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1. New taxa of Xylariales from Karst Ecosystems in Southwestern China

Authors: Liu LL, Ren YL, Habib K, Lu CT, Wu YP, Long SH, Lin Y, Zhang X, Kang YQ, Wijayawardene NN, Wang F, Elgorban AM, Al-Rejaie S, Samarakoon MC, Shen XC, Li QR

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The order *Xylariales* consists of fungi that are widely distributed and commonly found on decaying wood, fallen branches, and trunks. Despite the taxonomic and morphological challenges in accurately identifying species within this group, interest in *Xylariales* has increased in recent years, largely due to their ecological significance and and species diversity. Over the course of this study, dead branches of several plant hosts with fungal fruiting bodies were collected from Guizhou, Yunnan and Guangxi China. The collected specimens were described morphologically, and a multigene phylogeny was constructed based on internal transcribed spacer (ITS), 28S large subunit rDNA (LSU), RNA polymerase II second largest subunit (*rpb2*), and *β-tubulin* (*TUB2*), including a significant number of representative species of the main lineages in the *Xylariales*. These analyses led to the introduction of 24 new species: *Amphibambusa cerosissimae*, *Am. subbambusicola*, *Anthostomella guangxiensis*, *Arecophila guizhouensis*, *Ar. subguizhouensis*, *Biscogniauxia betulae*, *Cainia daweishanensis*, *Ca. shilihetanensis*, *Daldinia guizhouensis*, *Digitodochium damingshanense*, *D. xishuangbannense*, *D. zhangjiajiense*, *Fasciatispora guizhouensis*, *Helicogermslita nulliclypeata*, *Magnostiolata shiwandashanensis*, *Minuticlypeus yunnanensis*, *Nemania huangjingensis*, *Spirodecospora anshunensis*, *S. daweishanensis*, *S. jichuanenii*, *S. jinghongensis*, *Vamsapriya clypeata*, *V. damingshanensis*, and *V. shiwandashanensis*. Additionally, we report the occurrence of three new records in China, which includes *Amphibambusa bambusicola*, *Biscogniauxia petrensis*, and *Fasciatispora cocoes*. A new combination *Magnostiolata guizhouensis* (= *Anthostomella guizhouensis*) is proposed based on comparative morphological analysis and phylogenetic evidence. Morphologically similar species and phylogenetically close taxa are compared and discussed. Comprehensive morphological descriptions, illustrations, and a phylogenetic tree to show the placement of new taxa are provided.

Keywords: Anthostomella-like fungi – Ascomycetes – bambusicolous fungi – fungal systematics – new species

2. Towards an integrative morpho-molecular classification of the Lulworthiomycetidae

Authors: Dayarathne MC, Jones EBG, Rämä T, Hagestad OC, Abdel-Wahab MA, Bahkali AH, Prematunga C, Azevedo E, Hyde KD, Caeiro MF, Barata M, Sarma VV, Devadatha B, Guo SY, Sakayaroj J and Pang KL

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This study re-evaluates the classification of the *Lulworthiomycetidae* based on phylogenetic analyses of 18S, 28S and ITS (internal transcribed spacers and 5.8S) regions of rDNA and protein coding genes (TEF1α, RPB1, RPB2, TUB2, MCM7) along with comprehensive morphological comparisons. Based on the current phylogenetic data we consider the genus *Spathulospora* as a member of the *Lulworthiales*, *Lulworthiomycetidae*, and redundancy of the taxon *Spathulosporales*. This study confirms *Lulworthia* as polyphyletic with the characteristic filiform, long ascospores with an end chamber, which is found in many genera: *Halazoon*, *Halophilomyces*, *Lulwoana*, *Lulwoidea*, *Matsusporium*, *Paralulworthia*, *Paramoleospora*, *Rostrupiella*, and *Sammeyersia*. These genera can be distinguished by morphology, their asexual morphs and molecular phylogeny. The *Lulworthiomycetidae* includes 23 genera and 69 species. One new genus (*Lindriella*) and eight new species (*Hydea mangrovei*, *Lulworthia norwegica*, *Matsusporium japonica*, *Moromyces mangrovis*, *Paralulworthia lignicola*, *Rostrupiella longispora*, *Sammeyersia yanbuensis*, *S. thailandica*) are introduced, with four new combinations.

Keywords: 9 new taxa – ecology – marine Ascomycota – life below water – taxonomy

3. Morpho-molecular characterization and pathogenicity of fungi associated with sweet cherry (Prunus avium) trunk diseases in China

Authors: Zhang W, Chen P, Zhou Y, Manawasinghe IS, Ji S, Li X, Al-Otibi F, Hyde KD, Abeywickrama PD, and Yan J

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Karimi O et al. (2025)

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narathiwatensis, *Neoleptodontidium narathiwatense*, *Temera narathiwatensis*, and *Vamsapriya narathiwatensis*, which represent the first records of their respective genera on the host family *Arecaceae*. Each taxon is provided with detailed descriptions and illustrations, along with a concise summary for each family and genus. This study enhances our understanding of fungal diversity in peat swamp forests and validates the identification of species introduced in previous studies, which relied solely on morphological analysis. By incorporating molecular data, it ensures more accurate taxonomic placement.

Keywords: 25 new species – Dothideomycetes – molecular data – morphology – Sordariomycetes – taxonomy

15. Epidemiology, risk factors and virulence analysis of Candida infection in Southwest China

Authors: Wang D, Wang C, Wang YY, Pan WH, Luo G, Huang XH, Xue WW, Nie L, Chen CB and Kang YQ

Recieved: 24 April 2025, **Accepted:** 18 July 2025, **Published:** 30 July 2025

Fungal infections, especially invasive candidiasis caused by *Candida* species, have been shown to increase mortality rates among critically ill patients. However, there remains a dearth of epidemiological data on invasive *Candida* infections in Southwest China. This retrospective study sought to address this gap by investigating species distribution, underlying diseases, and risk factors among hospitalized patients with confirmed *Candida* infections in hospitals of Southwest China from 2019-2023. Additionally, we systematically analyzed the virulence properties of strains isolated from different clinical sources and action of cytokines involved in inflammatory and immune responses. A total of 4662 patients were included in the present study, with 174 identified as having bloodstream infection. Our data revealed that *Candida albicans* was the predominant infecting organism. Univariate analysis showed significant differences in ICU admission, respiratory dysfunction, solid tumors, neurological disorders, and gastrointestinal pathology between patients with *C. albicans* infections and those with non-*albicans Candida* infections. Multivariate analysis demonstrated that non-*albicans Candida* species are common pathogens in central venous catheter associated bloodstream infections [OR (2.488; 95% CI, 1.043-5.934)]. The invasive virulence determinants of the clinical *Candida* strains were also determined in vitro and in vivo (*Galleria mellonella* and murine models). And cytokine profiles in mice with *C. albicans* infections varied by the source of the isolate. The prevalence of non-albicans *Candida* infections in Southwest China is progressively rising annually, exacerbated by underlying comorbidities in infected individuals. Thus, our work underscores the significance of prompt identification, diagnosis and management of *Candida* infections in clinical practice.

Keywords: bloodstream infection – candidiasis – cytokine profiles – epidemiology – risk factors – virulence

16. Notes, outline, taxonomy and phylogeny of wood-inhabiting Agaricales

Authors: Dong JH, Chen ML, Chen M, Li Q, Zhu YJ, Zhang XC, Zhou CQ, Li W, Muhammad A, Zhou HM, Jabeen S, Zhao CL

Recieved: 18 March 2025, **Accepted:** 30 July 2025, **Published:** 13 August 2025

The order *Agaricales* covers fungi with diverse basidiomata types, and as one of the most species-rich orders within the phylum *Basidiomycota*, it comprises over 40,000 described species, whose basidiomata exhibit a remarkable spectrum of morphological diversity ranging from resupinate (corticioid) to conchate, cyphelloid, stereoid, clavarioid, agaricoid, gasteroid, sequestrate, or highly complex, with lamellate, smooth, wrinkled, odontoid, poroid hymenophore, demonstrating the broad adaptive evolutionary features. Such morphological plasticity not only reflects the functional complexity in ecological roles, reproductive strategies, and habitat adaptation but also provides the critical evidence for taxonomic delineation and phylogenetic reconstruction research. Traditionally, morphological characters have been used to identify and classify wood-inhabiting *Agaricales*, which has led to many taxonomic controversies. Modern molecular methods, based on DNA sequence data, have led to a more reliable and natural classification of wood-inhabiting *Agaricales*. The present study revises the taxonomy of the wood-inhabiting *Agaricales* based on both morphology and phylogeny. In total, 199 genera belong to the wood-inhabiting *Agaricales*, with 65 genera having brief notes provided. Of these, 40 families belong to wood-inhabiting *Agaricales* (eg., *Physalacriaceae*: 18; *Porotheleaceae*: 16; *Cyphellaceae*: 15; *Cyphellopsidaceae*: 12; *Omphalotaceae*: 11; *Mycenaceae*: 9; *Cystostereaceae*: 8; *Phyllotopsidaceae*: 7; *Pterulaceae*: 7; *Strophariaceae*: 7; *Crepidotaceae*: 6; *Nidulariaceae*: 6; *Psathyrellaceae*: 6; *Tubariaceae*: 6; *Campanellaceae*: 5; *Crepidotaceae*: 5; *Lyophyllaceae*: 5; *Clavariaceae*: 4; *Lichenomphaliaceae*: 4; *Marasmiaceae*: 4; *Pleurotaceae*: 4; *Radulomycetaceae*: 4; *Stephanosporaceae*: 3; *Bolbitiaceae*: 2; *Callistosporiaceae*: 2; *Fistulinaceae*: 2; *Hygrocybaceae*: 2; *Lycoperdaceae*: 2; *Sarcomyxaceae*: 2; *Schizophyllaceae*: 2; Typhulaceae: 2; Xeromphalinaceae: 2; Broomeiaceae: 1; Cantharellulaceae: 1; *Clitocybaceae*: 1; *Fayodiaceae*: 1; *Hygrophoraceae*: 1; *Mythicomycetaceae*: 1; *Resupinataceae*: 1; *Tricholomataceae*: 1). Multi-locus phylogeny, including 185 species of *Agaricales* within *Basidiomycota*, are carried out using the internal transcribed spacer (ITS) regions, translation elongation factor 1-α gene (tef1-α), RNA polymerase II largest subunit (rpb1), and the second subunit of RNA polymerase II (rpb2), and the results show that these species are phylogenetically placed in *Agaricales* (eg., 56 species in *Omphalotaceae*, 22 species in *Cyphellopsidaceae*, 16 species in *Marasmiaceae*, 10 species in *Campanellaceae*, 10 species in *Resupinataceae*). Based on morphology and multi-gene phylogeny, twelve new taxa are described in this study, including one new genus (*Sicyoideibasidia*) and eleven new species: *Campanella yunnanensis*, *Collybiopsis albobasidiosa*, *Co. cremea*, *Co. yunnanensis*, *Dendrothele fissurata*, *Gracilihypha albohymenia*, *G. yunnanensis*, *Marasmius wumengshanensis*, *Resupinatus tenuis*, *Sicyoideibasidia bambusicola*, and *S. punctata*. Detailed descriptions, morphological illustrations, and phylogenetic analysis results are provided for these new taxa.

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Notes, outline, taxonomy and phylogeny of wood-inhabiting *Agaricales*

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Abstract

The order *Agaricales* covers fungi with diverse basidiomata types, and as one of the most species-rich orders within the phylum *Basidiomycota*, it comprises over 40,000 described species, whose basidiomata exhibit a remarkable spectrum of morphological diversity ranging from resupinate (corticioid) to conchate, cyphelloid, stereoid, clavarioid, agaricoid, gasteroid, sequestrate, or highly complex, with lamellate, smooth, wrinkled, odontoid, poroid hymenophore, demonstrating the broad adaptive evolutionary features. Such morphological plasticity not only reflects the functional complexity in ecological roles, reproductive strategies, and habitat adaptation but also provides the critical evidence for taxonomic delineation and phylogenetic reconstruction research. Traditionally, morphological characters have been used to identify and classify wood-inhabiting *Agaricales*, which has led to many taxonomic controversies. Modern molecular methods, based on DNA sequence data, have led to a more reliable and natural classification of wood-inhabiting *Agaricales*. The present study revises the taxonomy of the wood-inhabiting *Agaricales* based on both morphology and phylogeny. In total, 199 genera belong to the wood-inhabiting *Agaricales*, with 65 genera having brief notes provided. Of these, 40 families belong to wood-inhabiting *Agaricales* (eg., *Physalacriaceae*: 18; *Porotheleaceae:* 16; *Cyphellaceae*: 15; *Cyphellopsidaceae*: 12; *Omphalotaceae*: 11; *Mycenaceae*: 9; *Cystostereaceae*: 8; *Phyllotopsidaceae*: 7; *Pterulaceae*: 7; *Strophariaceae*: 7; *Crepidotaceae*: 6; *Nidulariaceae*: 6; *Psathyrellaceae*: 6; *Tubariaceae*: 6; *Campanellaceae*: 5; *Crepidotaceae*: 5; *Lyophyllaceae*: 5; *Clavariaceae*: 4; *Lichenomphaliaceae*: 4; *Marasmiaceae*: 4; *Pleurotaceae*: 4; *Radulomycetaceae*: 4; *Stephanosporaceae*: 3; *Bolbitiaceae*: 2; *Callistosporiaceae*: 2; *Fistulinaceae*: 2; *Hygrocybaceae*: 2; *Lycoperdaceae*: 2; *Sarcomyxaceae*: 2; *Schizophyllaceae*: 2; *Typhulaceae*: 2; *Xeromphalinaceae*: 2; *Broomeiaceae*: 1; *Cantharellulaceae*: 1; *Clitocybaceae*: 1; *Fayodiaceae*: 1; *Hygrophoraceae*: 1; *Mythicomycetaceae*: 1; *Resupinataceae*: 1; *Tricholomataceae*: 1). Multi-locus phylogeny, including 185 species of *Agaricales* within *Basidiomycota*, are carried out using the internal transcribed spacer (ITS) regions, translation elongation factor 1-α gene (*tef*1-α), RNA polymerase II largest subunit (*rpb*1), and the second subunit of RNA polymerase II (*rpb*2), and the results show that these species are phylogenetically placed in *Agaricales* (eg., 56 species in *Omphalotaceae*, 22 species in *Cyphellopsidaceae,* 16 species in *Marasmiaceae*, 10 species in *Campanellaceae*, 10

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species in *Resupinataceae*). Based on morphology and multi-gene phylogeny, twelve new taxa are described in this study, including one new genus (*Sicyoideibasidia*) and eleven new species: *Campanella yunnanensis*, *Collybiopsis albobasidiosa*, *Co. cremea*, *Co. yunnanensis*, *Dendrothele fissurata*, *Gracilihypha albohymenia*, *G. yunnanensis*, *Marasmius wumengshanensis*, *Resupinatus tenuis*, *Sicyoideibasidia bambusicola*, and *S. punctata*. Detailed descriptions, morphological illustrations, and phylogenetic analysis results are provided for these new taxa.

Keywords – *Agaricales* – multi-locus – molecular phylogeny – new taxa – taxonomy – wood-decaying fungi

Outline of wood-inhabiting *Agaricales*

Order *Agaricales* Underw.
Suborder *Agaricineae* Fr.
Family *Bolbitiaceae* Singer
- *Rhodoarrhenia* Singer
- *Tubariella* E. Horak

Family *Crepidotaceae* (S. Imai) Singer
- *Crepidotus* (Fr.) Staude **(Note 1)**
- *Episphaeria* Donk
- *Nanstelocephala* Oberw. & R.H. Petersen
- *Pellidiscus* Donk
- *Pleuroflammula* Singer
- *Simocybe* P. Karst.

Family *Hymenogastraceae* Vittad. (= ***Chromocyphellaceae*** Knudsen)
- *Chromocyphella* De Toni & Levi (= *Phaeosolenia* Speg.)
- *Flammula* (Fr.) P. Kumm.
- *Galerina* Earle
- *Gymnopilus* P. Karst. (= *Pyrrhoglossum* Singer)
- *Synnematomyces* Kobayasi

Family *Lycoperdaceae* Chevall
- *Lycoperdopsis* Henn.
- *Morganella* Zeller

Family *Mythicomycetaceae* Vizzini, Consiglio & M. Marchetti
- *Stagnicola* Redhead & A.H. Sm.

Family *Nidulariaceae* Dumort.
- *Crucibulum* Tul. & C. Tul. **(Note 2)**
- *Cyathus* Haller **(Note 3)**
- *Mycocalia* J.T. Palmer **(Note 4)**
- *Nidula* V.S. White **(Note 5)**
- *Nidularia* Fr. **(Note 6)**
- *Retiperidiolia* Kraisit., Choeyklin, Boonprat. & M.E. Sm. **(Note 7)**

Family *Psathyrellaceae* Vilgalys, Moncalvo & Redhead (= ***Zerovaemycetaceae*** Gorovij)
- *Coprinellus* P. Karst.
- *Coprinopsis* P. Karst. (= *Rhacophyllus* Berk. & Broome, *Zerovaemyces* Gorovij)
- *Gasteroagaricoides* D.A. Reid
- *Heteropsathyrella* T. Bau & J.Q. Yan **(Note 8)**
- *Homophron* (Britzelm.) Örstadius & E. Larss.
- *Olotia* D. Wächt. & A. Melzer **(Note 9)**

Family *Strophariaceae* Singer & A.H. Sm.
- *Deconica* (W.G. Sm.) P. Karst.
- *Hemipholiota* (Singer) Bon

Hypholoma (Fr.) P. Kumm.
Kuehneromyces Singer & A.H. Sm.
Pholiota (Fr.) P. Kumm.
Pseudogymnopilus Raithelh.
Pyrrhulomyces E.J. Tian & Matheny **(Note 10)**
Family *Tubariaceae* Vizzini
Cyclocybe Velen.
Flammulaster Earle
Hemistropharia Jacobsson & E. Larss.
Phaeomarasmius Scherff.
Pleuromyces Dima, P.-A. Moreau & V. Papp **(Note 11)**
Tubaria (W.G. Sm.) Gillet

Suborder *Clavariineae* Olariaga, Huhtinen, Læssøe, J.H. Petersen & K. Hansen
Family *Clavariaceae* Chevall.
Clavaria Vaill. ex L.
Clavicorona Doty
Hyphodontiella Å. Strid
Mucronella Fr.

Suborder *Hygrophorineae* Aime, Dentinger & Gaya
Family *Cantharellulaceae* (Lodge, Redhead, Norvell & Desjardin) Vizzini, Consiglio & P. Alvarado
Pseudoarmillariella Singer **(Note 12)**
Family *Hygrocybaceae* (Padamsee & Lodge) Vizzini, Consiglio & P. Alvarado
Chromosera Redhead, Ammirati & Norvell
Chrysomphalina Clémençon
Family *Hygrophoraceae* Lotsy
Haasiella Kotl. & Pouzar
Family *Lichenomphaliaceae* (Lücking & Redhead) Vizzini, Consiglio & P. Alvarado
Arrhenia Fr.
Cora Fr.
Dictyonema C. Agardh ex Kunth
Lichenomphalia Redhead, Lutzoni, Moncalvo & Vilgalys

Suborder *Marasmiineae* Aime, Dentinger & Gaya
Family *Campanellaceae* J.S. Oliveira, Desjardin & Moncalvo
Brunneocorticium Sheng H. Wu **(Note 13)**
Campanella Henn. **(Note 14)**
Neocampanella Nakasone, Hibbett & Goranova
Tetrapyrgos E. Horak
Family *Cyphellaceae* Burnett
Asterocyphella W.B. Cooke
Baeospora Singer
Campanophyllum Cifuentes & R.H. Petersen
Cheimonophyllum Singer **(Note 15)**
Chondrostereum Pouzar
Cunninghammyces Stalpers
Cyphella Fr.
Gloeocorticium Hjortstam & Ryvarden
Gloeostereum S. Ito & S. Imai
Henningsomyces Kuntze

Lignomphalia Antonín, Borovička, Holec & Kolařík
Phaeoporotheleum (W.B. Cooke) W.B. Cooke
Pleurella E. Horak
Setigeroclavula R.H. Petersen
Thujacorticium Ginns

Family *Cystostereaceae* Jülich
Cericium Hjortstam
Crustomyces Jülich **(Note 16)**
Cystidiodontia Hjortstam
Cystostereum Pouzar **(Note 17)**
Effusomyces Yue Li, Nakasone & S.H. He **(Note 18)**
Parvobasidium Jülich
Rigidotubus J. Song, Y.C. Dai & B.K. Cui **(Note 19)**
Tenuimyces S.L. Liu & L.W. Zhou **(Note 20)**

Family *Marasmiaceae* Roze ex Kühner
Chaetocalathus Singer
Crinipellis Pat. **(Note 21)**
Marasmius Fr. (= *Amyloflagellula* Singer, *Hymenogloea* Pat.) **(Note 22)**
Metacampanella R.H. Petersen **(Note 23)**
Moniliophthora H.C. Evans, Stalpers, Samson & Benny **(Note 24)**
Paramarasmius Antonín & Kolařík **(Note 25)**

Family *Omphalotaceae* Bresinsky
Anthracophyllum Ces.
Collybiopsis (J. Schröt.) Earle (= *Marasmiellus* Murrill) **(Note 26)**
Gymnopanella Sand.-Leiva, J.V. McDonald & Thorn
Gymnopus (Pers.) Gray (= Caripia Kuntze)
Lentinula Earle
Mycetinis Earle **(Note 27)**
Neonothopanus R.H. Petersen & Krisai **(Note 28)**
Omphalotus Fayod
Paramycetinis R.H. Petersen **(Note 29)**
Pseudomarasmius R.H. Petersen & K.W. Hughes **(Note 30)**
Pusillomyces J.S. Oliveira

Family *Physalacriaceae* Corner
Armillaria (Fr.) Staude (= *Acurtis* Fr.; = *Rhizomorpha* Roth)
Cibaomyces Zhu L. Yang, Y.J. Hao & J. Qin
Cylindrobasidium Jülich
Cyptotrama Singer
Epicnaphus Singer
Flammulina P. Karst.
Gloiocephala Massee
Hymenopellis R.H. Petersen
Manuripia Singer
Mucidula Pat.
Oudemansiella Speg. (= *Cribbea* A.H. Sm. & D.A. Reid)
Physalacria Peck
Ponticulomyces R.H. Petersen
Pseudohiatula (Singer) Singer
Pseudotyphula Corner
Rhizomarasmius R.H. Petersen
Rhodotus Maire
Strobilurus Singer

Family *Porotheleaceae* Murrill

Acanthocorticium Baltazar, Gorjón & Rajchenb.
Calyptella Quél.
Chrysomycena Vizzini, Picillo, Perrone & Dovana **(Note 31)**
Clitocybula (Singer) Singer ex Métrod
Delicatula Fayod
Gerronema Singer
Hydropodia Vizzini & Consiglio **(Note 32)**
Hydropus Kühner ex Singer
Leucoinocybe Singer ex Antonín, Borovička, Holec & Kolařík
Marasmiellomycena De la Peña-Lastra, Mateos, Kolařík, Ševčíková & Antonín **(Note 33)**
Megacollybia Kotl. & Pouzar
Porotheleum Fr.
Pseudohydropus Vizzini & Consiglio **(Note 34)**
Pulverulina Matheny & K.W. Hughes **(Note 35)**
Trogia Fr.
Vizzinia Ševčíková & Kolařík **(Note 36)**

Family *Xeromphalinaceae* Vizzini, Consiglio & P. Alvarado

Heimiomyces Singer
Xeromphalina Kühner & Maire

Suborder *Mycenineae* R.L. Zhao, Vizzini & M.Q. He

Family *Mycenaceae* Overeem

Cruentomycena R.H. Petersen, Kovalenko & O.V. Morozova
Cynema Maas Geest. & E. Horak
Favolaschia (Pat.) Pat. **(Note 37)**
Flabellimycena Redhead
Hemimycena Singer
Mycena (Pers.) Roussel (= *Decapitatus* Redhead & Seifert) **(Note 38)**
Panellus P. Karst. (= *Scytinotus* P. Karst.)
Resinomycena Redhead & Singer
Roridomyces Rexer

Suborder *Phyllotopsidineae* Zhu L. Yang & G.S. Wang

Family *Phyllotopsidaceae* Locquin ex Olariaga, Huhtinen, Læssøe, J.H. Petersen & K. Hansen

Bulbillomyces Jülich (= *Aegerita* Pers.)
Cyphelloporia Karasiński, L. Nagy, Szarkándi, Holec & Kolařík
Macrotyphula R.H. Petersen
Phyllotopsis E.-J. Gilbert & Donk ex Singer
Pleurocybella Singer **(Note 39)**
Rectipilus Agerer **(Note 40)**
Tricholomopsis Singer

Family *Pterulaceae* Corner

Coronicium J. Erikss. & Ryvarden **(Note 41)**
Lepidomyces Jülich **(Note 42)**
Merulicium J. Erikss. & Ryvarden **(Note 43)**
Myrmecopterula Leal-Dutra, Dentinger & G.W. Griff. **(Note 44)**
Phaeopterula Henn. **(Note 45)**
Pterula Fr. **(Note 46)**
Pterulicium Corner (= *Deflexula* Corner) **(Note 47)**

Family *Radulomycetaceae* Leal-Dutra, Dentinger & G.W. Griff.

Aphanobasidium Jülich **(Note 48)**

Globuliciopsis Hjortstam & Ryvarden
Radulomyces M.P. Christ. **(Note 49)**
Radulotubus Y.C. Dai, S.H. He & C.L. Zhao **(Note 50)**
Family *Stephanosporaceae* Oberw. & E. Horak
Athelidium Oberw. **(Note 51)**
Cristinia Parmasto **(Note 52)**
Lindtneria Pilát **(Note 53)**

Suborder *Pleurotineae* Aime, Dentinger & Gaya
Family *Cyphellopsidaceae* Jülich (= ***Niaceae*** Jülich)
Calathella D.A. Reid
Dendrothele Höhn. & Litsch. **(Note 54)**
Digitatispora Doguet
Eoscyphella Silva-Filho, Stevani & Menolli **(Note 55)**
Flagelloscypha Donk
Gracilihypha Y. Yang & C.L. Zhao **(Note 56)**
Halocyphina Kohlm. & E. Kohlm.
Lachnella Fr.
Merismodes Earle (= *Cyphellopsis* Donk; = *Maireina* W.B. Cooke) **(Note 57)**
Nia R.T. Moore & Meyers
Pseudolasiobolus Agerer
Sicyoideibasidia J.H. Dong & C.L. Zhao ***gen. nov.*** **(Note 58)**
Family *Fistulinaceae* Lotsy
Fistulina Bull. **(Note 59)**
Porodisculus Murrill
Family *Pleurotaceae* Kühner
Hohenbuehelia Schulzer
Lignomyces R.H. Petersen & Zmitr. **(Note 60)**
Pleurotus (Fr.) P. Kumm.
Radulomycetopsis Dhingra, Priyanka & J. Kaur **(Note 61)**
Family *Resupinataceae* Jülich
Resupinatus Nees ex Gray **(Note 62)**

Suborder *Sarcomyxineae* Zhu L. Yang & G. S. Wang
Family *Sarcomyxaceae* Olariaga, Huhtinen, Læssøe, J.H. Petersen & K. Hansen
Sarcomyxa P. Karst.
Tectella Earle

Suborder *Schizophyllineae* Aime, Dentinger & Gaya
Family *Schizophyllaceae* Quél.
Auriculariopsis Maire
Schizophyllum Fr.

Suborder *Tricholomatineae* Aime, Dentinger & Gaya
Family *Callistosporiaceae* Vizzini, Consiglio, M. Marchetti & P. Alvarado
Callistosporium Singer (= *Pleurocollybia* Singer) **(Note 63)**
Macrocybe Pegler & Lodge **(Note 64)**
Family *Clitocybaceae* Vizzini, Consiglio & M. Marchetti
Lepistella T.J. Baroni & Ovrebo **(Note 65)**
Family *Fayodiaceae* Jülich
Conchomyces Overeem
Family *Lyophyllaceae* Jülich (= ***Asproinocybaceae*** T. Bau & G.F. Mou)

Clitolyophyllum Sesli, Vizzini & Contu
Fibulochlamys A.I. Romero & Cabral
Hypsizygus Singer
Ossicaulis Redhead & Ginns
Tricholosporum Guzmán
Family *Tricholomataceae* R. Heim ex Pouzar
Pseudotricholoma (Singer) Sánchez-García & Matheny

Suborder *Typhulineae* Vizzini, Consiglio & P. Alvarado
Family *Typhulaceae* Jülich
Lutypha Khurana, K.S. Thind & Berthier
Typhula (Pers.) Fr. (= *Tygervalleyomyces* Crous)

Suborder *Incertae sedis*
Family *Broomeiaceae* Zeller
Broomeia Berk.

INTRODUCTION

Agaricales is one of the fungal orders, composed of wood-inhabiting fungi within *Agaricomycetes*, *Basidiomycota* (He et al. 2024, Hyde et al. 2024a). This order was erected with the type family *Agaricaceae* (Chevallier 1826). More than 40,000 species have been assigned to *Agaricales* (Wang et al. 2023b), which comprises 560 genera, distributed across 62 families within 12 suborders (Table l, He et al. 2024, Hyde et al. 2024b, Oliveira et al. 2024, Vizzini et al. 2024).

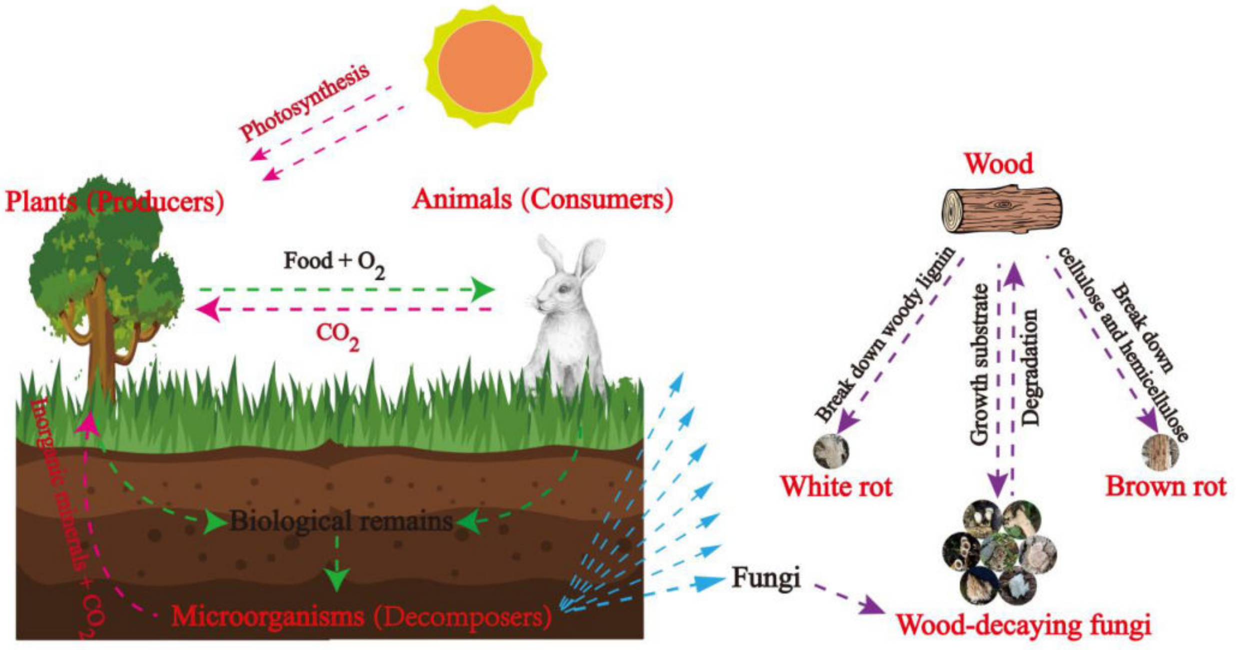

Figure 1 – The wood-inhabiting fungi contribute to the cycling of materials and the flow of energy in ecosystems.

Wood-inhabiting fungi are a morphologically, phylogenetically, and ecologically diverse group, playing an integral role in wood degradation and the matter cycle within the ecological system (Dong et al. 2024). Recognized as pivotal contributors to the intricate balance of forest ecosystems (Fig. 1), these fungi are renowned as "key players" due to their enzymatic prowess, effectively breaking down woody components like lignin, cellulose, and hemicellulose (Dai 2010, Dai et al. 2015, 2021, Cui et al. 2019, Hyde 2022, Dong et al. 2024, Spirin et al. 2024), and grow in various kinds of substrate as living trees, dead standing trees, fallen trunks, rotten wood, fallen branches, fallen twigs and stumps (M'Barek et al. 2020, Runnel et al. 2021, Wu et al. 2022a, Dong et al. 2023, 2024, Yuan et al. 2023, Cui et al. 2025, Liu et al. 2025a, b). Wood-inhabiting fungi possess the ability to degrade plant remains and various environmental contaminants through their extensive capabilities for degrading organic compounds (James et al. 2020). Hence, wood-inhabiting fungi, as important strategic biological resources, represent a captivating facet of biodiversity, showcasing a remarkable diversity of morphological, phylogenetic, and ecological diversity (Wu et al. 2019, Park et al. 2020, Dong et al. 2024, Ghobad-Nejhad et al. 2024).

Agaricales is the most conspicuous and largest group of macrofungi, characterized by highly diverse basidiomata types and nutritional modes (He et al. 2024). It is cosmopolitan in distribution and contains several basidiomata types, from resupinate (corticioid) to conchate, cyphelloid, stereoid, clavarioid, agaricoid (pileostipitate, with open or enclosed hymenophore), and gasteroid, sequestrate (epigeous or hypogeous) (Underwood 1889, He et al. 2024, Vizzini et al. 2024). Pileostipitate forms with protective veils (universal and partial) and lamellate hymenophores are the most frequent, but hymenophores can also be smooth, wrinkled, odontoid, or poroid (Vizzini et al. 2024). The four orders *Agaricales*, *Hymenochaetales, Polyporales,* and *Pucciniales* were the top with new families described (Hyde et al. 2024b). The fact that 2.8% of the genera in *Boletales* are monotypic and 1.9% have only two species, which is about three times higher than for *Agaricales* (0.9% and 0.6%, respectively, Hyde et al. 2024b), suggests that there is abundant species diversity and complexity in the order *Agaricales*. The accuracy of the infraorder classification of *Agaricales* was finally proposed, along with its suborders (Table 1), namely *Agaricineae*, *Clavariineae*, *Hygrophorineae*, *Marasmiineae*, *Mycenineae*, *Phyllotopsidineae*, *Pleurotineae*, *Pluteineae*, *Sarcomyxineae*, *Schizophyllineae*, *Typhulineae*, and *Tricholomatineae* (Dentinger et al. 2016, Olariaga et al. 2020, Wang et al. 2023b, He et al. 2024, Hyde et al. 2024b, Vizzini et al. 2024). It is overwhelmingly diverse morphologically and genetically, making it taxonomically challenging (Oliveira et al. 2020). Based on recent taxonomic revisions by He et al. (2024) and Vizzini et al. (2024), and the updated classification framework for fungi (Outline of fungi 2024) proposed by Hyde et al. (2024b), the currently recognized suborders, families, and number of genera within the order *Agaricales* are systematically presented in Table 1.

Table 1 Suborders, families, and genera number of ranks in *Agaricales* (Family *incertae sedis* is excluded).

Order	Suborders	families	Number of genera
Agaricales	*Agaricineae*	*Agaricaceae*	54
		Bolbitiaceae	16
		Cortinariaceae	12
		Crassisporiaceae	2
		Crepidotaceae	7
		Galeropsidaceae	5
		Hydnangiaceae	4
		Hymenogastraceae	12
		Inocybaceae	7
		Lycoperdaceae	13
		Mythicomycetaceae	2
		Nidulariaceae	6
		Psathyrellaceae	21
		Squamanitaceae	7
		Strophariaceae	14
		Tubariaceae	7
	Clavariineae	*Clavariaceae*	10

Order	Suborders	families	Number of genera
	Hygrophorineae	*Cantharellulaceae*	2
		Cuphophyllaceae	5
		Hygrocybaceae	9
		Hygrophoraceae	6
		Lichenomphaliaceae	7
	Marasmiineae	*Campanellaceae*	5
		Cyphellaceae	24
		Cystostereaceae	9
		Marasmiaceae	5
		Omphalotaceae	20
		Physalacriaceae	32
		Porotheleaceae	18
		Xeromphalinaceae	2
	Mycenineae	*Mycenaceae*	9
	Phyllotopsidineae	*Aphroditeolaceae*	1
		Phyllotopsidaceae	8
		Pterulaceae	8
		Radulomycetaceae	4
		Stephanosporaceae	5
	Pleurotineae	*Cyphellopsidaceae*	15
		Fistulinaceae	3
		Pleurotaceae	5
		Resupinataceae	1
	Pluteineae	*Amanitaceae*	7
		Limnoperdaceae	1
		Melanoleucaceae	2
		Pluteaceae	2
		Volvariellaceae	1
	Sarcomyxineae	*Sarcomyxaceae*	2
	Schizophyllineae	*Schizophyllaceae*	2
	Tricholomatineae	*Biannulariaceae*	3
		Callistosporiaceae	6
		Clitocybaceae	7
		Entolomataceae	9
		Fayodiaceae	5
		Lyophyllaceae	32
		Macrocystidiaceae	2
		Omphalinaceae	2
		Paralepistaceae	3
		PseudoClitocybaceae	6
		Pseudoomphalinaceae	1
		Tricholomataceae	10
	Typhulineae	*Typhulaceae*	2
	incertae sedis	*Broomeiaceae*	1
		Hemigasteraceae	2

The first sequence-based phylogenetic analyses of fungi were not explicitly focused on the internal structure of *Agaricales*; instead, they addressed fungal classification at higher ranks and/or investigated the origin of specific morphological types (Thorn et al. 2000, Hibbett & Donoghue 2001, Hibbett & Thorn 2001, Binder & Hibbett 2002, Hibbett & Binder 2002). The internal structure of order *Agaricales* was addressed explicitly at first employing sequences of nuclear rDNA, typically the 28S or large subunit (nrLSU), which successfully obtained significant support for multiple clades inside *Agaricales*, helping to delimit the phylogenetic concept of classical families (Moncalvo et al. 2000, 2002, Bodensteiner et al. 2004, Binder et al. 2005, 2006, Walther et al. 2005). Moncalvo et al. (2002) presented phylogenetic analyses of *Agaricales*, resolving 117 clades. Then, significant research of the first multilocus phylogeny was carried out in the order *Agaricales*, which found six clades as agaricoid, marasmioid, hygrophoroid, pluteoid, plicaturopsidoid, and tricholomatoid (Matheny et al. 2006), which allowed for producing a seminal reconstruction of the structure of *Agaricales*, obtaining statistical support for multiple major clades (now suborders). The analysis of additional information, obtained from nrLSU, SSU, *rpb*1, *rpb*2, and *tef1*-α sequences, revealed some changes to the previous results (in the positions of *Pluteus* and *Amanita*), but the new dataset also included a different selection of taxa (Matheny et al. 2007). The phylogenies in Zhao et al. (2017) and He et al. (2019) used even larger datasets containing all lineages of *Basidiomycotina*, in which both studies failed to obtain significant support for most suborders and families of *Agaricales*. The most recent compilation of names of *Agaricales* in a phylogenetic context was made by Kalichman et al. (2020). Based on the six-gene phylogenetic analyses of typhuloid taxa in *Agaricales*, Olariaga et al. (2020) introduced the new family *Phyllotopsidaceae* with the type genus *Phyllotopsis* and two other genera, *Macrotyphula* and *Pleurocybella*. The new families *Clitocybaceae* and *Omphalinaceae* (*Agaricales*) were established based on the molecular analyses (Vizzini et al. 2020). *Asproinocybaceae* was established by Mou & Bau (2021) to accommodate the genera *Asproinocybe* and *Tricholosporum*. A later study proposed *Phyllotopsidaceae* as a new suborder *Phyllotopsidineae* based on phylogenomic analyses of *Agaricales*, which found that *Macrotyphula* did not belong in *Phyllotopsidaceae* (Wang et al. 2023b). Recently, Vizzini et al. (2024) presented the systematic reorganization and classification of incertae sedis clitocyboid, pleurotoid, and tricholomatoid taxa based on an updated 6-gene phylogeny in the order *Agaricales*, in which they proposed a new suborder, *Typhulineae*, and six new families: *Aphroditeolaceae*, *Melanoleucaceae*, *Paralepistaceae*, *Pseudoomphalinaceae*, *Volvariellaceae*, and *Xeromphalinaceae*.

Basidiomata morphologies show a great diversity in the *Basidiomycota*, from naked lawns of basidia, to smooth, poroid, irpicoid, grandinoid, odontioid, hydnoid, tuberculate, floccose, coralloid, or highly complex, or the so-called pileate-stipitate basidiomata of well-known agarics (Nagy et al. 2023). Recent research on *Agaricomycetes* basidiomata morphogenesis has largely relied on comparative-omics techniques, which provided insights into the gene repertoire and the regulation of gene expression during basidiomata development (Royse et al. 2017). Research on basidiomata types has made significant progress in the fields of evolutionary and developmental biology, and phylogenetic studies have revealed trends in the evolution of morphologies. Meanwhile, developmental and genetic studies have identified several key genes underlying basidiomata development (Virágh et al. 2022). Despite considerable efforts in this area, the morphogenesis of *Basidiomycota* basidiomata remains poorly understood (Varga et al. 2019). One of the grand challenges of mycology is to understand how the diversity of basidiomata has evolved (Virágh et al. 2022). In recent years, mycologists have been interested in the evolution of basidiomata complexity, a topic that has garnered considerable attention (Nagy et al. 2023).

During investigations on wood-inhabiting fungi in southwestern China. We identified a genus and eleven species of the order *Agaricales* with diverse basidiomata morphologies that could not be assigned to any previously described genus or species. To clarify the placement and relationships of these genera and species, we carried out a phylogenetic and taxonomic study on the order *Agaricales* based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequences and ITS+nrLSU sequences. We present the morphological and molecular phylogenetic evidence that supports the 12 taxa are located in the order *Agaricales*.

MATERIALS AND METHODS

Sample collection and herbarium specimen preparation

Fresh basidiomata of the fungi growing on angiosperm branches were collected from Dali, Dehong, Diqing, and Zhaotong of Yunnan Province, China. The samples were photographed in situ, and detailed collection information was recorded (Rathnayaka et al. 2024). Fresh macroscopic details were also recorded in the field. Photographs were taken by a Jianeng 80D camera (Tokyo, Japan). All of the photos were focus stacked and merged using Helicon Focus Pro 7.7.5 software. Macroscopic details were recorded and transported to a field station where the fresh basidiomata were dried on an electronic food dryer at 40°C (Hu et al. 2022, Dong et al. 2024). Once dried, the specimens were sealed in an envelope and zip-lock plastic bags and labelled (Cui et al. 2019). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphological studies

The macro-morphological descriptions were based on field notes and photos captured in the field and lab. Petersen (1996) was followed for the colour terminology. The micro-morphological data were obtained from dried specimens observed under a light microscope with a magnification of 1000× oil (Zhao et al. 2023a, Dong et al. 2024). Sections were mounted in 5% KOH, 1% Congo Red solution, and 1% phloxine B ($C_{20}H_2Br_4C_{l4}Na_2O_5$), and we also used other reagents, including Cotton Blue and Melzer's reagent, to observe micromorphology following the method of Wu et al. (2022b). To show the variation in spore sizes, 5% of measurements were excluded from each end of the range and shown in parentheses. At least thirty basidiospores from each specimen were measured. Stalks were excluded from basidia measurements, and the hilar appendage was excluded from basidiospores measurements. The MycoBank number will be registered in the MycoBank database (http://www.mycobank.org).

The following abbreviations are used:
CB = Cotton Blue
CB+ = cyanophilous
CB– = acyanophilous
IKI = Melzer's reagent
IKI– = both inamyloid and non-dextrinoid
KOH = 5% potassium hydroxide water solution
L = mean spore length (arithmetic average for all spores)
W = mean spore width (arithmetic average for all spores)
n = a/b (number of spores (a) measured from the given number (b) of specimens)
Q = variation in the L/W ratios between the specimens studied
Q_m = represented the average Q of basidiospores measured ± standard deviation

Molecular procedures and phylogenetic analyses

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions. The gene fragments employed in this study are detailed in Table 2.

Table 2 A list of genes, primers, and sequences used in this study.

Fragment of amplification	Name of primer	Primer base sequence (5′-3′) b	References
ITS	ITS5	GGA AGT AAA AGT CGT AAC AAG G	White et al. (1990)
	ITS4	TCC TCC GCT TAT TGA TAT GC	
nrLSU	LR0R	ACC CGC TGA ACT TAA GC	Vilgalys & Hester (1990)
	LR7	TAC TAC CAC CAA GAT CT	Rehner & Samuels (1994)

Fragment of amplification	Name of primer	Primer base sequence (5′-3′) b	References
*tef*1-α	EF1-983F EF1-2218R	GCY CCY GGH CAY CGT GAY TTY AT ATG ACA CCR ACR GCR ACR GTY TG	Rehner & Buckley (2005)
*rpb*1	RPB1-Af RPB1-Cf	GAR TGY CCD GGD CAY TTY GG CCN GCD ATN TCR TTR TCC ATR TA	Matheny et al. (2002)
*rpb*2	bRPB2-6F bRPB2-7.1R	TGG GGY ATG GTN TGY CCY GC CCC ATR GCY TGY TTM CCC ATD GC	Matheny (2005)

[b] Degenerate base: R = A or G, Y = C or T, N = A or T or C or G, D = G or A or T, M = A or C, V = G or A. ITS, internal transcribed spacer region; nrLSU, the large nuclear ribosomal RNA subunit; *rpb*1, the largest subunit of RNA polymerase II; *rpb*2, the second subunit of RNA polymerase II; *tef*1-α, the translation elongation factor 1-a.

The PCR protocol for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, and 58 °C for 40 s. The PCR protocol for nrLSU and *tef*1-α was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for nrLSU and 59 °C for *tef*1-α for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR procedure for *rpb*1 was 94 °C for 2 min, followed by 10 cycles at 94 °C for 40 s, 60 °C for 40 s and 72 °C for 2 min, then followed by 37 cycles at 94 °C for 45 s, 55 °C for 1.5 min and 72 °C for 2 min, and a final extension of 72 °C for 10 min. The PCR procedure for *rpb*2 was 95 °C for 2.5 min, followed by 40 cycles at 95 °C for 30 s, 52 °C for 1 min, and 72 °C for 1 min, then followed by 40 cycles at 72 °C for 1.5 min, and final extension of 72 °C for 5 min (Dong et al. 2024). The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, Yunnan Province, P.R. China. All newly generated sequences were deposited in GenBank (Table 3).

Phylogenetic analyses followed the methods in Dissanayake et al. (2020). Newly generated sequence data were initially subjected to a BLAST search in NCBI to obtain the most probable closely related taxa in the GenBank (http://blast.ncbi.nlm.nih.gov/). Sequence data were retrieved from GenBank based on recent publications (https://www.ncbi.nlm.nih.gov/nuccore/). The sequences were aligned using MAFFT version 7 (Katoh et al. 2019) with the G-INS-I strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was initially aligned and later, ITS, nrLSU, *rpb*1, *rpb*2, and *tef*1-α sequences were combined using Mesquite version 3.51. FASTA data file formats were converted to PHYLIP and NEXUS formats using the online tool available on the ALTER website (http://sing.ei.uvigo.es/ALTER/, Glez-Peña et al. 2010). Phylogenetic trees were constructed based on randomized accelerated Maximum Likelihood (ML) and Bayesian Inference (BI) analyses.

Maximum Likelihood (ML) analysis was performed using the CIPRES Science Gateway (https://www.phylo.org/portal2/login!input.action, Miller et al. 2012) based on the dataset using the RA × ML-HPC BlackBox tool, with setting RA × ML halt bootstrapping automatically and 0.25 for maximum hours and obtaining the best tree using ML search. Other parameters in ML analysis used default settings, and statistical support values were obtained using nonparametric bootstrapping with 1,000 replicates. Bayesian inference (BI) analysis was performed on the dataset using MrBayes v3.2.7a (Ronquist et al. 2012). The best substitution model for the dataset was selected by ModelFinder v2.2.0 (Kalyaanamoorthy et al. 2017) using a Bayesian Information criterion, and the model was used for Bayesian analysis. Four Markov chains were run from random starting trees. Trees were sampled every 1,000th generation. The first 25% of sampled trees were discarded as burn-in, while the remaining trees were used to construct a 50% majority consensus tree and to calculate Bayesian posterior probabilities (BPPs).

Table 3 List of species, specimens, and GenBank accession numbers of sequences used in this study. * refers to type material, holotype; — refers to the data unavailability.

Species Name	**Sample No.**	**GenBank Accession No.**					**Country**	**References**
		ITS	**nrLSU**	***rpb*1**	***rpb*2**	***tef*1-α**		
Acanthocorticium brueggemannii	JMB2122	KT275193	KT275195	—	—	—	Brazil	Baltazar et al. (2015)
Akenomyces costatus	CBS:513.83	MH861635	MH873350	—	—	—	Netherlands	Vu et al. (2019)
Amanita brunnnescens	AFTOL-ID 673	AY789079	AY631902	AY788847	AY780936	AY881021	USA	Matheny et al. (2006)
Amanita subglobosa	HKAS:58837	JN943177	JN941152	JN994123	JQ031121	KJ482004	China	Vizzini et al. (2024)
Amylocorticium cebennense	CFMR: HHB-2808	GU187505	GU187561	—	GU187770	GU187675	USA	Vizzini et al. (2024)
Anthracophyllum archeri	AFTOL-ID 973	DQ404387	AY745709	DQ435799	DQ404387	DQ028586	USA	Matheny et al. (2006)
Anthracophyllum lateritium	TENN62043	FJ596892	—	—	—	—	USA	Hughes et al. (2009)
Aphanobasidium pseudotsugae	HHB-822	GU187509	GU187567	—	—	—	USA	Larsson (2007)
Aphanobasidium pseudotsugae	UC 2023153	KP814353	AY586696	GU187455	GU187781	GU187695	Sweden	Larsson (2007)
Apioperdon pyriforme	AFTOL-ID 480	AY854075	AF287873	AY860523	AY218495	AY883426	USA	Vizzini et al. (2024)
Asterophora lycoperdoides	CBS170.86	AF357037	AF223190	EF421021	DQ367431	DQ367424	Switzerland	Matheny et al. (2006)
Bolbitius vitellinus	AFTOL-ID 730	DQ200920	AY691807	DQ435802	DQ385878	DQ408148	USA	Matheny et al. (2006)
Camarophyllopsis	AFTOL-ID 1892	DQ4840	DQ4576	DQ5160	DQ4727	—	USA	Matheny et al. (2006)

Species Name	**Sample No.**	**GenBank Accession No.**					**Country**	**References**
		ITS	**nrLSU**	***rpb*1**	***rpb*2**	***tef*1-α**		
hymenocephala		66	79	70	26			
Campanella alba	BDC iNaturalist # 190272171	PQ498227	PQ498227	—	—	—	USA	Unpublished
Campanella alba	BDC iNaturalist # 190272171	PQ498227	PQ498227	—	—	—	USA	Unpublished
Campanella alba	BDC iNaturalist # 192505836	PQ498141	PQ498141	—	—	—	USA	Unpublished
Campanella buettneri	SFSU DED8276	NR_198033	NR_198033	—	—	—	USA	Desjardin & Perry (2017)
Campanella buettneri	DED 8276 (SFSU)	MF075136	MF075138	—	—	—	USA	Desjardin & Perry (2017)
Campanella burkei	SFSU: BAP 632	MF100970	—	—	—	—	USA	Desjardin & Perry (2017)
Campanella candida	PDD 102184	OQ282823	—	—	—	—	New Zealand	Unpublished
Campanella keralensis	AF 342	MW462889	—	—	—	—	India	Desjardin & Perry (2017)
Campanella pustulata	SMF2382	JX444164	—	—	—	—	Australia	Unpublished
Campanella pustulata	AQ793972	JX444168	—	—	—	—	Australia	Unpublished
Campanella simulans	AF 129	MW506836	—	—	—	—	India	Unpublished
Campanella subdendrophora	ATCC 42449	AY445121	AY445115	—	—	—	Sweden	Matheny et al. (2006)
Campanella tristis	JAC17081	PP407516	PP407538	—	—	—	New Zealand	Unpublished

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
Campanella tristis	PDD_88322	PP407517	—	—	—	—	New Zealand	Unpublished
Campanella yunnanensis	**CLZhao 33866 ***	**PV197911**	—	—	—	—	**China**	**Present study**
Campanella yunnanensis	**CLZhao 33868**	**PV197912**	—	**PV247734**	—	—	**China**	**Present study**
Catathelasma ventricosum	DAOM:225247	MN017537	MN017477	KP255480	MN018851	MN026906	Spain	Vizzini et al. (2024)
Chaetocalathus cocciformis	JAC12666	OQ282795	OQ282751	—	—	—	New Zealand	Matheny et al. (2006)
Chaetocalathus liliputianus	MCA485	AY916682	AY916680	AY916683	—	—	USA	Matheny et al. (2006)
Chaetocalathus liliputianus	MCA485	AY916682	AY916680	AY916683	—	—	USA	Matheny et al. (2006)
Cheimonophyllum candidissimum	AFTOL-ID 1765	DQ486687	DQ457654	DQ447888	DQ470831	GU187760	USA	Matheny et al. (2006)
Chondrostereum purpureum	AFTOL-ID 441	DQ200929	AF518607	—	AY218477	DQ457632	USA	Matheny et al. (2006)
Chromocyphella lamellata	AH 45802	MF623832	MF623831	MF652060	MF623837	MF948155	Spain	Moreno et al. (2017)
Chromocyphella meloana	LIP GG-201018-003	ON059375	ON059179	—	ON055277	ON055276	Spain	Gruhn et al. (2023)
Chromocyphella muscicola	ARAN-Fungi 3324	MF623834	MF623834	MF652062	—	MF948157	Spain	Moreno et al. (2017)
Clavaria zollingeri	AFTOL-ID 563	AY854071	AY639882	AH014578	AY780940	AY881024	USA	Matheny et al. (2006)
Clavulinopsis laeticolor	AFTOL-ID 984	DQ2022	AY7456	DQ4478	DQ3858	DQ0291	USA	Matheny et al. (2006)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
		67	93	90	80	98		
Collybiopsis albobasidiosa	**CLZhao 30216 ***	**PV197913**	**PV197933**	—	**PV247742**	—	**China**	**Present study**
Collybiopsis albobasidiosa	**CLZhao 30756**	**PV197914**	**PV197934**	—	**PV247743**	**PV231416**	**China**	**Present study**
Collybiopsis biformis	TENN 65189	KJ416249	KJ189569	—	—	—	USA	Petersen & Hughes (2014)
Collybiopsis brunneigracilis	AWW01-SFSU	AY639412	—	—	—	—	Indonesia	Wilson et al. (2004)
Collybiopsis californica	TENN-F-052617	MN413338	—	—	—	—	Canada	Phonrob et al. (2024)
Collybiopsis complicata	TENN-F-065811	OR500517	OR500517	—	—	—	USA	Petersen & Hughes (2024a)
Collybiopsis confluens	TENN-F-067864	KP710296	KJ189573	—	—	—	Germany	Petersen & Hughes (2016)
Collybiopsis cremea	**CLZhao 29915 ***	**PV197915**	**PV197935**	—	**PV247744**	—	**China**	**Present study**
Collybiopsis cremea	**CLZhao 29941**	**PV197916**	**PV197936**	—	**PV247745**	—	**China**	**Present study**
Collybiopsis cremea	**CLZhao 30022**	—	**PV197937**	—	**PV247746**	—	**China**	**Present study**
Collybiopsis dichroa	TENN-F-065569	MW396867	MW396867	—	—	—	USA	Petersen & Hughes (2021)
Collybiopsis disjuncta	TENN-F-069172	KJ416252	PP430330	—	—	—	USA	Petersen & Hughes (2014)
Collybiopsis enificola	TENN-F-069123	NR_137613	NG_059502	—	—	—	Canada	Petersen et al. (2014)

Species Name	**Sample No.**	**GenBank Accession No.**					**Country**	**References**
		ITS	**nrLSU**	***rpb*1**	***rpb*2**	***tef*1-α**		
Collybiopsis filamentipes	TENN-F-065861	MN897832	MN897832	—	—	—	USA	Petersen & Hughes (2021)
Collybiopsis furtiva	SFSU DED4425	DQ450031	AF042650	—	—	—	USA	Mata et al. (2007)
Collybiopsis gibbosa	URM 90012	KY061202	KY061202	—	—	—	Brazil	Phonrob et al. (2024)
Collybiopsis hasanskyensis	TENN-F-060730	MN897829	—	—	—	—	Russia	Petersen & Hughes (2021)
Collybiopsis indocta	TENN-F-054944	MW396870	MW396870	—	—	—	Argentina	Petersen & Hughes (2021)
Collybiopsis juniperin	TENN-F-058988	KY026661	KY026661	—	—	—	Argentina	Petersen & Hughes (2016)
Collybiopsis luxurians	TENN-F-050619	KJ416240	PP430331	—	—	—	Switzerland	Petersen & Hughes (2014)
Collybiopsis melanopus	SFSU: A.W. Wilson 54	NR_137539	NG_060624	—	—	—	Indonesia	Wilson et al. (2004)
Collybiopsis menehune	SFSU: DED5866	AY263426	—	—	—	—	Indonesia	Wilson et al. (2004)
Collybiopsis mesoamericana	TENN 058613	NR_119583	KY019632	—	—	—	Costa Rica	Schoch et al. (2014)
Collybiopsis minor	TENN-F-059993	MN413334	MW396880	—	—	—	USA	Petersen & Hughes (2021)
Collybiopsis minor	TENN-F-059993	MN413334	MW396880	—	—	—	USA	Mata et al. (2007)
Collybiopsis neotropica	TENN-F-058113	AF505769	—	—	—	—	Costa Rica	Phonrob et al. (2024)
Collybiopsis nonnulla	TENN-F-069193	MW396	MW3968	—	—	—	USA	Petersen & Hughes

Species Name	**Sample No.**	**GenBank Accession No.**					**Country**	**References**
		ITS	**nrLSU**	***rpb*1**	***rpb*2**	***tef*1-α**		
		873	73					(2021)
Collybiopsis parvula	TENN-F-058113	NR_119584	—	—	—	—	Costa Rica	Schoch et al. (2014)
Collybiopsis peronata	TENN-F-069322	KY026738	KY026738	—	—	—	USA	Petersen & Hughes (2016)
Collybiopsis polygramma	MHHNU 30912	MK214392	—	—	—	—	China	Unpublished
Collybiopsis quercophilia	TENN-F-069321	KY026737	KY026737	—	—	—	USA	Petersen & Hughes (2016)
Collybiopsis ramealis	TENN-F-069251	MW405779	MW396884	—	—	—	Slovakia	Petersen & Hughes (2021)
Collybiopsis readiae	TENN-F-053687	DQ450034	—	—	—	—	New Zealand	Mata et al. (2007)
Collybiopsis stenophylla	TENN-F-065943	MN413331	MW396886	—	—	—	USA	Zhang et al. (2023c)
Collybiopsis stenophyllus	TENN 59444	DQ450032	—	—	—	—	USA	Mata et al. (2007)
Collybiopsis subcyathiformis	URM90023	KY404982	KY404982	—	—	—	Brazil	Zhang et al. (2023c)
Collybiopsis subnuda	WRW08-462	KY026765	KY026765	—	—	—	USA	Petersen & Hughes (2016)
Collybiopsis trogioides	AWW51-SFSU	NR_152884	NG_228715	—	—	—	Indonesia	Petersen & Hughes (2024a)
Collybiopsis vaillantii	TENN-F-065115	KY026676	KY026676	—	—	—	USA	Petersen & Hughes (2016)
Collybiopsis villosipes	TENN-F-056252	DQ450058	—	—	—	—	USA	Mata et al. (2007)

Species Name	**Sample No.**	**GenBank Accession No.**					**Country**	**References**
		ITS	**nrLSU**	***rpb*1**	***rpb*2**	***tef*1-α**		
Collybiopsis villosipes	TENN-F-060951	KJ416255	FJ750264	—	—	—	New Zealand	Petersen & Hughes (2014)
Collybiopsis yunnanensis	**CLZhao 22508**	**PV197917**	**PV197938**				**China**	**Present study**
Collybiopsis yunnanensis	**CLZhao 22546 ***	**PV197918**	—	—	—	—	**China**	**Present study**
Collybiopsis yunnanensis	**CLZhao 22558**	**PV197919**	**PV197939**	—	**PV247747**	—	**China**	**Present study**
Collybiopsis yunnanensis	**CLZhao 22565**	**PV197920**	—	—	—	—	**China**	**Present study**
Coniolepiota spongodes	PNG012	HM488756	HM488774	—	HM488796	HM488883	USA	Vellinga et al. (2011)
Cortinarius aurilicis	TSJ1998-101	DQ083772	AY684152	DQ083826	DQ083880	—	Denmark	Frøslev et al. (2005)
Cortinarius iodes	IB19850061	AF389133	AY702013	AY857984	AY536285	—	USA	Matheny et al. (2006)
Cortinarius sodagnitus	TF2001-094	DQ083812	AY684151	DQ083867	DQ083920	—	Denmark	Matheny et al. (2006)
Cortinarius violaceus	AFTOL-ID 814	DQ486695	DQ457662	DQ447894	DQ470835	—	USA	Matheny et al. (2006)
Crepidotus applanatus	AFTOL-ID 817	DQ202273	AY380406	AY333303	AY333311	—	USA	Matheny et al. (2006)
Crinipellis birhizomorpha	BRNM751593	KF380831	KF380835	—	—	—	Korea	Antonín et al. (2014)
Crinipellis setipes	Bandala4031	JF930641	JF930642	—	—	—	Mexico	Antonín et al. (2014)
Crinipellis zonata	OKM 25450	AY9166	AY9166	AY9166		AY9166	USA	Aime et al. (2005)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
		92	90	93		94		
Crustomyces albidus	He 6164	ON117191	ON117175	—	—		China	Li et al. (2022)
Crustomyces pini-canadensis	HHB-11308	OP935222	OP995715	—	—	OP999050	USA	Paez et al. 2024
Dendrothele fissurata	**CLZhao 35015 ***	**PV197921**	—	—	—	—	**China**	**Present study**
Dendrothele griseocana	CBS:340.66	MH858816	—	—	—	—	Netherlands	Vu et al. (2019)
Dendrothele yunnanensis	CLZhao 17814	OR094484	OR449910	—	—	—	China	Dong et al. (2024)
Digitatispora marina	3027C	KM272371	KM272362	—	—	—	Norway	Silva-Filho et al. (2023)
Flagelloscypha japonica	NBRC 101830	LC146734	AB455964	—	—	—	Japan	Silva-Filho et al. (2023)
Flagelloscypha minutissima	CBS 823.88	AY571040	AY571006	—	—	—	USA	Silva-Filho et al. (2023)
Flammulina velutipes	AFTOL-ID 558	AY854073	AY639883	AY858966	AY786055	AY883423	USA	Matheny et al. (2006)
Gracilihypha abeliae	CLZhao 21445	PP819705	PP826257	—	—	—	China	Yang et al. (2025)
Gracilihypha abeliae	CLZhao 21485	PP819706	PP826258	—	—	—	China	Yang et al. (2025)
Gracilihypha albohymenia	**CLZhao 29603**	**PV197924**	—	**PV247738**	**PV247750**	—	**China**	**Present study**
Gracilihypha albohymenia	**CLZhao 31757**	**PV197925**	—	—	**PV368945**	—	**China**	**Present study**

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
Gracilihypha albohymenia	**CLZhao 32417**	**PV197926**	—	—	**PV368946**	**PV231420**	**China**	**Present study**
Gracilihypha albohymenia	**CLZhao 33069 ***	**PV197927**	—	**PV247739**	**PV368947**	—	**China**	**Present study**
Gracilihypha albohymenia	**CLZhao 33502**	**PV197928**	—	**PV247740**	**PV368948**	**PV231421**	**China**	**Present study**
Gracilihypha yunnanensis	**CLZhao 32826 ***	**PV197929**	**PV197943**	—	**PV368949**	—	**China**	**Present study**
Gymnopilus sapineus	PBM 1541 (WTU)	AF501560	AY380362	AY351789	AY337358	—	Australia	Matheny et al. (2006)
Gymnopus bicolor	AWW116	AY263423	AY639411	—	—	—	USA	Wilson et al. (2004)
Gymnopus dryophilus	AFTOL-ID 559	DQ241781	AY640619	DQ447903	DQ472717	DQ408152	USA	Matheny et al. (2006)
Gymnopus globulosus	HMJAU60307	OM030269	OM033406	—	—	—	China	Hu et al. (2022)
Gymnopus tiliicola	HMJAU60305	OM030276	OM033393	—	—	—	China	Hu et al. (2022)
Hebeloma velutipes	AFTOL-ID 980	AY818351	AY745703	DQ447904	DQ472718	GU187707	USA	Matheny et al. (2006)
Hohenbuehelia atrocoerulea	AMB:18080	KU355304	KU355389	—	KU355418	KU355439	Italy	Vizzini et al. (2024)
Hohenbuehelia faerberioides	Mertens	MG553638	MG553645	—	MW240980	MW240984	Spain	Vizzini et al. (2024)
Hohenbuehelia tremula	DAOM:180808	KU355357	KU355405	OR828361	KU355434	KU355465	Italy	Vizzini et al. (2024)
Hydnangium carneum	Trappe31123	KU6857	KU6858	—	KU6860	KU6861	USA	Vizzini et al. (2024)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
		41	92		38	44		
Laccaria ochropurpurea	AFTOL-ID 477	AF006598	AY700200	—	DQ472731	—	USA	Matheny et al. (2006)
Lachnella alboviolascens	PB332	AY571048	AY571012	—	—	—	USA	Silva-Filho et al. (2023)
Lachnella alboviolascens	Wu724	OR990018	—	—	—	—	China	Silva-Filho et al. (2023)
Lacrymaria velutina	AFTOL-ID 478	DQ490639	AY700198	—	DQ472733	—	USA	Matheny et al. (2006)
Lentinula edodes	OE-9	AY636053	AF261557	—	—	—	USA	Moncalvo et al. (2002)
Lentinula guzmanii	TENN 55247	NR_186965	—	—	—	—	USA	Unpublished
Limnoperdon incarnatum	IFO:30398	DQ097363	AF426958	—	—	—	USA	Matheny et al. (2006)
Limnoperdon sp.	CBS:160.95	OR863457	OR863524	—	OR828272	OR828327	Spain	Vizzini et al. (2024)
Lyophyllum decastes	JM87/16	AF357059	AF042583	DQ825418	DQ367433	DQ367426	Switzerland	Matheny et al. (2006)
Macrocystidia cucumis	AFTOL-ID 1343	DQ490640	DQ094787	—	—	—	USA	Matheny et al. (2006)
Macrocystidia cucumis	JX.1294733#45	OR863460	OR863527	—	OR828275	OR828330	Spain	Vizzini et al. (2024)
Macrolepiota dolichaula	AFTOL-ID 481	DQ221111	DQ411537	DQ447920	DQ385886	DQ435785	USA	Vizzini et al. (2024)
Macrotyphula phacorrhiza	DSH96-059	AF134710	AF393079	—	AY218525	—	Canada	Matheny et al. (2006)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
Macrotyphula juncea	IO.14.177	MT232353	MT232306	—	MT242337	MT242355	Spain	Vizzini et al. (2024)
Macrotyphula phacorrhiza	S:IO.14.200	MT232363	MT232314	—	—	MT242366	Spain	Vizzini et al. (2024)
Maireina filipendula	TL14226	KX772745	KX772745	—	—	—	Norway	Silva-Filho et al. (2023)
Maireina filipendula	TL2015-724890	KX772746	KX772746	—	—	—	Norway	Silva-Filho et al. (2023)
Maireina monacha	AM2106285	OP099548	OR197581	—	—	—	France	Mombert (2022)
Maireina subsphaerospora	AM2012151	OR234754	OR197582	—	—	—	Spain	Mombert (2022)
Maireina subsphaerospora	AM2004282	OP099549	OR234751	—	—	—	France	Mombert (2022)
Marasmius acerosus	TYS458	OR636634	OR656952	—	—	—	Canada	Oliveira et al. (2024)
Marasmius albopurpureus	N.K.Zeng 2253	MT822924	MT829107	—	—	—	China	Unpublished
Marasmius atrorubens	JO528	KP635207	KP635160	—	OR896447	PP026150	Brazil	Oliveira et al. (2024)
Marasmius bellus	JO299	KP635208	KP635161	—	OR896483	PP026086	Brazil	Oliveira et al. (2024)
Marasmius oreades	ZRL2015086	LT716048	KY418864	KY418972	KY419010	KY419066	China	Oliveira et al. (2024)
Marasmius oreades	AFTOL-ID 1559	DQ490641	DQ156126	DQ447921	—	—	USA	Matheny et al. (2006)
Marasmius pulcherripes	BRNM 714692	FJ91761	FJ91760	—	—	—	Korea	Antonín et al. (2012)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
		5	0					
Marasmius wumengshanensis	**CLZhao 32014 ***	**PV197930**	**PV197944**	—	—	—	**China**	**Present study**
Merismodes anomala	PB318	AY571035	AY570998	—	—	—	USA	Silva-Filho et al. (2023)
Merismodes anomala	PB323	AY571036	AY570999	—	—	—	USA	Silva-Filho et al. (2023)
Merismodes fasciculata	HHB-11894	AY571051	AY571015	—	—	—	USA	Silva-Filho et al. (2023)
Merismodes fasciculata	PB342	AY571052	AY571016	—	—	—	USA	Silva-Filho et al. (2023)
Moniliophthora aurantiaca	UTC 253824	JN692482	JN692483	—	—	—	USA	Antonín et al. (2014)
Moniliophthora perniciosa	DIS71	AY317136	AY916738	AY916740	—	AY916741	Brazil	Matheny et al. (2006)
Moniliophthora roreri	C21	AY916746	AY916744	—	—	—	USA	Antonín et al. (2014)
Mycena amabilissima	AFTOL-ID 1686	DQ490644	DQ457691	DQ447926	DQ474121	GU187727	USA	Matheny et al. (2006)
Mycena aurantiidisca	AFTOL-ID 1685	DQ490646	DQ470811	DQ447927	DQ474122	GU187728	USA	Matheny et al. (2006)
Mycetinis alliaceus	AFTOL-ID 556	AY854076	AY635776	—	—	—	USA	Matheny et al. (2006)
Mycetinis arbuscularis	HMJAU 60427	PP151533	PP151566	—	—	—	China	Li et al. (2024)
Mycetinis rufodiscus	HMJAU 60430	PP151522	PP639543	—	—	—	China	Li et al. (2024)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
Mythicomyces corneipes	AFTOL-ID 972	DQ404393	AY745707	DQ447929	DQ408110	DQ029197	USA	Matheny et al. (2006)
Naucoria vinicolor	AFTOL-ID 499	DQ536417	DQ536415	DQ536419	DQ536418		USA	Matheny et al. (2006)
Nia furcatipilosa	AH20191108-1	LC769762	LC769818	—	—	—	Japan	Nakagiri et al. (2024)
Nia furcatipilosa	AH20190926-1	LC769760	LC769816	—	—	—	Japan	Nakagiri et al. (2024)
Nia singaporensis	AN-1023	LC769779	—	—	—	—	Japan	Nakagiri et al. (2024)
Nia singaporensis	AN-1026	LC769780	LC769835	—	—	—	Japan	Nakagiri et al. (2024)
Nia sphaerocystis	AN-1851	LC769799	LC769854	—	—	—	Japan	Nakagiri et al. (2024)
Nia sphaerocystis	AH20191004-1	LC769802	LC769857	—	—	—	Japan	Nakagiri et al. (2024)
Nia vibrissa	AN-1825	LC769781	LC769836	—	—	—	Japan	Nakagiri et al. (2024)
Nia vibrissa	AH20190527-3	LC769783	LC769838	—	—	—	Japan	Nakagiri et al. (2024)
Nia vibrissa	AN-1825	LC769781	LC769836	—	—	—	Japan	Nakagiri et al. (2024)
Nia vibrissa	AH20190527-3	LC769783	LC769838	—	—	—	Japan	Nakagiri et al. (2024)
Omphalotus olearius	AFTOL-ID 1718	DQ494681	DQ470816	—	—	—	USA	Matheny et al. (2006)
Omphalotus olivascens	VT455	AF52506	AF26132	—	—	—	Austria	Matheny et al. (2006)

Species Name	**Sample No.**	**GenBank Accession No.**					**Country**	**References**
		ITS	**nrLSU**	***rpb*1**	***rpb*2**	***tef*1-α**		
		3	5					
Ossicaulis lignatilis	D604	DQ825426	AF261396	DQ825420	DQ825410	—	USA	Matheny et al. (2006)
Paragymnopus foliiphilus	TENN-F-68183	KY026705	KY026705	—	—	—	USA	Petersen & Hughes (2016)
Paragymnopus perforans	TENN-F-50319	KY026625	KY026625	—	—	—	Sweden	Petersen & Hughes (2016)
Paragymnopus pinophilus	TENN-F-69207	KY026725	KY026725	—	—	—	USA	Petersen & Hughes (2016)
Parvodontia luteocystidia	FP-102806	OP935224	OP995724	—	—	OP999041	USA	Paez et al. (2024)
Peyronelina glomerulata	NBRC 32867	—	AB455963	—	—	—	Japan	Silva-Filho et al. (2023)
Peyronelina glomerulata	NBRC 104522	—	AB455961	—	—	—	Japan	Silva-Filho et al. (2023)
Pleuroflammula flammea	AFTOL-ID 1381	DQ494685	AF367962	DQ447935	DQ474124	—	USA	Matheny et al. (2006)
Pleurotus dryinus	AMB:18868	OR863471	OR863538	OR828363	OR828286	OR828338	Spain	Vizzini et al. (2024)
Pleurotus fuscosquamulosus	A. Baglivo 13-07-2014	OR863472	—	—	OR828287	OR828339	Spain	Vizzini et al. (2024)
Pleurotus ostreatus	AFTOL-ID 564	AY854077	AY645052	AY862186	AY786062	—	USA	Matheny et al. (2006)
Pluteus romellii	AFTOL-ID 625	AY854065	AY634279	AY862187	AY786063	AY883433	USA	Matheny et al. (2006)
Pluteus variabilicolor	AMB:18872	OR863475	OR863541	OR828365	OR828290	OR828342	Spain	Matheny et al. (2006)

Species Name	**Sample No.**	**GenBank Accession No.**					**Country**	**References**
		ITS	**nrLSU**	***rpb*1**	***rpb*2**	***tef*1-α**		
Pluteus variabilicolor	AMB:18873	OR863476	OR863542	OR828366	OR828291	OR828343	Spain	Matheny et al. (2006)
Porotheleum fimbriatum	AFTOL-ID 1725	DQ490626	DQ457673	DQ447907	DQ472721	—	USA	Vizzini et al. (2024)
Porotheleum omphaliiforme	AMB 18842	OM422773	OM423650	—	—	—	Spain	Consiglio et al. (2021)
Psathyrella candolleana	AFTOL-ID 1507	DQ494689	DQ110874	—	—	—	USA	Matheny et al. (2006)
Pseudomarasmius glabrocystidiatus	BRNM 718676	NR_152899	NG_060647	—	—	—	Korea	Antonín et al. (2014)
Pseudomarasmius glabrocystidiatus	BRNM 718676	NR_152899	NG_060647	—	—	—	Korea	Antonín et al. (2014)
Pseudomarasmius nidus-avis	Bandala4052	MH560579		—	—	—	Mexico	César et al. (2018)
Pulverulina ulmicola	TENN 029208	NR_119887	HQ179668	—	—	—	USA	Consiglio et al. (2021)
Pulverulina ulmicola	TENN 065567	MT237476	MT237446	—	—	—	USA	Consiglio et al. (2021)
Radulomyces confluens	Cui 5977	KU535661	KU535669	—	—	—	China	Zhao et al. (2016)
Radulomyces confluens	He 2224	KU535662	KU535670	—	—	—	China	Zhao et al. (2016)
Radulotubus resupinatus	Cui 8383	KU535660	KU535668	—	—	—	China	Zhao et al. (2016)
Radulotubus resupinatus	Cui 8462	KU535657	KU535665	—	—	—	China	Zhao et al. (2016)
Rectipilus confertus	MO470781	PP83163	PP83789	—	—	—	USA	Unpublished

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
		6	9					
Rectipilus natalensis	PB312/RA	AY571058	AY571021	—	—	—	USA	Bodensteiner et al. (2004)
***Rectipilus* sp.**	**CLZhao 25824 ***	**PV197931**	**PV197945**	**PV247741**	**PV247751**	**PV231422**	**China**	**Present study**
Resupinatus applicatus	AMB:18098	MH137821	MH430596	—	—	MH449588	Spain	Vizzini et al. (2024)
Resupinatus europaeus	AMB:18075	KU355368	KU355409	—	—	KU355468	Italy	Vizzini et al. (2024)
Resupinatus griseopallidus	AMB:18277	MH137823	MH165881	—	—	—	Spain	Vizzini et al. (2024)
Resupinatus kavinae	AMB:19612	OR863477	OR863543	—	OR828293	OR828344	Spain	Vizzini et al. (2024)
Resupinatus niger	AMB:18095	KU355371	KU355413	—	—	KU355470	Italy	Vizzini et al. (2024)
Resupinatus rouxii	Z+ZT:971	MH137828	MH190787	—	—	MH449590	Spain	Vizzini et al. (2024)
Resupinatus striatulus	JA:Cussta8634	MH137829	MH430597	—	—	MH449591	Spain	Vizzini et al. (2024)
Resupinatus tenuis	**CLZhao 34892 ***	**PV197932**	**PV197946**	—	**PV247752**	**PV231423**	**China**	**Present study**
Resupinatus vetlinianus	TENN:F69285	KP026243	KP987309	—	—	—	USA	Vizzini et al. (2024)
Resupinatus yunnanensis	CLZhao 8651	OP901839	OP904197	—	—	—	China	Yang et al. (2023)
Rhodocollybia maculata	BRNM:699408	GU947370	—	—	—	—	Czech Republic	Unpublished

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	*rpb*1	*rpb*2	*tef*1-α		
Rhodocollybia maculata	AFTOL-ID 540	DQ404383	AY639880	—	—	—	USA	Matheny et al. (2006)
Rhodocybe mundula	AFTOL-ID 521	DQ494694	AY700182	DQ447937	DQ474128	—	USA	Matheny et al. (2006)
Rhodophana stangliana	KUN-HKAS:115926	MZ855876	MZ853562	MZ852813	MZ852825	MZ852801	China	Vizzini et al. (2024)
Sarcomyxa baishanzuensis	HKAS126474	OQ274990	OQ286059	—	OQ291100	—	China	Cai et al. (2023)
Sarcomyxa edulis	HKAS118864	OQ274994	OQ286065	—	OQ291106	OQ283017	China	Cai et al. (2023)
Sarcomyxa ochracea	HKAS126476	OQ274996	OQ286062	—	OQ291105	OQ283020	China	Cai et al. (2023)
Sarcomyxa serotina	AFTOL-ID 536	DQ494695	AY691887	DQ447938	DQ859892	GU187754	USA	Matheny et al. (2006)
Schizophyllum commune	DSH96-026	AF249390	AF334751		AY218515	—	USA	Matheny et al. (2006)
Schizophyllum radiatum	AFTOL-ID 516	AY571060	AY571023	DQ447939	DQ484052	—	USA	Matheny et al. (2006)
Sicyoideibasidia bambusicola	**CLZhao 31774 ***	**PV197922**	**PV197940**	**PV247735**	—	**PV231417**	**China**	**Present study**
Sicyoideibasidia bambusicola	**CLZhao 35394**	**PV197923**	**PV197941**	**PV247736**	**PV247748**	**PV231418**	**China**	**Present study**
Sicyoideibasidia punctata	**CLZhao 33271**	**PQ609290**		**PV247737**	—	—	**China**	**Present study**
Sicyoideibasidia punctata	**CLZhao 35563 ***	**PQ609291**	**PV197942**	—	**PV247749**	**PV231419**	**China**	**Present study**
Simocybe serrulata	AFTOL-ID 970	DQ4946	AY7457	DQ4479	DQ4840	GU1877	USA	Matheny et al. (2006)

Species Name	**Sample No.**	**GenBank Accession No.**					**Country**	**References**
		ITS	**nrLSU**	***rpb*1**	***rpb*2**	***tef*1-α**		
		96	06	40	53	55		
Stagnicola perplexa	ALV16926	MK351606	MK353790	—	MK359089	—	Spain	Vizzini et al. (2019a)
Tricholoma aestuans	AFTOL-ID 497	DQ494699	AY700197	—	DQ484055	—	USA	Matheny et al. (2006)
Tricholoma myomyces	KMS589	DQ825428	U76459	DQ842013	DQ367436	—	USA	Matheny et al. (2006)
Tricholomella constricta	HC84/75	DQ825429	AF223188	DQ825422	DQ825412	—	USA	Matheny et al. (2006)
Tubaria confragosa	AFTOL-ID 498	DQ267126	AY700190	DQ447944	DQ408113	—	USA	Matheny et al. (2006)
Typhula gyrans	S:IO.14.103	MT232360	KY224097	MT242323	MT242344	MT242363	Spain	Vizzini et al. (2024)
Typhula incarnata	IO.14.92	MT232362	MT232313	MT242325	MT242346	MT242365	Spain	Vizzini et al. (2024)
Typhula sclerotioides	S:IO.14.22	MT232365	MT232317	MT242327	MT242349	MT242369	Spain	Vizzini et al. (2024)
Woldmaria filicina	MO465010	PP831630	PP837898	—	—	—	USA	Unpublished
Xerophorus dominicanus	127428 (JBSD)	MN017550	MN017489	—	MN018855	MN026913	Spain	Vizzini et al. (2020)
Xerophorus donadinii	18222 (AMB)	MN017551	MN017490	—	—	MN026914	Spain	Vizzini et al. (2020)
Xerophorus olivascens	18226 (AMB)	MN017558	MN017496	—	MN018856	MN026916	Spain	Vizzini et al. (2020)

Phylogenetic trees were visualized and adjusted using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree), and the exports were edited using Adobe Illustrator CS6 software (Adobe Systems, USA). Branches of the consensus tree that received bootstrap support for Maximum Likelihood (ML) equal to or above 70%, and Bayesian Inference (BI) equal to or above 0.95, respectively.

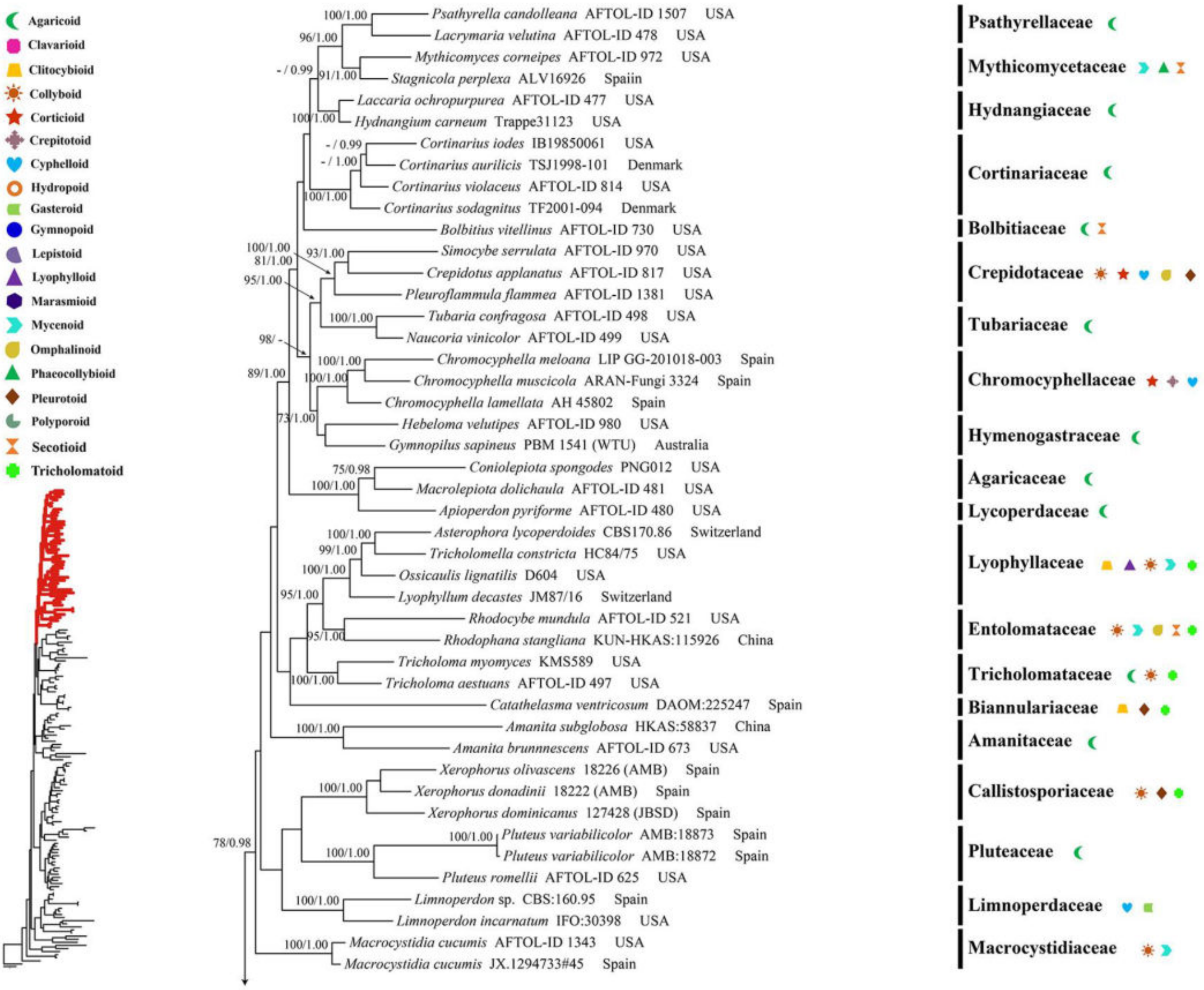

Figure 2 – Maximum likelihood tree illustrating the phylogeny of the wood-decaying fungi within the order *Agaricales* based on the combined ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, and Bayesian posterior probabilities ≥ 0.95, respectively.

RESULTS

Molecular phylogeny

The phylogeny of *Agaricales* based on combined ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2)

The combined ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α dataset (Fig. 2) included sequences from 154 fungal specimens representing 137 species. A total of four Markov chains were run for 2 million generations from random starting trees for eight million generations for the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α dataset, with trees and parameters sampled every 1,000 generations. ModelFinder v2.2.0 (Kalyaanamoorthy et al. 2017) was used to select the best-fit model based on the BIC criterion. The best model for the combined ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α dataset estimated and applied in the Bayesian analysis was GTR+F+I+G4. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies = 0.032530 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 316.5.

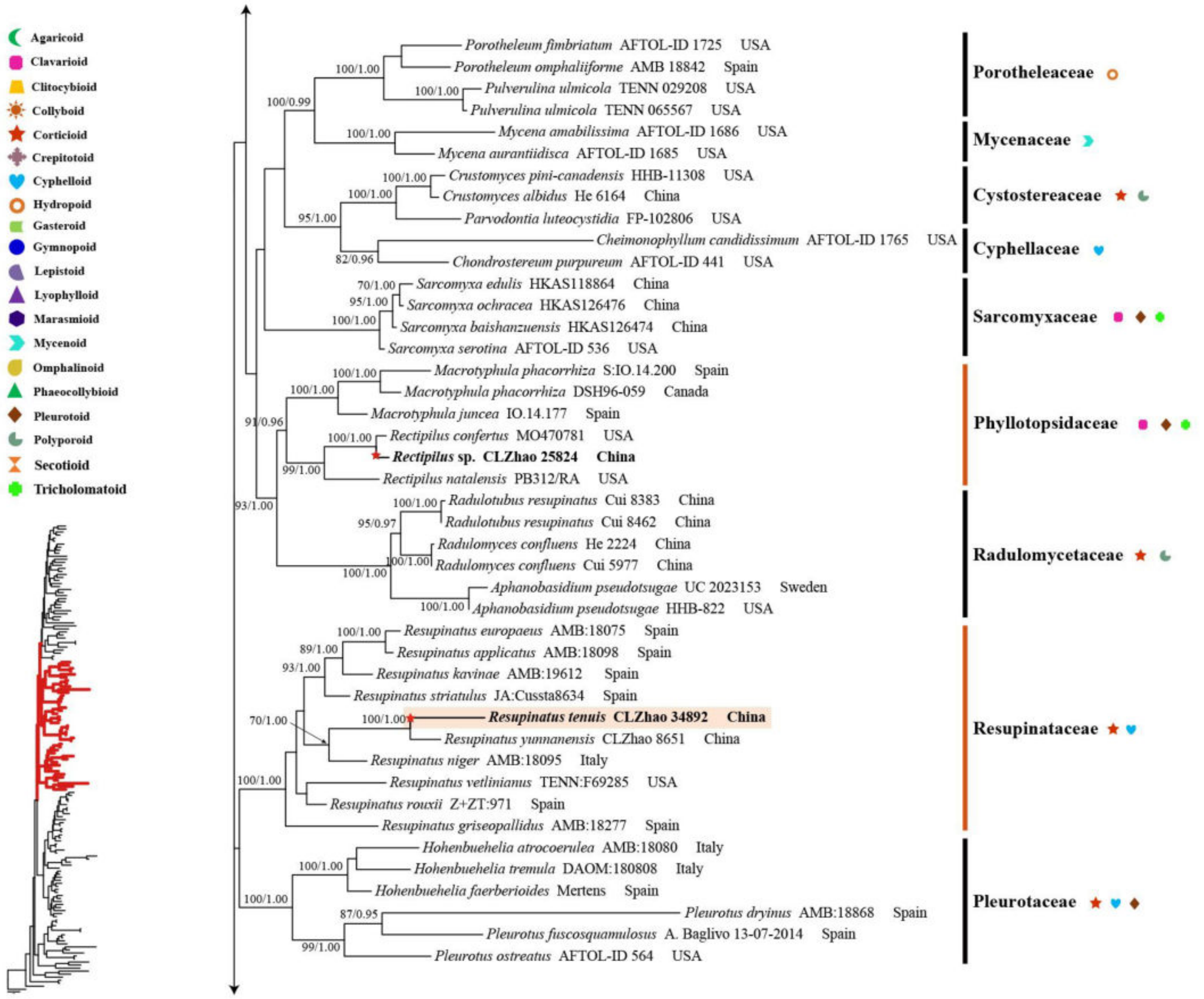

Figure 2 – Continued.

The phylogram, based on the combined ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequences analysis (Fig. 2), showed that the new genus *Sicyoideibasidia*, and eleven new species *Campanella yunnanensis*, *Collybiopsis albobasidiosa*, *Co. cremea*, *Co. yunnanensis*, *Dendrothele fissurata*, *Gracilihypha albohymenia*, *G. yunnanensis*, *Marasmius wumengshanensis*, *Resupinatus tenuis*, *Sicyoideibasidia bambusicola*, and *S. punctata*, were assigned to the families *Campanellaceae, Cyphellopsidaceae, Marasmiaceae, Omphalotaceae* and *Resupinataceae* within the order *Agaricales*. The specimen CLZhao 25824 is sterile; therefore, the lineage represented by it is not included in the subsequent taxonomic result.

The phylogeny of *Campanellaceae* and *Marasmiaceae* based on combined ITS+nrLSU sequence data (Fig. 3)

The combined ITS+nrLSU dataset (Fig. 3) included sequences from 29 fungal specimens representing 24 species. A total of four Markov chains were run for two independent runs from random starting trees, each for one million generations, using the ITS+nrLSU dataset. Trees and parameters were sampled every 1,000 generations. ModelFinder v2.2.0 (Kalyaanamoorthy et al.

2017) was used to select the best-fit model based on the BIC criterion. The best model for the combined ITS+nrLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G+F. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies = 0.017653 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 768.5.

The phylogenetic tree, based on combined ITS+nrLSU sequences (Fig. 3), revealed that the species *Campanella yunnanensis* was assigned to the genus *Campanella* within the family *Campanellaceae*, and *Marasmius wumengshanensis* was assigned to the genus *Marasmius* within the family *Marasmiaceae*. In addition, the taxon *C. yunnanensis* was sister to *C. burkei* Desjardin & B.A. Perry, and *M. wumengshanensis* was a sister to *M. bellus* Morgan ex Bres.

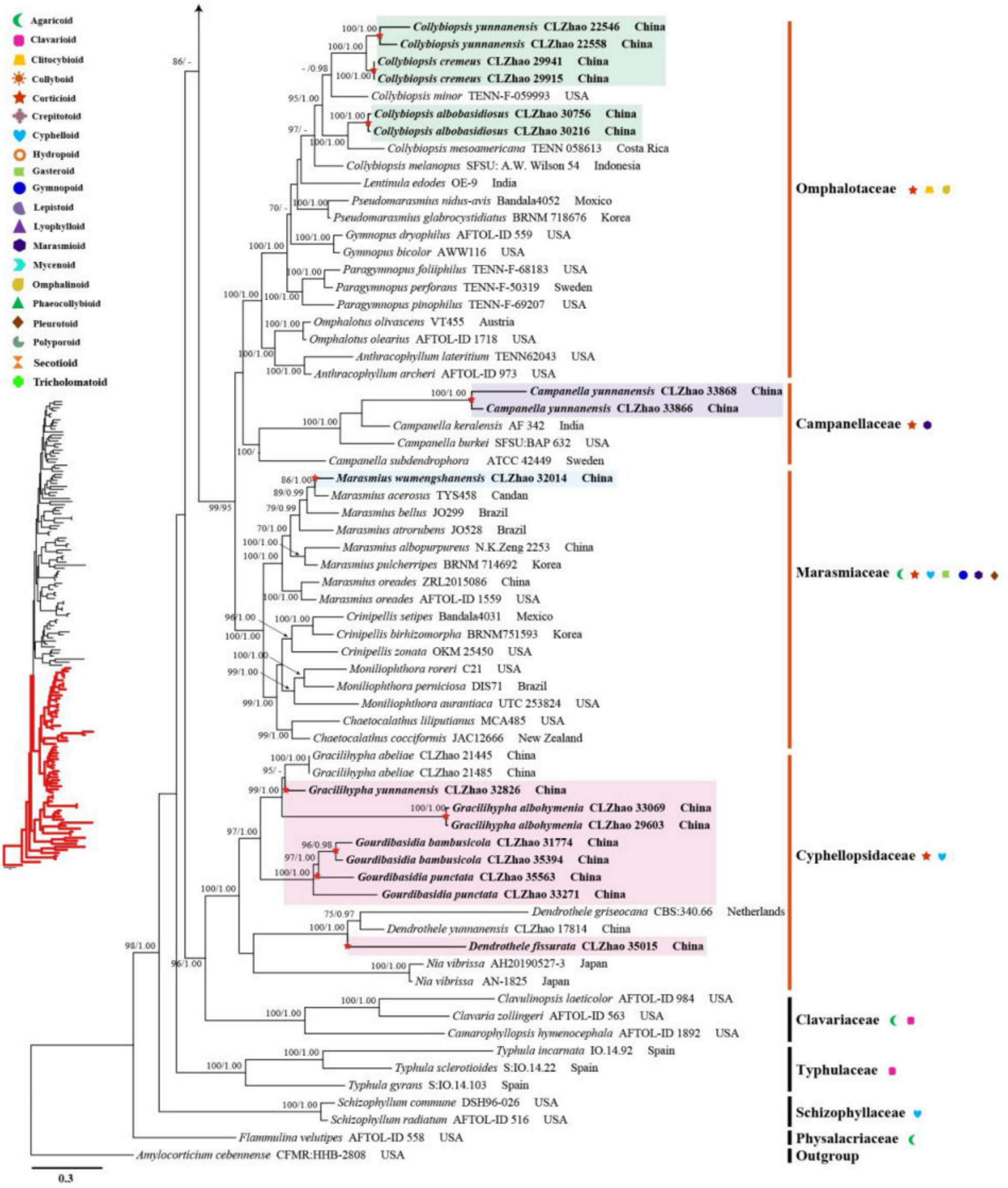

Figure 2 – Continued.

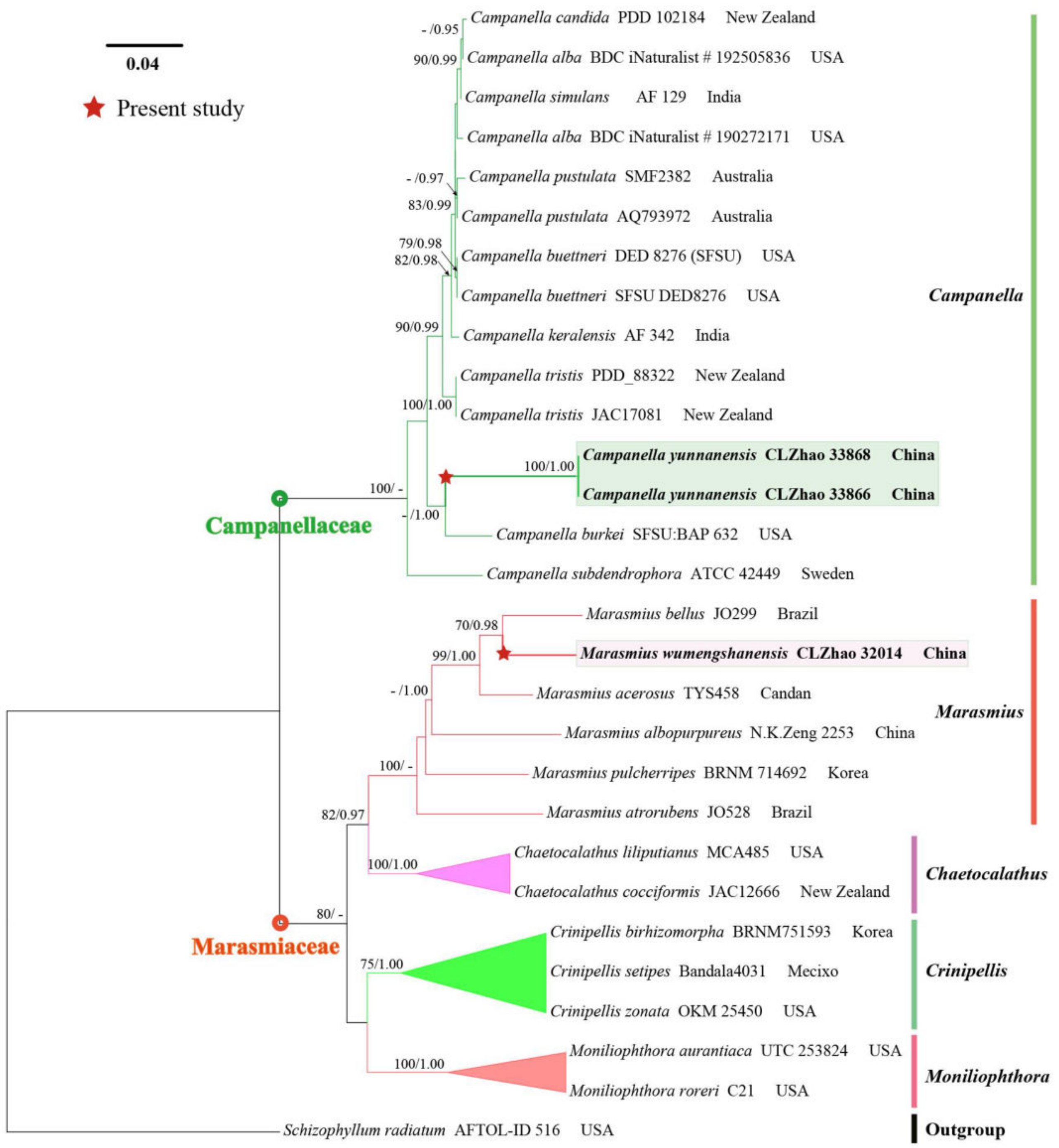

Figure 3 – Maximum likelihood tree illustrating the phylogeny of two new species within the families *Campanellaceae* and *Marasmiaceae* based on the combined ITS+nrLSU sequence data. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, and Bayesian posterior probabilities ≥ 0.95, respectively.

The phylogeny of *Omphalotaceae* based on combined ITS+nrLSU sequence data (Fig. 4)

The combined ITS+nrLSU dataset (Fig. 4) included sequences from 62 fungal specimens representing 57 species. A total of four Markov chains were run for two independent runs from random starting trees, each with 1.8 million generations for the ITS+nrLSU dataset, with trees and parameters sampled every 1,000 generations. ModelFinder v2.2.0 (Kalyaanamoorthy et al. 2017) was used to select the best-fit model based on the BIC criterion. The best model for the combined ITS+nrLSU dataset estimated and applied in the Bayesian analysis was GTR+F+I+G4. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies = 0.009319 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 169.5.

The phylogenetic tree, based on combined ITS+nrLSU sequences (Fig. 4), revealed that three new species, *Collybiopsis albobasidiosa*, *C. cremea*, and *C. yunnanensis* were assigned to the genus *Collybiopsis* within the family *Omphalotaceae*. In addition, *C. albobasidiosa* was sister to *C. villosipes* (Cleland) R.H. Petersen, and *C. cremea* was clustered with *C. yunnanensis*.

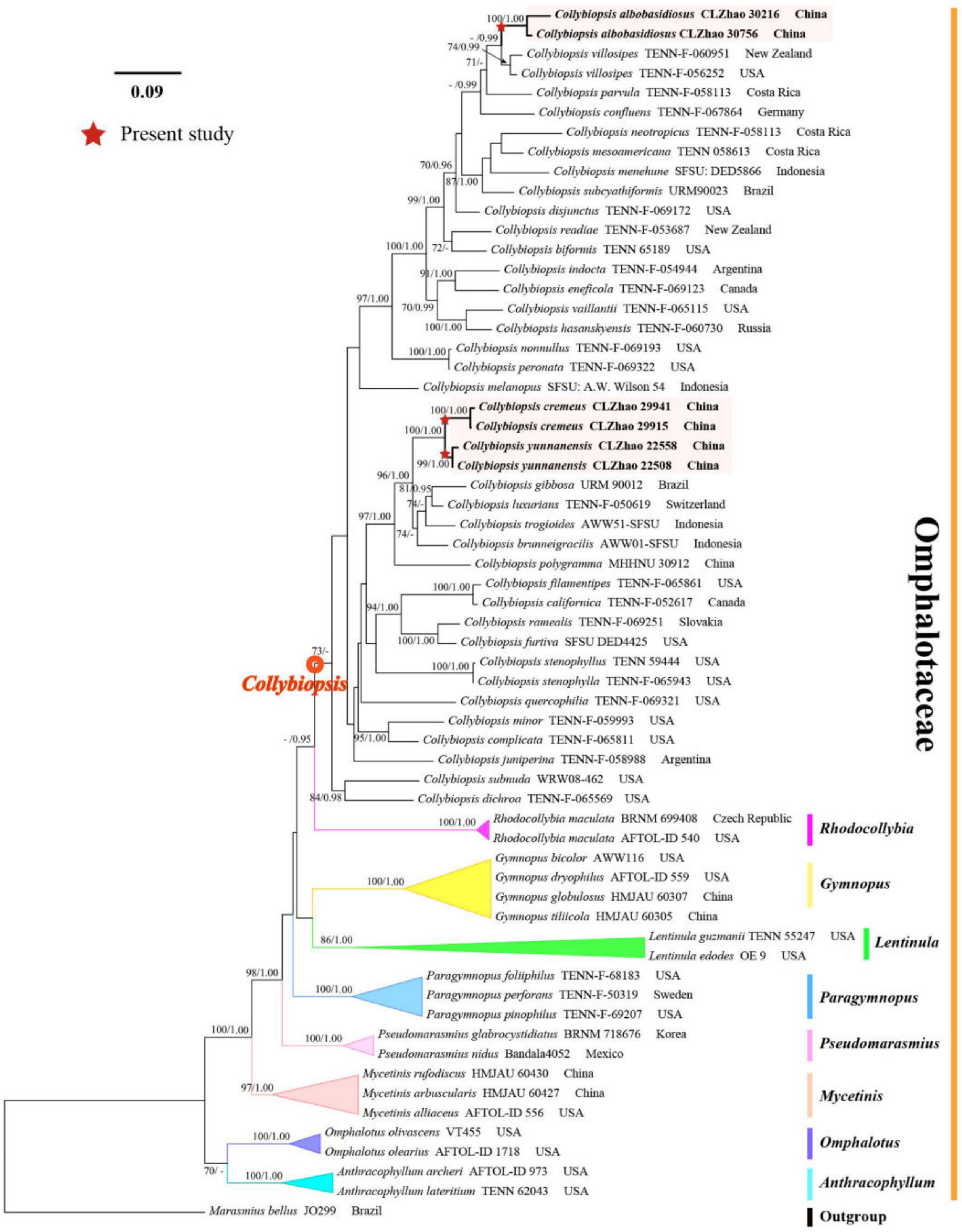

Figure 4 – Maximum likelihood tree illustrating the phylogeny of three new *Collybiopsis* species within the families *Omphalotaceae* based on the combined ITS+nrLSU sequence data. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, and Bayesian posterior probabilities ≥ 0.95, respectively.

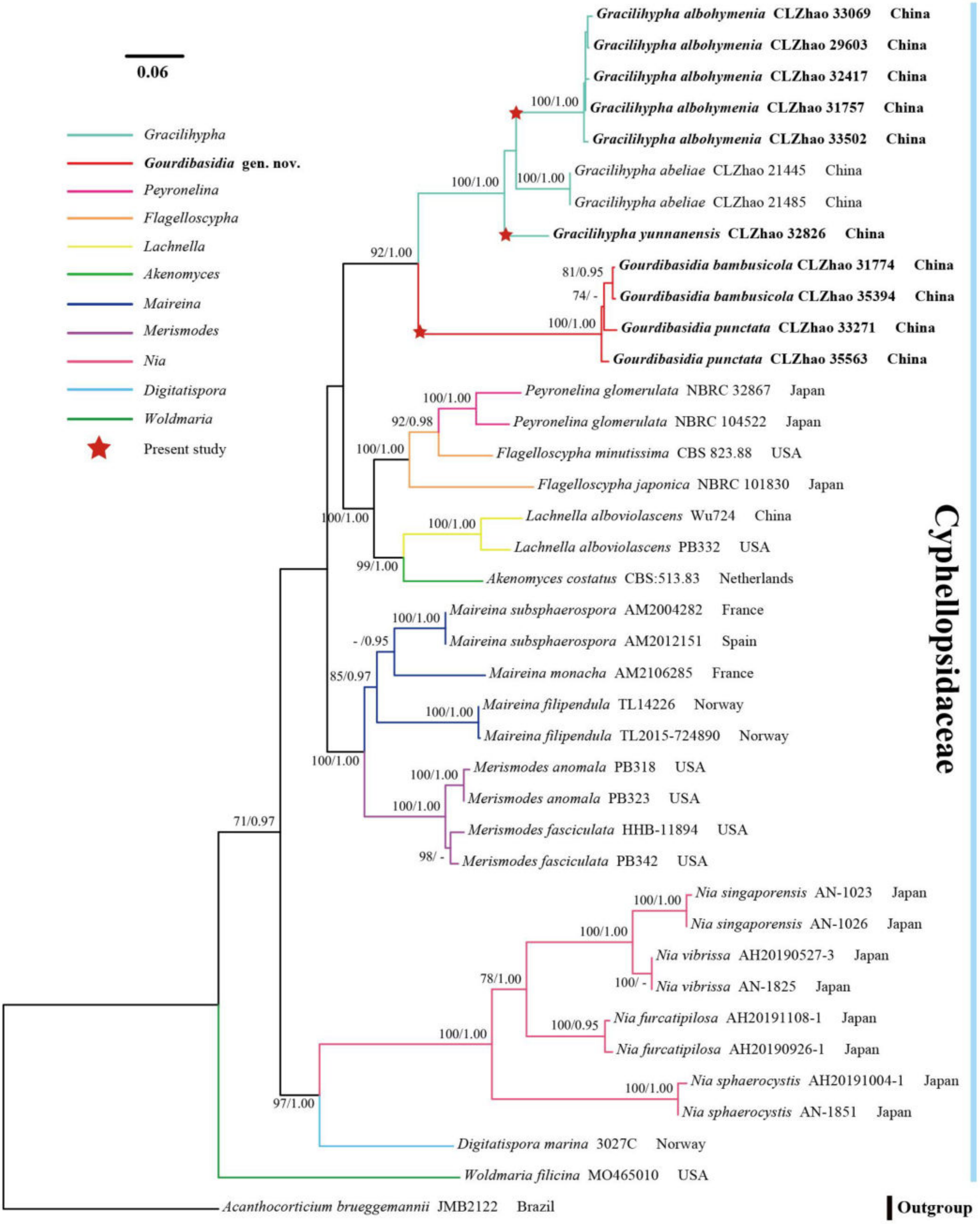

Figure 5 – Maximum likelihood tree illustrating the phylogeny of *Gracilihypha* and *Sicyoideibasidia* and related genera in *Cyphellopsidaceae* based on the combined ITS+nrLSU

sequence data. Branches are labeled with Maximum Likelihood bootstrap values ≥ 70%, and Bayesian posterior probabilities ≥ 0.95, respectively.

The phylogeny of *Cyphellopsidaceae* based on combined ITS+nrLSU sequence data (Fig. 5)

The combined ITS+nrLSU dataset (Fig. 5) included sequences from 39 fungal specimens representing 22 species. A total of four Markov chains were run for two independent runs from random starting trees, each for one million generations, using the ITS+nrLSU dataset. Trees and parameters were sampled every 1,000 generations. ModelFinder v2.2.0 (Kalyaanamoorthy et al. 2017) was used to select the best-fit model based on the BIC criterion. The best model for the combined ITS+nrLSU dataset estimated and applied in the Bayesian analysis was GTR+F+I+G4. Maximum Likelihood (ML) and Bayesian Inference (BI) analysis yielded a similar topology, with an average standard deviation of split frequencies of 0.006822 (BI) and an effective sample size (ESS) average ESS (avg. ESS) = 229.

The phylogenetic tree, based on combined ITS+nrLSU sequences (Fig. 5), showed that the new genus *Sicyoideibasidia* gen. nov. forms a strongly supported monophyletic lineage (BS = 100%, BPP = 1.00) within the family *Cyphellopsidaceae*, closely related to *Gracilihypha* Y. Yang & C.L. Zhao. Additionally, two new species, *G. albohymenia* and *G. yunnanensis*, were assigned to the genus *Gracilihypha*.

Taxonomy

Suborder *Agaricineae* Fr.
Family *Crepidotaceae* (S. Imai) Singer
Index Fungorum number: IF80655.
Type genus – *Crepidotus* (Fr.) Staude

Note 1 *Crepidotus* (Fr.) Staude
Index Fungorum number: IF17403.
Type species – *Crepidotus mollis* (Schaeff.) Staude

Notes – Fries (1821) initially categorized *Crepidotus* under *Agaricus* trib. *Crepidotus* Fr., which included pleurotoid taxa with fibrillose veil and pale or ferruginous basidiospores (Senn-Irlet 1995). However, *Crepidotus* was later raised to the generic rank by Staude (1857). The tribe *Crepidotus*, most of which have been transferred to two current genera as *Entoloma* (Fr.) P. Kumm. and *Tapinella* E.-J. Gilbert E.-J. Gilbert (Consiglio & Setti 2008, Na et al. 2022). Members of *Crepidotus* have typical pleurotoid basidiomata, characterized by a rudimentary stipe and dark-colored basidiospores (Capelari 2011, Guzmán-Dávalos et al. 2017, Kumar et al. 2020, Na et al. 2022). Various shapes can be found in the basidiomata, including semicircular, flabelliform, reniform, or spathuliform, and the lamellae spacing was relatively uniform and can be subventricose to rarely ventricose (Senn-Irlet 1995). The color of the basidiospore deposit has been regarded as one of the defining characteristics of *Crepidotus* (Senn-Irlet 1995). The basidiospores of *Crepidotus* can be categorized into two types: smooth and ornamented (Na et al. 2022). According to the classification of Consiglio & Setti (2008), the ornamented basidiospores are generally associated with clamped hyphae. In contrast, the smooth basidiospores mostly occur with hyphae without any clamp (Senn-Irlet 1995, Consiglio & Setti 2008, Na et al. 2022). This saprotrophic genus has a worldwide distribution, mostly on dead tree logs, and approximately 200 species have been documented under Crepidotus (Senn-Irlet 1995, Consiglio & Setti 2008, Kirk et al. 2008, Na et al. 2022). The diversity of this genus has also been studied in Asian countries, resulting in the discovery of numerous novel species (Na et al. 2022).

Family *Nidulariaceae* Dumort.
Index Fungorum number: IF81878.
Type genus – *Nidularia* Fr.

Note 2 ***Crucibulum*** Tul. & C. Tul.

Index Fungorum number: IF19081.

Type species – *Crucibulum vulgare* Tul. & C. Tul.

Notes – *Crucibulum* was introduced by Tulasne & Tulasne (1844), typified by the saprobic *C. vulgare* as the type species. The genus *Crucibulum* exhibits a typical cupulate form, a funicular attachment of the peridioles, and a splash dispersal mechanism (Hassett et al. 2013). Based on the phylogenetic analyses with SSU, nrLSU, *tef*1-α, and *rpb*2 sequence data, Kraisitudomsook et al. (2022) revealed the genus *Crucibulum* nested in /crucibulum clade, which formed a monophyletic lineage. Recently, Cooper (2023) proposed a new combined species, *Crucibulum lanosum* (Cooke) J.A. Cooper, previously described as *C. vulgare* var. *lanosum* Cooke. The taxonomic placement of *Crucibulum* is within the *Nidulariaceae*, in *Agaricales*.

Note 3 ***Cyathus*** Haller

Index Fungorum number: IF19085.

Type species– *Cyathus striatus* (Huds.) Willd.

Notes – The genus *Cyathus* was first introduced by Haller (1768) and typified by *C. striatus* (Duan et al. 2023). Due to their cup-like basidiomata resembling bird nests and lenticular periodioles resembling eggs, five genera, viz. *Cyathus*, *Crucibulum* Tul. & C. Tul., *Mycocalia* J.T. Palmer, *Nidula* V.S. White, and *Nidularia* Fr., were commonly known as bird's nest fungi (Brodie 1975, Gómez and Pérez-Silva1988, Zhao et al. 2008). The genus is characterized by having small-sized basidiomata with lenticular structures inside, named peridioles. Due to the arrangement of these structures, resembling small eggs inside a bird's nest, these organisms are known as "bird's nest fungi". The species of *Cyathus* are saprobic, typically growing on decaying wood, but they can also be found in manure, soil, leaves, or seeds (Duan et al. 2022). *Cyathus* is the most diverse genus of *Nidulariaceae*, with at least 60 described species to date (He et al. 2019, Boonmee et al. 2021, Duan et al. 2022). Comprehensive molecular systematic studies on *Cyathus* have been conducted over the last two decades (Matheny et al. 2006, Kraisitudomsook et al. 2021, 2022). An overview of the phylogeny of *Agaricales* based on a multilocus analysis of a six-gene region supermatrix revealed that the family *Nidulariaceae* was close to *Cystodermateae*, in which *Cyathus striatus* and *Crucibulum laeve* (Huds.) Kambly grouped together within the family *Nidulariaceae* (Matheny et al. 2006). Recent phylogenetic studies with all genera of the entire genus that comprises *Nidulariaceae* (*Cyathus*, *Crucibulum*, *Nidula*, *Nidularia*, *Mycocalia*, and the newly described *Retiperidiolia* Kraisit., Cheoyklin, Boonprat & M.E.Sm.) show that the family is a monophyletic group, forming a clade with *Squamanitaceae* Jülich (Kraisitudomsook et al. 2021, 2022). Zhao et al. (2008) had already demonstrated that inconsistencies exist within the internal clades of *Cyathus*, necessitating molecular data from type materials, as suggested by Kraisitudomsook et al. (2021). The striatum clade was re-nominated to the striatum supergroup and was divided into four new groups: aureum, badium, gigasporum, and minimum; and three subgroups: discoideus, stercoreus, and subglobisporus (Cruz et al. 2023, Góis et al. 2024). The taxonomic placement of *Cyathus* is located in the *Nidulariaceae* in the *Agaricales*.

Note 4 ***Mycocalia*** J.T. Palmer

Index Fungorum number: IF19226.

Type species – *Mycocalia denudata* (Fr.) J.T. Palmer

Notes – *Mycocalia* is a polyphyletic genus introduced by Palmer (1961) and typified by *M. denudata*. *Mycocalia* is of particular interest to mycologists due to its peculiar structure and unique dispersal strategy. The peridia of these species dehisce irregularly at maturity, and the peridioles then slowly exude out when wetted by rain or other precipitation (Brodie 1975). Morphologically, the genus *Mycocalia* is similar to *Nidularia* Fr., but differs in the microscopic features of their peridium structure and in the size of the basidiocarps (Brodie 1975). *Mycocalia denudata* (the type species), and *M. minutissima* were previously described as *Nidularia* from England, but both were transferred to *Mycocalia* by Palmer (1961). Subsequently, Cejp & Palmer (1963) described a new species, *M. sphagneti* J.T. Palmer, from England. Only two *Mycocalia* species have thus far been described from the tropics: *M. aquaphila* R. Cruz, L.T. Carmo, M.P. Martín, Gusmão & Baseia from Mesqueiro island in northern Brazil (Crous et al. 2018), and *M. reticulata*, from Sri Lanka (Petch 1919). Based on morphological and phylogenetic analyses, Kraisitudomsook et al. (2022) indicate that *Mycocalia* species belong to two distantly related clades, thereby determining the taxonomic and phylogenetic diversity of the genus *Mycocalia.* Therefore, Kraisitudomsook et al. (2022) proposed a novel genus, *Retiperidiolia* Kraisit., Choeyklin, Boonprat. & M.E. Sm. to accommodate this new lineage with two new combinations (*R. reticulata* and *R. aquaphila*). The taxonomic placement of *Mycocalia* is located in the *Nidulariaceae* within *Agaricales*.

Note 5 ***Nidula*** V.S. White

Index Fungorum number: IF19235.

Type species – *Nidula candida* (Peck) V.S. White

Notes – White (1902) introduced *Nidula* to accommodate *N. candida* as the type species. The present species can be readily classified within the *Nidulariaceae* family, commonly known as bird's nest fungi, based on its distinct cupulate form of basidiomata (Das & Zhao 2013). Moreover, the presence of a multilayered peridium with epiphragm/lid, absence of funiculus, and presence of transparent mucilaginous gel surrounding the peridioles confirms its placement in *Nidula* (Brodie 1975, Miller & Miller 1988). During a macrofungal survey, Das & Zhao (2013) encountered a striking bird's nest fungus. After thorough macro- and micromorphological studies and literature surveys, they proposed a new species *Nidula shingbaensis.* Based on the phylogenetic analyses with SSU, nrLSU, *tef*1-α, and *rpb*2 sequence data, Kraisitudomsook et al. (2022) revealed the genus *Nidula* nested in the /nidula-nidularia clade, in which is sister to the /mycocalia clade. The taxonomic placement of *Nidula* is located in the *Nidulariaceae* within *Agaricales*.

Note 6 ***Nidularia*** Fr.

Index Fungorum number: IF19237.

Type species – *Nidularia radicata* Fr. & Nordholm

Notes – *Nidularia radicata* was introduced by Fries (1817), as the type species of the genus *Nidularia*. The species distribution of this genus is worldwide, although many have been transferred to related genera (Palmer1961, Petch 1919, Kraisitudomsook et al. 2022). The genus *Nidularia* is similar to *Mycocalia*, but the peridium wall is composed of coenocytic skeletal hyphae in *Nidularia* species, but septate hyphae with clamp connections in *Mycocalia* species (Palmer 1961). Based on the phylogenetic analyses with SSU, nrLSU, *tef*1-α, and *rpb*2 sequence data, Kraisitudomsook et al. (2022) revealed that the genus *Nidularia*, nested in the /nidula-nidularia clade, is sister to the /mycocalia clade. No novel species within this genus have been formally described over the past five decades based on the MycoBank database (http:// www.mycobank.org, accessed on 10 March 2025) and the Index Fungorum (http:// www.indexfungorum.org, accessed on 10 March 2025). The taxonomic placement of *Nidularia* is within the *Nidulariaceae*, in *Agaricales*.

Note 7 ***Retiperidiolia*** Kraisit., Choeyklin, Boonprat. & M.E. Sm.

Index Fungorum number: IF842128.

Type species – *Retiperidiolia reticulata* (Petch) Kraisit., Choeyklin, Boonprat. & M.E. Sm.

Notes – *Retiperidiolia* was introduced to accommodate *R. aquaphila* (R. Cruz, L.T. Carmo, M.P. Martín, Gusmão & Baseia) and *R. reticulata* from the genus *Nidularia* (Kraisitudomsook et al. 2022). The genus type species was originally described from Sri Lanka by Petch (1919), who named it *Nidularia reticulata* Petch. Palmer (1961) later transferred it to the segregate genus *Mycocalia* J.T. Palmer based on the morphology of the peridium hyphae. Based on the morphological and phylogenetic analyses, Kraisitudomsook et al. (2022) indicated that *Mycocalia* species belonged to two distantly related clades and determined the taxonomic and phylogenetic diversity of the genus *Mycocalia*. Surprisingly, the new genus *Retiperidiolia* was established to accommodate a phylogenetically and morphologically distinct group of the bird's nest fungi viz. *R. aquaphila* and *R. reticulata.* The genus *Retiperidiolia* was more closely related to members of the genus *Cyathus* than the morphologically similar genera *Mycocalia* and *Nidularia* (Kraisitudomsook et al. 2022). The scientific fact shows that *Mycocalia* and *Retiperidiolia* are phylogenetically distant, yet share numerous morphological traits, indicating that they either evolved these traits independently or retained some of the ancestral characteristics of early bird's nest fungi (Kraisitudomsook et al. 2022). The taxonomic placement of *Retiperidiolia* belongs to *Nidulariaceae* in the order *Agaricales*.

Family *Psathyrellaceae* Vilgalys, Moncalvo & Redhead

Index Fungorum number: IF82127.

Type genus – *Psathyrella* (Fr.) Quél.

Note 8 *Heteropsathyrella* T. Bau & J.Q. Yan

Index Fungorum number: IF838372.

Type species– *Heteropsathyrella macrocystidia* T. Bau & J.Q. Yan

Notes – Bau & Yan (2021) introduced *Heteropsathyrella* as a monospecific genus based on *H. macrocystidia* as the type species. The type species was isolated as a saprobe on rotten wood in mixed forests of larch and birch in China (Bau & Yan 2021). Phylogenetic analyses based on ITS, nrLSU, *tef1*-α, and *tub*2 sequences (Bau & Yan 2021) indicated its phylogenetic position within the family *Psathyrellaceae*, and it grouped with three related genera: *Cystoagaricus* Singer, *Kauffmania* Örstadius & E. Larss., and *Typhrasa* Örstadius & E. Larss. Compared with the other genera of *Psathyrellaceae*, species of this genus can be distinguished by: psathyrelloid basidiomata, adnexed non-deliquescent lamellae, and monomorphic basidia; pseudoparaphyses are abundant; the pileipellis is composed of saccate to subglobose cells covered by a one-cell deep layer of periclinal hyphae, which are covered by scattered and irregular deposits dissolving in 5% KOH (Bau & Yan 2021). This is an agaricoid genus placed in the *Psathyrellaceae* within the *Agaricales*.

Note 9 *Olotia* D. Wächt. & A. Melzer

Index Fungorum number: IF831466.

Type species– *Olotia codinae* (Deschuyteneer, A. Melzer & Pérez-De-Greg.) D. Wächt. & A. Melzer

Notes – Wächter & Melzer (2020) introduced *Olotia* within the family *Psathyrellaceae* (*Agaricales*, *Agaricomycetes*, *Basidiomycota*) to accommodate a single species, *O. codinae*, originally described in the genus *Psathyrella*. Species of *Olotia* can be distinguished from *Psathyrella* by small, lignicolous basidiomata, frontally ellipsoid to slightly ovoid, dark, germ pore central basidiospores, clavate lamellae with edge predominantly lageniform, mostly spatula-shaped and strongly pediculated, walls often slightly thickened and brownish pigmented pleurocystidia (Wächter & Melzer 2020). Although its morphological characters align completely with *Pstahyrella* (Deschuyteneer et al. 2018), phylogenetic analysis based on ITS, nrLSU, *tef1*-α, and *tub*2 revealed its distinct position within *Psathyrellaceae* (Wächter & Melzer 2020).

Family *Strophariaceae* Singer & A.H. Sm.

Index Fungorum number: IF81444.

Type genus – *Stropharia* (Fr.) Quél.

Note 10 *Pyrrhulomyces* E.J. Tian & Matheny

Index Fungorum number: IF835046.

Type species – *Pyrrhulomyces astragalinus* (Fr.) E.J. Tian & Matheny

Notes – To resolve the non-monophyly of *Pholiota* (Fr.) P. Kumm., the new genus *Pyrrhulomyces* (*Strophariaceae*) was erected to accommodate *P. astragalinus* and its cryptic sister species, *P. amariceps* E.J. Tian & Matheny, from the Southern Appalachians in North America (Tian & Matheny 2020). The species of *Pyrrhulomyces* were usually associated with late stages of conifer wood decay (Tian & Matheny 2020). *Pyrrhulomyces* was phylogenetically closely related to *Stropharia* (Fr.) Quél. and *Hypholoma* (Fr.) P. Kumm., but it forms a separate clade apart from *Pholiota* (Tian & Matheny 2020). Compared with other genera of *Strophariaceae* (Tian & Matheny 2020), taxa of this genus are characterized by the blackening of basidiocarps with a bitter taste, smooth basidiospores without a germ pore under light microscopy, the presence of pleurochrysocystidia, an ixocutis, and rugulose spore ornamentation under the scanning electron microscope (Tian & Matheny 2020). Phylogenetic analyses based on ITS, nrLSU, *rpb*2, and *tef*1-α indicated its phylogenetic position in *Strophariaceae* (*Agaricales*, *Agaricomycetes)* (Tian & Matheny 2020)

Family *Tubariaceae* Vizzini

Index Fungorum number: IF512626.

Type genus – *Tubaria* (W.G. Sm.) Gillet

Note 11 *Pleuromyces* Dima, P.-A. Moreau & V. Papp

Index Fungorum number: IF824585.

Type species – *Pleuromyces hungaricus* V. Papp, Dima & P.-A. Moreau

Notes – *Pleuromyces* was introduced by Crous et al. (2018) to accommodate *P. hungaricus* as the type species. *Pleuromyces hungaricus* formed a distinct clade within *Tubariaceae* in the phylograms of Crous et al. (2018), and was well separated from other genera. *Pleuromyces hungaricus* forms a distinct clade and is well separated from other genera of *Tubariaceae*. Microscopical observations (spores smooth, thick-walled and subpored; pileipellis with coarsely incrusted hyphae) suggest closest affinities with species of *Phaeomarasmius* Scherff. and *Flammulaster* Earle, but the weak differentiation of the pileipellis is a distinctive feature for species of these genera (Crous et al. 2018).

Suborder *Hygrophorineae* Aime, Dentinger & Gaya

Family *Cantharellulaceae* (Lodge, Redhead, Norvell & Desjardin) Vizzini, Consiglio & P. Alvarado

Index Fungorum number: IF851144.

Type genus – *Cantharelluleae* Lodge, Redhead & Desjardin

Note 12 *Pseudoarmillariella* Singer

Index Fungorum number: IF18382.

Type species – *Pseudoarmillariella ectypoides* (Peck) Singer

Notes – *Pseudoarmillariella* Singer (1956) is a small genus comprising only three known species, distributed in North and Central America, China, and New Zealand (Horak 1971, Singer 1986, Kirk et al. 2008, Yang et al. 2013). The systematic position of the genus was previously unclear and had been long debated until recently. Based on morphological, anatomical, and molecular phylogenetic evidence, Norvell et al. (1994) and Redhead et al. (2002) defined the generic boundaries. Later, molecular phylogenetic studies indicated that *Pseudoarmillariella* was a member of the family *Hygrophoraceae* (Matheny et al. 2006, Lawrey et al. 2009). However, phylogenetic analyses of *Agaricales* based on multilocus sequences, Vizzini et al. (2024) transferred the genus *Pseudoarmillariella* to *Cantharellulaceae*. Later, the result was accepted by Hyde et al. (2024b).

Suborder *Marasmiineae* Aime, Dentinger & Gaya

Family *Campanellaceae* J.S. Oliveira, Desjardin & Moncalvo

Index Fungorum number: IF849979.

Type genus – *Campanella* Henn.

Note 13 ***Brunneocorticium*** Sheng H. Wu

Index Fungorum number: IF505727.

Type species – *Brunneocorticium pyriforme* Sheng H. Wu

Notes – *Brunneocorticium* was introduced by Wu et al. (2007) to accommodate *B. pyriforme* as the type species. This genus is characterized by having a smooth hymenial surface and by possessing a dimitic hyphal system with clamped generative hyphae, abundant yellowish-brown skeletal hyphae, 2-sterigmate basidia, and pear-shaped basidiospores (Wu et al. 2007). The molecular analysis also supported an independent status for *Brunneocorticium* from other corticioid genera with similar morphological features (Wu et al. 2007). Based on phylogenetic analysis, Wu et al. (2007) placed *Brunneocorticium* in the euagarics clade of *Homobasidiomycetes*, and closely related to agaricoid genera such as *Marasmiellus* and *Campanella* etc. However, the resupinate basidiocarp and dimitic hyphal system deviate strongly from the morphological concept of agaricoid organisms (Wu et al. 2007). *Cystostereum* Pouzar is another genus in the euagarics clade that also bears a resupinate basidiocarp and a dimitic hyphal system (Pouzar 1959). *Cystostereum* differs from *Brunneocorticium* by having an odontioid hymenial surface, 4-sterigmate basidia, and generally colorless skeletal hyphae (Pouzar 1959). Phylogenetic analyses of the order *Agaricales* based on multilocus sequences, Vizzini et al. (2024) transferred the genus *Brunneocorticium* to *Cantharellulaceae*. Later, the result was accepted by Hyde et al. (2024b). The taxonomic placement of *Brunneocorticium* is located in the family *Cantharellulaceae* within *Agaricales*.

Note 14 ***Campanella*** Henn.

Index Fungorum number: IF17229.

Type species– *Campanella buettneri* Henn.

Notes – The genus *Campanella* was introduced by Hennings (1895) and was typified by *C. buettneri*. The genus is characterized by small, lignicolous, pleurotoid basidiomata with a distinctive hymenophore composed of vein-like or ridge-like anastomosing lamellae, and smooth, colorless, inamyloid basidiospores (Singer 1975a, Farook & Manimohan 2014, Dai et al. 2022). Some molecular phylogenetic studies have shown that the genera *Campanella* and *Tetrapyrgos* E. Horak were distinct, monophyletic sister clades (Moncalvo et al. 2002, Aime & Phillips-Mora 2005, Matheny et al. 2006). Wilson & Desjardin (2005) provided nrLSU sequence data that showed that *Marasmiellus candidus* (Fr.) Singer was not closely related to *M. juniperinus* Murrill, but instead was sister to several species of *Tetrapyrgos*. Nakasone et al. (2009) phylogenetic analyses showed that the genus *Campanella* was distant from *Tetrapyrgos*. In a taxonomic revision of *Tetrapyrgos*, supported by ITS sequence data, Honan et al. (2015) reported *M. candidus* as the sister to *Campanella*, but embedded within *Tetrapyrgos*. A study of gymnopoid fungi using ITS sequence data revealed the discovery of a new species, *C. burkei*, reported by Desjardin & Perry (2017). In the present study, we describe one additional species, *Campanella yunnanensis*, from China, based on morphological characteristics and phylogenetic analyses inferred from ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequences data (Fig. 2) and ITS+nrLSU sequence data (Fig. 3).

Campanella yunnanensis J.H. Dong & C.L. Zhao, sp. nov. Figs. 6–8

Index Fungorum number: IF858336.

Etymology –Refers to the type locality, Yunnan Province, China.

Type – China, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates 27°40′ N, 104°15′ E, altitude 2000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 21 September 2023, CLZhao 33866 (SWFC).

Description – Basidiomata annual, resupinate, coriaceous, without odor or taste when fresh, becoming hard coriaceous upon drying, up to 15 cm long, 2 cm wide, 200 µm thick. Hymenial surface smooth, cracked, with a cream color when fresh, turning to a slightly buff color upon drying. Sterile margin cream, thinning out, up to 0.5 mm wide.

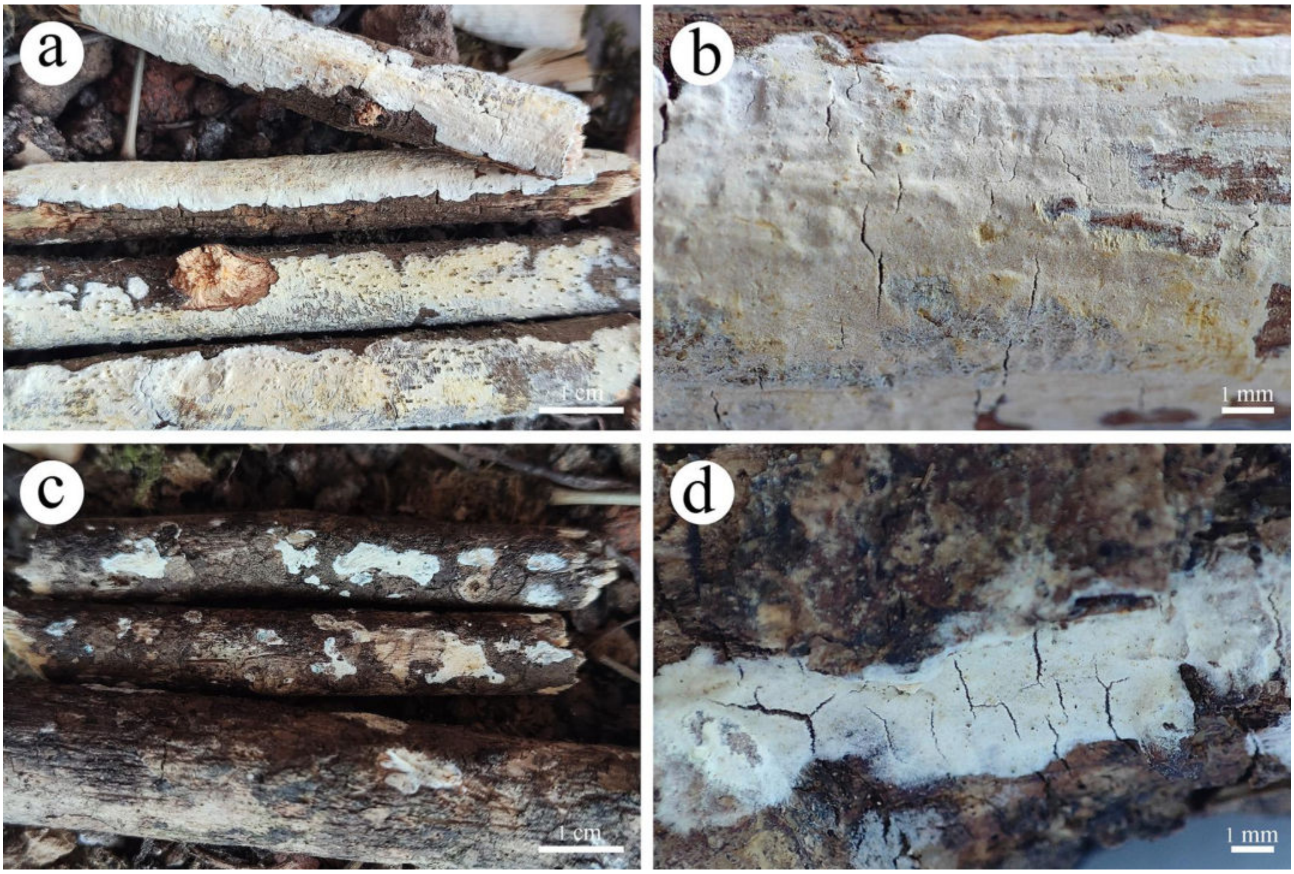

Figure 6 – Basidiomata of *Campanella yunnanensis* a, b CLZhao 33866 (holotype). c, d CLZhao 33868.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 1.5–2.5 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia capitate, colorless, thin-walled, 27.5–35.5 × 5–6.5 µm; cystidioles absent. Basidia clavate, slightly constricted, with 4 sterigmata and a basal clamp connection, 35.5–46 × 6.5–8 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores drop-shaped, colorless, thin-walled, smooth, with a few guttulae, IKI–, CB–, (8.5–)9–11 (–11.5) × 4.5–5.5(–5.8) µm, L = 9.94 µm, W = 5.01 µm, Q = 1.80–2.18, Q_m = 1.99 ± 0.15 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates 27°40′ N, 104°15′ E, altitude 2000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 21 September 2023, CLZhao 33868 (SWFC).

Notes – *Campanella yunnanensis* grouped in *Campanella* (*Campanellaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α data (Fig. 2). Based on the ITS+nrLSU data (Fig. 3), *C. yunnanensis* was sister to *C. burkei*. However, *C. burkei* can be delimited from *C. yunnanensis* by its gymnopoid basidiomata and longer basidiospores (14.5–18.5 × 5.2–6.5 µm *vs* 9–11 × 4.5–5.5 µm, Desjardin & Perry 2017).

Morphologically, *Campanella yunnanensis* resembles *C. gregaria* Bougher, *C. keralensis* V.A. Farook & Manim. in sharing the clavate basidia with 4-sterigmata. However, *C. gregaria* differentiates from *C. yunnanensis* by its flabelliform basidiomata, both shorter basidia (22–30 × 5–7 µm *vs* 35.5–46 × 6.5–8 µm), and basidiospores (4.9–6.1 × 4.2–5 µm *vs* 9–11 × 4.5–5.5 µm, Bougher 2007). *C. keralensis* differs from *C. yunnanensis* by its pleurotoid basidiomata, shorter basidia (27–35 × 7–8 µm *vs* 35.5–46 × 6.5–8 µm), and ellipsoid to broadly ellipsoid basidiospores (Farook & Manimohan 2014). Additionally, *C. yunnanensis* can be easily distinguished from most species of *Campanella* by its corticioid basidiomata, smooth, cracked, hymenial surface, and drop-shaped basidiospores measuring 9–11 × 4.5–5.5 µm.

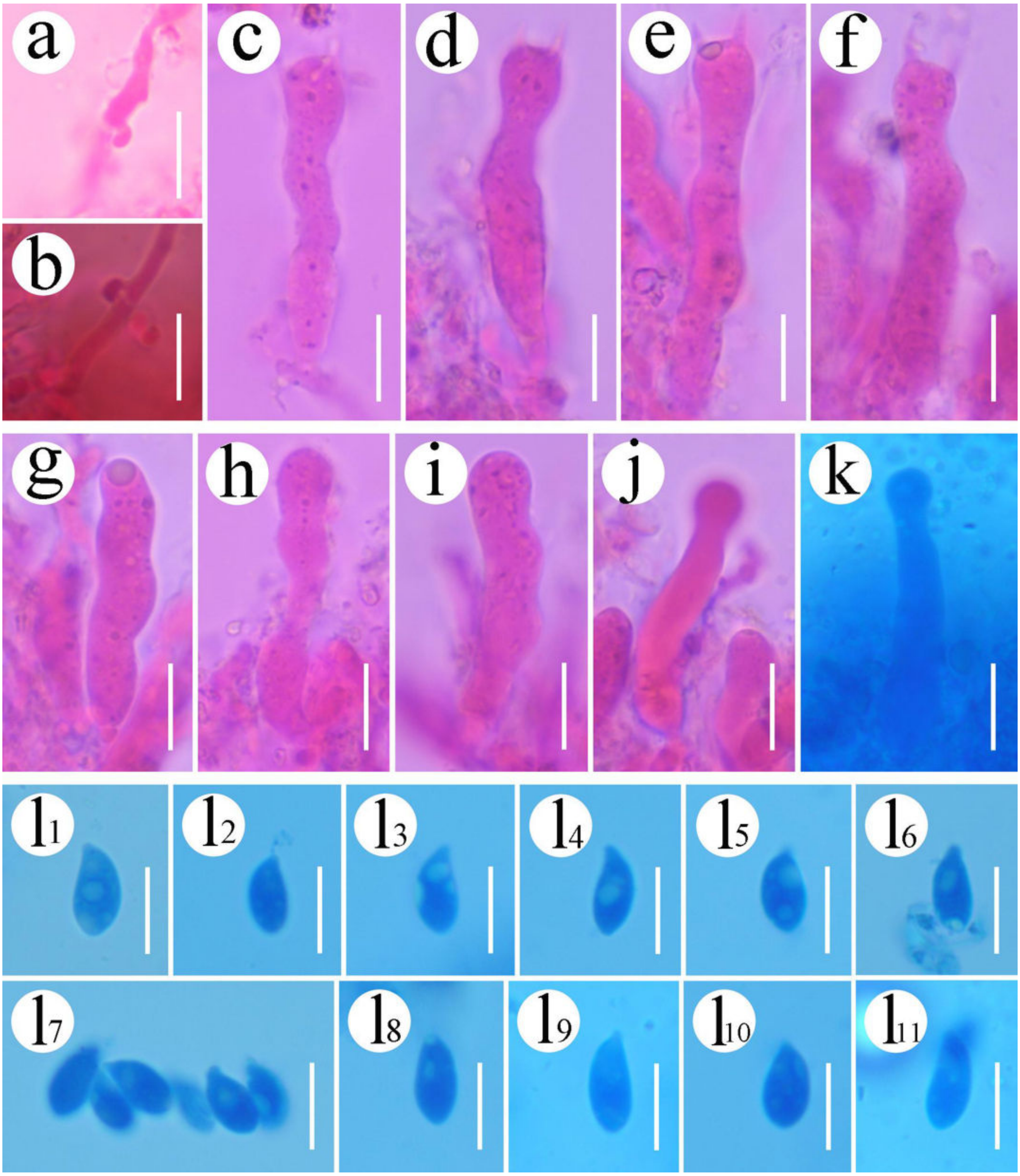

Figure 7 – Microscopic structures of *Campanella yunnanensis* (holotype, CLZhao 33866). a–b Generative hyphae. c–f Basidia. g–i Basidioles. j–k Capitate cystidia. l Basidiospores. Scale bars: a–l = 10 µm.

Family *Cyphellaceae* Burnett, Outl. Bot. (London): 233 (1835)

Index Fungorum number: IF80673.

Type genus – *Cyphella* Fr.

Note 15 *Cheimonophyllum* Singer

Index Fungorum number: IF17284.

Type species– *Cheimonophyllum haedinum* (Berk. & M.A. Curtis) Valade & P.-A. Moreau

Notes – *Cheimonophyllum* is a small saprobic genus belonging to the family *Cyphellaceae*, and consisting of four species from the temperate zone, with *C. candidissimum* (Sacc.) Singer (= *C. haedinum*) is the type species (He et al. 2019, Kalichman et al. 2020). Valade & Moreau (2022) transferred *Agaricus haedinus* Berk. & M.A. Curtis to *Cheimonophyllum*, and ITS sequence analysis supported that *C. candidissimum* was the same species as *C. haedinum*, which was published earlier. Therefore, the type species of *Cheimonophyllum* has been changed to *C. haedinum* (Valade & Moreau 2022). The genus is characterized by pleurotoid basidiomata, whitish to ivory lamellae, absence of stipe, hyaline globose to subglobose basidiospores, absence of pleurocystidia, cylindrical cheilocystidia with or without branches, trichodermal pileipillis, and presence of clamp connections (Delivorias & Gonou-Zagou 2008, Valade & Moreau 2022). Current molecular studies, based on ITS sequences, have confirmed that *Cheimonophyllum* belongs to the *Cyphellaceae* (Kalichman et al. 2020, Valade & Moreau 2022).

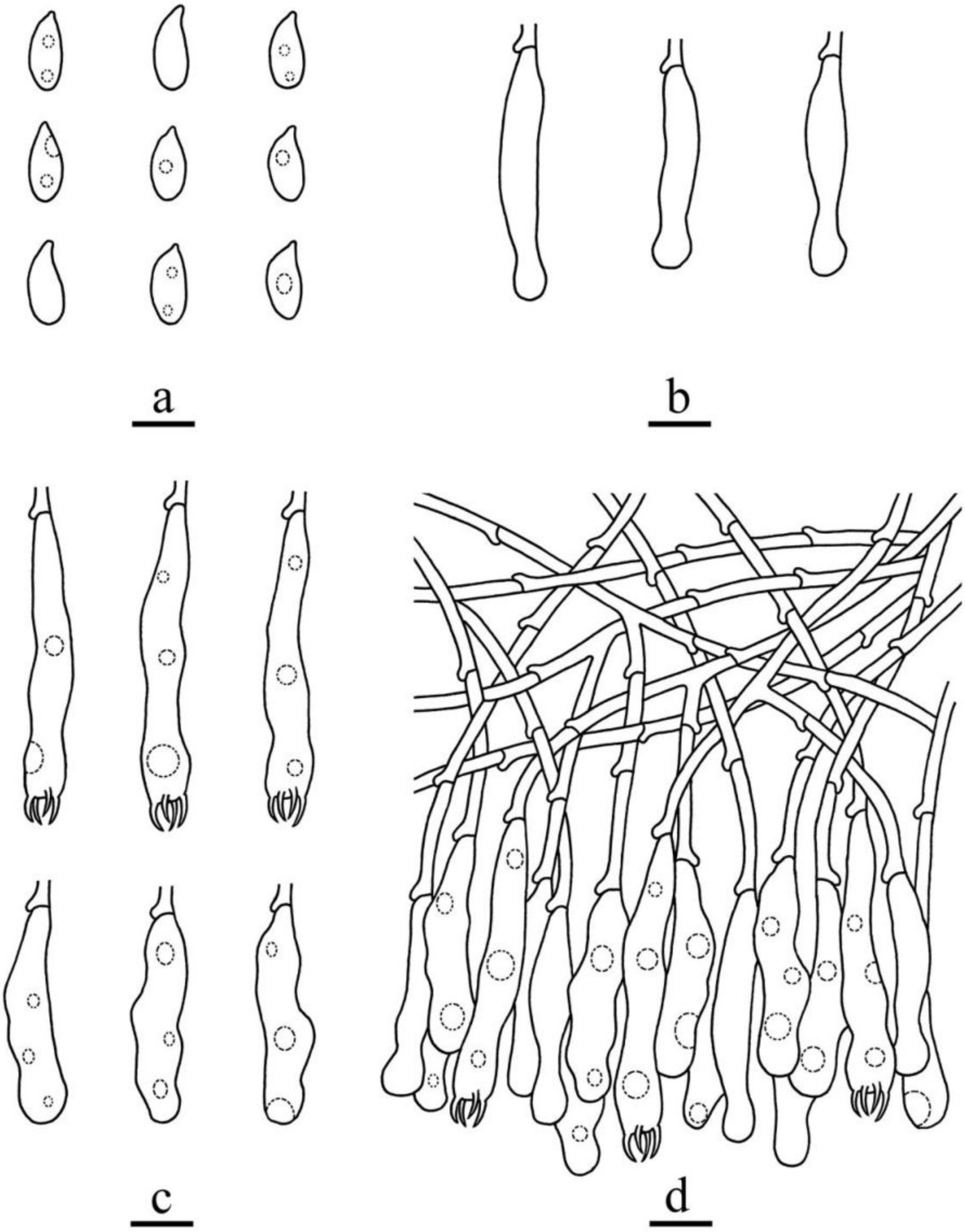

Figure 8 – Microscopic structures of *Campanella yunnanensis* (holotype, CLZhao 33866). a Basidiospores. b Basidia and basidioles c Capitate cystidia. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 µm.

Family *Cystostereaceae* Jülich

Index Fungorum number: IF81760.

Type genus – *Cystostereum* Pouzar

Note 16 *Crustomyces* Jülich

Index Fungorum number: IF25476.

Type species – *Crustomyces subabruptus* (Bourd. & Galzin) Jülich

Notes – The generic concept of *Crustomyces* was revised by Li et al. (2022) to include species with monomitic hyphal systems, poroid hymenophores, and thick-walled basidiospores. Therefore, the genus is characterized by annual or perennial, resupinate, widely effused, adnate, ceraceous to crustaceous, rarely membranous basidiomata, smooth, papillate to spinose or poroid hymenophore, a mono- or dimitic hyphal system, clavate basidia with four sterigmata, and subglobose, ellipsoid, short-cylindrical, thin- or thick-walled, smooth basidiospores (Li et al. 2022). Originally, two species were included in the genus, *C. subabruptus*, the generic type, and *C. pini-candensis* (Schwein.) Jülich (Jülich 1978). Li et al. (2022) phylogenetic analyses revealed that the genus *Crustomyces* is nested within the family *Cystostereaceae* and is sister to *Effusomyces*.

Note 17 *Cystostereum* Pouzar

Index Fungorum number: IF17451.

Type species – *Cystostereum murrayi* (Berk. & M.A. Curtis) Pouzar

Notes – The genus *Cystostereum* was introduced by Pouzar (1959), typified by *C. murrayi. Cystostereum* ar a genus of corticioid fungi in the family *Cystostereaceae*. Species in the *Cystosrereum* are characterized by perennial, pileate or mostly resupinate basidiomata, odontioid or tuberculate hymenophore, a dimitic hyphal system with clamped generative hyphae, narrowly clavate basidia with 4-sterigmata, and narrowly ellipsoid or subcylindrical, thin-walled, smooth basidiospores (Eriksson & Ryvarden 1975, Bernicchia & Gorjón 2010).

Note 18 *Effusomyces* Yue Li, Nakasone & S.H. He

Index Fungorum number: IF844194.

Type species – *Effusomyces thailandicus* Yue Li, Nakasone & S.H. He

Notes – This monotypic genus, *Effusomyces*, was typified by *E. thailandicus* (Li et al. 2022). Based on ITS and nrLSU sequence data, Li et al. (2022) proposed the genus *Effusomyces*, which was phylogenetically distinct from its sister genus *Crustomyces*. The genus *Effusomyces* grows on dead bamboo or angiosperm branches and has only been reported from Thailand (Li et al. 2022). The genus is characterized by annual, resupinate, widely effuse and inseparable from the substrate basidiomata, smooth, pale yellow or greyish yellow hymenophore, a monomitic hyphal system with clamped generative hyphae, lack of cystidia or gloeocystidia, and thin-walled basidiospores (Li et al. 2022). Although lacking distinctive morphological features, *Effusomyces* nested within the family *Cystostereaceae* and was sister to *Crustomyces* (Li et al. 2022).

Note 19 *Rigidotubus* J. Song, Y.C. Dai & B.K. Cui

Index Fungorum number: IF823702.

Type species – *Rigidotubus tephroleucus* J. Song, Y.C. Dai & B.K. Cui

Notes – *Rigidotubus* was introduced to accommodate the type species as *R. tephroleucus* from China (Song et al. 2018). The generic type of *Rigidotubus*, *R. tephroleucus*, was included with *Crustomyces subabruptus* in a strongly supported clade, demonstrating that they were congeneric (Li et al. 2022). *Crustomyces tephroleucus* (J. Song, Y.C. Dai & B.K. Cui) Yue Li, Nakasone &

S.H. He possesses a monomitic hyphal system and lacks cystidia and gloeocystidia, but has a tough, thick basidiome and poroid hymenophore (Song et al. 2018). Therefore, based on morphological characteristics and phylogenetic analyses, Li et al. (2022) transformed the genus *Rigidotubus* type *R. tephroleucus* to *Crustomyces* as *C. tephroleucus*. However, the genus *Rigidotubus* still was accepted by He et al. (2024) and Hyde et al. (2024b). In the present study, the research proposes to accept the name *Rigidotubus*.

Note 20 ***Tenuimyces*** S.L. Liu & L.W. Zhou

Index Fungorum number: IF901051.

Type species – *Tenuimyces bambusicola* S.L. Liu & L.W. Zhou.

Notes – Three corticioid specimens were collected by Liu et al. (2024a) from Southwest China, which form a distinct lineage with strong support within *Cystostereaceae* in phylogenetic analysis. Therefore, a new genus, *Tenuimyces*, was described base on these three specimens (Liu et al. 2024a). The genus is characterized by annual, resupinate, effused basidiomata with white to cream, smooth hymenophore, a monomitic hyphal system with clamp connections, subclavate basidia with 4-sterigmate, and broadly ellipsoid, hyaline, aculeate, slightly thick-walled basidiospores (Liu et al. 2024a).

Family ***Marasmiaceae*** Roze ex Kühner

Index Fungorum number: IF80977.

Type genus – *Marasmius* Fr.

Note 21 ***Crinipellis*** Pat.

Index Fungorum number: IF17405.

Type species – *Crinipellis scabella* (Alb. & Schwein.) Murrill

Notes – The genus *Crinipellis* (*Marasmiaceae*, *Agaricales*) was established by Patouillard (1900) with *C. scabella* as the type species (Singer 1943). This genus is characterized by the presence of thick-walled, dextrinoid, hair-like terminal cells in the pileipellis (Kerekes & Desjardin 2009). The *Crinipellis* species has been recognized as both a saprotrophic and a parasitic species (Singer 1943, Aime & Phillips-Mora 2005, Kerekes & Desjardin 2009). This genus comprises over 100 species and is considered to have a worldwide distribution (Kirk et al. 2008, Kerekes & Desjardin 2009, Antonín & Noodeloos 2010, Antonín et al. 2012, 2014, Hyde et al. 2024b).

Note 22 ***Marasmius*** Fr.

Index Fungorum number: IF18018.

Type species – *Marasmius rotula* (Scop.) Fr.

Notes – The genus *Marasmius*, typified by *M. rotula* (Fries 1836), is a member of the mushroom-forming fungi. *Marasmius* is a champion genus among the more diverse fungal genera in *Agaricales* (Bhunjun et al. 2022). With most species occurring in dense forests' litter across the Earth as a major decay driver on vegetal debris, and a few are adapted to open grasslands or are phytopathogenic, species diversity is greater in the tropical than in the temperate areas (Antonín & Buyck 2006, Antonín & Noordeloos 2010, Oliveira et al. 2024). In molecular phylogenetics based on ITS data within *Marasmius* s.str., the result showed that both phylogenetic analyses and morphological descriptions supported the classification of this genus (Wannathes et al. 2009, Tan et al. 2009, Antonín et al. 2012, 2014, Oliveira et al. 2020, Bhunjun et al. 2022). Based on the results in Wannathes et al. (2009) and Tan et al. (2009), Antonín & Noordeloos (2010) combined sect. *Sicci* in sect. *Globulares*. Oliveira et al. (2020) presented phylogenetic analyses combined ITS and nrLSU of sect. *Globulares* sensu, established new series and subsections based on several strongly supported subclades. According to previous studies, *Marasmius* s.str. includes sections *Globulares*, *Leveilleani*, *Marasmius*, *Neosessiles*, and *Sicci*, while no new sectional system was proposed (Oliveira et al. 2024). Based on results from multilocus phylogenetic analyses including SSU, nrLSU, ITS, *rpb*2, and *tef*1-α, Oliveira et al. (2024) proposed a family and genus delimitation, and they offered a revised infrageneric (subgenus-section-subsection-series) classification system. Due to the relevance of *Marasmius* in *Marasmiaceae*, all systematic treatments of the genus directly involve the family and the process of its establishment and circumscription (Oliveira et al. 2024). In the present study, based on ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and ITS+nrLSU sequence data (Fig. 3), a new species, *M. wumengshanensis* is described.

Marasmius wumengshanensis J.H. Dong & C.L. Zhao, sp. nov. Figs. 9–11

Index Fungorum number: IF858337.

Etymology –Refers to the locality (Wumengshan) of the type specimen.

Type – China, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates 27°40′ N, 104°15′ E, altitude 2000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 27 August 2023, CLZhao 32014 (SWFC).

Description – Basidiomata annual, resupinate, coriaceous, without odor or taste when fresh, becoming hard coriaceous upon drying, up to 10 cm long, 1.5 cm wide, and 150 µm thick. Hymenial surface tuberculate, cracked, slightly cream when fresh, turning to buff upon drying. Sterile margin indistinct, white to cream, up to 0.5 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, slightly thick-walled, branched, interwoven, 2–3.5 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia subcylindrical, colorless, thin-walled, with crystals at the apex, 24.5–30.5 × 3.5–5 µm; cystidioles tapering, colorless, thin-walled, 23–25.5 × 5–7.5 µm. Basidia clavate, slightly constricted, with 4 sterigmata and a basal clamp connection, 30–36 × 7.5–10.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (8–)8.5–10.3(–10.5) × (4.2–)4.5–6.2(–6.5) µm, L = 9.60 µm, W = 5.40 µm, Q = 1.57–1.91, Q_m = 1.79 ± 0.19 (n = 30/1).

Notes – *Marasmius wumengshanensis* grouped in *Marasmius* (*Marasmiaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2). Based on ITS+nrLSU sequence data (Fig. 3), *M. wumengshanensis* was sister to *M. bellus*. However, *M. bellus* is delimited from *M. wumengshanensis* by its pileate basidiomata (Berkeley 1856).

Morphologically, *Marasmius wumengshanensis* shares similarities with *M. hypochroides* Berk. & Broome, *M. nigrobrunneus* (Pat.) Sacc., *M. tubulatus* Petch, and *M. yunnanensis* Q.Y. Zhang, J. Si & H.J. Li in share the ellipsoid basidiospores. However, *M. hypochroides* differs from *M. wumengshanensis* by its pileate basidiomata, and shorter basidia (24–28 × 7–8 µm *vs* 30–36 × 7.5–10.5 µm, Manimohan & Leelavathy 1989); *M. nigrobrunneus* can be distinguished from *M. wumengshanensis* by its pileate basidiomata, and shorter basidia (23–30 × 6.5–8 µm *vs* 30–36 × 7.5–10.5 µm, Manimohan & Leelavathy 1989); *M. tubulatus* differentiates from *M. wumengshanensis* by its pileate basidiomata, and smaller basidia (20–22 × 5–7 µm *vs* 30–36 × 7.5–10.5 µm, Manimohan & Leelavathy 1989); *M. yunnanensis* differs from *M. wumengshanensis* by its pileate basidiomata, and shorter basidia (24–30 × 6–8 µm *vs* 30–36 × 7.5–10.5 µm, Zhang et al. 2023b). Additionally, *M. wumengshanensis* can be easily distinguished from most species of *Marasmius* by its corticioid basidiomata, tuberculate, cracked, and hymenial surface, as well as ellipsoid basidiospores measuring 8.5–10.3 × 4.5–6.2 µm.

Note 23 *Metacampanella* R.H. Petersen

Index Fungorum number: IF901403.

Type species – *Metacampanella dendrophora* (Singer) R.H. Petersen

Notes – *Metacampanella*, a genus within *Marasmiaceae*, was proposed by Petersen & Hughes (2024b) to accommodate a small group of species that are morphologically similar to *Tetrapyrgos* or *Campanella* but are molecularly distinct based on ITS and nrLSU sequence data. The type species is *Metacampanella dendrophora* (Petersen & Hughes 2024b). The genus is characterized by conchate, obcupulate to ob-saucer-shaped, sessile, pseudostipitate, or laterally stipitate basidiomata; a pileus that ranges from white to greenish or blue-greenish, and rarely pale pink. *Metacampanella* species typically colonize dead woody substrates, monocots such as bamboo, grass, sedge, or rush, and occasionally dicot rotting wood. Some members of this genus are also associated with grass endophytes (Petersen & Hughes 2024b). Currently, *Metacampanella* comprises nine species distributed across North, Central, and South America, Europe, China, and New Zealand (Hou et al. 2024, Petersen & Hughes 2024b).

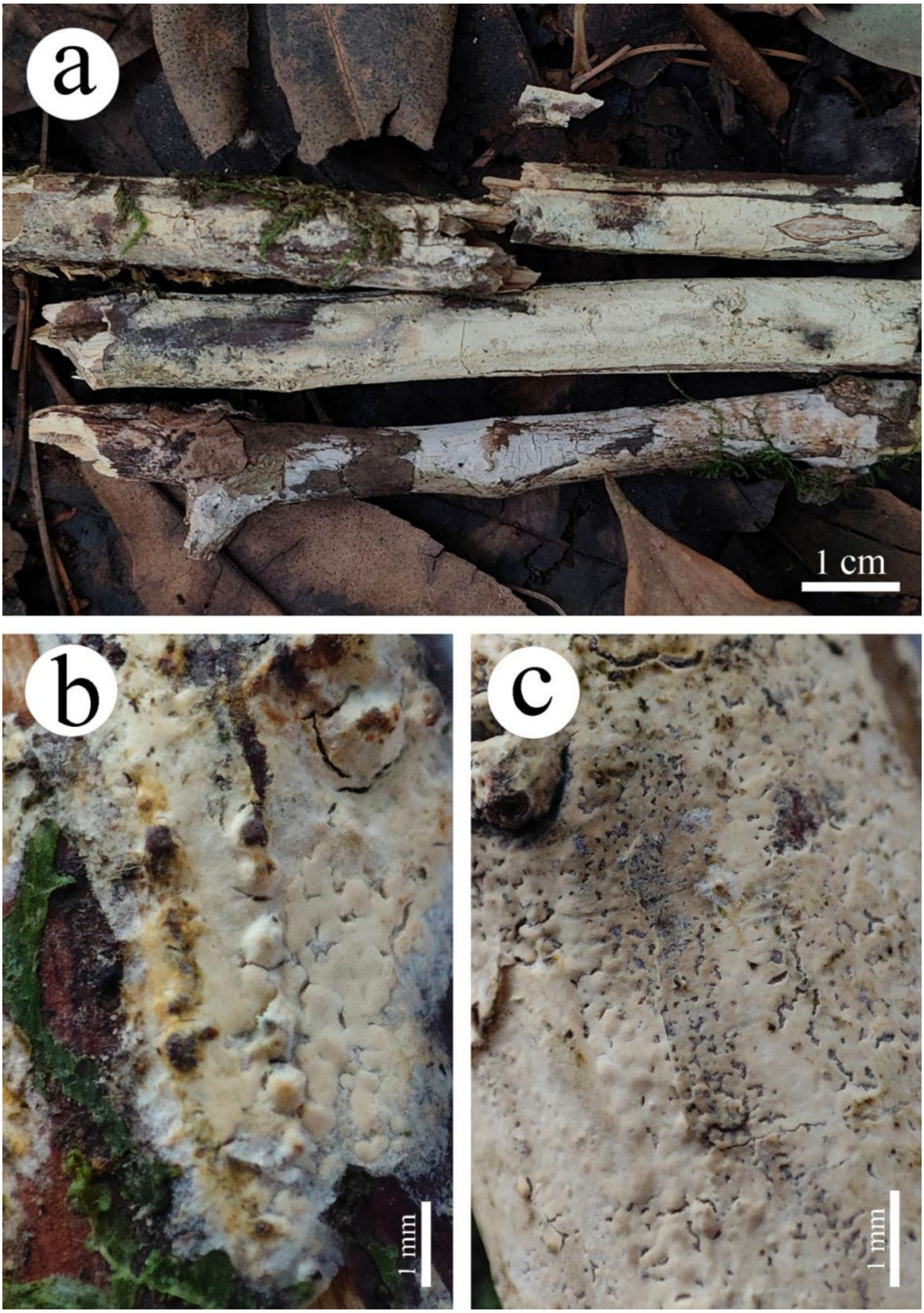

Figure 9 – Basidiomata of *Marasmius wumengshanensis* (holotype, CLZhao 32014).

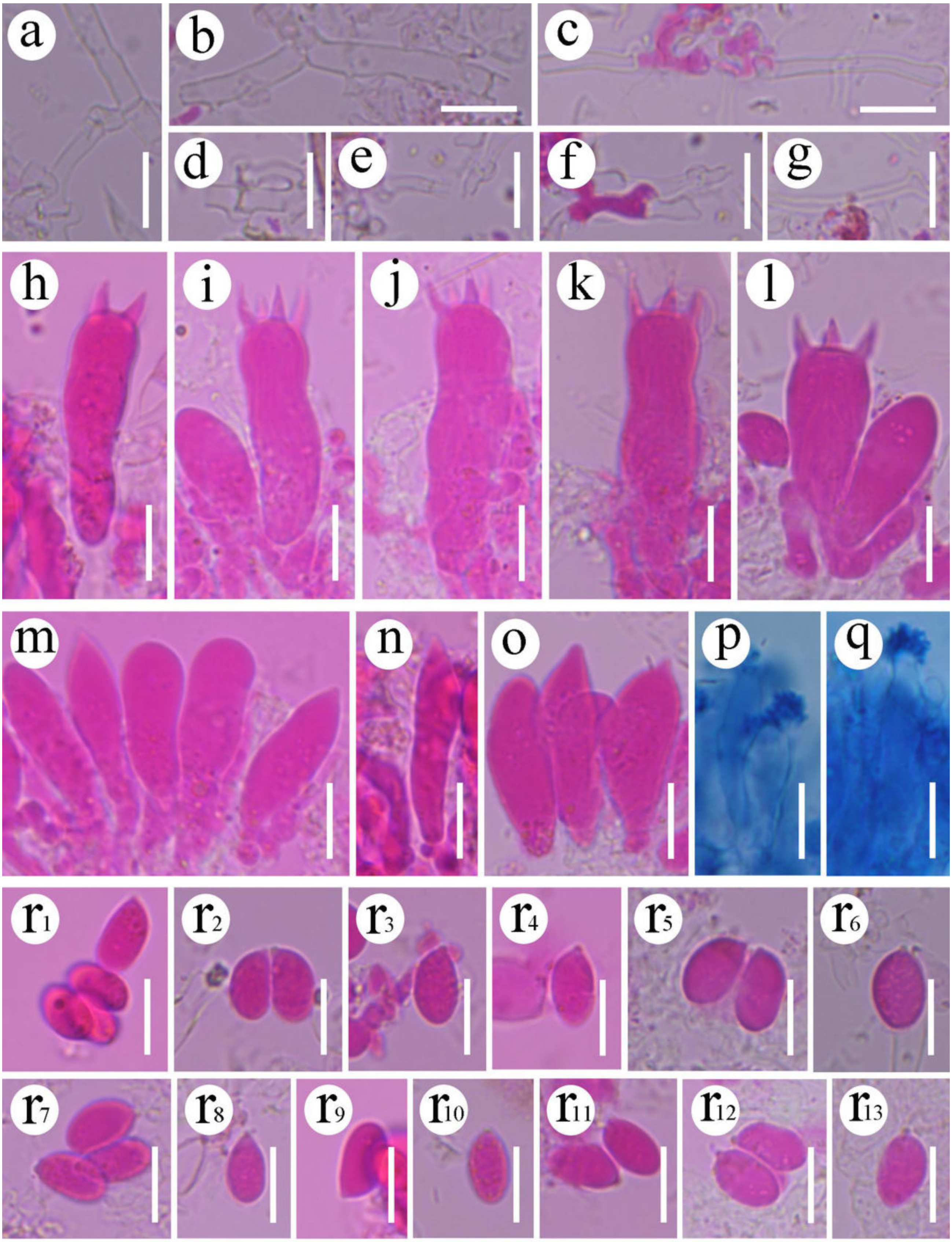

Figure 10 – Microscopic structures of *Marasmius wumengshanensis* (holotype, CLZhao 32014). a–g Generative hyphae. h–l Basidia. m A section of the hymenium and subhymenium. n–o Cystidioles. p–q Cystidia. r Basidiospores. Scale bars: a–r = 10 µm.

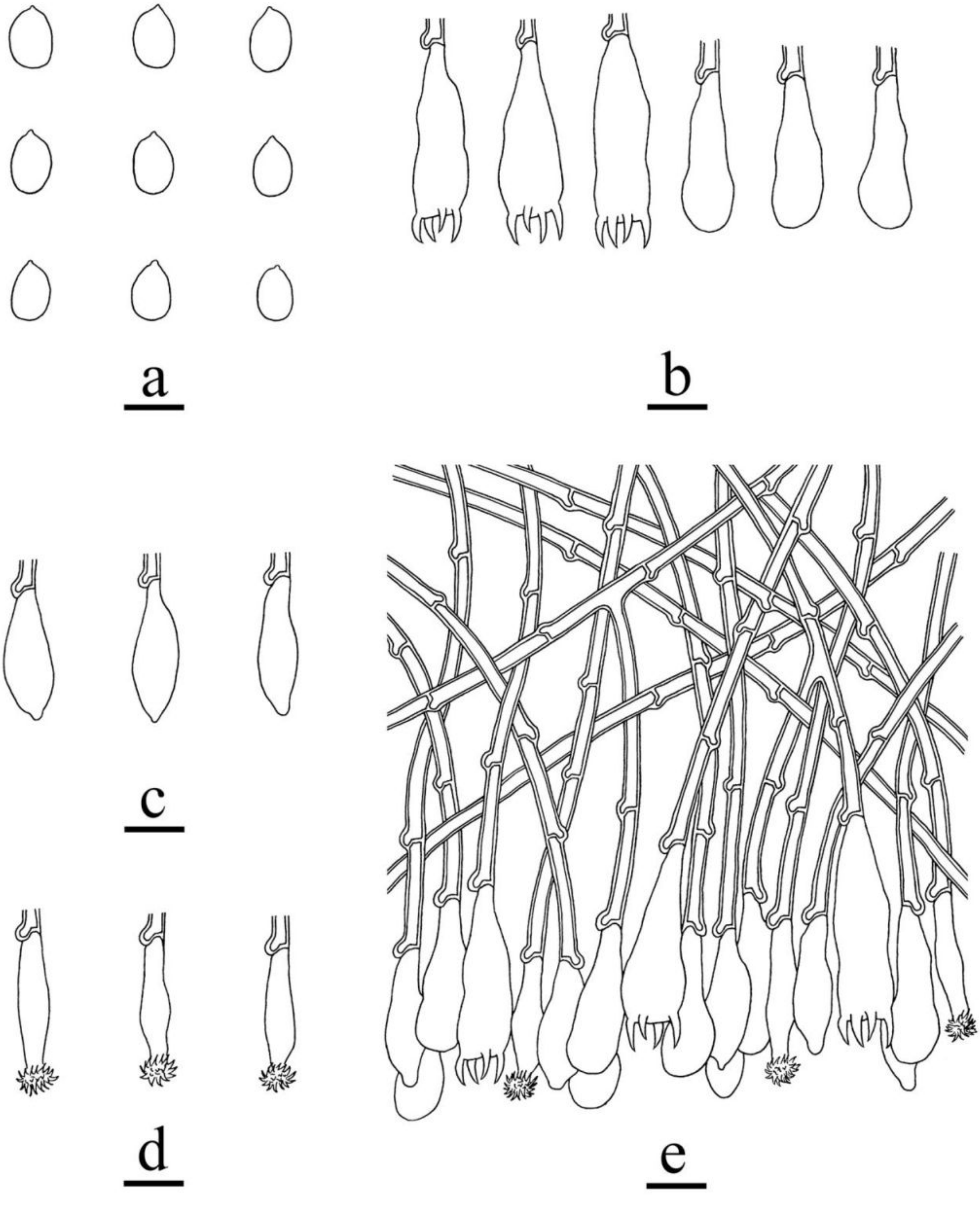

Figure 11 – Microscopic structures of *Marasmius wumengshanensis* (holotype, CLZhao 32014). a Basidiospores. b Basidia and basidioles. c Cystidioles. d Cystidia. e A section of the hymenium and subhymenium. Scale bars: a–e = 10 µm.

Note 24 *Moniliophthora* H.C. Evans, Stalpers, Samson & Benny.

Index Fungorum number: IF18070.

Type species – *Moniliophthora roreri* (Cif.) H.C. Evans, Stalpers, Samson & Benny

Notes – *Moniliophthora* was described by Evans et al. (1978) as an *incertae sedis*, monotypic genus of basidiomycetes, with *M. roreri* as the type (Niveiro et al. 2020). Later, based on phylogenetic studies, Aime & Phillips-Mora (2005) placed *M. roreri* within *Marasmiaceae*

(*Agaricales*), and included *M. perniciosa* (Stahel) Aime & Phillips-Mora in *Moniliophthora*. Many *Moniliophthora* species appear to have a biotrophic habit, including important pathogens of tropical crops such as cocoa (*Theobroma cacao*), while those of *Crinipellis* are primarily saprotrophic (Niveiro et al. 2020).

Note 25 *Paramarasmius* Antonín & Kolařík

Index Fungorum number: IF843224.

Type species – *Paramarasmius palmivorus* (Sharples) Antonín & Kolařík

Notes – *Paramarasmius* was introduced by Antonín et al. (2023) to accommodate *P. palmivorus* as the type species based on morphological characteristics and phylogenetic analyses of ITS and nrLSU sequence data. *Paramarasmius colocasiae* (Capelari & Antonín) W.H. Lu, Suwannar. & Kumla and *P. mesosporus* (Singer) Antonín, K. Hosaka & Kolařík are the other species accepted in the genus (Antonín et al. 2023, Lu et al. 2024). The type species was found on living or dead monocots in coastal sandy dunes across a wide range of climates, from tropical to subtropical and temperate areas (Antonín et al. 2023). The genus is characterized by single or in groups with convex or conical-convex pileus basidiomata, smooth, cylindrical stipitipellis, narrowly clavate caulocystidia, and smooth, thin-walled, ellipsoid to subglobose basidiospores (Antonín et al. 2023). The genus *Paramarasmius* differs from other related genera (*Marasmius*, *Crinipellis*, *Chaetocalathus*, and *Moniliphthora*) by forming the cutis pileipellis without setiform dextrinoid hairs (Antonín et al. 2023). The taxonomic placement of *Paramarasmius* is located in the family *Marasmiaceae* within *Agaricales*.

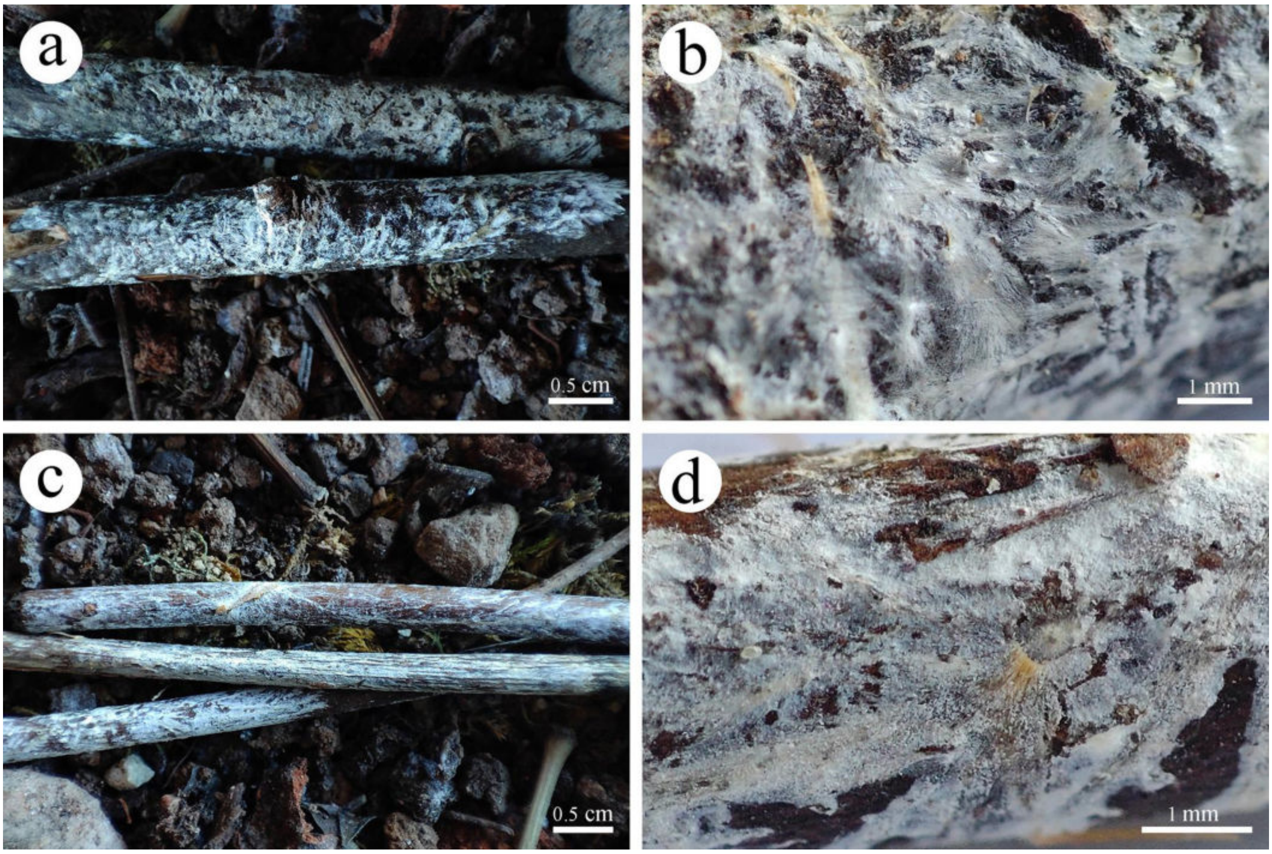

Figure 12 – Basidiomata of *Collybiopsis albobasidiosa* a, b CLZhao 30216 (holotype). c, d CLZhao 30756.

Family *Omphalotaceae* Bresinsky

Index Fungorum number: IF81085.

Type genus – *Omphalotus* Fayod

Note 26 *Collybiopsis* (J. Schröt.) Earle

Index Fungorum number: IF17341.

Type species – *Collybiopsis ramealis* (Bull.) Millsp.

Notes – The genus *Collybiopsis* was erected by Earle (1909) and is typified by *C. ramealis*. The genus is characterized by the collybioid, gymnopoid, marasmielloid, omphalioid, or pleurotoid basidiomata; free to decurrent lamellae; a central to eccentric, insititious to subinsititious stipe; the presence of caulocystidia; and coralloid or diverticulate terminal elements of pileipellis; and ellipsoid to oblong ellipsoid, inamyloid basidiospores with white spore prints (Murrill 1915, Singer 1973a, Antonín & Noordeloos 1993, Retnowati 2018, Oliveira et al. 2019, Kim et al. 2022). Initial molecular studies have segregated *Collybia* (Fr.) Staude and *Marasmius* Fr. and some species of both genera transferred into several genera such as *Gymnopus* Roussel, *Marasmiellus* Murril, *Rhodocollybia* Singer (Moncalvo et al. 2002, Mata et al. 2004a, b, Wilson & Desjardin 2005, Hughes et al. 2010). Wilson & Desjardin (2005) examined nrLSU-based phylogenetic relationships among the gymnopoid and marasmioid fungi and designated two unresolved clades, *gymnopus* and *marasmiellus*. Mata et al. (2007) used molecular data to examine structure within *Gymnopus*, arriving at clades A-N of "gymnopoid fungi", confirming placement of the generic type species of *Marasmiellus*, *Marasmiellus juniperinus* Murrill, within *Gymnopus* clade D. Species within clade D were transferred to *Marasmiellus* (Oliveira *et al*. 2019), then *Collybiopsis* (Petersen & Hughes 2021). Due to its relatively uncharacteristic basidiomata and slight variation in morphological characteristics, agaric taxonomists segregated several genera from *Gymnopus* (Pers.) Roussel; however, they still left a large complex assemblage, called *Marasmiellus* Murrill (Wilson & Desjardin 2005, Hughes et al. 2010, Oliveira et al. 2019, Petersen & Hughes 2017, 2021). Based on the advances in DNA sequencing techniques and analytic methods in the last decade, taxonomists agreed that *Collybiopsis* (J. Schröt.) Earle had clear priority over *Marasmiellus* (Petersen & Hughes 2021, Kim et al. 2022). As a result, *Collybiopsis* replaced *Marasmiellus* because the former has priority over the latter, and *C. ramealis* was assigned as the type species of the genus (Petersen & Hughes 2021, Liu et al. 2024c). Recently, based on a combination of morphological and molecular evidence, the fungal diversity within the genus *Collybiopsis* was analyzed (Zhang et al. 2023c, Li et al. 2024, Liu et al. 2024c, Petersen & Hughes 2024a, Phonrob et al. 2024, Wang et al. 2025). In the present study, based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and the ITS+nrLSU sequence data (Fig. 4), three new species, *Collybiopsis albobasidiosa*, *C. cremea*, and *C. yunnanensis*, are described.

Collybiopsis albobasidiosa J.H. Dong & C.L. Zhao, sp. nov. Figs. 12–14

Index Fungorum number: IF858338.

Etymology –Refers to the white basidiomata of the type specimen.

Type – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 23°48′ N, 97°38′ E, altitude 1000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 19 July 2023, CLZhao 30216 (SWFC).

Description – Basidiomata annual, resupinate, adnate, soft, membranaceous, without odor or taste when fresh, becoming coriaceous upon drying, up to 5 cm long, 1 cm wide, 100 µm thick. Hymenial surface smooth, flocculent, white when fresh, turning to white to slightly cream upon drying. Sterile margin white, fimbriate, up to 0.5 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, slightly thick-walled, branched, interwoven, 2.5–4 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Septate cystidia, colorless, thick-walled, firmly encrusted on the surface and almost entirely, 61–72.5 × 7.5–9 µm; cystidioles absent. Basidia subclavate, with 4 sterigmata and a basal clamp connection, 14.5–15.5 × 4–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores cylindrical, colorless, thin-walled, smooth, IKI–, CB–, (5.5–)6–8 × 2.8–4(–4.5) µm, L = 7.22 µm, W = 3.28 µm, Q = 2.01–2.52, Q_m = 2.21 ± 0.18 (n = 60/2).

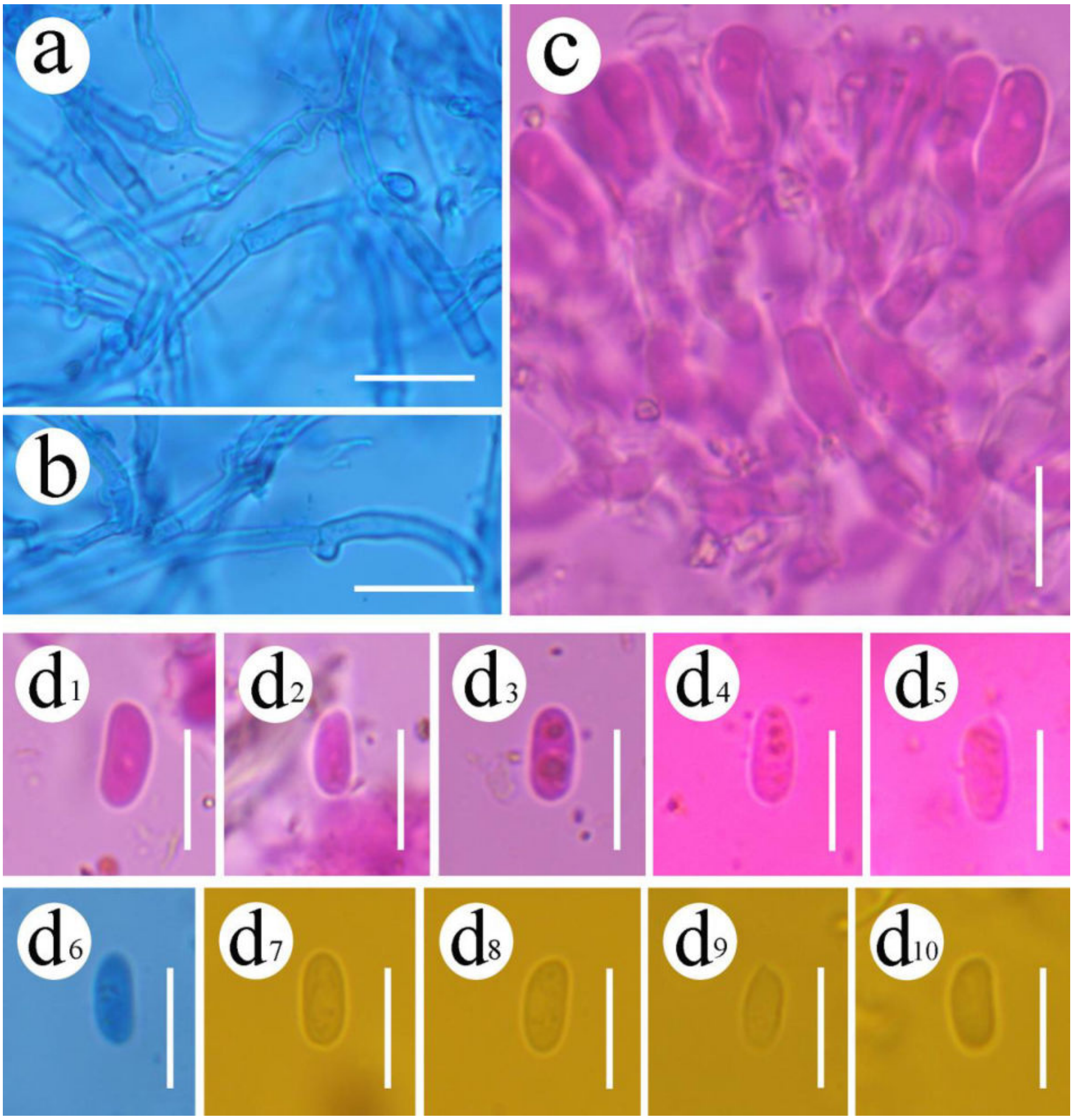

Figure 13 – Microscopic structures of *Collybiopsis albobasidiosa* (holotype, CLZhao 30216). a–b Generative hyphae. c A section of the hymenium and subhymenium. d Basidiospores. Scale bars: a–b= 20 µm; c–d = 10 µm.

Material examined (paratype) – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 23°48′ N, 97°38′ E, altitude 1000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 21 July 2023, CLZhao 30756 (SWFC).

Notes – *Collybiopsis albobasidiosa*, grouped in *Collybiopsis* (*Omphalotaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and ITS+nrLSU sequence data (Fig. 4), was closely associated with *C. confluens* (Pers.) R.H. Petersen, *C. parvula* (J.L. Mata, R.H. Petersen & K.W. Hughes) R.H. Petersen, and *C. villosipes* (Cleland) R.H. Petersen. However, *C. confluens* differs from *C. albobasidiosa* by its pileate basidiomata (Hughes & Petersen 2015); *C. parvula* differentiates from *C. albobasidiosa* by its pileate basidiomata with brown, larger basidia (20–38 × 4–10 µm *vs* 14.5–15.5 × 4–5.5 µm), and lacrymoid to narrowly ellipsoid basidiospores (Mata et al. 2007); *C. villosipes* can be distinguished from *C. albobasidiosa* by its brownish basidiomata, larger basidia (25–34 × 6.5–7.5 µm *vs* 14.5–15.5 × 4–5.5 µm, Desjardin et al. 1997).

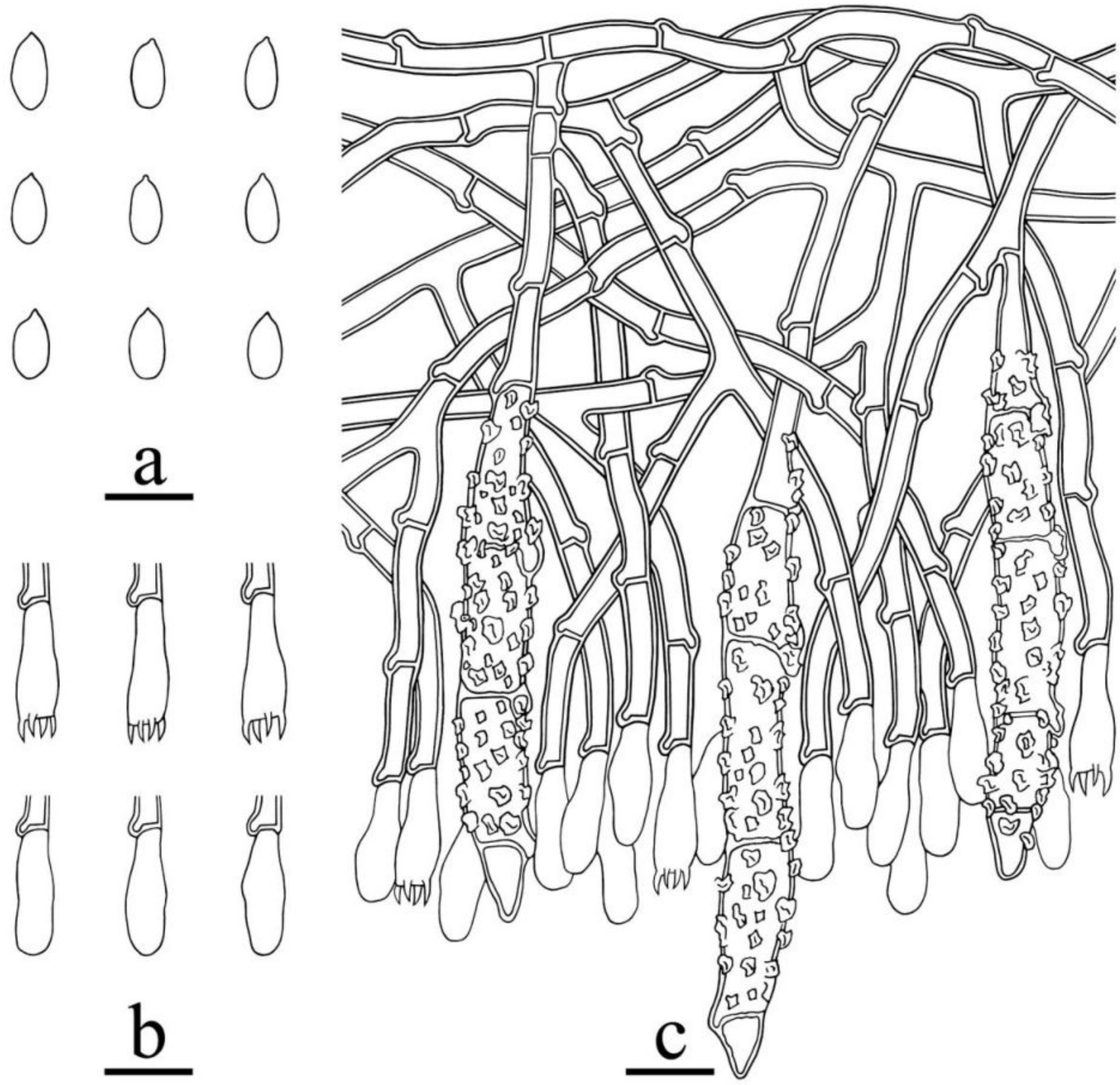

Figure 14 – Microscopic structures of *Collybiopsis albobasidiosa* (holotype, CLZhao 30216). a Basidiospores. b Basidia and basidioles. c A section of the hymenium and subhymenium. Scale bars: a–c = 10 µm.

Morphologically, *Collybiopsis albobasidiosa* shares similarities with *C. filamentipe* R.H. Petersen, *C. orientisubnuda* J.S. Kim & Y.W. Lim, and *C. undulata* J.S. Kim & Y.W. Lim in sharing the cylindrical basidiospores. However, *C. filamentipe* differs from *C. albobasidiosa* by its pileate basidiomata with pinkish buff, larger basidia (26–33 × 7–8 um *vs* 14.5–15.5 × 4–5.5 µm), and longer basidiospores (8–9 × 2.5–3.5 µm *vs* 6–8 × 2.8–4 µm, Petersen & Hughes 2021); *C. orientisubnuda* differentiates from *C. albobasidiosa* by its pileate basidiomata with brownish orange, longer basidia (19.8–28.7 × 3.7–7.3 um *vs* 14.5–15.5 × 4–5.5 µm, Kim et al. 2022); *C. undulata* can be distinguished from *C. albobasidiosa* by its pileate basidiomata with dark brown, longer basidia (15–22.3 × 3.6–6.8 um *vs* 14.5–15.5 × 4–5.5 µm, Kim et al. 2022).

Collybiopsis cremea J.H. Dong & C.L. Zhao, sp. nov. Figs. 15–17

Index Fungorum number: IF858339.

Etymology – Refers to the cream hymenial surface of the type specimen.

Type – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 23°48′ N, 97°38′ E, altitude 1000 m asl., on the dead stems of *Dendrocalamus sinicus* Chia et J.L. Su, leg. C.L. Zhao, 18 July 2023, CLZhao 29915 (SWFC).

Description – Basidiomata annual, resupinate, adnate, soft, membranaceous, without odor or taste when fresh, becoming coriaceous upon drying, up to 10 cm long, 5 cm wide, 100 µm thick. Hymenial surface smooth, white when fresh, turning to cream upon drying. Sterile margin cream, slightly fimbriate, up to 0.5 mm wide.

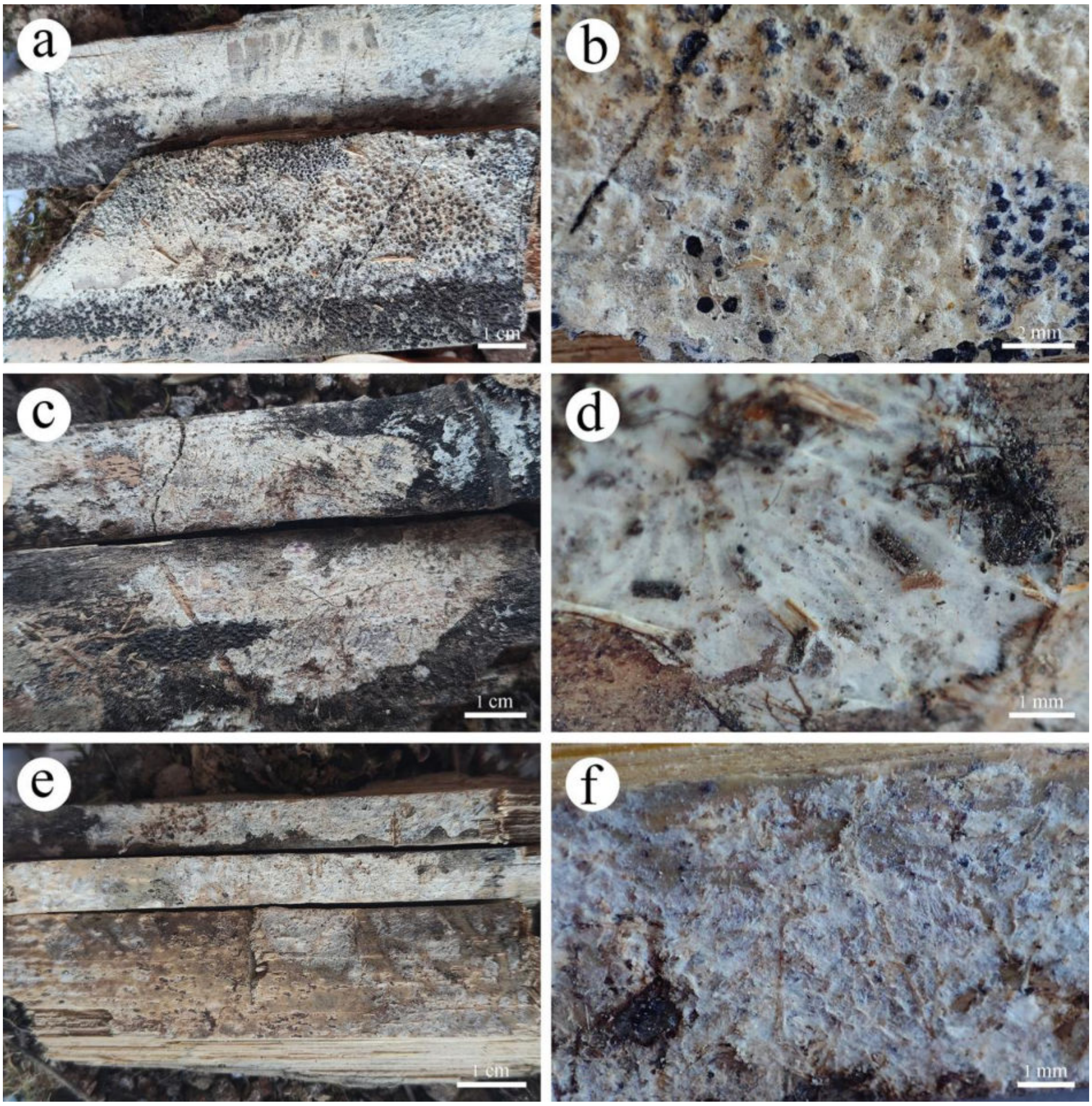

Figure 15 – Basidiomata of *Collybiopsis cremea* a, b CLZhao 29915 (holotype). c, d CLZhao 29941. e, f CLZhao 30022.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, slightly thick-walled, branched, interwoven, 2.5–4 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia capitate, colorless, thin-walled, 30–42.5 × 4.5–5.5 µm; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 13.5–18 × 4–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid, colorless, thick-walled, smooth, with a few guttulae, IKI–, CB+, (4.5–)4.7–5.8 × 3.3–3.8(–4) µm, L = 5.16 µm, W = 3.55 µm, Q = 1.30–1.61, Q_m = 1.45 ± 0.10 (n = 60/2).

Material examined (paratypes) – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 23°48′ N, 97°38′ E, altitude 1000 m asl., on the dead stems of *Dendrocalamus sinicus* Chia et J.L. Su, leg. C.L. Zhao, 18 July 2023, CLZhao 29941, CLZhao 30022 (SWFC).

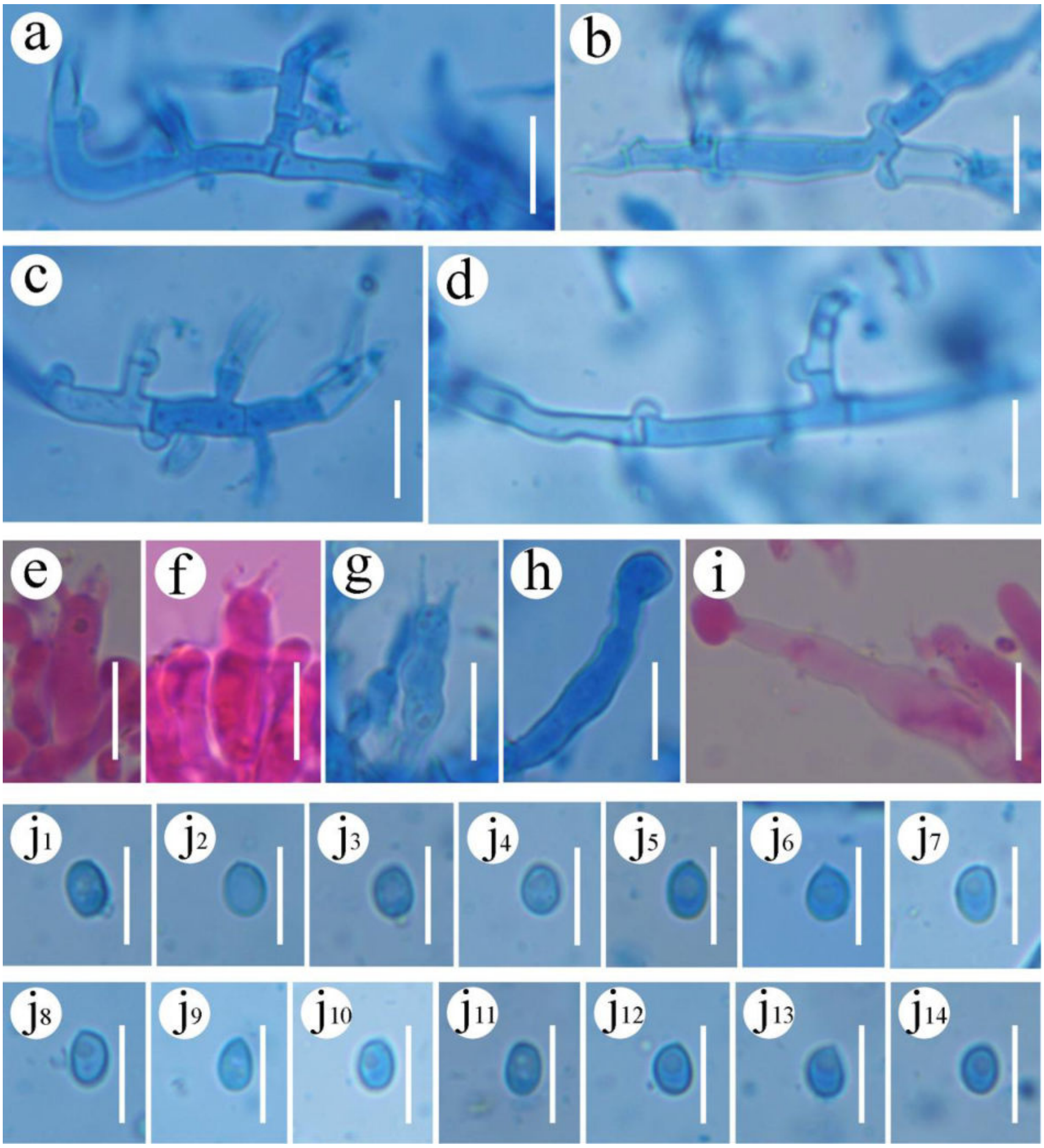

Figure 16 – Microscopic structures of *Collybiopsis cremea* (holotype, CLZhao 29915). a–d Generative hyphae. e–g Basidia. h–i Capitate cystidia. j Basidiospores. Scale bars: a–j = 10 µm.

Notes – *Collybiopsis cremea* grouped in *Collybiopsis* (*Omphalotaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and ITS+nrLSU sequence data (Fig. 4), was sister to *C. yunnanensis*. However, *C. yunnanensis* can be distinguished from *C. cremea* by its farinaceous basidiomata with straw-yellow, and larger basidiospores (6–6.8 × 4.2–5 µm *vs* 4.7–5.8 × 3.3–3.8 µm).

Morphologically, *Collybiopsis cremea* shares similarities with *C. bambusicola* Q.Y. Zhang, J. Si & H.J. Li, *C. complicata* R.H. Petersen, *C. gibbosa* (Corner) R.H. Petersen, *C. melanopus* (A.W. Wilson, Desjardin & E. Horak) R.H. Petersen, *C. minor* R.H. Petersen, and *C. ramealis* (Bull.) Millsp. in sharing the ellipsoid basidiospores. However, *C. bambusicola* differentiates from *C. cremea* by its brownish gray pileal surface, larger basidia (25–32 × 6–8 µm *vs* 13.5–18 × 4–5.5 µm), and longer basidiospores (6–8.3 × 3–4.3 µm *vs* 4.7–5.8 × 3.3–3.8 µm, Zhang et al. 2023c); *C. complicata* can be distinguished from *C. cremea* by its marasmielloid or gymnopoid basidiomata with snuff brown, larger basidia (35–60 × 7–9 µm *vs* 13.5–18 × 4–5.5 µm), and longer basidiospores (6.5–8.5 × 3–4 µm *vs* 4.7–5.8 × 3.3–3.8 µm, Petersen & Hughes 2024a); *C. gibbosa* differs from *C. cremea* by its grayish orange basidiomata, both larger basidia (22–30 × 5.5–7 µm *vs* 13.5–18 × 4–5.5 µm), and basidiospores (8–9.5 × 4–4.5 µm *vs* 4.7–5.8 × 3.3–3.8 µm, Phonrob et al. 2024); *C. melanopus* differentiates from *C. cremea* by its pileate basidiomata with beige, both longer basidia (23–30 × 5–7 µm *vs* 13.5–18 × 4–5.5 µm), and basidiospores (7–8.5 × 3.5–4.5 µm *vs* 4.7–5.8 × 3.3–3.8 µm, Phonrob et al. 2024); *C. minor* can be distinguished from *C. cremea* by its brown basidiomata, both larger basidia (30–43 × 7–9 µm *vs* 13.5–18 × 4–5.5 µm), and basidiospores (9–10 × 4–4.5 µm *vs* 4.7–5.8 × 3.3–3.8 µm, Petersen & Hughes 2021); *C. rameali*s differs from *C. cremea* by its ochraceous buff basidiomata, larger basidia (26–32 × 7–8.5 µm *vs* 13.5–18 × 4–5.5 µm), and longer basidiospores (7–10 × 2.5–4 µm *vs* 4.7–5.8 × 3.3–3.8 µm, Petersen & Hughes 2021).

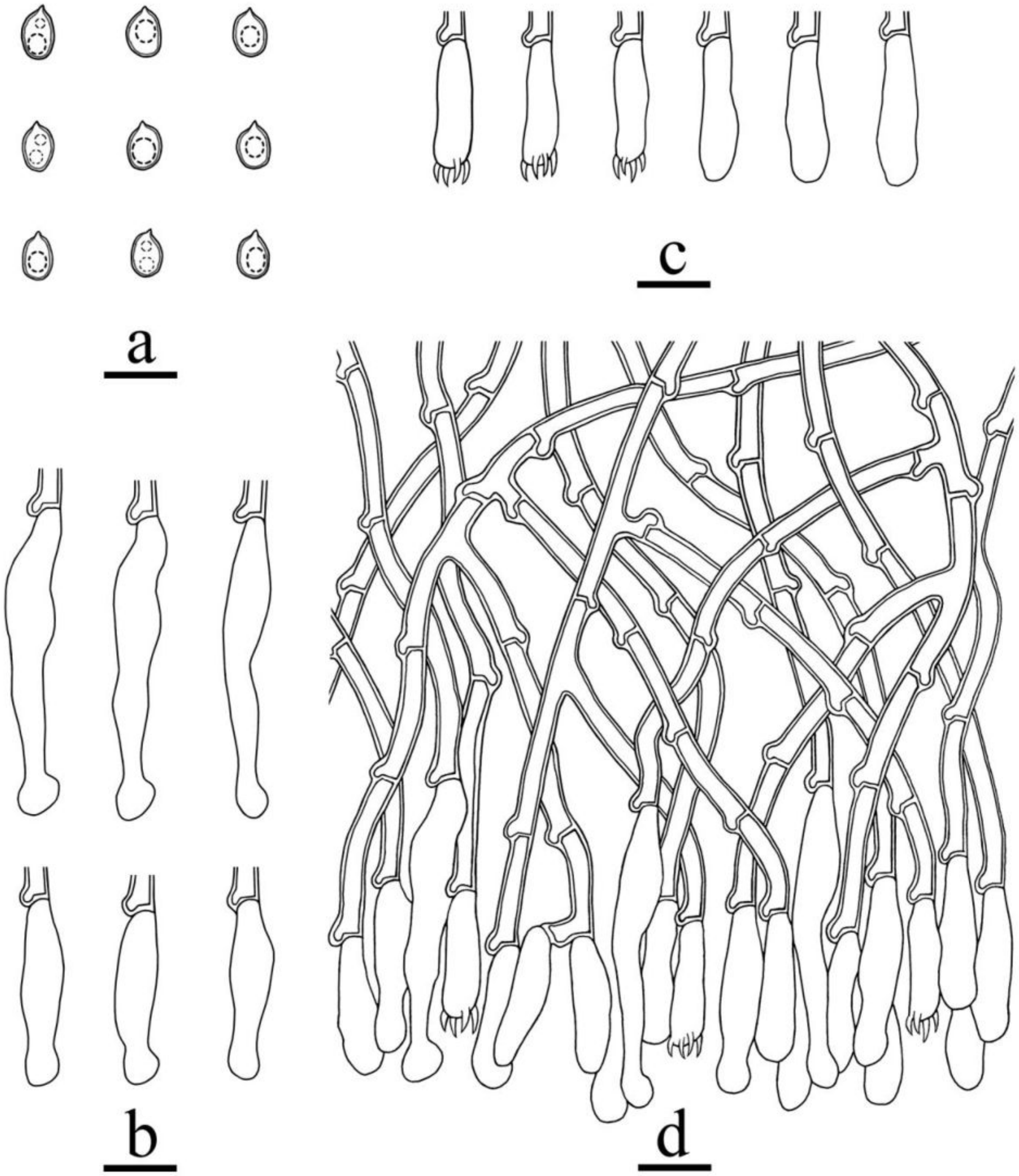

Figure 17 – Microscopic structures of *Collybiopsis cremea* (holotype, CLZhao 29915). a Basidiospores. b Capitate cystidia. c Basidia and basidioles. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 µm.

Collybiopsis yunnanensis J.H. Dong & C.L. Zhao, sp. nov. Figs. 18–20

Index Fungorum number: IF858340.

Etymology – Refers to the locality (Yunnan Province) of the type specimen.

Type – China, Yunnan Province, Dali, Weishan County, Qinghua Town, Green Peacock Provincial Nature Reserve, GPS coordinates 25°10′ N, 100°05′ E, altitude 2000 m asl., on the dead bamboo, leg. C.L. Zhao, 18 July 2023, CLZhao 22546 (SWFC).

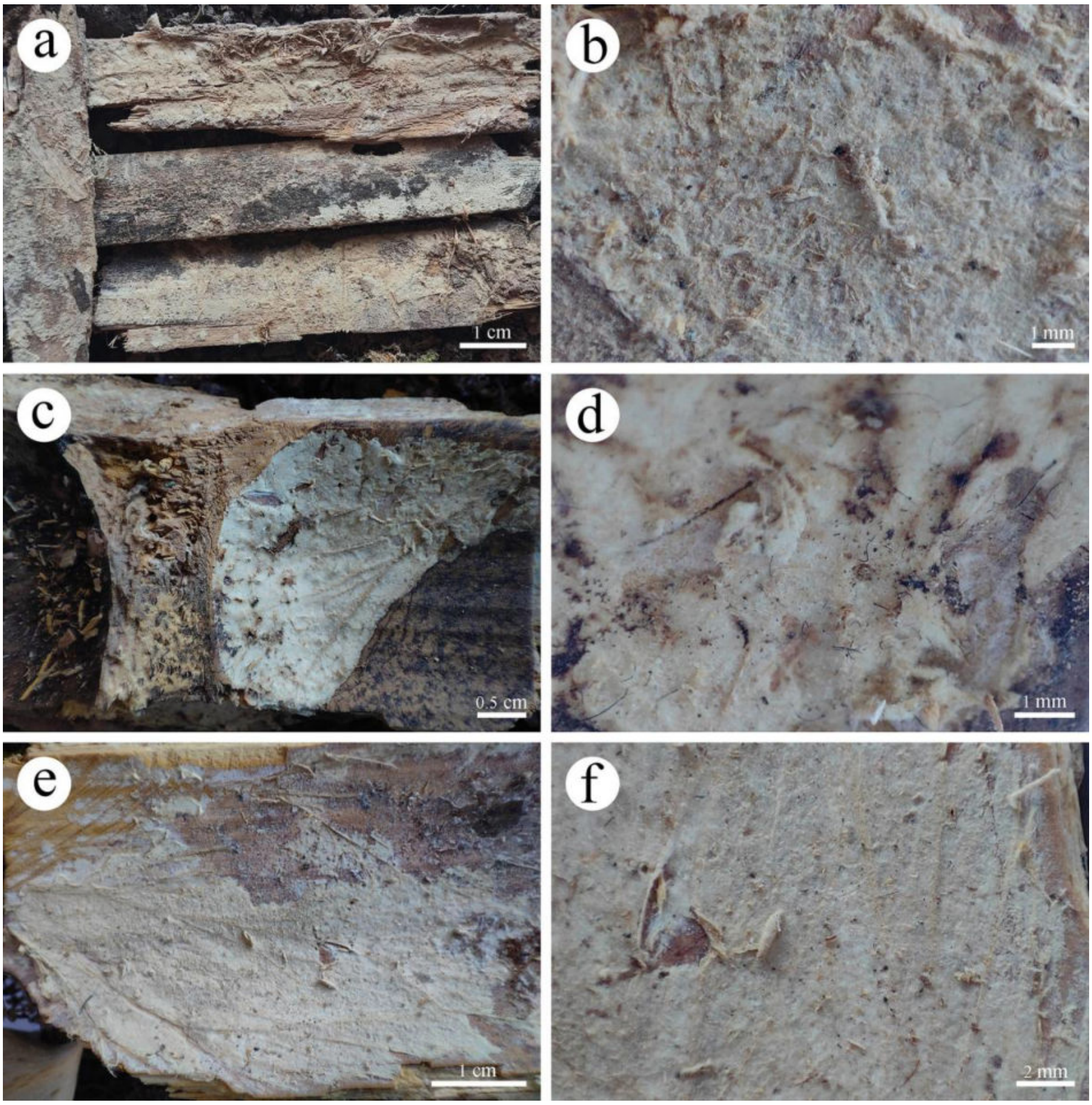

Figure 18 – Basidiomata of *Collybiopsis yunnanensis* a, b CLZhao 22546 (holotype). c, d CLZhao 22565. e, f CLZhao 22558.

Description – Basidiomata annual, resupinate, adnate, soft, membranaceous, without odor or taste when fresh, becoming farinaceous upon drying, up to 10 cm long, 5 cm wide, 150 µm thick. Hymenial surface smooth, white to slightly cream when fresh, turning to cream to straw-yellow upon drying. Sterile margin cream, slightly fimbriate, up to 0.5 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, slightly thick-walled, branched, interwoven, 2–3 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia capitate, colorless, slightly thick-walled, 16.5–26 × 4–6.5 µm; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 14–17.5 × 4–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid, colorless, slightly thick-walled, smooth, with one guttula, IKI–, CB+, 6–6.8 × 4.2–5(–5.2) µm, L = 6.44 µm, W = 4.71 µm, Q = 1.27–1.51, Q_m = 1.37 ± 0.07 (n = 90/3).

Material examined (paratypes) – China, Yunnan Province, Dali, Weishan County, Qinghua Town, Green Peacock Provincial Nature Reserve, GPS coordinates 25°10′ N, 100°05′ E, altitude 2000 m asl., on the dead bamboo, leg. C.L. Zhao, 18 July 2023, CLZhao 22508, CLZhao 22558, CLZhao 22565 (SWFC).

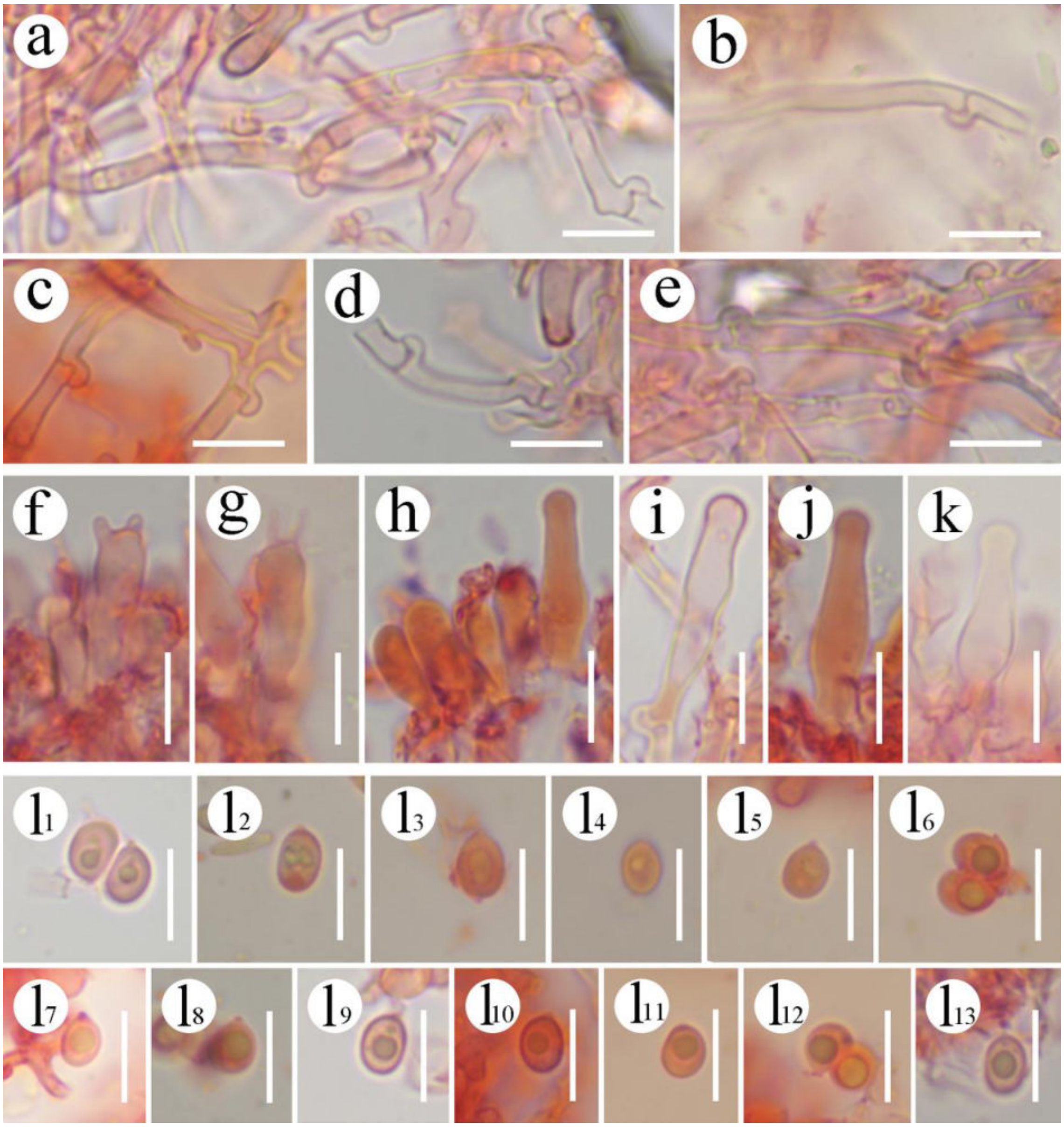

Figure 19 – Microscopic structures of *Collybiopsis yunnanensis* (holotype, CLZhao 22546). a–e Generative hyphae. f–g Basidia. h A section of the hymenium and subhymenium. i–k Capitate cystidia. l Basidiospores. Scale bars: a–l = 10 µm.

Notes – *Collybiopsis yunnanensis* grouped in *Collybiopsis* (*Omphalotaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and ITS+nrLSU sequence data (Fig. 4), was sister to *C. cremea*. However, *C. cremea* can be distinguished from *C. yunnanensis* by its coriaceous basidiomata with cream, and smaller basidiospores (4.7–5.8 × 3.3–3.8 µm *vs* 6–6.8 × 4.2–5 µm).

Morphologically, *Collybiopsis yunnanensis* shares similarities with *C. bambusicola*, *C. complicata*, *C. gibbosa*, *C. melanopus*, *C. minor*, and *C. ramealis* in sharing the ellipsoid basidiospores. However, *C. bambusicola* differentiates from *C. yunnanensis* by its brownish gray pileal surface, and larger basidia (25–32 × 6–8 µm *vs* 14–17.5 × 4–5.5 µm, Zhang et al. 2023c); *C. complicata* can be distinguished from *C. yunnanensis* by its marasmielloid or gymnopoid basidiomata with snuff brown, larger basidia (35–60 × 7–9 µm *vs* 14–17.5 × 4–5.5 µm), and narrower basidiospores (6.5–8.5 × 3–4 µm *vs* 6–6.8 × 4.2–5 µm, Petersen & Hughes 2024a); *C. gibbosa* differs from *C. yunnanensis* by its grayish orange basidiomata, larger basidia (22–30 × 5.5–7 µm *vs* 14–17.5 × 4–5.5 µm), and longer basidiospores (8–9.5 × 4–4.5 µm *vs* 6–6.8 × 4.2–5 µm, Phonrob et al. 2024); *C. melanopus* differentiates from *C. yunnanensis* by its pileate basidiomata with beige, both longer basidia (23–30 × 5–7 µm *vs* 14–17.5 × 4–5.5 µm), and basidiospores (7–8.5 × 3.5–4.5 µm *vs* 6–6.8 × 4.2–5 µm, Phonrob et al. 2024); *C. minor* can be distinguished from *C. yunnanensis* by its brown basidiomata, larger basidia (30–43 × 7–9 µm *vs* 14–17.5 × 4–5.5 µm), and longer basidiospores (9–10 × 4–4.5 µm *vs* 6–6.8 × 4.2–5 µm, Petersen & Hughes 2021); *C. ramealis* differs from *C. yunnanensis* by its ochraceous buff basidiomata, larger basidia (26–32 × 7–8.5 µm *vs* 14–17.5 × 4–5.5 µm), and longer basidiospores (7–10 × 2.5–4 µm *vs* 6–6.8 × 4.2–5 µm, Petersen & Hughes 2021).

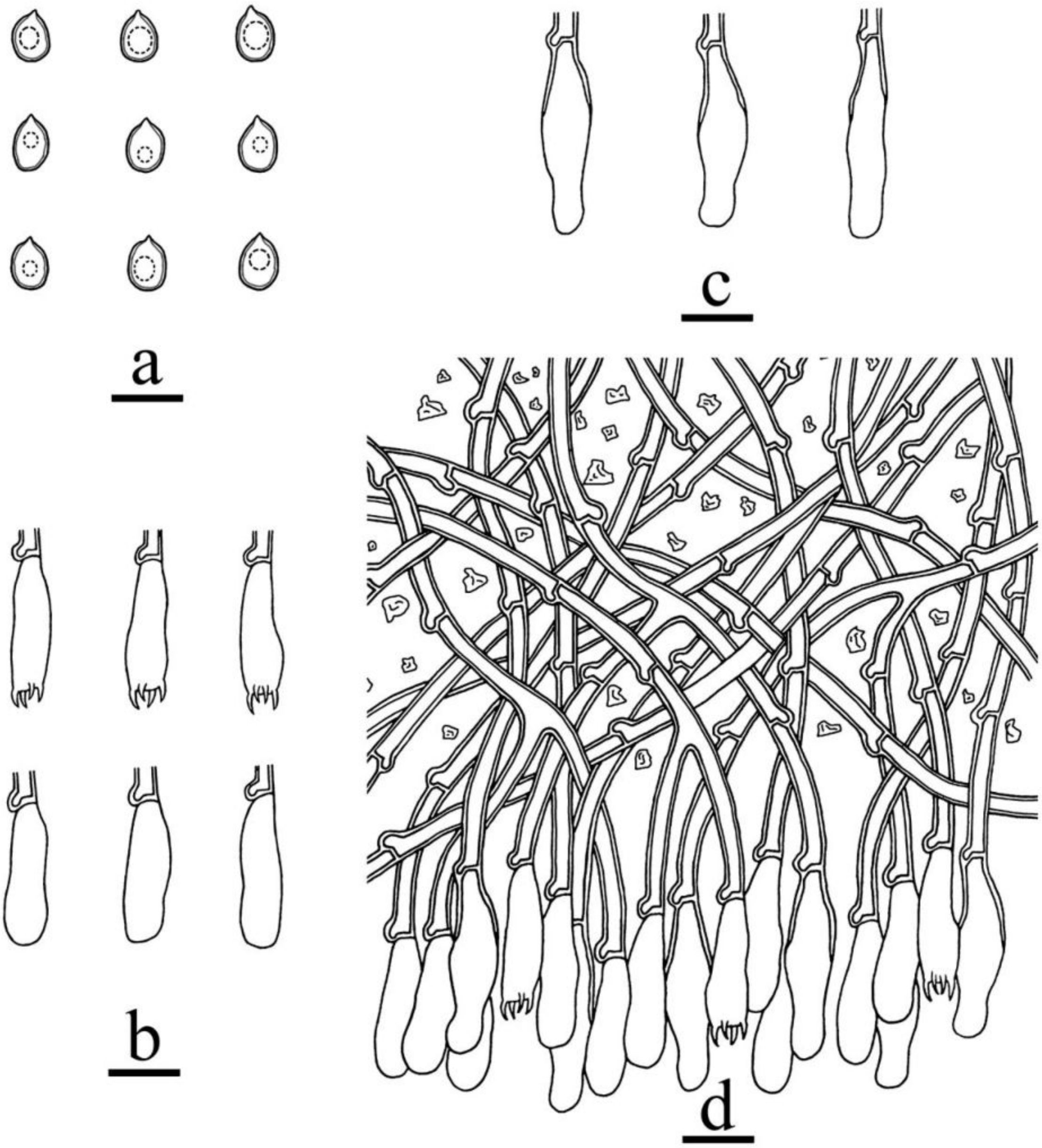

Figure 20 – Microscopic structures of *Collybiopsis yunnanensis* (holotype, CLZhao 22546). a Basidiospores. b Basidia and basidioles. c Capitate cystidia. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 µm.

Note 27 ***Mycetinis*** Earle

Index Fungorum number: IF18089.

Type species – *Mycetinis alliaceus* (Jacq.) Earle ex A.W. Wilson & Desjardin

Notes – *Mycetinis* was described by Earle (1909) to accommodate *M. alliaceus* as the type species, which is globally distributed and saprobic in nature (Peterson & Hughes 2017). The basidiomata of *Mycetinis* emit an odour of garlic-like to cabbage-like (Wilson & Desjardin 2005, Peterson & Hughes 2017). Molecular analysis (nrLSU) revealed a distinct clade comprising *Marasmius alliaceus* (Jacq.) Fr., *M. applanatipes* Desjardin, *M. copelandii* Peck, *M. opacus* Berk. & M.A. Curtis, and *M. scorodonius* (Fr.) Fr., which have been reclassified under the genus *Mycetinis* (Wilson & Desjardin 2005).

Note 28 ***Neonothopanus*** R.H. Petersen & Krisai

Index Fungorum number: IF28363.

Type species – *Neonothopanus nambi* (Speg.) R.H. Petersen & Krisai

Notes – The genus *Neonothopanus* was established by Petersen & Krisai-Greilhuber (1999) based on *Pleurotus nambi* (Speg.) Speg., which was first reported as *Agaricus nambi* Speg.

Two species were transferred to *Neonothopanus* based on specimens collected in Benin, Ghana, and Brazil (Capelari et al. 2011). Based on morphological study and molecular analysis, Capelari et al. (2011) believed that a specimen they found in central Brazil belonged to the genus *Neonothopanus*. Bua-art et al. (2011) studied the effects of bioactive compounds of *N. nambi* on root-knot nematodes. Later, Kanokmedhakul et al. (2012) found four new aristolane sesquiterpenes from *N. nambi.* Bondar et al. (2014) studied the luminescent system of *N. nambi* and its mechanism. Mogilnaya et al. (2016) studied the activities of total peroxidase and catalase during light emission. During the same year, Purtov et al. (2018) obtained high-purity luciferase from *N. nambi* for the first time, paving the way for research. In terms of numbers, *Neonothopanus* was a small genus, but it has potential as a valuable resource for interesting bioactive substances (Hu et al. 2021).

Note 29 ***Paramycetinis*** R.H. Petersen

Index Fungorum number: IF555792.

Type species – *Paramycetinis austrobrevipes* R.H. Petersen

Notes – *Paramycetinis* was introduced by Petersen & Hughes (2020), as the type species of *P. austrobrevipes*, which is from Australia. The genus *Paramycetinis* comprises two species related to *Mycetinis*, specifically *P. austrobrevipes* R.H. Petersen and *P. caulocystidiatus* R.H. Petersen. Both *Paramycetinis* species are characterized by luxuriant rhizomorphs, with basidiomata arising occasionally as side branches but also separately from rhizomorphs, clavate basidia with 4-sterigmate spores, and thin-walled, smooth, inamyloid basidiospores with white or off-white deposits (Petersen & Hughes 2020).

Note 30 ***Pseudomarasmius*** R.H. Petersen & K.W. Hughes

Index Fungorum number: IF555729.

Type species – *Pseudomarasmius pallidocephalus* (Gilliam) R.H. Petersen

Notes – Petersen & Hughes (2020) introduced *Pseudomarasmius* to accommodate four species and four others previously placed in *Marasmius*. Oliveira et al. (2019) resolved a clade they named /pallidocephalus (not a genus name). Subsequently, this clade was proposed as *Pseudomarasmius* by Petersen & Hughes (2020). *Pseudomarasmius* encompasses significant basidiomata variation, but nrLSU and ITS-based phylogenies support its taxa in a monophyletic clade that occupies a position related to *Rhodocollybia* (Petersen & Hughes 2020). The genus differs from *Marasmius* by the presence of diverticulate hyphae in the pileipellis and the absence of clamp connections (Petersen & Hughes 2020).

Family *Porotheleaceae* Murrill

Index Fungorum number: IF81214.

Type genus – *Porotheleum* Fr.

Note 31 *Chrysomycena* Vizzini, Picillo, Perrone & Dovana

Index Fungorum number: IF832697

Type species – *Chrysomycena perplexa* Picillo, Vizzini & Perrone

Notes – *Chrysomycena* was proposed in *Porotheleaceae* by Vizzini et al. (2019b) to accommodate *C. perplexa* from Italy, based on morphological characteristics and phylogenetic analyses of ITS and nrLSU sequences. However, with more taxon sampling from Portugal and Spain with the evidence by sequence data analyses, Villarreal et al. (2021) discovered *C. dunicola* (M. Villarreal, Esteve-Rav., Barrasa & A. Ortega), M. Villarreal, Esteve-Rav., F. Sánchez & Pérez de Gregorio (≡ *Mycena dunicola* M. Villarreal, Esteve-Rav., Barrasa & A. Ortega). Also, they suggested that *C. perplexa* should be synonymized under *C. dunicola* based on morphology and phylogenetic analysis. *Chrysomycena* is characterized by a habitus from collybioid to clitocyboid, a pileic fibrillary surface, abundant rhizomorphs at the base of the stipe, a sub-hymenidermic to subtrichodermic pileipellis (at least in the middle of the pileus), non-amyloid spores, and widely clavate cheilocystidia (Vizzini et al. 2019b). *Chrysomycena* species can be found in *Pinus* forests, coastal areas, or dunes in Mediterranean areas such as Italy, Portugal, and Spain (Vizzini et al. 2019b, Villarreal et al. 2021). The taxonomic placement of *Chrysomycena* is in the family *Porotheleaceae* within *Agaricales*.

Note 32 *Hydropodia* Vizzini & Consiglio

Index Fungorum number: IF843200.

Type species – *Hydropodia subalpina* (Höhn.) Vizzini, Consiglio & M. Marchetti

Notes – The genus *Hydropus* Kühner ex Singer is polyphyletic in *Porotheleaceae* (Consiglio et al. 2021). Phylogenetic analyses of *Porotheleaceae* based on ITS and nrLSU sequences showed *Hydropus subalpinus* (Höhn.) formed a distinct clade in the family (Consiglio et al. 2021). Thus, *Hydropodia* was proposed with the type species *H. subalpine* (Consiglio et al. 2021). The following were identified by Consiglio et al. (2021) as synonyms of the new combination *Hydropodia subalpine* as *Mycena subalpina* Höhn., Sber. Akad. Wiss. Wien, *Hemimycena subalpina* (Höhn.) Singer, *Marasmiellus subalpinus* (Höhn.) Singer, *Hydropus subalpinus*, and *Collybia pseudoradicata* J.E. Lange & F.H. Møller. Species of this genus form a mycenoid to collybioid basidiomata (Consiglio et al. 2021). The taxonomic placement of *Hydropodia* is within *Porotheleaceae*, in the *Agaricales*.

Note 33 *Marasmiellomycena* De la Peña-Lastra, Mateos, Kolařík, Ševčíková & Antonín

Index Fungorum number: IF839731.

Type species – *Marasmiellomycena pseudoomphaliiformis* Antonín & Ševčíková

Notes – *Marasmiellomycena* was introduced by Senanayake et al. (2023) to accommodate *M. pseudoomphaliiformis* as the type. This genus contains agaricoid, saprotrophic species with omphaloid or marasmioid basidiomata, well-developed lamellae, thin stipe, smooth spores, indistinct or absent cheilocystidia, absent pleurocystidia, and present clamp connections (Senanayake et al. 2023). *Marasmiellomycena omphaliiformis* was the other accepted species of the genus, initially described as *Marasmius omphaliiformis* (Kühner & Romagnesi 1954), but phylogenetic analyses have placed it in the *Porotheleaceae*. Consiglio et al. (2021) combined *Marasmius omphaliiformis* with *Porotheleum* Fr., despite its different morphology, as a member of the cypheloid genus *Porotheleum* sensu stricto, by sharing its lignicolous habitat, the presence of clamp connections, a sarcodimitic structure sensu Redhead (1987), and some metachromatic elements. Phylogenetic analyses of *Porotheleaceae* based on ITS and nrLSU sequences showed *Marasmiellomycena* formed a distinct clade in the family (Senanayake et al. 2023). Na et al. (2024) confirmed the *Marasmiellomycena* as a separate genus by ITS, nrLSU, and *rpb*2 analyses, described one new species, *M. tomentosa* Q. Na & Y.P. Ge, and combined *Porotheleum albodescendens* J.A. Cooper into *Marasmiellomycena*. Thus, this genus is known from Asia (China), Europe, and North America, where it grows on dead wood and decaying leaves (Senanayake et al. 2023, Na et al. 2024). The taxonomic placement of *Marasmiellomycena* is in the family *Porotheleaceae* within *Agaricales*.

Note 34 *Pseudohydropus* Vizzini & Consiglio

Index Fungorum number: IF843195.

Type species – *Pseudohydropus floccipes* (Fr.) Vizzini & Consiglio

Notes – *Pseudohydropus* was introduced by Consiglio et al. (2021) to accommodate *P. floccipes* as the type. This is an agaricoid genus, saprotrophic, lignicolous, found on buried wood (Consiglio et al. 2021). Currently, four species of *Pseudohydropus* have been described worldwide by Consiglio et al. (2021). Phylogenetic analyses based on ITS and nrLSU sequences indicated its phylogenetic position within *Porotheleaceae* as sister to a clade consisting of *Porotheleum* Fr. and *Pulverulina* Matheny & K.W. Hughes (Consiglio et al. 2021). Compared with the other genera within *Porotheleaceae*, species of *Pseudohydropus* are distinguished by their mycenoid habit, globose to largely ellipsoid, inamyloid basidiospores, presence of hymenial cystidia (cheilo- and pleurocystidia), caulocystidia and pileocystidia, and a pileipellis as xero- to ixocutis with abundant, clavate pileocystidia (Consiglio et al. 2021). The taxonomic placement of *Pseudohydropus* is in the family *Porotheleaceae* within *Agaricales*.

Note 35 *Pulverulina* Matheny & K.W. Hughes

Index Fungorum number: IF835131.

Type species – *Pulverulina ulmicola* (H.E. Bigelow) Matheny & K.W. Hughes

Notes – Matheny et al. (2020) introduced *Pulverulina* to accommodate the monotypic lineage *Clitocybe ulmicola* H.E. Bigelow in *Porotheleaceae*. The genus is characterized by small, clitocyboid, pileate-stipitate basidiomata with a tough, pruinose stipe, distant decurrent lamellae; smooth inamyloid basidiospores, long, abundant caulocystidia, interwoven lamellar trama, and lignicolous habit on the bark of living trees (Matheny et al. 2020). Na et al. (2024) confirmed *Pulverulina* as a separate genus by ITS, nrLSU, and *rpb*2 analyses, and described one new species, *Pulverulina flavoalba* Q. Na & Y.P. Ge. The taxonomic placement of *Pulverulina* is in the *Porotheleaceae* in the *Agaricales*.

Note 36 *Vizzinia* Ševčíková & Kolařík

Index Fungorum number: IF900586.

Type species – *Vizzinia nigripes* (Angelini, Vizzini, Consiglio & M. Marchetti) Ševčíková & Kolařík

Notes – *Vizzinia* was introduced by Senanayake et al. (2023) to accommodate *Vizzinia nigripes* as the type. This genus contains two species originally described under *Porotheleum* sensu (Consiglio et al. 2021). This broad concept of *Porotheleum* encompasses cypheloid *Porotheleum* sensu stricto and also agaricoid species with marasmielloid or gerronematoid basidioma types, characterized by pale spores, the presence of clamp connections, and a lignicolous habitat (Senanayake et al. 2023). Phylogenetic analyses of *Porotheleaceae* based on ITS and nrLSU sequences showed *Vizzinia* formed a distinct clade in the family *Porotheleaceae*. Based on a multi-locus (ITS, nrLSU, and *rpb*2) analysis, Na et al. (2024) confirmed that *Vizzinia* was monophyletic and represents a separate genus. The taxonomic placement of *Vizzinia* is in the family *Porotheleaceae* (*Agaricales*).

Suborder *Mycenineae* R.L. Zhao, Vizzini & M.Q. He

Family *Mycenaceae* Overeem

Index Fungorum number: IF505549.

Type genus – *Mycena* (Pers.) Roussel

Note 37 ***Favolaschia*** (Pat.) Pat.

Index Fungorum number: IF17578.

Type species – *Favolaschia gaillardia* (Pat.) Pat.

Notes – The genus *Favolaschia*, typified by *F. gaillardia* (Patouillard 1887), belongs to the *Mycenaceae* (*Agaricales*) (Moncalvo et al. 2002, Bodensteiner et al. 2004). It is characterised by gelatinous basidiomata with poroid hymenophore, a monomitic hyphal system, a gelatinous hyphal structure, the presence of gloeocystidia and acanthocystidia, which are terminal, mostly swollen tips of hyphae covered by outgrowths (Clémençon 1977), and amyloid basidiospores (Singer 1945, 1974, Gillen et al. 2012, Capelari et al. 2013, Magnago et al. 2013). *Favolaschia* species have a worldwide distribution and prefer humid climates, with the highest species diversity in subtropical to tropical zones (Singer 1974, Gillen et al. 2012, Capelari et al. 2013). The basidiomata primarily found on the decaying parts of monocotyledonous plants, as well as on ferns, and cause white rot (Singer 1974, Gillen et al. 2012). Singer (1974) divided *Favolaschia* into two sections, based on morphological studies, namely section *Favolaschia* Singer and section *Anechinus* Singer. Later, Johnston et al. (2006), Gillen et al. (2012), and Magnago et al. (2013) confirmed the two sections by phylogenetic analyses. Recently, the species diversity, taxonomy, and phylogenies of *Favolaschia* have been extensively studied in China (Zhang & Dai 2021, Zhang et al. 2023a, 2024b)

Note 38 ***Mycena*** (Pers.) Roussel

Index Fungorum number: IF18084.

Type species – *Mycena galericulata* (Scop.) Gray

Notes – The genus *Mycena* was introduced by Roussel (1806), typified by *M. galericulata*, is a polyphyletic genus, containing poroid and lamellate mushrooms, predominantly saprobic and distributed worldwide (Hyde et al. 2024b). The sections *Amparoina* (T. Bau & Q. Na, Calodontes, Fr. ex Berk.) Quél., *Fragilipedes* (Fr.) Quél., *Sacchariferae* Kühner ex Singer, and *Supinae* Konrad & Maubl. were phylogenetically recognized with a base in ITS, nrLSU, and mtSSU sequences (Na & Bau 2019). New species have been described based on the morphology and the ITS, nrLSU, mtSSU, *tef*1-α, *rpb*1, and *rpb*2 regions (e.g., Na & Bau 2019, Cortés-Pérez et al. 2019, Chang et al. 2020, Oliveira et al. 2021, Na et al. 2022, Zhang et al. 2024a). Research utilizing *Mycena* genomes has offered new insights about the evolution of fungal bioluminescence, as well as understanding its adaptability and lifestyles (Harder et al. 2024). The taxonomic placement of *Mycena* is within the *Mycenaceae* in the *Agaricales*.

Suborder ***Phyllotopsidineae*** Zhu L. Yang & G.S. Wang

Family ***Phyllotopsidaceae*** Locquin ex Olariaga, Huhtinen, Læssøe, J.H. Petersen & K. Hansen

Index Fungorum number: IF831374.

Type genus – *Phyllotopsis* E.-J. Gilbert & Donk ex Singer

Note 39 ***Pleurocybella*** Singer

Index Fungorum number: IF18302.

Type species – *Pleurocybella porrigens* (Pers.) Singer

Notes – Singer (1947) established the genus *Pleurocybella* to accommodate *P. porrigens*, a widely distributed species in the temperate northern hemisphere. Singer (1986) included a total of six species in *Pleurocybella*; however, only two of these had been officially transferred to the genus at the time: namely *P. porrigens* and *P. vinosofusca* (Bres.) Singer (Singer 1986). The remaining four species were accepted by Singer (1973b) in the genus *Nothopanus*, namely *N. noctilucens* (Le´v.) Singer, *N. panelloides* (Dennis) Singer, *N. tropicalis* Singer, and *N. amarescens* Singer. The latter three species were transferred subsequently to *Pleurocybella* (Raithelhuber 1992). The taxonomic placement of *Pleurocybella* is in the family *Phyllotopsidaceae* within *Agaricales*.

Note 40 ***Rectipilus*** Agerer

Index Fungorum number: IF18450.

Type species – *Rectipilus fasciculatus* (Pers.) Agerer

Notes – *Rectipilus* was introduced by Agerer (1973) with *R. fasciculatus* as the type species. *Rectipilus* is a cyphelloid genus with currently eleven species (Agerer 1973, 1979, Cooke 1989, Vila et al. 1999, Gorjón & de Jesus 2014, Lucas & Dentinger 2015). It was morphologically and phylogenetically very closely related to *Henningsomyces* Kuntze, producing similar, more or less tubular basidiomata (Agerer 1973). *Henningsomyces* produces somewhat gelatinous basidiomata (Agerer 1983), but the most important anatomical character to separate the two genera is the branching pattern of the surface hyphae. All species of *Henningsomyces* produce consistently branched surface hyphae, whereas those of *Rectipilus* species are usually non-ramified, a feature which is considered taxonomically important at the generic level among cyphelloid fungi (Agerer 1973, 1983, Bodensteiner et al. 2004). Both, *Rectipilus* and *Henningsomyces* have non-pigmented and non-encrusted surface hyphae, a character that morphologically separates them from a large number of cyphelloid genera (Agerer 1983). The phylogenetic study by Bodensteiner et al. (2004) suggests that there are two clades, each comprising a mixture of *Rectipilus* and *Henningsomyces* species, indicating that the inclusion of more species in the analyses was still required to elucidate their phylogenetic relationships. The taxonomic placement of *Rectipilus* is in the family *Phyllotopsidaceae* within *Agaricales*.

Family *Pterulaceae* Corner

Index Fungorum number: IF81309.

Type genus – *Pterula* Fr.

Note 41 *Coronicium* J. Erikss. & Ryvarden

Index Fungorum number: IF17382.

Type species – *Coronicium gemmiferum* (Bourdot & Galzin) J. Erikss. & Ryvarde

Notes – *Coronicium* was originally described to accommodate *C. gemmiferum*, a species with a distinct kind of cystidia apically encrusted with a cap-like layer of resinous brown substance (Eriksson & Ryvarden 1975). Jülich (1975) added to deviating species with no encrusted cystidia, *C. alboglaucum* (Bourdot & Galzin) Jülich and *C. thymicola* (Bourdot & Galzin) Jülich, the latter also differing in the simple-septate hyphae. Gilbertson & Hemmes (2004) study revealed that an additional species *C. molokaiense* Gilb. & Hemmes was described. *Coronicium* was similar to *Pterula* Fr. more or less in sharing ellipsoid to navicular basidiospores (Larsson 2007). Both genera *Coronicium* and *Merulicium* J. Erikss. & Ryvarden form resupinate basidiomata, but differ in the hyphal system present (monomitic in *Coronicium*, dimitic in *Merulicium*). Despite the morphological distinctiveness from the rest of *Pterulaceae*, there is a trend in morphology and strong phylogenetic support for the placement of the *Coronicium* superclade among the *Pterula*/*Myrmecopterula* and *Pterulicium* clades within *Pterulaceae* (Leal-Dutra et al. 2020). Additionally, Leal-Dutra et al. (2020) reported that the phylogenetic analysis result revealed the genus *Coronicium* to be sister to *Merulicium* and form a monospecific clade. The taxonomic placement of *Coronicium* is located in the family *Pterulaceae* within *Agaricales*.

Note 42 *Lepidomyces* Jülich

Index Fungorum number: IF17935.

Type species – *Lepidomyces subcalceus* (Litsch.) Jülich

Notes – Larsson (2007) suggested that *Lepidomyces* had affinities to *Aphanobasidium* Jülich and could possibly be placed in the family *Pterulaceae*. However, no sequence data are available for the genus. *Lepidomyces* was described as bearing pleurobasidia as in *Aphanobasidium*, but also leptocystidia as in *Coronicium* J. Erikss. & Ryvarden and *Merulicium* J. Erikss. & Ryvarden (Leal-Dutra et al. 2020). Given its morphological similarities to *Aphanobasidium* and the *Coronicium* superclade, Leal-Dutra et al. (2020) retained *Lepidomyces* as *incertae sedis* until molecular data are available to confirm its phylogenetic position. However, the genus *Lepidomyces* placing in the family *Pterulaceae*, which accepted by He et al. (2019, 2024) and Hyde et al. (2024b). In the present study, we accepted the previous studies, which *Lepidomyces* placing in the family *Pterulaceae* (He et al. 2019, 2024, Hyde et al. 2024b)

Note 43 ***Merulicium*** J. Erikss. & Ryvarden

Index Fungorum number: IF18048.

Type species – *Merulicium fusisporum* (Romell) J. Erikss. & Ryvarden

Notes – The monotypic genus *Merulicium* was introduced by Eriksson & Ryvarden (1976) to accommodate *M. fusisporum.* Traditionally, the genus *Merulicium* was placed in *Corticiaceae*, and subsequently, Larsson (2007) suggested a transfer to the family *Pterulaceae* within *Agaricales* based on the molecular evidence. *Merulicium* differs from other athelioid species in its dimitic hyphal system, characterized by dextrinoid skeletal hyphae, and fusiform, smooth, thin-walled basidiospores (Eriksson & Ryvarden 1976). Leal-Dutra et al. (2020) reported that the phylogenetic analysis result revealed the genus *Merulicium* to be the sister to *Coronicium* and form a monospecific clade, and among the *Pterula*/*Myrmecopterula* and *Pterulicium* clades within *Pterulaceae*. The taxonomic placement of *Merulicium* is in the family *Pterulaceae* within *Agaricales*.

Note 44 ***Myrmecopterula*** Leal-Dutra, Dentinger & G.W. Griff.

Index Fungorum number: IF831048.

Type species – *Myrmecopterula moniliformis* (Henn.) Leal-Dutra, Dentinger & G.W. Griff.

Notes – The genus *Myrmecopterula* was introduced by Leal-Dutra et al. (2020) to accommodate *M. moniliformis* as the type species, based on morphological characteristics and phylogenetic analysis of ITS, nrLSU, and *rpb*2 sequence data. The species of *Myrmecopterula* are usually associated with ant nests, growing on living or dead nests, or are cultivated by the ants (Leal-Dutra et al. 2020). Phylogenetic analyses of combined ITS, nrLSU, and *rpb*2 confirmed its phylogenetic position in the family *Pterulaceae* (Leal-Dutra et al. 2020). *Myrmecopterula* formed a distinct clade sister to *Pterula*, and this distinct clade was erected as a new genus to accommodate ant-associated taxa previously grouped in *Pterula* (Leal-Dutra et al. 2020). In comparison to other species in *Pterulaceae*, the species in this genus are characterized by bushy, pteruloid, white-cream to light-brown, and surface greyish basidiomata, concolorous or stipe darker than the hymenophore, developing from cottony subiculum with mycelial cords; sterile stipe surface; dimitic hyphal system; relatively small basidiospores usually less than 7 μm wide (Leal-Dutra et al. 2020). To date, there are three species in this genus, and it is presently unclear whether the existing mutualistic association found in *Myrmecopterula nudihortorum* and *M. velohortorum* is ancestral, suggesting that free-living taxa may have escaped the mutualism (Leal-Dutra et al. 2020). The taxonomic placement of *Myrmecopterula* is located in the family *Pterulaceae* within *Agaricales*.

Note 45 ***Phaeopterula*** Henn.

Index Fungorum number: IF18237.

Type species – *Phaeopterula juruensis* Henn.

Notes – Hennings (1904) introduced *Phaeopterula* within *Pterulaceae* (*Agaricales*) with *P. juruensis* as the type species. The generic name *Phaeopterula* was originally proposed as a subgenus of *Pterula* to accommodate *P. hirsuta* (Henn.) Sacc. & D. Sacc. and *P. juruensis* Henn. (Hennings 1900, 1904). Based on the combined ITS, nrLSU, and *rpb*2 sequence data, Leal-Dutra et al. (2020) phylogenetic analyses proposed the reintroduction of the following to distinguish these brown pigmented taxa from *Pterula* s. str. *Phaeopterula* includes *P. anomala* (P. Roberts) Leal-Dutra, Dentinger & G.W. Griff., *P. stipata* (Corner) Leal-Dutra, Dentinger & G.W. Griff., and *P. juruensis*, and other species, which all have dark brown basidiomata.

Note 46 ***Pterula*** Fr.

Index Fungorum number: IF18422.

Type species – *Pterula plumosa* (Schwein.) Fr.

Notes – Fries (1825) described *Pterula* with *P. plumosa* as the type species. The genus *Pterula* has very bushy coralloid basidiomata, usually robust and taller than those of *Pterulicium*, with a stipe that is concolorous with the hymenophore and lacking a cottony subiculum (Leal-Dutra et al. 2020). *Pterula* has a predominantly pantropical and pan-subtropical distribution, with occurrences reported on all continents except Antarctica (Corner 1970). There was strong phylogenetic support for the placement of the genus *Pterula* among *Pterula*/*Myrmecopterula* and *Pterulicium* clades, and closely related to *Myrmecopterula* within *Pterulaceae* (Leal-Dutra et al. 2020). The taxonomic placement of *Pterula* is in the family *Pterulaceae* within *Agaricales*.

Note 47 *Pterulicium* Corner

Index Fungorum number: IF18423.

Type species – *Pterulicium xylogenum* (Berk. & Broome)

Notes – Corner (1950) described *Pterulicium* with *P. xylogenum* as the type species. Some *Pterulicium* species also show transitions in their morphology to a resupinate state (Leal-Dutra et al. 2020). Corner (1950) showed that *Pterulicium xylogenum* could form monomitic corticioid patches independent of the coralloid state and even in its absence, thus appearing to be truly corticioid. Furthermore, the experimental studies on *P. echo* (D.J. McLaughlin & E.G. McLaughlin), Leal-Dutra, Dentinger & G.W. Griff. show a dimitic, resupinate, fertile corticioid phase both on agar and when cultured on cocoa twigs (McLaughlin & McLaughlin 1972, McLaughlin et al. 1978, McLaughlin & McLaughlin 1980). There was strong phylogenetic support for the placement of the genus *Pterulicium* among *Pterula*/*Myrmecopterula* and *Pterulicium* clades, and closely related to *Coronicium* and *Merulicium* within *Pterulaceae* (Leal-Dutra et al. 2020). The taxonomic placement of *Pterulicium* is within the family *Pterulaceae* in *Agaricales*.

Family *Radulomycetaceae* Leal-Dutra, Dentinger & G.W. Griff.

Index Fungorum number: IF831047.

Type genus *Radulomyces* M.P. Christ.

Note 48 *Aphanobasidium* Jülich

Index Fungorum number: IF17085

Type species – *Aphanobasidium subnitens* (Bourdot & Galzin) Jülich

Notes – *Aphanobasidium* was introduced by Jülich (1979) to accommodate *A. subnitens* as the type species. Four resupinate genera were transferred to the family *Pterulaceae* as *Aphanobasidium*, *Coronicium*, *Merulicium*, and *Radulomyces* M.P. Christ. (Larsson et al. 2004, Larsson 2007). Three genera (i.e., *Aphanobasidium*, *Radulomyces*, and *Radulotubus*) formed a strongly supported clade, and they were sisters to the *Pterula-Deflexula-Pterulicium-Merulicium-Coronicium* clade based on the sequence analyses of the ITS+nrLSU data (Zhao et al. 2016). Based on phylogenetic analyses inferred from ITS+nrLSU+*rpb*2 sequence data, Leal-Dutra et al. (2020) transferred the genus *Aphanobasidium* to *Radulomycetaceae* from *Pterulaceae*. The taxonomic placement of *Aphanobasidium* is located in the family *Radulomycetaceae* in the *Agaricales*.

Note 49 *Radulomyces* M.P. Christ.

Index Fungorum number: IF18442.

Type species – *Radulomyces confluens* (Fr.) M.P. Christ.

Notes – *Radulomyces* was introduced by Christiansen (1960) and is typified by *R. confluens*. Larsson et al. (2004) showed that *Coronicium alboglaucum* (Bourdot & Galzin) Jülich, *Radulomyces confluens*, *R. molaris* (Chaillet ex Fr.) M.P. Christ., and *R. rickii* (Bres.) M.P. Christ. nested within the euagarics clade. The placement of two genera *Aphanobasidium* Jülich and *Radulomyces*, was previously assigned to the family *Pterulaceae* based on phylogenetic reconstructions of corticioid taxa (Larsson et al. 2004, Larsson 2007). Phylogenetically, *Radulomyces* belonged in the *Pterulaceae* (*Agaricales*) and was most closely related to

Radulotubus Y.C. Dai, S.H. He & C.L. Zhao, and *Aphanobasidium* (Zhao et al. 2016). These three genera formed a strongly supported clade and were sisters to the *Pterula-Deflexula-Pterulicium-Merulicium-Coronicium* clade based on the demonstrated sequence analyses of the ITS+nrLSU data (Zhao et al. 2016). Based on the ITS+nrLSU+*rpb*2 sequence data, Leal-Dutra et al. (2020) phylogenetic analyses showed strong support for the segregation of *Radulomycetaceae* from *Pterulaceae*. Thus, Leal-Dutra et al. (2020) proposed the introduction of a new family for these three genera (i.e., *Aphanobasidium*, *Radulomyces*, and *Radulotubus*) instead of placing them in *Pterulaceae*, as they were distinct from nearly all the other members of *Pterulaceae* clearly by morphology and phylogeny. Subsequently, Dong et al. (2024, 2025a) confirmed the phylogenetic analysis of the family *Radulomycetaceae*, which segregated from *Pterulaceae* using ITS+nrLSU sequence data, with six species reported. In the present study, based on ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α phylogenetic analysis (Fig. 2), we confirm that these three genera (i.e., *Aphanobasidium*, *Radulomyces*, and *Radulotubus*) are nested within *Radulomycetaceae*, which is the sister family to *Pterulaceae*. This finding corroborates previous molecular phylogenetic studies (Leal-Dutra et al. 2020, Dong et al. 2024, 2025a)

Note 50 ***Radulotubus*** Y.C. Dai, S.H. He & C.L. Zhao

Index Fungorum number: IF815760.

Type species – *Radulotubus resupinatus* Y.C. Dai, S.H. He & C.L. Zhao

Notes– Zhao et al. (2016) introduced the monotypic genus *Radulotubus*, assigning *R. resupinatus* as its type species, based on a comprehensive phylogenetic analysis of ITS and nrLSU sequence data, along with morphological characteristics. Phylogenetically, *Radulotubus* was most closely related to the genera *Aphanobasidium* and *Radulomyces*, which formed a strongly supported clade and were sisters to the *Pterula-Deflexula-Pterulicium-Merulicium-Coronicium* clade based on the demonstrated sequence analyses of the ITS+nrLSU data (Zhao et al. 2016). Based on the ITS+nrLSU+*rpb*2 sequence data, Leal-Dutra et al. (2020) proposed the introduction of a new family, *Radulomycetaceae*, for these three genera (i.e., *Aphanobasidium*, *Radulomyces*, and *Radulotubus*) instead of placing them in *Pterulaceae*, as they were distinct from nearly all the other members of *Pterulaceae* clearly by morphology and phylogeny. Recent phylogenetic analyses have confirmed that this finding is consistent with previous studies (Dong et al. 2024, 2025a). The taxonomic placement of *Radulotubus* is located in the *Radulomycetaceae* in the *Agaricales*.

Family ***Stephanosporaceae*** Oberw. & E. Horak

Index Fungorum number: IF81422.

Type genus – *Stephanospora* Pat.

Note 51 ***Athelidium*** Oberw.

Index Fungorum number: IF17119.

Type species – *Athelidium aurantiacum* (M.P. Christ.) Oberw.

Notes – *Athelidium* was a small genus of corticioid fungi originally created to accommodate the sole species *Xenasma aurantiacum* M.P. Christ. (Oberwinkler 1966). The genus is characterized by, among others, the orange-yellow hymenial surface, clampless septa, cylindrical to clavate, slightly constricted basidia, and thin-walled, smooth, inamyloid spores (Eriksson & Ryvarden 1975, Bernicchia & Gorjón 2010). The resupinate polypore *Athelidium* was previously considered to belong to *Stephanosporaceae* (Oberwinkler 1966, Kirk et al. 2008), despite the spores of the genus lacking ornamentation and a corona (Ghobad-Nejhad & Yurchenko 2012, Zíbarová & Tejklová 2019). *Athelidium* was a monotypic genus phylogenetically related to *Cristinia* Parmasto and *Lindtneria* Pilát in the family *Stephanosporaceae*; however, the relationship is unclear because it shares morphologically only the yellow-orange basidiomata (Larsson 2007).

Note 52 ***Cristinia*** Parmasto

Index Fungorum number: IF17408.

Type species – *Cristinia helvetica* (Pers.) Parmasto

Notes – Parmasto (1968) described *Cristinia* with *C. helvetica* as the type species. The genus is characterized by resupinate basidiomata, granular to irregularly raduloid hymenophore, a monomitic hyphal system with clamp connections or simple septa, subclavate or cylindrical basidia with 4-sterigmata, and subglobose to somewhat angular, smooth, thick-walled basidiospores (Bernicchia & Gorjón 2010). The systematic position of the genus was in the vicinity of *Hypochnicium* J. Erikss. (Eriksson & Ryvarden 1975). Molecular data by Binder et al. (2005) suggest possible relationships between *Cristinia*; and *Lindtneria* and *Stephanospora*, which share cyanophilous granulation in the basidia and cyanophilous spore walls. Based on the basis of cyanophilous basidiospores and granules in the basidia, the species *Cristinia tubulicystidiata* J. Kaur, Dhingra & Hallenberg was described by Kaur et al. (2014).

Note 53 ***Lindtneria*** Pilát

Index Fungorum number: IF17983.

Type species – *Lindtneria trachyspora* (Bourdot & Galzin) Pilát

Notes – *Lindtneria* was introduced by Pilát (1938) to accommodate *L. trachyspora* as type species. The genus is characterized by a smooth, merulioid to poroid or hydnoid hymenophore, a monomitic hyphal system with septate clamped and non-clamped hyphae (usually both), basidia with distinct cyanophilous granulations, and cyanophilous and ornamented basidiospores (Bernicchia & Gorjón 2010, Ryvarden & Melo 2014). Oberwinkler & Horak (1979) noted the morphological similarities between *Lindtneria* and the gastroid genus *Stephanospora* Patouillard, which also features cyanophilous and ornamented basidiospores, and proposed a new family, *Stephanosporaceae*, to accommodate these two genera. Their relationship was later confirmed by molecular analyses, which also showed that *Stephanosporaceae* was a member of *Agaricales* and also includes the corticioid genera *Athelidium* Oberwinkler and *Cristinia* Parmasto (Martin et al. 2004, Larsson 2007, Lebel et al. 2015). Phylogenetic analyses based on ITS and nrLSU sequence data, as well as the morphological characteristics, support *Lindtneria asiae-orientalis* S.L. Liu & S.H. He as a new species in the genus *Lindtneria* (Liu et al. 2016). Until now, 15 species were accepted in *Lindtneria* (Hyde et al. 2024b), among which four species, *Lindtneria asiae-orientalis*, *L. chordulata* (D.P. Rogers) Hjortstam, *L. flava* Parmasto, and *L. trachyspora* (Bourdot & Galzin) Pilát, were recorded in China (Dai 2011, 2012, Liu et al. 2016).

Suborder ***Pleurotineae*** Aime, Dentinger & Gaya

Family ***Cyphellopsidaceae*** Jülich

Index Fungorum number: IF81759.

Type genus – *Cyphellopsis* Donk

Note 54 ***Dendrothele*** Höhn. & Litsch.

Index Fungorum number: IF17484.

Type species – *Dendrothele papillosa* Höhn. & Litsch.

Notes – The genus *Dendrothele* was erected by Höhnel & Litschauer (1907) and was typified by *D. papillosa*. Goranova et al. (2003) demonstrated that *Dendrothele* was polyphyletic with taxa distributed among 11 lineages in the hymenochaetoid, russuloid, corticioid, and agaricoid clades. Molecular studies have shown that *D. griseocana* (Bres.) Bourdot & Galzin, the generic type of *Dendrothele*, is embedded in the *Agaricales* clade and closely related to *Lachnella* Fr. and *Cyphellopsis* Donk (Bodensteiner et al. 2004, Binder et al. 2005). One distinct clade recovered by Bodensteiner et al. (2004), and named as the Nia clade, comprised several cyphelloid genera, the marine species *Nia vibrissa* R.T. Moore & Meyers, and two species of *Dendrothele*, of which is the generic type *D. griseo-cana*. *Dendrothele* is a highly polyphyletic genus, with representatives occurring in the orders *Corticiales* K.H. Larss., *Russulales* Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David and possibly *Polyporales*. (Larsson 2007). A phylogenetic study of *Dendrothele sensu stricto* from New Zealand was conducted, which reported 13 species (Nakasone & Burdsall 2011).

Based on the phylogenetical and morphological analysis with ITS+nrLSU sequences data, Dong et al. (2024) revealed that a new species, *D. yunnanensis* J.H. Dong & C.L. Zhao, was proposed. In the present study, based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2), a new species, *D. fissurata* is reported.

Dendrothele fissurata J.H. Dong & C.L. Zhao, sp. nov. Figs. 21–23

Index Fungorum number: IF858341.

Etymology – Refers to the cracked hymenophore of the type specimen.

Type – China, Yunnan Province, Diqing, Weixi County, Zhonglu Town, GPS coordinates 27°50′ N, 99°05′ E, altitude 1500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 15 October 2023, CLZhao 35015 (SWFC).

Description – Basidiomata annual, resupinate, adnate, membranous, without odor or taste when fresh, becoming hard coriaceous upon drying, up to 8 cm long, 1 cm wide, 150 µm thick. Hymenial surface smooth, cracked, and white when fresh, turning to a slightly cream color upon drying. Sterile margin white to cream, abrupt, up to 0.5 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, difficult to discern, colorless, thin-walled, rarely branched, 2–3 µm in diameter; IKI–, CB–; tissues unchanged in KOH; dendrohyphidia numerous, 1–1.5 µm in diameter; subhymenial hyphae densely covered by crystals. Cystidia subfusiform, colorless, slightly thick-walled, 13–25 × 8–10 µm; cystidioles absent. Basidia barreled, slightly thick-walled and sinuous, with 2–3 sterigmata and a basal clamp connection, with a few guttulae, 20.5–27.5 × 7.5–12 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subcylindrical, thin- to thick-walled, colorless, smooth, IKI–, CB–, (4.5–)4.7–5(–5.3) × 2.5–3(–3.2) µm, L = 4.90 µm, W = 2.84 µm, Q = 1.54–1.87, Q_m = 1.73 ± 0.11 (n = 30/1).

Notes – *Dendrothele fissurata* grouped in *Dendrothele* (*Cyphellopsidaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2), *D. fissurata* is closely related to *D. griseocana* (Bres.) Bourdot & Galzin and *D. yunnanensis* J.H. Dong & C.L. Zhao. However, *D. griseocana* can be delimited from *D. fissurata* by its greyish to ochraceous basidiomata, and subglobose to ellipsoid, larger basidiospores (9–11 × 7–8 µm *vs* 4.7–5 × 2.5–3 µm, Bernicchia & Gorjón 2010); *D. yunnanensis* can be delimited from *D. fissurata* by its longer basidia (31–40 × 6–8 µm *vs* 20.5–27.5 × 7.5–12 µm), and subglobose to globose, larger basidiospores (7.5–9 × 6–7.8 µm *vs* 4.7–5 × 2.5–3 µm, Dong et al. 2024).

Morphologically, *Dendrothele fissurata* shares similarities with *D. alliacea* (Quél.) P.A. Lemke, *D. ampullospora* (G. Cunn.) Nakasone& Burds., and *D. australis* Nakasone & Burds. share the cylindrical basidiospores. However, *D. alliacea* differs from *D. fissurata* by its tuberculate hymenial surface, longer basidia (30–60 × 8–10 µm *vs* 20.5–27.5 × 7.5–12 µm), and larger basidiospores (16–18 × 6–7 µm *vs* 4.7–5 × 2.5–3 µm, Bernicchia & Gorjón 2010); *D. ampullospora* can be distinguished from *D. fissurata* by its pale-yellow to greyish orange basidiomata, longer basidia (28–55 × 11–17 µm *vs* 20.5–27.5 × 7.5–12 µm), and larger basidiospores (14–18 × 8.5–10 µm *vs* 4.7–5 × 2.5–3 µm, Nakasone & Burdsall 2011); *D. australis* differentiates from *D. fissurata* by its yellowish to pale orange basidiomata, longer basidia (43–65 × 9–13 µm *vs* 20.5–27.5 × 7.5–12 µm), and larger basidiospores (15–16.5 × 8–11 µm *vs* 4.7–5 × 2.5–3 µm, Nakasone & Burdsall 2011).

Note 55 *Eoscyphella* Silva-Filho, Stevani & Menolli

Index Fungorum number: IF849403.

Type species – *Eoscyphella luciurceolata* Silva-Filho, Stevani & Desjardin

Notes – *Eoscyphella* was introduced by Silva-Filho et al. (2023) to accommodate the bioluminescent *E. luciurceolata* as a monotypic species, based on the morphological characteristics and phylogenetic analysis of ITS and nrLSU sequence data. The genus is characterized by the absence of conspicuous long hairs on the receptacle, regularly bi-spored basidia, the absence of clamp connections, the consistent presence of pigmented and encrusted external hyphae, and subglobose to broadly ellipsoid basidiospores (Silva-Filho et al. 2023). The genus contains bioluminescent and non-bioluminescent representatives. The genus *Woldmaria* forms a sister clade with *Eoscyphella* based on the phylogenetic analysis of ITS and nrLSU sequence data (Silva-Filho et al. 2023). The taxonomic placement of *Eoscyphella* is in the family *Cyphellopsidaceae* within *Agaricales.*

Note 56 ***Gracilihypha*** Y. Yang & C.L. Zhao

Index Fungorum number: IF854077.

Type species – *Gracilihypha abeliae* Y. Yang & C.L. Zhao

Notes – The genus *Gracilihypha* Y. Yang & C.L. Zhao was erected by Yang et al. (2025) and is typified by *G. abeliae* Y. Yang & C.L. Zhao. A phylogenetical analysis in the family *Cyphellopsidaceae* (previously classified as *Niaceae*) using ITS+nrLSU+mtSSU+*rpb*1+*rpb*2+*tef*1-α sequence data, as presented by Yang et al. (2025), proposed a new genus, *Gracilihypha*, closely related to *Merismodes* Earle. Morphologically, *Gracilihypha* is characterized by the coriaceous and cracked hymenophore, a monomitic hyphal system with very thin generative hyphae, fusiform cystidia, ellipsoid to subglobose and thin-walled basidiospores that are distinguished from known genera in *Merismodes* (Yang et al. 2025).

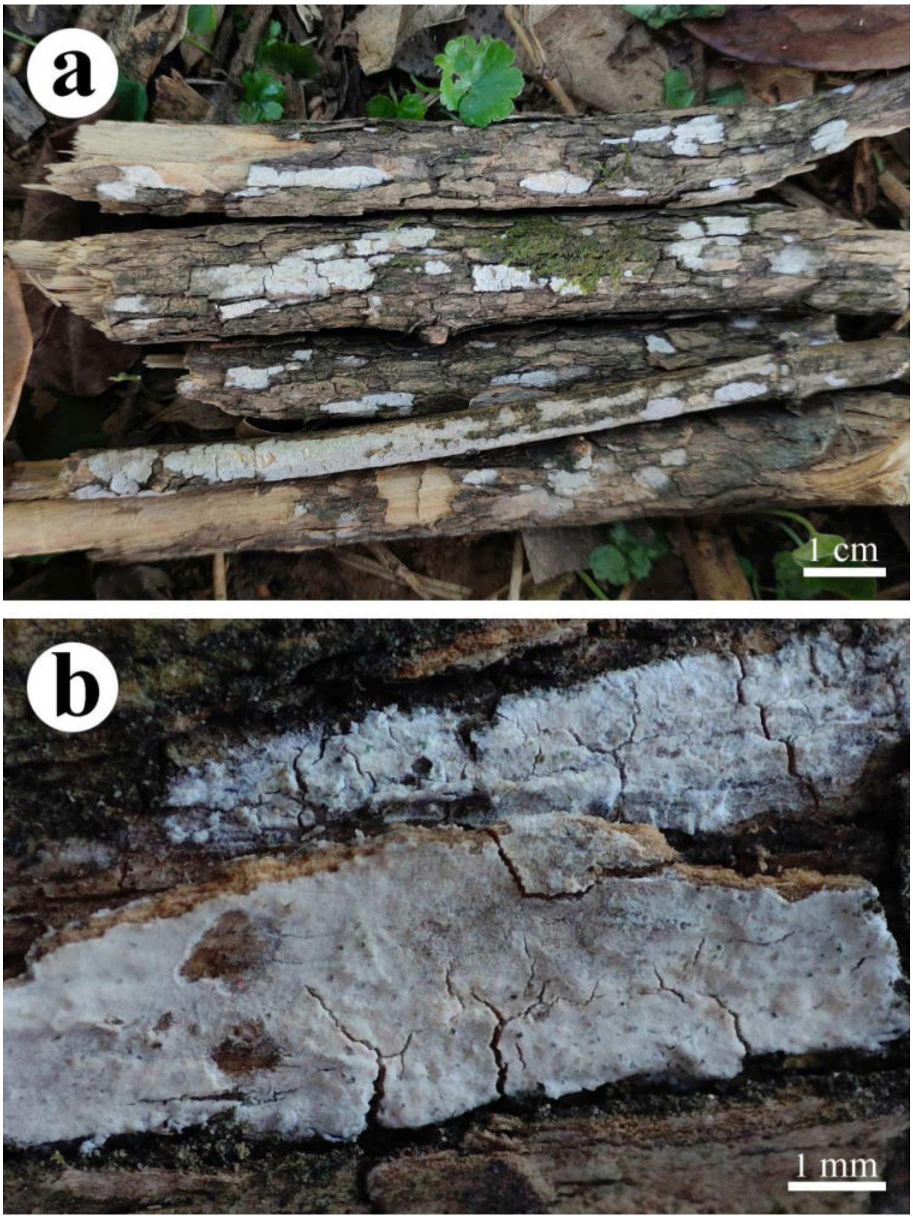

Figure 21 – Basidiomata of *Dendrothele fissurata* (holotype, CLZhao 35015).

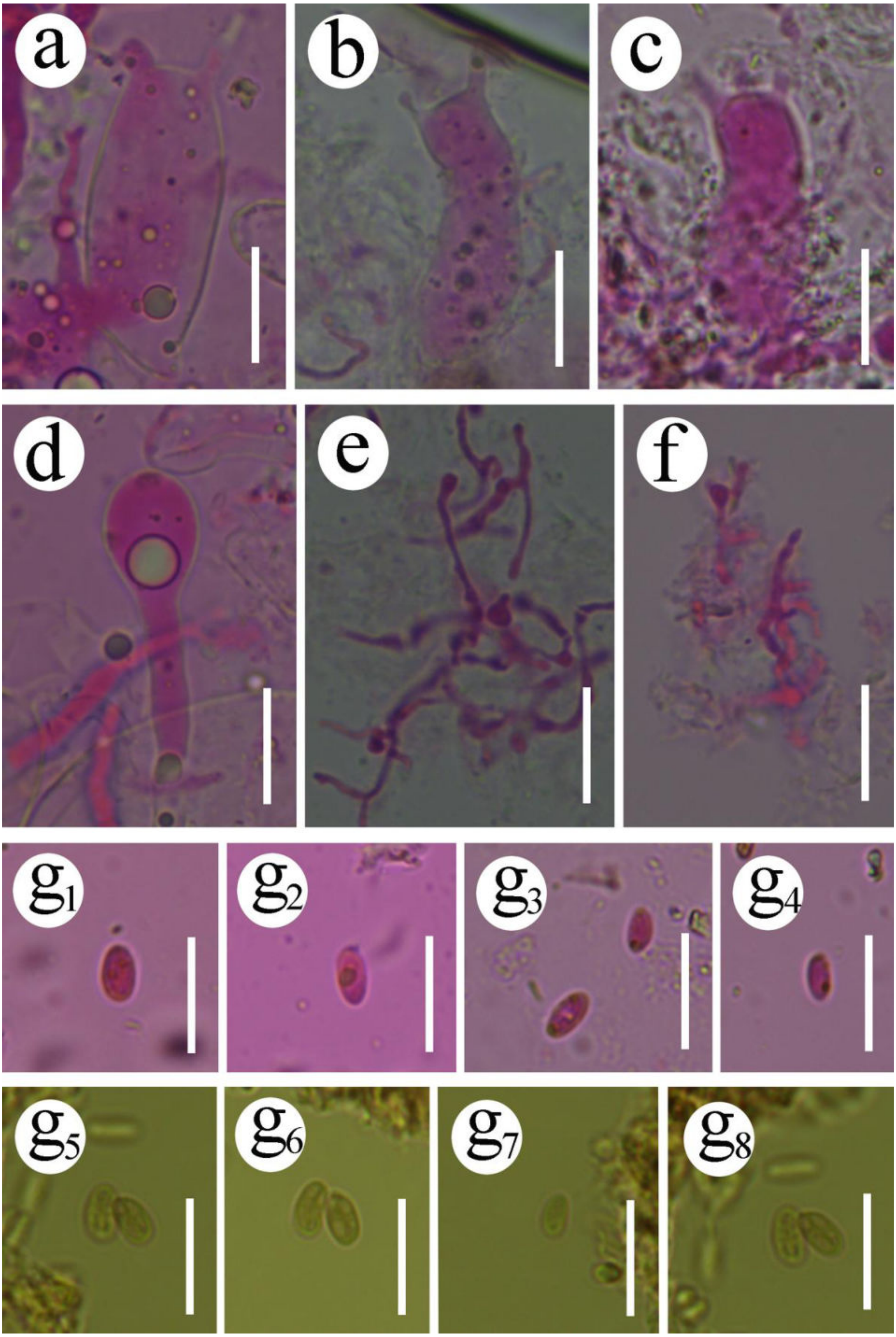

Figure 22 – Microscopic structures of *Dendrothele fissurata* (holotype, CLZhao 35015). a–c Basidia. d Cystidia. e–f Dendrohyphidia. g Basidiospores. Scale bars: a–g = 10 µm.

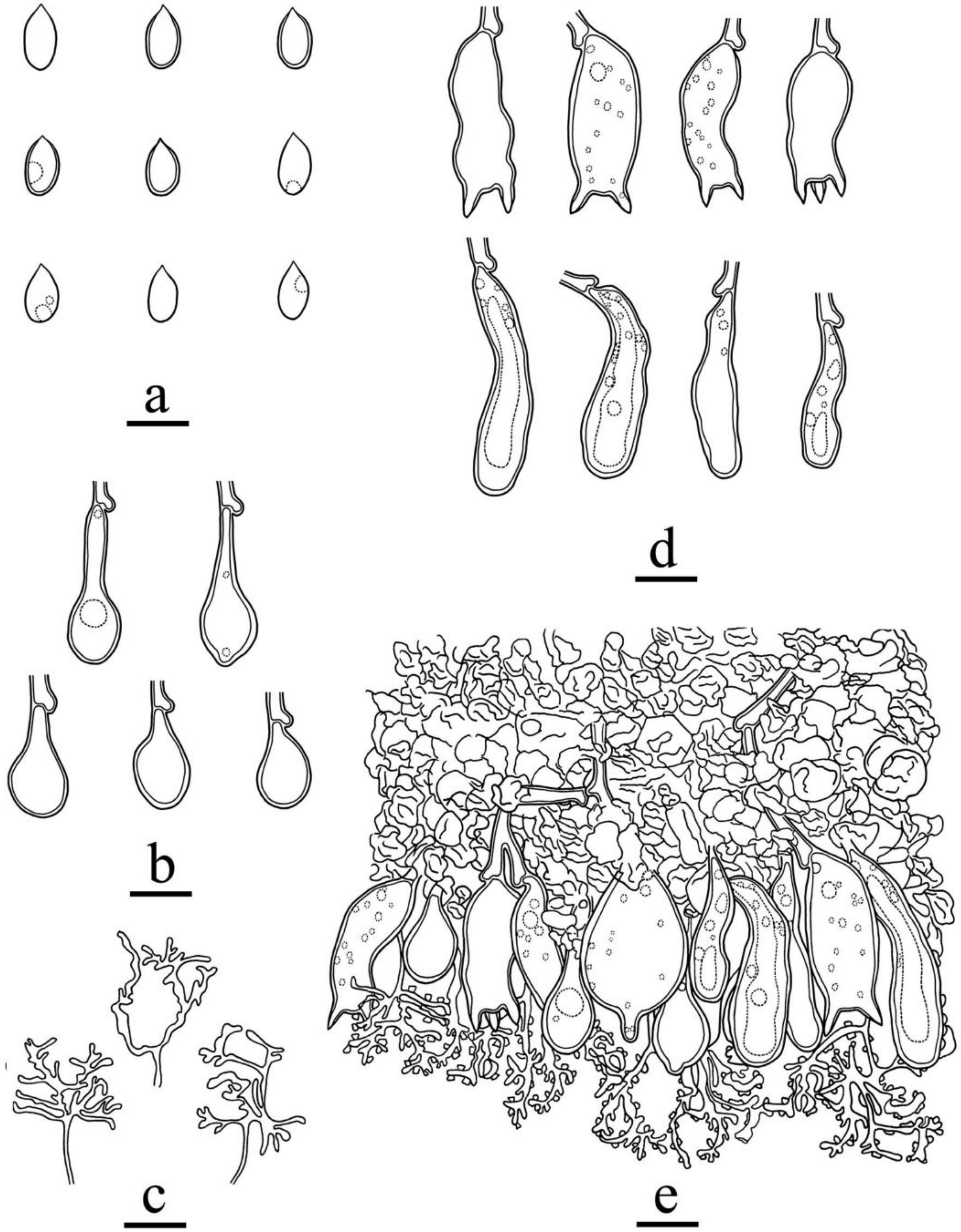

Figure 23 – Microscopic structures of *Dendrothele fissurata* (holotype, CLZhao 35015). a Basidiospores. b Cystidia. c Dendrohyphidia. d Basidia and basidioles. e A section of the hymenium and subhymenium. Scale bars: a = 5 µm; b–d = 10 µm.

Gracilihypha albohymenia J.H. Dong & C.L. Zhao, sp. nov. Figs. 24–26

Index Fungorum number: IF858348.

Etymology – Refers to the white hymenial surface of the type specimen.

Type – China, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates 27°40′ N, 104°15′ E, altitude 2000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 18 September 2023, CLZhao 33069 (SWFC).

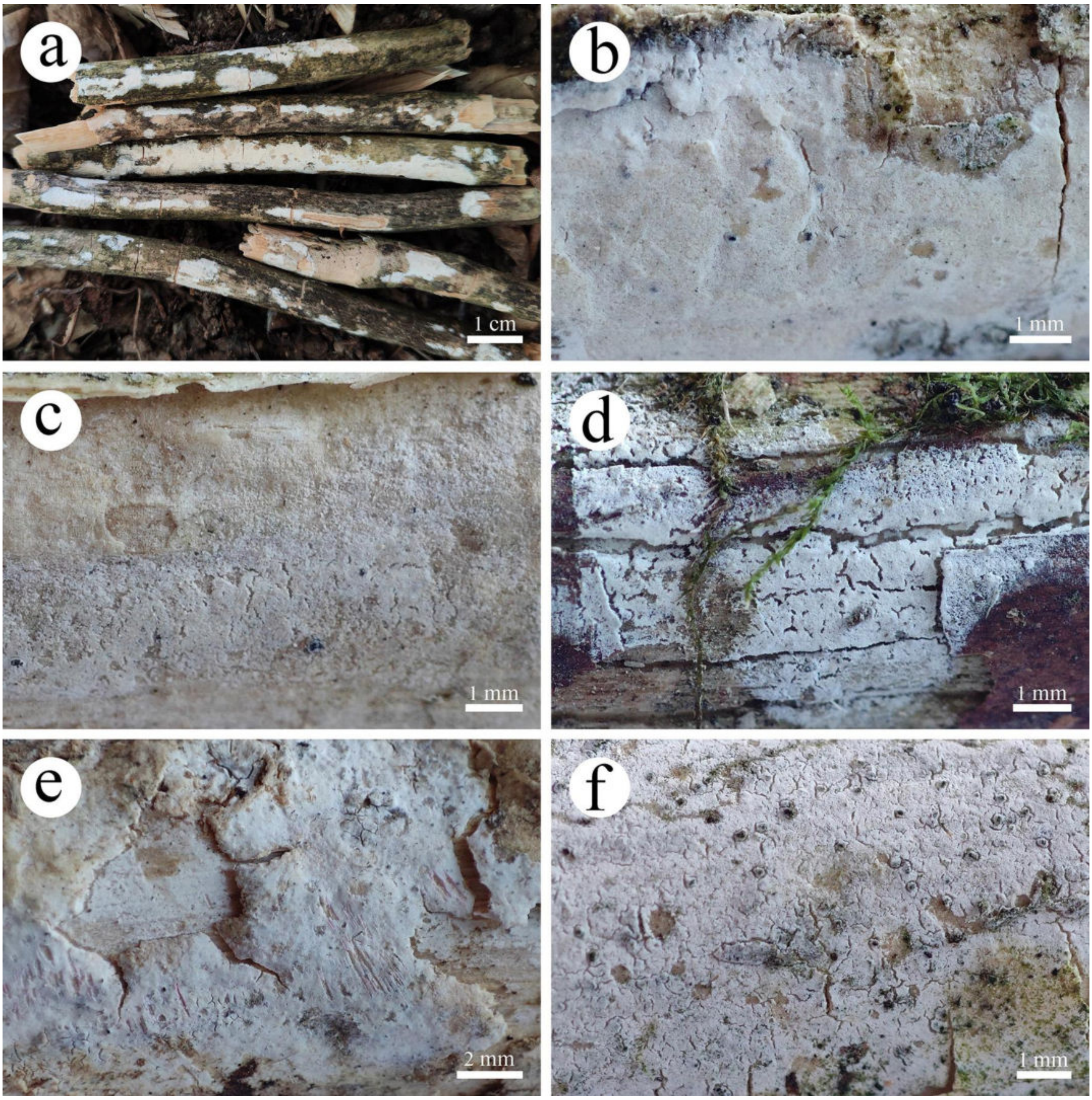

Figure 24 – Basidiomata of *Gracilihypha albohymenia* a, b CLZhao 33069 (holotype). c CLZhao 29603. d CLZhao 31757. e CLZhao 32417. f CLZhao 33502.

Description – Basidiomata annual, resupinate, adnate, membranaceous, without odor or taste when fresh, becoming farinaceous upon drying, up to 10 cm long, 2 cm wide, 150 µm thick. Hymenial surface smooth, cracked, white when fresh, turning to slightly cream upon drying. Sterile margin white, narrow, up to 0.5 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled, branched, interwoven, 1.5–3 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia fusiform, colorless, thin-walled, 32.5–40 × 10.5–14.5 µm; cystidioles absent. Basidia clavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, 31.5–52 × 8.5–

14.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid to subglobose, colorless, thick-walled, smooth, IKI–, CB+, (10–)10.5–13.5(–14) × (8.5–)8.7–12.5 µm, L = 12.12 µm, W = 10.46 µm, Q = 1.08–1.30, Q_m = 1.16 ± 0.06 (n = 120/4).

Material examined (paratypes) – China, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates 27°40′ N, 104°15′ E, altitude 2000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 12 July 2023, CLZhao 29603; 26 August 2023, CLZhao 31757; 28 August 2023, CLZhao 32417; 20 September 2023, CLZhao 33502 (SWFC).

Notes – *Gracilihypha albohymenia* grouped in *Gracilihypha* (*Cyphellopsidaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and ITS+nrLSU sequence data (Fig. 5), forming a monophyletic lineage closely associated with *G. abelia* and *G. yunnanensis.* However, *G. abelia* differs from *G. albohymenia* by its coriaceous basidiomata, and thin-walled basidiospores (Yang et al. 2025); *G. yunnanensis* differentiates from *G. albohymenia* by its furfuraceous basidiomata, and smaller cystidia (20–32.5 × 8.5–10.5 µm *vs* 32.5–40 × 10.5–14.5 µm).

Gracilihypha yunnanensis J.H. Dong & C.L. Zhao, sp. nov. Figs. 27–29

Index Fungorum number: IF858349.

Etymology –Refers to the type locality, Yunnan Province, China.

Type – China, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates 27°40′ N, 104°15′ E, altitude 2000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 29 August 2023, CLZhao 32826 (SWFC).

Description – Basidiomata annual, resupinate, adnate, soft, membranaceous, without odor or taste when fresh, becoming furfuraceous upon drying, up to 3 cm long, 1.5 cm wide, 100 µm thick. Hymenial surface smooth, cracked, white when fresh, and upon drying. Sterile margin white, narrow, up to 0.5 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 1.5–2.5 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia fusiform, colorless, thin-walled, 20–32.5 × 8.5–10.5 µm; cystidioles absent. Basidia clavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, 30–35.5 × 6.5–10 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid to subglobose, colorless, thick-walled, smooth, IKI–, CB+, (8.5–)9–11.5(–11.7) × (7–)7.3–9(–9.5) µm, L = 10.11 µm, W = 7.92 µm, Q = 1.16–1.40, Q_m = 1.28 ± 0.07 (n = 30/1).

Notes – *Gracilihypha yunnanensis* grouped in *Gracilihypha* (*Cyphellopsidaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and ITS+nrLSU sequence data (Fig. 5), forming a monophyletic lineage closely associated with *G. abelia* and *G. albohymenia.* However, *G. abelia* differs from *G. yunnanensis* by its coriaceous basidiomata, and thin-walled basidiospores (Yang et al. 2025); *G. albohymenia* differentiates from *G. yunnanensis* by its farinaceous basidiomata and larger cystidia (32.5–40 × 10.5–14.5 µm *vs* 20–32.5 × 8.5–10.5 µm).

Note 57 *Merismodes* Earle

Index Fungorum number: IF18047.

Type species – *Merismodes fasciculata* (Schwein.) Earle

Notes – *Merismodes* was established by Earle (1909), with *M. fasciculata* as the type species, and contains 13 accepted species (Silva-Filho et al. 2023, Yang et al. 2025). The typical feature of this genus is the structure of cyphelloid receptacle, cupulate to tubular basidiomata, covered with yellow brown to brown hairs, and subglobose, ellipsoid, cylindrical, allantoid, or subfusiform basidiospores (Silva-Filho et al. 2023). Based on the morphological characteristics and phylogenetic analysis, Yang et al. (2025) described two new species as *Merismodes wumengshanensis* Y. Yang & C.L. Zhao and *M. yunnanensis* Y. Yang & C.L. Zhao with ITS+nrLSU+mtSSU+*rpb*1+*rpb*2+*tef*1-α sequence data.

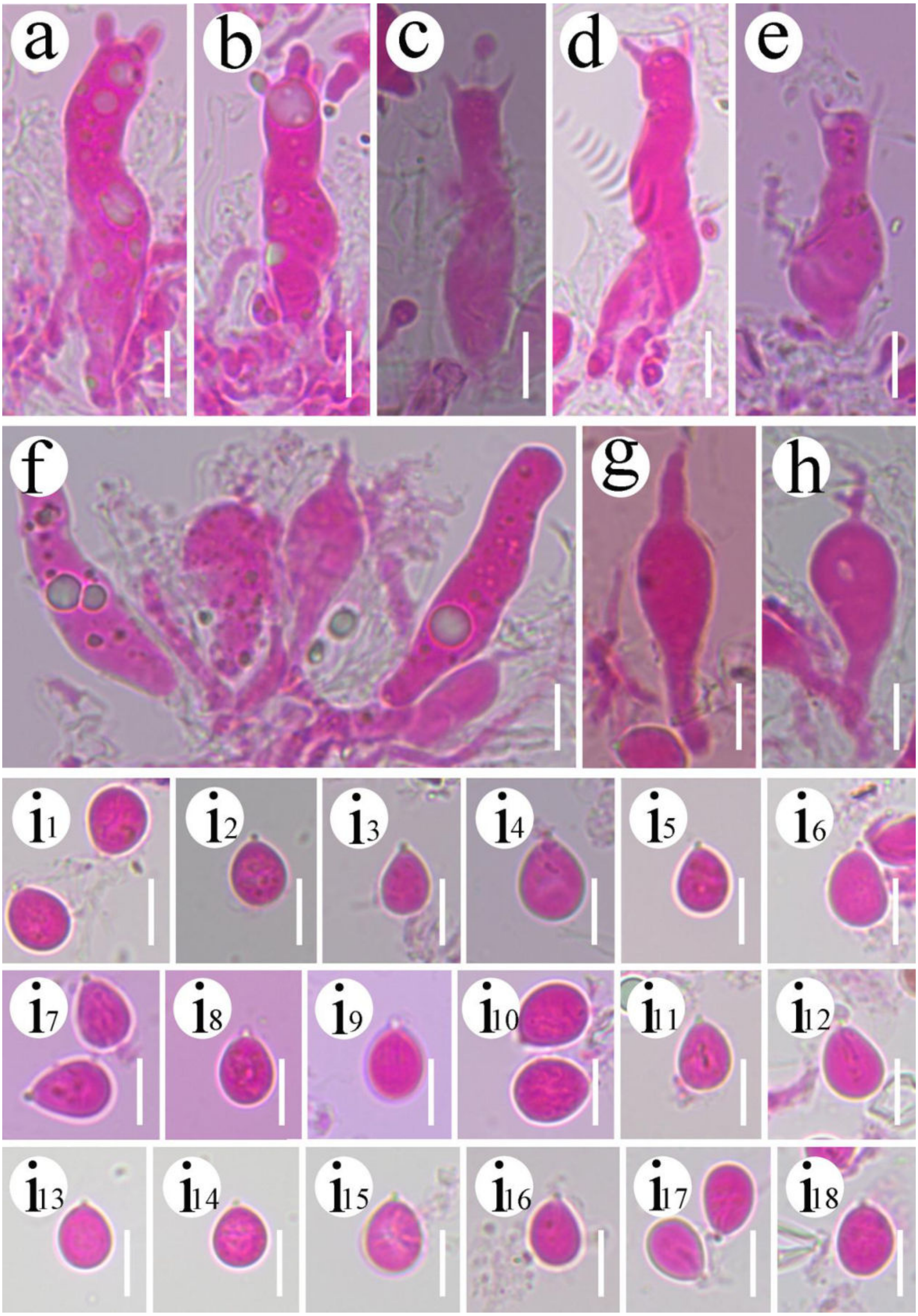

Figure 25 – Microscopic structures of *Gracilihypha albohymenia* (holotype, CLZhao 33069). a–e Basidia. f A section of the hymenium and subhymenium. g–h Cystidia. i Basidiospores. Scale bars: a–i = 10 µm.

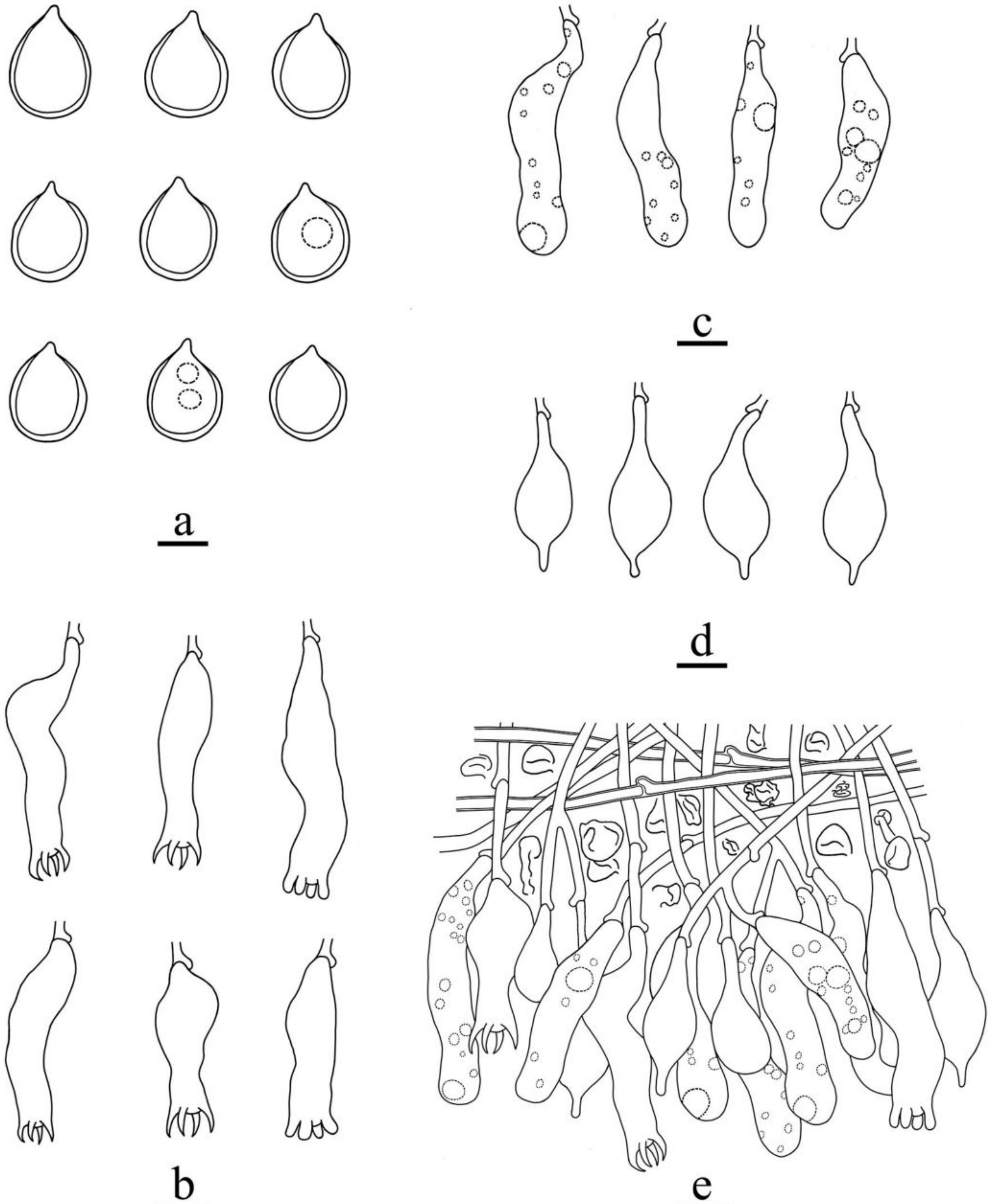

Figure 26 – Microscopic structures of *Gracilihypha albohymenia* (holotype, CLZhao 33069). a Basidiospores. b Basidia. c Basidioles. d Cystidia. e A section of the hymenium and subhymenium. Scale bars: a = 5 µm; b–d = 10 µm.

Note 58 ***Sicyoideibasidia*** J.H. Dong & C.L. Zhao, gen. nov.

Index Fungorum number: IF858342.

Etymology –Refers to the gourd-shaped basidia.

Type –*Sicyoideibasidia bambusicola* J.H. Dong & C.L. Zhao

Description – Basidiomata annual, resupinate, adnate, membranaceous. Hymenial surface somooth, grandinoid. Hyphal system monomitic; generative hyphae with clamp connections, thin- to slightly thick-walled. Cystidia tubular, cystidioles absent. Basidia gourd-shaped, slightly constricted in the middle, with 4 sterigmata and a basal clamp connection. Basidiospores cylindrical, colorless, thick-walled, smooth, IKI–, CB+.

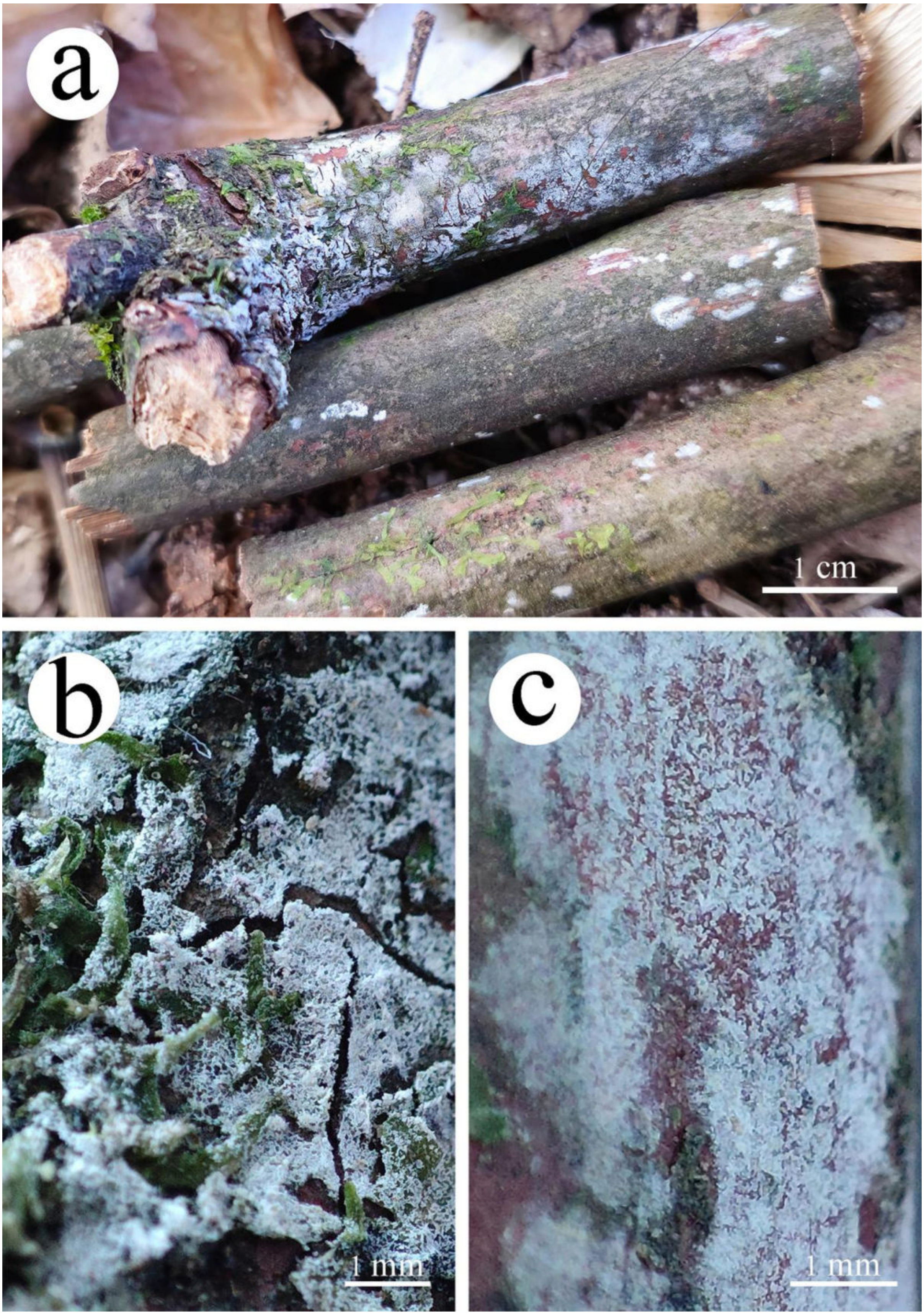

Figure 27 – Basidiomata of *Gracilihypha yunnanensis* (holotype, CLZhao 32826).

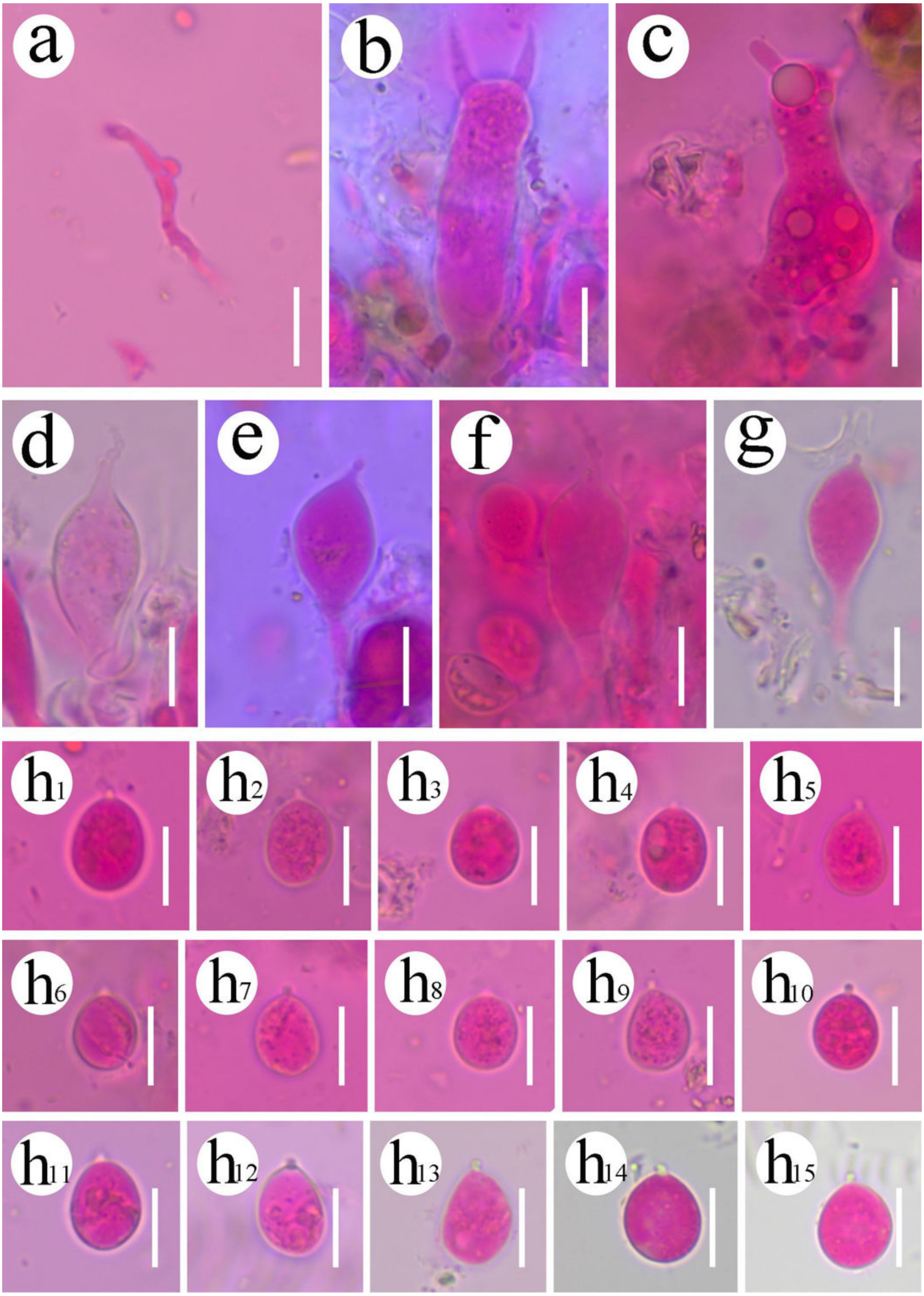

Figure 28 – Microscopic structures of *Gracilihypha yunnanensis* (holotype, CLZhao 32826). a Generative hypha. b–c Basidia. d–g Cystidia. h Basidiospores. Scale bars: a–h = 10 µm.

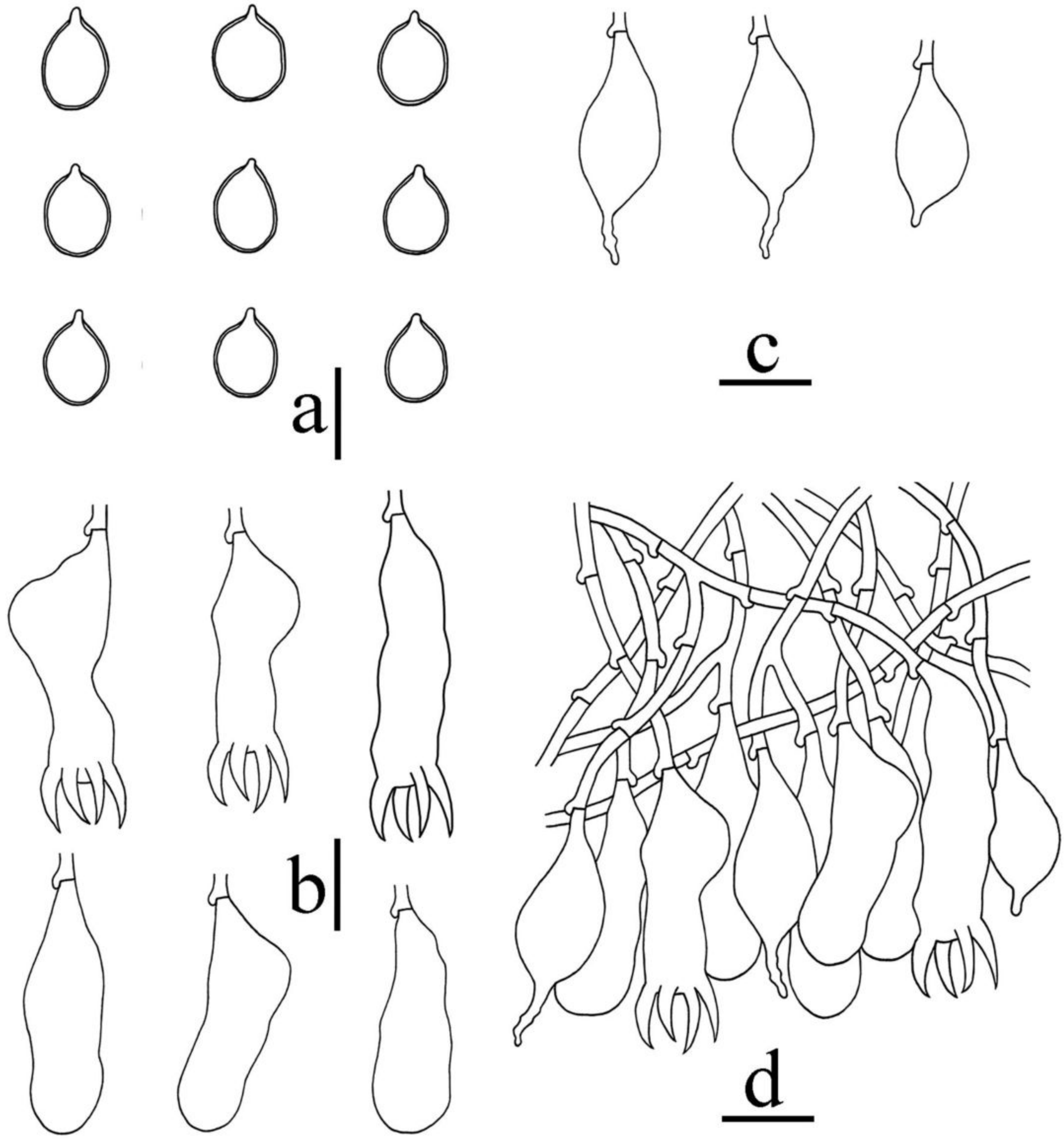

Figure 29 – Microscopic structures of *Gracilihypha yunnanensis* (holotype, CLZhao 32826). a Basidiospores. b Basidia and basidioles. c Cystidia. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 µm.

Notes – In our phylogenetic analyses based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and ITS+nrLSU sequence data (Fig. 5), *Sicyoideibasidia* is identified as a monophyletic group (BS = 100%, BPP = 1.00), typified by *S. bambusicola*. The new genus *Sicyoideibasidia* falls within the family *Cyphellopsidaceae* (*Agaricales*) and is closely related to *Gracilihypha* Y. Yang & C.L. Zhao. In addition, based on the phylogenetic and morphological analysis, two new species are described in the genus *Gourdibasidia.* However, *Gracilihypha* can be distinguished from *Sicyoideibasidia* by its cracked hymenial surface, clavate basidia, and broadly ellipsoid to subglobose, thin-walled basidiospores (Yang et al. 2025).

Sicyoideibasidia bambusicola J.H. Dong & C.L. Zhao, sp. nov. Figs. 30–32

Index Fungorum number: IF858345.

Etymology – Refers to the bamboo substrate of the type specimen.

Typus – China, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates 27°40′ N, 104°15′ E, altitude 2000 m asl., on the dead bamboo, leg. C.L. Zhao, 26 August 2023, CLZhao 31774 (SWFC).

Description – Basidiomata annual, resupinate, adnate, membranaceous, without odor or taste when fresh, becoming coriaceous upon drying, up to 10 cm long, 3 cm wide, 150 µm thick. Hymenial surface grandinoid, cracked, cream when fresh, turning to cream to straw-buff upon drying. Sterile margin cream, thinning out, up to 0.5 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled, branched, interwoven, 2–3 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia tubular, colorless, thin-walled, 20–28.5 × 4–6.5 µm; cystidioles absent. Basidia gourd-shaped, slightly constricted in the middle, with 4 sterigmata and a basal clamp connection, 20.5–28.5 × 4.5–9 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores cylindrical, colorless, thick-walled, smooth, IKI–, CB+, (9.5–)9.8–12.2(–12.5) × 5.5–7(–7.5) µm, L = 11.13 µm, W = 6.12 µm, Q = 1.55–2.10, Q_m = 1.83 ± 0.18 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Zhaotong, Daguan County, Wumengshan National Nature Reserve, GPS coordinates 27°50′ N, 103°45′ E, altitude 2500 m asl., on the dead bamboo, leg. C.L. Zhao, 6 November 2023, CLZhao 35394 (SWFC).

Notes – Based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and the ITS+nrLSU sequence data (Fig. 5), the newly proposed genus *Sicyoideibasidia* is identified as a monophyletic group within the family *Cyphellopsidaceae* (*Agaricales*). The hylogenetic analyses result (Figs. 2, 4) showed that *S. bambusicola* is closely related to *S. punctata*. However, *S. punctata* can be distinguished from *S. bambusicola* by its farinaceous basidiomata with cream, smooth, punctate hymenial surface, and longer cystidia (29–35.5 × 5.5–7.5 µm *vs* 20–28.5 × 4–6.5 µm).

Sicyoideibasidia punctata J.H. Dong & C.L. Zhao, sp. nov. Figs. 33–35

Index Fungorum number: IF858346.

Etymology – Refers to the punctate hymenial surface of the type specimen.

Typus – China, Yunnan Province, Zhaotong, Yongshan County, Mugan Town, Wumengshan National Nature Reserve, GPS coordinates 28°10′ N, 104°25′ E, altitude 2500 m asl., on the dead bamboo, leg. C.L. Zhao, 7 November 2023, CLZhao 35563 (SWFC).

Description – Basidiomata annual, resupinate, adnate, membranaceous, without odor or taste when fresh, becoming farinaceous upon drying, up to 3 cm long, 1 cm wide, 100 µm thick. Hymenial surface smooth, punctate, white when fresh, turning to cream upon drying. Sterile margin white, narrow, up to 0.5 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled, branched, interwoven, 1.5–2.5 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia tubular, colorless, thin-walled, 29–35.5 × 5.5–7.5 µm; cystidioles absent. Basidia gourd-shaped, slightly constricted in the middle, with 4 sterigmata and a basal clamp connection, 20.5–30.5× 7.5–10.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores cylindrical, colorless, thick-walled, smooth, IKI–, CB+, (8.7–)9–12(–12.5) × 5.5–6.8(–7) µm, L = 10.46 µm, W = 6.03 µm, Q = 1.47–1.93, Q_m = 1.74 ± 0.14 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Zhaotong, Yiliang County, Xiaocaoba Town, Wumengshan National Nature Reserve, GPS coordinates 27°40′ N, 104°15′ E, altitude 2000 m asl., on the dead bamboo, leg. C.L. Zhao, 19 September 2023, CLZhao 33271 (SWFC).

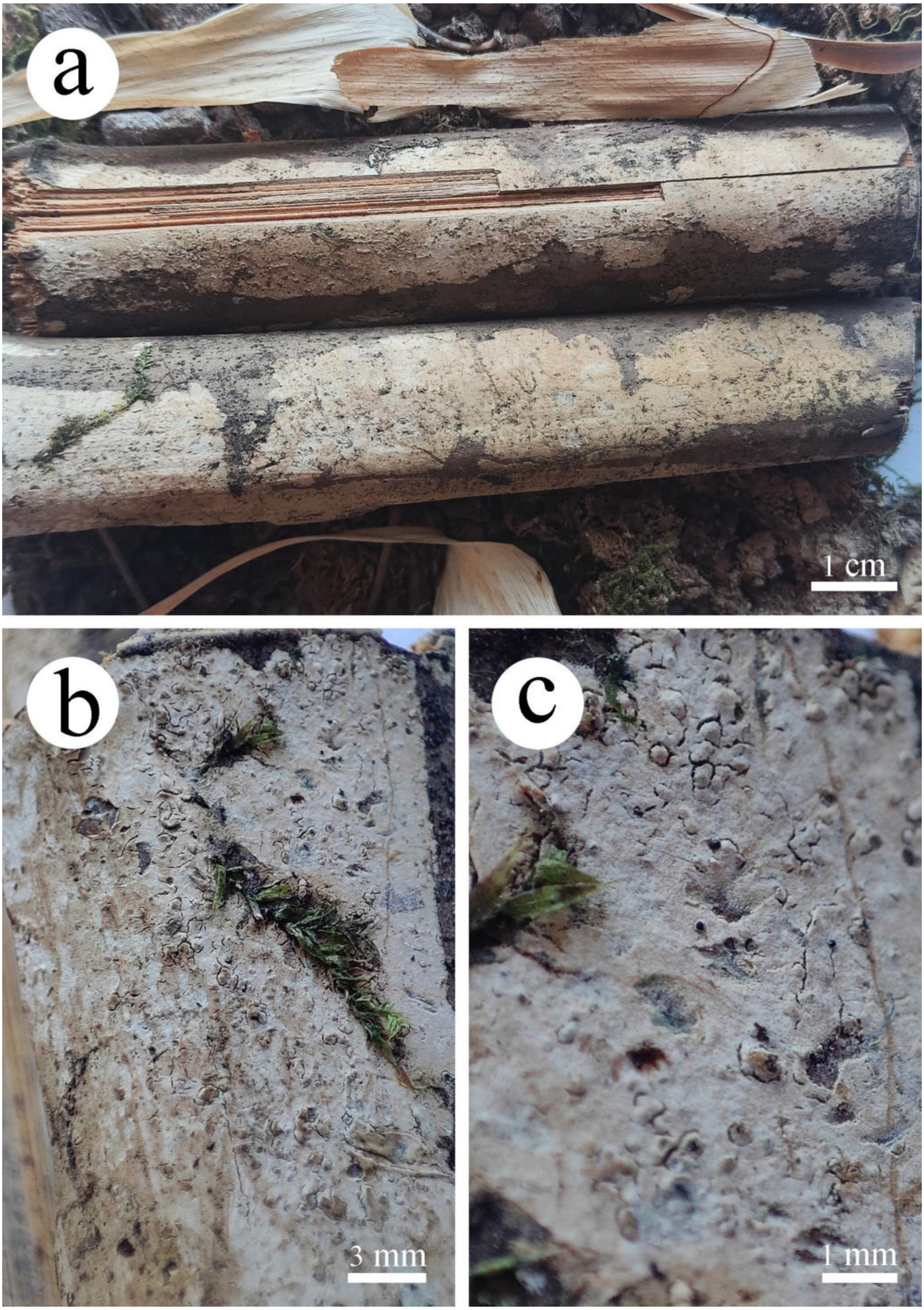

Figure 30 – Basidiomata of *Sicyoideibasidia bambusicola* (holotype, CLZhao 31774).

Notes – Based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2) and the ITS+nrLSU sequence data (Fig. 5), the newly proposed genus *Sicyoideibasidia* is identified as a monophyletic group within the family *Cyphellopsidaceae* (*Agaricales*). The phylogenetic analyses result (Figs. 2, 4) shows that *S. punctata* is closely related to *S. bambusicola*. However, *S. bambusicola* can be distinguished from *S. punctata* by its coriaceous basidiomata with straw-buff, grandinoid, cracked hymenial surface, and shorter cystidia (20–28.5 × 4–6.5 µm *vs* 29–35.5 × 5.5–7.5 µm).

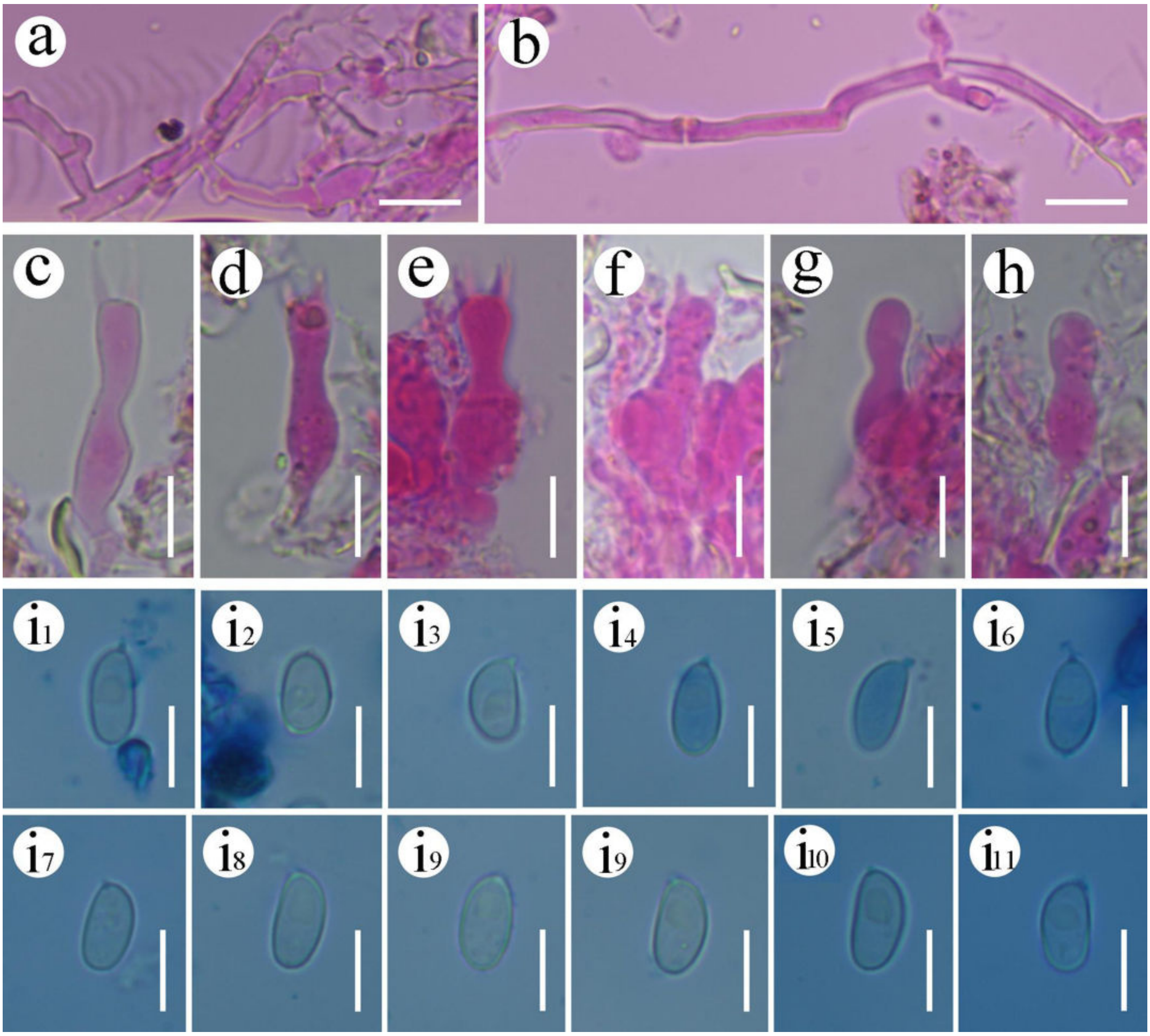

Figure 31 – Microscopic structures of *Sicyoideibasidia bambusicola* (holotype, CLZhao 31774). a–b Generative hyphae. c–f Basidia. g–h Basidioles. i Basidiospores. Scale bars: a–i = 10 µm.

Family *Fistulinaceae* Lotsy

Index Fungorum number: IF80774.

Type genus – *Fistulina* Bull.

Note 59 *Fistulina* Bull.

Index Fungorum number: IF17591.

Type species – *Fistulina hepatica* (Schaeff.) With.

Notes – *Fistulina* was established by Bulliard (1791) and typified by *Fistulina hepatica*. The genus is characterized by annual, pileate to lateral stipitate basidiocarps with reddish to brownish upper surface and context with red sap when fresh, separated tubes closely packed, a monomitic hyphal system with clamp connections, some with simple septa, cystidial elements present at dissepimental edges, hyaline, thin- to thick-walled basidiospores that are cyanophilous, and the degradation of hardwoods as a brown rot (Ryvarden & Melo 2017). It is a cosmopolitan genus with ten accepted species, eight from the Southern Hemisphere and four from the Northern Hemisphere (González et al. 2021, Wu et al. 2022b). Although *Fistulina* is considered a polypore genus, it consists of separate tubes, a feature distinct from the true polypores (Zhou et al. 2022). Phylogenetically, *Fistulina* was closely related to *Porodisculus* Murrill in the euagarics clade (Bodensteiner et al. 2004, Binder et al. 2005, Song et al. 2015, Sun et al. 2019, González et al. 2021).

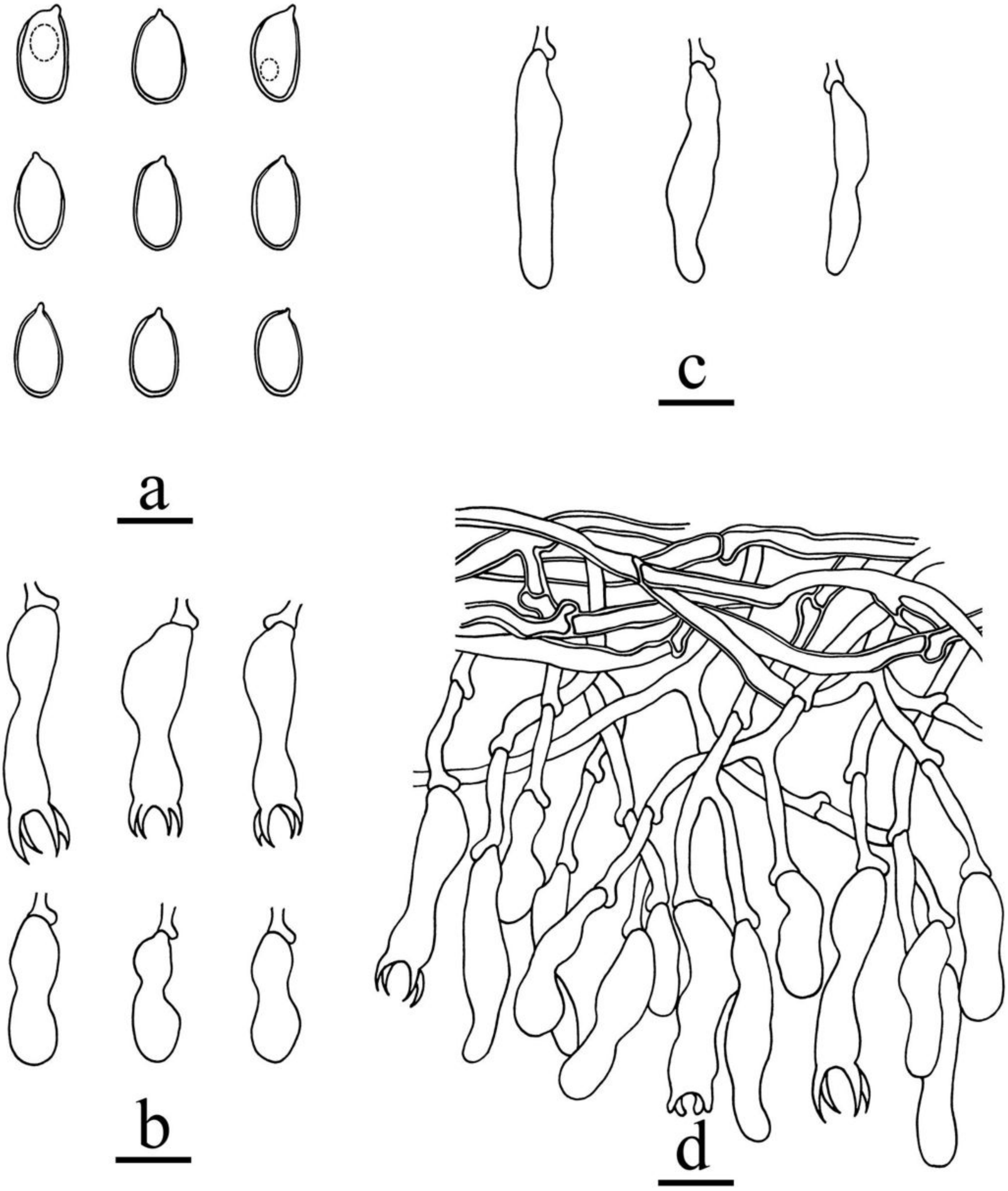

Figure 32 – Microscopic structures of *Sicyoideibasidia bambusicola* (holotype, CLZhao 31774). a Basidiospores. b Basidia and basidioles. c Cystidia. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 µm.

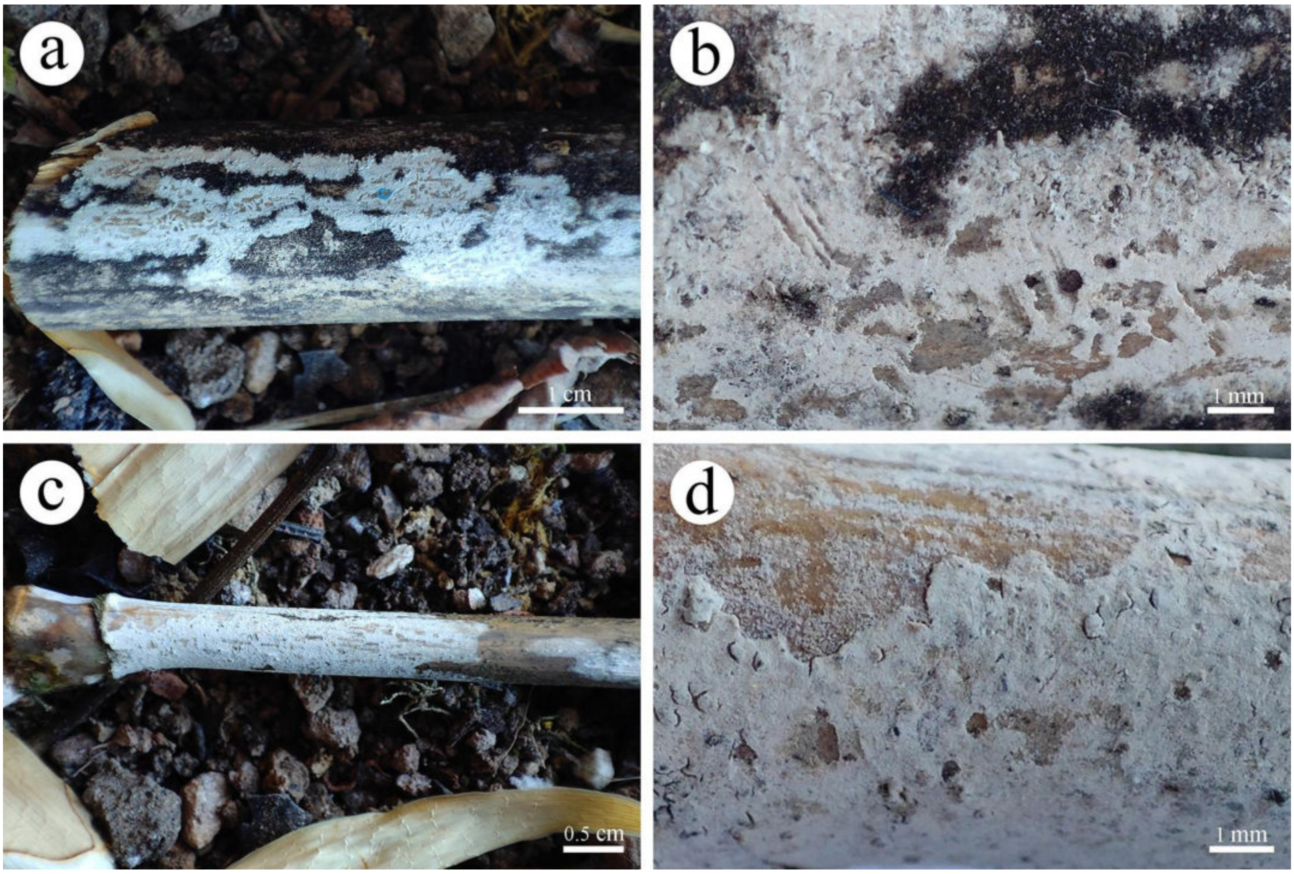

Figure 33 – Basidiomata of *Sicyoideibasidia punctata* a, b CLZhao 35563 (holotype). c, d CLZhao 33271.

Family *Pleurotaceae* Kühner

Index Fungorum number: IF81191.

Type genus – *Pleurotus* (Fr.) P. Kumm.

Note 60 *Lignomyces* R.H. Petersen & Zmitr.

Index Fungorum number: IF811172.

Type species – *Lignomyces vetlinianus* (Domański) R.H. Petersen & Zmitr.

Notes – *Lignomyces* was established by Petersen et al. (2015) and typified by *L. vetlinianus*. The phylogenetic analysis based on nrLSU includes diverse genera with pleurotoid basidiomata, as well as genera identified as potentially related through a BLAST query of GenBank. Petersen et al. (2015) phylogenetic analysis revealed that the genus *Lignomyces* is the nearest sister group to *Resupinatus*, but *Resupinatus* appears polyphyletic. Based on the ITS sequence, Petersen et al. (2015) resolved a single species, initially described as *Resupinatus violaceogriseus* G. Stev. but transferred to *Marasmiellus* by Horak (1971), as the sister to *Lignomyces* sequences. Available descriptive material on this taxon suggests that *Resupinatus violaceogriseus* is taxonomically distinct from *Lignomyces vetlinianus*, based on diverticulate pileus cuticle hyphae and cheilocystidia, as well as its geographic distribution, which appears to be limited to New Zealand (Petersen et al. 2015).

Note 61 *Radulomycetopsis* Dhingra, Priyanka & J. Kaur

Index Fungorum number: IF560517.

Type species – *Radulomycetopsis cystidiata* Dhingra, Priyanka & J. Kaur

Notes – The corticioid genus *Radulomycetopsis* (*Agaricomycetes*) was introduced by Dhingra et al. (2012) to accommodate *R. cystidiata* as the type species, which is from India. *Radulomycetopsis* resembles *Radulomyces* in producing simple to somewhat branched hyphoid structures in the hymenium, similar basidia, and broadly ellipsoid to subglobose basidiospores that are thin- to slightly thick-walled, non-amyloid, acyanophilous, and with oil-rich protoplasm (Dhingra et al. 2012). *Radulomycetopsis* differs in having dark-colored fruitbodies, hyphae without clamps, and the presence of cystidia — a combination of features that supports an independent genus (Dhingra et al. 2012). The taxonomic placement of *Radulomycetopsis* is located in the family *Pleurotaceae* within *Agaricales*.

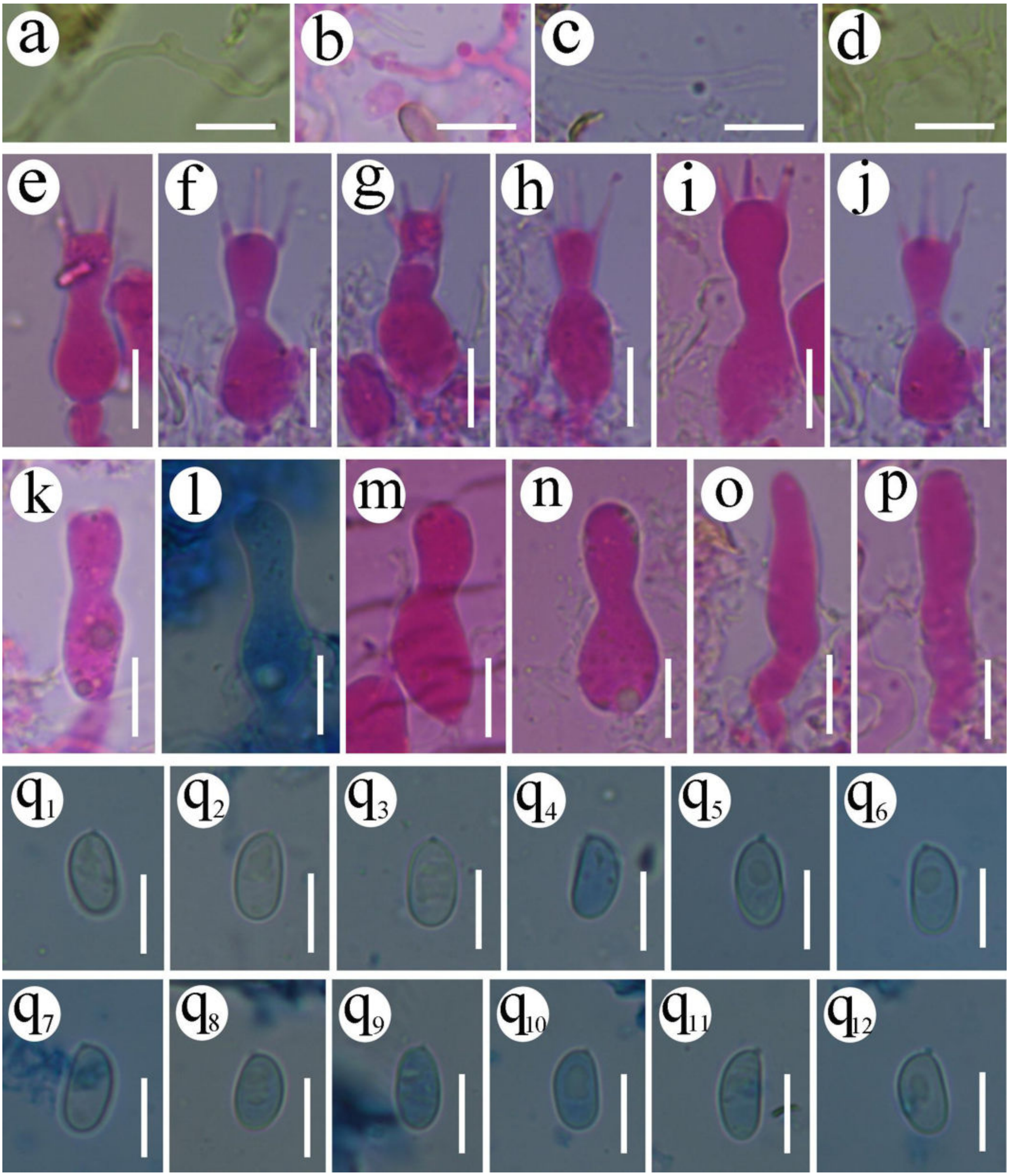

Figure 34 – Microscopic structures of *Sicyoideibasidia* punctata (holotype, CLZhao 35563). a–d Generative hyphae. e–j Basidia. k–n Basidioles. o–p Cystidia. q Basidiospores. Scale bars: a–q = 10 µm.

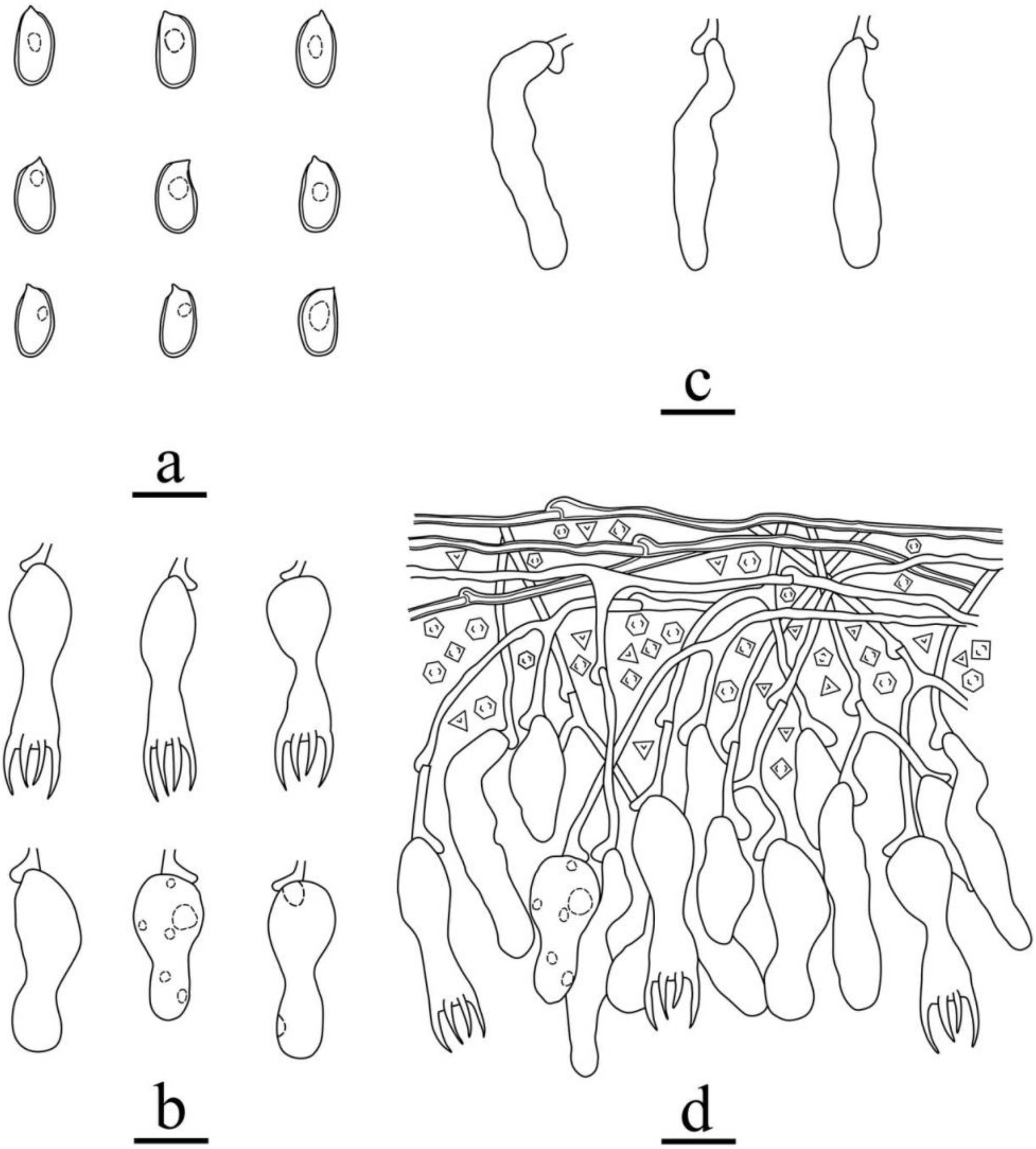

Figure 35 – Microscopic structures of *Sicyoideibasidia punctata* (holotype, CLZhao 35563). a Basidiospores. b Basidia and basidioles. c Cystidia. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 µm.

Family *Resupinataceae* Jülich

Index Fungorum number: IF80034.

Type genus – *Resupinatus* Nees ex Gray

Note 62 *Resupinatus* Nees ex Gray, Nat. Arr. Brit. Pl. (London) 1: 617 (1821)

Index Fungorum number: IF18455.

Type species – *Resupinatus applicatus* (Batsch) Gray 1821

Notes – *Resupinatus* was introduced by Gray (1821) and is typified by *R. applicatus* (Batsch) Gray. The genus is characterized by the resupinate basidiomata with lamellate, poroid, or cyphelloid hymenophore, a monomitic hyphal system with clamp connections, clavate or subclavate basidia with 2- or 4-spored, smooth, globose or subglobose to oblong or cylindric basidiospores (Gray 1821, Bijeesh et al. 2020). Majority rule consensus tree from Bayesian analysis indicated that the species of *Resupinatus* grouped into the resupinatus clade, in which this monophyletic group also included members of *Asterotus* Singer and the cyphelloid genus *Stigmatolemma* Kalchbr. (Thorn et al. 2005). Phylogeny analysis of a super-matrix of three nuclear gene regions (ITS, nrLSU and *tef*1-α) showed that two sequences known as *Hohenbuehelia nigra* (Schwein.) Singer was placed with strong support in the sister genus *Resupinatus* with the species *R. niger* (Schwein.) Murrill (Consiglio et al. 2018). Phylogenetic analysis of *Resupinatus* species inferred from ITS sequences showed that a merulioid hymenophore taxon as *R. odoratus* C.K. Pradeep, C. Bijeesh & A.M. Kumar was reported (Bijeesh et al. 2020). Based on a combination of morphological and molecular evidence, the fungal diversity within the genus *Resupinatus* was analyzed, including *R. porrigens* J.Z. Xu & Yu Li, *R. reviviscens* Carpouron & Raspé, and *R. yunnanensis* Yang Yang & C.L. Zhao (Yang et al. 2023, Carpouron et al. 2024, Liu et al. 2024a). In the present study, based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2), a new species, *R. tenuis*, is introduced.

Resupinatus tenuis J.H. Dong & C.L. Zhao, sp. nov. Figs. 36–38

Index Fungorum number: IF858350.

Etymology – Refers to the tenuous basidiomata of the type specimen.

Typus – China, Yunnan Province, Diqing, Weixi County, Zhonglu Town, GPS coordinates 27°50′ N, 99°05′ E, altitude 1500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 14 October 2023, CLZhao 34892 (SWFC).

Description – Basidiomata annual, resupinate to cupulate, adnate, soft gelatinous, without odor or taste when fresh, becoming fragile upon drying, up to 3 cm long, 1 cm wide, 100 µm thick, cups globose or depressed-globose, up to 100 µm in diameter, aggregated in groups, 7–10 per mm, covered in a dense mat of hairs. Hymenial surface cyphelloid, grey when fresh, turning to mouse-grey to grey-black upon drying. Sterile margin indistinct and slightly cream; subiculum felty, loosely attached to the substrate and densely packed, up to 0.1 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled, branched, interwoven, 2–3 µm in diameter, presence of crystal-encrusted hyphae; IKI–, CB–; tissues unchanged in KOH. Cystidia absent; cystidioles tapering, colorless, thin-walled, 16–22 × 3.5–5.5 µm. Basidia clavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, with a few guttulae, 20.5–26.5 × 8.5–10 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, with one guttula, IKI–, CB–, (7.3–)7.5–9 × (4.8–)5–6 µm, L = 8.15 µm, W = 5.28 µm, Q = 1.43–1.65, Q_m = 1.55 ± 0.08 (n = 30/1).

Notes – The species *Resupinatus tenuis* was grouped in *Resupinatus* (*Resupinataceae*, *Agaricales*) based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α data (Fig. 2), and *R. tenuis* was sister to *R. yunnanensis*. However, *R. yunnanensis* can be distinguished from *R. tenuis* by its greyish to pale mouse-grey basidiomata, narrower basidia (12–36.5 × 4–8 µm *vs* 20.5–26.5 × 8.5–10 µm, Yang et al. 2023).

Morphologically, *Resupinatus tenuis* shares similarities with *R. reviviscens*, *R. alboniger* (Pat.) Singer, Beih., *R. hyalinus* (Singer) Thorn, Moncalvo & Redhead, and *R. vinosolividus* (Segedin) J.A. Cooper in sharing the ellipsoid basidiospores. However, *R. reviviscens* differs from *R. tenuis* by its pileate basidiomata, narrower basidia (18.2–28.8 × 4.5–7 *vs* 20.5–26.5 × 8.5–10 µm), and smaller basidiospores (4.4–6.8 × 3.2–5 µm *vs* 7.5–9 × 5–6 µm, Carpouron et al. 2024); *R. alboniger* can be distinguished from *R. tenuis* by its brown hymenophore and irregular finger-like cystidia (23–35 × 8–10 µm, Gonou-Zagou et al. 2011); *R. hyalinus* differentiates from *R. tenuis* by its hairs surface and finger-like cystidia (Mcdonald 2015); *R. vinosolividus* differs from *R. tenuis* by its cheilocystidia at edge of basidiomata on top surface (Mcdonald 2015).

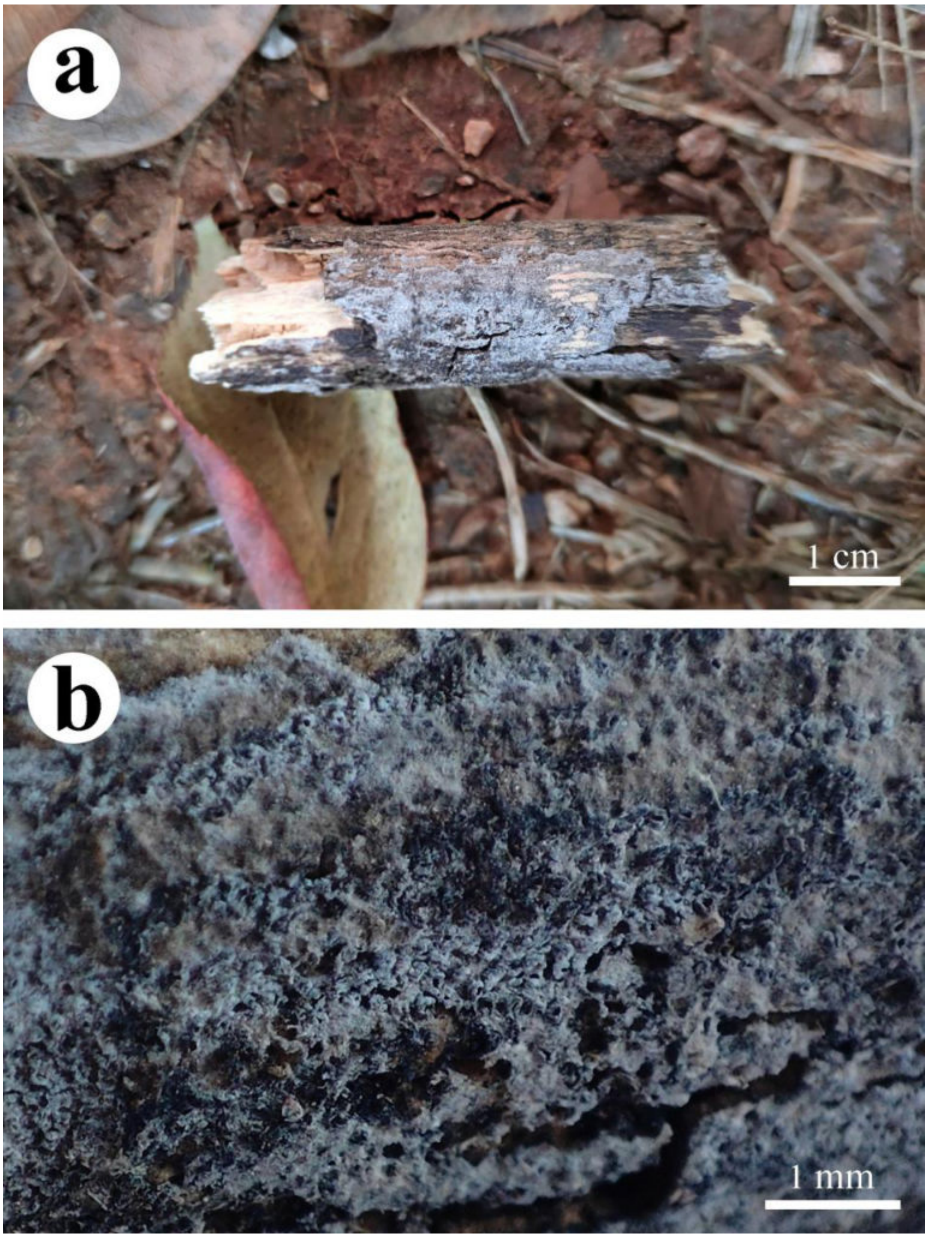

Figure 36 – Basidiomata of *Resupinatus tenuis* (holotype, CLZhao 34892).

Suborder *Tricholomatineae* Aime, Dentinger & Gaya
Family *Callistosporiaceae* Vizzini, Consiglio, M. Marchetti & P. Alvarado
Index Fungorum number: IF831396.
Type genus – *Callistosporium* Singer

Note 63 *Callistosporium* Singer
Index Fungorum number: IF17217.
Type species – *Callistosporium palmarum* (Murrill) Singer

Notes – The genus *Callistosporium* was described by Singer (1944) for *C. palmarum* (basionym: *Gymnopus palmarum* Murrill), a species known only from the type collection.

Since then, several new *Callistosporium* taxa have been recognized, and new combinations made. There are about 30 *Callistosporium* species names published (Vizini et al. 2020). A close phylogenetic relationship between *Pleurocollybia* Singer and *Callistosporium* was later suggested by the genetic works by Moncalvo et al. (2002) and Lavorato et al. (2015). Both genera *Pleurocollybia* and *Callistosporium* were significantly related to the so-called /callistosporioid clade, as well as by Ammirati et al. (2007), Sánchez-García et al. (2016), Sánchez-García & Matheny (2017), and Alvarado et al. (2018a, b).

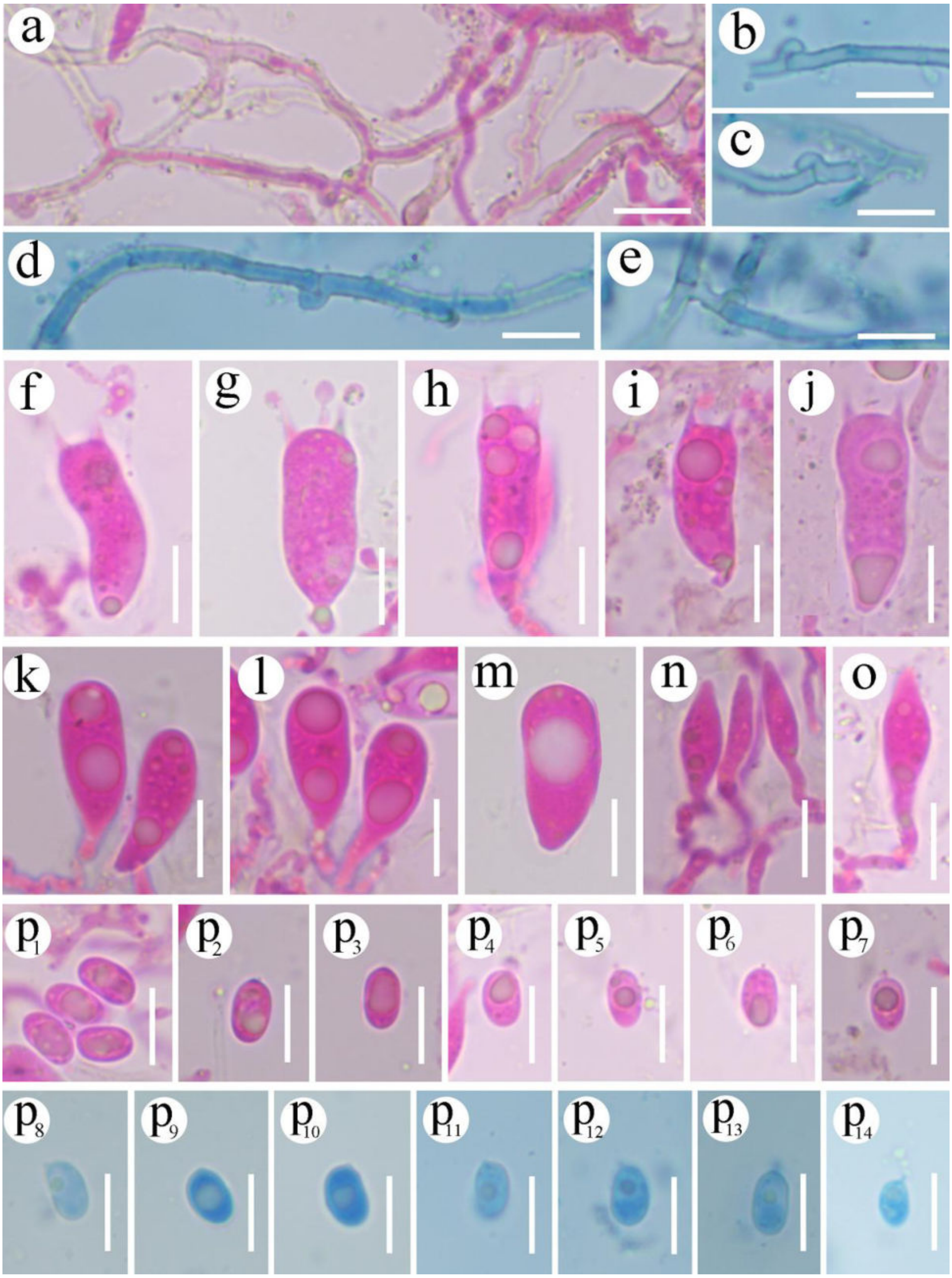

Figure 37 – Microscopic structures of *Resupinatus tenuis* (holotype, CLZhao 34892). a–e Generative hyphae. f–j Basidia. k–m Basidioles. n–o Cystidioles. p Basidiospores. Scale bars: a–p = 10 µm.

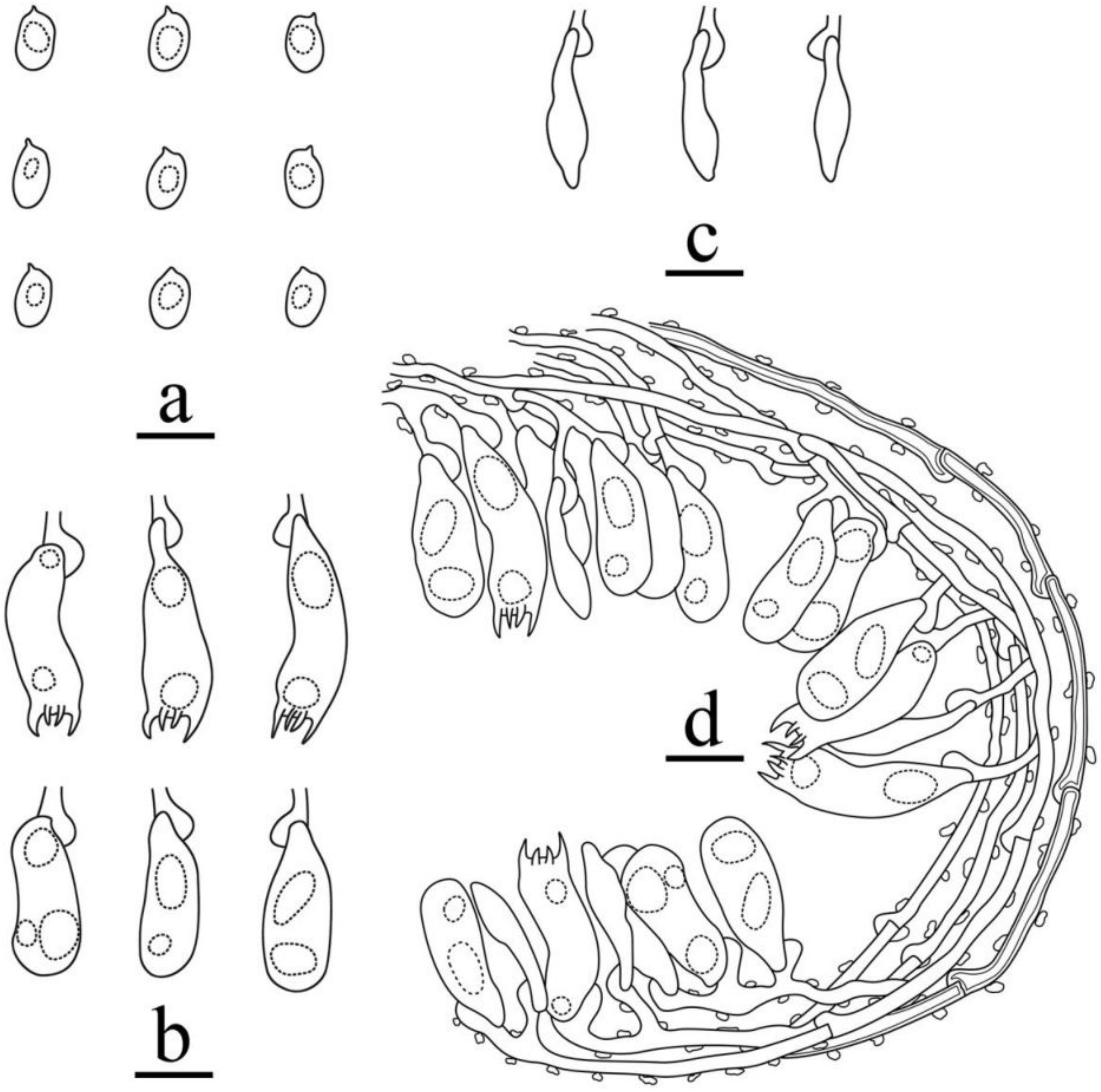

Figure 38 – Microscopic structures of *Resupinatus tenuis* (holotype, CLZhao 34892). a Basidiospores. b Basidia and basidioles. c Cystidioles. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 µm.

Note 64 *Macrocybe* Pegler & Lodge

Index Fungorum number: IF27740.

Type species – *Macrocybe titans* (H.E. Bigelow & Kimbr.) Pegler, Lodge & Nakasone

Notes – *Macrocybe* was introduced by Pegler et al. (1998) to accommodate *M. titans* as type species. Most species of *Macrocybe* were previously classified within *Tricholoma* sect. *Leucorigida* Singer by Singer (1986) because of the presence of clamp connections, an interwoven cutis, whitish basidiomata, and a non-mycorrhizal lifestyle. However, *Tricholoma mongolicum* S. Imai, the type species of section *Leucorigida*, was suggested to be a species of *Calocybe* Kühner ex Donk by Pegler et al. (1998), which provided genetic support to combine species of *Tricholoma* sect. *Leucorigida* with massive basidiomata, saprotrophic habit, and growing in subtropical to tropical areas, is placed in the new genus *Macrocybe*. Moncalvo et al. (2002) found that the nrLSU rDNA sequences of *Macrocybe* were significantly related to those of the callistosporioid clade.

Family *Clitocybaceae* Vizzini, Consiglio & M. Marchetti

Index Fungorum number: IF557869.

Type genus – *Clitocybe* (Fr.) Staude

Note 65 ***Lepistella*** T.J. Baroni & Ovrebo

Index Fungorum number: IF510737.

Type species – *Lepistella ocula* T.J. Baroni & Ovrebo

Notes – *Lepistella* was introduced by Ovrebo & Baroni (2007) to accommodate *L. ocula* as the type species. The genus is characterized by small size, brown broadly depressed glabrous pileus with the dark brown disc, adnate or subcurrent crowded lamellae, central to eccentric stipe, and habit of growing in dense clusters on downed decaying logs or stumps, and strongly verrucose small basidiospores (Ovrebo & Baroni 2007). *Lepistella* has an unusual feature not seen in any other fungus we had studied in the past: corrugated-collapsed and obscurely gelatinizing hyphae making up most of the lamella trama and pileus context (Ovrebo & Baroni 2007). Based on multi-locus sequences, Vizzini et al. (2024) phylogenetic analyses revealed that the genus *Lepistella* belonged to the family *Clitocybaceae*. Later, the result was accepted by Hyde et al. (2024b).

DISCUSSION

Fungi are closer to humans than to plants, and thus can be treated as a kind of strategic biological resource (Ming et al. 2023, Zhao et al. 2023b). The application potential of fungi is as essential as their natural ability to recognize fungi (Dai et al. 2021). Climate change and the destruction of natural habitats are also threatening species, and many may become extinct before they are even discovered (Hyde et al. 2024c). Studies on the biodiversity of fungi and their applications are essential, as they may lead to new products (Hyde et al. 2024a, Chen et al. 2025, Zhou et al. 2025). Therefore, for future utilization, it is now urgent to recognize and conserve fungi.

In the present study, we present morphological and molecular phylogenetic evidence that supports the eleven new species and a new genus in their taxa, based on the ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α sequence data (Fig. 2). The specimen CLZhao 25824 lacks reproductive structures, precluding morphological species determination; therefore, this lineage has been tentatively assigned to the genus *Resupinatus* (designated as *Resupinatus* sp.) based on molecular phylogenetic evidence.

Ancestral basidiomata of the *Agaricomycotina* were probably crust-like, 'resupinate' forms (Hibbett & Binder 2002, Hibbett 2004, Varga et al. 2019), which then evolved into increasingly more complex forms, including derived 'pileate-stipitate' types, which are differentiated into a cap, stipe, and hymenophore (spore-bearing surface, Varga et al. 2019). Extensive mycological studies have confirmed that the genera *Campanella*, *Collybiopsis*, and *Marasmius* all exhibit the mushroom-forming growth pattern typical of the order *Agaricales* (Matheny et al. 2006, Oliveira et al. 2024, Vizzini et al. 2024). Surprisingly, in our phylogenetic analysis (Fig. 2), the research using multiple gene loci revealed that five novel corticioid species, *Campanella yunnanensis*, *Collybiopsis albobasidiosa*, *Co. cremea*, *Co. yunnanensis*, and *Marasmius wumengshanensis* were nested within the three genera. While displaying marked macro-morphological divergence from congeneric taxa, these five species retain strong micro-morphological correspondence, characterized by diagnostic features of their respective genera. Our findings demonstrate significant morphological diversity in basidiomata of wood-inhabiting fungi, establishing a crucial foundation for elucidating the evolutionary origins and diversification mechanisms that drive basidiomata polymorphism in these organisms.

Similar to the order *Auriculariales*, with continuous study, several corticioid genera, e.g., *Adustochaete* Alvarenga & K.H. Larss., *Alloexidiopsis* L.W. Zhou and S.L. Liu, *Amphistereum* Spirin & Malysheva, *Crystallodon* Alvarenga, *Heteroradulum* Lloyd ex. Spirin and Malysheva, *Metulochaete* Alvarenga, *Nodulochaete* J.H. Dong & C.L. Zhao, *Proterochaete* Spirin & Malysheva, *Punctochaete* J.H. Dong & C.L. Zhao, and *Sclerotrema* Spirin & Malysheva have been established and described based on morphological and phylogenetic studies (Malysheva & Spirin 2017, Alvarenga et al. 2019, Alvarenga & Gibertoni 2021, Liu et al. 2022, Dong et al. 2025b, c). All examined species exhibit longitudinal basidia that persist even in the absence of gelatinous basidiocarps. In our current study (Fig. 2), the result revealed notable diversity in basidiomata types within the order *Agaricales*, with thirteen families (or more) within this order exhibiting three or more distinct basidiomata types. Within the studied fungal families, members of the family *Marasmiaceae* demonstrated the highest degree of morphological diversification in basidiomata types, with taxonomic analysis revealing the presence of no fewer than seven distinct basidiomata types (Fig. 2). The types of basidiomata in the order *Agaricales* (Fig. 2), the resupinate basidiomata include corticioid type e.g., *Campanellaceae*, *Chromocyphellaceae*, *Crepidotaceae*, *Cyphellopsidaceae* (as *Niaceae*), *Cystostereaceae*, *Marasmiaceae*, *Omphalotaceae*, *Pleurotaceae*, *Radulomycetaceae*, *Resupinataceae*, and *Stephanosporaceae*, and also cyphelloid type e.g., *Crepidotaceae*, *Cyphellaceae*, *Limnoperdaceae*, and *Schizophyllaceae*. The potential correlation between corticioid basidiomata morphology and phylogenetic relationships remains unresolved within the present study. However, in the future study, employing integrative morphological and molecular phylogenetic approaches is warranted to rigorously assess the hypothesized association between these morphological characteristics and evolutionary lineages. Therefore, combining morphological and molecular phylogenetic analyses is warranted to rigorously test the relationship between these morphological characteristics and evolutionary lineages. The distinct diversity in basidiomata within the order *Agaricales* represents an evolutionary outcome shaped by long-term natural selection and adaptive radiation. Studying these basidiomata types not only enhances our understanding of fungal evolutionary mechanisms but also establishes a scientific foundation for bioprospecting initiatives and ecosystem management practices.

The evolutionary history of fungal basidiocarps and the mechanisms underlying their development have long been a central focus for mycologists (Hibbett & Binder 2002, Hibbett 2004, 2007, Matheny et al. 2006, Chen et al. 2015, Nagy et al. 2018, 2023, Varga et al. 2019, Virágh et al. 2022, Zhao et al. 2023c, Yang et al. 2025). Pileate-stipitate forms have arisen repeatedly from simpler morphologies (e.g., resupinate or coral-like) during evolution (Matheny et al. 2006, Hibbett 2007, Varga et al. 2019, Zhao et al. 2025). However, this diversity arose; what explains the dominance of pileate-stipitate species in the class, and whether basidiomata morphology impacts diversification rates are not known (Varga et al. 2019). In the present study (Fig. 2), we confirmed notable diversity in basidiomata types within the order *Agaricales*. Therefore, this necessitated the integration of molecular data for a more robust classification. Future research endeavors should integrate genomics data with phylogenetic frameworks to elucidate the molecular regulatory networks underlying macro-scale phenotypic variations among species within the same taxonomic family/genus, thereby unraveling the dynamic interplay between phenotypic diversification and the evolutionary trajectories of genetic elements.

Significant progress has been achieved in elucidating phylogenetic relationships within *Agaricales* through the integration of morphological characteristics, multi-locus sequence analyses, and genomic approaches (Moncalvo et al. 2002, Bodensteiner et al. 2004, Thorn et al. 2005, Matheny et al. 2006, Dentinger et al. 2016, Azevedo et al. 2018, Abdel-Wahab et al. 2019, Oliveira et al. 2019, 2020, 2024, Varga et al. 2019, Kalichman et al. 2020, Ke et al. 2020, Olariaga et al. 2020, Sánchez-García et al. 2020, Vizzini et al. 2020, 2024, Bellanger et al. 2021, Consiglio et al. 2021, Mou & Bau 2021, Bandini et al. 2022, He et al. 2023, 2024, Karasiński et al. 2023, Silva-Filho et al. 2023, Wang et al. 2023b, Dong et al. 2024, Kraisitudomsook et al. 2024).

The family *Campanellaceae*

While our phylogenetic tree topologies align with those presented in Moncalvo et al. (2002), Matheny et al. (2006), Koch et al. (2018), and Oliveira et al. (2019), it should be noted that their circumscription of the family *Marasmiaceae* encompasses *Campanella* and related genera, an interpretation accepted in He et al. (2019, 2024). However, a recent phylogenetic analysis by Oleviria et al. (2024) revealed distinct evolutionary relationships between the /*Marasmiaceae* and /*Campanellaceae* clades when evaluated within a subordinal phylogenetic framework. (Oleviria et al. 2024) provided a comprehensive reconstruction of *Marasmiineae* phylogeny, demonstrating that these lineages maintain separate phylogenetic identities, which led to their reclassification as two distinct families rather than being grouped as a single taxonomic unit. Oleviria et al. (2024) phylogenetic grouping integrates molecular evidence revealing that the family *Campanellaceae* is taxonomically composed of the genera *Brunneocorticium* Sheng H. Wu, *Campanella*, *Neocampanella* Nakasone, Hibbett & Goranova, *Tetrapyrgos* E. Horak, and *Marasmiellus candidus* (Fr.) Singer (type of *Marasmiellus* sect. *Candidi* Singer). The maximum likelihood (ML) phylogenetic reconstruction based on ITS, nrLSU, SSU, *rpb*2, and *tef1*-α sequence data revealed a strongly supported sister relationship between the families *Marasmiaceae* s.str. and *Campanellaceae* (Oleviria et al. 2024), it is uncertain whether *Marasmiaceae* is sister to *Campanellaceae* or *Omphalotaceae*, or whether these two latter groups are sister to each other. Notably, the families *Campanellaceae*, *Marasmiaceae* s.str. and *Omphalotaceae* form a highly supported clade (Oleviria et al. 2024). *Campanellaceae* differs from *Marasmiaceae* in the absence of brightly pigmented pilei, the hymenophore nearly always having interveined or reticulate lamellae, the stipe never being chitinous when present, in the basidiospores having a bulge or tetrahedral shape in some cases, and being gelatinized in the mushroom-forming groups (Oleviria et al. 2024). Additionally, *Campanellaceae* also differs in that some groups are purely resupinate (*Neocampanella*, Nakasone et al. 2009) or form white threads often with bud-like ornamentation (*Brunneocorticium*, Wu et al. 2007). In this study, based on ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α phylogenetic analysis (Fig. 2), we confirm that *Campanellaceae*, *Marasmiaceae* s.str. and *Omphalotaceae* form a well-supported clade (BS=99%, PP=0.95), though their precise sister relationships remain unresolved. This finding corroborates the current molecular phylogenetic study (Oleviria et al. 2024). Therefore, comprehensive phylogenetic investigations incorporating extensive sampling, multi-locus genetic markers, and advanced sequencing technologies are critically needed to elucidate the precise evolutionary relationships among *Campanellaceae*, *Marasmiaceae* s.str. and *Omphalotaceae*.

The family *Cyphellopsidaceae* (= *Niaceae*)

In current taxonomic frameworks, the families *Cyphellopsidaceae* and *Niaceae* were recognized as the primary taxonomic names associated with the *Nia* clade (Jülich 1982, Bodensteiner et al. 2004). *Cyphellopsidaceae* was the most diverse family and the largest lineage of cyphelloid forms confirmed with molecular data (Bodensteiner et al. 2004). The genera *Calathella* D.A. Reid. *Cyphellopsis* Donk, *Merismodes* Earle (abbreviated here as Me.), and *Woldmaria* W.B. Cooke were previously classified in *Cyphellopsidaceae* (Jülich 1982). *Niaceae* was erected in the same work (Jülich 1982) to accommodate the genus *Nia* R.T. Moore & Meyers, typified by the marine species *Nia vibrissa* R.T. Moore & Meyers. Binder et al. (2001), placed *N. vibrissa* in the euagaric clade, and Hibbett & Binder (2001) confirmed its placement in the euagaric clade along with two additional marine basidiomycetes, *Calathella mangrovei* E.B.G. Jones & Agerer and *Halocyphina villosa* Kohlm. & E. Kohlm. The family *Cyphellopsidaceae* encompasses the genera *Akenomyces* G. Arnaud ex D. Hornby, *Calathella*, *Cyphellopsis*, *Dendrothele*, *Digitatispora* Doguet, *Eoscyphella* Silva-Filho, Stevani & Menolli, *Flagelloscypha* Donk, *Gracilihypha*, *Halocyphina* Kohlm. & E. Kohlm., *Lachnella* Fr., *Maireina*, *Merismodes*, *Nia*, *Peyronelina* P.J. Fisher, J. Webster & D.F. Kane, *Phaeodepas* D.A. Reid, *Pseudolasiobolus* Agerer, and *Woldmaria* (Bodensteiner et al. 2004, Matheny et al. 2006, Yamaguchi et al. 2009, Henkel et al. 2010, Azevedo et al. 2018, Abdel-Wahab et al. 2019 Silva-Filho et al. 2023, Hyde et al. 2024b, Yang et al. 2025). The name *Cyphellopsidaceae* was legitimized over *Niaceae* by Knudsen & Vesterholt (2012); however, the name *Niaceae* was still being used by some authors (e.g., Abdel-Wahab et al. 2019, Kalichman et al. 2020, Yang et al. 2025). The phylogenomic analyses, as reported by Wang et al. (2023b), revealed a significant evolutionary relationship; the family *Cyphellopsidaceae* was closely related to the families *Schizophyllaceae* and *Fistulinaceae*. The newly described genus *Eoscyphella* was confirmed from molecular phylogenies in the family *Cyphellopsidaceae* (Silva-Filho et al. 2023). Yang et al. (2025) proposed the novel genus *Gracilihypha* within the family *Cyphellopsidaceae* based on a multilocus phylogenetic analysis combined with ITS+nrLSU+mtSSU+*rpb*1+*rpb*2+*tef*1-α sequence data. Our phylogenetic analyses, combining ITS and nrLSU (Fig. 5), revealed that *Merismodes* was clustered with *Maireina*, supporting the proposal by Silva-Filho et al. (2023). Our multilocus phylogenetic analysis based on a combined dataset of ITS+nrLSU+mtSSU+*rpb*1+*rpb*2+*tef*1-α (Fig. 2), revealed that the family *Cyphellopsidaceae* was closely related to *Schizophyllaceae* and *Fistulinaceae*. This finding contrasts with the results of the previous studies (Silva-Filho et al. 2023, Wang et al. 2023b, Vizzini et al. 2024), and the discrepancy may be due to the unstable topology, as the selection of representative sequences is not comprehensive. Therefore, phylogenetic analysis of *Agaricales* should prioritize the inclusion of a more comprehensive set of related taxonomic groups.

The families *Marasmiaceae* and *Omphalotaceae*

The suborder *Marasmiineae* was formally proposed by Dentinger et al. (2016) for the clade containing families *Cyphellaceae*, *Marasmiaceae*, *Mycenaceae*, *Omphalotaceae*, *Physalacriaceae*, and *Porotheleaceae* (Antonín et al. 2019, Vizzini et al. 2019b, 2022, Matheny et al. 2020, Consiglio et al. 2021, Qin et al. 2025). This decision was later confirmed by Varga et al. (2019), Ke et al. (2020), and Olariaga et al. (2020). However, phylogenetic analysis by Moncalvo et al. (2002) and Thorn et al. (2005) found that the family *Mycenaceae* was unrelated to Marasmiineae. Interestingly, some phylogenomic studies found a significant monophyletic origin between *Mycenaceae* and the remaining families of *Marasmiineae* (Ke et al. 2020). Dentinger et al. (2016) conducted a phylogenomic analysis of the *Agaricales*, establishing the suborder *Marasmiineae*, equivalent to the Marasmioid clade described by Matheny et al. (2006). Later, a study implemented a multilocus *(rpb*1, *rpb*2, and 18S, 25S, and 5.8S ribosomal RNA genes) phylogenetic analysis in *Agaricales*, recognizing the clade *Marasmiaceae* as the sister to the clade *Omphalotaceae*, both within the Marasmioid major clade (Dentinger et al. 2016). In some studies, *Marasmiineae* (or the Marasmioid clade) included also *Schizophyllineae* (Thorn et al. 2005, Matheny et al. 2006, Varga et al. 2019, Olariaga et al. 2020, Sánchez-García et al. 2020). In the present study, based on ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α phylogenetic analysis (Fig. 2), it is confirmed that *Marasmiaceae* is the sister to the clade *Omphalotaceae*, which is consistent with previous studies (Dentinger et al. 2016, Oleviria et al. 2024). Additionally, our phylogenetic analysis (Fig. 2) revealed that the *Mycenaceae* family exhibited a close phylogenetic relationship with *Porotheleaceae* but showed no significant evolutionary association with Marasmiineae. This finding contrasts with the results of the previous studies (Antonín et al. 2019, Vizzini et al. 2019b, 2022, Matheny et al. 2020, Consiglio et al. 2021), and the discrepancy may be due to the unstable topology and lower support values. Hence, using more gene segments and scientific methods to study the order *Agaricales* is a current trend.

The family *Resupinataceae*

Traditionally, the genus *Resupinatus*, typified by *R. applicatus*, has always been considered closely related to *Hohenbuehelia* Schulzer (Singer 1948, 1975b, 1986, Kühner 1980). The similarities between the two genera were so striking as to induce Kühner (1980) to consider *Hohenbuehelia* a subgenus of *Resupinatus*. Kühner (1980) included only *Resupinatus* (with *Hohenbuehelia* as a subgenus) inside the tribe *Resupinateae* Singer of *Pleurotaceae*. Jülich (1982) established the family *Resupinataceae* for *Resupinatus*. Finally, Singer (1986) widened the concept of his tribe *Resupinateae* to include the lamellate genera *Agaricochaete* Eichelb., *Hohenbuehelia*, and *Resupinatus*, and the cyphelloid genera *Aphyllotus* Singer, *Stigmatolemma* Kalchbr., and *Stromatocyphella* W.B. Cooke. With the aid of molecular phylogenetic studies, *Asterotus*, *Lignomyces*, *Rhodocyphella*, *Stigmatolemma*, and *Stromatocyphella* are later synonyms of *Resupinatus* (Thorn et al. 2000, 2005, McDonald 2015, Consiglio & Setti 2018, McDonald & Thorn 2019). Numerous phylogenetic studies have supported a close relationship between *Resupinatus*, *Hohenbuehelia* Schulzer, and *Pleurotus* (Fr.) P. Kumm. within *Pleurotaceae*, consistent with morphological observations (Matheny et al. 2006, Justo et al. 2011). However, *Resupinatus* also exhibits distinct differences from the latter two genera, suggesting its placement close to but not within *Pleurotaceae*, as indicated by Mcdonald (2015) and Consiglio et al. (2018). Correspondingly, some scholars (Jülich 1982, Kalichman et al. 2020) have proposed placing *Resupinatus* in a standalone family, the *Resupinataceae*. The systematic position of *Resupinatus* (tribe *Resupinateae* s.str.) has remained a persistent taxonomic ambiguity in previous studies (Moncalvo et al. 2002, Bodensteiner et al. 2004, Binder et al. 2005, Thorn et al. 2005, Matheny et al. 2006, Petersen et al. 2015, Consiglio & Setti 2017, Varga et al. 2019, Sánchez-García et al. 2020, Vizzini et al. 2022, Karasiński et al. 2023). Despite extensive phylogenetic investigations, extant literature reveals a conspicuous absence of robust evidence delineating the genus *Resupinatus* evolutionary affiliations, with unresolved topological relationships. It is only recently that a comprehensive study of *Agaricales* (Vizzini et al. 2024) provided significant phylogenetic evidence supporting the resurrection of *Resupinataceae*. In this study, based on ITS+nrLSU+*rpb*1+*rpb*2+*tef*1-α phylogenetic analysis (Fig. 2), it is evident that the family *Resupinataceae* forms a monophyletic clade, indicating a sister relationship with *Pleurotaceae*. This result conforms to the previous molecular phylogenetic analyses by Vizzini *et al*. (2024).

The philosophy and science behind the concept of species numbers warrant a different perspective. Undoubtedly, progress has been made to date, culminating in a better understanding of fungal diversity and its estimates, but further work is needed (Hyde et al. 2024c). Further research is needed to understand fungal diversity and distribution, including their specialisation and substrate preference across different nutritional guilds (Hyde et al. 2024c). Despite significant advances in species diversity among wood-inhabiting fungi in China (Cui et al. 2019, Shen et al. 2019, Sun et al. 2020, 2022, Cao et al. 2021, Savchenko et al. 2021, Ji et al. 2022, Dong et al. 2023, 2024, 2025a, Liu et al. 2023a, b, Mao et al. 2023, Wang et al. 2023a, 2024, Zhang et al. 2023, Zhao et al. 2023a, 2024, Spirin et al. 2024, Yang et al. 2025), the systematic studies still need to be conducted for many groups of wood-inhabiting fungi. In the present study, we have compiled sequence data for wood-inhabiting fungi in the order *Agaricales*. Our focus has been intensified on exploring the molecular systematics of wood-inhabiting *Agaricales* from China, and other parts of Asia. Additionally, we have explored their topological relationships through the analysis of phylogenetic trees and provided detailed morphological descriptions and phylogenetic analyses of these fungal species, while also contributing to the enrichment of fungal diversity in East Asia.

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DECLARATION ON CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

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