8–)3.0–3.2(–3.5) μm, L = 5.18 μm, W = 3.16 μm, Q = 1.64 (n = 30/1).

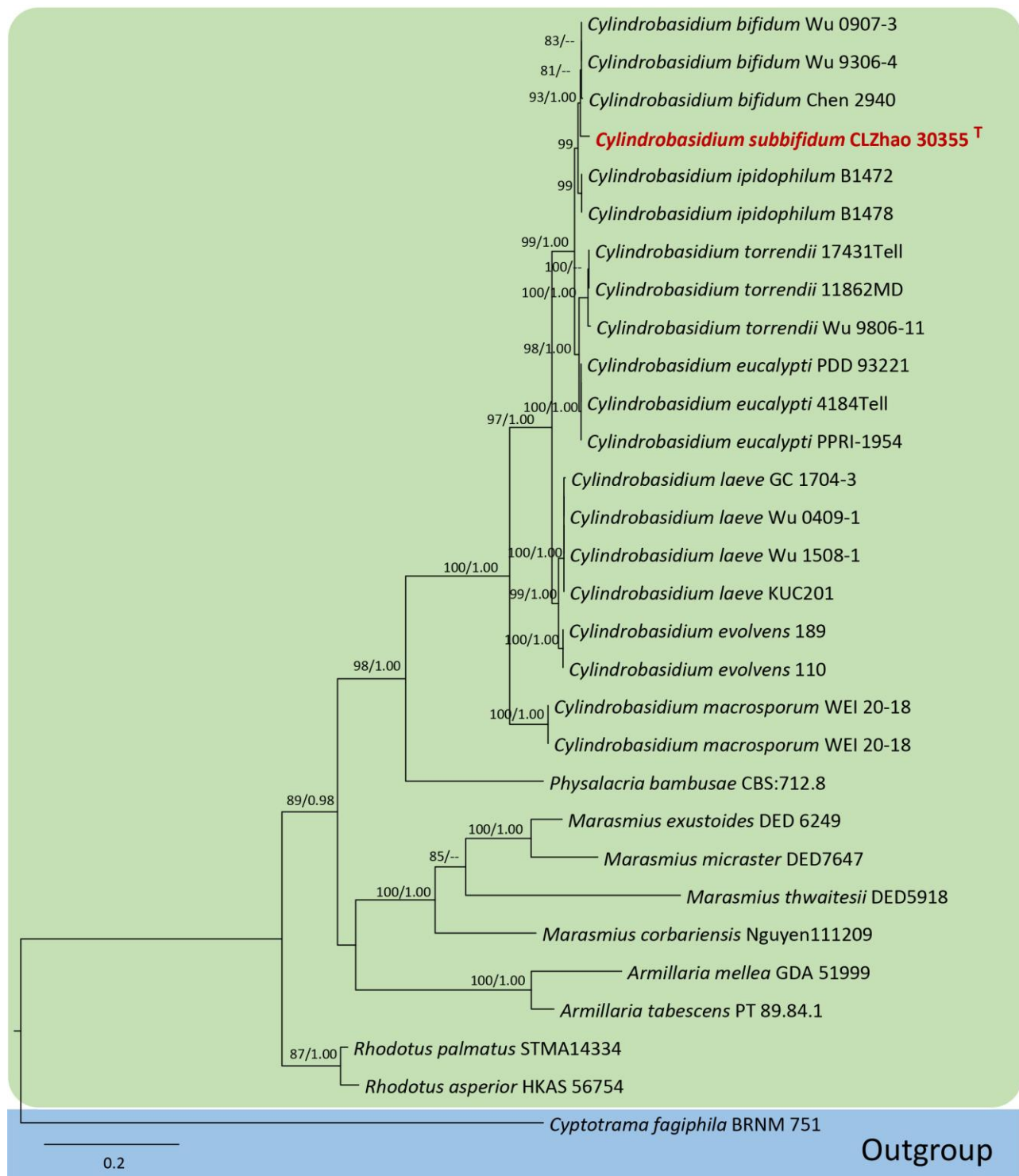


Figure 30 – Phylogram generated from maximum likelihood analysis based on ITS sequence data. Thirty specimens were included in the combined sequence analyses, which comprised 919 characters with gaps. *Cyptotrama fagiphila* (BRNM 751) was used as the outgroup. The final ML optimization likelihood is -5990.441. The alignment dataset includes 523 distinct patterns, 158 singleton sites and 419 constant sites. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.95 are given above or below the nodes. The taxon from the current study is in red-bold, and the type specimen is indicated with ^T.

Material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, on the fallen angiosperm branch, leg. C.L. Zhao, 19 July 2023, CLZhao 30355 (SWFC, holotype).

GenBank accession numbers – ITS: MW413326.

Notes – In the phylogeny, our new collection *Cylindrobasidium subbifidum* (CLZhao 30355) grouped within *Cylindrobasidium*, forming a separate lineage sister to *Cy. bifidum* (Wu 0907-3, Wu 9306-4, and Chen 2940) with 93% ML and 1.00 BYPP bootstrap support (Fig. 30). Phylogenetically, our collection shares similar morphologies to *Cy. bifidum* in having cream and adnate basidiomata, but the latter has wider basidiospores (3.6–4.2 μm vs. 3.0–3.2 μm , Lin et al. 2021). Thus, based on morphology and phylogenetic evidence we conclude our collection is a new species, *Cylindrobasidium subbifidum* collected from Yunnan Province, China.

Atheliales Jülich

Atheliaceae Jülich

Athelopsis Oberw. ex Parmasto.

Index Fungorum number: IF 17121; Facesoffungi number: FoF 18419

Notes – *Athelopsis* was introduced by Parmasto (1968) and was typified by *At. glaucina* ($\equiv$ *Corticium glaucinum*) found on dead wood of *Castanea stiva* in France. The genus is characterized by the pellicular basidiomes, with yellowish or green tints and ellipsoid, allantoid to cylindrical basidiospores (Bernicchia & Gorjón 2010, Gorjón et al. 2011, Liu et al. 2024). *Athelopsis* is similar to *Athelia* in micromorphology, but differs in its basidia arranged in a compacted layer (Bernicchia & Gorjón 2010, Gorjón et al. 2011, Liu et al. 2024). Currently, there are 17 species of *Athelopsis* listed in Species Fungorum (2025) and only two species have molecular data (GenBank 2025). In this study, *A. albofarinaceus* sp. nov. was introduced from China based on the ITS+nLSU sequence data (Fig. 32) and morphological characteristics (Fig. 33).

Athelopsis albofarinaceus Q. Yuan & C.L. Zhao, sp. nov.

Fig. 33

Index Fungorum number: IF 904404; Facesoffungi number: FoF 18420

Diagnosis – Differs from other *Athelopsis* species by the farinaceous basidiomata, smooth hymenial surface, a monomitic hyphal system with clamped generative hyphae and cylindrical basidiospores measuring 12.5–16 $\times$ 3–4 μm .

Etymology – *albofarinaceus* (Lat.): referring to the white hymenial surface with farinaceous hymenophore.

Basidiomata annual, resupinate, effused, thin, loosely adnate, farinaceous, without odor and taste when fresh, and up to 7 cm long, 2 cm wide, 50–100 μm thick. *Hymenial surface* smooth, whitish to grayish when fresh, turn to white upon drying. Sterile margin thinning out, concolorous. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, 2.5–4.5 μm in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* tapering, colorless, thin-walled, 22–37.5 $\times$ 5.5–7.5 μm . *Basidia* subclavate, with 4 sterigmata and a basal clamp connection, 17.5–24.5 $\times$ 7–8.5 μm . *Basidioles* dominant, similar to basidia in shape, but slightly smaller. *Basidiospores* cylindrical, colorless, thin-walled, smooth, CB–, IKI–, 12.5–16(–17) $\times$ 3–4(–4.5) μm , L = 14.24 μm , W = 3.62 μm , Q = 3.93 (n = 30/1).

Material examined – China. Yunnan Province, Zhaotong, Wumeng Mountain National Nature Reserve, GPS coordinates 27°77' N, 104°29' E, altitude 2900 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 25 August 2023, CLZhao 31353 (SWFC, holotype).

GenBank accession numbers – ITS: PV254829, LSU: OQ411117.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 32) revealed that our species *Athelopsis albofarinaceus* (CLZhao 31353) grouped with the other *Athelopsis* taxa, forming a separate lineage in a monophyletic clade, with 100% ML and 1.00 BYPP bootstrap support. *Athelopsis albofarinaceus* resembles *At. glaucina* and *At. subglaucina* in having cylindrical basidiospores. However, *At. glaucina* (type species) can be distinguished from *At. albofarinaceus* by its pellicular hymenophore, and its smaller basidia (12–13 $\times$ 6–6.5 μm , Ginns 1982). Also,

At. subglaucina differs from *At. albofarinaceus* due to its smaller basidia ($14\text{--}16 \times 6\text{--}7\text{ }\mu\text{m}$) and its small basidiospores ($8.5\text{--}10 \times 2.5\text{--}3\text{ }\mu\text{m}$, Liu et al. 2024). Thus, based on morphology and multigene phylogenetic evidence, we introduce *At. albofarinaceus* as a new species, collected from Yunnan Province, China.

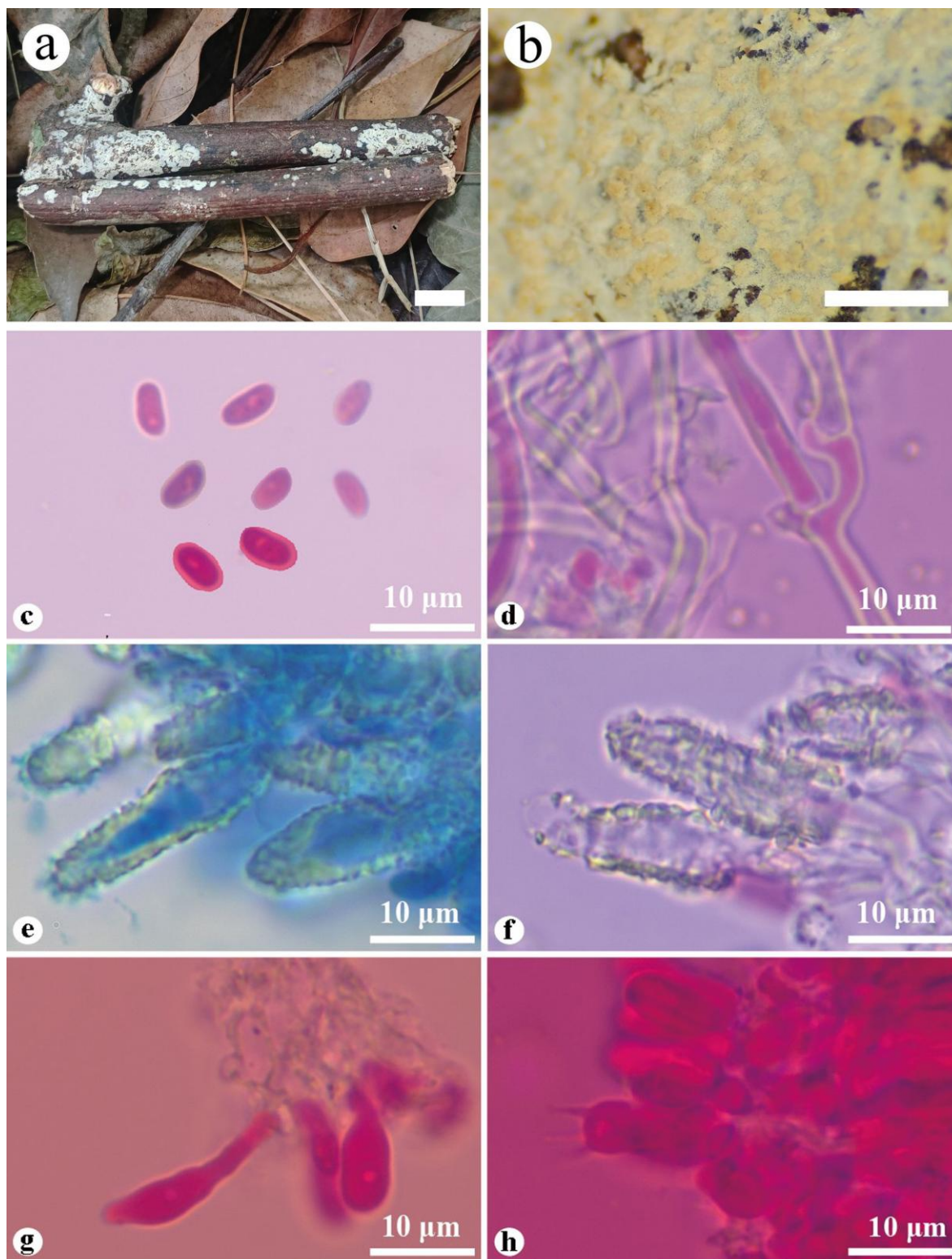


Figure 31 – Basidiomata and microscopic structures of *Cyindrobasidium subbifidum* (CLZhao 30335, holotype). a, The front view of the basidiomata on the host substrates. b Characteristic of hymenophore. c Basidiospores. d Hyphae. e, f Metuloid cystidia. g Hymenial cystidia. h A cross-section of basidiomata. Scale bars: a = 1 cm, b = 1 mm, c–h = 10 μm .

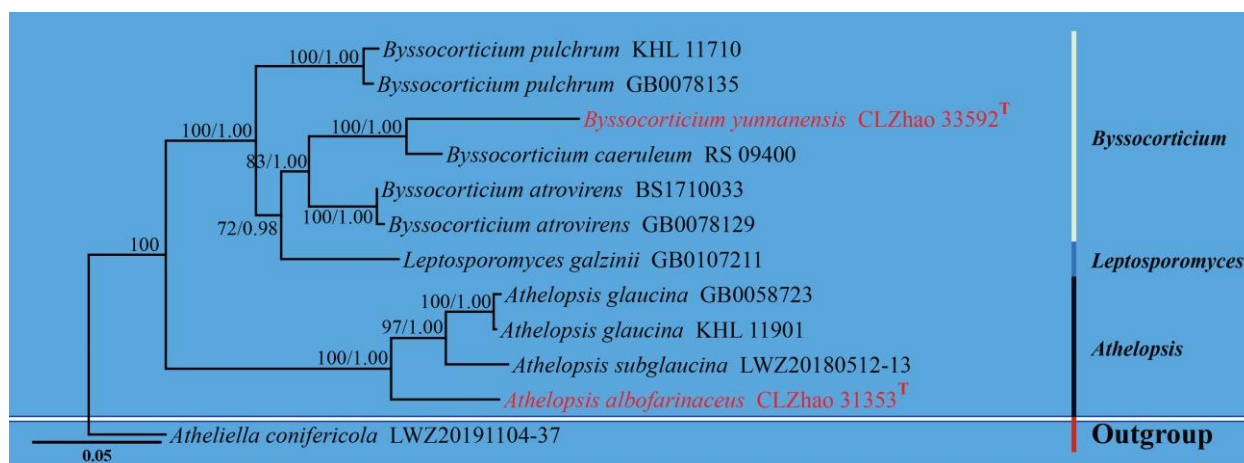


Figure 32 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and nLSU sequence data of *Byssocorticiaceae*. Twelve specimens are included in the combined analyses. The tree topology of the ML analysis is similar to the Bayesian analysis. The best RAXML tree with a final likelihood value of -6401.632 is presented. The evolutionary model GTR+GAMMA is applied for all the genes. The matrix had 537 distinct alignment patterns, with 26.22% of undetermined characters or gaps. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Atheliella conifericola* (LWZ20191104-37). Newly generated sequences are in red-bold and the type collections are indicated with ^T.

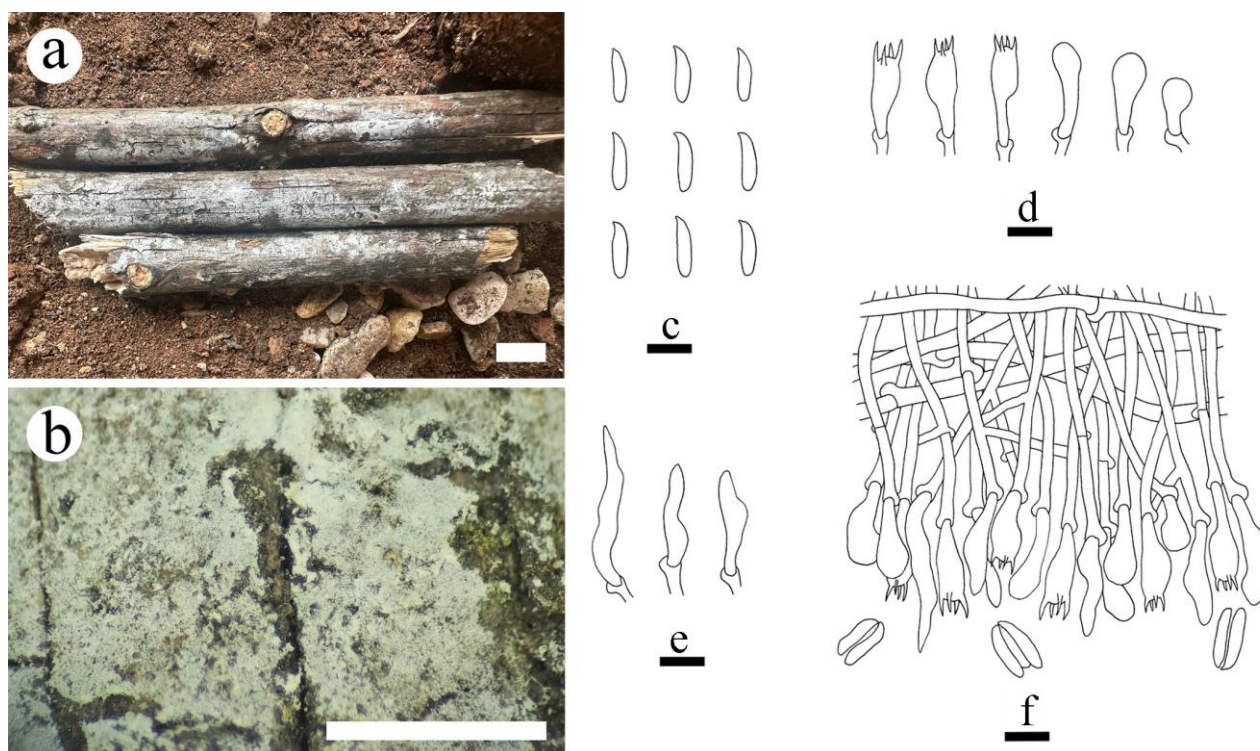


Figure 33 – Basidiomata and microscopic structures of *Athelopsis albofarinaceus* (CLZhao 31353, holotype). a, b Basidiomata on the host substrates. c Basidiospores, d Basidia and basidioles. e Cystidia. f A section of hymenium. Scale bars: a = 1 cm, b = 2 mm, c–f = 10 μm.

Byssocorticium Bondartsev & Singer

Index Fungorum number: IF 17207; Facesoffungi number: FoF 18421

Notes – *Byssocorticium* was typed by *By. atrovirens* and is characterized by the pellicular basidiomes, usually with bluish green or yellow and broadly ellipsoid to globose basidiospores

(Maekawa 2021). This genus is micro-morphologically similar to *Piloderma*, but differs in the total lack of clamps in the latter genus (Eriksson & Ryvarden 1973, Maekawa 2021, Liu et al. 2024). Currently, there are seven species of *Byssocorticium* accepted (Hyde et al. 2024d, Species Fungorum 2025) and three species with sequence data. In this study, we introduce *Byssocorticium yunnanense* sp. nov. collected on woody substrate from China, based on the ITS+nLSU sequence data (Fig. 32) and morphological characteristics (Fig. 34).

***Byssocorticium yunnanense* Q. Yuan & C.L. Zhao, sp. nov.**

Fig. 34

Index Fungorum number: IF 904405; Facesoffungi number: FoF 18422

Diagnosis – Differs from other *Byssocorticium* species by the soft, felt-like basidiomata, arachnoid hymenial surface, a monomitic hyphal system with simple septa, generative hyphae and global to ellipsoid basidiospores measuring $5\text{--}5.5 \times 4\text{--}5.5 \mu\text{m}$.

Etymology – *yunnanense* (Lat.): referring to the locality (Yunnan Province) of the type specimen.

Basidiomata annual, resupinate, soft, felt-like, loosely attached to the substrate, without odor and taste when fresh, and up to 5 cm long, 3 cm wide, 150–200 μm thick. *Hymenial surface* arachnoid, turquoise blue when fresh, turn to clay blue to dark ink-blue upon drying. Sterile margin blue, up to 1 mm wide. *Hyphal system* monomitic, generative hyphae with simple septa, colorless, thin-walled, rarely branched, 2–3.5 μm in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* absent. *Basidia* clavate, with 4 sterigmata and a basal simple septum, $16.5\text{--}32 \times 5\text{--}7.5 \mu\text{m}$. *Basidiospores* global to ellipsoid, colorless, thin-walled, smooth, CB–, IKI–, $(4.5\text{--})5\text{--}5.5 \times 4\text{--}5.5 \mu\text{m}$, $L = 5.30 \mu\text{m}$, $W = 4.94 \mu\text{m}$, $Q = 1.07$ ($n = 30/1$).

Material examined – China, Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, GPS coordinates $27^{\circ}77' \text{N}$, $104^{\circ}29' \text{E}$, altitude 2900 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 20 September 2023, CLZhao 33592 (SWFC, holotype).

GenBank accession numbers – ITS: PV254828, LSU: OQ411117.

Notes – The combined ITS+nLSU phylogenetic analyses revealed that our species *Byssocorticium yunnanense* (CLZhao 33592) formed a separate lineage sister to *By. caeruleum* (RS 09400) with 100% ML and 1.00 BYPP bootstrap support (Fig. 32). Although *By. caeruleum* resembles *By. yunnanense* in many characters and it can be delimited by having pyriform basidiospores (Kotiranta et al. 2012). Thus, based on morphology and multigene phylogenetic evidence we introduce *By. yunnanense* as a new species from Yunnan Province, China.

***Amylocorticiales* K.H. Larss., Manfr. Binder & Hibbett**

***Amylocorticiaceae* Jülich**

***Amyloenasma* (Oberw.) Hjortstam & Ryvarden**

Index Fungorum number: IF 28987; Facesoffungi number: FoF 18423

Notes – *Amyloenasma* was introduced by Hjortstam & Ryvarden (2005) and was typified by *Am. grisellum*. This genus was segregated from *Phlebiella* independently by Hjortstam & Ryvarden (2005) ranking the subgenus *Amyloenasma* to the generic level. It includes species with pleurobasidia and smooth amyloid basidiospores. The taxonomic placement of *Amyloenasma* is unclear, however, it could belong to *Amylocorticiaceae* because the amyloid spore wall is indicative of this group. But it differs from other genera included in *Amylocorticiaceae* by morphology of the basidia, typically pleurobasidiate (Larsson 2007). Currently, *Amyloenasma* consists of six accepted species (He et al. 2024, Hyde et al. 2024d, Species Fungorum 2025). In this study, *Amyloenasma cremeum* sp. nov. and *Amyloenasma tenuissimum* sp. nov. are introduced from China based on the ITS+nLSU sequence data (Fig. 35) and morphological characteristics (Fig. 36).

***Amyloenasma cremeum* Qi. Yuan & C.L. Zhao, sp. nov.**

Fig. 36

Index Fungorum number: IF 904406; Facesoffungi number: FoF 18424

Diagnosis – Differs from other *Amyloxenasma* species by the membranous basidiomata, smooth hymenial surface, a monomitic hyphal system with clamped generative hyphae and with a median constriction basidia measuring $15\text{--}30 \times 6\text{--}9.5\ \mu\text{m}$.

Etymology – *cremeum* (Lat.): referring to the color of the cream surface of hymenophore.

Basidiomata annual, resupinate, adnate, membranous, without odor or taste when fresh, up to 8.9 cm long, 1.1 cm wide, 50–100 μm thick. *Hymenial surface* smooth, white when fresh, turning to cream upon drying. Sterile margin thin, white, thinning out, up to 1 mm wide. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 3–4.5 μm in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* and *Cystidioles* absent. *Basidia* clavate, with a median constriction, slightly thick-walled, with 4 sterigmata and a basal clamp connection, with oily contents, $15\text{--}30 \times 6\text{--}9.5\ \mu\text{m}$; basidioles abundant, in shape similar to basidia, but slightly smaller. *Basidiospores* allantoid, colorless, thin-walled, smooth, with oil drop, IKI–, CB–, $(7\text{--})7.5\text{--}10.5\text{--}(11) \times 3\text{--}5\ \mu\text{m}$, $L = 8.55\ \mu\text{m}$, $W = 3.79\ \mu\text{m}$, $Q = 2.22\text{--}2.5\ \mu\text{m}$ ($n = 90/3$).

Material examined – China, Yunnan Province, Zhaotong, Wumenshan National Nature Reserve, GPS coordinates $25^{\circ}67'\text{ N}$, $103^{\circ}66'\text{ E}$, altitude 2410 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 20 September 2023, CLZhao 33591 (SWFC, holotype); Yunnan Province, Zhaotong, Yongshan County, Mungan Town, Wumenshan National Nature Reserve GPS coordinates: $28^{\circ}23'\text{ N}$, $103^{\circ}63'\text{ E}$, altitude 1180 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 7 November 2023, CLZhao 35457, CLZhao 35509 (SWFC, paratypes).

GenBank accession numbers – CLZhao 33591: ITS = PV501100, LSU = OQ411117; CLZhao 35457: ITS = PV501101, LSU = PV569514; CLZhao 35509: ITS = PV501102

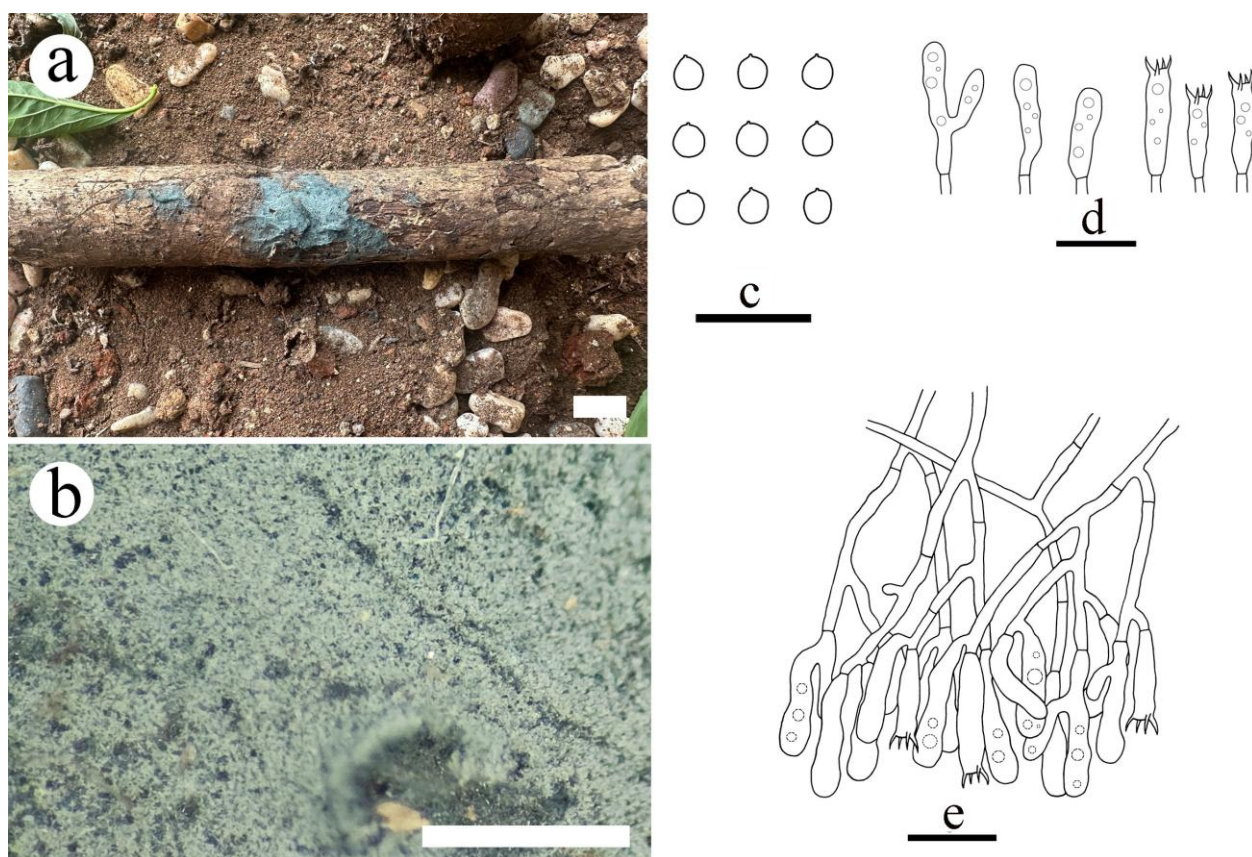


Figure 34 – Basidiomata and microscopic structures of *Byssocorticium yunnanense* (CLZhao 33592, holotype). a, b Basidiomata on the host substrate. c Basidiospores. d Basidia and basidioles. e A section of hymenium. Scale bars: a = 1 cm, b = 2 mm, c–e = 20 μm .

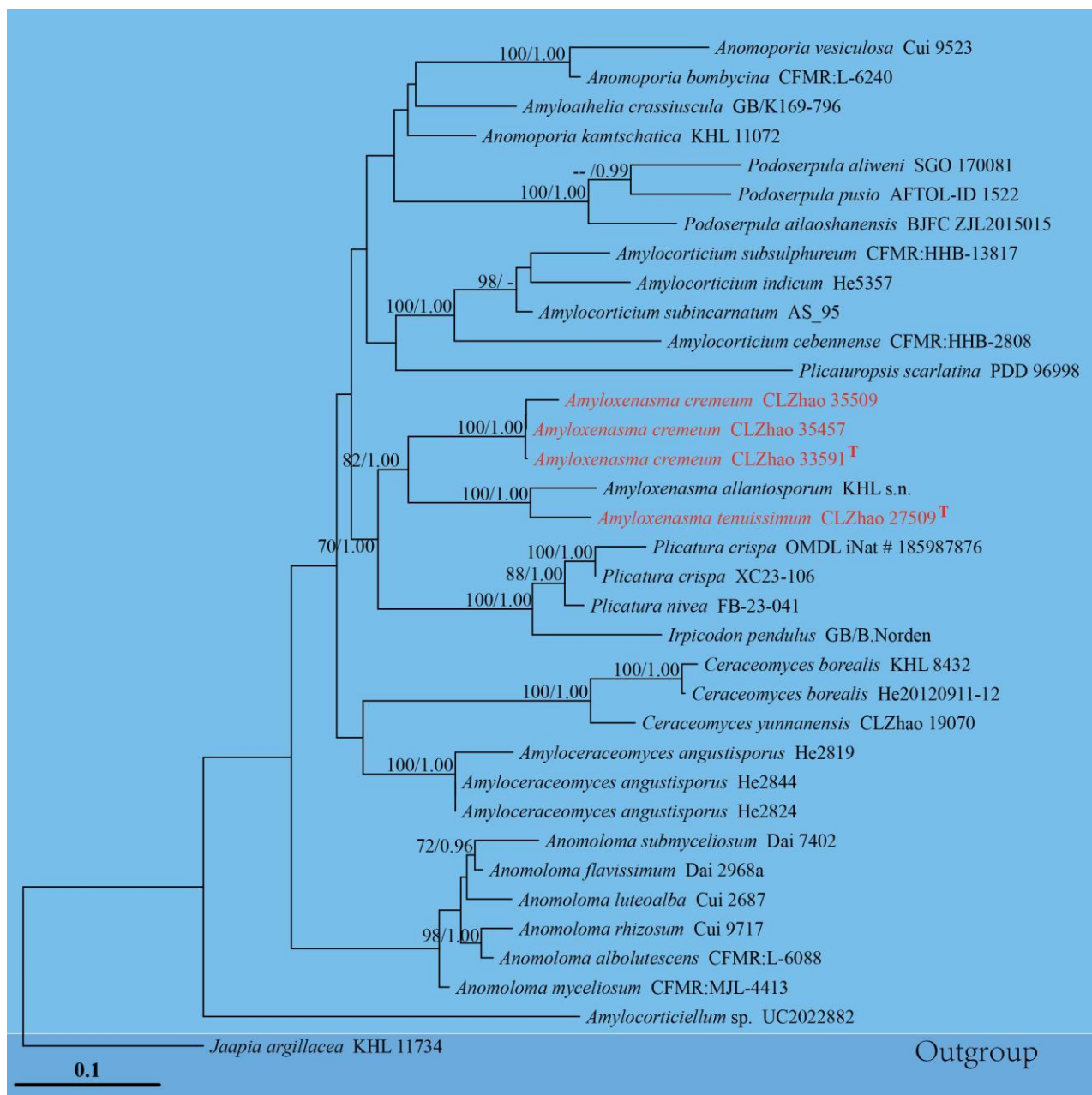


Figure 35 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and nLSU sequence data of *Amylocorticiaceae*. Thirty-five specimens are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAXML tree with a final likelihood value of -14820.786 is presented. The evolutionary model GTR+R3+F is applied for all the genes. The matrix had 1079 distinct alignment patterns, with 28.28% of undetermined characters or gaps. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Jaapia argillacea* (KHL 11734). The newly generated sequences are in red-bold and the type collections are indicated in ^T.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 35) revealed that our specimens of *Amyloxenasma cremeum* (CLZhao 33591, CLZhao 35457, and CLZhao 35509) grouped within *Amyloxenasma*, forming a monophyletic clade with 100% ML and 1.00 BYPP bootstrap support. *Amyloxenasma cremeum* resembles *Am. elongatisporum* and *Am. allantosporum* by having allantoid basidiospores. However, morphologically, *Am. allantosporum* can be distinguished from *Am. cremeum* by its slightly tuberculate hymenial surface, and smaller basidiospores ($4.5\text{--}6 \times 1.5\text{--}2.2 \mu\text{m}$, Bernicchia & Gorjón 2010). Also, *Am. elongatisporum* differs

from *Am. cremeum* due to its pruinose hymenophore, and narrower basidiospores ($5.5\text{--}8.5 \times 1.2\text{--}1.5\ \mu\text{m}$, Duhem & Schultheis 2012). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Am. cremeum* as a new species, collected from Yunnan Province, China.

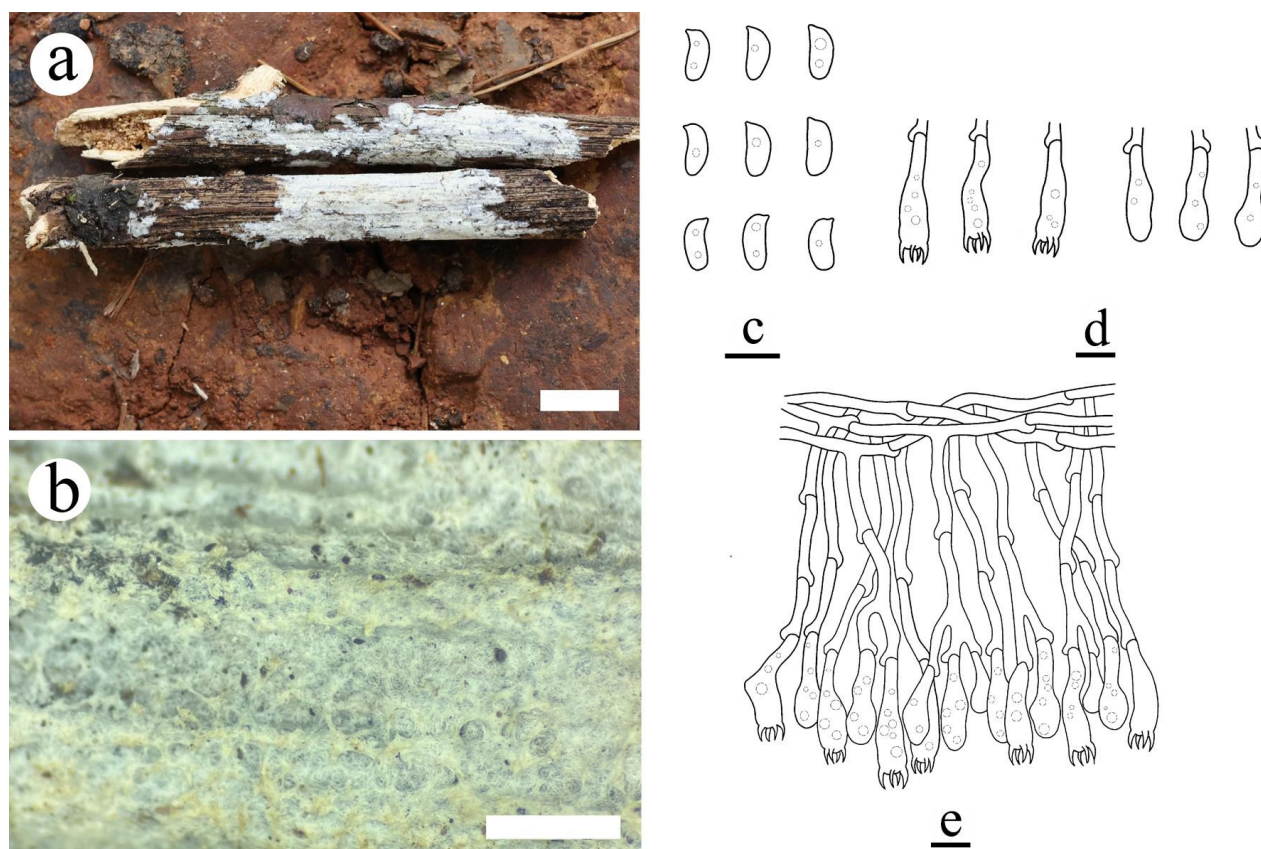


Figure 36 – Basidiomata and microscopic structures of *Amyloxenasma cremeum* (CLZhao 33591, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e A section of hymenium. Scale bars: a = 1 cm, b = 1 mm, c = 5 μm , d, e = 10 μm .

Amyloxenasma tenuissimum Qi. Yuan & C.L. Zhao, sp. nov.

Fig. 37

Index Fungorum number: IF 904407; Facesoffungi number: FoF 18425

Diagnosis – Differs from other *Amyloxenasma* species by the pellicular basidiomata with smooth, incanus to rubricans hymenial surface, a monomitic hyphal system with clamped generative hyphae and cylindrical to clavate basidia measuring $15\text{--}24 \times 5.5\text{--}8\ \mu\text{m}$.

Etymology – *tenuissimum* (Lat.): refers to the thin basidiomata of the type specimens.

Basidiomata annual, resupinate, adnate, pellicular, coriaceous, without odor or taste when fresh, up to 8.4 cm long, 1.7 cm wide, $50\text{--}100\ \mu\text{m}$ thick. **Hymenial surface** smooth, incanus when fresh, turning to rubricans upon drying. Sterile margin thin, gray, thinning out, up to 1 mm wide. **Hyphal system** monomitic, generative hyphae with clamp connections, colorless, slightly thick-walled, frequently branched, interwoven, $2\text{--}4.5\ \mu\text{m}$ in diam.; IKI–, CB–, tissues unchanged in KOH. **Cystidia** and **Cystidioles** absent. **Basidia** cylindrical to clavate, with a median constriction, slightly thick-walled, with 4 sterigmata and a basal clamp connection, with oily contents, $15\text{--}24 \times 5.5\text{--}8\ \mu\text{m}$. **Basidioles** abundant, in shape similar to basidia, but slightly smaller. **Basidiospores** suballantoid, colorless, thin-walled, smooth, with oil drop, IKI–, CB–, $(6\text{--})6.5\text{--}8.5(9) \times 3\text{--}4.5(5)\ \mu\text{m}$, $L = 7.47\ \mu\text{m}$, $W = 3.77\ \mu\text{m}$, $Q = 1.98\ \mu\text{m}$ ($n = 30/1$).

Material examined – China, Yunnan Province, Qujing, Zhanyi District, Dapo Town, Lijia Tomb, GPS coordinates $25^{\circ}67' \text{ N}$, $103^{\circ}66' \text{ E}$, altitude 2410 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 7 March 2023, CLZhao 27509 (SWFC, holotype).

GenBank accession numbers – ITS: PV501099, LSU: OQ411117.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 35) revealed that our species *Amyloxenasma tenuissimum* (CLZhao 27509) grouped within *Amyloxenasma*, forming a sister lineage to *Am. tenuissimum* (KHL s.n. Sweden) with 100% ML and 1.00 BYPP bootstrap support. However, *Am. allantosporum* can be delimited from *Am. tenuissimum* by its slightly tuberculate hymenial surface, and its smaller basidiospores ($4.5\text{--}6 \times 1.5\text{--}2.2\ \mu\text{m}$, Bernicchia & Gorjón 2010). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Am. tenuissimum* as a new species, collected from Yunnan Province, China.

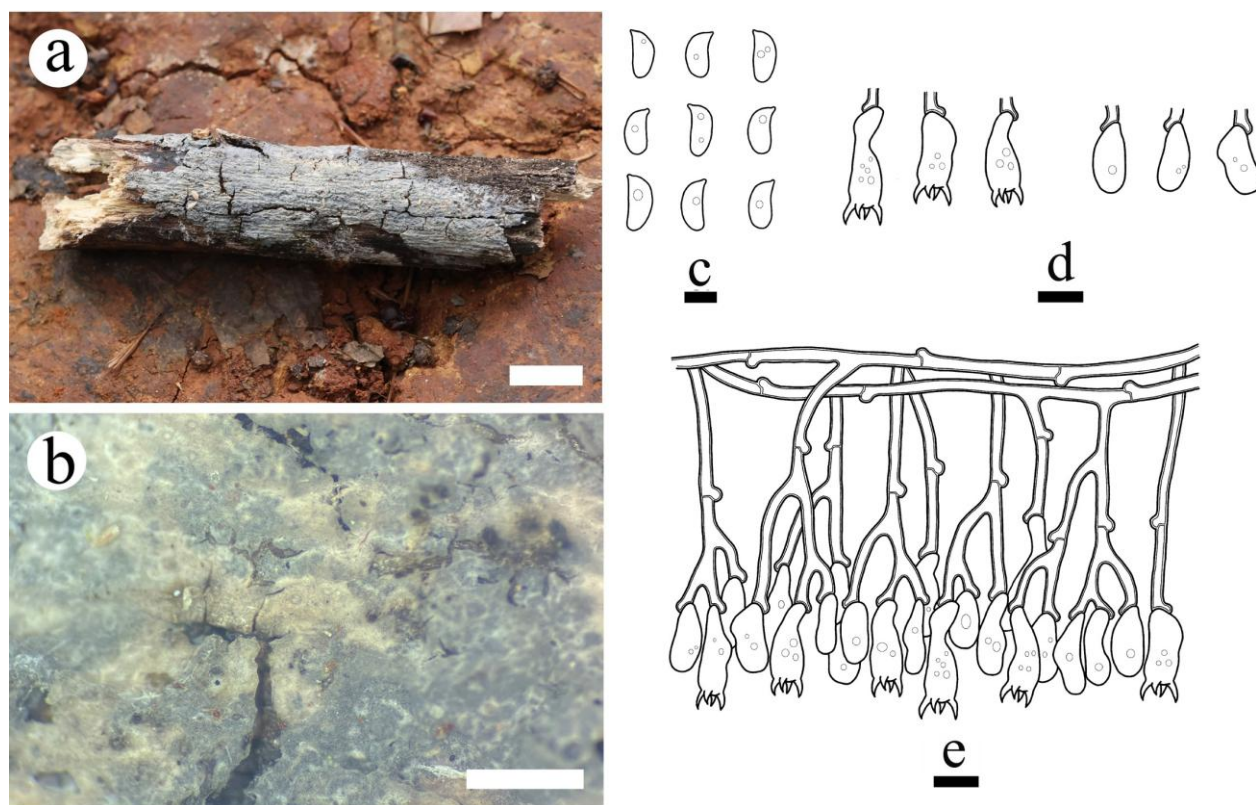


Figure 37 – Basidiomata and microscopic structures of *Amyloxenasma tenuissimum* (CLZhao 27509, holotype). a, b Basidiomata on the host substrate. c Basidiospores. d Basidia and basidioles. e A section of hymenium. Scale bars: a = 1 cm, b = 1 mm, c = 5 μm , d, e = 10 μm .

Boletales E.-J. Gilbert

Sclerodermataceae Corda

Scloderma Pers.

Index Fungorum number: IF 19309; Facesoffungi number: FoF 18426

Notes – *Scloderma* was described by Persoon (1801) and typified by *Sc. verrucosum*. This is an easily recognizable genus of gasteroid fungi which produces macroscopic sporocarps called “earthballs” (Jeffries 1999). *Scloderma* is characterized by the subglobose, pyriform, or subturbinate basidiomata, a firm peridium, which dehisces at maturity, and globose, colored, and ornamented basidiospores (Guzmán et al. 1970). *Scloderma* play a vital role in maintaining plant diversity, ecosystem stability, and afforestation, and were found to be one of the most species-rich groups throughout the tropics (Read & Perez-Moreno 2003, Sanon et al. 2009, Kumla et al. 2013, Corrales et al. 2022, Wu et al. 2023, Wang et al. 2024b). They form ectomycorrhiza with plants in the families, viz. *Cistaceae*, *Dipterocarpaceae*, *Fagaceae*, *Juglandaceae*, *Myrtaceae*, *Mimosaceae*, and *Pinaceae*. Currently, ca. 140 are listed in Species Fungorum (2025) under *Scloderma*. In this study, *Scloderma roseobrunneum* sp. nov. is introduced from China based on the ITS sequence data (Fig. 38) and morphological characteristics (Figs 39, 40).

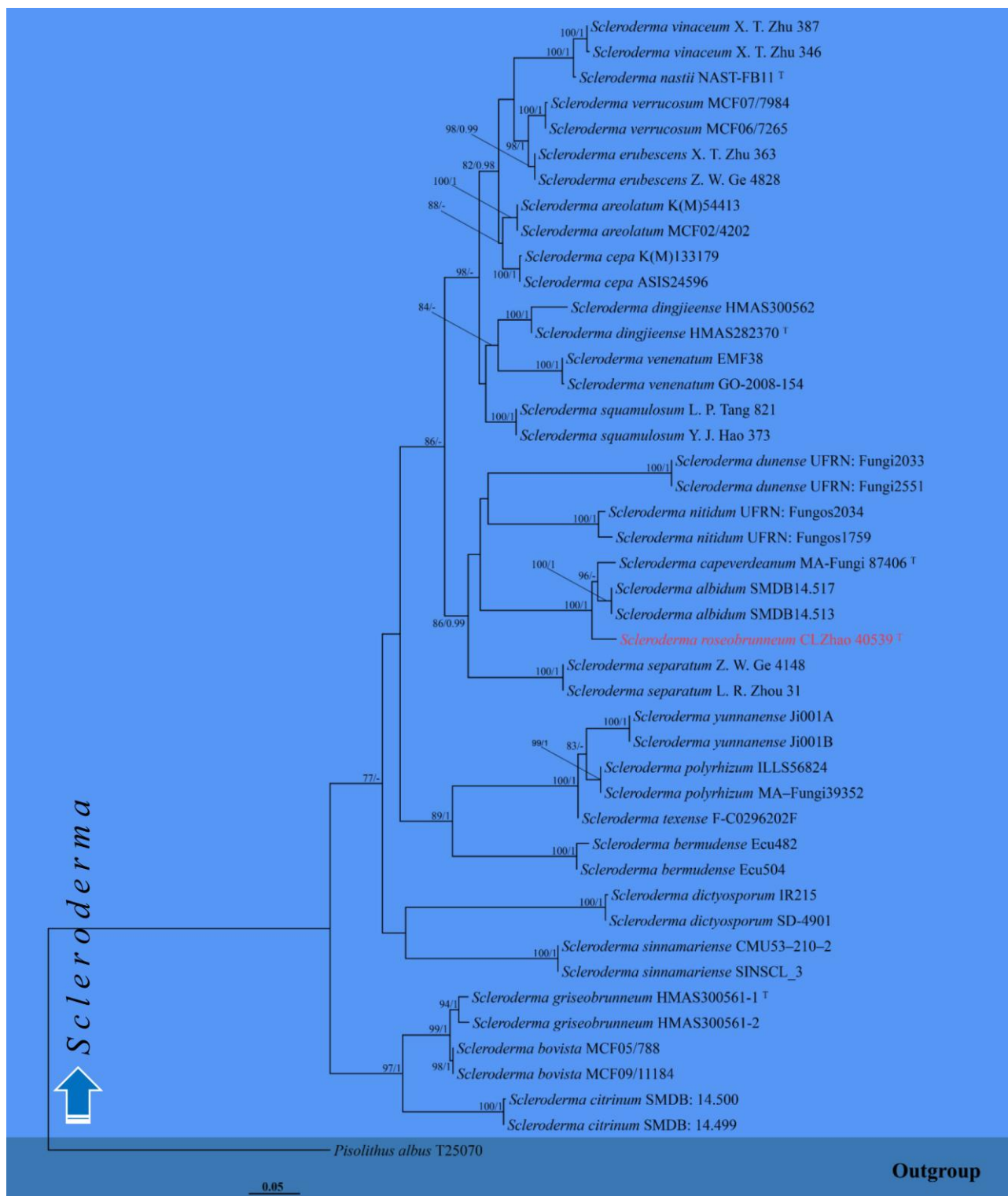


Figure 38 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and nLSU sequence data of *Scleroderma*. Forty-five specimens are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5551.268 is presented. The evolutionary model TIM+G4+F is applied for all the genes. The matrix had 485 distinct alignment patterns, with 24.07% of undetermined characters or gaps. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Pisolithus albus* (T25070). Newly generated sequences are in red-bold with ^T indicated as the type collections.

Scleroderma roseobrunneum X. Yang & C.L. Zhao, sp. nov.

Figs 39, 40

Index Fungorum number: IF 904408; Facesoffungi number: FoF 18427

Diagnosis – Differs from other *Scleroderma* species by the pinkish to brown of the basidiomata when dry, gleba compact, hyphae of rhizomorphs with simple septa, and globose to subglobose basidiospores measuring 9.7–12.0 µm.

Etymology – *roseobrunneum* (Lat.): referring to the pinkish to brown of the basidiomata of the type specimen when dry.

Basidiomata epigeous, globose to subglobose, 14 mm in diam., 15 mm in height. *Peridium* is leathery, thin, roughly 0.1 mm thick. *Surface* is rough, curry-yellow to honey-yellow when fresh, pinkish to brown of the basidiomata when dry. *Gleba* compact, dark brown. *Base* with numerous white to whitish rhizomorphs. *Hyphal structure* hyphae of rhizomorphs bifurcating, with simple septa, and inflated near the septa, thin-walled, 2.5–4.3 µm in diam. *Peridium* composed of subcylindric hyphae, evenly and tightly arranged, simple septa, 2.0–4.5 µm in diam. *Gleba* made up of hyaline hyphae, 1.7–3.5 µm in diam., and globose to moniliform expanded cells measuring, 1.5–4.5 µm in diam. *Basidiospores* globose to subglobose, (8.9–)9.7–12.0(–14.0) µm in diam. (not including ornamentation), 10.5 µm on average, grayish brown to brown, densely covered with spines or narrow pyramidal warts tapering to sharp points, and ornamentation 1.5–3.0 µm in height.

Material examined – China, Hainan Province, Sanya, Hainan Tropical Ocean University, 18°18'35.4"N, 109°32'4.06"E, altitude 15 m, on the ground, 27 September 2024, CLZhao 40539 (SWFC, holotype).

GenBank accession numbers – ITS: PV809771.

Notes – The combined ITS phylogenetic analyses revealed that our species *Scleroderma roseobrunneum* (CLZhao 40539) grouped within *Scleroderma*, forming a sister lineage to *S. albidum* (SMDB14.517, SMDB14.513) and *Sc. capeverdeanum* (MA-Fungi 87406) clade with 100% ML and 1.00 BYPP bootstrap support (Fig. 38). *Scleroderma roseobrunneum* resembles *Sc. albidum* and *Sc. capeverdeanum* in having echinulate basidiospores. However, *Sc. albidum* can be distinguished from *Sc. roseobrunneum* by its basidiomata stellate dehiscence, and its basidiospores (12.0–14.5 µm in diam., Nouhra et al. 2012). Also, *S. capeverdeanum* differs from *Sc. roseobrunneum* due to its peridium with brown squamules and its small ornamentation (0.5–1 µm, Crous et al. 2016b). The new species is only found growing in Hainan Province. Thus, based on morphological characters and multigene phylogenetic evidence, we introduce *Sc. roseobrunneum* as a new species.

Cantharellales Gäum.

Hydnaceae Chevall.

Burgella Diederich & Lawrey

Index Fungorum number: IF 511585; Facesoffungi number: FoF 18428

Notes – *Burgella* (*Hydnaceae*, *Cantharellales*) was introduced by Diederich & Lawrey (2007) as a lichenicolous genus and it was typified by *Bu. flavoparmeliae* collected from the USA. The study by Diederich & Lawrey (2007) has shown that *Burgella flavoparmeliae* and *Sistotrema oblongisporum* were as the sister group of the lichenized genus *Multiclavula*. *Burgella flavoparmeliae* was only distantly related to the type species of the genus *Burgoa*, that appeared in a different place in the order *Cantharellales*, and the research revealed that *Bu. flavoparmeliae* should not be included in *Burgoa*, and the description of a new genus as *Burgella* (Diederich & Lawrey 2007, Diederich et al. 2014). Based on MycoBank (2025) and Index Fungorum (2025), the *Burgella* consists of four accepted species. In this study, *Burgella yunnanensis* sp. nov. is introduced from China, based on the ITS+nLSU sequence data (Fig. 41) and morphological characteristics (Fig. 42).

Burgella yunnanensis Q. Zhou & C.L. Zhao, sp. nov.

Fig. 42

Index Fungorum number: IF 859085; Facesoffungi number: FoF 18429

Diagnosis – *Burgella yunnanensis* is characterized by the resupinate, pellicular basidiomata, a monomitic hyphal system with clamped generative hyphae and allantoid basidiospores ($9.5\text{--}13 \times 3\text{--}6 \mu\text{m}$).

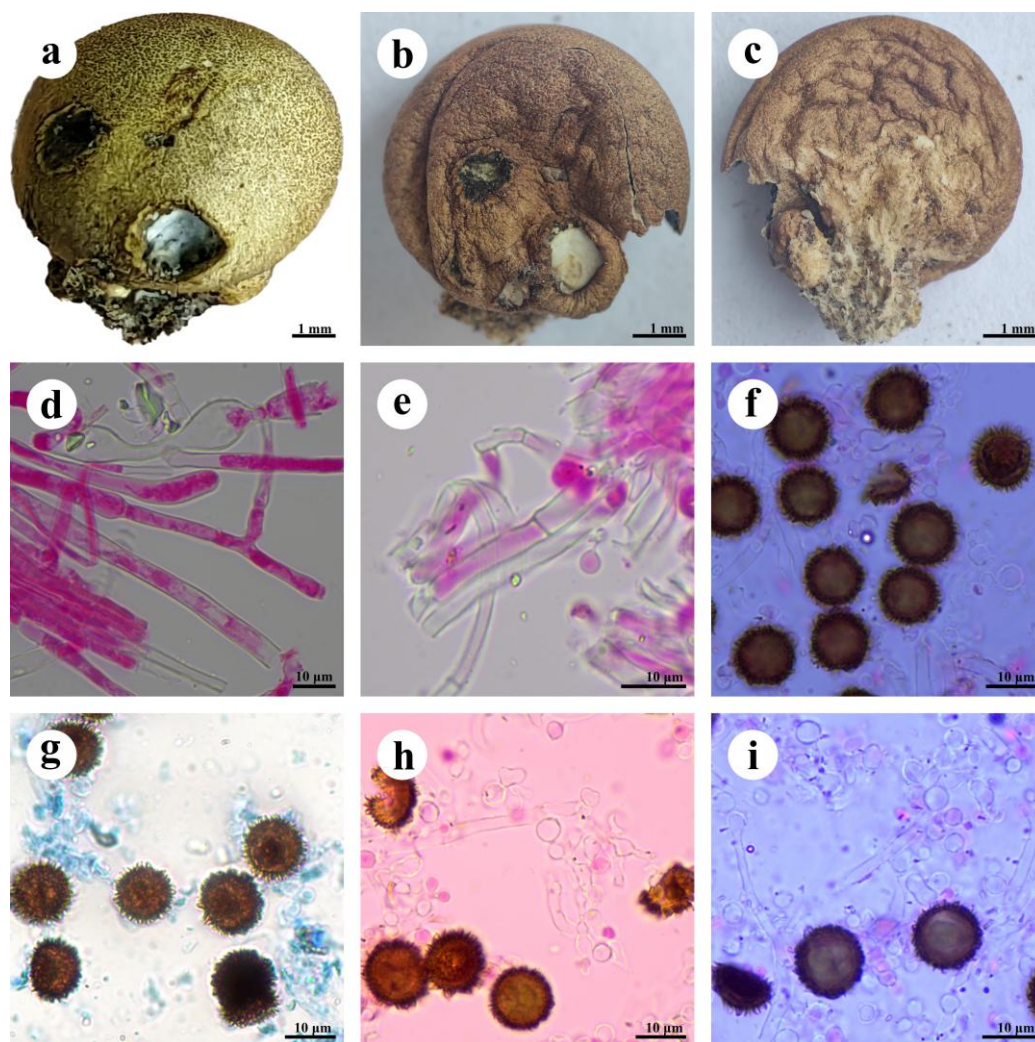


Figure 39 – Basidiomata and microscopic structures of *Scleroderma roseobrunneum* (CLZhao 40539, holotype). a–c Basidiomes. d Hyphae of rhizomorphs. e Peridium hyphae. f, g Basidiospores. h–i Gleba hyphae. Scale bars: a–c = 1 mm, d–i = 10 μm .

Etymology – *yunnanensis* (Lat.): referring to the type locality (Yunnan Province) of the specimen.

Basidiomata annual, resupinate, adnate, pellicular, pruinose upon drying, without odor or taste when fresh, up to 10.5 cm long, 1.5 cm wide, 20–50 μm thick. *Hymenial surface* smooth, farinaceous, white when fresh, turning to incanus upon drying. Sterile margin thin, white, thinning out, up to 1 mm wide. *Hyphal system* monomitic, generative hyphae with clamp connections, sometimes with oily contents, colorless, slightly thick-walled, frequently branched, interwoven, 3–5 μm in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* and *Cystidioles* absent. *Basidia* suburniform to urniform, slightly thick-walled, with 6 sterigmata and a basal clamp connection, $9.5\text{--}13 \times 3\text{--}6 \mu\text{m}$. *Basidioles* abundant, in shape similar to basidia, but slightly smaller. *Basidiospores* allantoid, colorless, thin-walled, smooth, with oil drop, IKI–, CB–, $3\text{--}5 \times 1.5\text{--}2.5 \mu\text{m}$, $L = 4 \mu\text{m}$, $W = 1.82 \mu\text{m}$, $Q = 2.2 \mu\text{m}$ ($n = 30/1$).

Material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: $25^{\circ}52' \text{ N}$, $97^{\circ}38' \text{ E}$, altitude 1000 m asl., on angiosperm fallen branch, leg. C.L. Zhao, 2 July 2024, CLZhao 37344 (SWFC, holotype).

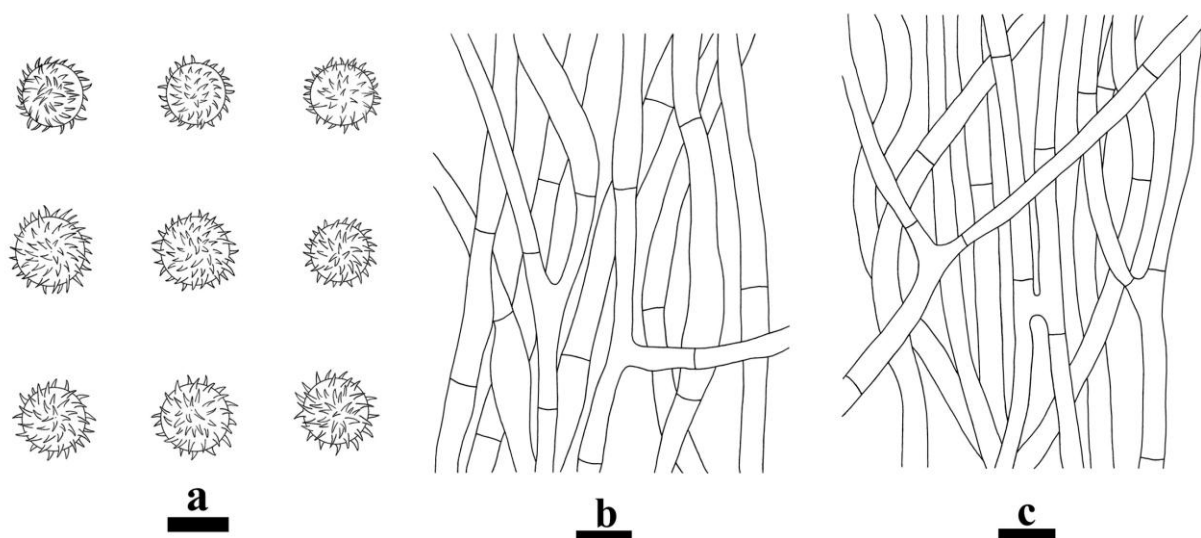


Figure 40 – *Scleroderma roseobrunneum* (CLZhao 40539, holotype). a Basidiospores b Hyphae of rhizomorphs c Peridium hyphae. Scale bars: a–c = 10 μ m.

GenBank accession numbers – ITS: PV475867.

Notes – The phylogram based on the combined ITS+nLSU data (Fig. 41) revealed that our species *Burgella yunnanensis* (CLZhao 37344) clustered within *Burgella*, forming a closely related sister lineage to *Bu. lutea* (Etayo 27623) with 97% ML, 98% MP and 1.00 BYPP bootstrap support. These collections show close phylogenetic affinity to *Bu. albofarinacea*, *Bu. flavoparmeliae*, and *Bu. fissurata*. *Burgella lutea* distinguishes from *Bu. yunnanensis* by the superficial, yellow to orange-yellow, roundish bulbils (Diederich et al. 2014). The type species of the genus, *Bu. flavoparmeliae* is distinguished from *Bu. yunnanensis* by the irregularly shaped, coralloid, orange agglomerations of bulbils and generative hyphae with septa, both situations present on the same hyphae at neighboring septa (Diederich & Lawrey 2007). Also, *Bu. fissurata* differs from *Bu. yunnanensis* by its umbrella-shaped cystidia, smaller basidia with 4 sterigmata ($6\text{--}11.5 \times 2\text{--}4.5$ μ m), and narrowly ellipsoid and smaller basidiospores ($(2.5\text{--})3\text{--}4 \times 1\text{--}2$ μ m, Cai & Zhao 2023); and *Bu. albofarinacea* differs from *Bu. yunnanensis* by the coriaceous hymenial surface, bigger basidia with 8 sterigmata ($10.5\text{--}22 \times 3.5\text{--}7$ μ m), and bigger basidiospores ($4.5\text{--}6.5 \times 2\text{--}4$ μ m, Cai & Zhao 2023). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Bu. yunnanensis* as a new species.

Sistotrema Fr.

Index Fungorum number: IF 18551; Facesoffungi number: FoF 14852

Notes – *Sistotrema* was introduced by Fries (1821) to accommodate *Si. confluens* as the type species. This genus is characterized by resupinate or pileate-stipitate, soft basidiomata, smooth, grandinioid, hydroid, or poroid hymenophore with various characteristic textures (pellicular, membranous, or ceraceous), a monomitic hyphal system with oily inclusions, uniform basidia with (4)6–8 sterigmata, and smooth, thin-walled basidiospores containing cytoplasmic oil droplets (Eriksson et al. 1984, Bernicchia & Gorjón 2010). The continuous taxonomic studies have revealed that *Sistotrema* is highly polyphyletic (Nilsson et al. 2006, Larsson 2007, Hibbett et al. 2014). Kotiranta & Larsson (2013) conducted preliminary phylogenetic studies on *Sistotrema* and proposed a new species, *Si. luteoviride*. The nuclear DNA sequence analysis of the phylogenetic diversity of bulbil-forming lichenicolous fungi in *Cantharellales* by Lawrey et al. (2016) revealed that the type species, *Si. conuens*, grouped closely with the genus *Cantharellus*. A comprehensive phylogenetic analysis based on a multiple-marker dataset for the entire *Hydnaceae sensu stricto* indicated that *Sistotrema* along with its sister genus *Hydnum*. formed a fully supported lineage that was closely related to *Craterellus*. and *Cantharellus* (Cao et al. 2021). Phylogenetic trees obtained

using the ITS and nLSU and *rpb2* sequences showed that *Sistotrema* grouped with *Hydnum*; however, the generic boundary was unclear (Sugawara et al. 2022). A study of wood-rotting fungi with nLSU sequence data has shown that a new species *Si. yunnanense* was reported (Cai & Zhao 2023). In the present study, we describe two novel species *Sistotrema fissuratum* sp. nov. and *Sistotrema albofarinaceum* sp. nov. from China, based on the phylogenetic analyses inferred from ITS sequence data (Fig. 43) and morphological characteristics (Figs 44, 45).

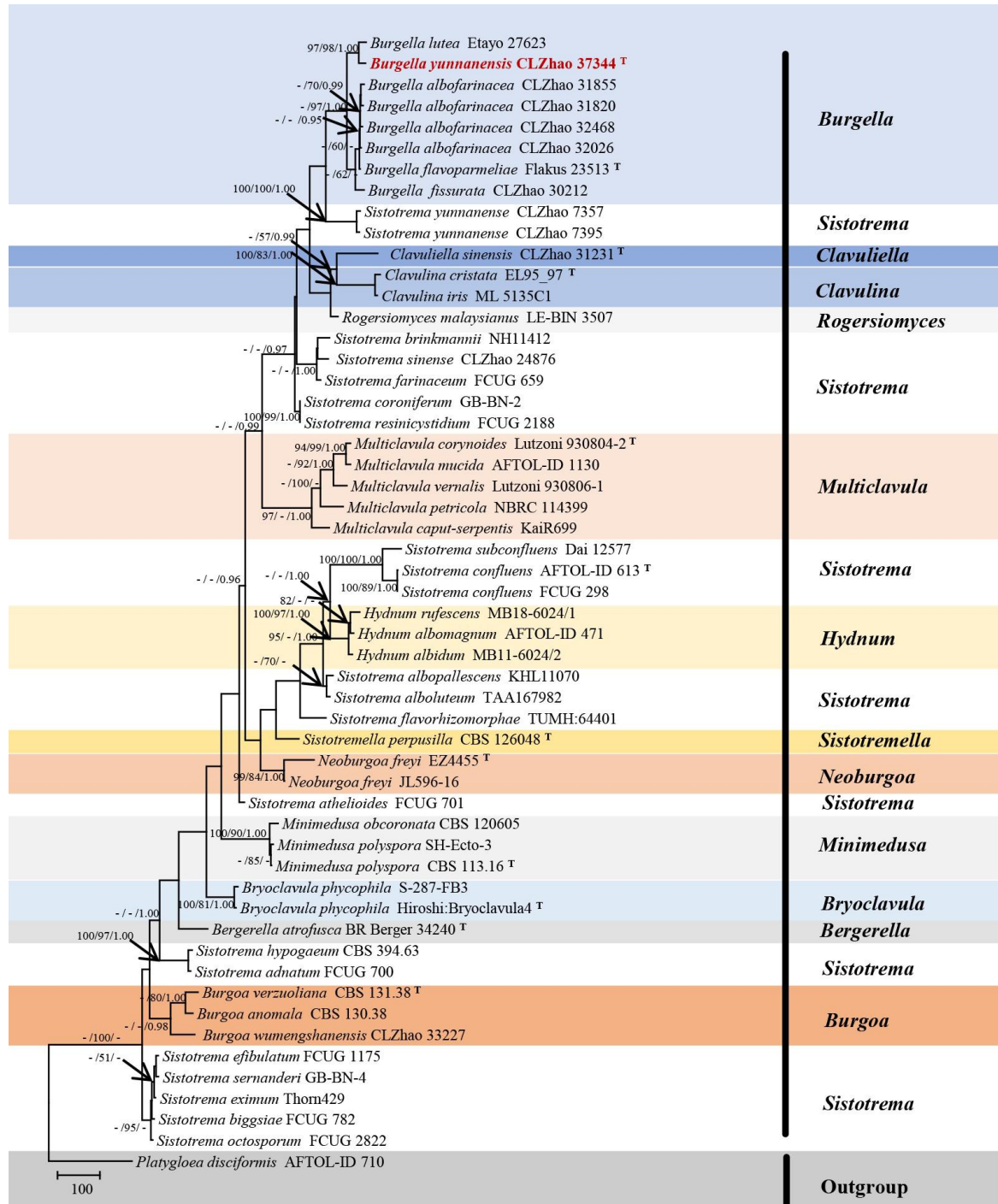


Figure 41 – Phylogram generated from maximum parsimony strict consensus tree analysis based on the ITS+nLSU sequence data. Fifty-three specimens are included in the analyses. Bayesian analysis and ML analysis resulted in a similar topology as in the MP analysis. The dataset had an aligned length of 2367 characters, of which 1333 characters were constant, 431 were variable and parsimony-uninformative and 596 were parsimony-informative. Maximum parsimony analysis yielded 6 equally parsimonious trees (TL = 3760, CI = 0.4428, HI = 0.5572 RI = 0.4688 and RC =

0.2076). The best model of nucleotide evolution for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was found to be GTR+I+G. The Bayesian analysis had an average standard deviation of split frequencies = 0.022662 (BI) and the effective sample size (ESS) across the two runs is double the average ESS (avg. ESS) = 497. Bootstrap support values for ML $\geq$ 70%, MP $\geq$ 50%, and Bayesian posterior probabilities $\geq$ 0.95 are given near nodes, respectively. The tree was rooted with *Platyglea disciformis* (AFTOL-ID 710). The newly generated sequences are indicated in red-bold and the type collections are indicated with ^T.

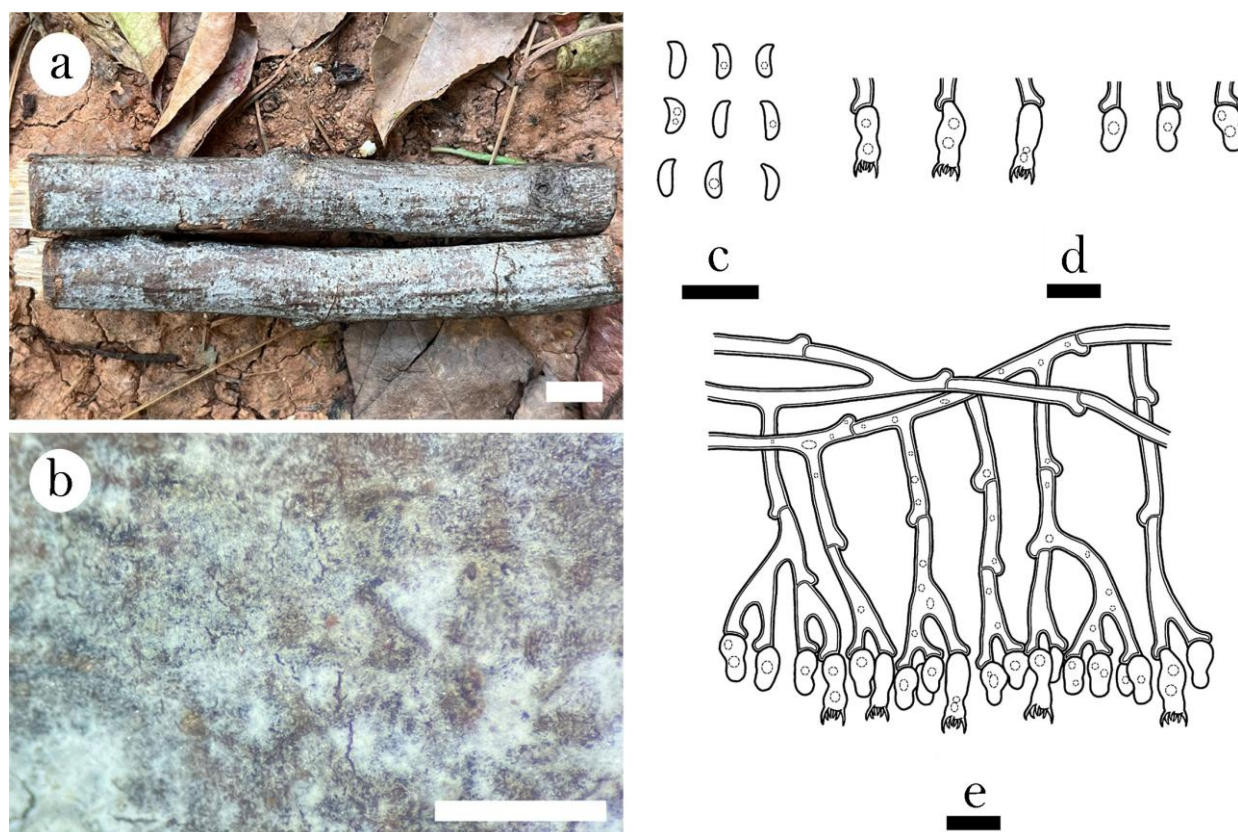


Figure 42 – Basidiomata and microscopic structures of *Burgella yunnanensis* (CLZhao 37344, holotype). a Basidiomata on the substrate. b Macroscopic characteristics of hymenophore. c basidiospores. d basidia and basidioles. e A section of hymenium. Scale bars: a = 1 cm, b = 1 mm, c–e = 10 μ m.

Sistotrema albofarinaceum Q. Li & C.L. Zhao, sp. nov.

Fig. 44

Index Fungorum number: IF 904409; Facesoffungi number: FoF 18430

Diagnosis – Differs from other *Sistotrema* species by the farinaceous basidiomata with cream to pale-grey, smooth hymenial surface, a monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring $2.5\text{--}3.2 \times 2\text{--}2.5 \mu\text{m}$.

Etymology – *albofarinaceum* (Lat.): referring to the white-farinaceous hymenophore of the type specimen.

Basidiomata annual, resupinate, adnate, strongly attached to the wood, membranous, farinaceous, without odor or taste when fresh, becoming coriaceous upon drying, up to 8 cm long, 2 cm wide, 50–100 μ m thick. **Hymenial surface** smooth, white when fresh, turning to cream to pale-grey upon drying. Sterile margin slightly cream, thinning out, up to 0.5 mm wide. **Hyphal system** monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 2–3 μ m in diam.; IKI–, CB–, tissues unchanged in KOH. **Cystidia** and **Cystidioles** absent. **Basidia** subcylindrical, slightly constricted, with 4 sterigmata and a basal clamp connection, $12\text{--}18.5 \times 2.5\text{--}5 \mu\text{m}$. **Basidioles** dominant, in shape similar to basidia, but slightly smaller.

Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, with 1–2 guttulate, $2.5\text{--}3.2(-3.4) \times 2\text{--}2.5\text{ }\mu\text{m}$, $L = 2.96\text{ }\mu\text{m}$, $W = 2.32\text{ }\mu\text{m}$, $Q = 1.13\text{--}1.42$, $Q_m = 1.28 \pm 0.09$ ($n = 60/2$).

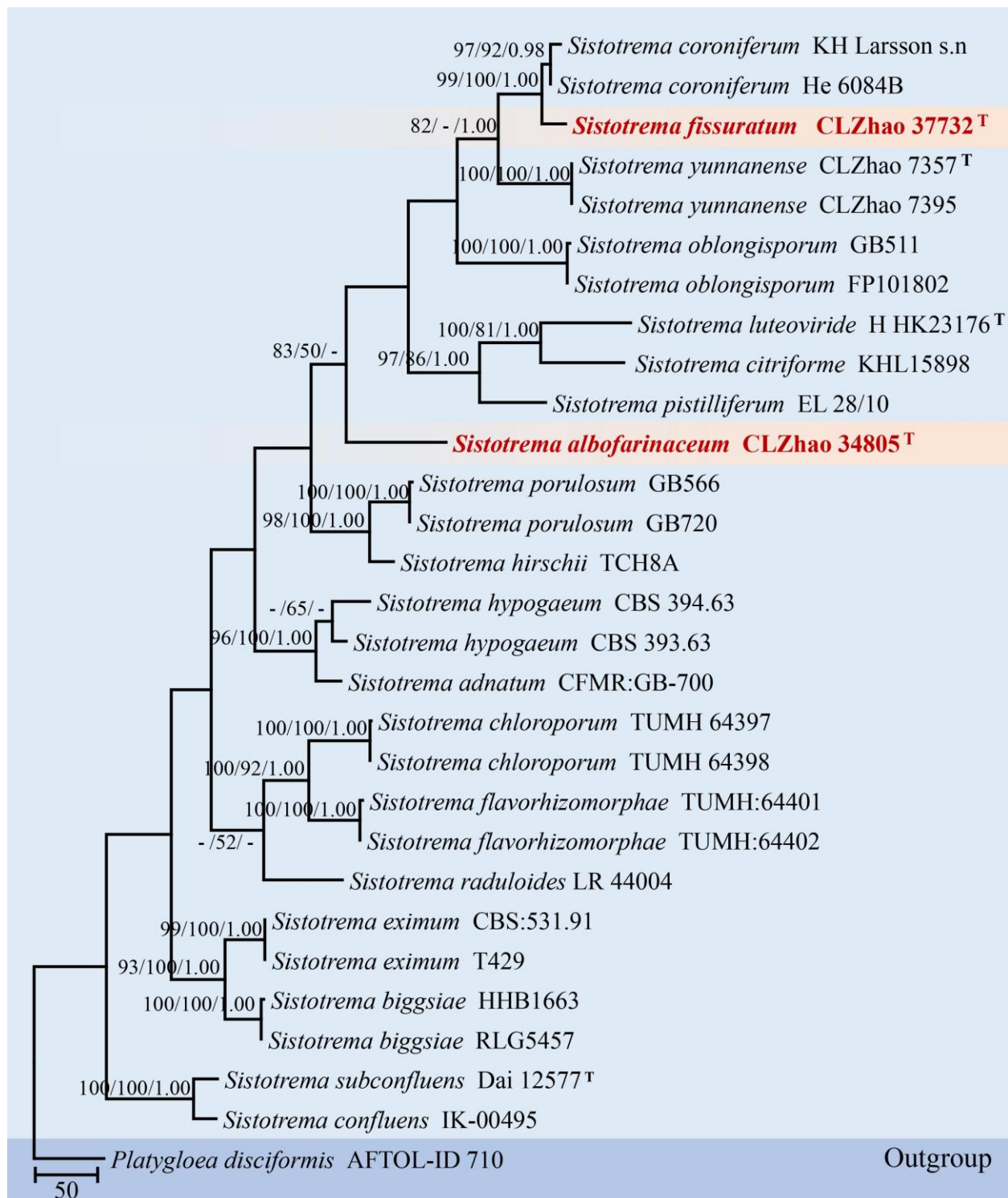


Figure 43 – Phylogram generated from maximum parsimony strict consensus tree analysis based on the ITS sequence data of *Sistotrema* species. Twenty-nine specimens are included in the analyses. The tree topology of the maximum parsimony analysis is similar to the maximum likelihood and Bayesian analysis. Constant characters were 236. Parsimony-informative characters were 394 whereas parsimony-uninformative characters were 136. Bootstrap support values for ML $\geq 70\%$, MP $\geq 50\%$, and Bayesian posterior probabilities ≥ 0.95 are given near nodes, respectively. The tree was rooted with *Platygloea disciformis* (AFTOL-ID 710). The newly generated sequences are indicated in red-bold, and the type collections are indicated with ^T.

Material examined – China, Yunnan Province, Diqing, Weixi County, Zhonglu Town, Lagaluo, 27°17' N, 99°16' E, altitude 1600 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 14 October 2023, CLZhao 34805 (SWFC, holotype).

GenBank accession numbers – ITS: PV569135

Notes – The phylogenetic analyses based on the ITS sequence data (Fig. 43) revealed that our species *Sistotrema albofarinaceum* (CLZhao 34805) grouped within *Sistotrema*, forming a distinct, monophyletic and basal lineage with 83% ML and 50% MP bootstrap support. The type species of the genus, *Si. confluens* shares similar morphologies to our species, however it can be distinguished from *Si. albofarinaceum* by its uniform basidia with 6–8 sterigmata and longer basidiospores ($4.5\text{--}6.5 \times 3.5\text{--}6 \mu\text{m}$ vs. $2.5\text{--}3.2 \times 2\text{--}2.5 \mu\text{m}$, Bernicchia & Gorjón 2010). A detailed morphological comparison between our new species and the phylogenetically closely related species are presented in Table 2. Based on these morphological characteristics and phylogenetic evidence, we introduce *Si. albofarinaceum* as a new species.

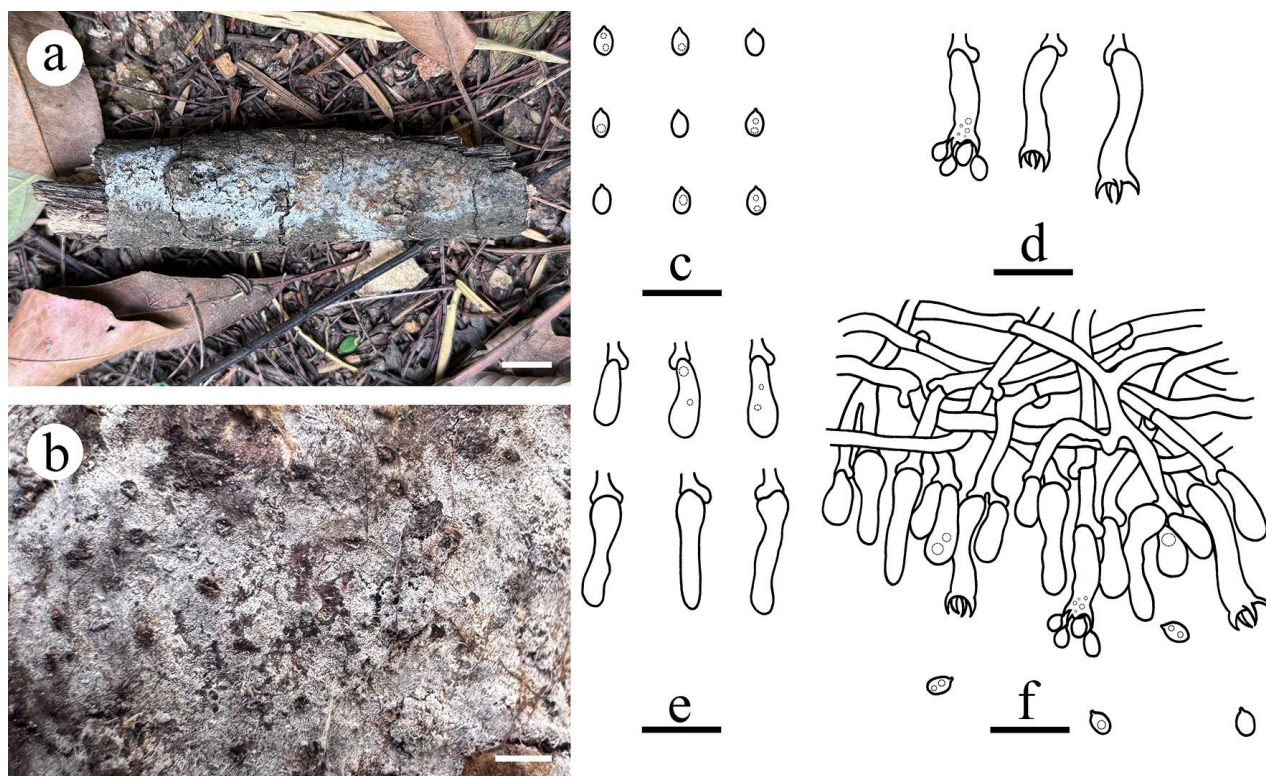


Figure 44 – Basidiomata and microscopic structures of *Sistotrema albofarinaceum* (holotype, CLZhao 34805). a Basidiomata on the substrate. b Macroscopic characteristics of hymenophore. c Basidiospores. d Basidia. e Basidioles. f section of hymenium. Scale bars: a = 1 cm, b = 1 mm, c–f = 10 μm .

Sistotrema fissuratum J.H. Dong & C.L. Zhao, sp. nov.

Fig. 45

Index Fungorum number: IF 904410; Facesoffungi number: FoF 18431

Diagnosis – Differs from other *Sistotrema* species by the coriaceous basidiomata with cream to slightly buff, smooth hymenial surface, a monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring $3.5\text{--}4.6 \times 2.3\text{--}3 \mu\text{m}$.

Etymology – *fissuratum* (Lat.): referring to the cracked hymenophore of the type specimen.

Basidiomata annual, resupinate, coriaceous, without odor or taste when fresh, becoming hard coriaceous upon drying, up to 10 cm long, 5 cm wide, 100–200 μm thick. *Hymenial surface* smooth, cracked, cream when fresh, turning to cream to slightly buff upon drying. *Sterile margin* cream, thinning out, slightly fimbriate, up to 1 mm wide. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 3–5 μm in diam.;

IKI–, CB–, tissues unchanged in KOH. *Gloeocystidia* colorless, thin-walled, sinuous, $37\text{--}90.5 \times 7.5\text{--}10.5 \mu\text{m}$. *Cystidioles* absent. *Basidia* suburniform to subcylindrical, slightly constricted, with 6-sterigmata and a basal clamp connection, $14\text{--}19 \times 4.5\text{--}6.5 \mu\text{m}$. *Basidioles* dominant, in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, $3.5\text{--}4.6(4.8) \times (2\text{--})2.3\text{--}3 \mu\text{m}$, $L = 4.01 \mu\text{m}$, $W = 2.64 \mu\text{m}$, $Q = 1.40\text{--}1.70$, $Q_m = 1.52 \pm 0.09$ ($n = 30/1$).

Material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, $23^{\circ}48' \text{N}$, $97^{\circ}38' \text{E}$, altitude 1000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 4 July 2024, CLZhao 37732 (SWFC, holotype).

GenBank accession numbers – ITS: PV569136

Notes – The phylogenetic analyses based on the ITS sequence data (Fig. 43) revealed that our species *Sistotrema fissuratum* (CLZhao 37732) grouped within *Sistotrema*, forming a separate lineage sister to *Si. coroniferum* (He 6084B and KH Larsson s.n.) with 99% ML 100 MP, and 1.00 BYPP bootstrap support. However, *Si. coroniferum* can be delimited from *Si. fissuratum* by its longer basidiospores ($5\text{--}6 \times 2\text{--}2.5 \mu\text{m}$ vs. $3.5\text{--}4.6 \times 2.3\text{--}3 \mu\text{m}$, Bernicchia & Gorjón 2010). A detailed morphological comparison between our new species *Si. fissuratum* and similar species are presented in Table 2. Based on these morphological characteristics and phylogenetic evidence, we introduce *Si. fissuratum* as a new species.

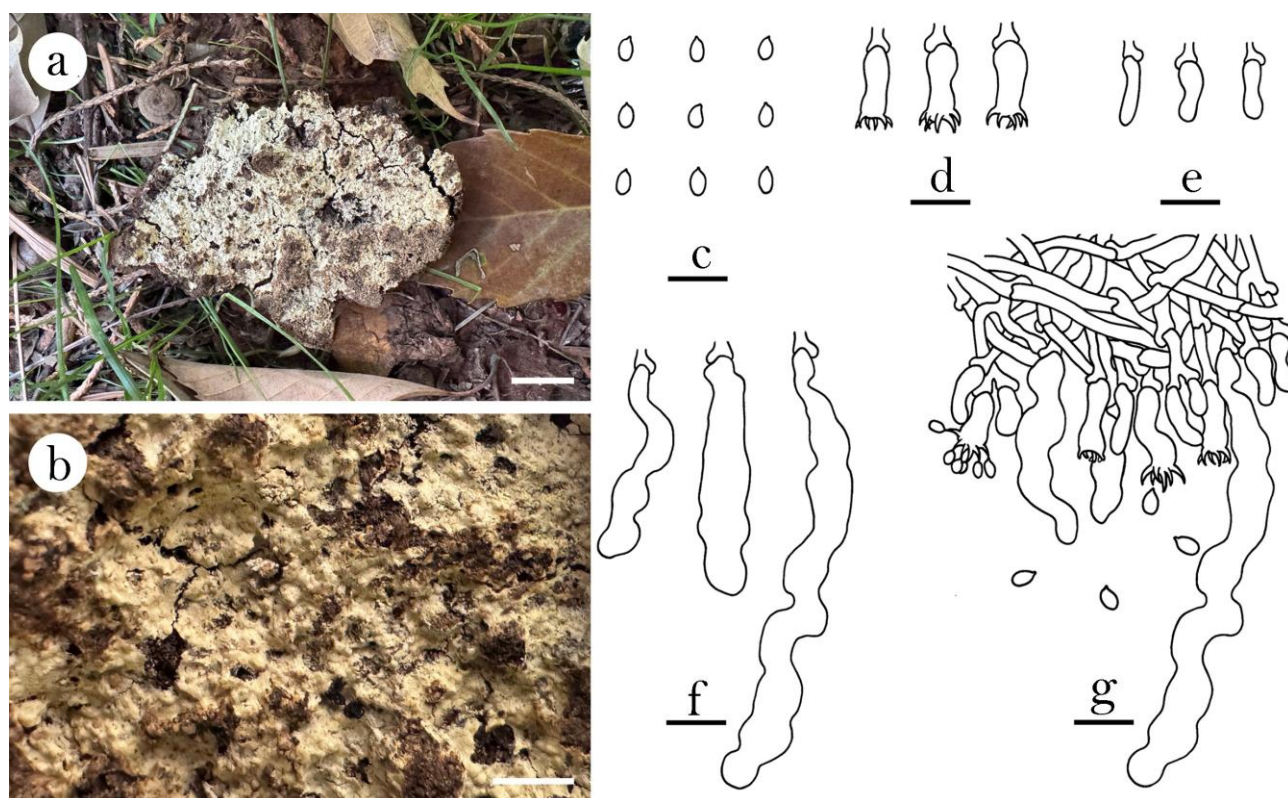


Figure 45 – Basidiomata and microscopic structures of *Sistotrema fissuratum* (holotype, CLZhao 37732). a Basidiomata on the substrate. b Macroscopic characteristics of hymenophore. c Basidiospores. d Basidia. e Basidioles. f Gloeocystidia. g A section of hymenium. Scale bars: a = 1 cm, b = 2 mm, c–g = 10 μm .

Corticiales K.H. Larss.

Punctulariaceae Donk T

Punctularia Pat.

Index Fungorum number: IF 18429; Facesoffungi number: FoF 18432

Notes – *Punctularia* was established by Patouillard (1895), with *Pu. atropurpurascens* ($\equiv$ *Pu. tuberculosa*) as the type species. The key morphological characteristics of this genus are the

structure of resupinate to effused-reflexed basidiomata, gelatinous when fresh, rigid upon drying, tuberculate or radial ridges hymenophore, a monomitic hyphal system with clamped generative hyphae, yellowish to brown dendrohyphidia, and thin-walled, smooth, ellipsoid, acyanophilous basidiospores (Bernicchia & Gorjón 2010). Currently, *Punctularia* contains four accepted species as listed *Pu. atropurpurascens*, *Pu. bambusicola*, *Pu. nigrodontea* and *Pu. strigosozonata* (Index Fungorum 2025, Yang et al. 2025b). In this study, *Punctularia fragilis* sp. nov. was introduced from China based on the ITS+nLSU sequence data (Fig. 46) and morphological characteristics (Fig. 47).

Table 2 A morphological comparison between two new *Sistotrema* species and similar species in the genus *Sistotrema*.

Species name	Hymenial surface	Basidia (µm)	Basidiospores (µm)	References
<i>Sistotrema albofarinaceum</i>	Smooth/ cream to pale-grey	Subcylindrical, 4-sterigmata; 12–18.5 × 2.5–5	Ellipsoid; 3.5–4.6 × 2.3–3	Present study
<i>Si. brinkmannii</i>	Grandinioid/ whitish to cream	Uniform, 6–8-sterigmata; 15–20 × 4–6	Suballantoid; 4–5 × 2–2.5	Bernicchia & Gorjón (2010)
<i>Si. chloroporum</i>	Poroid/ whitish to cream	Uniform, 4–6 sterigmata; 15.5–27 × 7–9	Subglobose to broadly ellipsoid; 4.5–6.5 × 3.5–6	Sugawara et al. (2022)
<i>Si. confluens</i>	Smooth/ whitish to cream	Uniform, 6–8 sterigmata; 15–20 × 4–6	Narrowly ellipsoid to suballantoid; 4.5–6 × 2–2.5	Bernicchia & Gorjón (2010)
<i>Si. coroniferum</i>	Smooth/ whitish	Uniform, 6-sterigmata; 15–20 × 4–5	Subcylindrical; 5–6 × 2–2.5	Bernicchia & Gorjón (2010)
<i>Si. diademiferum</i>	Smooth to porulose/ whitish	Uniform, 6 sterigmata; 15–20 × 5–7	Ovoid to subglobose; 3.5–5 × 3–3.5	Bernicchia & Gorjón (2010)
<i>Si. fissuratum</i>	Smooth/ cream to slightly buff	Subuniform to subcylindrical; 6-sterigmata; 14–19 × 4.5–6.5	Ellipsoid; 2.5–3.2 × 2–2.5	Present study
<i>Si. flavorhizomorphae</i>	Hydnoid, to irpicoid/ cream to pale ocher	Uniform, 6–8-sterigmata; 10.5–20 × 5–6.5	Globose to ovoid; 3–3.5 × 2.5–3	Sugawara et al. (2022)
<i>Si. luteoviride</i>	Smooth/ yellowish or yellowish green	Uniform or subcylindrical, 6-sterigmata; 21–36 × 6–8	Broadly ellipsoid; 5–5.6 × 3–3.6	Kotiranta & Larsson (2013)
<i>Si. macabouense</i>	Smooth/ yellowish and porulose	Uniform, 4–6-sterigmata; 17–22 × 6–7	Subglobose; 5–6 × 4–5	Gruhn et al. (2017)
<i>Si. macrosporum</i>	Smooth, tuberculate	Subuniform to uniform, 4-sterigmate; 20–34 × 8–9	Narrowly ellipsoid to suballantoid; 8–11.5 × 3–3.7	Kaur et al. (2019)
<i>Si. subconfluens</i>	Smooth/ buff to cinnamon-buff	Uniform, 6-sterigmata (occasionally 2 or 4); 10–18 × 4–7	Short-cylindrical to oblong ellipsoid; 3.9–4.2 × 2–2.3	Zhou & Qin (2013)
<i>Si. yunnanense</i>	Smooth/ white to pale cream	Subuniform to uniform, 4-sterigmata; 13.5–24 × 2.5–5.5	Subcylindrical to oblong ellipsoid; 4.5–6.5 × 3–4	Cai & Zhao (2023)

Punctularia fragilis Y. Yang & C.L. Zhao, sp. nov.

Fig. 47

Index Fungorum number: IF 904411; Facesoffungi number: FoF 18433

Diagnosis – Differs from other *Punctularia* species by the fragile basidiomata with white to cinnamon-buff to slightly brown hymenophore surface, a hyphal system monomitic with clamped generative hyphae, and ellipsoid basidiospores (4–5 × 3–3.5 µm).

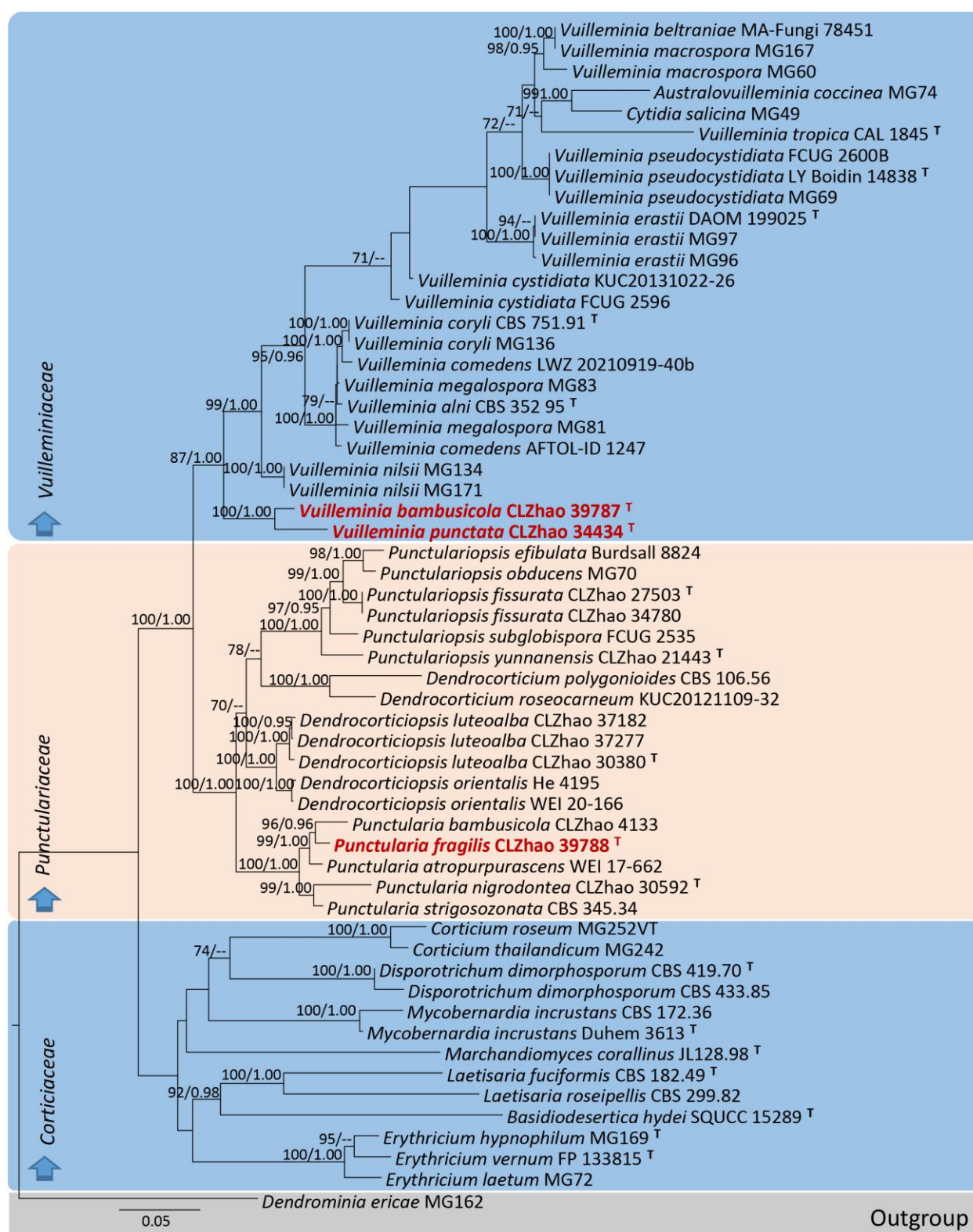


Figure 46 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and nLSU sequence data of *Corticiales*. Thirty-nine specimens are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -16454.287 is presented. The evolutionary model GTR+F+I+G4 is applied for all the genes. The matrix had 1066 distinct alignment patterns. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Dendrominia ericae* (MG162). The newly generated sequences are in red-bold, and the type collections are indicated with ^T.

Etymology – *fragilis* (Lat.): referring to the fragile basidiomata when dry.

Basidiomata annual, resupinate, adnate but easily separable from substrate, membranous, without odor or taste when fresh, up to 10 cm long, 4 cm wide, and 50–300 µm thick. *Hymenophore surface* smooth, white to cinnamon-buff when fresh, cinnamon-buff to slightly brown when drying. *Sterile margin* white to cream, up to 2 mm wide. *Hyphal system* monomitic, generative hyphae with clamp connections, IKI–, CB–, tissues unchanged in KOH. *Subiculum* absent or indistinct, subhymenial generative hyphae hyaline, more or less interwoven, thin-walled, frequently branched, 1.5–2.5 µm in diam., subhymenial generative hyphae colorless, thick-walled, branched, 2–3.5 µm in diam. *Cystidia* absent. *Dendrohyphidia* numerous, colorless, thin-walled. *Basidia* subclavate, flexuous, thin-walled, with 4 sterigmata and a basal clamp connection, 10–17 × 3–4.5 µm. *Basidioles* numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, 4–5(–5.5) × 3–3.5(–4) µm, L = 4.58 µm, W = 3.31 µm, Q = 1.38 (n = 30/1).

Material examined – China, Yunnan Province, Dehong, Mang City, Tongbiguan Provincial Nature Reserve, 25°50'N, 97°36'E; altitude 1000 m, on the fallen angiosperm branches, 8 Jul 2024, CLZhao 39788 (SWFC, holotype).

GenBank accession numbers – ITS: PV475634, LSU: PV490570.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 46) revealed that our species *Punctularia fragilis* (CLZhao 39788) grouped within the genus *Punctularia*, forming a sister lineage to *Pu. bambusicola* C.L. Zhao (CLZhao 4133) with 96% ML and 0.96 BYPP bootstrap support. These two species have a close phylogenetic affinity with *Pu. atropurpurascens* (WEI 17-662). However, *Punctularia bambusicola* differs from *Pu. fragilis* by its gelatinous to rigid basidiomata, resupinate, tuberculate with rose tints, pink to purple hymenophore surface, larger basidia (17.5–21.5 × 4–5.5 µm) and basidiospores (6.5–8.5 × 3.5–5 µm; Guan et al. 2021a). Also, *Pu. atropurpurascens* can be distinguished from *Pu. fragilis* by its reddish-brown to dark purplish-brown or bluish hymenial surface and larger basidia (40–65 × 5–6 µm, Yang et al. 2025b). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Pu. fragilis* as a new species.

***Vuilleminiaceae* Maire ex Lotsy**

***Vuilleminia* Maire**

Index Fungorum number: IF 18743; Facesoffungi number: FoF 18434

Notes – *Vuilleminia* was introduced by Maire (1902) to accommodate *Vuilleminia comedens* (as *Corticium comedens*). The genus is characterized by ceraceous to latexy, resupinate basidiomata with a smooth to tuberculate hymenophore, a monomitic hyphal system with clamp connections, and thin-walled, dendrohyphidia present and allantoid to ellipsoid basidiospores (Bernicchia & Gorjón 2010). Species of this genus are common in Europe on dead or decaying but attached branches of woody angiosperms (Ghobad-Nejhad et al. 2010). Currently, *Vuilleminia* contains 13 species (Crous et al. 2023b). In this study, we described the new species *Vuilleminia bambusicola* sp. nov. and *V. punctata* are introduced from China based on the ITS+nLSU sequence data (Fig. 46) and morphological characteristics (Figs 48, 49).

***Vuilleminia bambusicola* L. Wang & C.L. Zhao, sp. nov.**

Fig. 48

Index Fungorum number: IF 904412; Facesoffungi number: FoF 18435

Diagnosis – Differs from other *Vuilleminia* species by the membranaceous basidiomata with white to cream, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 8–10 × 5.5–7 µm.

Etymology – *bambusicola* (Lat.): referring to growing of the type specimen on bamboo.

Basidiomata annual, resupinate, adnate, inseparable from substrate, membranous, without odor or taste when fresh, up to 10 cm long, 3 cm wide, and 50–200 µm thick. *Hymenophore surface* smooth, white when fresh, white to cream when drying. *Sterile margin* white, up to 1 mm. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently

branched, interwoven, 2.5–3.5 μm in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* absent. *Dendrohyphidia* numerous, colorless, thin-walled. *Basidia* clavate, flexuous, thin-walled, with 4 sterigmata and a basal clamp connection, 32–53 $\times$ 5.5–10.5 μm , *Basidioles* numerous, similar to basidia in shape but smaller. *Basidiospores* ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (7.5–)8–10(–10.5) $\times$ 5.5–7(–7.5) μm , $L = 9.01 \mu\text{m}$, $W = 6.41 \mu\text{m}$, $Q = 1.41$ ($n = 30/1$).



Figure 47 – Basidiomata and microscopic structures of *Punctularia fragilis* (CLZhao 39788, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e *Dendrohyphidia*. f A section of the hymenium. Scale bars: a = 1 cm, b = 2 mm, c–f = 10 μm .

Material examined – China, Yunnan Province, Dehong, Mang, Tongbiguan Provincial Nature Reserve, 25°50'N, 97°36'E; altitude 1000 m, on the fallen angiosperm branches, 8 Jul 2024, CLZhao 39787 (SWFC, holotype).

GenBank accession numbers – ITS: PV475632, LSU: PV490569.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 46) revealed that our species *Vuilleminia bambusicola* (CLZhao 39787) clustered within *Vuilleminia*. It formed a basal lineage to the genus and was sister to *V. punctata* (CLZhao 34434) with 100% ML and 1.00 BYPP bootstrap support. *Vuilleminia punctata* can be delimited from *V. bambusicola* by its leptocystidia and gloeocystidia present, shorter basidia (22–32 $\times$ 5.5–8 μm). Also, *Vuilleminia comedens* can be delimited from *V. bambusicola* by its gelatinous to ceraceous basidiomata, cream to ochraceous white hymenophore surface, longer basidia (70–120 $\times$ 5–8 μm), and larger allantoid basidiospores (18–23 $\times$ 5–7 μm , Ghobad-Nejhade et al. 2010). Thus, based on morphological evidence and multigene phylogenetic analysis, we introduce *V. bambusicola* as a new species.

Vuilleminia punctata L. Wang & C.L. Zhao, sp. nov.

Fig. 49

Index Fungorum number: IF 904413; Facesoffungi number: FoF 18436

Diagnosis – Differs from other *Vuilleminia* species by the coriaceous to membranous basidiomata with white to buff, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 7–8.5 $\times$ 4–5 μm .

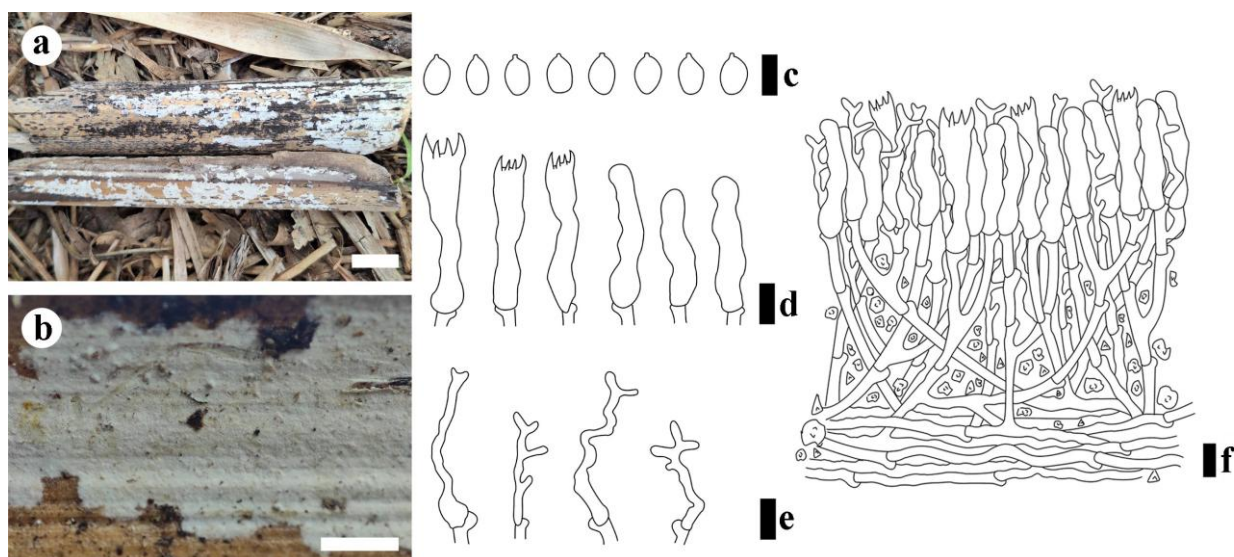


Figure 48 – Basidiomata and microscopic structures of *Vuilleminia bambusicola* (CLZhao 39787, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e Dendrohyphidia. f A section of the hymenium. Scale bars: a = 1 cm, b = 2 mm, c–f = 10 μ m.

Etymology – *punctata* (Lat.): referring to the punctate or dotted basidiomata when dry.

Basidiomata annual, resupinate, adnate, inseparable from substrate, coriaceous to membranaceous, without odor or taste when fresh, up to 15 cm long, 2 cm wide, and 50–600 μ m thick. *Hymenophore surface* smooth, white when fresh, white to buff when drying, cracked. *Sterile margin* white, up to 1 mm. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 3–4 μ m in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* of two types: (1) leptocystidia fusoid to conical, colorless, thin-walled, with a basal clamp connection, 32–44 $\times$ 4–6.5 μ m; (2) gloeocystidia tubular to vesicular, colorless, thin-walled, with a basal clamp connection, 13–22 $\times$ 6.5–8 μ m. *Basidia* cylindrical, thin-walled, with 4 sterigmata and a basal clamp connection, 22–32 $\times$ 5.5–8 μ m. *Basidioles* numerous, similar to basidia in shape but smaller. *Basidiospores* ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, 7–8.5(–9) $\times$ (3.5–)4–5 μ m, L = 7.86 μ m, W = 4.41 μ m, Q = 1.79 (n = 30/1).

Material examined – China, Yunnan Province, Diqing, Weixi, Songpo Village, 27°16'N, 99°15'E; altitude 2250 m, on the fallen angiosperm branches, 13 October 2023, CLZhao 34434 (SWFC, holotype).

GenBank accession numbers – ITS: PV475633.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 46) revealed that the sample of our species *Vuilleminia punctata* (CLZhao 34434) grouped within *Vuilleminia*, formed a basal lineage to the genus and sister to *V. bambusicola* (CLZhao 39787) with 100% ML and 1.00 BYPP bootstrap support. However, *Vuilleminia bambusicola* differs from *V. punctata* by its absence of cystidia, and longer basidia (32–53 $\times$ 5.5–10.5 μ m). Also, *V. comedens* can be distinguished from *V. punctata* by its gelatinous to ceraceous basidiomata, cream to ochraceous white hymenophore surface, longer basidia (70–120 $\times$ 5–8 μ m), and larger allantoid basidiospores (18–23 $\times$ 5–7 μ m, Ghobad-Nejhade et al. 2010). Thus, based on morphology and multigene phylogenetic evidence, we introduce *V. punctata* as a new species.

Hymenochaetales Oberw.

Hymenochaetaceae Donk

Hymenochaete Lév.

Index Fungorum number: IF 17816; Facesoffungi number: FoF 17683

Notes – *Hymenochaete*, the type genus of *Hymenochaetaceae* was established by Lévillé (1846) mainly based on the presence of setae in the hymenium and typified by *Hym. rubiginosa*.

Burt (1918) was the first to recognize the three distinct layers within the basidiomata of *Hymenochaete*: a setal layer (containing the setae), a context/subiculum (hyphal layer without setae) and a cortex (consisting of agglutinated hyphae; in several cases, a tomentum is developed covering the cortex). Based on the specific occurrence of these three layers within taxa, Léger (1998) divided *Hymenochaete* into four sections. The genus is characterized by basidiomata mostly annual, rarely perennial, resupinate, effused-reflexed to pileate, rarely stipitate, usually thin, membranous or coriaceous to hard corky, sometimes brittle; hymenial surface mostly smooth, rarely hydroid, lamellate, poroid or verruculose, mostly cracked with age, usually brown, darkening in KOH; hyphal system monomitic; generative hyphae simple-septate, mostly hyaline to yellowish, thin- to thick-walled; setal hyphae and setae present in some species; hyphidia present in some species; basidiospores mostly ellipsoid, oblong-ellipsoid to cylindrical, rarely allantoid or subglobose, hyaline, thin-walled, smooth, negative in Melzer's reagent and Cotton Blue; on angiosperm and gymnosperm wood, and causing a white rot (Dai 2010, He & Dai 2012, Wu et al. 2022a). *Hymenochaete* is a genus with smoothest hymenophore in *Hymenochaetaceae* which was extensively and systematically studied both in China and the world (Dai 2010, He & Dai 2012, Wu et al. 2022a), and its evolution was analyzed by Zhao et al. (2025c). The species of the genus are medicinal fungi and forest pathogens (Wu et al. 2019b, Yuan et al. 2023, Ghobad-Nejhad et al. 2024). To date, 225 species have been accepted in the world (Liu et al. 2025a). In this study, *Hymenochaete malaysiana* sp. nov. was introduced from Malaysia based on the ITS+nLSU+mtSSU sequence data (Fig. 50) and morphological characteristics (Fig. 51).

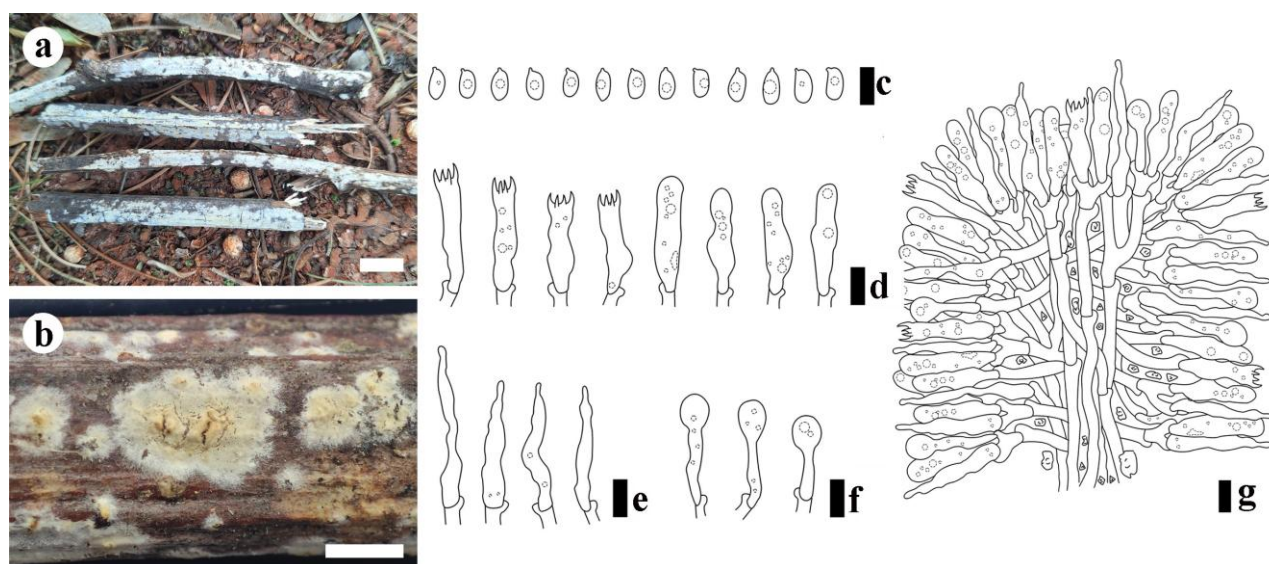


Figure 49 – Basidiomata and microscopic structures of *Vuilleminia punctata* (CLZhao 34434, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e Leptocystidia. f Gloeocystidia. g A section of the hymenium. Scale bars: a = 1 cm, b = 2 mm, c–g = 10 µm.

***Hymenochaete malaysiana* Z.B. Liu, sp. nov.**

Fig. 51

Index Fungorum number: IF 903802; Facesoffungi number: FoF 17684

Diagnosis – The new species differs from other *Hymenochaete* species by the light vinaceous gray to lilac to brownish vinaceous hymenophore surface with verruculose, a hyphal system monomitic with hyaline to orange-yellow generative hyphae bearing simple septa, and oblong-ellipsoid to allantoid basidiospores.

Etymology – *malaysiana* (Lat.): referring to the species being found in Malaysia.

Basidiomata annual, resupinate, adnate, inseparable from substrate, corky and without odor or taste when fresh, first as small colonies, then confluent up to 8 cm long, 4 cm wide, 0.4 mm thick at center. **Hymenophore surface** verruculose, light vinaceous gray when fresh, lilac to

brownish vinaceous upon drying, uncracked when fresh, cracked upon drying; margin straw yellow. *Tissues* darkening in KOH. *Tomentum*, cortex and hyphal layer absent; setal layer present. An agglomeration of crystals abundant in the setal layer. *Hyphal system* monomitic, all septa without clamp connections. *Generative hyphae* hyaline to orange-yellow, thin- to thick-walled, agglutinated, frequently branched, interwoven, 1–2 µm in diam. *Setae* abundant, subulate, thick-walled, brown, with obtuse tips, projecting up to 80 µm above the hymenium, (80–)82–103(–104) × 9–12 µm. *Hyphidia* absent. *Basidia* clavate, thin-walled, bearing four sterigmata and a simple septum at the base, 16–24 × 4–5 µm, *Basidioles* in shape similar to basidia, but smaller. *Basidiospores* oblong-ellipsoid to allantoid, hyaline, thin-walled, smooth, IKI–, CB–, 6–8 × 2.5–3 µm, L = 6.67 µm, W = 2.9 µm, Q = 2.21–2.42 (n = 60/2).

Material examined – Malaysia, Kuala Lumpur, Kota Damansara Community Forest Reserve, on dead liana branch, 6 December 2019, He 6380 (BJFC 033324, holotype), *ibid.*, on dead angiosperm branch, He 6423 (BJFC 033367, paratype).

GenBank accession numbers – He 6380: ITS = OR287565, LSU = OR287640; He 6423: ITS = OR287564, LSU = OR287639, mtSSU = OR295575.

Notes – The combined ITS+nLSU+mtSSU phylogenetic analyses (Fig. 50) revealed that the collections of our species *Hymenochaete malaysiana* (He 6380, He 6423) grouped within *Hymenochaete*, forming a separate clade sister to *Hym. cylindrospora* (He 773, Dai 14890) with 94% ML and 1.00 BYPP bootstrap support. Also, the clade with *Hym. malaysiana* and *Hym. cylindrospora* are closely related to *Hym. vaginata* (He 6380, He 6423). Morphologically, *Hym. malaysiana* is characterized by resupinate basidiomata, a verruculose hymenophore surface, the absence of a tomentum, cortex and hyphal layer, setae measuring 82–103 × 9–12 µm, and oblong-ellipsoid to allantoid basidiospores measuring 6–8 × 2.5–3 µm. *Hymenochaete cylindrospora* differs from *Hym. malaysiana* by having bigger basidiospores (9–11 × 3–3.2 vs. 6–8 × 2.5–3 µm) and *Hym. vaginata* differs from *Hym. malaysiana* by having narrower basidiospores (7–8 × 2.5 vs. 6–8 × 2.5–3 µm, Cunningham 1957). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Hym. malaysiana* as a new species.

***Polyporales* Gäum.**

***Hyphodermataceae* Jülich**

***Hyphoderma* Wallr.**

Index Fungorum number: IF 17823; Facesoffungi number: FoF 2835

Notes – *Hyphoderma* represents one of the most species-rich and taxonomically complicated genera among wood-inhabiting fungi, typified by *Hyp. setigerum* (Donk 1957, Nilsson et al. 2003, Kirk et al. 2008, Yurchenko & Wu 2015). *Hyphoderma* species can cause white-rot (Wu 1997), and it is one of the most important fungal groups in the forest ecosystem (Floudas et al. 2012, Yang et al. 2024b). This genus is characterized by the resupinate to effuse-reflexed basidiomata with ceraceous consistency, smooth to tuberculate or hydroid hymenophore, a monomitic hyphal structure (rarely dimitic) with clamp connections on generative hyphae, presence of cystidia or not, suburniform to subcylindrical and cylindrical basidia, and smooth, thin-walled, ellipsoid to subglobose basidiospores (Bernicchia & Gorjón 2010). A total of 214 specific and infraspecific names are listed under *Hyphoderma* in Index Fungorum (2025) and MycoBank (2025), whereas 136 species have been accepted worldwide (Donk 1957, Nakasone 2008, Baltazar et al. 2016, Martín et al. 2018, Guan et al. 2021b, Guan & Zhao 2021, Ma et al. 2021, Duan et al. 2023, Yang et al. 2023a, Su et al. 2024, Li et al. 2025, Yang et al. 2025b). In this study, *Hyphoderma fragilissimum* sp. nov., *Hyphoderma punctatum* sp. nov., and *Hyphoderma yingjiangense* sp. nov. are introduced from China based on the ITS+nLSU sequence data (Fig. 52) and morphological characteristics (Figs 53, 54, 55, 56).

***Hyphoderma fragilissimum* Y.L. Deng & C.L. Zhao, sp. nov.**

Figs 53, 54

Index Fungorum number: IF 858754; Facesoffungi number: FoF 18437

Diagnosis – *Hyphoderma fragilissimum* is characterized by the membranous basidiomata with white to cream hymenial surface hypochnoid, a hyphal system monomitric with clamped generative hyphae, and ellipsoid to ovoid basidiospores measuring $13.8\text{--}18.6 \times 10\text{--}12.9 \mu\text{m}$.

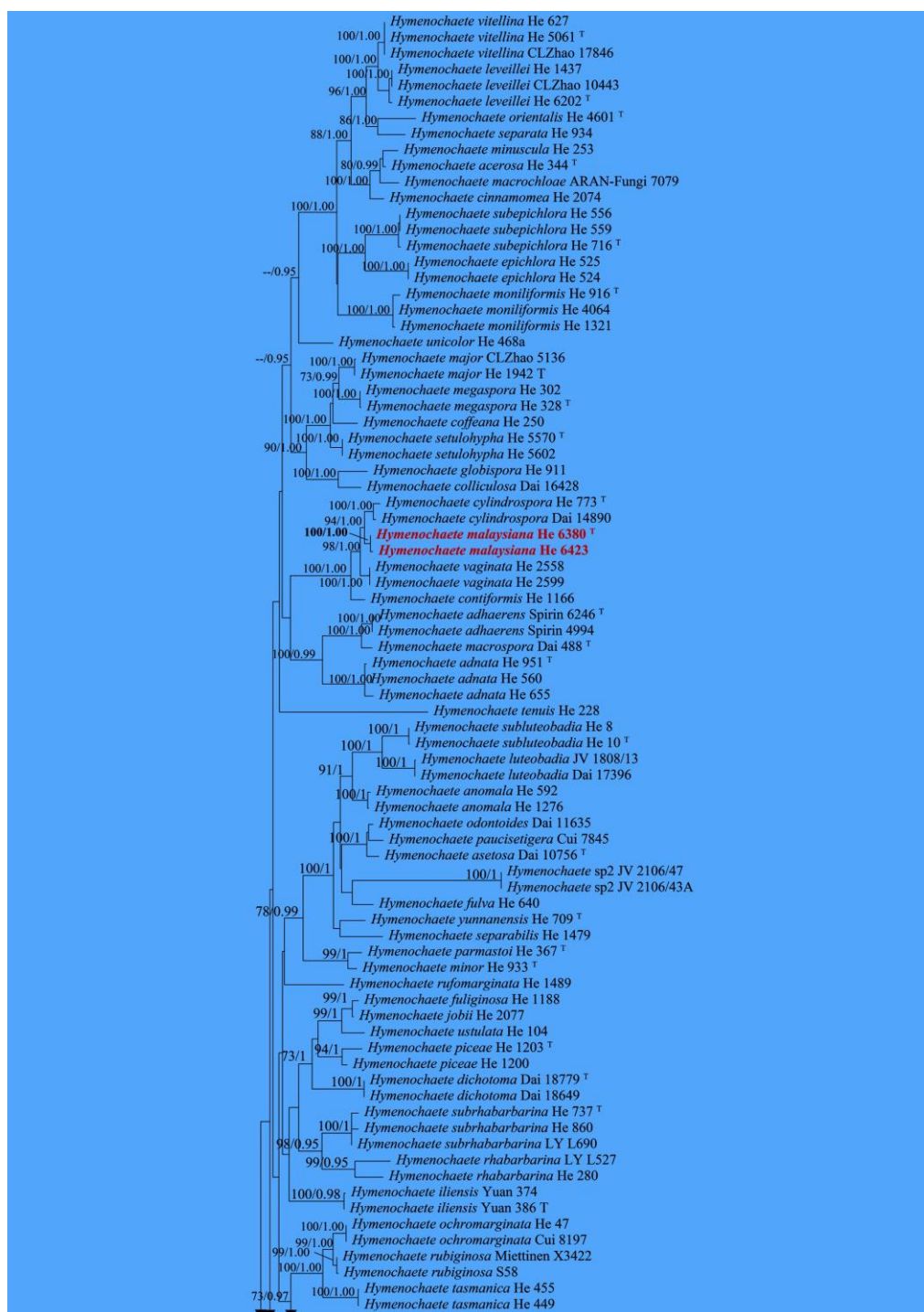


Figure 50 – Phylogram generated from maximum likelihood analysis based on combined ITS+LSU+mtSSU sequences. Two hundred and twelve specimens of *Hymenochaete* are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near the nodes, respectively. The tree was rooted with *Hydnoporia olivacea* (Miettinen X3403, Miettinen X3273). The newly generated sequences are indicated in red-bold, and the holotype, paratype and epitype collections are indicated with ^T, ^{PT}, and ^{ET}, respectively.

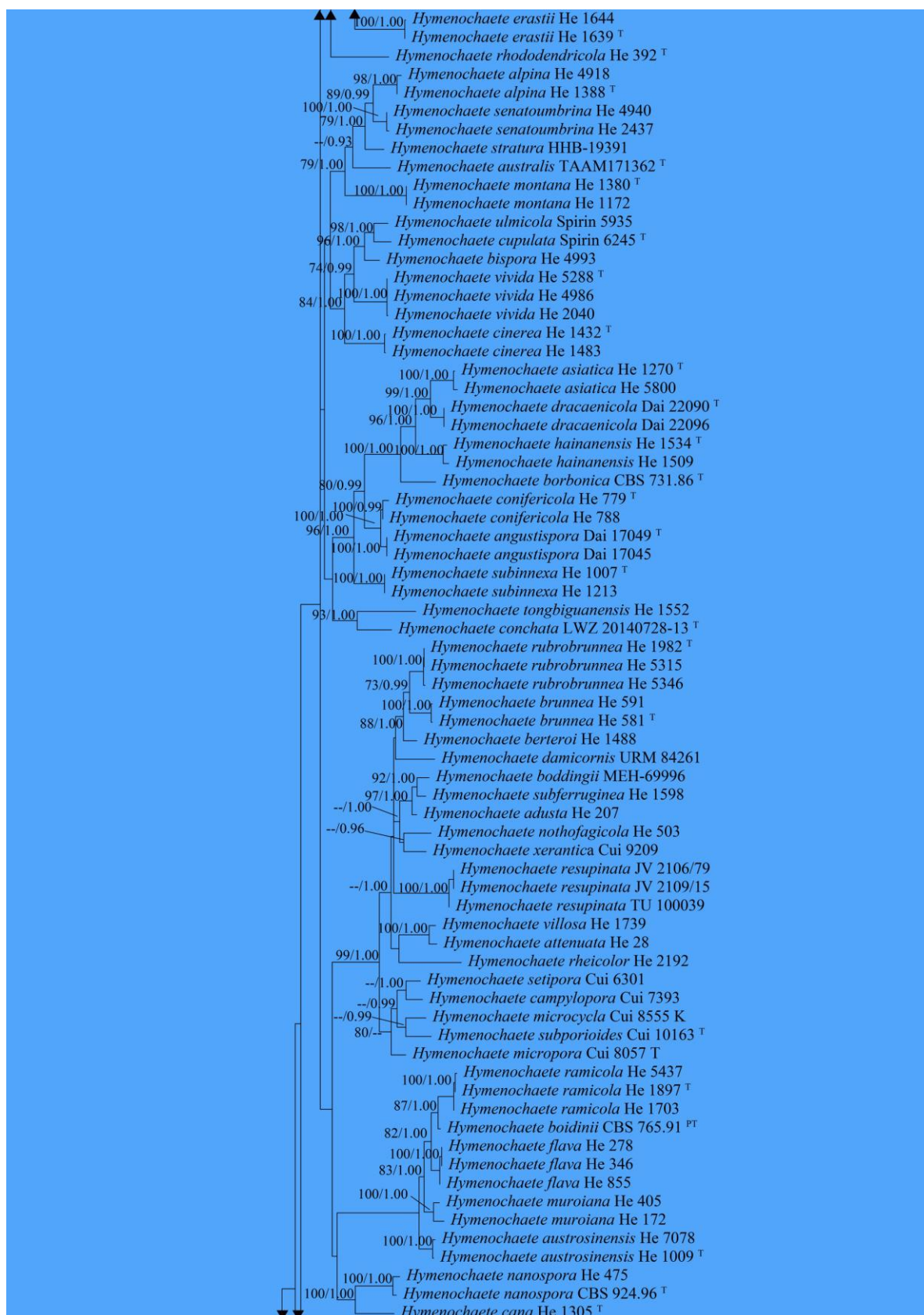


Figure 50 – Continue.

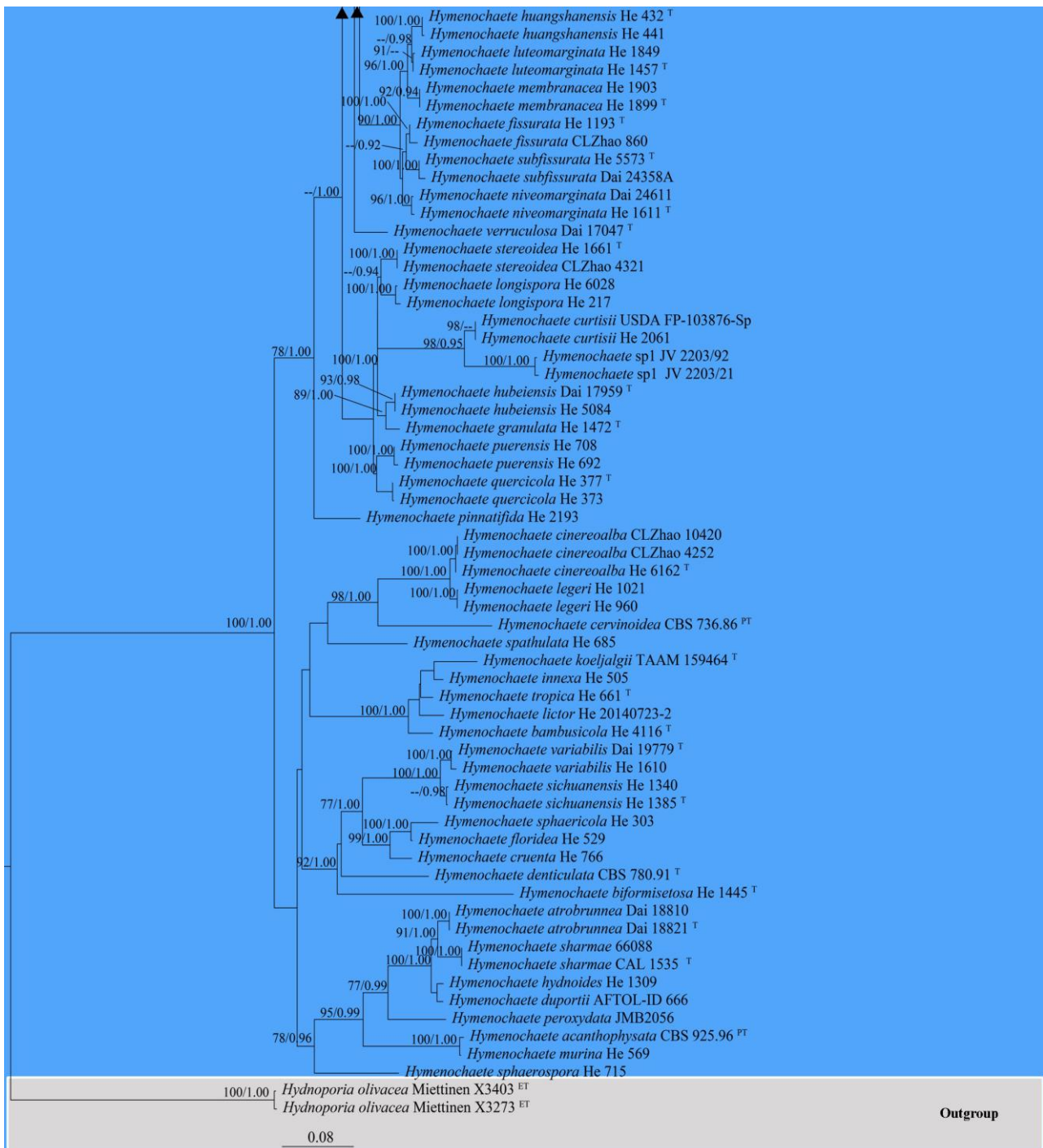


Figure 50 – Continue.

Etymology – *fragilissimum* (Lat.): referring to the fragile basidiomata of the type specimen.

Basidiomata annual, resupinate, closely adnate, membranous, thin, without odor or taste when fresh, up to 10 cm long, 3.5 cm wide, and 100 µm thick. *Hymenial surface* smooth, thin, slightly cream to cream when fresh, cream to buff to apricot-orange upon drying. *Sterile margin* slightly cream, up to 1 mm. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, smooth, moderately branched, 6–8 µm in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* cylindrical, 40–51 × 10.6–12.7 µm. *Basidia* cylindrical, with a basal clamp connection and two sterigmata, 30–45 × 8–12.9 µm. *Basidioles* numerous, in shape similar to basidia but smaller. *Basidiospores* ellipsoid to ovoid, colorless, thin-walled, smooth, IKI–, CB–, (13–)13.8–18.6(–18.9) × (9.7–)10–12.9(–13.1) µm, L = 16.41 µm, W = 11.49 µm, Q = 1.43 (n = 30/1).

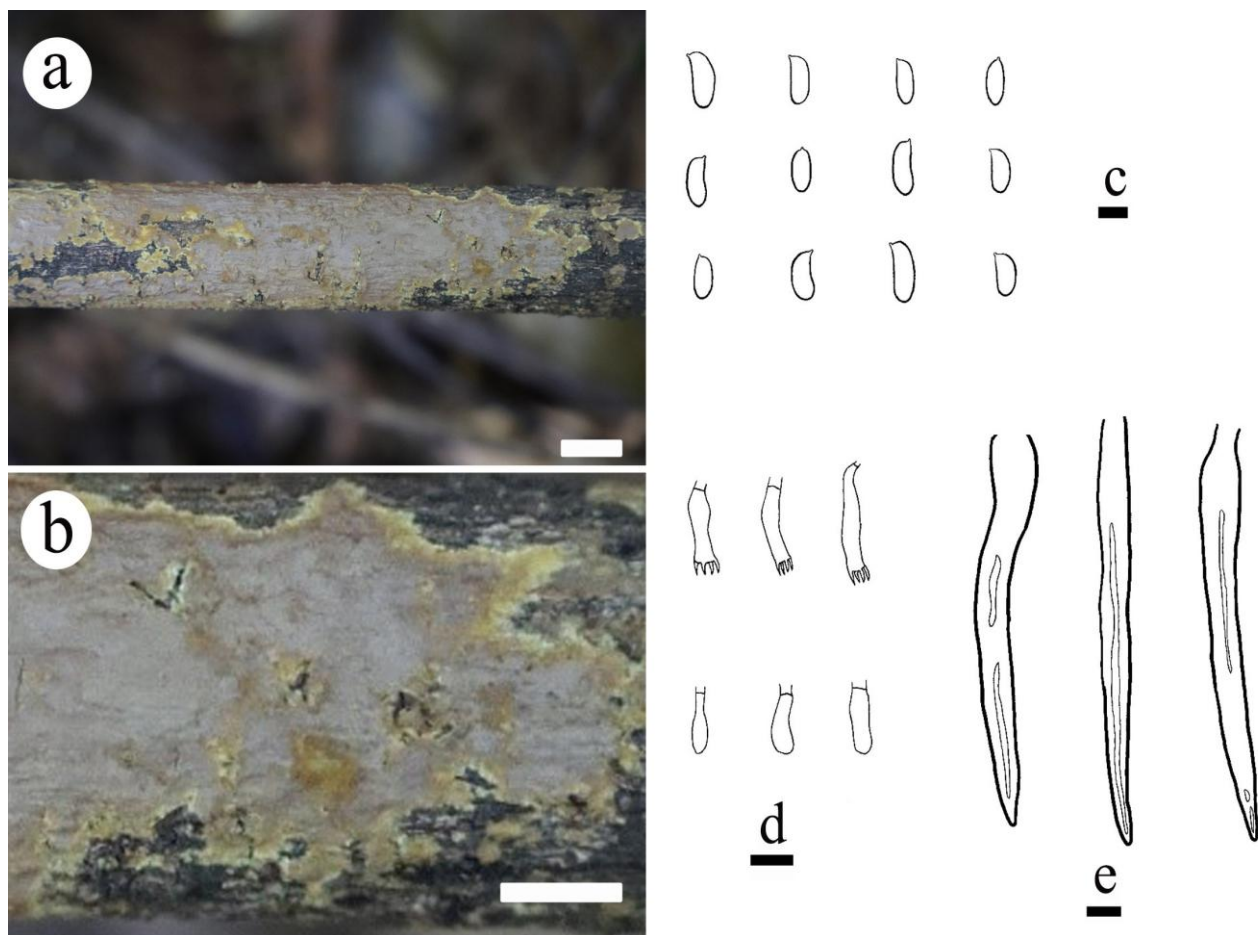


Figure 51 – Basidiomata and microscopic structures of *Hymenochaete malaysiana* (He 6380, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e Setae. Drawings by Zhan-Bo Liu. Scale bar a, b = 1 cm, c = 5 μ m, d, e = 10 μ m.

Material examined – China, Yunnan Province, Wenshan City, Pingba Town, Wenshan National Nature Reserve, GPS coordinates: 23°24' N, 104°09' E, altitude 2200 m asl., on *Picea* stump (*Pinaceae*), leg. C.L. Zhao, 28 July 2019, CLZhao 17245 (SWFC, holotype).

GenBank accession numbers – ITS: PV147166; LSU: PV185848.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 52) revealed that our species of *Hyphoderma fragilissimum* (CLZhao 17245) grouped within *Hyphoderma*, forming a distinct lineage sister to *Hyp. obtusiforme* (KHL1464, KHL11105) and *Hyp. obtusum* (JS17804) with 78% ML bootstrap support. Morphologically, *Hyp. obtusiforme* is distinguished from *Hyp. fragilissimum* by its narrower clavate to suburniform basidia (30–40 $\times$ 6–8 μ m), and smaller narrowly ellipsoid basidiospores (10–12 $\times$ 5–6 μ m, Eriksson & Ryvarden 1975); whereas *Hyp. obtusum* differs from *Hyp. fragilissimum* by its white to cream colored or rose-greyish hymenial surface, narrower clavate to suburniform basidia (30–40 $\times$ 6–8 μ m), and smaller basidiospores (8–10 $\times$ 5–6 μ m, Eriksson 1958). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Hyp. fragilissimum* as a new species.

Hyphoderma punctatum W. Li & C.L. Zhao, sp. nov.

Fig. 55

Index Fungorum number: IF 860786; Facesoffungi number: FoF 14010

Diagnosis – Differs from other *Hyphoderma* species by the membranous basidiomata, smooth hymenial surface, a monomitic hyphal system with clamped generative hyphae and with a median constriction basidia measuring 19–20 $\times$ 4.5–5 μ m.



Figure 52 – Phylogram generated from maximum parsimony strict consensus tree analysis based on the combined ITS and LSU sequence data of *Hyphoderma* (ITS = 696, LSU = 1350). Forty-one species were included in the combined sequence analyses. The tree topology of the maximum parsimony analysis is similar to the maximum likelihood and Bayesian analysis. Constant

characters were 1394. Parsimony-informative characters were 513 whereas parsimony-uninformative characters were 139. Bootstrap support values for $ML \geq 70\%$, $MP \geq 50\%$, and Bayesian posterior probabilities ≥ 0.95 are given near nodes, respectively. The tree was rooted with *Diplomitoporus crustulinus* (FD-137). The newly generated sequences are indicated in red-bold, and the type collections are indicated with ^T.

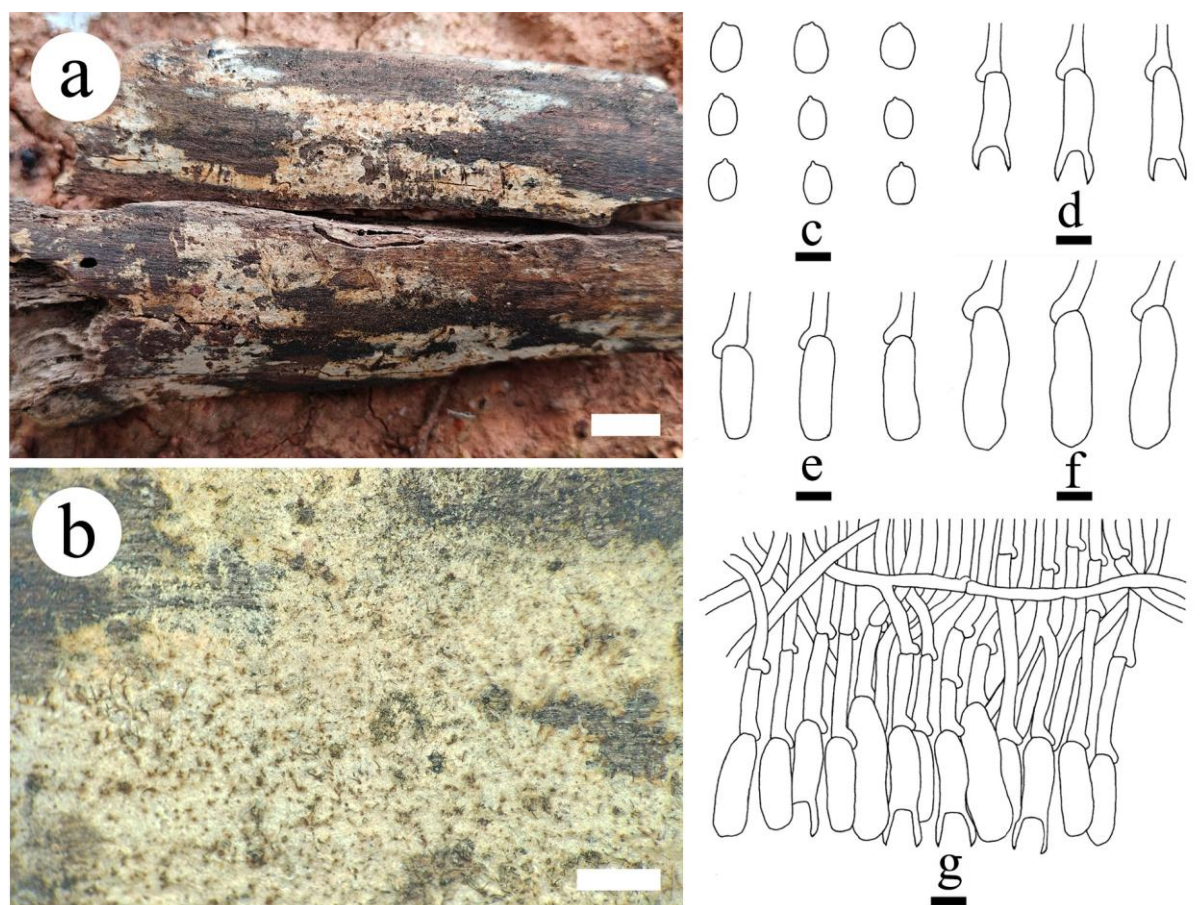


Figure 53 – Basidiomata and microscopic structures of *Hyphoderma fragilissimum* (CLZhao 17245, holotype). a Basidiomata on the substrates. b Characters of hymenophore. c Basidiospores. d Basidia. e Basidioles. f Cystidia. g A section of the hymenium. Scale bars: Scale bars: a = 1 cm, b = 1 mm, c–g = 10 μ m.

Etymology – *punctatum* (Lat.): referring to the punctate hymenophore surface.

Basidiomata annual, resupinate, adnate, membranous, without odor or taste when fresh, up to 8.5 cm long, 1.4 cm wide, 50–100 μ m thick. *Hymenial surface* smooth, white when fresh, turning to cream upon drying. *Sterile margin* thin, white, thinning out, up to 1 mm wide. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 3–3.5 μ m in diam.; IKI–, CB–, tissues unchanged in KOH. *Halocystidia* capitate, 34–37 $\times$ 5.5–6 μ m. *Basidia* clavate, with a median constriction, slightly thick-walled, with 4 sterigmata and a basal clamp connection, with oily contents, 19–20 $\times$ 4.5–5 μ m. *Basidioles* abundant, in shape similar to basidia, but slightly smaller. *Basidiospores* cylindrical to allantoid, colorless, thin-walled, smooth, with oil drop, IKI–, CB–, 7–8.5 $\times$ (2.5–)3–3.5(–4) μ m, $L = 7.71 \mu$ m, $W = 3.36 \mu$ m, $Q = 2.33 \mu$ m ($n = 30/1$).

Material examined – China, Yunnan Province, Zhaotong, Wumenshan National Nature Reserve, GPS coordinates 25°67' N, 103°66' E, altitude 2410 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 18 September 2023, CLZhao 33051 (SWFC, holotype).

GenBank accession numbers – ITS: PV469675

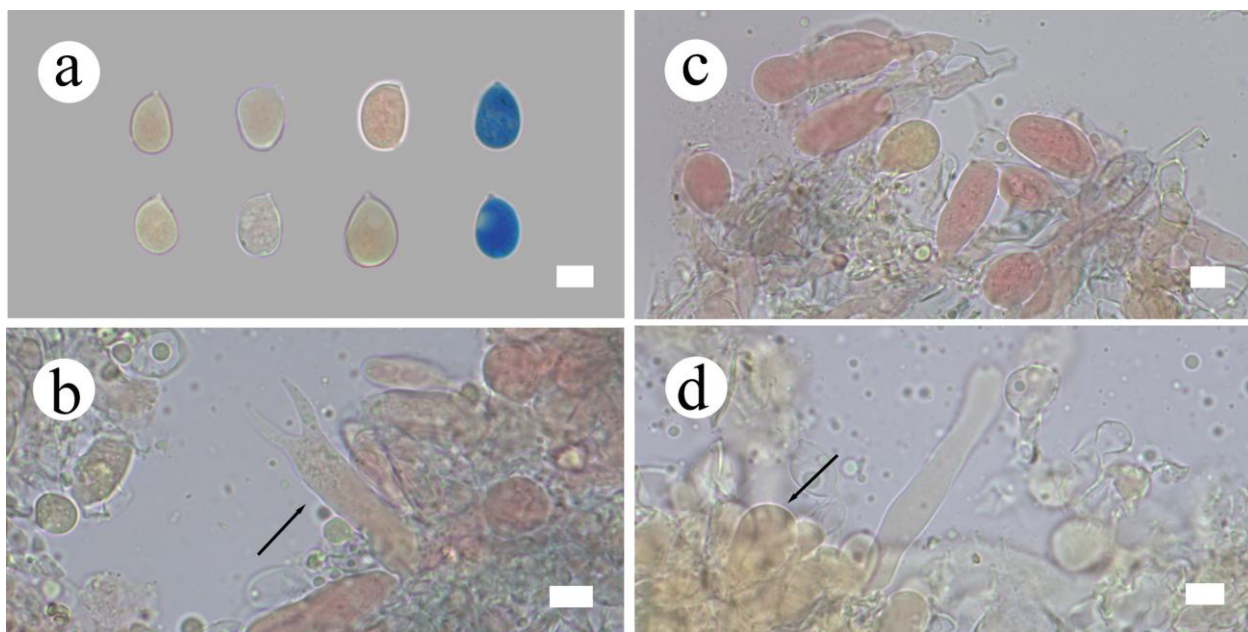


Figure 54 – a–d Sections of hymenium of *Hyphoderma fragilissimum* (CLZhao 17245, holotype). a Basidiospores. b Basidioles. c Basidia (arrowed). d Cystidia (arrowed). Scale bars: a–d = 10 μ m.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 52) revealed that our species *Hyphoderma Punctatum* (CLZhao 33051) grouped within *Hyphoderma*, forming a distinct monophyletic lineage sister to *Hyp. microporoides* (CLZhao 8695, CLZhao 6857) with 100% MP and 1.00 BYPP bootstrap support. *Hyphoderma Punctatum* resembles *Hyp. microporoides* in having cylindrical to allantoid basidiospores and capitate halocystidia. However, *Hyp. microporoides* can be distinguished from *Hyp. Punctatum* by its bigger basidiospores ($8.5\text{--}10\text{--}10.5 \times 2.5\text{--}3.5\text{--}4 \mu\text{m}$, Guan & Zhao 2021). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Hyp. Punctatum* as a new species.

Hyphoderma yingjiangense X.J. Zhang & C.L. Zhao, sp. nov.

Fig. 56

Index Fungorum number: IF 860726; Facesoffungi number: FoF 18438

Diagnosis – The new species differs from other *Hyphoderma* by the soft coriaceous to coriaceous basidiomata with white to slightly cream hymenial surface, a hyphal system monomitic with generative hyphae bearing simple-septa, and cylindrical basidiospores measuring $13\text{--}17 \times 5\text{--}7 \mu\text{m}$.

Etymology – *yingjiangense* (Lat.): referring to the locality (Yingjiang County) of the type specimen.

Basidiomata annual, resupinate, soft coriaceous when fresh, turn to coriaceous upon drying, without odor or taste, up to 10 cm long, 1 cm wide, 50–100 μ m thick. *Hymenial surface* smooth, white when fresh, white to slightly cream upon drying. *Sterile margin* white, up to 1 mm. *Hyphal system* monomitic, generative hyphae with simple-septa, colorless, thin-walled, unbranched, interwoven, 3.5–4.2 μ m in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* and *cystidioles* absent. *Basidia* barreled, with 4 sterigmata and a basal simple septum, with oil drops, $30.8\text{--}41 \times 8.6\text{--}17.8 \mu\text{m}$. *Basidioles* dominant, similar to basidia in shape, but slightly smaller. *Basidiospores* cylindrical, colorless, thin-walled, smooth, with oil drops, IKI–, CB–, $(12\text{--})13\text{--}17\text{--}(17.5) \times 5\text{--}7 \mu\text{m}$, $L = 15.46 \mu\text{m}$, $W = 6.18 \mu\text{m}$, $Q = 2.30\text{--}2.50$ ($n = 60/2$).

Material examined – China. Yunnan Province, Baoshan, Tengchong, Laifengshan Nature Forest Park, GPS coordinates: $25^{\circ}25' \text{ N}$, $98^{\circ}13' \text{ E}$, altitude 1921 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 5 July 2024, CLZhao 37815 (SWFC, holotype); Yunnan Province, Dehong, Mang City, Mengga Town, Tongbiguan Provincial Nature Reserve, GPS coordinates: $24^{\circ}28' \text{ N}$,

97°31' E, altitude 1125 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 29 June 2024, CLZhao 36602 (SWFC, paratype).

GenBank accession numbers – CLZhao 36602: ITS = PV470535, CLZhao 37815: ITS = PV470536.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 52) revealed that the collections of our species *Hyphoderma yingjiangense* (CLZhao 36602, CLZhao 37815) grouped within other *Hyphoderma* specimens, forming a distinct clade sister to *Hyp. crystallinum* (CLZhao 9338, CLZhao 9374) with 98% ML, 94% MP, and 1.00 BYPP bootstrap support. *Hyphoderma weishanense* is also closely related to these taxa. *Hyphoderma crystallinum* is distinguished from *Hyp. yingjiangense* by its cream hymenium surface and smaller basidia ($21\text{--}31.5 \times 5\text{--}7 \mu\text{m}$ vs $30.8\text{--}41 \times 8.6\text{--}17.8 \mu\text{m}$, Guan & Zhao 2021). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Hyp. yingjiangense* as a new species.

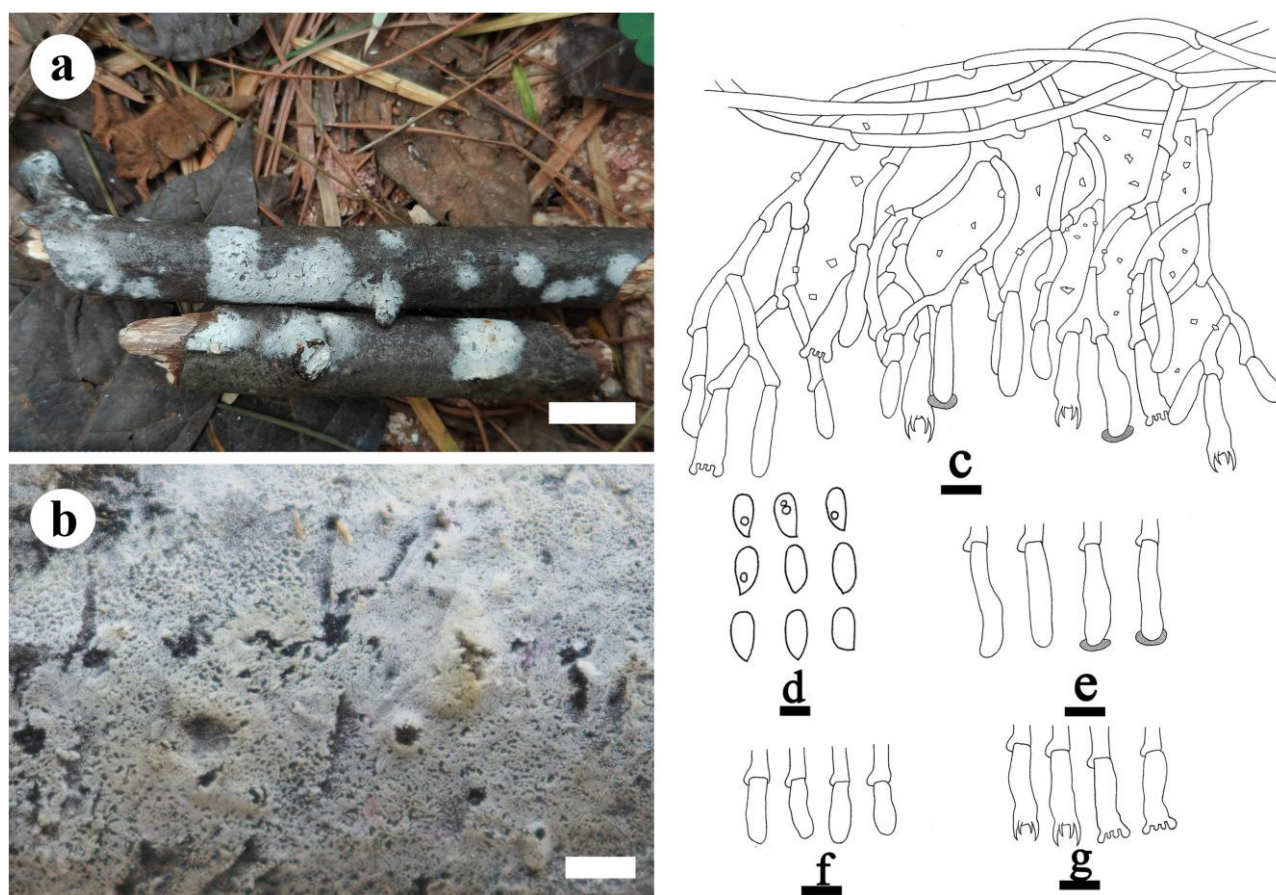


Figure 55 – Basidiomata and microscopic structures of *Hyphoderma punctatum* (CLZhao 33051, holotype). a, b Basidiomata. c A section of hymenium. d Basidiospores. e Cystidia. f Basidioles. g Basidia. Scale bars: a = 1 cm, b = 1 mm, c–g = 10 μm .

Incrustoporiaceae Jülich

Skeletocutis Kotl. & Pouzar

Index Fungorum number: IF18554; Facesoffungi number: FoF 15428

Notes – *Skeletocutis* was established as a monotypic genus with the type *Sk. amorpha* by Kotlába & Pouzar (1958) and segregated it from *Gloeoporus*, due to its upper layer of trama consisting solely of loosely interwoven skeletal hyphae, a dimitic hyphal system, and the absence of inter hyphal mucus. The genus is characterized by basidiomata annual to perennial, resupinate to pileate. Hyphal system dimitic to trimitic; generative hyphae with clamps. *Cystidia* absent, and cystidioles present in most species. Basidiospores colorless, cylindrical to ellipsoid, negative in Melzer's reagent (Kotlába & Pouzar 1958). It is a taxonomically complex polypore genus due to the

presence of tiny basidiospores in many species (Bian et al. 2016). Phylogenetically, *Skeletocutis* has close affinity to *Tyromyces*, *Ceriporiopsis* and *Piloporia* and they cluster within the *Tyromyces* clade (Binder et al. 2005, 2013). *Skeletocutis* is a cosmopolitan genus, however, most species have been found in boreal and temperate forests from the northern hemisphere and the southern hemisphere (Gilbertson & Ryvarden 1987, Niemelä 1998, Cui 2013, Liu et al. 2025c). Recent studies on *Skeletocutis* have yielded numerous new species and combinations (Du & Dai 2020, Jayawardena et al. 2022, Dong et al. 2024, Liu et al. 2025a), currently the genus consists of 117 species and 86 registered species have been accepted worldwide (Species Fungorum 2025). In this study, three new species of *Skeletocutis* are introduced from China based on morphological characteristics and phylogenetic analyses inferred from ITS and LSU sequences (Figs 57, 58, 59).

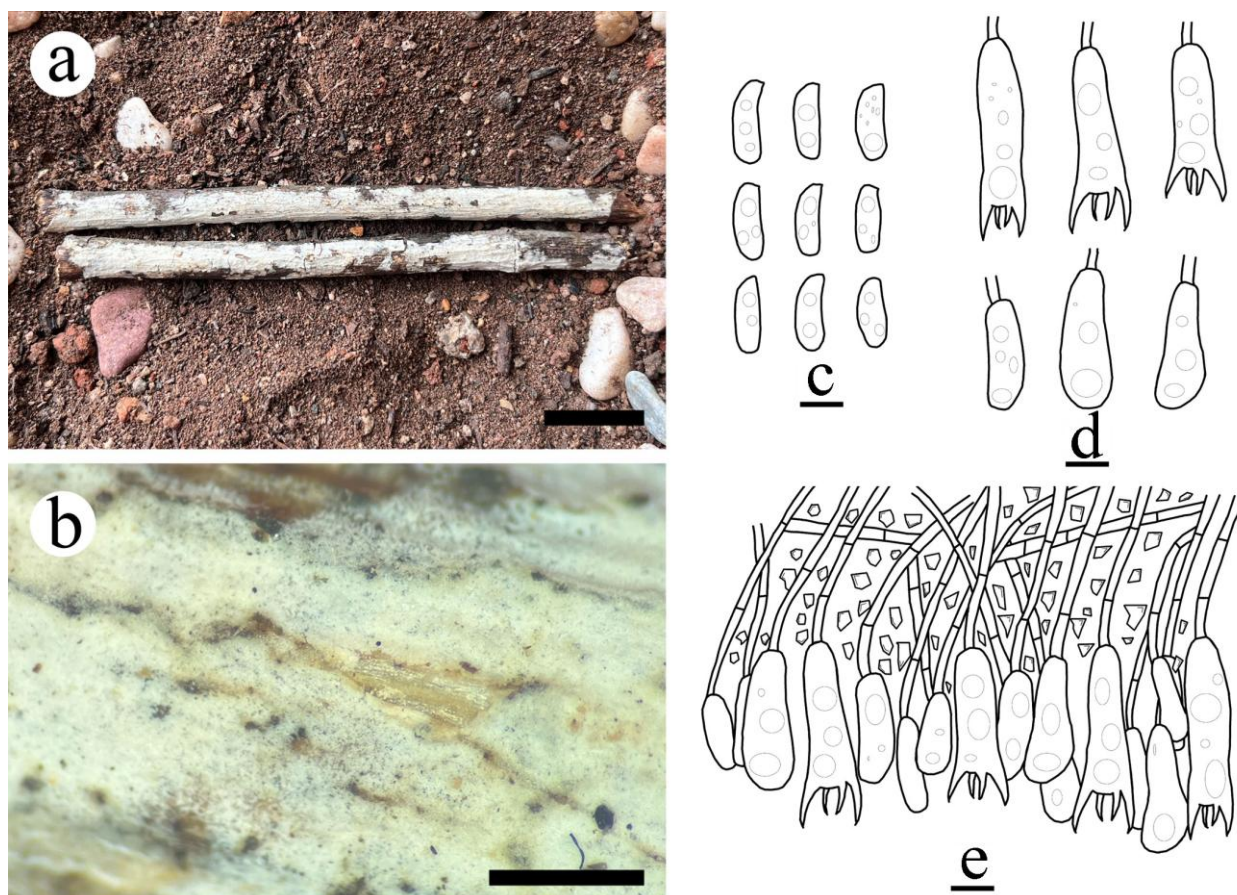


Figure 56 – Basidiomata and microscopic structures of *Hyphoderma yingjiangense* (holotype, CLZhao 37815). a Basidiomata on the substrate. b Macroscopic characteristics of hymenophore. c Basidiospores. d Basidia and basidioles. e A section of the hymenium. Scale bars: a = 1 cm, b = 1 mm, c–e 10 µm.

Skeletocutis fissurata Y.L. Deng & C.L. Zhao, sp. nov.

Figs 58, 59

Index Fungorum number: IF 858755; Facesoffungi number: FoF 18439

Diagnosis – *Skeletocutis fissurata* is characterized by the adnate, hard corky, fragile basidiomata with buff to cinnamon-buff to greyish-brown poroid surface, dimitic hyphal system with clamped generative hyphae and allantoid basidiospores.

Etymology – *fissurata* (Lat.): referring to the cracking hymenial surface of the type specimen.

Basidiomata annual, resupinate, adnate, hard corky, fragile, without odor or taste when fresh, becoming coriaceous upon drying, up to 5 cm long, 4 cm wide, 2 mm thick. **Poroid surface** buff to cinnamon-buff when fresh, cinnamon-buff to greyish brown upon drying. **Pores** round to angular, 6–8 per mm, up to 1 mm deep, 0.1 mm in diam., dissepiments thin. **Tubes** concolorous with a poroid surface. **Context** cream, up to 1 mm thick. **Sterile margin** distinct when juvenile, cream to

buff, up to 1 mm wide. *Hyphal system* dimitic, generative hyphae with clamp connections, skeletal hyphae dominant; IKI–, CB–, tissues unchanged in KOH. *Subiculum* generative hyphae colorless, thin-walled, 3.5–4 µm in diam.; skeletal hyphae dominant, distinctly thick-walled, thickness 1.5–2.5 µm, unbranched, interwoven, 4–5 µm in diam. *Tubes* generative hyphae colorless, thin-walled, sharp-pointed encrustations, especially at dissepiment edge, occasionally branched and bearing crystals, 3–3.5 µm in diam., skeletal hyphae dominant, distinctly thick-walled with a narrow lumen to subsolid, unbranched, subparallel along the tubes, 3.5–4.5 µm in diam. *Cystidia* absent. *Cystidioles* abundant, bottle-shaped, with a conical apex, almost as size as basidia, 5–9 × 3–4 µm. *Basidia* barreled, with 4 sterigmata and a basal clamp connection, 5–9 × 2–4 µm. *Basidioles* infrequent, in shape similar to basidia, but slightly smaller. *Basidiospores* allantoid, colorless, thin-walled, smooth, CB–, IKI–, (3.9–)4.4–6.8(–7.4) × (2–)2.2–3.5(–4.2) µm, L = 5.50 µm, W = 2.75 µm, Q = 2.0–2.2 (n = 60/2).

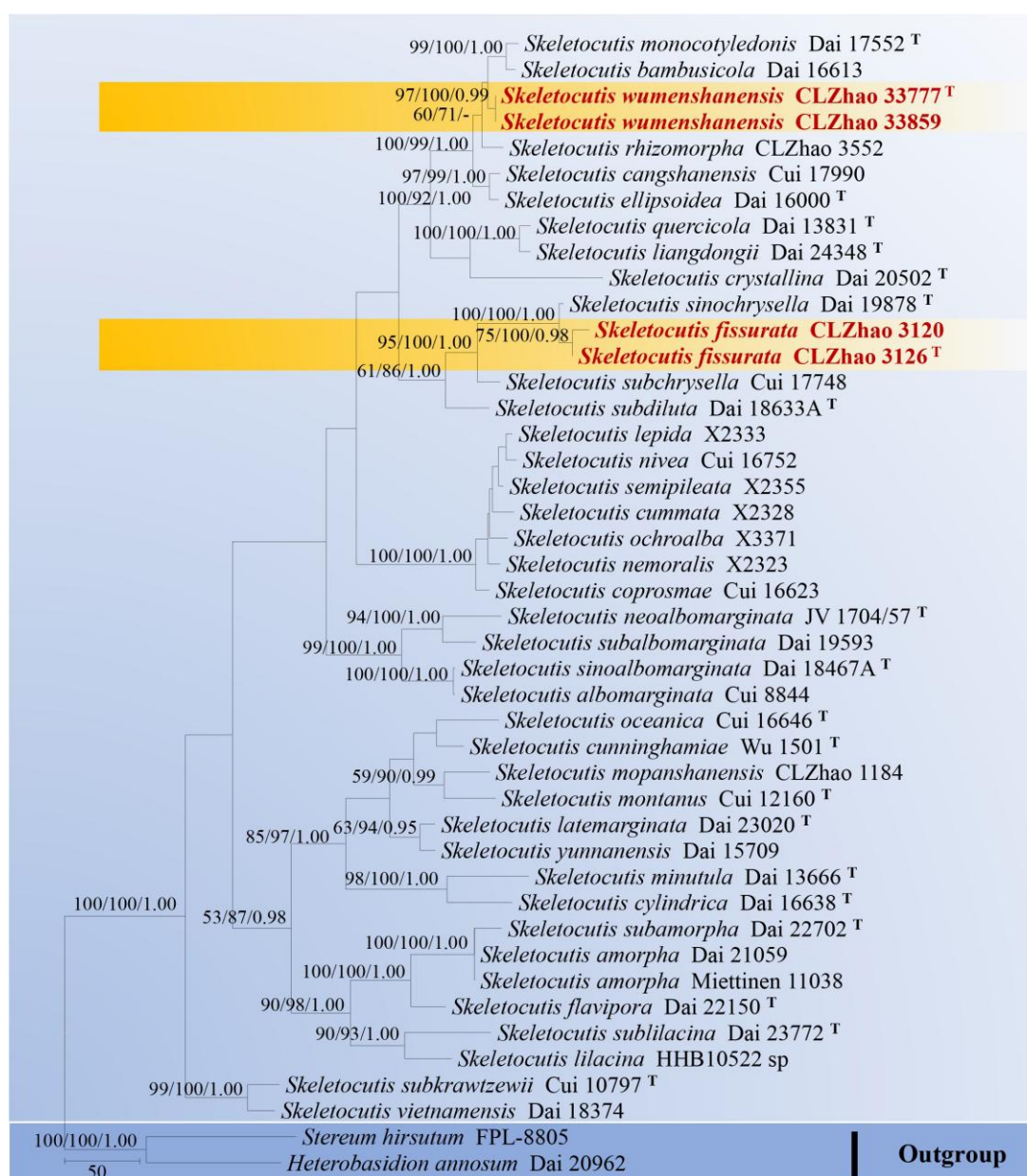


Figure 57 – Phylogram generated from maximum parsimony strict consensus tree analysis based on the combined ITS and nLSU sequence data of *Incrustoporiaceae* species. Forty-four specimens are included in the combined analyses. The tree topology of the maximum parsimony analysis is similar to the maximum likelihood and Bayesian analysis. Constant characters were 1448. Parsimony-informative characters were 151 whereas parsimony-uninformative characters were 476.

Bootstrap support values for ML $\geq 50\%$, MP $\geq 70\%$, and Bayesian posterior probabilities ≥ 0.95 are given near nodes, respectively. The tree was rooted with *Heterobasidion annosum* (Dai 20962) and *Stereum hirsutum* (FPL-8805). The newly generated sequences are in red-bold and the type collections are indicated in with ^T.

Material examined – China, Yunnan Province, Puer, Laiyanghe Forest Park, GPS coordinates: 22°61' N, 101°09' E, altitude 1500 m asl., on the angiosperm trunk, leg. C.L. Zhao, 30 September 2017, CLZhao 3126 (SWFC, holotype), *ibid.*, CLZhao 3120 (SWFC, isotype).

GenBank accession numbers – CLZhao 3126: ITS = PQ811406; CLZhao 3120: ITS = PQ811407, LSU: PV185844.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 57) revealed that the collections of our species *Skeletocutis fissurata* (CLZhao 3120, CLZhao 3126) grouped within *Skeletocutis* sister to *Sk. sinochrysella* (Dai 19878) with 75% MP, 100% ML and 0.98 BYPP bootstrap support. The clade of *Skeletocutis fissurata* and *Sk. sinochrysella* shows a close phylogenetic affinity to *Sk. subchrysella* (Cui 17748) and *Sk. subdiluta* (Dai 18633A). Morphologically, *Sk. sinochrysella* is distinguished from *Sk. fissurata* by its pore surface locally verruculose, buff yellow to cinnamon and shiny, thin-walled generative hyphae, and smaller basidiospores allantoid ($2.9\text{--}3.1 \times 1\text{--}1.2 \mu\text{m}$, Liu et al. 2025a). *Skeletocuti subchrysella* is characterized by its pore surface white to cream to cinnamonbuff, thin-walled generative hyphae, larger basidia, $10.3\text{--}15.6 \times 3.2\text{--}4.5 \mu\text{m}$, and smaller basidiospores ($2.7\text{--}3.2 \times 0.7\text{--}1 \mu\text{m}$, Jayawardena et al. 2022). *Skeletocuti subdiluta* is distinguished from *Sk. fissurata* by a pore surface that is white to cream to honey yellow and shiny, hyphal structure trimitic; generative hyphae bearing clamps, and smaller basidiospores ($3.1\text{--}3.7 \times 0.6\text{--}0.7 \mu\text{m}$, Liu et al. 2025a). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Sk. fissurata* as a new species.

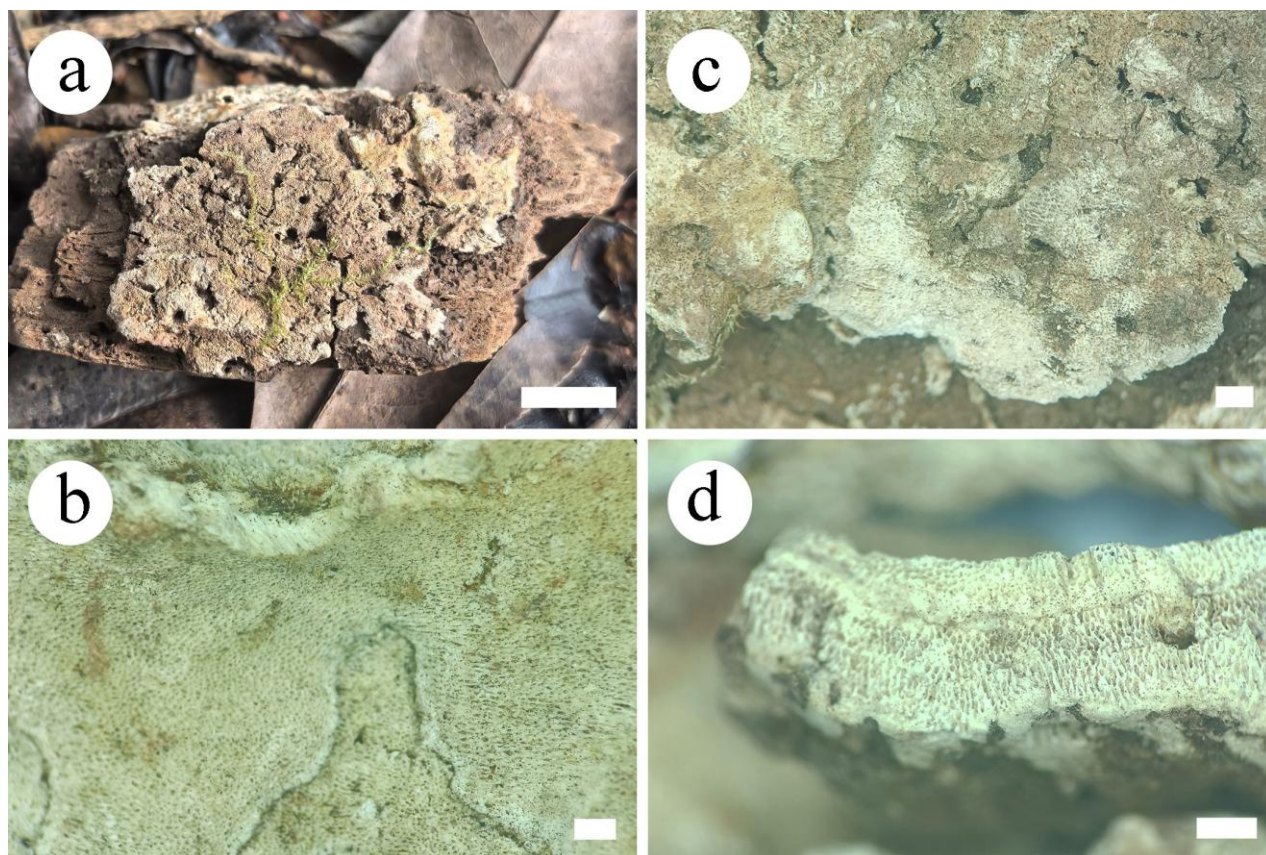


Figure 58 – Macro-morphology of *Skeletocutis fissurata* (CLZhao 3126, holotype). a Basidiomata on the substrate. b–d Characters of hymenophore. Scale bars: a = 1 cm, b–d = 1 mm.

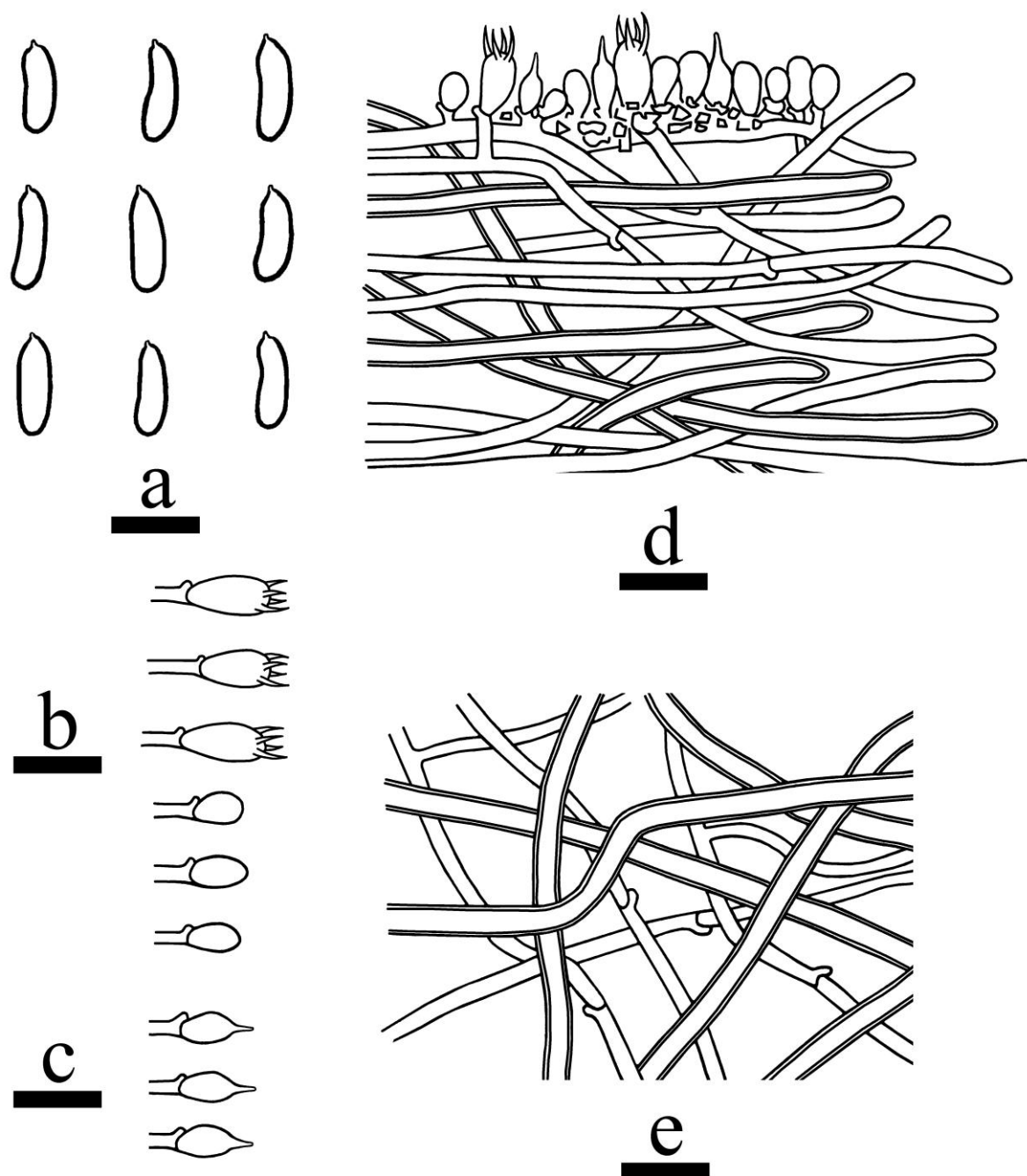


Figure 59 – Microscopic structures of *Skeletocutis fissurata* (CLZhao 3126, holotype). a Basidiospores. b Basidia and basidioles. c Cystidioles. d A section of the hymenium. e Hyphal from context. Scale bars: a = 5 μ m, b–e = 10 μ m.

Skeletocutis wumenshanensis Y.L. Deng & C.L. Zhao, sp. nov.

Fig. 60

Index Fungorum number: IF 858757; Facesoffungi number: FoF 18440

Diagnosis – *Skeletocutis wumenshanensis* is characterized by the adnate, fragile basidiomata with smooth, cream to curry-yellow poroid hymenial surface, a dimorphic hyphal system with clamped generative hyphae and allantoid basidiospores.

Etymology – *wumenshanensis* (Lat.): referring to the locality (Wumengshan National Nature Reserve) of the type specimen.

Basidiomata annual, resupinate, adnate, fragile, without odor or taste when fresh, up to 8 cm long, 1.5 cm wide, 1 mm thick. *Pore surface* cream to buff-yellow when fresh, buff-yellow to

curry-yellow upon drying. *Pores* round, 6–8 per mm, up to 0.2 mm deep, dissepiments thin, tubes concolorous with poroid surface. *Context* cream, up to 0.5 mm thick. Sterile margin distinct when juvenile, cream, up to 1 mm wide. *Hyphal system* dimitic, generative hyphae with clamp connections, skeletal hyphae dominant, IKI–, CB–, tissues unchanged in KOH. *Subiculum* generative hyphae colorless, thin to thick-walled, occasionally branched and bearing crystals, 2–3.5 µm in diam.; skeletal hyphae dominant, distinctly thick-walled, unbranched, interwoven, 2.5–3.5 µm in diam. *Tubes* generative hyphae, colorless, thin-walled, sharp-pointed encrustations, especially at dissepiment edge, occasionally branched and bearing crystals, 2–3 µm in diam.; skeletal hyphae dominant, distinctly thick-walled with a narrow lumen to subsolid, unbranched, subparallel along the tubes, 2.5–3 µm in diam. *Cystidia* absent. *Cystidioles* abundant, bottle-shaped, with a conical apex, almost as size as basidia, 7–11.5 × 3–5 µm. *Basidia* clavate, with 4 sterigmata and a basal clamp connection, 7–12 × 3–5 µm. *Basidioles* similar to basidia in shape, but slightly smaller. *Basidiospores* allantoid, colorless, thin-walled, smooth, usually with two oils, CB–, IKI–, (2.8–)3.2–4.4(–5.2) × (1.2–)1.6–2(–2.4) µm, L = 3.54 µm, W = 1.77 µm, Q = 1.91–2.09 (n = 60/2).

Material examined – China, Yunnan Province, Zhaotong, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates: 27°33'N, 103°27'E, altitude 2300 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 21 September 2023, CLZhao 33777 (SWFC, holotype); *ibid.*, CLZhao 33859 (SWFC, isotype).

GenBank accession numbers – CLZhao 33777: ITS = PQ811410, LSU = PV185846; CLZhao 33859: ITS = PQ811411, LSU = PV185847, mtSSU = PV283187.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 57) revealed that the collections of our species *Skeletocutis wumenshanensis* (CLZhao 33777, CLZhao 33859) grouped within *Skeletocutis* sister to *Sk. bambusicola* (Dai 16613) and *Sk. monocotyledona* (Dai 17552) with 97%MP, 100% ML and 0.99 BYPP bootstrap support. *Skeletocutis rhizomorpha* (CLZhao 3552) shows a close affinity to these three species. Morphologically, *Sk. bambusicola* is distinguished from *Sk. wumenshanensis* by its shorter basidiospores (2.2–2.8 × 1.4–1.8 µm, Zhou & Qin 2013). *Skeletocutis rhizomorpha* differs from *Sk. wumenshanensis* by its cream to buff poroid surface, and smaller basidiospores (2–2.7 × 1–1.5 µm, Dong et al. 2024). *Skeletocutis monocotyledona* is distinguished from *Sk. wumenshanensis* by having white, cream to buff yellow pore surface, narrower clavate cystidioles, 10–12 × 2–3 µm, and smaller ellipsoid basidiospores (2.7–3.4 × 1.7–1.8 µm, Liu et al. 2025a). Further, *Sk. cangshanensis* differs from *Sk. wumenshanensis* by its white to buff-yellow pore surface, thin- to slightly thick-walled generative hyphae, and smaller cylindrical basidiospores (2.7–3.5 × 0.8–1.5 µm, Jayawardena et al. 2022). *Skeletocutis ellipsoidea* can be characterized by having cream or buff pore surface, and smaller, ellipsoid basidiospores (2.9–3.3 × 1.6–1.9 µm, Liu et al. 2025a). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Sk. wumenshanensis* as a new species.

***Meruliaceae* Rea**

***Physisporinus* P. Karst.**

Index Fungorum number: IF 18281; Facesoffungi number: FoF 18441

Notes – *Physisporinus* was introduced by Karsten (1889) and typified by *Phy. vitreus*. This genus is characterized by annual or stratified, having a perennial habit, resupinate, effused-reflexed to rarely pileate or with a short stipe basidiomata, a white to brightly colored pore surface when fresh and often changing color when bruised or dried, a monomitic hyphal system with simple septa on generative hyphae, thin- to thick-walled and encrusted hyphoid cystidia and fusoid or mastoid cystidioles present in most species, ovoid, ellipsoid, subglobose to globose and thin-walled basidiospores with the negative reaction in Melzer's reagent and Cotton Blue. Species of *Physisporinus* are important wood decaying agents that cause a white rot on both angiosperm and gymnosperm substrate from living trees to rotten wood and have a distribution from boreal to tropical forests (Chen & Dai 2021, Wu et al. 2017, Wang et al. 2024c). Binder et al. (2013) first investigated the phylogeny of *Physisporinus* and revealed that the genus was nested in the residual polyporoid clade, and treated it in *Meripilaceae* under *Polyporales*. Wang et al. (2024c), further

studied *Physisporinus* based on more samples from Asia, Australia, Europe, and North and Central America. Phylogenies based on a two-loci DNA fragments dataset (ITS+nLSU) and a six loci DNA fragments dataset (ITS+nLSU+*tef1*- α +*rpb2*+nSSU+mtSSU) are carried out (Wang et al. 2024c). Currently, 37 species are accepted in the genus *Physisporinus* by Wang et al. (2024c). In this study, a novel wood-inhabiting fungus *Physisporinus pingbianensis* sp. nov. is introduced from China based on the ITS+nLSU sequence data (Fig. 61) and morphological characteristics (Fig. 62).

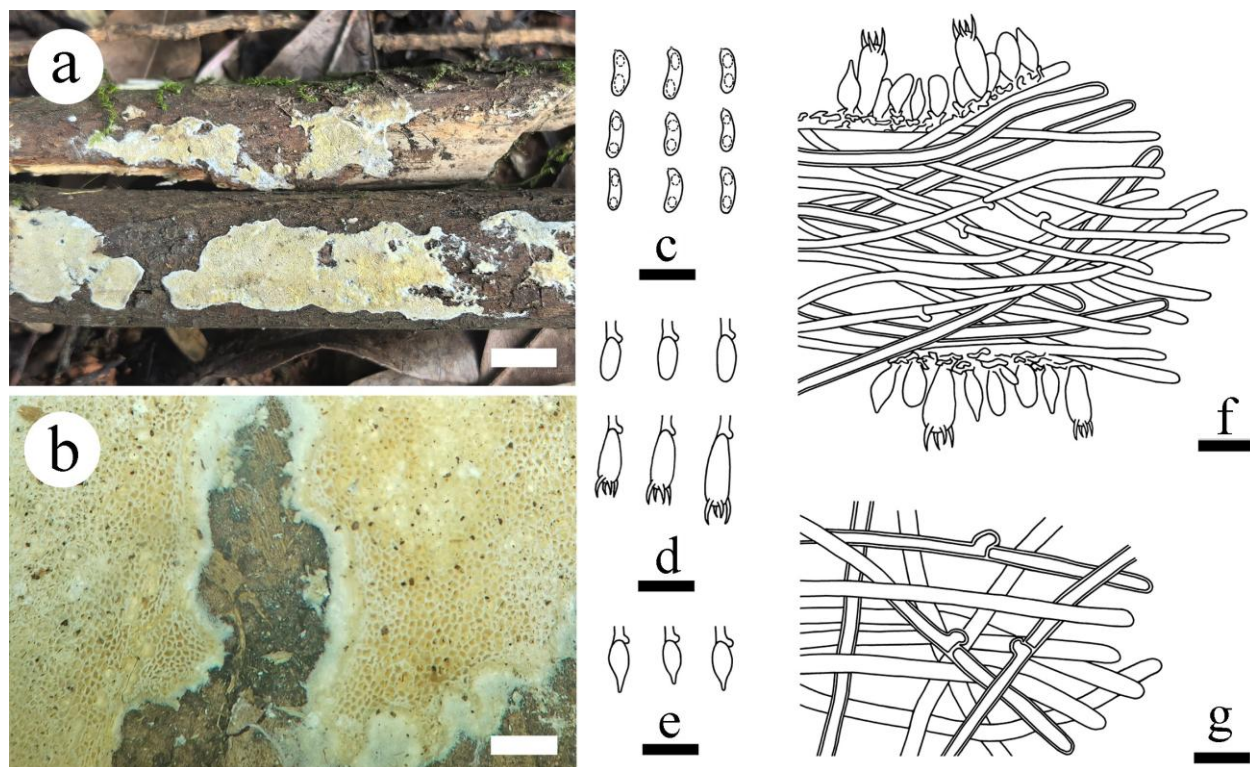


Figure 60 – Basidiomata and microscopic structures of *Skeletocutis wumenshanensis* (CLZhao 33777, holotype). a Basidiomata on the substrate. b Characters of hymenophore. c Basidiospores. d Basidia and basidioles. e Cystidioles. f A section of the hymenium. g Hyphal from context. Scale bars: a = 1 cm, b = 1 mm, c–g = 10 μ m.

***Physisporinus pingbianensis* Z.R. Gu & C.L. Zhao, sp. nov.**

Fig. 62

Index Fungorum number: IF 904414; Facesoffungi number: FoF 18442

Diagnosis – Differs from other *Physisporinus* species by its buff to honey-yellow basidiomata when dry, a monomitic hyphal system with simple septa, and globose basidiospores measuring $3.2\text{--}4 \times 3\text{--}3.8 \mu\text{m}$.

Etymology – *pingbianensis* (Lat.): referring to the locality (Pingbian County) of the type specimen.

Basidiomata annual, closely adnate, corky, without odor or taste when fresh, up to 12 cm long, 2 cm wide, and 0.5 mm thick. **Hymenophore surface** cream to slightly buff when fresh, buff to honey yellow when dry; pores angular, 7–9 per mm; dissepiments thin. **Context** curry-yellow, corky when dry, up to 0.1 mm thick. **Tubes** concolorous with pore surface, hard corky when dry, up to 0.4 mm long. **Sterile margin** narrow, cream to buff, up to 1 mm wide. **Hyphal system** monomitic, generative hyphae simple septate, colorless, thin- to thick-walled, smooth, unbranched, interwoven. **Trametal hyphae** thick-walled, unbranched, subparallel along the tubes, 3–4 μ m in diam.; IKI–, CB–, tissues unchanged in KOH. **Contextual hyphae** thick-walled with a wide lumen, unbranched, rarely simple septate, interwoven, 3–6.5 μ m in diam. **Hyphoid cystidia** capitate, apically encrusted, colorless, thick-walled, smooth, $38.8\text{--}83.9 \times 5.8\text{--}7.2 \mu\text{m}$. **Basidia** clavate, with a simple septate connection and four sterigmata, $12.3\text{--}20.7 \times 5.4\text{--}5.6 \mu\text{m}$. **Basidioles** numerous, similar to basidia in

shape but smaller. *Basidiospores* globose, colorless, thin-walled, smooth, with one small guttules, IKI–, CB–, (3.1–)3.2–4(–4.3) × 3–3.8(–4.1) μm, L = 3.49 μm, W = 3.42 μm, Q = 1.019–1.024 (n = 60/2).

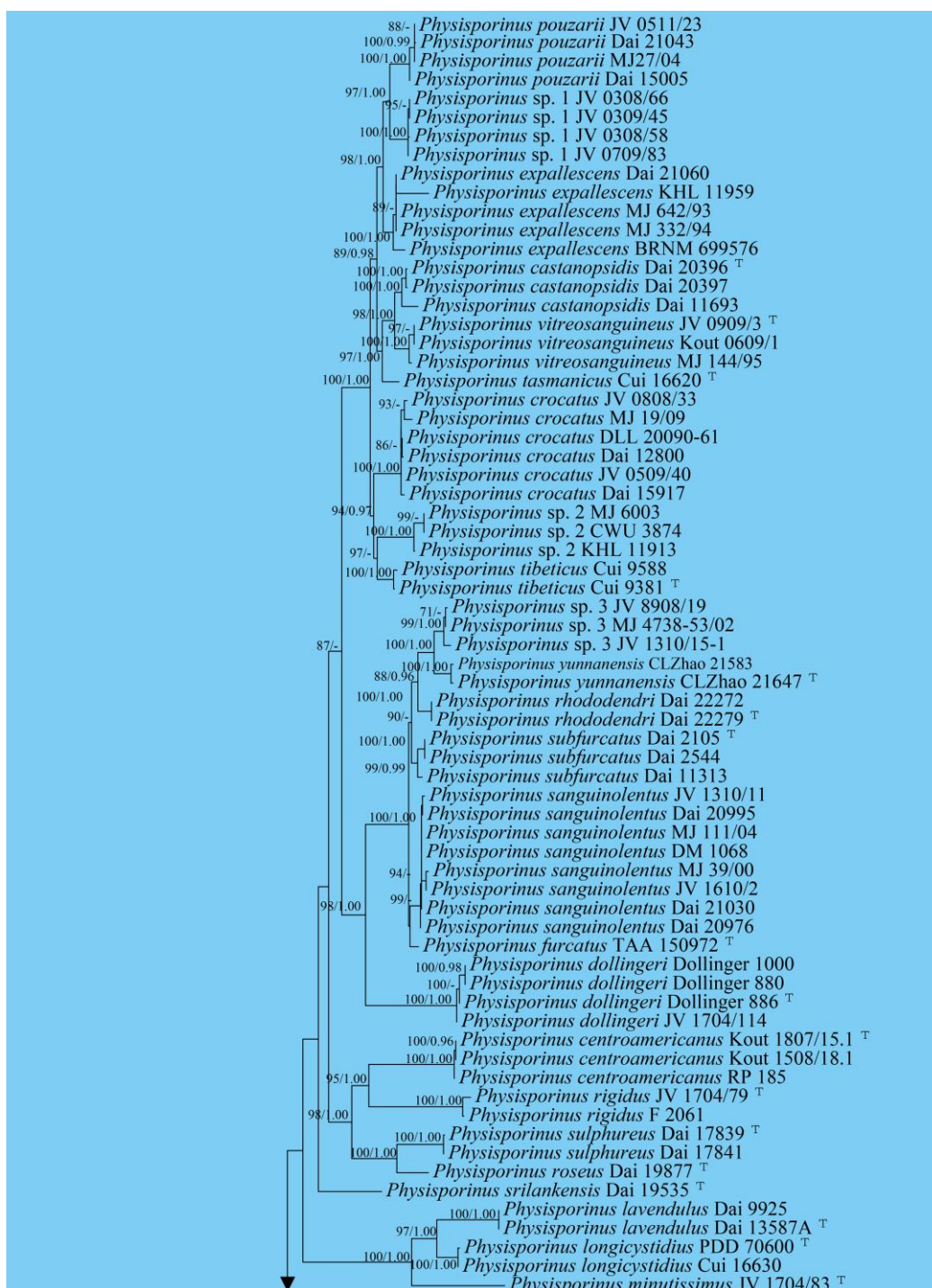


Figure 61 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and nLSU sequence data of *Physisporinus*. One hundred and eleven specimens are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -12416.328 is presented. The evolutionary model TIM2+F+I+G4 is applied for all the genes. The matrix had 654 distinct alignment patterns. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Hyphoderma setigerum* (FD 312). The newly generated sequences are indicated in red-bold, and the type collections are indicated with ^T.

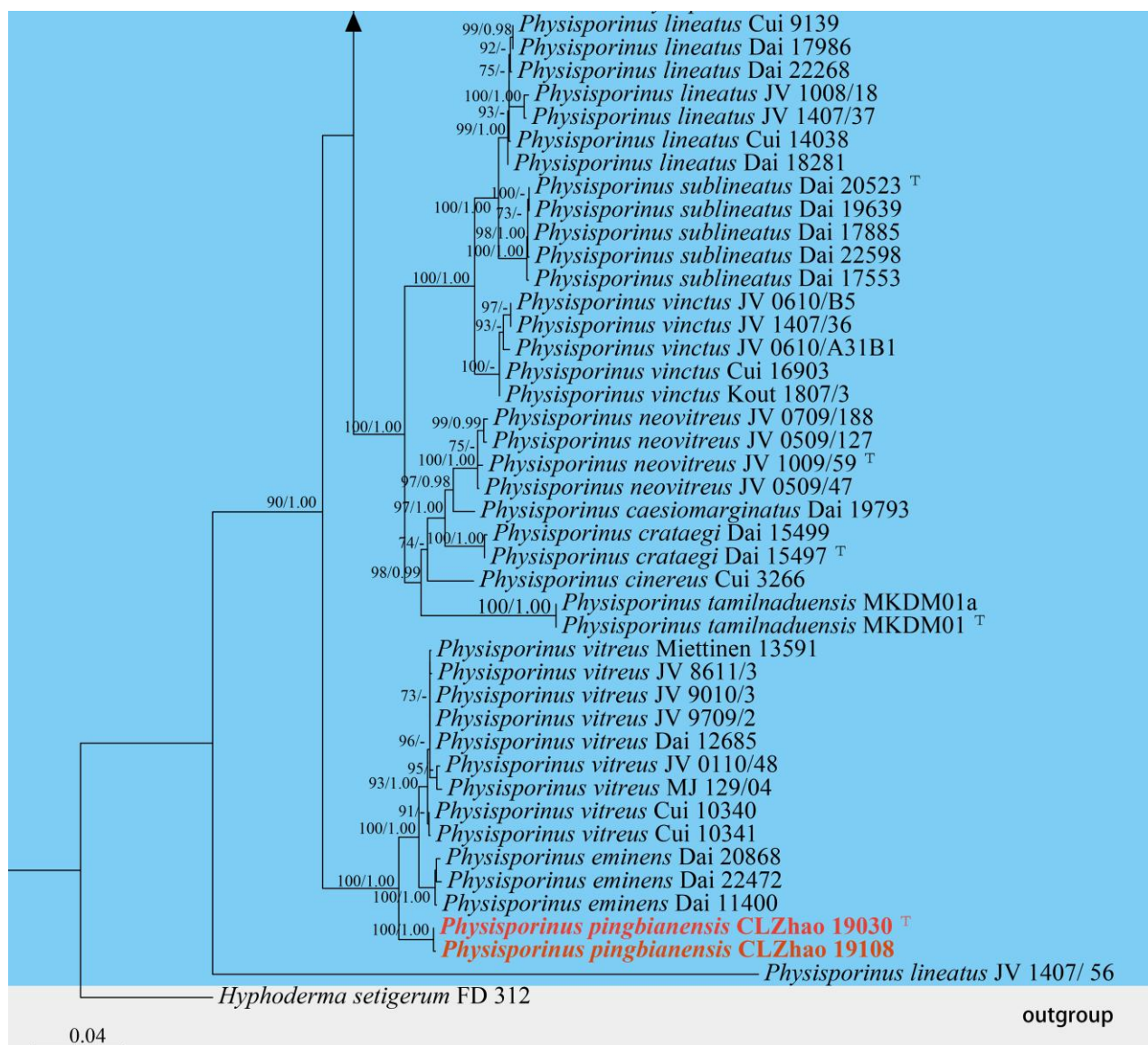


Figure 61 – Continue.

Material examined – China, Yunnan Province: Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates: 22°92'N, 103°69'E, altitude 1900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 9 June 2020, CLZhao 19030 (SWFC, holotype); *ibid.*, CLZhao 19108 (SWFC, isotype).

GenBank accession numbers – CLZhao 19030: ITS = PV727078, LSU = PV727080; CLZhao 19108: ITS = PV727079.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 61) revealed that the collections of our species *Physisporinus pingbianensis* (CLZhao 19030, CLZhao 19108) grouped within *Physisporinus*, forming a sister clade to the collections of *Phy. eminens* and *Phy. vitreus* with 100% ML and 1.00 BYPP bootstrap support. *Physisporinus eminens* differs from *Phy. pingbianensis* by its wider basidia (6–8 µm) and larger basidiospores (4.2–6 × 3.9–5.2 µm, Wang et al. 2024c). Also, *Phy. vitreus* can be distinguished from *Phy. pingbianensis* by its hymenial surface that white to bluish-white when fresh, ochraceous to pale pinkish-brown when dried, and larger basidiospores (5–5.5 × 4–4.5 µm, Wang et al. 2024c). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Phy. pingbianensis* as a new species.

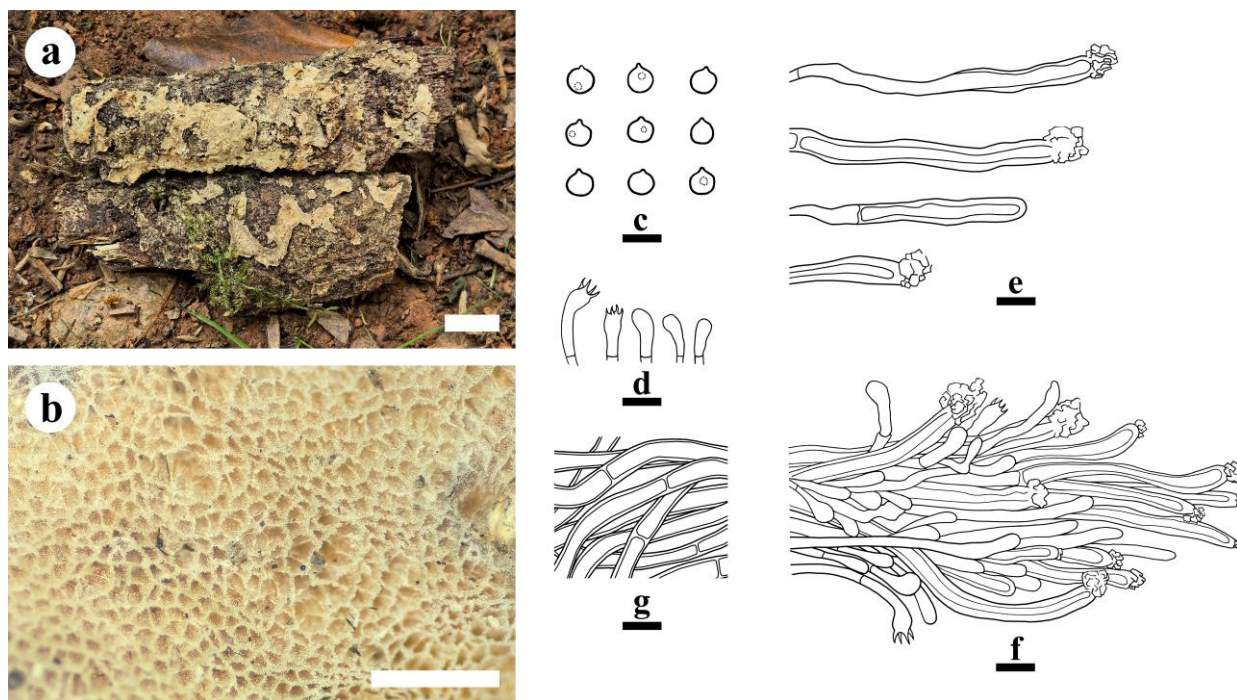


Figure 62 – Basidiomata and microscopic structures of *Physisporinus pingbianensis* (CLZhao 19030, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e Hyphoid cystidia. f A section of the hymenium. g Hyphae from context. Scale bars: a = 1 cm, b = 1 mm, c = 5 μ m, d–f = 10 μ m.

Phanerochaetaceae Jülich

Phanerochaete P. Karst

Index Fungorum number: IF 18245; Facesoffungi number: FoF 15445

Notes – *Phanerochaete* was introduced by Karsten (1889) and typified by *Pha. alnea*. The basidiomata of *Phanerochaete* s.s. are typically membranous, in which the hymenophore is usually smooth, but tuberculate, grandinoid, odontoid to hydroid or even poroid hymenophore occur in some species (Chen et al. 2021, Wang & Zhao 2021, Deng et al. 2024, Luo et al. 2024a). *Phanerochaete* shares similar morphologies to *Irpicaceae* but differs in its mostly present cystidia (Justo et al. 2017). These species are causing white rot in wood, widely distributed from boreal to tropical forests in the world (Luo et al. 2024a). Currently, 208 species of *Phanerochaete* are registered in Index Fungorum (2025), but 121 species have been accepted worldwide. In this study, *Phanerochaete yingjiangensis* sp. nov. is introduced from China based on the ITS sequence data (Fig. 63) and morphological characteristics (Fig. 64).

Phanerochaete yingjiangensis W.Y. Xiao & H.M. Zhou, sp. nov.

Fig. 64

Index Fungorum number: IF 860762; Facesoffungi number: FoF 18443

Diagnosis – Differs from other *Phanerochaete* species by the membranous basidiomata, smooth hymenial surface, a monomitic hyphal system with simple separate and cylindrical basidiospores measuring (4.5–)5.0–6.5 $\times$ 3.5–4.0 μ m.

Etymology – *yingjiangensis* (Lat.): referring to the locality (Yingjiang County) of the type specimen.

Basidiomata annual, resupinate, thin, membranous, and up to 1.5 cm long, 0.7 cm wide, 50–100 μ m thick. *Hymenial surface* smooth, yellow when fresh turn to white upon drying. *Sterile margin* indistinct, concolorous. *Hyphal system* monomitic, generative hyphae with simple septa, colorless, thin-walled, frequently branched, 3.0–5.0 μ m in diam., IKI–, CB–, tissues unchanged in KOH, intensely covered with granular crystals. *Cystidia* absent. *Basidia* subclavate to clavate, with 4 sterigmata and a basal simple septum, 23.5–27.0 $\times$ 3.0–4.0 μ m. *Basidioles* dominant, similar to

basidia in shape, but slightly smaller. *Basidiospores* cylindrical, colorless, thin-walled, smooth, CB–, IKI–, $5.0\text{--}7.0 \times 3.0\text{--}4.0 \mu\text{m}$, $L = 6.29 \mu\text{m}$, $W = 3.60 \mu\text{m}$, $Q = 1.75$ ($n = 120/4$).

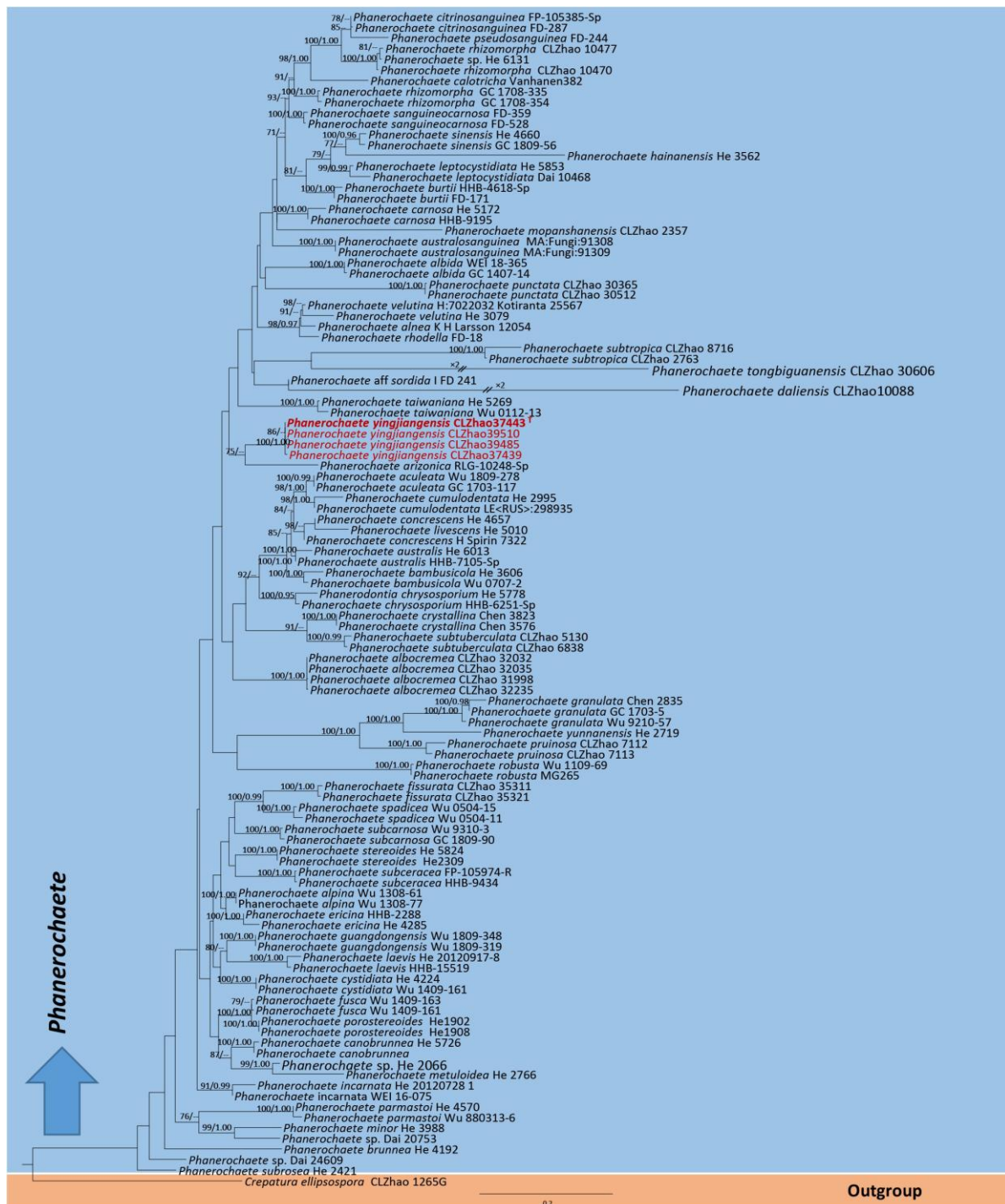


Figure 63 – Phylogram generated from the maximum likelihood analysis based on the combined ITS sequence data of *Phanerochaete*. One hundred and ten specimens are included in the final analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -10708.966 is presented. The evolutionary model TVM+F+I+G4 is applied. The matrix had 599 distinct alignment patterns, with 34.48% of undetermined characters or gaps. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Crepatura ellipsospora* (CLZhao 126). The newly generated sequences are in red-bold and ^T indicates the type material.

Material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 23°48'N, 97°38'E, altitude 1500 m asl., on fallen angiosperm branch of, leg. C.L. Zhao, 8 July 2024, CLZhao 37443 (SWFC, holotype); *ibid.*, CLZhao 37439, CLZhao 39485 CLZhao 39510 (SWFC, isotypes).

GenBank accession numbers – CLZhao 37443: ITS = PV820773, CLZhao 37439: ITS = PV820772; CLZhao 39485: ITS = PV820774; CLZhao 39510: ITS = PV820775.

Notes – The ITS phylogenetic analyses (Fig. 63) revealed that the collections of our species *Phanerochaete yingjiangensis* (CLZhao 37439, CLZhao 37443, CLZhao 39485, CLZhao 39510) grouped with the other taxa of *Phanerochaete*, forming a separate monophyletic clade sister to *Pha. arizonica* (RLG-10248-Sp) with 75% ML bootstrap support. *Phanerochaete yingjiangensis* resembles *Pha. arizonica* in having heavily encrusted with hyaline to pale yellow crystals. However, *Pha. arizonica* can be distinguished from *Pha. yingjiangensis* by bigger basidia $35\text{--}45 \times 5.5\text{--}8\ \mu\text{m}$, Burdsall 1985). Thus, based on morphology and phylogenetic evidence, we introduce *Pha. yingjiangensis* as a new species.

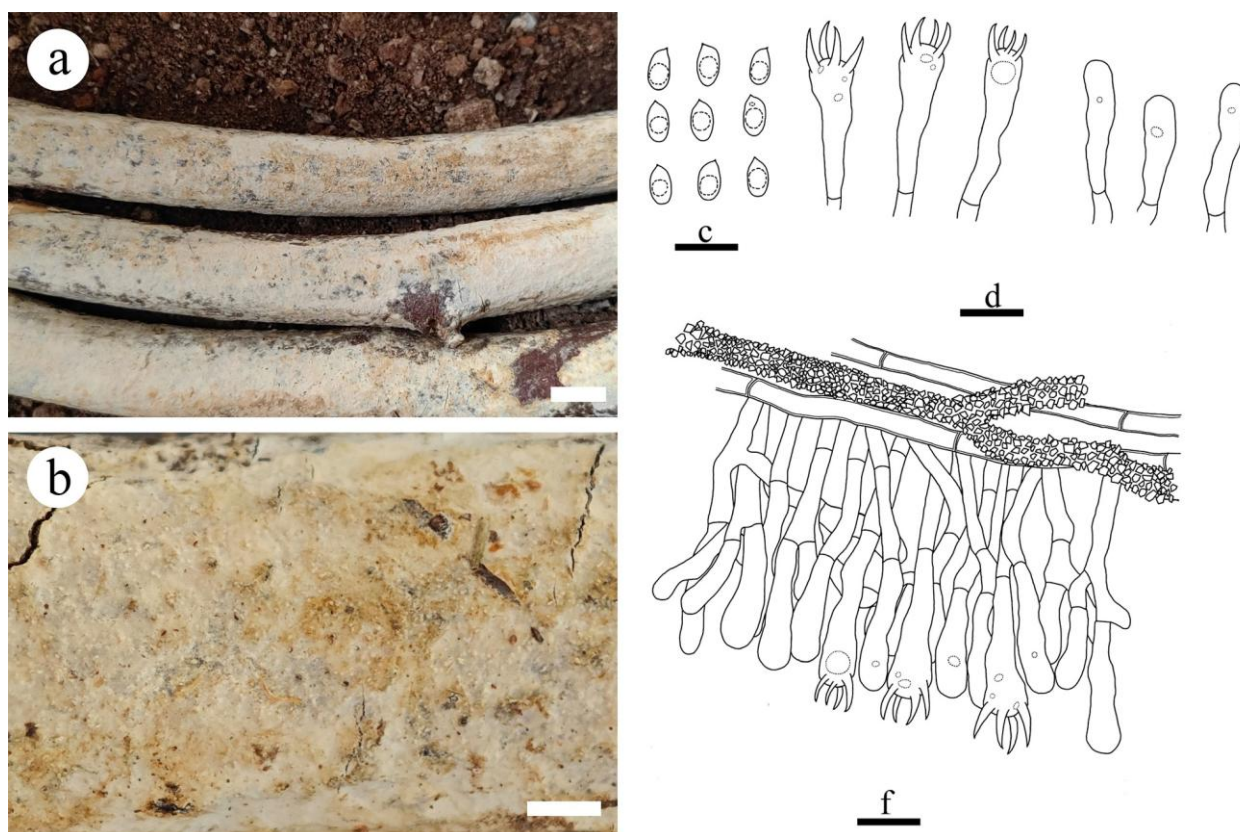


Figure 64 – Basidiomata and microscopic structures of *Phanerochaete yingjiangensis* (CLZhao 37443, holotype). a, b Basidiomata on the host substrates. c Basidiospores, d Basidia and basidioles. e A section of hymenium. Scale bars: a = 1 cm, b = 1 mm, c–f = 10 μm .

Polyporaceae Fr. ex Corda

Cerioporus Quélet.

Index Fungorum number: IF 17266; Facesoffungi number: FoF 18444

Notes – *Cerioporus* was introduced by Quélet in 1886 and the genus was typified by *Ce. squamosus*. With the emergence of the molecular data, this genus has become more narrowly defined as many species were transferred to other genera, families and orders (Zmitrovich & Kovalenko 2016, Zmitrovich 2018). The taxonomic studies for *Cerioporus* contributed to the definition of *Cerioporus* in its strict sense (Zmitrovich 2018). Zmitrovich et al. (2017) provided a taxonomic revision of *Cerioporus squamosus* and restored a separate species, *Ce. rangiferinus*, using comparative morphology and ITS rDNA sequence data analyses. The species of the genus are

widely distributed throughout the world (Wu et al. 2022b, Zhao et al. 2024). Based on Index Fungorum (2025), *Cerioporus* consists of 47 species and 21 registered species have been accepted worldwide (Zmitrovich & Kovalenko 2016, Zmitrovich et al. 2017, Zmitrovich 2018, Yang et al. 2024b). In this study, *Cerioporus nigromarginatus* sp. nov. is introduced from China, based on the ITS+nLSU sequence data (Fig. 65) and morphological characteristics (Figs 66, 67).

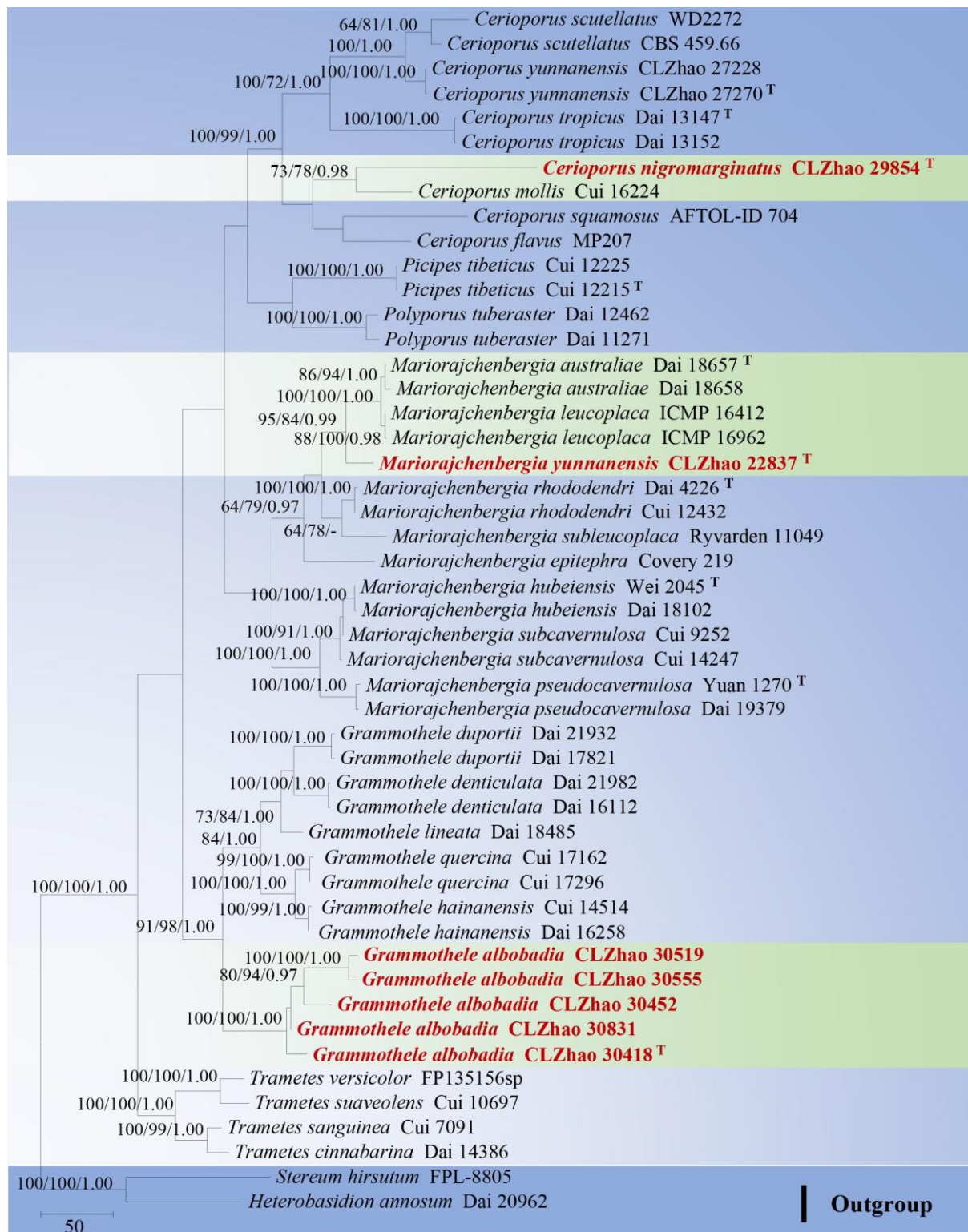


Figure 65 – Phylogram generated from maximum parsimony strict consensus tree analysis based on the combined ITS and nLSU sequence data of *Polyporaceae* species. Forty-nine specimens are included in the combined analyses. The tree topology of the maximum parsimony analysis is

similar to the maximum likelihood and Bayesian analysis. Constant characters were 1369. Parsimony-informative characters were 150 whereas parsimony-uninformative characters were 488. Bootstrap support values for ML $\geq 70\%$, MP $\geq 50\%$, and Bayesian posterior probabilities ≥ 0.95 are given near nodes, respectively. The tree was rooted with *Heterobasidion annosum* (Dai 20962) and *Stereum hirsutum* (FPL-8805). The newly generated sequences are indicated in red-bold, and the type collections are indicated with ^T.

Cerioporus nigromarginatus Y.L. Deng & C.L. Zhao, sp. nov.

Figs 66, 67

Index Fungorum number: IF 858758; Facesoffungi number: FoF 18445

Diagnosis – *Cerioporus nigromarginatus* is characterized by the resupinate, osseous basidiomata with cream to pale pink pore surface, brownish black to black sterile margin, a dimitic hyphal system with clamped generative hyphae and ellipsoid to cylindrical basidiospores ($5.5\text{--}7.5 \times 3\text{--}4 \mu\text{m}$).

Etymology – *nigromarginatus* (Lat.): referring to the brownish black to black sterile margin of the type specimen.

Basidiomata annual, resupinate, osseous, without odor or taste when fresh, up to 7 cm long, 3 cm wide and 4 mm thick at base. *Pore surface* cream to pale pink when fresh, becoming olivaceo-bubalinus to avellaneus when dry, pores round, 5–7 per mm. *Context* cream, corky, up to 3 mm thick. *Tubes* pale cream, hard corky, up to 2 mm long. *Sterile margin* brownish black to black, up to 1 mm. *Hyphal system* dimitic, generative hyphae with clamp connections, thin-walled, colorless, $2\text{--}3 \mu\text{m}$ in diam. *Skeletal hyphae* dominant in context, thick-walled with a narrow lumen to subsolid, colorless, $3\text{--}5 \mu\text{m}$ in diam., all hyphae occasionally branched, flexuous, interwoven; IKI–, CB–, tissues unchanged in KOH. *Cystidia* absent. *Cystidioles* present, fusoid, the tip forms a long beak, colorless, thin-walled, $18\text{--}28 \times 4\text{--}5 \mu\text{m}$. *Basidia* clavate, with four sterigmata and a basal clamp connection, $17\text{--}23 \times 3\text{--}5 \mu\text{m}$. *Basidioles* similar to basidia in shape, but slightly smaller. *Basidiospores* cylindrical, colorless, thin-walled, smooth, IKI–, CB–, $5.5\text{--}7.5 \times 3\text{--}4 \mu\text{m}$, $L = 6.56 \mu\text{m}$, $W = 3.49 \mu\text{m}$, $Q = 2.07$ ($n = 30/1$).

Material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: $25^{\circ}52' \text{N}$, $97^{\circ}38' \text{E}$, altitude 1000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 18 July 2023, CLZhao 29854 (SWFC, holotype).

GenBank accession numbers – ITS: PQ811394, LSU: PV185840, mtSSU: PV283181, *rpb2*: PV339604.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 65) revealed that our species *Cerioporus nigromarginatus* (CLZhao 29854) clustered within *Cerioporus* sister to *Ce. mollis* (Cui 16224) with 73% MP, 78% ML and 0.98 BYPP bootstrap support. This clade shows a close phylogenetic affinity to the clade of *Ce. squamosus* (AFTOL-ID 704) and *Ce. flavus* (MP 207). Morphologically, *Ce. mollis* is distinguished from *Ce. nigromarginatus* by having imbricate basidiomata, trimitic hyphal system, generative hyphae with clamps, contextual skeletal hyphae yellowish, thick-walled, binding hyphae thick-walled, longer basidiospores ($8\text{--}11 \times 3\text{--}3.5 \mu\text{m}$). Also, *Ce. squamosus* differs from *Ce. nigromarginatus* by stipitate basidiomata, larger basidia ($40\text{--}70 \times 9\text{--}12 \mu\text{m}$), and subellipsoid basidiospores ($14\text{--}17 \times 5\text{--}6 \mu\text{m}$, Núñez & Ryvarden 1995). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Ce. nigromarginatus* as a new species.

Grammothele Berk. & M.A. Curtis

Index Fungorum number: IF 17692; Facesoffungi number: FoF 18446

Notes – *Grammothele* was described by Berkeley & Curtis (1868) and typified by *Gram. lineata* (Ryvarden 1991). This genus is characterized by annual, resupinate, adnate, effused basidiomata, irregularly irpicoid to poroid and then partly labyrinthine to sinuous hymenial surface, hyphal system dimitic; generative hyphae with clamps, dendrohyphidia absent or present, basidiospores ellipsoid to cylindrical, smooth and non-amyloid to dextrinoid (Berkeley & Curtis 1868). It is a mostly subtropical and tropically distributed genus with more or less poroid hymenial

surface consisting of shallow pores, the hymenium of this genus species is often restricted to the bottom of the pores (Wu et al. 2016). Mao et al. (2023) made a comprehensive study on *Grammothele* s.l. *Grammothele*, *Pseudogrammothele* and *Theleporus* species share similar morphological characteristics also with hymenia restricted to the horizontal surface of basidiomata (Ryvarden & Johansen 1980, Ryvarden 2015, Wu et al. 2016). *Pseudogrammothele* differs from *Grammothele* and *Theleporus* by its basidiome is easily separated from the substrate, distinct pores, duplex subiculum and large and cyanophilous basidiospores with guttules (Mao et al. 2023). *Theleporus* differs from *Grammothele* species by the presence of dextrinoid skeletal hyphae, hydroid to distinctly poroid basidiocarps and darker pore surface (Zhou & Dai 2012, Ryvarden 2014, Wu et al. 2016). Based on Index Fungorum (2025), *Grammothele* consists of 40 species and 24 registered species have been accepted worldwide (Ryvarden & Johansen 1980, Ryvarden 2014, Wu et al. 2016, Jayawardena et al. 2022). In this study, *Grammothele albobadia* sp. nov. is introduced from China, based on the ITS+nLSU sequence data (Fig. 65) and morphological characteristics (Figs 68, 69).

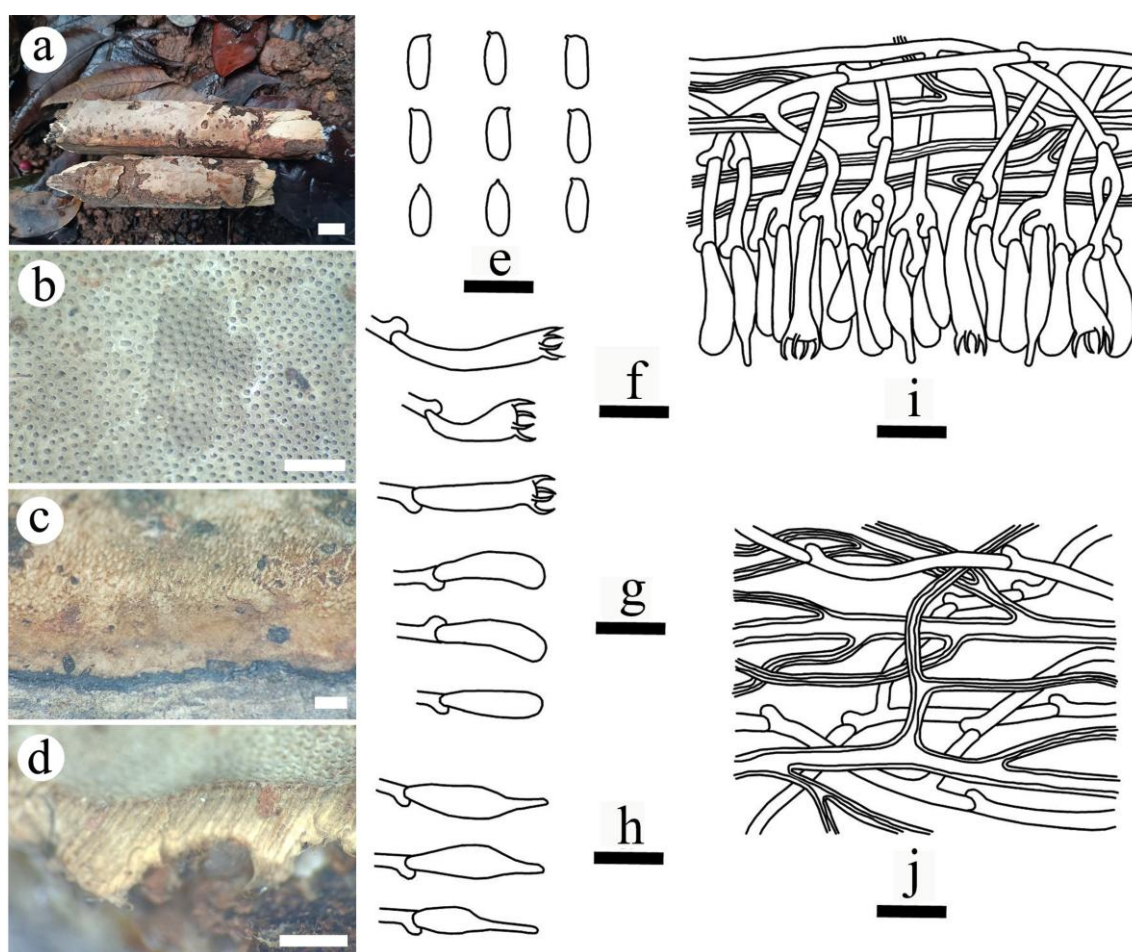


Figure 66 – Basidiomata and microscopic structures of *Cerioporus nigromarginatus* (CLZhao 29854, holotype). a Basidiomata on the host substrate. b–c Characters of pore. d Characters of tube. e Basidiospores. f Basidia. g Basidioles. h Cystidioles. i A section of the hymenium. j Hyphae from context. Scale bars: a = 1 cm, b–d = 1 mm, e–j = 10 µm.

Grammothele albobadia Y.L. Deng & C.L. Zhao, sp. nov.

Figs 68, 69

Index Fungorum number: IF 858759; Facesoffungi number: FoF 18447

Diagnosis – *Grammothele albobadia* is distinguished from other species of *Grammothele* by the resupinate, coriaceous basidiomata with white to cream hymenial surface, a dimitic hyphal system with clamped generative hyphae and oblong ellipsoid to cylindrical basidiospores.

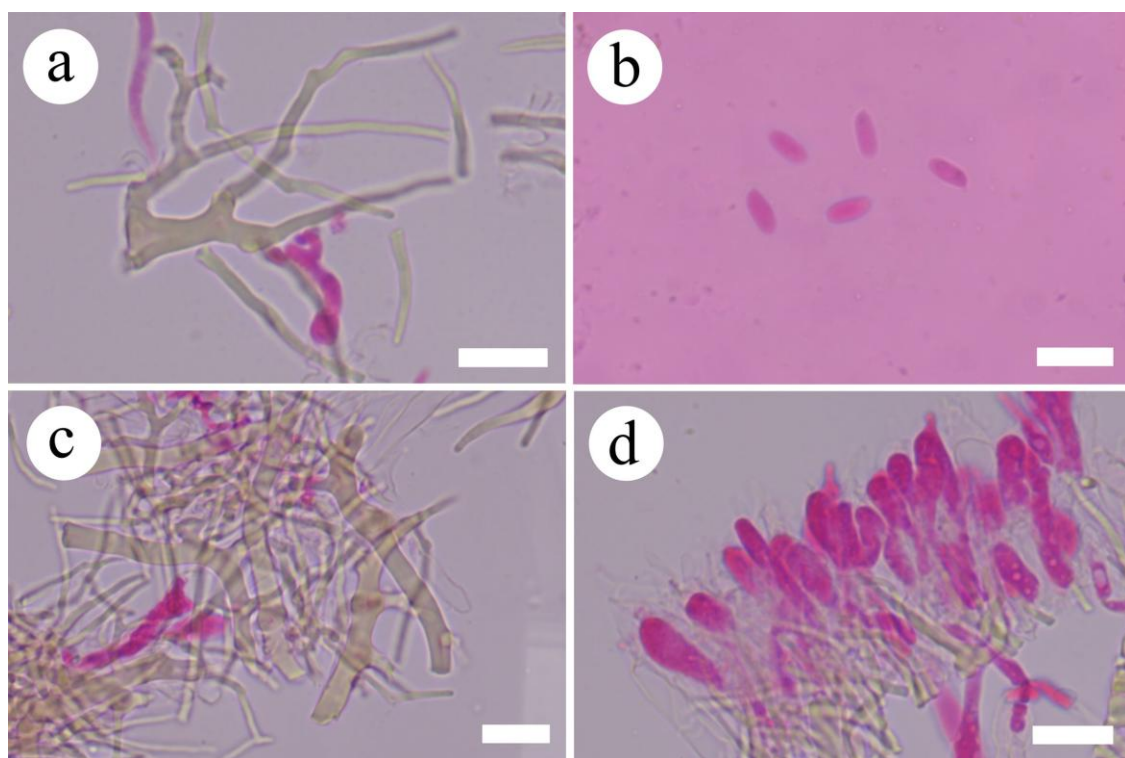


Figure 67 – Sections of hymenium of *Cerioporus nigromarginatus* (CLZhao 29854, holotype). a, c Hyphae from context. b Basidiospores. d A section of the hymenium. Scale bars: a–d = 10 μ m.

Etymology – *albobadia* (Lat.): referring to white hymenial surface of the type specimen.

Basidiomata annual, resupinate, coriaceous, without odor or taste when fresh, up to 8 cm long, 2.5 cm wide and 100–130 μ m thick. *Hymenial surface* smooth, white when fresh, becoming cream when dry. *Sterile margin* distinctly, thin, white, up to 2 mm. *Hyphal system* dimitic, generative hyphae with clamp connections, thin-walled, colorless, 2–3 μ m in diam. *Skeletal hyphae* dominant in context, thick-walled, colorless, 3–4 μ m in diam., occasionally branched, flexuous, interwoven, IKI–, CB–, tissues unchanged in KOH. *Cystidia* absent. *Cystidioles* present, fusoid to clavate, the apical neck contracted, forming a mastoid shape, colorless, thin-walled, 13–20 $\times$ 5–8.5 μ m. *Dendrohyphidia* colorless, richly branched, thin-walled. *Basidia* clavate, base slender, with four sterigmata and a basal clamp connection, 14.5–23 $\times$ 5–7 μ m. *Basidioles* similar to basidia in shape, but slightly smaller. *Basidiospores* oblong ellipsoid to cylindrical, colorless, thin-walled, smooth, IKI–, CB–, (10.7–)11–13.8(–14.2) $\times$ (4.2–)4.6–7 μ m, L = 12.47 μ m, W = 5.86 μ m, Q = 2.11–2.14 (n = 150/5).

Material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 25°52' N, 97°38' E, altitude 1000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 19 July 2023, CLZhao 30418 (SWFC, holotype); *ibid.*, CLZhao 30452, CLZhao 30519, CLZhao 30555, and CLZhao 30831 (SWFC, isotypes).

GenBank accession numbers – CLZhao 30418: ITS = PQ811396, mtSSU = PV283182, *rpb2* = PV339606; CLZhao 30452: mtSSU = PV283183; CLZhao 30519: LSU = PV185842, MTSSU: PV283184, *rpb2*: PV339607; CLZhao 30555 LSU: PV185843, mtSSU: PV283185, *rpb2*: PV339608; CLZhao 30831: ITS = PQ811397, mtSSU = PV283186.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 65) revealed that our five specimens of *Grammothele albobadia* (CLZhao 30519, CLZhao 30555, CLZhao 30452, CLZhao 30831 and CLZhao 30418; type specimen) grouped within *Grammothele*, forming a monophyletic clade sister to the clade consisting of *Gram. duportii* (Dai 21932, Dai 17821), *Gram. denticulate* (Dai 21982, Dai 16112), *Gram. lineata* (Dai 18485), *Gram. quercina* (Cui 17162, Cui 17296), and *Gram. hainanensis* (Cui 14514, Dai 16258) with 91% MP, 98% ML and 1.00 BYPP bootstrap support. Morphologically, *Gram. albobadia* is similar to *Gram. hainanensis* by resupinate

basidiomata, a dimitic hyphal system, generative hyphae with clamp connections, thin-walled, dominant skeletal hyphae that are thick-walled and flexuous. However, *Gram. hainanensis* can be easily distinguished from *Gram. albobadia* by larger two kinds of cystidioles, $30\text{--}70 \times 2\text{--}4 \mu\text{m}$, and smaller cylindrical basidiospores ($7\text{--}8.1 \times 2.3\text{--}2.9 \mu\text{m}$, Wu et al. 2016). Thus, based on morphology and multigene phylogenetic evidence we introduce *Gram. albobadia* as a new species.

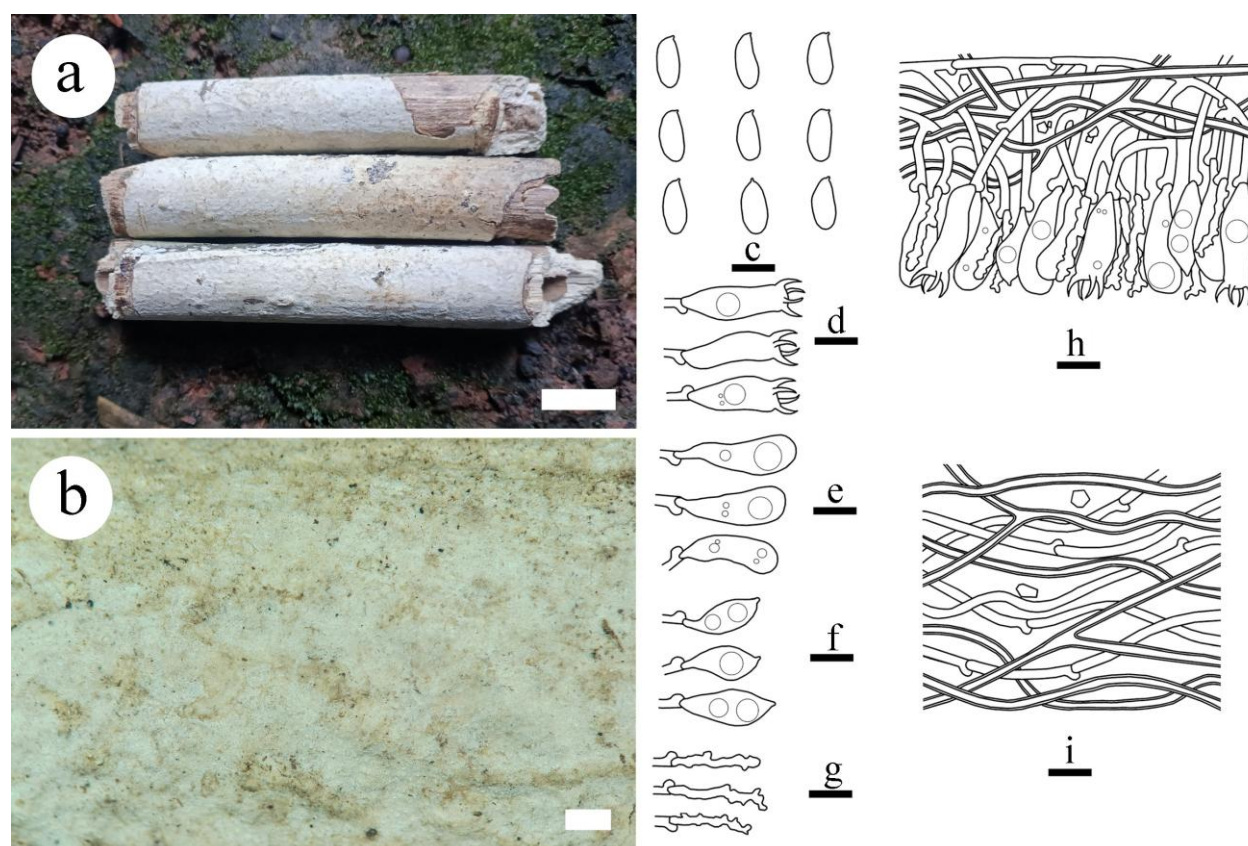


Figure 68 – Basidiomata and microscopic structures of *Grammothele albobadia* (holotype, CLZhao 30555). a Basidiomata on the substrate. b Macroscopic characteristics of hymenophore. c Basidiospores. d Basidia. e Basidioles. f Cystidioles. g Dendrohyphidia. h A section of the hymenium. i Hyphae from context. Scale bars: a = 1 cm, b = 1 mm, c–i = 10 μm .

Mariorajchenbergia Gibertoni & C.R.S. Lira

Index Fungorum number: IF 832795; Facesoffungi number: FoF 18448

Notes – *Mariorajchenbergia* was established to replace *Megasporoporiella* by Lira et al. (2021) and validated legitimately with type species, *Ma. subcavernulosa*. The genus is characterized by basidiomata that are annual and resupinate. Pore surface cream, pale yellowish to honey yellow, gray. Pores angular, 1–5 mm. Hyphal system dimitic with clamped generative hyphae. Skeletal hyphae non-dextrinoid to strongly dextrinoid, acyanophilous, moderately to frequently branched. Basidiospores cylindrical to oblong-ellipsoid, ellipsoid in one species, colorless, thin-walled, smooth, IKI–, CB–. Most species with polyhedric crystals in subhymenium, hymenium, and hyphal pegs in the tubes. Dendrohyphidia present in some species and many specimens of the genus have a few basidiospores (Lira et al. 2021, Wang et al. 2022a). Lira et al. (2021) revised the definition of *Megasporoporia sensu lato* and proposed *Jorgewrightia* and *Mariorajchenbergia*, which confirmed the four clades nested in *Megasporoporia sensu lato*, viz. clades of *Jorgewrightia*, *Mariorajchenbergia*, *Megasporia*, and *Megasporoporia sensu stricto* (Lira et al. 2021). *Dichomitus*, *Jorgewrightia*, *Mariorajchenbergia*, *Megasporia* and *Megasporoporia* have mostly resupinate pale-colored basidiomata, poroid hymenial surface, usually dextrinoid branched skeletal hyphae, and cylindrical basidiospores. Differentiating them based only on

morphology is challenging; therefore, molecular analyses using at least two regions (ITS and LSU), along with geographical distribution data, are necessary to accurate identification (Lira et al. 2021). Later, Wang et al. (2022a) studied the diversity and phylogeny of *Megasporoporia sensu lato*, and proposed two new combinations *Ma. epitephra* and *Ma. leucoplaca* with and one new species *Ma. subleucoplaca* based on a 4-gene (ITS+nLSU+mtSSU+tef1- α) phylogeny. Based on Index Fungorum (2025), *Mariorajchenbergia* consists of 8 species and 7 registered species have been accepted and known from temperate and subtropical China (Lira et al. 2021, Wang et al. 2021, 2022a). In the present study, *Mariorajchenbergia yunnanensis* sp. nov. is introduced from China, based on the ITS+nLSU sequence data (Fig. 65) and morphological characteristics (Fig. 70, 71).

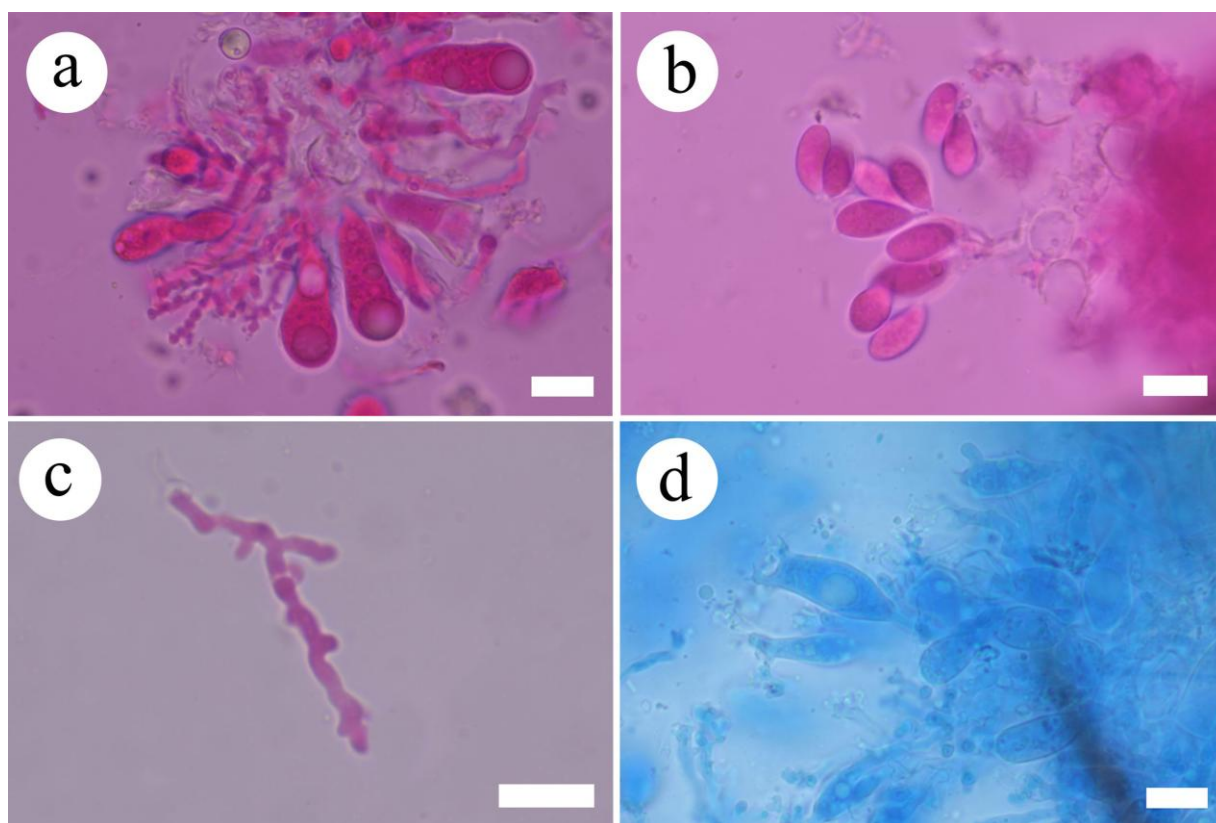


Figure 69 – a–d Sections of hymenium of *Grammothele albobadia* (holotype, CLZhao 30555). Scale bars: a–d = 10 μ m.

Mariorajchenbergia yunnanensis Y.L. Deng & C.L. Zhao, sp. nov.

Figs 70, 71

Index Fungorum number: IF 858760; Facesoffungi number: FoF 18449

Diagnosis – *Mariorajchenbergia yunnanensis* is characterized by the osseous basidiomata with cream to cinnamon-buff to ochroleucous pore surface, a dimitic hyphal system with clamped generative hyphae and ellipsoid to cylindrical basidiospores measuring $10\text{--}14 \times 6\text{--}7.5 \mu\text{m}$.

Etymology – *yunnanensis* (Lat.): referring to the locality province (Yunnan Province) of the type specimen.

Basidiomata annual, resupinate, osseous, without odor or taste when fresh, becoming hard corky upon drying, up to 7 cm long, 2.5 cm wide and 2 mm thick at the center. **Pore surface** smooth, cream to cinnamon-buff when fresh, becoming cream to slightly orange to ochroleucous when dry, pores round to angular, 4–5 per mm, dissepiments thick, entire, up to 0.1 mm thick. **Sterile margin** distinct, cream to ochroleucous, up to 2 mm wide. **Tubes** pale cream, hard corky, up to 1 mm long. **Hyphal system** dimitic, generative hyphae with clamp connections, thin-walled, colorless, $2.5\text{--}3.5 \mu\text{m}$ in diam. **Skeletal hyphae** dominant in context, thick-walled with a narrow lumen to subsolid, colorless, $3\text{--}4 \mu\text{m}$ in diam., all hyphae occasionally branched, flexuous, interwoven, IKI–, CB–, tissues unchanged in KOH. **Cystidia** absent. **Cystidioles** present, tubular to

fusoid, colorless, thin-walled, smooth, $21\text{--}34 \times 6\text{--}7.5\ \mu\text{m}$. *Basidia* clavate, with four sterigmata and a basal clamp connection, $23\text{--}38.5 \times 9\text{--}15\ \mu\text{m}$, with abundant oily substance. *Basidioles* similar to basidia in shape, but slightly smaller. *Basidiospores* ellipsoid to cylindrical, colorless, thin-walled, smooth, sometimes with one or two oil drops, IKI–, CB–, $(9.5\text{--})10\text{--}14(\text{--}14.3) \times (5.5\text{--})6\text{--}7.5(\text{--}8)\ \mu\text{m}$, $L = 12.30\ \mu\text{m}$, $W = 6.73\ \mu\text{m}$, $Q = 1.82$ ($n = 30/1$).

Material examined – China, Yunnan Province, Lingcang, Fengqing County, GPS coordinates: $23^{\circ}48'$ N, $100^{\circ}05'$ E, altitude 2900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 20 July 2022, CLZhao 22837 (SWFC, holotype).

GenBank accession numbers – ITS: PQ811395, LSU: PV185841, *rpb2*: PV339605.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 65) revealed that our species *Mariorajchenbergia yunnanensis* (CLZhao 22837) clustered within *Mariorajchenbergia*, forming a distinct lineage sister to the clade that consists of *Ma. australiae* (Dai 18657, Dai 18658) and *Ma. leucoplaca* (ICMP 16412, ICMP 16962) with 95% MP, 84% ML and 0.99 BYPP bootstrap support. Morphologically, *Ma. australiae* differs from *Ma. yunnanensis* by its pore surface white to cream to vinaceous buff to fulvous, pores 3–4 per mm, narrower basidiospores ($11.8\text{--}15 \times 4\text{--}6\ \mu\text{m}$, Lira et al. 2021, Wang et al. 2021). Also, *Ma. leucoplaca* can be easily distinguished from *Ma. yunnanensis* by basidiomata effused forming linear areas, hymenial surface white to cream or pallid alutaceous, pores not in strata, round, often oblique, 2–4 per mm, or in some specimens 2–3, generative hyphae thick-walled, smaller basidia $16\text{--}22 \times 5\text{--}8\ \mu\text{m}$, bearing 2–4 sterigmata, and narrower longelliptical or narrowly obovate basidiospores ($10\text{--}16 \times 4\text{--}6\ \mu\text{m}$, Wang et al. 2022b). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Ma. yunnanensis* as a new species.

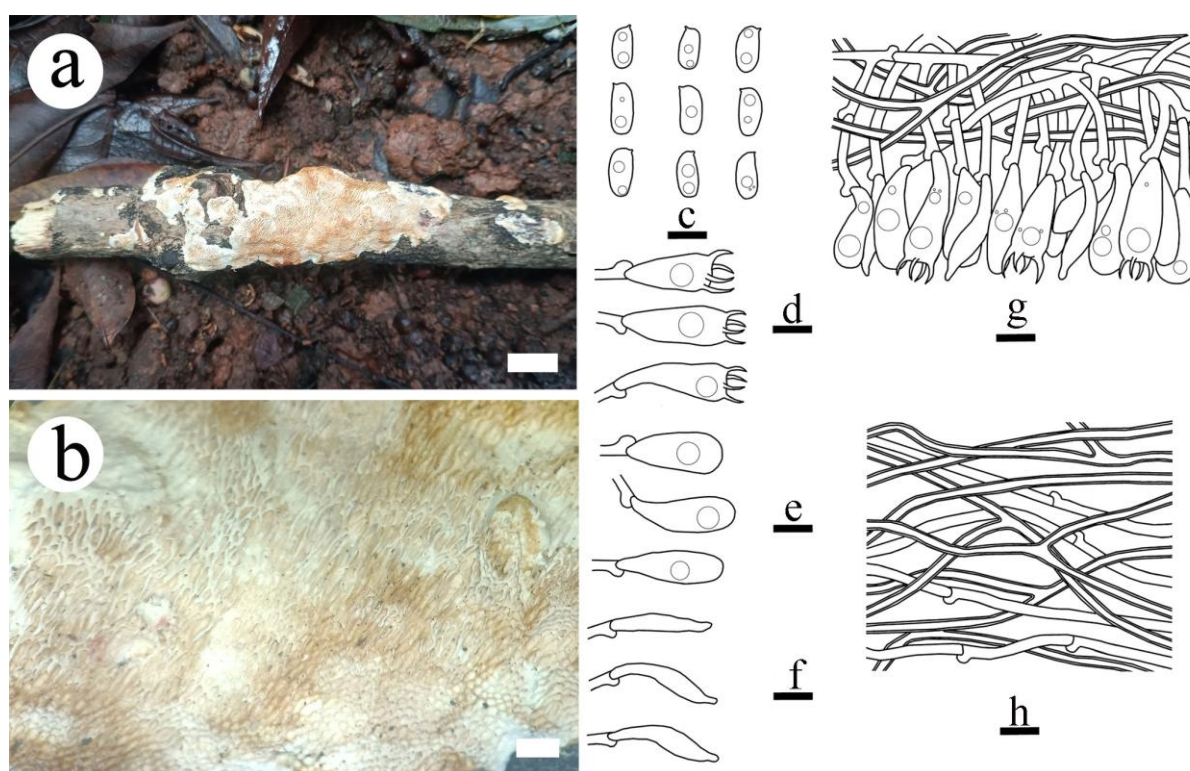


Figure 70 – Basidiomata and microscopic structures of *Mariorajchenbergia yunnanensis* (holotype, CLZhao 22837). a Basidiomata on the substrate. b Characters of hymenophore. c Basidiospores. d Basidia. e Basidioles. f Cystidioles. g A section of the hymenium. h Hyphae from context. Scale bars: a, b = 1 cm, a–f = 10 μm .

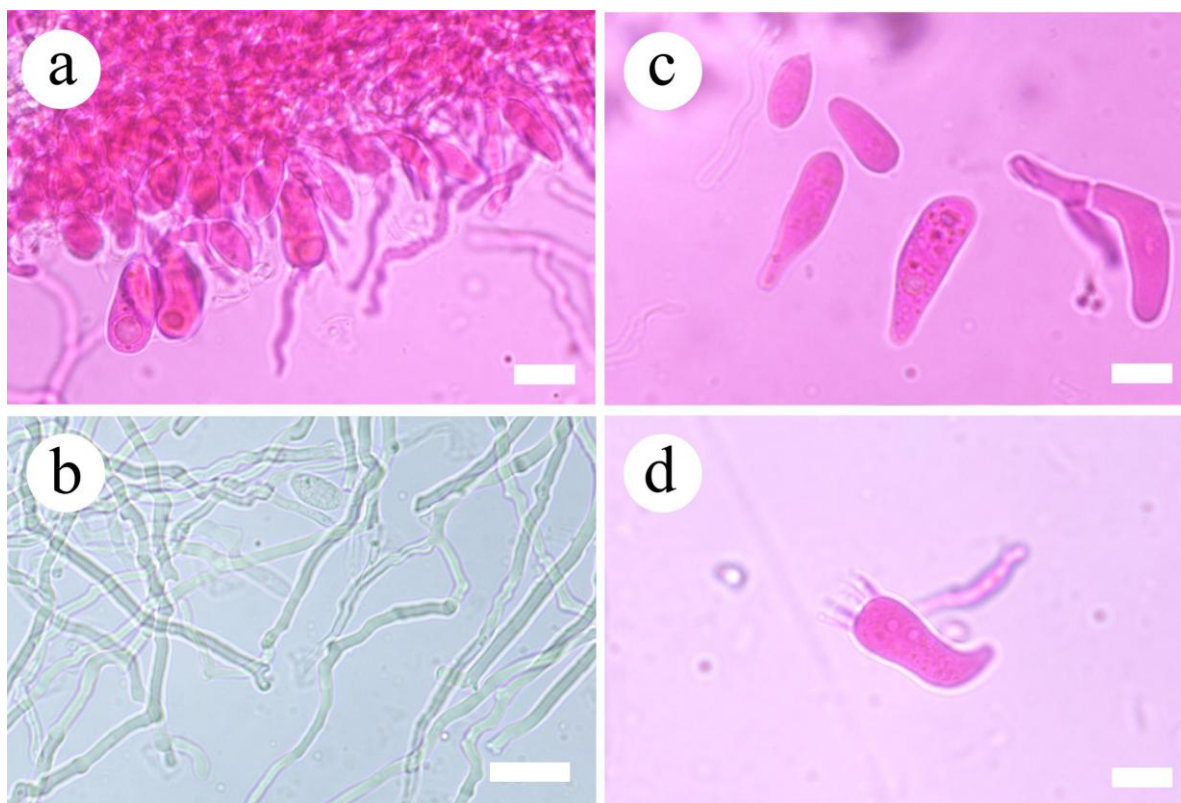


Figure 71 – a–d Sections of hymenium of *Mariorajchenbergia yunnanensis* (holotype, CLZhao 22837). a A section of the hymenium. b Hyphae from context. c Basidioles. d Basidia. Scale bars: a–d = 10 μ m.

Microporellus Murrill

Index Fungorum number: IF 18062; Facesoffungi number: FoF 18450

Notes – *Microporellus*, a tropical taxon, was established by Murrill (1905) and *Mi. dealbatus* as the type species. These key characteristics of this genus are having sessile to stipitate basidiomata, a trimitic hyphal system and coralloid dichophytic elements along the dissepiments (Ryvarden & Johansen 1980, Motato-Vásquez & Gugliotta 2016). *Microporellus* is easily confused with *Perenniporia*; however, the latter genus exhibits distinct structures of skeletal hyphae and basidiospores morphology (Robledo et al. 2009, Motato-Vásquez & Gugliotta 2016). Based on ITS and nLSU phylogenetic analyses by Zhao & Cui (2013), *Microporellus* forms a group that can be recognized as a separate genus. Nevertheless, the phylogeny of *Microporellus* remains unclear with the family *Hymenochaetaceae*. Currently, around 25 species are accepted in *Microporellus* worldwide (Hyde et al. 2024c, Index Fungorum 2025). In this study, a novel species, *Microporellus oblongosporus* is introduced from China, based on the ITS and LSU sequence data (Fig. 72) and morphological characteristics (Fig. 73).

Microporellus oblongosporus Z.R. Gu, H.M. Zhou & C.L. Zhao, sp. nov.

Fig. 73

Index Fungorum number: IF 856057; Facesoffungi number: FoF 18451

Diagnosis – Differs from *Microporellus subadusta* by wider basidiospores.

Etymology – *oblongosporus* (Lat.): referring to the oblong basidiospores.

Basidiomata annual, pileate, sessile, imbricate, effused-reflexed, or sometimes umbonate, soft, coriaceous and flexible when dry, up to 9 cm long, 6 cm wide, and 0.2 mm thick. *Hymenial surface* fluffy, with striations in a ring pattern, brown-yellow when fresh, turn to brown-yellow to earthy brown when dry. *Hyphal system* dimitic, generative hyphae distinct, with clamp connections, hyaline, thin-walled, 1.73–2.87 μ m in diam.; IKI–, CB–. *Skeletal hyphae* yellowish to yellowish brown, thick-walled, 4.0–4.8 μ m in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* and *cystidioles* absent. *Basidia* clavate with a slight median constriction, hyaline, thin-walled, with four

sterigmata and a basal clamp connection, $22.9\text{--}32.4 \times 4\text{--}4.5\ \mu\text{m}$. *Basidioles* similar to basidia in shape, but slightly smaller. *Basidiospores* oblong to ellipsoid, hyaline, thin-walled, $(5.1\text{--})5.3\text{--}7.0 \times (2.2\text{--})2.4\text{--}3(3.1)\ \mu\text{m}$, $L = 6.31\ \mu\text{m}$, $W = 2.62\ \mu\text{m}$, $Q = 2.41$ ($n = 30/1$).

Type of rot – White rot.

Material examined – China, Yunnan Province, Yuxi, XinPing County, GPS coordinates $23^{\circ}38'N$, $101^{\circ}16'E$, altitude 2000 m asl., on the fallen angiosperm trunk, leg. C.L. Zhao, 18 January 2018, CLZhao 6336 (SWFC, holotype); Yunnan Province, Wenshan, Xichou County, Wenshan National Nature Reserve, GPS coordinates $23^{\circ}21'N$, $104^{\circ}41'E$, altitude 1400 m asl., on the fallen angiosperm trunk, leg. C.L. Zhao, 15 January 2019, CLZhao 10964 (SWFC, paratype).

GenBank accession numbers – CLZhao 6336: ITS = PQ362236, LSU = PQ363280; CLZhao 10964: ITS = PQ362237.

Notes – The phylogenetic analysis based on ITS and nLSU sequences revealed that the collections of our species *Microporellus oblongosporus* (CLZhao 10964 and CLZhao 6336) grouped within other specimens of *Microporellus*, forming a separate clade closely related to *Mi. obovatus* with 100% ML and 1.00 BYPP bootstrap support (Fig. 72). *Microporellus oblongosporus* is characterized by pileate, sessile and brown basidiomata, a dimitic system, oblong to ellipsoid basidiospores ($5.3\text{--}7.0 \times 2.4\text{--}3\ \mu\text{m}$). Morphologically, *Mi. oblongosporus* is similar to *Mi. subadustus* by pileate, sessile and brown basidiomata, but the latter has wider basidiospores ($3.5\text{--}4\ \mu\text{m}$ vs. $2.4\text{--}3\ \mu\text{m}$, Zheng & Bi 1987). It can be distinguished from phylogenetically closely related *Mi. obovatus* by its shorter basidiospores ($3.5\text{--}5\ \mu\text{m}$ vs. $5.3\text{--}7.0\ \mu\text{m}$, Núñez & Ryvarden 2001). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Mi. oblongosporus* as a new species.

***Lopharia* Kalchbr. & MacOwan**

Index Fungorum number: IF 17993; Facesoffungi number: FoF 18452

Notes – Hjortstam & Ryvarden (1990) compiled the first nomenclature of *Lopharia* which is an important group of the wood-decaying fungi (Gu et al. 2025). *Lopharia* s.s. was typified by *L. lirellosa* (= *Radulum mirabile*); the species listed in Welden's monograph (2010) were combined with *Porostereum* by Hjortstam & Ryvarden (1990), as well as Ryvarden (2010). Both genera are classified within Polyporales, with *Lopharia* belonging to *Polyporaceae* (Justo et al. 2017). *Lopharia* is stereoid fungi, and the key morphologies of this genus are resupinate and effused-reflexed basidiomata, a monomitic or dimitic hyphal system, generative hyphae with clamp connection, presence of the large basidia and basidiospores and large, encrusted, hyaline, thick-walled lamprocystidia (Kalchbrenner 1881, Liu et al. 2018). Based on a three-gene phylogeny (nrLSU, nrITS, and *rpb1*) and morphological analyses, taxonomic placement of *Lopharia* was confirmed within *Polyporaceae* (Justo et al. 2017, He et al. 2024). Based on MycoBank (2025) and Index Fungorum (2025), *Lopharia* has registered 40 specific and infraspecific names, and 18 species are widely recognized (Hyde et al. 2024d, Gu et al. 2025). In this study, *Lopharia fissurata* is introduced from China based on the ITS+nLSU sequence data (Fig. 74) and morphological characteristics (Fig. 75).

***Lopharia fissurata* J.L. Zhang & C.L. Zhao, sp. nov.**

Fig. 75

Index Fungorum number: IF 904415; Facesoffungi number: FoF 18453

Diagnosis – It differs from other *Lopharia* species by its coriaceous and cracked basidiomata, a monomitic hyphal system with clamp connections, and oblong ellipsoid basidiospores measuring $5\text{--}5.6 \times 2.1\text{--}2.4\ \mu\text{m}$.

Etymology – *fissurata* (Lat.): referring to the holotype having a cracked hymenial surface.

Basidiomata annual, resupinate, coriaceous, without odor or taste when fresh, up to 7.7 cm long, 1.9 cm wide, less than 1 mm thick. *Hymenial surface* cream to slightly pink when fresh, pinkish buff to slightly clay-buff when dry, cracking. *Sterile margin* narrow, cream, up to 1 mm wide. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequent branching, interwoven, $1.7\text{--}2.3\ \mu\text{m}$ in diam.; IKI–, CB–, tissues unchanged in KOH, but

it's hard to see clearly. *Lamprocystidia* abundant, arising from subhymenium, subulate, heavily encrusted with crystals, thin-walled, embedded in subhymenium or exerted, $30\text{--}50 \times 8\text{--}12\ \mu\text{m}$; capitate cystidia, colorless, thin-walled, $9\text{--}18 \times 3\text{--}5\ \mu\text{m}$. *Basidia* clavate, with a basal clamp connection and four sterigmata, $16\text{--}27 \times 4\text{--}5\ \mu\text{m}$. *Basidioles* dominate in hymenium, similar to basidia but smaller. *Basidiospores* oblong ellipsoid, colorless, thin-walled, smooth, containing guttules, IKI–, CB–, $5\text{--}5.6\text{--}(5.7) \times (2.0\text{--}) 2.1\text{--}2.4\text{--}(2.5)\ \mu\text{m}$, $L = 5.21\ \mu\text{m}$, $W = 2.25\ \mu\text{m}$, $Q = 2.31$ ($n = 30/1$).

Type of rot – white rot

Material examined – China, Yunnan Province, Diqing Prefecture, Weixi County, Weideng Township, Fuchuan Village, $27^{\circ}16'N$, $99^{\circ}15'E$, altitude 1700 m asl., on the fallen angiosperm branch, 12 October 2023 (CLZhao 34262, holotype).

GenBank accession numbers – ITS: PV839362, LSU: PV839363.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 74) revealed that our species *Lopharia fissurata* (CLZhao 34262) grouped within other specimens of *Lopharia*, forming a separate lineage sister to *L. minispora* (CLZhao 21694, CLZhao 21779, CLZhao 21787) with 96% ML and 1.00 BYPP bootstrap support. Morphologically, *L. fissurata* resembles *L. minispora* in having cream to ochraceous (when fresh), cracked basidiomata, and lamprocystidia. In contrast, the hymenial surface of *L. fissurata* is pinkish buff to slightly clay-buff when dry, while *L. minispora* is ochraceous to slightly brown when dry. Also, *L. minispora* distinguishes from *L. fissurata* by its larger basidiospores ($5.5\text{--}6.7 \times 2.7\text{--}3.3\ \mu\text{m}$), broader basidia ($22\text{--}28 \times 5\text{--}7\ \mu\text{m}$), and the former has subulate, heavily encrusted with crystals, while the latter has capitate cystidia (Gu et al. 2025). The key morphological differences of *Lopharia* species are provided in Table 3. Thus, based on morphology and multigene phylogenetic evidence, we introduce *L. fissurata* as a new species.

Sebacinales M. Weiss, Selosse, Rexer, A. Urb. & Oberw.

Sebacinaceae K. Wells & Oberw.

Sebacina Tul. & C. Tul.

Index Fungorum number: IF 18534; Facesoffungi number: FoF 18454

Notes – Tulasne & Tulasne (1871) erected *Sebacina* to transfer *Se. incrustans* (*Corticium corticium*; type species) based on longitudinally septate basidia. This genus is characterized by the ellipsoid, ovoid to globose basidia, longitudinally septate, two to four-celled, primary basidiospores are smooth and thin-walled. In addition, thick-walled spores with irregular spore walls are commonly present. (Oberwinkler et al. 2014, Weiß et al. 2016, Crous et al. 2024). Previously, *Sebacina* consisted of fungi with resupinate or lacking fruitbodies. Later, Wells & Oberwinkler (1982) introduced *Sebacinaceae*, and the several genera including *Sebacina* which present erect and branched or funnel-shaped or pustulate-confluent fruitbodies were placed within the family. Currently, more than 60 species are accepted into this genus (Hyde et al. 2024d). In this study, *Sebacina yunnanensis* sp. nov. is introduced from China based on the ITS sequence data (Fig. 76) and morphological characteristics (Fig. 77).

Sebacina yunnanensis Q.Q. Jiang & C.L. Zhao, sp. nov.

Fig. 77

Index Fungorum number: IF 904416; Facesoffungi number: FoF 18455

Diagnosis – Differs from other *Sebacina* species by the gelatinous basidiomata, smooth hymenial surface, a monomitic hyphal system with simple septate generative hyphae and ellipsoid basidiospores measuring $(8.5\text{--})9\text{--}11.5\text{--}(13) \times (5.5\text{--})6\text{--}7\text{--}(7.5)\ \mu\text{m}$.

Etymology – *yunnanensis* (Lat.): referring to the locality (Yunnan Province) of the holotype.

Basidiomata annual, growing on decaying wood, strictly resupinate and strongly gelatinous when fresh, drying out to inconspicuous, easily separable, up to 10 cm long, 6 cm wide, 10–30 mm thick. *Hymenial surface* smooth, gelatinous, composed of basidia and hyphidia, white when fresh, white to cream on drying. *Hyphal system* monomitic, generative hyphae with simple septa, colorless, thin-walled, occasionally branched, interwoven, densely packed hyphae are interspersed with air spaces, $1.5\text{--}3.5\ \mu\text{m}$ in diam.; IKI–, CB–, tissues unchanged in KOH. *Cystidia* and

Cystidioles absent. *Basidia* ellipsoid to ovoid, longitudinally septate, two to four-celled, $12\text{--}15.5 \times 10\text{--}13.5 \mu\text{m}$. *Basidioles* dominant, similar to basidia in shape, but slightly smaller. *Basidiospores* ellipsoid, slightly curved, colorless, thin-walled, sometimes with one oil drop, IKI–, CB–, $(8.5\text{--})9\text{--}11.5(-13) \times (5.5\text{--})6\text{--}7(-7.5) \mu\text{m}$, $L = 10.11 \mu\text{m}$, $W = 6.47 \mu\text{m}$, $Q = 1.56$ ($n = 30/1$).

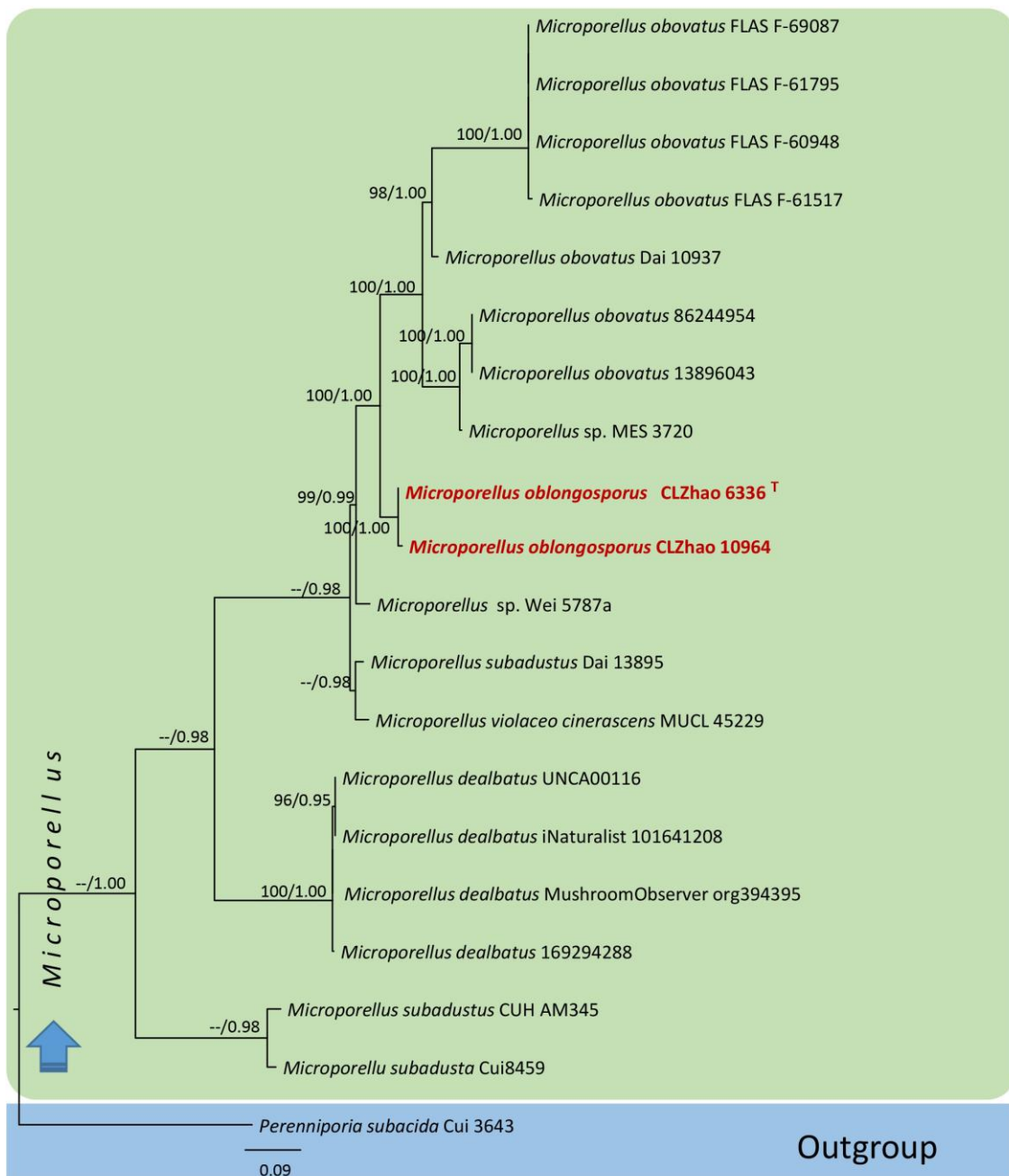


Figure 72 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data of *Microporellus*. Twenty specimens were included in the combined sequence analyses, which comprised 1840 characters with gaps (ITS = 600, LSU = 1240). Single-gene analyses were also performed, and the topology and clade stability were compared with those from the combined gene analyses. *Perenniporia subacida* (Cui 3643) was used as the outgroup. The final ML optimization likelihood is -7474.124. The alignment dataset includes 543 distinct patterns, 389 singleton sites and 1045 constant sites. Bootstrap support values for ML (first set) equal to or greater than 96%, BYPP equal to or greater than 0.95 are given above or below the nodes. The newly generated sequences of the current study are in red-bold, and the type collection is indicated with ^T.

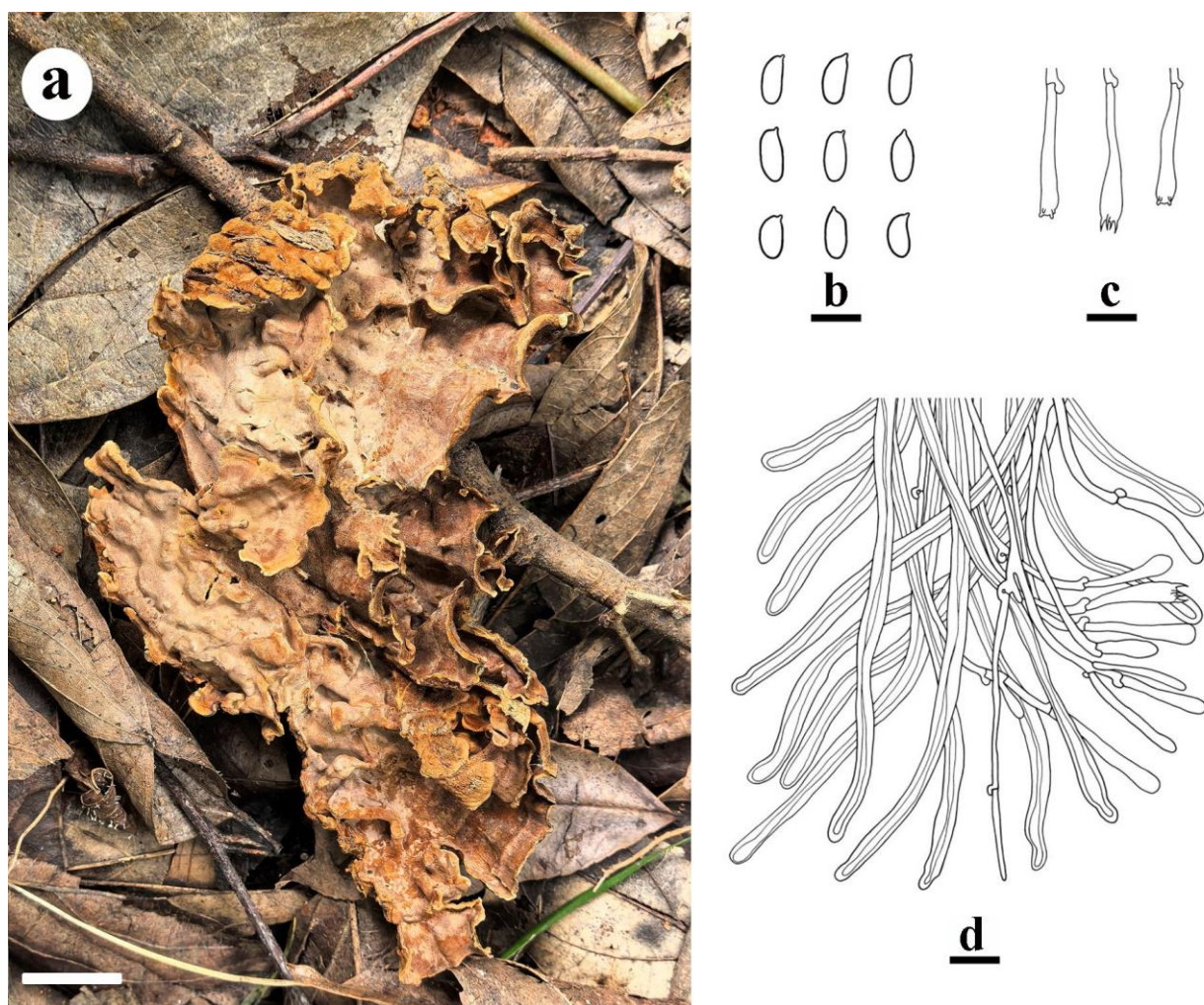


Figure 73 – Basidiomata and Microscopic structures of *Microporellus oblongosporus* (CLZhao 6336, holotype). a Basidiomata. b Basidiospores. c Basidia. d A cross-section of basidiomata. Scale bars: a = 1 mm, b = 5 μ m, c–d = 10 μ m.

Material examined – China. Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates: 27°30' N, 104°10' E, altitude 1750 m asl., on the root of *Hydrangea macrophylla* (Hydrangeaceae), leg. H.M. Zhou, 14 October 2024, HM Zhou 954 (SWFC, holotype).

GenBank accession numbers – ITS: PV648694.

Notes – The combined ITS phylogenetic analyses revealed that our species *Sebacina yunnanensis* (HM Zhou 954) formed a separate lineage sister to *Se. cystidiata* (TUB 020024, 020025, 020026, and 020027) with 83% ML bootstrap support (Fig. 76). *Sebacina yunnanensis* resembles *Se. cystidiata* in having gelatinous basidiomata when fresh. *Sebacina cystidiata* differs from *Se. yunnanensis* by the absence of cystidia, and its wider basidiospores (7–9 $\times$ 10–16–(20) μ m), with multipolar germ tube formation, possibly also functioning as resting spores (Oberwinkler et al. 2014). Also, *Se. yunnanensis* resembles *Se. spongicarpa* in having gelatinous basidiomata when fresh. However, *Se. spongicarpa* can be distinguished from *Se. yunnanensis* by its smaller basidia (10–19 $\times$ 8–18 μ m), and smaller basidiospores (10–19 $\times$ 8–18 μ m, Crous et al. 2024). Further, *S. yunnanensis* resembles *S. epigaea* in having ellipsoid basidiospores and without cystidia and flagelliform dikaryophyses. However, *Se. epigaea* can be distinguished from *Se. yunnanensis* by its pale grey basidiomata, and its strongly gelatinizing hyphae, slightly coralloid dikaryophyses (Riess et al. 2013). Thus, based on morphology and phylogenetic evidence, we introduce *Se. yunnanensis* as a new species.

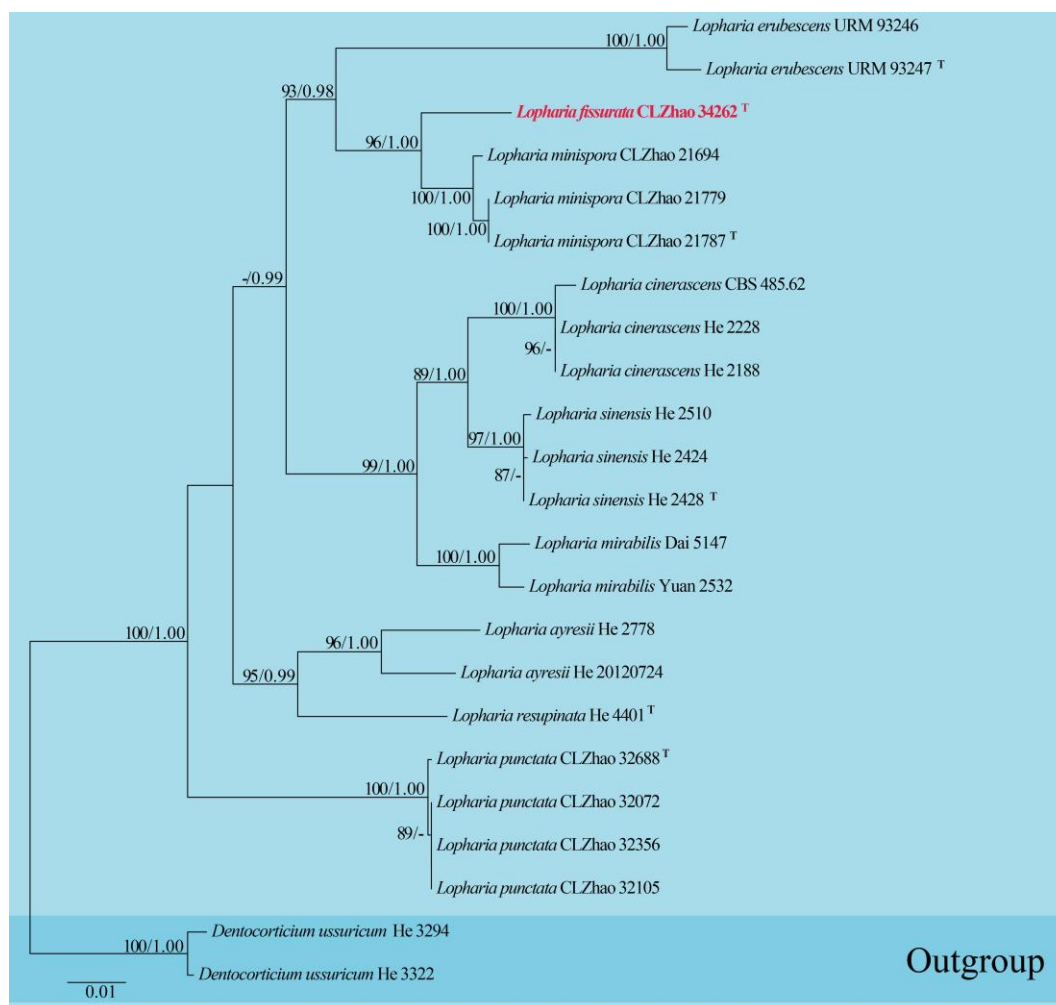


Figure 74 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and nLSU sequence data of *Lopharia*. Twenty-three specimens are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5541.761167 is presented. The evolutionary model GTR+F+I+G4 is applied for both genes. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Dentocorticium ussuricum* (He 3294, He 3322). The newly generated sequence is indicated in red-bold, and the type collections are indicated with ^T.

Thelephorales Corner ex Oberw.

Thelephoraceae Chevall.

Thelephora Ehrh. ex Willd.

Index Fungorum number: IF 18640; Facesoffungi number: FoF 18456

Notes – *Thelephora* was established by Willdenow (1787) and typified by *Th. terrestris*. It is an ectomycorrhizal genus in *Thelephoraceae* consists of some edible and medicinal species which have a worldwide distribution mainly in the northern temperate and tropical regions of Asia, Europe, and North America (Liu et al. 2021, Yang et al. 2023b). *Thelephora* species have different shapes of basidiocarps such as stereoid, coral-like, merismatoid, spathulate-rosulate and basidiospores with tuberculate or echinulate ornamentation, supporting to differentiate it from other *Thelephoraceae* genera (Yang et al. 2023b). Further, the genus is characterized by a smooth to slightly wrinkled hymenophore often cyanescent in KOH, glabrous to strigose, even or faintly ribbed or papillose pileus surface, continuous hymenium, monomitic hyphal system with clamped generative hyphae, 4-spored basidia and subhyaline to brownish, typically muricate, verruculose or echinulate, and inamyloid basidiospores (Liu et al. 2021). *Thelephora* shares similar morphology

with *Tomentella*. Kõljalg et al. (2024) and Song et al. (2025) merged *Tomentella* into *Thelephora* and proposed 191 and 4 new combinations, respectively. Based on the previous studies, approximately 452 accepted *Thelephora* species have been described worldwide (Song et al. 2025). In this study, *Thelephora tropica* sp. nov. is introduced from China based on the ITS sequence data (Fig. 78) and morphological characteristics (Figs 79, 80).

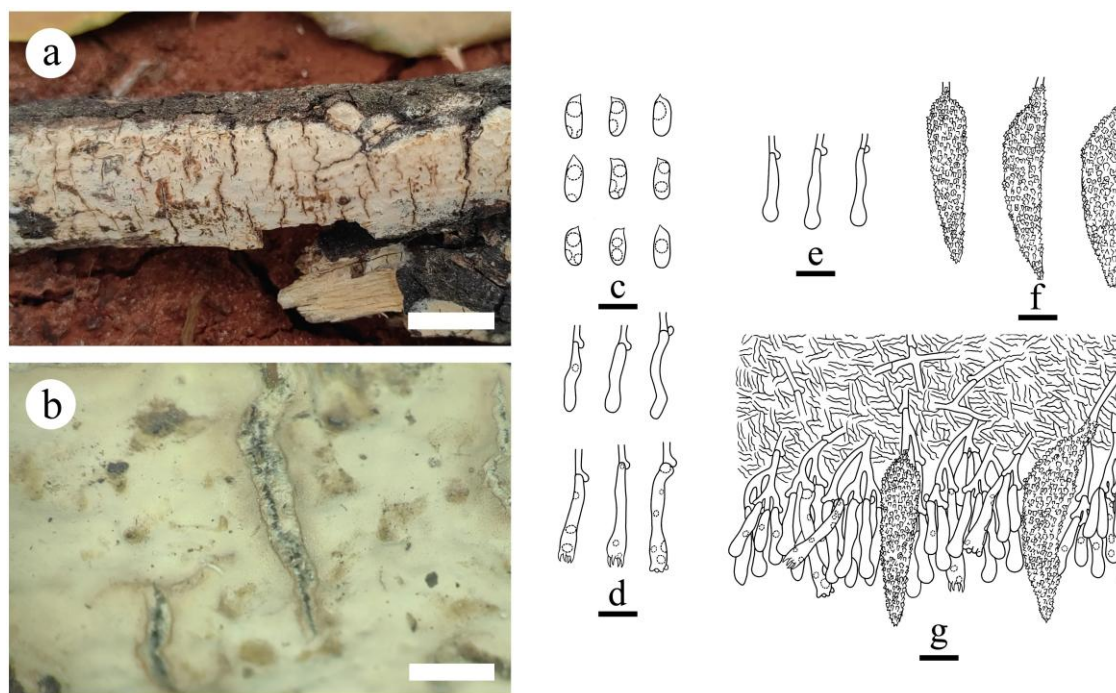


Figure 75 – Basidiomata and microscopic structures of *Lopharia fissurata* (CLZhao 34262, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e Capitulate cystidia. f Lamprocystidia. g A cross-section of hymenium. Scale bars: a = 1 cm, b = 1 mm, c = 5 µm, d–g = 10 µm.

Table 3 The key morphological differences in the dimensions of *Lopharia* species.

Species	Basidiomata	Size of Basidiospores (µm)	Hyphal System	Location	References
<i>Lopharia ayresii</i>	membranous	10–13 × 5.8–7	monomitic	Mauritius	Boidin & Gilles (1991)
<i>L. cinerascens</i>	coriaceous	8–16 × 5–8	dimitic	USA	Cunningham (1956)
<i>L. cystidiosa</i>	—	6.6–9.1 × 4.5–5.8	monomitic	India	Boidin (1969)
<i>L. erubescens</i>	ceraceous	5–6 × 1.5–2.5 µm	monomitic	Brazil	Xavier de Lima et al. (2020)
<i>L. fissurata</i>	coriaceous	5–5.6 × 2.1–2.4	monomitic	China	Present study
<i>L. minispora</i>	coriaceous	5.5–6.7 × 2.7–3.3	monomitic	China	Gu et al. (2025)
<i>L. mirabilis</i>	coriaceous	10–16 × 6–8	dimitic	Sri Lanka	Liu et al. (2018)
<i>L. pseudocinerascens</i>	ceraceous	8–14 × 4.5–6.5	dimitic	Central African Republic	Boidin & Gilles (2002)
<i>L. punctata</i>	membranous	9.5–12 × 7.5–10.1	monomitic	China	Gu et al. (2025)
<i>L. resupinata</i>	ceraceous	7–9 × 4–5	dimitic	China	Liu et al. (2018)
<i>L. sinensis</i>	coriaceous	11–14 × 6.5–8	dimitic	China	Liu et al. (2018)

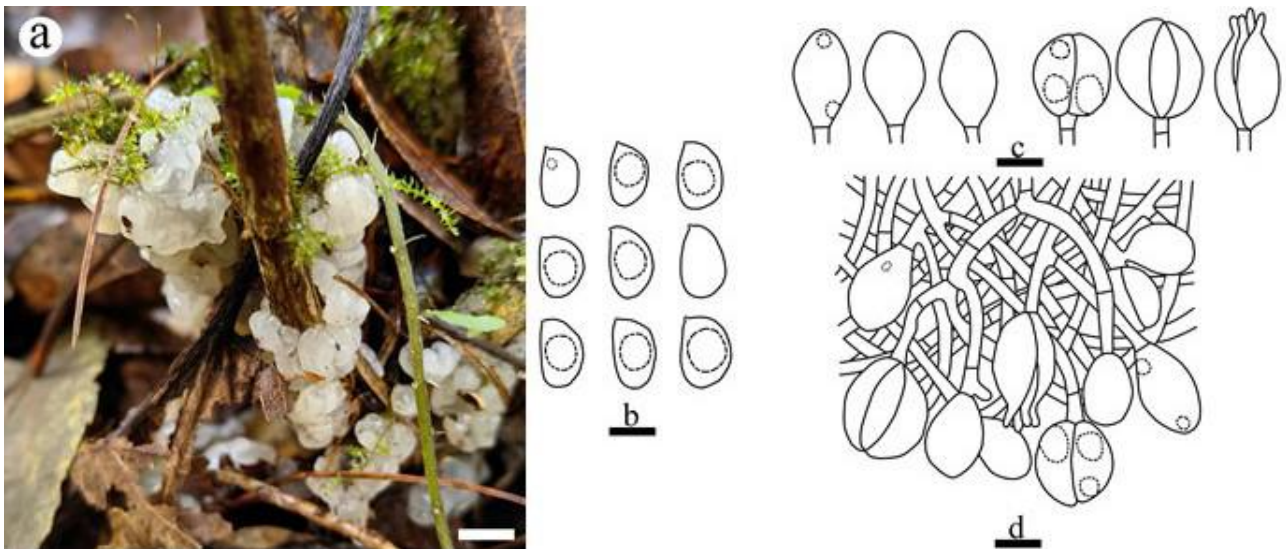


Figure 77 – Basidiomata and microscopic structures of *Sebacina yunnanensis* (CLZhao 954, holotype). a Basidiomata on the host substrates. b Basidiospores. c Basidia and basidioles. d A section of hymenium. Scale bars: a = 1 cm, b–d = 10 μ m.

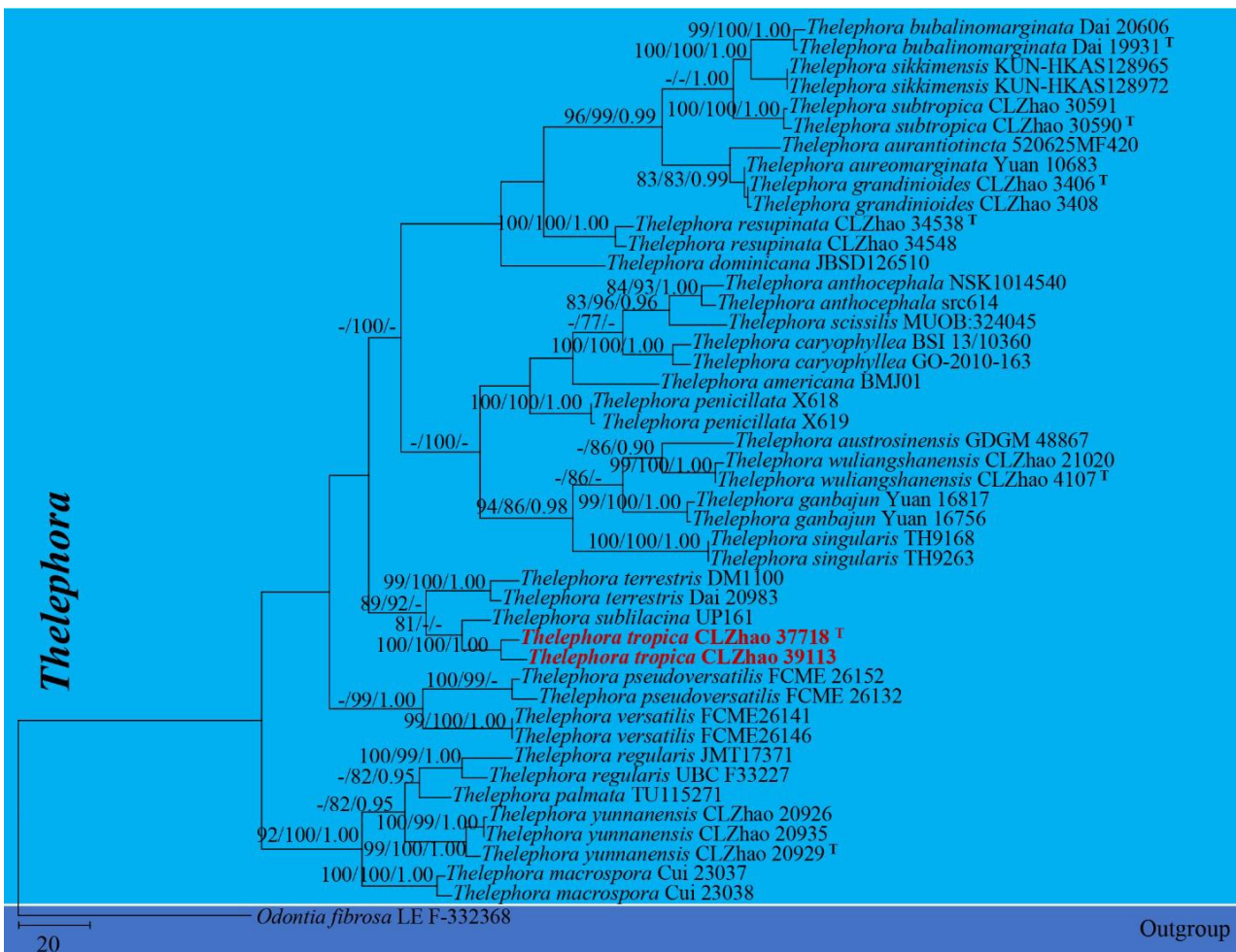


Figure 78 – Phylogram generated from maximum parsimony strict consensus tree analysis based on the ITS sequence data of species in *Thelephora*. Twenty-seven species were included in the analyses. The tree topology of the maximum parsimony analysis is similar to the maximum likelihood and Bayesian analysis. Constant characters were 853. Parsimony-informative characters were 426 whereas parsimony-uninformative characters were 536. Bootstrap support values for ML

$\geq 70\%$, MP $\geq 70\%$, and Bayesian posterior probabilities ≥ 0.95 are given near nodes, respectively. The tree was rooted with *Odontia fibrosa* (LE F-332368). The newly generated sequences are in red-bold and the type collections are indicated with ^T.

Basidiomata annual, resupinate, arachnoid, without odor or taste when fresh, and up to 10.5 cm long, 2.5 cm wide, 0.2–0.3 mm thick. *Hymenial surface* smooth, slightly buff when fresh, buff to cinnamon buff upon drying. *Sterile margin* narrow, slightly buff, up to 1 mm. *Hyphal system* monomitic, generative hyphae with clamp connections, pale brown, thin-walled, moderately branched, interwoven, 5.2–8.0 μm in diam.; IKI–, CB–, brown-black to black in KOH. *Cystidia* and *Cystidioles* absent. *Basidia* clavate, with 4 sterigmata and a basal clamp connection, $23.26\text{--}46.25 \times 9.11\text{--}14.63 \mu\text{m}$. *Basidiole* subclavate, slightly smaller than basidia. *Basidiospores* subglobose to globose, nodulose to verrucose, yellowish-brown, thick-walled, IKI–, CB–, $9\text{--}11(12) \times 7\text{--}9.5(10) \mu\text{m}$, L = 9.96 μm , W = 8.48 μm , Q = 1.13–1.17 (n = 60/2).

Material examined – China. Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 24°28' N, 97°31' E, altitude 1125 m asl., on the dead bamboo (*Poaceae*), leg. C.L. Zhao, 4 July 2024, CLZhao 37718 (SWFC, holotype), Yunnan Province, Tengchong, Tuantian Town, Gaoligongshan National Nature Reserve, GPS coordinates: 26°23' N, 98°44' E, altitude 3020 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 7 July 2024, CLZhao 39133 (SWFC, paratype).

GenBank accession numbers – CLZhao 37718: ITS = PV475848, CLZhao 39133: ITS = PV475849.

Notes – The phylogenetic analyses inferred from ITS dataset indicated that the collections of our species (CLZhao 37718, CLZhao 39113) nested within other *Thelephora* species, and formed a separate clade sister to *Thelephora sublilacina* (UP161) with 100% ML, 100% MP and 1.00 BYPP bootstrap support (Fig. 78). However, *Th. tropica* is distinguishable from *Th. sublilacina* by its basidium fruit, which is coral-shaped and brownish (Ellis & Everhart 1896). *Thelephora tropica* is distinguishable from *Th. tenuifarinea* by having the olivaceous hymenium surface and smaller basidiospores ($7\text{--}9 \times 6\text{--}8$ vs. $9\text{--}11 \times 7\text{--}9.5 \mu\text{m}$, Zhang et al. 2024a). Also, *Th. tropica* is distinct from *Th. bubalinomarginata* by its cream to pinkish buff hymenium surface and smaller basidiospores ($6.5\text{--}8.5 \times 5.5\text{--}7$ vs. $9\text{--}11 \times 7\text{--}9.5 \mu\text{m}$, Song 2025). Further, *Th. tropica* shares similar characteristics to *Th. subtropica* and *Tomentella wumenshanensis* by having the subglobose to globose, yellowish-brown, nodulose to verrucose, thick-walled basidiospores. However, *Th. tropica* is distinguished from *Th. subtropica* by its pale gray-brown hymenial surface, and smaller basidia ($6\text{--}8 \times 5\text{--}7.5$ vs. $9\text{--}11 \times 7\text{--}9.5 \mu\text{m}$) (Zhu et al. 2024). *Thelephora tropica* differs from *Th. wumenshanensis* by its white to yellowish-brown to orange-brown hymenial surface, and smaller basidiospores ($7.5\text{--}9.5 \times 6\text{--}8$ vs. $9\text{--}11 \times 7\text{--}9.5 \mu\text{m}$, Zhang et al. 2024b). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Th. tropica* as a new species.

Trechisporales K.H. Larss.

Hydnodontaceae Jülich = *Subulicystidiaceae* Jülich.

Index Fungorum number: IF 81729; Facesoffungi number: FoF 15464

Type genus – *Hydnodon* Banker = *Trechispora* P. Karst.

Notes – *Hydnodontaceae* was established by Jülich (1981) to accommodate *Hydnodon*. Later, based on morpho-molecular evidence *Hydnodon* is considered a synonym of *Trechispora*. Currently, 11 genera are accepted in this family (Liu et al. 2022a). Species of this family have been reported on wood or ground. The key morphologies of the family are having resupinate, effused, stipitate or clavarioid basidiomes; smooth, grandinioid, odontoid, hydroid or poroid to partly irpicoid hymenophore, mycelial cords present or absent; monomitic to dimitic hyphal system, all septa with clamp connections, subicular hyphae with or without ampullate septa; cystidia present in some species, mostly absent; cylindrical with two to four sterigmata basidia often with a slight median constriction; smooth or ornamented, subglobose, ellipsoid, subangular or fusiform, inamyloid, acyanophilous basidiospores; and sometimes conidiospores are present (Liu et al.

2022b). In considering the taxonomy, *Hydnodontaceae* and *Subulicystidiaceae* (as well as *Litschauerellaceae*, see *Litschauerella* under excluded genera from *Trechisporales*) were published simultaneously by Jülich (1981). Under these circumstances, the choice of name is governed by Art. 11.5 of the Shenzhen Code (Turland et al. 2018) and the first effectively published choice establishes priority. Hibbett et al. (2014) listed *Subulicystidiaceae* as a synonym of *Hydnodontaceae*, thereby establishing the priority of the latter name (Liu et al. 2022b). In this study, we introduce *Grandicium tenuissimum* gen. nov. et sp. nov. and *Membranothymium grandinioides* gen. nov. et sp. nov. to the family, based on multi-gene phylogenetic evidence of ITS+nLSU sequences (Fig. 81) combined with morphological characteristics (Figs 82, 83).

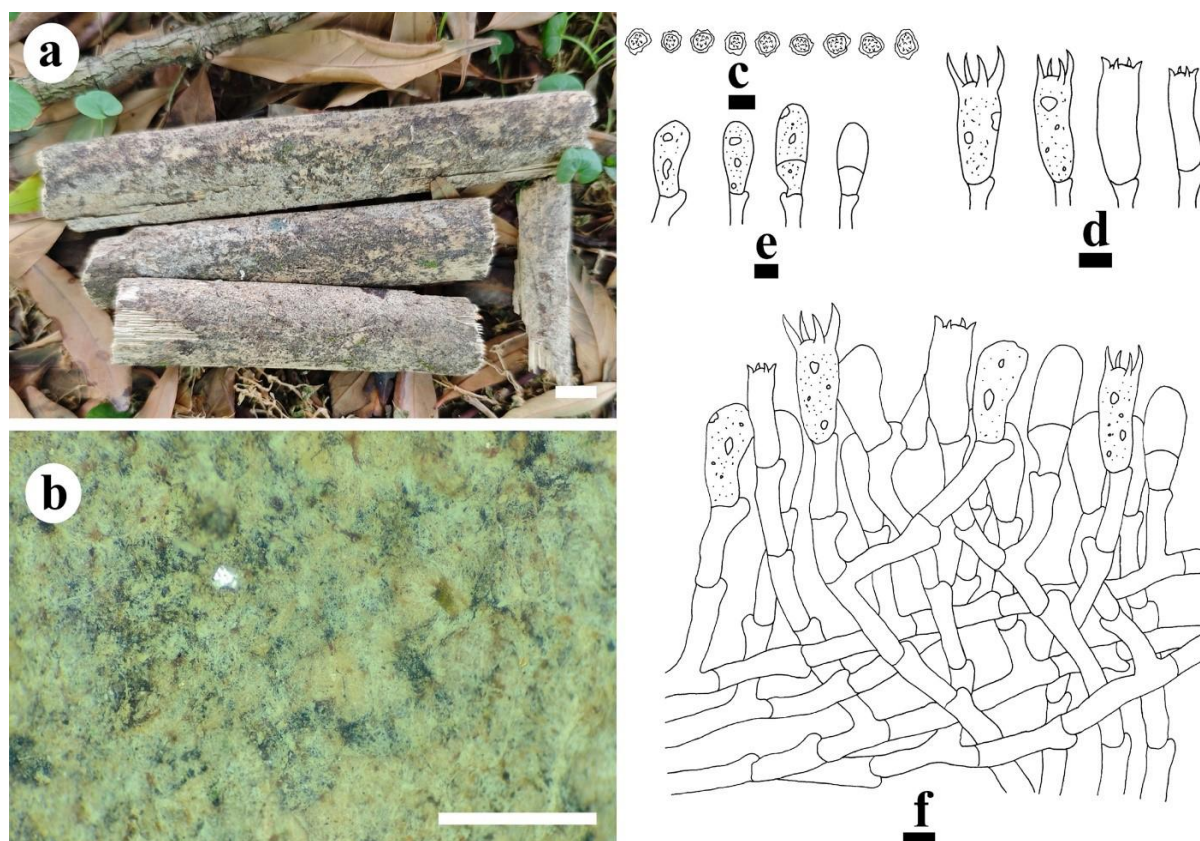


Figure 79 – Basidiomata and microscopic structures of *Thelephora tropica* (holotype, CLZhao 37718): a Basidiomata on the substrate. b Macroscopic characteristics of hymenophore. c Basidiospores. d Basidia. e Basidioles. f A section of the hymenium. Scale bars: a = 1 cm, b = 1 mm, c–f = 10 μ m.

Grandicium Y.F. Dai & C.L. Zhao, gen. nov.

Index Fungorum number: IF 860709; Facesoffungi number: FoF 18458

Type species – *Grandicium tenuissimum* Y.F. Dai & C.L. Zhao

Etymology – *grandicium* (Lat.): referring to the grandinioid hymenial surface of type specimens.

Basidiomata annual, resupinate, adnate, thin, membranous, hymenial surface grandinioid. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled. *Cystidia* abundant, subulate, colorless, multi-rooted, distinctly thick-walled. *Basidia* subclavate, colorless, thin-walled. *Basidiospores* subglobose, colorless, thin-walled, smooth, frequently with oil drops, CB–, IKI–.

Notes – The combined ITS+nLSU phylogenetic analysis (Fig. 81, Clade B) revealed that our two collections of *Grandicium* clustered within *Hydnodontaceae*, forming a monophyletic clade sister to the specimens representing *Pteridomyces* with 83% in ML and 1.00 in BYPP statistical support. Morphologically, *Grandicium* shares characters fits with *Hydnodontaceae*

description. *Pteridomyces* is distinguished from its phylogenetically closely related *Grandicium* by having cylindrical, allantoid or navicular basidiospores (Liu et al. 2022b). Thus, based on multi-gene phylogeny and morphological comparison, we introduce *Grandicium* as a new genus in *Hydnodontaceae* and the genus is typified by *Gran. tenuissimum*.

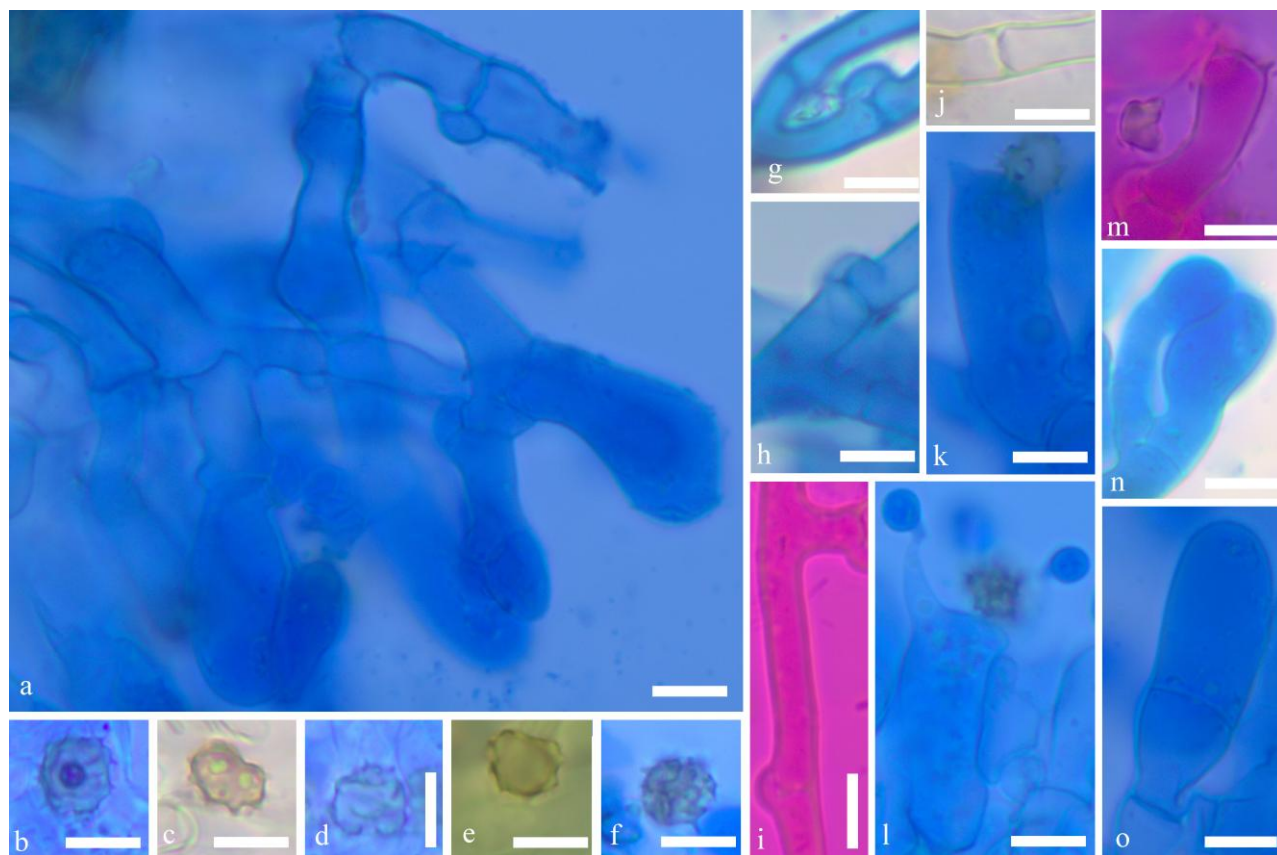


Figure 80 – *Thelephora tropica* (CLZhao 37718, holotype). a Sections of hymenium of *Thelephora tropica*. b–f Basidiospores. g, h Generative hyphae with clamp connections. i, j Partial hyphal sections. k–m Some basidia sections. n–o Some basidioles section. Scale bars: a–o = 10 μ m.

Grandicium tenuissimum Y.F. Dai & C.L. Zhao, sp. nov.

Fig. 82

Index Fungorum number: IF 860711; Facesoffungi number: FoF 18459

Diagnosis – Differs from other species by the thin basidiomata, pale cream hymenial surface, subclavate basidia (24.5–38.5 $\times$ 9–13.5 μ m) and subglobose basidiospores (7–11.5 $\times$ 5–10 μ m).

Etymology – *tenuissimum* (Lat.): referring to the thin basidiomata of type specimens.

Basidiomata annual, resupinate, adnate, thin, membranous, without odor and taste when fresh, and up to 11.5 cm long, 1.8 cm wide, 60–100 μ m thick. **Hymenial surface** grandinioid, white when fresh, turn to pale cream upon drying. **Sterile margin** thinning out, pale cream. **Hyphal system** monomitic, generative hyphae with clamp connections, colorless, thin-walled, occasionally branched, 2–3 μ m in diam.; IKI–, CB–, tissues unchanged in KOH. **Crystals** abundant in hymenium. **Cystidia** abundant, subulate, colorless, broad-base and very acute apex, multi-rooted, distinctly thick-walled, 62–85 $\times$ 8–13 μ m, projecting beyond hymenium. **Basidia** subclavate, colorless, thin-walled, with 4 sterigmata and a basal clamp connection, frequently with oil drops, 24.5–38.5 $\times$ 9–13.5 μ m. **Basidioles** similar to basidia in shape, but slightly smaller. **Basidiospores** subglobose, colorless, thin-walled, smooth, frequently with oil drops, CB–, IKI–, 7–11.5(–12.5) $\times$ 5–10(–10.5) μ m, L = 9.18 μ m, W = 7.37 μ m, Q = 1.18–1.36 (n = 60/2).

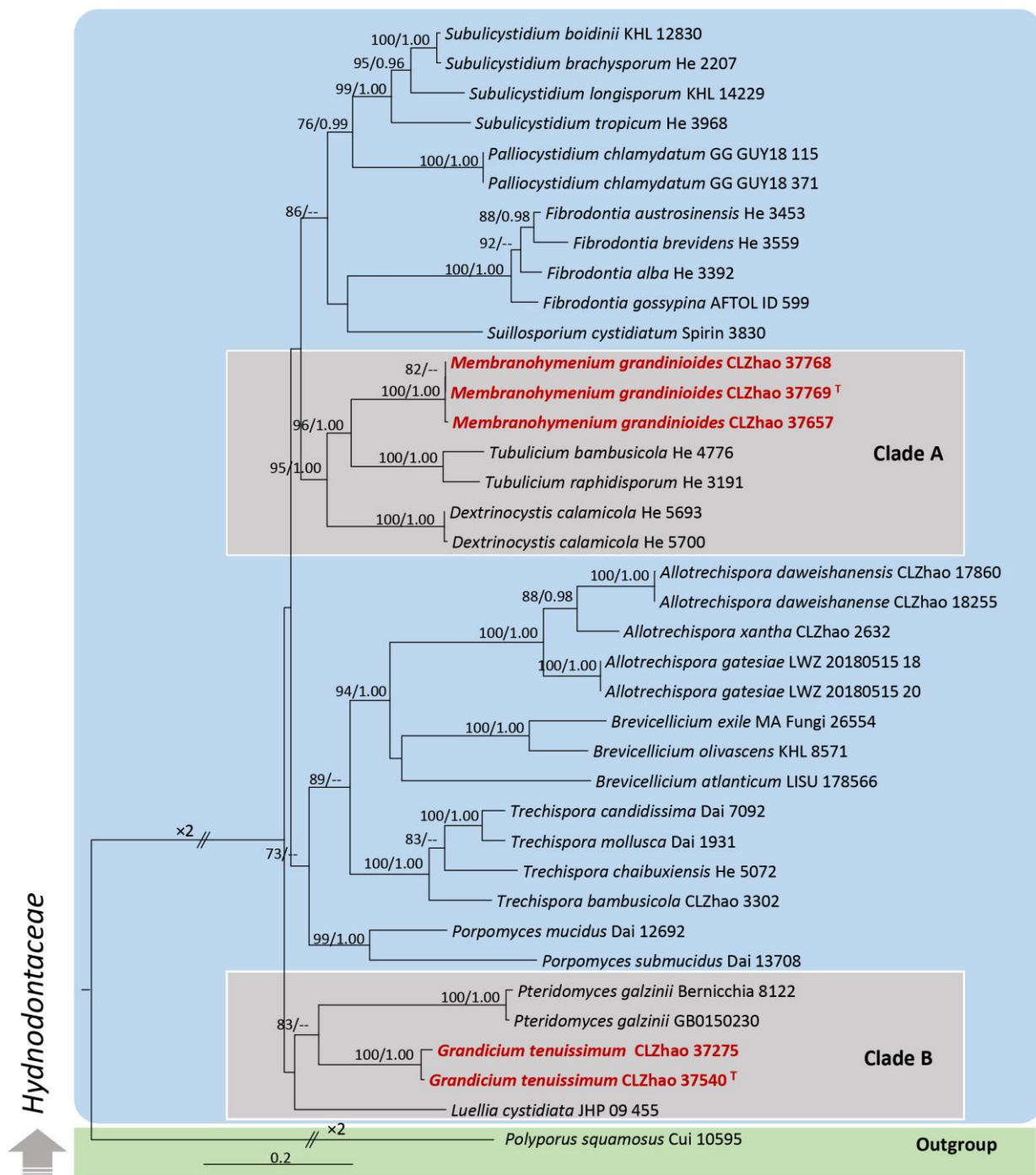


Figure 81 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and nLSU sequence data of *Hydnodontaceae*. Thirty-eight specimens are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -15819.045 is presented. The matrix had 826 distinct alignment patterns, with 22.17% of undetermined characters or gaps. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The newly generated sequences are indicated in red-bold, and the type collections are indicated with ^T.

Material examined – China. Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 23°48' N, 97°38' E, altitude 1500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 3 July 2024, CLZhao 37540 (SWFC, holotype); *ibid.*, 2 July 2024, CLZhao 37275 (SWFC, paratype).

GenBank accession numbers – CLZhao 37275: ITS = PX108623, LSU = PV975048; CLZhao 37540: ITS = PX108624, LSU = PV975049.

Notes – The combined ITS+nLSU phylogenetic analysis (Fig. 81, Clade B) revealed that the two collections of our species *Grandicium tenuissimum* (CLZhao 37540, CLZhao 37275) formed a distinct, monophyletic clade closely related to *Pteridomyces*; *Pteridomyces galzinii* (type species) Bernicchia 8122 and GB0150230. However, *Pteridomyces galzinii* can be distinguished from *Gran. tenuissimum* by its smaller basidia ($9\text{--}15 \times 4\text{--}5\ \mu\text{m}$, Eriksson & Ryvarden 1975, Jülich 1979). Thus, based on morphology and multigene phylogenetic evidence of ITS+nLSU sequences, we introduce *Gran. tenuissimum* as a new species.

Membranhymenium Y. Xu & C.L. Zhao, gen. nov.

Index Fungorum number: IF 860712; Facesoffungi number: FoF 18460

Type species – *Membranhymenium grandinioides* Y. Xu & C.L. Zhao

Etymology – *membranhymenium* (Lat.): referring to type specimens having a membranous hymenial surface.

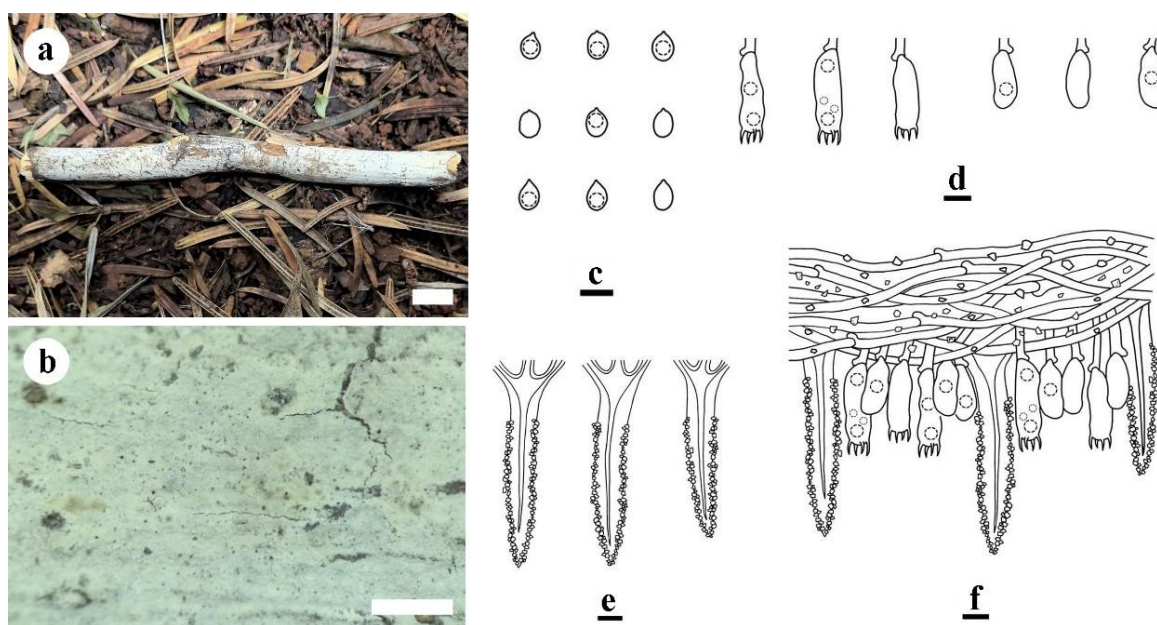


Figure 82 – Basidiomata and microscopic structures of *Grandicium tenuissimum* (CLZhao 37540, holotype). a, b Basidiomata on the host substrate. c Basidiospores. d Basidia and basidioles. e Subulate cystidia. f A section of hymenium. Scale bars: a = 1 cm, b = 1 mm. c–f = 10 μm .

Basidiomata annual, resupinate, adnate, thin, membranous, hymenial surface grandinioid. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled. *Cystidia* of two types, subulate cystidia, colorless, multi-rooted, thick-walled; fusiform cystidia, colorless, thin-walled. *Basidia* subclavate, colorless, thin-walled. *Basidiospores* cylindrical to allantoid, colorless, thin-walled, smooth, CB–, IKI–.

Notes – The combined ITS+nLSU phylogenetic analysis (Fig. 81, Clade A) revealed that our three collections of *Membranhymenium* clustered within *Hydnodontaceae*, and formed a monophyletic clade sister to the specimens representing *Tubulicium* with 96% in ML and 1.00 in BYPP statistical support. Morphologically, *Membranhymenium* shares characters fits with *Hydnodontaceae* description. *Tubulicium* is distinguished from its phylogenetically closely related *Membranhymenium* by having smooth, more or less arachnoid hymenophore surface, and narrowly fusiform to vermicular basidiospores (Liu et al. 2022b). Thus, based on multi-gene phylogeny and morphological comparison, we introduce *Membranhymenium* as a new genus in *Hydnodontaceae* and the genus is typified by *Me. grandinioides*.

Membranhymenium grandinioides Y. Xu & C.L. Zhao, sp. nov.

Fig. 83

Index Fungorum number: IF 860713; Facesoffungi number: FoF 18461

Diagnosis – Differs from other species by the thin basidiomata, cream hymenial surface, subclavate basidia ($7.5\text{--}17.5 \times 5\text{--}8.5 \mu\text{m}$), and cylindrical to allantoid basidiospores ($6.5\text{--}10.5 \times 1.5\text{--}3 \mu\text{m}$).

Etymology – *grandinioides* (Lat.): referring to the grandinioid hymenial surface of type specimens.

Basidiomata annual, resupinate, adnate, thin, membranous, without odor and taste when fresh, and up to 10 cm long, 2.5 cm wide, $55\text{--}100 \mu\text{m}$ thick. *Hymenial surface* grandinioid, pale cream when fresh, turn to cream upon drying. Sterile margin thinning out, concolorous. *Hyphal system* monomitic; generative hyphae with clamp connections, colorless, thin-walled, occasionally branched, $1\text{--}2.5 \mu\text{m}$ in diam.; IKI–, CB–, tissues unchanged in KOH. *Crystals* abundant in hymenium.

Cystidia of two types: (1) subulate, colorless, broad-base and very acute apex, multi-rooted, thick-walled, $30.5\text{--}60.5 \times 4\text{--}5.5 \mu\text{m}$, projecting beyond the hymenium. (2) fusiform, colorless, thin-walled, frequently with oil drops, $13\text{--}18.5 \times 7.5\text{--}17 \mu\text{m}$. *Basidia* subclavate, colorless, thin-walled, with 4 sterigmata and a basal clamp connection, frequently with oil drops, $7.5\text{--}17.5 \times 5\text{--}8.5 \mu\text{m}$. *Basidioles* similar to basidia in shape, but slightly smaller. *Basidiospores* cylindrical to allantoid, colorless, thin-walled, smooth, frequently with oil drops, CB–, IKI–, $(6.0\text{--}) 6.5\text{--}10.5\text{--}(11.5) \times 1.5\text{--}3.0 \mu\text{m}$, $L = 8.41 \mu\text{m}$, $W = 2.20 \mu\text{m}$, $Q = 3.65\text{--}4.00$ ($n = 60/2$).

Material examined – China. Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, $23^{\circ}48' \text{N}$, $97^{\circ}38' \text{E}$, altitude 1500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 4 July 2024, CLZhao 37769 (SWFC, holotype); *ibid.*, CLZhao 37657, CLZhao 37768 (SWFC, isotypes).

GenBank accession numbers – CLZhao 37657: ITS = PX108625; CLZhao 37768: ITS = PX108626; CLZhao 37769: ITS = PX108627, LSU = PV975050.

ITS: PX108625 (CLZhao 37657), PX108626 (CLZhao 37768), PX108627 (CLZhao 37769); LSU: PV975050 (CLZhao 37769).

Notes – The combined ITS+nLSU phylogenetic analysis (Fig. 81, Clade A) revealed that the three collections of our species, *Membranhymenium grandinioides* (CLZhao 37769, 37657, 37768) formed a monophyletic clade closely related to *Tubulicium* specimens; *Tubulicium bambusicola* (He 4776) and *Tu. raphidisporum* (He 3191). However, *Tubulicium bambusicola* can be distinguished from *Me. grandinioides* by its smooth hymenophore surface and its bigger, narrowly fusiform to vermicular basidiospores ($20\text{--}29 \times 2.2\text{--}3 \mu\text{m}$, Liu et al. 2019). Thus, based on morphology and multigene phylogenetic evidence of ITS+nLSU sequences, we introduce *Me. grandinioides* as a new species.

Trechispora P. Karst.

Index Fungorum number: IF 18664; Facesoffungi number: FoF 18462

Notes – *Trechispora* (*Hydnodontaceae*) was introduced by Karsten (1890) and typified by *Tre. onusta*, which is characterized by resupinate to effused basidiomata; a smooth to hydroid to poroid hymenophore; ampullaceous septa; short cylindric basidia; and smooth to verrucose or aculeate basidiospores (Bernicchia & Gorjón 2010, Luo et al. 2024b). *Trechispora* is similar to *Scytinopogon* in micromorphology, but *Scytinopogon* is formally recognized as a synonym of *Trechispora* (de Meiras-Ottoni et al. 2021). Currently, 161 records of intraspecific names in *Trechispora*, are listed in MycoBank (2025) and Index Fungorum (2025), respectively. In this study, *Trechispora alborhizomorpha* sp. nov. and *Trechispora mangensis* sp. nov. are introduced from China based on the ITS sequence data (Fig. 84) and morphological characteristics (Figs 85, 86).

Trechispora alborhizomorpha X.C. Zhang & C.L. Zhao, sp. nov.

Fig. 85

Index Fungorum number: MB 860779; Facesoffungi number: FoF 18463

Diagnosis – Differs from other *Trechispora* species by the membranous basidiomata, membranous hymenial surface, thin-walled hyphae and subglobose to ellipsoid basidiospores smooth measuring $3.5\text{--}4 \times 2.65\text{--}3\text{ }\mu\text{m}$.

Etymology – *alborhizomorpha* (Lat.): referring to the white color rhizomorph of basidiomata of the type specimen.

Basidiomata annual, resupinate, flocculant, thin, growing adnate but easily separable, up to 8 cm long, 2 cm wide, $100\text{--}400\text{ }\mu\text{m}$ thick. *Hymenial surface* arachnoid, whitish to grayish when fresh, turn to cream upon drying. *Sterile margin* indistinct, slightly white, $0.1\text{--}0.2\text{ mm}$ wide. *Hyphal system* monomitic; generative hyphae with clamp connections, colorless, thin-walled, occasionally branched, interwoven, $2.5\text{--}3\text{ }\mu\text{m}$ in diam.; IKI–, CB–, tissues unchanged in KOH; ampullate septa frequently present in subiculum and hymenium with crystals, up to $5\text{ }\mu\text{m}$ wide. *Cystidia* and *Cystidioles* absent. *Basidia* clavate, with two or four sterigmata and a basal clamp connection, $9.5\text{--}14 \times 4\text{--}5.5\text{ }\mu\text{m}$. *Basidioles* dominant, similar to basidia in shape, but slightly smaller. *Basidiospores* ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, $3.5\text{--}4 \times (2.61\text{--})2.65\text{--}3\text{ }\mu\text{m}$, $L = 3.71\text{ }\mu\text{m}$, $W = 2.79\text{ }\mu\text{m}$, $Q = 1.33$ ($n = 30/1$).

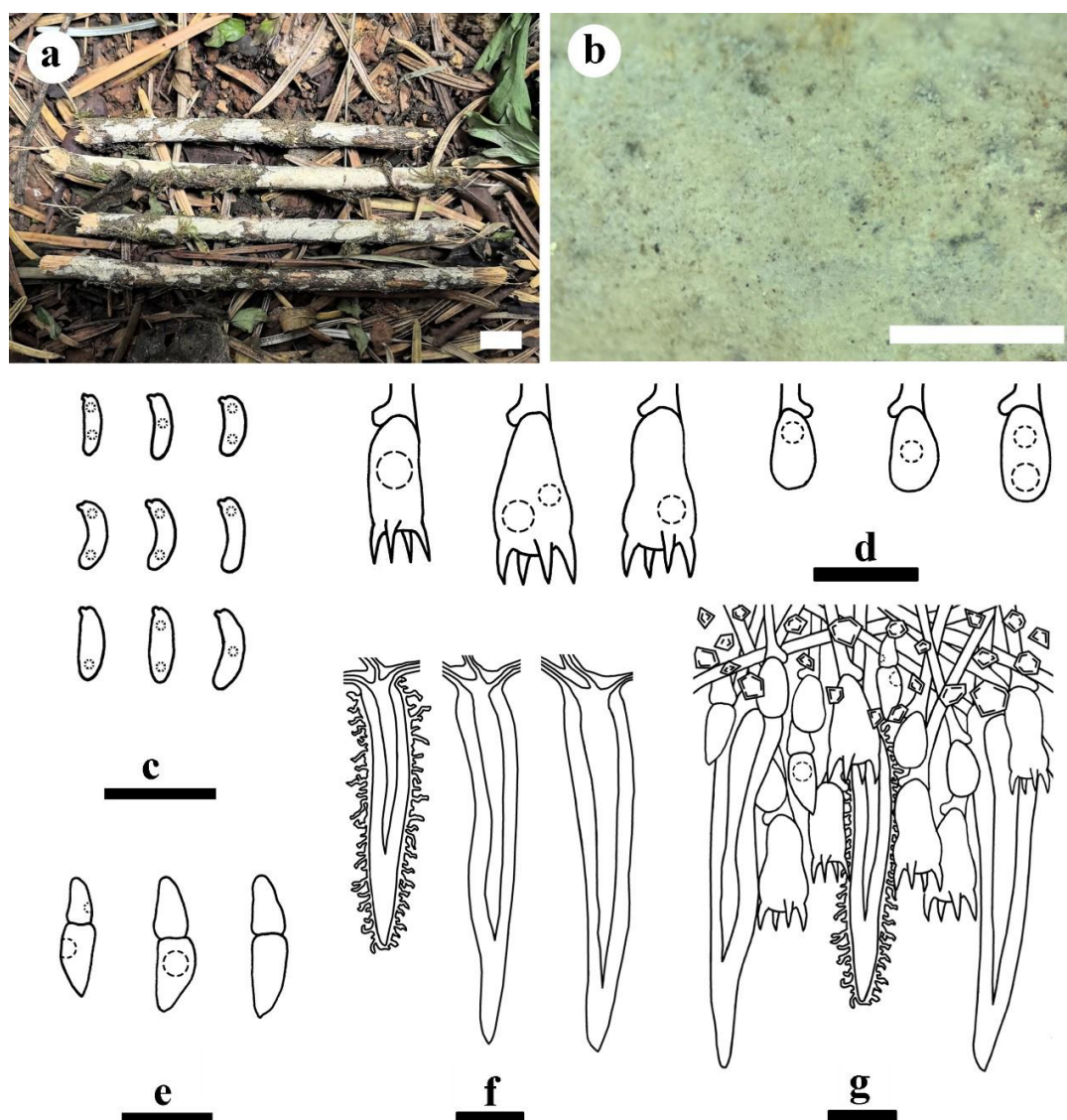


Figure 83 – Basidiomata and microscopic structures of *Membranhymenium grandinioides* (CLZhao 37769, holotype). a, b Basidiomata on the host substrate. c Basidiospores. d Basidia and basidioles. e Subulate cystidia. f Fusiform cystidia. g A section of hymenium. Scale bars: a = 1 cm, b = 1 mm, c–g = $10\text{ }\mu\text{m}$.

Material examined – China. Yunnan Province, Baoshan, Tengchong, Laifengshan National Forest Park, GPS coordinates 25°30' N, 98°16' E, altitude 1600 m asl., on a fallen angiosperm branch, leg. C.L. Zhao, 6 July 2024, CLZhao 37978 (SWFC, holotype).

GenBank accession numbers – ITS: PV591026.

Notes – The ITS phylogenetic analyses (Fig. 84) revealed that our species *Trechispora alborhizomorpha* (CLZhao 37978) formed a separate lineage sister to *Tre. cohaerens* (HHB-19445). Although *Tre. cohaerens* resembles many characters, it can be delimited from *Tre. alborhizomorpha* by having thick-walled and narrow basidiospores ($3.5\text{--}4 \times 2.2\text{--}2.5\ \mu\text{m}$, Larsson 1992). *Trechispora alborhizomorpha* resembles *Tre. albofarinosa* and *Tre. laevispora* in having ellipsoid basidiospores. However, *Tre. albofarinosa* can be distinguished from *Tre. alborhizomorpha* by its hymenial surface flocculence, and its smaller basidia ($6.5\text{--}10 \times 3.5\text{--}5\ \mu\text{m}$, Luo et al. 2024b). Also, *Tre. laevispora* differs from *Tre. albofarinosa* due to its small basidiospores ($2.6\text{--}3.2 \times 1.9\text{--}2.2\ \mu\text{m}$, Liu et al. 2022b). Thus, based on morphology and phylogenetic evidence, we introduce *Tre. alborhizomorpha* as a new species.

Trechispora mangensis J.Q. Su & C.L. Zhao, sp. nov.

Fig. 86

Index Fungorum number: MB 860780; Facesoffungi number: FoF 18464

Diagnosis – Differs from other *Trechispora* species by the flocculence basidiomata with the grandinioid hymenial surface, and nephroid to ellipsoid basidiospores measuring $(3.1\text{--})3.4\text{--}4.3\text{--}(4.4) \times (2.0\text{--})2.1\text{--}2.8\text{--}(2.9)\ \mu\text{m}$.

Etymology – *mangensis* (Lat.): referring to the locality (Mang City) of the type specimen.

Basidiomata annual, resupinate, thin, growing adnate but easily separable, up to 17 cm long, 2 cm wide, 100–400 μm thick. *Hymenial surface* smooth, flocculence, gray when fresh, gray to cream when drying, Sterile margin indistinct, slightly white, 0.2–0.5 mm wide. *Hyphal system* monomitic, generative hyphae with clamp connections, colorless, thin-walled, occasionally branched, interwoven, 1.5–2.6 μm in diam.; IKI–, CB–, tissues unchanged in KOH; subhymenial hyphae covered by crystals. *Cystidia* and *Cystidioles* absent. *Basidia* barreled, with four sterigmata and a basal clamp connection, $8.2\text{--}10.6 \times 3.7\text{--}4.4\ \mu\text{m}$. *Basidioles* dominant, similar to basidia in shape, but slightly smaller. *Basidiospores* nephroid to ellipsoid, colorless, thin-walled, ornamented, IKI–, CB–, $(3.1\text{--})3.4\text{--}4.3\text{--}(4.4) \times (2.0\text{--})2.1\text{--}2.8\text{--}(2.9)\ \mu\text{m}$, $L = 3.79\ \mu\text{m}$, $W = 2.48\ \mu\text{m}$, $Q = 1.53$ ($n = 30/1$).

Material examined – China. Yunnan Province, Dehong, Mang City, Tongbiguan Provincial Nature Reserve, GPS coordinates 24°25' N, 98°38' E, altitude 1400 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 29 June 2024, CLZhao 36340 (SWFC, holotype).

GenBank accession numbers – ITS: PV591025.

Notes – The ITS phylogenetic analyses (Fig. 84) revealed that our species *Trechispora mangensis* (CLZhao 36340) grouped with the other specimens of *Trechispora*, forming a separate lineage with 0.90 BYPP bootstrap support. *Trechispora mangensis* resembles *Tre. dentata* and *Tre. perminispora* in having ellipsoid basidiospores. However, *Tre. dentata* can be distinguished from *Tre. mangensis* by its hymenial surface irpicoid, and its large basidia ($10\text{--}15 \times 4\text{--}5\ \mu\text{m}$, Liu et al. 2022a). Also, *Tre. perminispora* differs from *Tre. mangensis* due to its hymenophore grandinioid with numerous small aculei and its small basidiospores ($2.6\text{--}3 \times 1.8\text{--}2.1\ \mu\text{m}$, Liu et al. 2024). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Tre. mangensis* as a new species.

Tubulicium Oberw.

Index Fungorum number: IF 18692; Facesoffungi number: FoF 18465

Notes – *Tubulicium* originated as *Peniophora vermifera* (Oberwinkler 1965), and is primarily characterized by resupinate basidiomata with a hispidulous hymenial surface, nodose-septate hyphae, and multirooted lycocystidia covered with dendroid-branching hyphae (Bernicchia & Gorjón 2010, Ushijima et al. 2019). *Tubulicium* is included in the trechisoroid clade, but there are no common morphological characters to support this phylogenetic relationship (Bernicchia &

Gorjón 2010). Currently, ten *Tubulicium* species are accepted (Hyde et al. 2024d, Species Fungorum 2025). In this study, we introduce a new species *Tubulicium yunnanense* from China based on the ITS+nLSU sequence data (Fig. 87), and detailed morphological data (Fig. 88).

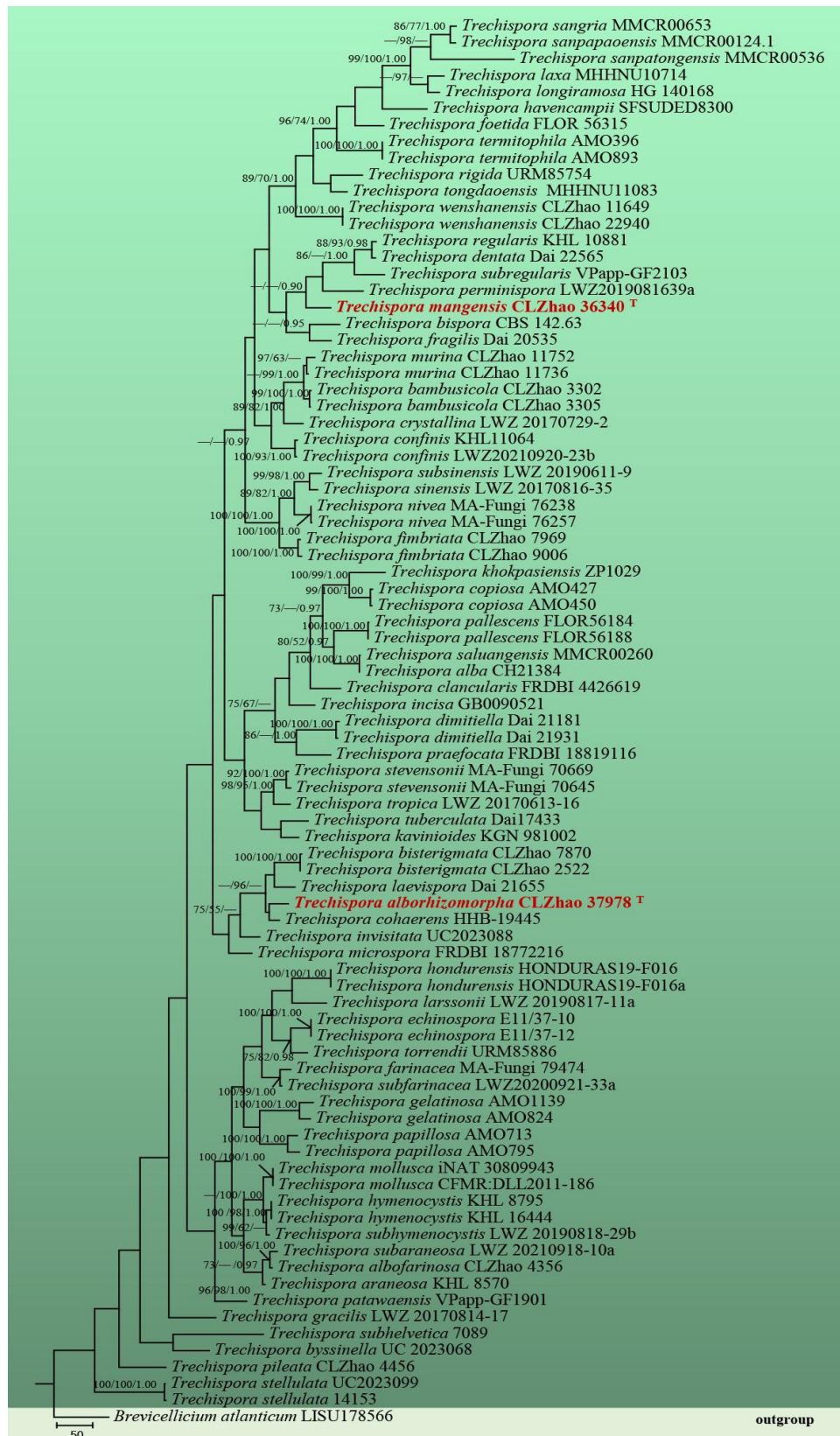


Figure 84 – Phylogram generated from maximum parsimony strict consensus tree analysis based on the ITS sequence data of *Trechispora* species. Eighty-five specimens are included in the analyses. The tree topology of the maximum parsimony analysis is similar to the maximum

likelihood and Bayesian analysis. The dataset had an aligned length of 840 characters, of which 229 characters are constant, 163 are variable and parsimony uninformative, and 448 are parsimony informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 4620, CI = 0.2675, HI = 0.7325, RI = 0.4741, and RC = 0.1268). Bootstrap support values for ML $\geq$ 70%, MP $\geq$ 50%, and Bayesian posterior probabilities $\geq$ 0.95 are given near nodes, respectively. The tree was rooted with *Brevicellicium atlanticum* (LISU178566). The newly generated sequences are indicated in red-bold and type collections are indicated with ^T.

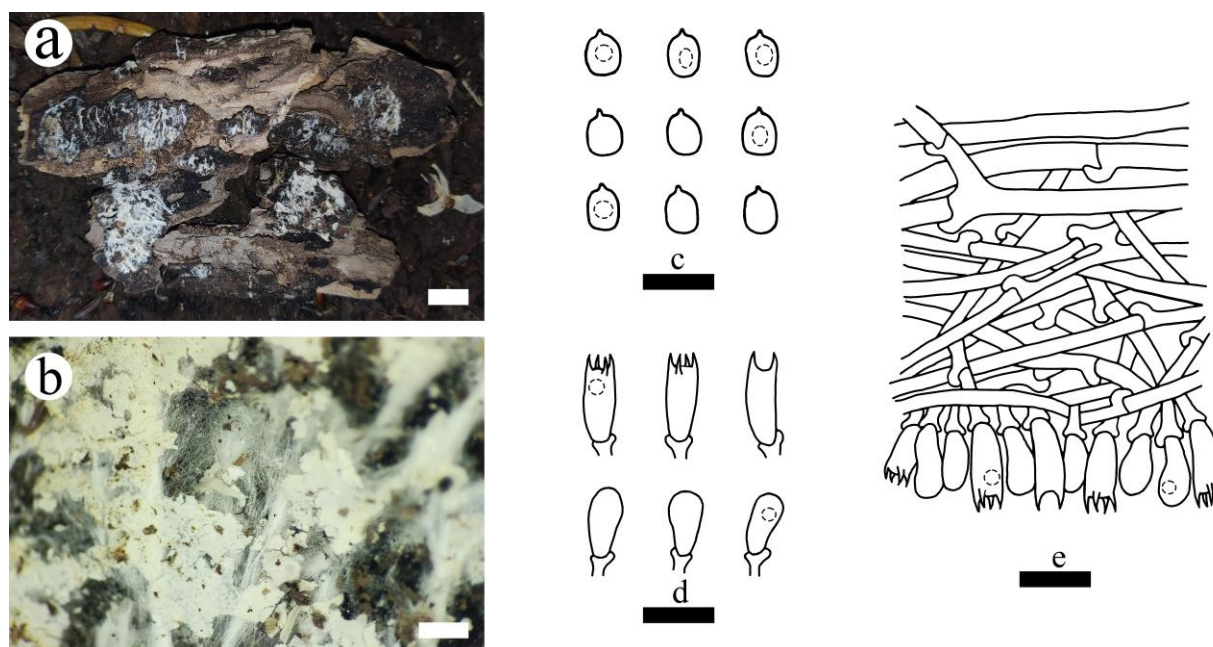


Figure 85 – Basidiomata and microscopic structures of *Trechispora alborhizomorpha* (CLZhao 37978, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e A section of hymenium. Scale bars: a = 1 cm, b = 1 mm, c = 5 μ m, d, e = 10 μ m.

Tubulicium yunnanense S.Y. He & C.L. Zhao, sp. nov.

Fig. 88

Index Fungorum number: IF 904418; Facesoffungi number: FoF 18466

Diagnosis – Differs from other *Tubulicium* species by the membranaceous basidiomata with velutinous hymenial surface, monomitic hyphal system with clamped generative hyphae and narrowly fusiform to vermicular basidiospores measuring 20–34 $\times$ 3–4 μ m.

Etymology – *yunnanense* (Lat.): Referring to the locality (Yunnan Province) of the type specimen.

Basidiomata annual, resupinate, closely adnate, smooth, without odor or taste when fresh, up to 10 cm long, 2 cm wide and 200 μ m thick. **Hymenial surface** velutinous by the projecting cystidia, cream when fresh, pale pink to pink when dry. **Sterile margin** cream, up to 1 mm wide. **Hyphal system** monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 2–3 μ m in diam.; IKI–, CB–, tissues unchanged in KOH. **Cystidia** subulate, abundant, projecting, cylindrical to slightly sinuous, multi-rooted, colorless, slightly amyloid, covered with dendroid branching hyphae, thin-walled, 119–147 $\times$ 12.5–16.5 μ m. **Basidia** barrelled, colorless, thin-walled, with 4-sterigmata and a basal clamp connection, 15–26 $\times$ 10–12.5 μ m. **Basidioles** dominant, in shape similar to basidia, but slightly smaller. **Basidiospores** narrowly fusiform to vermicular, bi-apiculate, colorless, smooth, thin-walled, occasionally with oil drops, IKI–, CB–; (17–)20–34(–36) $\times$ (2.5–)3–4(–4.5) μ m, L = 27.53 μ m, W = 3.56 μ m, Q = 6.42–7.75 (n = 60/2).

Material examined – China, Yunnan Province, Dehong, Mang City, Yingjiang County, Tongbiguan Provincial Nature Reserve, 27°52' N, 97°38' E, altitude 1000 m, on dead bamboo (*Poaceae*), 3 July 2024, CLZhao 37459 (SWFC, holotype); Yunnan Province, Tengchong, Tuanjie

Town, Gaoligongshan National Nature Reserve, 25°27'36" N, 98°46'12" E, altitude 1600 m, on the fallen angiosperm branches, 7 July 2024, CLZhao 39116 (SWFC, paratype).

GenBank accession numbers – CLZhao 37459: ITS = PV475577, LSU = PV646273; CLZhao 39116: ITS = PV475578.

Notes – The combined ITS+nLSU phylogenetic analyses (Fig. 87) revealed that the specimens of our new species *Tubulicium yunnanense* (CLZhao 37459 and CLZhao 39116) grouped within *Tubulicium* sister to *Tu. bambusicola* (He 4776, He 4058) with 99% ML and 1.00 BYPP bootstrap support. *Tubulicium bambusicola* differs to *Tu. yunnanense* by its pale-orange to greyish-orange hymenophore surface and smaller, narrow basidiospores ($20\text{--}29 \times 2.2\text{--}3 \mu\text{m}$, Liu et al. 2019). Thus, based on morphology and multigene phylogenetic evidence, we introduce *Tu. yunnanense* as a new species.

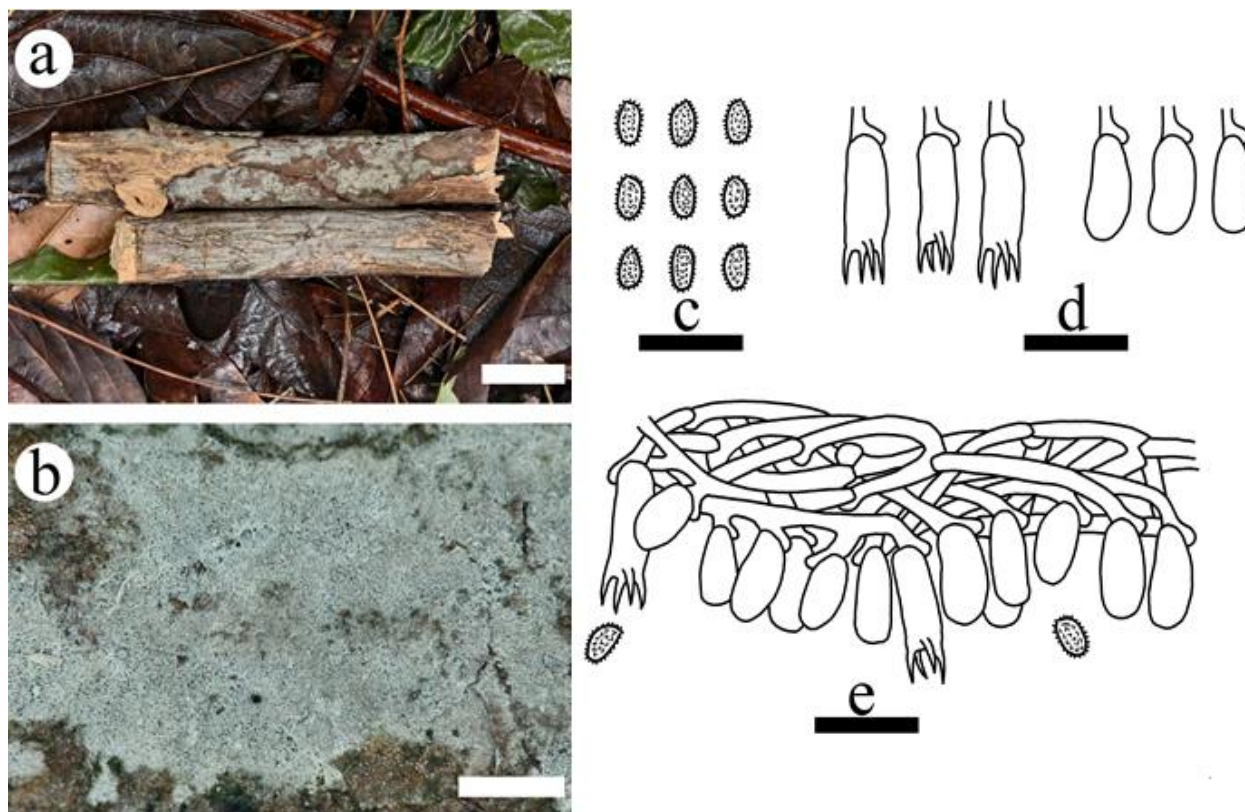


Figure 86 – Basidiomata and microscopic structures of *Trechispora mangensis* (CLZhao 36340, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e A section of hymenium. Scale bars: a = 2 cm, b = 1 mm, c–e = 10 μm .

Class *Tremellomycetes* Doweld

Filobasidiales Jülich

Piskurozymaceae Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout

Solicoccozyma Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout

Index Fungorum number: IF 812197; Facesoffungi number: FoF 18611

Notes – Six *Cryptococcus* (formerly classified within the *aerius* clade) which were phylogenetically distinct from the type species, lead to their reclassification as a novel genus, *Solicoccozyma*, with *So. aerius* designated as the type species (Liu et al. 2015). Most members of *Solicoccozyma* are soil-dwelling and exclusively exist in yeast form. These organisms are characterized by their frequent production of thick polysaccharide capsules and their capacity to accumulate substantial lipid reserves. Notably, they exhibit a strong ability to assimilate aldaric acids and low-molecular-weight aromatic compounds, including L-malic, L-tartaric, saccharic, mucic, caffeic, gentisic, p-coumaric, protocatechuic, and hydroxybenzoic acids. Currently, nine species are recognized

within this genus (Liu et al. 2015). In this study, the new species *Solicoccozyma humicola* sp. nov. is proposed and one new geographical record of *Solicoccozyma aerea* is introduced from soil habitats in China based on morphology and phylogenetic analyses (Figs 89, 90, 91)

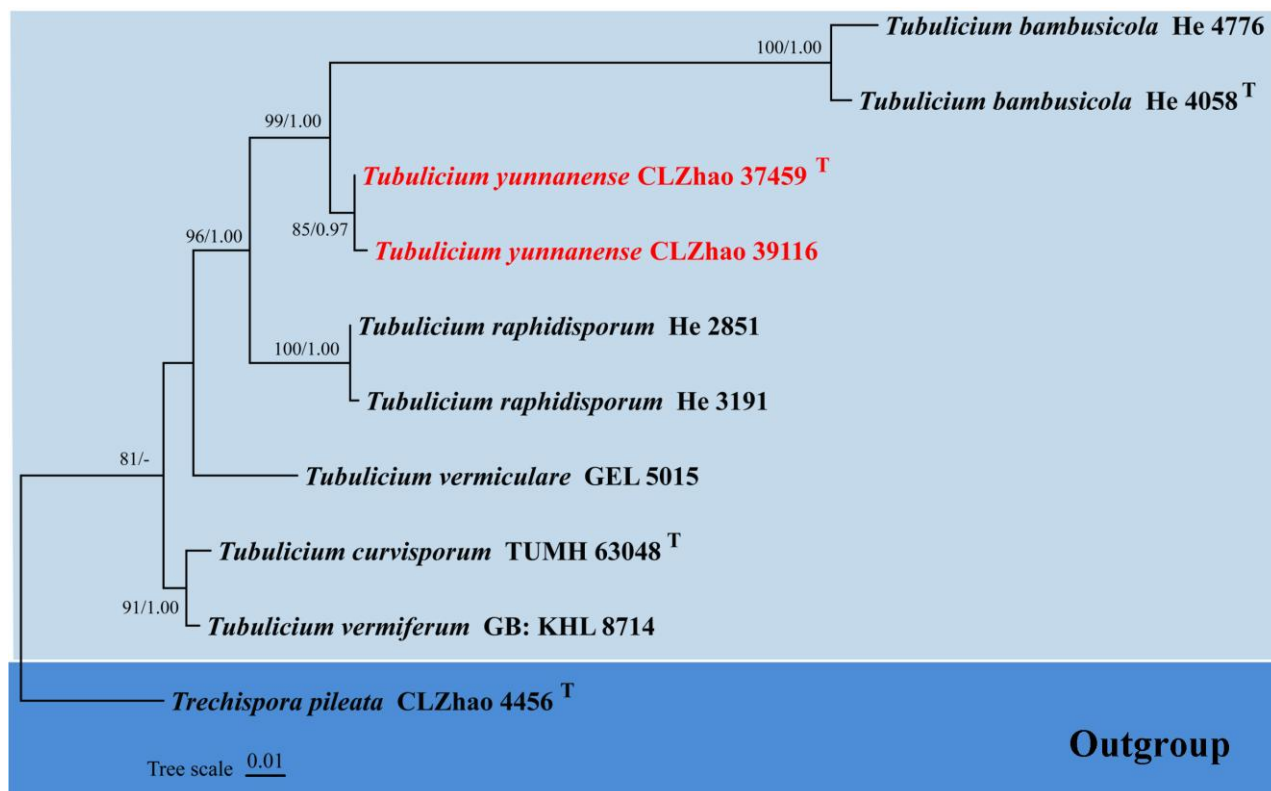


Figure 87 – Phylogram generated from the maximum likelihood analysis based on the combined ITS and nLSU sequence data of *Tubulicium*. Seven species are included in the combined analyses. The tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5107.742 is presented. The evolutionary model GTR+F+G4 is applied for all the genes. The matrix had 217 distinct alignment patterns. Bootstrap support values for ML greater than 80% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree was rooted with *Trechispora pileata* (CLZhao 4456). The newly generated sequences are in red-bold, and the type collections are indicated with ^T.

Solicoccozyma aerea (Saito) Yurkov, Stud. Mycol. 81: 121 (2015)

Fig. 90

Index Fungorum number: IF 812198; Facesoffungi number: FoF 18612

Saprobic in soil. After 7 days of growth in YM broth at 17°C, cells are 3.1–5.5 µm diam., globose to ellipsoid, hyaline, single. Budding is polar and a sediment is formed. After 1 month at 17°C, a ring and a sediment are present. After 5 days of growth in YM agar at 17°C, colonies are cream-colored, butyrous, smooth and glistening with an entire margin, round. Pseudohyphae are not observed. Cells are 3.1–5.3 µm diam. After 5 days of growth in OA at 17°C, colonies are sandgelb, butyrous with an entire margin, round. Pseudohyphae are not observed. Cells are 3.3–5.4 µm diam.

Material examined – China, Xizang Autonomous Region, Rikaze City, Dingri County, Qomolangma Nature Reserve, from frozen soil, 5 August 2023, Ning Jiang & Kuang Zhao, cultures, XZ6L, XZ12.

GenBank accession numbers – XZ6L: ITS = PP965526, LSU = PP965522; XZ12: ITS = PP965527, LSU = PP965523.

Notes – The multigene phylogenetic analysis (Fig. 89, Clade A) revealed that the strains of our species (XZ6L, XZ12) grouped within *Solicoccozyma* together with the strain of the ex-type strain of *S. aerea* (CBS 155). Our two strains of *Solicoccozyma* were isolated from frozen soils in

Xizang, China and identified as *So. aeria* based on exactly matched sequences with its ex-type strains CBS 155 were found in the air from Japan. *Solicoccozyma aeria* is a basidiomycetous yeast. The strains analyzed in this study were isolated from frozen soils in sparsely populated plateau regions, suggesting that this fungal species may be ancient in origin (Liu et al. 2015). We introduce *So. aeria* as a new geographical record isolated in China.

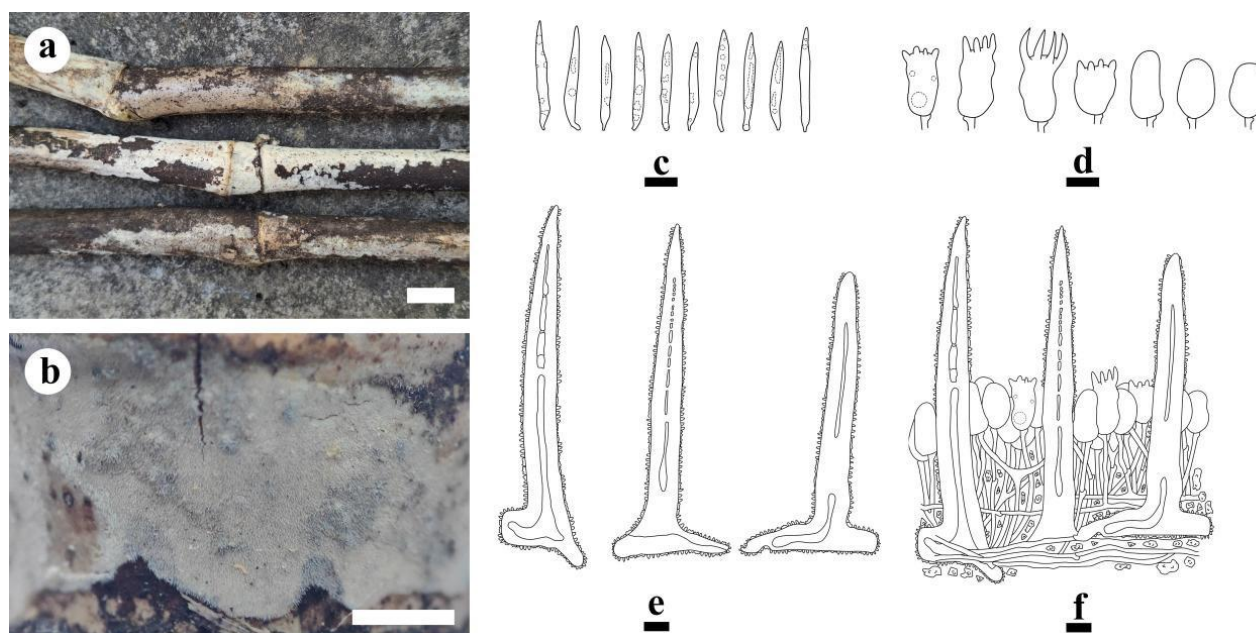


Figure 88 – Basidiomata and microscopic structures of *Tubulicium yunnanense* (CLZhao 37459, holotype). a, b Basidiomata on the host substrates. c Basidiospores. d Basidia and basidioles. e Cystidia. f A section of the hymenium. Scale bars: a = 1 cm, b = 2 mm, c–f = 10 μ m.

Solicoccozyma humicola Ning Jiang, sp. nov.

Fig. 91

Index Fungorum number: IF 904419; Facesoffungi number: FoF 18613

Etymology – Referring to the habitat (soil) where the holotype was found.

Saprobic in soil. After 7 days of growth in YM broth at 17°C, cells are 2.2–5.2 μ m diam., globose to ellipsoid, hyaline, single. *Budding* is polar and a sediment is formed. After 1 month at 17°C, a ring and a sediment are present. After 5 days of growth in YM agar at 17°C, colonies are cream-colored, butyrous, smooth and glistening with an entire margin, round. *Pseudohyphae* are not observed. *Cells* are 2.3–5.4 μ m diam. After 5 days of growth in OA at 17°C, colonies are white, butyrous, irregular. *Pseudohyphae* are not observed. *Cells* are 2.6–5.3 μ m diam. Glucose fermentation is absent. D-Glucose, D-galactose, L-sorbose, D-glucosamine, D-xylose, L-arabinose, D-arabinose, D-ribose, L-rhamnose, sucrose, maltose, cellobiose, lactose, melibiose, raffinose, melezitose, ribitol, galactitol, D-mannitol, D-glucitol, salicin, D-gluconate, myo-inositol are assimilated as sole carbon sources. Inulin, glycerol, erythritol, methanol and ethanol are not assimilated. Ammonium sulfate, potassium nitrate, sodium nitrite, L-lysine, ethylamine hydrochloride and cadaverine dihydrochloride are assimilated as sole nitrogen sources. Maximum growth temperature is 34 °C. Growth in vitamin-free medium is positive. Starch-like substances are not produced. Urease activity is positive. Diazonium Blue B reaction is positive.

Material examined – China, Xizang Autonomous Region, Rikaze City, Dingri County, Qomolangma Nature Reserve, from frozen soil, 5 August 2023, Ning Jiang & Kuang Zhao, (CFCC 3586, holotype) preserved in a metabolically inactive state; additional collection: *ibid.*, culture, CFCC 3589.

GenBank accession numbers – CFCC 3586: ITS = PP965528, LSU = PP965525; CFCC 3589: ITS = PP965529, LSU = PP965526.

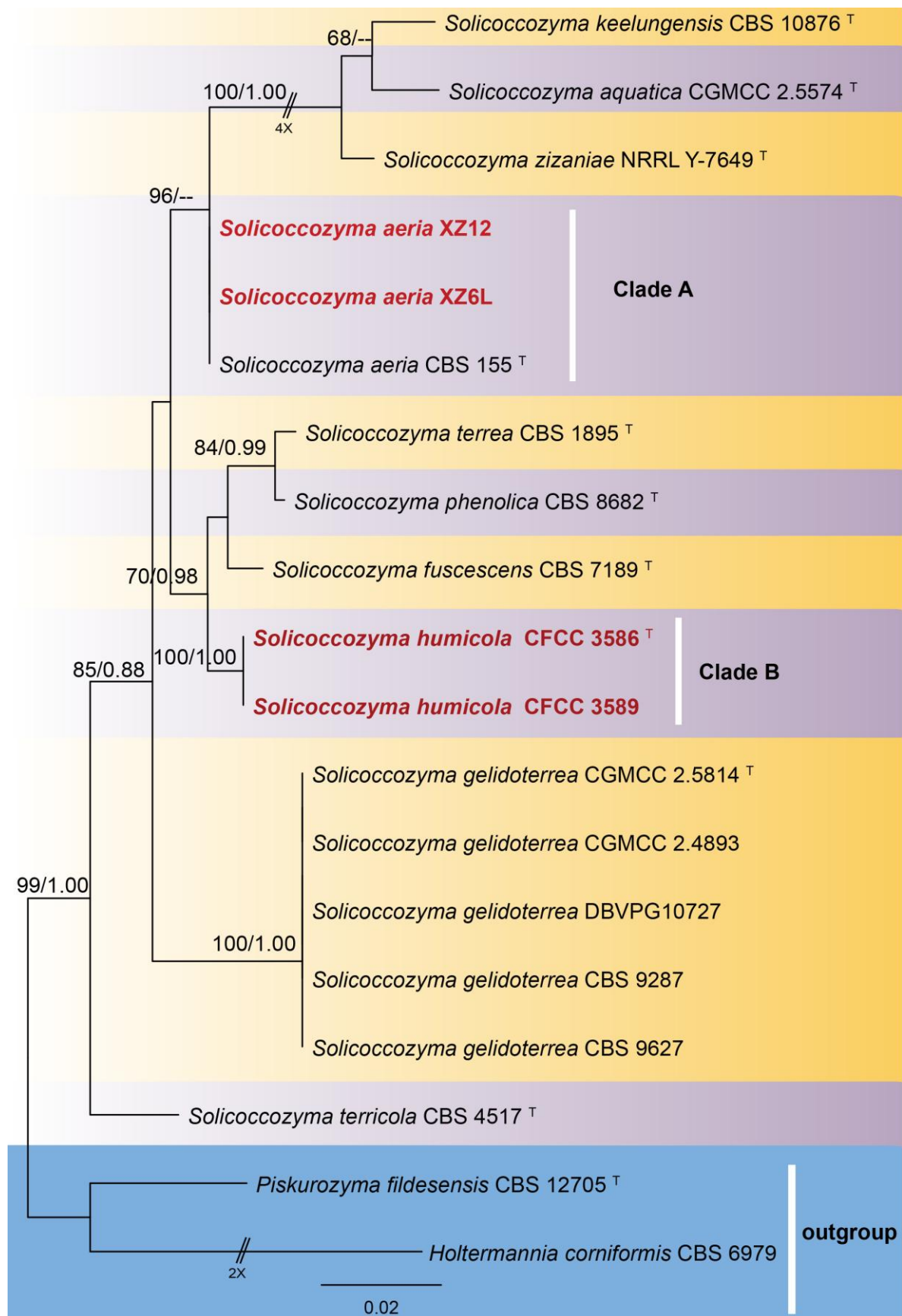


Figure 89 – Phylogram generated from maximum likelihood analysis based on combined LSU sequence data. Nineteen strains were included in the combined sequence analyses, which comprised 638 characters with gaps. *Piskurozyma fildesensis* (CBS 12705) and *Holtermannia corniformis* (CBS 6979) strains were used as the outgroup taxa. The final ML optimization

likelihood is -1796.200505. The matrix included 141 distinct alignment patterns, with 5.16% undetermined characters or gaps. Bootstrap support values for ML (first set) equal to or greater than 68%, BYPP equal to or greater than 0.95 are given above or below the nodes. The strains from the current study are in red-bold, and the type strains are indicated with ^T.

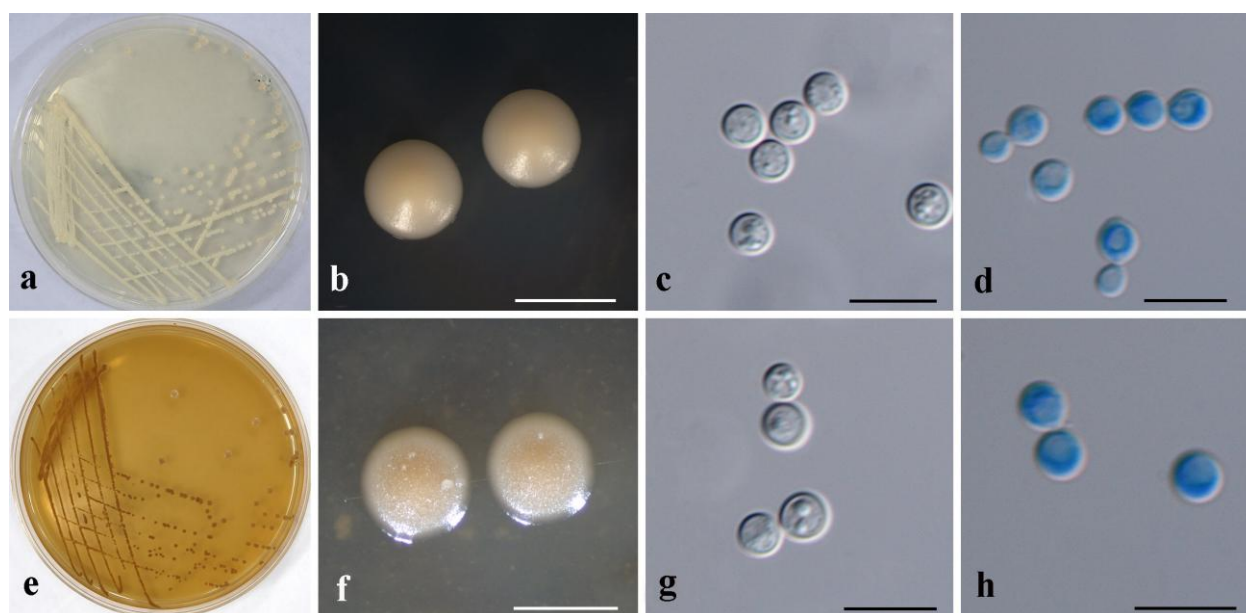


Figure 90 – *Solicoccozyma aerea* (XZ6L, a new geographical record). a, b Colonies formed on YA. c Cells formed on YA immersed in water. d Cells formed on YA immersed in cotton blue. e, f Colonies formed on OA. g. Cells formed on OA immersed in water. h. Cells formed on OA immersed in cotton blue. Scale bars: b, f = 300 μ m, c, d, g, h = 10 μ m.

Notes – The multigene phylogenetic analysis (Fig. 89, Clade B) revealed that the strains of our species *Solicoccozyma humicola* (CFCC 3586, CFCC 3589) formed a separate clade closely related to the strains of *So. fuscescens* (CBS 7189), *So. phenolica* (CBS 8682), and *So. terrea* (CBS 1895) with 70% ML and 0.98 BYPP bootstrap support. They share some similar morphological characters to our species, however, differences in LSU sequence data (9 bp from *So. fuscescens*, 10 bp from *So. phenolica* and 12 bp from *So. terrea*) are revealed (Fonseca et al. 1999). Thus, based on the phylogenetic evidence, we conclude our collection is a new species, *Solicoccozyma humicola* collected from frozen soil in China.

Phylum *Mucoromycota* Doweld

Subphylum *Mucoromycotina* Benny

Class *Mucoromycetes* Doweld

Mucorales Dumort.

Cunninghamellaceae Naumov ex R.K. Benj.

Cunninghamella Matr.

Index Fungorum number: IF 20150; Facesoffungi number: FoF 18614

Notes – *Cunninghamella* was introduced by Matruchot (1903) and typified with *Cu. echinulata* (Alcorn & Yeage 1938, Ding et al. 2025). The key morphologies of the genus are sporangiophores branching patterns, shapes and dimensions of terminal and lateral vesicles and sporangiola (Ding et al. 2025). There have been extensive studies on *Cunninghamella* in recent years. Zhao et al. (2023b) conducted a comprehensive investigation on the diversity and systematics of *Mucoromycota* in China, documenting six new species and one new combination in the genus *Cunninghamella*. Subsequently, Freitas et al. (2024) reported a novel *Cunninghamella* species from Brazil, while Ding et al. (2025) described seven additional new species from China. In the present study, we identify and characterize *Cunninghamella variabilis* sp. nov. from Fujian

Province, China, based on multigene phylogenetic evidence (Fig. 92) and morphological characters (Fig. 93).

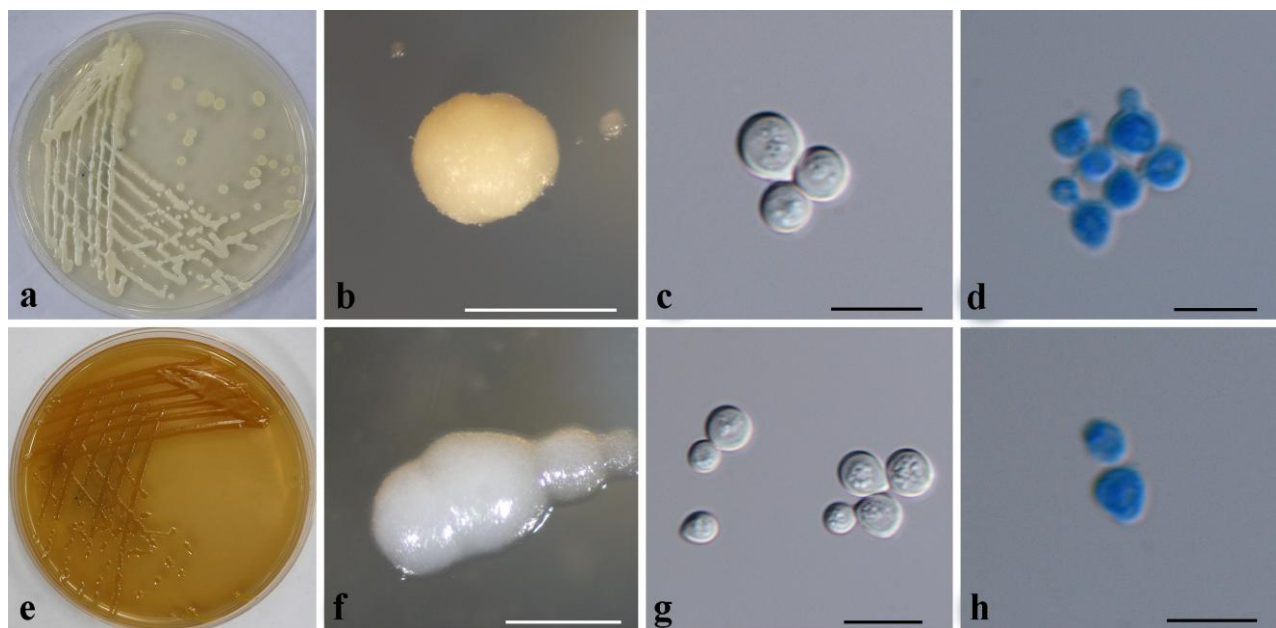


Figure 91 – *Solicoccozyma humicola* (CFCC 3586, holotype). a, b Colonies formed on YA. c Cells formed on YA immersed in water. d Cells formed on YA immersed in cotton blue. e, f Colonies formed on OA. g Cells formed on OA immersed in water. h Cells formed on OA immersed in cotton blue. Scale bars: b, f = 300 μ m, c, d, g, h = 10 μ m.

Cunninghamella variabilis W.X. Liu, F. Li & X.Y. Liu, sp. nov.

Fig. 93

Index Fungorum number: IF 904066; Facesoffungi number: FoF 17964

Etymology – *variabilis* (lat.): referring to the variable shape of vesicles.

Colonies on PDA at 25°C for 5 d, growing fast, attaining 85 mm in diam., exhibiting an average growth rate of 16.5–17.0 mm/d, white at first, becoming pale gray when mature, velvety, regularly and concentrically zonate with ring, and comparatively regular in reverse with a wavy edge. *Hyphae* branched, mostly subhyaline, dark gray, mostly aseptate, rarely septate, and 4.2–22.9 μ m in diam. *Stolons* present, branched, mostly hyaline, smooth, septate, and 4.6–17.8 μ m in diam. *Rhizoids* root-like, subhyaline, branched. *Sporangiophores* arising from stolons or aerial hyphae, smooth, erect, gently bent, or recumbent, hyaline or subhyaline, unbranched or simply branched, primary branches 31.0–129.7 μ m long and 5.6–14.3 μ m wide, longer than secondary branches, sometimes 2 in whorls, main axes usually aequilate, 3.5–13.9 μ m in diam., and always terminating in a vesicle. *Vesicles* hyaline or subhyaline, pale gray or light brown, pyriform, subglobose, squircle or rounded rectangle, axially 12.7–46.4 μ m long and 9.6–42.9 μ m wide, and laterally 6.6–37.1 μ m long and 5.0–32.5 μ m wide. *Pedicels* on vesicles 1.7–3.3 μ m long. *Sporangiola* globose or ellipsoidal, subhyaline, brown or grayish green, mostly densely covered with slender spines, rarely smooth, 4.5–16.3 μ m in diam., and growing on vesicles with pedicels. *Chlamydospores* absent. *Zygospores* not observed.

Material examined – China, Fujian Province, Sanming City, Sanyuan District, Sanyuan National Forest Park, Geshi Oak Scenic Area, 120 meters northeast to the Visitor Center, in the soil, 24 October 2024, Yang Jiang, (HMAS 353947, holotype); ex-type CGMCC3.28895=XG12244-12.

GenBank accession numbers – ITS-PV490640, LSU-PV603421, *tef1*- α -PV700502.

Notes – Phylogenetic analyses (Fig. 92) employing ITS, LSU rDNA, and *tef1*- α sequences demonstrate that the strains of the newly discovered taxon (CGMCC3. 28895, XG12244-12) grouped within *Cunninghamella* sister to *Cu. verrucosa* (CGMCC 3.16260) with 45% ML and 0.81

BYPP. However, comprehensive morphological comparisons clearly distinguish it from *Cu. verrucosa* by its broader hyphae (4.2–22.9 vs. 2.8–15.7 μm in diam.), larger axial vesicles (12.7–46.4 $\times$ 9.6–42.9 vs. 10.8–31.6 $\times$ 7.5–20.8 μm), shorter pedicels (1.7–3.3 vs. 2.6–6.1 μm), and smaller sporangiola (4.5–16.3 vs. 10.9–17.6 μm , Wang et al. 2022c). These diagnostic morphological characters, combined with molecular evidence, robustly support the recognition of *Cu. variabilis* as a distinct species.

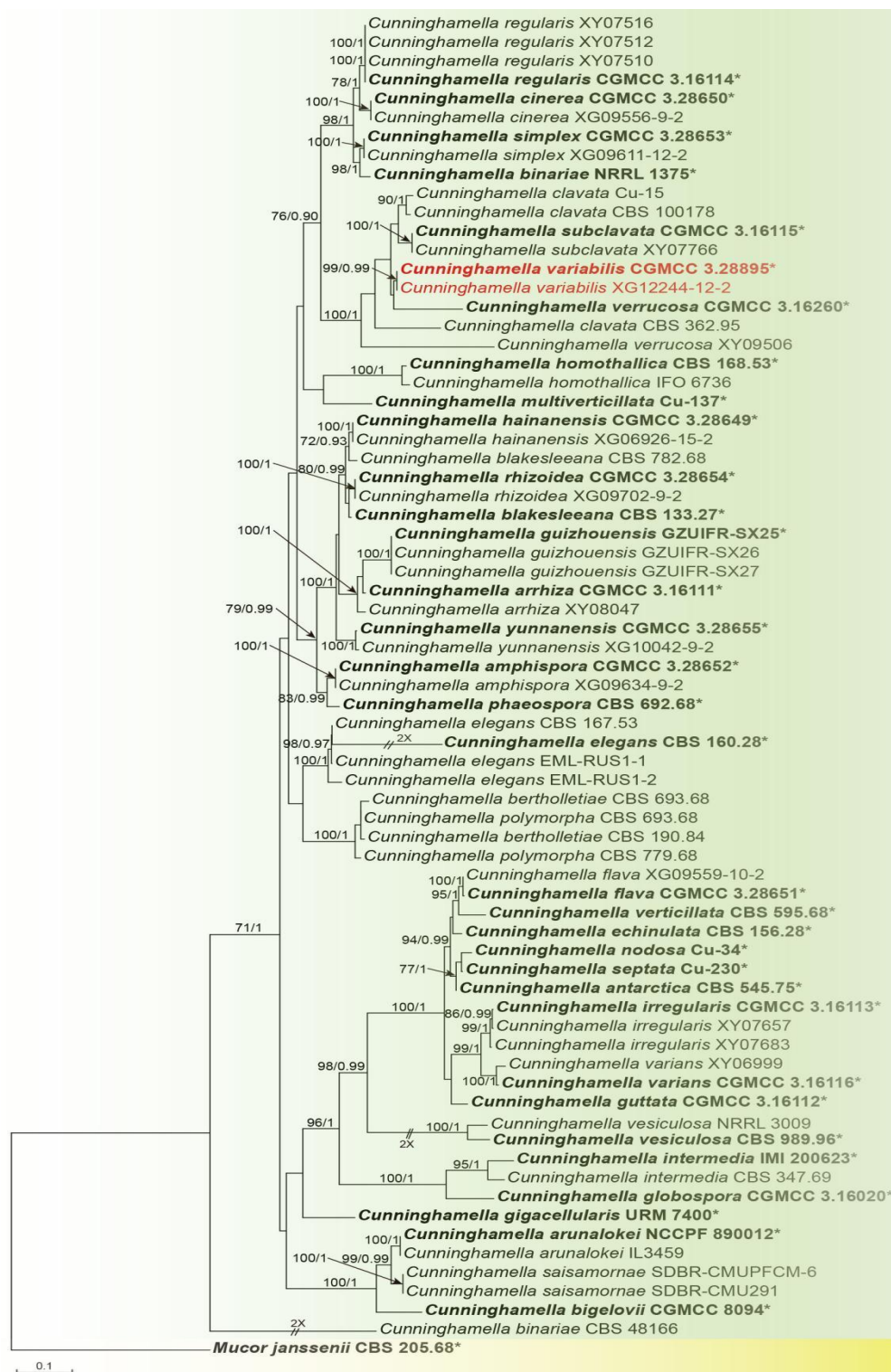


Figure 92 – Phylogram generated from maximum likelihood analysis based on ITS-LSU-*tef1-α* sequence data of *Cunninghamella*. *Mucor janssenii* (CBS 205.68) was used as the outgroup. Seventy-one strains were included in the combined sequence analyses, which comprised 4274

characters with gaps. The best RAxML tree with a final likelihood value of -27837.331510 is presented. The evolutionary model GTR+I+G is applied for all the genes. The matrix had 1884 distinct alignment patterns, with 59.89% of undetermined characters or gaps. Bootstrap support values for ML greater than 70% (left side) and Bayesian posterior probabilities greater than 0.90 (right side) are given near the nodes, respectively. The tree was rooted with *Mucor janssenii* (CBS 205.68). Newly generated sequences are in red-bold and the bold strains marked with an asterisk “*” represent ex-types or ex-holotypes. Branches shortened to fit the page are represented by double slashes “//” and the number of folds “×”. The scale at the bottom left indicates 0.1 substitutions per site.



Figure 93 – *Cunninghamella variabilis* (HMAS 353947, holotype). a, b Colonies on PDA (a: obverse, b: reverse). c, h Branched sporangiophores. d, e Single sporangiophores. f, g Vesicles bearing pedicels and sporangioles. i Rhizoids. j, k Sporangioles. Scale bars: c–k 10 μ m.

Phylum *Amoebozoa* L  he
 Eumycetozoa L.S. Olive
 Class *Dictyosteliomycetes* Doweld

Dictyosteliales L.S. Olive ex P.M. Kirk, P.F. Cannon & J.C. David

Dictyosteliaceae Rostaf. ex Cooke

Dictyostelium Bref.

Index Fungorum number: IF 12072; Facesoffungi number: FoF 18615

Note – Dictyostelids (cellular slime molds), a phylogenetically distinct group of terrestrial protists within the *Amoebozoa*, are among the most abundant and ecologically widespread microbial groups in ecosystems, with 12 recognized genera (Sheikh et al. 2018, Liu et al. 2025b). *Dictyosteliaceae* is the most species-rich group in *Dictyosteliales*, consisting of two genera, viz. *Dictyostelium* and *Polysphondylium* (Zhang et al. 2024c). *Dictyostelium* was introduced by Brefeld (1869) and typified by *D. mucoroides* isolated from a dung sample of rabbit and horse in France. Currently, more than 50 *Dictyostelium* species are accepted (Hyde et al. 2024d, Index Fungorum 2025) and many Chinese collections are available among them (Zhang et al. 2024c). In this study, *Dictyostelium gracilidiscobasis* is introduced from China based on the SSU sequence data (Fig. 94) and morphological characteristics (Fig. 95).

Dictyostelium gracilidiscobasis J.L. Jin, Z.J. Zhang, P. Liu & Y. Li sp. nov.

Fig. 95

Index Fungorum number: IF 572499; Facesoffungi number: FoF 18616

Etymology – The name refers to the slender sorophores and discoid bases.

When cultured at 23°C on non-nutrient agar with *Escherichia coli*. *Sorocarps* solitary, erect, inclined or prone, usually unbranched, usually 1.772–7.184 mm in length, prostrate individuals can exceed 1 cm in length, with strong phototropism. *Sorophores* colorless and slender, usually consisting of one or two rows of cells, tips are enlarged clavate or capitate, 3.036–8.583 µm wide, bases clavate, conical or round, often mucus attached, sometimes forming a base disc, 9.566–25.388 (56.380) µm wide. *Sori* globose or lemon-shaped, milky white translucent, 103–350 (500) µm in diam. *Spores* elliptical, with polar or non-polar particles distributed in the spore, 5.870–8.400 × 3.568–4.829 µm, a few spores length can reach 12 µm, the length-width ratio of 1.65–2.01. Aggregations mounds or radiate. *Pseudoplasmodia* migrating with stalk.

Material examined – China, Jilin Province, Songyuan City, Ningjiang District, Xincheng Township, isolated from 5–10 cm soil layer, soil samples collected from a cornfield, Soil No. 7812, altitude 145.6 m, coordinates 45°11'43.08"N, 124°50'53.16"E, 26 August 2023, (HMJAU MR465, holotype); ex-type, strain SY2 2D2, Jilin Province, Changchun City, in Gongzhuling City, isolated from 0–5 cm soil layer, soil samples collected from uncultivated weed land, Soil No. 7197, altitude 199.8 m, coordinates 43°30'23.76"N, 124°47'27.6"E, 25 August 2022, (HMJAU MR466, paratype); ex-paratype strain GC4 1D3.

GenBank accession numbers – SY2 2D2: SSU = PV476740; GC4 1D3: SSU = PV476739.

Note – Molecular phylogeny based on SSU rRNA supported the position of this species within *Dictyostelium*. In the molecular phylogenetic tree (Fig. 94), the strains of *D. gracilidiscobasis* (SY2 2D2 and GC4 1D3) are closely related to *D. giganteum* (Hagiwara 1992), *D. brunneum* (Raper 1984), *D. gargantum* (Vadell et al. 2011), *D. longigracilis* (Zhang et al. 2024c), and *D. robustum* (Hagiwara 1996). However, it exhibits significant morphological differences from these species (Table 4). The spores of *D. gracilidiscobasis* possess distinct polar granules, whereas the spores of *D. giganteum*, *D. brunneum*, *D. longigracilis*, and *D. robustum* without polar granules. The sorophore bases of *D. gracilidiscobasis* are mucilaginous and form disc-shaped structures, a feature absent in the five species of *Dictyostelium*. The sorocarps of *D. gracilidiscobasis* are white and translucent, whereas those of *D. brunneum* turn brown over time. The aggregations of *D. gracilidiscobasis* are either radial or mound-shaped, while the aggregations of *D. brunneum*, *D. gargantum*, and *D. robustum* are all radial. The spores of *D. gracilidiscobasis* (5.8–8.4 × 3.5–4.8 µm) are larger than those of *D. giganteum* (5.0–8.2 × 2.6–3.6 µm), *D. brunneum* (7.0–10.0 × 3.0–4.0 µm), *D. gargantum* (6.0–11.5 × 3.0–4.0 µm), and *D. robustum* (7.1–9.6 × 3.2–4.4 µm). The morphological comparison combined with phylogenetic analysis, allows us to establish our isolates as a new species as *Dictyostelium gracilidiscobasis*.

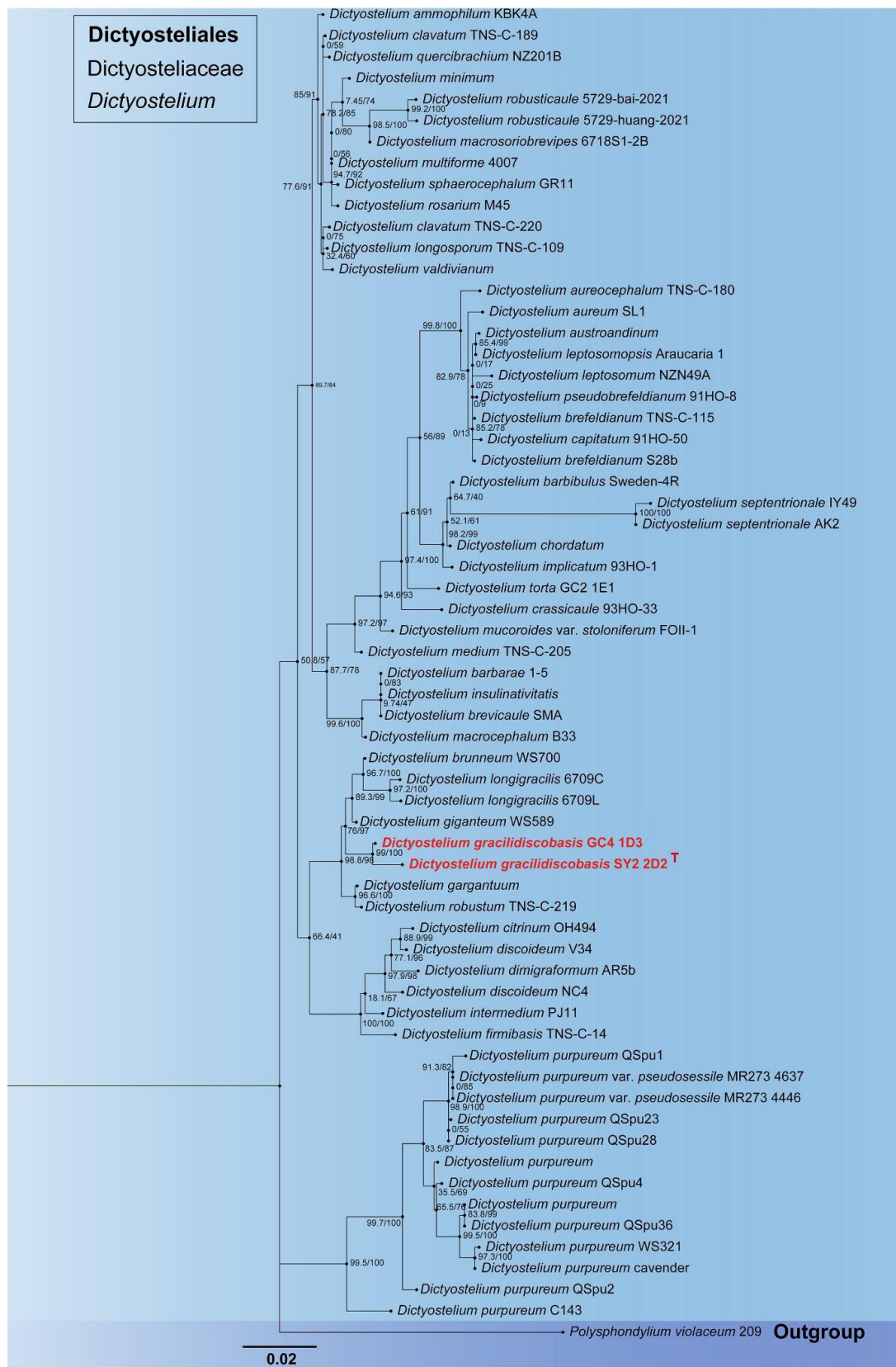


Figure 94 – Phylogram generated from the maximum-likelihood (ML) analysis based on SSU sequence data of *Dictyostelium* species, with Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT support%) (left) and ultrafast bootstrap support (UFB%) (right) near the corresponding node. SY2 2D2 and GC4 1D3 strains are included in the analysis. The scale bar represents substitutions per site. The tree was rooted with *Polysphondylium violaceum* (strain 209). Newly generated sequences are highlighted in bold-red and the ex-type strain is indicated with ^T.

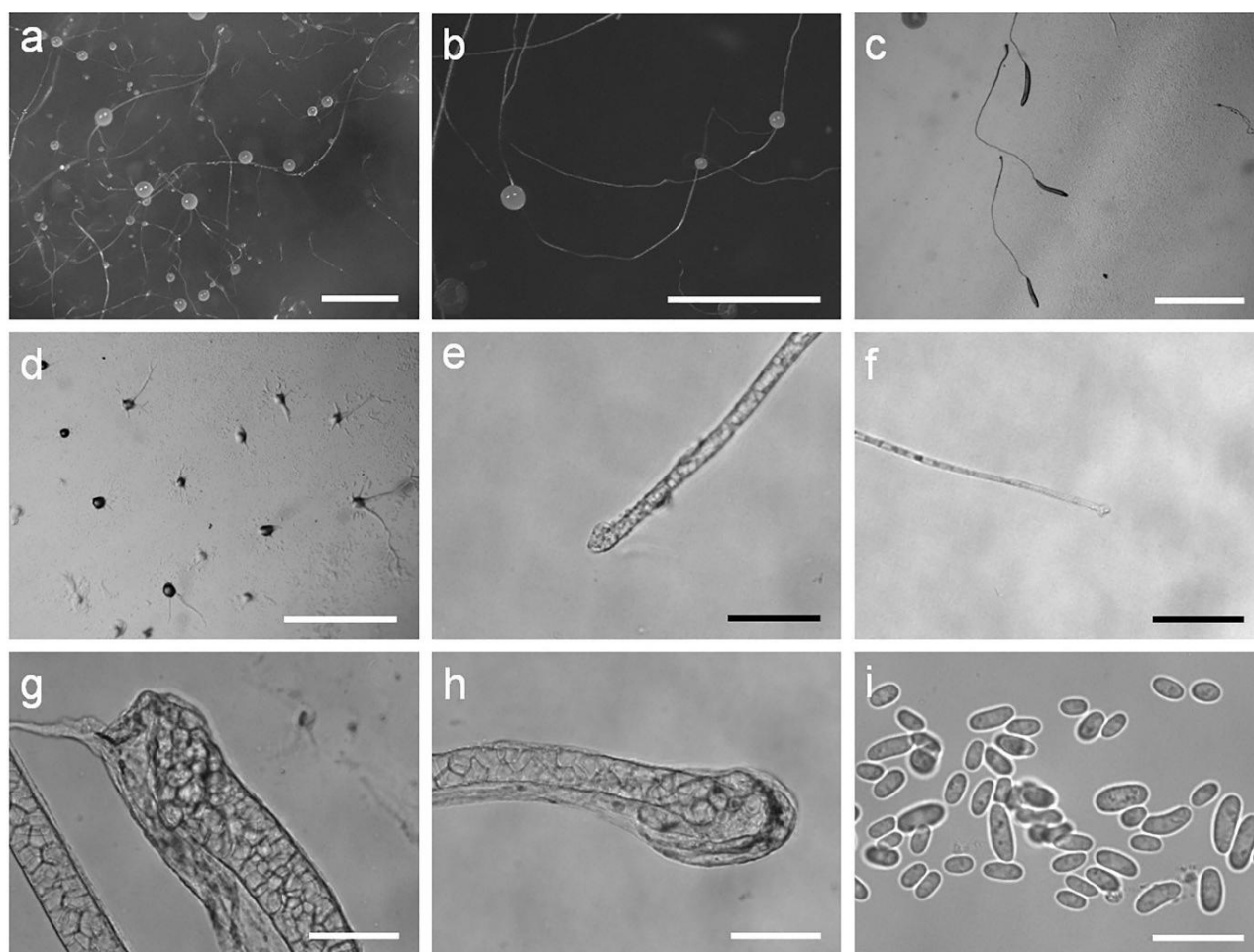


Figure 95 – Macro and micromorphological characteristics of *Dictyostelium gracilidiscobasis* (Strain SY2 2D2, ex-type). a, b Sorocarps. c Pseudoplasmodia. d Aggregations. e, f Sorophore tips. g, h Sorophore bases. i Spores. Scale bars: a–d = 2 mm, e–h = 50 μ m, i = 20 μ m.

Table 4 The key morphological differences in the dimensions of *Dictyostelium gracilidiscobasis*.

Species	Sorocarps (mm)	Sorophores tips (μ m)	Sorophores bases (μ m)	Sori (μ m)	Spores (μ m)	References
<i>D. gracilidiscobasis</i>	1.772–7.184	3.036–8.583	9.566–25.388 (56.380)	103–350 (500)	5.870–8.400 $\times$ 3.568–4.829	Present study
<i>D. giganteum</i>	17–25	—	—	—	5–8.2 $\times$ 2.6–3.6	Hagiwara (1992)
<i>D. brunneum</i>	3–8	—	—	200–300	7–10 $\times$ 3–4	Raper (1984)
<i>D. gargantum</i>	3–8	20–35	30–50	250–500	6–11.5 $\times$ 3–4	Vadell et al. (2011)
<i>D. longigracilis</i>	2.375–10.71	5.539–8.011	16.922–39.985	158–426	5.673–9.330 $\times$ 3.050–3.814	Zhang et al. (2024c)
<i>D. robustum</i>	0.4–11.6	2–12	45–180	50–400 (–640)	7.1–9.6 $\times$ 3.2–4.4	Hagiwara (1996)

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CONFLICT OF INTEREST

We would like to disclose that some of the co-authors of this manuscript are members of the editorial board of the *Mycosphere* journal. These authors were not be involved in the peer review process or any editorial decisions related to this manuscript.

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