

Notes, taxonomy, and phylogeny of wood-inhabiting fungi in Russulales

Yinglian Deng^{1,2}, Meng Chen², Sicheng Zhang², Kaisheng Wang², Wanting Liu², Yuhan Qiu², Youtong Dou², Xiangfu Liu^{3,4}, Arachchige Subodini Nuwanthika Wijesinghe², Hongmin Zhou^{1,2}, Sana Jabeen⁵ and Changlin Zhao^{1,2,4,6*}

¹ Key Laboratory of Forest Disaster Warning and Control in Universities of Yunnan Province, Southwest Forestry University, Kunming 650224, China

² College of Forestry, Southwest Forestry University, Kunming 650224, China

³ School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand

⁴ Modern Industry School of Edible Fungi, Southwest Forestry University, Kunming 650224, China

⁵ Department of Botany, Division of Science and Technology, University of Education, Township, Lahore, Punjab, Pakistan

⁶ Department Microbial Drugs (MWIS), Helmholtz-Centre for Infection Research, 38124 Braunschweig, Germany

* Correspondence: fungi@swfu.edu.cn (Zhao C)

Abstract

The order Russulales includes fungi with diverse basidiomata types. As one of the most species-rich orders within the phylum Basidiomycota, it comprises over 4,000 described species. These members are important forestry fungi, occurring on both angiosperms and gymnosperms, richly colonizing different substrates ranging from living trees, to rotten wood, to ground in almost all forest ecosystems worldwide. However, numerous species still remain to be discovered, and the taxonomy and phylogeny of Russulales is still understudied. To narrow down this study gap to some extent, an in-depth study of taxonomy and phylogenetic relationships of Russulales was conducted. Specimens collected from East Asia were studied, and taxonomic placements of the taxa were confirmed based on morphological and molecular systematic methods. This study represents the most comprehensive analysis to date of wood-inhabiting fungi in Russulales subjected to multi-gene phylogenetic analysis with combined ITS, LSU, mtSSU, *rpb2*, and *tef1- α* sequence data. A comprehensive outline for wood-inhabiting fungi in Russulales is provided, with 14 families and 77 genera having brief notes provided. Two new families, Aleurocystidiellaceae and Gloeodontiaceae, are established to accommodate the genera *Aleurocystidiellum* and *Gloeodontia*, respectively, and one new genus, *Subulicystidiella* is also recognized in the phylogenetic tree of Russulales. Additionally, the family Gloeocystidiellaceae was reactivated to contain *Gloeocystidiellum* s. str. The divergence time inferred from ITS, LSU, *rpb2*, and *tef1- α* sequence data revealed that the order Russulales occurred at a mean crown age of 222.49 Mya (203.38–288.24 Mya, 95% HPD), and the divergence time of the two new families, Aleurocystidiellaceae and Gloeodontiaceae, are 140.94 (87.46–196.71 Mya, 95% HPD) and 178.7 Mya (139.36–218.13 Mya, 95% HPD), respectively. Further, 26 new species belong to six families within the order Russulales were described and illustrated. These are *Aleurodiscus yunnanensis*, *Asterostroma fimbriata*, *Baltazaria pingbianensis*, *Confertotrama cremea*, *C. yunnanensis*, *Dentipellis yingjiangensis*, *Gloeocystidiellum membranaceum*, *G. punctatum*, *Gloeodontia sinensis*, *Gloiothele fragilima*, *G. tuberculata*, *Laxitextum cremeum*, *Megalocystidium bambusinum*, *Stereum convolutomarginatum*, *S. rigidohymeneum*, *S. yunnanense*, *Subulicystidiella murina*, *Vararia asiana*, *V. bambusicola*, *V. bannaensis*, *V. ferruginosa*, *V. lacerata*, *V. membranacea*, *V. muscicola*, *V. pingbianensis*, and *V. wumengshanensis*. This study expands the taxonomic framework of Russulales with the contribution of the present new collections from different Chinese sites.

Citation: Deng Y, Chen M, Zhang S, Wang K, Liu W, et al. 2026. Notes, taxonomy, and phylogeny of wood-inhabiting fungi in Russulales. *Mycosphere* 17: e003 <https://doi.org/10.48130/mycosphere-0026-0003>

Outline of the order Russulales

Order Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David 2001

Family Albatrellaceae Nuss 1980

Albatrellopsis Teixeira 1993

Albatrellus Gray 1821 (= *Ovinus* (Lloyd) Torrend 1920, *Polyporus* sect. *Ovinus* Lloyd 1911)

(Note 1)

Byssoporia M.J. Larsen & Zak 1978

(Note 2)

Leucogaster R. Hesse 1882

Leucophleps Harkn. 1899 (= *Creomeogaster* Mattir. 1924, *Leucophleps* Harkn. 1899)

Mycolevis A.H. Sm. 1965

Polyporoletus Snell 1936

(Note 3)

Scutigera Paulet 1808

Family Aleurocystidiellaceae Y.L. Deng & C.L. Zhao, fam. nov.

(Note 4)

Aleurocystidiellum P.A. Lemke 1964

(Note 5)

Family Auriscalpiaceae Maas Geest. 1963

Artomyces Jülich 1982

(Note 6)

Auriscalpium Gray 1821 (= *Pleurodon* Quéél. ex P. Karst. 1881)

(Note 7)

Dentipratulum Domański 1965

(Note 8)

Gloiodon P. Karst. 1879 (= *Leaia* Banker 1906, *Sclerodon* P. Karst. 1889)

(Note 9)

Lentinellus P. Karst. 1879 (= *Hemicybe* P. Karst. 1879)

Stalpersia Parmasto 2001

Family Bondarzewiaceae Kotl. & Pouzar 1957 (= **Hybogasteraceae** Jülich 1982)

(Note 10)

Amylaria Corner 1955

(Note 11)

- Amylonotus* Ryvarden 1975 (Note 12)
Amyloporus Ryvarden 1973 (= *Rigidoporopsis* I. Johans. & Ryvarden 1979) (Note 13)
Bondarzewia Singer 1940 (= *Hybogaster* Singer 1964) (Note 14)
Heterobasidion Bref. 1888 (= *Spiniger* Stalpers 1974, *Spongioides* Lázaro Ibiza 1916) (Note 15)
Laurilia Pouzar 1959 (Note 16)
Lauriliella Nakasone & S.H. He 2017 (Note 17)
Stecchericum D.A. Reid 1963 (Note 18)
Family Echinodontiaceae Donk 1961 (= **Amylostereaceae** Boidin, Mugnier & Canales 1998)
Amylostereum Boidin 1958 (= *Lloydellopsis* Pouzar 1959, *Trichocarpus* P. Karst. 1889) (Note 19)
Echinodontiellum S.H. He & Nakasone 2017 (Note 20)
Echinodontium Ellis & Everh. 1900 (= *Hydnofomes* Henn. 1900, *Hydnophysa* Clem. 1909) (Note 21)
Larssoniporia Y.C. Dai, Jia J. Chen & B.K. Cui 2015 (Note 22)
Subulicystidiella Y.L. Deng & C.L. Zhao gen. nov. (Note 23)
Family Gloeocystidiellaceae Jülich 1982
Gloeocystidiellum Donk 1931 (Note 24)
Family Gloeodontiaceae Y.L. Deng & C.L. Zhao fam. nov.
Gloeodontia Boidin 1966 (Note 25)
Family Hericiaceae Donk 1964
Dentipellicula Y.C. Dai & L.W. Zhou 2013 (Note 27)
Dentipellis Donk 1962 (= *Amylodontia* Nikol. 1967) (Note 28)
Heridium Pers. 1794 (= *Creolophus* P. Karst. 1879, *Dryodon* Qué. ex P. Karst. 1881, *Friesites* P. Karst. 1879, *Heridium* Schrank 1786, *Hericius* Juss. 1789, *Manina* Banker 1912, *Martela* Adans. 1763, *Martella* Endl. 1836, *Medusina* Chevall. 1826) (Note 29)
Laxitextum Lentz 1956 (Note 30)
Pseudowrightporia Y.C. Dai, Jia J. Chen & B.K. Cui 2015 (Note 31)
Wrightporiopsis Y.C. Dai, Jia J. Chen & B.K. Cui 2015 (Note 32)
Family Peniophoraceae Lotsy 1907 (= **Lachnocladiaceae** D.A. Reid 1965)
Amylofungus Sheng H. Wu 1996 (Note 34)
Asterostroma Masee 1889 (Note 35)
Asterostromella Höhn. & Litsch. 1907
Baltazaria Leal-Dutra, Dentinger & G.W. Grif 2018 (Note 36)
Dendrophora (Parmasto) Chamuris 1987 (Note 37)
Dichostereum Pilát 1926 (Note 38)
Duportella Pat. 1915 (Note 39)
Entomocorticium H.S. Whitney, Bandoni & Oberw. 1987 (Note 40)
Gloiothele Bres. 1920 (Note 41)
Lachnocladium Lév. 1846 (= *Eriocladus* Lév. 1846, *Stelligera* R. Heim 1938, *Stelligera* R. Heim ex Doty 1948) (Note 42)
Metulodontia Parmasto 1968
Parapterulicium Corner 1952 (Note 43)
Peniophora Cooke 1879 (= *Cryptochaete* P. Karst. 1889, *Gloeopeniophora* Höhn. & Litsch. 1907, *Sterellum* P. Karst. 1889) (Note 44)
Sceptrolum K.H. Larss. 2014
Scytinostroma Donk 1956 (= *Licrostroma* P.A. Lemke 1964 = *Michenera* Berk. & M.A. Curtis 1868) (Note 45)
Vararia P. Karst. 1898 (= *Denrophysellum* Parmasto 1968) (Note 46)
Vesiculomyces E. Hagstr. 1977
Family Russulaceae Lotsy 1907
Boidinia Stalpers & Hjortstam 1982 (Note 47)
Gloeopeniophorella Rick 1934 (Note 48)
Lactarius Pers. 1797 (= *Agaricus* subdiv. *Galorrhues* Fr. 1818, *Arcangiella* Cavara 1900, *Galorrhues* (Fr.) Fr. 1825, *Gastrolactarius* R. Heim 1971, *Gastrolactarius* R. Heim ex J.M. Vidal 2005, *Gloeocybe* Earle 1909, *Hypophyllum* Earle 1909, *Lactariella* J. Schröt. 1889, *Zelleromyces* Singer & A.H. Sm. 1960) (Note 49)
Lactifluus (Pers.) Roussel 1806 (= *Lactariopsis* Henn. 1901, *Pleurogala* Redhead & Norvell 1993) (Note 50)
Multifurca Buyck & V. Hofst. 2008 (Note 51)
Pseudoxenasma K.H. Larss. & Hjortstam 1976 (Note 52)
Russula Pers. 1796 (= *Bucholtzia* Lohweg 1924, *Cystangium* Singer & A.H. Sm. 1960, *Dixophyllum* Earle 1909, *Elasmomyces* Cavara 1897, *Gymnomyces* Masee & Rodway 1898, *Hypochanum* Kalchbr. 1876, *Lactarellis* Earle 1909, *Macowanites* Kalchbr. 1882, *Martellia* Mattir. 1900, *Omphalomyces* Battarra ex Earle 1909, *Phaeohygrocybe* Henn. 1901, *Russulina* J. Schröt. 1889)
Family Stereaceae Pilát 1930 (Note 53)
Acanthobasidium Oberw. 1965 (Note 54)
Acanthofungus Sheng H. Wu, Boidin & C.Y. Chien 2000
Acanthophysellum Parmasto 1967 (Note 55)
Acanthophysium (Pilát) G. Cunn. 1963
Aleurobotrys Boidin 1986
Aleurodiscus Rabenh. ex J. Schröt. 1888 (= *Aleurobotrys* Boidin 1985, *Aleurodiscus* Cooke 1885, *Aleurodiscus* Rabenh. 1874, *Gloeomyces* Sheng H. Wu 1996, *Gloeosoma* Bres. 1920, *Nodularia* Peck 1871)
Aleuromyces Boidin & Gilles 2002
Amylohyphus Ryvarden 1978
Amylosporomyces S.S. Rattan 1977 (Note 57)
Conferticium Hallenb. 1980 (Note 58)
Confertotrama Nakasone & S.H. He 2025 (Note 59)
Coniophorafomes Rick 1934
Dextrinocystidium Sheng H. Wu 1996

<i>Gelatinostereum</i> S.H. He, S.L. Liu & Y.C. Dai 2025	(Note 60)
<i>Gloeocystidiopsis</i> Jülich 1982	(Note 61)
<i>Gloeomyces</i> Sheng H. Wu 1996	(Note 62)
<i>Gloeosoma</i> Bres. 1920	(Note 63)
<i>Megalocystidium</i> Jülich 1978	(Note 64)
<i>Neoleurodiscus</i> Sheng H. Wu 2010	(Note 65)
<i>Scotoderma</i> Jülich 1974	
<i>Stereodiscus</i> Rajchenb. & Pildain 2021	(Note 66)
<i>Stereum</i> Hill ex Pers. 1794 (= <i>Haematostereum</i> Pouzar 1959)	(Note 67)
<i>Xylobolus</i> P. Karst. 1881	(Note 68)
Family Terrestriporiaceae Y.C. Dai, B.K. Cui, F. Wu, Y. Yuan & Jia J. Chen 2020	(Note 69)
<i>Terrestriporia</i> Y.C. Dai, B.K. Cui, F. Wu, Y. Yuan & Jia J. Chen 2020	(Note 70)
Family Wrightporiaceae Jülich 1982	
<i>Wrightporia</i> Pouzar 1966	(Note 71)
Russulales genera incertae sedis	
<i>Dentipellopsis</i> Y.C. Dai & L.W. Zhou 2013	(Note 72)
<i>Dichantharellus</i> Corner 1966	
<i>Dichopleuropus</i> D.A. Reid 1965	
<i>Gloeoaerostroma</i> Rick 1938	
<i>Gloehyphochnicium</i> (Parmasto) Hjortstam 1987	(Note 73)
<i>Haloaleurodiscus</i> N. Maek., Suhara & K. Kinjo 2005	(Note 74)
<i>Laeticutis</i> Audet 2010	
<i>Neoalbatrellus</i> Audet 2010	(Note 75)
<i>Perplexostereum</i> Ryvarden & S. Tutka 2014	(Note 76)
<i>Polypus</i> Audet 2010	
<i>Scopulodontia</i> Hjortstam 1998	
<i>Scytinostromella</i> Parmasto 1968 (= <i>Confertobasidium</i> Jülich 1972)	
<i>Xeroceps</i> Audet 2010	

Introduction

Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David is one of the significant fungal orders, comprising wood-inhabiting fungi within Agaricomycetes, Basidiomycota^[1–4]. The concept of Russulales was initially proposed in 1969, and later accepted and amended by Kirk^[4], and it was erected with the type family Russulaceae Lotsy^[4]. Approximately 4,500 species have been ascribed to Russulales, which contains 98 genera, within 11 families^[1,4–7]. Members of Russulales exhibit a wide range of ecological strategies including saprotrophic wood rotting, tree root and heartwood pathogens, ectomycorrhizal, and association with insects as entomogenous fungi^[4,8]. The genus *Heterobasidium* Bref. was indigenous to many areas and an important ecological factor involved in nutrient cycling, forest regeneration, and forest succession, such as *Heterobasidium occidentale* Otrösina & Garbel. and *H. irregulare* Garbel. & Otrösina as entry plant quarantine fungi in North America, and *H. abietinum* Niemelä & Korhonen, *H. annosum* (Fr.) Bref., and *H. parviporum* Niemelä & Korhonen as entry plant quarantine fungi in Europe^[4,9–13]. Species of *Albatrellus* have been reported as significant ectomycorrhizal fungi^[4,14]. They also formed mutualistic symbiotic relationships with plants, especially Pinaceae^[4,15], and some angiosperms^[4,16], aiding in nutrient uptake and enhancing plant growth^[17]. *Albatrellus ovinus* (Schaeff.) Kotl. & Pouzar is a common edible mushroom reported in Europe and North America^[17–19].

Russulales is the most conspicuous and largest group of macrofungi, characterized by highly diverse basidiomata types which can range from agaricoid to discoid, clavarioid, polyporoid, corticioid, and even gasteroid^[1,9–11,20–22]. Among Russulales, the hymenophore types encompass lamellate, hydroid, poroid, labyrinthoid, grandinoid, and a smooth configuration^[17,23,24]. Many species of Russulales share two key morphological characteristics: (1) basidiospore walls exhibit an amyloid reaction combined with an ornamented outline (although there are a few exceptions that have non-amyloid or smooth walls); (2) many of these species possess gloeoplerous hyphae or gloeocystidia containing sesquiterpenes that can be stained by sulphuric benzaldehydes^[25,26]. However, it is worth

noting that in certain genera within the order, these elements may be absent or transformed into homologous structures like lactiferous hyphae^[1].

The morphology of the basidiomata and hymenophore, together with habitat, are often regarded as important characteristics of the order Russulales^[26–28]. Resupinate basidiomata are common in Echinodontiaceae Donk (=Amylostereaceae Boidin, Mugnier & Canales), Peniophoraceae Lotsy, Stereaceae Pilát and Terrestriporiaceae Y.C. Dai, B.K. Cui, F. Wu, Y. Yuan & Jia J. Chen, and rarely present in Hericiaceae Donk and Russulaceae Lotsy^[3,21,29–34]. Pileate basidiomata are predominantly found in Albatrellaceae Nuss, Auriscalpiaceae Maas Geest., Bondarzewiaceae Kotl. & Pouzar, Hericiaceae and Russulaceae; while gasteroid basidiomata are mainly present in Hybogasteraceae Jülich and Russulaceae, rarely in Albatrellaceae^[17,35]. Clavarioid basidiomata are present in Auriscalpiaceae, Bondarzewiaceae and Peniophoraceae, while effused-reflexed basidiomata are infrequently scattered in Auriscalpiaceae, Echinodontiaceae, Hericiaceae, Peniophoraceae, and Stereaceae^[1,3,12,25,28].

Fungal classification was traditionally based on comparative morphology, anatomy, biochemistry, physiology, and ecology^[2,5,6,36,37]. The systematics of fungi has been revolutionized by advancements in molecular biology, phylogenetics, and bioinformatics. Nowadays, morphology integrated with DNA sequence-based classification and identification has become the standard approach in fungal taxonomy^[35,38–43]. In the past few decades, evidence supporting the monophyly of Russulales has been gathered through both morphological characteristics and DNA sequence phylogenetic analyses^[1,6,10,42]. Miller et al.^[27] first explored the molecular phylogeny of Russulales with an emphasis on the agaricoid, gasteroid and pleurotoid taxa in family Russulaceae, according to the current accepted classification^[25], which indicated that these taxa were not clustered strictly according to their basidiomata morphology. Larsson & Larsson^[26] subsequently sampled some additional species producing corticioid basidiomata, and the resulting phylogeny suggested 13 major clades in the order with strong

or moderate bootstrap support, as /peniophorales, /amylostereaceae, /gloeocystidiellum I, /gloeocystidiellum II, /auriscalpiaceae, /gloeodontia, /aleurocystidiellum, /hericiaceae, /bondarzewiaceae, /albatrellus, /scytinostromella, /russulales, and /stereales. Following these studies, Russulales was classified into 12 families and 80 genera on the basis of molecular and morphological characters. However, many taxa remain unsampled in phylogenetic analyses of Russulales, and phylogenies of many sampled taxa were not resolved. Some genera such as *Gloeocystidiellum* Donk and *Wrightoporia* Pouzar, are morphologically well defined, whereas they were inferred as polyphyletic or paraphyletic^[28]. Previous research suggested that species of *Wrightoporia* s.l. were mainly placed in the Bondarzewiaceae clade, and the Wrightoporiaceae clade based on ITS and nLSU sequences^[10,26,44]. Phylogenetic studies have supported the monophyletic status of only a few genera, such as *Aleurocystidiellum* P.A. Lemke and *Wrightoporia*, and these genera correspond to two families of their own^[11,21,45,46]. Other genera still require deeper analysis, since they were either intermingled with other taxa or possess or lack characters that intermingle with those present in other genera^[1,19,21,46]. Thus, the question remained as to whether to treat them in a broad or narrow sense^[46].

Some studies have shown a relatively constant relationship between differences in the amino acid sequences and divergence time of species^[47,48]. Recently, divergence time was used as an important criterion for the classification and estimation of evolutionary time of Basidiomycota^[1,5,13,49–51]. The phylogenomic analysis suggested that the subphyla diverged in a time range of 443–490 Mya (million years), classes in a time range of 312–412 Mya, and orders in a time range of 102–361 Mya, families diverged in a time range of 50–289 Mya, 76–224 Mya, and 62–156 Mya in Agaricomycotina, Pucciniomycotina, and Ustilaginomycotina, respectively^[1]. The Bayesian evolutionary analysis based on the combined ITS + nLSU + *rpb1* + *rpb2* + *tef1- α* dataset indicated an ancient divergence of the family Terrestrisporiaceae from Albatrellaceae during the Cretaceous (124.68 ± 0.39 Mya (million years ago))^[21]. Nevertheless, there is no comprehensive study focused on the divergence times of Russulales and its lower classification ranking.

According to geographical regions, numerous new fungal species have been found in southwest China and low-latitude tropical and subtropical regions^[20]. These regions have many hills and mountains, extensive vegetation coverage, a high fungi species richness, a mild climate, and abundant rainfall, all of which are conducive to fungal growth, and contribute to a rich species diversity^[20,52]. In recent years, several studies have been conducted on wood-inhabiting fungi in Yunnan Province, China^[20,36,51,53,54]. However, there are still many new taxa that have not been discovered yet, due to the unique geographical environment and vegetation types in Yunnan Province. In this study, the taxon sampling of wood-inhabiting fungi is expanded to investigate taxonomy and phylogeny of new samples within Russulales collected from Yunnan Province. Based on a combination of morphological and molecular evidence of internal transcribed spacer (ITS) region, the large subunit nuclear ribosomal RNA gene (nLSU), the small subunit of mitochondrial rRNA gene (mtSSU), the second largest subunit of RNA polymerase II (*rpb2*), and the translation elongation factor 1- α gene (*tef1- α*) markers, two new families, a new genus, and 26 new species are proposed. The data available to date were used to construct a time-framed phylogenomic tree of Russulales. Based on the recent taxonomic revisions by He et al.^[1] and Liu et al.^[42], and the updated classification of fungi (Outline of Fungi 2024) by Hyde et al.^[7], the currently recognized suborders, families, and number of genera within order Russulales are systematically presented in Table 1.

Table 1. Number of genera within families of Russulales.

Order	Families	Number of genera
Russulales	Albatrellaceae	8
	Aleurocystidiellaceae	1
	Auriscalpiaceae	6
	Bondarzewiaceae	8
	Echinodontiaceae	5
	Gloeocystidiellaceae	1
	Gloeodontiaceae	1
	Hericiaceae	6
	Peniophoraceae	17
	Russulaceae	7
	Stereaceae	23
	Terrestrisporiaceae	1
	Wrightoporiaceae	1
Incertae sedis	13	

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata of the fungi growing on angiosperm branches, and on the ground were collected from Dali, Dehong, Diqing, Honghe, Lincang, Lijiang, Puer, Qujing, Wenshan, Tengchong, Xishuangbanna, and Zhaotong in Yunnan Province, China. Voucher specimens were dried in an electric food dehydrator at 40 °C, and then deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China. The samples were photographed *in situ*, and fresh macroscopic details were recorded. Photographs were recorded by a Jianeng 80D camera (Tokyo, Japan). All photos were stacked and merged using Helicon Focus Pro 7.7.5 software.

Morphological studies

Macromorphological descriptions and color terminology are based on field notes and photos captured in the field or laboratory, and follow those of a previous study^[36]. Micromorphological characters were obtained from the dried specimens observed using a light microscope following a previous study^[36]. The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB = cotton blue, CB- = acyanophilous, CB+ = cyanophilous, IKI = Melzer's reagent, IKI+ = amyloid, IKI- = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n = a/b (number of spores [a] measured from given number [b] of specimens)^[55].

Molecular procedures and phylogenetic analyses

The EZNA HP Fungal DNA Kit (Omega Biotechnologies Co., Kunming, China) was used with some modifications to extract DNA from the dried specimens. The DNA samples were kept at -20 °C. The thermal cycling conditions for each locus are provided in Table 2. The amplified fragments were internal transcribed spacer ITS (ITS5 and ITS4), the large subunit nuclear ribosomal RNA gene nLSU (LR0R and LR7), the small subunit of mitochondrial rRNA gene mtSSU (MS1 and MS2), the translation elongation factor 1- α gene *tef1- α* (*ef1-983 F* and *ef1-2218R*), RNA polymerase II largest subunit *rpb1* (*rpb1-Af* and *rpb1-Cf*), and the second large subunit of RNA polymerase II *rpb2* (*brpb2-6F* and *brpb2-7.1R*)^[56–60]. The components of a 30 μ L volume PCR mixture were 12.5 μ L of double distilled water, 15 μ L of PCR Master Mix (Sangon Biotech Shanghai Co., Shanghai, China),

Table 2. Gene regions and respective primers used in the study.

Gene region	Primer pairs	Sequence (5'–3')	Annealing temperature (°C)	Ref.
ITS	ITS5	GGAAGTAAAAGTCGTAACAAGG	55	[56]
	ITS4	TCCTCCGCTTATTGATATGC		
nLSU	LR0R	ACCCGCTGAACCTAAGC	48	[61]
	LR7	TACTACCACCAAGATCT		
mtSSU	MS1	CAGCAGTCAAGAATATTAGTCAA TG	52	[56]
	MS2	GCGGATTATCGAATTAATAAC		
<i>tef1-α</i>	<i>ef1-983F</i>	GCYCCYGGHCAYCGTGAYTTYAT	60	[62]
	<i>ef1-2218R</i>	ATGACACCACRACRGRACRGTYTG		
<i>rpb1</i>	<i>rpb1-Af</i>	GARTGYCCDGGDCAYTTYGG	52	[59,60]
	<i>rpb1-Cf</i>	CCNGCDATNCRTRTCCATRTA		
<i>rpb2</i>	<i>brpb2-6F</i>	TGGGGYATGGTNTGYCCYGC	52	[58]
	<i>brpb2-7.1R</i>	CCCATRGCYTYTMMCCCATDGC		

1 µL of each primer and 1 µL of template DNA. The amplification followed the protocol of Dong et al.^[52]. Amplified PCR products were examined through 1.5% agarose gel electrophoresis stained with GoldenView, and sent to Qingke Co., China, for sequencing. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, China. The sequences were reviewed and manually modified with Chromas v.1.0.1.1 to remove low-quality base calls from both ends. All newly generated sequences were subsequently deposited in GenBank (Table 2).

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 procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min and, 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR procedure for mtSSU was as follows: initial denaturation at 94 °C for 2 min, followed by 35 cycles at 94 °C for 45 s, 52 °C for 45 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for *tef1-α* was as follows: initial denaturation at 94 °C for 2.5 min, denaturation at 94 °C for 45 s, annealing at 60 °C for 50 s (minus 1 °C per cycle), extension at 72 °C for 2 min, repeat for 6 cycles starting at step 2, denaturation at 94 °C for 30 s, annealing at 55 °C for 50 s, extension at 72 °C for 1.5 min, repeat for 34 cycles starting at step 6, leave at 72 °C for 5 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^[20,53]. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, China. The newly generated fungal sequences in this study were deposited in GenBank.

Phylogenetic analyses

Phylogenetic analyses followed the methods described in Dissanayake et al.^[63]. 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 (www.ncbi.nlm.nih.gov/nucleotide). The sequences were aligned using MAFFT version 7^[64] with the G-INS-I strategy. The alignment was adjusted manually using AliView version 1.27^[65]. The dataset was initially aligned and later, ITS, nLSU, mtSSU, *rpb2*, and

tef1-α sequences were combined using Mesquite version 3.51. FASTA data file formats were converted to NEXUS formats using the online tool available on the ALTER website (<http://sing.ei.uvigo.es/ALTER/>)^[66]. Phylogenetic trees were constructed based on randomized accelerated maximum likelihood (ML) and Bayesian inference (BI) analyses.

Maximum likelihood analysis was performed using the CIPRES Science Gateway (www.phylo.org/portal2/logininput.action)^[67] 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 analysis was performed on the dataset using MrBayes v3.2.7a^[68]. The best substitution model for the dataset was selected by ModelFinder v2.2.0^[69] 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). Phylogenetic trees were visualized and adjusted using FigTree v1.4.0 (<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 ML equal to or above 70%, and BI equal to or above 0.95, are indicated.

Divergence time estimation

Three fossil calibrations, *Archaeomarasmius leggetti* Hibbett, D. Grimaldi and Donoghue, *Quatsinoporites cranhamii* S. Y. Sm., Currah and Stockey, and *Paleopyrenomycites devonicus* Taylor, Hass, Kerp, M. Krings and Hanlin, were used in the divergence time estimation. *Archaeomarasmius leggetti* was used as the representative of the minimum age of Agaricales at 90 Mya^[70]; *Q. cranhamii* was the representative of the minimum age of Hymenochaetaceae at 125 Mya^[52]; *P. devonicus* was used as the representative of the minimum age between Basidiomycota and Ascomycota at 400 Mya^[71,72]. Divergence time was estimated with the BEAST v2.6.5 software package with ITS, nLSU, *rpb2* and *tef1-α* sequences representing main lineages in Basidiomycota (Table 3). According to these time points, the offset age with a gamma distribution prior (scale = 20, shape = 1) for Agaricales was set as 90 Mya, and for Hymenochaetaceae as 125 Mya. After 20 million generations. The log file was analyzed in Tracer v1.6 to confirm that the estimated effective sample size (ESS) is ≥ 200³. The first 10% of the sampled trees every 1000th generation were removed as burn-in. The resulting log file was checked for chain convergence using Tracer 1.5.

Genealogical concordance phylogenetic species recognition (GCP SR) analysis

The pairwise homoplasy index (PHI) test was conducted in certain cases of species delineation when necessary. We used the genealogical concordance phylogenetic species recognition analysis (GCP SR) to check for significant recombination events^[73]. The data were analyzed using the PHI test in SplitsTree 4 to determine the recombination level with closely related species^[74–76]. ITS and LSU datasets with closely related species were used for the analyses. The pairwise homoplasy index lower than 0.05 ($\Phi_w \leq 0.05$) indicates significant recombination in the dataset. The relationships between closely related taxa were visualized by constructing split graphs from the concatenated datasets using the LogDet transformation and split decomposition options.

Table 3. Taxa used in molecular clock analysis.

Order/family	Species	Sample no.	GenBank accession no.				Ref.
			ITS	nLSU	<i>rpb2</i>	<i>tef1-α</i>	
Agaricales	<i>Asterophora lycoperdoides</i>	CBS 170.86	AF357037	AF223190	DQ367431	DQ367424	[77]
	<i>Gymnopilus picreus</i>	ZRL2015011	LT716066	KY418882	KY419027	KY419077	[77]
Amylocorticiales	<i>Amylocorticiium cebennense</i>	HHB-2808	GU187505	GU187561	GU187770	GU187675	[78]
	<i>Anomoloma myceliosum</i>	MJL-4413	GU187500	GU187559	GU187766	GU187677	[78]
Atheliales	<i>Athelia arachnoidea</i>	CBS 418.72	GU187504	GU187557	GU187769	GU187672	[78]
	<i>Leptosporomyces raunkiaerii</i>	HHB-7628	GU187528	GU187588	GU187791		[78]
Auriculariales	<i>Auricularia heimuer</i>	Xiaoheimao	LT716074	KY418890	KY419035	KY419083	[78]
	<i>Exidia</i> sp.	PBM2527	DQ241774	AY700191		DQ408144	[78]
Boletales	<i>Coniophora arida</i>	FP104367	GU187510	GU187573	GU187775	GU187684	[78]
	<i>Gomphidius roseus</i>	MB 95-038	DQ534570	DQ534669	GU187818	GU187702	[78]
Dacrymycetales	<i>Calocera cornea</i>	AFTOL 438	AY789083	AY701526	AY536286	AY881019	[78]
Geastrales	<i>Dacryopinax spathularia</i>	AFTOL 454	AY854070	AY701525	AY857981	AY881020	[78]
	<i>Geastrum taylorii</i>	OSC59760		DQ218520	DQ219060	DQ219235	[79]
Gomphales	<i>Schenella pityophila</i>	OSC59743		DQ218519	DQ219057	DQ219232	[79]
	<i>Clavariadelphus truncatus</i>	OSC67280		AY574649	DQ219064	DQ219240	[78]
Hymenochaetales	<i>Kavinia alboviridis</i>	0102140		AY574692	DQ219073	DQ219250	[78]
	<i>Fomitiporia mediterranea</i>	AFTOL688	AY854080	AY684157	AY803748	AY885149	[78]
Hysterangiales	<i>Phellinus hartigii</i>	Dai 11766	KT203287	KT203308	KJ651721		[78]
	<i>Aroramycetes gelatinosporus</i>	H4010		DQ218524	DQ218941	DQ219118	[78]
Jaapiales	<i>Chondrogaster pachysporus</i>	OSC49298		DQ218538	DQ218958	DQ219136	[78]
	<i>Jaapia argillacea</i>	CBS252.74	GU187524	GU187581	GU187788	GU187711	[78]
Polyporales	<i>Fomitopsis pinicola</i>	AFTOL 770	AY854083	AY684164	AY786056	AY885152	[78]
	<i>Polyporus squamosus</i>	Cui 10595	KU189778	KU189809	KU189988	KU189925	[78]
Russulales/Albatrellaceae	<i>Albatrellus ovinus</i>	PS11795	MW269673	MW269685	MW290304	MW290320	[26]
	<i>Byssoporia terrestris</i>	Hjm18172	EU118608	EU118608			[45]
-/Aleurocystidiellaceae	<i>Polyporoletus sublividus</i>	JA 030918	DQ389663	DQ389663			[80]
	<i>Aleurocystidiellum bernicchiai</i>	MR12636	MT831037	MT831017			[46]
	<i>Aleurocystidiellum bernicchiai</i>	SPG3217		MT831016			[46]
	<i>Aleurocystidiellum subcruentatum</i>	He2886	KU559341	KU574847		KU992720	[81]
	<i>Aleurocystidiellum subcruentatum</i>	HHB-17353-sp	KU559360	KU574818			[81]
	<i>Aleurocystidiellum tsugae</i>	He4025	KY706211	KY706223			[81]
-/Auriscalpiaceae	<i>Aleurocystidiellum tsugae</i>	He4024	KY706210	KY706222			[81]
	<i>Auriscalpium vulgare</i>	HKAS93484	MK211170	KY485984	KY495319	KY474614	Unpublished
-/Bondarzewiaceae	<i>Dentipratulum bialoviesense</i>	GG1645	AF506389	AF506389			[26]
	<i>Lentinellus cochleatus</i>	KG960928	AF506417	AF506417			[26]
-/Bondarzewiaceae	<i>Bondarzewia occidentalis</i>	HHB-14803	KM243329	KM243332	KX066163	KX066142	[46]
	<i>Heterobasidion annosum</i>	Korhonen 06129/6	KJ583211	KJ583225	KF006499	KX252741	[46]
-/Echinodontiaceae	<i>Laurilia sulcata</i>	He20120916-7	KY172894	KY172909			[82]
	<i>Lauriliella taxodii</i>	FP-105464-Sp	KY172896	KY172912			[82]
-/Echinodontiaceae	<i>Amylostereum chailletii</i>	NH8031	AF506406	AF506406			[26]
	<i>Echinodontiellum japonicum</i>	Dai 7378	KY172887	KY172902			[82]
	<i>Echinodontium tinctorium</i>	HHB-12866-Sp	KY172888	KY172903		MH550371	[26]
	<i>Larssoniporia tropicalis</i>	Ryvarden 45363	KJ513294	KJ807089			[44]
-/Gloeocystidiellaceae	<i>Subulicystidiella murina</i>	CLZhao 30728	PV771055	PX418375			Present study
	<i>Subulicystidiella murina</i>	CLZhao 35801*	PV441140	PV441154			Present study
-/Gloeocystidiellaceae	<i>Gloeocystidiellum clavuligerum</i>	He3376	KY860377	KY860434			Unpublished
	<i>Gloeocystidiellum granulatum</i>	He4301	KY860391	KY860449			Unpublished
	<i>Gloeocystidiellum membranaceum</i>	CLZhao 37038	PV940928	PX070092	PX432797	PX439082	Present study
	<i>Gloeocystidiellum porosellum</i>	Hjm 8851	AY048878	AY048878			Unpublished
	<i>Gloeocystidiellum porosum</i>	HHB-15589-Sp	MK625627	MK625555		MN031003	Unpublished
	<i>Gloeocystidiellum punctatum</i>	CLZhao 20755*	PP356586	PP785346			Present study
-/Gloeodontiaceae	<i>Gloeocystidiellum purpureum</i>	Wu9310-45	AF441338	AF441338			[26]
	<i>Gloeodontia columbiensis</i>	NH 11118	AF506444	AF506444			[26]
	<i>Gloeodontia pyramidata</i>	Ryvarden 15502	AF506446	AF506446			[26]
	<i>Gloeodontia sinensis</i>	CLZhao 34748	PV147171	PV185857		PV400175	Present study
	<i>Gloeodontia subasperispora</i>	GB/KHL8695	AF506404	AF506404			[26]
	<i>Gloeodontia discolor</i>	KHL 10099	AF506445	AF506445			[26]
	<i>Gloeodontia eriobotryae</i>	Dai 12080	JQ349116	JQ349103			[30]
	<i>Gloeodontia yunnanensis</i>	CLZhao 10504	MN908252	MN908254			[83]
-/Hericiaceae	<i>Dentipellis fragilis</i>	Dai14767	MH085943	MH085958			Unpublished
	<i>Hericium americanum</i>	DAOM21467	AF506458	AF506458			[26]

(to be continued)

Table 3. (continued)

Order/family	Species	Sample no.	GenBank accession no.				Ref.
			ITS	nLSU	<i>rpb2</i>	<i>tef1-α</i>	
–/Peniophoraceae	<i>Laxitextum bicolor</i>	Dai14056	KY860393	KY860451			[82]
	<i>Asterostroma muscicola</i>	He4397	MK625630	MK625563		MN030965	[82]
	<i>Baltazaria galactina</i>	He4999	MK625618	MK625547		MN030977	[84]
	<i>Dichostereum boidinii</i>	He4410	MH538315	MH538331		MH550361	[43]
	<i>Gloiothele lamellosa</i>	CBS 404.83	AF506487	AF506487			[26]
	<i>Lachnocladium schweinfurthianum</i>	KM49740	MH260033	MH260051			[85]
	<i>Peniophora quercina</i>	CBS 408.50	MH856688	MH868205			[84]
	<i>Scytinostroma portentosum</i>	EL 11-99	AF506470	AF506470			[26]
	<i>Vararia trinidadensis</i>	CBS:650.84	MH873495	MH873495			[84]
	–/Russulaceae	<i>Lactarius torminosus</i>	CBS 197.72	MH860447	MH872175		
<i>Multifurca ochricompacta</i>		JJ2010.08 (PC0723658)	MH063879	MH063844	MH061176		[86]
<i>Russula delica</i>		FH12-272	KF432955	KR364224	KR364340		[61]
–/Stereaceae	<i>Acanthobasidium delicatum</i>	CBS 233.86	MH861948	MH873638			[84]
	<i>Aleurobotrys botryosus</i>	DAOM211598	AF506398	AF506398			[26]
	<i>Aleurodiscus amorphus</i>	Ghobad- Nejhad2464	KU559342	KU574832		KU992717	[81]
	<i>Confertotrama rugulosa</i>	LodgeSJ 110.1	AF506441	AF506441			[87]
	<i>Gelatinostereum phlebioides</i>	He4492	MW533096	MW528942			Unpublished
	<i>Gloeosoma vitellinum</i>	646cc	MT831039	MT831019			[46]
	<i>Megalocystidium leucoxanthum</i>	HK9808	AF506420	AF506420			[26]
	<i>Stereodiscus antarcticus</i>	MR11265	MT831048	MT831028			[46]
	<i>Stereum hirsutum</i>	He3504	MK625629	MK625557		MN031010	Unpublished
	<i>Xylobolus frustulatus</i>	He2231	MH121216	KU574825		KU992704	[81]
–/Terrestriporiaceae	<i>Terrestriporia alba</i>	Dai 18548	MT068564	MT068560	MW290307	MW290324	[21]
	<i>Terrestriporia alba</i>	Dai 18556	MT068565	MT068561	MW290308	MW290325	[21]
–/Wrightoporiaceae	<i>Wrightoporia avellanea</i>	LR 41710	AF506488	AF506488			[26]
Wrightoporiaceae	<i>Wrightoporia subavellanea</i>	Dai 11484	KJ513295	KJ807085			[26]
Sebacinales	<i>Sebacina</i> sp.	AFTOL 1517	DQ911617	DQ521412			[78]
	<i>Tremellodendron pallidum</i>	AFTOL 699	DQ411526	AY745701	DQ408132	DQ029196	[78]
Sordariales	<i>Neurospora crassa</i>	OR74A	HQ271348	AF286411	AF107789	XM959775	[78]
Thelephorales	<i>Boletopsis leucomelaena</i>	PBM2678	DQ484064	DQ154112	GU187820	GU187763	[78]
	<i>Thelephora ganbajun</i>	ZRL20151295	LT716082	KY418908	KY419043	KY419093	[78]

Results

Molecular phylogeny

Russulales phylogeny based on the ITS + nLSU + mtSSU + *rpb2* + *tef1-α* sequences data (Fig. 1)

The aligned dataset encompassed 104 specimens representing 99 taxa. *Cerioporus squamosus* (Huds.) Quél. and *Trametes suaveolens* (L.) Fr. retrieved from GenBank were used as outgroup taxa (Fig. 1) in previous analysis by Liu et al.^[88]. Trees and parameters were sampled every 1,000 generations. ModelFinder v2.2.0^[69] was used to select the best-fit model based on the BIC criterion. The best model for the combined ITS, nLSU, mtSSU, *rpb2*, and *tef1-α* dataset was estimated as GTR + I + G, and it was applied in the Bayesian analysis. Maximum likelihood (ML) and Bayesian inference (BI) analyses yielded a similar topology, with an average standard deviation of split frequencies of 0.009610 (BI), and an effective sample size (ESS) average ESS (avg. ESS) = 754. The phylogram, based on the combined ITS + nLSU + mtSSU + *rpb2* + *tef1-α* sequence analysis (Fig. 1), showed that Russulales formed 13 distinct lineages, Albatrellaceae, Aleurocystidiellumaceae, Auriscalpiaceae, Bondarzewiaceae, Echinodontiaceae, Gloeocystidiellaceae, Gloeodontiaceae, Hericiaceae, Peniophoraceae, Russulaceae, Stereaceae, Terrestriporiaceae, and Wrightoporiaceae.

The divergence time of the order Russulales based on combined ITS + nLSU + *rpb2* + *tef1-α* sequences data (Fig. 2)

The ITS, nLSU, *rpb2*, and *tef1-α* dataset included 92 collections, of which 59 belonged to Russulales. This dataset resulted in a concatenated alignment of 5,419 characters with GTR + I + G as the best-fit evolutionary model. Chain convergence was indicated by the ESS 499. The result (Fig. 2) showed that Russulales occurred in a mean crown age of 222.49 Mya (179.97–262.75 Mya, 95% HPD). The initial diversification between Hericiaceae and Aleurocystidiellaceae at 140.94 Mya (87.46–196.71 Mya, 95% HPD). The family Gloeodontiaceae occurred in a mean stem age of 178.7 Mya (139.36–218.13 Mya, 95% HPD). Subsequently, the new genus *Subulicystidiella* is grouped into family Echinodontiaceae and occurred in a mean stem age of 114.84 Mya (71.1–161.48 Mya, 95% HPD). The estimated divergence times for other nodes are summarized in Table 4.

Family Gloeocystidiellaceae phylogeny based on combined ITS + nLSU sequences data (Fig. 3)

The aligned dataset encompassed 43 specimens representing 20 taxa, including the two new species, *Gloeocystidiellum membranaceum*, *G. punctatum*, and *Laurilia sulcata* (Burt) Pouzar was retrieved from GenBank as an outgroup in using the concatenated ITS + nLSU sequences dataset analysis (Fig. 3) following the previous study analysis^[89]. The best fit model was estimated as TIM3ef + I + G for the ITS + nLSU dataset, and it was applied in the Bayesian analysis. Four Markov chains were run twice from a random starting

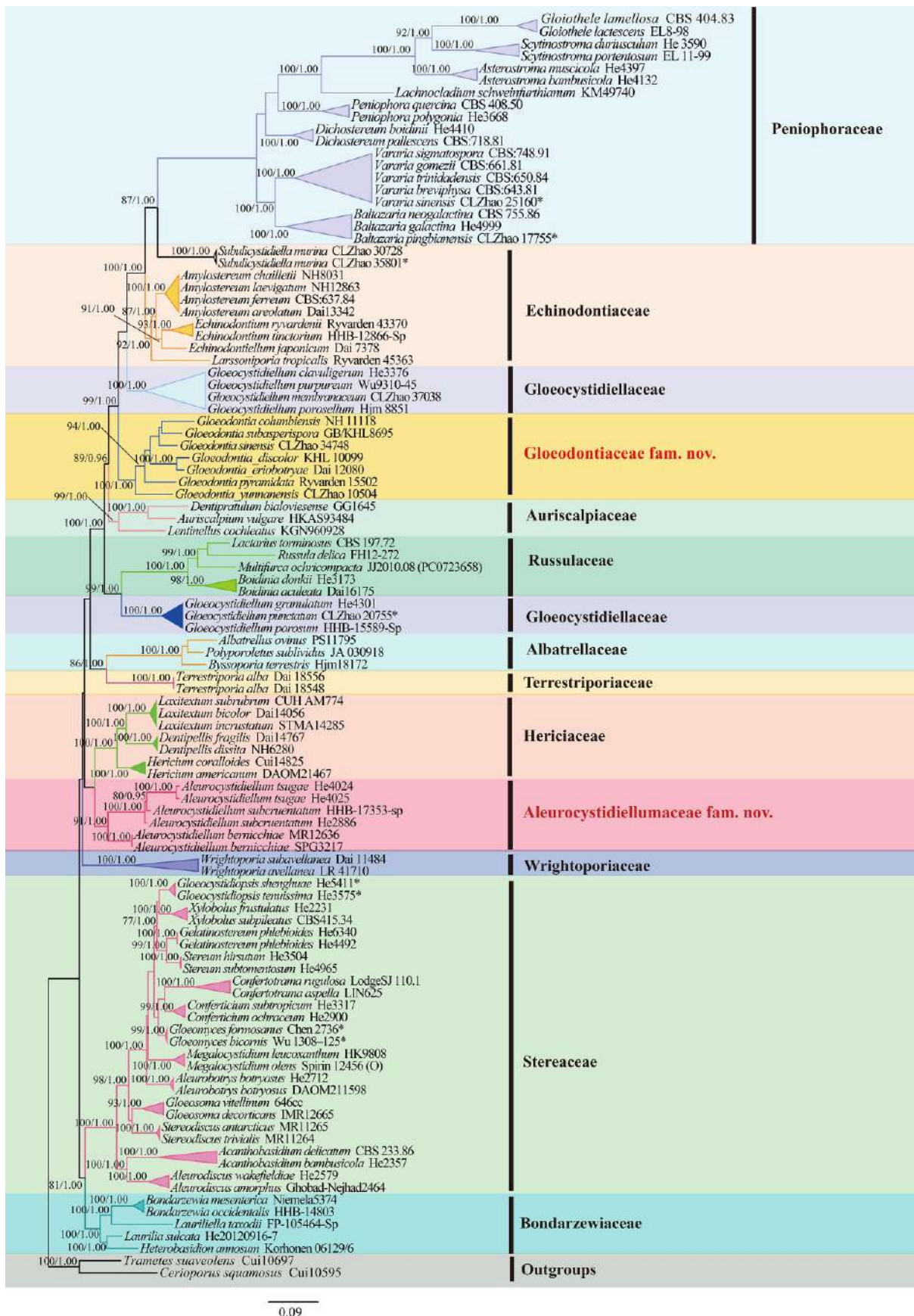


Fig. 1 Maximum likelihood strict consensus tree illustrating the phylogeny of the species of Russulales based on ITS + nLSU + mtSSU + rpb2 + tef1- α sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, and Bayesian posterior probabilities more than 0.95, respectively.

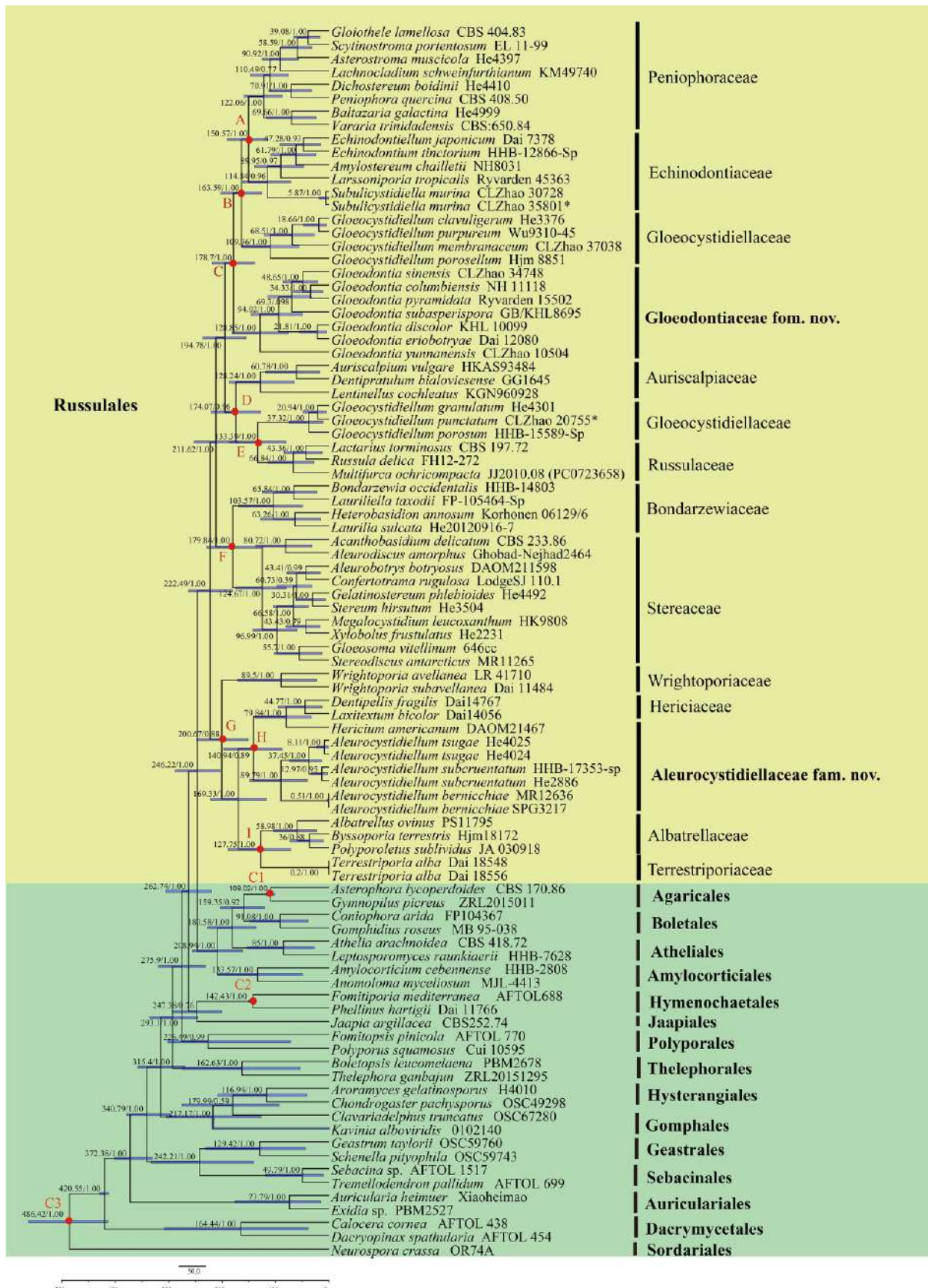


Fig. 2 Divergence time estimation of families within Russulales from molecular clock analysis sampling tree based on the combined sequence dataset of ITS, nLSU, *rbp2*, and *tef1-α*. Posterior probabilities not less than 0.80, and the mean ages of each node are annotated. The 90% highest posterior densities of divergence time estimation are marked by horizontal bars.

Table 4. Estimated divergence time of each node.

Node	Means of stem age (Mya)	95% HPD (Mya) posterior probabilities
A: Peniophoraceae/Echinodontiaceae	150.57	113.56–190.2
B: Gloeocystidiellaceae	163.59	125.46–202.89
C: Gloeodontiaceae	178.7	139.36–218.13
D: Auriscalpiaceae	174.07	128.22–221.01
E: Gloeocystidiellaceae/Russulaceae	133.39	79.96–186.84
F: Bondarzewiaceae/Stereaceae	179.84	126.6–228.84
G: Wrightoporiaceae	200.67	150.99–248.34
H: Hericiaceae/Aleurocystidiellaceae	140.94	87.46–196.71
I: Albatrellaceae/Terrestriporiaceae	127.75	71.29–188.91
C1: Hymenochaetales	142.43	135.31–150.67
C2: Agaricales	109.02	101.26–117.85
C3: Ascomycota/Basidiomycota	486.42	413.94–727.32

tree, for 0.35 million generations of the datasets (Fig. 3) with trees and parameters sampled every 1,000 generations. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.009945 (BI), and the effective sample size (ESS) across the two runs is double of the average ESS (avg ESS) = 1224. The phylogram depicts an overall topology of the genus *Gloeocystidiellum* Donk (Fig. 3) and reveals that *G. membranaceum* Y.L. Deng & C.L. Zhao, and *G. punctatum* Y.L. Deng & C.L. Zhao are grouped into this genus and *G. membranaceum* is retrieved as a sister to *G. porosellum* Hjortstam, and closely clustered with *G. bisporum* Boidin, Lanq. & Gilles. In addition, *G. punctatum* formed a separate clade.

Family Hericiaceae phylogeny based on combined ITS + nLSU sequences data (Fig. 4)

The aligned dataset encompassed 75 specimens representing 53 taxa. *Albatrellus ovinus* (Schaeff.) Kotl. & Pouzar and *A. subrubescens* (Murrill) Pouzar were retrieved from GenBank as the outgroup taxa in using the concatenated ITS + nLSU sequences dataset analysis (Fig. 4), following a previous analysis^[11]. The estimated best fit model was GTR + I + G for the ITS + nLSU dataset, and it was applied in the Bayesian analysis. Four Markov chains were run twice from a random starting tree, for 0.25 million generations of the datasets (Fig. 3) with trees and parameters sampled every 1,000 generations. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis, with an average standard deviation of split frequencies = 0.009780 (BI), and the effective sample size (ESS) across the two runs is double of the average ESS (avg ESS) = 268.

The phylogram depicts an overall topology of family Hericiaceae (Fig. 4), and shows that *Dentipellis yingjiangensis* and *Laxitextum cremeum* are grouped into genera *Dentipellis* Donk and *Laxitextum* Lentz, respectively. *Dentipellis yingjiangensis* Y.L. Deng & C.L. Zhao is retrieved as a sister to *D. rhizomorpha* Yuan Yuan & Y.C. Dai, and closely related to *D. fragilis* (Pers.) Donk, and *D. dissita* (Berk. & Cooke) Maas Geest. In addition, *Laxitextum cremeum* Y.L. Deng & C.L. Zhao is closely related to *L. subrubrum* R. Saha, A.K. Dutta & K. Acharya, *L. bicolor* (Pers.) Lentz, and *L. incrustatum* Hjortstam & Ryvardeen. Furthermore, *Subulicystidiella* Y.L. Deng & C.L. Zhao clustered together within family Echinodontiaceae, and closely related to *Larssoniporia* Y.C. Dai, Jia J. Chen & B.K. Cui, and *Amylostereum* Boidin.

Family Peniophoraceae phylogeny based on combined ITS and nLSU sequence data (Fig. 5)

The aligned dataset encompassed 149 specimens representing 89 taxa. *Stereum ostrea* (Blume & T. Nees) Fr., and *S. hirsutum* (Willd.)

Pers. were retrieved from GenBank as the outgroup taxa in the concatenated ITS + nLSU sequences dataset analysis (Fig. 5) following the method of Deng et al.^[33]. The estimated best fit model was GTR + I + G for the ITS + nLSU dataset, and it was applied in the Bayesian analysis. Four Markov chains were run twice from a random starting tree, for 7.66 million generations of the datasets (Fig. 5) with trees and parameters sampled every 1,000 generations. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis, with an average standard deviation of split frequencies = 0.010000, and the effective sample size (ESS) across the two runs is double of the average ESS (avg ESS) = 2,852.

The phylogram depicts an overall topology of family Peniophoraceae (Fig. 5), and supports the introduction of 13 new species. *Asterostroma fimbriatum* Y.L. Deng & C.L. Zhao is grouped into *Asterostroma*, and retrieved as a sister to *A. muscicola* (Berk. & M.A. Curtis) Masee. *Baltazaria pingbianensis* Y.L. Deng & C.L. Zhao is grouped into *Baltazaria*, and closely related to *B. galactina* (Fr.) Leal-Dutra, Dentinger & G.W. Griff, and *B. neogalactina* (Boidin & Lanq.) Leal-Dutra, Dentinger & G.W. Griff. Two new species *Gloiothele fragilima* Y.L. Deng & C.L. Zhao, and *G. tuberculata* Y.L. Deng & C.L. Zhao are grouped into *Gloiothele*. They are sister to *G. citrina* (Pers.) Ginns & G.W. Freeman, and *G. lamellosa* (Henn.) Bres. and *G. lactescens* (Berk.) Hjortstam., respectively. Nine new *Vararia* species are grouped into genus *Vararia*, in which, *V. asiana* Y.L. Deng & C.L. Zhao is sister to *V. dawei-shanensis* L. Zou & C.L. Zhao, and closely related to *V. rhombospora* Boidin & Lanq; *V. bambusicola* Y.L. Deng & C.L. Zhao is sister to *V. bannaensis* Y.L. Deng & C.L. Zhao; *V. ferruginosa* Y.L. Deng & C.L. Zhao is related to *V. cinnamomea* Boidin, Lanq. & Gilles as a sister; *V. lacerata* Y.L. Deng & C.L. Zhao is sister to *V. muscicola* Y.L. Deng & C.L. Zhao; *V. membranacea* Y.L. Deng & C.L. Zhao is sister to *V. punctata* Y.L. Deng & C.L. Zhao; *V. muscicola* is sister to *V. lacerata*; *V. pingbianensis* is closely related to *V. gomezii* Boidin & Lanq., *V. sigmatospora* Boidin, Gilles & Lanq., and *V. trinidadensis* A.L. Welden. *V. wumengshanensis* Y.L. Deng & C.L. Zhao is grouped as sister to *V. gallica* (Bourdot & Galzin) Boidin.

Family Stereaceae phylogeny based on combined ITS and nLSU sequences data (Fig. 6)

The aligned dataset encompassed 170 specimens representing 100 taxa. *Laurilia sulcata* was retrieved from GenBank as the outgroup taxon in the concatenated ITS+nLSU sequences dataset analysis (Fig. 6) following a previous analysis^[87]. The estimated best fit model was GTR + I + G for the ITS + nLSU dataset, and it was applied in the Bayesian analysis. Four Markov chains were run twice from a random starting tree, for 5.115 million generations of the datasets (Fig. 6) with trees and parameters sampled every 1,000 generations. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.009977, and the effective sample size (ESS) across the two runs is double of the average ESS (avg ESS) = 2255.

The phylogram depicts an overall topology of family Stereaceae (Fig. 6), and eight new species are introduced. *Aleurodiscus yunnanensis* Y.L. Deng & C.L. Zhao is grouped within the genus *Aleurodiscus* and is closely related to *A. wakefieldiae* Boidin & Beller, and *A. subroseus* S.H. He & Y.C. Dai. Two new species, *Confertotrama cremea* Y.L. Deng & C.L. Zhao and *C. yunnanensis* Y.L. Deng & C.L. Zhao grouped with *C. aspella* (Hjortstam) Nakasone & S.H. He, *C. rajchenbergii* (Gorjón & Hallenb.) Nakasone & S.H. He, and *C. rugulosa* (Berk. & M.A. Curtis) Nakasone & S.H. He forming a clade. *Gloeodontia sinensis* Y.L. Deng & C.L. Zhao is grouped into *Gloeodontia* and closely related to *G. columbiensis* Burt ex Burds. & Lombard, and *G. subasperispora* (Litsch.) E. Larss. & K.H. Larss. *Megalocystidium bambusinum* Y.L. Deng & C.L. Zhao formed a separate lineage,

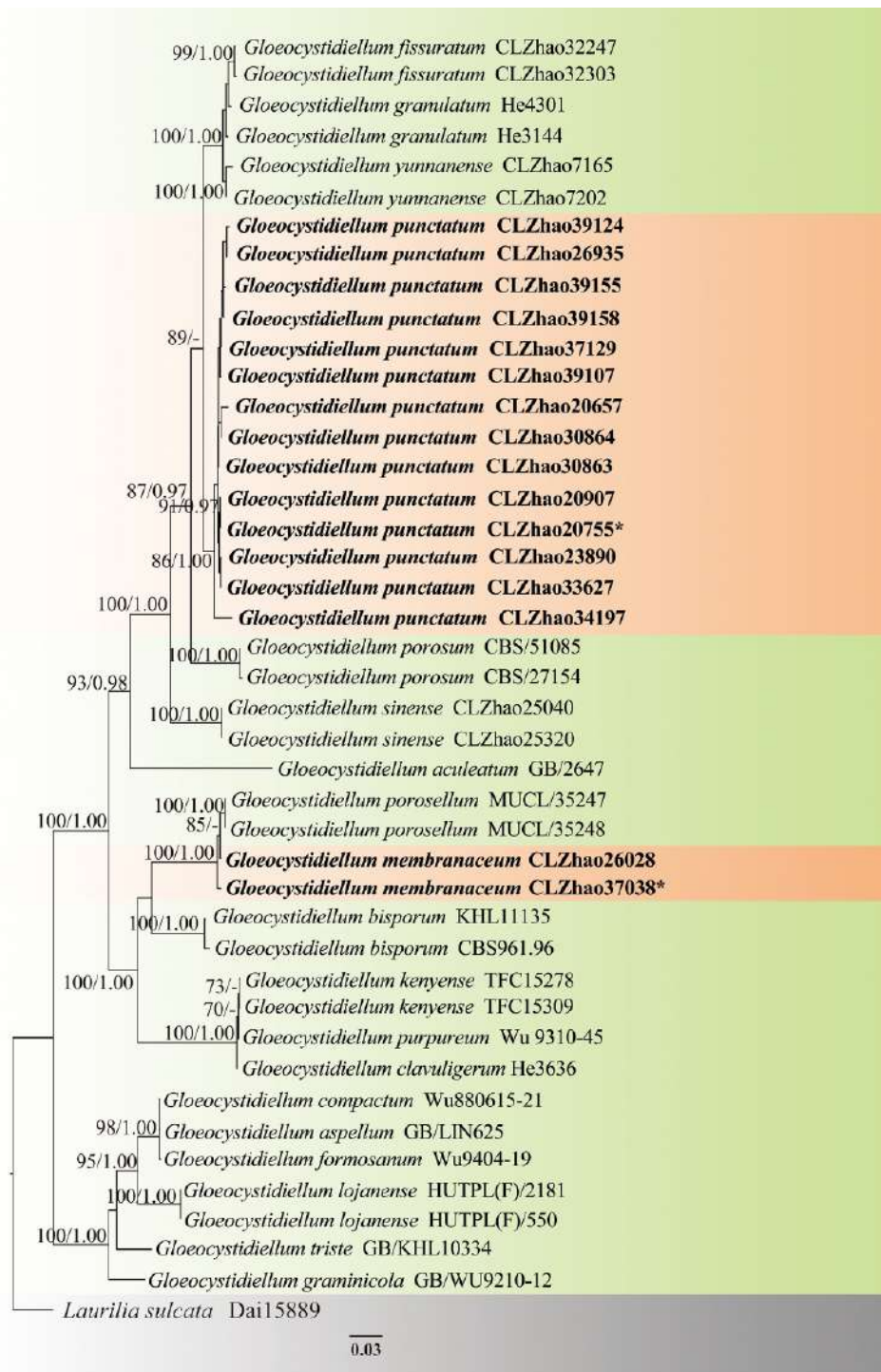


Fig. 3 Maximum likelihood strict consensus tree illustrating the phylogeny of two new species of *Gloeocystidiellum* based on ITS and nLSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, and Bayesian posterior probabilities more than 0.95, respectively. The new species are in bold, and type specimens are indicated with an asterisk (*).

closely related to *M. effusum* S.H. He and *M. brunneum* S.H. He. The three new species, *Stereum convolutomarginatum* Y.L. Deng & C.L. Zhao, *S. rigidohymenium* Y.L. Deng & C.L. Zhao, and *S. yunnanense* Y.L. Deng & C.L. Zhao are grouped within the genus *Stereum* and closely related to *S. ochraceoflavum* (Schwein.) Sacc. and *S. vellereum* Berk., *S. insigne* Bres., and *S. lobatum* (Kunze ex Fr.) Fr., respectively.

Taxonomy:

Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David

Family Albatrellaceae

Nuss 1980

Index Fungorum number: IF80437

Type genus – *Albatrellus* Gray

Notes – Albatrellaceae is characterized by annual, resupinate, pileate-stipitate or gasteroid basidiomata, poroid or locular (gasteroid fungi) hymenophore, monomitic hyphal system, with or without clamp connections, inamyloid or amyloid hyphae, smooth or appearing slightly rough, with a double wall separated by inter-wall pillar or aleveolate, hyaline, inamyloid or amyloid basidiospores.

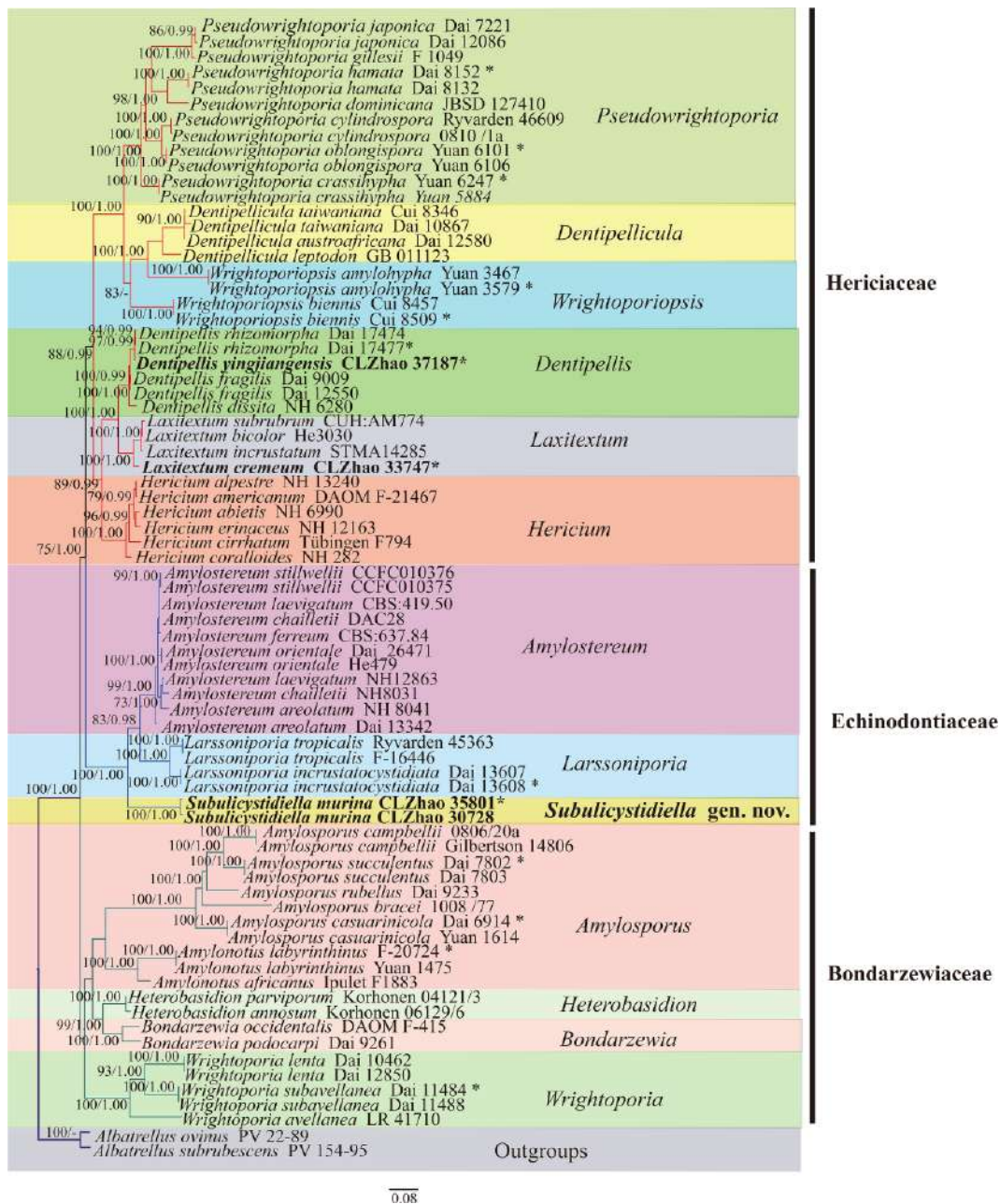


Fig. 4 Maximum likelihood strict consensus tree illustrating the phylogeny of species of family Hericiaceae, and related families based on ITS and nLSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, and Bayesian posterior probabilities more than 0.95, respectively. The new species are in bold, and type specimens are indicated with an asterisk (*).

Currently, eight genera are accepted in family Albatrellaceae^[1,7,17].

Note 1 *Albatrellus* Gray

Index Fungorum number: IF17035

Type species – *Albatrellus albidus* Gray 1821

Notes – *Albatrellus* is a mushroom genus belonging to Russulales, and holds a unique taxonomic status due to its poroid basidiomata^[16,90]. The important identifying features of *Albatrellus* are a poroid hymenophore of mostly white or cream colour, usually inflated hyphae, and smooth and mostly amyloid basidiospores. Initially, the taxonomy of *Albatrellus* was based on morphological studies, and the genus was treated as a polypore^[91–93]. Previous phylogenetic studies of Russulales revealed some *Albatrellus* species clustered in the russuloid clade^[26,94,95]. The taxonomy of European and North American *Albatrellus* has been carried out by various mycologists^[15,91–93,96]. Recently, Zhou et al.^[17] conducted

multi-locus phylogenetic analyses based on seven gene loci (ITS, nLSU, *tef1-α*, *rpb1*, *rpb2*, mtSSU, and nucSSU), and showed that *Albatrellus* formed a polyphyletic group and belonged to family Albatrellaceae. Species within *Albatrellus*, specifically those in *Albatrellus sensu stricto*, are significant ectomycorrhizal fungi^[14]. Some *Albatrellus* species also have edible and medicinal functions (antioxidative and antitumor activities), such as *A. ovinus* (Schaeff.) Kotl. & Pouzar which is a common edible mushroom in Europe and North America^[19,97–99]. Based on Index Fungorum (2025), *Albatrellus* consists of 54 registered names of which 32 species are accepted worldwide.

Note 2 *Byssoporia* M.J. Larsen & Zak 1978

Index Fungorum number: IF17210

Type species – *Byssoporia terrestris* (DC.) M.J. Larsen & Zak 1978

Notes – *Byssoporia* was typified by *B. terrestris* (Pers.) M.J. Larsen &

Zak, a genus proposed for *Poria terrestris* Pers. and its varieties^[100]. It is characterized by effused basidiomata, basidia with 4 sterigmata, and ellipsoid to subglobose basidiospores^[100]. Based on the MycoBank database (2025), and Index Fungorum (2025), *Byssoporia* has seven taxa, but only *B. terrestris* is accepted^[100]. The species diversity of this genus needs to be further explored. Based on the ITS and nLSU dataset, the phylogeny of Russulales showed that *Byssoporia* grouped together with *Albatrellus* and *Polyporoletus* into family Albatrellaceae^[10].

Note 3 *Polyporoletus* Snell

Index Fungorum number: IF18333

Type species – *Polyporoletus sublividus* Snell

Notes – *Polyporoletus* inferred from the specific spores and typified by *P. sublividus* Snell. The genus is characterized by annual fascicular basidiomata, hymenophore with gray to bluish-gray or olive gray pores, monomitic hyphal system, cylindrical basidia and ellipsoid to subglobose basidiospores^[96]. Based on the MycoBank database (2025), and Index Fungorum (2025), *Polyporoletus* has four species, *P. bulbosus* Audet, *P. neotropicus* M. Mata & Ryvarde, *P.*

sublividus, and *P. sylvestris* (Overh. ex Pouzar) Audet. Based on morphological characteristics and the phylogenetic analysis of ITS1, 5.8S, ITS2 sequence data, *Polyporoletus* was closely related to *Albatrellopsis* Teixeira in family Albatrellaceae^[96].

Note 4 Family *Aleurocystidiellaceae* Y.L. Deng & C.L. Zhao, fam. nov.

Index Fungorum number: IF861354

Type genus – *Aleurocystidiellum* P.A. Lemke

Description – Basidiomata annual to perennial, cupulate to substereoid, margin determinate, subcoriaceous, hymenophore smooth, abhymenial sterile surface glabrous. Hyphal system monomitic or dimitic, generative hyphae with clamps. Basidia subclavate with 4-sterigmata and a basal clamp. Basidiospores ovoid to broadly ellipsoid, apiculate, thick-walled, minutely verruculose amyloid in Melzer's^[46,101].

Notes – Lemke^[101] proposed the genus *Aleurocystidiellum*, and it could not be assigned to any recognized family in Russulales. Rajchenberg et al.^[46] proposed two new species combinations, *A. bernicchia* (Gorjón, Gresl. & Rajchenb.) Rajchenb. & Pildain, and *A.*

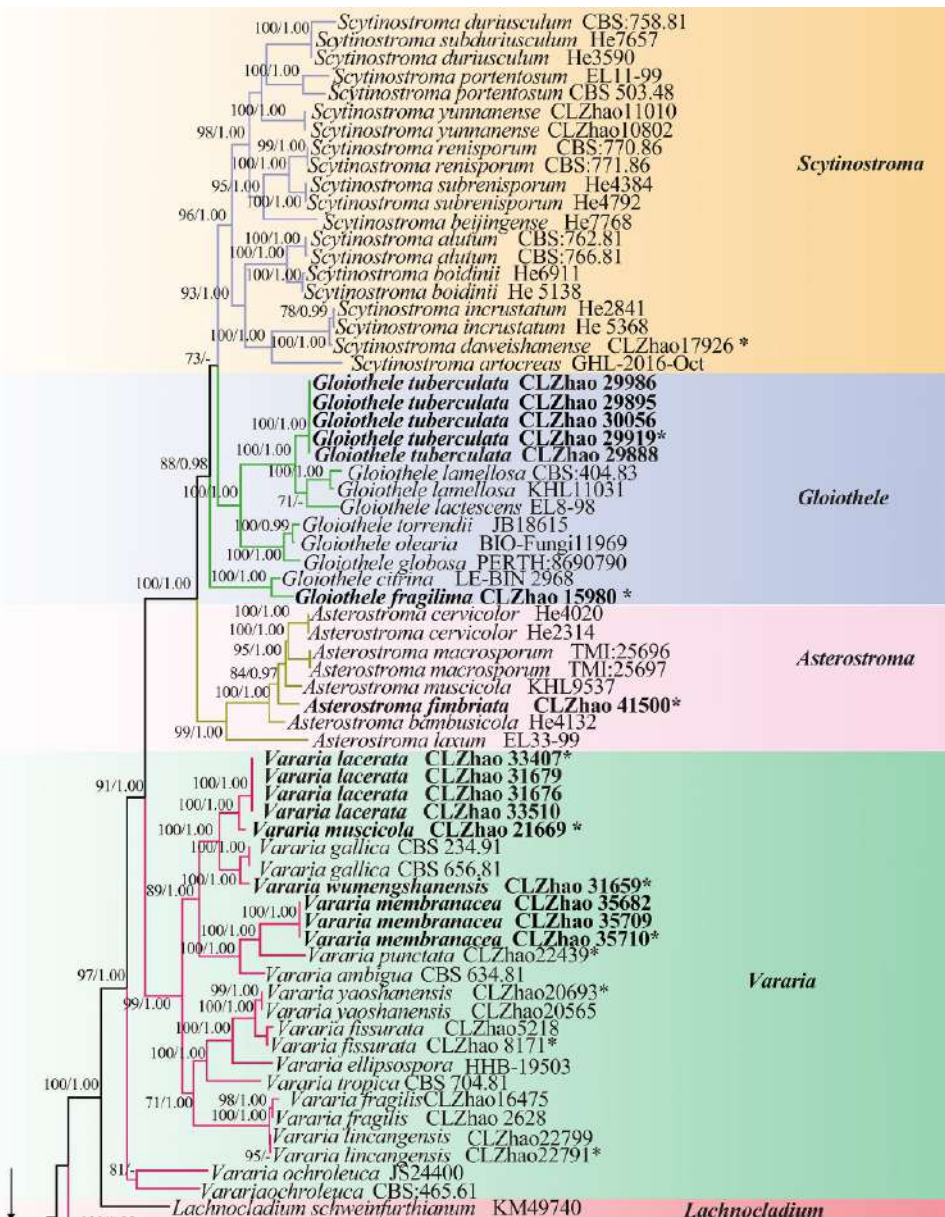


Fig. 5 (to be continued)

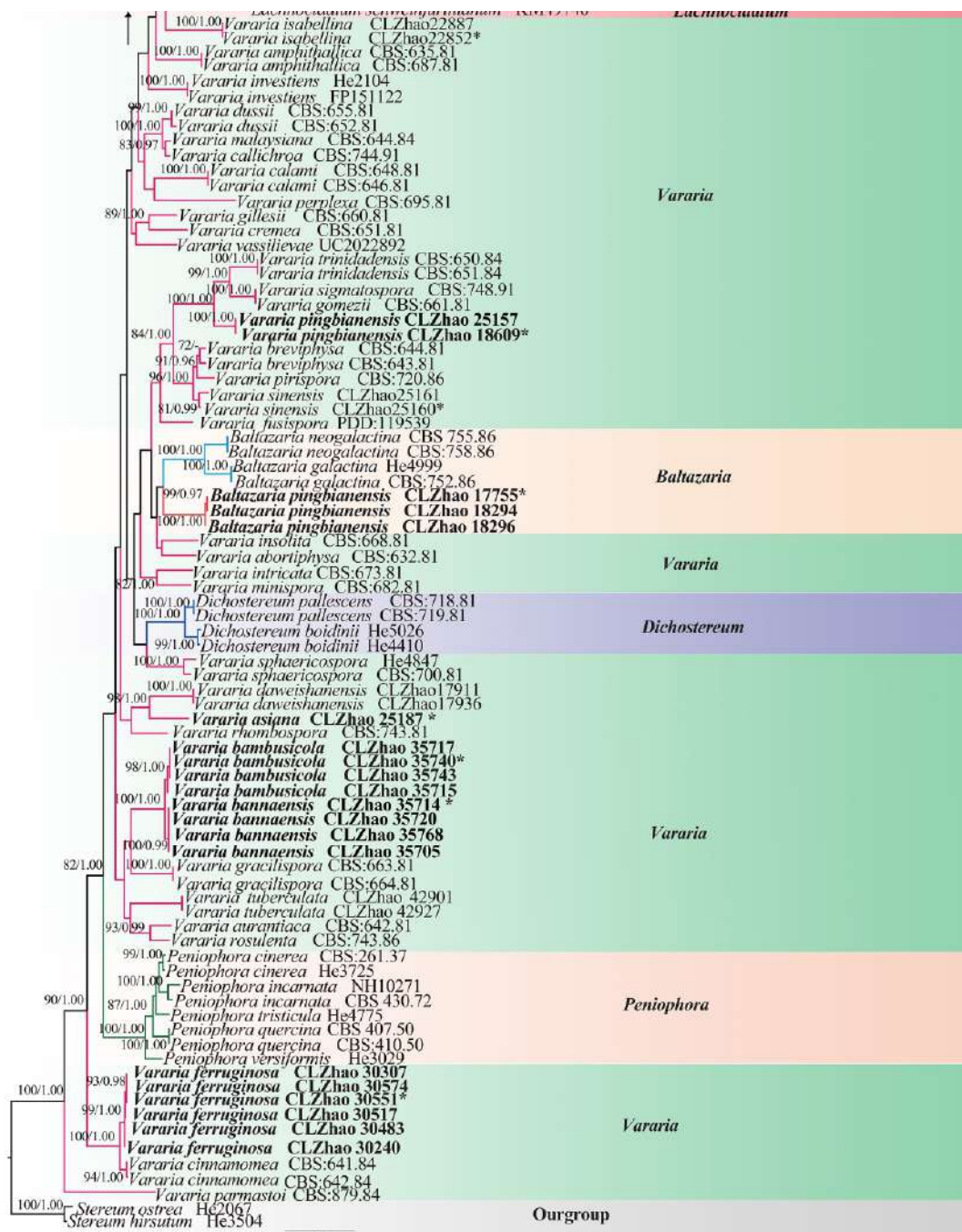


Fig. 5 Maximum likelihood strict consensus tree illustrating the phylogeny of species of family Peniophoraceae based on ITS and nLSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, and Bayesian posterior probabilities more than 0.95, respectively. The new species are in bold, and type specimens are indicated with an asterisk (*).

hallenbergii (Gorjón, Gresl. & Rajchenb.) Rajchenb. & Pildain based on morphology and phylogenetic analyses. However, a phylogenetic tree analysis indicated that *Aleurocystidiellum* formed a separate clade, and did not affiliate in any recognized family of Russulales. In this study, based on combined ITS + nLSU + *rpb2* + *tef1-α* sequence dataset of Russulales in the phylogenetic analyses as well as the divergence time (Figs 1, 2), *Aleurocystidiellum* formed a distinct lineage with strong support within Russulales. The divergence time of the *Aleurocystidiellum* clade is 140.94 Mya, with a 95% highest posterior density (HPD) of 87.46–196.71 Mya, 95% HPD. Therefore, the new family Aleurocystidiellaceae is introduced for this genus.

Note 5 *Aleurocystidiellum* P.A. Lemke 1964

Index Fungorum number: IF17039

Type species – *Aleurocystidiellum subcruentatum* (Berk. & M.A. Curtis) P.A. Lemke

Notes – *Aleurocystidiellum* was established by Lemke^[101] to include dimorphic species with discoid basidiomata and large, minutely verrucose, amyloid spores with *A. subcruentatum* (Berk. & M.A. Curtis) P.A. Lemke as the type species. *Aleurocystidiellum subcruentatum* was previously placed in *Aleurodiscus* based on its discoid basidiomata and the amyloid basidiospores^[101]. Previously, *Aleurodiscus disciformis* (DC.) Pat. was transferred to *Aleurocystidiellum*^[26]. Morphologically, *A. disciforme* (DC.) Tellería has moniliform gloeocystidia rather than skeletocystidia as in *A. subcruentatum* (Berk. & M.A. Curtis) P.A. Lemke, otherwise these two species are

highly similar. The two species formed a distinct clade distant from *Aleurodiscus* s.s. in the phylogenetic trees in previous studies^[101–103]. *Aleurodiscus tsugae* Yasuda ex Lloyd was originally described from Japan on bark of *Tsuga*, and then found on *Pinus* in Japan, the Russian Far East and northeastern China^[102,104]. Careful morphological and molecular studies of the Chinese specimens of *Aleurodiscus tsugae* indicated that it belongs to the genus *Aleurocystidiellum*, and thus a new combination was proposed^[104].

Family Auriscalpiaceae Maas Geest. 1963

Index Fungorum number: IF80506

Type genus –*Auriscalpium* Gray

Notes – Auriscalpiaceae is characterized by annual, resupinate, effused-reflexed, pileate-sessile, pileate-stipitate to clavarioid basidiomata, hydroid, poroid, labyrinthine to daedaleoid, meruloid and lamellate hymenophore. Monomitic to dimitic hyphal system, generative hyphae with clamp-connections, inamyloid or amyloid, skeletal hyphae when present dextrinoid (*Amylonotus*), gloeoplerous hyphae and gloecystidia present or absent, with asperulate,

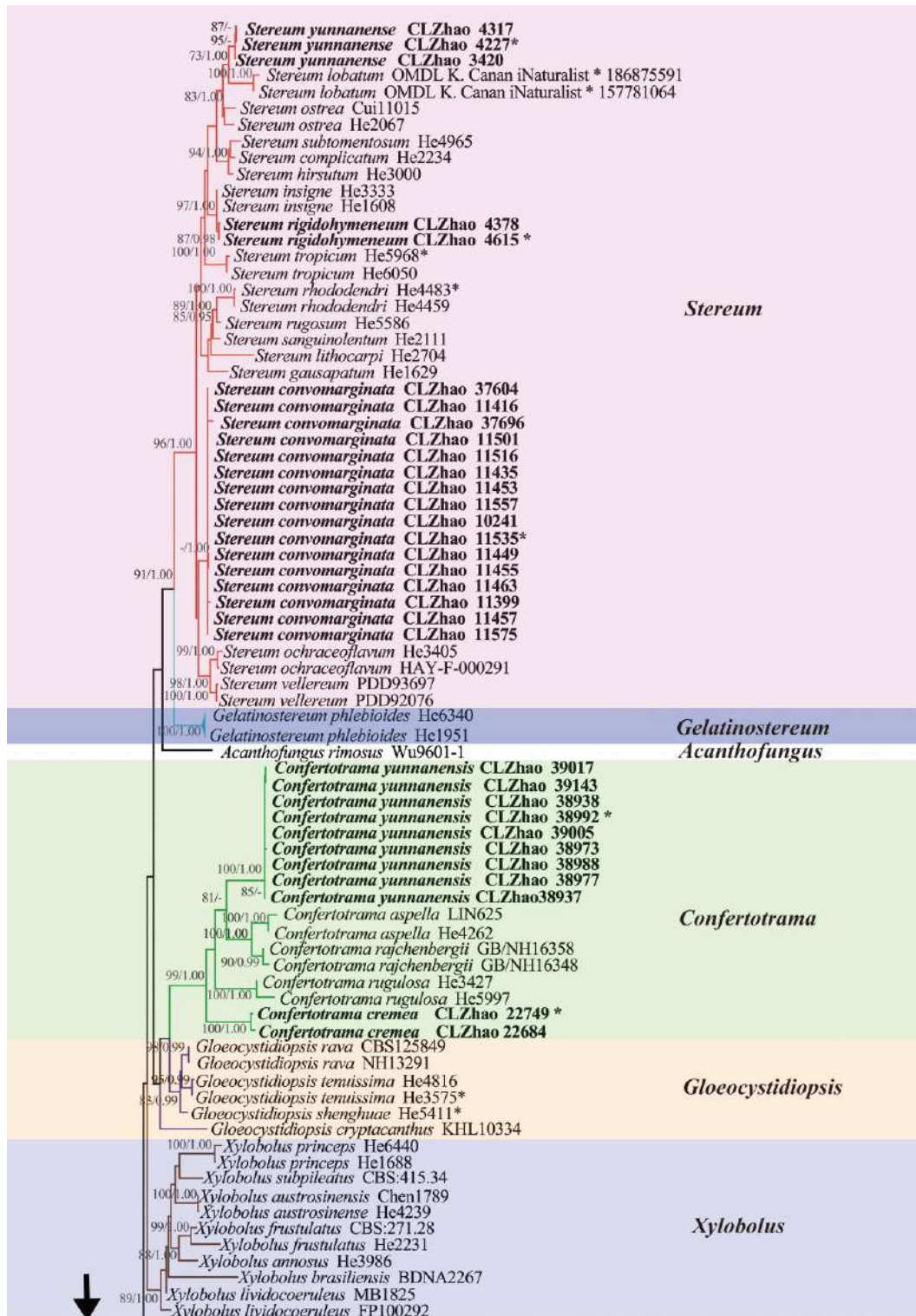


Fig. 6 (to be continued)

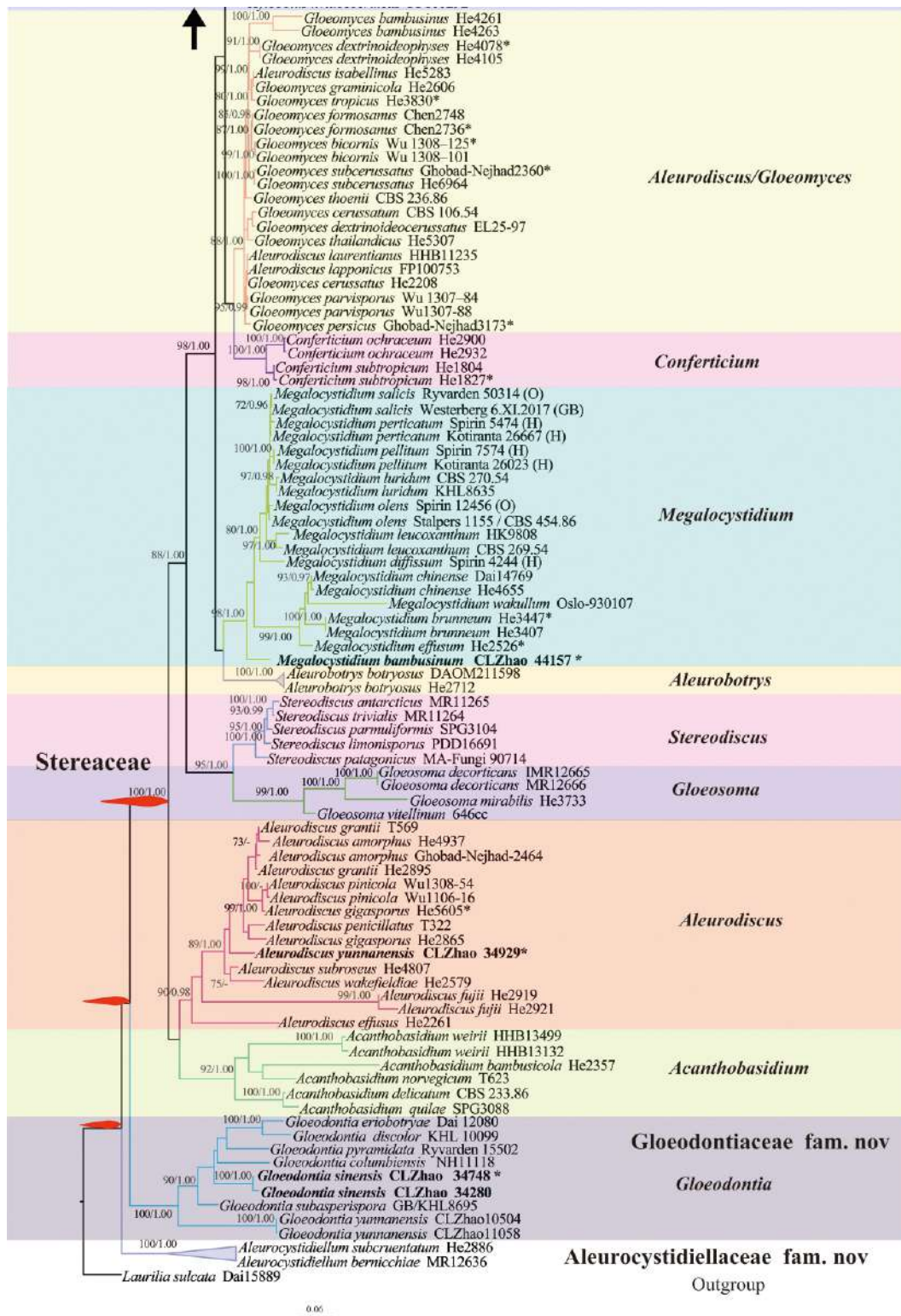


Fig. 6 Maximum likelihood strict consensus tree illustrating phylogeny of species of family Stereaceae and related families based on ITS and nLSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, and Bayesian posterior probabilities more than 0.95, respectively. The new species are in bold, and type specimens are indicated with an asterisk (*).

spinulose, verrucose, hyaline to pigmented, amyloid basidiospores. The species of this family are wood decaying or ectomycorrhizal fungi^[1].

Note 6 *Artomyces* Jülich

Index Fungorum number: IF17104

Type species – *Artomyces pyxidatus* (Pers.) Jülich

Notes – Jülich^[105] introduced *Artomyces*, and typified it with *A. pyxidatus* (Pers.) Jülich, proposing *Artomyces* as a distinct genus separate from *Clavicornia* Doty. Lickey et al.^[106] conducted a comprehensive phylogenetic and taxonomic study for *Artomyces*, accepting 15 species within the genus based on a combination of morphology, nuclear ribosomal internal transcribed spacer DNA

(nrITS DNA) sequences, and mating studies. In addition, they described seven new species. Kneal & Smith^[107] described a new species *A. nothofagi* R.J. Kneal & M.E. Sm., based on morphology and phylogeny. Subsequently, Dong et al.^[52] proposed two new species, *A. niveus* J.H. Dong & C.L. Zhao and *A. yunnanensis* J.H. Dong & C.L. Zhao, based on morphological and molecular evidence. Cai et al.^[108] reported three new species, *A. brunneoalbus* Zhu L. Yang & Q. Cai, *A. hirtipes* Zhu L. Yang & Q. Cai, and *A. pteruloides* Zhu L. Yang & Q. Cai, based on morphological characteristics, ecological traits and molecular phylogenetic evidence in the family Auriscalpiaceae. To date, *Artomyces* consists of 24 registered names of which 22 species are accepted worldwide (Index Fungorum 2025).

Note 7 Auriscalpium Gray

Index Fungorum number: IF17139

Type species – *Auriscalpium vulgare* Gray

Notes – *Auriscalpium* (Auriscalpiaceae, Russulales) has about eight widely distributed species, and is characterized by pale to dark brown basidiocarps that are laterally to centrally stipitate and amyloid-ornamented basidiospores^[109]. The genus is commonly known as 'the cone tooth', and *A. vulgare* is widely reported from the Northern Hemisphere^[109]. It is the only known species of *Auriscalpium* which grows and reproduces on cones of various conifers; all other species inhabit soil or deadwood^[26,109–111]. Wang & Yang^[112] described two species, *A. microsporium* P.M. Wang & Zhu L. Yang, and *A. orientale* P.M. Wang & Zhu L. Yang inferred from morphological characteristics and molecular markers (ITS, nLSU, and *rpb2*). Currently, 19 species are accepted in *Auriscalpium* (Index Fungorum 2025).

Note 8 Dentipratulum Domański

Index Fungorum number: IF17488

Type species – *Dentipratulum bialoviesense* Domański

Notes – Domański^[113] described the genus *Dentipratulum* with *D. bialoviesense* Domański to accommodate this mucronelloid fungus. Domański^[113] placed *Dentipratulum* in family Hericiaceae, but the presence of sulfocystidia detected by Boidin & Gilles^[114] indicated its affinity to family Auriscalpiaceae. The genus is characterized by basidiomata forming clusters of downwards-growing individual spines, scattered or crowded, pointed and unbranched; spines connected with very thin, rudimentary, discontinuous or continuous subiculum; monomitic hyphal system, generative hyphae with clamp connections, hyaline or rarely brownish in subiculum, thin to slightly thick-walled; gloeopleurous hyphae and presenting gloeocystidia, sulfopositive; clavate basidia with 2–4 sterigmata; and broadly ellipsoidal to globose basidiospores, slightly thick-walled, apiculate, ornamented, strongly amyloid, acyanophilous^[115]. Macro-morphological similarities of the basidiomata of *Dentipratulum* and *Mucronella* Fr. are not reflected in their phylogenetic relationships, with *Mucronella* belonging to order Agaricales^[116]. Based on the MycoBank database (2025), and Index Fungorum (2025), *Dentipratulum* has only three species, viz. *D. bialoviesense* Domański, found in the Białowieża Primeval Forest in Poland, and later reported from several locations in Eurasia; *D. crystallinum* Karasiński from the Kuril Islands and France; and *D. khuranae* Karasiński & Piątek from India^[116].

Note 9 Gloiodon P. Karst.

Index Fungorum number: IF17677

Type species – *Gloiodon strigosus* (Sw.) P. Karst.

Notes – *Gloiodon* was introduced by Karsten and typified by *G. strigosus* (Sw.) P. Karst. This genus is characterized by dark brown, effused-reflexed, or sessile basidiomata; spines with very dark but acquiring a whitish or bluish bloom from the ripening spores; dimitic hyphal system with thin-walled generative hyphae and clamp connections; clavate basidia with four spores, and a basal

clamp; broadly ellipsoid basidiospores, minutely spinulose, and amyloid^[117,118]. *Gloiodon* includes five known species, *G. hirtus* (Fr.) P. Karst., *G. nigrescens* (Petch) Maas Geest., *G. occidentalis* Ginns, *G. stratosus* (Berk.) Banker and *G. strigosus*^[12]. According to MycoBank and He et al.^[1], this genus belongs to family Bondarzewiaceae. However, based on the phylogenomic relationships and divergence times of combined ITS + nLSU + mtSSU + *tef1-α* + *rpb2* dataset *Gloiodon* grouped into Auriscalpiaceae.

Note 10 Family Bondarzewiaceae Kotl. & Pouzar 1957 (=Hybogasteraceae Jülich 1982)

Index Fungorum number: IF80527

Type genus – *Bondarzewia* Singer

Notes – The family Bondarzewiaceae was originally introduced to accommodate wood-rotting mushrooms, with type genus *Bondarzewia* Singer^[12,21]. Bondarzewiaceae is characterized by annual to perennial, resupinate, effused-reflexed, pileatesessile, pileate-stipitate to clavarioid basidiomata, smooth, tuberculate, poroid, hydroid hymenophore. The hyphal system is monomitic, pseudodimitic to dimitic, generative hyphae with or without clamp-connections, inamyloid, skeletal hyphae inamyloid or dextrinoid (*Amyloporus*), gloeopleurous hyphae and gloeocystidia present or absent, with asperulate, spinulose, verrucose, echinulate, ridges or crests, hyaline to pigmented, amyloid basidiospores. The family comprises wood decaying fungi^[1]. Later, other genera, such as *Amylaria* Corner, *Amyloporus* Ryvarden, *Heterobasidion* Bref., and *Echinodontium* Ellis and Everh., were added to the family^[26]. However, it was later suggested that *Echinodontium* is sister to *Amylostereum* Boidin and it has been treated under Echinodontiaceae Donk^[45,94,119]. Members of this family are widespread and found in tropical, subtropical, and temperate climates^[1]. Ecologically, these species are mostly associated with wood as decaying fungi; however, some such as *Bondarzewia berkeleyi* (Fr.) Bondartsev and Singer, *B. montana* (Quél.) Singer, *Heterobasidion annosum* (Fr.) Bref., and *H. parviporum* Niemelä and Korhonen, are plant pathogens^[1,5,45,120,121].

Note 11 Amylaria Corner

Index Fungorum number: IF17062

Type species – *Amylaria himalayensis* Corner

Notes – *Amylaria*, typified by *A. himalayensis*. It is characterized by clavarioid basidiomata, hyphal system dimitic with clamped generative hyphae, clavate to subventricose basidia with 2–4 sterigmata and amyloid ellipsoidal basidiospore^[1,25]. *Amylaria* is a monotypic, clavarioid genus reported from Bhutan and Nepal^[25]. The genus has been placed in Bondarzewiaceae according to recent systematics reports^[1]. However, Hussain et al.^[12] declared that the systematic position of this taxon in Bondarzewiaceae is questionable due to lack of sequence data and limited reports of the genus have been made after the original description.

Note 12 Amylonotus Ryvarden

Index Fungorum number: IF17069

Type species – *Amylonotus africanus* Ryvarden

Notes – *Amylonotus* was proposed by Ryvarden^[122] based on *A. africanus*, but species in the genus were later treated in *Wrightoporia* by David & Rajchenberg^[123]. A phylogeny based on ITS + nLSU sequence data revealed that *A. labyrinthinus* (= *Wrightoporia labyrinthina* T. Hatt.), and *A. africanus* (= *W. pouzarii* A. David & Rajchenb.) formed a well-supported lineage within family Bondarzewiaceae clade, distant from *W. lenta* (Overh. & J. Lowe) Pouzar, and closely related to species of *Bondarzewia* Singer and *Heterobasidion* Bref.^[10,11]. *Amylonotus* is characterized by its effused-reflexed or resupinate, sessile, pileate, soft coriaceous to brittle basidiomata with cinnamon to dark brown pileal surface; pale orange, isabelline, pale cinnamon to brown pore surface; hyphal

system dimitic with clamped generative hyphae; thin- to slightly thick-walled, ellipsoid to subglobose, finely asperulate basidiospores^[122]. Five species have been recorded in *Amylonotus*, viz. *A. africanus* Ryvarden, *A. gyroporus* (Corner) Y.C. Dai, Jia J. Chen & B.K. Cui, *A. labyrinthinus* (T. Hatt.) Y.C. Dai, Jia J. Chen & B.K. Cui, *A. ramosus* (A. David & Rajchenb.) Y.C. Dai, Jia J. Chen & B.K. Cui and *A. tenuis* G.Y. Zheng & Z.S. Bi^[10,11,122,123].

Note 13 *Amylosporus* Ryvarden

Index Fungorum number: IF17072

Type species – *Amylosporus graminicola* (Murrill) Ryvarden

Notes – *Amylosporus* was introduced in 1973, initially typified with *A. graminicola*^[124]. Later, *A. graminicola* was synonymized with *A. campbellii* (Berk.) Ryvarden, with the latter becoming the type species of the genus, introduced to include species having both simple septate and multi-clamped generative hyphae, and finely asperulate and amyloid basidiospores^[125]. *Amylosporus wrightii* Rajchenb. is a taxonomic synonym of *A. bracei* (Murrill) A. David & Rajchenb. Based on ITS + nLSU sequence data and morphological characteristics, Chen et al.^[10] proposed that *Wrightoporia casuarinicola* Y.C. Dai & B.K. Cui, *W. efibulata* I. Lindblad & Ryvarden and *W. rubella* Y.C. Dai are characterized by their generative hyphae lacking clamp connections, which fits the newly defined *Amylosporus* (clamp connections are absent in hymenium). Currently, there are 14 species of *Amylosporus*, namely *A. annosus* Y.C. Dai, P. Du & X.H. Ji, *A. auxiliadora* Drechsler-Santos & Ryvarden, *A. bracei* (Murrill) A. David & Rajchenb., *A. campbellii*, *A. casuarinicola* (Y.C. Dai & B.K. Cui) Y.C. Dai, Jia J. Chen & B.K. Cui, *A. daedaliformis* G.Y. Zheng & Z.S. Bi, *A. efibulatus*, *A. guaraniticus* Campi & Robledo, *A. rubellus*, *A. ryvardenii* Stalpers, *A. succulentus* Jia J. Chen & L.L. Shen, *A. sulcatus* F.C. Huang & Bin Liu, *A. wadinaheezicus* S. Hussain, Al-Sadi, Al-Yahya'ei, Al-Kharousi & Al-Owaisi, *A. wrightii* Rajchenb.^[10,12,126]. Initially, the genus was placed in Wrightoporiaceae Jülich, but recently it was treated under Bondarzewiaceae^[1,5,12,121].

Note 14 *Bondarzewia* Singer

Index Fungorum number: IF17176

Type species – *Bondarzewia montana* (Qué.) Singer

Notes – *Bondarzewia* was established based on *B. montana*, now considered a synonym of *B. mesenterica* (Schaeff.) Kreisel, originally described from *Abies* in the Pyrenees mountains (*B. mesenterica* in Germany). It is a remarkable genus because the species usually have relatively large and imbricate basidiomata. Some species are edible and have medicinal potential, such as *B. mesenterica*^[11,12,14,127,128], while others are plant pathogens^[120]. The genus is characterized by annual growth habit, pileate basidiomata with poroid hymenophores and it is morphologically similar to many species of order Polyporales. However, it has strongly amyloid and ornamented basidiospores and recent phylogenetic analyses revealed that it belongs to Russulales^[12,26,28,45,128,129]. Chen et al.^[11] conducted a taxonomic study of *Bondarzewia* based on many samples covering a wide geographic range. With the aid of morphological and phylogenetic analyses of ITS and nuc 28S rDNA D1-D2 domain (28S) sequences, three new species were described and three new combinations were proposed^[11]. Hussain et al.^[12] estimated the divergence time of Bondarzewiaceae (Russulales) based on ITS-28S dataset, revealed that the species diversified approximately 114 million years ago (Mya). The clade consisted of *Bondarzewia*, *Heterobasidion*, *Gloiodon*, *Laurilia*, *Lauriliella*, and *Wrightoporia*, which estimated stem age of the clade is approximately 90 Mya.

Note 15 *Heterobasidion* Bref.

Index Fungorum number: IF17745

Type species – *Heterobasidion annosum* (Fr.) Bref.

Notes – *Heterobasidion* was typed by *H. annosum*. It is characterized by effused-reflexed to sessile basidiomata, dimitic hyphal

system with dextrinoid skeletal hyphae, generative hyphae without clamp connections, and finely asperulate and nonamyloid basidiospores, and is distributed in both Northern and Southern Hemispheres^[9]. Based on ITS, nLSU, *rpb1*, *rpb2*, *gapdh*, *atp6*, and mtSSU, Chen et al.^[13] suggested that ancestral *Heterobasidion* species originated in Eurasia during the Early Miocene, followed by dispersal and speciation to other continents during the Middle Miocene and Early Pliocene. *Heterobasidion* is a global complex of woody plant pathogens and saprobes whose host range comprises over 200 plant taxa, most of which are conifers^[13]. *Heterobasidion* has a negative impact on conifers, both ecologically and economically, by reducing site productivity and the amount of harvestable timber^[9,12]. *Heterobasidion abietinum* Niemelä and Korhonen, distributed in Italy, is associated with *Abies alba* and *Picea abies*; *H. amyloideum* Y.C. Dai, Jia J. Chen and Korhonen with *Abies* in China; *H. annosum* from Italy and Russia, associated with different species of *Pinus*; *H. araucariae* P.K. Buchanan with trees of *Araucaria cunninghamii*, reported from Australia; *H. armandii* Y.C. Dai, Jia J. Chen and Yuan Yuan with *Pinus armandii*, found in China; *H. australe* Y.C. Dai and Korhonen from China, associated with *Pinus* species; *H. insulare* (Murrill) Ryvarden from China in association with *Pinus massoniana*; *H. irregulare* Garbel and Orosina is a South American species associated with *Pinus*; *H. linzhiense* Y.C. Dai and Korhonen is a Chinese species associated with *Abies* and *Picea*; *H. occidentale* is pathogenic to various conifer hosts; *H. orientale* Tokuda, T. Hatt. and Y.C. Dai associated with fallen conifer trunk, reported from China; *H. parviporum* Niemelä and Korhonen associated with *Picea abies*, distributed in Europe and Asia; *H. subinsulare* Y.C. Dai, Jia J. Chen and Yuan Yuan is reported from China, associated with wood of *Pinus*; *H. subparviporum* Y.C. Dai, Jia J. Chen and Yuan Yuan with wood of *Abies* and *Picea*, reported from China; and *H. tibeticum* Y.C. Dai, Jia J. Chen and Korhonen with *Pinus* wood from China^[9,12].

Note 16 *Laurilia* Pouzar

Index Fungorum number: IF17912

Type species – *Laurilia sulcata* (Burt) Pouzar

Notes – *Laurilia* is a monotypic genus with *L. sulcata*, characterized by effuse-reflexed basidiomata with smooth to tuberculate hymenophore, and a trimitic hyphal system^[81]. *Laurilia sulcata* is widely distributed in boreal conifer forests in the northern hemisphere^[81]. It is characterized by having basidiomata of perennial, leathery or ligneous, resupinate, effused and confluent, or partly pileate, especially on vertical sides of the substrate; hyphal system is trimitic with skeletal and binding hyphae with thick walls and few clamps, and thin-walled, fibulate generative hyphae; tinder-layer mainly dimitic, composed largely of horizontal, brown, thick-walled skeletal hyphae; metuloid cystidia numerous, thick-walled, encrusted; clavate basidia with 4 sterigmata and basal clamp; and globose spores, somewhat thick-walled, echinulate and amyloid^[130]. Only two species, *L. sulcata* and *L. taxodii* (Lentz & H.H. McKay) Pouzar are accepted (Index Fungorum 2025).

Note 17 *Lauriliella* S.H. He & Nakasone

Index Fungorum number: IF819211

Type species – *Lauriliella taxodii* (Lentz & H.H. McKay) S.H. He & Nakasone

Notes – *Lauriliella* was established by He & Nakasone, and typified by *L. taxodii* (= *Stereum taxodii* Lentz & H.H. McKay). It is a perennial genus with effused-reflexed, pileate or umbonate, woody basidiomata, hymenophore smooth to tuberculate, basidia with basal clamp connections, basidiospores broadly ellipsoid to subglobose, hyaline, thick-walled, echinulate, and amyloid^[81]. The genus comprises two species, *L. taxodii* and *L. taiwanensis* S.H. He & Nakasone. *Lauriliella taxodii* is distributed in USA, causing white stringy rot or brown powdery rot in living *Taxodium distichum*.

Similarly, *L. taiwanensis* is reported from China, causing white rot in living *Chamaecyparis formosensis*^[81]. With the transfer of *Laurilia taxodii* into *Lauriliella*, *Laurilia* becomes monotypic. Although similar, *Laurilia* and *Lauriliella* can be distinguished by several critical features. *Laurilia* causes a white stringy rot or white pocket rot in dead coniferous wood, whereas *Lauriliella* creates large pockets of decayed wood scattered in the heartwood of *Taxodium* and *Chamaecyparis* which is somewhat stringy or laminated. The hymenophore is light yellow or pink to salmon-colored in *Laurilia* but gray, orange, or brown in *Lauriliella*. Microscopically, unbranched skeletal hyphae are dominant in the context of *Lauriliella*, whereas in *Laurilia* unbranched skeletal and richly branched binding hyphae are present. Davidson et al.^[131] and Nakasone^[132] noted the differences in cultures, with *L. sulcata* growing faster, producing strong oxidase reactions, and developing conidia (Spiniger anamorph). In contrast, *L. taxodii* cultures grew very slowly and produced no or weak oxidase reactions and produced chlamydospores.

Note 18 *Stecchericum* D.A. Reid

Index Fungorum number: IF18581

Type species – *Stecchericum fistulatum* (G. Cunn.) D.A. Reid

Notes – *Stecchericum* was established by D.A. Reid based on *S. seriatum* (Lloyd) Maas Geest. (= *S. fistulatum* G. Cunn.) as the type. It is characterized by pileate basidiomata, hydroid hymenophore, monomitic to imperfectly dimitic hyphae system, tubular and thick-walled gloeocystidia, and finely asperulate, strongly amyloid basidiospores^[133]. This genus resembles *Steccherinum* Gray in macroscopic characters, and they could be easily confused with each other in the field. But *Steccherinum* has encrusted skeletocystidia and smooth, non-amyloid basidiospores^[133]. According to MycoBank, *Stecchericum* belongs to Wrightporiaceae; however, recent studies^[1,5,134] classified it in Bondarzewiaceae. The known species are *S. abditum* Maas Geest., found on rotten log in Australia, *S. acanthophysium* T. Hatt. and Ryvarden on hardwood reported from Japan, *S. isabellinum* Corner associated with fallen wood in the Amazon forest, *S. rusticum* Maas Geest., on dead wood in Singapore, *S. seriatum* were found in Singapore and Malaysia, and *S. dimiticum* Douanla-Meli associated with angiosperm wood, reported from Cameroon^[135].

Family Echinodontiaceae Donk 1961

Index Fungorum number: IF80722

Type genus – *Echinodontium* Ellis & Everh.

Notes – Echinodontiaceae is characterized by annual to perennial, resupinate, effused-reflexed to pileate-sessile basidiomata, smooth, poroid to hydroid hymenophore, monomitic, pseudodimitic to dimitic hyphal system, generative hyphae with or without clamp-connections, inamyloid, skeletal hyphae inamyloid or dextrinoid (*Larssoniporia*), gloeocystidia present or incrusting cystidia absent or present, with smooth, asperulate, spinulose, verrucose, hyaline to pigmented, amyloid basidiospores. This family consists of wood decaying fungi^[1].

Note 19 *Amylostereum* Boidin

Index Fungorum number: IF17073

Type species – *Amylostereum chailletii* (Pers.) Boidin

Notes – *Amylostereum* with *A. chailletii* as its type is a fascinating genus, as some species are symbionts of mycophagous horntails^[136]. Species are characterized by numerous thick-walled and apically encrusted cystidia in hymenium and context, nodose-septate generative hyphae and distinctly amyloid basidiospores^[137]. Six species, *A. areolatum* (Chaillat ex Fr.) Boidin, *A. chailletii*, *A. ferreum* (Berk. & M.A. Curtis) Boidin & Lanq., *A. laevigatum* (Fr.) Boidin, *A. orientale* S.H. He & Hai J. Li, *A. stillwellii* Slippers, K.N.E. Fitz & J.D. Allison, are recognized worldwide, all associated with gymnosperm hosts^[138–140].

Traditionally, *Amylostereum* has been placed in family Stereaceae due to its morphological similarity to *Stereum* Hill ex Pers.^[141,142]. However, phylogenetic analysis based on DNA sequences showed that *Amylostereum* is close to *Echinodontium* Ellis & Everh. and should be placed in the monotypic family Amylostereaceae^[138,139]. However, divergence times showed that *Amylostereum* was placed in family Echinodontiaceae^[1]. The present study, based on the ITS, nLSU, mtSSU, *rpb2*, and *tef1-α* dataset, confirmed that *Amylostereum* formed an independent lineage in Echinodontiaceae.

Note 20 *Echinodontiellum* S.H. He & Nakasone

Index Fungorum number: IF819204

Type species – *Echinodontiellum japonicum* (Imazeki) S.H. He & Nakasone

Notes – *Echinodontiellum* was established by S.H. He & Nakasone to accommodate *E. japonicum* (= *Echinodontium japonicum* Imazeki). It is characterized by perennial, resupinate to slightly effused-reflexed basidiomata, gray to olive gray and dentate hymenophore, dimitic hyphal system, thin- to thick-walled generative hyphae nodose-septate, with scattered secondary simple septa, thick-walled to subsolid skeletal hyphae light brown, clavate, hyaline to light brown, thick-walled cystidia apically encrusted, blunt, embedded or slightly projected, clavate basidia with four sterigmata, and a basal clamp connection, and ellipsoid, thick-walled, echinulate, amyloid basidiospores^[81]. Morphological differences between *Echinodontium* Ellis & Everh and *Echinodontiellum* are few but significant. Basidiomata of *Echinodontiellum* are effused to effused-reflexed, whereas they are effused-reflexed to pileate, rarely effused, in *Echinodontium*. The context in *Echinodontiellum* is cinnamon to olive gray or brownish gray that darkens in KOH. In comparison, the context of *Echinodontium* species are brick red or brownish orange turning maroon in KOH or pale brown to brown (in *Echinodontium ryvardenii* Bernicchia & Piga). Furthermore, *Echinodontiellum japonicum* is sister to *Echinodontium* s.s. and segregated into a separate genus because of ecological, basidiomata, and molecular criteria^[81].

Note 21 *Echinodontium* Ellis & Everh.

Index Fungorum number: IF17540

Type species – *Echinodontium tinctorium* (Ellis & Everh.) Ellis & Everh.

Notes – Species of *Echinodontium* sensu lato are characterized by conspicuous basidiomata, dentate to smooth hymenophores, encrusted cystidia, and ornamented, amyloid basidiospores^[81]. Based on a concatenated dataset of ITS and 28S sequences of taxa in Russulales, *E. tinctorium*, *E. tsugicola* (Henn. & Shirai) Imazeki, and *E. ryvardenii* were confirmed in family Echinodontiaceae^[81]. *Echinodontium sulcatum* (Burt) H.L. Gross and *E. taxodii* (Lentz & H.H. McKay) H.L. Gross were also placed in *Laurilia* Pouzar and *Lauriliella* S.H. He & Nakasone in some studies^[81,143]. Currently, only five species, *E. ballouii* (Banker) H.L. Gross, *E. japonicum* Imazeki, *E. ryvardenii*, *E. tinctorium*, and *E. tsugicola* are accepted (Index Fungorum 2025). Tabata et al.^[138] demonstrated that *Echinodontium* and *Amylostereum* were phylogenetically related, and belonged in Echinodontiaceae. This was confirmed by subsequent studies^[10,81,94,144,145].

Note 22 *Larssoniporia* Y.C. Dai, Jia J. Chen & B.K. Cui

Index Fungorum number: IF812223

Type species – *Larssoniporia tropicalis* (Cooke) Y.C. Dai, Jia J. Chen & B.K. Cui

Notes – *Larssoniporia* was proposed to accommodate *L. tropicalis* (*Wrightporia tropicalis* (Cooke) Ryvarden) and *L. incrustatocystidiata* Y.C. Dai, Jia J. Chen & B.K. Cui^[10]. *Larssoniporia* is characterized by its woody hard basidiomata with tough tubes, dextrinoid skeletal hyphae, presence of cystidia with crystals at tips, and gloeocystidia, finely asperulate and amyloid basidiospores, and is tropical in distribution^[10]. Phylogeny of Russulales inferred from ITS and 28S

sequence data, placed *Larssoniporia* into family Echinodontiaceae^[81].

Note 23 *Subulicystidiella* Y.L. Deng & C.L. Zhao gen. nov.

Index Fungorum number: IF861371

Type species – *Subulicystidiella murina* Y.L. Deng & C.L. Zhao.

Etymology – referring to the subulate cystidia of the type species.

Notes – *Subulicystidiella* is characterized by annual, resupinate, membranous basidiomata, closely adnate, smooth, gray to charcoal gray hymenial surface, a monomitic hyphal system, thin-walled, generative hyphae with clamp connections, subulate, yellowish brown, thick-walled, cystidia with acute tips, encrusted with crystals in the apical part, thin-walled, smooth, barrelled cystidia with a clamp connection at base, cylindrical basidia with four sterigmata and a basal clamp connection thin-walled, smooth, globose basidiospores. Our study, based on ITS + nLSU + mtSSU + *rpb2* + *tef1-α* sequence data and ITS + nLSU sequence data, showed that *Subulicystidiella* clustered within family Echinodontiaceae, closely related to *Larssoniporia* and *Amylostereum*, and formed a separate clade. However, morphologically, *Larssoniporia* differs from *Subulicystidiella* by its hard basidiomata with tough tubes, hyphal system dimitic, dextrinoid skeletal hyphae, and finely asperulate basidiospores^[10]. *Amylostereum* can be distinguished from *Subulicystidiella* by its thick-walled and apically encrusted cystidia in hymenium and context, nodose-septate generative hyphae and distinctly amyloid basidiospores^[10]. Thus, a new genus *Subulicystidiella* is introduced, based on phylogenetic analyses and morphological characteristics (Figs. 7, 8).

Subulicystidiella murina Y.L. Deng & C.L. Zhao, sp. nov. Figures 7, 8

Index Fungorum number: IF861374

Diagnosis – *Subulicystidiella murina* differs from other species by the membranous basidiomata, gray to charcoal gray hymenial surface, hyphal system monomitic with clamped generative hyphae, and globose basidiospores.

Etymology – referring to the murine hymenial surface of the type specimens.

Type – China, Yunnan Province, Xishuangbanna, Wild Elephant Valley, 22°17' N, 100°85' E, 900 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 25 January, 2024, CLZhao 35801 (SWFC).

Description – Basidiomata annual, resupinate, membranous, closely adnate, thin, without odor or taste when fresh, up to 5.5 cm long, 1.5 cm wide, 150 μm thick. Hymenial surface smooth, gray

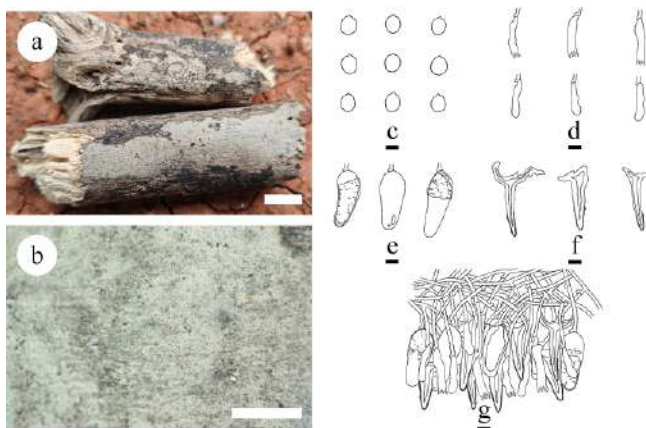


Fig. 7 Basidiomata and microscopic structures of *Subulicystidiella murina* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Barrelled gloeocystidia. (f) Subulate cystidia (g) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 μm, (d)–(g) = 10 μm.

when fresh, gray to charcoal gray upon drying. Sterile margin gray, thinning out, up to 1 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, smooth, moderately branched, 2.5–5.5 μm in diameter, IKI–, CB–; tissues unchanged in KOH. Cystidia with two types: (1) subulate cystidia, numerous, some slightly sigmoid, yellowish brown, thick-walled, with acute tips, encrusted with crystals in the apical part, 18–60 × 7–49 μm, projecting up to 36 μm above the hymenium; (2) barrelled cystidia, colorless, thin-walled, smooth, filled with refractive material, with a clamp connection at base, 41–57 × 6–10 μm. Basidia cylindrical, with one oil drop, four sterigmata, and a basal clamp connection, 20–34 × 5–8.5 μm; basidioles numerous, in shape similar to basidia but smaller. Basidiospores globose, colorless, thin-walled, smooth, with some oil drops, CB–, IKI–, (5.3–)5.7–7.4(–7.8) × (4.3–)4.6–6.3(–6.9) μm, L = 6.42 μm, W = 5.55 μm, Q = 1.16 (n = 60/2).

Additional material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71' N, 94°52' E, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 21 July 2023, CLZhao 30728 (SWFC).

GenBank accession numbers – CLZhao 35801 ITS: PV441140, LSU: PV441154, mtSSU: PV461163; CLZhao 30728 ITS: PV771055, LSU: PX418375, mtSSU: PV774692.

Family Gloeocystidiellaceae Jülich 1982

Index Fungorum number: IF81775

Type genus – *Gloeocystidiellum* Donk

Notes – *Gloeocystidiellaceae* is characterized by annual resupinate, effused-reflexed basidiomata, smooth, rarely grandinoid or odontoid hymenial surface, a monomitic hyphal system with nodose or simple-septate generative hyphae, gloeocystidia, subcylindrical to clavate basidia with four sterigmata and suballantoid, ellipsoid, subglobose or globose, verrucose or aculeate basidiospores^[45].

Note 24 *Gloeocystidiellum* Donk

Index Fungorum number: IF17663

Type species – *Gloeocystidiellum porosum* (Berk. & M.A. Curtis) Donk

Notes – A corticioid genus *Gloeocystidiellum* belonging to order Russulales was established by Donk with *G. porosum* as its type species. The genus is characterized by smooth, rarely grandinoid or odontoid hymenial surface, a monomitic hyphal system with

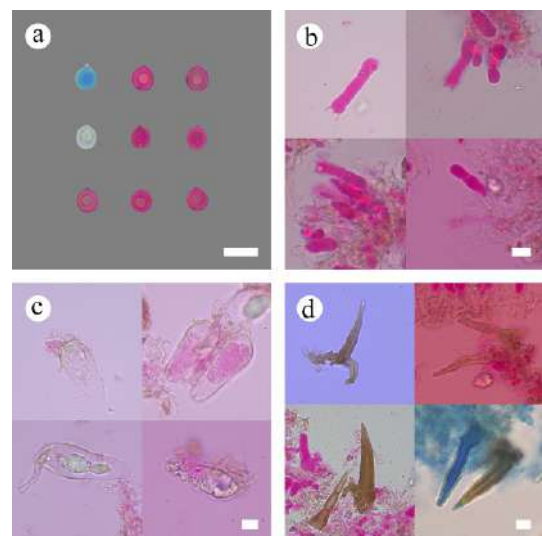


Fig. 8 Sections of hymenium of *Subulicystidiella murina* (holotype). (a) Basidiospores. (b) Basidia and basidioles. (c) Barrelled cystidia. (d) Subulate cystidia. Scale bars: (a)–(d) = 10 μm.

nodose or simple-septate generative hyphae, gloeocystidia, subcylindrical to clavate basidia with four sterigmata and suballantoid, ellipsoid, subglobose or globose, verrucose or aculeate basidiospores^[146]. Recently, molecular studies involving *Gloeocystidiellum* based on single-gene or multi-gene datasets have been carried out^[3,147–151]. Phylogenetic relationships of russuloid basidiomycetes revealed that the species of *Gloeocystidiellum* formed two clades based on analyses of nuclear 5.8S, ITS2, and nLSU rDNA genes, in which the generic type species *G. porosum* grouped into clade I^[26]. The high phylogenetic diversity among corticioid homobasidiomycetes showed that *G. subasperisporum* (Litsch.) J. Erikss. & Ryvar den nested into the russuloid clade and closely grouped with *Gloeodontia discolor* (Berk. & M.A. Curtis) Boidin^[116]. Phylogenetic relationships inferred from 5.8S and nLSU rDNA sequences showed that *Gloeocystidiellum* is clustered into family Gloeocystidiellaceae and closely related to Russulaceae within Russulales^[45]. Analyses based on ITS and nLSU sequences indicated that *Gloeocystidiellum* clustered with Russulaceae Litsy and *Gloeodontia* clade^[82,150]. In this study, analyses inferred from ITS + nLSU + mtSSU + *rpb2* + *tef1-α* sequences (Figs 1, 3) showed that *Gloeocystidiellum* is polygeneic, formed two single clades and then grouped with *Gloeodontia* clade and Russulaceae. Thus, *Gloeocystidiellum* is placed into family Gloeocystidiellaceae. Also, two new species, *G. membranaceum* and *G. punctatum* found in China are introduced, based on phylogeny and morphological characteristics.

Gloeocystidiellum membranaceum Y.L. Deng & C.L. Zhao, sp. nov. Figures 9, 10

Index Fungorum number: IF860765

Diagnosis – Differs other species by the white to cream, smooth hymenial surface, a dimitic hyphal system with clamped generative hyphae, cylindrical basidia, and ellipsoid basidiospores.

Etymology – referring to the membranous hymenial surface of the type specimen.

Type – China, Yunnan Province, Dehong, Mang City, Tongbiguan Provincial Nature Reserve, 25°50' N, 97°36' E; 1,000 m asl, on fallen angiosperm branch, 30 June, 2024, CLZhao 37038 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, membranous, without odor or taste when fresh, up to 10 cm long, 1 cm wide, and 150 μm thick. Hymenial surface smooth, white to cream when fresh, buff to pale brown upon drying. Sterile margin thin, white, up to 1 mm.

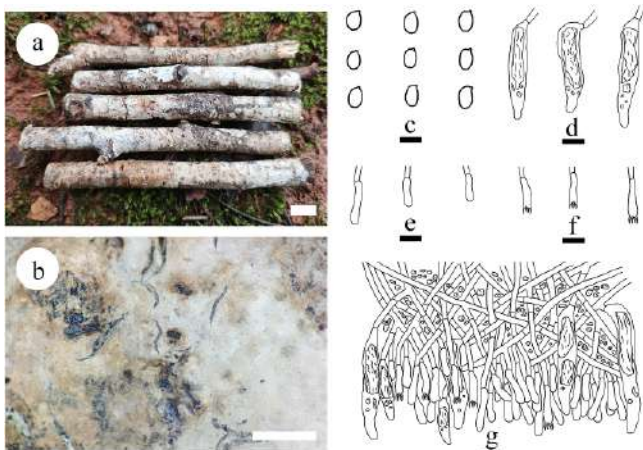


Fig. 9 Basidiomata and microscopic structures of *Gloeocystidiellum membranaceum* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Gloeocystidia. (e) Basidioles. (f) Basidia. (g) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 μm, (d)–(g) = 10 μm.

Hyphal system monomitic, generative hyphae bearing simple septa, colorless, thin-walled, branched, 2.5–4.5 μm in diameter, IKI-, CB-; tissues unchanged in KOH. Gloeocystidia abundant, cylindrical, basally inflated and slightly tapering towards the apices, thin-walled, 26.5–72.5 × 6–12.5 μm. Basidia cylindrical, colorless, thin-walled, with a basal simple septum and four sterigmata, 13–23 × 3–5 μm, basidioles dominant, similar in shape to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI+, CB-, (3.8–)4.4–5.3(–5.8) × (2.5–)3.2–3.9(–4.4) μm, L = 4.82 μm, W = 3.48 μm, Q = 1.35–1.39 (n = 60/2).

Additional material examined – China, Yunnan Province, Qujing, Qilin District, Cuishan Park, 25°54' N, 103°69' E; 1,875 m asl, on fallen angiosperm branch, 4 November, 2022, CLZhao 26028 (SWFC).

GenBank accession numbers – CLZhao 37038 ITS: PV940928, LSU: PX070092, *rpb2*: PX432797, *rpb1*: PX441306, *tef1-α*: PX439082; CLZhao 26028 ITS: PV940927.

Notes – Based on the multigene phylogeny (Figs 1, 3), *Gloeocystidiellum membranaceum* clustered together with *G. bisporum*, *G. clavuligerum* (Höhn. & Litsch.) Nakasone, *G. kenyense* Hjortstam, and *G. porosum*. However, morphologically, *G. bisporum* differs from *G. membranaceum* by having basidia with two sterigmata, oval to subglobose basidiospores^[152]; *G. clavuligerum* differs by its cream to ochraceous hymenophore, generative hyphae with clamp connections (Nakasone 1982); *G. kenyense* has larger fusiform cystidia (20–100 × 8–18 μm), and subcylindrical basidia^[153]; *G. porosum* has pale cream coloured, smooth basidiomata, thin-walled, subfusiform cystidia, constricted basidia^[154].

Gloeocystidiellum punctatum Y.L. Deng & C.L. Zhao, sp. nov. Figure 11

Index Fungorum number: IF852412

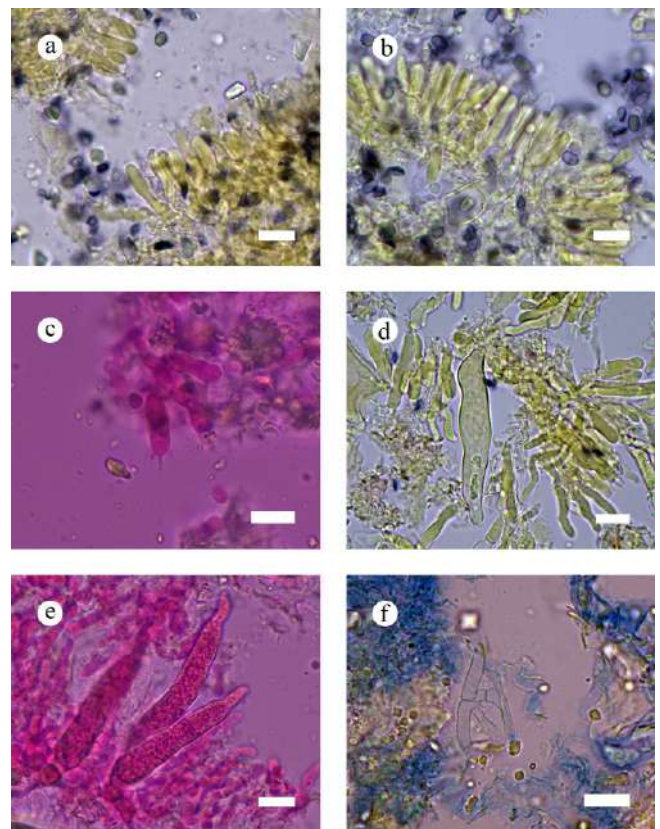


Fig. 10 Sections of hymenia of *Gloeocystidiellum membranaceum* (holotype). (a)–(c) Basidiospores and basidia. (d) Gloeocystidia. (e) Hyphae from context. (f) Section of hymenium. Scale bars: (a)–(f) = 10 μm.

Diagnosis – Differs from other species in the genus by grandinoid, white to cream hymenial surface, thin-walled generative hyphae with clamp connections, and thin-walled ellipsoid basidiospores.

Etymology – referring to the punctate basidiomata.

Type – China, Yunnan Province, Zhaotong, Qiaojia County, Yaoshan Town, Yaoshan National Nature Reserve, 27°08' N, 103°09' E, 2,220 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 23 August, 2020, CLZhao 20755 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, ceraceous, up to 6 cm long, 1.9 cm wide, and 0.2 mm thick. Hymenial surface grandinoid, white to cream when fresh, cream upon drying. Sterile margin thin, slightly cream, up to 1 mm.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, 1.5–3.8 μm in diameter, IKI-, CB-; tissues unchanged in KOH. Gloeocystidia abundant, tubular, basally inflated and slightly tapering towards the apices, thick-walled, thinning towards apex, 51.5–106 μm long, 8.5–15 μm wide, the protoplasmic content granular and yellowish in KOH. Basidia subclavate, colorless, thin-walled, with a basal clamp connection and four sterigmata, 16–24 \times 3.5–5 μm , basidioles dominant, similar shape to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, verruculose, IKI+, CB-, 4–6.5 \times 2.5–4.5 μm , L = 5.03 μm , W = 3.64 μm , Q = 1.3–1.47 (n = 60/2).

Additional material examined – China, Yunnan Province, Zhaotong, Qiaojia County, Yaoshan Town, Yaoshan National Nature Reserve, 27°08' N, 103°09' E, 2,220 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 23 August, 2020, CLZhao 20657 and CLZhao 20907 (SWFC); Yiliang County, Luozehe Town, Li Jiaping Village, 27°49' N, 103°91' E, 1,700 m asl, on dead bamboo, leg. C.L. Zhao, 25 August, 2022, CLZhao 23890 (SWFC); Qujing City, Qilin District, Cuihan, 25°54' N, 103°69' E, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 6 November, 2022, CLZhao 26935 (SWFC); Zhaotong, Wumeng Mountain National Nature Reserve, 27°32' N, 103°72' E, 2,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 2 September, 2023, CLZhao 33627 (SWFC); Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71' N, 97°94' E, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 21 July, 2023, CLZhao 30863, and CLZhao 30864 (SWFC); Diqing, Weixi County, Weideng Town, Fuchuan Village, 27°10' N, 99°16' E, 2,000 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 12 October, 2023, CLZhao 34197 (SWFC); Dehong, Mang City, Mengjia Town, Sanxian Cave Park, 24°38' N, 98°62' E, 1,370 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 30 June, 2024, CLZhao 37129 (SWFC); Tengchong, Tuantian Town, Gaoligong Mountain National Nature Reserve, 25°55' N,

98°58' E, 2,600 m asl, on fallen angiosperm branch, 7 July, 2024, CLZhao 39107, CLZhao 39124, CLZhao 39155, and CLZhao 39158 (SWFC).

GenBank accession numbers – CLZhao 20755 ITS: PP356586, LSU: PP785346, mtSSU: PV774693; CLZhao 20907 ITS: PP356587, LSU: PP785347, mtSSU: PV774694; CLZhao 23890 ITS: PV771056, LSU: PV771607, mtSSU: PV774695; CLZhao 26935 ITS: PV771057; CLZhao 33627 ITS: PP356588; CLZhao 30863 ITS: PV771058, LSU: PP785348, mtSSU: PV774696; CLZhao 30864 ITS: PV771059, LSU: PP785349, mtSSU: PV774697; CLZhao 34197 ITS: PV771060; CLZhao 37129 ITS: PV771061, LSU: PV771608, mtSSU: PV774698; CLZhao 39107 ITS: PV771062, LSU: PV771609, mtSSU: PV774699; CLZhao 39124 ITS: PV771063, LSU: PV771610, mtSSU: PV774700; CLZhao 39155 ITS: PV771064, LSU: PV771611, mtSSU: PV774701; CLZhao 39158 ITS: PV771065, LSU: PV771612, mtSSU: PV774702.

Notes – The phylogram (Fig. 3) revealed that *Gloeocystidiellum punctatum* is nested within the *Gloeocystidiellum* clade, as a sister to *G. porosum*. However, morphologically, *G. porosum* has yellowish to isabelline, smooth hymenophore, thin- to slightly thick-walled, tubular to sinuous gloeocystidia (80–150 \times 8–15 μm), and subcylindrical to ellipsoid basidiospores (5–6 \times 2.5–3 μm). Morphologically, *G. kenyense*, *G. lojanense* A. Jaram., D. Cruz & Decock and *G. yunnanense* Y.L. Zhao & C.L. Zhao are similar to *G. punctatum*. However, *G. kenyense* differs in its cream to ochraceous basidiomata, smaller gloeocystidia (35–85 \times 7–16 μm), and longer cylindrical basidia (21–27 \times 4–5 μm)^[149]; *G. lojanense* can be distinguished by its bright grayish white and slightly light yellow hymenial surface, thin- to thick-walled generative hyphae, smaller gloeocystidia (80–90 \times 7–8 μm), larger basidia (25–35 \times 5–6 μm), and longer basidiospores (6.5–8 μm \times 3.4–4.5 μm)^[149]; *G. yunnanense* is distinct by having smaller clavate (25–48.2 \times 6.4–9.6 μm) and tubular (22.6–47.2 \times 4.1–9.5 μm) gloeocystidia, basidia (12.5–14.5 \times 3.5–4.5 μm), and basidiospores (3.9–4.7 \times 3–3.5 μm)^[150].

Note 25 Family Gloeodontiaceae Y.L. Deng & C.L. Zhao, fam. nov.

Index Fungorum number: IF 861348

Type genus – *Gloeodontia* Boidin

Etymology – referring to the type genus *Gloeodontia*.

Description – Basidiomata resupinate or effused-reflexed, ceraceous to membranous consistency. Hymenophore smooth to odontoid. Hyphal system monomitic; generative hyphae with clamp connections. Cystidia present, Basidia cylindrical to urniform with four sterigmata, thin to thick-walled. Basidiospores ellipsoid to globose, asperulate, acyanophilous, and amyloid.

Notes – *Gloeodontia* was created by Boidin^[155] and could not be assigned to any recognized family of Russulales, and it was treated as incertae sedis. Recent research have reported some new species based on morphology and phylogenetic analyses. However, phylogenetic tree analysis indicated that *Gloeodontia* formed a separate clade, and it was not placed in any recognized family of Russulales^[30,82]. In this study, based on combined ITS, nLSU, mtSSU, *rpb2*, and *tef1- α* data of Russulales, the phylogenetic analyses and divergence time (Figs 1, 2) also showed that *Gloeodontia* could not be assigned to any recognized family. The divergence time of the *Gloeodontia* clade occurred in 178.7 Mya with a 95% highest posterior density (HPD) of 139.36–218.13 Mya. Thus, the genus is placed into the new family Gloeodontiaceae.

Note 26 *Gloeodontia* Boidin

Index Fungorum number: IF17666

Type species – *Gloeodontia discolor* (Berk. & M.A. Curtis) Boidin

Notes – *Gloeodontia* Boidin was typified by *G. discolor* (Berk. & M.A. Curtis) Boidin^[155], and characterized by a combination of resupinate or effused-reflexed basidiomata of ceraceous to

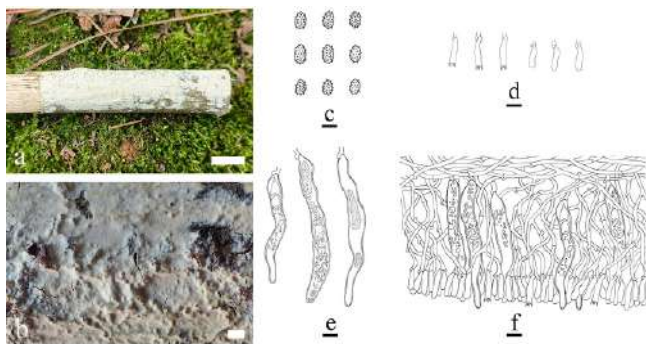


Fig. 11 Basidiomata and microscopic structures of *Gloeocystidiellum punctatum* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidioles. (e) Basidia. (f) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 μm , (d)–(f) = 10 μm .

membranous consistency, smooth to odontoid hymenophore, a monomitic or dimittic hyphal system, clamped hyphae, presence of cystidia, cylindrical to urniform basidia, and colorless to pale yellow, thick-walled, asperulate, ellipsoid to globose, acyanophilous and amyloid basidiospores^[155]. Phylogenetic relationships of russuloid basidiomycetes with an emphasis on non-gilled taxa revealed that four species of *Gloeodontia* formed a monophyletic clade that grouped with Russulales and Stereales clades^[26,30,84], and additionally, a new combination *G. subasperispora* was proposed^[26]. Leal-Dutra et al.^[84] studied Lachnocladiaceae and Peniophoraceae (Russulales) and showed that *Gloeodontia* formed a single clade and then grouped with the clades, Amylostereaceae, Auriscalpiaceae, Bondarzewiaceae, *Gloeocystidiellum*, Russulaceae, and Stereaceae. Nine species have been accepted in the genus^[26,30,84]. In this study, a new species *G. sinensis* is proposed based on ITS + nLSU + mtSSU + *rpb2* + *tef1-α* and ITS + nLSU data (Figs 1, 6), and morphological characteristics (Figs 12, 13).

Gloeodontia sinensis Y.L. Deng & C.L. Zhao, sp. nov. Figures 12, 13
Index Fungorum number: IF860766

Diagnosis – Differs from other species by the coriaceous basidiomata with white to cream hymenial surface odontoid, a monomitic hyphal system with clamped generative hyphae, and ellipsoid, verrucose basidiospores (3.4–4.5 × 2.4–3.4 μm).

Etymology – referring to the locality (China) of the type specimen.

Type – China, Yunnan Province, Diqing, Weixi County, Weideng Town, Fuchuan village, 27°09'N, 99°17'E, 1,910 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 12 October, 2023, CLZha0 34280 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, coriaceous, without odor or taste when fresh, up to 8 cm long, 2 cm wide, and 150 μm thick. Hymenial surface odontoid, thin, white to cream when fresh, cream to buff upon drying. Sterile margin white, up to 1 mm.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, smooth, moderately branched, 2–3 μm in diameter, IKI–, CB–; tissues unchanged in KOH. Cystidia cylindrical with a mastoid at the tip, 10–15 × 4–5 μm. Basidia cylindrical, with a basal clamp connection and four sterigmata, 11–18 × 3–4 μm; basidioles numerous, in shape similar to basidia but smaller. Basidiospores ellipsoid, colorless, thin-walled, verrucose, amyloid, CB–, (3.3–)3.4–4.5(–4.8) × (2.3–)2.4–3.4(–3.7) μm, L = 3.98 μm, W = 2.87 μm, Q = 1.38–1.39 (n = 60/2).

Additional material examined – China, Yunnan Province, Diqing, Weixi County, Zhonglu Town, Lagaluo village, 27°15'N, 99°15'E,

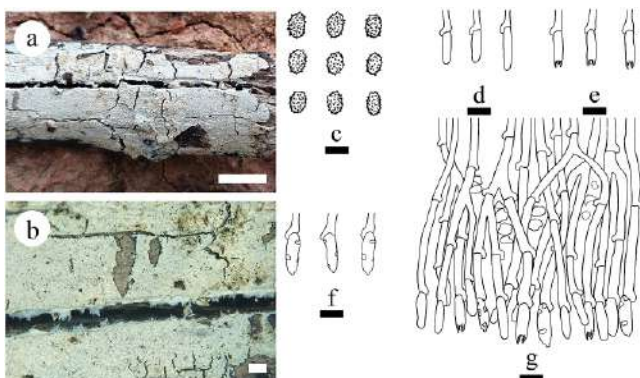


Fig. 12 Basidiomata and microscopic structures of *Gloeodontia sinensis* (holotype). (a) Basidiomata on the substrate. (b) Characteristics of hymenophore. (c) Basidiospores. (d) Basidioles. (e) Basidia. (f) Cystidia. (g) Section of the hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 μm, (d)–(g) = 10 μm.

3100 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 14 October, 2023, CLZha0 34748 (SWFC).

GenBank accession numbers – CLZha0 34280 ITS: PV147170, LSU: PV185856, mtSSU: PV283189, *rpb1*: PX441307; CLZha0 34748 ITS: PV147171, LSU: PV185857, mtSSU: PV399821, *tef1-α*: PV400175.

Notes – The phylogenetic analyses (Figs 1, 6) revealed that *Gloeodontia sinensis* clustered within the genus *Gloeodontia*, and is closely related to *G. columbiensis* and *G. subasperispora*. However, *G. columbiensis* differs from *G. sinensis* by having thick-walled, cylindrical cystidia, both larger thin-walled, vesicular to cylindrical gloeocystidia (20–60 × 5–8 μm), clavate basidia (15–35 × 5–6 μm), and ellipsoid basidiospores (5.5–7 × 3.5–4.5 μm)^[156]; *G. subasperispora* can be distinguished from *G. sinensis* by its greyish-white to pale ochraceous, smooth hymenial surface, longer yellowish gloeocystidia (20–30 × 3–5 μm)^[26]. Morphologically, *G. sinensis* is reminiscent of *G. yunnanensis* C.L. Zhao by thin-walled generative hyphae with clamp connections, sharing asperulate basidiospores. However, *G. yunnanensis* has cream to buff to brownish vinaceous smooth hymenial surface, larger obclavate gloeocystidia (32–57 × 6–9 μm), and thick-walled, subglobose to globose basidiospores measuring 3.3–4.3 × 2.5–3.5 μm^[82].

Family Hericiaceae Donk 1964

Index Fungorum number: IF80854

Type genus – *Hericium* Pers.

Notes – Hericiaceae is characterized by annual, resupinate, effused-reflexed, pileate-sessile to flabelliform basidiomata, smooth, poroid to hydroid hymenophore, monomitic or dimittic hyphal system, generative hyphae with clamp-connections, inamyloid or amyloid, skeletal hyphae inamyloid or dextrinoid (*Pseudowrightoporia*, *Wrightoporiopsis*), gloeoplerous hyphae and gloeocystidia present or absent, with asperulate, spinulose or echinulate, hyaline, amyloid basidiospores. The members of this family include wood decaying fungi^[1].

Note 27 *Dentipellicula* Y.C. Dai & L.W. Zhou

Index Fungorum number: IF564153

Type species – *Dentipellicula taiwaniana* (Sheng H. Wu) Y.C. Dai & L.W. Zhou

Notes – *Dentipellicula* was segregated from *Dentipellis* and proposed for two hydroid fungal species, *Dentipellis leptodon*

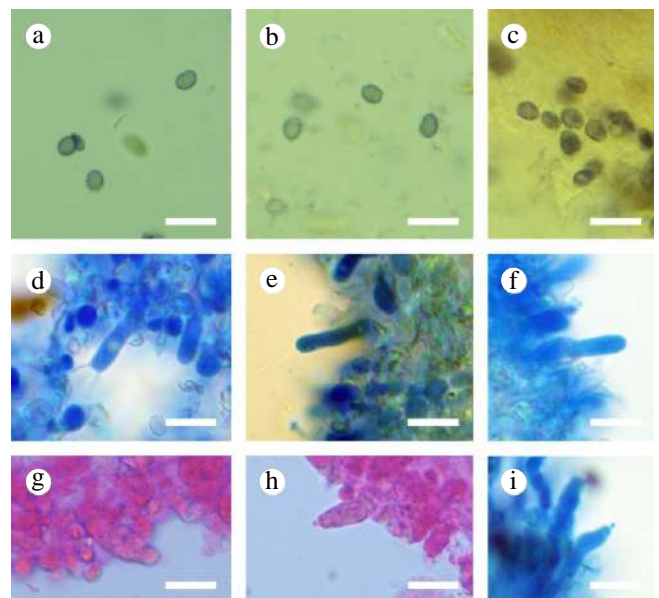


Fig. 13 Sections of hymenium of *Gloeodontia sinensis* (holotype). (a)–(c) Basidiospores. (d)–(f) Basidia and basidioles. (g)–(i) Cystidia. Scale bars: (a)–(i) = 10 μm.

(Mont.) Maas Geest. and *Dentipellis taiwaniana* Y.C. Dai, G.M. Gates, X.H. Ji & P. Du which were transferred to the genus *Dentipellicula* with the latter designated as the generic type. *Dentipellicula* is characterized by its annual, effused-reflexed to pileate basidiomata, hydroid hymenophore, soft corky, cream to ivory yellow to buff to cinnamon-buff spines, a monomitic hyphal system; generative hyphae with clamp connections, slightly thick-walled, minutely rough basidiospores^[30]. Chen et al.^[157] proposed *D. austroafricana* Jia J. Chen, L.L. Shen & Y.C. Dai, which was recognized in the *Dentipellicula* clade and distant from *Dentipellis* based on combined ITS and nLSU sequences. Another species, *D. guyanensis* Yuan Yuan, M. Zhou, Jia J. Chen & Vlasák shares several morphological characteristics with other *Dentipellicula* species, such as an annual growth habit, a monomitic hyphal system with non-amyloid, non-dextrinoid and acyanophilous generative hyphae^[30,158].

Note 28 *Dentipellis* Donk

Index Fungorum number: IF17487

Type species – *Dentipellis fragilis* (Pers.) Donk

Notes – *Dentipellis* was typified by *D. fragilis*. This genus was introduced to accommodate the species characterized by an annual growth habit, hydroid basidiomata, soft spines, a monomitic hyphal structure with clamp connections and cyanophilous hyphae, and amyloid rough basidiospores^[30,159]. Zhou & Dai^[30] demonstrated that *Dentipellis* was polyphyletic and segregated *D. leptodon* (Mont.) Maas Geest. and *D. taiwaniana* Sheng H. Wu from *Dentipellis* based on ITS and nLSU rDNA sequences. Chen et al.^[11] maintained that *Dentipellis* remained polyphyletic based on ITS and nLSU rDNA sequences, therefore, a broad concept for *Dentipellis* s.l. was adopted^[160]. Recently, based on molecular and morphological analyses, more new taxa were described in *Dentipellis* sensu lato^[157,160,161]. All *Dentipellis* spp. were found from the northern hemisphere^[120,157,160,161]. In the present study, a new species *D. yingjiangensis* is described based on morphological and molecular systematics analysis inferred from ITS + nLSU data (Fig. 4).

Dentipellis yingjiangensis Y.L. Deng & C.L. Zhao, sp. nov. Figures 14, 15

Index Fungorum number: IF860767

Diagnosis – *Dentipellis yingjiangensis* differs from other species by the inseparable, leather basidiomata, cream to yellowish-brown hymenial surface odontoid, hyphal system monomitic; generative hyphae with clamp connections, and ellipsoid basidiospores.

Etymology – referring to the locality (Yingjiang) of the type specimen.

Type – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71'N, 94°52'E, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 2 July, 2024, CLZhao 37187 (SWFC).

GenBank accession numbers – CLZhao 37187 ITS: PV441141, LSU: PV441155, mtSSU: PV461164, rpb1: PX441308

Description – Basidiomata annual, resupinate, inseparable, leather, without odor or taste when fresh, up to 7 cm long, 3 cm wide, 150 µm thick. Hymenial surface odontoid, fresh spines soft, white to cream, becoming fragile, cream to yellowish-brown when dry. Sterile margin cottony, buff to clay-buff, up to 1 mm wide. Subiculum very thin, soft corky, buff, up to 1 mm thick.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, smooth, moderately branched, 2.5–4 µm in diameter, IKI–, CB–; tissues unchanged in KOH. Gloeocystidia with three types: (1) cylindrical to fusoid gloeocystidia numerous, colorless, thin-walled, the top overflows and shrinks in a beak-like shape, 31–61 × 5–6.5 µm; (2) mushroom-shaped gloeocystidia, colorless, thin-walled, 17–32 × 2–4 µm; and (3) long cylindrical gloeocystidia, colorless, thin-walled, 82–131.5 × 5–7 µm. Basidia

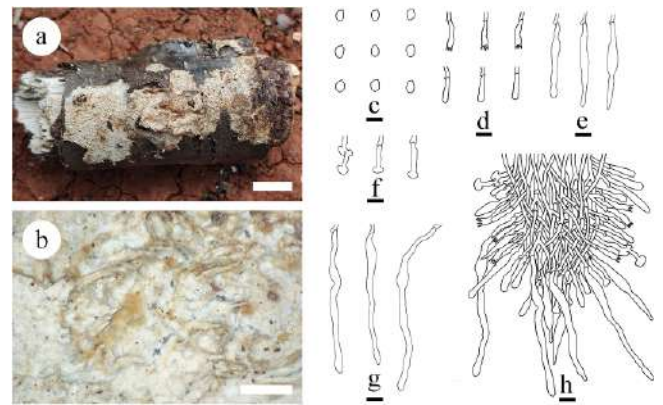


Fig. 14 Basidiomata and microscopic structures of *Dentipellis yingjiangensis* (holotype). (a) Basidiomata on the substrate. (b) Characteristics of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Fusiform gloeocystidia. (f) Mushroom-shaped gloeocystidia. (g) Long cylindrical gloeocystidia. (h) Section of hymenium. Scale bars: (a) = 1 cm; (b) = 1 mm, (c) = 5 µm, (d)–(h) = 10 µm.

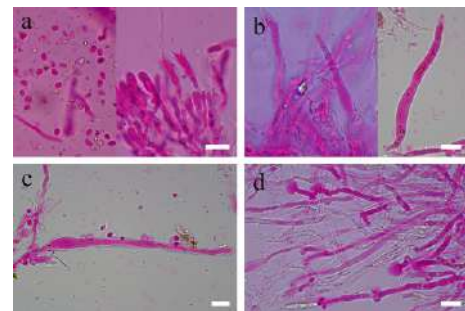


Fig. 15 Sections of hymenium of *Dentipellis yingjiangensis* (holotype). (a) Basidiospores, basidia, and basidioles. (b), (c) Fusiform gloeocystidia. (d) Mushroom-shaped gloeocystidia. Scale bars: (a)–(d) = 10 µm.

cylindrical, with one oil drops, with 4 sterigmata and a basal clamp connection, 14–31 × 3–5 µm; basidioles numerous, in shape similar to basidia but smaller. Basidiospores broadly ellipsoid, colorless, thin-walled, smooth, with some oil drops, IKI–, CB–, (3.3–)3.5–4.7(–4.4) × 2.1–2.9(–3.1) µm, L = 3.79 µm, W = 2.51 µm, Q = 1.49–1.53 (n = 30/1).

Notes – *Dentipellis yingjiangensis* groups in *Dentipellis* (Hericiaceae) based on the ITS + nLSU data (Fig. 4). Phylogenetic analysis shows that *D. yingjiangensis* is sister to *D. rhizomorpha*, and closely related to *D. fragilis*, and *D. dissita*. However, morphologically, *D. rhizomorpha* can be delimited from *D. yingjiangensis* by its cottony margin with white rhizomorphs, thin- to thick-walled generative hyphae, present fusoid cystidioles (18–22 × 2.5–3 µm), clavate basidia (20–23 × 3.5–4 µm), and thick-walled, minutely rough, ellipsoid basidiospores (3.5–4.1 × 2.6–3 µm)^[160]. *Dentipellis fragilis* differs by having thin, soft, fragile basidiomata, narrow, thin-walled, cystidioles, moniliform at their apices, slender basidia, mostly four-spored but often also with only two sterigmata, larger broadly ellipsoid to subglobose, thick-walled, minutely warted basidiospores (5–5.5 × 4.2–4.9 µm)^[162]. *Dentipellis dissita* differs by its effuse basidiomata with buff to pale flesh hymenial surface, pale yellow or concolorous margin with spines, thin to thick-walled generative hyphae with single clamp connections, slenderly clavate to cylindrical basidia (26–35 × 4.6–6 µm), and broadly ellipsoid to subglobose, thick-walled, minutely warted basidiospores^[162].

Note 29 *Hericium* Pers.

Index Fungorum number: IF17740

Type species – *Hericium hystrix* Pers.

Notes – *Hericium coralloides* (Scop.) Pers as the type species to establish the genus *Hericium*. Later, several species of *Hericium* were discovered and to date, 34 species are accepted^[163–166]. Most of *Hericium* species are reported from America and Eurasia in higher latitude ecosystems. A phylogeny of *Hericium* species from North America, together with key taxa from Europe, was accomplished using sequence data from ITS, nLSU, *tef1-α*, and *rpb2* sequences^[166]. In China, five *Hericium* species have been reported, viz. *H. abietis* (Weir ex Hubert) K.A. Harrison, *H. cirrhatum* (Pers.) Nikol., *H. coralloides* (Scop.) Pers., *H. erinaceus* (Bull.) Pers., and *H. yunnanense* S.M. Tang & S.H. Li^[165,166].

Note 30 *Laxitextum* Lentz

Index Fungorum number: IF17914

Type species – *Laxitextum bicolor* (Pers.) Lentz

Notes – *Laxitextum* (Hericiaceae, Russulales, Basidiomycota) is a small genus of stereoid fungi^[167]. *Laxitextum* species can be differentiated from other stereoid genera by distinctive characteristics like resupinate to subpileate basidiomata, brown, tomentose, zonate pileus upper surface; white when fresh, smooth hymenial surface; a monomitic type of hyphal system with thin-walled, clamped generative hyphae; numerous, subulate gloeocystidia; and subglobose to ellipsoid, echinulate and amyloid basidiospores^[42,167–169]. Based on Index Fungorum (2025), *Cerioporus* has nine specific names with only five species accepted worldwide, viz. *L. bicolor*, *L. globisporum* Henkel & Ryvarde, *L. incrustatum*, *L. lutescens* Hjortstam & Ryvarde, and *L. subrubrum*^[42,167–170]. In the present study, a new species *L.*

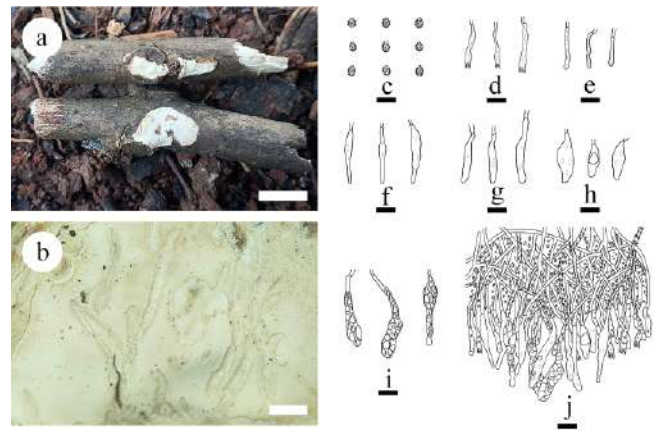


Fig. 16 Basidiomata and microscopic structures of *Laxitextum cremeum* (holotype). (a) Basidiomata on the substrate. (b) Characteristics of hymenophore. (c) Basidiospores. (d) Basidia. (e) Basidioles. (f) Subcylindrical gloeocystidia. (g) Narrowly subcylindrical gloeocystidia. (h) Bottled gloeocystidia. (i) Piriform gloeocystidia. (j) Section of hymenium. Scale bars: (a) = 1 cm; (b) = 1 mm, (c) = 5 μm, (d)–(j) = 10 μm.

cremeum is introduced from China, characterized by morphological traits and analyzed phylogenetically using multi-gene analyses.

Laxitextum cremeum Y.L. Deng & C.L. Zhao, sp. nov. **Figures 16, 17**
Index Fungorum number: IF860768

Diagnosis – *Laxitextum cremeum* differs from other species by the coriaceous basidiomata with white to cream hymenial surface, a

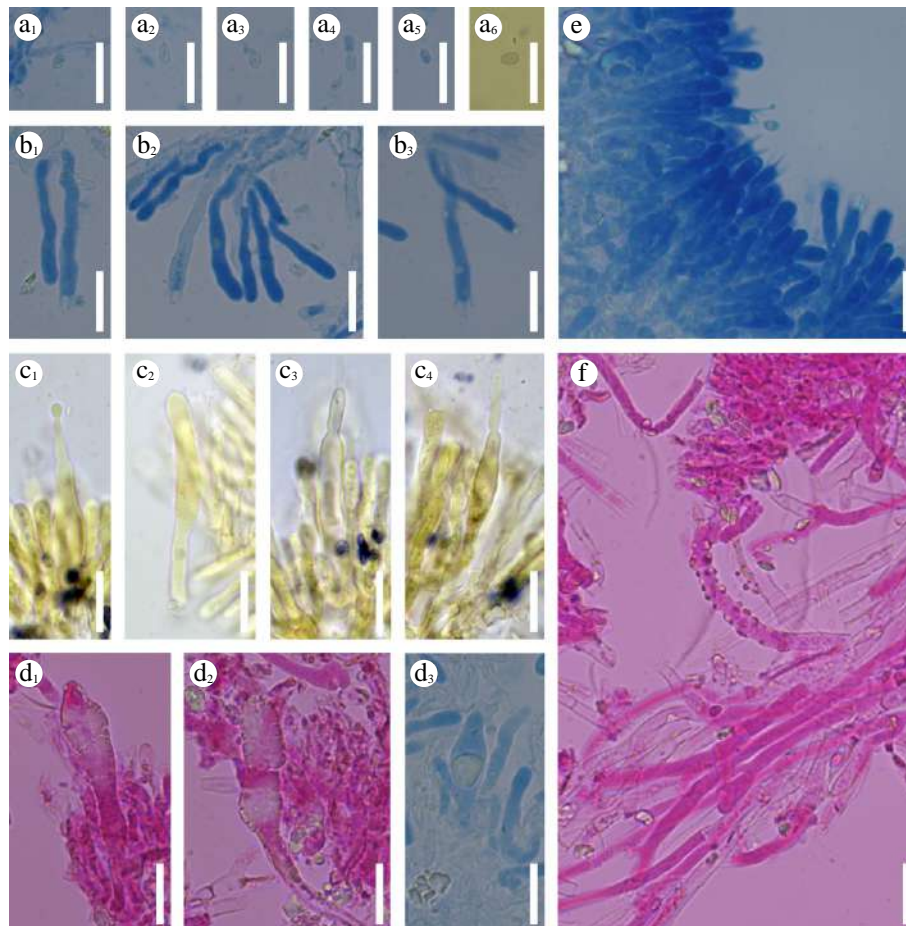


Fig. 17 Sections of hymenium of *Laxitextum cremeum* (holotype). a₁–a₆ Basidiospores. b₁–b₃ Basidia and basidioles. c₁–c₄ subcylindrical gloeocystidia. d₁–d₃ Piriform gloeocystidia. (e) Section of hymenium. (f) Generative hyphae. Scale bars: (a)–(f) = 10 μm.

hyphal system monomitic with generative hyphae bearing simple septa, and apiculate ellipsoid basidiospores measuring 2.5–3.3 × 1.8–2.4 µm.

Etymology – referring to the cream color of the hymenial surface.

Type – China, Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, 27°33'N, 103°27'E, 1,910 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 21 September, 2023, CLZhao 33747 (SWFC).

GenBank accession numbers – CLZhao 33747 ITS: PV147169, LSU: PV185855, mtSSU: PV399820, *rpb2*: PV339601, *rpb1*: PX441309, *tef1-α*: PV400174

Description – Basidiomata annual, resupinate, closely adnate, sessile, coriaceous, soft-spongy when fresh and brittle on drying, without odor or taste when fresh, up to 1.5 cm long, 1 cm wide, 0.1 mm thick. Hymenial surface smooth, thin, white to cream when fresh, cream upon drying. Sterile margin white to cream, thinning out, up to 2 mm.

Hyphal system monomitic; generative hyphae bearing simple septa, colorless, thin-walled, smooth, moderately branched, 2–2.5 µm in diameter, IKI–, CB–; tissues unchanged in KOH. Subhymenial hyphae densely covered by crystals. Gloeocystidia with four types: (1) subcylindrical, the tip contracts to form a long beak, colorless, thin-walled, smooth, filled with refractive oil-like matter, 23–36.5 × 3.5–5 µm; (2) narrowly subcylindrical, colorless, thin-walled, smooth, 27–39 × 4–5 µm; (3) bottled, filled with refractive matter, colorless, thin-walled, smooth, 12–28 × 5–9.5 µm; and (4) pyriform, consisting of a crystal overlay, occasionally the tip contracts to globular, colorless, thin-walled, smooth, 30–45.5 × 7–8 µm. Basidia narrowly subcylindrical, with four sterigmata and a basal simple septum, filled with oil-like matter, 20–28 × 3–3.5 µm; basidioles numerous, in shape similar to basidia but smaller. Basidiospores ellipsoid, colorless, thin-walled, finely echinulate, CB–, strongly amyloid in Melzer's reagent, (2.4–)2.5–3.3(–3.4) × (1.7–)1.8–2.4(–2.6) µm, L = 2.94 µm, W = 2.04 µm, Q = 1.45 (n = 30/1).

Notes – The phylogram based on combined ITS+nLSU data (Fig. 4) revealed that *Laxitextum cremeum*, is clustered within *Laxitextum* (Hericiaceae), forming a clade with *L. subrubrum*, *L. bicolor* and *L. incrustatum*. Morphologically, *L. subrubrum* can be delimited from *L. cremeum* by having pileate, sessile, soft-spongy, brittle basidiomata, thin- to thick-walled generative hyphae with clamp connections, larger pale orange, lanceolate gloeocystidia with apex moniliform (102–156 × 8.5–15 µm), both larger narrowly clavate basidia with 4-sterigmate and a basal clamp connection (23.5–38 × 5.5–9 µm), and ellipsoid, apiculate basidiospores (4.7–5.9 × 3.1–3.5 µm)^[42]. *Laxitextum bicolor* differs from *L. cremeum* by its resupinate or subpileately reflexed, upper side brown basidiomata, thin to thick-walled light brown generative hyphae with clamp connections, larger fusiform, subulate cystidia with a moniliform apical appendix (40–100 × 5–10 µm), wider narrowly clavate basidia with 4-sterigmate and a basal clamp connection (20–30 × 3.5–5 µm), and longer oblong-ellipsoid, finely echinulate basidiospores (4.5–5 × 2.5 µm)^[168]. *Laxitextum incrustatum* can be distinguished from *L. cremeum* by having effuse basidiomata, white to pallid, cottony to matted tomentose margin, thin- to thick-walled, pale yellow generative hyphae with clamp connections, larger tubular or with a bulbous swelling gloeocystidia with moniliform at the apex (45–170 × 5–10 µm), both larger slenderly clavate basidia with four sterigmata (28–40 × 5.0–6.0 µm), and slightly thick-walled, broadly ellipsoid to subglobose, verrucose basidiospores (4.6–5.2 × 3.4–3.8 µm)^[168].

Note 31 *Pseudowrightoporia* Y.C. Dai, Jia J. Chen & B.K. Cui

Index Fungorum number: IF812226

Type species – *Pseudowrightoporia cylindrospora* (Ryvarden) Y.C. Dai, Jia J. Chen & B.K. Cui

Notes – *Pseudowrightoporia* was proposed to accommodate five species, *P. africana* (I. Johans. & Ryvarden) Y.C. Dai, Jia J. Chen & B.K. Cui, *P. aurantipora* (T. Hatt.) Y.C. Dai, Jia J. Chen & B.K. Cui, *P. gillesii* (A. David & Rajchenb.) Y.C. Dai, Jia J. Chen & B.K. Cui, *P. solomonensis* (Corner) Y.C. Dai, Jia J. Chen & B.K. Cui, and *P. straminea* (T. Hatt.) Y.C. Dai, Jia J. Chen & B.K. Cui, which were segregated from *Wrightoporia*^[10]. *Pseudowrightoporia* is characterized by soft corky to corky basidiomata, usually with shining pores, corky to fibrous-corky tubes, a dimitic hyphal structure, oblong, broadly ellipsoid, ellipsoid to subglobose, finely asperulate and amyloid basidiospores, and a subtropical to tropical distribution^[10]. Several new species and new combinations have been proposed, *P. crassihypha* Y.C. Dai, Jia J. Chen & B.K. Cui, *P. cylindrospora*, *P. hamata* Y.C. Dai, Jia J. Chen & B.K. Cui, *P. japonica* (Núñez & Ryvarden) Y.C. Dai, Jia J. Chen & B.K. Cui, *P. oblongispora* Y.C. Dai, Jia J. Chen & B.K. Cui. Subsequently, *P. dominicana* Angelini, Losi & Vizzini was described from the Dominican Republic based on morphological and molecular data (ITS and nLSU sequence analyses)^[31].

Note 32 *Wrightoporiopsis* Y.C. Dai, Jia J. Chen & B.K. Cui

Index Fungorum number: IF812239

Type species – *Wrightoporiopsis neotropica* (Ryvarden) Y.C. Dai, Jia J. Chen & B.K. Cui

Notes – *Wrightoporiopsis* was established by Chen et al.^[10] and was typified by *W. neotropica*. *Wrightoporiopsis* is characterized by pileate, yellow to yellowish-brown basidiomata, a dimitic hyphal system with generative hyphae bearing clamp connections, skeletal hyphae usually dextrinoid, basidiospores ellipsoid to subglobose, hyaline, finely asperulate, strongly amyloid, and causing a white rot^[10]. Some taxa were previously treated under *Wrightoporia* Pouzar.^[10,44,171] Later, five species, *Wrightoporiopsis amylohypha* Y.C. Dai, Jia J. Chen & B.K. Cui, *W. biennis* (Jia J. Chen & B.K. Cui) Y.C. Dai, Jia J. Chen & B.K. Cui, *W. irregularis* Y.C. Dai, Qian Chen & X.H. Ji, *W. neotropica* and *W. roseocontexta* (Ryvarden & Iturr.) Y.C. Dai, Jia J. Chen & B.K. Cui, were accepted in the genus^[10]. Phylogenetic analysis demonstrated that *Wrightoporiopsis* was distant from *Wrightoporia* sensu stricto, and these two genera in fact belong to two families, Hericiaceae and Wrightoporiaceae, respectively^[10].

Note 33 Family Peniophoraceae Lotsy 1907

Index Fungorum number: IF81123

Type genus – *Peniophora* Cooke

Notes – Peniophoraceae (Russulales) was established by Lotsy, with the type genus *Peniophora*. Peniophoraceae is characterized by basidiomata annual, resupinate, orbicular, discoid, effused-reflexed, to clavarioid. Hymenial surfaces smooth, grandinoid, tuberculate or raduloid. Hyphal system monomitic to dimitic, generative hyphae with or without clamp connections, IKI–. Skeletal hyphae or dichohyphae when present dextrinoid or inamyloid binding hyphae as 'bovista-type', dextrinoid, asterosetae present. Gloeoplerous hyphae and gloeocystidia present or absent, lamprocystidia present or absent, smooth, asperulate, spinulose, verrucose, hyaline to pigmented, IKI– basidiospores, or IKI+ suprahilar plage or IKI+ basidiospores^[1,172]. Leal-Dutra et al.^[84] demonstrated the inclusion of *Parapterulicium* and *Baltazaria* in family Peniophoraceae based on morphological and molecular characters. It is a large and rather heterogeneous family with seventeen genera, viz. *Amylofungus* Sheng H. Wu, *Asterostroma*, *Baltazaria*, *Dendrophora*, *Dichostereum*, *Duportella* Pat., *Entomocorticium*, *Gloiothele* Bres., *Lachnocladium*, *Licrostroma*, *Metulodontia* Parmasto, *Parapterulicium*, *Peniophora*, *Sceptrulum*, *Scytinostroma*, *Vararia*, and *Vesiculomyces* E. Hagstr. currently accepted^[1,173]. *Peniophora* and *Vararia*, have the highest number of taxa in this family, in which they play fundamental ecological roles to drive carbon cycling in forest soils, acting as decomposers^[25,174].

Note 34 *Amylofungus* Sheng H. Wu

Index Fungorum number: IF27556

Type species – *Amylofungus corrosus* (G. Cunn.) Sheng H. Wu

Notes – *Amylofungus* was established by Sheng H. Wu^[175], and typed by *A. corrosus* (= *Corticium corrosus* G. Cunn.). It is characterized by resupinate, effuse basidiomata, smooth hymenial surface, generative hyphae simple-septate, amyloid, numerous, clavate or cylindrical, amyloid gloeocystidia, utriform basidia, four sterigmata, amyloid, globose or subglobose, smooth, thin-walled, amyloid basidiospores^[175]. Another species *A. globosporus* (Maekawa) Sheng H. Wu was transferred from *Vesiculomyces globosporus* N. Maek., it has characters typical of the genus *Amylofungus* Sheng H. Wu, i.e., amyloid reaction for all elements in the basidioma: hyphae, gloeocystidia, basidia, and basidiospores. Simple-septate hyphae, utriform basidia, and smooth basidiospores are also important characters of the species in this genus^[175,176].

Note 35 *Asterostroma* Massee

Index Fungorum number: IF17113

Type species – *Asterostroma apalum* (Berk. & Broome) Massee

Notes – The corticioid genus *Asterostroma*, belonging to order Russulales, was established by Massee with *A. apalum* as its type species. The genus is characterized by resupinate and felted-membranous basidiomata, gloeocystidia, and dextrinoid astrosetae^[177], and based on the astrosetae, *Asterostroma* was placed in family Lachnocladiaceae^[178]. *Asterostroma* belongs to Peniophoraceae of russuloid lineage in recent phylogenetic analysis of 5.8S + nLSU sequence data^[28,45,53,179]. According to the morphological characters of the basidiospores in *Asterostroma*^[180], this genus can be divided into two subgenera *Austroasterostroma* Parmasto (smooth and amyloid basidiospores) and *Asterostroma* (ornamented and amyloid basidiospores)^[23,34]. In recent years, three clades were correlated with two sections and a monotypic lineage: the sect. *Asterostroma* clade, which includes *A. bambusicola*, *A. cervicolor* (Berk. & M.A. Curtis) Massee, *A. macrosporum* N. Maek. & Suhara, *A. medium* Bres., *A. muscicola* (Berk. & M.A. Curtis) Massee, and *A. ochroleucum* Bres. ex Torrend; sect. *Laevispora* Parmasto contains *A. vararioides* S.L. Liu & S.H. He and *A. laxum* Bres.; and a monotypic lineage consisting of *A. andinum* Pat.^[53,179,181]. In the present study, based on morphological traits (Figs 18, 19) and analyzed phylogeny using multiple gene regions, a new species *Asterostroma fimbriatum* is described.

Asterostroma fimbriatum Y.L. Deng & C.L. Zhao, sp. nov. Figures 18, 19

Index Fungorum number: IF860769

Diagnosis – *Asterostroma fimbriatum* differs from other species by the felted-membranous to pellicular basidiomata, cream to slightly buff hymenial surface, a dimitic hyphal system with generative hyphae bearing simple septa, and subglobose to globose echinulate basidiospores.

Etymology – referring to fimbriate sterile margin of the basidiomata.

Type – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71' N, 94°52' E, 1,500 m asl, on dead bamboo, leg. C.L. Zhao, 21 November, 2024, CLZhao 41500 (SWFC).

GenBank accession numbers – CLZhao 41500 ITS: PV940929, LSU: PX070093, mtSSU: PX243671, rpb2: PX432789

Description – Basidiomata annual, resupinate, rhizomorphic, without odor and taste when fresh, up to 9 cm long, 2 cm wide, and 90 µm thick. Hymenial surface smooth, cream when fresh, cream to buff to slightly brown upon drying. Sterile margin thinning out, fimbriate, cream, up to 1 mm wide.

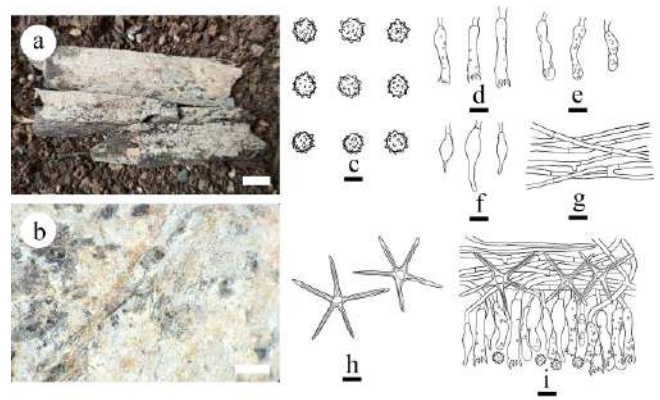


Fig. 18 Basidiomata and microscopic structures of *Asterostroma fimbriatum* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia. (e) Basidioles. (f) Gloeocystidia. (g) Hyphae from context. (h) Asterosetae. (i) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 µm, (d)–(i) = 10 µm.

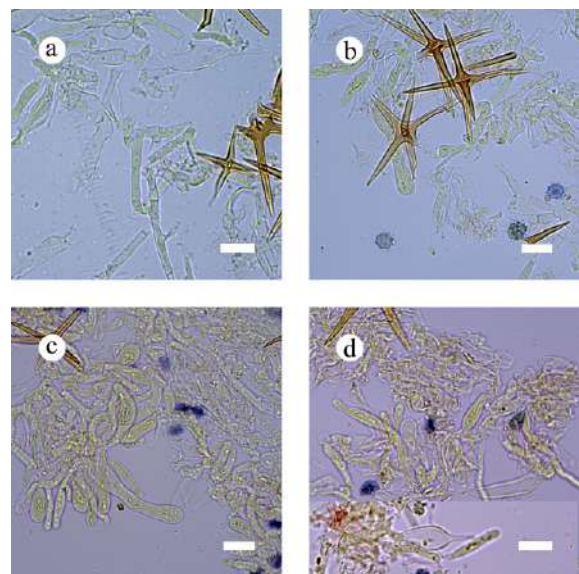


Fig. 19 Sections of hymenium of *Asterostroma fimbriatum* (holotype). (a) Basidia. (b) Basidiospores. (c) Basidioles. (d) Gloeocystidia. Scale bars: (a)–(d) = 10 µm.

Hyphal system dimitic; generative hyphae bearing simple septa, moderately branched, colorless, thin-walled, 3–4 µm in diameter; IKI–, CB–; tissues unchanged in KOH. Asterosetae in subiculum abundant, predominant, yellowish brown, thick-walled, regularly star-shaped, 3–9 µm in diameter, dextrinoid, rays up to 76 µm long, with acute tips, CB–; IKI–, tissues unchanged in KOH. Asterohyphidia in hymenium similar to asterosetae in the subiculum, but smaller and less regularly shaped, 3–5 µm in diameter, rays up to 40 µm long. Gloeocystidia subulate to fusiform, thin-walled, with a basal simple septum, 15.6–24.7 × 4.6–8.2 µm; cystidioles absent. Basidia subcylindrical, colorless, with four sterigmata and a basal simple septum, 16–35 × 4.7–7.6 µm; basidioles dominant, similar to basidia in shape, but slightly smaller. Basidiospores subglobose to globose, with a distinct apiculus, spines conical, colorless, thin-walled, echinulate, with one oil drop, IKI+, CB–, (4.7)–4.9–6(–8) × (4.5)–4.8–6(–7.8) µm, L = 5.55 µm, W = 5.34 µm, Q = 1.04 (n = 30/1).

Notes – Based on ITS + nLSU sequence data (5), *Asterostroma fimbriatum* is grouped within *Asterostroma* (Peniophoraceae), and it is closely related to *A. bambusicola*, *A. cervicolor*, *A. macrosporum*, *A. muscicola*, and *A. laxum*. However, morphologically, *A. bambusicola*

can be delimited from *A. fimbriatum* by its membranaceous to pellicular, soft basidiomata, brownish yellow, greyish brown, light brown to brownish red hymenophore, larger subulate gloeocystidia (40–70 × 6–11 µm)^[179]. *Asterostroma cervicolor* differs from *A. fimbriatum* by having larger gloeocystidia (40–50 × 4–6 µm), and basidia (30–40 × 4.5–5.5 µm)^[180]. *Asterostroma macrosporium* differs from *A. fimbriatum* by its effused, soft, felt-like basidiomata, buff, ochreous to fulvous hymenial surface, thin- to slightly thick-walled generative hyphae, both larger subcylindrical, ventricose to subfusiform gloeocystidia (40–80 × 10–17 µm), and subcylindrical to utriform basidia (38–65 × 8–9.5 µm), globose basidiospores (8.5–11 × 7.5–9 µm)^[181]. *Asterostroma muscicola* can be distinguished from *A. fimbriatum* by having larger gloeocystidia (20–70 × 8–12 µm), utriform basidia with 2–4 sterigmata (18–24 × 5–6 µm)^[177]. *Asterostroma laxum* differs from *A. fimbriatum* by its effused, membranaceous basidiomata, cream to ochraceous hymenophore, larger irregularly cylindrical gloeocystidia (40–100 × 6–10 µm), utriform basidia with 4-sterigmata, and a simple basal septum (40–80 × 6–8 µm), and smooth, subglobose basidiospores^[177].

Note 36 *Baltazaria* Leal-Dutra, Dentinger & G.W. Grif

Index Fungorum number: IF825233

Type species – *Baltazaria galactina* (Fr.) Leal-Dutra, Dentinger & G.W. Grif.

Notes – *Baltazaria* was proposed by Leal-Dutra et al.^[84], and typified by *B. galactina*, to accommodate *B. octopodites* (Corner) Leal-Dutra, Dentinger & G.W. Grif. (= *Parapterulicium octopodites* Corner), *B. galactina* (= *Scytinostroma galactinum* (Fr.) Donk), *B. neogalactina* (Boidin & Lanq.) Leal-Dutra, Dentinger & G.W. Grif., (= *S. neogalactinum* Boidin & Lanq.) and *B. eurasiaticogalactina* (Boidin & Lanq.) Leal-Dutra, Dentinger & G.W. Grif. (= *S. eurasiaticogalactinum* Boidin & Lanq.) within Peniophorales^[84]. This genus is characterized by corticioid, adherent to effused, coriaceous, or membranaceous to hard basidiomata, white, cream or pale ochraceous hymenial surface. Context densely homogeneous with thick-walled and dextrinoid skeletal-binding hyphae, sometimes bearing rows of short papillae or skeletodendrohyphidia^[84]. In the present study, based on the characterization of morphological traits (Fig. 20) and analyzed phylogeny using multiple gene analyses (Figs 1, 5), the new species *Baltazaria pingbianensis* is described.

Baltazaria pingbianensis Y.L.Deng & C.L. Zhao, sp. nov.

Index Fungorum number: IF856165, Fig. 20

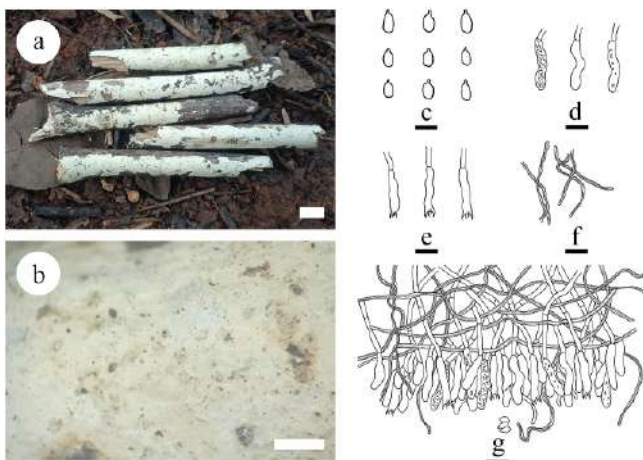


Fig. 20 Basidiomata and microscopic structures of *Baltazaria pingbianensis* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidioles. (e) Basidia. (f) Skeletal hyphae. (g) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 µm, (d)–(g) = 10 µm.

Diagnosis – Differs from other species by its membranous basidiomata, a dimitic hyphal system with generative hyphae bearing simple septa, fibriform skeletal hyphae, cylindrical basidia, and ovoid basidiospores.

Etymology – referring to the locality (Pingbian) of the type specimen.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°51' N, 103°41' E, 2,360 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 1 August 2019, CLZhao 17755 (SWFC).

Description – Basidiomata annual, resupinate, membranous, soft, and adnate, up to 130 mm long, 20 mm wide, and 90 µm thick. Hymenial surface smooth, white when fresh, white to slightly cream upon drying. Sterile margin narrow, whitish, up to 1 mm wide.

Hyphal system dimitic; generative hyphae bearing simple septa, colorless, rarely branched, thin-walled, 2–2.5 µm in diameter, CB–; tissues unchanged in KOH. Skeletal hyphae fibriform, white to yellowish, moderately dextrinoid, thick-walled, 1–2 µm in diameter. Cystidia and cystidioles absent. Basidia cylindrical, colorless, thin-walled, with four sterigmata and a simple septum at base, 18–28 × 3–5 µm, basidioles dominant, in shape similar to basidia, but slightly smaller, with a refractive oil-like matter. Basidiospores oblong ellipsoid, with a beaklike extension, thin-walled, colorless, smooth, IKI–, CB–, 3.5–5 × 2–3 µm, L = 4.38 µm, W = 2.52 µm, Q = 1.83–2.11 (n = 60/3).

Additional Material Examined – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°51' N, 103°41' E, 2,360 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 3 August, 2019, CLZhao 18294 and CLZhao 18296 (SWFC).

GenBank accession numbers – CLZhao 17755 ITS: OR048814, LSU: OR510674, mtSSU: OR539677, *tef1-α*: PQ726901; CLZhao 18294 ITS: OR048816; CLZhao 18296 ITS: OR048815

Notes – The phylogenetic analysis based on ITS + nLSU sequence data (Figs 1, 5) shows that *Baltazaria pingbianensis* is closely related to *B. galactina* and *B. neogalactina* within family Peniophoraceae. However, morphologically, *B. galactina* differs from *B. pingbianensis* by its resupinate, effused, membranaceous basidiomata, cream to isabelline or pale yellowish hymenophore, generative hyphae with clamps, hyaline to yellowish, thick-walled skeletal-binding hyphae, cylindrical gloeocystidia (30–120 × 2–5.5 µm), clavate to subcylindrical basidia with four sterigmata and a basal clamp, narrowly ellipsoid to subcylindrical basidiospores^[84]. *Baltazaria neogalactina* can be distinguished from *B. pingbianensis* by having beige to beige ombré, isabelle, cannelle hymenophore, and larger ellipsoid basidiospores (4.5–6 × 3–3.5 µm)^[182]

Note 37 *Dendrophora* (Parmasto) Chamuris

Index Fungorum number: IF25097

Type species – *Dendrophora versiformis* (Berk. & M.A. Curtis) Chamuris

Notes – *Dendrophora* was initially typified by *D. versiformis*, but the species was transferred to *Peniophora*. The genus is characterized by resupinate, effuse-reflexed or rarely sessile basidiomata, smooth, finely pruinose or velutinous, grey to brown, hymenial surface brown to black, tomentose to felty hymenophore, hyphal system monomitic (or pseudodimitic), subhyaline to brown, thin- to thick-walled generative hyphae with clamp connections, heavily encrusted cystidia (lamprocystidia), subhyaline to brown dendrohyphidia, narrowly clavate basidia with four sterigmata, and a basal clamp, and smooth, thin-walled, cylindrical to allantoid basidiospores^[183]. *Dendrophora* species share similar characters with the species of *Peniophora*. *Dendrophora* mainly differs in the brown dendrohyphidia. It is phylogenetically classified in family

Peniophoraceae^[45]. Only two species are accepted, *D. albobadia* (Schwein.) Chamuris, and *D. erumpens* (Burt) Chamuris.

Notes 38 *Dichostereum* Pilát

Index Fungorum number: IF17504

Type species – *Dichostereum durum* (Bourdot & Galzin) Pilát

Notes – *Dichostereum*, typified with *D. durum*, is a small and well-delimited corticioid genus in Russulales. It is characterized by resupinate basidiomata with smooth or grandinioid hymenophore, dimitic hyphal system with dextrinoid dichohyphae and clamped generative hyphae, gloeocystidia and ellipsoid or subglobose, ornamented basidiospores with a strong amyloid reaction in Melzer's reagent^[45]. Previously, *Dichostereum* was placed in Lachnocladiaceae, which included genera with dextrinoid skeletal hyphae^[184]. However, recent DNA-based phylogenetic analyses, showed that *Dichostereum* formed a monophyletic lineage within family Peniophoraceae, which included genera with or without dextrinoid hyphae^[26,28,45]. *Dichostereum* was once treated as a subgenus of *Vararia* (Peniophoraceae, Russulales) in some studies since the two genera are very similar in morphology except that the latter has smooth basidiospores^[185,186]. Boidin & Lanquetin^[187] emended the description of *Dichostereum*, and retained it as a separate genus. Later, Boidin & Lanquetin^[188] monographed the genus and provided a key to its 11 species based on evidence of morphology, distribution, and inter compatibility tests of cultures. Based on limited taxon sampling, their results showed that *D. effusatum* (Cooke & Ellis) Boidin & Lanq. and *D. granulosum* (Pers.) Boidin & Lanq. were widely distributed, while the other species seemed to be rather endemic^[188]. Few studies on the genus have been carried out since then and many regions including East Asia need further collecting and studies^[182]. Previously, five species, *D. austrosinense* S.H. He & S.L. Liu, *D. boidinii* S.H. He & S.L. Liu, *D. boreale* (Pouzar) Ginns & M.N.L. Lefebvre, *D. eburneum* S.H. He & S.L. Liu, and *D. pallidum* (Schwein.) Boidin & Lanq. were reported in temperate China^[43,173]. According to Index Fungorum (2025), and Mycobank (2025), *Dichostereum* has 18 specific and infraspecific names, and the number of accepted species is 15.

Note 39 *Duportella* Pat.

Index Fungorum number: IF17533

Type species – *Duportella velutina* Pat.

Notes – *Duportella* (Russulales, Basidiomycota) is a small genus of corticioid fungi currently including 20 records of intraspecific names. However, only eight species, *D. kuehneri* (Boidin & Lanq.) Hjortstam, *D. kuehneroides* Boidin, Lanq. & Gilles, *D. lassa* Spirin & Kout, *D. raimundoi* Pat., *D. renispora* Boidin, Lanq. & Gilles, *D. schomburgkii* (Berk.) G. Cunn., *D. tristicula* (Berk. & Broome) Reinking, and *D. velutina* have been accepted worldwide. The species mostly have a tropical distribution. Many species of *Duportella* have been transferred to *Peniophora*^[189–191]. This genus is characterized by resupinate, effused to effuse-reflexed, adnate basidiomata, greyish, reddish, violaceous, ochraceous or blackish hymenophore, monomitic or dimitic hyphal system, hyphae usually with clamps or some simple-septa, brown, apically encrusted pseudocystidia and gloeocystidia usually SA+, cylindrical to subclavate basidia with four sterigmata, and with a basal clamp, ellipsoid to ovoid or globose, cylindrical to allantoid, smooth, thin-walled basidiospores^[192]. *Duportella* is characterized among *Peniophora* s.l. by the brown encrusted pseudocystidia and by presence of skeletal or skeletoid hyphae. *Duportella* is closely related to *Peniophora* and *Dendrophora* and it is classified in family Peniophoraceae^[45,191].

Note 40 *Entomocorticium* H.S. Whitney, Bandoni & Oberw.

Index Fungorum number: IF23076

Type species – *Entomocorticium dendroctoni* H.S. Whitney 1987

Notes – *Entomocorticium* is comprised of 12 species, all associated with Scolytinae beetles^[193–195]. *Entomocorticium dendroctoni*, the type species of the genus, was described based exclusively on morphological characters to accommodate a cryptic species that was observed growing intermingled with a blue stain fungus^[193]. Hsia & Harrington^[196] were the first to show that *Entomocorticium* was a diverse fungal lineage associated solely with a group of phloem-inhabiting bark beetles that feed heavily on fungi. In addition to *E. dendroctoni*, they identified nine putative species based on their mt-SSU, ITS, and IGS-1 phylogenetic analyses. They also suggested that the *Entomocorticium* clade was relatively young, likely having recently diversified, and remained uncharacterized until the early 2000s.

Note 41 *Gloiothele* Bres.

Index Fungorum number: IF17678

Type species – *Gloiothele lamellosa* (Henn.) Bres.

Notes – *Gloiothele* was introduced by Bresadola^[197] and it was typified by *G. lamellosa*, which deviates from other members of the genus by its coarsely hydroid-tuberculate hymenophore^[198]. It comprises resupinate basidiomata with simple septate, generative hyphae, true gloeocystidia generated from gloeoplerous hyphae, and smooth, thin-walled, amyloid basidiospores. It belongs to order Russulales and is most closely related to *Asterostroma*, *Scytinostroma*, and *Vesiculomyces*^[26]. *Vesiculomyces* is separated from *Gloiothele* by the absence of sulfovanillin reaction in gloeocystidia^[26,199]. According to Index Fungorum (2025, www.indexfungorum.org), *Gloiothele* has 18 specific names, with 14 species accepted worldwide^[20,26,198–201]. Two species were reported from Amazon Rainforest, *G. incrustata* Gorjón and *G. lactescens* growing on a frondose trees^[202]. *Gloiothele torrendii* (Bres.) Boidin & H. Michel was originally described as *Corticium torrendii* Bres., and grows exclusively on olive trees^[198,201]. From China, *G. yunnanensis* Yang Yang & C.L. Zhao was reported on the fallen branch of angiosperms^[20]. In the present study, based on morphological traits and phylogeny using multi-gene sequences, two new species *G. fragilima* and *G. tuberculata* are described.

***Gloiothele fragilima* Y.L. Deng & C.L. Zhao, sp. nov. Figures 21, 22**

Index Fungorum number: IF860770

Diagnosis – *Gloiothele fragilima* differs from other species by the cream to slightly yellowish hymenial surface, a monomitic hyphal system with simple septa generative hyphae, and globose basidiospores measuring 6.6–8.3 × 6.2–7.7 μm.

Etymology – referring to fragile basidiomata of the species.

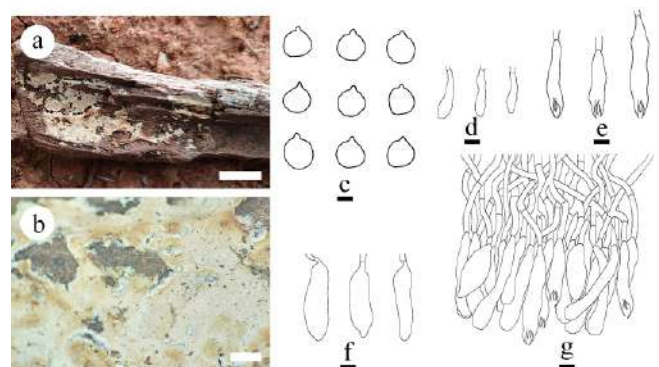


Fig. 21 Basidiomata and microscopic structures of *Gloiothele fragilima* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidioles. (e) Basidia. (f) Gloeocystidia. (g) Section of hymenium. Scale bars: (a) = 1 cm; (b) = 1 mm, (c) = 5 μm, (d)–(g) = 10 μm.

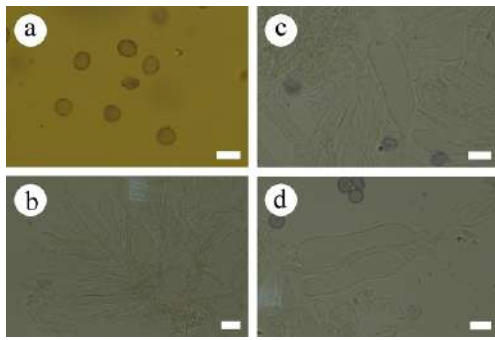


Fig. 22 Sections of hymenium of *Gloiothele fragilima* (holotype). (a) Basidiospores. (b) Section of hymenium. (c), (d) Gloeocystidia. Scale bars: (a)–(d) = 10 µm.

Type – China, Yunnan Province, Wenshan, Bozhu Town, Wenshan National Nature Reserve, 23°36' N, 104°25' E; 1,500 m asl, on trunk of *Camellia*, leg. C.L. Zhao, 23 July, 2019, CLZhao 15980 (SWFC).

GenBank accession numbers – CLZhao 15980 ITS: PV147168, mtSSU: PV399819

Description – Basidiomata annual, membranous, adnate, up to 6 cm long, 2 cm wide, and 100 µm thick. Hymenial surface smooth, cream to slightly yellowish when fresh, slightly yellowish upon drying. Sterile margin distinct, narrow, white, up to 2 mm.

Hyphal system monomitic; generative hyphae bearing simple septa, rarely branched, colorless, thin-walled, 3–5 µm in diameter, IKI–, CB–; tissues unchanged in KOH. Gloeocystidia fusoid to barrelled, colorless, thin-walled, smooth, contract into a mastoid shape at the top, 48.4–69.3 × 11.2–17.2 µm. Basidia subcylindrical, with four sterigmata and a basal simple septum, thin-walled, smooth, 41.1–49.2 × 9–10.5 µm; basidioles in shape similar to basidia, but slightly smaller. Basidiospores globose, thin-walled, colorless, smooth, amyloid, CB–, (6.5–)6.6–8.3(–8.4) × (5.9–)6.2–7.7(–8) µm, L = 7.57 µm, W = 6.98 µm, Q = 1.08 (n = 30/1).

Notes – The combined ITS + nLSU phylogenetic analyses (Fig. 5) revealed that *Gloiothele fragilima* is grouped within *Gloiothele*, sister to *G. citrina*. However, morphologically, *G. citrina* can be distinguished from *G. fragilima* by its widely effuse, margin indeterminate basidiomata with yellowish hymenial surface, irregularly cylindrical to vesicular gloeocystidia, wider tubular to narrowly clavate basidia (30–40 × 5–7 µm), and smaller subglobose basidiospores (4.5–7 × 4–6 µm)^[203].

Gloiothele tuberculata Y.L. Deng & C.L. Zhao, sp. nov. Figures 23, 24

Index Fungorum number: IF860771

Diagnosis – *Gloiothele tuberculata* differs from other species by the coriaceous basidiomata with tubercles hymenial surface white to cream, and broadly ellipsoid to globose basidiospores (5.6–8.9 × 4.3–6.8 µm).

Etymology – referring to tuberculous hymenial surface of the type specimens.

Type – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71' N, 94°52' E, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 18 July 2023, CLZhao 29919 (SWFC).

Description – Basidiomata annual, adnate, coriaceous, up to 8 cm long, 5 cm wide, and 200 µm thick. Hymenial surface tuberculate, white to cream when fresh, cream upon drying. Sterile margin distinct, white, up to 2 mm.

Hyphal system monomitic; generative hyphae bearing simple septa, rarely branched, colorless, thin-walled, 2–3.5 µm in diameter, IKI–, CB–; tissues unchanged in KOH. Gloeocystidia with two types:

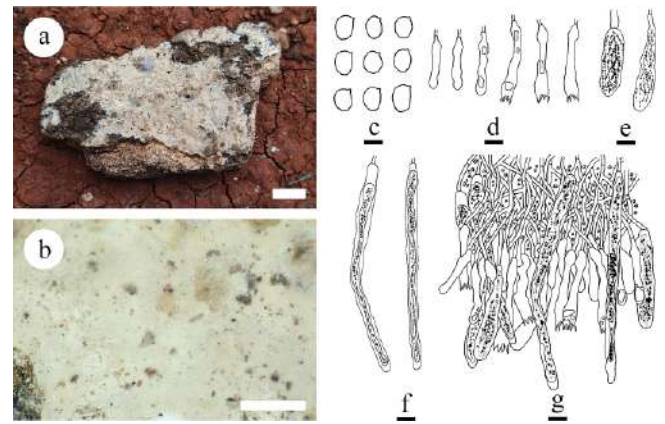


Fig. 23 Basidiomata and microscopic structures of *Gloiothele tuberculata* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Barrelled gloeocystidia. (f) Long cylindrical gloeocystidia. (g) Section of hymenium. Scale bars: (a) = 1 cm; (b) = 1 mm; (c) = 5 µm; (d)–(g) = 10 µm.

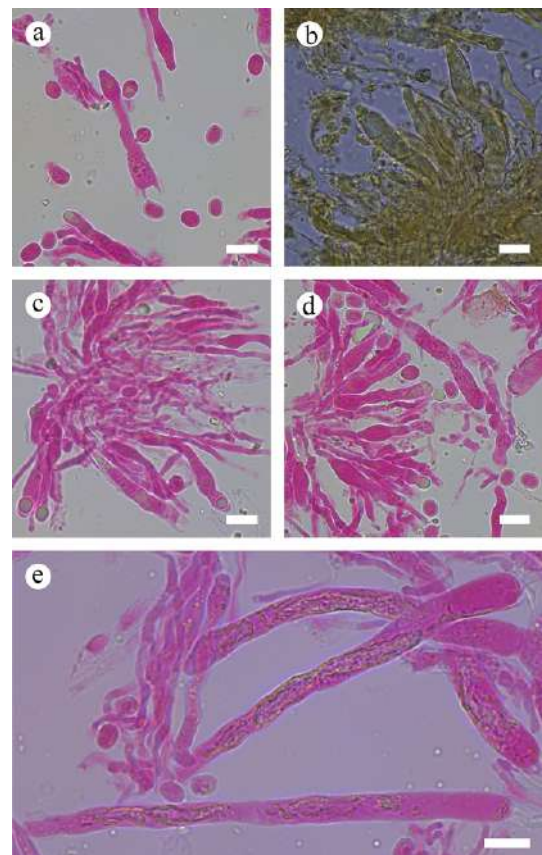


Fig. 24 Sections of hymenium of *Gloiothele tuberculata* (holotype). (a) Basidiospores and basidia. (b), (e) Gloeocystidia. (c), (d) Section of hymenium. Scale bars: (a)–(e) = 10 µm.

(1) barrelled, colorless, thin-walled, smooth, filled with a lot of refracted matter, 29.4–53.3 × 9.2–11.8 µm; and (2) long cylindrical, colorless, thin-walled, smooth, filled with a lot of refracted matter, 75.4–117.5 × 6.1–12.3 µm. Basidia subcylindrical, swollen at the base, with four sterigmata and a basal simple septum, thin-walled, smooth, 34.7–49.6 × 5.2–8.4 µm; basidioles in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid to globose, thin-walled, colorless, smooth, amyloid, CB–, (4.9–)5.6–8.9(–9.5) × (4.1–)4.3–6.8(–7.1) µm, L = 6.85 µm, W = 5.17 µm, Q = 1.26–1.38 (n = 150/6).

Additional material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71' N, 94°52' E, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 18 July, 2023, CLZhao 29888, CLZhao 29895, CLZhao 29986, and CLZhao 30056 (SWFC).

GenBank accession numbers – CLZhao 29919 ITS: PV441136, LSU: PV441151, MTSSU: PV461161, *rpb2*: PV648922, *tef1-α*: PV648916; CLZhao 29888 ITS: PV441135, LSU: PV441150, MTSSU: PV461160; CLZhao 29895 ITS: PV441137; CLZhao 29986 ITS: PV441138, LSU: PV441152, MTSSU: PV461162, *tef1-α*: PV648917; CLZhao 30056 ITS: PV441139, LSU: PV441153, *rpb2*: PV648923, *tef1-α*: PV648918

Notes – In the multi-locus phylogeny, *Gloiothele tuberculata* grouped within *Gloiothele*, forming a separate lineage sister to *G. lamellosa* and *G. lactescens*. However, morphologically, *G. lamellosa* differs from *G. tuberculata* by its isabelline basidiomata, both larger irregularly cylindrical gloeocystidia (80–250 × 10–20 μm), and claviformes basidia (40–60 × 6–8 μm)^[197]. *Gloiothele lactescens* can be distinguished from *G. tuberculata* by its smooth yellowish hymenial surface, both longer, tubular, and sinuous gloeocystidia (100–150 × 5–8 μm), and narrowly clavate basidia (45–60 × 6–7 μm)^[200].

Note 42 *Lachnocladium* Lév.

Index Fungorum number: IF17889

Type species – *Lachnocladium brasiliense* (Lév.) Pat.

Notes – *Lachnocladium* was typed by *L. brasiliense* (= *Eriocladus brasiliensis* Lév.). It is characterized by annual, often caespitose basidiomata usually strongly ramified with rather slender branch; hymenium unilateral on the underside; section shows distinct medulla and paler cortex; pale ochre or yellowish to brown; apices paler and sterile; a dimittic hyphal system; generative hyphae with simple septate, abundant dichophyses; often present gloeoplerous hyphae; always present gloeocystidia, hyaline, thin-walled; small basidia with (2–)4 sterigmata; hyaline basidiospores that are very small, smooth, not amyloid^[204]. The distinctive characters of *Lachnocladium* are coriaceous and more or less hairy covering of fructifications; by these characters the genus can be distinguished from *Clavaria* Vaill. ex L.

Note 43 *Parapterulicium* Corner

Index Fungorum number: IF18185

Type species – *Parapterulicium subarbusculum* Corner

Notes – *Parapterulicium* was introduced to accommodate two Brazilian species, *P. simplex* Corner, and *P. subarbusculum* of coralloid fungi with affinities to Pterulaceae (Agaricales). Despite the coralloid habit and the presence of skeletal hyphae, other features such as the presence of gloeocystidia, dichophyses, and papillate hyphal ends differentiate this genus from Pterulaceae sensu stricto. Fieldwork in Brazil resulted in the rediscovery of two coralloid fungi identifiable as *Parapterulicium*, the first verified collections of this genus since Corner's original work in the 1950s. Molecular phylogenetic analyses of ITS and nLSU sequences from these modern specimens revealed affinities with order Russulales, rather than Pterulaceae. The presence of distinctive hyphal elements, homologous to the defining features of Peniophoraceae, is consistent with the phylogenetic evidence and thus clearly distinguished *Parapterulicium* and its type species *P. subarbusculum* from Pterulaceae, placing this genus within Peniophoraceae (Russulales)^[84].

Note 44 *Peniophora* Cooke

Index Fungorum number: IF18201

Type species – *Peniophora quercina* (Pers.) Cooke

Notes – *Peniophora* was introduced in 1879, and typified by *P. quercina*, which was the first corticioid genus described on the basis of microscopic characteristics^[205]. It was initially introduced to accommodate *Corticium* Pers. and *Stereum* Hill species which have lamprocystidia (metuloids) in the hymenium. It is a cosmopolitan

genus with a wide distribution from boreal to tropical areas, causing a white rot on both angiosperms and gymnosperms. The genus is characterized by having membranaceous, ceraceous, or coriaceous basidiomata with a smooth hymenophore, a monomitic hyphal system with simple-septate or nodose-septate generative hyphae, both encrusted cystidia and gloeocystidia, and thin-walled, smooth basidiospores^[206]. Based on analyses of ITS sequences of Aphyllophorales, Boidin^[207] found that the species of *Peniophora* s.l. formed a relatively strongly supported group that they named 'Peniophorales'. Later, phylogenetic studies showed that *Peniophora* s.l. belongs to Peniophoraceae, Russulales^[26,28,45]. According to the phylogenetic analyses of ITS + nLSU sequence data, the morphological characters of *Peniophora* s.l. are used to delimit the three genera, *Peniophora* s.s., *Dendrophora*, and *Duportella*^[206].

Note 45 *Scytinostroma* Donk

Index Fungorum number: IF18530

Type species – *Scytinostroma portentosum* (Berk. & M.A. Curtis) Donk

Notes – *Scytinostroma* was established by Donk^[146], and typified by *S. portentosum*. Initially, the sexual morph of *Michenera* Berk. & M.A. Curtis which was typified by *M. artocreas*, was described as *Licrostroma* P.A. Lemke that was typified by *L. subgiganteum* (Berk.) P.A. Lemke by Lemke^[101]. Lyman^[208] had earlier demonstrated that cultures derived from basidiospores of *Corticium subgiganteum* Berk., the basionym of *L. subgiganteum*, produced spores he referred to as *Michenera*. However, he was unable to induce the cultures to form hymenia and basidiospores. Molecular data place *L. subgiganteum* with *Scytinostroma aluta*, *S. portentosum*, the type of *Scytinostroma*^[45,209] and *S. caudisporum*^[210]. Based on a morphological study, Stalpers et al.^[211] transferred two species of *Michenera* Berk. & M.A. into *Scytinostroma* and treated the former genus as a synonym of the latter. Thus, *Scytinostroma*, *Michenera*, and *Licrostroma* are synonyms. Li et al.^[212] conducted phylogenetic analyses of Peniophoraceae based on concatenated ITS1-5.8S-ITS2-nLSU sequence data, with a focus on samples of *Scytinostroma* s.s. in different localities, and introduced four new species viz., *S. beijingense* Yue Li, S.L. Liu & S.H. He, *S. boidinii* Yue Li, S.L. Liu & S.H. He, *S. subduriusculum* Yue Li, S.L. Liu & S.H. He, and *S. subrenisporum* Yue Li, S.L. Liu & S.H. He. Recently, Dong et al.^[52] reported a new species *S. dawweishanense* J.H. Dong & C.L. Zhao from China based on morphological characteristics and phylogenetic analyses inferred from ITS + nLSU sequences. *Scytinostroma* includes 44 names based on MycoBank (2025) and Index Fungorum (2025).

Note 46 *Vararia* P. Karst.

Index Fungorum number: IF18724

Type species – *Vararia investiens* (Schwein.) P. Karst.

Notes – *Vararia* is a corticioid wood-inhabiting genus with a wide distribution, typified by *V. investiens*. It was described by Karsten as a subgenus of *Xerocarpus* P. Karst. for *X. alutarius* (Berk. & M. A. Curtis) P. Karst., which was later found to be a synonym of *Radulum investiens* Schwein^[213]. The genus is characterized by resupinate basidiomata, a dimittic hyphal structure with simple-septate or clamped generative hyphae and often dextrinoid dichohyphae in Melzer's reagent, presence of gloeocystidia, and variously shaped smooth basidiospores with or without an amyloid reaction^[214–216]. The species of *Vararia* are found on fallen angiosperm branches, dead wood or herbaceous stems or occasionally on gymnosperm wood^[217]. Based on MycoBank (2025) and Index Fungorum (2025), *Vararia* has 107 specific and infraspecific names, with up to 83 accepted species, occurring mainly in tropical and subtropical areas of the world^[33,218–221]. However, *Vararia* is still poorly studied in China, 18 species have been reported^[33,218–222]. In the present study, eight new wood-inhabiting species belonging to order Russulales,

namely, *Vararia asiana*, *V. bambusicola*, *V. bannaensis*, *V. ferruginosa*, *V. lacerata*, *V. membranacea*, *V. muscicola* and *V. wumengshanensis* are proposed based on a combination of morphoanatomical characteristics and molecular phylogenetic data. Additionally, an identification key to 25 species of *Vararia* in China is provided.

Vararia asiana Y.L. Deng & C.L. Zhao, sp. nov. Figures 25, 26, 27a
Index Fungorum number: IF859280

Diagnosis – *Vararia asiana* differs from other species by its membranous, soft basidiomata with a smooth, cream to slightly yellowish hymenial surface, generative hyphae bearing simple septa, and broadly ellipsoidal basidiospores (2.5–4 × 1.5–2.5 μm).

Etymology – referring to the continent where the species was found.

Type – China, Yunnan Province, Lincang, Yun County, Dumu Village. 24°23' N, 101°9' E; 1,960 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 20 October, 2022, CLZhao 25187 (SWFC).

GenBank accession numbers – CLZhao 25187 ITS: OR102488, LSU: OR510680, *tef1-α*: PV400170.

Description – Basidiomata annual, membranous, adnate, up to 60 mm long, 20 mm wide, and 60 μm thick. Hymenial surface smooth, cream to slightly yellowish when fresh, slightly yellowish to yellowish upon drying. Sterile margin distinct, narrow, white, up to 2 mm.

Hyphal system dimittic; generative hyphae bearing simple septa, rarely branched, colorless, thin-walled, with some crystals, 1.5–2.5 μm in diameter, IKI–, CB–; tissues unchanged in KOH. Dichohyphae predominate, frequently branched, capillary, white to yellowish, thick-walled, 2–2.5 μm in diameter, dichotomously to irregularly branched with main branch and acute tips, moderately dextrinoid in Melzer's reagent. Hymenium skeletal hyphae fibriform, colorless, thick-walled (0.3–0.5 μm thick), 2.5–3 μm in diameter. Gloeocystidia fusiform to subcylindrical, colorless, thin-walled, smooth, with a narrow or shizophapillate apex, 15–21 × 5–7 μm. Basidia subcylindrical, with four sterigmata and a basal simple septum, thin-walled, smooth, 20–29 × 6–7.5 μm; basidioles in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid, thin-walled, colorless, smooth, occasionally with one or two guttules, IKI–, CB–, 2.5–4 × 1.5–2.5 μm, L = 3.21 μm, W = 2.09 μm, Q = 1.54 (n = 30/1).

Notes – The phylogenetic analyses (Fig. 5) revealed that *Vararia asiana* clustered within the genus *Vararia* sister to *V. daweshanensis*, and closely related to *V. rhombospora*. However, morphologically, *V. daweshanensis* differs from *V. asiana* by its pale yellowish hymenial surface, generative hyphae with clamps, colorless, thin- to thick-walled, and larger allantoid basidiospores (9–13 × 3.5–5 μm)^[221]. Furthermore, *V. rhombospora* differs from *V. asiana* in having both larger basidia (30–38 × 5–7 μm) and basidiospores (15–17 × 5–6.2 μm)^[187]. Morphologically, *V. asiana* is similar to *V. investiens* and *V. isabellina* Y.L. Deng & C.L. Zhao by having a smooth hymenial surface, and basidia with four sterigmata. However, *V. investiens* has a yellowish-cream to ochraceous hymenial surface, generative hyphae with clamps, larger fusiform gloeocystidia (40–80 × 4–8 μm), utriform basidia (30–50 × 4–5 μm), and fusoid basidiospores (8–12 × 3–3.5 μm)^[215]. *Vararia isabellina* can be distinguished from *V. asiana* by having cream to isabelline to slightly brown hymenial surface, thin to slightly thick-walled generative hyphae bearing simple-septa, larger spindle to subcylindrical gloeocystidia (38–47 × 8–13 μm), basidia (33–39 × 7–9 μm), and sub-fusiform to navicular basidiospores (9–13 × 5–8 μm)^[33]. The PHI (Figs 5, 27a) analysis reveals no recombination in the new species compared to the closely related taxa. Thus, based on morphology and multigene phylogenetic evidence, *V. asiana* is introduced as a new species.

Vararia bambusicola Y.L. Deng & C.L. Zhao, sp. nov. Figures 27b, 28, 29

Index Fungorum number: IF859281

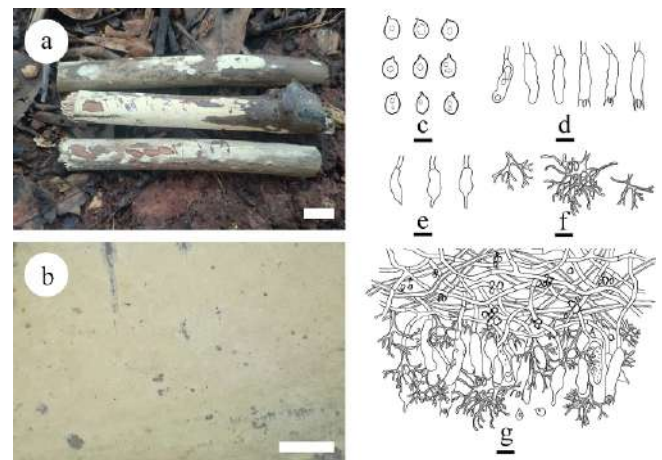


Fig. 25 Basidiomata and microscopic structures of *Vararia asiana* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Gloeocystidia. (f) Dichohyphae. (g) Section of the hymenium. Scale bars: a = 1 cm, b = 1 mm, c = 5 μm, d–g = 10 μm.

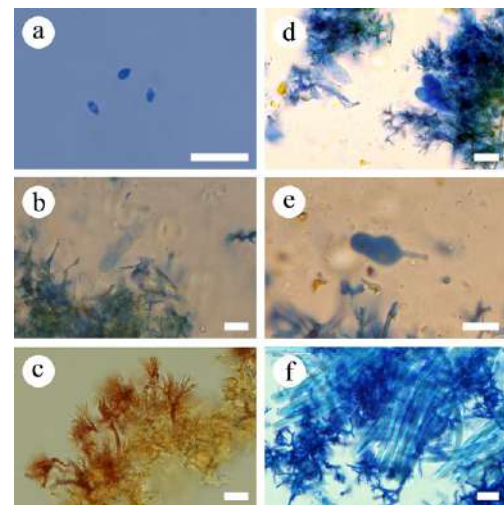


Fig. 26 Sections of the hymenium of *Vararia asiana* (holotype). (a) Basidiospores. (b) Basidia. (c) Dichohyphae. (d) Basidioles. (e) Gloeocystidia. (f) Skeletal hyphae. Scale bars: (a)–(f) = 10 μm.

Diagnosis – *Vararia bambusicola* differs from other species by its coriaceous basidiomata, a pink to salmon to peach hymenial surface, generative hyphae bearing simple septa, and three types of gloeocystidia (urniform, mushroom-shaped, and fusiform), as well as ellipsoid basidiospores.

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

Type – China, Yunnan Province, Dehong, Xishuangbanna, Jinghong City, Rubber Plantation, 21°90' N, 100°76' E, 552.7 m asl, on dead bamboo, leg. C.L. Zhao, 25 January 2024, CLZhao 35740 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, coriaceous, without odor or taste when fresh, up to 10 cm long, 1.5 cm wide, and 120 μm thick. Hymenial surface smooth, pink to salmon when fresh, becoming salmon to peach when dry. Sterile margin pink, thinning out, up to 1 mm.

Hyphal system dimittic; generative hyphae bearing simple septa, colorless, thin-walled, smooth, frequently branched, 2.5–3 μm in diameter. Hymenium skeletal hyphae fibriform, thin-walled, colorless, 2 μm in diameter, IKI–, CB–; tissues unchanged in KOH.

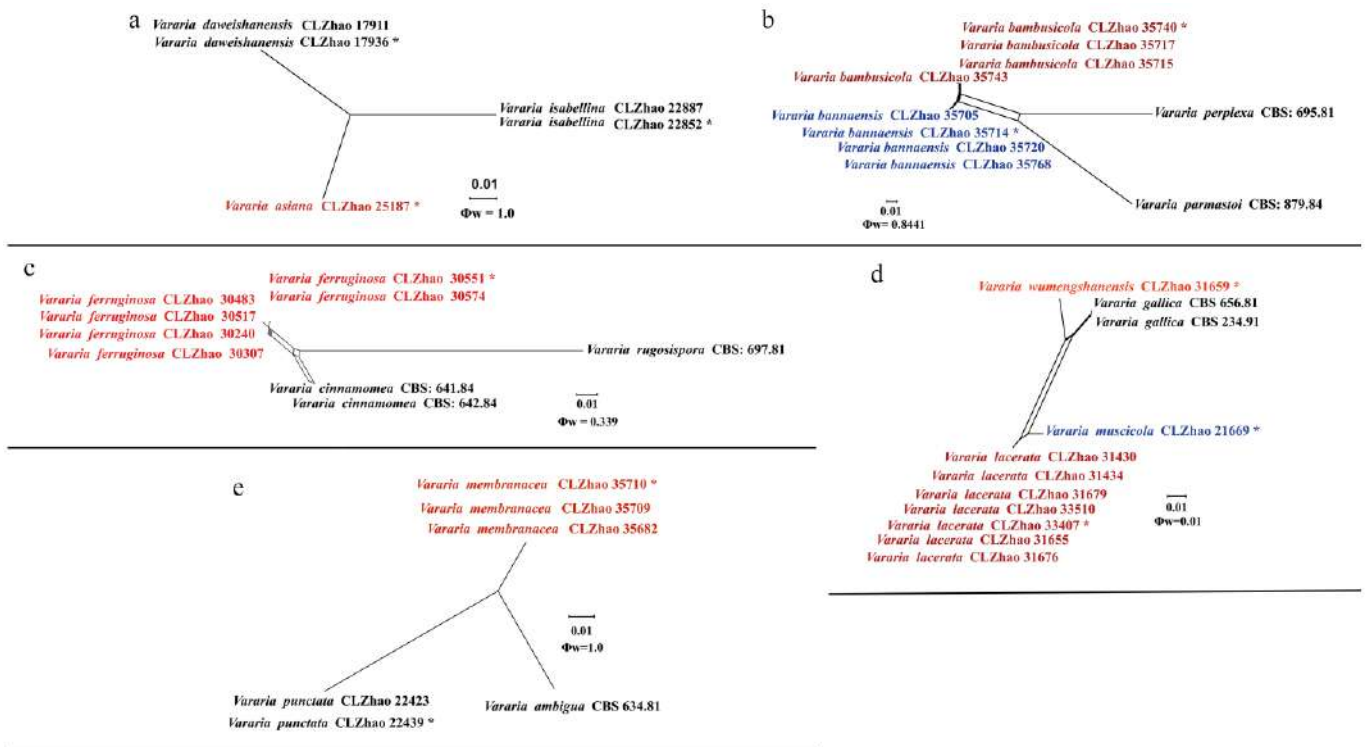


Fig. 27 Pairwise homoplasy index (PHI) test of the new species of *Vararia* and closely related species using both LogDet transformation and splits decomposition. PHI test results $\Phi_w \leq 0.05$ indicate that there is significant recombination within the dataset. The new taxa are in bold red type.

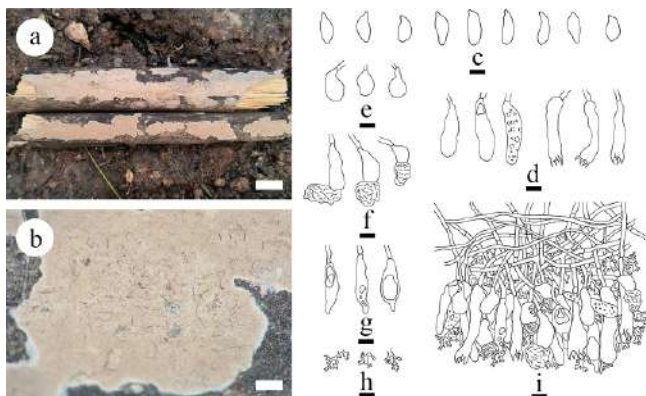


Fig. 28 Basidiomata and microscopic structures of *Vararia bambusicola* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Uniform gloeocystidia. (f) Mushroom-shaped gloeocystidia. (g) Fusiform gloeocystidia. (h) Dichohyphae. (i) Section of the hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c)–(i) = 10 μm .

Dichohyphae predominant, thin-walled, yellowish, capillary, frequently branched, dichotomously to irregularly branched with main branch and blunt tips, 2.5–3 μm in diameter, weakly to moderately dextrinoid in Melzer's reagent, CB–; tissues unchanged in KOH. Gloeocystidia of three types: (1) urniform gloeocystidia, colorless, thin-walled, smooth, 16.3–28 \times 10–14 μm ; (2) mushroom-shaped gloeocystidia, colorless, thin-walled, smooth, 21.3–37 \times 12.7–13 μm , flocculent at the top, up to 11–32 \times 8–17 μm ; and (3) fusiform gloeocystidia, colorless, thin-walled, smooth, swelling of the base and shrinkage apex, slightly flexuous, filled with refractive matter, 35.4–47.3 \times 7.8–14.1 μm . Basidia cylindrical to clavate, slightly flexuous, with a basal simple septum and four sterigmata, 29–57 \times 8.5–12.3 μm ; basidioles numerous, in shape similar to basidia but

smaller, filled with refractive oil-like matter. Basidiospores cylindrical to fusiform, colorless, thin-walled, smooth, CB–, IKI+, (20.1–)22.1–25.1(–26) \times (8.6–)8.7–10.1(–10.8) μm , L = 23.19 μm , W = 9.4 μm , Q = 2.47 (n = 120/4).

Additional material examined – China, Yunnan Province, Xishuangbanna, Jinghong City, Rubber Plantation, 21°90' N, 100°76' E, 552.7 m asl, on dead bamboo, leg. C.L. Zhao, 25 January 2024, CLZhao 35715, CLZhao 35717, CLZhao 35743 (SWFC).

GenBank accession numbers – CLZhao 35740 ITS: PV637442, LSU: PV637449, mtSSU: PV637456, *rpb1*: PX441310, *rpb2*: PV648921, *tef1- α* : PV648915; CLZhao 35715 ITS: PV637440, LSU: PV637447, mtSSU: PV637454; CLZhao 35717 ITS: PV637441, LSU: PV637448, mtSSU: PV637455, *tef1- α* : PV648914; CLZhao 35743 ITS: PV637443, LSU: PV637450, mtSSU: PV637457

Notes – The phylogenetic analyses (Fig. 5) reveal that the specimens of *Vararia bambusicola* grouped within *Vararia* and are sister to *V. bannaensis*. However, morphologically, *V. bannaensis* is distinguished from *V. bambusicola* by its white to pinkish buff to cinnamon buff hymenial surface, two types gloeocystidia (urniform, 9–20 \times 8–14 μm and subcylindrical to fusiform, 23–42 \times 6–10 μm), smaller subclavate basidia (20.5–26 \times 5.5–7 μm), and smaller fusiform to ellipsoid basidiospores (11.8–16.1 \times 5.6–7.7 μm). Morphologically, *V. bambusicola* is similar to *V. perplexa* Boidin, Lanq. & Gilles and *V. parmastoi* Boidin & Lanq. by sharing resupinate, adnate, coriaceous basidiomata and smooth hymenial surface. However, *V. perplexa* has narrower utriform basidia (30–35 \times 5–6 μm) and smaller basidiospores (12.5–16 \times 3–4.2 μm) [216]. *V. parmastoi* can be distinguished from *V. bambusicola* by narrower basidia (35–42 \times 4–5 μm) and smaller basidiospores (6–7.5 \times 1.8–2.4 μm) [223]. The PHI analysis reveals no significant evidence of genetic recombination among these species (Fig. 27b). Thus, based on morphology and multigene phylogenetic evidence, we introduce *V. bambusicola* as a new species.

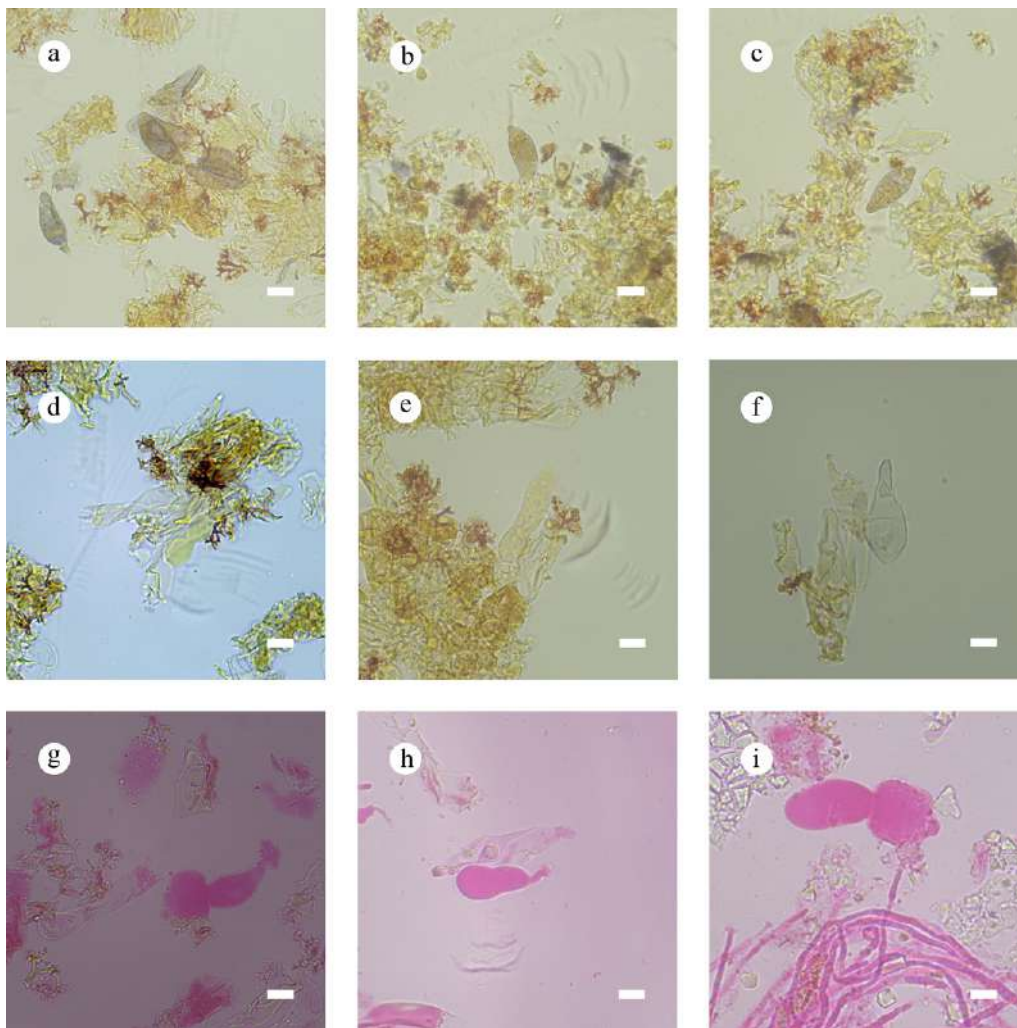


Fig. 29 Sections of the hymenium of *Vararia bambusicola* (holotype). (a)–(c) Basidiospores. (d) Basidia. (e) Basidioles. (f)–(i) Gloeocystidia. Scale bars: (a)–(i) = 10 µm.

Vararia bannaensis Y.L. Deng & C.L. Zhao, sp. nov. [Figures 27b, 30, 31](#)

Index Fungorum number: IF859282

Diagnosis – *Vararia bannaensis* differs from other species by thin, membranous basidiomata, white to pinkish buff to cinnamon buff hymenial surface, urniform, and subcylindrical to fusiform gloeocystidia, and fusiform basidiospores.

Etymology – referring to the locality (Xishuangbanna) of the type specimen.

Type – China, Yunnan Province, Dehong, Xishuangbanna, Jinghong City, Rubber Plantation, 21°90' N, 100°76' E, 552.7 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 25 January, 2024, CLZhao 35714 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, thin, membranous, without odor or taste when fresh, up to 7 cm long, 2 cm wide, and 100 µm thick. Hymenial surface smooth, white when fresh and becoming pinkish buff to cinnamon buff when dry. Sterile margin white, thinning out, up to 2 mm. Hyphal system dimittic; generative hyphae bearing simple septa, colorless, thin-walled, smooth, frequently branched, 2–3.4 µm in diameter, IKI–, CB–; tissues unchanged in KOH. Dichohyphae predominant, thin-walled, yellowish, capillary, frequently branched, dichotomously to irregularly branched with main branch and blunt tips, 1.5–2.3 µm in diameter, weakly to moderately dextrinoid in Melzer's reagent, CB–;

tissues unchanged in KOH. Gloeocystidia with two types: (1) urniform gloeocystidia, colorless, thin-walled, smooth, 9–20 × 8–14 µm; and (2) subcylindrical to fusiform gloeocystidia, with a long beak in the apical part, colorless, thin-walled, smooth, 23–42 × 6–10 µm. Basidia subclavate, flexuous, with a basal simple septum and four sterigmata, 20.5–26 × 5.5–7 µm; basidioles numerous, in shape similar to basidia but smaller. Basidiospores fusiform to ellipsoid, colorless, thin-walled, smooth, CB–, IKI+, (9.5–)11.8–16.1(–17.2) × (4.8–)5.6–7.7(–8.3) µm, L = 14.30 µm, W = 6.56 µm, Q = 2.09–2.28 (n = 120/4).

Additional material examined – China, Yunnan Province, Xishuangbanna, Jinghong City, Rubber Plantation, 21°90' N, 100°76' E, 552.7 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 25 January, 2024, CLZhao 35705, CLZhao 35720, CLZhao 35768 (SWFC).

GenBank accession numbers – CLZhao 35714 ITS: PV441143, LSU: PV441157, *rpb2*: PV648920; CLZhao 35705 ITS: PV441142, LSU: PV441156, mtSSU: PV461165, *rpb2*: PV648919; CLZhao 35720 ITS: PV441144, LSU: PV441158, mtSSU: PV461166, *rpb2*: PX432799; CLZhao 35768 ITS: PV441145, LSU: PV441159, mtSSU: PV461167, *rpb2*: PX432800

Notes – The phylogram ([Fig. 5](#)) revealed that *Vararia bannaensis* is grouped within *Vararia* and sister to *V. bambusicola*. However, morphologically, *V. bambusicola* is distinguished from *V. bannaensis* by pink to salmon to peach hymenial surface, three types of

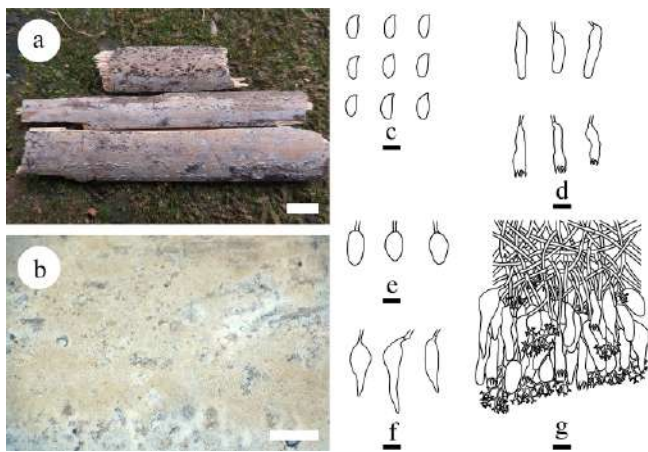


Fig. 30 Basidiomata and microscopic structures of *Vararia bannaensis* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (d) Basidia and basidiospores. (e), (f) Gloeocystidia. (g) Section of the hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c)–(g) = 10 µm.

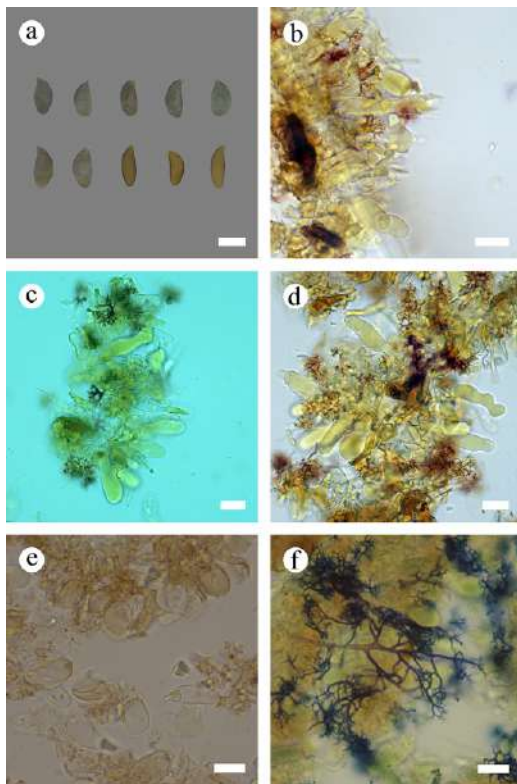


Fig. 31 Sections of hymenium of *Vararia bannaensis* (holotype). (a) Basidiospores. (b) Basidia. (c)–(e) Basidioles and gloeocystidia. (f) Dichohyphae. Scale bars: (a)–(f) = 10 µm.

gloeocystidia (urniform, $16.3\text{--}28 \times 10\text{--}14$ µm; mushroom-shaped, $21.3\text{--}37 \times 12.7\text{--}13$ µm, fusiform, $35.4\text{--}47.3 \times 7.8\text{--}14.1$ µm), larger cylindrical basidia ($29\text{--}57 \times 8.5\text{--}12.3$ µm), and ellipsoid basidiospores ($22.1\text{--}25.1 \times 8.7\text{--}10.1$ µm). Morphologically, *V. bannaensis* is similar to *V. perplexa* and *V. parmastoi* sharing resupinate, adnate, coriaceous basidiomata and smooth hymenial surface. However, morphologically, *V. perplexa* differs from *V. bannaensis* in having longer utriform basidia ($30\text{--}35 \times 5\text{--}6$ µm) and narrower basidiospores ($12.5\text{--}16 \times 3\text{--}4.2$ µm)^[216]. *V. parmastoi* can be distinguished from *V. bannaensis* by longer basidia ($35\text{--}42 \times 4\text{--}5$ µm) and smaller basidiospores ($6\text{--}7.5 \times 1.8\text{--}2.4$ µm)^[223]. To validate the

species delineation, PHI analysis was performed. The analysis reveals no significant evidence of genetic recombination among these species (Fig. 27b). Thus, based on morphology and multigene phylogenetic evidence, *V. bannaensis* is introduced as a new species.

Vararia ferruginosa Y.L. Deng & C.L. Zhao, sp. nov. Figures 27c, 32, and 33

Index Fungorum number: IF859283

Diagnosis – *Vararia ferruginosa* differs from other species by the ferruginous to yellowish-brown hymenial surface, a dimitic hyphal system with generative hyphae bearing simple septa, and ellipsoid basidiospores.

Etymology – referring to the ferruginous color of the hymenial surface of the specimens.

Type – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, $24^{\circ}71' N$, $94^{\circ}52' E$, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 19 July, 2023, CLZhao 30551 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, coriaceous, without odor or taste when fresh, up to 6 cm long, 1.5 cm wide, and 100 µm thick. Hymenial surface smooth, slightly ferruginous when fresh and ferruginous to yellowish-brown when dry. Sterile margin cream, thinning out, up to 1 mm.

Hyphal system dimitic; generative hyphae bearing simple septa, colorless, thin-walled, smooth, frequently branched, $2.2\text{--}3.2$ µm in diameter. Hymenium skeletal hyphae fibriform, thick-walled, colorless, $2\text{--}3$ µm in diameter, IKI–, CB–; tissues unchanged in KOH. Dichohyphae predominant, thick-walled, yellowish, capillary, frequently branched, dichotomously to irregularly branched with main branch and acute tips, $1.5\text{--}3.5$ µm in diameter, weakly to moderately dextrinoid in Melzer's reagent, CB–; tissues unchanged in KOH. Gloeocystidia obclavate, colorless, thin-walled, smooth, $14\text{--}25 \times 3\text{--}6$ µm. Basidia fusiform to subcylindrical, flexuous, with a basal simple septum and four sterigmata, $15\text{--}28 \times 3\text{--}5.3$ µm; basidiospores numerous, in shape similar to basidia but smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, CB–, $(5.1\text{--})5.9\text{--}8.8\text{--}(9) \times (2.7\text{--})3.1\text{--}5.1\text{--}(5.3)$ µm, $L = 7.43$ µm, $W = 4.25$ µm, $Q = 1.71\text{--}1.89$ ($n = 180/6$).

Additional material examined – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, $24^{\circ}71' N$, $94^{\circ}52' E$, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 19 July 2023, CLZhao 30240, CLZhao 30307, CLZhao 30483, CLZhao 30517, and CLZhao 30574 (SWFC).

GenBank accession numbers – CLZhao 30551 ITS: PV147175; CLZhao 30240 ITS: PV147172, LSU: PV185858, mtSSU: PV283190; CLZhao 30307 ITS: PV147177; LSU: PV185859, mtSSU: PV283192, *rpb2*: PV339603, *tef1-α*: PV400177; CLZhao 30483 ITS: PV147173, mtSSU: PV399822; CLZhao 30517 ITS: PV147174, mtSSU: PV399823; CLZhao 30574 ITS: PV147176, LSU: PV185860, mtSSU: PV283191, *rpb2*: PV339602, *tef1-α*: PV400176

Notes – The phylogenetic analyses (Fig. 5) revealed that the six specimens of *Vararia ferruginosa* grouped within *Vararia* and are related to *V. cinnamomea* as sister. Morphologically, *V. cinnamomea* can be distinguished from *V. ferruginosa* by larger subcylindrical basidia ($45\text{--}65 \times 8\text{--}10$ µm), and oblong to subellipsoid basidiospores ($9\text{--}13 \times 5\text{--}7.2$ µm)^[223]. Morphologically, *V. ferruginosa* is similar to *V. rugosipora* Boidin, Lanq. & Gilles by sharing smooth hymenial surface and generative hyphae bearing simple septa. However, *V. rugosipora* differs by larger basidia ($50\text{--}55 \times 9\text{--}11$ µm), and oval to oblong basidiospores ($12\text{--}16 \times 7\text{--}8$ µm)^[216]. The PHI analysis reveals the absence of recombination in the new species compared to the closely related taxa (Fig. 27c). Thus, based on morphology and multigene phylogenetic evidence, *V. ferruginosa* is introduced as a new species.

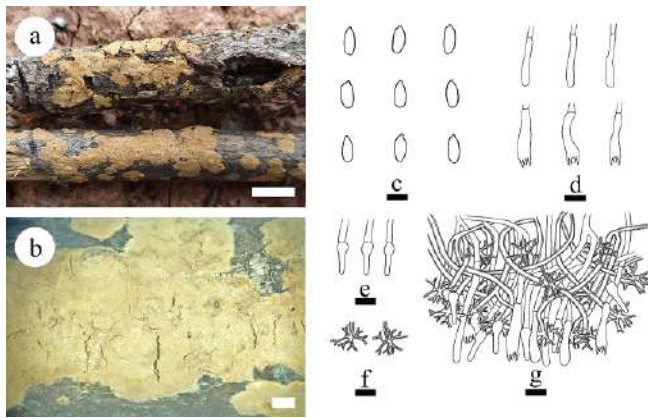


Fig. 32 Basidiomata and microscopic structures of *Vararia ferruginosa* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Gloeocystidia. (f) Dichohyphae. (g) Section of the hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 µm; (d)–(g) = 10 µm.

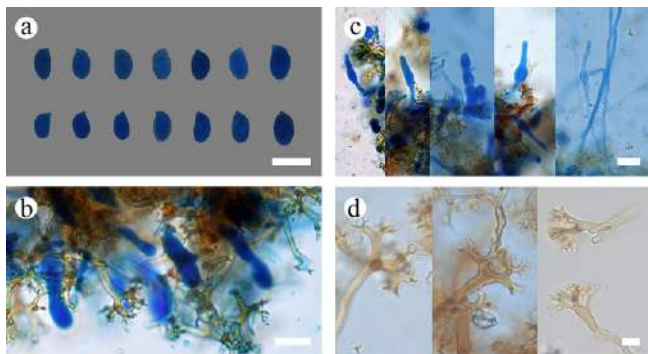


Fig. 33 Sections of the hymenium of *Vararia ferruginosa* (holotype). (a) Basidiospores. (b) Basidioles. (c) Gloeocystidia. (d) Dichohyphae. Scale bars: (a)–(d) = 10 µm.

Vararia lacerata Y.L. Deng & C.L. Zhao, sp. nov. [Figures 27d, 34, and 35](#)

Index Fungorum number: IF859284

Diagnosis – *Vararia lacerata* differs from other species by a cream to buff hymenial surface, a dimitic hyphal system with generative hyphae bearing simple septa, and broadly ellipsoid basidiospores.

Etymology – referring to the lacerate hymenial surface of the specimens.

Type – China, Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, 27°77' N, 104°25' E, 1,900 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 20 September, 2023, CLZhao 33407 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, cracked, coriaceous, without odor or taste when fresh, up to 7 cm long, 2 cm wide, and 400 µm thick. Hymenial surface smooth, cream to buff in appearance when fresh, becoming buff upon drying. Sterile margin cream to buff, thinning out, up to 2 mm. Hyphal system dimitic; generative hyphae bearing simple septa, colorless, thin-walled, smooth, rarely branched, interwoven, 1.5–2 µm in diameter. Dichohyphae predominant, yellowish, capillary, frequently branched, thin-walled, dichotomously to irregularly branched with main branch and acute tips, weakly to moderately dextrinoid in Melzer's reagent, CB–; tissues unchanged in KOH. Gloeocystidia with two types: (1) urniform, colorless, thin-walled, smooth, 12.5–16.5 × 3.5–5.5 µm; (2) capitate, colorless, thin-walled, smooth, 10.5–13 × 5–6 µm. Basidia subcylindrical to subclavate, flexuous, with a basal simple septum and four sterigmata, 34.5–37.5 × 4–5.5 µm, basidi-

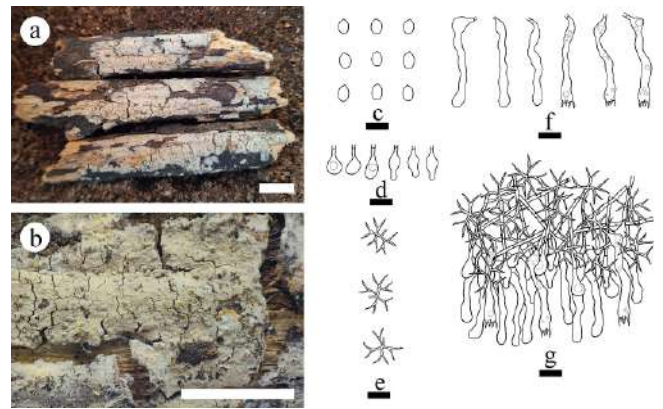


Fig. 34 Basidiomata and microscopic structures of *Vararia lacerata* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Gloeocystidia. (f) Section of the hymenium. (g) Dichohyphae. Scale bars: (a) = 1 cm, (b) = 1 mm, (c)–(g) = 10 µm.

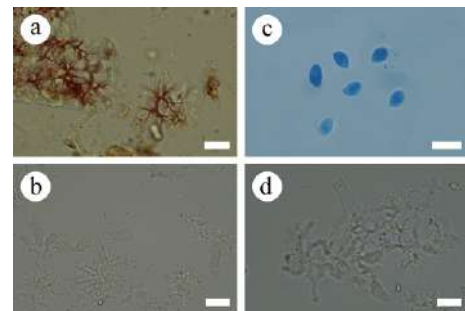


Fig. 35 Sections of the hymenium of *Vararia lacerata* (holotype). (a) Dichohyphae. (b) Gloeocystidia. (c) Basidiospores. (d) Basidia. Scale bars: (a)–(d) = 10 µm.

oles numerous, in shape similar to basidia but smaller. Basidiospores broadly ellipsoid, colorless, thin-walled, smooth, amyloid, CB–, 6–7.5(–8) × 3.5–5(–5.5) µm, L = 6.89 µm, W = 4.30 µm, Q = 1.47–1.60 (n = 120/4).

Additional material examined – China, Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, 27°77' N, 104°25' E, 1,900 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 25 August, 2023, CLZhao 31430, CLZhao 31434; 26 August, 2023, CLZhao 31655, CLZhao 31676, CLZhao 31679; 20 September, 2023, CLZhao 33510 (SWFC).

GenBank accession numbers – CLZhao 33407 ITS: PQ811403, LSU: PV185851; CLZhao 31430 ITS: PQ811398; CLZhao 31434 ITS: PQ811399, LSU: PV384143, mtSSU: PV399816; CLZhao 31655 ITS: PQ811400; CLZhao 31676 ITS: PQ811401, LSU: PV185849, mtSSU: PV399817, *rpb2*: PV339596; CLZhao 31679 ITS: PQ811402, LSU: PV185850, *tef1-α*: PV400171, *rpb2*: PV339597; CLZhao 33510 ITS: PQ811404, LSU: PV185852, *tef1-α*: PV400172, *rpb2*: PV339598

Notes – The phylogenetic analyses ([Fig. 5](#)) revealed that *V. lacerata* clustered within *Vararia*, and sister to *V. muscicola*. However, morphologically, *V. muscicola* is distinguished from *V. lacerata* by having coriaceous, fragile basidiomata growing on mossy rotting wood, white to cream hymenial surface, subcylindrical to fusiform and cylindrical (24–40 × 4–8 µm) to subclavate (12–18 × 6–7 µm) gloeocystidia, shorter fusiform to subcylindrical basidia (14–39 × 5–7 µm). The PHI test confirmed the absence of recombination in the new species compared to the closely related taxa ([Fig. 27d](#)). Thus, based on morphology and multigene phylogenetic evidence, *V. lacerata* is introduced as a new species.

Vararia membranacea Y.L. Deng & C.L. Zhao, sp. nov. **Figures 27e, 36, and 37**

Index Fungorum number: IF859285

Diagnosis – *Vararia membranacea* differs from other species by thin, membranous basidiomata, white to slightly cream to slightly greyish hymenial surface, gloeocystidia of two types (urniform and fusiform), and ellipsoid basidiospores.

Etymology – referring to the membranous basidiomata of the type specimen.

Type – China, Yunnan Province, Dehong, Xishuangbanna, Jinghong City, Rubber Plantation, 21°90' N, 100°76' E, 552.7 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 25 January, 2024, CLZhao 35710 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, thin, membranous, without odor or taste when fresh, up to 13 cm long, 1 cm wide, and 90 µm thick. Hymenial surface smooth, white to slightly cream when fresh, and becoming cream to slightly greyish when dry. Sterile margin cream, thinning out, up to 0.5 mm wide.

Hyphal system dimittic; generative hyphae bearing simple septa, colorless, thin-walled, smooth, frequently branched, 2.3–3.2 µm in diameter. Dichohyphae predominant, thick-walled, yellowish, capillary, frequently branched, dichotomously to irregularly branched with main branch and blunt tips, 1–2 µm in diameter, weakly to moderately dextrinoid in Melzer's reagent, CB–; tissues unchanged in KOH. Gloeocystidia with two types: (1) urniform gloeocystidia, colorless, thin-walled, smooth, 10–18 × 7–10 µm; and (2) fusiform gloeocystidia, colorless, thin-walled, smooth, 26.1–36.3 × 4.2–7.9 µm. Basidioles cylindrical, slightly flexuous, thin-walled, smooth, thin-walled, smooth, 17–29 × 5–8 µm. Basidiospores ellipsoid, colorless, thin-walled, smooth, CB–, IKI+, (6.8–)8.1–9.2(–9.4) × (4.6–)4.8–6.9(–7.5) µm, L = 8.53 µm, W = 5.70 µm, Q = 1.49 ± 0.04 (n = 30/3).

Additional material examined – China, Yunnan Province, Xishuangbanna, Jinghong City, Rubber Plantation, 21°90' N, 100°76' E, 552.7 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 25 January, 2024, CLZhao 35682, CLZhao 35709 (SWFC).

GenBank accession numbers – CLZhao 35710 ITS: PV637446, LSU: PV637453, mtSSU: PV637460, *rpb1*: PX441313, *rpb2*: PX432803, *tef1-α*: PX439084; CLZhao 35682 ITS: PV637444, LSU: PV637451, mtSSU: PV637458, *rpb1*: PX441311, *rpb2*: PX432801; CLZhao 35709 ITS: PV637445, LSU: PV637452, mtSSU: PV637459, *rpb1*: PX441312, *rpb2*: PX432802, *tef1-α*: PX439083

Notes – The phylogram (**Fig 5**) revealed that *Vararia membranacea* grouped within *Vararia*, and is sister to *V. punctata*, and shows a close phylogenetic affinity to *V. ambigua* Boidin, Lanq. & Gilles. However, morphologically, *V. punctata* is distinguished from *V. membranacea* by its thick-walled, clavate to cylindrical gloeocystidia (12–21 × 5–9 µm)^[33]. *V. ambigua* can be distinguished from *V. membranacea* by utriform basidia (27–40 × 3.5–4 µm), shorter basidiospores (6–7.3 × 3.4–5 µm)^[216]. The PHI analysis revealed no significant evidence of genetic recombination among these species (**Fig. 27e**). Thus, based on morphology and multigene phylogenetic evidence, we introduce *V. membranacea* as a new species.

Vararia muscicola Y.L. Deng & C.L. Zhao, sp. nov. **Figures 27d, 38, 39**

Index Fungorum number: IF859286

Diagnosis – *Vararia muscicola* differs from other species by the membranous, fragile basidiomata with a white to cream hymenial surface, generative hyphae bearing simple septa, and ellipsoid basidiospores (5.8–8.9 × 3.5–5.5 µm).

Etymology – referring to it dwelling on moss, on rotting wood.

Type – China, Yunnan Province, Lijiang, Helongtan Park, Xiangshan, 26°88' N, 100°22' E, 2,600 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 21 July, 2021, CLZhao 21669 (SWFC).

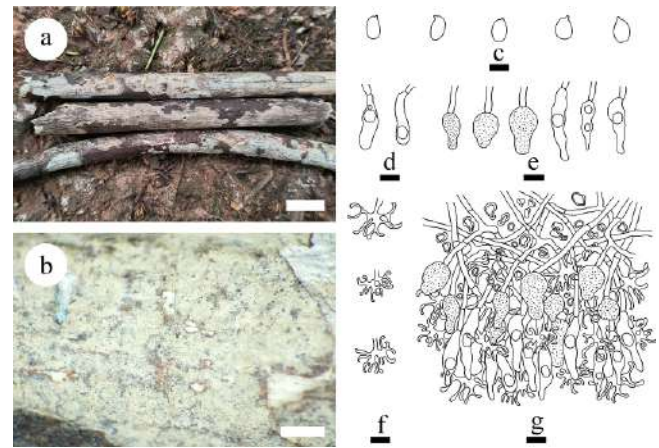


Fig. 36 Basidiomata and microscopic structures of *Vararia membranacea* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidioles. (e) Gloeocystidia. (f) Dichohyphae. (g) Section of the hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c)–(g) = 10 µm.

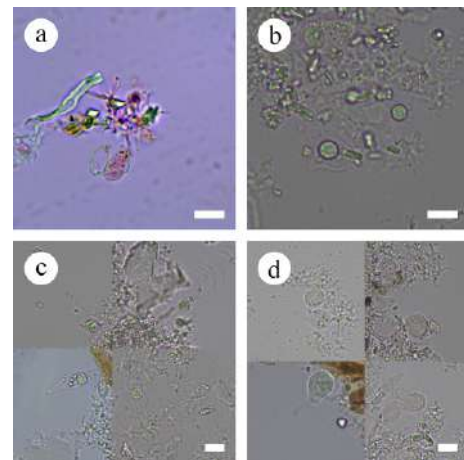


Fig. 37 Sections of the hymenium of *Vararia membranacea* (holotype). (a) Basidiospores. (b) Basidioles. (c), (d) Gloeocystidia. Scale bars: (a)–(d) = 10 µm.

GenBank accession numbers – CLZhao 21669 ITS: PV147167, LSU: PV185854, mtSSU = PV399818, *rpb2*: PV339600

Description – Basidiomata annual, resupinate, closely adnate, membranous, fragile, growing on mossy rotting wood, without odor or taste when fresh, up to 8 cm long, 2.5 cm wide, and 200 µm thick. Hymenial surface smooth, thin, white to cream when fresh, cream upon drying. Sterile margin white, thinning out, up to 2 mm wide.

Hyphal system dimittic; generative hyphae bearing simple septa, colorless, thin-walled, smooth, frequently branched, with some crystals, interwoven, 1.6–2 µm in diameter. Hymenium skeletal hyphae fibriform, thick-walled, colorless, 1.5–2.2 µm in diameter, IKI–, CB–; tissues unchanged in KOH. Dichohyphae predominant, slightly thick-walled, yellowish, capillary, frequently branched, dichotomously to irregularly branched with main branch and acute tips, 1–1.6 µm in diameter, weakly to moderately dextrinoid in Melzer's reagent, CB–; tissues unchanged in KOH. Gloeocystidia two types: (1) subcylindrical to fusiform, with a narrow or shizopapillate apex, colorless, with some refractive matter, thin-walled, smooth, 24–40 × 4–8 µm; and (2) cylindrical to subclavate, colorless, thin-walled, smooth, with some refractive matter, 12–18 × 6–7 µm. Basidia fusiform to subcylindrical, flexuous, with some refractive matter, with a basal simple septum and four sterigmata, 14–39 × 5–7 µm;

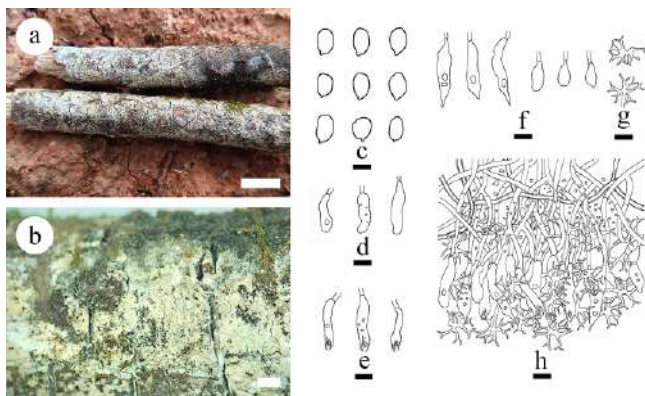


Fig. 38 Basidiomata of and microscopic structures *Vararia muscicola* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidioles. (e) Basidia. (f) Gloeocystidia. (g) Dichohyphae. (h) Section of the hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 μ m, (d)–(h) = 10 μ m.

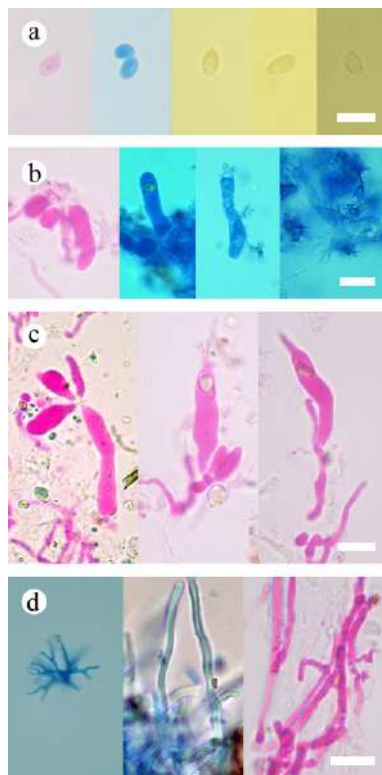


Fig. 39 Sections of the hymenium of *Vararia muscicola* (holotype). (a) Basidiospores. (b) Basidia and basidioles. (c) Gloeocystidia. (d) Hyphae. Scale bars: (a)–(d) = 10 μ m.

basidioles numerous, in shape similar to basidia but smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, CB⁻, (5.2–)5.8–8.9 \times (3.1–)3.5–5.5(–5.7) μ m, L = 7.21 μ m, W = 4.77 μ m, Q = 1.51 (n = 30/1).

Notes – The phylogenetic analyses (Fig. 5) revealed that *V. muscicola* is clustered within *Vararia* and sister to *V. lacerata*. However, morphologically, *V. lacerata* is distinguished from *V. muscicola* by coriaceous basidiomata with cream to buff hymenial surface, uniform (12.5–16.5 \times 3.5–5.5 μ m) and capitata (10.5–13 \times 5–6 μ m) gloeocystidia, narrower subcylindrical to subclavate basidia (34.5–37.5 \times 4–5.5 μ m), and broadly ellipsoid basidiospores (6–7.5 \times 3.5–5 μ m). The PHI test confirmed the absence of recombination in the new species compared to the closely related taxa (Fig. 27d).

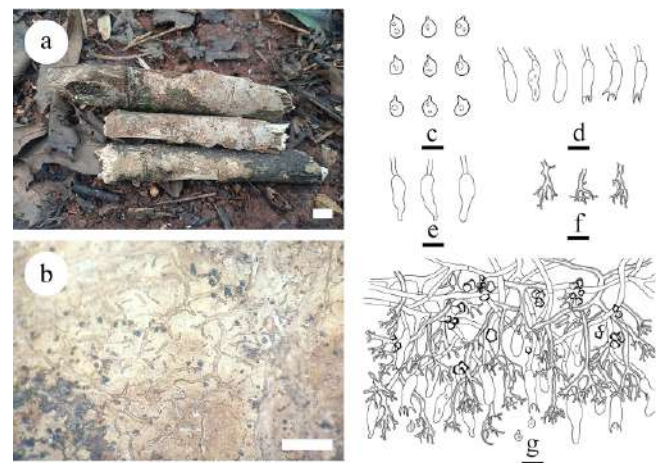


Fig. 40 Basidiomata of and microscopic structures *Vararia pingbianensis* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Cystidia. (f) Dichohyphae hyphae. (g) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm. Bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 μ m, (d)–(g) = 10 μ m.

Thus, *V. muscicola* is introduced as a new species, based on both morphological and multigene phylogenetic evidence.

Vararia pingbianensis Y.L. Deng & C.L. Zhao, sp. nov. [Figure 40](#)

Index Fungorum number: IF856163

Diagnosis – *Vararia pingbianensis* differs from other species by resupinate, membranous basidiomata, a dimittic hyphal system, thin-walled generative hyphae bearing simple septa, slightly thick-walled, hyaline to light buff dichohyphae predominate in hymenium, thin-walled, ellipsoidal basidiospores.

Etymology – referring to the locality (Pingbian) of the type specimens.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°51' N, 103°41' E, 2,360 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 7 June, 2020, CLZhao 18609 (SWFC).

Description – Basidiomata annual, resupinate, membranous, closely adnate, up to 20 cm long, 2 cm wide, and 150 μ m thick. Hymenial surfaces smooth, sparsely and deeply cracked with age, cream to rose pink when fresh, slightly brown to dark brown upon drying. Sterile margin slightly brown, up to 0.5 mm. Hyphal system dimittic, generative hyphae bearing simple septa, thin-walled, 2–3 μ m in diameter, IKI⁻, CB⁻; tissues unchanged in KOH. Dichohyphae predominate in hymenium, frequently branched, capillary, colorless to light buff, thick-walled, 1–1.5 μ m in diameter, weakly to moderately dextrinoid. Skeletal hyphae in context rarely branched, interwoven, colorless, slightly thick-walled, 1–2 μ m in diameter. Cystidia pyramid, smooth, colorless, thin-walled, the apex papillaceous, 22.5–25.0 \times 6–7 μ m. Basidia barred-shaped, with four sterigmata and a basal simple septum, thin-walled, smooth, 16.5–23.0 \times 4.5–5.5 μ m, basidioles in shape similar to basidia, but slightly smaller, occasionally with some guttules. Basidiospores ellipsoid, with a distinct apiculus, thin-walled, colorless, smooth, occasionally with one or two oil drops, IKI⁻, CB⁻, 4–6 \times 2.5–4.0 μ m, L = 4.90 μ m, W = 3.21 μ m, Q = 1.51–1.53 (n = 30/2).

Additional material examined – China, Yunnan Province, Lincang, Yun County, Dumu Village. 24°23' N, 101°9' E; 1,960 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 20 October, 2022, CLZhao 25157 (SWFC).

GenBank accession numbers – CLZhao 18609 ITS: OR195736, LSU: OR539690; CLZhao 25157 ITS: OR195737, LSU: OR510677, mtSSU: OR539689; *tef1- α* : PQ774593

Notes – The phylogenetic tree (Fig. 5) inferred from the ITS + nLSU sequences shows that *V. pingbianensis* is grouped within the genus *Vararia*, and closely related to *V. gomezii*, *V. sigmatospora*, and *V. trinidadensis*. However, morphologically, *V. gomezii* differs from *V. pingbianensis* by having both larger fusiform basidia ($30\text{--}40 \times 7\text{--}8 \mu\text{m}$), and subellipsoid basidiospores ($12\text{--}14 \times 4.5\text{--}5.5 \mu\text{m}$)^[216]; *V. sigmatospora* can be distinguished by its larger basidiospores ($13\text{--}22 \times 2.5\text{--}3.5 \mu\text{m}$)^[182]; while *V. trinidadensis* has larger gloecystidia ($27\text{--}50 \times 7\text{--}12 \mu\text{m}$), narrower fusiform basidia ($25\text{--}30 \times 4.2\text{--}5 \mu\text{m}$), longer fusiform, and subcylindrical basidiospores ($13\text{--}14.8 \times 2.5\text{--}3.2 \mu\text{m}$)^[224]. Thus, based on both morphological and multigene phylogenetic evidence, *V. pingbianensis* is introduced as a new species.

Vararia wumengshanensis Y.L. Deng & C.L. Zhao, sp. nov. Figures 27d, 41, 42

Index Fungorum number: IF859287

Diagnosis – *Vararia wumengshanensis* differs from other species by its white to cream-colored hymenial surface, generative hyphae bearing simple septa, gloecystidia of two types (ventricose and obclavate), and subcylindrical to narrowly smooth ellipsoid basidiospores.

Etymology – referring to the locality (Wumengshan National Nature Reserve) of the type species.

Type – China, Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, $27^{\circ}77'N$, $104^{\circ}25'E$, 1,900 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 26 August, 2023, CLZhao 31659 (SWFC).

GenBank accession numbers – CLZhao 31659 ITS: PQ811405, LSU: PV185853, mtSSU; PV283188, rpb2: PV339599, tef1- α : PV400173

Description – Basidiomata annual, resupinate, closely adnate, membranous, without odor or taste when fresh, up to 8 cm long, 2 cm wide, and 300 μm thick. Hymenial surface smooth, thin, white to cream when fresh, cream upon drying. Sterile margin white to cream, thinning out, up to 2 mm wide.

Hyphal pattern dimittic; generative hyphae bearing simple septa, colorless, thin-walled, smooth, rarely branched, interwoven, with some crystals, 2–3.5 μm in diameter. Dichohyphae predominant, yellowish, capillary, frequently branched, thick-walled, dichotomously to irregularly branched with main branch and acute tips, weakly to moderately dextrinoid in Melzer's reagent, CB–; tissues unchanged in KOH. Gloecystidia with two types: (1) ventricose, with a shizopapilla in the apical part, filled with refractive oil-like matter, colorless, thin-walled, smooth, $16\text{--}19.5 \times 5.5\text{--}7.5 \mu\text{m}$; and (2) obclavate, colorless, thin-walled, smooth, $15\text{--}18 \times 5.5\text{--}7 \mu\text{m}$. Basidia subcylindrical to subclavate, flexuous, with a basal simple septum and four sterigmata, $33.5\text{--}40 \times 4.5\text{--}6 \mu\text{m}$; basidioles numerous, in shape similar to basidia but smaller. Basidiospores subcylindrical to

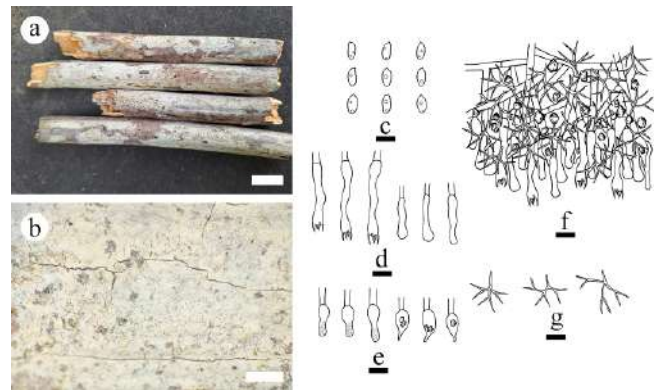


Fig. 41 Basidiomata and microscopic structures of *Vararia wumengshanensis* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Gloecystidia. (f) Section of the hymenium. (g) Dichohyphae. Scale bars: (a) = 1 cm, (b) = 1 mm, (c)–(g) = 10 μm .

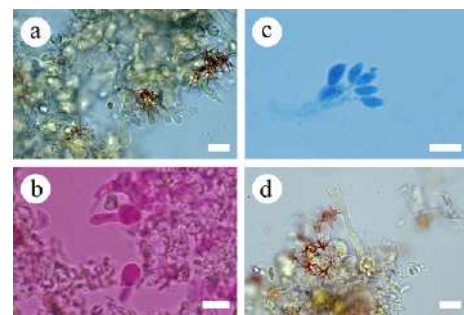


Fig. 42 Sections of the hymenium of *Vararia wumengshanensis* (holotype). (a) Section of the hymenium. (b) Gloecystidia. (c) Basidiospores. (d) Basidia. Scale bars: (a)–(d) = 10 μm .

narrowly ellipsoid, colorless, thin-walled, smooth, amyloid, CB–, $(7\text{--})7.5\text{--}9.5\text{--}10.5 \times (3.5\text{--})4\text{--}5\text{--}(5) \mu\text{m}$, $L = 8.77 \mu\text{m}$, $W = 4.12 \mu\text{m}$, $Q = 2.07$ ($n = 30/1$).

Notes – The phylogenetic analyses (Figs 5) revealed that *V. wumengshanensis* clustered within *Vararia* and is sister to *V. gallica*. However, morphologically, *V. gallica* differs from *V. wumengshanensis* by whitish hymenial surface, ventricose gloecystidia with a shizopapilla in the apical part ($15\text{--}20 \times 4\text{--}7 \mu\text{m}$), wider utriform basidia ($20\text{--}40 \times 5\text{--}7 \mu\text{m}$), and longer fusiform to narrowly ellipsoid basidiospores with a very prominent apiculus ($10\text{--}12 \times 3\text{--}5.5 \mu\text{m}$)^[225]. The PHI test confirmed the absence of recombination in the new species compared to the closely related taxa (Fig. 27d). Thus, *V. wumengshanensis* is introduced as a new species, based on both morphological and multigene phylogenetic evidence.

Key to 25 species of *Vararia* s.l. in China

- | | | |
|---|---|------------------------------|
| 1 | Generative hyphae with clamp connections | 2 |
| – | Generative hyphae with simple septa | 8 |
| 2 | Basidia with 2 sterigmata | 3 |
| – | Basidia with 4 sterigmata | 4 |
| 3 | Subcylindrical to fusiform basidiospores ($12\text{--}17 \times 4.5\text{--}5.5 \mu\text{m}$), slightly thick-walled gloecystidia two types: subglobose ($15\text{--}30 \times 6\text{--}8 \mu\text{m}$), and subcylindrical or gradually narrower ($25\text{--}40 \times 4.5\text{--}6 \mu\text{m}$) | <i>Vararia amphithallica</i> |
| – | Fusiform to cylindrical basidiospores ($18\text{--}22 \times 6\text{--}7.2 \mu\text{m}$), thick-walled, ventricose, gloecystidia with an apical papilla ($20\text{--}40 \times 9\text{--}12 \mu\text{m}$) | <i>V. bispora</i> |
| 4 | Thin to thick-walled generative hyphae, subcylindrical basidia ($26\text{--}46 \times 5\text{--}8 \mu\text{m}$), ellipsoid to ovoid to subcylindrical gloecystidia ($9\text{--}23 \times 7\text{--}10.5 \mu\text{m}$) | <i>V. dawuishanensis</i> |
| – | Thin-walled generative hyphae | 5 |
| 5 | Gloecystidia two types: thin-walled, subglobose ($11\text{--}23 \times 6\text{--}12 \mu\text{m}$), and subulate ($25.5\text{--}43 \times 7\text{--}11 \mu\text{m}$), ellipsoid to broadly ellipsoid basidiospores ($5\text{--}10 \times 3\text{--}7 \mu\text{m}$) | <i>V. fissurata</i> |
| – | Gloecystidia one type | 6 |
| 6 | Basidiospores < 5 μm wide | <i>V. investiens</i> |

–	Basidiospores > 5 µm wide	7
7	Broadly ellipsoid basidiospores (12–16 × 9.5–13 µm), clavate basidia (70–110 × 10–16 µm), clavate gloeocystidia (50–100 × 4–9 µm)	<i>V. montana</i>
–	Spherical basidiospores (8–10 × 7.5–8.5 µm), cylindrical to clavate basidia (40–45 × 6–7.5 µm), subcylindrical to fusiform gloeocystidia (48–80(–105) × 7–11(–14) µm)	<i>V. sphaericospora</i>
8	Dichohyphae distinctly thick-walled	9
–	Dichohyphae thin-walled or slightly thick-walled	20
9	Generative hyphae thin- to slightly thick-walled	10
–	Generative hyphae thin-walled	14
10	Gloeocystidia one type	11
–	Gloeocystidia two or three types	12
11	Gloeocystidia clavate to cylindrical, thick-walled (12–21 × 5–9 µm), subcylindrical basidia with 4 sterigmata (11–25 × 4–7 µm), ellipsoid basidiospores (6–10 × 4–6 µm), white to cream hymenial surface	<i>V. punctata</i>
–	Gloeocystidia spindle to subcylindrical (38–47 × 8–13 µm), basidiospores sub-fusiform to navicular (9–13 × 5–8 µm), subcylindrical basidia with four sterigmata (33–39 × 7–9 µm), spindle to subcylindrical gloeocystidia (38–47 × 8–13 µm), cream to isabelline to slightly brown hymenial surface	<i>V. isabellina</i>
12	Gloeocystidia three types: subcylindrical (16.5–58.5 × 4–10 µm), fusiform (18.5–43.5 × 7–9 µm), and tapering (27.5–42 × 5.5–9 µm), slightly thick-walled, ellipsoid basidiospores (5.9–11.5 × 4.7–8.6 µm), cylindrical basidia (17.5–32 × 5–9.5 µm), thin- to slightly thick-walled	<i>V. yunnanensis</i>
–	Thin-walled ellipsoid basidiospores	13
13	Gloeocystidia two types: elliptical to ovoid (5.8–16 × 3.5–7 µm), subulate (16.5–27 × 4–7 µm), subcylindrical basidia with 4 sterigmata (13–23.5 × 3–4.5 µm), ellipsoid basidiospores (3.5–5.5 × 2.5–3.5 µm), buff to ochraceous hymenial surface	<i>V. fragilis</i>
–	Gloeocystidia two types: thick-walled, fusiform (28.5–50 × 6–12.5 µm), subglobose (11–27 × 7–11 µm), ellipsoid basidiospores (7.6–10.8 × 5.7–7.8 µm), subclavate to subcylindrical basidia (23–46 × 5–8 µm)	<i>V. yaoshanensis</i>
14	Thick-walled fibriform skeletal hyphae absent	15
–	Thick-walled fibriform skeletal hyphae present	16
15	Hymenial surface white to cream, gloeocystidia ventricose (16–19.5 × 5.5–7.5 µm) and obclavate (15–18 × 5.5–7 µm), subcylindrical to subclavate basidia (33.5–40 × 4.5–6 µm), subcylindrical to narrowly ellipsoid basidiospores (7.5–9.5 × 4–5 µm)	<i>V. wumengshanensis</i>
–	Hymenial surface white to slightly cream to slightly greyish, gloeocystidia urniform (10–18 × 7–10 µm) and fusiform (26.1–36.3 × 4.2–7.9 µm), ellipsoid basidiospores (8.1–9.2 × 4.8–6.9 µm)	<i>V. membranacea</i>
16	Gloeocystidia two types: subcylindrical to fusiform (24–40 × 4–8 µm), cylindrical to subclavate (12–18 × 6–7 µm), fusiform to subcylindrical basidia with 4 sterigmata (14–39 × 5–7 µm), ellipsoid basidiospores (5.8–8.9 × 3.5–5.5 µm), white to cream hymenial surface	<i>V. muscicola</i>
–	Gloeocystidia one type	17
17	Basidia clavate	18
–	Basidia fusiform to subcylindrical	19
18	Basidia larger (25–35 × 6–7 µm), hymenial surface white to slightly pink, gloeocystidia subulate (17–35 × 6–7 µm), sub-fusiform to navicular basidiospores (6–11 × 4–6 µm)	<i>V. sinensis</i>
–	Basidia smaller (11–17.5 × 2–4 µm), hymenial surface white to cream, gloeocystidia subglobose, and clavate to fusiform (6.5–16 × 3–5 µm), ellipsoid basidiospores (3.5–5.5 × 2.5–4 µm)	<i>V. lincangensis</i>
19	Basidia subcylindrical (20–29 × 6–7.5 µm), hymenial surface cream to yellowish, gloeocystidia fusiform to subcylindrical (15–21 × 5–7 µm), broadly ellipsoid basidiospores (2.5–4 × 1.5–2.5 µm)	<i>V. asiana</i>
–	Basidia fusiform to subcylindrical (15–28 × 3–5.3 µm), hymenial surface ferruginous to yellowish-brown, gloeocystidia obclavate (14–25 × 3–6 µm), basidiospores ellipsoid (5.9–8.8 × 3.1–5.1 µm)	<i>V. ferruginosa</i>
20	Thick-walled fibriform skeletal hyphae present	21
–	Thick-walled fibriform skeletal hyphae absent	22
21	Gloeocystidia three types: urniform (16.3–28 × 10–14 µm), mushroom-shaped (21.3–37 × 12.7–13 µm), fusiform (35.4–47.3 × 7.8–14.1 µm), cylindrical to clavate basidia (29–57 × 8.5–12.3 µm), cylindrical to fusiform basidiospores (22.1–25.1 × 8.7–10.1 µm)	<i>V. bambusicola</i>
–	Gloeocystides absent, oblong to subellipsoid basidiospores (9–13 × 5–7.2 µm), subcylindrical basidia (45–65 × 8–10 µm)	<i>V. cinnamomea</i>
22	Rose to orange subfusiform basidiospores ((14–)16–19(–21.5) × 4.2–6 µm), cylindrical basidia (30–53 × 6.5–7.5 µm), thick-walled, subcylindrical gloeocystides (50–65 × 6–7(–8.5) µm)	<i>V. breviphysa</i>
–	Basidiospores colorless	23
23	Gloeocystidia subcylindrical to fusiform (26–40 × 4.5–9 µm), cylindrical basidiospores (6–8 × 2–3 µm), cylindrical basidia (30–40 × 4–5 µm)	<i>V. racemosa</i>
–	Gloeocystidia two types	24
24	Hymenial surface cream to buff, gloeocystidia two types: urniform (12.5–16.5 × 3.5–5.5 µm), capitate (10.5–13 × 5–6 µm); subcylindrical to subclavate basidia (34.5–37.5 × 4–5.5 µm), broadly ellipsoid basidiospores (6–7.5 × 3.5–5 µm)	<i>V. lacerata</i>
–	Hymenial surface white to pinkish buff to cinnamon buff, gloeocystidia two types: urniform (9–20 × 8–14 µm), subcylindrical to fusiform (23–42 × 6–10 µm), subclavate basidia (20.5–26 × 5.5–7 µm), fusiform to ellipsoid basidiospores (11.8–16.1 × 5.6–7.7 µm)	<i>V. bannaensis</i>

Family Russulaceae Lotsy 1907

Index Fungorum number: IF81358

Type genus – *Russula* Pers.

Notes – Russulaceae is characterized by annual, resupinate, corticioid, pleurotoid, cantharelloid (*Multifurca*), agaricoid, gasteroid (sequestrate), and some with veiled basidiomata, with or without milk, smooth, lamellate, regularly forked and globular or irregular hymenophore. Also, they have a monomitic to dimitic hyphal system, generative hyphae with or without clamp-connections, heteromerous trama in context, lamellae and stipe with sphaero-

cysts and hyphae mixed (*Lactarius*, *Russula* and some sequestrate fungi), gloeoplerous hyphae and gloeocystidia present or absent, lamprocystidia present or absent, pseudocystidia and macrocystidia present or absent, with asperulate, spinulose, verrucose, echinulate, ridges or crests, subreticulate to reticulate, amyloid basidiospores. Wood decay or ectomycorrhizal fungi belong to this family^[1].

Note 47 *Boidinia* Stalpers & Hjortstam

Index Fungorum number: IF17162

Type species – *Boidinia furfuracea* (Bres.) Stalpers & Hjortstam

Notes – *Boidinia* was segregated from *Gloeocystidiellum* as a monotypic genus^[226], and typified by *B. furfuracea*. It is characterized by annual, resupinate, separable, thin, porulose or furfuraceous, sometimes pellicular to soft membranaceous basidiomata and thin to thick-walled, globose or subglobose, echinulate or verrucose, ornamentation disappearing in KOH, strongly amyloid basidiospores with distinct apiculus as the main diagnostic features. Later authors have pointed to the suburniform shape of basidia with 1–2 sterigmata, and a basal clamp connection as an additional characteristic^[105,203,227]. Several species subsequently have been placed in *Boidinia*. Both *Boidinia* and *Gloeopeniophorella* belong to family Russulaceae. Contrary to *Lactarius* and *Russula* that are mycorrhizal, *Boidinia* is saprobic and it clusters in a basal position in the clade, suggesting that the ancestor in the russuloid clade to the agaricoid forms had a corticioid basidiome and was saprotrophic^[26,228].

Note 48 *Gloeopeniophorella* Rick

Index Fungorum number: IF22169

Type species – *Gloeopeniophorella rubroflava* Rick

Notes – *Gloeopeniophorella* was introduced with a single species *G. rubroflava*^[229], but has been largely ignored since its introduction. This genus is characterized by resupinate basidiomata, a smooth to tuberculate hymenophore surface, a monomitic hyphal system with simple-septate generative hyphae, present lamprocystidia and gloeocystidia, and amyloid ellipsoid basidiospores^[180]. *Gloeopeniophorella* is characterized among *Gloeocystidiellum* s.l. by the presence of lamprocystidia. Boidin^[152] restudied the type specimen and concluded that it shares similarities with *Gloeocystidiellum convolvens* (P. Karst.) Donk and *G. laxum* Sheng H. Wu, and they also made the appropriate combinations. To date, *Gloeopeniophorella* includes five species, namely *G. bambusicola* Yang Yang & C.L. Zhao, *G. griseolutea* Rick, *G. rubroflava*, *G. sacrata* (G. Cunn.) Hjortstam & Ryvarden, and *G. singularis* (Boidin, Lanq. & Gilles) Hjortstam & Ryvarden. It belongs to family Russulaceae, closely related to *Boidinia* based on ITS+nLSU sequence data^[20,26,45].

Note 49 *Lactarius* Pers.

Index Fungorum number: IF17895

Type species – *Lactarius torminosus* (Schaeff.) Pers

Note 50 *Lactifluus* (Pers.) Roussel

Notes – *Lactarius* is a well-known ectomycorrhizal genus that is characterized by the presence of latex, hence the common name milk caps^[230]. Until recently, species identification of *Lactarius* was based on morphological characteristics such as latex color, and color change, pileus features, spore ornamentation, the presence/absence of cystidia and pileipellis structures^[231]. Classification of *Lactarius* species has historically been problematic, as mycologists often use different morphological characters for infrageneric classification. Pileipellis structures have been the most frequently used character for infrageneric classification in *Lactarius*^[230]. The genus has long been recognized as one of two major groups (together with the larger genus *Russula* Pers.) in family Russulaceae. A recent multi-locus phylogenetic study revealed that species identified as *Lactarius* spp. represent three genera: *Multifurca* Buyck & V. Hofst, *Lactarius*, and *Lactifluus* (Pers.) Roussel^[86,230–235].

Index Fungorum number: IF17896

Type species – *Lactifluus piperatus* (L.) Roussel

Notes – *Lactifluus* belongs to Russulaceae (Russulales) and is a genus of milk caps, predominantly found in subtropical and tropical regions^[174,232,233,236]. The genus was previously classified under *Lactarius* due to the presence of latex exudation when the basidiomata are damaged. Although there are no synapomorphic characters to distinguish between them, some morphologies tend to be well-represented in either *Lactarius* or *Lactifluus*^[237,238]. Upon closer inspection, *Lactifluus* and *Lactarius* have some key morphological

differences. Although no synapomorphic characteristic has been found to consistently distinguish both genera, the distinction can usually be made on a combination of characters and trends. First, *Lactifluus* species, relative to *Lactarius*, are more likely to have dry pilei with a velvety to pruinose texture. Also, *Lactifluus* species lack zonate, hairy, viscid, or scrobiculate pilei^[236,237,239,240]. After the proposal to conserve *Lactifluus* as a separate genus, *Lactifluus* was divided into six subgenera, 13 sections, and several unclassified species^[234,235,241]. A multi-locus phylogeny using global samples revealed a new classification scheme of the genus and consequently four subgenera were proposed; *Lactifluus* subg. *Gymnocarpi* (R. Heim ex Verbeke) De Crop, subg. *Lactariopsis* (Henn.) Verbeke, subg. *Lactifluus* (Pers.) Roussel, and subg. *Pseudogymnocarpi* (Verbeke) De Crop^[241]. Each subgenus was further divided into four or more sections, together with undescribed clades and species in isolated phylogenetic positions^[240].

Note 51 *Multifurca* Buyck & V. Hofst.

Index Fungorum number: IF511332

Type species – *Multifurca ochricompacta* (Bills & O.K. Mill.) Buyck & V. Hofst.

Notes – *Multifurca* was described to accommodate a well-supported monophyletic clade comprising species of *Russula* subsect. *Ochricompactae* Bills & O.K. Mill. and *Lactarius furcatus* Coker. Mainly based on *Russula* subsect. *Ochricompactae* and sharing the same type with the subsection, as a 'hybrid' of the two genera, the small genus can nevertheless be recognized by a combination of various characters: concentrically zonate pale-colored pileus, regularly forked gills that are yellow to salmon at maturity, zonate context, dark-colored spore print, and very small and faintly ornamented spores. The known geographic distribution of *Multifurca* species are from southeastern North America, Central America, Oceania, and Southeast and South Asia^[232,242]. *Multifurca* is of phylogenetic importance for the phylogeny of Russulaceae as it is the only genus that exhibits features that are reminiscent of the earlier diversified resupinate genera *Gloeocystidiellum* Donk and *Boidinia* Stalpers & Hjortstam^[232,242]. Two species *M. furcata* (Coker) Buyck & V. Hofst. and *M. zonaria* (Buyck & Desjardin) Buyck & V. Hofst., which were originally described from USA and Thailand, respectively, were found to exist in subtropical-tropical China^[242]. *Multifurca stenophylla* (Berk.) T. Lebel, C.W. Dunk & T.W. May was described and illustrated by Lebel et al.^[243]. Subsequently, using samples from different localities and three loci (ITS, 28S rDNA and *rpb2*), Wang et al.^[85] demonstrated that *Multifurca* is split into two highly supported major clades that are here recognized at the subgeneric level: subg. *Furcata* subg. nov. exclusively included lactarioid species, while subg. *Multifurca* included species with a russuloid habit. Meanwhile, using phylogenetic species recognition and comparison of genetic distances five new and six previously described species were recognized^[85]. So far, 12 species have been accepted in the genus (Index Fungorum 2025).

Note 52 *Pseudoxenasma* K.H. Larss. & Hjortstam

Index Fungorum number: IF18416

Type species – *Pseudoxenasma verrucisporum* K.H. Larss. & Hjortstam

Notes – *Pseudoxenasma verrucisporum* has clear affinities to Russulales, and occurs as a sister taxon to that clade in phylogenetic trees^[26]. However, the connection is not supported by bootstrap. *Pseudoxenasma* was established as a monotypic genus because it has pleurobasidia (lateral basidia), a feature not known from any other genus with ornamented amyloid spores and sulfo-positive cystidia. In some species with a dense, more or less gelatinized hyphal texture, generative hyphae tend to grow horizontally in the hymenium and produce basidia laterally. Both gelatinization of the

hyphae and lateral production of basidia seem to facilitate quick response to favorable conditions for sporulation. *Pseudoxenasma* grows on dead but still attached branches of *Picea abies* and is often found fertile in mild periods of winter; its globose, coarsely ornamented, and strongly amyloid spores fit well with the general spore morphology in Russulales^[26].

Note 53 Family Stereaceae Pilát 1930

Index Fungorum number: IF81424

Type genus – *Stereum* Hill ex Pers. 1794

Notes – Stereaceae, typified by *Stereum*, formed a well-supported monophyletic clade in Russulales^[26,28,45]. Stereaceae is characterized by annual, resupinate, discoid, cupulate, stereoid, auricularioid (gelatinous to fleshy, *Gloeosoma*) pulvinate, disciform, effused-reflexed, pileate-sessile to flabelliform basidiomata, smooth, rugose to tuberculate hymenophore. It also shows a monomitic to dimittic hyphal system, generative hyphae with or without clamp-connections, amyloid (*Amylohyphus*) or inamyloid; skeletal hyphae occasionally branched, nonamyloid, nondextrinoid or binding hyphae distributed in the subiculum (*Gloeomyces*); gloeoplerous hyphae and gloeocystidia present or absent, pseudocystidia present or absent, Skeletocystidia present or not, amyloid (*Amylohyphus*), dextrinoid (*Dextrinocystidium*) or not, acanthophyses present or absent, acanthobasidia present or absent, botryophyses with tips amyloid present in *Aleurobotrys*; with smooth, asperulate, spinulose, verrucose, echinulate, aculeate, ridges or crests, subreticulate to reticulate, inamyloid (*Amylohyphus*) or amyloid basidiospores^[1]. Species in the family are all saprobic, causing a white rot (or white pocket rot in some species) on both conifers and hardwoods. Although mushrooms and polypores are commonly present in different clades within the order Russulales, so far, Stereaceae contains only corticioid and stereoid wood-inhabiting fungi with a smooth or occasionally tuberculate or merulioid hymenophores. Micro-morphologically, all species in the family have gloeocystidia (skeletocystidia in *Stereum*), and amyloid basidiospores with smooth or ornamented walls^[26]. Species in the family mostly belong to *Stereum*, *Xylobolus* P. Karst., *Aleurodiscus* s. lat., and *Gloeocystidiellum* s. lat. While taxa of *Stereum* s. str. and *Xylobolus* formed monophyletic clades in published phylogenetic trees, the latter two genera were highly polyphyletic, which left the generic arrangements within Stereaceae partly unresolved^[26,87,103,244,245]. Recently, phylogenetic analyses based on a concatenated ITS1-5.8S-ITS2 (ITS) and the D1-D2 domains of nuc 28S rDNA (LSU) sequence data of Stereaceae, reported two new genera, *Confertotrama* and *Gelatinostereum*, nine new species and 20 new combinations^[87]. In the study, based on the ITS + nLSU + *rpb2* + *tef1-α* dataset, the divergence time of family Stereaceae occurred in a mean crown age of 179.84 Mya, with a 95% highest posterior density (HPD) of 126.6–228.84 Mya.

Note 54 Acanthobasidium Oberw. 1965

Index Fungorum number: IF17002

Type species – *Acanthobasidium delicatum* (Wakef.) Oberw. ex Jülich

Notes – *Acanthobasidium* was segregated from *Aleurodiscus* s.l. based on various morphological characters and supported by phylogenetic analyses^[103]. It is characterized by thin, delicate basidiomata, a monomitic hyphal system with clamped generative hyphae, gloeocystidia moniliform, acanthocystidia and/or acanthophyses, acanthobasidia present, basidia with spines and usually ornamented subglobose basidiospores^[246]. *Acanthobasidium* is a well-circumscribed group of species displaying good phylogenetic support. The presence of acanthobasidia is not unique within *Aleurodiscus* s. lat.^[247]; however, it is a strong indication of relationship with the genus^[46,246]. Recently, *Acanthobasidium weirii* (Burt) L.D. Dai & S.H. He was proposed as a new combination, and *A. bambusicola*

L.D. Dai & S.H. He was described and illustrated by Dai & He^[80]. *Acanthobasidium quilae* (Gorjón, Gresl. & Rajchenb.) Rajchenb. & Pildain was proposed based on morphology and phylogenetic analyses of ITS and 28S^[46]. Currently, seven species are accepted in *Acanthobasidium* (Index Fungorum 2025).

Note 55 Acanthophysellum Parmasto

Index Fungorum number: IF17004

Type species – *Acanthophysellum lividocoeruleum* (P. Karst.) Parmasto

Notes – *Acanthophysellum* was introduced to accommodate resupinate basidiomata, a monomitic hyphal system; generative hyphae with clamps or with simple-septa, present gloeocystidia and acanthocystidia, clavate to cylindrical basidia with 2–4 sterigmata, and cylindrical or ellipsoid to allantoid, smooth non-amyloid basidiospores, with *Corticium lividocoeruleum* P. Karst. as the generic type species^[248]. However, the statement about non-amyloid spores must be regarded as a typographical error because later introduced *Acanthophysellum* in the tribe Aleurodisceae defined by the amyloid basidiospores. *Corticium lividocoeruleum* and *Thelephora frustulata* Pers., the generic type of *Xylobolus*, are phylogenetically and morphologically closely related^[26], and this connection could suggest that *Acanthophysellum* should be regarded as synonym of *Xylobolus*. However, *Acanthophysellum* differs from *Xylobolus* in some morphological characters and in having white rot (white pocket rot in *Xylobolus*), phenoloxidase positive reaction and nuclear behavior astatocoenocytic (holocoenocytic in *Xylobolus*). Genus *Acanthophysium* is a synonym of *Xylobolus*, but conserved *Acanthophysellum*. Xu et al.^[87] showed that *C. lividocoeruleum* is the type species of *Acanthophysellum*, but phylogenetic analyses showed that it nested within the *Xylobolus* lineage. Morphologically, *X. lividocoeruleus* shared characters with other species in the genus a pseudo-parenchymatic subhymenium, numerous acanthohyphidia and smooth basidiospores, but is unique for its resupinate basidiomata, nodose-septate hyphae and typical gloeocystidia. With this disposition, *Acanthophysellum* becomes a synonym of *Xylobolus*. Although, four species, *A. canadense* (Skolko) Sheng H. Wu, Boidin & C.Y. Chie, *A. fennicum* (Laurila) Bernicchia & Gorjón, *A. propinquum* (Boidin & Gilles) Boidin & Gilles, and *A. verecundum* Duhem are remaining in the genus *Acanthophysellum*.

Note 56 Aleurodiscus Rabenh. ex J. Schröt.

Index Fungorum number: IF840214

Type species – *Aleurodiscus amorphus* (Pers.) J. Schröt.

Notes – *Aleurodiscus* belongs to family Stereaceae (Russulales). *Aleurodiscus* s.l. is characterized by cupulate, effused or effused-reflexed basidiomata, a monomitic or dimittic hyphal system with simple-septate or clamped generative hyphae, smooth or ornamented amyloid basidiospores, and sterile organs such as acanthophyses, gloeocystidia, hyphidia, and dendrohyphidia may be present^[102,103]. However, it has long been a complicated and unsettled problem as how to delimit the segregated genera among *Aleurodiscus* s.l.^[19,26,28,45,103,244], due to highly variable diagnostic characters among species. In recent times, new species of *Aleurodiscus* s.l. have been proposed by Ryvarden et al.^[249], Gorjón et al.^[148], Maninder et al.^[250], Dai & He^[80], Dai et al.^[251,252], Ghobad-Nejhad & Langer^[253], Tian et al.^[254], and Wu et al.^[19]. Although *Aleurodiscus* s.l. had been divided into several small genera, based on different combinations of morphological characters, the phylogenetic analyses did not fully support these separations^[80,103]. Accordingly, the inter- and intrageneric phylogeny of *Aleurodiscus* s.l. in Stereaceae is still unclear and no reliable morphological characters can be used to recognize the small segregated genera. Thus, the broad concept of the genus has often been adopted by mycologists when describing new species^[102,148,251,252].

Aleurodiscus yunnanensis Y.L. Deng & C.L. Zhao, sp. nov. Figures 43, 44

Index Fungorum number: IF860772

Diagnosis – *Aleurodiscus yunnanensis* differs from other species by the punctate basidiomata, white to cream hymenial surface smooth, a dimittic hyphal system, generative hyphae bearing simple septa, and broadly ellipsoid to globose basidiospores.

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

Type – China, Yunnan Province, Diqing, Weixi County, Zhonglu Town, Lagaluo village, 27°15' N, 99°15' E, 3,100 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 14 October, 2023, CLZhao 34929 (SWFC).

GenBank accession numbers – CLZhao 34929 ITS: PV940926, LSU: PX070091, *rpb2*: PX432788, *rpb1*: PX441314, *tef1- α* : PX439085

Description – Basidiomata resupinate, adnate, membranous, punctate, without odor and taste when fresh, up to 7 cm long, 1 cm wide, and 120 μ m thick. Hymenial surface smooth, white to cream when fresh, cream to slightly buff upon drying. Sterile margin white, thinning or fairly determinate, arachnoid or shortly filamentous, up to 2 mm wide.

Hyphal system dimittic; generative hyphae bearing simple septa, interwoven, moderately branched, colorless, thin-walled, usually with small oily drops, 2–3 μ m in diameter. Quasi-binding hyphae numerous, embedded in woody substrate, richly ramified, thin-walled, rarely branched, colorless, IKI–, CB–; tissues unchanged in KOH. Gloeocystidia numerous, immersed or slightly projecting, irregularly cylindrical, clavate, moniliform, flexuous, usually moniliform toward apices or with a schizopapillate constriction, sometimes laterally or apically protruding, usually with several big oily drops, colorless, 34.5–50 \times 11–17 μ m, thin-walled, weakly to moderately dextrinoid in Melzer's reagent, CB–; tissues unchanged in KOH. Basidia cylindrical to subclavate, usually laterally with several aculei, with four sterigmata and a basal simple septum, 33–65.5 \times 8–19 μ m; basidioles numerous, in shape similar to basidia but smaller, 28–44.5 \times 5–10 μ m. Basidiospores broadly ellipsoid to globose, thin-walled, colorless, smooth to echinulate, with several minute oily drops, IKI+, CB–, (14–)14.7–17(–18) \times (8.5–)9.7–12.5(–14) μ m, L = 15.88 μ m, W = 11.02 μ m, Q = 1.44 (n = 30/1).

Notes – The phylogenetic analysis (Fig. 6) revealed that *Aleurodiscus yunnanensis* is grouped within the genus *Aleurodiscus* in family Stereaceae, and closely related to *A. wakefieldiae* and *A. subroseus*. However, morphologically, *A. wakefieldiae* differs from *A. yunnanensis* by its bright pink to cream to pale ochraceous hymenophore, generative hyphae with clamps, hyphoid to distinctly clavate acanthophyses (30–80 \times 4–12 μ m), both larger slightly thick-walled and slightly moniliform gloeocystidia with a few constrictions, negative in sulphoaldehyde solution (90–180 \times 5–12 μ m), clavate basidia (80–180 \times 10–20 μ m), and ellipsoid ornamented basidiospores (20–28 \times 14–20 μ m)^[185]. *Aleurodiscus subroseus* can be distinguished from *A. yunnanensis* by pinkish white to pale orange to brownish orange hymenophore, generative hyphae with clamp connections, both larger slightly thick-walled and moniliform gloeocystidia with one to several constrictions (45–70 \times 6–12 μ m), slightly thick-walled, subclavate to subcylindrical acanthophyses (acanthocystidia) (30–60 \times 6–20 μ m), and clavate basidia (52–80 \times 13–17 μ m), and wider basidiospores (16–20 \times 11–14 μ m)^[254]. Thus, morphology and multi-gene phylogenetic analysis confirmed that the present collection is a new species, *Aleurodiscus yunnanensis*.

Note 57 *Amylosporomyces* S.S. Rattan

Index Fungorum number: IF17071

Type species – *Amylosporomyces echinosporus* S.S. Rattan

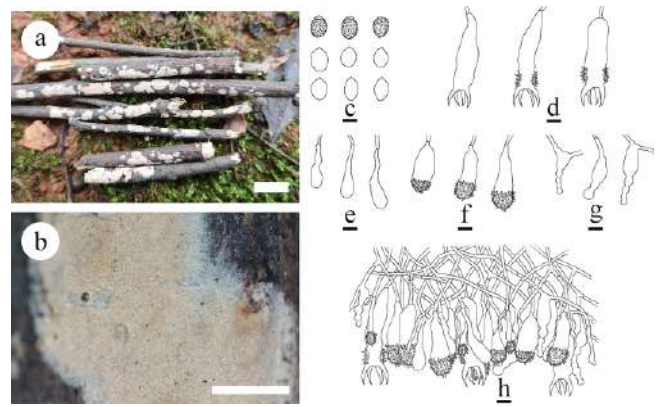


Fig. 43 Basidiomata and microscopic structures of *Aleurodiscus yunnanensis* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Clavate gloeocystidia. (f) Acanthocystidia. (g) Moniliform cystidia. (h) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c)–(h) = 10 μ m.

Notes – Hjortstam & Ryvarden^[227] referred *Gloeocystidiellum subasperisporum* to *Amylosporomyces*, a genus described as lacking any kind of cystidia^[255]. It is characterized by effuse basidiomata with white, pallid to pale yellow, lignicolous or corticolous hymenial surface, a monomittic hyphal system; generative hyphae with clamp connections, suburniform basidia with four sterigmata, and reniform, verruculose, amyloid basidiospores^[255]. Only two species, *A. camelicolor* Khara and *A. echinosporus* S.S. Rattan, are accepted in *Amylosporomyces*^[26].

Note 58 *Conferticium* Hallenb.

Index Fungorum number: IF17349

Type species – *Conferticium insidiosum* (Bourdot & Galzin) Hallenb.

Notes – *Conferticium* (Stereaceae, Russulales) was erected in 1980 and typified by *C. insidiosum*, which is characterized by the resupinate basidiomata with membranaceous to ceraceous, smooth to tuberculate hymenophore, a monomittic simple-septate hyphae, and the numerous cylindrical, sinuous gloeocystidia^[256]. Based on MycoBank (2025) and Index Fungorum (2025), nine specific and infraspecific names are registered under *Conferticium*, of which seven species are widely recognized^[256,257]. Phylogenetic relationships of russuloid basidiomycetes with emphasis on aphylophoralean taxa revealed that *C. ochraceum* (Fr.) Hallenb. did not cluster with *C. ravum* (Burt) Ginns & G.W. Freeman, but it occurred on a single clade^[9,26]. The research showed that the similarities in basidiomata structures and basidia regeneration among species in *Conferticium* were of uncertain value for genus characterization^[26]. Sequences of ITS and nLSU nrRNA gene regions of the studied samples were generated, in which *C. ochraceum* nested into family Stereaceae, and then grouped with *Gloeocystidiellum*, *Stereum*, and *Gloeomyces* Sheng H. Wu^[150,256,257].

Note 59 *Confertotrama* Nakasone & S.H. He

Index Fungorum number: IF843412

Type species – *Confertotrama rugulosa* (Berk. & M.A. Curtis) Nakasone & S.H. He

Notes – *Confertotrama* was established by Xu et al.^[87], and typed by *C. rugulosa*. Larsson & Larsson^[26] indicated that *Megalocystidium chelidonium* (Pat.) Boidin, Lanq. & Gilles, *Boidinia macrospora* Sheng H. Wu, *Gloeocystidiellum aspellum* Hjortstam, *G. compactum* Sheng H. Wu and *G. formosanum* Sheng H. Wu formed a strongly supported lineage (chelidonium) in Stereaceae. Phylogenetic analyses also recovered this lineage inferring from ITS + nLSU data^[87]. Morphologically, these species have some similar characteristics, such as yellowish basidiomata with compact texture, clamped generative

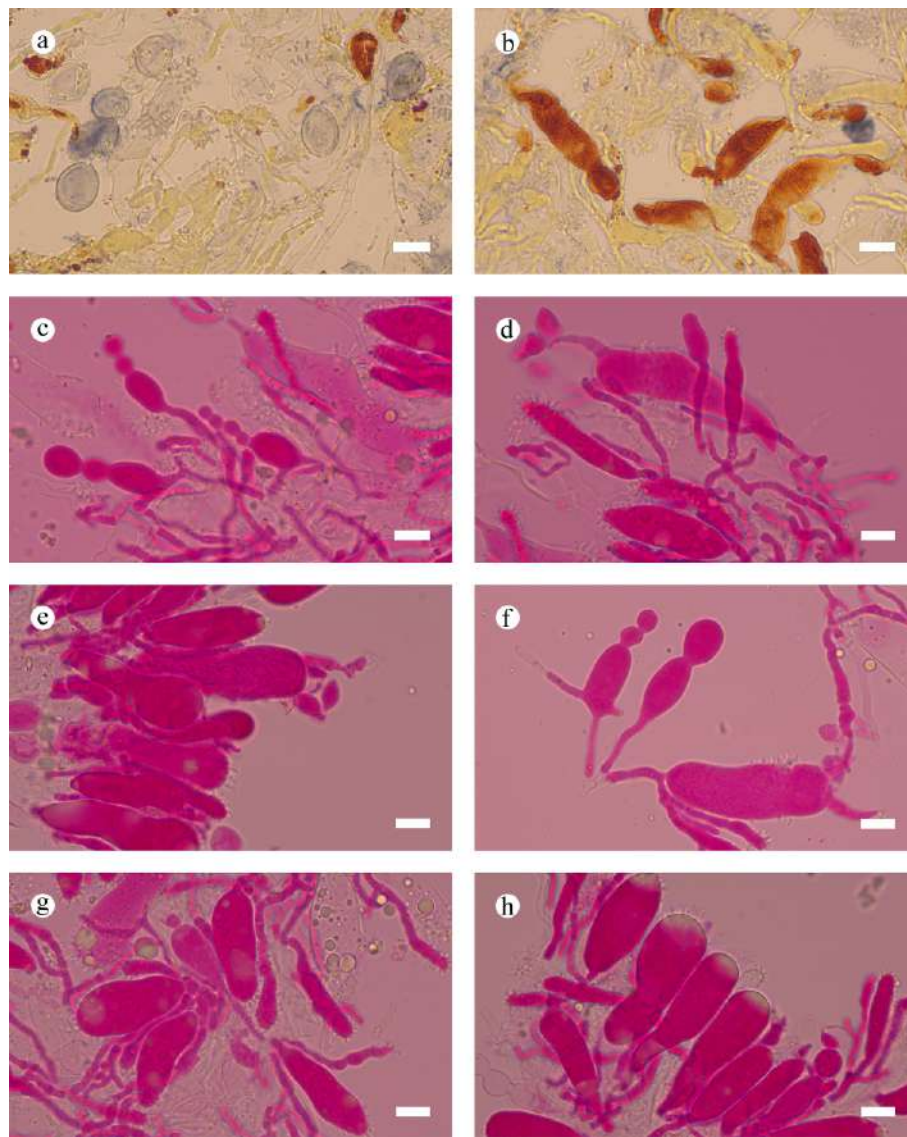


Fig. 44 Sections of hymenium of *Aleurodiscus yunnanensis* (holotype). (a) Basidiospores. (b), (g), (h) Clavate gloeocystidia and acanthocystidia. (c) Moniliform cystidia. (d)–(f) Basidia and basidioles. Scale bars: (a)–(h) = 10 μ m.

hyphae and numerous large gloeocystidia with a positive sulphovanillin reaction. Basidiospores are reported as smooth in *M. chelidonium* and verrucose to indistinctly verrucose in the other species^[26]. Since there are no other morphological characters that can be used to separate *M. chelidonium* from other species, Xu et al.^[87] treated the lineage as a single genus and propose the new generic name *Confertotrama*, and proposed four newly combined species, namely *C. aspella* (Hjortstam) Nakasone & S.H. He, *C. macrospora* (Sheng H. Wu) Nakasone & S.H. He, *C. rajchenbergii* (Gorjón & Hallenb.) Nakasone & S.H. He, and *C. rugulosa*. In the present study, based on morphology and phylogenetic evidence, two new species are introduced, *C. yunnanensis* and *C. cremea* collected from China.

Confertotrama cremea Y.L. Deng & C.L. Zhao, sp. nov. **Figures. 45, 46**
Index Fungorum number: IF860773

Diagnosis – *Confertotrama cremea* differs from other species by the resupinate coriaceous basidiomata with cream to slightly cream hymenial surface with tuberculate, a monomitic hyphal system with clamped generative hyphae, three types cystidia, and ellipsoid basidiospores (5.8–7.2 \times 3.4–4.4 μ m).

Etymology – referring to the cream basidiomata of the type species.

Type – China, Yunnan Province, Dali, Weishan County, Leqiu Town, Zhongyao village, 24°57'N, 100°16'E, 1,910 m asl, on angiosperm trunk, leg. C.L. Zhao, 19 July 2022, CLZhao 22749 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, coriaceous, without odor or taste when fresh, up to 7 cm long, 3 cm wide, and 200 μ m thick. Hymenial surface tuberculate, cracking, slightly cream when fresh, cream upon drying. Sterile margin cream, up to 2 mm.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, smooth, moderately branched, 2–2.5 μ m in diameter, IKI–, CB–; tissues unchanged in KOH; subhymenial hyphae densely covered by crystals. Cystidia with three types: (1) Halocystidia, colorless, thin-walled, smooth, 15–27 \times 4–5 μ m; (2) Cylindrical cystidia, filled with refractive matter, colorless, thin-walled, smooth, 37–48 \times 5–6 μ m; and (3) Tubular cystidia, filled with refractive matter, colorless, thin to slightly thick-walled at the top, smooth, 72–105 \times 7–10 μ m. Basidia cylindrical to subclavate, with a basal clamp connection and four sterigmata, 25–28 \times 5–6.5 μ m; basidioles numerous, in shape similar to basidia but smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, amyloid, CB–,

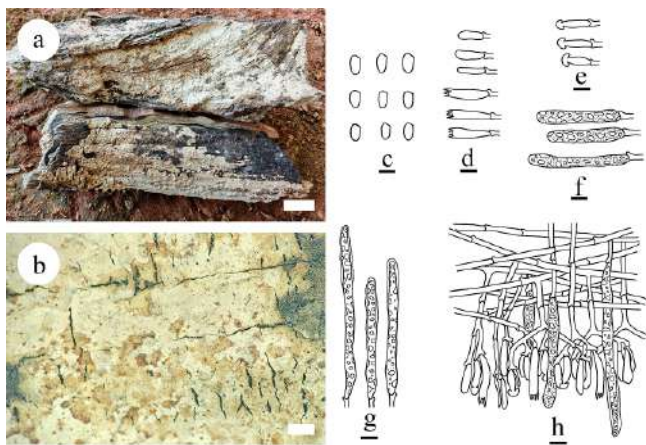


Fig. 45 Basidiomata and microscopic structures of *Confertotrama cremea* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidia and basidioles. (e) Halocystidia cystidia. (f) Cylindrical cystidia. (g) Tubular cystidia. (h) Section of the hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c) = 5 μm , (d)–(h) = 10 μm .

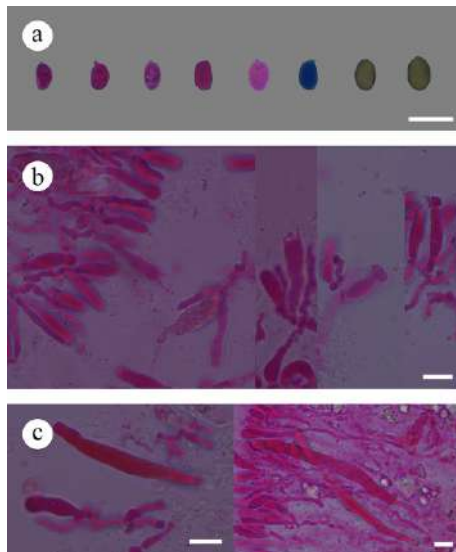


Fig. 46 Sections of hymenium of *Confertotrama cremea* (holotype). (a) Basidiospores. (b) Basidia and basidioles. (c) Cystidia. Scale bars: (a)–(c) = 10 μm .

(5.3–)5.8–7.2(–7.9) \times (3.3–)3.4–4.4(–4.6) μm , L = 6.52 μm , W = 3.83 μm , Q = 1.70–1.71 (n = 60/2).

Additional material examined – China, Yunnan Province, Dali, Weishan County, Leqiu Town, Zhongyao village, 24°57' N, 100°16' E, 1,910 m asl, on angiosperm trunk, leg. C.L. Zhao, 19 July, 2022, CLZhao 22684 (SWFC).

GenBank accession numbers – CLZhao 22749 ITS: PV147178, LSU: PV384144, mtSSU: PV283193, *rpb1*: PX441315; CLZhao 22684 ITS: PV147179, LSU: PV384145, mtSSU: PV399824, *rpb1*: PX441316, *rpb2*: PV648924

Notes – Based on the ITS + nLSU sequence data (Fig. 6), *Confertotrama cremea* grouped within genus *Confertotrama*, forming a separate clade, and closely related to *C. rugulosa*. However, *C. rugulosa* differs from *C. cremea* by having folded hymenophore and strongly encrusted cystidia and has considerably smaller spores^[258]. Based on morphology and multi-gene phylogeny, we introduced this collection as a new species, *Confertotrama cremea*.

Confertotrama yunnanensis Y.L. Deng & C.L. Zhao, sp. nov. Figures 47, 48

Index Fungorum number: IF860774

Diagnosis – Differs from other species by the slightly ferruginous to yellowish-brown hymenial surface smooth, a hyphal system monomitic with clamped generative hyphae, allantoid basidiospores.

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

Type – China, Yunnan Province, Tengchong, Tuantian Town, Gaoligong Mountain National Nature Reserve, 25°55' N, 98°58' E, 2,600 m asl, on fallen angiosperm branch, 7 July, 2024, CLZhao 38992 (SWFC).

Description – Basidiomata annual, resupinate, closely adnate, coriaceous, without odor or taste when fresh, up to 6 cm long, 2 cm wide, and 100 μm thick. Hymenial surface smooth, slightly ferruginous when fresh and ferruginous to yellowish-brown when dry, cracked. Sterile margin slightly ferruginous, up to 1 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thick-walled, branched, 2–3.5 μm in diameter, IKI–, CB–; tissues unchanged in KOH. Hyphidia arising from generative hyphae, rarely branched, colorless, thin-walled, 1–3 μm in diameter. Gloeocystidia cylindrical numerous, embedded, colorless, thick-walled, containing granular refractive material, 36–45 \times 5–7.5 μm ; cystidia fusiform, colorless, thin-walled, with several contractions at the apex, 16.5–25 \times 2–3 μm . Basidia clavate, colorless, thin-walled, with a basal clamp connection and four sterigmata, 18.5–25 \times 4.5–6 μm ; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores allantoid, colorless, thin-walled, smooth, IKI–, CB–, (6.8–)8–13.4(–15.2) \times (2.8–)3.2–4.3(–4.6) μm , L = 10.89 μm , W = 3.77 μm , Q = 2.76–3.03 (n = 270/9).

Additional material examined – China, Yunnan Province, Tengchong, Tuantian Town, Gaoligong Mountain National Nature Reserve, 25°55' N, 98°58' E, 2,600 m asl, on fallen angiosperm branch, 7 July 2024, CLZhao 38937, CLZhao 38938, CLZhao 38973, CLZhao 38977, CLZhao 38988, CLZhao 39005, CLZhao 39017, CLZhao 39143 (SWFC).

GenBank accession numbers – CLZhao 38992 ITS: PX243636, LSU: PX243652, mtSSU: PX243667, *rpb2*: PX432794; CLZhao 38937 ITS: PX243633, LSU: PX243649, mtSSU: PX243664, *rpb2*: PX432790; CLZhao 38938 ITS: PX243632, LSU: PX243648, mtSSU: PX243663, *rpb2*: PX432791; CLZhao 38973 ITS: PX243633, LSU: PX243649, mtSSU: PX243664, *rpb2*: PX432792; CLZhao 38977 ITS: PX243634, LSU: PX243650, mtSSU: PX243665, *rpb2*: PX432793; CLZhao 38988

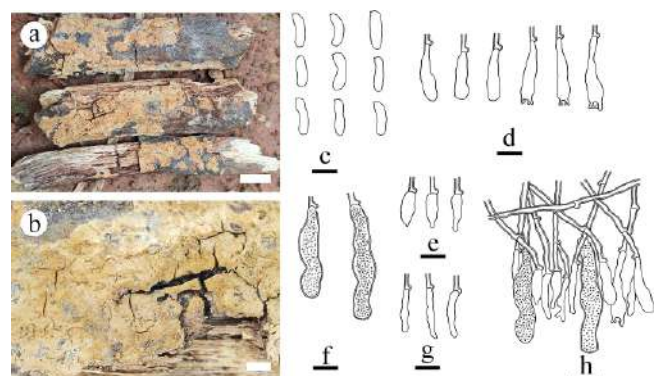


Fig. 47 Basidiomata and microscopic structures of *Confertotrama yunnanensis* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidioles and basidia. (e), (f) Cystidia. (g) Hyphidia. (h) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 2 mm, (c)–(h) = 10 μm .

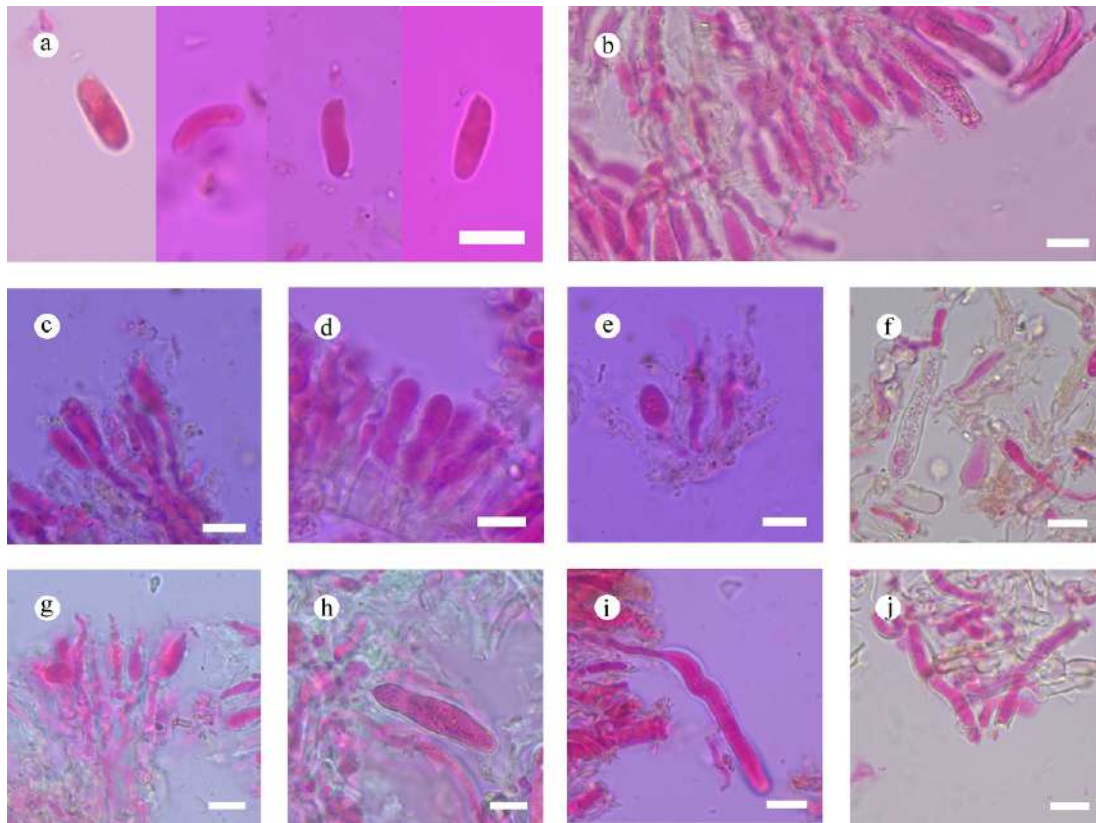


Fig. 48 Sections of hymenium of *Confertotrama yunnanensis* (holotype). (a) Basidiospores. (b) Section of hymenium. (c) Basidia and basidioles. (e)–(i) Cystidia. (j) Trametal hyphae. Scale bars: (a)–(j) = 10 μ m.

ITS: PX243635, LSU: PX243651, mtSSU: PX243666; CLZhao 39005 ITS: PX243637, LSU: PX243653, mtSSU: PX243668, *rpb2*: PX432795; CLZhao 39017 ITS: PX243638, LSU: PX243654, mtSSU: PX243669; CLZhao 39143 ITS: PX243639, LSU: PX243655, mtSSU: PX243670, *rpb2*: PX432796.

Notes – The multi-locus phylogeny (Fig. 6) revealed that *Confertotrama yunnanensis* formed a separate lineage sister to *C. aspella* and *C. rajchenbergii*. However, morphologically, *C. aspella* differs from *C. yunnanensis* by having greyish orange to light orange hymenial surface, larger basidia (25–35 \times 6–7 μ m), and shorter ellipsoid, verrucose basidiospores (7–8 \times 3.5–4 μ m)^[87]. *Confertotrama rajchenbergii* can be distinguished from *C. yunnanensis* by its yellowish ochraceous basidiomata, larger cylindrical gloeocystidia (40–70 \times 5.5–7.5 μ m), and shorter cylindrical to ellipsoid, verruculose, basidiospores with a straight adaxial side (6–7 \times 3–3.5 μ m)^[87]. Based on morphological differences and evidence from the phylogenetic analysis, we introduce our collections, as a new species *Confertotrama yunnanensis*.

Note 60 *Gelatinostereum* S.H. He, S.L. Liu & Y.C. Dai

Index Fungorum number: IF843417

Type species – *Gelatinostereum phlebioides* S.H. He, S.L. Liu & Y.C. Dai

Notes – *Gelatinostereum* was introduced by Xu et al.^[87], and typified by *G. phlebioides*. It is characterized by resupinate to effused-reflexed, gelatinous, hygrophanous basidiomata, smooth, tuberculate to merulioid, greyish orange, brownish orange, light brown to brown hymenophore, dimittic hyphal system, generative hyphae simple-septate, smooth, amyloid basidiospores. *Gelatinostereum* is similar to *Stereum* by sharing effused-reflexed basidiomata, a dimittic hyphal system with simple-septate generative hyphae and smooth amyloid basidiospores but differs in having gelatinous and brittle

basidiomata with a smooth to merulioid hymenophore and thickened subhymenium, thin-walled gloeocystidia and numerous hyphidia. In the phylogenetic tree inferring from ITS + nLSU data, *Gelatinostereum* formed a sister lineage to *Stereum* with high support values^[87].

Note 61 *Gloeocystidiopsis* Jülich

Index Fungorum number: IF17664

Type species – *Gloeocystidiopsis flammea* (Boidin) Jülich

Notes – *Gloeocystidiopsis* was introduced for *Gloeocystidiellum*-like species, and exhibits resupinate, effused basidiomata with cereaceous to firm-membranaceous hymenial surface, simple septate hyphae and a coenocytic nuclear behavior^[105]. Two species, *G. flammea* and *G. heimii* (Boidin) Jülich, were originally included. Wu^[175] moved *G. heimii* to *Conferticium* Hallenb. mainly based on his assumption on the dense hyphal structure in this species is typical for *Conferticium* but not present in the type of *Gloeocystidiopsis*. Recent research has introduced three species, viz. *G. tenuissima* (L.D. Dai & S.H. He) S.H. He & Y.F. Cao, *G. shenghuae* S.H. He & Y.F. Cao, and *G. rava* (Burt) S.H. He & Y.F. Cao based on morphology and phylogenetic evidence^[87].

Note 62 *Gloeomyces* Sheng H. Wu

Index Fungorum number: IF27592

Type species – *Gloeomyces graminicola* Sheng H. Wu

Notes – *Gloeomyces graminicola*, the type of *Gloeomyces*, lacks acanthophyses and has simple septate hyphae, while the other two species in the genus have hyphae that are nodose septate. Morphologically, species of *Gloeomyces* are characterized by having resupinate basidiomata, well-developed acanthohyphidia, and smooth basidiospores^[102]. They could be compared to binding hyphae but are few and do not lend any tough consistency to the basidioma. With these characteristics *Gloeomyces* looks quite

different from the other two species in the clade^[26]. The colored thick-walled binding hyphae in some species might be a special form of the acanthophyses. *Aleurodiscus* s. str. can be easily separated from *Gloeomyces* by possessing ornamented basidiospores or thick-walled smooth basidiospores in *A. fujii* (Sheng H. Wu) S.H. He & Yun L. Xu. Based on morphological and molecular evidence, a new species, *G. subcerussatus* S.H. He & Ghob.-Nehj. was described and illustrated, and 11 new combinations were proposed in *Gloeomyces*^[87]. More species of *Aleurodiscus* s. lat. will be moved to *Gloeomyces* after sequencing of authentic specimens^[87].

Note 63 *Gloeosoma* Bres.

Index Fungorum number: IF17672

Type species – *Gloeosoma vitellinum* (Lév.) Bres.

Notes – *Gloeosoma* was introduced by Bresadola^[197] and typified by *G. vitellinum*. It is characterized by having discoid, cupulate to large and auricularioid, gelatinous to fleshy basidiomata becoming cartilaginous to hard, pink to salmon-colored hymenial surface, a monomitic hyphal system with clamped generative hyphae, present acanthocystidia and gloeocystidia, clavate basidia with four sterigmata, aculeate to echinulate, amyloid basidiospores^[46,197]. *Gloeosoma* was defined as a taxon growing on dead branches of Nothofagaceae in Patagonia, and remained monotypic over the years. A lack of information on *G. vitellinum* in phylogenetic studies precluded any conclusion regarding its taxonomic status. It was a matter of personal decision whether to accept the genus or consider it as the synonym of *Aleurodiscus*, as the microscopic characters were quite typical of the latter in a broad sense. The present study includes sequences of *G. vitellinum* for the first time and showed that together with *G. zealandicum* (Cooke & W. Phillips) Rajchenb., Pildain & C. Riquelme, *G. mirabile* (Berk. & M.A. Curtis) Rajchenb., Pildain & C. Riquelme, and *G. decorticans* Rajchenb., Pildain & C. Riquelme, they formed a well-defined group of species with strong phylogenetic support. This group clustered in the Stereaceae clade but was distant from *Aleurodiscus amorphus* (Pers.) J. Schröt., the type species of *Aleurodiscus*. The latter differs from *Gloeosoma* morphologically by the simple-septate generative hyphae^[46,87].

Note 64 *Megalocystidium* Jülich

Index Fungorum number: IF18027

Type species – *Megalocystidium leucoxanthum* (Bres.) Jülich

Notes – *Megalocystidium* is a genus of corticioid fungi typified by *M. leucoxanthum* (syn. *Corticium leucoxanthum* Bres.). Initially the genus was introduced to accommodate three species, and *Megalocystidium* currently embraces 15 species^[87,259,260]. As redefined in phylogenetic studies, it belongs to family Stereaceae in order Russulales and encompasses crust-like fungi with effused basidiomata, clamped hyphae, long and deeply rooted gloeocystidia, without acanthohyphidia, as well as narrowly ellipsoid or cylindrical, smooth, strongly amyloid basidiospores^[45,116]. Spirin et al.^[260] transferred *Peniophora diffissa* Sacc., which has abundant acanthohyphidia, into the genus. Xu et al.^[87] showed *M. chinensis* (Pilát) S.H. He & Nakasone, *M. wakullum* (Burd., Nakasone & G.W. Freeman) E. Larss. & K.H. Larss. and other two undescribed species with simple-septate generative hyphae and acanthohyphidia formed a sister subclade to the *M. leucoxanthum* subclade.

***Megalocystidium bambusinum* Y.L. Deng & C.L. Zhao, sp. nov.**

Figures 49, 50

Index Fungorum number: IF860775

Diagnosis – Differs from other species by the white to cream hymenial surface smooth, a dimitic hyphal system with clamped generative hyphae, ellipsoid basidiospores (7.2–10.3 × 4–6.5 μm).

Etymology – referring to grow on bamboo of the type specimen.

Type – China, Yunnan Province, Dehong, Ruili County, Tongbiguan Provincial Nature Reserve, 23°38' N, 97°51' E, 1,500 m asl, on

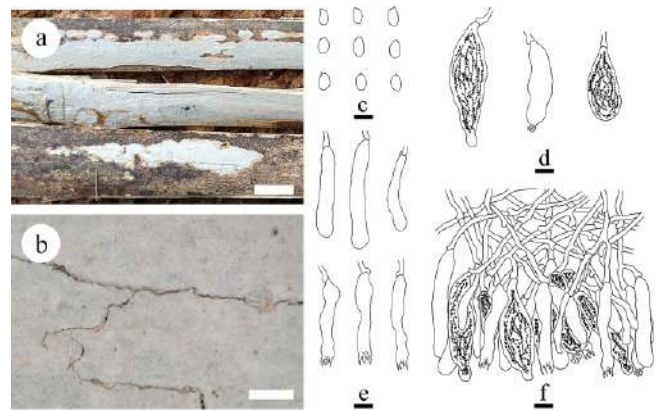


Fig. 49 Basidiomata and microscopic structures of *Megalocystidium bambusinum* (holotype). (a) Basidiomata on the substrate. (b) Section of hymenophore. (c) Basidiospores. (d) Basidioles and basidia. (e) Gloeocystidia. (f) Section of hymenium. Scale bars: (a) = 1 cm, (b) = 1 mm, (c)–(f) = 10 μm.

dead bamboo, leg. C.L. Zhao, 14 January, 2025, CLZhao 44157 (SWFC).

GenBank accession numbers – CLZhao 44157 ITS: PX243630, LSU: PX243646, mtSSU: PX243661, *rpb2*: PX432798, *tef1-α*: PX439086

Description – Basidiomata annual, resupinate, closely adnate, membranous, without odor or taste when fresh, up to 10 cm long, 1.5 cm wide, and 90 μm thick. Hymenial surface smooth, white when fresh, cream upon drying. Sterile margin thin, white, up to 1 mm wide.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, branched, 2.5–4 μm in diameter, IKI–, CB–; tissues unchanged in KOH. Gloeocystidia numerous, vesicular to racket-shaped, embedded, colorless, thin-walled, containing granular refractive material, with several contractions at the apex, 24–66 × 9.5–21 μm. Basidia cylindrical, flexuous, colorless, thin-walled, with a basal clamp connection and four sterigmata, 43–54.5 × 6–9 μm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI+, CB–, (6.9–)7.2–10.3(–10.8) × (3.5–)4–6.5(–7) μm, L = 8.95 μm, W = 5.08 μm, Q = 1.76 (n = 30/1).

Notes – The phylogeny (Fig. 6) revealed that *Megalocystidium bambusinum* formed a separate lineage and closely related to *M. effusum* and *M. brunneum*. However, morphologically, *M. effusum* differs from *M. bambusinum* by having a pale orange to light orange to greyish orange hymenophore, slightly thick-walled generative hyphae without clamps, slightly thick-walled, subclavate to subcylindrical pseudocystidia, subulate acutocystidia, smaller slightly thick-walled, cylindrical to clavate basidia (30–35 × 4–4.5 μm), and narrower oblong ellipsoid to subcylindrical basidiospores (7.5–10 × 2–3.5 μm)^[87]; while *M. brunneum* has a greyish brown to brownish orange to light brown hymenophore, thin- to thick-walled generative hyphae without clamps, slightly thick-walled, vesicular to racket-shaped gloeocystidia, and longer subcylindrical to subfusiform basidiospores (10–12 × 4–5 μm)^[87]. Based on these morphological and phylogenetic information, it is concluded that the present collection is a new species, *Megalocystidium bambusinum*.

Note 65 *Neoaleurodiscus* Sheng H. Wu

Index Fungorum number: IF513514

Type species – *Neoaleurodiscus fujii* Sheng H. Wu

Notes – Wu et al.^[244] described the new genus, *Neoaleurodiscus*, based on the type species *N. fujii* collected from Mount Fuji in Japan on *Rhododendron*. Later Dai & He^[80] also found this species in

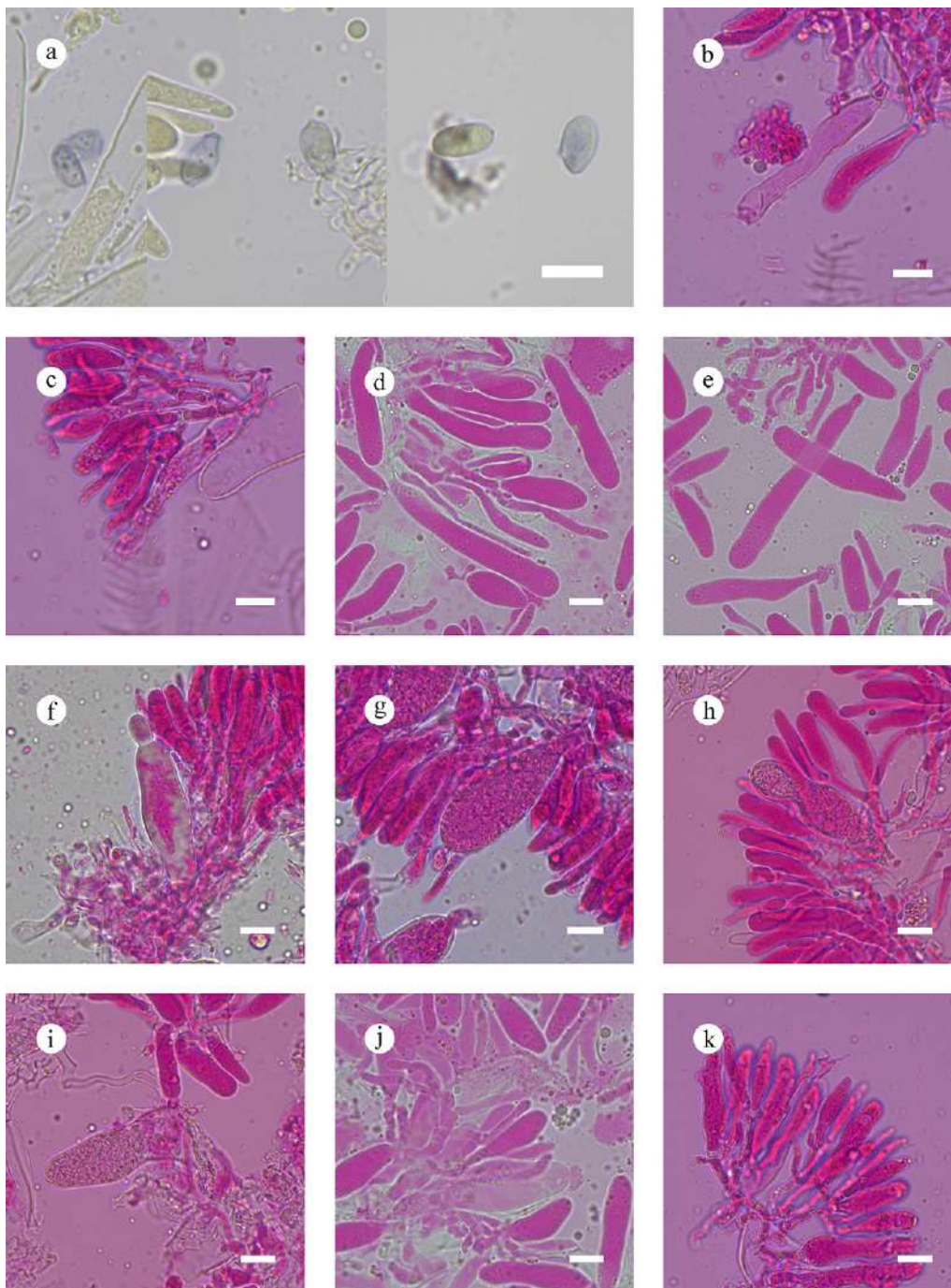


Fig. 50 Sections of hymenium of *Megalocystidium bambusinum* (holotype). (a) Basidiospores. (b), (c) Basidia. (d), (e) Basidioles. (f)–(j) Gloeocystidia. (k) Section of hymenium. Scale bars: (a)–(k) = 10 μm .

southwestern China. Morphologically, the genus mainly differs from *Aleurodiscus* s. str. by having thick-walled smooth basidiospores. However, the phylogenetic results by Xu et al.^[87] and Rajchenberg et al.^[46] showed that *N. fujii* was nested within the *Aleurodiscus* s. str. lineage with strong support values. According to the phylogenetic delimitation of *Aleurodiscus* s. str., the genus is still morphologically heterogeneous with simple- or nodose-septate hyphae, smooth or ornamented basidiospores, and with or without acanthohyphidia. More evidence is needed to prove whether this delimitation of *Aleurodiscus* s. str. is natural and reasonable.

Note 66 *Stereodiscus* Rajchenb. & Pildain
Index Fungorum number: IF836692

Type species – *Stereodiscus antarcticus* (Speg.) Rajchenb. & Pildain
Notes – *Stereodiscus* was established by Rajchenberg et al.^[46] and typified by *S. antarcticus*. *Stereodiscus* is characterized by smooth, thin-walled, cylindric, broadly ellipsoid to citriform basidiospores up to 25 μm long and absence of any of the typical cystidia in *Aleurodiscus* s. lat., i.e., acanthocystidia, acanthophyses, gloeocystidia, and dendrohyphidia. However, skeletocystidia are present in three species (*S. antarcticus*, *S. parmuliformis* [G. Cunn.] Rajchenb. & Pildain, and *S. trivialis* [Speg.] Rajchenb. & Pildain). The hyphal system is monomitic with simple-septate hyphae, except in the recently described *S. patagonicus* (as *Aleurodiscus*), which features scattered clamps on the hyphae and at the bases of basidia^[245]. The

latter is consistent with its phylogenetic position, as it is excluded from the main cluster of species. Otherwise, the five species grouped with strong support^[46]. Rajchenberg et al.^[46] showed *Stereodiscus* to be distantly related to species of *Stereum*, showing features that could be synapomorphic within Stereaceae. Both *Gloeosoma* and *Stereodiscus* were shown to be phylogenetically related to each other, but distant from other clades in Stereaceae, and from other genera segregated from *Aleurodiscus* s. lat. A recent study proposed a new species, *S. pseudotrivialis* Gorjón & Gresl. based on morphological and molecular evidence^[261].

Note 67 *Stereum* Hill ex Pers.

Index Fungorum number: IF18596

Typ species – *Stereum hirsutum* (Willd.) Pers.

Stereum convolutomarginatum Y.L. Deng & C.L. Zhao, sp. nov.

Figures 51, 52

Notes – *Stereum* (Stereaceae) was established in 1794 and typified with *S. hirsutum*. It is among the oldest described corticioid fungi and is characterized by annual to perennial, resupinate, effused, effuse-reflexed to pileate basidiomata often umbonate, seldom wholly resupinate; glabrous to tomentose or hirsute upper sterile surface, with appressed hairs and shiny, in concentric bands or completely to expose underlying cutis; smooth to slightly tuberculate hymenial surface, sometimes with concentric ridges, or with radial wrinkles on the marginal zone, usually with light colours, bruises red, orange-yellow or yellow; a dimitic hyphal system, generative hyphae with simple septa, thin- to thick-walled, skeletal hyphae; several kinds of cystidia, oleiferous pseudocystidia, skeletocystidia, acutocystidia, acanthocystidia; clavate to tubular basidia, with 4-sterigmata, simple septa at the base; and ellipsoid to cylindrical, smooth, thin-walled, amyloid basidiospores^[26,262]. *Stereum* and *Xylobolus* are closely related genera which form the core of family Stereaceae, which share pseudocystidia, but the latter has shorter and more ellipsoid basidiospores. Furthermore, *Xylobolus* has a brown context and a dense zone separating the context from a usually brown tomentum^[263]. Three new species are introduced, *S. convolutomarginatum*, *S. rigidohymeneum* and *S. yunnanense* found in China, based on the ITS + nLSU data (Fig. 6), and morphological characteristics.

Index Fungorum number: IF860776

Diagnosis – *Stereum convolutomarginatum* differs from other species by the resupinate to effused, coriaceous basidiomata, cream to buff hymenial surface smooth, convolitional margin, a dimitic hyphal system, generative hyphae bearing simple septa, and ellipsoid basidiospores.

Etymology – referring to the convolitional sterile margin of the specimens.

Type – China, Yunnan Province, Wenshan, Malipo County, Pingzhai Village, Forest farm, 104°42' E, 23°7'32" N, 1,057 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 18 January, 2019, CLZhao 11535 (SWFC).

Description – Basidiomata annual, resupinate to effused, coriaceous, first orbicular, later fusing together, without odour or taste when fresh, becoming hard coriaceous upon drying, up to 10.5 cm long, 2 cm wide, and 1 mm thick. Upper surface tomentose or hirsute, with appressed hairs, in concentric bands or completely to expose underlying cutis, cream when fresh, becoming cream to buff becoming, projecting up to 2 cm, 3 cm wide at center. Hymenial surface smooth, cream to buff when fresh, becoming buff to fawn upon drying. Sterile margin cream, convolitional, up to 2 mm wide.

Hyphal system dimitic; generative hyphae bearing simple septa, colorless, thick-walled, smooth, moderately branched, 2.8–3.3 μm in diameter. Skeletal hyphae dominant, colorless, distinctly thick-walled, narrow chamber, smooth, 5–5.5 μm in diameter, IKI–, CB–; tissues unchanged in KOH. Acanthocystidia dominant, subclavate to subcylindrical, colorless, 20–34.4 × 4.7–7.9 μm. Basidia barrelled, with four sterigmata and a basal simple septum, 22.8–29.4 × 4.2–8 μm; basidioles numerous, in shape similar to basidia but smaller. Basidiospores oblong ellipsoid, colorless, thin-walled, smooth, CB–, amyloid, (6.9–)8.9–13(–14.1) × (3.1–)3.9–5.6(–6.5) μm, L = 10.69 μm, W = 4.79 μm, Q = 4.57–4.76 (n = 420/14).

Additional material examined – China, Yunnan Province, Dali, Nanjian County, Lingbao Mountain National Forest Park, 100°30' E,

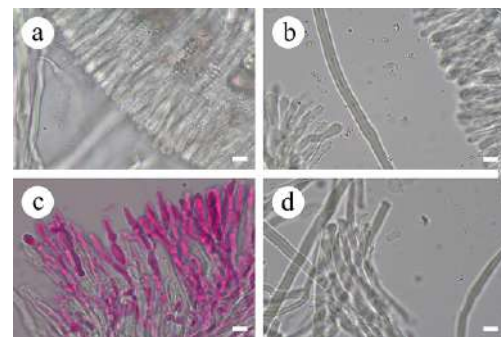


Fig. 52 Sections of hymenium of *Stereum convolutomarginatum* (holotype). (a), (c) Section of hymenium. (b) Skeletal hyphae. (d) Basidiospores. Scale bars: (a)–(d) = 10 μm.

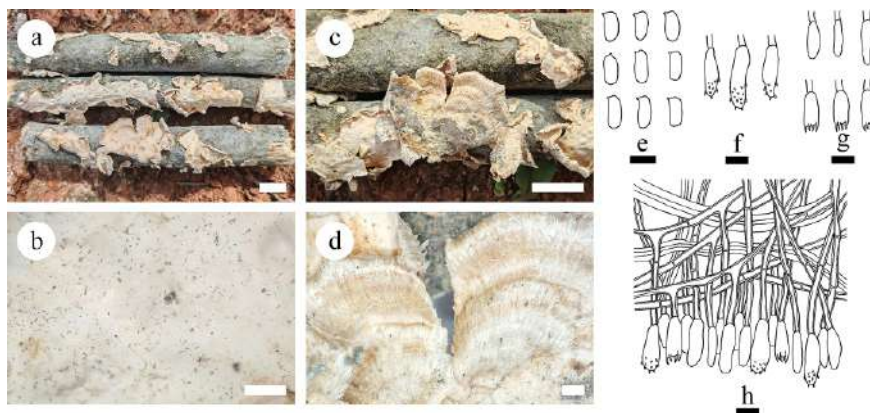


Fig. 51 Basidiomata and microscopic structures of *Stereum convolutomarginatum* (holotype). (a), (c) Basidiomata on the natural substrates. (b), (d) A character hymenophore. (e) Basidiospores. (f) Acanthocystidia. (g) Basidia and basidioles. (h) Section of hymenium. Scale bars: (a), (c) = 1 cm, (b), (d) = 1 mm, (e)–(h) = 10 μm.

24°46' N, 2,000 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 9 January, 2019, CLZhao 10241 (SWFC); Wenshan, Malipo County, Pingzhai Village, Forest farm, 104°42' E, 23°7' N, 1,057 m asl., on fallen angiosperm branch, leg. C.L. Zhao, 18 January, 2019, CLZhao 11416, CLZhao 11435, CLZhao 11449, CLZhao 11453, CLZhao 11455, CLZhao 11463, CLZhao 11501, CLZhao 11557, and CLZhao 11575; on angiosperm trunk, CLZhao 11399, CLZhao 11457 and CLZhao 11516 (SWFC); Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, 24°71' N, 94°52' E, 1,500 m asl, on fallen angiosperm branch, leg. C.L. Zhao, 4 July, 2024, CLZhao 37604 and CLZhao 37696 (SWFC).

GenBank accession numbers – CLZhao 11535 ITS: PV283209; CLZhao 10241 ITS: PV283198; CLZhao 11416 ITS: PV283200; CLZhao 11435 ITS: PV283201, mtSSU: PV399825, *rpb2*: PV648927; CLZhao 11449 ITS: PV283202, LSU: PV384149, mtSSU: PV399826, *rpb1*: PX441317, *tef1- α* : PV400178; CLZhao 11453 ITS: PV283203; CLZhao 11455 ITS: PV283204, LSU: PV384150, mtSSU: PV399827, *rpb1*: PX441318; CLZhao 11463 ITS: PV283206, LSU: PV384152, mtSSU: PV399828; CLZhao 11501 ITS: PV283207; CLZhao 11557 ITS: PV283210; CLZhao 11575 ITS: PV283211, LSU: PV384153; CLZhao 11399 ITS: PV283199, LSU: PV384148; CLZhao 11457 ITS: PV283205, LSU: PV384151, *rpb1*: PX441319; CLZhao 11516 ITS: PV283208; CLZhao 37604 ITS: PX415429, LSU: PX418376, *tef1- α* : PX439087; CLZhao 37696 ITS: PX415428

Notes – Phylogenetic analysis (Fig. 6) indicated that *Stereum convolutomarginatum* grouped within *Stereum*, forming a separate lineage, closely related to *S. ochraceoflavum* and *S. vellereum*. However, morphologically, *S. ochraceoflavum* differs from *S. convolutomarginatum* by its effuse-reflexed basidiomata, cream to pale yellowish orange hymenophore, slightly thick-walled, hyaline to yellowish pseudocystidia (80–100 × 5–7 μ m), acutocystidia (25–35 × 3–4 μ m), and smaller cylindrical to narrowly ellipsoid basidiospores (6–9 × 1.5–2.5 μ m)^[264]. *Stereum vellereum* can be distinguished from *S. convolutomarginatum* by its both smaller acutocystidiolles (15–22 × 3.5–5 μ m), and subcylindrical basidiospores (5–7 × 2–3 μ m)^[265]. Based on these morphological and phylogenetic evidence, we introduce our collection as a new species, *Stereum convolutomarginatum*.

Stereum rigidohymeneum Y.L. Deng & C.L. Zhao, sp. nov. Figures 53, 54

Index Fungorum number: IF860777

Diagnosis – *Stereum rigidohymeneum* differs from other species by the perennial, rigid basidiomata, effused to pileate, cream to light orange hymenial surface with tuberculate, a dimittic hyphal system, generative hyphae bearing simple septa, ellipsoid basidiospores.

Etymology – referring to the rigid hymenial surface of the specimens.

Type – China, Yunnan Province, Puer, Jingdong County, Wuliang Mountain, 100°29' E, 24°38' N, 1,800 m asl, on angiosperm trunk, leg. C.L. Zhao, 6 October, 2017, CLZhao 4615 (SWFC).

Description – Basidiomata perennial, effused to pileate, separate from the substrate, coriaceous, rigid, without odor or taste when fresh. Pileus projecting up to 5 cm, 12 cm wide, and 4 cm thick at center. Hymenial surface slightly tuberculate, cream when fresh, cream to light orange upon drying; sterile margin brownish orange, distinct, up to 0.3 cm wide. Pileal surface brown to black, aquamarinus, in concentric bands or completely to expose underlying cutis, woody hard. Sterile margin blunt, up to 4 mm wide.

Hyphal system dimittic; generative hyphae bearing simple septa, colorless, thick-walled, smooth, moderately branched, 2.5–3 μ m in diameter. Skeletal hyphae dominant, colorless, distinctly thick-walled, smooth, unbranched, straight, with scattered secondary simple septa, 4.9–5.3 μ m in diameter, IKI–, CB–; tissues unchanged in KOH. Acanthocystidia dominant, cylindrical, colorless, 13.8–16.4 × 2.5–3.2 μ m. Basidia clavate to cylindrical, with four sterigmata and a basal simple septum, 13.3–16 × 2.7–4 μ m; basidioles numerous, in shape similar to basidia but smaller. Basidiospores cylindrical to

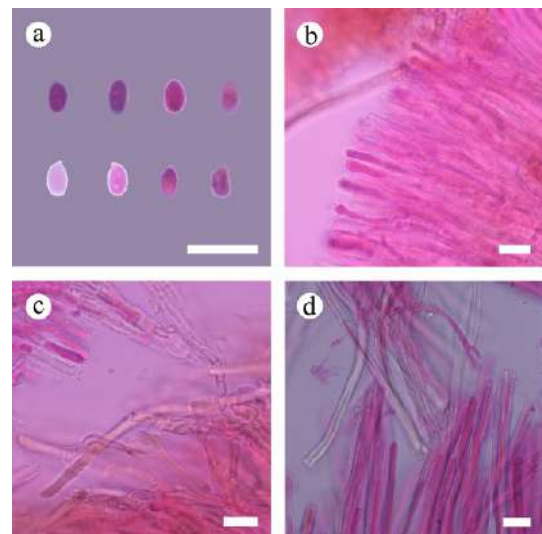


Fig. 54 Sections of hymenium of *Stereum rigidohymeneum* (holotype). (a) Basidiospores. (b), (c) Acanthocystidia. (d) Skeletal hyphae. Scale bars: (a)–(d) = 10 μ m.

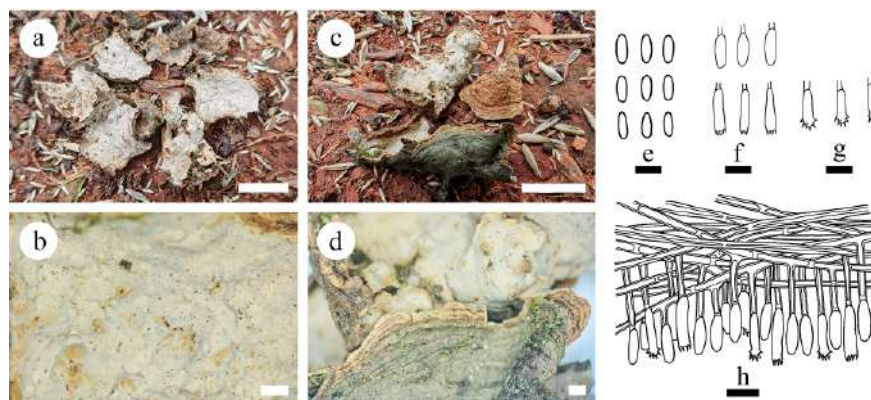


Fig. 53 Basidiomata and microscopic structures of *Stereum rigidohymeneum* (holotype). (a), (b) Section of hymenophore. (c), (d) The back of the basidiomata. (e) Basidiospores. (f) Basidia and basidioles. (g) Acanthocystidia. (h) Section of hymenium. Scale bars: (a), (c) = 1 cm, (b), (d) = 1 mm, (e) = 5 μ m, (f)–(h) = 10 μ m.

ellipsoid, colorless, thin-walled, smooth, CB-, amyloid, $(3.6-3.9-5.8(-6.7) \times (1.3-1.7-2.7(-3.3)) \mu\text{m}$, $L = 4.64 \mu\text{m}$, $W = 2.16 \mu\text{m}$, $Q = 1.85-2.43$ ($n = 60/2$).

Additional material examined – China, Yunnan Province, Puer City, Jingdong County, Wuliang Mountain, $100^{\circ}29' \text{ E}$, $24^{\circ}38' \text{ N}$, 1,800 m asl, on angiosperm trunk, leg. C.L. Zhao, 6 October, 2017, CLZhao 4378 (SWFC).

GenBank accession numbers – CLZhao 4615 ITS: MT214936; CLZhao 4378 ITS: MT214935, mtSSU: PV283197

Notes – In the multi-locus phylogeny (Fig. 6), the new collection of *Stereum rigidohymeneum* grouped within *Stereum*, and sister to *S. insigne*. However, morphologically, *S. insigne* can be distinguished from *S. rigidohymeneum* by its effuse-reflexed, coriaceous to corky basidiomata, thin- to thick-walled, hyaline to yellowish brown generative hyphae, thick-walled, brown pseudocystidia tubular with obtuse apex, both larger hyaline to brown acanthocystidia ($20-30 \times 4-5 \mu\text{m}$), and narrowly clavate basidia ($25-30 \times 4-5 \mu\text{m}$)^[266]. Thus, based on morphological characters and phylogenetic analysis, the present collections are introduced as a new species, *Stereum rigidohymeneum*.

Stereum yunnanense Y.L. Deng & C.L. Zhao, sp. nov. Figures 55, 56

Index Fungorum number: IF860778

Diagnosis – *Stereum yunnanense* differs from other species by the perennial, effused to pileate basidiomata, slightly cream to cream hymenial surface, cream to brownish orange pileal surface with short tomentum, ellipsoid basidiospores ($4.7-8 \times 2.4-3.2 \mu\text{m}$).

Etymology – referring to the locality province (Yunnan) of the type specimen.

Type – China, Yunnan Province, Puer City, Jingdong County, Wuliang Mountain, $100^{\circ}29' \text{ E}$, $24^{\circ}38' \text{ N}$, 1,800 m asl, on angiosperm trunk, leg. C.L. Zhao, 5 October, 2017, CLZhao 4227 (SWFC).

Description – Basidiomata perennial, effused to pileate, separate from the substrate, coriaceous, without odor or taste when fresh. Pileus projecting up to 3.5 cm, 4.5 cm wide, and 1 mm thick at center. Hymenial surface smooth, slightly cream when fresh, becoming cream, sterile margin brownish orange, distinct, up to 1 mm wide. Pileal surface short tomentum, cream when fresh, becoming cream to brownish orange, in concentric bands or completely to expose underlying cutis. Sterile margin blunt, lightly orange, up to 1 mm wide.

Hyphal system dimitic; generative hyphae bearing simple septa, colorless, thick-walled, smooth, moderately branched, $2.5-3 \mu\text{m}$ in diameter. Skeletal hyphae dominant, colorless, distinctly thick-walled, smooth, unbranched, straight, with scattered secondary simple septa, $4.5-10 \mu\text{m}$ in diameter, IKI-, CB-; tissues unchanged in

KOH. Cystidia dominant, cylindrical to fusiform, colorless, $14-21 \times 3.5-5 \mu\text{m}$. Basidia cylindrical, with four sterigmata and a basal simple septum, $12-15 \times 3.5-4.5 \mu\text{m}$; basidioles numerous, in shape similar to basidia but smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, amyloid, CB-, $(4.6-4.7-6(-8)) \times (2.2-2.4-3.2(-3.5)) \mu\text{m}$, $L = 5.2 \mu\text{m}$, $W = 2.84 \mu\text{m}$, $Q = 1.72-2.06$ ($n = 90/3$).

Additional material examined – China, Yunnan province, Puer City, Xieqipo Park, $101^{\circ}5' \text{ E}$, $24^{\circ}0' \text{ N}$, 1,302 m asl, fallen angiosperm branch, leg. C.L. Zhao, 1 October, 2017, CLZhao 3420; Jingdong County, Wuliang Mountain, $100^{\circ}29' \text{ E}$, $24^{\circ}38' \text{ N}$, 1,800 m asl, on angiosperm trunk, leg. C.L. Zhao, 5 October, 2017, CLZhao 4317 (SWFC).

GenBank accession numbers – CLZhao 4227 ITS: MT214932, LSU: PV384146, mtSSU: PV283194, *rpb2*: PV648925; CLZhao 3420 ITS: MT214929, LSU: PV384147, mtSSU: PV283195, *rpb2*: PV648926; CLZhao 4317 ITS: MT214930, mtSSU: PV283196

Notes – Phylogenetic analysis (Fig. 6) indicated that *Stereum yunnanense* grouped within *Stereum*, sister to *S. lobatum*. However, morphologically, *S. lobatum* differs from *S. yunnanense* by having pseudoacanthophyses ($16-27 \times 2.5-3 \mu\text{m}$), and subcylindrical basidiospores ($5.2-7 \times 2-3 \mu\text{m}$)^[267]. Thus, based on morphology and phylogenetic analysis, we concluded our collection is a new species, *Stereum yunnanense*.

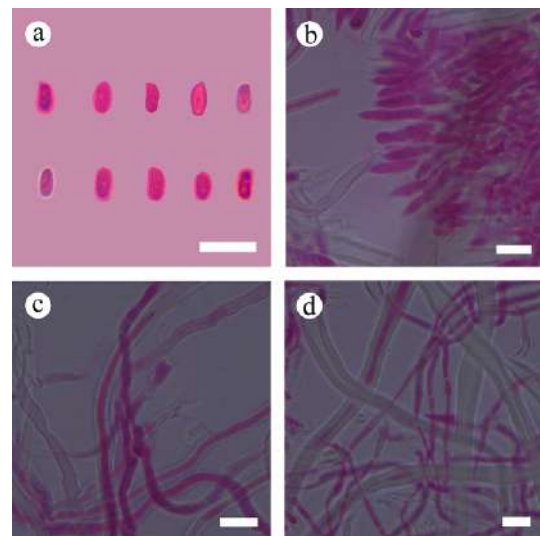


Fig. 56 Sections of hymenium of *Stereum yunnanense* (holotype). (a) Basidiospores. (b) Section of hymenium. (c) Basidia. (d) Skeletal hyphae. Scale bars: (a)–(d) = 10 μm .

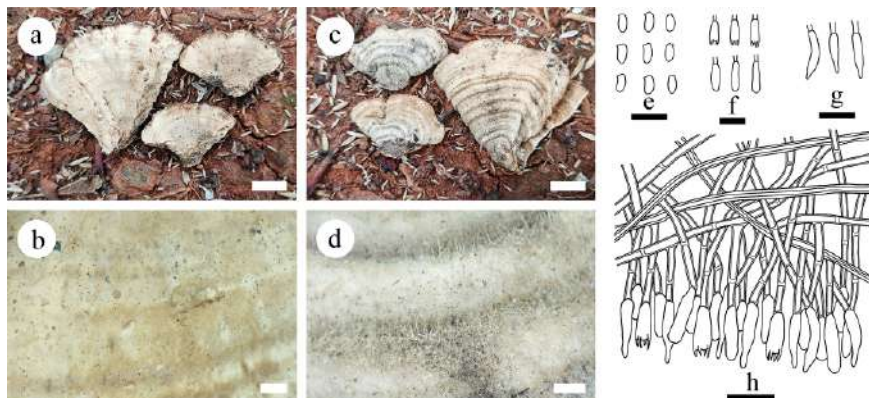


Fig. 55 Basidiomata and microscopic structures of *Stereum yunnanense* (holotype). (a), (b) Section of hymenophore. (c), (d) The back of the basidiomata. (e) Basidiospores. (f) Basidia and basidioles. (g) Cystidia. (h) Section of hymenium. Scale bars: (a), (c) = 1 cm, (b), (d) = 1 mm, (e)–(h) = 10 μm .

Note 68 *Xylobolus* P. Karst.

Index Fungorum number: IF18770

Type species – *Xylobolus frustulatus* (Pers.) P. Karst.

Notes – *Xylobolus* is a small, globally distributed wood-inhabiting genus classified within family Stereaceae (Russulales)^[268]. The type species of the genus is *X. frustulatus*, a distinctive corticioid species that grows on dead or decaying oak wood, and forms perennial basidiomata, which crack into small, angular polygons^[269]. Another species *X. subpileatus* which has been widely studied, causes white rot in angiosperms, and grows mainly in southeastern USA, with a smaller distribution. The basidiomata of *X. subpileatus* are perennial, and acanthocystidia and can be observed in its hymenium under microscopic examination; this species was described from South Carolina by Berkeley & Curtis^[266], but it has since been reported from all continents except Antarctica. In Europe, *X. subpileatus* is mostly distributed in southern regions, and is considered a rare species in several countries^[266]. There are few taxonomic studies on *Xylobolus*, although the chemical composition of *Xylobolus* has been studied^[269].

Note 69 Family Terrestriporiaceae Y.C. Dai, B.K. Cui, F. Wu, Y. Yuan & Jia J. Chen 2020

Index Fungorum number: IF834539

Type genus – *Terrestriporia* Y.C. Dai, B.K. Cui, F. Wu, Y. Yuan & Jia J. Chen

Notes – Terrestriporiaceae was established to accommodate *Terrestriporia* in order Russulales, based on its distinct lineage in the phylogenetic analysis^[21]. The family is characterized by annual, resupinate basidiomata, a poroid hymenophore, monomitic hyphal structure, mostly simple septate generative hyphae, but occasionally with clamp connections, presence of gloeoplerous hyphae, and hyaline, thin-walled, smooth, amyloid basidiospores. The combined phylogeny of ITS, nLSU, *rpb1*, *rpb2*, and *tef1- α* sequence data, demonstrated that Terrestriporiaceae is related to Albatrellaceae, but showed no affinity to the other families of Russulales. Albatrellaceae includes mycorrhizal species that are mostly stipitate^[21].

Note 70 *Terrestriporia* Y.C. Dai, B.K. Cui, F. Wu, Y. Yuan & Jia J. Chen

Index Fungorum number: IF834540

Type species – *Terrestriporia alba* Y.C. Dai, B.K. Cui, F. Wu & Jia J. Chen

Notes – *Terrestriporia* was established by Wu et al.^[21] and typified by *T. alba*. It is characterized by annual, resupinate basidiomata, poroid and white hymenophore, a monomitic hyphal structure, mostly simple septate generative hyphae, but occasionally with clamp connections, with gloeoplerous hyphae and gloeocystidioles, and hyaline, thin-walled, smooth, amyloid, acyanophilous basidiospores^[21]. *Terrestriporia* resembles *Anomoporia* Pouzar and *Anomoloma* Niemelä & K.H. Larss. by sharing annual and resupinate basidiomata, a monomitic hyphal structure, and hyaline, thin-walled, smooth and amyloid basidiospores^[16], but the latter two genera have clamp connections only, lack gloeoplerous hyphae and cystidioles, and belong to Amylocorticiales^[21].

Family Wrightoporiaceae Jülich 1982

Index Fungorum number: IF80052

Type genus – *Wrightoporia* Pouzar

Note 71 *Wrightoporia* Pouzar

Index Fungorum number: IF18750

Type species – *Wrightoporia lenta* (Overh. & J. Lowe) Pouzar

Notes – The type species of *Wrightoporia* is *W. lenta*^[92]. According to the recent studies, *Wrightoporia* s.str. is distinguished by an annual growth pattern, resupinate to effused-reflexed basidiomata, soft and cottony at fresh condition, membranous to cottony at dry condition, rounded to angular pores, mostly having rhizomorph margins, finely asperulate basidiospores, mostly found on dead logs

of gymnosperms, rarely on angiosperms. There are six species distributed in Asia: *W. austrosinensis* Y.C. Dai, *W. avellanea* (Bres.) Pouzar, *W. borealis* Y.C. Dai, *W. lenta*, *W. srilankensis* Y.C. Dai and Yuan Yuan, and *W. subavellanea* Jia J. Chen and B.K. Cui^[10,44,270]. Cystidia are absent in most of these species, however, cystidia and cystidiols are present in *W. austrosinensis*^[173]. *Wrightoporia* is a large and diverse genus of wood decaying tropical polypores and has been shown to be polyphyletic^[45]. The systematic position of the genus has been in flux, initially it was placed in Wrightoporiaceae, and later transferred to Hericiaceae^[259]. According to Index Fungorum (2025) and recent studies, the genus has been placed in Bondarzewiaceae^[1,5,121]. The generic circumscription has recently been revised and placed it into family Wrightoporiaceae^[10,270]. Interestingly, in a recent phylogenetic analysis, *W. austrosinensis* formed an independent lineage outside of the genus^[270]. A similar phylogenetic position of *W. austrosinensis* outside of *Wrightoporia* was observed by Hussain et al.^[12]. Perhaps this species should be included either in *Amyloporus* or be treated as an independent genus^[12].

Russulales genera incertae sedis

Note 72 *Dentipellopsis* Y.C. Dai & L.W. Zhou

Index Fungorum number: IF564151

Type species – *Dentipellopsis dacrydiicola* Y.C. Dai & L.W. Zhou

Notes – *Dentipellopsis* was erected to accommodate a newly described species *D. dacrydiicola* by Zhou & Dai^[30]. The genus is characterized by annual, resupinate basidiomata, hydroid hymenophore, a monomitic hyphal system; generative hyphae with clamp connections, and distinctly thick-walled, densely echinulate, strongly amyloid basidiospores^[30]. *Dentipellopsis* is similar to *Dentipellis* in macro-morphology but differs from the latter by its distinctly thick-walled and cyanophilous basidiospores. Furthermore, the two genera are not closely related, and *Dentipellopsis* was isolated from all accepted families in Russulales in the phylogeny using ITS and nLSU rDNA sequence data. Therefore, its family level taxonomic position is uncertain, and Zhou & Dai^[30] named this clade as *Dentipellopsis* family for convenience.

Note 73 *Gloehypochnicium* (Parmasto) Hjortstam

Index Fungorum number: IF15544

Type species – *Gloehypochnicium analogum* (Bourdot & Galzin) Hjortstam

Notes – *Gloehypochnicium* (Russulales) is typified by *G. analogum*, and it is characterized by the resupinate basidiomata with smooth to tuberculate hymenophore, a monomitic hyphal system with clamps on generative hyphae, the numerous cylindrical, sinuous gloeocystidia, and globose to ellipsoid, thick-walled, warted basidiospores^[1,5,6]. Based on MycoBank (2025) and Index Fungorum (2025), *Gloehypochnicium* has three species, *G. analogum*, *G. versutum* (Burt) Tellería, M. Dueñas, Melo & M.P. Martín, and *G. yunnanense* Lu Wang & C.L. Zhao. The taxonomic status of the genus is unclear, and it was only placed in order Russulales, and it is a mystery genus, and lacks new taxa in the genus for nearly a decade^[1,5,6]. The phylogeny of *Gloehypochnicium* is ambiguous due to a lack of molecular evidence and morphological data. The phylogenetic tree inferred from ITS + nLSU sequences revealed that *Gloehypochnicium* grouped within order Russulales^[20].

Note 74 *Haloaleurodiscus* N. Maek., Suhara & K. Kinjo

Index Fungorum number: IF28938

Type species – *Haloaleurodiscus mangrovei* N. Maek., Suhara & K. Kinjo

Notes – *Haloaleurodiscus* was described from Japanese mangrove forests with one species, *H. mangrovei*. The genus is morphologically characterized by having resupinate basidiomata, nodose-septate hyphae, sulphoaldehyde-positive gloeocystidia, dendrohyphidia and amyloid basidiospores with minute warts. These morphological characters are similar to those of *Aleurodiscus* s. lat., but *H. mangrovei* differs from *Aleurodiscus* primarily in occurring in white pocket-rot and is not closely related based on ribosomal DNA sequence analyses. Molecular data suggested that this species is phylogenetically placed in the root of the 'Peniophorales' clade^[271].

Note 75 *Neoalbatrellus* Audet

Index Fungorum number: IF511206

Type species – *Neoalbatrellus caeruleoporus* (Peck) Audet

Notes – *Neoalbatrellus* was separated from *Albatrellus* s. l. by Audet^[96], and typified by *N. caeruleoporus*. It was distinguished from *Albatrellus* s.s. by several peculiar features such as the unique hymeniderm, and blue, black, and brown color of the basidiomata^[96,272]. Four species, *N. caeruleoporus*, *N. odoratus* Yuan Y. Chen & B.K. Cui, *N. subcaeruleoporus* Audet & B.S. Luther, and *N. yasudae* (Lloyd) Audet, have been recorded^[96,272,273]. The phylogenetic tree based on ITS and nLSU dataset revealed that the genera *Albatrellopsis*, *Polypus*, *Xeroceps*, *Neoalbatrellus*, and *Xanthoporus* clustered within separate lineages with high branch supports^[273]. However, *Albatrellopsis* differs from *Neoalbatrellus* by its large, convex and highly confluent basidiomata, clamped generative hyphae and small, amyloid basidiospores^[96,274,275]. *Polyporus* is characterized by pale yellow petaloid pileus sharing a common base, its fragrant odor when fresh, and thin-walled, non-amyloid basidiospores^[96,274,275]. *Xeroceps* showed unique fuliginous to black pileus, clamped generative hyphae and larger basidiospores than *Neoalbatrellus*^[96,274,275], whereas *Xanthoporus* is distinguished from *Neoalbatrellus* by its yellowish-ochraceous to yellowish-brown pileus, clamped generative hyphae, and thin-walled basidiospores^[96]. *Albatrellopsis* differs from *Neoalbatrellus* by its large, convex and highly confluent basidiomata, clamped generative hyphae and small, amyloid basidiospores^[96,275].

Note 76 *Perplexostereum* Ryvarden & S. Tutka

Index Fungorum number: IF807398

Type species – *Perplexostereum endocrocinum* (Berk.) Ryvarden & Tutka

Notes – Ryvarden^[276] proposed *Perplexostereum* for *Stereum endocrocinum* Berk. Like *Echinodontium* and *Laurilia*. *Perplexostereum* develops large, pileate basidiocarps, ornamented amyloid basidiospores, and inhabits gymnosperms but differs in lacking encrusted cystidia. Phylogenetic tree, based on sequence data of the nuc rDNA ITS1-5.8S-ITS2 (ITS) and D1–D2 domains of nuc 28S rDNA (28S), *Perplexostereum* formed a distinct clade from Echinodontiaceae and Bondarzewiaceae within Russulales^[81].

Discussion

Fungi include mushrooms, molds, lichens, yeasts, and zoosporic forms that occur as free-living or symbiotic organisms in every ecosystem on Earth, and about 155,000 species of fungi have been described, and possibly millions more remain to be named^[2,7,121]. Fungal systematists have made remarkable progress toward resolving the major branches of the phylogeny, although some deep nodes have proven recalcitrant, in which fungal taxonomists steadily describe about 3,000 new species per year, and fungal molecular ecologists routinely detect many thousands of unidentifiable 'dark fungi' through metagenomic analyses^[277]. In recent years, numerous taxa of wood-inhabiting fungi have been reported and

documented worldwide^[2,7,20,54,121,134]. Over the past ten years, global studies have explored the diversity, ecology, and systematics of wood-inhabiting fungi, with different studies emphasizing various taxonomic groups^[37,52,134,220]. However, many fungi in unexplored geographic areas are threatened by climate change, forest expansion, deforestation, and human interactions. Therefore, numerous extant taxa may become extinct before they are discovered^[7]. Consequently, it is now urgent to recognize and conserve fungal biodiversity as it may result in new discoveries^[2]. Additionally, the diversity of wood-inhabiting fungi in the Yunnan-Guizhou Plateau of China holds significant importance.

Fungi include model systems for cell and molecular biology and they represent one of the few clades that has evolved complex multicellularity, which they have done at least eight times during their billion-year history^[277]. Fruiting bodies (sporocarps, sporophores or basidiomata) of Russulales are among the most complex structures produced by fungi and these sexual reproductive organs facilitate efficient spore dispersal. While in simple Basidiomycota have spores that are born on naked basidia, mushroom-forming fungi have evolved complex three-dimensional structures that offer tremendous advantages in effective spore dispersal^[278]. Ancestral basidiomata of the Agaricomycotina were probably crust-like, 'resupinate' forms^[279,280], 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)^[280]. Extensive mycological studies have confirmed that the species of Russulales exhibit pileate, clavarioid, and gasteroid basidiomata^[1]. The diversity of Russulaceae is extremely rich, including discoid, claviform, resupinate-effuse and gasteroid basidiomata, with smooth, pleated, poroid, and odontoid hyphal surface^[17,281]. The distribution of corticioid basidiomata in Russulales was early studied by Larsson^[45]. According to He et al.^[1], the resupinate basidiomata are present in seven families Echinodontiaceae, Hericiaceae, Peniophoraceae, Russulaceae (*Boidinia* and *Gloeopeniophorella* were separate from *Gloeocystidiellum* s.l.), Stereaceae and Terrestriporiaceae. Surprisingly, in the present summary, the resupinate basidiomata type of Russulales, are distributed in 13 branches (families), In addition to the above families, Albatrellaceae, Aleurocystidiellaceae fam. nov., Auriscalpiaceae, Bondarzewiaceae (*Laurilia* and *Lauriliella*), Gloeocystidiellaceae, Gloeodontiaceae fam. nov., and Wrightoporiaceae are included. Meanwhile, In the present study, we propose a new genus and two new families, and we introduce 26 new species with resupinate basidiomata. These taxa belong to six families, Amylostereaceae, Gloeocystidiellaceae, Gloeodontiaceae, Hericiaceae, Peniophoraceae, and Stereaceae, based on morphology, molecular phylogenetic analyses, and divergence time estimates.

Aleurocystidiellaceae

Lemke^[101] established *Aleurocystidiellum* which could not be assigned to any recognized family of Russulales, and its family level classification was treated as incertae sedis. Subsequently, phylogenetic studies supported the monophyletic status of only a small group of the genus *Aleurocystidiellum*, and it was shown that the genus corresponds to a family of its own inferred from ITS + 28S sequence data^[10,21,45,46]. Furthermore, *Aleurocystidiellum* is similar to *Aleurodiscus* (Stereaceae) by sharing the characters of discoid to effused-reflexed basidiomata, moniliform gloeocystidia and verrucose basidiospores. However, species of *Aleurodiscus* can be distinguished from *Aleurocystidiellum* by the presence of numerous acanthocystidia. In the present study, for phylogenetic analyses, *Aleurocystidiellum* species were placed in an alignment of ITS and 28S

sequences of Stereaceae and allied fungi, as previously generated by Wu et al.^[103], Dai & He^[80], Phookamsak et al.^[245], Rajchenberg et al.^[46], and Xu et al.^[87]. The phylogram depicts an overall topology of family Stereaceae (Fig. 6), and order Russulales (Fig. 1), confirming that *Aleurocystidiellum* cannot be placed into any recognized family, including Stereaceae. The analysis of divergence times was also carried out (Fig. 2), which reveals the divergence time of the *Aleurocystidiellum* clade and Hericiaceae at 140.94 Mya with a 95% highest posterior density (HPD) of 87.46–196.71 Mya, 95% HPD, which is similar to the differentiation time of each family in Russulales. Thus, the family name Aleurocystidiellaceae was proposed.

Echinodontiaceae

The family Echinodontiaceae includes four genera, *Amylostereum*, *Echinodontiellum*, *Echinodontium*, and *Larssoniporia*. Except for *Larssoniporia*, which has a poroid basidiomata, the other three genera have corticioid basidiomata^[10]. The divergence time of family Echinodontiaceae and the genus *Subulicystidiella* are at 150.57 Mya (113.56–190.2 Mya, 95% HPD), and 114.84 Mya (125.46–202.89 Mya, 95% HPD), based on ITS + nLSU + *rpb2* + *tef1- α* sequence data (Fig. 2). Inference from the ITS + nLSU + mtSSU + *rpb2* + *tef1- α* (Fig. 1) sequence data showed that *Subulicystidiella* formed a monophyletic clade with statistical support of 87/1.00, and the ITS + nLSU (Fig. 4) sequence data showed that *Subulicystidiella* formed an alone clade with statistical support of 100/100. These indicate that *S. murina* is distinct from all other species sampled in the phylogenetic analysis. However, due to the limited taxa of *Subulicystidiella*, the topology may be influenced by taxon sampling. Meanwhile, morphologically, *Subulicystidiella* was similar to the genus *Amylostereum* (Echinodontiaceae) by its dimitic hyphal system, thick-walled, yellowish brown subulate, encrusted cystidia, and smooth basidiospores, but the latter has effused-reflexed basidiomata, first as small colonies, later confluent, azonate, pale mouse gray to grayish-brown hymenophore, and distinctly amyloid basidiospores^[39]. In addition, the type genus *Echinodontium* of the family Echinodontiaceae is characterised by annual to perennial, resupinate, effused-reflexed to pileate-sessile basidiomata, dimitic hyphal system, generative hyphae with or without clamp-connections, skeletal hyphae inamyloid or dextrinoid, gloeocystidia present or incrustated cystidia absent or present, with smooth basidiospores^[1]. The characteristics of the new genus *Subulicystidiella* are consistent with those of Echinodontiaceae. Thus, we introduce *Subulicystidiella* as a new genus and belongs to this family Echinodontiaceae based on phylogenetic analyses and morphological characteristics.

Gloeocystidiellaceae

The family Gloeocystidiellaceae was established by Jülich^[105], and typified by the genus *Gloeocystidiellum* which was established in 1931 based on morphological classification, including all monophyletic species characterized by gloeocystidia and amyloid basidiospores. All species in this group are corticioid basidiomata and include only the genus *Gloeocystidiellum*, and the genus is not recovered as monophyletic based on the phylogenetic evidence. The situation in *Gloeocystidiellum* s. lat. is similar to *Aleurodiscus* s. lat., but its lineages have wider distributions in Russulales with only certain species nested within Stereaceae^[3,45,89,149,151]. A complete taxonomy and phylogenetic study of the family focusing on the phylogenetic relationships at generic level is urgently needed. We attempted to classify *Gloeocystidiellum* into Stereaceae, but from molecular evidence did not support this view. The result also confirms that *Gloeocystidiellum* is polygenic, and does not place it

in any recognized family of Russulales. The divergence time of family Gloeocystidiellaceae is at 133.39 Mya with a 95% highest posterior density (HPD) of 79.96–186.84 Mya, 95% HPD, based on ITS + nLSU + *rpb2* + *tef1- α* sequence data (Fig. 2). Therefore, based on the divergence times and the molecular phylogenetic relationship, family Gloeocystidiellaceae accommodates *Gloeocystidiellum* s. str. based on the type sequences.

Peniophoraceae

Previous studies of family Peniophoraceae (Russulales) have shown that *Vararia* was closely related to *Asterostroma*, *Baltazaria*, *Dichostereum*, and *Scytinostroma*^[33,34,43,172,219,221]. In the present study, the phylogenetic analysis of *Vararia* and other related genera, inferred from the dataset of ITS + nLSU + mtSSU + *rpb2* + *tef1- α* (Fig. 1), reveals that *Vararia* forms different clades, and three genera *Baltazaria*, *Dichostereum*, and *Peniophora* are distributed within *Vararia*. According to the lineage delimitation, some genera are morphologically well-circumscribed, but some have wide ranges in several aspects, and most genera exhibit their specific characteristics. *Asterostroma* is strongly supported to a single clade characterized by asterosetae and ornamented basidiospores. *Baltazaria* and *Dichostereum* are both monotypic, in which the former is characterized by fibriform skeletal hyphae without simple septa and smooth basidiospores, the latter is characterized by dichohyphae and ornamented basidiospores. *Scytinostroma* s. str. comprises species with fibriform skeletal hyphae, abundant gloeocystidia and smooth basidiospores. *Vararia* s. str. remains a complex assemblage of species with diverse morphology characterized by dichohyphae, gloeocystidia and smooth basidiospores. At present, we prefer to treat it in a rather broad sense to avoid more lineages and new names. *Peniophora* s. str. is characterized by the numerous cystidia encrusted with crystals and smooth basidiospores.

Recalcitrant nodes notwithstanding, reconstructing most of the major branches of the fungal tree of life appears to be a tractable problem but, the goal of achieving a complete catalog of fungi is aspirational at best^[277]. Most major branches of the fungal tree of life have been resolved and the Russulales will follow as more barcodings are sequenced. The harder part, for which no immediate solution is apparent, will be to resolve the fine branches of the phylogeny in detail within Russulales and translate their structure into an accessible classification for different families of Russulales.

The present study addressed and resolved several important taxonomic and phylogenetic issues, and provides a solution framework for further studies on the phylogeny of wood-inhabiting fungi in Russulales. Additional taxa in Russulales should be included into the phylogenetic analyses to improve the generic delimitation with better and more accurate taxonomic resolution. The present study aims to fill the knowledge gap concerning wood-inhabiting fungi within Russulales by introducing new taxa, and providing detailed morphological characteristics, comprehensive descriptions and phylogenetic analyses of these fungal species. In addition, this work contributes to the enrichment of fungal diversity in Asia, particularly expanding the knowledge of Chinese fungal diversity. Further, we suggest that future investigations on the species diversity of Russulales should be prioritized in habitats in underexplored regions and hosts such as monocots in subtropical and tropical areas to uncover the hidden fungal diversity.

Ethical statements

No ethical statement was reported.

Author contributions

The authors confirm contribution to the paper as follows: study conception and design: Zhao CL; data collection: Zhao CL, Deng YL, Chen M, Zhang SC; investigation: analysis and interpretation of results: Deng YL, Chen M, Zhang SC, Wang KS, Liu WT, Qiu YH, Dou YT, Wijesinghe SN, Zhou HM, Jabeen S, Liu XF, Zhao CL.; draft manuscript preparation: Deng YL, Chen M, Zhang SC, Wang KS, Liu WT, Qiu YH, Dou YT, Wijesinghe SN, Zhou HM, Jabeen S, Liu XF, Zhao CL. All authors reviewed the results and approved the final version of the manuscript.

Data availability

All data generated or analyzed during this study are included in this published article.

Acknowledgments

The research was supported by the Forestry and Grass Science and Technology Innovation Joint Project of Yunnan Province (Project No. 202404CB090008), High-level Talents Program of Yunnan Province (YNQR-QNRC-2018-111), Modern Industry School of Edible-fungi, Southwest Forestry University (SYJ25), the Science Foundation of Education Department of Yunnan Province (2025Y0845), Science and Technology Projects of Yunnan Universities Serving Key Industries (FWCY-BSPY2025093), Southwest Forestry University Graduate Research Innovation Fund Project (YJS-KCJJ-2025-03), and Yunnan Province College Students Innovation and Entrepreneurship Training Program (Project No. S202510677111).

Conflict of interest

The authors declare that there is no conflict of interest.

Dates

Received 18 November 2025; Revised 27 December 2025; Accepted 29 December 2025; Published online 19 March 2026

References

- He MQ, Cao B, Liu F, Boekhout T, Denchev TT, et al. 2024. Phylogenomics, divergence times and notes of orders in Basidiomycota. *Fungal Diversity* 126(1):127–406
- Hyde KD, Baldrian P, Chen Y, Thilini Chethana KW, De Hoog S, et al. 2024. Current trends, limitations and future research in the fungi? *Fungal Diversity* 125(1):1–71
- Wang L, Zhu Y, He S, Jabeen S, Zhao C. 2025. Additions to the coriaceous families Peniophoraceae and Stereaceae (Russulales): six novel wood-inhabiting taxa in the genera *Conferticium*, *Gloeocystidiellum*, and *Peniophora* from southwest China. *MycKeys* 115:273
- Ainsworth GC. 2008. Ainsworth & Bisby's dictionary of the fungi. Oxfordshire, Wallingford: CABI
- He MQ, Zhao RL, Hyde KD, Begerow D, Kemler M, et al. 2019. Notes, outline and divergence times of Basidiomycota. *Fungal Diversity* 99(1):105–367
- He MQ, Zhao RL, Liu DM, Denchev TT, Begerow D, et al. 2022. Species diversity of Basidiomycota. *Fungal Diversity* 114(1):281–325
- Hyde K, Noorabadi M, Thiagaraja V, Mq H, Johnston P, et al. 2024. The 2024 Outline of Fungi and fungus-like taxa. *Mycosphere* 15(1):5146–6239
- Hibbett DS, Bauer R, Binder M, Giachini AJ, Hosaka K, et al. 2014. Agaricomycetes. In *Systematics and evolution. The mycota (A comprehensive treatise on fungi as experimental systems for basic and applied research)*, eds. McLaughlin D, Spatafora J. vol. 7. Berlin: Springer. pp.373–429 doi: 10.1007/978-3-642-55318-9_14
- Yuan Y, Chen JJ, Korhonen K, Martin F, Dai YC. 2021. An updated global species diversity and phylogeny in the forest pathogenic genus *Heterobasidion* (Basidiomycota, Russulales). *Frontiers in Microbiology* 11:596393
- Chen JJ, Cui BK, Dai YC. 2016. Global diversity and molecular systematics of *Wrightoporia* s.l. (Russulales, Basidiomycota). *Persoonia – Molecular Phylogeny and Evolution of Fungi* 37(1):21–36
- Chen J, Cui B, He S, Cooper JA, Barrett MD, et al. 2016. Molecular phylogeny and global diversity of the remarkable genus *Bondarzewia* (Basidiomycota, Russulales). *Mycologia* 108(4):697–708
- Hussain S, Al-Kharousi M, Al-Maqbali D, Al-Owaisi AA, Velazhahan R, et al. 2024. Notes on the ecology and distribution of species of the genera of *Bondarzewiaceae* (Russulales and Basidiomycota) with an emphasis on *Amylosporus*. *Journal of Fungi* 10(9):625
- Chen JJ, Cui BK, Zhou LW, Korhonen K, Dai YC. 2015. Phylogeny, divergence time estimation, and biogeography of the genus *Heterobasidion* (Basidiomycota, Russulales). *Fungal Diversity* 71(1):185–200
- Pouzar Z. 1975. Two rare Japanese species of the genus *Albatrellus* (Polyporaceae). *Folia Geobotanica et Phytotaxonomica* 10(2):197–203
- GINNS J. 1997. The taxonomy and distribution of rare or uncommon species of *Albatrellus* in western North America. *Canadian Journal of Botany* 75(2):261–273
- Ryvarden L, Melo I. 2014. Poroid fungi of Europe. *Synopsis Fungorum* 31:1–455
- Zhou HM, Dai YC, Bian LS, Liu HG, Vlasák J, et al. 2025. Diversity, divergence time, and biogeography of the genus *Albatrellus* (Agaricomycetes, Russulales). *Mycology* 16(2):738–776
- Zhou HM, Wu YD, Dai YC. 2021. A new species of *Albatrellus sensu stricto* (Albatrellaceae, Russulales) from China. *Phytotaxa* 510(1):43–52
- Wu F, Zhou LW, Yang ZL, Bau T, Li TH, et al. 2019. Resource diversity of Chinese macrofungi: edible, medicinal and poisonous species. *Fungal Diversity* 98(1):1–76
- Yang Y, Xu Y, Wang L, Jiang QQ, Su JQ, 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
- Wu F, Yuan Y, Chen JJ, Cui BK, Zhou M, et al. 2020. Terrestriporiaceae fam. nov., a new family of Russulales (Basidiomycota). *Mycosphere* 11(1):2755–2766
- Herrera M, Montoya L, Bandala VM. 2018. Two *Lactarius* species (subgenus *Plinthogalus*) in ectomycorrhizal association with tropical *Quercus* trees in eastern Mexico. *Mycologia* 110(6):1033–1046
- Zhou HM, Gu ZR, Zhao CL. 2024. Molecular phylogeny and morphology reveal a new species of *Asterostroma* from Guizhou Province, China. *Phytotaxa* 635(2):173–181
- Caboň M, Li GJ, Saba M, Kolařík M, Jančovičová S, et al. 2019. Phylogenetic study documents different speciation mechanisms within the *Russula globispora* lineage in boreal and arctic environments of the Northern Hemisphere. *IMA Fungus* 10(1):5
- Kirk PM, Cannon PF, Minter DW, Stalpers JA. 2008. Dictionary of the Fungi. 10th Edition. Wallingford: CAB International. pp. 771
- Larsson E, Larsson KH. 2003. Phylogenetic relationships of russuloid basidiomycetes with emphasis on aphyllporalean taxa. *Mycologia* 95(6):1037–1065
- Miller SL, McClean TM, Walker JF, Buyck B. 2001. A molecular phylogeny of the Russulales including agaricoid, gasteroid and pleurotoid taxa. *Mycologia* 93(2):344–354
- Miller SL, Larsson E, Larsson KH, Verbeken A, Nuytinck J. 2006. Perspectives in the new Russulales. *Mycologia* 98(6):960–970
- Yoon SI, Kim SY, Lim YW, Jung HS. 2003. Phylogenetic evaluation of stereoid fungi. *Journal of Microbiology and Biotechnology* 13(3):406–414
- Zhou LW, Dai YC. 2013. Taxonomy and phylogeny of wood-inhabiting hydroid species in Russulales: two new genera, three new species and two new combinations. *Mycologia* 105(3):636–649
- Vizzini A, Angelini C, Losi C, Ercole E. 2018. Diversity of polypores in the Dominican Republic: *Pseudowrightoporia dominicana* sp. nov. (Hericiaceae, Russulales). *MycKeys* 34:35

- [32] Liu ZB, Yuan Y. 2022. A new species of *Xenasmatella* (Polyporales, Basidiomycota) from southern China. *Phytotaxa* 556(2):185–192
- [33] Deng Y, Jabeen S, Zhao C. 2024. Species diversity and taxonomy of *Vararia* (Russulales, Basidiomycota) with descriptions of six species from Southwestern China. *Mycosphere* 103:97
- [34] Deng Y, Li J, Zhao C, Zhao J. 2024. Four new fungal species in forest ecological system from southwestern China. *Journal of Fungi* 10(3):194
- [35] Liu F, Hu ZD, Zhao XM, Zhao WN, Feng ZX, et al. 2024. Phylogenomic analysis of the *Candida auris*-*Candida haemuli* clade and related taxa in the *Metschnikowiaceae*, and proposal of thirteen new genera, fifty-five new combinations and nine new species. *Persoonia – Molecular Phylogeny and Evolution of Fungi* 52(1):22–43
- [36] Dong JH, Chen ML, Chen M, Li Q, Zhu YJ, et al. 2025. Notes, outline, taxonomy and phylogeny of wood-inhabiting Agaricales. *Mycosphere* 16(1):2599–2711
- [37] Liu ZB, Yuan Y, Dai Y, Liu HG, Vlasák J, et al. 2025. Global diversity and systematics of Hymenochaetales with non-poroid hymenophore. *Fungal Diversity* 131(1):1–97
- [38] Hibbett DS, Binder M, Bischoff JF, Blackwell M, Cannon PF, et al. 2007. A higher-level phylogenetic classification of the Fungi. *Mycological Research* 111(5):509–547
- [39] Xu J. 2020. Fungal species concepts in the genomics era. *Genome* 63(9):459–468
- [40] Li Y, He SH, Chen CC, Nakasone KK, Ma HX. 2022. Global taxonomy and phylogeny of *Irpicaceae* (Polyporales, Basidiomycota) with descriptions of seven new species and proposals of two new combinations. *Frontiers in Microbiology* 13:911978
- [41] Ding XX, Xu X, Cui YY, Kost G, Wang PM, et al. 2023. A fifty-locus phylogenetic analysis provides deep insights into the phylogeny of *Tricholoma* (Tricholomataceae, Agaricales). *Persoonia – Molecular Phylogeny and Evolution of Fungi* 50(1):1–26
- [42] Liu SL, Wang XW, Li GJ, Deng CY, Rossi W, et al. 2024. Fungal diversity notes 1717–1817: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 124(1):1–216
- [43] Liu SL, He SH. 2018. Taxonomy and phylogeny of *Dichostereum* (Russulales), with descriptions of three new species from southern China. *Mycosphere* 40:111
- [44] Chen JJ, Cui BK. 2014. Studies on *Wrightoporia* from China 3. *Wrightoporia subavellanea* sp. nov. based on morphological characters and rDNA sequence data. *Phytotaxa* 175(4):225–234
- [45] Larsson KH. 2007. Re-thinking the classification of corticioid fungi. *Mycological Research* 111(9):1040–1063
- [46] Rajchenberg M, Pildain MB, de Errasti A, Riquelme C, Becerra J, et al. 2021. Species and genera in *Aleurodiscus* sensu lato as viewed from the Southern Hemisphere. *Mycologia* 113(6):1264–1277
- [47] Zuckerkandl E. 1962. Molecular disease, evolution, and genic heterogeneity. *Horizons in Biochemistry*: 189–225
- [48] Doolittle RF, Blombäck B. 1964. Amino-acid sequence investigations of fibrinopeptides from various mammals: evolutionary implications. *Nature* 202:147–152
- [49] Zhao RL, Zhou JL, Chen J, Margaritescu S, Sánchez-Ramírez S, et al. 2016. Towards standardizing taxonomic ranks using divergence times – a case study for reconstruction of the *Agaricus* taxonomic system. *Fungal Diversity* 78(1):239–292
- [50] Zhao RL, Li GJ, Sánchez-Ramírez S, Stata M, Yang ZL, 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(1):43–74
- [51] Wang XW, Varga T, Li QS, Nagy LG, Zhou LW. 2025. Complex evolutionary history of the fungal order *Hymenochaetales* revealed by analyses of trait evolution and diversification. *Mycosphere* 16(1):517–535
- [52] Dong JH, Li Q, Yuan Q, Luo YX, Zhang XC, et al. 2024. Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. *Mycosphere* 15(1):1110–1293
- [53] Dong J, Deng Q, Chen M, Chen D, Zhou C, et al. 2025. Molecular phylogeny and morphology reveal four new wood-inhabiting fungi of *Asterostroma* and *Radulomyces* (Basidiomycota) from Southwestern China. *Mycosphere* 112:35
- [54] Wijesinghe SN, Deng YL, Yuan Q, Zhou HM, Wang L, et al. 2025. Mycosphere Notes 572–624: Exploring the hidden diversity of fungi and fungi-like taxa in different terrestrial microhabitats. *Mycosphere* 16(1):2975–3129
- [55] Lücking R, Aime MC, Robbertse B, Miller AN, Aoki T, et al. 2021. Fungal taxonomy and sequence-based nomenclature. *Nature Microbiology* 6(5):540–548
- [56] White TJ, Bruns T, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In *PCR Protocols: a guide to methods and applications*, Innis MA, Gelfand DH, Sninsky JJ, White TJ. London, UK: Academic Press. pp. 315–322 doi: 10.1016/b978-0-12-372180-8.50042-1
- [57] Rehner SA, Samuels GJ. 1994. Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. *Mycological Research* 98(6):625–634
- [58] Liu YJ, Whelen S, Hall BD. 1999. Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. *Molecular Biology and Evolution* 16(12):1799–1808
- [59] Matheny PB, Liu YJ, Ammirati JF, Hall BD. 2002. Using RPB1 sequences to improve phylogenetic inference among mushrooms (Inocybe, Agaricales). *American Journal of Botany* 89(4):688–698
- [60] Matheny PB, Wang Z, Binder M, Curtis JM, Lim YW, et al. 2007. Contributions of rpb2 and tef1 to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). *Molecular Phylogenetics and Evolution* 43(2):430–451
- [61] Vilgalys R, Hester M. 1990. Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172(8):4238–4246
- [62] Rehner SA, Buckley E. 2005. A *Beauveria* phylogeny inferred from nuclear ITS and EF1- α sequences: evidence for cryptic diversification and links to *Cordyceps* teleomorphs. *Mycologia* 97(1):84–98
- [63] Dissanayake AJ, Bhunjun CS, Maharachchikumbura S, Liu JK. 2020. Applied aspects of methods to infer phylogenetic relationships amongst fungi. *Mycosphere* 11(1):2652–2676
- [64] Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics* 20(4):1160–1166
- [65] Larsson A. 2014. AliView: a fast and lightweight alignment viewer and editor for large datasets. *Bioinformatics* 30(22):3276–3278
- [66] Glez-Peñ A D, Gi Mez-Blanco D, Reboiro-Jato M, Fdez-Riverola F, Posada D. 2010. ALTER: program-oriented conversion of DNA and protein alignments. *Nucleic Acids Research* 38:W14–W18
- [67] 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, Illinois, USA, July 16–20, 2012*. New York, United States: Association for Computing Machinery. pp. 1–39. doi: 10.1145/2335755.2335836
- [68] Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, et al. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61(3):539–542
- [69] Kalyaanamoorthy S, Minh BQ, Wong TKF, Von Haeseler A, Jermini LS. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods* 14(6):587–589
- [70] Hibbett D, Grimaldi D, Donoghue M. 1997. Fossil mushrooms from *Miocene* and *Cretaceous* ambers and the evolution of Homobasidiomycetes. *American Journal of Botany* 84(7):981–991
- [71] Taylor TN, Hass H, Kerp H, Krings M, Hanlin RT. 2005. Perithecial ascomycetes from the 400 million year old Rhynie chert: an example of ancestral polymorphism. *Mycologia* 97(1):269–285
- [72] Berbee ML, Taylor JW. 2010. Dating the molecular clock in fungi—how close are we? *Fungal Biology Reviews* 24(1-2):1–16
- [73] Quaedvlieg W, Binder M, Groenewald JZ, Summerell BA, Carnegie AJ, et al. 2014. Introducing the consolidated species concept to resolve species in the *Teratosphaeriaceae*. *Persoonia – Molecular Phylogeny and Evolution of Fungi* 33(1):1–40

- [74] Bruen TC, Philippe H, Bryant D. 2006. A simple and robust statistical test for detecting the presence of recombination. *Genetics* 172(4):2665–2681
- [75] Huson DH, Bryant D. 2006. Application of phylogenetic networks in evolutionary studies. *Molecular Biology and Evolution* 23(2):254–267
- [76] Huson DH, Bryant D. 2024. The SplitsTree App: interactive analysis and visualization using phylogenetic trees and networks. *Nature Methods* 21(10):1773–1774
- [77] Wang XW, Liu SL, Zhou LW. 2023. An updated taxonomic framework of *Hymenochaetales* (Agaricomycetes, Basidiomycota). *Mycosphere* 14(1):452–496
- [78] Hosaka K, Bates ST, Beever RE, Castellano MA, Colgan III W, et al. 2006. Molecular phylogenetics of the gomphoid-phalloid fungi with an establishment of the new subclass Phallomycetidae and two new orders. *Mycologia* 98(6):949–959
- [79] Elith J, Phillips SJ, Hastie T, Dudík M, Chee YE, et al. 2011. A statistical explanation of MaxEnt for ecologists. *Diversity and Distributions* 17(1):43–57
- [80] Dai LD, He SH. 2016. New species and new records of *Aleurodiscus* s.l. (Basidiomycota) in China. *Mycological Progress* 15(7):717–730
- [81] Liu SL, Zhao Y, Dai YC, Nakasone KK, He SH. 2017. Phylogeny and taxonomy of *Echinodontium* and related genera. *Mycologia* 109(4):568–577
- [82] Chen L, Shi ZJ, Wu CH, Zhao CL. 2020. *Gloeodontia yunnanensis* sp. nov. (Russulales, Basidiomycota) from China, evidenced by morphological characters and phylogenetic analyses. *Phytotaxa* 432(2):111–118
- [83] Vu D, Groenewald M, De Vries M, Gehrmann T, Stielow B, 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(1):135–154
- [84] Leal-Dutra CA, Neves MA, Griffith GW, Reck MA, Clasen LA, et al. 2018. Reclassification of *Parapterulicium* Corner (Pterulaceae, Agaricales), contributions to Lachnocladiaceae and Peniophoraceae (Russulales) and introduction of *Baltazaria* gen. nov. *MycKeys* 37:39–56
- [85] Wang XH, Halling RE, Hofstetter V, Lebel T, Buyck B. 2018. Phylogeny, biogeography and taxonomic re-assessment of *Multifurca* (Russulaceae, Russulales) using three-locus data. *PLoS One* 13(11):e0205840
- [86] Wisitrasameewong K, Nuytink J, Hyde KD, Verbeken A. 2014. *Lactarius* subgenus *Russularia* (Russulaceae) in Southeast Asia, 1: species with very distant gills. *Phytotaxa* 158(1):23–42
- [87] Xu YL, Cao YF, Liu SL, Nakasone KK, He SH. 2025. Taxonomy and phylogeny of *Stereaceae* (Russulales, Basidiomycota): two new genera, nine new species and twenty new combinations. *Persoonia-Molecular Phylogeny and Evolution of Fungi* 54(1):119–145
- [88] Liu S, Zhou JL, Song J, Sun YF, Dai YC, et al. 2023. *Climacocystaceae* fam. nov. and *Gloeoporellaceae* fam. nov., two new families of Polyporales (Basidiomycota). *Frontiers in Microbiology* 14:1115761
- [89] Zhang S, Dong J, Zhang X, Li Y, Liu R, et al. 2025. *Gloeocystidiellum sinense* sp. nov. (Stereaceae, Russulales), a wood-inhabiting fungus from Yunnan Province, China. *New Zealand Journal of Botany* 63(2-3):370–381
- [90] Cui BK, Wang Z, Dai YC. 2008. *Albatrellus piceiphilus* sp. nov. on the basis of morphological and molecular characters. *Fungal Diversity* 28:41–48
- [91] Pouzar Z. 1966. A new species of the genus *Albatrellus* (Polyporaceae). *Folia Geobotanica et Phytotaxonomica Bohemoslovaca* 1:274–276
- [92] Pouzar Z. 1966. Studies in the taxonomy of the Polypores II. *Folia Geobotanica et Phytotaxonomica* 1(1):356–375
- [93] Pouzar Z. 1972. Contribution to the knowledge of the genus *Albatrellus* (Polyporaceae). I. A conspectus of species of the North Temperate Zone. *Česká Mykologie* 26:194–200
- [94] Binder M, Hibbett DS. 2002. Higher-level phylogenetic relationships of Homobasidiomycetes (mushroom-forming fungi) inferred from four rDNA regions. *Molecular Phylogenetics and Evolution* 22(1):76–90
- [95] Wang Z, Binder M, Dai YC, Hibbett DS. 2004. Phylogenetic relationships of Sparassis inferred from nuclear and mitochondrial ribosomal DNA and RNA polymerase sequences. *Mycologia* 96(5):1015–1029
- [96] Audet S. 2010. Essai de découpage systématique du genre *Scutigera* (Basidiomycota): *Albatrellopsis*, *Albatrellus*, *Polyporoletus*, *Scutigera* et description de six nouveaux genres. *Mycotaxon* 111(1):431–464
- [97] Nukata M, Hashimoto T, Yamamoto I, Iwasaki N, Tanaka M, et al. 2002. Neogrifolin derivatives possessing anti-oxidative activity from the mushroom *Albatrellus ovinus*. *Phytochemistry* 59(7):731–737
- [98] Li ZP, Shang Y, Xiang L, Lu XM. 2014. Antioxidant activities in vitro of polysaccharide from *Albatrellus caeruleoporos*. *Science and Technology of Food Industry* 35:115–118
- [99] Wei Q, Li ZP. 2016. Study on antioxidant activities of flavonoids from *Albatrellus ovinus*. *Journal of Anhui Science and Technology University* 30:35–38
- [100] Larsen MJ, Zak B. 1978. *Byssoporia* gen. nov.: taxonomy of the mycorrhizal fungus *Poria terrestris*. *Canadian Journal of Botany* 56(9):1122–1129
- [101] Lemke PA. 1964. The genus *Aleurodiscus* (sensu lato) in North America. *Canadian Journal of Botany* 42(6):723–768
- [102] Núñez M, Ryvarde L. 1997. The genus *Aleurodiscus* (Basidiomycotina). *Synopsis Fungorum* 12:1–164
- [103] Wu SH, Hibbett DS, Binder M. 2001. Phylogenetic analyses of *Aleurodiscus* s.l. and allied genera. *Mycologia* 93(4):720–731
- [104] Dai LD. 2017. A new species and a new combination of *Aleurodiscus* s.l. (Russulales, Basidiomycota). *Mycosphere* 8(7):908–916
- [105] Julich W. 1981. Higher taxa of Basidiomycetes. *Bibliotheca Mycologica* 85:1–485
- [106] Lickey EB, Hughes KW, Petersen RH. 2003. Phylogenetic and taxonomic studies in *Artomyces* and *Clavicornora* (Homobasidiomycetes: Auriscalpiaceae). *Sydowia* 55(2):181–254
- [107] Kneal R, Smith ME. 2015. *Artomyces nothofagi* sp. nov., a clavarioid fungus from a Chilean Nothofagus forest. *Mycotaxon* 130:653–660
- [108] Cai Q, He S, Li GM, Fan XP, Li YC, et al. 2025. The genus *Artomyces* (Auriscalpiaceae, Basidiomycota) from the Gaoligong Mountains and adjacent areas, southwestern China. *Mycologia* 117(3):516–531
- [109] Ryvarde L. 2001. The genus *Auriscalpium*. *Harvard Papers in Botany* 6:193–198
- [110] Hall D, Stuntz DE. 1971. Pileate hydneae of the puget sound area. I. white-spored genera: *Auriscalpium*, *Herichium*, *Dentinum* and *Phellodon*. *Mycologia* 63(6):1099–1128
- [111] Petersen RH, Cifuentes J. 1994. Notes on mating systems of *Auriscalpium vulgare* and *A. villipes*. *Mycological Research* 98(12):1427–1430
- [112] Wang PM, Yang ZL. 2019. Two new taxa of the *Auriscalpium vulgare* species complex with substrate preferences. *Mycological Progress* 18(5):641–652
- [113] Domański S. 1965. Wood-inhabiting fungi in Białowieża virgin forest in Poland. II. The mucronelloid fungus of the *Herichium*-group: *Dentipratulum bialoviesense*, gen. et sp. nov.. *Acta Mycologica* 1(1):5–11
- [114] Boidin J, Gilles G. 1990. Corticiés si intéressants ou nouveaux pour la France (Basidiomycotina). *Bulletin Trimestriel de la Société Mycologique de France* 106(4):135–167
- [115] Karasiński D, Piątek M. 2017. The genus *Dentipratulum* (Russulales, Auriscalpiaceae): comparative morphology and SEM imaging spore ornamentation split one into three species. *Mycological Progress* 16(2):109–116
- [116] Larsson KH, Larsson E, Køljalg U. 2004. High phylogenetic diversity among corticioid homobasidiomycetes. *Mycological Research* 108(9):983–1002
- [117] Banker HJ. 1913. Type studies in the Hydneae—VI. The genera *Creolophus*, *Echinodontium*, *Gloiodon*, and *Hydnodon*. *Mycologia* 5(6):293–298
- [118] Desjardin DE, Ryvarde L. 2003. The genus *Gloiodon*. *Sydowia* 55(2):153–161
- [119] Hibbett DS, Binder M. 2002. Evolution of complex fruiting-body morphologies in homobasidiomycetes. *Proceedings of the Royal Society of London. Series B: Biological Sciences* 269(1504):1963–1969
- [120] Dai YC, Cui BK, Yuan HS, Li BD. 2007. Pathogenic wood-decaying fungi in China. *Forest Pathology* 37(2):105–120
- [121] Wijayawardene NN, Mešić A, Pošta A, Tkalčec Z, Thines M. 2022. Outline of Fungi and fungus-like taxa—2021. *Mycosphere* 13:53–453

- [122] Ryvarden L. 1975. Studies in the Aphyllophorales of Africa 2. Some new species from East Africa. *Norwegian Journal of Botany* 22(1):25–34
- [123] David A, Rajchenberg M. 1987. A reevaluation of *Wrightoporia* and *Amylonotus* (Aphyllophorales, Polyporaceae). *Canadian journal of botany* 65(1):202–209
- [124] Ryvarden L. 1973. New genera in the Polyporaceae. *Nordic Journal of Botany* 20:1–5
- [125] Ryvarden L. 1977. Type studies in the Polyporaceae, 10. Species described by JM Berkeley, either alone or with other authors from 1844 to 1855. *Nordic Journal of Botany* 24:213–230
- [126] Huang FC, Liu B, Wu H, Qin PS, Li JF. 2018. *Amylosporus sulcatus* sp. nov. (Russulales, Basidiomycota) from Southern China. *Mycobiology* 46(4):311–316
- [127] Rajchenberg M. 2003. Taxonomic studies on selected Austral polypores. *Australian Systematic Botany* 16(4):473–485
- [128] Song J, Chen J, Wang M, Chen Y, Cui B. 2016. Phylogeny and biogeography of the remarkable genus *Bondarzewia* (Basidiomycota, Russulales). *Scientific Reports* 6(1):34568
- [129] Dai Y, Cui B, Liu X. 2010. *Bondarzewia podocarpi*, a new and remarkable polypore from tropical China. *Mycologia* 102(4):881–886
- [130] Eriksson J, Ryvarden L. 1976. The Corticiaceae of North Europe 4. *Hyphodermella–Mycoacia*. Oslo, Norway: *Fungiflora* pp. 787–794
- [131] Davidson RW, Lentz PL, McKay HH. 1960. The fungus causing pecky cypress. *Mycologia* 52(2):260–279
- [132] Nakasone KK. 1990. Cultural studies and identification of wood-inhabiting Corticiaceae and selected Hymenomycetes from North America. *Mycologia Memoir* 15:1–412
- [133] Geesteranus RAM. 1971. Hydnoneous fungi of the eastern old world. *Verhandelingen der Koninklijke Nederlandse Akademie van Wetenschappen, Afdeling Natuurkunde, Sectie* 260(3):1–176
- [134] Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L, Haelewaters D, et al. 2020. Outline of fungi and fungus-like taxa. *Mycosphere Online: Journal of Fungal Biology* 11(1):1060–1456
- [135] Douanla-Meli C, Langer E. 2009. Fungi of Cameroon 1. New corticioid species (Basidiomycetes). *Mycotaxon* 107(1):95–103
- [136] Slippers B, Coutinho TA, Wingfield BD, Wingfield MJ. 2003. A review of the genus *Amylostereum* and its association with woodwasps. *South African Journal of Science* 99(1):70–74
- [137] Bergeron MJ, Leal I, Foord B, Ross G, Davis C, et al. 2011. Putative origin of clonal lineages of *Amylostereum areolatum*, the fungal symbiont associated with *Sirex noctilio*, retrieved from *Pinus sylvestris*, in eastern Canada. *Fungal Biology* 115(8):750–758
- [138] Tabata M, Harrington TC, Chen W, Abe Y. 2000. Molecular phylogeny of species in the genera *Amylostereum* and *Echinodontium*. *Mycoscience* 41(6):585–593
- [139] He SH, Li HJ. 2013. *Amylostereum orientale* sp. nov. (Basidiomycota, Russulales) and first report of *A. areolatum* in China based on morphological and molecular characters. *Nordic Journal of Botany* 31(6):728–733
- [140] Visagie CM, Yilmaz N, Allison JD, Barreto RW, Boekhout T, et al. 2024. New and interesting fungi. 7. *Fungal Systematics and Evolution* 13:441
- [141] Donk MA. 1964. A conspectus of the families of Aphyllophorales. *Persoonia-Molecular Phylogeny and Evolution of Fungi* 3(2):199–324
- [142] Baxter AP, Rong IH, Schutte AL. 1995. *Amylostereum areolatum* (Aphyllophorales: Stereaceae) in South Africa. *South African Journal of Botany* 61(6):352–354
- [143] Stalpers JA. 1996. The aphyllophoraceous fungi 2. Keys to the species of the Hericiales. *Studies in Mycology* 40:1–185
- [144] Hibbett DS, Gilbert LB, Donoghue MJ. 2000. Evolutionary instability of ectomycorrhizal symbioses in basidiomycetes. *Nature* 407:506–508
- [145] Hibbett DS, Donoghue MJ. 2001. Analysis of character correlations among wood decay mechanisms, mating systems, and substrate ranges in homobasidiomycetes. *Systematic Biology* 50(2):215–242
- [146] Donk MA. 1957. The generic names proposed for Hymenomycetes. VII: "Theleporaceae". *Taxon* 6:17–28
- [147] Larsson E, Hallenberg N. 2001. Species delimitation in the *Gloeocystidiellum porosum-clavuligerum* complex inferred from compatibility studies and nuclear rDNA sequence data. *Mycologia* 93(5):907–914
- [148] Gorjón SP, Greslebin AG, Rajchenberg M. 2013. The genus *Aleurodisca* s.l. (Stereaceae, Russulales) in the Patagonian Andes. *Mycological Progress* 12(1):91–108
- [149] Jaramillo-Riofrio A, Decock C, Suárez JP, Benítez Á, Castillo G, et al. 2022. Screening of antibacterial activity of some resupinate fungi, reveal *Gloeocystidiellum lojanense* sp. nov. (Russulales) against *E. coli* from Ecuador. *Journal of Fungi* 9(1):54
- [150] Zhao YL, Zhao CL. 2023. A corticioid fungus, *Gloeocystidiellum yunnannense* sp. nov. (Russulales) with characteristic gloeocystidia from southern China. *Nova Hedwigia* 116:155–170
- [151] Zhu Y, Dong J, Shen K, Yang S, Zhao C, et al. 2025. Molecular phylogeny and morphology reveal a new species of *Gloeocystidiellum* (Stereaceae, Russulales) from Southwestern China. *Phytotaxa* 725(1):11–23
- [152] Boidin J. 1997. Le genre *Gloeocystidiellum* sensu lato (Basidiomycotina). *Bulletin de la Société Mycologique de France* 113:1–80
- [153] Hjortstam K. 1987. Studies in tropical Corticiaceae (Basidiomycetes) VII. Specimens from East Africa collected by L. Ryvarden. II. *Mycotaxon* 28(1):19–37
- [154] Hjortstam K. 1984. Notes on Corticiaceae (Basidiomycetes). XIII. *Mycotaxon* 19:503–513
- [155] Boidin J. 1966. Basidiomycètes Auriscalpiaceae de la république Centrafricaine. *Cahiers de la Maboké* 4:18–25
- [156] Bursdall Jr HH, Lombard FF. 1976. The genus *Gloeodontia* in North America. *Memoirs of the New York Botanical Garden* 28(1):16–31
- [157] Chen JJ, Shen LL, Dai YC. 2015. *Dentipellicula austroafricana* sp. nov. supported by morphological and phylogenetic analyses. *Mycotaxon* 130(1):17–25
- [158] Zhou M, Chen JJ, Vlasák J, Yuan Y. 2021. *Dentipellicula guyanensis* sp. nov. (Hericiaceae, Basidiomycota) from French Guiana. *Phytotaxa* 478(2):261–267
- [159] Dai Y. 2009. Notes on *Dentipellis* (Russulales, Basidiomycota). *Mycosystema* 28:668–671
- [160] Yuan Y, Ren GJ, Dai YC. 2018. *Dentipellis rhizomorpha* sp. nov. supported by morphological and phylogenetic analyses. *Nova Hedwigia* 107(1–2):131–140
- [161] Shen LL, Wang M. 2017. Morphological characteristics and molecular data reveal two new species of *Dentipellis* from China. *Phytotaxa* 323(1):69
- [162] Donk MA. 1962. Notes on resupinate Hymenomycetes—VI. *Persoonia-Molecular Phylogeny and Evolution of Fungi* 2(2):217–238
- [163] Jumbam B, Haelewaters D, Koch RA, Dentinger BTM, Henkel TW, et al. 2019. A new and unusual species of *Hericium* (Basidiomycota: Russulales, Hericiaceae) from the Dja Biosphere Reserve, Cameroon. *Mycological Progress* 18(10):1253–1262
- [164] Van der Merwe B, Herrmann P, Jacobs K. 2023. *Hericium opheliae* sp. nov., a novel species of *Hericium* (Basidiomycota: Russulales, Hericiaceae) from the Southern Afrotemperate forests of South Africa. *Mycology* 14(2):133–141
- [165] Wang S, Zhao L, Chen D, Luo H, Tang S, et al. 2024. *Hericium yunnannense* (Hericiaceae, Russulales), a new edible mushroom from Yunnan, China. *Phytotaxa* 665(3):253–262
- [166] Koga J, Thorn RG, Langer E. 2025. A multilocus phylogeny of *Hericium* (Hericiaceae, Russulales). *Persoonia* 55:141–157
- [167] Henkel TW, Ryvarden L. 2021. A synopsis of the wood-decay genus *Laxitextum* (Hericiaceae, Russulales, Basidiomycota) and a new species from Cameroon. *Edinburgh Journal of Botany* 78:1–9
- [168] Hjortstam K, Ryvarden L. 1981. Studies in tropical Corticiaceae (Basidiomycetes) III. Two new species of *Laxitextum*. *Mycotaxon* 13:35–40
- [169] Lee JS, Jung HS. 2006. Taxonomic study on Korean Aphyllophorales (5)—on some unrecorded genera and species. *Mycobiology* 34(4):166–175
- [170] Mudalungu CM, Richter C, Wittstein K, Ali Abdalla M, Matasyoh JC, et al. 2016. *Laxitextines* A and B, cyathane xylosides from the tropical fungus *Laxitextum incrustatum*. *Journal of Natural Products* 79(4):894–898
- [171] Ryvarden L, Iturriaga T. 2003. Studies in neotropical polypores 10. New polypores from Venezuela. *Mycologia* 95(6):1066–1077

- [172] Deng YL, Zhao CL. 2023. The molecular phylogeny and morphology revealed a new wood-rotting fungus *Vararia yunnanensis* (Peniophoraceae, Russulales) in Yunnan Province, China. *Phytotaxa* 583(1):39–49
- [173] Dai YC. 2011. A revised checklist of corticioid and hydroid fungi in China for 2010. *Mycoscience* 52(1):69–79
- [174] Tedersoo L, Bahram M, Jairus T, Bechem E, Chinoya S, et al. 2011. Spatial structure and the effects of host and soil environments on communities of ectomycorrhizal fungi in wooded savannas and rain forests of Continental Africa and Madagascar. *Molecular Ecology* 20(14):3071–3080
- [175] Wu SH. 1995. Two new genera of corticioid basidiomycetes with gloeocystidia and amyloid basidiospores. *Mycologia* 87(6):886–890
- [176] Wu S. 1997. Two new combinations: *Amylofungus globosporus* and *Gloeomyces moniliformis*. *Mycotaxon* 64:361–364
- [177] Masee G. 1889. A monograph of the Thelephoræ—Part I. *Botanical Journal of the Linnean Society* 25(170):107–155
- [178] Hallenberg N. 1985. The Lachnocladiaceae and Coniophoraceae of North Europe. *Fungiflora, Oslo*. pp. 96
- [179] Liu SL, Tian Y, Nie T, Thawthong A, Hyde KD, et al. 2017. Updates on East Asian *Asterostroma* (Russulales, Basidiomycota): new species and new records from Thailand and China. *Mycological Progress* 16(6):667–676
- [180] Boidin J, Lanquetin P, Gilles G. 1997. Contribution à la connaissance du genre *Asterostroma* Masee 1889 (Basidiomycotina). *Bulletin trimestriel de la Société mycologique de France* 113(4):269–301
- [181] Suhara H, Maekawa N, Ushijima S, Kinjo K, Hoshi Y. 2010. *Asterostroma* species (Basidiomycota) from mangrove forests in Japan. *Mycoscience* 51(1):75–80
- [182] Boidin J, Lanquetin P. 1987. Le Genre *Scytinostroma* Donk. *Bibliotheca Mycologica* 114:1–130
- [183] Chamuris GP. 1987. Notes on stereoid fungi I: the genus *Dendrophora*, stat. nov., and *Peniophora malenconii* subsp. americana, subsp. nov. ("Sterium heterosporum"). *Mycotaxon* 28(2):543–552
- [184] Reid DA. 1965. A monograph of the stipitate stereoid fungi. *Taxon* 14(8):289
- [185] Boidin J. 1967. Basidiomycètes Lachnocladiaceae résumés de la république Centrafricaine. *Cahiers de la Maboké* 5:23–35
- [186] Lanquetin P. 1973. Utilisation des cultures dans la systématique des *Vararia* Karst subg. *Dichostereum* (Pilat) Boid. (Basidiomycètes Lachnocladiaceae). *Publications de la Société Linnéenne de Lyon* 42(7):167–192
- [187] Boidin J, Lanquetin P. 1977. Les genres *Dichostereum* et *Vararia* en Guadeloupe (Basidiomycetes, Lachnocladiaceae). *Mycotaxon* 6:277–336
- [188] Boidin J, Lanquetin P. 1980. Contribution à l'étude du genre *Dichostereum* Pilat (Basidiomycètes Lachnocladiaceae). *Bulletin de la Société Mycologique de France* 96:381–406
- [189] Hjortstam K, Ryvarden L. 2004. Some new and noteworthy corticioid fungi (Basidiomycotina, Aphyllophorales) from Japan. *Synopsis Fungorum* 18:8–13
- [190] Andreassen M, Hallenberg N. 2009. A taxonomic survey of the Peniophoraceae. *Synopsis Fungorum* 26:56–119
- [191] Spirin V, Kout J. 2015. *Duportella lassa* sp. nov. from Northeast Asia. *Mycotaxon* 130(2):483–488
- [192] Patouillard N. 1915. Champignons des Philippines communiqués par CF Baker, II. *Philippine Journal of Science Section C Botany* 10:85–98
- [193] Whitney HS, Bandoni RJ, Oberwinkler F. 1987. *Entomocorticium dendrotoni* gen. et sp. nov. (Basidiomycotina), a possible nutritional symbiote of the mountain pine beetle in lodgepole pine in British Columbia. *Canadian Journal of Botany* 65(1):95–102
- [194] Araújo JPM, Li Y, Six D, Rajchenberg M, Smith ME, et al. 2021. Diversity and evolution of *Entomocorticium* (Russulales, Peniophoraceae), a genus of bark beetle mutualists derived from free-living, wood rotting *Peniophora*. *Journal of Fungi* 7(12):1043
- [195] Harrington TC, Batzer JC, McNew DL. 2021. Corticioid basidiomycetes associated with bark beetles, including seven new *Entomocorticium* species from North America and *Cylindrobasidium ipidophilum*, comb. nov. *Antonie Van Leeuwenhoek* 114(5):561–579
- [196] Hsiao PT, Harrington TC. 2003. Phylogenetics and adaptations of basidiomycetous fungi fed upon by bark beetles (Coleoptera: Scolytidae). *Symbiosis* 34(2):111–132
- [197] Hjortstam K, Ryvarden L. 2007. Checklist of corticioid fungi (Basidiomycotina) from the tropics, subtropics and the southern hemisphere. *Synopsis fungorum* 22:27–146
- [198] Larsson K, Melo I, Salcedo I. 2020. *Gloiothele olearia*—a new name for a known species. *Synopsis Fungorum* 41:12–15
- [199] Boidin J, Lanquetin P. 1983. Basidiomycètes Aphyllophorales épithéloïdes étalés. *Pascal and Francis Bibliographic Databases* 16:461–499
- [200] Ghobad-Nejhad M. 2009. A new species and new combinations in the corticioid genus *Gloiothele* (Basidiomycota). *Mycotaxon* 110(1):261–270
- [201] Chacón S, Tapia F, Jarvio D. 2018. Four interesting aphyllophoroid species in the tropical northern region of Veracruz, Mexico. *Mycotaxon* 133(1):153–163
- [202] Gorjón SP, De Jesus MA. 2012. Some new species and new records of corticioid fungi (Basidiomycota) from the Brazilian Amazon. *Phytotaxa* 67(1):38–54
- [203] Ginns H. 1994. The Gloeocystidiellaceae (Basidiomycota, Hericiales) of North America. *Bibliotheca Mycologica* 157:1–118
- [204] Corner E.J.H. 1950. A monograph of *Clavaria* and allied genera. Dawson of Pall Mall, London. pp. 740
- [205] Parmasto E. 1986. On the origin of Hymenomyces (What are corticioid fungi?). *Windahlia* 16:3–19
- [206] Xu YL, Tian Y, He SH. 2023. Taxonomy and phylogeny of *Peniophora* sensu lato (Russulales, Basidiomycota). *Journal of Fungi* 9(1):93
- [207] Boidin J. 1998. Taxonomie moléculaire des Aphyllophorales. *Mycotaxon* 66:445–491
- [208] Lyman GF. 1907. Culture studies on the polymorphism of Hymenomyces. *Proceedings of the Boston Society of Natural History* 33:125–209
- [209] Giraldo A, Crous PW, Schumacher RK, Cheewangkoon R, Ghobad-Nejhad M, et al. 2017. The Genera of Fungi—G3: *Aleurocystis*, *Blastocervulus*, *Clypeophysalospora*, *Licrostroma*, *Neohendersonia* and *Spumatoria*. *Mycological Progress* 16(4):325–348
- [210] Leal-Dutra CA, Griffith GW, Neves MA, McLaughlin DJ, McLaughlin EG, et al. 2020. Reclassification of Pterulaceae Corner (Basidiomycota: Agaricales) introducing the ant-associated genus *Myrmecopterulagen* nov., *Phaeopterula* Henn. and the corticioid *Radulomycetaceafam* nov. *IMA Fungus* 11(2):1–24
- [211] Stalpers JA, Redhead SA, May TW, Rossmann AY, Crouch JA, et al. 2021. Competing sexual-asexual generic names in Agaricomycotina (Basidiomycota) with recommendations for use. *IMA Fungus* 12(1):22
- [212] Li Y, Xu WQ, Liu SL, Yang N, He SH. 2023. Species diversity and taxonomy of *Scytinostroma* sensu stricto (Russulales, Basidiomycota) with descriptions of four new species from China. *MycKeys* 98:133–152
- [213] Karasinski D. 2010. Polish resupinate Russulales: the genus *Vararia*. *Acta Mycologica* 45(1):45–56
- [214] Karnste PA. 1898. Kritisk af versigt af Finlands Basidsvampar. *Biology* 3:1–36
- [215] Boidin J, Lanquetin P. 1975. *Vararia* subgenus *Vararia* (Basidiomycètes Lachnocladiaceae): étude spéciale des espèces d'Afrique intertropicale. *Bulletin de la Société Mycologique de France* 4(91):457–513
- [216] Boidin J, Lanquetin P, Gilles G. 1980. Application du concept biologique de l'espèce aux Basidiomycètes: le genre *Vararia* (section *Vararia*) au Gabon. 4(1): 265–384
- [217] Yurchenko E, Riebesehl J, Langer E. 2017. Clarification of *Lyomyces sambuci* complex with the descriptions of four new species. *Mycological Progress* 16(9):865–876
- [218] Nakasone KK. 2015. Taxonomic studies in *Chrysoderma*, *Corneromyces*, *Dendrophysellum*, *Hyphoradulum*, and *Mycobonia*. *Mycotaxon* 130(2):369–397
- [219] Liu SL, He SH. 2016. The genus *Vararia* (Russulales, Basidiomycota) in China. *Two new species and two new Chinese records*. *Nordic Journal of Botany* 34(5):553–558
- [220] Dai Y, Yang Z, Cui B, Wu G, Yuan H, et al. 2021. Diversity and systematics of the important macrofungi in Chinese forests. *Mycosystema* 40:770–805

- [221] Zou L, Zhang X, Deng Y, Zhao C. 2022. Four new wood-inhabiting fungal species of Peniophoraceae (Russulales, Basidiomycota) from the Yunnan-Guizhou Plateau, China. *Journal of Fungi* 8(11):1227
- [222] Manawasinghe IS, Hyde KD, Wanasinghe DN, Karunarathna SC, Maharachchikumbura SSN, et al. 2025. Fungal diversity notes 1818–1918: taxonomic and phylogenetic contributions on genera and species of fungi. *Fungal Diversity* 130(1):1–261
- [223] Boidin J, Lanquetin P. 1984. Compléments au genre *Vararia* P. Karst. (basidiomycetes). *Persoonia-Molecular Phylogeny and Evolution of Fungi* 12(3):243–262
- [224] Welden AL. 1965. West Indian species of *Vararia* with notes on extralimital species. *Mycologia* 57(4):502–520
- [225] Boidin J, Lanquetin P, Terra P, Gomez CE. 1976. *Vararia* subgenus *Vararia* (Basidiomycetes Lachnocladiaceae): deuxième partie: caractères culturels. *Bulletin de la Société Mycologique de France* 2(92):247–277
- [226] Hjortstam K. 1986. Notes on Corticiaceae (Basidiomycetes). *XIV. Mycotaxon* 25(1):273–277
- [227] Hjortstam K, Ryvarden L. 1988. Notes on the Corticiaceae of Northern China. *Acta Mycologica Sinica* 2(7):77–88
- [228] Larsson K, Larsson E, Ryvarden L, Spirin V. 2020. Some new combinations of corticioid fungi (Basidiomycota, Agaricomycetes). *Synopsis Fungorum* 40:113–117
- [229] Rick JE. 1934. Monographia Thelephoracearum resupinarum Riograndensium. *Brotéria Série Trimestral: Ciências Naturais* 3(2):66–80
- [230] Lee H, Wissitrassameewong K, Park MS, Verbeken A, Eimes J, et al. 2019. Taxonomic revision of the genus *Lactarius* (Russulales, Basidiomycota) in Korea. *Fungal Diversity* 95(1):275–335
- [231] Tang SM, Wisitrassameewong K, Yu FM, Ye L, Gao L, et al. 2022. *Lactarius pseudoaurantiozonatus* (Russulales), A new Species of *Lactarius* subgenus *Lactarius* from China. *Chiang Mai Journal of Science* 49:1307–1316
- [232] Buyck B, Hofstetter V, Eberhardt U, Verbeken A, Kauff F. 2008. Walking the thin line between *Russula* and *Lactarius*: the dilemma of *Russula* subsect. *Ochricompactae*. *Fungal Diversity* 28(28):15–40
- [233] Buyck B, Hofstetter V, Verbeken A, Walleyn R. 2010. Proposal 1919: To conserve *Lactarius* nom. cons. (Basidiomycota) with a conserved type. *Mycotaxon* 111:504–508
- [234] Verbeken A, Nuytinck J, Buyck B. 2012. New combinations in *Lactifluus*. 1. *L. subgenera edules, Lactariopsis, and russulopsis*. *Mycotaxon* 118(1):447–453
- [235] Verbeken A, Van de Putte K, De Crop E. 2012. New combinations in *Lactifluus*. 3. *L. subgenera Lactifluus and Piperati*. *Mycotaxon* 120(1):443–450
- [236] McNeill J, Turland NJ, Monro AM, Lepschi BJ. 2011. XVIII International Botanical Congress: preliminary mail vote and report of Congress action on nomenclature proposals. *Taxon* 60:1507–1520
- [237] Lee H, Wissitrassameewong K, Park MS, Fong JJ, Verbeken A, et al. 2021. Taxonomic Revision of the Genus *Lactifluus* (Russulales, Basidiomycota) of South Korea. *Mycobiology* 49(4):308–345
- [238] Xu XH, Chen AM, Yao N, Wen TC, Pei Y, et al. 2023. Three New Species of *Lactifluus* (Basidiomycota, Russulaceae) from Guizhou Province, Southwest China. *Journal of Fungi* 9(1):122
- [239] Verbeken A, Nuytinck J. 2013. Not every milkcap is a *Lactarius*. *Scripta Botanica Belgica* 51:162–168
- [240] Chakraborty D, Tudu D, Ghosh A, Wisitrassameewong K. 2025. New insights into *Lactifluus* sect. *Gerardii*: a novel taxon from Meghalaya, India. *Phytotaxa* 716:4
- [241] De Crop E, Hampe F, Wisitrassameewong K, Stubbe D, Nuytinck J, et al. 2018. Novel diversity in *Lactifluus* section *Gerardii* from Asia: five new species with pleurotoid or small agaricoid basidiocarps. *Mycologia* 110(5):962–984
- [242] Wang X, Liu P. 2010. *Multifurca* (Russulales), a genus new to China. *Cryptogamie* 31(1):9
- [243] Lebel T, Dunk CW, May TW. 2013. Rediscovery of *Multifurca stenophylla* (Berk.) T. Lebel, CW Dunk & TW May comb. nov. (Russulaceae) from Australia. *Mycological Progress* 12(3):497–504
- [244] Wu SH, Wang DM, Yu SY. 2010. *Neoleurodiscus fujii*, a new genus and new species found at the timberline in Japan. *Mycologia* 102(1):217–223
- [245] Phookamsak R, Hyde KD, Jeewon R, Bhat DJ, Gareth Jones EB, et al. 2019. Fungal diversity notes 929–1035: taxonomic and phylogenetic contributions on genera and species of fungi. *Fungal Diversity* 95(1):1–273
- [246] Oberwinkler F. 1965. Primitive Basidiomyceten: revision einiger Formenkreise von Basidienpilzen mit plastischer Basidie. *Berger* 1–72.
- [247] Wu SH, Wei CL, Lin YT, Chang CC, He SH. 2019. Four new East Asian species of *Aleurodiscus* with echinulate basidiospores. *MycKeys* 52:71
- [248] Parmasto E. 1967. Descriptions taxorum novorum. *Combinaciones novae. Eesti NSV Tead Akad Toim Ser Biol* 16:377–394
- [249] Ryvarden L, Sanyal SK, Dhingra GS. 2012. *Aleurodiscus indicus* (Agaricomycetes) sp. nov. from India. *Synopsis Fungorum* 30:14–16
- [250] Maninder K, Avneet PS, Dhingra GS, Ryvarden L. 2014. *Aleurodiscus himalaicus* (Agaricomycetes) sp. nov. from India. *Synopsis Fungorum* 32:5–7
- [251] Dai LD, Zhao Y, He SH. 2017. Three new species of *Aleurodiscus* s.l. (Russulales, Basidiomycota) on bamboos from East Asia. *Cryptogamie, Mycologie* 38(2):227–239
- [252] Dai LD, Wu SH, Nakasone KK, Burdsall HH, He SH. 2017. Two new species of *Aleurodiscus* s.l. (Russulales, Basidiomycota) on bamboo from tropics. *Mycoscience* 58(3):213–220
- [253] Ghobad-Nejhad M, Langer E. 2018. A new species in *Aleurodiscus* sl (Stereaceae, Russulales) from Iran. *Phytotaxa* 351(4):264
- [254] Tian Y, Ghobad-Nejhad M, He SH, Dai YC. 2018. Three new species of *Aleurodiscus* s.l. (Russulales, Basidiomycota) from southern China. *MycKeys* 37:93
- [255] Rattan SS. 1977. The resupinate Aphyllophorales of the North Western Himalayas. *Bibliotheca Mycologica* 60:1–427
- [256] Shen L, Wang K, Xia H, Liu S, Yao L, et al. 2024. Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species of *Conferticum* (Stereaceae, Basidiomycota) from southwest China. *Phytotaxa* 677(1):77–86
- [257] Yang A, Wang L, Hu Y, Jiang Y, Shi G, et al. 2025. Morphological characteristics and phylogenetic analyses revealed five new species (Basidiomycota) from Southwestern China. *MycKeys* 114:177
- [258] Hjortstam K. 1990. Corticioid fungi described by M.J. Berkeley. II: Species from Cuba. *Mycotaxon* 39:415–423
- [259] Jülich W. 1978. Studies in resupinate Basidiomycetes—V. *Some new genera and species. Persoonia-Molecular Phylogeny and Evolution of Fungi* 10(1):137–140
- [260] Spirin V, Volobuev S, Malysheva V, Miettinen O, Kotiranta H, et al. 2021. Identity of the subalpine–subarctic corticioid fungus *Megalocystidium leucoxanthum* (Russulales, Basidiomycota) and six related species. *Plant Ecology and Evolution* 154(2):231–244
- [261] Gorjón SP, Greslebin AG. 2024. *Stereodiscus pseudotrivialis* (Russulales, Basidiomycota), a new species from the Patagonian Andes of Argentina. *Phytotaxa* 636(2):152–162
- [262] Welden AL. 1954. Some tropical American stipitate stereums. *Bulletin of the Torrey Botanical Club* 81:422–439
- [263] Ghobad-Nejhad M, Langer E, Gorjón SP. 2025. Morphological and phylogenetic evidence reveal a new species in *Stereum* (Russulales, Basidiomycota). *Nova Hedwigia* 121(1-2):139–151
- [264] Saccardo PA. 1887. *Sylloge hymenomycetum*, vol. I. Agaricineae. *Sylloge Fungorum* 5:1–1146
- [265] Hooker JD. 1847. The botany of the Antarctic voyage of HM discovery ships Erebus and Terror in the years 1839–1843: under the command of Captain Sir James Clark Ross. Vol. 1. pp. 1–378
- [266] Berkeley MJ, Curtis MA. 1849. Decades of fungi. Decades XXI–XXII. North and South Carolina Fungi. *Hooker's Journal of Botany and Kew Garden Miscellany* 1:97–104
- [267] Boidin J, Gilles G. 1986. Basidiomycètes Aphyllophorales de l'île de la Réunion. *Bulletin trimestriel de la Société Mycologique de France* 102(3):273–319
- [268] Cao Y, He S. 2020. *Xylobolus austrosinensis* sp. nov. (Stereaceae, Russulales) and notes on the genus. *Phytotaxa* 452:200–208
- [269] Felegyi K, Garádi Z, Studzińska-Sroka E, Papp V, Boldizsár I, et al. 2023. Anticholinesterase and antityrosinase secondary metabolites from the fungus *Xylobolus subpileatus*. *Molecules* 29(1):213

- [270] Zhou M, Chen J, Yuan Y. 2020. A new species of *Wrightoporia* (Wrightoporiaceae, Basidiomycota) from Sri Lanka. *Phytotaxa* 437(2):105–112
- [271] Maekawa N, Suhara H, Kinjo K, Kondo R, Hoshi Y. 2005. *Haloaleurodiscus mangrovei* gen. sp. nov. (Basidiomycota) from mangrove forests in Japan. *Mycological research* 109(7):825–832
- [272] Audet S, Luther BS. 2016. *Neoalbatrellus subcaeruleoporus* sp. nov. (Scutigeraceae) from western North America. *Mycotaxon* 130(4):1191–1202
- [273] Chen YY, Wang M, Zhang B, Cui BK. 2017. *Neoalbatrellus odoros* sp. nov. (Albatrellaceae, Russulales) from Southwest China. *Phytotaxa* 309(3):217–228
- [274] Zheng HD, Liu PG. 2006. *Albatrellus yunnanensis*, a new species from China. *Mycotaxon* 97:145–151
- [275] Zheng HD, Liu PG. 2008. Additions to our knowledge of the genus *Albatrellus* (Basidiomycota) in China. *Fungal Diversity* 32:157–170
- [276] Ryvarden L. 2014. *Perplexostereum* Ryvarden & Tutka nov. gen. *Synopsis Fungorum* 32:72–75
- [277] Hibbett D, Nagy LG, Nilsson RH. 2025. Fungal diversity, evolution, and classification. *Current Biology* 35(11):463–469
- [278] Nagy LG, Vonk PJ, Künzler M, Földi C, Virágh M, et al. 2023. Lessons on fruiting body morphogenesis from genomes and transcriptomes of Agaricomycetes. *Studies in Mycology* 104(1):1–85
- [279] 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
- [280] Varga T, Krizsán K, Földi C, Dima B, Sánchez-García M, et al. 2019. Megaphylogeny resolves global patterns of mushroom evolution. *Nature Ecology and Evolution* 3(4):668–678
- [281] Liu S, Zhu M, Keyhani NO, Wu Z, Lv H, et al. 2024. Three new species of Russulaceae (Russulales, Basidiomycota) from southern China. *Journal of Fungi* 10(1):70



Copyright: © 2026 by the author(s). Published by Maximum Academic Press, Fayetteville, GA. This article is an open access article distributed under Creative Commons Attribution License (CC BY 4.0), visit <https://creativecommons.org/licenses/by/4.0/>.