

ARTICLE

Notes, outline, taxonomy and phylogeny of wood-inhabiting *Agaricales***Dong JH^{1,2}, Chen ML², Chen M², Li Q², Zhu YJ², Zhang XC², Zhou CQ³, Li W³, Muhammad A², Zhou HM², Jabeen S⁴, Zhao CL^{1,2*}**

¹ The Key Laboratory of Forest Resources Conservation and Utilization in the Southwest Mountains of China Ministry of Education, Key Laboratory of National Forestry and Grassland Administration on Biodiversity Conservation in Southwest China, Yunnan Provincial Key Laboratory for Conservation and Utilization of In-forest Resource, Southwest Forestry University, Kunming 650224, P.R. China

² College of Forestry, Southwest Forestry University, Kunming 650224, P.R. China

³ Management and Conservation Bureau, Yunnan Wumeng Mountain National Nature Reserve, Zhaotong, 657000, P.R. China

⁴ Department of Botany, Division of Science and Technology, University of Education, Township, Lahore, Punjab, Pakistan

Citation – Dong JH, Chen ML, Chen M, Li Q, Zhu YJ, Zhang XC, Zhou CQ, Li W, Muhammad A, Zhou HM, Jabeen S, Zhao CL. 2025 – Notes, outline, taxonomy and phylogeny of wood-inhabiting *Agaricales*. *Mycosphere* 16(1), 2599–2711, Doi 10.5943/mycosphere/16/1/16

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 (corticoid) 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; *Sarcomyaceae*: 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

Submitted: 18 March 2025; **Accepted:** 30 July 2025; **Published:** 13 August 2025

***Corresponding Author:** Changlin Zhao – e-mail – fungi@swfu.edu.cn; fungichanglinz@163.com

Accepted by: Samantha C. Karunarathna

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.
Pyrrohulomyces 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.
Clavicornia 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 Cléménçon

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
Phaeoporothelium (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.

Calyprella 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

Pseudotracheloma (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 1, He et al. 2024, Hyde et al. 2024b, Oliveira et al. 2024, Vizzini et al. 2024).

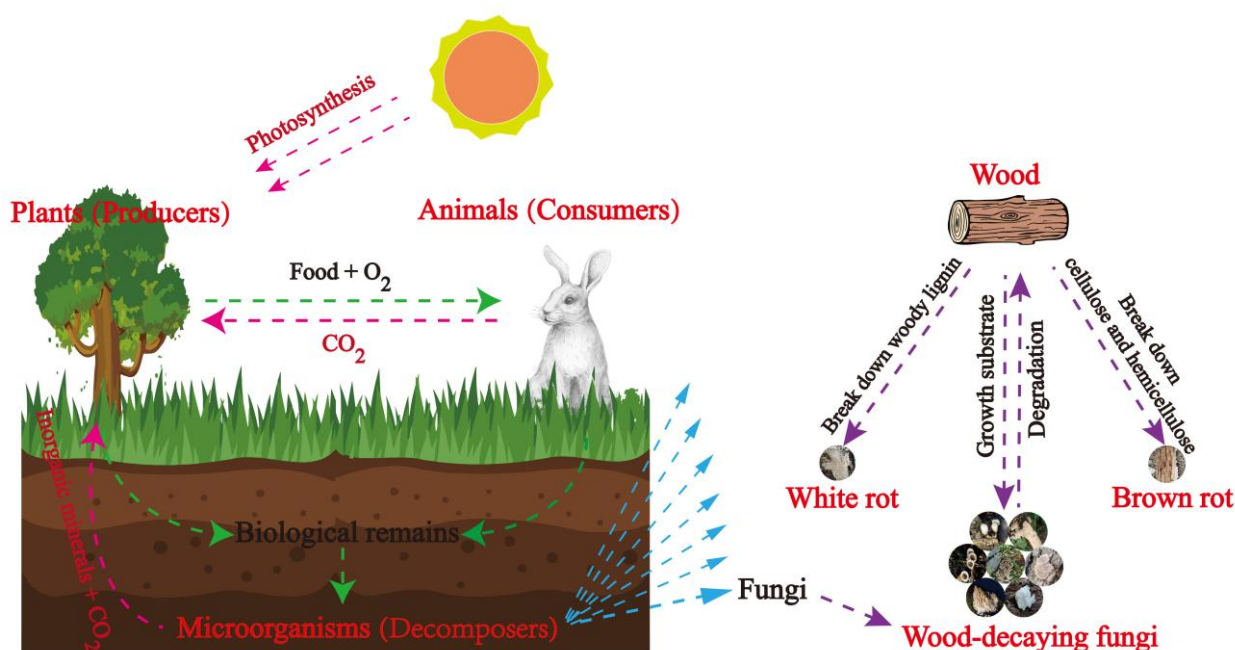


Figure 1 – The wood-inhabiting fungi contribute to the cycling of materials and the flow of energy in ecosystems.

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 (corticoid) 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
<i>Agaricales</i>	<i>Agaricineae</i>	<i>Agaricaceae</i>	54
		<i>Bolbitiaceae</i>	16
		<i>Cortinariaceae</i>	12
		<i>Crassisporiaceae</i>	2
		<i>Crepidotaceae</i>	7
		<i>Galeropsidaceae</i>	5
		<i>Hydnangiaceae</i>	4
		<i>Hymenogastraceae</i>	12
		<i>Inocybaceae</i>	7
		<i>Lycoperdaceae</i>	13
		<i>Mythicomycetaceae</i>	2
		<i>Nidulariaceae</i>	6
		<i>Psathyrellaceae</i>	21
		<i>Squamanitaceae</i>	7
		<i>Strophariaceae</i>	14
		<i>Tubariaceae</i>	7
	<i>Clavariineae</i>	<i>Clavariaceae</i>	10

Order	Suborders	families	Number of genera
	<i>Hygrophorineae</i>	<i>Cantharellulaceae</i>	2
		<i>Cuphophyllaceae</i>	5
		<i>Hygrocybaceae</i>	9
		<i>Hygrophoraceae</i>	6
		<i>Lichenomphaliaceae</i>	7
	<i>Marasmiineae</i>	<i>Campanellaceae</i>	5
		<i>Cyphellaceae</i>	24
		<i>Cystostereaceae</i>	9
		<i>Marasmiaceae</i>	5
		<i>Omphalotaceae</i>	20
		<i>Physalacriaceae</i>	32
		<i>Porotheleaceae</i>	18
		<i>Xeromphalinaceae</i>	2
	<i>Mycenineae</i>	<i>Mycenaceae</i>	9
	<i>Phyllotopsidineae</i>	<i>Aphroditeolaceae</i>	1
		<i>Phyllotopsidaceae</i>	8
		<i>Pterulaceae</i>	8
		<i>Radulomycetaceae</i>	4
		<i>Stephanosporaceae</i>	5
	<i>Pleurotineae</i>	<i>Cyphellopsidaceae</i>	15
		<i>Fistulinaceae</i>	3
		<i>Pleurotaceae</i>	5
		<i>Resupinataceae</i>	1
	<i>Pluteineae</i>	<i>Amanitaceae</i>	7
		<i>Limnoperdaceae</i>	1
		<i>Melanoleucaceae</i>	2
		<i>Pluteaceae</i>	2
		<i>Volvariellaceae</i>	1
	<i>Sarcomyxineae</i>	<i>Sarcomyxaceae</i>	2
	<i>Schizophyllineae</i>	<i>Schizophyllaceae</i>	2
	<i>Tricholomatineae</i>	<i>Biannulariaceae</i>	3
		<i>Callistosporiaceae</i>	6
		<i>Clitocybaceae</i>	7
		<i>Entolomataceae</i>	9
		<i>Fayodiaceae</i>	5
		<i>Lyophyllaceae</i>	32
		<i>Macrocystidiaceae</i>	2
		<i>Omphalinaceae</i>	2
		<i>Paralepistaceae</i>	3
		<i>PseudoClitocybaceae</i>	6
		<i>Pseudoomphalinaceae</i>	1
		<i>Tricholomataceae</i>	10
	<i>Typhulineae</i>	<i>Typhulaceae</i>	2
	<i>incertae sedis</i>	<i>Broomeiaceae</i>	1
		<i>Hemigasteraceae</i>	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, *rpb1*, *rpb2*, and *tefl-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, odontoid, hydroid, 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+*rpb1*+*rpb2*+*tefl-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 (C₂₀H₂Br₄C₁₄Na₂O₅), 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
<i>tef1-α</i>	EF1-983F	GCY CCY GGH CAY CGT GAY TTY AT	Rehner & Buckley (2005)
	EF1-2218R	ATG ACA CCR ACR GCR ACR GTY TG	
<i>rpb1</i>	RPB1-Af	GAR TGY CCD GGD CAY TTY GG	Matheny et al. (2002)
	RPB1-Cf	CCN GCD ATN TCR TTR TCC ATR TA	
<i>rpb2</i>	bRPB2-6F	TGG GGY ATG GTN TGY CCY GC	Matheny (2005)
	bRPB2-7.1R	CCC ATR GCY TGY TTM CCC ATD GC	

^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; *rpb1*, the largest subunit of RNA polymerase II; *rpb2*, the second subunit of RNA polymerase II; *tef1-α*, the translation elongation factor 1-α.

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 *tef1-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 *tef1-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 *rpb1* 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 *rpb2* 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/nucleotide/>). 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, *rpb1*, *rpb2*, and *tef1-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	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Acanthocortici</i> <i>brueggemannii</i>	JMB2122	KT2751 93	KT27519 5	—	—	—	Brazil	Baltazar et al. (2015)
<i>Akenomyces costatus</i>	CBS:513.83	MH8616 35	MH8733 50	—	—	—	Netherlands	Vu et al. (2019)
<i>Amanita brunnnescens</i>	AFTOL-ID 673	AY7890 79	AY6319 02	AY7888 47	AY7809 36	AY8810 21	USA	Matheny et al. (2006)
<i>Amanita subglobosa</i>	HKAS:58837	JN94317 7	JN94115 2	JN9941 23	JQ03112 1	KJ48200 4	China	Vizzini et al. (2024)
<i>Amylocortici</i> <i>cebennense</i>	CFMR: HHB-2808	GU1875 05	GU1875 61	—	GU1877 70	GU1876 75	USA	Vizzini et al. (2024)
<i>Anthracophyllum archeri</i>	AFTOL-ID 973	DQ4043 87	AY7457 09	DQ4357 99	DQ4043 87	DQ0285 86	USA	Matheny et al. (2006)
<i>Anthracophyllum lateritium</i>	TENN62043	FJ59689 2	—	—	—	—	USA	Hughes et al. (2009)
<i>Aphanobasidium</i> <i>pseudotsugae</i>	HHB-822	GU1875 09	GU1875 67	—	—	—	USA	Larsson (2007)
<i>Aphanobasidium</i> <i>pseudotsugae</i>	UC 2023153	KP81435 3	AY5866 96	GU1874 55	GU1877 81	GU1876 95	Sweden	Larsson (2007)
<i>Apioperdon pyriforme</i>	AFTOL-ID 480	AY8540 75	AF28787 3	AY8605 23	AY2184 95	AY8834 26	USA	Vizzini et al. (2024)
<i>Asterophora lycoperdoides</i>	CBS170.86	AF35703 7	AF22319 0	EF4210 21	DQ3674 31	DQ3674 24	Switzerland	Matheny et al. (2006)
<i>Bolbitius vitellinus</i>	AFTOL-ID 730	DQ2009 20	AY6918 07	DQ4358 02	DQ3858 78	DQ4081 48	USA	Matheny et al. (2006)
<i>Camarophyllopsis</i>	AFTOL-ID 1892	DQ4840	DQ4576	DQ5160	DQ4727	—	USA	Matheny et al. (2006)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>hymenocephala</i>		66	79	70	26			
<i>Campanella alba</i>	BDC iNaturalist #	PQ49822	PQ49822	—	—	—	USA	Unpublished
	190272171	7	7					
<i>Campanella alba</i>	BDC iNaturalist #	PQ49822	PQ49822	—	—	—	USA	Unpublished
	190272171	7	7					
<i>Campanella alba</i>	BDC iNaturalist #	PQ49814	PQ49814	—	—	—	USA	Unpublished
	192505836	1	1					
<i>Campanella buettneri</i>	SFSU DED8276	NR_198	NR_198	—	—	—	USA	Desjardin & Perry (2017)
		033	033					
<i>Campanella buettneri</i>	DED 8276 (SFSU)	MF0751	MF0751	—	—	—	USA	Desjardin & Perry (2017)
		36	38					
<i>Campanella burkei</i>	SFSU: BAP 632	MF1009	—	—	—	—	USA	Desjardin & Perry (2017)
		70						
<i>Campanella candida</i>	PDD 102184	OQ2828	—	—	—	—	New Zealand	Unpublished
		23						
<i>Campanella keralensis</i>	AF 342	MW462	—	—	—	—	India	Desjardin & Perry (2017)
		889						
<i>Campanella pustulata</i>	SMF2382	JX44416	—	—	—	—	Australia	Unpublished
		4						
<i>Campanella pustulata</i>	AQ793972	JX44416	—	—	—	—	Australia	Unpublished
		8						
<i>Campanella simulans</i>	AF 129	MW506	—	—	—	—	India	Unpublished
		836						
<i>Campanella subdendrophora</i>	ATCC 42449	AY4451	AY4451	—	—	—	Sweden	Matheny et al. (2006)
		21	15					
<i>Campanella tristis</i>	JAC17081	PP40751	PP40753	—	—	—	New Zealand	Unpublished
		6	8					

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Campanella tristis</i>	PDD_88322	PP40751 7	—	—	—	—	New Zealand	Unpublished
<i>Campanella yunnanensis</i>	CLZhao 33866 *	PV1979 11	—	—	—	—	China	Present study
<i>Campanella yunnanensis</i>	CLZhao 33868	PV1979 12	—	PV2477 34	—	—	China	Present study
<i>Catathelasma ventricosum</i>	DAOM:225247	MN0175 37	MN0174 77	KP2554 80	MN0188 51	MN0269 06	Spain	Vizzini et al. (2024)
<i>Chaetocalathus cocciformis</i>	JAC12666	OQ2827 95	OQ2827 51	—	—	—	New Zealand	Matheny et al. (2006)
<i>Chaetocalathus liliputianus</i>	MCA485	AY9166 82	AY9166 80	AY9166 83	—	—	USA	Matheny et al. (2006)
<i>Chaetocalathus liliputianus</i>	MCA485	AY9166 82	AY9166 80	AY9166 83	—	—	USA	Matheny et al. (2006)
<i>Cheimonophyllum candidissimum</i>	AFTOL-ID 1765	DQ4866 87	DQ4576 54	DQ4478 88	DQ4708 31	GU1877 60	USA	Matheny et al. (2006)
<i>Chondrostereum purpureum</i>	AFTOL-ID 441	DQ2009 29	AF51860 7	—	AY2184 77	DQ4576 32	USA	Matheny et al. (2006)
<i>Chromocyphella lamellata</i>	AH 45802	MF6238 32	MF6238 31	MF6520 60	MF6238 37	MF9481 55	Spain	Moreno et al. (2017)
<i>Chromocyphella meloana</i>	LIP GG-201018-003	ON0593 75	ON0591 79	—	ON0552 77	ON0552 76	Spain	Gruhn et al. (2023)
<i>Chromocyphella muscicola</i>	ARAN-Fungi 3324	MF6238 34	MF6238 34	MF6520 62	—	MF9481 57	Spain	Moreno et al. (2017)
<i>Clavaria zollingeri</i>	AFTOL-ID 563	AY8540 71	AY6398 82	AH0145 78	AY7809 40	AY8810 24	USA	Matheny et al. (2006)
<i>Clavulinopsis laeticolor</i>	AFTOL-ID 984	DQ2022	AY7456	DQ4478	DQ3858	DQ0291	USA	Matheny et al. (2006)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Collybiopsis albobasidiosa</i>	CLZhao 30216 *	67 PV1979	93 PV19793	90 —	80 PV2477	98 —	China	Present study
		13	3		42			
<i>Collybiopsis albobasidiosa</i>	CLZhao 30756	PV1979	PV19793	—	PV2477	PV2314	China	Present study
		14	4		43	16		
<i>Collybiopsis biformis</i>	TENN 65189	KJ41624	KJ18956	—	—	—	USA	Petersen & Hughes (2014)
		9	9					
<i>Collybiopsis brunneigracilis</i>	AWW01-SFSU	AY6394	—	—	—	—	Indonesia	Wilson et al. (2004)
		12						
<i>Collybiopsis californica</i>	TENN-F-052617	MN4133	—	—	—	—	Canada	Phonrob et al. (2024)
		38						
<i>Collybiopsis complicata</i>	TENN-F-065811	OR5005	OR5005	—	—	—	USA	Petersen & Hughes (2024a)
		17	17					
<i>Collybiopsis confluens</i>	TENN-F-067864	KP71029	KJ18957	—	—	—	Germany	Petersen & Hughes (2016)
		6	3					
<i>Collybiopsis cremea</i>	CLZhao 29915 *	PV1979	PV19793	—	PV2477	—	China	Present study
		15	5		44			
<i>Collybiopsis cremea</i>	CLZhao 29941	PV1979	PV19793	—	PV2477	—	China	Present study
		16	6		45			
<i>Collybiopsis cremea</i>	CLZhao 30022	—	PV19793	—	PV2477	—	China	Present study
			7		46			
<i>Collybiopsis dichroa</i>	TENN-F-065569	MW396	MW3968	—	—	—	USA	Petersen & Hughes (2021)
		867	67					
<i>Collybiopsis disjuncta</i>	TENN-F-069172	KJ41625	PP43033	—	—	—	USA	Petersen & Hughes (2014)
		2	0					
<i>Collybiopsis enificola</i>	TENN-F-069123	NR_137	NG_059	—	—	—	Canada	Petersen et al. (2014)
		613	502					

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Collybiopsis filamentipes</i>	TENN-F-065861	MN8978 32	MN8978 32	—	—	—	USA	Petersen & Hughes (2021)
<i>Collybiopsis furtiva</i>	SFSU DED4425	DQ4500 31	AF04265 0	—	—	—	USA	Mata et al. (2007)
<i>Collybiopsis gibbosa</i>	URM 90012	KY0612 02	KY0612 02	—	—	—	Brazil	Phonrob et al. (2024)
<i>Collybiopsis hasanskyensis</i>	TENN-F-060730	MN8978 29	—	—	—	—	Russia	Petersen & Hughes (2021)
<i>Collybiopsis indocta</i>	TENN-F-054944	MW396 870	MW3968 70	—	—	—	Argentina	Petersen & Hughes (2021)
<i>Collybiopsis juniperin</i>	TENN-F-058988	KY0266 61	KY0266 61	—	—	—	Argentina	Petersen & Hughes (2016)
<i>Collybiopsis luxurians</i>	TENN-F-050619	KJ41624 0	PP43033 1	—	—	—	Switzerland	Petersen & Hughes (2014)
<i>Collybiopsis melanopus</i>	SFSU: A.W. Wilson 54	NR_137 539	NG_060 624	—	—	—	Indonesia	Wilson et al. (2004)
<i>Collybiopsis menehune</i>	SFSU: DED5866	AY2634 26	—	—	—	—	Indonesia	Wilson et al. (2004)
<i>Collybiopsis mesoamericana</i>	TENN 058613	NR_119 583	KY0196 32	—	—	—	Costa Rica	Schoch et al. (2014)
<i>Collybiopsis minor</i>	TENN-F-059993	MN4133 34	MW3968 80	—	—	—	USA	Petersen & Hughes (2021)
<i>Collybiopsis minor</i>	TENN-F-059993	MN4133 34	MW3968 80	—	—	—	USA	Mata et al. (2007)
<i>Collybiopsis neotropica</i>	TENN-F-058113	AF50576 9	—	—	—	—	Costa Rica	Phonrob et al. (2024)
<i>Collybiopsis nonnulla</i>	TENN-F-069193	MW396	MW3968	—	—	—	USA	Petersen & Hughes

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Collybiopsis parvula</i>	TENN-F-058113	873 NR_119 584	73 —	—	—	—	Costa Rica	(2021) Schoch et al. (2014)
<i>Collybiopsis peronata</i>	TENN-F-069322	KY0267 38	KY0267 38	—	—	—	USA	Petersen & Hughes (2016)
<i>Collybiopsis polygramma</i>	MHHNU 30912	MK2143 92	—	—	—	—	China	Unpublished
<i>Collybiopsis quercophila</i>	TENN-F-069321	KY0267 37	KY0267 37	—	—	—	USA	Petersen & Hughes (2016)
<i>Collybiopsis ramealis</i>	TENN-F-069251	MW405 779	MW3968 84	—	—	—	Slovakia	Petersen & Hughes (2021)
<i>Collybiopsis readiae</i>	TENN-F-053687	DQ4500 34	—	—	—	—	New Zealand	Mata et al. (2007)
<i>Collybiopsis stenophylla</i>	TENN-F-065943	MN4133 31	MW3968 86	—	—	—	USA	Zhang et al. (2023c)
<i>Collybiopsis stenophyllus</i>	TENN 59444	DQ4500 32	—	—	—	—	USA	Mata et al. (2007)
<i>Collybiopsis subcyathiformis</i>	URM90023	KY4049 82	KY4049 82	—	—	—	Brazil	Zhang et al. (2023c)
<i>Collybiopsis subnuda</i>	WRW08-462	KY0267 65	KY0267 65	—	—	—	USA	Petersen & Hughes (2016)
<i>Collybiopsis trogioides</i>	AWW51-SFSU	NR_152 884	NG_228 715	—	—	—	Indonesia	Petersen & Hughes (2024a)
<i>Collybiopsis vaillantii</i>	TENN-F-065115	KY0266 76	KY0266 76	—	—	—	USA	Petersen & Hughes (2016)
<i>Collybiopsis villosipes</i>	TENN-F-056252	DQ4500 58	—	—	—	—	USA	Mata et al. (2007)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Collybiopsis villosipes</i>	TENN-F-060951	KJ41625 5	FJ75026 4	—	—	—	New Zealand	Petersen & Hughes (2014)
<i>Collybiopsis yunnanensis</i>	CLZhao 22508	PV1979 17	PV19793 8	—	—	—	China	Present study
<i>Collybiopsis yunnanensis</i>	CLZhao 22546 *	PV1979 18	—	—	—	—	China	Present study
<i>Collybiopsis yunnanensis</i>	CLZhao 22558	PV1979 19	PV19793 9	—	PV2477 47	—	China	Present study
<i>Collybiopsis yunnanensis</i>	CLZhao 22565	PV1979 20	—	—	—	—	China	Present study
<i>Coniolepiota spongodes</i>	PNG012	HM4887 56	HM4887 74	—	HM4887 96	HM4888 83	USA	Vellinga et al. (2011)
<i>Cortinarius aurilicis</i>	TSJ1998-101	DQ0837 72	AY6841 52	DQ0838 26	DQ0838 80	—	Denmark	Frøslev et al. (2005)
<i>Cortinarius iodes</i>	IB19850061	AF38913 3	AY7020 13	AY8579 84	AY5362 85	—	USA	Matheny et al. (2006)
<i>Cortinarius sodagnitus</i>	TF2001-094	DQ0838 12	AY6841 51	DQ0838 67	DQ0839 20	—	Denmark	Matheny et al. (2006)
<i>Cortinarius violaceus</i>	AFTOL-ID 814	DQ4866 95	DQ4576 62	DQ4478 94	DQ4708 35	—	USA	Matheny et al. (2006)
<i>Crepidotus applanatus</i>	AFTOL-ID 817	DQ2022 73	AY3804 06	AY3333 03	AY3333 11	—	USA	Matheny et al. (2006)
<i>Crinipellis birhizomorpha</i>	BRNM751593	KF38083 1	KF38083 5	—	—	—	Korea	Antonín et al. (2014)
<i>Crinipellis setipes</i>	Bandala4031	JF93064 1	JF93064 2	—	—	—	Mexico	Antonín et al. (2014)
<i>Crinipellis zonata</i>	OKM 25450	AY9166	AY9166	AY9166		AY9166	USA	Aime et al. (2005)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Crustomyces albidus</i>	He 6164	92 ON1171	90 ON1171	93 —	—	94	China	Li et al. (2022)
<i>Crustomyces pini-canadensis</i>	HHB-11308	91 OP93522	75 OP99571	—	—	OP99905	USA	Paez et al. 2024
<i>Dendrothele fissurata</i>	CLZhao 35015 *	2 PV1979	5 —	—	—	0	China	Present study
<i>Dendrothele griseocana</i>	CBS:340.66	21 MH8588	—	—	—	—	Netherlands	Vu et al. (2019)
<i>Dendrothele yunnanensis</i>	CLZhao 17814	16 OR0944	—	—	—	—	China	Dong et al. (2024)
<i>Digitatispora marina</i>	3027C	84 KM2723	10 KM2723	—	—	—	Norway	Silva-Filho et al. (2023)
<i>Flagelloscypha japonica</i>	NBRC 101830	71 LC14673	62 AB4559	—	—	—	Japan	Silva-Filho et al. (2023)
<i>Flagelloscypha minutissima</i>	CBS 823.88	4 AY5710	64 AY5710	—	—	—	USA	Silva-Filho et al. (2023)
<i>Flammulina velutipes</i>	AFTOL-ID 558	40 AY8540	06 AY6398	AY8589	AY7860	AY8834	USA	Matheny et al. (2006)
<i>Gracilihypha abeliae</i>	CLZhao 21445	73 PP81970	83 PP82625	66 —	55 —	23	China	Yang et al. (2025)
<i>Gracilihypha abeliae</i>	CLZhao 21485	5 PP81970	7 PP82625	—	—	—	China	Yang et al. (2025)
<i>Gracilihypha albohymenia</i>	CLZhao 29603	6 PV1979	8 —	PV2477	PV2477	—	China	Present study
<i>Gracilihypha albohymenia</i>	CLZhao 31757	24 PV1979	—	38 —	50 PV3689	—	China	Present study
		25			45			

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Gracilhypha albohymenia</i>	CLZhao 32417	PV1979 26	—	—	PV3689 46	PV2314 20	China	Present study
<i>Gracilhypha albohymenia</i>	CLZhao 33069 *	PV1979 27	—	PV2477 39	PV3689 47	—	China	Present study
<i>Gracilhypha albohymenia</i>	CLZhao 33502	PV1979 28	—	PV2477 40	PV3689 48	PV2314 21	China	Present study
<i>Gracilhypha yunnanensis</i>	CLZhao 32826 *	PV1979 29	PV19794 3	—	PV3689 49	—	China	Present study
<i>Gymnopilus sapineus</i>	PBM 1541 (WTU)	AF50156 0	AY3803 62	AY3517 89	AY3373 58	—	Australia	Matheny et al. (2006)
<i>Gymnopus bicolor</i>	AWW116	AY2634 23	AY6394 11	—	—	—	USA	Wilson et al. (2004)
<i>Gymnopus dryophilus</i>	AFTOL-ID 559	DQ2417 81	AY6406 19	DQ4479 03	DQ4727 17	DQ4081 52	USA	Matheny et al. (2006)
<i>Gymnopus globulosus</i>	HMJAU60307	OM0302 69	OM0334 06	—	—	—	China	Hu et al. (2022)
<i>Gymnopus tiliicola</i>	HMJAU60305	OM0302 76	OM0333 93	—	—	—	China	Hu et al. (2022)
<i>Hebeloma velutipes</i>	AFTOL-ID 980	AY8183 51	AY7457 03	DQ4479 04	DQ4727 18	GU1877 07	USA	Matheny et al. (2006)
<i>Hohenbuehelia atrocoerulea</i>	AMB:18080	KU3553 04	KU3553 89	—	KU3554 18	KU3554 39	Italy	Vizzini et al. (2024)
<i>Hohenbuehelia faerberioides</i>	Mertens	MG5536 38	MG5536 45	—	MW240 980	MW240 984	Spain	Vizzini et al. (2024)
<i>Hohenbuehelia tremula</i>	DAOM:180808	KU3553 57	KU3554 05	OR8283 61	KU3554 34	KU3554 65	Italy	Vizzini et al. (2024)
<i>Hydnangium carneum</i>	Trappe31123	KU6857	KU6858	—	KU6860	KU6861	USA	Vizzini et al. (2024)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Laccaria ochropurpurea</i>	AFTOL-ID 477	41 AF00659	92 AY7002	—	38 DQ4727	44 —	USA	Matheny et al. (2006)
<i>Lachnella alboviolascens</i>	PB332	8 AY5710	00 AY5710	—	31 —	—	USA	Silva-Filho et al. (2023)
<i>Lachnella alboviolascens</i>	Wu724	48 OR9900	12 —	—	—	—	China	Silva-Filho et al. (2023)
<i>Lacrymaria velutina</i>	AFTOL-ID 478	18 DQ4906	— AY7001	—	— DQ4727	—	USA	Matheny et al. (2006)
<i>Lentinula edodes</i>	OE-9	39 AY6360	98 AF26155	—	33 —	—	USA	Moncalvo et al. (2002)
<i>Lentinula guzmanii</i>	TENN 55247	53 NR_186	7 —	—	—	—	USA	Unpublished
<i>Limnoperdon incarnatum</i>	IFO:30398	965 DQ0973	— AF42695	—	—	—	USA	Matheny et al. (2006)
<i>Limnoperdon</i> sp.	CBS:160.95	63 OR8634	8 OR8635	—	— OR8282	— OR8283	USA	Vizzini et al. (2024)
<i>Lyophyllum decastes</i>	JM87/16	57 AF35705	24 AF04258	— DQ8254	72 DQ3674	27 DQ3674	Spain	Matheny et al. (2006)
<i>Macrocyttidia cucumis</i>	AFTOL-ID 1343	9 DQ4906	3 DQ0947	18 —	33 —	26 —	Switzerland	Matheny et al. (2006)
<i>Macrocyttidia cucumis</i>	JX.1294733#45	40 OR8634	87 OR8635	—	— OR8282	— OR8283	USA	Matheny et al. (2006)
<i>Macrolepiota dolichaula</i>	AFTOL-ID 481	60 DQ2211	27 DQ4115	— DQ4479	75 DQ3858	30 DQ4357	Spain	Vizzini et al. (2024)
<i>Macrotyphula phacorrhiza</i>	DSH96-059	11 AF13471	37 AF39307	20 —	86 AY2185	85 —	USA	Vizzini et al. (2024)
		0 —	9 —	—	25 —	—	Canada	Matheny et al. (2006)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Macrotyphula juncea</i>	IO.14.177	MT2323 53	MT2323 06	—	MT2423 37	MT2423 55	Spain	Vizzini et al. (2024)
<i>Macrotyphula phacorrhiza</i>	S:IO.14.200	MT2323 63	MT2323 14	—	—	MT2423 66	Spain	Vizzini et al. (2024)
<i>Maireina filipendula</i>	TL14226	KX7727 45	KX7727 45	—	—	—	Norway	Silva-Filho et al. (2023)
<i>Maireina filipendula</i>	TL2015-724890	KX7727 46	KX7727 46	—	—	—	Norway	Silva-Filho et al. (2023)
<i>Maireina monacha</i>	AM2106285	OP09954 8	OR1975 81	—	—	—	France	Mombert (2022)
<i>Maireina subsphaerospora</i>	AM2012151	OR2347 54	OR1975 82	—	—	—	Spain	Mombert (2022)
<i>Maireina subsphaerospora</i>	AM2004282	OP09954 9	OR2347 51	—	—	—	France	Mombert (2022)
<i>Marasmius acerosus</i>	TYS458	OR6366 34	OR6569 52	—	—	—	Canada	Oliveira et al. (2024)
<i>Marasmius albopurpureus</i>	N.K.Zeng 2253	MT8229 24	MT8291 07	—	—	—	China	Unpublished
<i>Marasmius atrorubens</i>	JO528	KP63520 7	KP63516 0	—	OR8964 47	PP02615 0	Brazil	Oliveira et al. (2024)
<i>Marasmius bellus</i>	JO299	KP63520 8	KP63516 1	—	OR8964 83	PP02608 6	Brazil	Oliveira et al. (2024)
<i>Marasmius oreades</i>	ZRL2015086	LT71604 8	KY4188 64	KY4189 72	KY4190 10	KY4190 66	China	Oliveira et al. (2024)
<i>Marasmius oreades</i>	AFTOL-ID 1559	DQ4906 41	DQ1561 26	DQ4479 21	—	—	USA	Matheny et al. (2006)
<i>Marasmius pulcherripes</i>	BRNM 714692	FJ91761	FJ91760	—	—	—	Korea	Antonín et al. (2012)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Marasmius wumengshanensis</i>	CLZhao 32014 *	5 PV1979 30	0 PV19794 4	—	—	—	China	Present study
<i>Merismodes anomala</i>	PB318	AY5710 35	AY5709 98	—	—	—	USA	Silva-Filho et al. (2023)
<i>Merismodes anomala</i>	PB323	AY5710 36	AY5709 99	—	—	—	USA	Silva-Filho et al. (2023)
<i>Merismodes fasciculata</i>	HHB-11894	AY5710 51	AY5710 15	—	—	—	USA	Silva-Filho et al. (2023)
<i>Merismodes fasciculata</i>	PB342	AY5710 52	AY5710 16	—	—	—	USA	Silva-Filho et al. (2023)
<i>Moniliophthora aurantiaca</i>	UTC 253824	JN69248 2	JN69248 3	—	—	—	USA	Antonín et al. (2014)
<i>Moniliophthora perniciosa</i>	DIS71	AY3171 36	AY9167 38	AY9167 40	—	AY9167 41	Brazil	Matheny et al. (2006)
<i>Moniliophthora roreri</i>	C21	AY9167 46	AY9167 44	—	—	—	USA	Antonín et al. (2014)
<i>Mycena amabilissima</i>	AFTOL-ID 1686	DQ4906 44	DQ4576 91	DQ4479 26	DQ4741 21	GU1877 27	USA	Matheny et al. (2006)
<i>Mycena aurantiidisca</i>	AFTOL-ID 1685	DQ4906 46	DQ4708 11	DQ4479 27	DQ4741 22	GU1877 28	USA	Matheny et al. (2006)
<i>Mycetinis alliaceus</i>	AFTOL-ID 556	AY8540 76	AY6357 76	—	—	—	USA	Matheny et al. (2006)
<i>Mycetinis arbuscularis</i>	HMJAU 60427	PP15153 3	PP15156 6	—	—	—	China	Li et al. (2024)
<i>Mycetinis rufodiscus</i>	HMJAU 60430	PP15152 2	PP63954 3	—	—	—	China	Li et al. (2024)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Mythicomycetes corneipes</i>	AFTOL-ID 972	DQ4043 93	AY7457 07	DQ4479 29	DQ4081 10	DQ0291 97	USA	Matheny et al. (2006)
<i>Naucoria vinicolor</i>	AFTOL-ID 499	DQ5364 17	DQ5364 15	DQ5364 19	DQ5364 18		USA	Matheny et al. (2006)
<i>Nia furcatipilosa</i>	AH20191108-1	LC76976 2	LC76981 8	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia furcatipilosa</i>	AH20190926-1	LC76976 0	LC76981 6	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia singaporensis</i>	AN-1023	LC76977 9	—	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia singaporensis</i>	AN-1026	LC76978 0	LC76983 5	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia sphaerocystis</i>	AN-1851	LC76979 9	LC76985 4	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia sphaerocystis</i>	AH20191004-1	LC76980 2	LC76985 7	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia vibrissa</i>	AN-1825	LC76978 1	LC76983 6	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia vibrissa</i>	AH20190527-3	LC76978 3	LC76983 8	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia vibrissa</i>	AN-1825	LC76978 1	LC76983 6	—	—	—	Japan	Nakagiri et al. (2024)
<i>Nia vibrissa</i>	AH20190527-3	LC76978 3	LC76983 8	—	—	—	Japan	Nakagiri et al. (2024)
<i>Omphalotus olearius</i>	AFTOL-ID 1718	DQ4946 81	DQ4708 16	—	—	—	USA	Matheny et al. (2006)
<i>Omphalotus olivascens</i>	VT455	AF52506	AF26132	—	—	—	Austria	Matheny et al. (2006)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Ossicaulis lignatilis</i>	D604	3 DQ8254	5 AF26139					
		26	6	20	10			
<i>Paragymnopus foliophilus</i>	TENN-F-68183	KY0267	KY0267	—	—	—	USA	Petersen & Hughes (2016)
		05	05					
<i>Paragymnopus perforans</i>	TENN-F-50319	KY0266	KY0266	—	—	—	Sweden	Petersen & Hughes (2016)
		25	25					
<i>Paragymnopus pinophilus</i>	TENN-F-69207	KY0267	KY0267	—	—	—	USA	Petersen & Hughes (2016)
		25	25					
<i>Parvodontia luteocystidia</i>	FP-102806	OP93522	OP99572	—	—	OP99904	USA	Paez et al. (2024)
		4	4			1		
<i>Peyronelina glomerulata</i>	NBRC 32867	—	AB4559	—	—	—	Japan	Silva-Filho et al. (2023)
			63					
<i>Peyronelina glomerulata</i>	NBRC 104522	—	AB4559	—	—	—	Japan	Silva-Filho et al. (2023)
			61					
<i>Pleuroflammula flammea</i>	AFTOL-ID 1381	DQ4946	AF36796	DQ4479	DQ4741	—	USA	Matheny et al. (2006)
		85	2	35	24			
<i>Pleurotus dryinus</i>	AMB:18868	OR8634	OR8635	OR8283	OR8282	OR8283	Spain	Vizzini et al. (2024)
		71	38	63	86	38		
<i>Pleurotus fuscusquamulosus</i>	A. Baglivo 13-07-2014	OR8634	—	—	OR8282	OR8283	Spain	Vizzini et al. (2024)
		72			87	39		
<i>Pleurotus ostreatus</i>	AFTOL-ID 564	AY8540	AY6450	AY8621	AY7860	—	USA	Matheny et al. (2006)
		77	52	86	62			
<i>Pluteus romellii</i>	AFTOL-ID 625	AY8540	AY6342	AY8621	AY7860	AY8834	USA	Matheny et al. (2006)
		65	79	87	63	33		
<i>Pluteus variabilicolor</i>	AMB:18872	OR8634	OR8635	OR8283	OR8282	OR8283	Spain	Matheny et al. (2006)
		75	41	65	90	42		

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Pluteus variabilicolor</i>	AMB:18873	OR8634 76	OR8635 42	OR8283 66	OR8282 91	OR8283 43	Spain	Matheny et al. (2006)
<i>Porothelium fimbriatum</i>	AFTOL-ID 1725	DQ4906 26	DQ4576 73	DQ4479 07	DQ4727 21	—	USA	Vizzini et al. (2024)
<i>Porothelium omphaliiforme</i>	AMB 18842	OM4227 73	OM4236 50	—	—	—	Spain	Consiglio et al. (2021)
<i>Psathyrella candolleana</i>	AFTOL-ID 1507	DQ4946 89	DQ1108 74	—	—	—	USA	Matheny et al. (2006)
<i>Pseudomarasmius glabrocystidiatus</i>	BRNM 718676	NR_152 899	NG_060 647	—	—	—	Korea	Antonín et al. (2014)
<i>Pseudomarasmius glabrocystidiatus</i>	BRNM 718676	NR_152 899	NG_060 647	—	—	—	Korea	Antonín et al. (2014)
<i>Pseudomarasmius nidus-avis</i>	Bandala4052	MH5605 79	—	—	—	—	Mexico	César et al. (2018)
<i>Pulverulina ulmicola</i>	TENN 029208	NR_119 887	HQ1796 68	—	—	—	USA	Consiglio et al. (2021)
<i>Pulverulina ulmicola</i>	TENN 065567	MT2374 76	MT2374 46	—	—	—	USA	Consiglio et al. (2021)
<i>Radulomyces confluens</i>	Cui 5977	KU5356 61	KU5356 69	—	—	—	China	Zhao et al. (2016)
<i>Radulomyces confluens</i>	He 2224	KU5356 62	KU5356 70	—	—	—	China	Zhao et al. (2016)
<i>Radulotubus resupinatus</i>	Cui 8383	KU5356 60	KU5356 68	—	—	—	China	Zhao et al. (2016)
<i>Radulotubus resupinatus</i>	Cui 8462	KU5356 57	KU5356 65	—	—	—	China	Zhao et al. (2016)
<i>Rectipilus confertus</i>	MO470781	PP83163	PP83789	—	—	—	USA	Unpublished

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Rectipilus natalensis</i>	PB312/RA	6 AY5710	9 AY5710	—	—	—	USA	Bodensteiner et al. (2004)
<i>Rectipilus</i> sp.	CLZhao 25824 *	58 PV1979 31	21 PV19794 5	— PV2477 41	— PV2477 51	— PV2314 22	China	Present study
<i>Resupinatus applicatus</i>	AMB:18098	MH1378 21	MH4305 96	—	—	MH4495 88	Spain	Vizzini et al. (2024)
<i>Resupinatus europaeus</i>	AMB:18075	KU3553 68	KU3554 09	—	—	KU3554 68	Italy	Vizzini et al. (2024)
<i>Resupinatus griseopallidus</i>	AMB:18277	MH1378 23	MH1658 81	—	—	—	Spain	Vizzini et al. (2024)
<i>Resupinatus kavinae</i>	AMB:19612	OR8634 77	OR8635 43	—	OR8282 93	OR8283 44	Spain	Vizzini et al. (2024)
<i>Resupinatus niger</i>	AMB:18095	KU3553 71	KU3554 13	—	—	KU3554 70	Italy	Vizzini et al. (2024)
<i>Resupinatus rouxii</i>	Z+ZT:971	MH1378 28	MH1907 87	—	—	MH4495 90	Spain	Vizzini et al. (2024)
<i>Resupinatus striatulus</i>	JA:Cussta8634	MH1378 29	MH4305 97	—	—	MH4495 91	Spain	Vizzini et al. (2024)
<i>Resupinatus tenuis</i>	CLZhao 34892 *	PV1979 32	PV19794 6	—	PV2477 52	PV2314 23	China	Present study
<i>Resupinatus vetlinianus</i>	TENN:F69285	KP02624 3	KP98730 9	—	—	—	USA	Vizzini et al. (2024)
<i>Resupinatus yunnanensis</i>	CLZhao 8651	OP90183 9	OP90419 7	—	—	—	China	Yang et al. (2023)
<i>Rhodocollybia maculata</i>	BRNM:699408	GU9473 70	—	—	—	—	Czech Republic	Unpublished

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Rhodocollybia maculata</i>	AFTOL-ID 540	DQ4043 83	AY6398 80	—	—	—	USA	Matheny et al. (2006)
<i>Rhodocybe mundula</i>	AFTOL-ID 521	DQ4946 94	AY7001 82	DQ4479 37	DQ4741 28	—	USA	Matheny et al. (2006)
<i>Rhodophana stangliana</i>	KUN-HKAS:115926	MZ8558 76	MZ8535 62	MZ8528 13	MZ8528 25	MZ8528 01	China	Vizzini et al. (2024)
<i>Sarcomyxa baishanzuensis</i>	HKAS126474	OQ2749 90	OQ2860 59	—	OQ2911 00	—	China	Cai et al. (2023)
<i>Sarcomyxa edulis</i>	HKAS118864	OQ2749 94	OQ2860 65	—	OQ2911 06	OQ2830 17	China	Cai et al. (2023)
<i>Sarcomyxa ochracea</i>	HKAS126476	OQ2749 96	OQ2860 62	—	OQ2911 05	OQ2830 20	China	Cai et al. (2023)
<i>Sarcomyxa serotina</i>	AFTOL-ID 536	DQ4946 95	AY6918 87	DQ4479 38	DQ8598 92	GU1877 54	USA	Matheny et al. (2006)
<i>Schizophyllum commune</i>	DSH96-026	AF24939 0	AF33475 1		AY2185 15	—	USA	Matheny et al. (2006)
<i>Schizophyllum radiatum</i>	AFTOL-ID 516	AY5710 60	AY5710 23	DQ4479 39	DQ4840 52	—	USA	Matheny et al. (2006)
<i>Sicyoideibasidia bambusicola</i>	CLZhao 31774 *	PV1979 22	PV19794 0	PV2477 35	—	PV2314 17	China	Present study
<i>Sicyoideibasidia bambusicola</i>	CLZhao 35394	PV1979 23	PV19794 1	PV2477 36	PV2477 48	PV2314 18	China	Present study
<i>Sicyoideibasidia punctata</i>	CLZhao 33271	PQ6092 90		PV2477 37	—		China	Present study
<i>Sicyoideibasidia punctata</i>	CLZhao 35563 *	PQ6092 91	PV19794 2		PV2477 49	PV2314 19	China	Present study
<i>Simocybe serrulata</i>	AFTOL-ID 970	DQ4946	AY7457	DQ4479	DQ4840	GU1877	USA	Matheny et al. (2006)

Species Name	Sample No.	GenBank Accession No.					Country	References
		ITS	nrLSU	<i>rpb1</i>	<i>rpb2</i>	<i>tef1-a</i>		
<i>Stagnicola perplexa</i>	ALV16926	96 MK3516	06 MK3537	40 —	53 MK3590	55 —	Spain	Vizzini et al. (2019a)
<i>Tricholoma aestuans</i>	AFTOL-ID 497	06 DQ4946	90 AY7001	—	89 DQ4840	—	USA	Matheny et al. (2006)
<i>Tricholoma myomyces</i>	KMS589	99 DQ8254	97 U76459	—	55 DQ3674	—	USA	Matheny et al. (2006)
<i>Tricholomella constricta</i>	HC84/75	28 DQ8254	—	13 DQ8254	36 DQ8254	—	USA	Matheny et al. (2006)
<i>Tubaria confragosa</i>	AFTOL-ID 498	29 DQ2671	8 AY7001	22 DQ4479	12 DQ4081	—	USA	Matheny et al. (2006)
<i>Typhula gyrans</i>	S:IO.14.103	26 MT2323	90 KY2240	44 MT2423	13 MT2423	—	Spain	Vizzini et al. (2024)
<i>Typhula incarnata</i>	IO.14.92	60 MT2323	97 MT2323	23 MT2423	44 MT2423	63 MT2423	Spain	Vizzini et al. (2024)
<i>Typhula sclerotioides</i>	S:IO.14.22	62 MT2323	13 MT2323	25 MT2423	46 MT2423	65 MT2423	Spain	Vizzini et al. (2024)
<i>Woldmaria filicina</i>	MO465010	65 PP83163	17 PP83789	27 —	49 —	69 —	USA	Unpublished
<i>Xerophorus dominicanus</i>	127428 (JBSD)	0 MN0175	8 MN0174	—	—	—	Spain	Vizzini et al. (2020)
<i>Xerophorus donadinii</i>	18222 (AMB)	50 MN0175	89 MN0174	—	55 —	13 MN0269	Spain	Vizzini et al. (2020)
<i>Xerophorus olivascens</i>	18226 (AMB)	51 MN0175	90 MN0174	—	—	14 MN0269	Spain	Vizzini et al. (2020)
		58	96		56	16		

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.

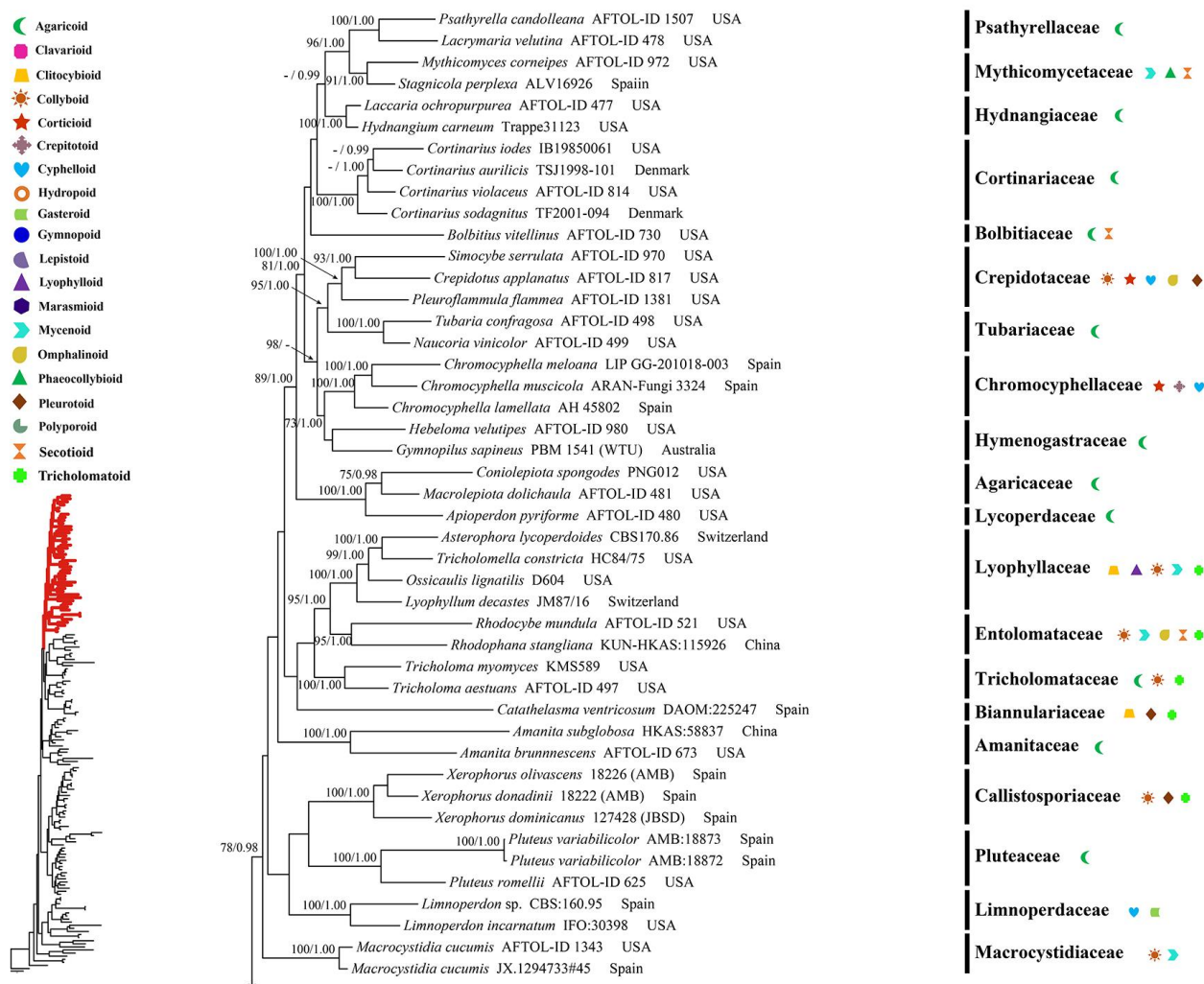


Figure 2 – Maximum likelihood tree illustrating the phylogeny of the wood-decaying fungi within the order *Agaricales* based on the combined ITS+nrLSU+*rpb1*+*rpb2*+*tef1-α* sequence data. Branches are labeled with Maximum Likelihood bootstrap values $\geq 70\%$, and Bayesian posterior probabilities ≥ 0.95 , respectively.

RESULTS

Molecular phylogeny

The phylogeny of *Agaricales* based on combined ITS+nrLSU+*rpb1*+*rpb2*+*tef1-α* sequence data (Fig. 2)

The combined ITS+nrLSU+*rpb1*+*rpb2*+*tef1-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+*rpb1*+*rpb2*+*tef1-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+*rpb1*+*rpb2*+*tef1-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.

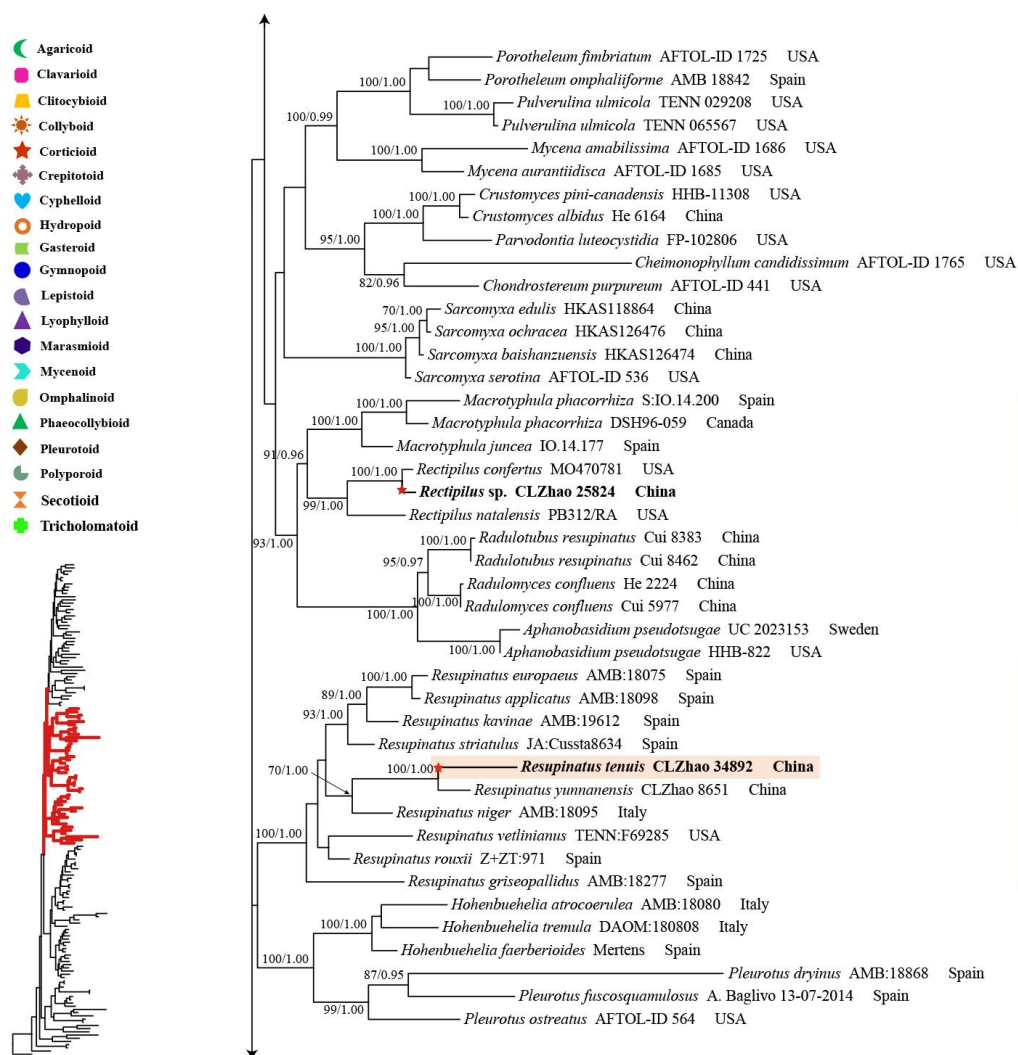


Figure 2 – Continued.

The phylogram, based on the combined ITS+nrLSU+*rpb1*+*rpb2*+*tef1-α* sequences analysis (Fig. 2), showed that the new genus *Sicyoideibasidia*, and eleven new species *Campanella yunnanensis*, *Collybiopsis albobasidiosa*, *Co. crema*, *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.

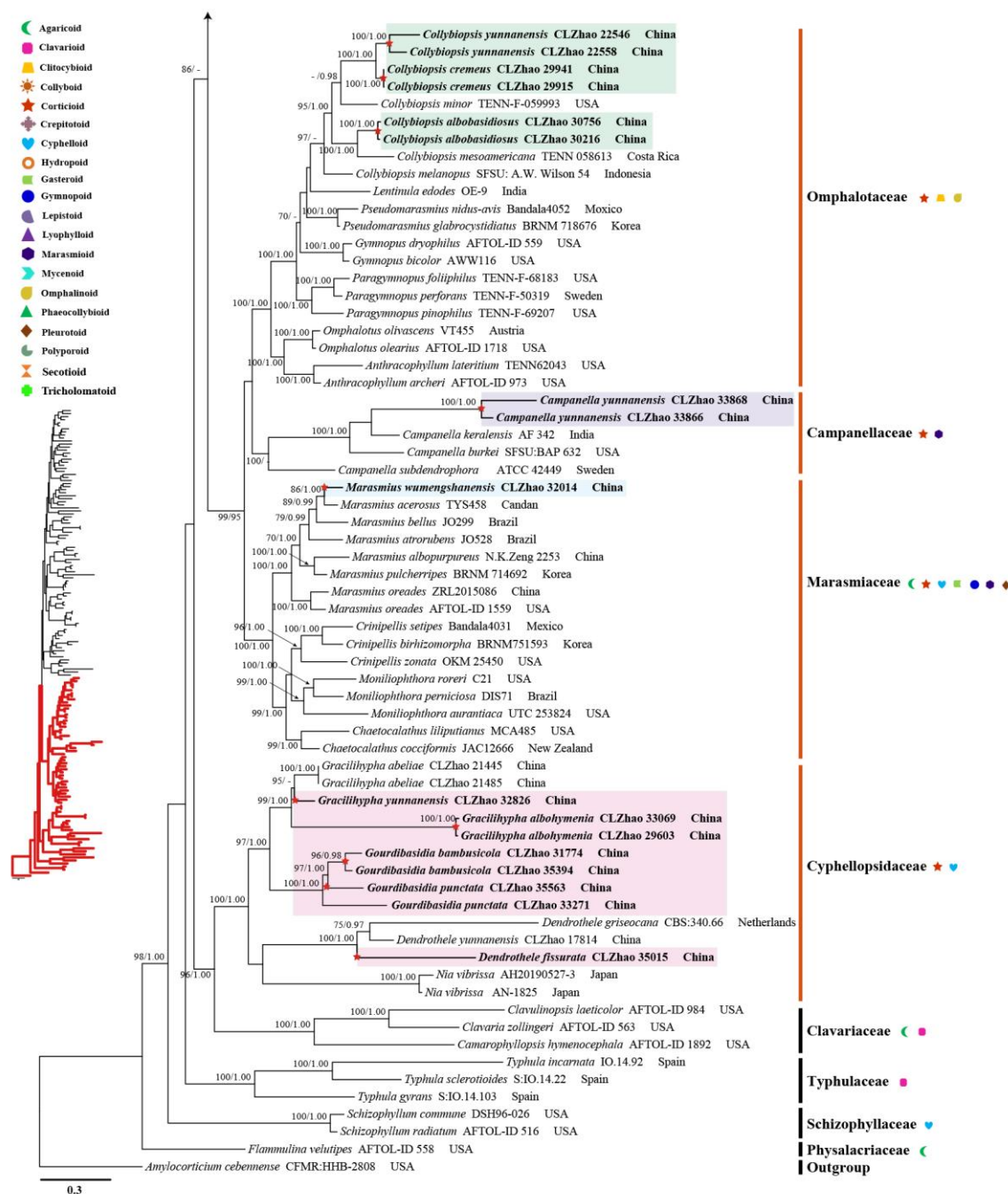


Figure 2 – Continued.

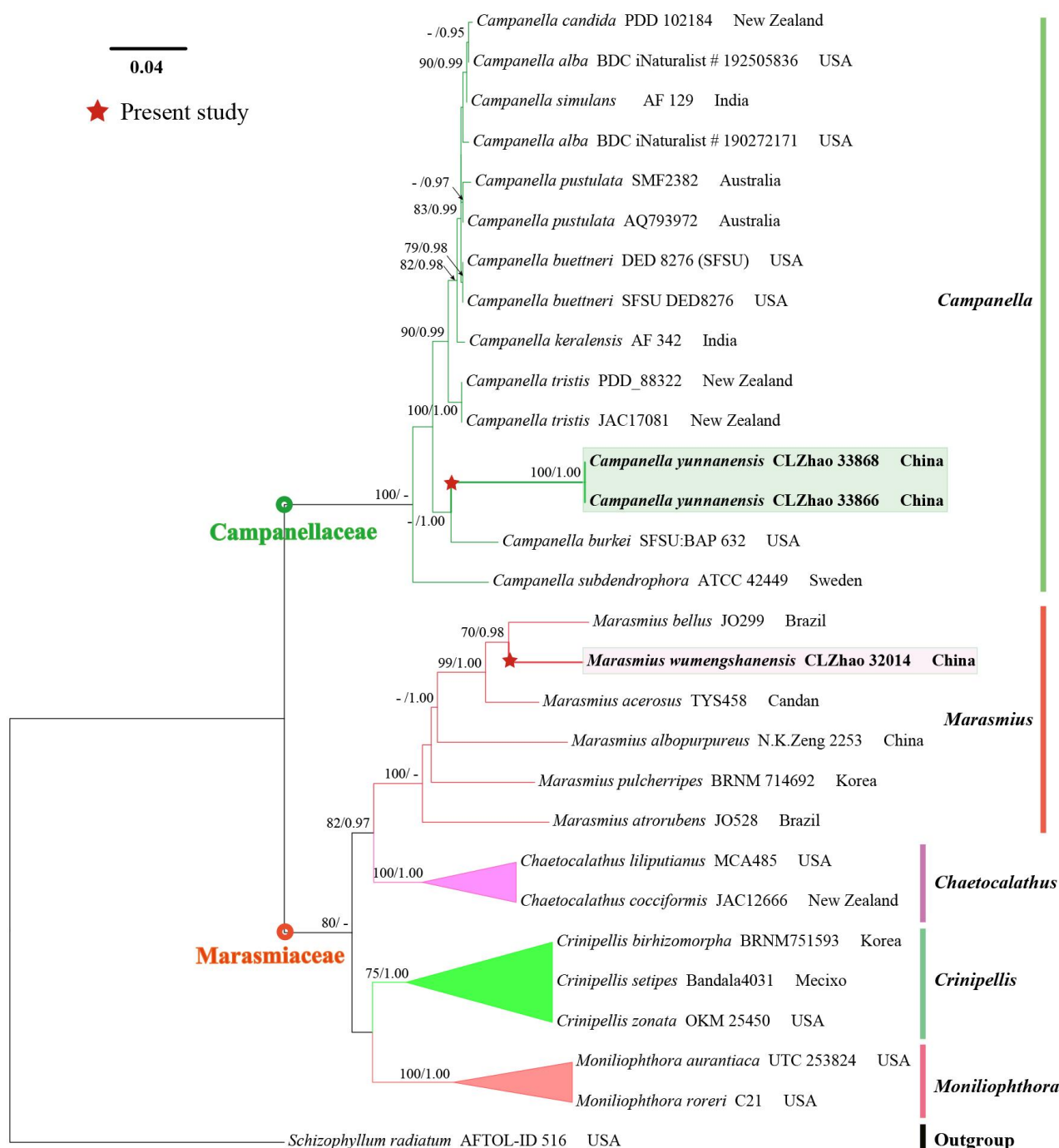


Figure 3 – Maximum likelihood tree illustrating the phylogeny of two new species within the families *Campanellaceae* and *Marasmiaceae* based on the combined ITS+nrLSU sequence data. Branches are labeled with Maximum Likelihood bootstrap values $\geq 70\%$, and Bayesian posterior probabilities ≥ 0.95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

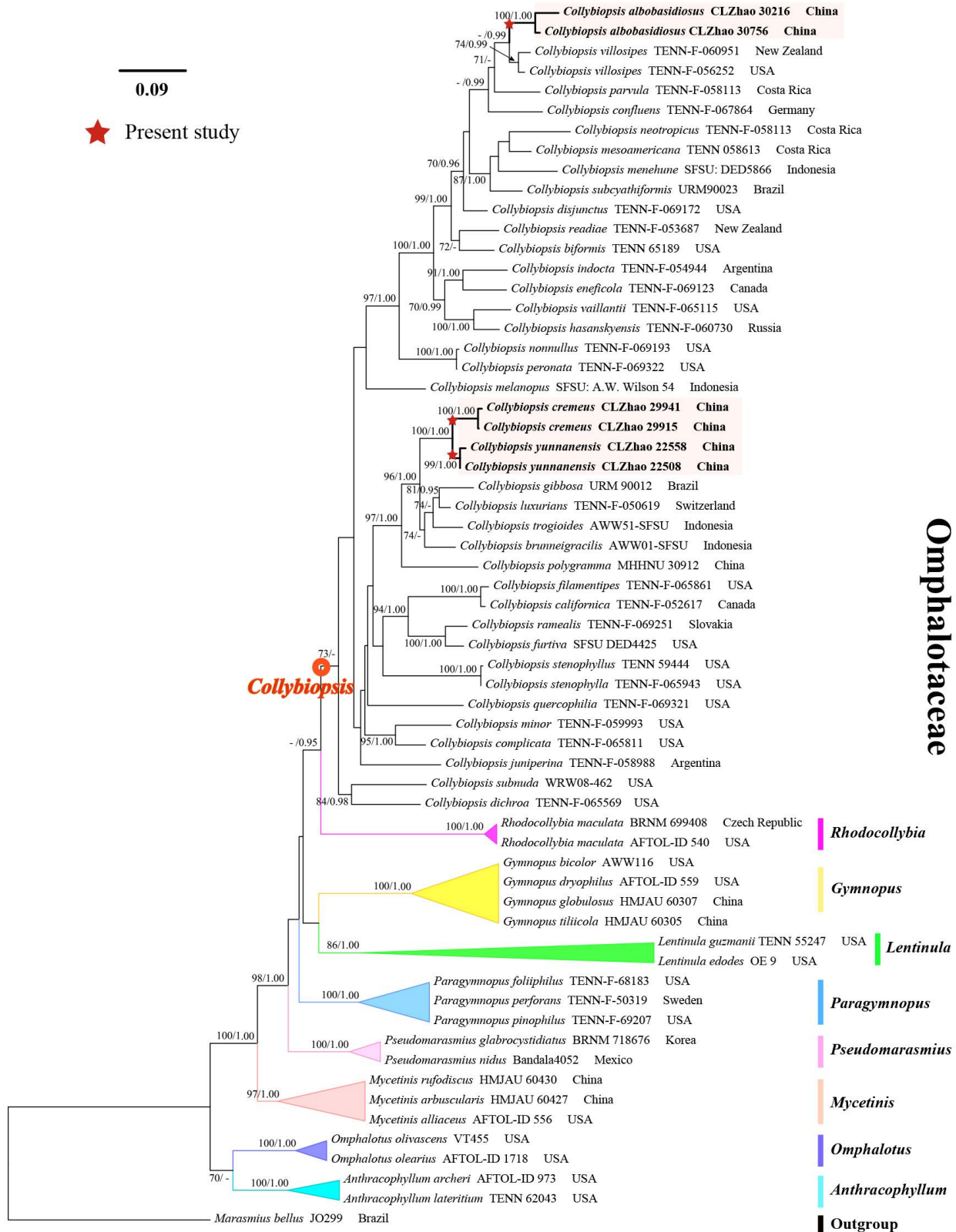


Figure 4 – Maximum likelihood tree illustrating the phylogeny of three new *Collybiopsis* species within the families *Omphalotaceae* based on the combined ITS+nrLSU sequence data. Branches are labeled with Maximum Likelihood bootstrap values $\geq 70\%$, and Bayesian posterior probabilities ≥ 0.95 ,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

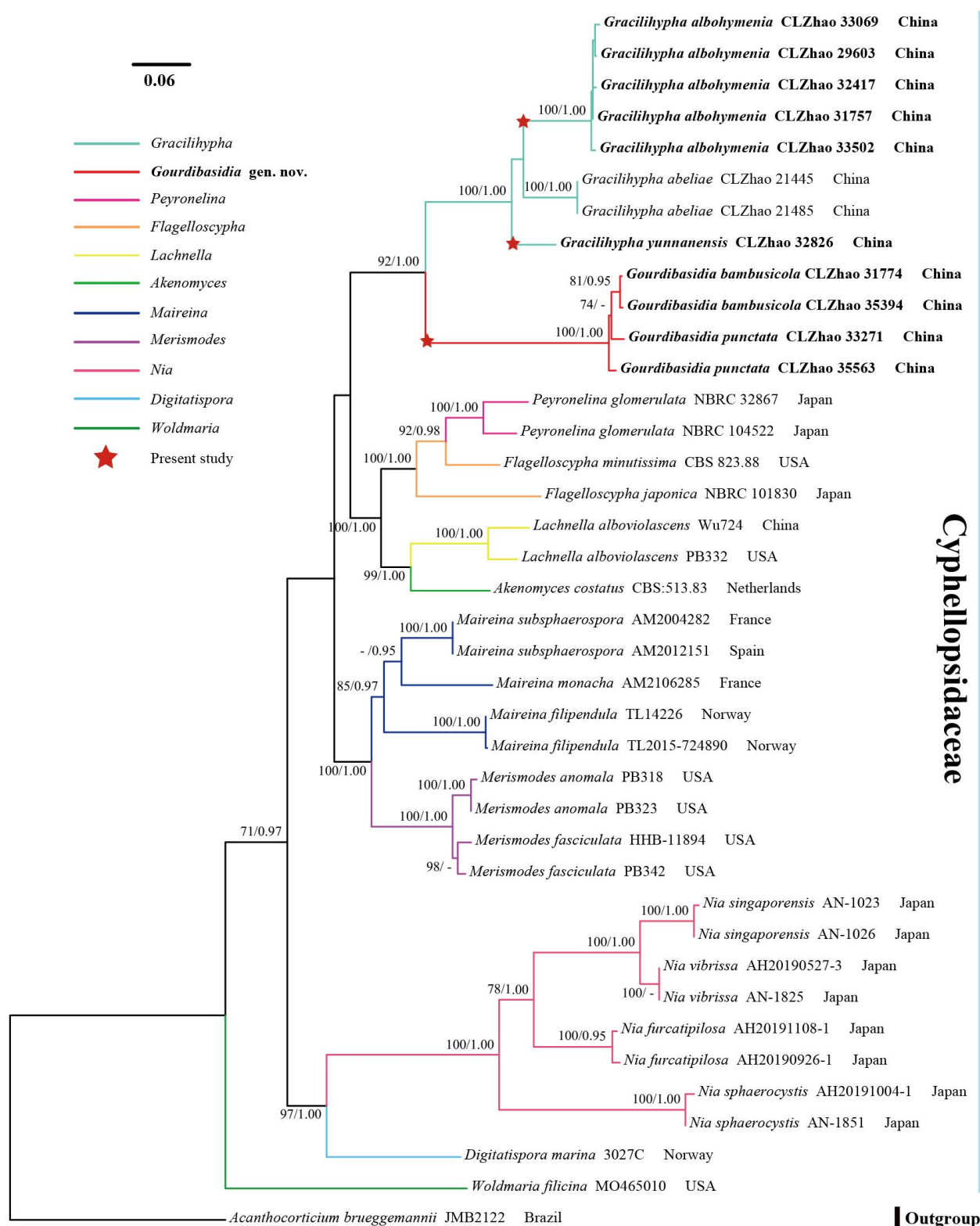


Figure 5 – Maximum likelihood tree illustrating the phylogeny of *Gracilihypha* and *Sicyoideibasidia* and related genera in *Cyphellopsidaceae* based on the combined ITS+nrLSU

sequence data. Branches are labeled with Maximum Likelihood bootstrap values $\geq 70\%$, 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, *tef1*- α , and *rpb2* 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 peridioles 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-Silva 1988, 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, *tef1-α*, and *rpb2* 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 (Palmer 1961, 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, *tef1-α*, and *rpb2* 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](http://www.mycobank.org), accessed on 10 March 2025) and the Index Fungorum ([http:// www.indexfungorum.org](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 *tub2* 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-deliquestent 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 *Psathyrella* (Deschuyteneer et al. 2018), phylogenetic analysis based on ITS, nrLSU, *tef1-α*, and *tub2* 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, *rpb2*, and *tefl-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 incrustated 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 odontoid 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+*rpb1+rpb2+tef1-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.

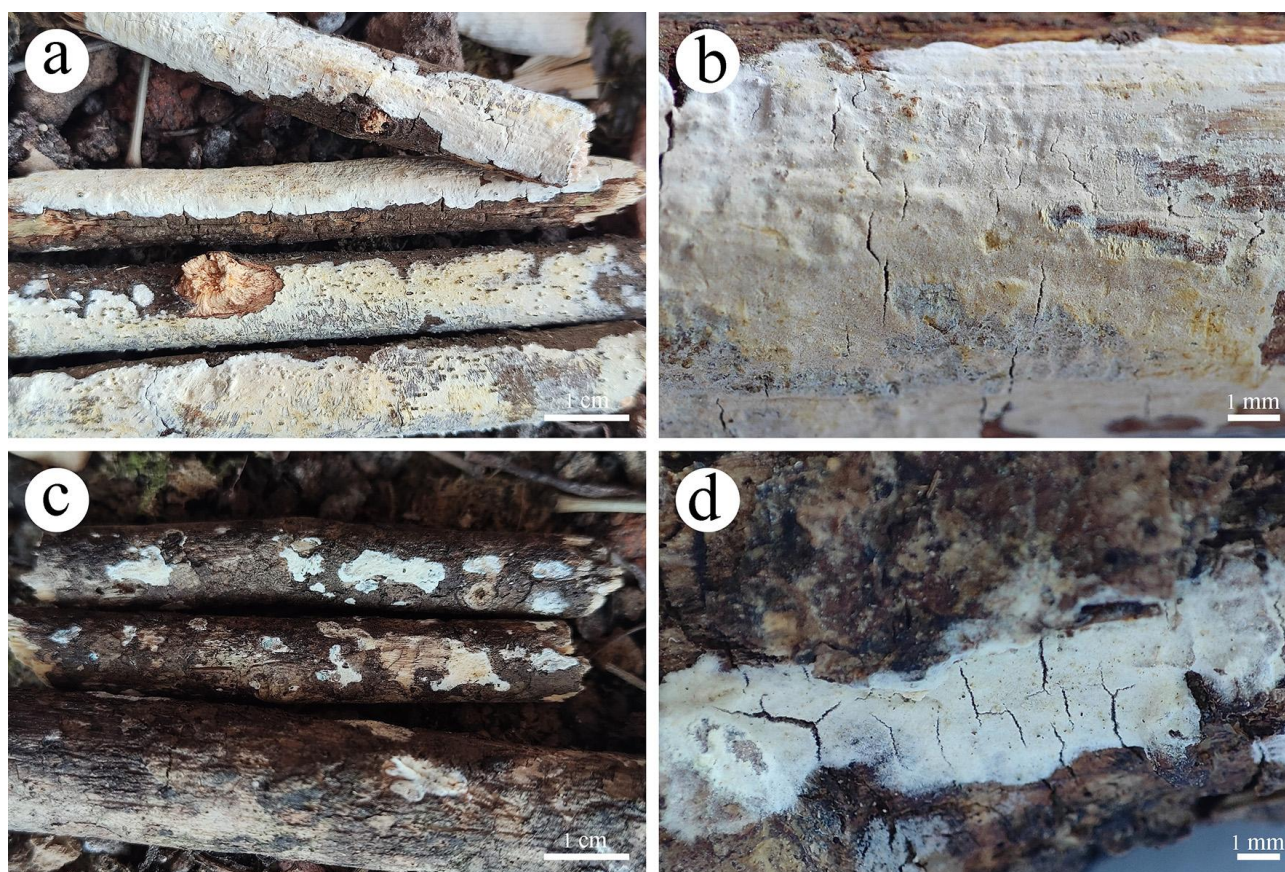


Figure 6 – Basidiomata of *Campanella yunnanensis* a, b CLZhao 33866 (holotype). c, d CLZhao 33868.

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 $\times$ 5–6.5 μm ; cystidioles absent. Basidia clavate, slightly constricted, with 4 sterigmata and a basal clamp connection, 35.5–46 $\times$ 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) $\times$ 4.5–5.5 (–5.8) μm , $L = 9.94 \mu\text{m}$, $W = 5.01 \mu\text{m}$, $Q = 1.80\text{--}2.18$, $Q_m = 1.99 \pm 0.15$ ($n = 60/2$).

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+*rpb1*+*rpb2*+*tef1*- 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 $\times$ 5.2–6.5 μm vs 9–11 $\times$ 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 $\times$ 5–7 μm vs 35.5–46 $\times$ 6.5–8 μm), and basidiospores (4.9–6.1 $\times$ 4.2–5 μm vs 9–11 $\times$ 4.5–5.5 μm , Bougher 2007). *C. keralensis* differs from *C. yunnanensis* by its pleurotoid basidiomata, shorter basidia (27–35 $\times$ 7–8 μm vs 35.5–46 $\times$ 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 $\times$ 4.5–5.5 μm .

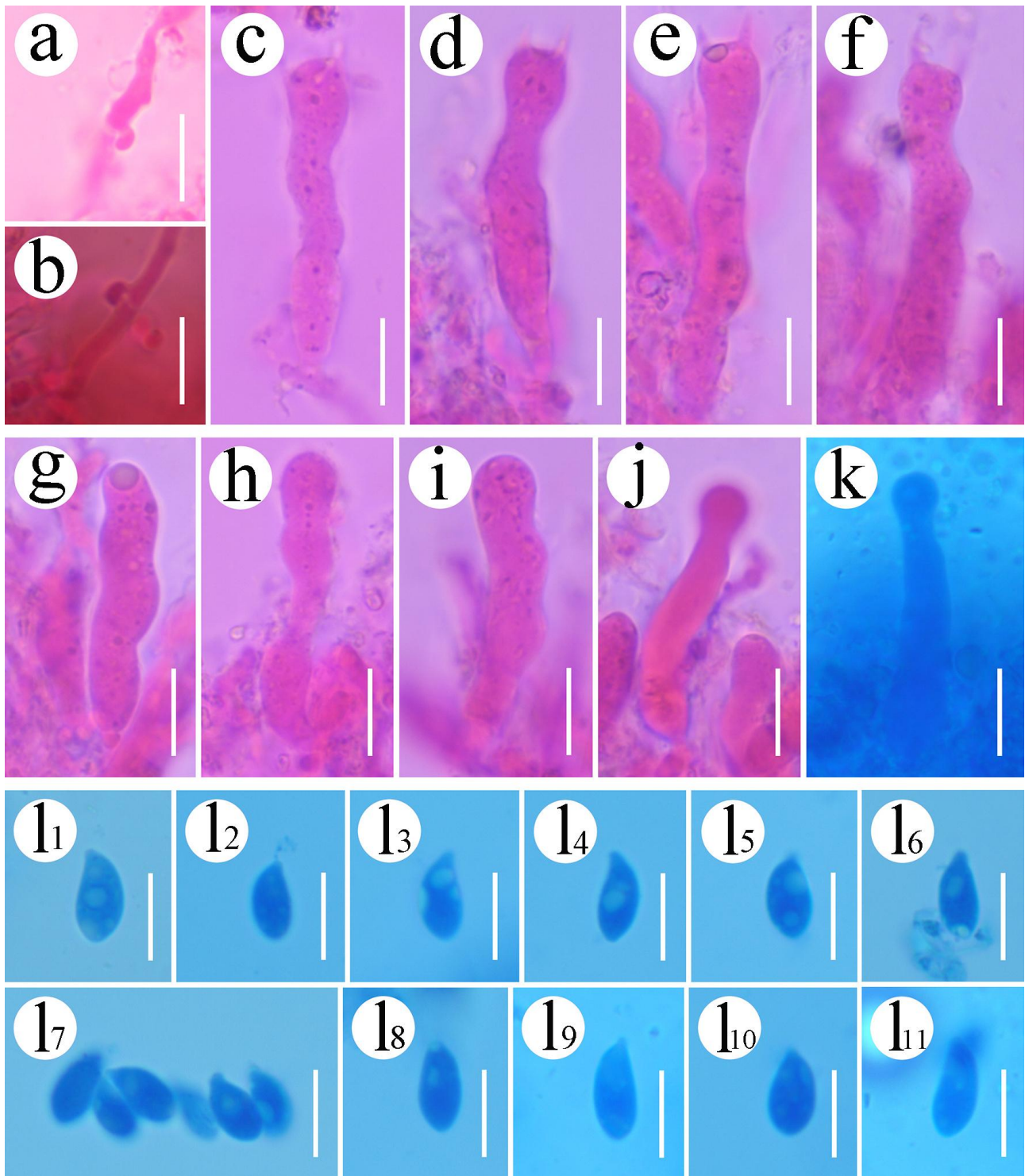


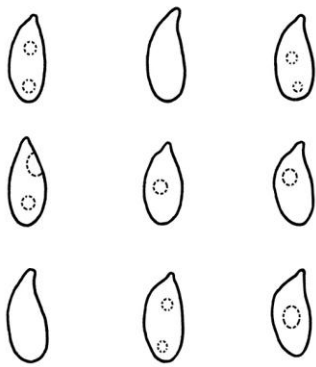
Figure 7 – Microscopic structures of *Campanella yunnanensis* (holotype, CLZhao 33866). a–b Generative hyphae. c–f Basidia. g–i Basidioles. j–k Capitate cystidia. l Basidiospores. Scale bars: a–l = 10 μm.

Family *Cyphellaceae* Burnett, Outl. Bot. (London): 233 (1835)
 Index Fungorum number: IF80673.
 Type genus – *Cyphella* Fr.

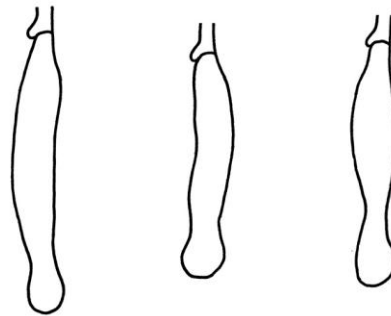
Note 15 *Cheimonophyllum* Singer
 Index Fungorum number: IF17284.

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

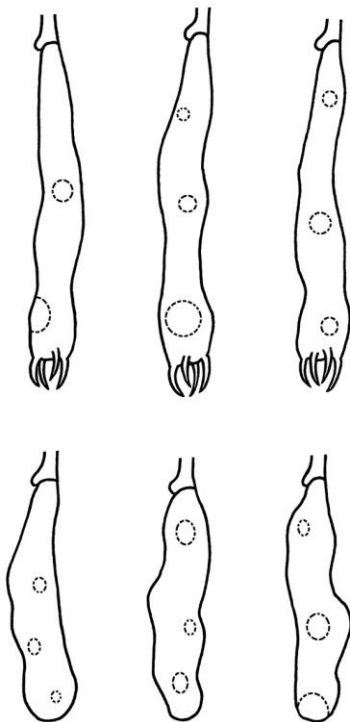
Notes – *Cheimonophyllum* is a small saprobic genus belonging to the family *Cyphellaceae*, and consisting of four species from the temperate zone, with *C. candidissimum* (Sacc.) Singer (= *C. haedinum*) is the type species (He et al. 2019, Kalichman et al. 2020). Valade & Moreau (2022) transferred *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).



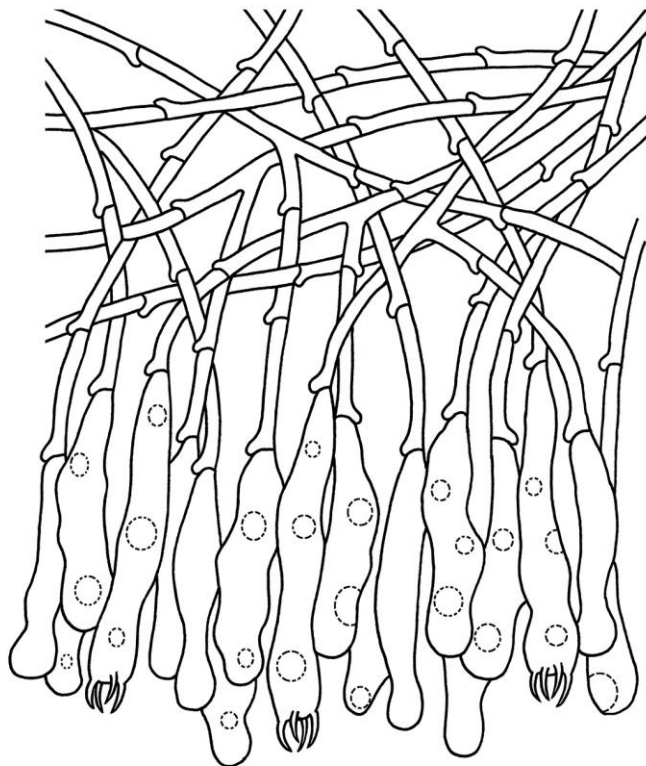
a



b



c



d

Figure 8 – Microscopic structures of *Campanella yunnanensis* (holotype, CLZhao 33866). a Basidiospores. b Basidia and basidioles c Capitulate 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 dimorphic 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* as a genus of corticioid fungi in the family Cystostereaceae. Species in the *Cystostereum* are characterized by perennial, pileate or mostly resupinate basidiomata, odontoid or tuberculate hymenophore, a dimorphic 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 gloecystidia, 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 gloecystidia, 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 & Noordeloos 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, *rpb2*, and *tefl-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+*rpb1*+*rpb2*+*tef1*- 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 μ m 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 μ m in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia subcylindrical, colorless, thin-walled, with crystals at the apex, 24.5–30.5 $\times$ 3.5–5 μ m; cystidioles tapering, colorless, thin-walled, 23–25.5 $\times$ 5–7.5 μ m. Basidia clavate, slightly constricted, with 4 sterigmata and a basal clamp connection, 30–36 $\times$ 7.5–10.5 μ m; 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) $\times$ (4.2–)4.5–6.2(–6.5) μ m, L = 9.60 μ m, W = 5.40 μ m, Q = 1.57–1.91, Q_m = 1.79 $\pm$ 0.19 (n = 30/1).

Notes – *Marasmius wumengshanensis* grouped in *Marasmius* (*Marasmiaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb1*+*rpb2*+*tef1*- 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 $\times$ 7–8 μ m vs 30–36 $\times$ 7.5–10.5 μ m, Manimohan & Leelavathy 1989); *M. nigrobrunneus* can be distinguished from *M. wumengshanensis* by its pileate basidiomata, and shorter basidia (23–30 $\times$ 6.5–8 μ m vs 30–36 $\times$ 7.5–10.5 μ m, Manimohan & Leelavathy 1989); *M. tubulatus* differentiates from *M. wumengshanensis* by its pileate basidiomata, and smaller basidia (20–22 $\times$ 5–7 μ m vs 30–36 $\times$ 7.5–10.5 μ m, Manimohan & Leelavathy 1989); *M. yunnanensis* differs from *M. wumengshanensis* by its pileate basidiomata, and shorter basidia (24–30 $\times$ 6–8 μ m vs 30–36 $\times$ 7.5–10.5 μ m, 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 $\times$ 4.5–6.2 μ m.

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).

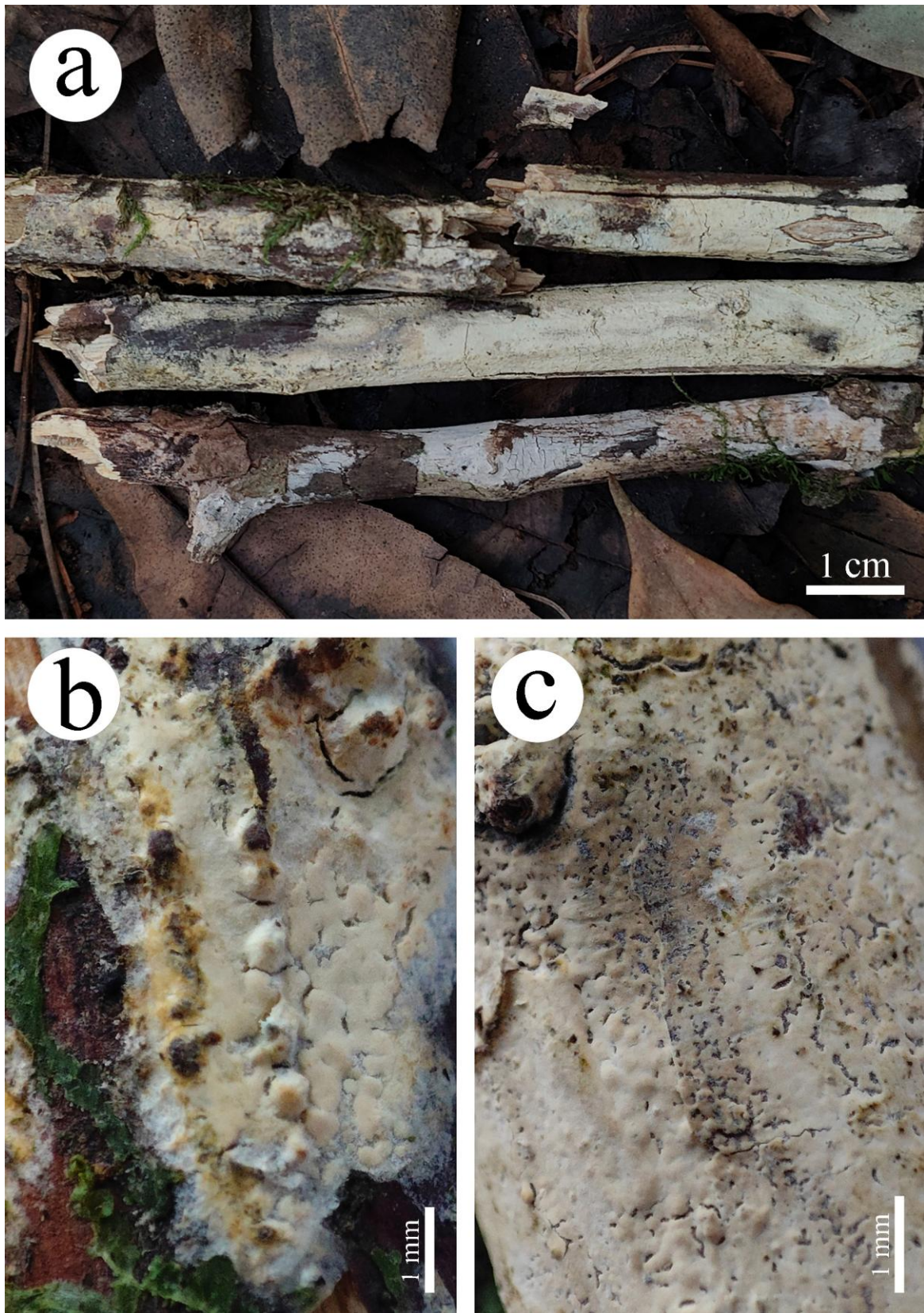


Figure 9 – Basidiomata of *Marasmius wumengshanensis* (holotype, CLZhao 32014).

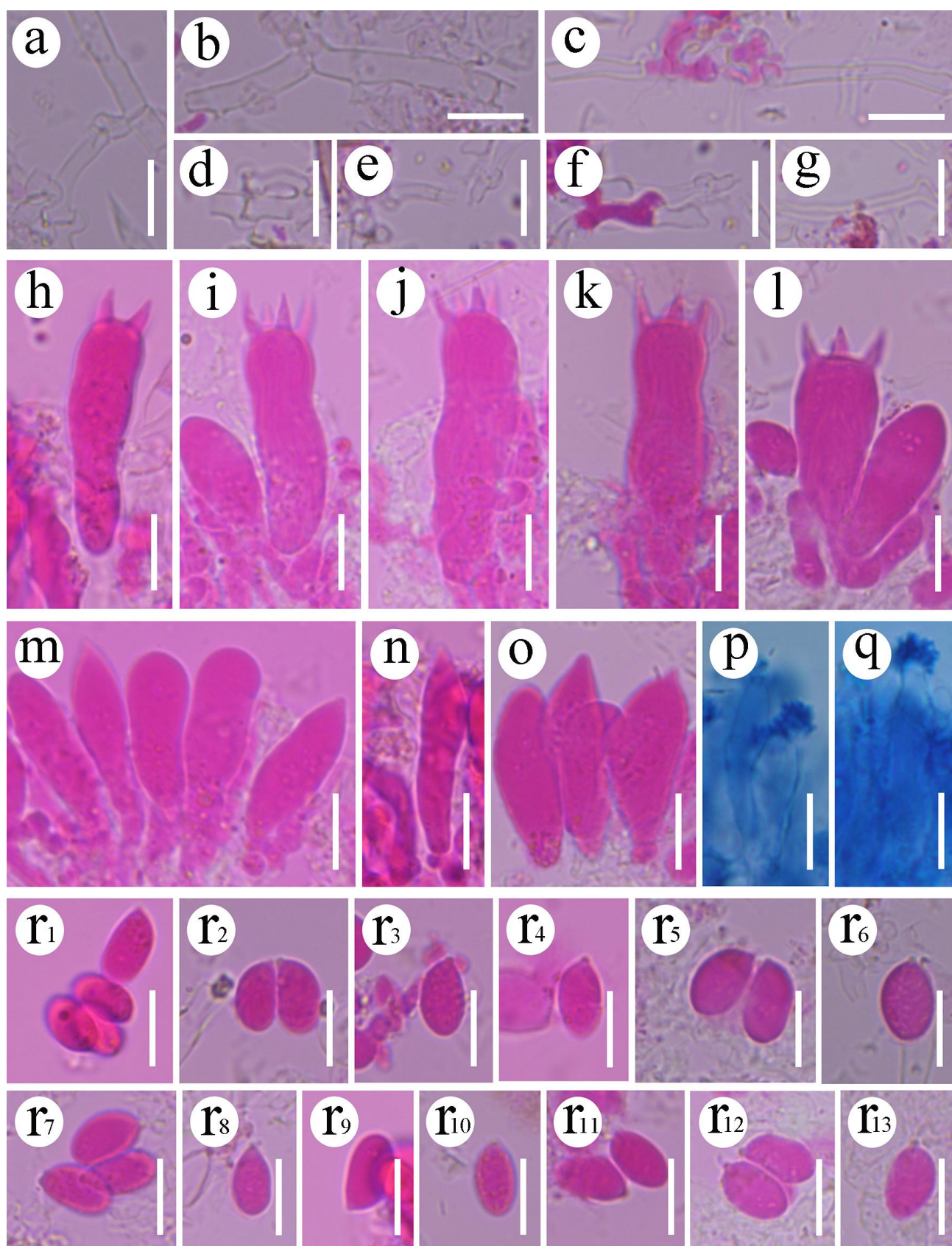


Figure 10 – Microscopic structures of *Marasmius wumengshanensis* (holotype, CLZhao 32014). a–g Generative hyphae. h–l Basidia. m A section of the hymenium and subhymenium. n–o Cystidioles. p–q Cystidia. r Basidiospores. Scale bars: a–r = 10 μm.

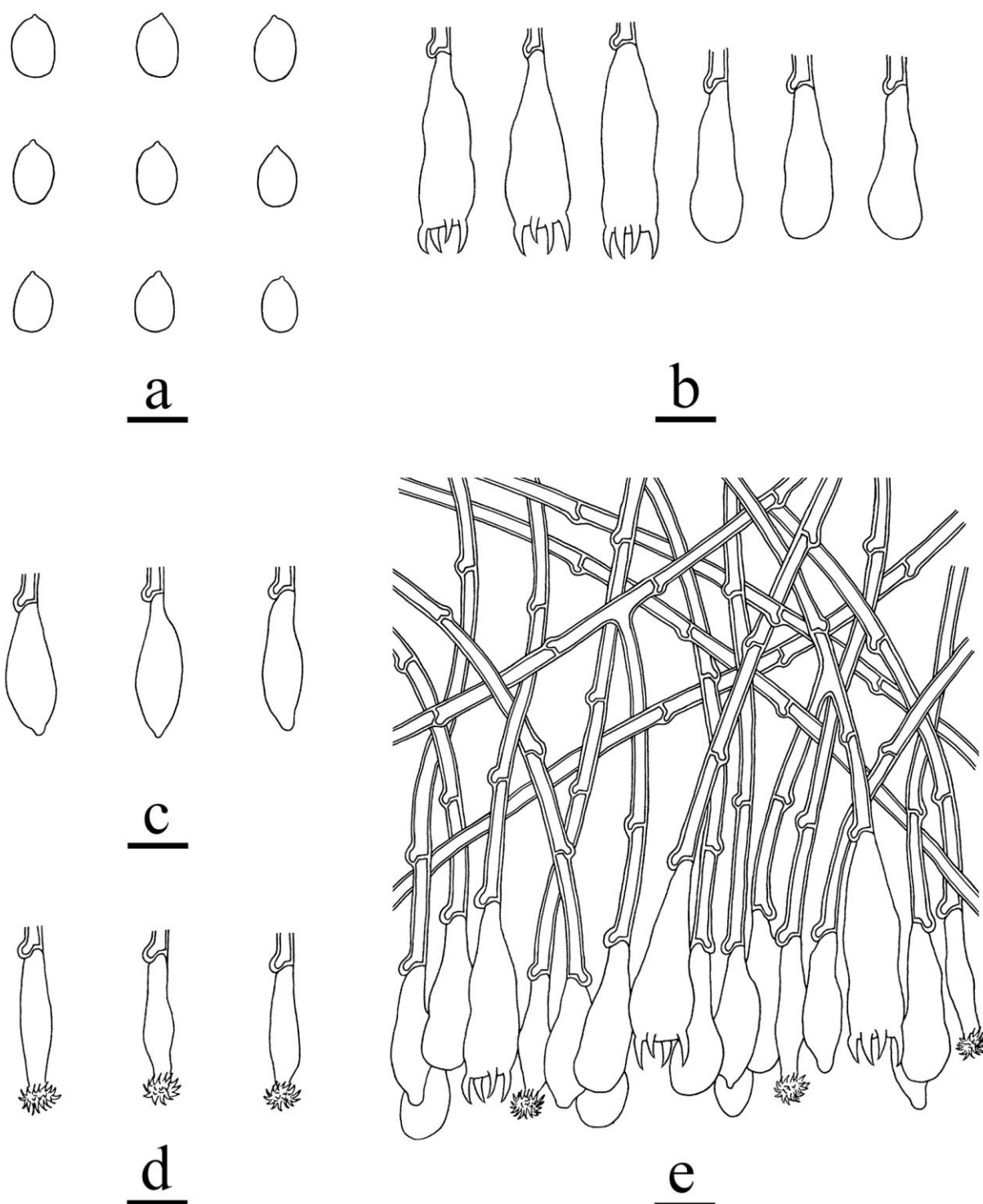


Figure 11 – Microscopic structures of *Marasmius wumengshanensis* (holotype, CLZhao 32014). a Basidiospores. b Basidia and basidioles. c Cystidioles. d Cystidia. e A section of the hymenium and subhymenium. Scale bars: a–e = 10 μ m.

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*.

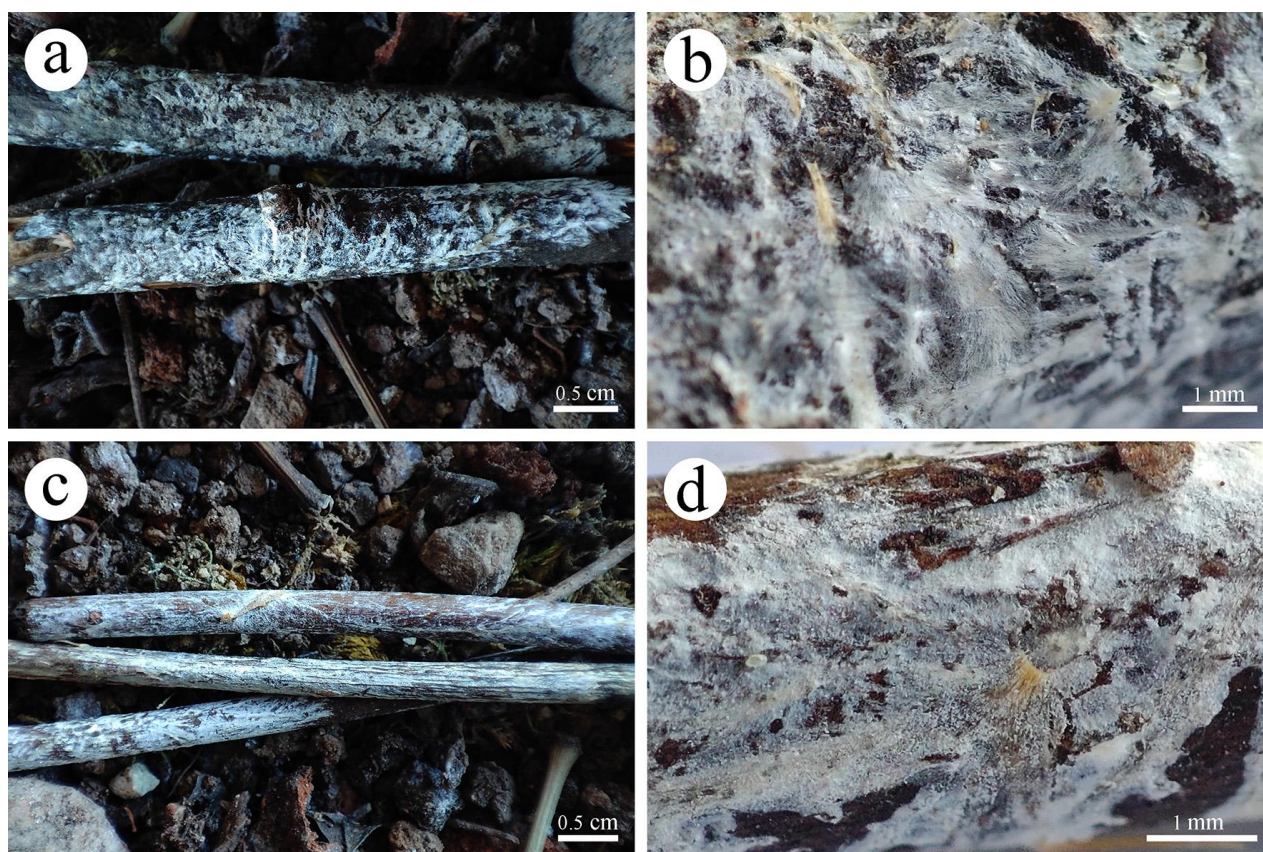


Figure 12 – Basidiomata of *Collybiopsis albobasidiosa* a, b CLZhao 30216 (holotype). c, d CLZhao 30756.

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* Murrill, *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+*rpb1*+*rpb2*+*tefl-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).

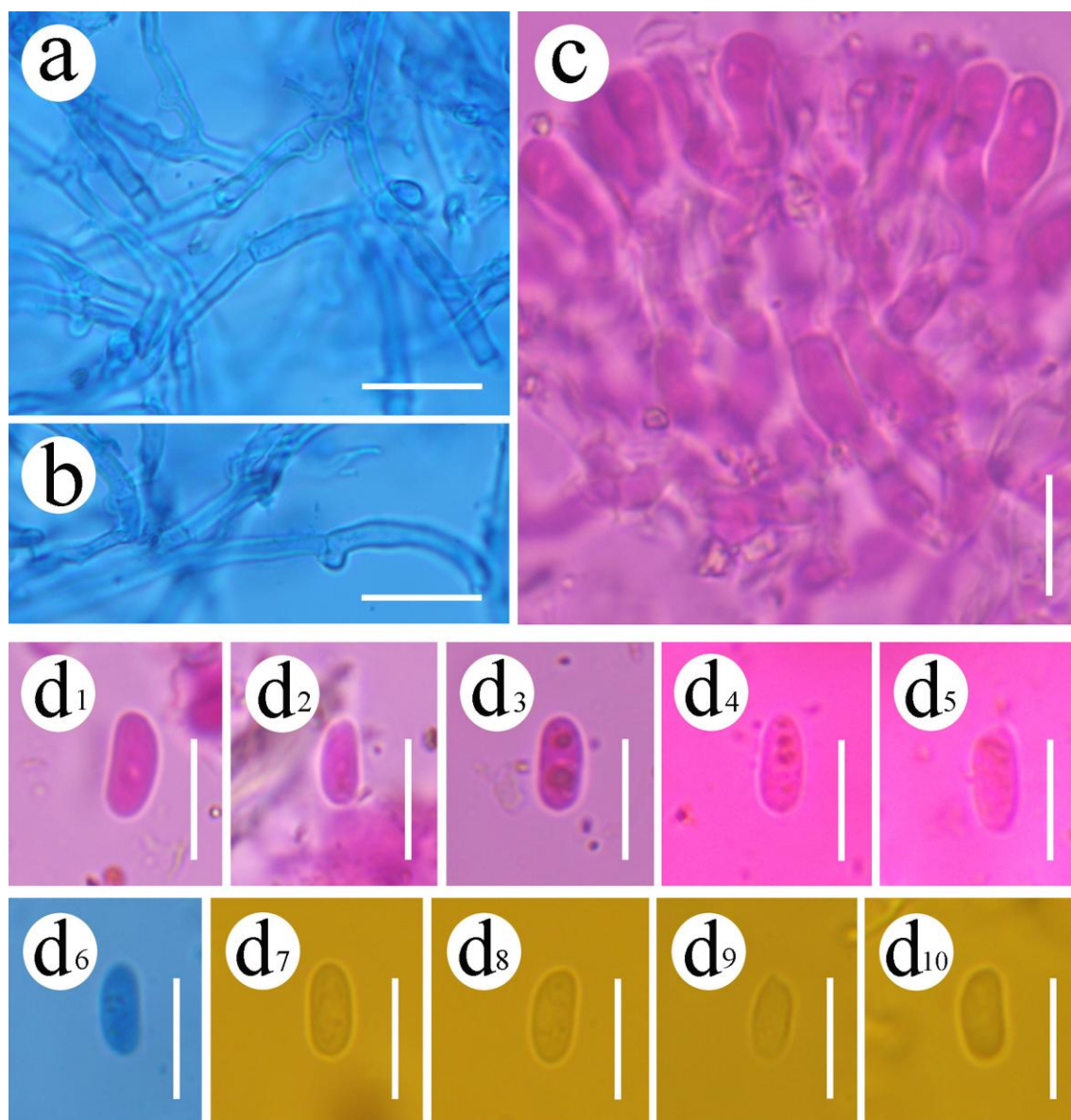


Figure 13 – Microscopic structures of *Collybiopsis albobasidiosa* (holotype, CLZhao 30216). a–b Generative hyphae. c A section of the hymenium and subhymenium. d Basidiospores. Scale bars: a–b= 20 μ m; c–d = 10 μ m.

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+*rpb1*+*rpb2*+*tef1*- 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 $\times$ 4–10 μ m vs 14.5–15.5 $\times$ 4–5.5 μ m), 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 $\times$ 6.5–7.5 μ m vs 14.5–15.5 $\times$ 4–5.5 μ m, Desjardin et al. 1997).

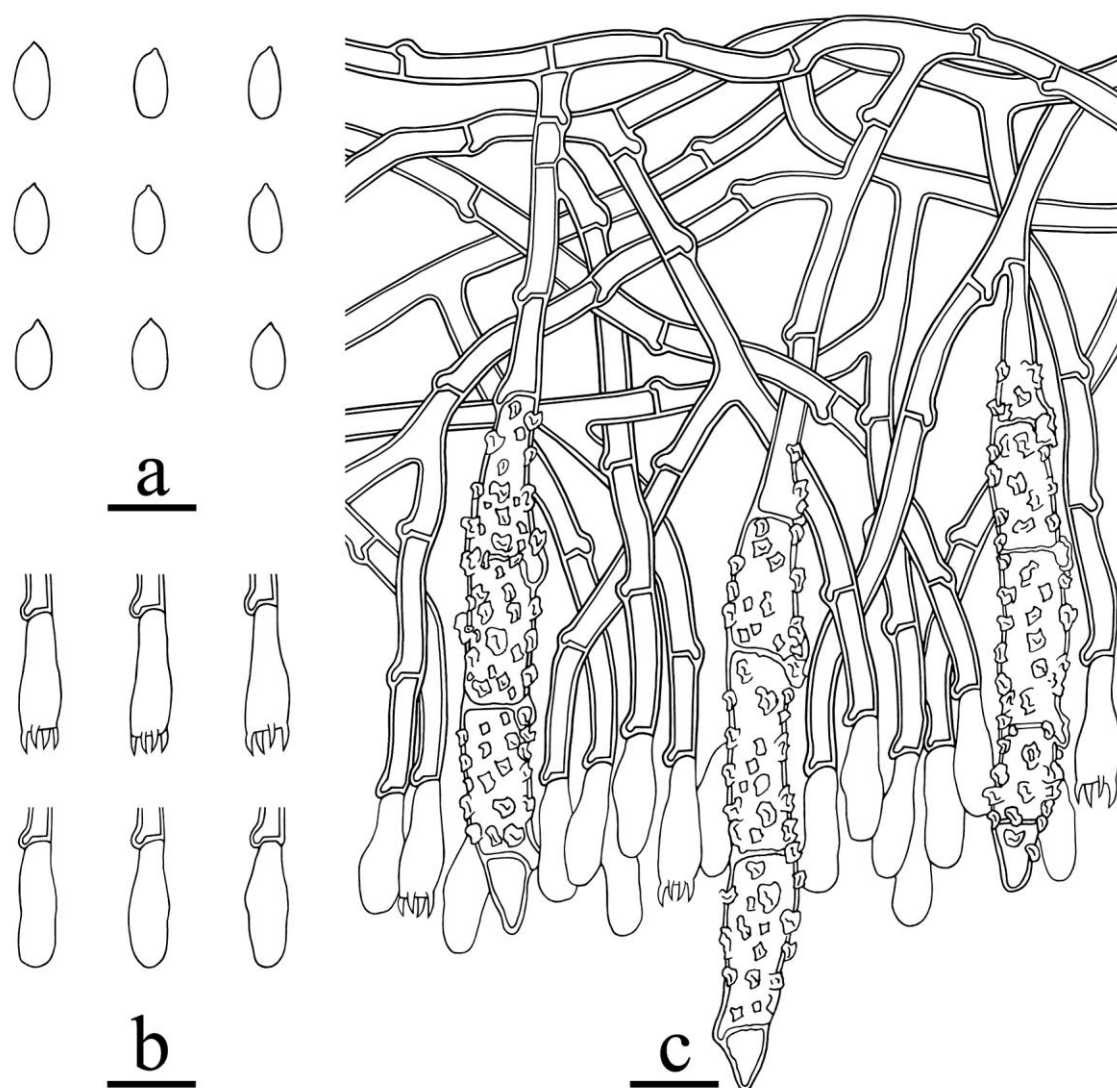


Figure 14 – Microscopic structures of *Collybiopsis albobasidiosa* (holotype, CLZhao 30216). a Basidiospores. b Basidia and basidioles. c A section of the hymenium and subhymenium. Scale bars: a–c = 10 μm .

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 ($26\text{--}33 \times 7\text{--}8 \mu\text{m}$ vs $14.5\text{--}15.5 \times 4\text{--}5.5 \mu\text{m}$), and longer basidiospores ($8\text{--}9 \times 2.5\text{--}3.5 \mu\text{m}$ vs $6\text{--}8 \times 2.8\text{--}4 \mu\text{m}$, Petersen & Hughes 2021); *C. orientisubnuda* differentiates from *C. albobasidiosa* by its pileate basidiomata with brownish orange, longer basidia ($19.8\text{--}28.7 \times 3.7\text{--}7.3 \mu\text{m}$ vs $14.5\text{--}15.5 \times 4\text{--}5.5 \mu\text{m}$, Kim et al. 2022); *C. undulata* can be distinguished from *C. albobasidiosa* by its pileate basidiomata with dark brown, longer basidia ($15\text{--}22.3 \times 3.6\text{--}6.8 \mu\text{m}$ vs $14.5\text{--}15.5 \times 4\text{--}5.5 \mu\text{m}$, 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, $23^{\circ}48' \text{N}$, $97^{\circ}38' \text{E}$, 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 μ m thick. Hymenial surface smooth, white when fresh, turning to cream upon drying. Sterile margin cream, slightly fimbriate, up to 0.5 mm wide.

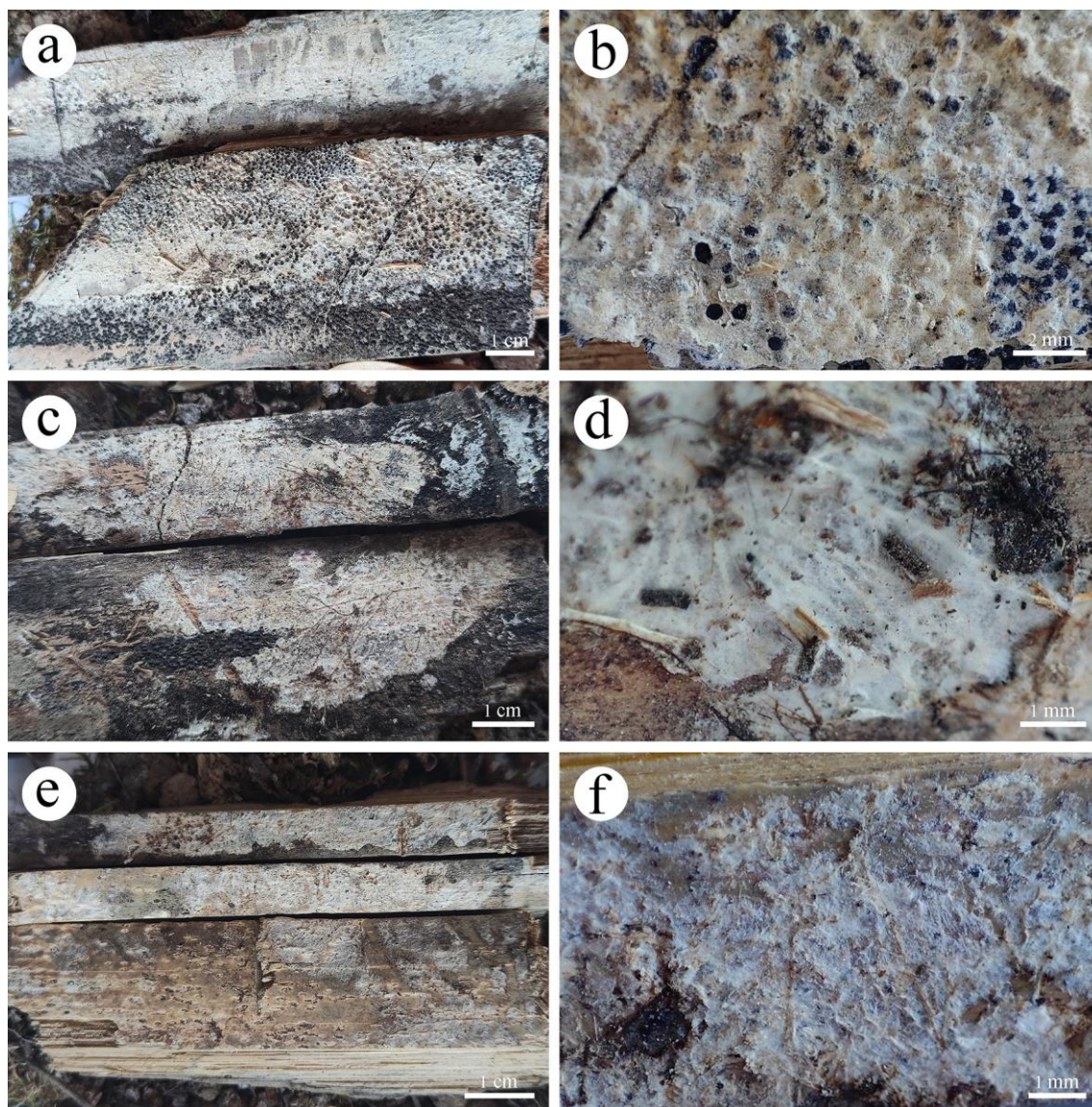


Figure 15 – Basidiomata of *Collybiopsis cremea* a, b CLZhao 29915 (holotype). c, d CLZhao 29941. e, f CLZhao 30022.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, slightly thick-walled, branched, interwoven, 2.5–4 μ m in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia capitate, colorless, thin-walled, 30–42.5 $\times$ 4.5–5.5 μ m; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 13.5–18 $\times$ 4–5.5 μ m; 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 $\times$ 3.3–3.8(–4) μ m, L = 5.16 μ m, W = 3.55 μ m, Q = 1.30–1.61, Q_m = 1.45 $\pm$ 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).

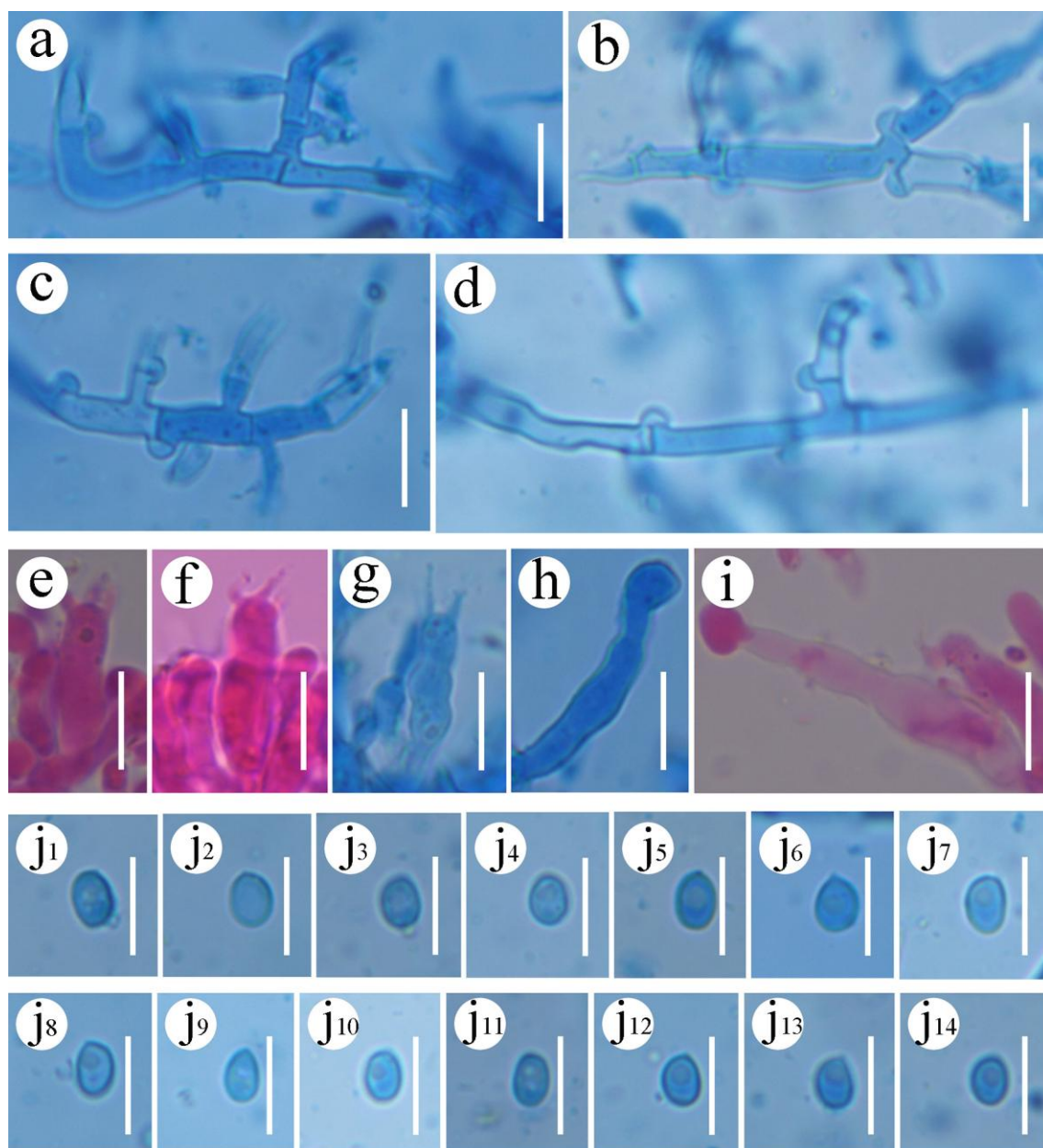


Figure 16 – Microscopic structures of *Collybiopsis crema* (holotype, CLZhao 29915). a–d Generative hyphae. e–g Basidia. h–i Capitate cystidia. j Basidiospores. Scale bars: a–j = 10 μ m.

Notes – *Collybiopsis crema* grouped in *Collybiopsis* (*Omphalotaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb1*+*rpb2*+*tef1*- 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. crema* by its farinaceous basidiomata with straw-yellow, and larger basidiospores ($6\text{--}6.8 \times 4.2\text{--}5 \mu\text{m}$ vs $4.7\text{--}5.8 \times 3.3\text{--}3.8 \mu\text{m}$).

Morphologically, *Collybiopsis crema* 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. crema* by its brownish gray pileal surface, larger basidia ($25\text{--}32 \times 6\text{--}8 \mu\text{m}$ vs $13.5\text{--}18 \times 4\text{--}5.5 \mu\text{m}$), and longer basidiospores ($6\text{--}8.3 \times 3\text{--}4.3 \mu\text{m}$ vs $4.7\text{--}5.8 \times 3.3\text{--}3.8 \mu\text{m}$, Zhang et al. 2023c); *C. complicata* can be distinguished from *C. crema* by its marasmielloid or gymnopoid basidiomata with snuff brown, larger basidia ($35\text{--}60 \times 7\text{--}9 \mu\text{m}$ vs $13.5\text{--}18 \times 4\text{--}5.5 \mu\text{m}$), and longer basidiospores ($6.5\text{--}8.5 \times 3\text{--}4 \mu\text{m}$ vs $4.7\text{--}5.8 \times 3.3\text{--}3.8 \mu\text{m}$, Petersen & Hughes 2024a); *C. gibbosa*

differs from *C. cremea* by its grayish orange basidiomata, both larger basidia ($22\text{--}30 \times 5.5\text{--}7 \mu\text{m}$ vs $13.5\text{--}18 \times 4\text{--}5.5 \mu\text{m}$), and basidiospores ($8\text{--}9.5 \times 4\text{--}4.5 \mu\text{m}$ vs $4.7\text{--}5.8 \times 3.3\text{--}3.8 \mu\text{m}$, Phonrob et al. 2024); *C. melanopus* differentiates from *C. cremea* by its pileate basidiomata with beige, both longer basidia ($23\text{--}30 \times 5\text{--}7 \mu\text{m}$ vs $13.5\text{--}18 \times 4\text{--}5.5 \mu\text{m}$), and basidiospores ($7\text{--}8.5 \times 3.5\text{--}4.5 \mu\text{m}$ vs $4.7\text{--}5.8 \times 3.3\text{--}3.8 \mu\text{m}$, Phonrob et al. 2024); *C. minor* can be distinguished from *C. cremea* by its brown basidiomata, both larger basidia ($30\text{--}43 \times 7\text{--}9 \mu\text{m}$ vs $13.5\text{--}18 \times 4\text{--}5.5 \mu\text{m}$), and basidiospores ($9\text{--}10 \times 4\text{--}4.5 \mu\text{m}$ vs $4.7\text{--}5.8 \times 3.3\text{--}3.8 \mu\text{m}$, Petersen & Hughes 2021); *C. ramealis* differs from *C. cremea* by its ochraceous buff basidiomata, larger basidia ($26\text{--}32 \times 7\text{--}8.5 \mu\text{m}$ vs $13.5\text{--}18 \times 4\text{--}5.5 \mu\text{m}$), and longer basidiospores ($7\text{--}10 \times 2.5\text{--}4 \mu\text{m}$ vs $4.7\text{--}5.8 \times 3.3\text{--}3.8 \mu\text{m}$, Petersen & Hughes 2021).

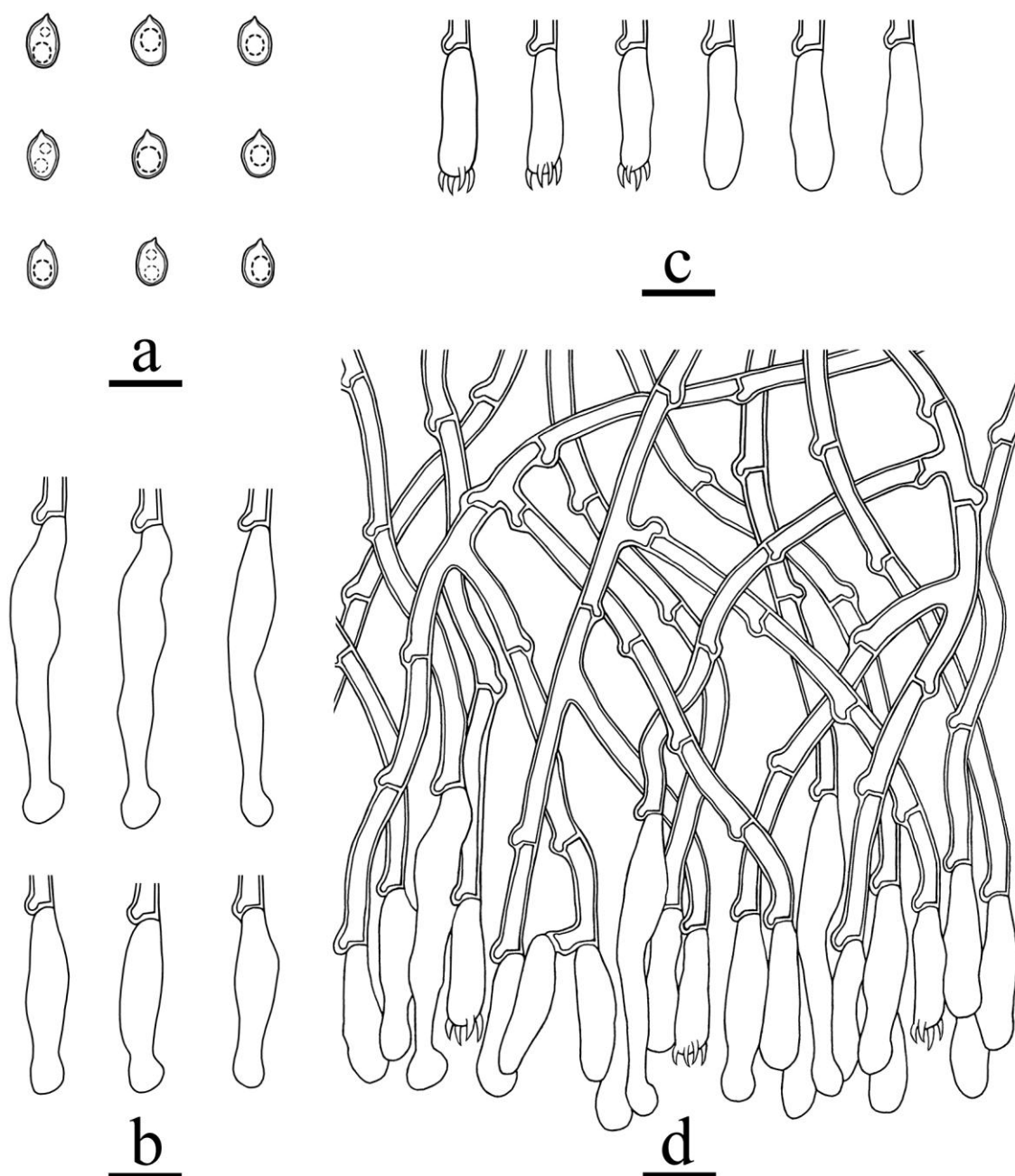


Figure 17 – Microscopic structures of *Collybiopsis cremea* (holotype, CLZhao 29915). a Basidiospores. b Capitulate cystidia. c Basidia and basidioles. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 μm .

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).

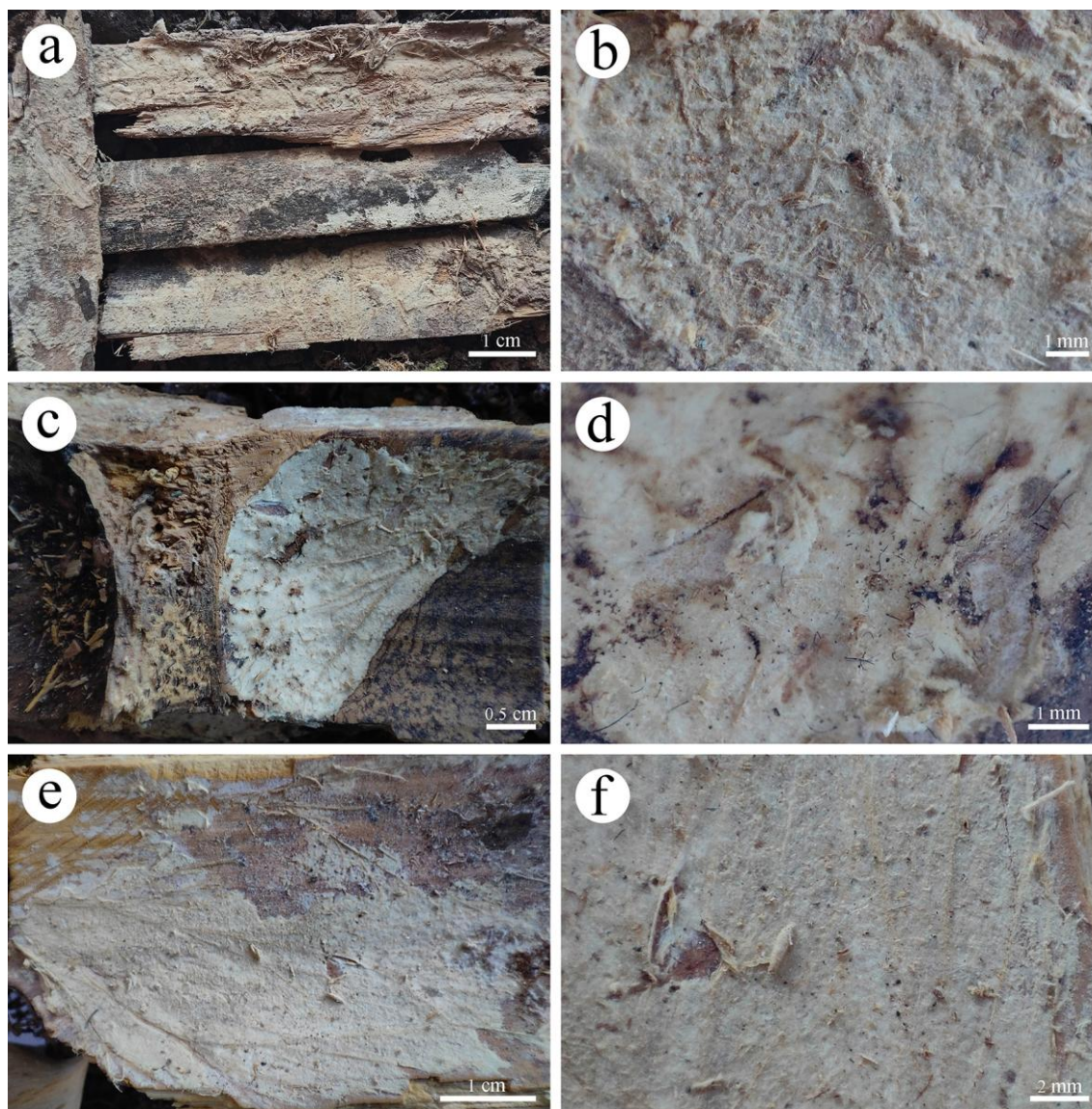


Figure 18 – Basidiomata of *Collybiopsis yunnanensis* a, b CLZhao 22546 (holotype). c, d CLZhao 22565. e, f CLZhao 22558.

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 μ m 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 μ m in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia capitate, colorless, slightly thick-walled, 16.5–26 $\times$ 4–6.5 μ m; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 14–17.5 $\times$ 4–5.5 μ m; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid, colorless, slightly

thick-walled, smooth, with one guttula, IKI–, CB+, $6\text{--}6.8 \times 4.2\text{--}5(5.2) \mu\text{m}$, $L = 6.44 \mu\text{m}$, $W = 4.71 \mu\text{m}$, $Q = 1.27\text{--}1.51$, $Q_m = 1.37 \pm 0.07$ ($n = 90/3$).

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

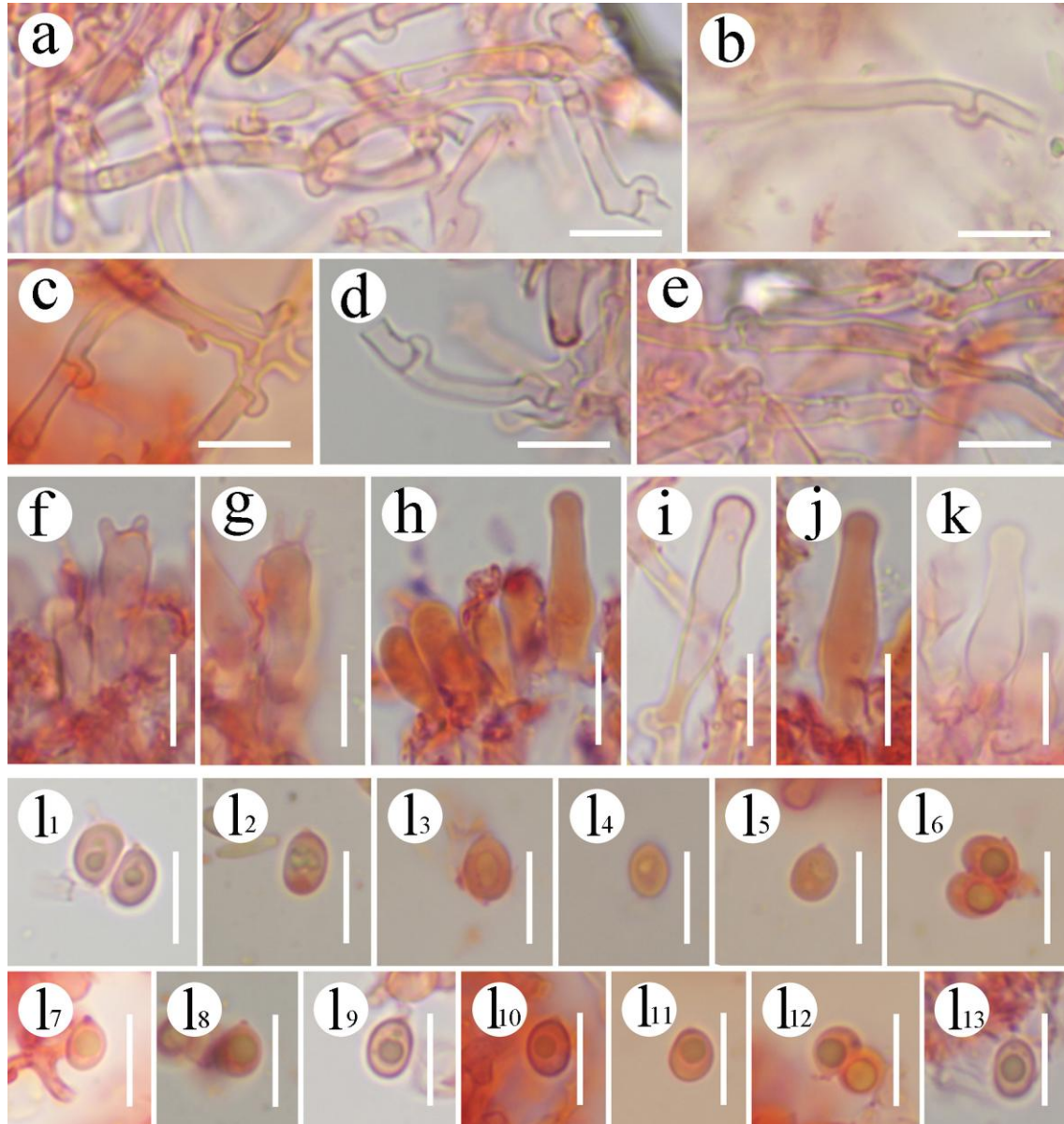


Figure 19 – Microscopic structures of *Collybiopsis yunnanensis* (holotype, CLZhao 22546). a–e Generative hyphae. f–g Basidia. h A section of the hymenium and subhymenium. i–k Capitate cystidia. l Basidiospores. Scale bars: a–l = 10 μm .

Notes – *Collybiopsis yunnanensis* grouped in *Collybiopsis* (*Omphalotaceae*, *Agaricales*) based on the ITS+nrLSU+*rpb1*+*rpb2*+*tefl- 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 ($4.7\text{--}5.8 \times 3.3\text{--}3.8 \mu\text{m}$ vs $6\text{--}6.8 \times 4.2\text{--}5 \mu\text{m}$).

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 ($25\text{--}32 \times 6\text{--}8 \mu\text{m}$ vs $14\text{--}17.5 \times 4\text{--}5.5 \mu\text{m}$, Zhang et al. 2023c); *C. complicata* can be distinguished from *C. yunnanensis* by its marasmieloid or gymnopoid basidiomata with snuff brown, larger basidia ($35\text{--}60 \times 7\text{--}9 \mu\text{m}$ vs $14\text{--}17.5 \times 4\text{--}5.5 \mu\text{m}$), and narrower basidiospores ($6.5\text{--}8.5 \times 3\text{--}4 \mu\text{m}$ vs $6\text{--}6.8 \times 4.2\text{--}5 \mu\text{m}$, Petersen & Hughes 2024a); *C. gibbosa* differs from *C. yunnanensis* by its grayish orange basidiomata, larger basidia ($22\text{--}30 \times 5.5\text{--}7 \mu\text{m}$ vs $14\text{--}17.5 \times 4\text{--}5.5 \mu\text{m}$), and longer basidiospores ($8\text{--}9.5 \times 4\text{--}4.5 \mu\text{m}$ vs $6\text{--}6.8 \times 4.2\text{--}5 \mu\text{m}$, Phonrob et al. 2024); *C. melanopus* differentiates from *C. yunnanensis* by its pileate basidiomata with beige, both longer basidia ($23\text{--}30 \times 5\text{--}7 \mu\text{m}$ vs $14\text{--}17.5 \times 4\text{--}5.5 \mu\text{m}$), and basidiospores ($7\text{--}8.5 \times 3.5\text{--}4.5 \mu\text{m}$ vs $6\text{--}6.8 \times 4.2\text{--}5 \mu\text{m}$, Phonrob et al. 2024); *C. minor* can be distinguished from *C. yunnanensis* by its brown basidiomata, larger basidia ($30\text{--}43 \times 7\text{--}9 \mu\text{m}$ vs $14\text{--}17.5 \times 4\text{--}5.5 \mu\text{m}$), and longer basidiospores ($9\text{--}10 \times 4\text{--}4.5 \mu\text{m}$ vs $6\text{--}6.8 \times 4.2\text{--}5 \mu\text{m}$, Petersen & Hughes 2021); *C. ramealis* differs from *C. yunnanensis* by its ochraceous buff basidiomata, larger basidia ($26\text{--}32 \times 7\text{--}8.5 \mu\text{m}$ vs $14\text{--}17.5 \times 4\text{--}5.5 \mu\text{m}$), and longer basidiospores ($7\text{--}10 \times 2.5\text{--}4 \mu\text{m}$ vs $6\text{--}6.8 \times 4.2\text{--}5 \mu\text{m}$, Petersen & Hughes 2021).

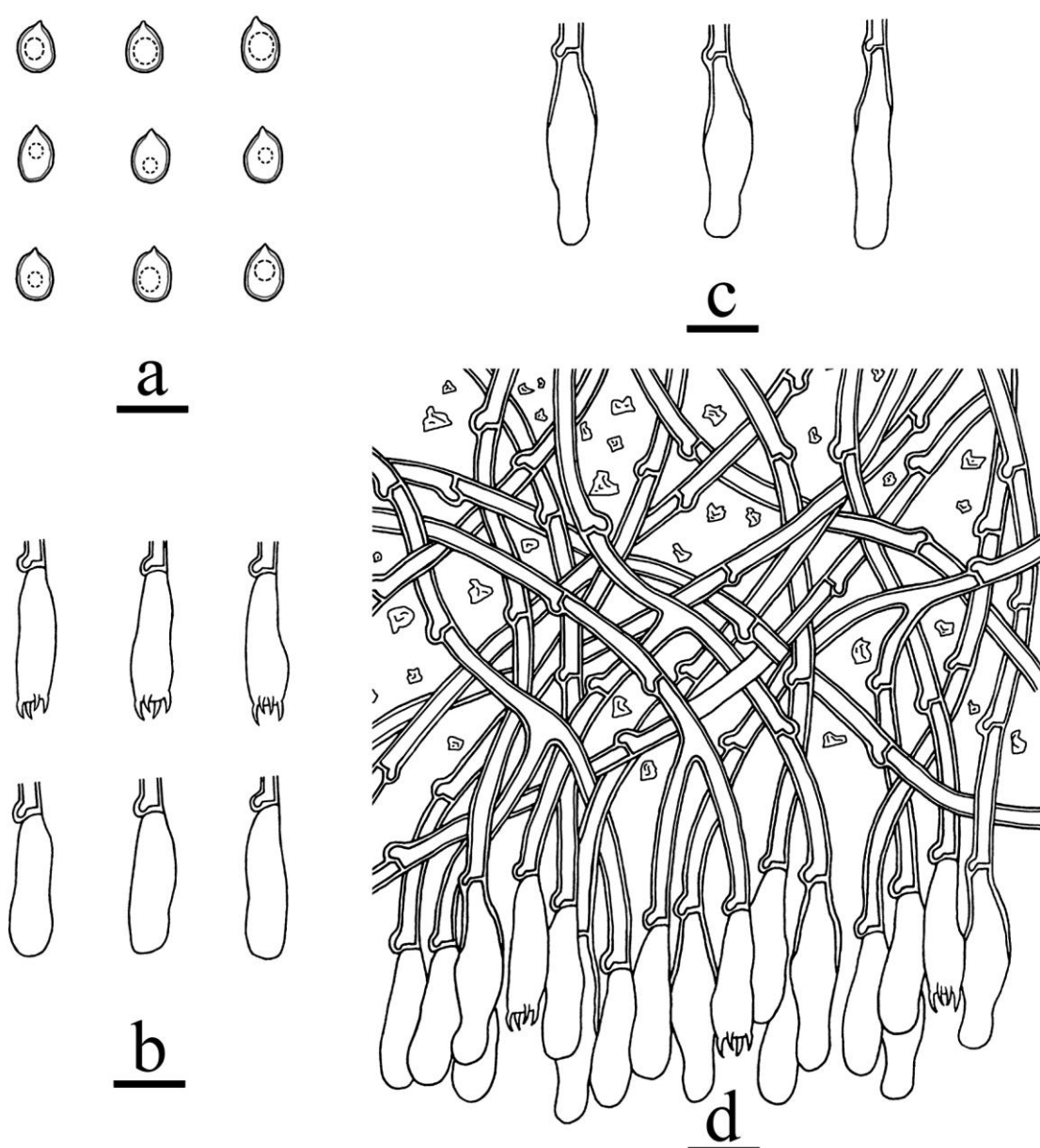


Figure 20 – Microscopic structures of *Collybiopsis yunnanensis* (holotype, CLZhao 22546). a Basidiospores. b Basidia and basidioles. c Capitata cystidia. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 μm .

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 ($\equiv$ *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 pseudomphaliiformis* Antonín & Ševčíková

Notes – *Marasmiellomycena* was introduced by Senanayake et al. (2023) to accommodate *M. pseudomphaliiformis* as the type. This genus contains agaricoid, saprotrophic species with omphaloid or marasmiod 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 *rpb2* analyses,

described one new species, *M. tomentosa* Q. Na & Y.P. Ge, and combined *Porothelium albodescendens* J.A. Cooper into *Marasmiellomyces*. 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 *Marasmiellomyces* is in the family *Porothelaceae* within *Agaricales*.

Note 34 *Pseudohydrops* Vizzini & Consiglio

Index Fungorum number: IF843195.

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

Notes – *Pseudohydrops* 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 *Pseudohydrops* have been described worldwide by Consiglio et al. (2021). Phylogenetic analyses based on ITS and nrLSU sequences indicated its phylogenetic position within *Porothelaceae* as sister to a clade consisting of *Porothelium* Fr. and *Pulverulina* Matheny & K.W. Hughes (Consiglio et al. 2021). Compared with the other genera within *Porothelaceae*, species of *Pseudohydrops* 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 *Pseudohydrops* is in the family *Porothelaceae* 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 *Porothelaceae*. 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 *rpb2* analyses, and described one new species, *Pulverulina flavoalba* Q. Na & Y.P. Ge. The taxonomic placement of *Pulverulina* is in the *Porothelaceae* 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 *Porothelium* sensu (Consiglio et al. 2021). This broad concept of *Porothelium* encompasses cypheloid *Porothelium* 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 *Porothelaceae* based on ITS and nrLSU sequences showed *Vizzinia* formed a distinct clade in the family *Porothelaceae*. Based on a multi-locus (ITS, nrLSU, and *rpb2*) analysis, Na et al. (2024) confirmed that *Vizzinia* was monophyletic and represents a separate genus. The taxonomic placement of *Vizzinia* is in the family *Porothelaceae* (*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 (Cléménçon 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, *tefl*- α , *rpb1*, and *rpb2* 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. & Ryvar den

Index Fungorum number: IF17382.

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

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 & Ryvar den 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. & Ryvar den 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. & Ryvar den and *Merulicium* J. Erikss. & Ryvar den (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 *rpb2* 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 *rpb2* 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 *rpb2* 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+*rpb2* 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+*rpb2* 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+*rpb1+rpb2+tef1-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+*rpb2* 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 & Ryvar den 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, Zibarová & Tejkllová 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 hydroid 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 Höhnelt & 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+*rpb1+rpb2+tef1-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+*rpb1+rpb2+tef1-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+*rpb1*+*rpb2*+*tef1*- 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).

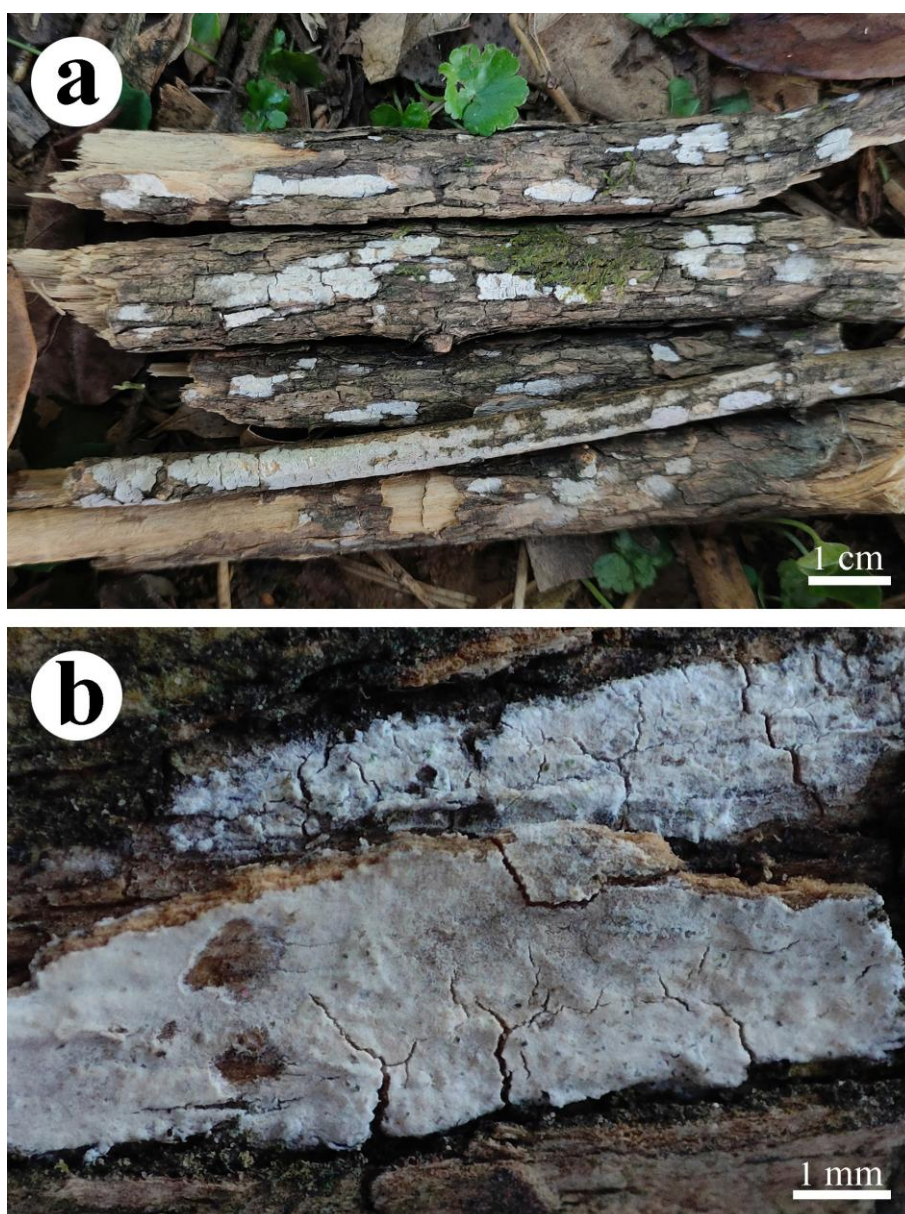


Figure 21 – Basidiomata of *Dendrothele fissurata* (holotype, CLZhao 35015).

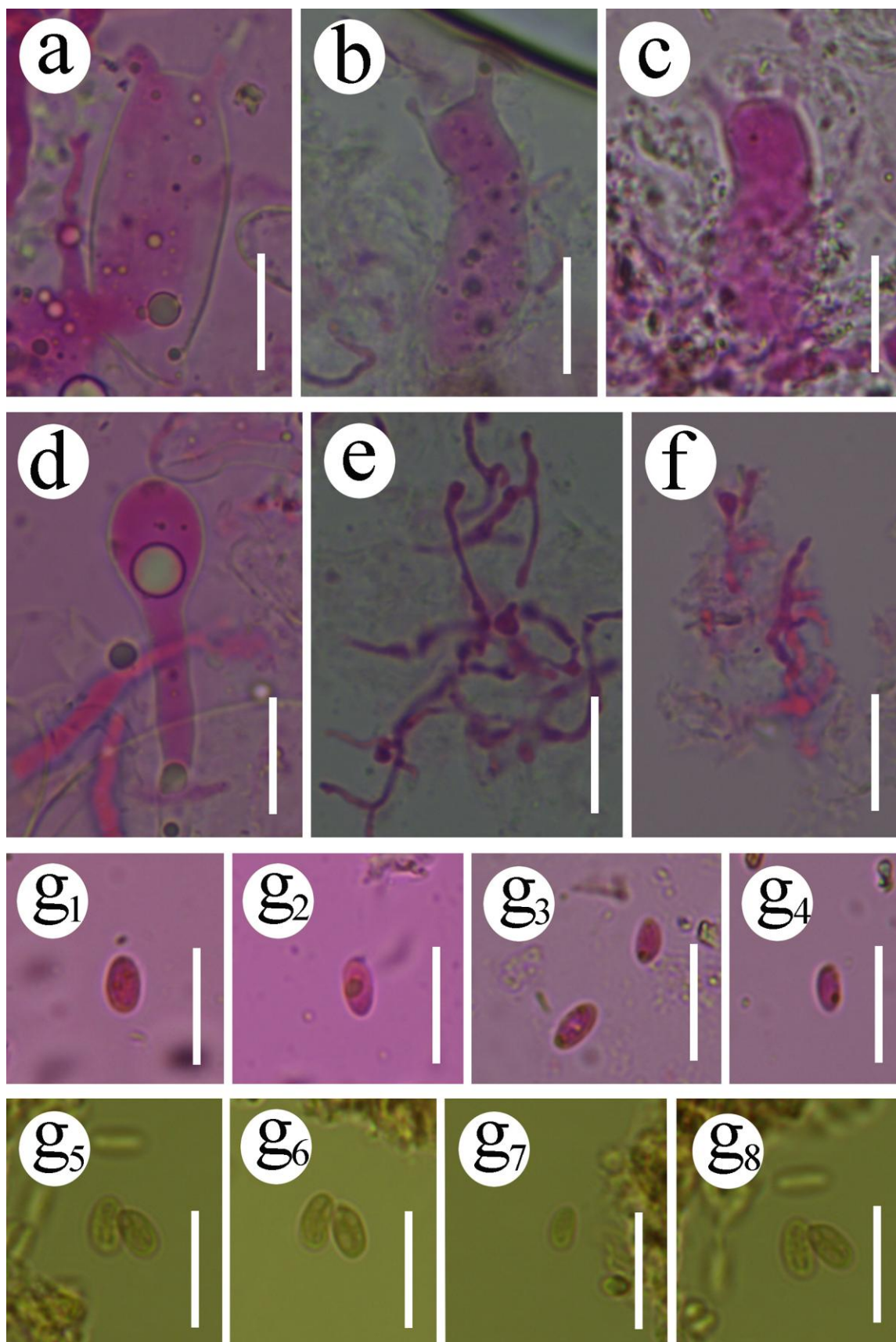


Figure 22 – Microscopic structures of *Dendrothele fissurata* (holotype, CLZhao 35015). a–c Basidia. d Cystidia. e–f Dendrohyphidia. g Basidiospores. Scale bars: a–g = 10 μm.

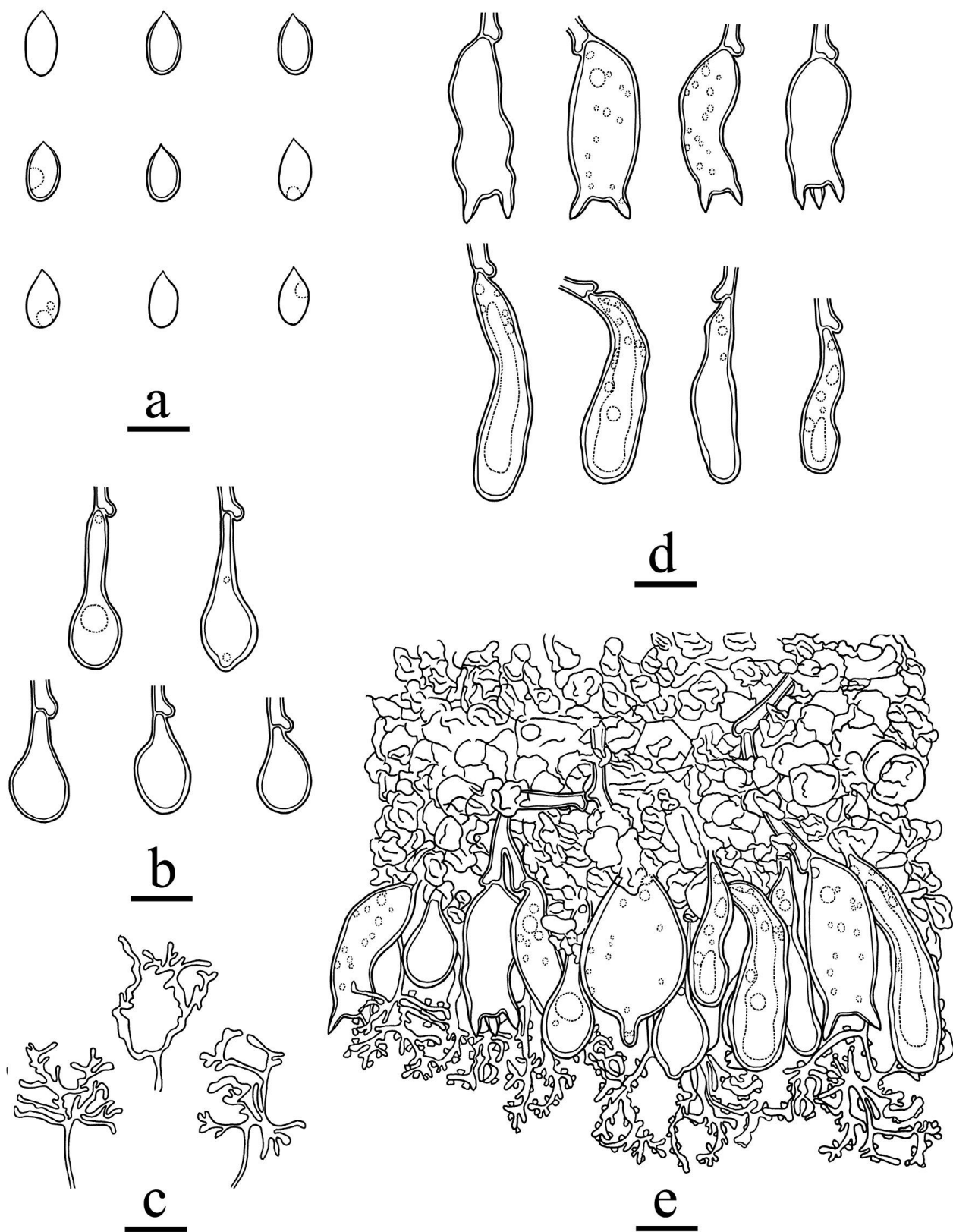


Figure 23 – Microscopic structures of *Dendrothele fissurata* (holotype, CLZhao 35015). a Basidiospores. b Cystidia. c Dendrohyphidia. d Basidia and basidioles. e A section of the hymenium and subhymenium. Scale bars: a = 5 μm ; b–d = 10 μm .

Gracilihypha albohymenia J.H. Dong & C.L. Zhao, sp. nov.
Index Fungorum number: IF858348.

Figs. 24–26

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).

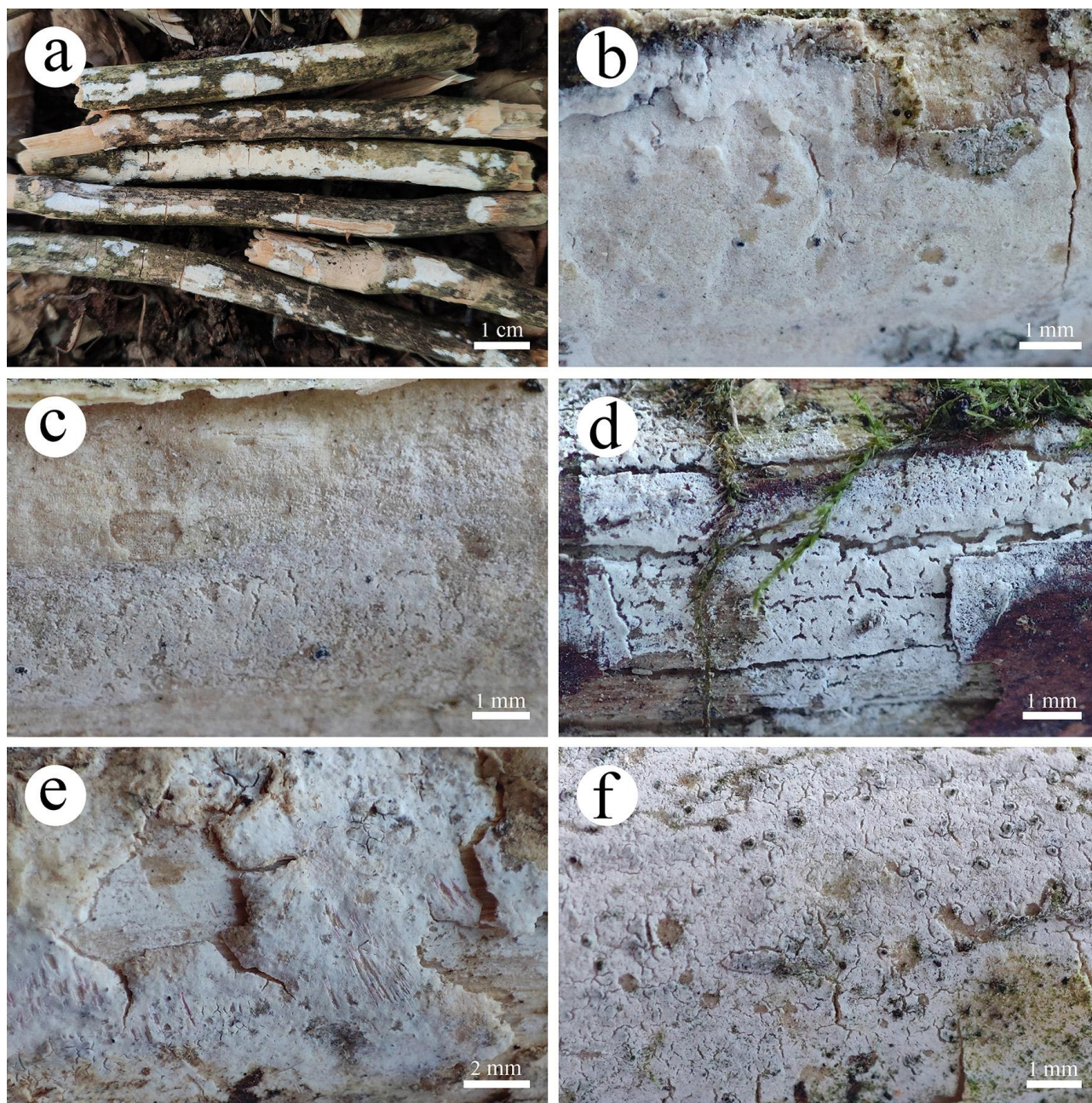


Figure 24 – Basidiomata of *Gracilihypha albohymenia* a, b CLZhao 33069 (holotype). c CLZhao 29603. d CLZhao 31757. e CLZhao 32417. f CLZhao 33502.

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 μ m 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 μ m in diameter; IKI–, CB–; tissues unchanged in KOH. Cystidia fusiform, colorless, thin-walled, 32.5–40 $\times$ 10.5–14.5 μ m; cystidioles absent. Basidia clavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, 31.5–52 $\times$ 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) $\times$ (8.5–)8.7–12.5 μm , L = 12.12 μm , W = 10.46 μm , Q = 1.08–1.30, $Q_m = 1.16 \pm 0.06$ (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+rpb1+rpb2+tef1- 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 $\times$ 8.5–10.5 μm vs 32.5–40 $\times$ 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 $\times$ 8.5–10.5 μm ; cystidioles absent. Basidia clavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, 30–35.5 $\times$ 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) $\times$ (7–)7.3–9(–9.5) μm , L = 10.11 μm , W = 7.92 μm , Q = 1.16–1.40, $Q_m = 1.28 \pm 0.07$ (n = 30/1).

Notes – *Gracilihypha yunnanensis* grouped in *Gracilihypha* (Cyphellopsidaceae, Agaricales) based on the ITS+nrLSU+rpb1+rpb2+tef1- 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 $\times$ 10.5–14.5 μm vs 20–32.5 $\times$ 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+rpb1+rpb2+tef1- α sequence data.

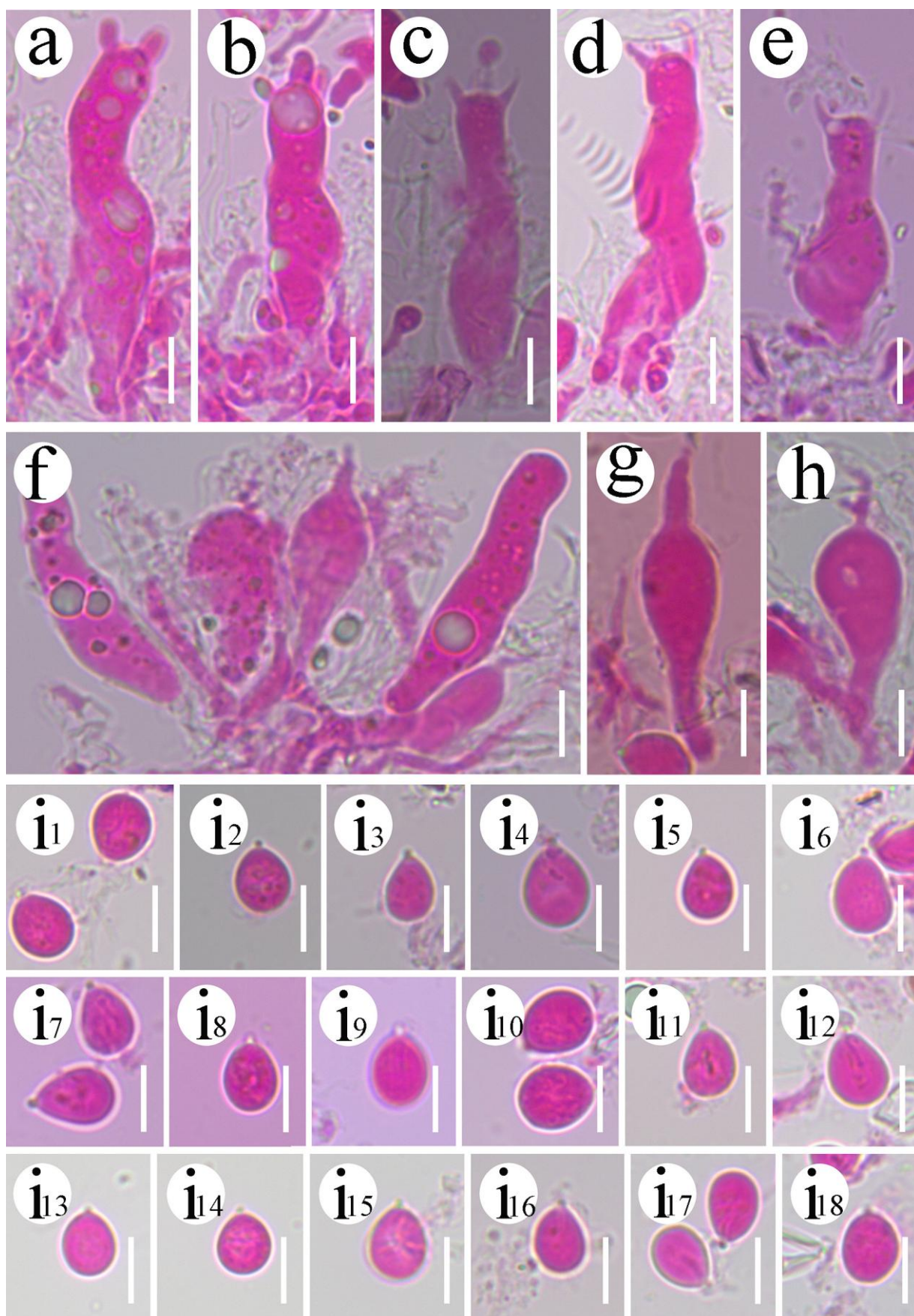


Figure 25 – Microscopic structures of *Gracilihypha albohymenia* (holotype, CLZhao 33069). a–e Basidia. f A section of the hymenium and subhymenium. g–h Cystidia. i Basidiospores. Scale bars: a–i = 10 μ m.

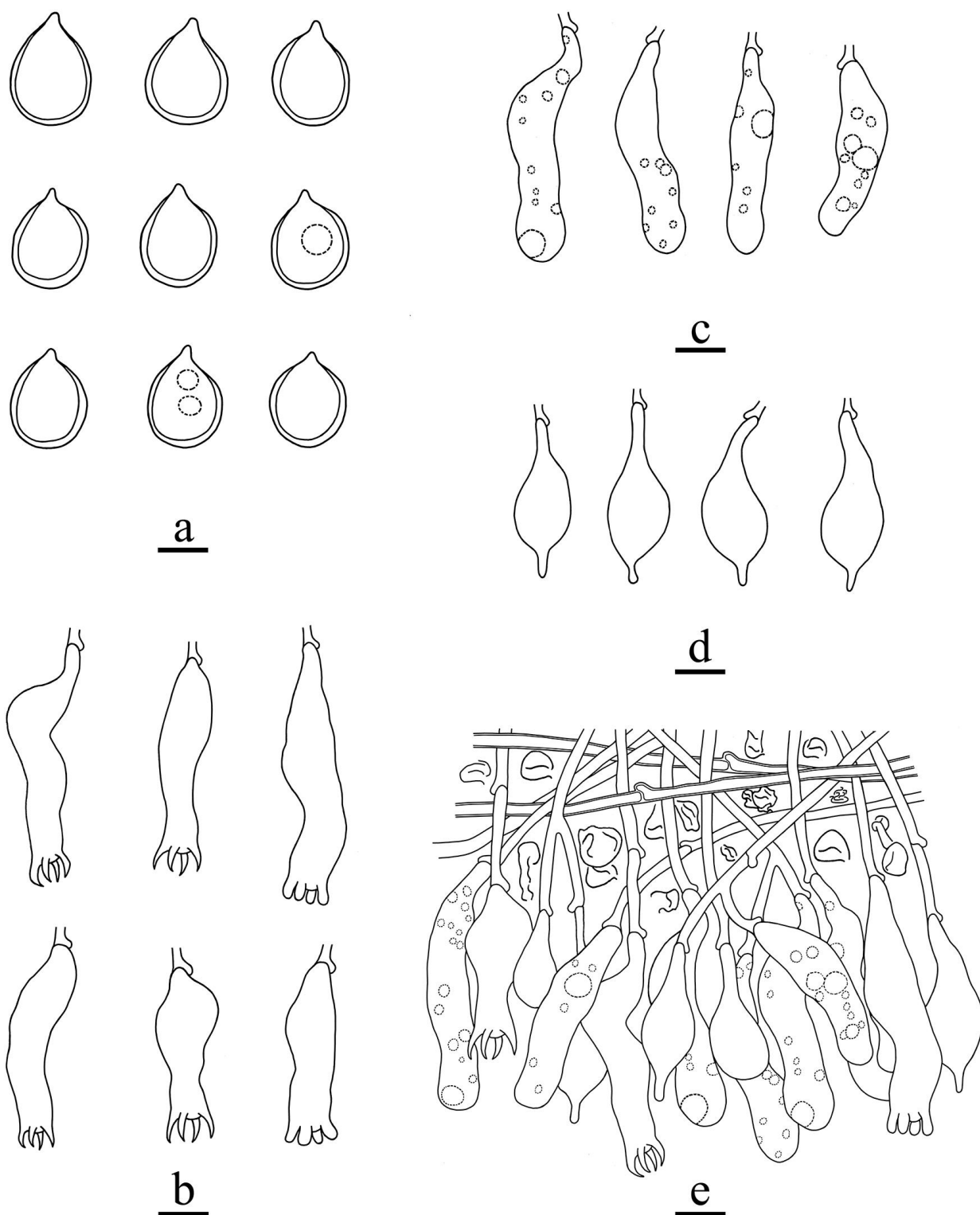


Figure 26 – Microscopic structures of *Gracilihypha albohymenia* (holotype, CLZhao 33069). a Basidiospores. b Basidia. c Basidioles. d Cystidia. e A section of the hymenium and subhymenium. Scale bars: a = 5 μ m; b–d = 10 μ m.

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 smooth, graninoid. 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).

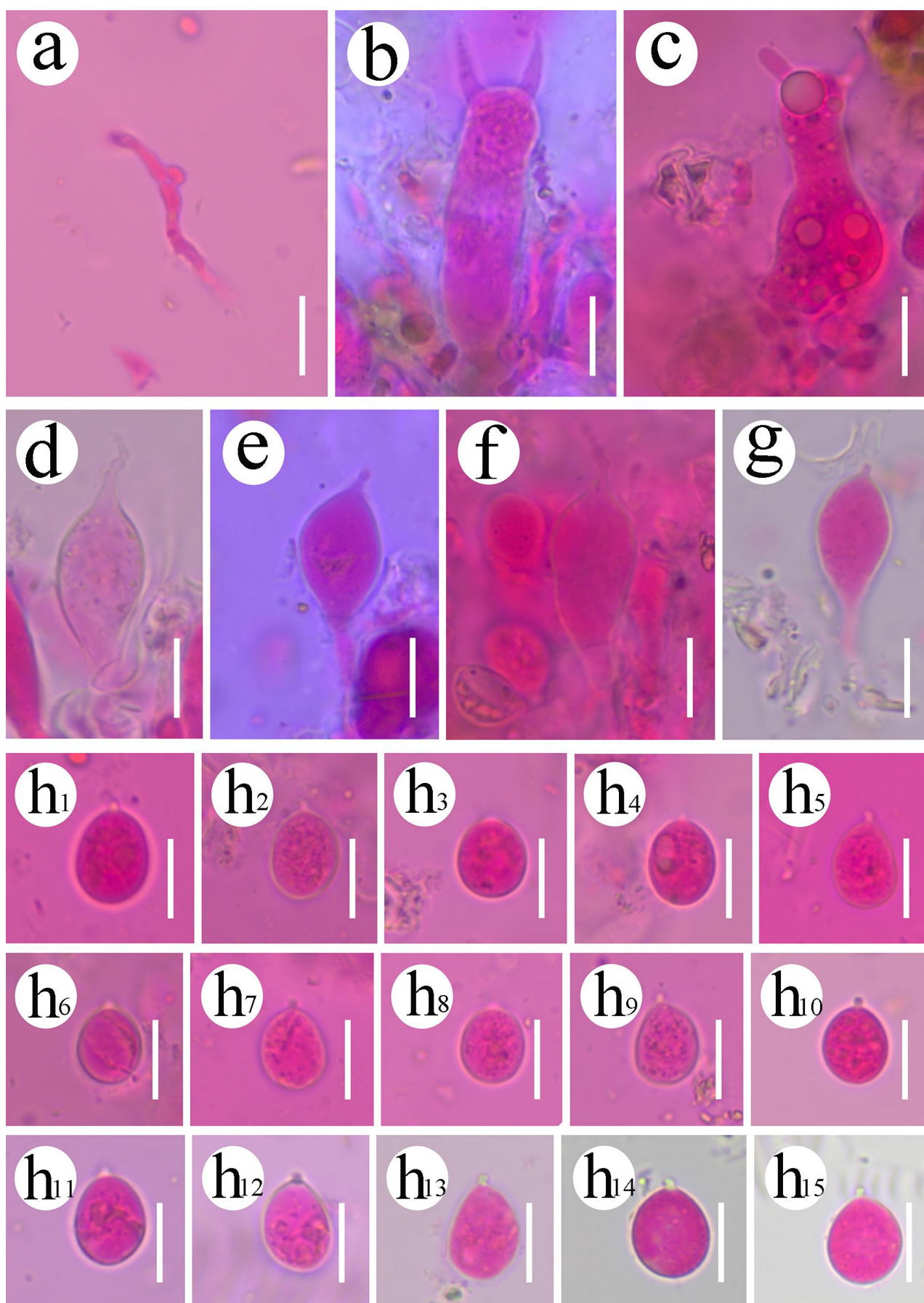


Figure 28 – Microscopic structures of *Gracilihypha yunnanensis* (holotype, CLZhao 32826). a Generative hypha. b–c Basidia. d–g Cystidia. h Basidiospores. Scale bars: a–h = 10 μ m.

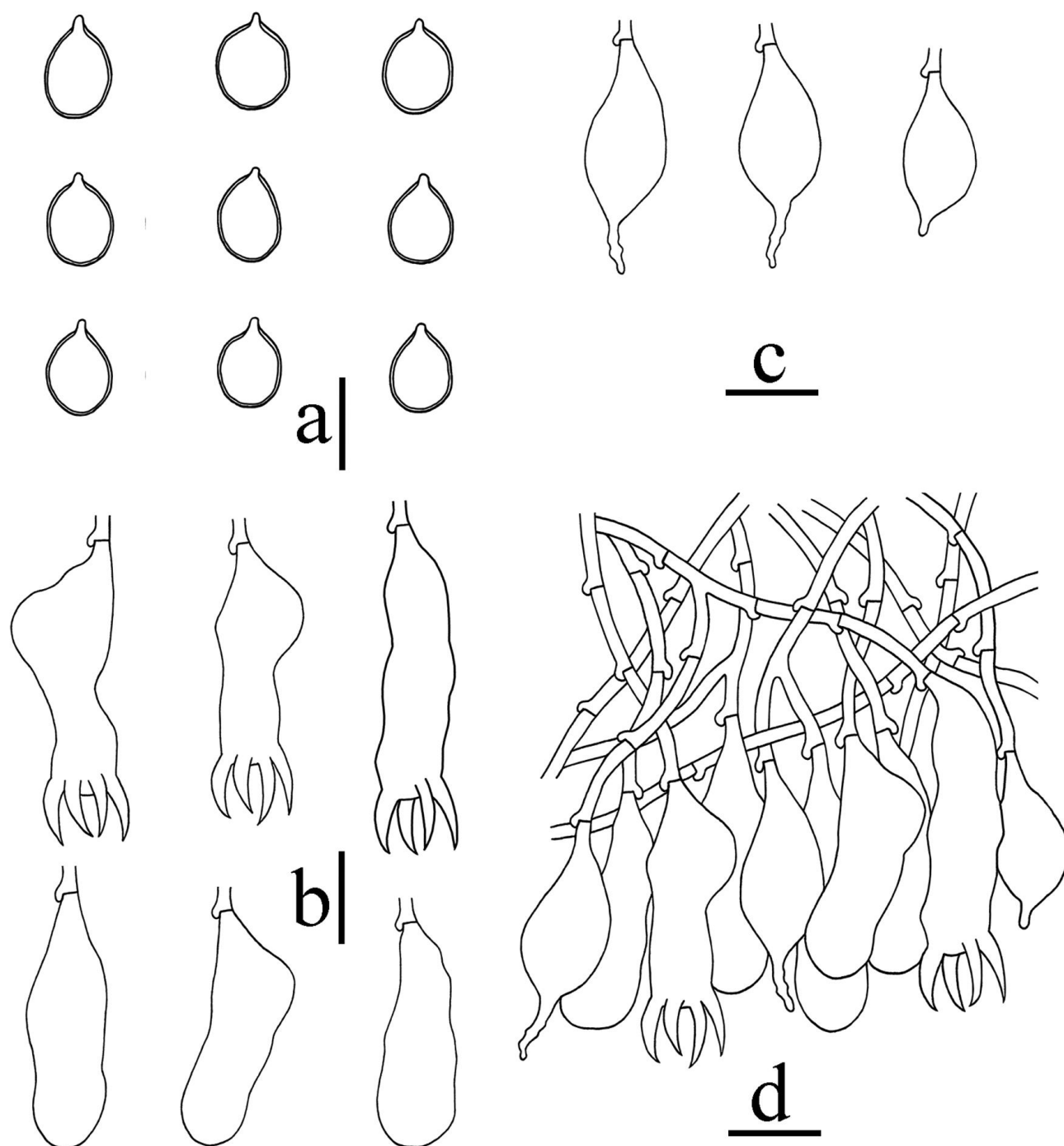


Figure 29 – Microscopic structures of *Gracilihypha yunnanensis* (holotype, CLZhao 32826). a Basidiospores. b Basidia and basidioles. c Cystidia. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 μ m.

Notes – In our phylogenetic analyses based on the ITS+nrLSU+rpb1+rpb2+tef1- 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 graninoid, 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, Dagan 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+*rpb1*+*rpb2*+*tef1*-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) 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, Mugu 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).

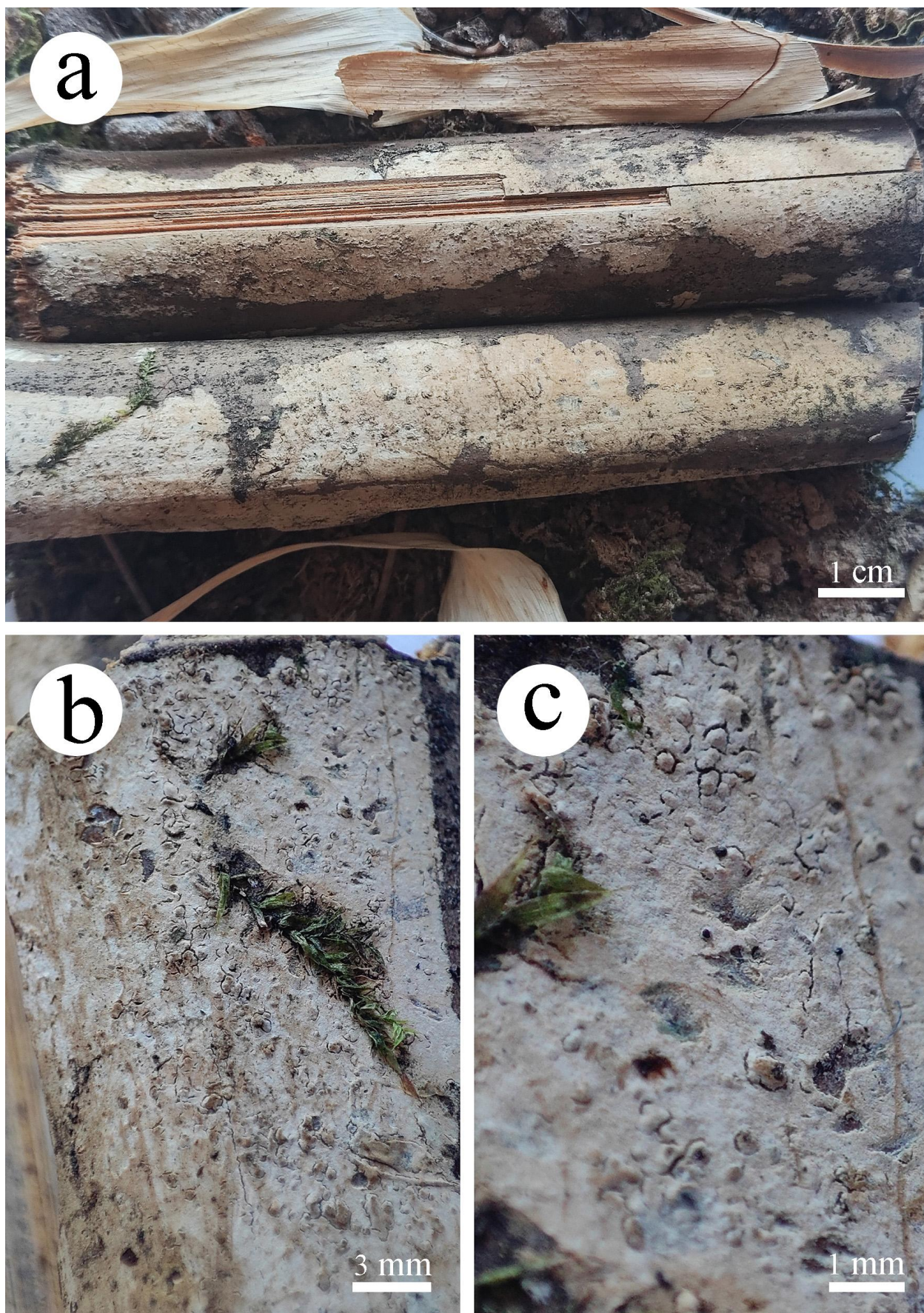


Figure 30 – Basidiomata of *Sicyoideibasidia bambusicola* (holotype, CLZhao 31774).

Notes – Based on the ITS+nrLSU+*rpb1*+*rpb2*+*tef1*- 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 ($20\text{--}28.5 \times 4\text{--}6.5 \mu\text{m}$ vs $29\text{--}35.5 \times 5.5\text{--}7.5 \mu\text{m}$).

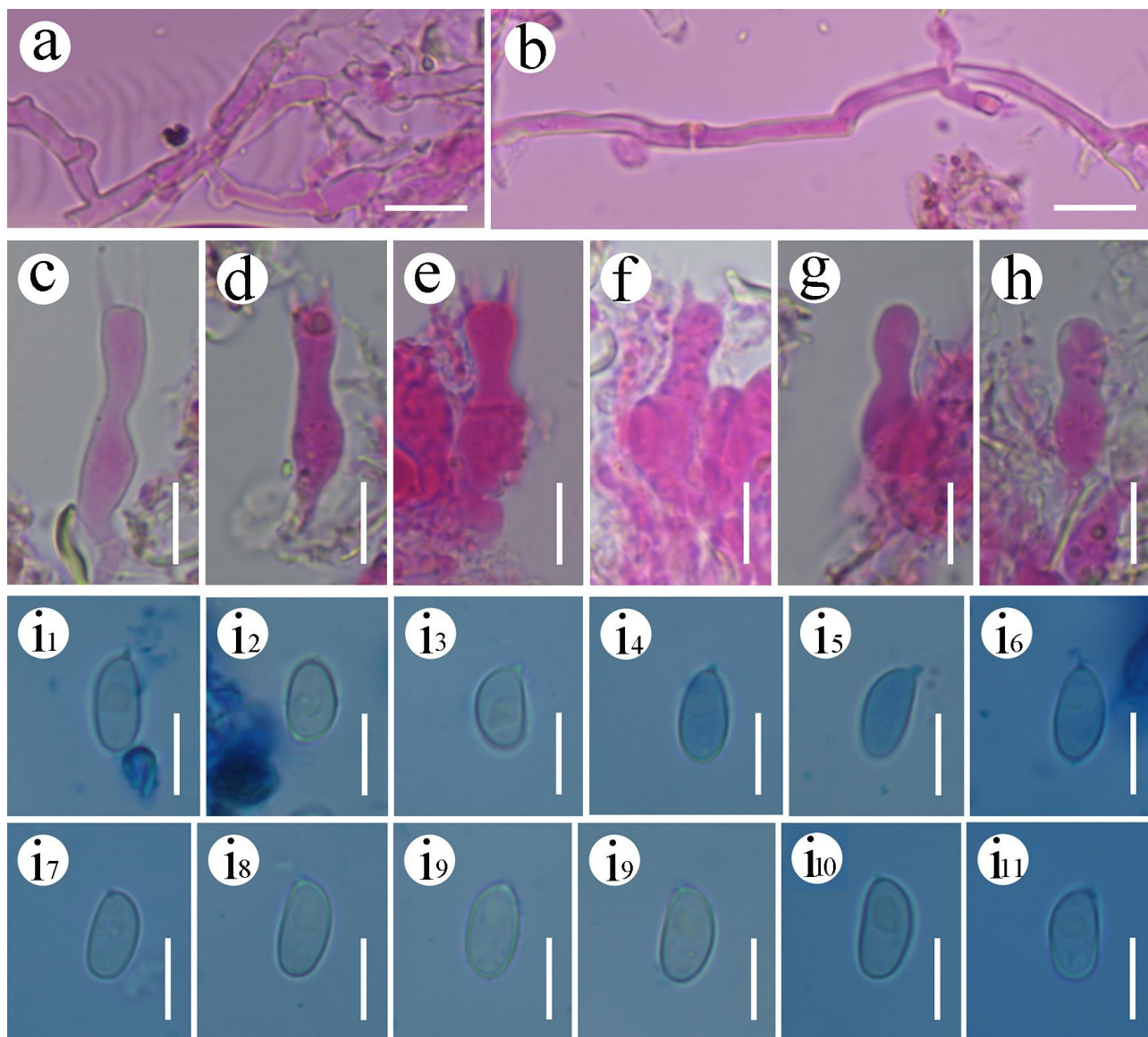


Figure 31 – Microscopic structures of *Sicyoideibasidia bambusicola* (holotype, CLZhao 31774). a–b Generative hyphae. c–f Basidia. g–h Basidioles. i Basidiospores. Scale bars: a–i = 10 μm .

Family *Fistulinaceae* Lotsy

Index Fungorum number: IF80774.

Type genus – *Fistulina* Bull.

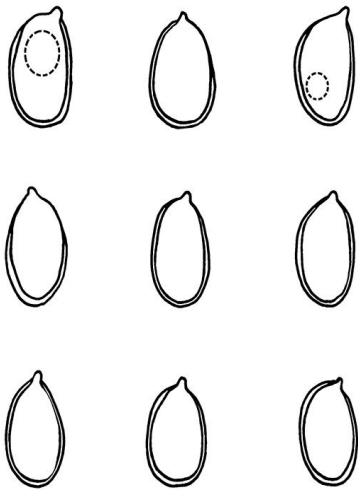
Note 59 *Fistulina* Bull.

Index Fungorum number: IF17591.

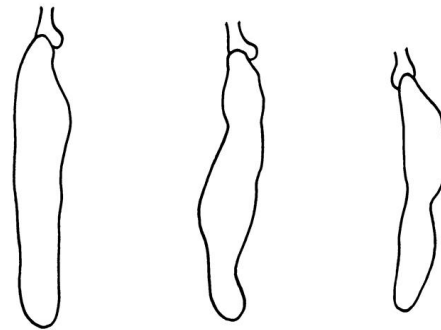
Type species – *Fistulina hepatica* (Schaeff.) With.

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

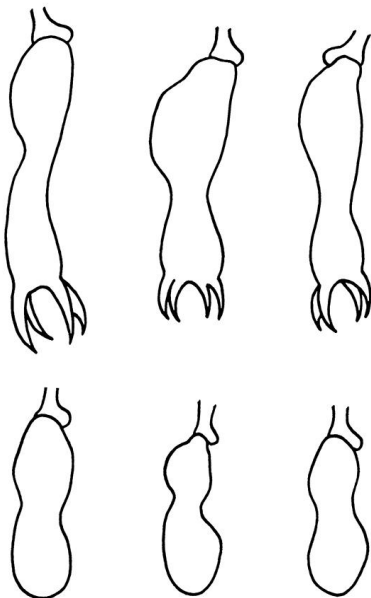
hyphal system with clamp connections, some with simple septa, cystidial elements present at dissepimental edges, hyaline, thin- to thick-walled basidiospores that are cyanophilous, and the degradation of hardwoods as a brown rot (Ryvarden & Melo 2017). It is a cosmopolitan genus with ten accepted species, 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).



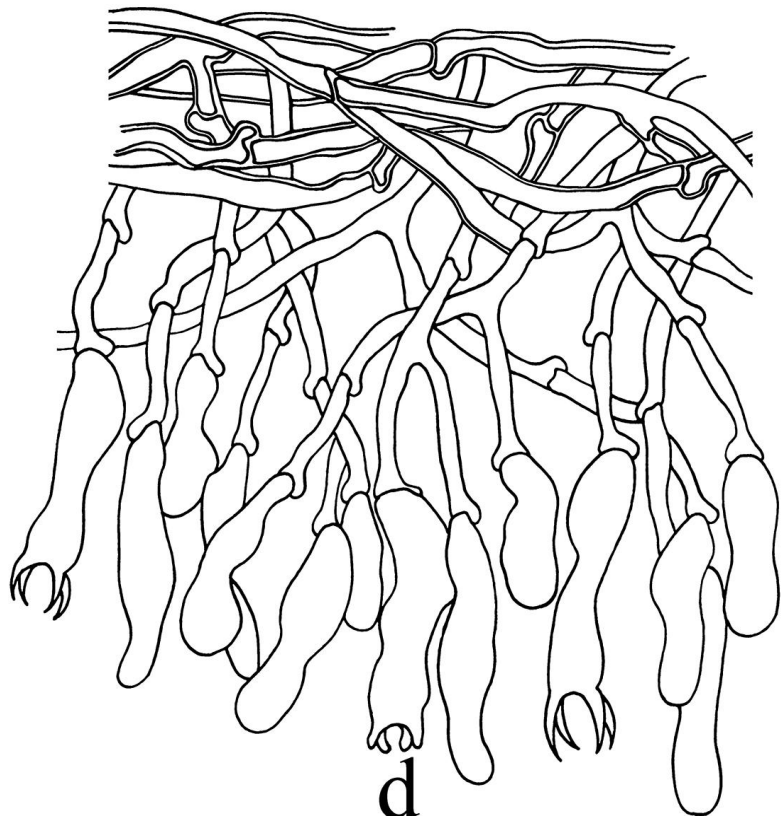
a



c



b



d

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*.

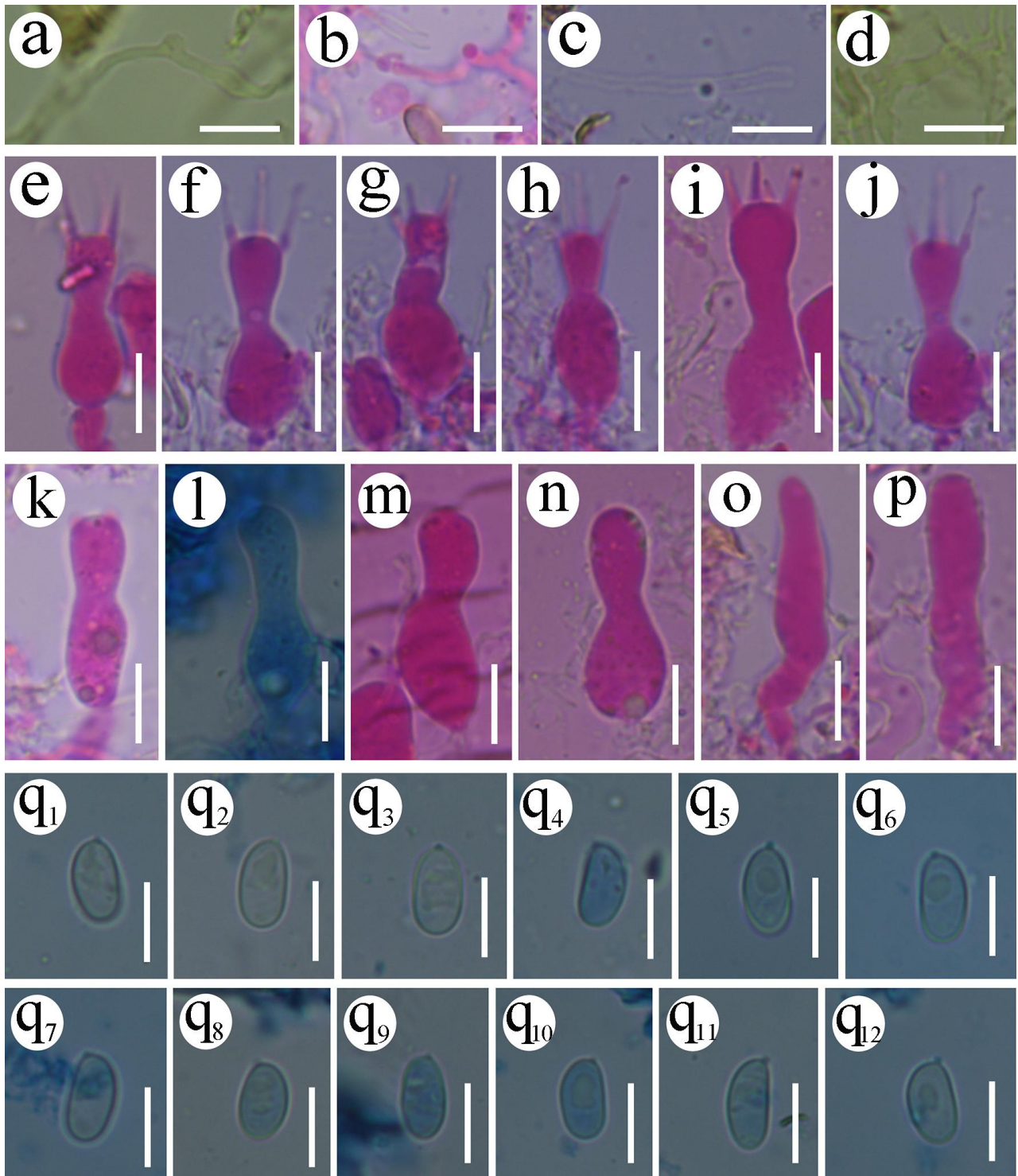


Figure 34 – Microscopic structures of *Sicyoideibasidia punctata* (holotype, CLZhao 35563). a–d Generative hyphae. e–j Basidia. k–n Basidioles. o–p Cystidia. q Basidiospores. Scale bars: a–q = 10 μ m.

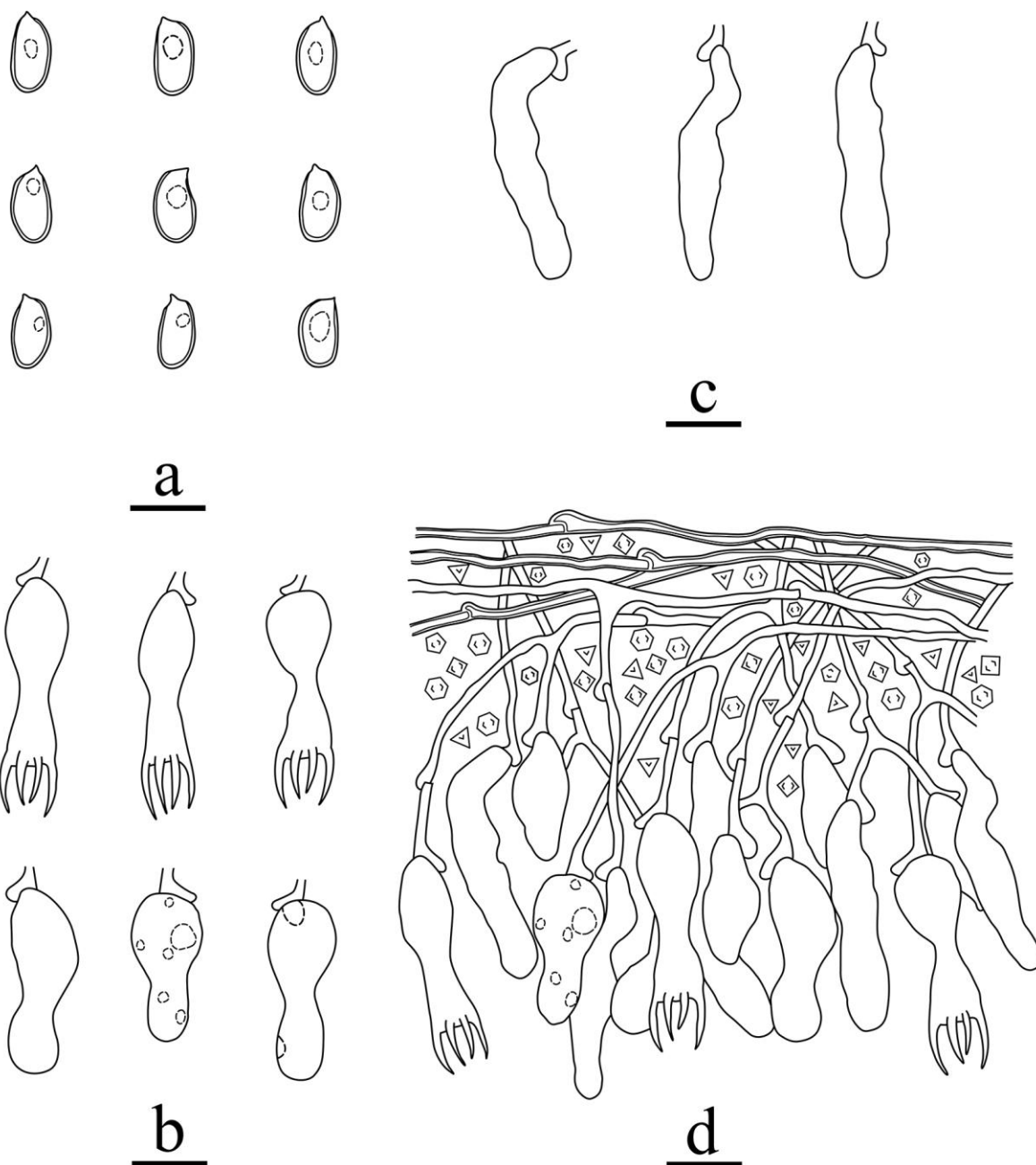


Figure 35 – Microscopic structures of *Sicyoideibasidia punctata* (holotype, CLZhao 35563). a Basidiospores. b Basidia and basidioles. c Cystidia. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 μ m.

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 *tef1-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 merulioioid 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* Carpouren & Raspé, and *R. yunnanensis* Yang Yang & C.L. Zhao (Yang et al. 2023, Carpouren et al. 2024, Liu et al. 2024a). In the present study, based on the ITS+nrLSU+*rpb1*+*rpb2*+*tef1-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+*rpb1*+*rpb2*+*tef1-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. vinosolivoidus* (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, Carpouren 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).

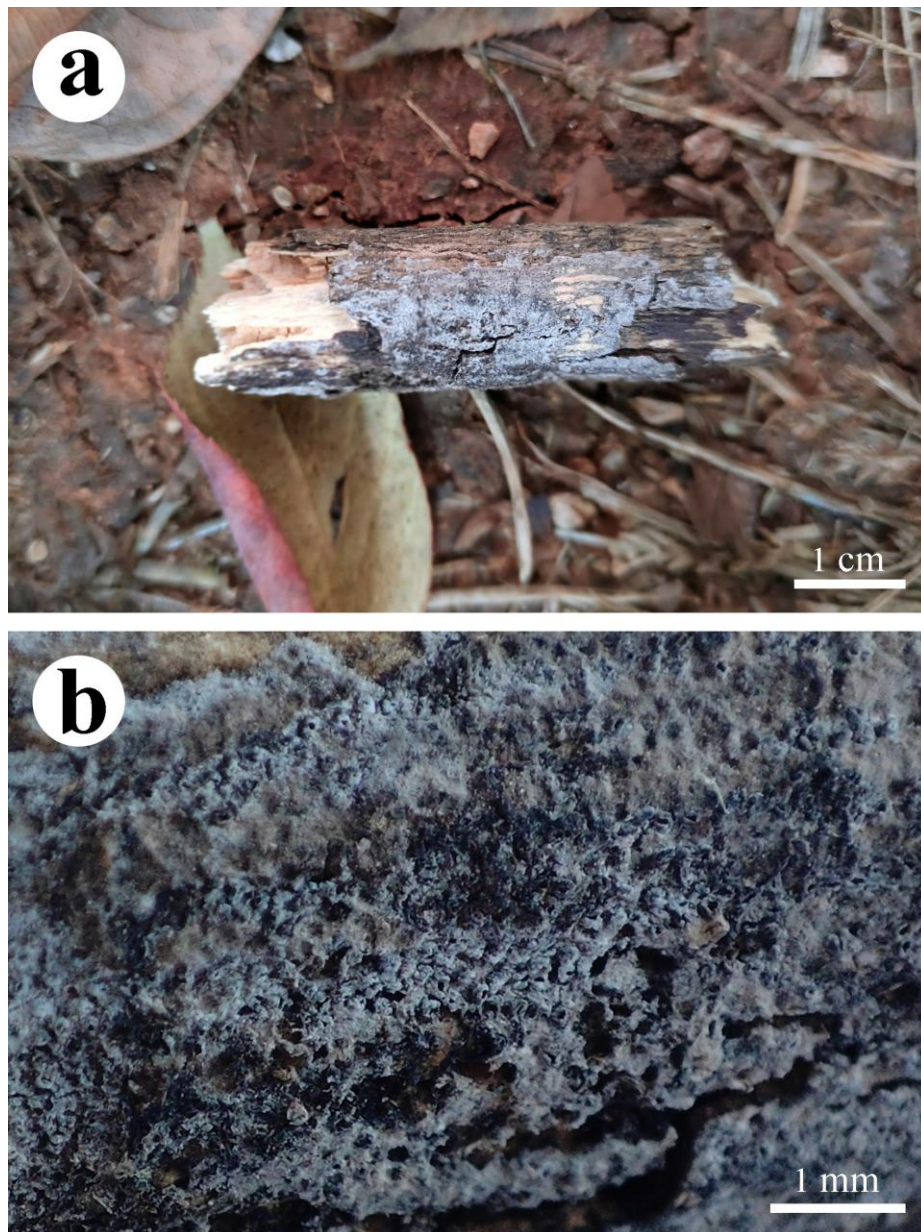


Figure 36 – Basidiomata of *Resupinatus tenuis* (holotype, CLZhao 34892).

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).

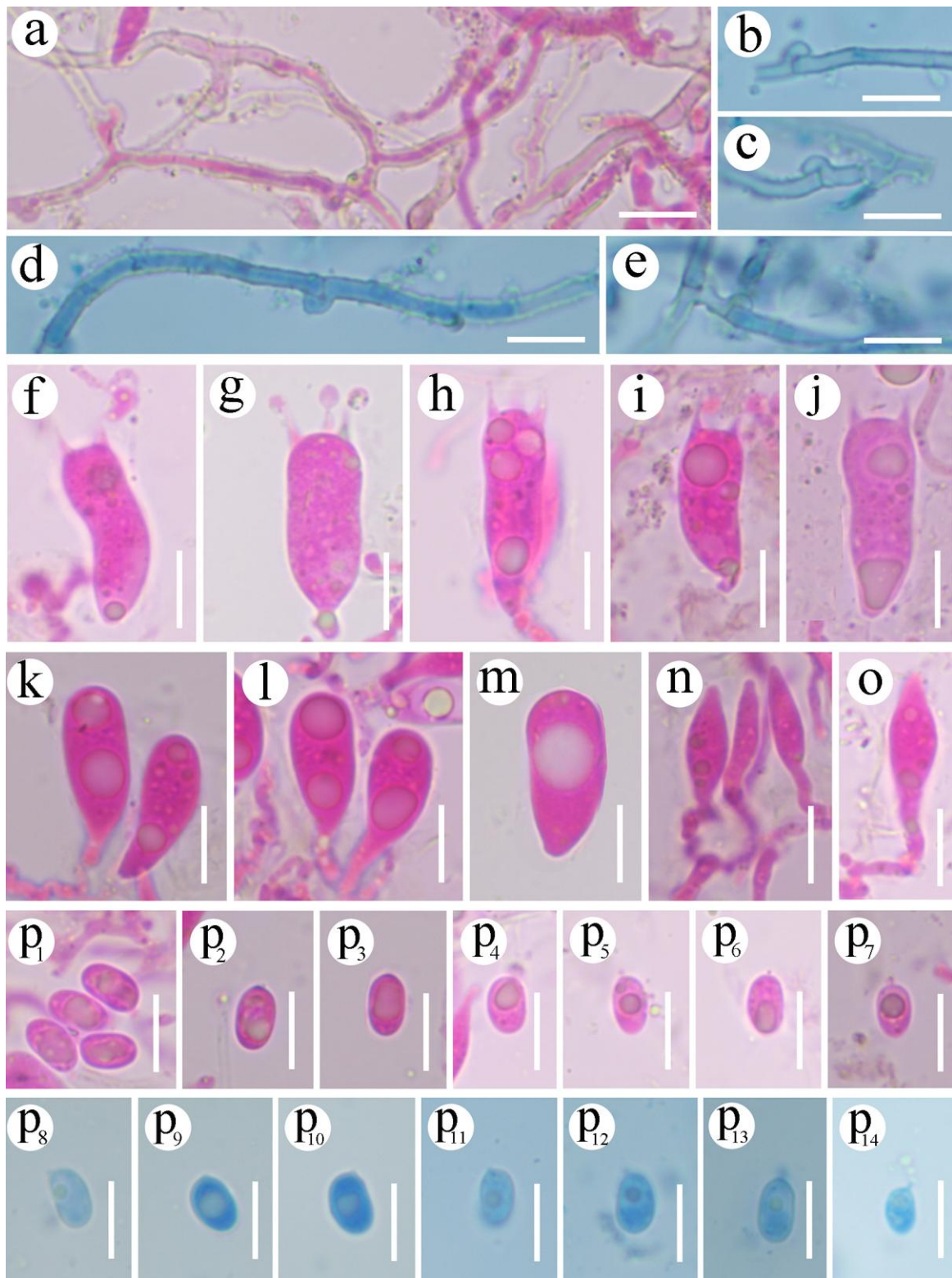


Figure 37 – Microscopic structures of *Resupinatus tenuis* (holotype, CLZhao 34892). a–e Generative hyphae. f–j Basidia. k–m Basidioles. n–o Cystidioles. p Basidiospores. Scale bars: a–p = 10 μm.

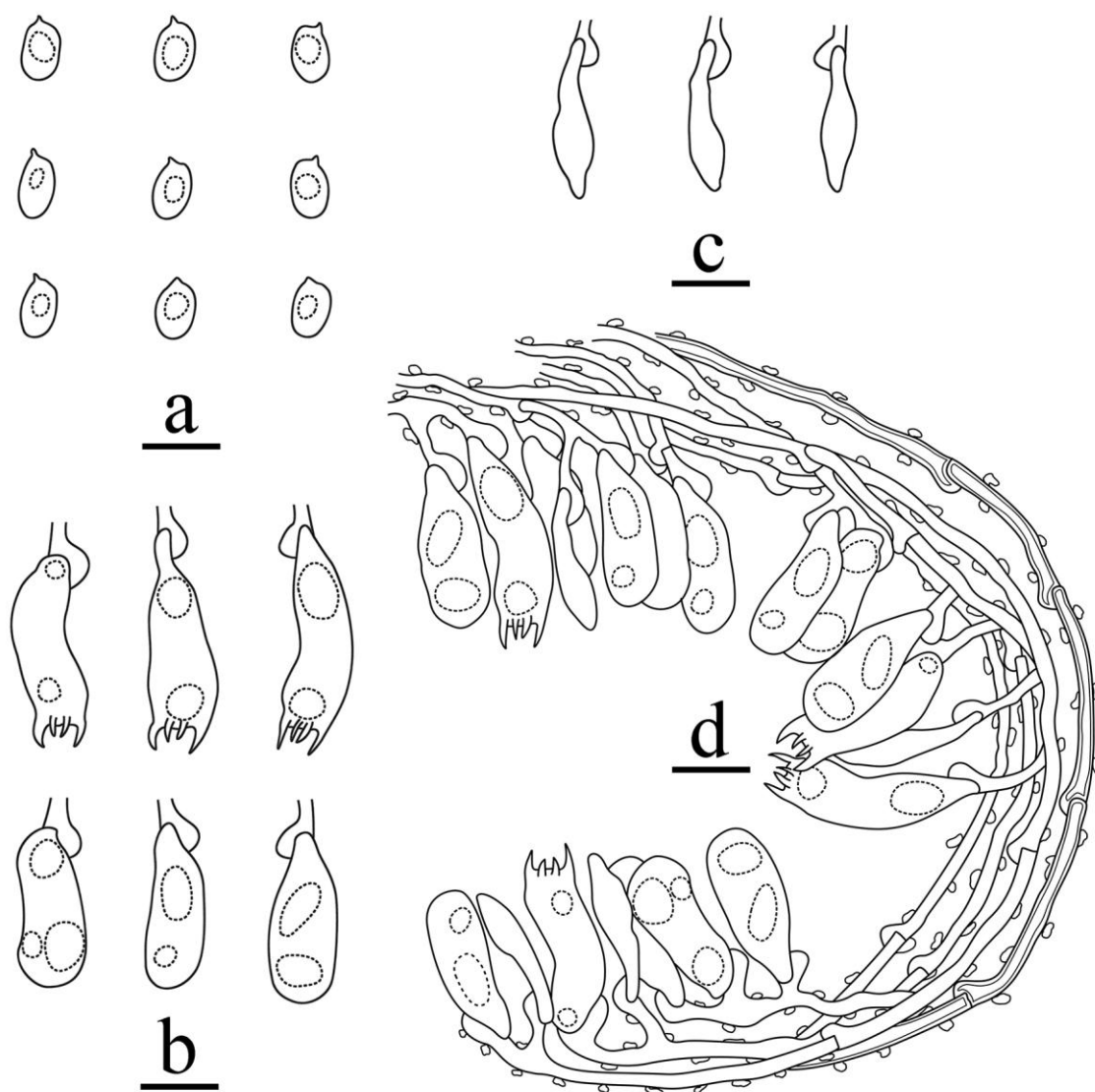


Figure 38 – Microscopic structures of *Resupinatus tenuis* (holotype, CLZhao 34892). a Basidiospores. b Basidia and basidioles. c Cystidioles. d A section of the hymenium and subhymenium. Scale bars: a–d = 10 μ m.

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+*rpb1+rpb2+tefl-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, *rpb2*, and *tefl-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+*rpb1*+*rpb2*+*tefl-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+*rpb1*+*rpb2*+*tefl-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+*rpb1+rpb2+tefl-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 (*rpb1*, *rpb2*, 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+*rpb1+rpb2+tefl-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+*rpb1*+*rpb2*+*tefl-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.

ACKNOWLEDGEMENTS

The research was supported by the National Natural Science Foundation of China (Project Nos. 32170004, U2102220), the Forestry and Grass Science and Technology Innovation Joint Project of Yunnan Province (Project No. 202404CB090008), the Forestry Innovation Programs of Southwest Forestry University (Grant No: LXXK-2023Z07), the High-level Talents Program of Yunnan Province (YNQR-QNRC-2018-111), the Research Project of Key Laboratory of Forest Disaster Warning and Control in Universities of Yunnan Province (ZKJS-S-202208), and the Yunnan Province College Students Innovation and Entrepreneurship Training Program (Project no. S202410677022).

DECLARATION ON CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

REFERENCES

- Abdel-Wahab MA, Jones EBG, Abdel-Aziz FA, Bahkali AH. 2019 – *Nia lenicarpa* sp. nov. (*Niaceae*, *Agaricales*) from Red Sea mangroves in Saudi Arabia with comments on *Nia vibrissa*. *Phytotaxa* 406, 157–168.
- Agerer R. 1973 – *Rectipilus*, eine neue Gattung cyphelloider Pilze. *Persoonia* 7, 389–436.
- Agerer R. 1979 – Typusstudien an cyphelloiden Pilzen 2. *Rectipilus erubescens*. *Sydowia* 32, 1–4.
- Agerer R. 1983 – Typus studien an cyphelloiden Pilzen 4. *Lachnella* Fr. s.l. *Mitteilungen aus der Botanischen Staatssammlung München* 19, 163–334.
- Aime MC, Phillips-Mora W. 2005 – The causal agents of witches' broom and frosty pod rot of cacao (chocolate, *Theobroma cacao*) form a new lineage of *Marasmiaceae*. *Mycologia* 97, 1012–1022.

- Alvarado P, Moreau PA, Dima B, Vizzini A et al. 2018a – *Pseudoclitocybaceae* fam. nov. (*Agaricales*, *Tricholomatineae*), a new arrangement at family, genus and species level. *Fungal Diversity* 90, 109–133.
- Alvarado P, Moreau PA, Sesli E, Khodja LY et al. 2018b – Phylogenetic studies on *Bonomyces* (*Tricholomatineae*, *Agaricales*) and two new combinations from *Clitocybe*. *Cryptogamie Mycologie* 39, 149–168.
- Alvarenga RLM, Gibertoni TB. 2021 – *Crystallodon* Alvarenga gen. nov., a new genus of the *Auriculariales* from the Neotropics. *Cryptogamie Mycologie* 42, 17–24.
- Alvarenga RLM, Spirin V, Malysheva V, Gibertoni TB et al. 2019 – Two new genera and six other novelties in *Heterochaete* sensu lato (*Auriculariales*, *Basidiomycota*). *Botany* 97, 439–451.
- Ammirati JF, Parker AD, Matheny PB. 2007 – *Cleistocybe*, a new genus of *Agaricales*. *Mycoscience* 48, 282–289.
- Antonín V, Borovička J, Holec J, Piltaver A et al. 2019 – Taxonomic update of *Clitocybula* sensu lato with a new generic classification. *Fungal Biology* 123, 431–447.
- Antonín V, Buyck B. 2006 – *Marasmius* (*Basidiomycota*, *Marasmiaceae*) in Madagascar and the Mascarenes. *Fungal Diversity* 23, 17–50.
- Antonín V, Hosaka K, Kolařík M. 2023 – Taxonomy and phylogeny of *Paramarasmius* gen. nov. and *Paramarasmius mesosporus*, a worldwide distributed fungus with a strict ecological niche. *Plant Biosystems-An International Journal Dealing with all Aspects of Plant Biology* 157, 286–293.
- Antonín V, Noordeloos ME. 1993 – A monograph of *Marasmius*, *Collybia*, and related genera in Europe: *Marasmius*, *Setulipes*, and *Marasmiellus*. *Libri botanici* 8, 1–229.
- Antonín V, Noordeloos ME. 2010 – A monograph of marasmioid and collybioid fungi in Europe. IHW-Verlag, Eching, pp. 1–480.
- Antonín V, Ryoo R, Ka KH. 2014 – Marasmioid and gymnopoid fungi of the Republic of Korea 7. *Gymnopus* sect. *Androsacei*. *Mycological Progress* 13, 703–718.
- Antonín V, Ryoo R, Shin HD. 2012 – Marasmioid and gymnopoid fungi of the Republic of Korea 4. *Marasmius* sect. *Sicci*. *Mycological Progress* 11, 615–638.
- Azevedo E, Barata M, Caeiro MF. 2018 – Morphological and phylogenetic analyses of *Nia vibrissa*, a marine *Basidiomycota* collected in Portuguese waters. *Regional Studies in Marine Science* 23, 53–59.
- Baltazar JM, Gorj SP, Pildain B M, Rajchenberg M et al. 2015 – *Acanthocorticium brueggemannii*, a new corticioid genus and species related to cyphelloid fungi in the euagarics clade (*Agaricales*, *Basidiomycota*). *Botany* 93, 453–463.
- Bandini D, Oertel B, Eberhardt U. 2022 – More smooth-spored species of *Inocybe* (*Agaricales*, *Basidiomycota*): type studies and 12 new species from Europe. *Persoonia* 48, 91–149.
- Bau T, Yan JQ. 2021 – A new genus and four new species in the *Psathyrella* s.l. clade from China. *MycoKeys* 80, 115–131.
- Bellanger JM, Lebeuf R, Sesli E, Loizides M et al. 2021 – *Hygrophorus* sect. *Olivaceoumbrini*: new boundaries, extended biogeography and unexpected diversity unravelled by transatlantic studies. *Persoonia* 46, 272–312.
- Berkeley MJ. 1856 – Decades of fungi. Decades LI - LIV. Rio Negro fungi. *Hooker's Journal of Botany and Kew Garden Miscellany* 8, 129–144.
- Bernicchia A, Gorjón SP. 2010 – *Fungi Europaei* 12: *Corticiaceae* s.l. Edizioni Candusso, Alassio, Italy, pp. 1–1008.
- Bhunjun CS, Niskanen T, Suwannarach N, Wannathes N et al. 2022 – The numbers of fungi: are the most speciose genera truly diverse? *Fungal Diversity* 114, 387–462.
- Bijeesh C, Kumar AM, Pradeep CK. 2020 – A new species of *Resupinatus* (*Agaricomycetes*) with merulioid hymenophore from India. *Phytotaxa* 464, 167–174.
- Binder M, Hibbett DS. 2002 – Higher-level phylogenetic relationships of *Homobasidiomycetes* (mushroom-forming fungi) inferred from four rDNA regions. *Molecular Phylogenetics and Evolution* 22, 76–90.

- Binder M, Hibbett DS, Larsson KH, Larsson E et al. 2005 – The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (*Homobasidiomycetes*). *Systematics and Biodiversity* 3, 113–157.
- Binder M, Hibbett DS, Molitoris HP. 2001 – Phylogenetic relationships of the marine gasteromycete *Nia vibrissa*. *Mycologia* 93, 679–688.
- Binder M, Hibbett DS, Wang Z, Farnham WF et al. 2006 – Evolutionary relationships of *Mycaureola dilseae* (*Agaricales*), a basidiomycete pathogen of a subtidal rhodophyte. *American Journal of Botany* 93, 547–556.
- Bodensteiner P, Binder M, Moncalvo JM, Agerer R et al. 2004 – Phylogenetic relationships of cyphelloid homobasidiomycetes. *Molecular Phylogenetics and Evolution* 33, 501–515.
- Bondar VS, Puzyr AP, Purtov K, Petunin AI et al. 2014 – Isolation of luminescence system from the luminescent fungus *Neonothopanus nambi*. *Doklady Biochemistry and biophysics* 455, 346–348.
- Boonmee S, Wanasinghe DN, Calabon MS, Huanraluek N et al. 2021 – Fungal Diversity notes 1387–1511: taxonomic and phylogenetic contribution on genera and species of fungal taxa. *Fungal Diversity* 111, 1–335.
- Bougher NL. 2007 – The genus *Campanella* in Western Australia. *Mycotaxon* 99, 327–336.
- Brodie HJ. 1975 – *The Bird's Nest Fungi*. University of Toronto Press, Canada. pp. 1–999.
- Bua-art S, Saksirirat W, Hiransalee A, Kanokmedhakul S et al. 2011 – Effect of bioactive compound from luminescent mushroom (*Neonothopanus nambi* Speg.) on root-knot nematode (*Meloidogyne incognita* Chitwood) and non-target organisms. *Asia-Pacific Journal of Science and technology* 16, 331–341.
- Bulliard P. 1791 – Histoire des champignons de la France: Ou, traité élémentaire renfermant dans un ordre méthodique les descriptions et les figures des champignons qui croissent naturellement en France, Vol. 1. Paris: Chez l'Auteur, 1–368.
- Cai Q, Lin WF, Liu JW, Zhou Y et al. 2023 – Two new species of *Sarcomyxa* (*Agaricales*) from China. *Mycological Progress* 22, 38.
- Cao T, Hu YP, Yu JR, Wei TZ et al. 2021 – A phylogenetic overview of the *Hydnaceae* (*Cantharellales*, *Basidiomycota*) with new taxa from China. *Studies in Mycology* 99, 100121.
- Capelari M. 2011 – New species and new records of *Crepidotus* from the northwest region of São Paulo state, Brazil. *Mycotaxon* 115, 145–153.
- Capelari M, Desjardin DE, Perry BA, Asai T et al. 2011 – *Neonothopanus gardneri*: a new combination for a bioluminescent agaric from Brazil. *Mycologia* 103(6), 1433–1440.
- Capelari M, Karstedt F, de Oliveira JJS. 2013 – *Favolaschia* in remnants of the Atlantic Forest, Brazil. *Mycoscience* 55, 12–20.
- Carpouron JE, Appadoo MA, Chomnunti P, Raspé O. 2024 – Taxonomy, phylogeny and ecology of a new bambusicolous *Resupinatus* species (*Agaricales*, *Resupinataceae*) from Northern Thailand. *Phytotaxa* 677, 195–206.
- Cejp K, Palmer JT. 1963 – The genera *Nidularia* Fr. and *Mycocalia* J. T. Palmer in Czechoslovakia and *Mycocalia sphagneti* J.T. Palmer sp. nov. from England. *Česká Mykology* 17, 113–133.
- César E, Bandala VM, Montoya L, Ramos A. 2018 – A new *Gymnopus* species with rhizomorphs and its record as nesting material by birds (Tyrannidae) in the subtropical cloud forest from eastern Mexico. *MycoKeys* 21(42), 21–34.
- Chang C, Chen C, Lin W, Kao HW. 2020 – *Mycena jingyinga*, *Mycena luguensis*, and *Mycena venus*: three new species of bioluminescent fungi from Taiwan. *Taiwan Journal of Biodiversity* 65, 396–406.
- Chen J, Liu HG, Chang P, Yuan Y et al. 2025 – Insight into the *Gastrodia elata* microbiome and its relationship with secondary metabolites. *Industrial Crops & Products* 223, 120248.
- Chen JJ, Cui BK, Zhou LW, Korhonen K et al. 2015 – Phylogeny, divergence time estimation, and biogeography of the genus *Heterobasidion* (*Basidiomycota*, *Russulales*). *Fungal Diversity* 71, 185–200.
- Chevallier FF. 1826 – Flore Générale des Environs de Paris. 1, 1–674.

- Christiansen MP. 1960 – Danish resupinate fungi. Part II. *Homobasidiomycetes*. Dansk botanisk Arkiv 19, 57–388.
- Cléménçon H. 1977 – Anatomie der Hymenomyceten (Anatomy of the *Hymenomycetes*). In: Flück-Wirth T (Ed.) Universität Lausanne, Lausanne, Switzerland. pp. 1–996.
- Consiglio G, Setti L. 2008 – Il genere *Crepidotus* in Europa. Vicenza: A. M. B. Fondazione Centro Studi Micologici. pp. 1–334.
- Consiglio G, Setti L. 2017 – Prolegomena to the systematics of family *Pleurotaceae* in the monograph “I Generi *Hohenbuehelia* e *Resupinatus* in Europa”. Rivista di Micologia 60, 237–253.
- Consiglio G, Setti L. 2018 – The genera *Hohenbuehelia* and *Resupinatus* in Europe. Monografie di Pagine di Micologia. Vol. 3. Associazione Micologica Bresadola, Centro Studi Micologici, Trento/Vicenza, Italy, pp. 1–448.
- Consiglio G, Setti L, Thorn RG. 2018 – New species of *Hohenbuehelia*, with comments on the *Hohenbuehelia atrocoerulea* – *Nematoctonus robustus* species complex. Persoonia 41, 202–212.
- Consiglio GA, Vizzini J, Cooper M, Marchetti M et al. 2021 – The agaricoid members of the genus *Porotheleum* (*Porotheleaceae*, *Agaricales*), *Porotheleum* emend., *Porotheleaceae* s. stricto, and new genera for *Agaricus floccipes* and *Mycena subalpina*. Revista di Micologia 64, 99–152.
- Cooke WB. 1989 – The cyphelloid fungi of Ohio. Memoirs of the New York Botanical Garden 49, 158–172.
- Cooper JA. 2023 – Nomenclatural novelties. Index Fungorum 531, 1–4.
- Corner E.J.H. 1950 – A monograph of *Clavaria* and allied genera. Annals of Botany Memoirs 1, 1–740.
- Corner E.J.H. 1970 – Supplement to “a monograph of *Clavaria* and allied genera”. Beihefte zur Nova Hedwigia 33, 1–299.
- Cortés-Pérez A, Desjardin DE, Perry BA, Ramírez-Cruz V et al. 2019 – New species and records of bioluminescent *Mycena* from Mexico. Mycologia 111(2), 319–338.
- Crous PW, Wingfield MJ, Burgess TI, Hardy GESJ et al. 2018 – Fungal Planet description sheets: 716–784. Persoonia 40, 240–393.
- Cruz RHSF, Góis JS, Marinho P, Baseia LG et al. 2023 – Rearranging the bird’s nest fungi: molecular review of internal clades in *Cyathus* (*Nidulariaceae*, *Basidiomycota*). IMA Fungus 14, 8.
- Cui BK, Li HJ, Ji X, Zhou JL et al. 2019 – Species diversity, taxonomy and phylogeny of *Polyporaceae* (*Basidiomycota*) in China. Fungal Diversity 97, 137–392.
- Cui YJ, Wu YD, Jiang YH, Zhu AH et al. 2025 – Diversity of macrofungi in southeast Xizang 1. the wood-decay fungi. Mycology 16(2), 635–669.
- Dai YC. 2010 – *Hymenochaetaceae* (*Basidiomycota*) in China. Fungal Diversity 45, 131–343.
- Dai YC. 2011 – A revised checklist of corticioid and hydroid fungi in China for 2010. Mycoscience 52, 69–79.
- Dai YC. 2012 – Polypore diversity in China with an annotated checklist of Chinese polypores. Mycoscience 53, 49–80.
- Dai YC, Cui BK, Si J, He SH et al. 2015 – Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. Mycological Progress 14, 1–9.
- Dai YC, Wu F, Si J, Yuan Y et al. 2022 – Resources and diversity of wood-decaying fungi in Yunnan. Beijing: Science Press, pp. 1–574.
- Dai YC, Yang ZL, Cui BK, Wu G et al. 2021 – Diversity and systematics of the important macrofungi in Chinese forests. Mycosystema 40, 770–805.
- Das K, Zhao RL. 2013 – *Nidula shingbaensis* sp. nov., a new bird’s nest fungus from India. Mycotaxon 125, 53–58.
- Delivorias P, Gonou-Zagou Z. 2008 – On *Cheimonophyllum candidissimum* from Greece with notes on its implied aphyllophoroid ancestry. Mycotaxon 104, 1–8.

- Dentinger BTM, Gaya E, O'Brien H, Suz LM et al. 2016 – Tales from the crypt: genome mining from fungarium specimens improves resolution of the mushroom tree of life. *Biological Journal of the Linnean Society* 117, 11–32.
- Desjardin DE, Halling RE, Perry BA. 1997 – *Gymnopus villosipes*-a common collybioid agaric from California. *Mycotaxon* 64, 141–148.
- Deschuyteneer D, Melzer A, Pérez-De-Gregorio MÀ. 2018 – *Psathyrella codinae*, a new species from Spain. *Bulletin de l'Association des Mycologues francophones de Belgique* 11, 4–8.
- Desjardin DE, Perry BA. 2017 – The gymnopoid fungi (*Basidiomycota*, *Agaricales*) from the Republic of São Tomé and Príncipe, West Africa. *Mycosphere* 8(9), 1317–1391.
- Dhingra GS, Kaur J. 2012 – *Radulomycetopsis* (*Agaricomycetes*), a new corticioid genus from India. *Mycotaxon* 119, 133–136.
- Dissanayake AJ, Bhunjun CS, Maharachchikumbura SS, Liu JK. 2020 – Applied aspects of methods to infer phylogenetic relationships amongst fungi. *Mycosphere* 11, 2652–76.
- Dong J, Deng Q, Chen M, Chen D et al. 2025a – Molecular phylogeny and morphology reveal four new wood-inhabiting fungi of *Asterostroma* and *Radulomyces* (*Basidiomycota*) from Southwestern China. *Mycosystema* 112, 35–58.
- Dong JH, Gu JY, Zhao CL. 2023 – Diversity of wood-decaying fungi in Wenshan Area, Yunnan Province, China. *Mycosystema* 42, 638–662.
- Dong JH, Li Q, Su JQ, Zhao CL. 2025b – *Punctochaete murina* gen. et sp. nov. (*Agaricomycetes*, *Basidiomycota*) from southwestern China. *European Journal of Taxonomy* 981, 96–113.
- Dong JH, Li Q, Yuan Q, Luo YX et al. 2024 – Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. *Mycosphere* 15, 1110–1293.
- Dong JH, Xu Y, Jiang QQ, Hosen MI et al. 2025c – A new genus and two new species of *Auriculariales* (*Basidiomycota*) from southwest China, evidenced by morphological characteristics and phylogenetic analyses. *Mycological Progress* 24, 1–17.
- Duan ZY, Yang X, Li Q, Yao L et al. 2023 – *Cyathus tongxinianus* sp. nov. (*Basidiomycota*) from China. *Phytotaxa* 622, 1–16.
- Duan ZY, Yu J, Zhao CL. 2022 – Molecular phylogeny and morphology reveal a new wood-rotting fungal species, *Cyathus wenshanensis* sp. nov. from the Yunnan-Guizhou Plateau. *Studies in Fungi* 7, 1–10.
- Earle FS. 1909 – The genera of North American gill fungi. *Bulletin of the New York Botanical Garden* 5, 373–451.
- Eriksson J, Ryvarden L. 1975 – The *Corticiaceae* of North Europe 3. *Coronicium* – *Hyphoderma*. *Fungiflora*, Oslo. pp. 1–259.
- Eriksson J, Ryvarden L. 1976 – The *Corticiaceae* of North Europe 4. *Hyphodermella* – *Mycoacia*. *Fungiflora*, Oslo. pp. 547–886.
- Evans HC, Stalpers JA, Samson RA, Benny L. 1978 – On the taxonomy of *Monilia roreri*, an important pathogen of *Theobroma cacao* in South America. *Canada Journal of Botany* 56, 2528–2532.
- Farook VA, Manimohan P. 2014 – The genus *Campanella* (*Marasmiaceae*, *Agaricales*): A new species and a new combination and species status. *Current Research in Environmental & Applied Mycology* 4(2), 157–161.
- Fries EM. 1821 – *Systema mycologicum*. Vol. 1. Sweden, Lundin, pp. 1–520.
- Fries EM. 1825 – *Systema Orbis Vegetabilis*. 1, 1–369.
- Fries EM. 1836 – *Corpus Florarum provincialium suecicae* 1. *Floram Scanicam*. pp. 1–432.
- Fries EM, Nordholm J. 1817 – *Symbolae Gasteromycorum*. 1, 1–8.
- Frøslev TG, Matheny PB, Hibbett DS. 2005 – Lower-level relationships in the mushroom genus *Cortinarius* (*Basidiomycota*, *Agaricales*): a comparison of RPB1, RPB2, and ITS phylogenies. *Molecular Phylogenetics and Evolution* 37(2), 602–618.
- Ghobad-Nejhad M, Yurchenko E. 2012 – Three new corticioid species (*Basidiomycota*) from the Caucasus region. *Synopsis Fungorum* 30, 5–13.

- Ghobad-Nejhad M, Zhou LW, Tomšovský M, Angelini P et al. 2024 – Unlocking nature's pharmacy: diversity of medicinal properties and mycochemicals in the family *Hymenochaetaceae* (*Agaricomycetes*, *Basidiomycota*). *Mycosphere* 15(1), 6347–6438.
- Gilbertson RL, Hemmes DE. 2004 – New species of lignicolous basidiomycetes from Hawaii. *Memoirs of the New York Botanical Garden* 89, 81–92.
- Gillen K, Laessle T, Kirschner R, Piepenbring M. 2012 – *Favolaschia* species (*Agaricales*, *Basidiomycota*) from Ecuador and Panama. *Nova Hedwigia* 96, 117–165.
- Glez-Peña D, Gómez-Blanco D, Reboiro-Jato M, Fdez-Riverola F et al. 2010 – ALTER: program-oriented conversion of DNA and protein alignments. *Nucleic Acids Research* 38, 14–18.
- Góis JD, do Nascimento PH, Cruz R, Marinho P et al. 2024 – Two new taxa and a new record of a rare species for the genus *Cyathus* (*Nidulariaceae*, *Basidiomycota*) from Brazilian Amazon Forest. *Plant Biosystems – An International Journal Dealing with all Aspects of Plant Biology* 158, 354–364.
- Gómez CL, Pérez-Silva E. 1988 – Especies de *Nidulariales* (*Gasteromycetes*) comunes en México. *Scientia Fungorum* 161–183.
- Gonou-Zagou Z, Triantafyllou M, Floudas D, Delivorias P. 2011 – The genus *Resupinatus* Nees ex Gray in Greece. *Nova Hedwigia* 92, 513–522.
- González GC, Barroetaveña C, Visnovsky SB, Pildain MB. 2021 – A new species, phylogeny, and a worldwide key of the edible wood decay *Fistulina* (*Agaricales*). *Mycological Progress* 20(5), 733–746.
- Goranova G, Binder M, Hibbett DS. 2003 – Molecular phylogenetics indicate that the corticioid genus *Dendrothele* is highly polyphyletic. *Inoculum* 54, 22.
- Gorjón SP, de Jesus MA. 2014 – *Rectipilus stromatoides* sp. nov. (*Agaricales*, *Basidiomycota*), a new cyphelloid fungus from the Brazilian Amazon. *Mycosphere* 5, 393–396.
- Gray SF. 1821 – A natural arrangement of British plants. 1. Baldwin, Cradock & Joy, London, Baldwin, pp. 1–824.
- Gruhn G, Moreno G, Mourgues Y, Alvarado P. 2023 – A new species in *Chromocyphella* from France. *Nordic Journal of Botany* 2023(6), 1–7.
- Guzmán-Dávalos L, Pradeep CK, Vrinda KB, et al. 2017 – A new stipitate species of *Crepidotus* from India and Thailand, with notes on other tropical species. *Mycologia* 109(5), 804–814.
- Haller AV. 1768 – *Historia stirpium indigenarum Helvetiae inchoate*. Sumptibus Societatis typographicae 3, 236.
- Harder CB, Miyauchi C, Virágh M, Kuo A et al. 2024 – Extreme overall mushroom genome expansion in *Mycena* s.s. irrespective of plant hosts or substrate specializations. *Cell Genomics* 4(7), 100586.
- Hassett MO, Fischer MWF, Sugawara ZT, tolze-Rybczynski J et al. 2013 – Splash and grab: biomechanics of peridiole ejection and function of the funicular cord in bird's nest fungi. *Fungal Biology* 117(10), 708–714.
- He MQ, Zhao RL, Hyde KD, Begerow D et al. 2019 – Notes, outline and divergence times of *Basidiomycota*. *Fungal Diversity* 99(1), 105–367.
- He MQ, Cao B, Liu F, Boekhout T et al. 2024 – Phylogenomics, divergence times and notes of orders in *Basidiomycota*. *Fungal Diversity* 126, 127–406.
- He ZM, Chen ZH, Bau T, Wang GS et al. 2023 – Systematic arrangement within the family *Clitocybaceae* (*Tricholomatineae*, *Agaricales*): phylogenetic and phylogenomic evidence, morphological data and muscarine-producing innovation. *Fungal Diversity* 123, 1–47.
- Henkel TW, Smith ME, Aime MC. 2010 – *Guyanagaster*, a new wood-decaying sequestrate genus of *Agaricales* from the Guiana Shield. *American Journal of Botany* 97, 1474–1484.
- Hennings P. 1895 – *Fungi camerunenses* 1. *Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie*. 22, 72–111.
- Hennings P. 1900 – *Fungi monsunenses*. In: Warburg O (ed) *Monsunia; Beiträge zur Kenntniss der Vegetation des Süd- und Ostasiatischen Monsungebietes.*, vol 1. W. Engelmann, Leipzig, pp. 1–38.

- Hennings P. 1904 – Fungi amazonici II, a cl. Ernesto Ule collecti. *Hedwigia* 43, 242–273.
- Hibbett DS. 2004 – Trends in morphological evolution in *Homobasidiomycetes* inferred using maximum likelihood: a comparison of binary and multistate approaches. *Systematic Biology* 53(6), 889–903.
- Hibbett DS. 2007 – After the gold rush, or before the flood? Evolutionary morphology of mushroom-forming fungi (*Agaricomycetes*) in the early 21st century. *Mycological Research* 111(9), 1001–1018.
- Hibbett DS, Binder M. 2001 – Evolution of marine mushrooms. *Biology Bulletin* 201, 319–322.
- Hibbett DS, Binder M. 2002 – Evolution of complex fruiting-body morphologies in homobasidiomycetes. *Proceedings of the Cambridge Philosophical Society-Biological Science* 269, 1963–1969.
- Hibbett DS, Donoghue MJ. 2001 – Analysis of character correlations among wood decay mechanisms, mating systems, and substrate ranges in *Homobasidiomycetes*. *Systematic Biology* 50, 215–242.
- Hibbett DS, Thorn RG. 2001 – *Homobasidiomycetes*. In: *The Mycota, Vol. VII. Part B., Systematics and Evolution* (McLaughlin DJ, McLaughlin EG, Lemke PA, eds). Springer-Verlag, Berlin, Germany, 121–168.
- Höhnelt F, Litschauer V. 1907 – Beiträge zur Kenntnis der Corticieen (II. Mitteilung – Sitzungsber Kaiserl Akad Wiss Wien Math-Naturwiss Cl Abt 1. 116, 739–852.
- Honan AH, Desjardin DE, Perry BA, Horak E et al. 2015 – Towards a better understanding of *Tetrapyrgos* (*Basidiomycota*, *Agaricales*): new species, type studies, and phylogenetic inferences. *Phytotaxa* 231, 101–132.
- Horak E. 1971 – A contribution towards the revision of the *Agaricales* (fungi) from New Zealand. *New Zealand Journal of Botany* 9, 403–462.
- Hou WN, Burenbaatar G, Bau T. 2024 – Two new species of *Metacampanella* (*Agaricales*, *Marasmiaceae*) from China and Mongolia. *MycKeys* 108, 227–247.
- Hu J, Zhao G, Tuo Y, Rao G et al. 2022 – Morphological and molecular evidence reveal eight new species of *Gymnopus* from northeast China. *Journal of Fungi* 8(4), 349.
- Hu JJ, Li Y, Li X, Sossah F. 2021 – New findings of *Neonothopanus* (*Marasmiaceae*, *Basidiomycota*) from Ghana. *Phytotaxa* 512, 57–67.
- Hu Y, Karunarathna SC, Li H, Galappaththi MC et al. 2022 – The impact of drying temperature on basidiospore size. *Diversity* 25, 14(4), 239.
- Hughes KW, Mather DA, Petersen RH. 2010 – A new genus to accommodate *Gymnopus acervatus* (*Agaricales*). *Mycologia* 102(6), 1463–1478.
- Hughes K, Petersen RH. 2015 – Transatlantic disjunction in fleshy fungi III: *Gymnopus confluens*. *MycKeys* 9, 37–63.
- Hughes KW, Petersen RH, Lickey EB. 2009 – Using heterozygosity to estimate a percentage DNA sequence similarity for environmental species' delimitation across basidiomycete fungi. *New Phytologist* 182(4), 795–798.
- Hyde KD. 2022 – The numbers of fungi. *Fungal Diversity* 114, 1.
- Hyde KD, Baldrian P, Chen Y, Kandawatte TC et al. 2024a – Current trends, limitations and future research in the fungi? *Fungal Diversity* 125, 1–71.
- Hyde KD, Noorabadi MT, Thiagaraja V, He MQ et al. 2024b – The 2024 Outline of Fungi and fungus-like taxa. *Mycosphere* 15, 5146– 6239.
- Hyde KD, Saleh A, Aumentado HDR, Boekhout T et al. 2024c – Fungal numbers: global needs for a realistic assessment. *Fungal Diversity* 128, 191–225.
- James TY, Stajich JE, Hittinger CT, Rokas A. 2020 – Toward a fully resolved fungal tree of life. *Annual Review of Microbiology* 74, 291–313.
- Ji X, Zhou JL, Song CG, Xu TM et al. 2022 – Taxonomy, phylogeny and divergence times of *Polyporus* (*Basidiomycota*) and related genera. *Mycosphere* 13, 1–52.
- Johnston PR, Whitton SR, Buchanan PK, Park D et al. 2006 – The basidiomycete genus *Favolaschia* in New Zealand. *New Zealand Journal of Botany* 44, 65–87.

- Jülich W. 1975 – Studies in resupinate *Basidiomycetes* - 3. Persoonia 8, 291–305.
- Jülich W. 1978 – Studies in resupinate *Basidiomycetes* - 5. Some new genera and species. Persoonia 10, 137–140.
- Jülich W. 1979 – Studies in resupinate *Basidiomycetes* - 6. On some new taxa. Persoonia 10, 325–336.
- Jülich W. 1982 – Higher taxa of *Basidiomycetes*. Bibliotheca Mycologica 85, 1–485.
- Justo A, vizzini A, Minnis AM, Jr NM et al. 2011 – Phylogeny of the *Pluteaceae* (*Agaricales*, *Basidiomycota*): taxonomy and character evolution. Fungal Biology 115, 1–20.
- Kalichman J, Kirk PM, Matheny PB. 2020 – A compendium of generic names of agarics and *Agaricales*. Taxon 69(10), 425–447.
- Kalyaanamoorthy S, Minh BQ, Wong TKF, Haeseler AV et al. 2017 – ModelFinder: Fast model selection for accurate phylogenetic estimates. Nature Methods 14(6), 587–589.
- Kanokmedhakul S, Lekphrom R, Kanokmedhakul K, Hahnvajjanawong C et al. 2012 – Cytotoxic sesquiterpenes from luminescent mushroom *Neonothopanus nambi*. Tetrahedron 68, 8261–8266.
- Karasiński D, Nagy LG, Szarkándi JG, Dvořák D et al. 2023 – *Cyphelloporia bialoviesensis* (Fungi, *Agaricales*) - a new genus and species for a giant cyphelloid fungus from Białowieża virgin forest in Poland. Phytotaxa 589(2), 119–136.
- Katoh K, Rozewicki J, Yamada KD. 2019 – MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20, 1160–1166.
- Kaur J, Dhingra GS, Hallenberg N. 2014 – *Cristinia tubulicystidiata* sp. nov. from India. Mycotaxon 127, 89–92.
- Ke HM, Lee HH, Lin CI, Liu YC et al. 2020 – *Mycena* genomes resolve the evolution of fungal bioluminescence. Proceedings of the National Academy of Sciences USA 117(49), 31267–31277.
- Kerekes JF, Desjardin DE. 2009 – A monograph of the genera *Crinipellis* and *Moniliophthora* from Southeast Asia including molecular phylogeny of the nrITS region. Fungal Diversity 37, 101–152.
- Kim JS, Cho Y, Park KH, Park JH et al. 2022 – Taxonomic study of *Collybiopsis* (*Omphalotaceae*, *Agaricales*) in the Republic of Korea with seven new species. MycoKeys 88, 79–108.
- Kirk PM, Cannon PF, Minter DW, Minter DM. 2008 – Ainsworth & Bisby's Dictionary of the fungi. 10th edition. CAB International, Wallingford, pp. 1–771.
- Knudsen H, Vesterholt J. 2012 – Funga Nordica, 2nd ed.; Nordsvamp: Copenhagen, Denmark.
- Koch RA, Lodge DJ, Sourell S, Nakasone K, et al. 2018 – Tying up loose threads: revised taxonomy and phylogeny of an avian-dispersed Neotropical rhizomorph-forming fungus. Mycological Progress 17, 989–998.
- Kraisitudomsook N, Ahrendt S, Riley R, LaButti K et al. 2024 – On the origin of bird's nest fungi, Phylogenomic analyses of fungi in the *Nidulariaceae* (*Agaricales*, *Basidiomycota*). Molecular Phylogenetics and Evolution 193, 108010.
- Kraisitudomsook N, Choeyklin R, Boonpratuang T, Pobkwamsuk M et al. 2022 – Hidden in the tropics: *Retiperidiolia* gen. nov., a new genus of bird's nest fungi (*Nidulariaceae*), and asystematic study of the genus *Mycocalia*. Mycological Progress 21, 1–12.
- Kraisitudomsook N, Healy RA, Smith ME. 2021 – Molecular systematics and taxonomic overview of the bird's nest fungi (*Nidulariaceae*). Fungal Biology 125, 693–703.
- Kühner R. 1980 – Les Hyménomycètes agaricoïdes (*Agaricales*, *Tricholomatales*, *Plutéales*, *Russulales*). Etude générale et classification. Bulletin de la Société linnéenne de Lyon, numéro spécial 49. Société linnéenne de Lyon, Lyon, France. pp. 1–550.
- Kühner R, Romagnesi H. 1954 – Compléments a la Flore Analytique, 3. Espèces nouvelles, critiques ou rares de Pleurotacées, Marasmiacées et Tricholomacées. Bulletin de la Société des Naturalistes d'Oyonnax 8, 71–131.
- Kumar AM, Aime MC, Vrinda KB, Pradeep CK. 2020 – Two new species and a new record of *Crepidotus* (*Agaricomycetes*) from India. Australian Systematic Botany 33, 380–391.

- Larsson A. 2014 – AliView: a fast and lightweight alignment viewer and editor for large data sets. *Bioinformatics* 30, 3276–3278.
- Larsson KH. 2007 – Re-thinking the classification of corticioid fungi. *Mycological Research* 111, 1040–1063.
- Larsson KH, Larsson E, Kõljalg U. 2004 – High phylogenetic diversity among corticioid Homobasidiomycetes. *Mycological Research* 108, 983–1002.
- Lavorato C, Vizzini A, Ge ZW, Marco C. 2015 – Redescription of *Clitocybe umbrinopurpurascens* (*Basidiomycota*, *Agaricales*) and revision of *Neohygrophorus* and *Pseudoomphalina*. *Phytotaxa* 219, 43–57.
- Lawrey JD, Lücking R, Sipman HJM, Chaves JL et al. 2009 – High concentration of basidiolichens in a single family of agaricoid mushrooms (*Basidiomycota*: *Agaricales*: *Hygrophoraceae*). *Mycological Research* 113, 1154–1171.
- Leal-Dutra CA, Griffith GW, Neves MA, McLaughlin DJ et al. 2020 – Reclassification of *Pterulaceae* Corner (*Basidiomycota*: *Agaricales*) introducing the ant-associated genus *Myrmecopterula* gen. nov., *Phaeopterula* Henn. and the corticioid *Radulomycetaceae* fam. nov. *IMA Fungus* 11, 1–24.
- Lebel T, Castellano MA, Beever RE. 2015 – Cryptic diversity in the sequestrate genus *Stephanospora* (*Stephanosporaceae*: *Agaricales*) in Australasia. *Fungal Biology* 119, 201–228.
- Li JP, Oliveira JJS, Pan MC, Deng CY et al. 2024 – Notes on all genera of *Omphalotaceae*: expanding the taxonomic spectrum in China and revisiting historical type specimens. *Mycosphere* 15, 1522–1594.
- Li Y, Nakasone KK, Chen CC, Zhao CL et al. 2022 – Taxonomy and phylogeny of *Cystostereaceae* (*Agaricales*, *Basidiomycota*): a new genus, five new species, and three new combinations. *Journal of Fungi* 8, 1229.
- Liu S, Chen YY, Sun YF, He XL et al. 2023a – Systematic classification and phylogenetic relationships of the brown-rot fungi within the Polyporales. *Fungal Diversity* 118, 1–94.
- Liu S, Shen LL, Xu TM, Song CG et al. 2023b – Global diversity, molecular phylogeny and divergence times of the brown-rot fungi within the Polyporales. *Mycosphere* 14, 1564–1664.
- Liu SL, Liu DM, Zhou LW. 2024a – The future is now: how to conserve fungi. *Biological Diversity* 1, 6–8.
- Liu SL, Shen ZQ, Li QZ, Liu XY et al. 2022 – *Alloexidiopsis* gen. nov., a revision of generic delimitation in *Auriculariales* (*Basidiomycota*). *Frontiers in Microbiology* 13, 894641.
- Liu SL, Wang XW, Li GJ, Deng CY et al. 2024b – Fungal diversity notes 1717–1817: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 124, 1–216.
- Liu SL, Wu F, He SH. 2016 – *Lindtneria asiae-orientalis* sp. nov. (*Stephanosporaceae*, *Basidiomycota*) from China based on morphological and molecular characters. *Phytotaxa* 260(3), 283–290.
- Liu XC, Lin ZJ, Liang YS, Cao LX et al. 2024c – *Collybiopsis baiyunensis* sp. nov. (*Omphalotaceae*, *Agaricales*) from Baiyun Mountain, Southern China. *Phytotaxa* 640, 183–195.
- Liu ZB, Liu HG, Vlasák J, Gates GM et al. 2025a – Global diversity and phylogeny of *Incrustoporiaceae* (*Polyporales*, *Basidiomycota*) with an emphasis on *Skeletocutis*. *Mycology* 1–58.
- Liu ZB, Yuan Y, Dai YC, Liu HG et al. 2025b – Global diversity and systematics of *Hymenochaetaceae* with non-poroid hymenophore. *Fungal Diversity* 131, 1–97.
- Lu WH, Nutaratat P, Kumla J, Tibpromma S et al. 2024 – Morphological and molecular identification of two new *Marasmiellus* species (*Omphalotaceae*, *Agaricales*) from Thailand. *MycoKeys* 109, 31–48.
- Lucas A, Dentinger BTM. 2015 – *Rectipilus afibulatus* – a new cyphelloid mushroom (*Agaricales*) from Great Britain. *Kew Bulletin* 70, 58.

- Magnago AC, Trierveiler-Pereira L, Neves MA. 2013 – Contributions towards the knowledge of *Favolaschia* (Mycenaceae, Agaricomycetes) from Brazil. *Mycosphere* 4, 1071–1078.
- Malysheva V, Spirin V. 2017 – Taxonomy and phylogeny of the *Auriculariales* (Agaricomycetes, Basidiomycota) with stereoid basidiocarps. *Fungal Biology* 121(8), 689–715.
- Manimohan P, Leelavathy KM. 1989 – *Marasmius* species new to India. *Sydowia* 41, 185–199.
- Mao WL, Wu YD, Liu HG, Yuan Y et al. 2023 – A contribution to *Porogramme* (Polyporaceae, Agaricomycetes) and related genera. *IMA Fungus* 14, 5.
- Martin MP, Raidl S, Telleria MT. 2004 – Molecular analyses confirm the relationship between *Stephanospora caroticolor* and *Lindtneria trachyspora*. *Mycotaxon* 90, 133–140.
- Mata JL, Halling RE, Petersen RH. 2004a – New species and mating system reports in *Gymnopus* (Agaricales) from Costa Rica. *Fungal Diversity* 16, 113–129.
- Mata JL, Hughes KW, Petersen RH. 2004b – Phylogenetic placement of *Marasmiellus juniperinus*. *Mycoscience* 45(3), 214–221.
- Mata JL, Hughes KW, Petersen RH. 2007 – An investigation of *Omphalotaceae* (Fungi: Euagarics) with emphasis on the genus *Gymnopus*. *Sydowia* 58, 191–289.
- Matheny PB. 2005 – Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (*Inocybe*, Agaricales). *Molecular Phylogenetics and Evolution* 35, 1–20.
- Matheny PB, Curtis JM, Hofstetter V, Aime MC et al. 2006 – Major clades of Agaricales: a multilocus phylogenetic overview. *Mycologia* 98(6), 982–995.
- Matheny PB, Hughes KW, Kalichman J, Lebeuf R. 2020 – *Pulverulina*, a new genus of Agaricales for *Clitocybe ulmicola*. *Southeastern Naturalist* 19, 447–459.
- Matheny PB, Liu YJ, Ammirati JF, Hall B. 2002 – Using RPBI sequences to improve phylogenetic inference among mushrooms (*Inocybe*, Agaricales). *American Journal of Botany* 89, 688–698.
- Matheny PB, Wang Z, Binder M, Curti JM et al. 2007 – Contributions of rpb2 and tef1 to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). *Molecular Phylogenetics and Evolution* 43, 430–451.
- M'Barek HN, Arif S, Taidi B, et al. 2020 – Consolidated bioethanol production from olive mill waste: wood-decay fungi from central Morocco as promising decomposition and fermentation biocatalysts. *Biotechnology Reports* 28, e00541.
- McDonald JL. 2015 – Morphological and molecular systematics of *Resupinatus* (Basidiomycota). The University of Western Ontario, London. pp. 1–319.
- McDonald JV, Thorn RG. 2019 – Nomenclatural novelties. *Index Fungorum* 425, 1.
- McLaughlin DJ, McLaughlin EG. 1972 – Pure culture studies of fruiting and sporulation in a clavarioid fungus, *Pterula* sp. *Mycologia* 64, 599–608.
- McLaughlin DJ, McLaughlin EG. 1980 – A new species of *Pterula* (Aphylllophorales) with corticioid characteristics. *Canadian Journal of Botany* 58, 1327–1333.
- McLaughlin EG, McLaughlin DJ, Adson DE. 1978 – Developmental anatomy of adimitic basidiomycete, *Pterula* sp. *Canadian Journal of Botany* 56, 288–296.
- Miller MA, Pfeiffer W, Schwartz T. 2012 – The CIPRES science gateway. In *Proceedings of the 1st Conference of the Extreme Science and Engineering Discovery Environment: Bridging from the Extreme to the Campus and Beyond*, Chicago, IL, USA. pp. 1–39.
- Miller OKJ, Miller HH. 1988 – *Gasteromycetes*—morphological and developmental features with keys to the orders, families and genera. Mad River Press, Eureka, California, USA. pp. 1–157.
- Ming B, Zhou LW, Tong YJ, Yin F. 2023 – “Risk assessment and warning system for strategic biological resources in China.” *The Innovation Life* 1, 100004.
- Mogilnaya OA, Ronzhin NO, Bondar VS. 2016 – Comparative evaluation of total peroxidase and catalase activities during light emission of luminous fungus *Neonothopanus nambi*. *Mycosphere* 7(4), 499–510.
- Mombert A. 2022 – Bulletin Mycologique et Botanique Dauphiné-Savoie. 246, 37–42.
- Moncalvo JM, Lutzoni FM, Rehner SA, Johnson J et al. 2000 – Phylogenetic relationships of agaric fungi based on nuclear large subunit ribosomal DNA sequences. *Systematic Biology* 49, 278–305.

- Moncalvo JM, Vilgalys R, Redhead SA, Johnson JE et al. 2002 – One hundred and seventeen clades of Euagarics. *Molecular Phylogenetics and Evolution* 23(3), 357–400.
- Moreno G, Prieto M, Esteve-Raventós F, Olariaga I. 2017 – Phylogenetic assessment of *Chromocyphellaceae* (Agaricineae, Basidiomycota) and a new lamellate species of *Chromocyphella*. *Mycologia* 109(4), 578–587.
- Mou GF, Bau T. 2021 – *Asproinocybaceae* fam. nov. (Agaricales, Agaricomycetes) for accommodating the genera *Asproinocybe* and *Tricholosporum*, and description of *Asproinocybe sinensis* and *Tricholosporum guangxiense* sp. nov. *Journal of Fungi* 7, 1086.
- Murrill W. 1915 – *Agaricaceae* (pars). *Flora of North America* 9, 286–296.
- Na Q, Bau T. 2019 – Recognition of *Mycena* sect. *Amparoina* sect. nov. (Mycenaceae, Agaricales), including four new species and revision of the limits of sect. *Sacchariferae*. *Mycoskeys* 52, 103–124.
- Na Q, Liu Z, Zeng H, Cheng X, Cheng XH et al. 2022 – *Crepidotus yuanchui* sp. nov. and *C. caspari* found in subalpine areas of China. *Mycoscience* 63, 1–11.
- Na Q, Zeng H, Hu Y, Ding H et al. 2024 – Morphological and phylogenetic analyses reveal five new species of *Porotheleaceae* (Agaricales, Basidiomycota) from China. *MycoKeys* 105, 49–95.
- Nagy LG, Kovács GM, Krizsán K. 2018 – Complex multicellularity in fungi: evolutionary convergence, single origin, or both? *Biological Reviews* 93, 1778–1794.
- Nagy LG, Vonk PJ, Künzler M, Földi C et al. 2023 – Lessons on fruiting body morphogenesis from genomes and transcriptomes of *Agaricomycetes*. *Studies in Mycology* 104, 1–85.
- Nakagiri A, Hakotani A, Shino R, Miyazaki K et al. 2024 – Taxonomic and life cycle reappraisals of the marine basidiomycete *Nia vibrissa* complex, with descriptions of three new *Nia* species. *Mycologia* 116, 59–91.
- Nakasone KK, Burdsall JHH. 2011 – The genus *Dendrothele* (Agaricales, Basidiomycota) in New Zealand. *New Zealand Journal of Botany* 49, 107–131.
- Nakasone KK, Hibbett DS, Goranova G. 2009 – *Neocampanella*, a new corticioid fungal genus, and a note on *Dendrothele bispora*. *Botany* 87, 875–882.
- Niveiro N, Ramírez NA, Michlig A, Lodge DJ et al. 2020 – Studies of Neotropical tree pathogens in *Moniliophthora*: a new species, *M. mayarum*, and new combinations for *Crinipellis ticoi* and *C. brasiliensis*. *MycoKeys* 66, 39–54.
- Norvell LL, Redhead SA, Ammirati JF. 1994 – *Omphalina sensulato* in the North America 1-2. 1: *Omphalina wynniae* and the genus *Chrysomphalina*. 2: *Omphalina* sensu Bigelow. *Mycotaxon* 50, 379–407.
- Oberwinkler F. 1966 – Primitive Basidiomyceten. Revision einiger Formenkreise von Basidienpilzen mit plastischer Basidie. *Sydowia* 19, 1–72.
- Oberwinkler F, Horak E. 1979 – *Stephanosporaceae*, eine neue familie der Basidiomycetes mit aphylllophoralen un gastroiden fruchtkorpern. *Plant Systematics and Evolution* 131, 157–164.
- Olariaga I, Huhtinen S, Læssøe T, Petersen JH et al. 2020 – Phylogenetic origins and family classification of typhuloid fungi, with emphasis on *Ceratellopsis*, *Macrotyphula* and *Typhula* (Basidiomycota). *Studies in Mycology* 96, 155–184.
- Oliveira JJ, Vargas-Isla R, Cabral TS, Rodrigues DP et al. 2019 – Progress on the phylogeny of the *Omphalotaceae*: *Gymnopus* s. str., *Marasmiellus* s. str., *Paragymnopus* gen. nov. and *Pusillomyces* gen. nov. *Mycological Progress* 18(5), 713–739.
- Oliveira JJS, Desjardin DE, Jenkinson TS, Margaritescu S et al. 2024 – Taxonomic revision of *Marasmius* Fr. and *Marasmiaceae* Roze ex Kühner based on multigene phylogenetics and morphological evidence. *Fungal Diversity* 127, 1–54.
- Oliveira JJS, Moncalvo JM, Margaritescu S, Capelari M. 2020 – A morphological and phylogenetic evaluation of *Marasmius* sect. *globulares* (*globulares-sicci* complex) with nine new taxa from the Neotropical Atlantic Forest. *Persoonia* 44, 240–277.
- Oliveira JJS, Vargas-Isla R, Cabral TS, Cardoso JS et al. 2021 – The Amazonian luminescent *Mycena cristinae* sp. nov. from Brazil. *Mycoscience* 62, 395–405.

- Ovrebo CL, Baroni TJ. 2007 – New taxa of *Tricholomataceae* and *Entolomataceae* (*Agaricales*) from Central America. *Fungal Diversity* 27, 157–170.
- Paez CA, Smith JA, Nakasone KK, Bec S et al. 2024 – *Parvodontia relampaga* sp. nov.: A *Cystostereaceae* fungal pathogen that is the causal agent of relampago blight of woody plants in Florida, USA. *Fungal Biology* 128, 1758–1770.
- Palmer JT. 1961 – Observations on *Gasteromycetes* IX. The conservation of *Nidularia* Fr. and the separation of *Mycocalia* J.T. Palmer, gen. nov. *Taxon* 10, 54–60.
- Park JH, Pavlov IN, Kim MJ, Park MS et al. 2020 – Investigating wood decaying fungi diversity in Central Siberia, Russia using ITS sequence analysis and interaction with host trees. *Sustainability* 12, 2535.
- Parmasto E. 1968 – Conspectus systematis *Corticacearum*. 1–261.
- Patouillard N. 1887 – Etude sur le genre *Laschia* Fr. *Journal de Botanique* 15, 225–231.
- Patouillard N. 1900 – Essai taxonomique sur les familles et les genres des Hyménomycètes. Lucien Declume, Lons-le-Saunier. pp. 1–197.
- Pegler DN, Lodge DJ, Nakasone KK. 1998 – The pantropical genus *Macrocybe* gen. nov. *Mycologia* 90, 494–504.
- Petch T. 1919 – *Gasteromyceta zeylanicae*. *Ann R Bot Gard Perad* 7, 57–78.
- Petersen JH. 1996 – Farvekort. The Danish mycological society's colour-chart. Foreningen til Svampekundskabens Fremme Greve. pp. 1–6.
- Petersen R, Hughes K. 2014 – New north American species of *Gymnopus*. *North American Fungi* 9, 1–22. Petersen RH, Hughes KW. 2016 – *Micromphale* sect. *Perforantia* (*Agaricales*, *Basidiomycetes*); expansion and phylogenetic placement. *Mycology* 18, 1–122.
- Petersen RH, Hughes KW. 2017 – An investigation on *Mycetinis* (Euagarics, *Basidiomycota*). *Mycology* 24, 1–138.
- Petersen RH, Hughes KW. 2020 – Two new genera of gymnopoid/marasmioid euagarics. *Mycotaxon* 135, 1–95.
- Petersen RH, Hughes KW. 2021 – *Collybiopsis* and its type species, *Co. ramealis*. *Mycotaxon* 136, 263–349.
- Petersen RH, Hughes KW. 2024a – Two new species of *Collybiopsis* (*Agaricales*, *Omphalotaceae*) from Eastern North America. *Mycology* 107, 95–124.
- Petersen RH, Hughes KW. 2024b – *Metacampanella* gen. nov.: the *Campanella dendrophora* complex. *Mycology* 16(1), 210–237.
- Petersen RH, Hughes KW, Voitek A. 2014 – *Gymnopus eneficola*—species nova from Newfoundland. *Omphalina* 5, 5–12.
- Petersen RH, Krisai-Greilhuber I. 1999 – Type specimen studies in *Pleurotus*. *Persoonia* 17(2), 201–219.
- Petersen RH, Psurtseva N, Zmitrovich I, Chachula P et al. 2015 – *Lignomyces*, a new genus of pleurotoid *Agaricomycetes*. *Mycologia* 107, 1045–1054.
- Phonrob W, Kumla J, Suwannarach N, Pumin N et al. 2024 – Five new records of *Collybiopsis* (*Agaricales*, *Omphalotaceae*) in Thailand: a significant addition to the species diversity and global distribution of the genus. *Phytotaxa* 650, 213–235.
- Pilát A. 1938 – *Lindtneria* g.n., a new genus of the *Phylacteriaceae* with polyporoid hymenophore. *Studia Botanica Cechoslovaca* 1, 71–73.
- Pouzar Z. 1959 – New genera of higher fungi III. *Ceská Mykologie* 13, 10–19.
- Purtov KV, Gorokhovatsky AY, Kotlobay AA, Osipova ZM et al. 2018 – Isolation and purification of fungal luciferase from *Neonothopanus nimbi*. *Doklady Biochemistry and Biophysics* 480, 177–180.
- Qin GF, Qin WM, Wang HC, Zhao J et al. 2025 – Phylogeny and species diversity of *Armillaria* in China based on morphological, mating test, and GCPSR criteria. *Mycology* 16(2), 777–811.
- Raithelhuber J. 1992 – Agaric flora of South America (6). *Metrodiana* 20, 151–200.

- Rathnayaka AR, Tennakoon DS, Jones GE, Wanasinghe DN et al. 2025 – Significance of precise documentation of hosts and geospatial data of fungal collections, with an emphasis on plant-associated fungi. *New Zealand Journal of Botany* 63(2-3), 462–489.
- Redhead SA. 1987 – The *Xerulaceae* (*Basidiomycetes*), a family with sarcodimitic tissues. *Canadian Journal of Botany* 65, 1551–1562.
- Redhead SA, Lutzoni F, Moncalvo JM, Vilgalys R. 2002 – Phylogeny of agarics: partial systematics solutions for coreomphalinoid genera in the *Agaricales* (euagarics). *Mycotaxon* 83, 19–57.
- Rehner SA, Buckley E. 2005 – A *Beauveria* phylogeny inferred from nuclear ITS and EF1-alpha sequences: evidence for cryptic diversification and links to *Cordyceps teleomorphs*. *Mycologia* 97, 84–98.
- Rehner SA, Samuels GJ. 1994 – Taxonomy and phylogeny of *Gliocladium* analyzed from nuclear large subunit ribosomal DNA sequences. *Mycological Research* 98(6), 625–634.
- Retnowati A. 2018 – The species of *Marasmiellus* (*Agaricales: Omphalotaceae*) from Java and Bali. *Gardens’ Bull Singapore* 70(1), 191–258.
- Ronquist F, Teslenko M, van der Mark, Ayres DL et al. 2012 – MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61, 539–542.
- Roussel HFA. 1806 – Flore du Calvados et terrains adjacents, composée suivant la méthode de Jussieu Ed. 2. pp. 1–372.
- Royse DJ, Baars J, Tan Q. 2017 – Current overview of mushroom production in the world. *Edible and Medicinal Mushrooms: Technology and Applications* 2, 5–13.
- Runnel K, Miettinen O, Lohmus A. 2021 – Polypore fungi as a flagship group to indicate changes in biodiversity – a test case from Estonia. *IMA Fungus* 12(1), 1–31.
- Ryvarden L, Melo I. 2014 – Poroid fungi of Europe. *Synopsis Fungorum* 31, 1–455.
- Ryvarden L, Melo I. 2017 – Poroid fungi of Europe. *Synopsis Fungorum* 37, 1–431.
- Sánchez-García M, Henkel TW, Aime MC, Smith ME et al. 2016 – *Guyanagarika*, a new ectomycorrhizal genus of *Agaricales* from the Neotropics. *Fungal Biology* 120(12), 1540–1553.
- Sánchez-García M, Matheny PB. 2017 – Is the switch to an ectomycorrhizal state an evolutionary key innovation in mushroom-forming fungi? A case study in the *Tricholomatineae* (*Agaricales*). *Evolution* 71, 51–65.
- Sánchez-García M, Ryberg M, Khan FK, Varga T et al. 2020 – Fruiting body form, not nutritional mode, is the major driver of diversification in mushroom-forming fungi. *Proceedings of the National Academy of Sciences USA* 117, 32528–32534.
- Savchenko A, Zamora JC, Shirouzu T, Spirin V et al. 2021 – Revision of *Cerinomyces* (*Dacrymycetes, Basidiomycota*) with notes on morphologically and historically related taxa. *Studies in Mycology* 99, 100117.
- Schoch CL, Robbertse B, Robert V, Vu D et al. 2014 – Finding needles in haystacks: linking scientific names, reference specimens and molecular data for fungi. *Database (Oxford)* 2014, bau061.
- Senanayake IC, Rossi W, Leonardi M, Weir A et al. 2023 – Fungal diversity notes 1611–1716: taxonomic and phylogenetic contributions on fungal genera and species emphasis in south China. *Fungal Diversity* 12, 1–243.
- Senn-Irlet B 1995 – The genus *Crepidotus* (Fr.) Staude in Europe. *Persoonia-Molecular Phylogeny and Evolution of Fungi* 16, 1–80.
- Shen LL, Wang M, Zhou JL, Xing JH et al. 2019 – Taxonomy and phylogeny of *Postia*. Multi-gene phylogeny and taxonomy of the brown-rot fungi: *Postia* (*Polyporales, Basidiomycota*) and related genera. *Persoonia* 42, 101–126.
- Silva-Filho AGS, Mombert A, Nascimento CC, Nóbrega BB et al. 2023 – *Eoscyphella luciurceolata* gen. and sp. nov. (*Agaricomycetes*) shed light on *Cyphellopsidaceae* with a new lineage of bioluminescent fungi. *Journal of Fungi* 9, 1004.

- Singer R. 1943 – A monographic study of the genera *Crinipellis* and *Chaetocalathus*. Lilloa 8, 441–534.
- Singer R. 1944 – New genera of fungi 1. Mycologia 36, 358–368.
- Singer R. 1945 – The *Laschia*-complex (*Basidiomycetes*). Lloydia 8, 170–230.
- Singer R. 1947 – New genera of fungi 3. Mycologia 39, 77–89.
- Singer R. 1948 – Diagnoses fungorum novorum *Agaricalium*. Sydowia 2, 26–42.
- Singer R. 1956 – New genera of fungi 7. Mycologia 48, 719–727.
- Singer R. 1973a – The genera *Marasmiellus*, *Crepidotus* and *Simocybe* in the neotropics. Beihefte zur Nova Hedwigia 44, 1–517.
- Singer R. 1973b – Diagnoses fungorum novorum *Agaricalium* 3. Beih Sydowia 7, 1–106.
- Singer R. 1974 – A monograph of *Favolaschia*. Beihefte zur Nova Hedwigia 50, 1–108.
- Singer R. 1975a – The *Agaricales* in modern taxonomy. 3rd ed. J. Cramer, Vaduz, Liechtenstein.
- Singer R. 1975b – The Neotropical species of *Campanella* and *Aphyllotus* with notes on some species of *Marasmiellus*. Nova Hedwigia 26, 847–895.
- Singer R. 1986 – The *Agaricales* in modern taxonomy. 4th ed. Koeltz Scientific Books, Koenigstein, Germany. pp. 1–981.
- Song J, Han ML, Cui BK. 2015 – *Fistulina subhepatica* sp. nov. from China inferred from morphological and sequence analyses. Mycotaxon 130(1), 47–56.
- Song J, Xing JH, Ji X, Sun YF et al. 2018 – *Rigidotubus tephroleucus* gen. et sp. nov. (*Cystostereaceae*, *Agaricales*) evidenced by morphological characters and phylogenetic analyses. Phytotaxa 333, 259–266.
- Spirin V, Runnel K, Vlasák J, Viner I et al. 2024 – The genus *Fomitopsis* (*Polyporales*, *Basidiomycota*) reconsidered. Studies in Mycology 107, 149–249.
- Staude F. 1857 – Die Schwämme Mitteldeutschlands, insbesondere des Herzogthums Coburg. Druck der Dietz'schen Hofbuchdruckerei. pp. 1–134.
- Sun YF, Costa-Rezende DH, Xing JH, Zhou JL et al. 2020 – Multi-gene phylogeny and taxonomy of *Amauroderma* s. lat. (*Ganodermataceae*). Persoonia 44, 206–239.
- Sun YF, Liu S, Cui BK. 2019 – Morphological and phylogenetic analyses reveal a new species of *Fistulina* (*Fistulinaceae*, *Agaricales*) from Australia. Phytotaxa 420, 233–240.
- Sun YF, Xing JH, He XL, Wu DM et al. 2022 – Species diversity, systematic revision and molecular phylogeny of *Ganodermataceae* (*Polyporales*, *Basidiomycota*) with an emphasis on Chinese collections. Studies in Mycology 101, 287–415.
- Tan YS, Desjardin DE, Perry BA, Vikineswary S et al. 2009 – *Marasmius* sensu stricto in Peninsular Malaysia. Fungal Diversity 37, 9–100.
- Thorn RG, Moncalvo JM, Reddy CA, Vilgalys R. 2000 – Phylogenetic analyses and the distribution of nematophagy support a monophyletic *Pleurotaceae* within the polyphyletic pleurotoid-lentinoid fungi. Mycologia 92, 241–252.
- Thorn RG, Moncalvo JM, Redhead SA, Lodge DJ et al. 2005 – A new poroid species of *Resupinatus* from Puerto Rico, with a reassessment of the cyphelloid genus *Stigmatolemma*. Mycologia 97, 1140–1151.
- Tian E, Matheny PB. 2020 – A phylogenetic assessment of *Pholiota* and the new genus *Pyrhulomyces*. Mycologia 113(1), 146–167.
- Tulasne LR, Tulasne C. 1844 – Recherches sur l'organisation et le mode de fructification des champignons de la tribu des Nidulariées, suivies d'un essai monographique. Annales des Sciences Naturelles. Botanique. Sér. 1, 41–107.
- Underwood LM. 1899 – Moulds, mildews and mushrooms. pp. 1–236.
- Valade F, Moreau PA. 2022 – Validité et légitimité de *Cheimonophyllum candidissimum* (Berk. Etm. Curtis) Singer. Bulletin Trimestriel de la Société Mycologique de France 138, 209–226.
- Varga T, Krizsán K, Földi C, Dima B et al. 2019 – Megaphylogeny resolves global patterns of mushroom evolution. Nature Ecology & Evolution 3, 668–678.
- Vellinga EC, Sysouphanthong P, Hyde KD. 2011 – The family *Agaricaceae*: phylogenies and two new white-spored genera. Mycologia 103, 494–509.

- Vila J, Esteve-Raventós F, Llimona X. 1999 – *Rectipilus cistophilus* Esteve-Rav. et Vila sp. nov., un nuevo hongo cifeloides mediterráneo. *Revista catalana de micología* 22, 1–4.
- Vilgalys R, Hester M. 1990 – Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172, 4238–4246.
- Villarreal M, Esteve-Raventós F, Sánchez F, Pérez-Dz-Gregorio MA. 2021 – *Chrysomyceia dunicola* comb. nov. (*Agaricales*, *Porothelaceae*), un nombre prioritario sobre *Chrysomyceia perplexa*. *Boletín de la Sociedad Micológica de Madrid* 45, 43–52.
- Virág M, Merényi Z, Csernetics Á, Földi C et al. 2022 – Evolutionary morphogenesis of sexual fruiting bodies in *Basidiomycota*: toward a new evo-devo synthesis. *Microbiology and Molecular Biology Reviews* 86, 19–21.
- Vizzini A, Alvarado P, Consiglio G, Marchetti M et al. 2024 – Family matters inside the order *Agaricales*: systematic reorganization and classification of incertae sedis clitocyboid, pleurotoid and tricholomatoid taxa based on an updated 6-gene phylogeny. *Studies in Mycology* 107, 67–148.
- Vizzini A, Consiglio G, Marchetti M. 2019a – *Mythicomyetaceae* fam. nov. (*Agaricineae*, *Agaricales*) for accommodating the genera *Mythicomyces* and *Stagnicola*, and *Simocybe parvispora* reconsidered. *Fungal Systematics and Evolution* 3(1), 41–56.
- Vizzini A, Consiglio G, Marchetti M, Alvarado P. 2020 – Insights into the *Tricholomatineae* (*Agaricales*, *Agaricomycetes*): a new arrangement of *Biannulariaceae* and *Callistosporium*, *Callistosporiaceae* fam. nov., *Xerophorus* stat. nov., and *Pleurocollybia* incorporated into *Callistosporium*. *Fungal Diversity* 101, 211–59.
- Vizzini A, Consiglio G, Marchetti M, Borovička J et al. 2022 – New data in *Porothelaceae* and *Cyphellaceae*: epitypification of *Prunulus scabripes* Murrill, the status of *Mycopan* Redhead, Moncalvo & Vilgalys and a new combination in *Pleurella* Horak emend. *Mycological Progress* 21, 44.
- Vizzini A, Picillo B, Perrone L, Dovana F. 2019b – *Chrysomyceia perplexa* gen. et sp. nov. (*Agaricales*, *Porothelaceae*), a new entity from the Lazio region”. *Rivista Micologica Romana, Bollettino dell’Associazione Micologica Ecologica Romana* 107, 96–107.
- Vu D, Groenewald M, de Vries M, Gehrman T et al. 2019 – Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. *Studies in Mycology* 92, 135–154.
- Wächter D, Melzer A. 2020 – Proposal for a subdivision of the family *Psathyrellaceae* based on a taxon rich phylogenetic analysis with iterative multigene guide tree. *Mycological Progress* 19, 1151–1265.
- Walther G, Garnica S, Weiß M. 2005 – The systematic relevance of conidiogenesis modes in the gilled *Agaricales*. *Mycological Research* 109, 525–544.
- Wang CG, Zhao H, Liu HG, Zeng GY et al. 2023a – A multigene phylogeny clarifies species diversity, taxonomy, and divergence times of *Ceriporia* and other related genera in *Irpicaceae* (*Polyporales*, *Basidiomycota*). *Mycosphere* 14, 1665–1729.
- Wang CG, Dai YC, Kout J, Gates GM et al. 2024 – Multi-gene phylogeny and taxonomy of *Physisporinus* (*Polyporales*, *Basidiomycota*). *Mycosphere* 15, 1455–1521.
- Wang GS, Cai Q, Hao YJ, Bau T et al. 2023b – Phylogenetic and taxonomic updates of *Agaricales*, with an emphasis on *Tricholomopsis*. *Mycology* 15, 180–209.
- Wang K, Du Z, Hong P, Zhao MJ et al. 2025 – Taxonomy of *Collybiopsis* spp. and *Gymnopus* spp. in China. *Journal of Liaocheng University (Natural Science Edition)* 38, 76–91.
- Wannathes N, Desjardin DE, Hyde KD, Perry BA et al. 2009 – A monograph of *Marasmius* (*Basidiomycota*) from Northern Thailand based on morphological and molecular (ITS sequences) data. *Fungal Diversity* 37, 209–306.
- White TJ, Bruns T, Lee S, Taylor J. 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis M.A., Gelfand D.H., Sninsky J.J., White T.J., editor. *PCR protocols: a guide to methods and applications*. San Diego: Academic Press; pp. 315–322.

- White VS. 1902 – The *Nidulariaceae* of North America. Bulletin of the Torrey Botanical Club 29, 251–280.
- Wilson AW, Desjardin DE. 2005 – Phylogenetic relationships in the gymnopoid and marasmioid fungi (*Basidiomycota*, euagarics clade). Mycologia 97, 667–679.
- Wilson AW, Desjardin DE, Horak E. 2004 – *Agaricales* of Indonesia. 5. The genus *Gymnopus* from Java and Bali. Sydowia 56, 137–210.
- Wu, F, Man XW, Tohtirjap A, Dai YC. 2022a – A comparison of polypore funga and species composition in forest ecosystems of China, North America, and Europe. Forest Ecosystems 9, 100051.
- Wu F, Zhou LW, Vlasák J, Dai YC. 2022b – Global diversity and systematics of *Hymenochaetaceae* with poroid hymenophore. Fungal Diversity 113, 1–192.
- Wu F, Zhou LW, Yang ZL, Bau T et al. 2019 – Resource diversity of Chinese macrofungi: edible, medicinal and poisonous species. Fungal Diversity 98, 1–76.
- Wu SH, Wang DM, Tschene E. 2007 – *Brunneocorticium pyriforme*, a new corticioid fungal genus and species belonging to the euagarics clade. Mycologia 99, 302–309.
- Yamaguchi K, Degawa Y, Nakagiri A. 2009 – An aero-aquatic fungus, *Peyronelina glomerulata*, is shown to have teleomorphic affinities with cyphelloid basidiomycetes. Mycoscience 50, 156–164.
- Yang Y, Li R, Liu CM, Zhao CL. 2023 – Morphological and molecular identification for two new species of wood-inhabiting macrofungi (*Basidiomycota*) from Yunnan-Guizhou Plateau, China. Phytotaxa 591, 1–18.
- Yang Y, Xu Y, Wang L, Jiang QQ et al. 2025 – Multigene phylogeny of seven wood-inhabiting fungal orders in *Basidiomycota*, and proposal of a new genus and thirteen new species. Mycosphere 16(1), 245–295.
- Yang ZL, Feng B, Hao YJ. 2013 – *Pseudoarmillariella bacillaris*, a new species with bacilliform basidiospores in Asia. Mycosystema 32, 127–132.
- Yuan Y, Bian LS, Wu YD, Chen JJ et al. 2023 – Species diversity of pathogenic wood-rotting fungi (*Agaricomycetes*, *Basidiomycota*) in China. Mycology 14(3), 204–226.
- Zhang H, Xiao YX, Tan Z M, Shen AR et al. 2024a – *Mycena brunnescens* (*Basidiomycota*, *Mycenaceae*), a new species of *Mycena* sect. *Pterigenae* from China. Biodiversity Data Journal 12, e125570.
- Zhang QY, Dai YC. 2021 – Taxonomy and phylogeny of the *Favolaschia calocera* complex (*Mycenaceae*) with descriptions of four new species. Forests 12, 1397.
- Zhang QY, Liu HG, Li WY, Zhang X et al. 2024b – Three new species of *Favolaschia* (*Mycenaceae*, *Agaricales*) from South China. In: Wijayawardene N, Karunarathna S, Fan X-L, Li Q-R (Eds) Taxonomy and secondary metabolites of wood-associated fungi. MycoKeys 104, 71–89.
- Zhang QY, Liu HG, Papp V, Zhou M et al. 2023a – New insights into the classification and evolution of *Favolaschia* (*Agaricales*, *Basidiomycota*) and its potential distribution, with descriptions of eight new species. Mycosphere 14, 777–814.
- Zhang QY, Si J, Li HJ. 2023b – A new *Marasmius* species (*Agaricales*, *Marasmiaceae*) with sessile basidiomata growing on wood, from Yunnan, China. Phytotaxa 578, 169–179.
- Zhang QY, Zhou M, Shi FM, Si J et al. 2023c – *Collybiopsis bambusicola* sp. nov. in Yunnan Province, Southwestern China. Phytotaxa 578, 125–135.
- Zhao CL, Chen H, He SH, Dai YC. 2016 – *Radulotubus resupinatus* gen. et sp. nov. with a poroid hymenophore in *Pterulaceae* (*Agaricales*, *Basidiomycota*). Nova Hedwigia 103, 265–278.
- Zhao CL, Qu MH, Huang RX, Karunarathna SC. 2023a – Multi-Gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (*Polyporales*, *Basidiomycota*). Journal of Fungi 9, 320.
- Zhao H, Nie Y, Zong TK, Wang K et al. 2023b – Species diversity, updated classification and divergence times of the phylum Mucoromycota. Fungal Diversity 123, 49–157.

- Zhao H, Vlasák J, Yuan Y. 2023c – Outline, phylogenetic and divergence times analyses of the genus *Haploporus* (*Polyporales*, *Basidiomycota*): two new species are proposed. *MycoKeys* 98, 233–252.
- Zhao H, Wu F, Maurice S, Pavlov IN et al. 2025 – Large-scale phylogenomic insights into the evolution of the *Hymenochaetales*. *Mycology* 16(2), 617–634.
- Zhao H, Wu YD, Yang ZR, Liu HG et al. 2024 – Polypore fungi and species diversity in tropical forest ecosystems of Africa, America and Asia, and a comparison with temperate and boreal regions of the Northern Hemisphere. *Forest Ecosystems* 11, 100200.
- Zhao RL, Desjardin DE, Soyong K, Hyde KD. 2008 – A new species of bird's nest fungi: characterisation of *Cyathus subglobisporus* sp. nov. based on morphological and molecular data. *Persoonia* 21, 71–76.
- Zhao RL, Li GJ, Sánchez-Ramírez S, Stata M et al. 2017 – A six-gene phylogenetic overview of *Basidiomycota* and allied phyla with estimated divergence times of higher taxa and a phyloproteomics perspective. *Fungal Diversity* 84, 43–74.
- Zhou HM, Dai YC, Bian LS, Liu HG et al. 2025. Diversity, divergence time, and biogeography of the genus *Albatrellus* (*Agaricomycetes*, *Russulales*). *Mycology* 16(2), 738–776.
- Zhou M, Liu ZB, Lim YW, Cho Y et al. 2022 – Two new species of *Fistulina* (*Agaricales*, *Basidiomycota*) from the Northern Hemisphere. *Frontiers in Microbiology* 13, 1063038.
- Zíbarová L, Tejklová T. 2019 – Notes on corticioid fungi of the Czech Republic 2. *Athelidium caucasicum* (*Stephanosporaceae*, *Agaricales*). *Czech Mycology* 71, 91–98.