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ARTICLE

Multigene phylogeny of seven wood-inhabiting fungal orders in *Basidiomycota*, and proposal of a new genus and thirteen new species

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Abstract

The wood-inhabiting fungal orders play a central role in understanding the diversity in *Basidiomycota*, and their significance in the recycling of organic matter and nutrient cycling. Typically they are categorized as the white-rot and brown-rot fungi. In the present study, wood-inhabiting fungi were collected from various locations in Yunnan Province, China. These collections were further identified using comprehensive analysis of combined morphological characters and phylogenetic analyses encompassed the internal transcribed spacer (ITS) regions, the large subunit nuclear ribosomal RNA gene (nLSU), small subunit mitochondrial rRNA gene sequences (mtSSU), translation elongation factor 1-α gene (*tef*1-α), RNA polymerase II largest subunit (*rpb1*), and the second subunit of RNA polymerase II (*rpb2*). Based on these, this study presents a new genus, *Gracilihypha*, and thirteen new species from seven orders and eight families as *Coniophoropsis sinensis*, *Gloeopeniophorella bambusicola*, *Gloiothele yunnanensis*, *Gracilihypha abeliae*, *Hyphoderma asianum*, *H. qujingense*, *Hyphodontia daweishanensis*, *Kneiffiella qujingensis*, *Merismodes wumengshanensis*, *M. yunnanensis*, *Peniophora fissurata*, *Punctulariopsis asiana*, and *Sertulicium yunnanense*. Furthermore, this multi-locus approach allowed for a robust assessment of the evolutionary relationships within the fungal community. To enhance accessibility and understanding, herein we include illustrated descriptions of the newly proposed taxa and comprehensive notes on the genera. Our study will provide new insight into the diversity of wood-inhabiting fungi while contributing new species to basidiomycete.

Keywords – *Agaricomycetes*, basidiomata morphogenesis, ecology, fungal classification, multiple genes, new taxa

INTRODUCTION

Fungi are eukaryotic microorganisms that play key ecological roles as decomposers, mutualists, or pathogens (Hyde et al. 2024). The classification of the fungal kingdom has been updated continuously, with the frequent inclusion of data from DNA sequences and by using both fresh material and cultures. Furthermore, mycologists re-collect historic taxa and types to accomplish taxonomy and phylogeny in 19 phyla of fungi as *Aphelidiomycota*, *Ascomycota*, *Basidiobolomycota*, *Basidiomycota*, *Blastocladiomycota*, *Calcarisporiellomycota*,

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Chytridiomycota, *Entomophthoromycota*, *Entorrhizomycota*, *Glomeromycota*, *Kickxellomycota*, *Monoblepharomycota*, *Mortierellomycota*, *Mucoromycota*, *Neocallimastigomycota*, *Olpidiomycota*, *Rozellomycota*, *Sanchytriomycota*, and *Zoopagomycota* (Wijayawardene et al. 2024). Classification of the fungi has proven challenging due to the small number of known as compared to estimated species and a lack of sequence data for many extant taxa (Hyde et al. 2021). The wood-inhabiting fungi, a diverse group in terms of morphology, phylogeny, and ecology, are integral to the wood degradation and the matter cycle in the ecological system. They are considered the "key player" in wood decomposition, as they produce a variety of enzymes that break down woody lignin, cellulose, and hemicellulose, thereby playing a crucial role in the ecological system (Zhao et al. 2023).

Wood-inhabiting fungi are cosmopolitan and rich in diversity, growing in tropical, subtropical and temperate regions, exhibit diverse morphological features in their basidiomata (Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014, Dai et al. 2021, Zhao et al. 2023). The research analyses of species publication rates in the past twelve years and the species numbers in currently recognized families of *Basidiomycota* predicted more than 54,000 species in *Basidiomycota* described by 2030 (He et al. 2022). Basidiomata morphogenesis has been a subject of intense research; however, despite tremendous efforts in this area, the morphogenesis of *Basidiomycota* fruiting bodies needs to be better understood. How basidiomata complexity evolved has interested mycologists for decades and has received considerable attention recently (Nagy et al. 2023). Basidiomata morphologies show a great diversity in the *Basidiomycota*, from naked lawns of basidia, to smooth, poroid, irpicoid, grandinoid, odontioid, hydnoid, tuberculate, floccose, coralloid or highly complex, or the so called pileate-stipitate fruiting bodies of well-known agarics (Nagy et al. 2023). One of the grand challenges of mycology is to understand how the diversity of basidiomata has evolved (Virágh et al. 2022). The development of basidiomata is one of the most complex morphogenetic processes in fungi. A significant body of previous research has focused on understanding the underlying genetics and has made significant progress in cataloguing genes related to the initiation, morphogenesis, defence, and pigmentation of fruiting bodies, among others (Kües & Navarro-González 2015, Nagy et al. 2018, Virágh et al. 2022). Research on basidiomata has made tremendous progress in evolutionary and developmental biology fields, phylogenetic studies uncovered trends in how morphologies evolved, while developmental and genetic studies revealed some key genes underlying fruiting body development (Virágh et al. 2022). A recent study provided a catalogue of conserved fruiting body development genes based on a literature review and a meta-analysis of developmental transcriptomes of 12 mushroom-forming fungi (Nagy et al. 2023). However, available knowledge is still patchy and lacks key details in multiple aspects, such as conserved events in basidiomata morphogenesis and corresponding genes or causes and evolutionary trends of morphological differentiation of basidiomata (Nagy et al. 2023).

Fruiting bodies (sporocarps, sporophores or basidiomata) of fungi (*Agaricomycetes*) are among the most complex structures produced by fungi and they are sexual reproductive organs that facilitate spore dispersal, while in simple basidiomycota spores are born on naked basidia, mushroom-forming fungi evolved complex three-dimensional structures that offer tremendous advantages in spore dispersal efficiency (Nagy et al. 2023). Unlike the vegetative hyphae, fruiting bodies grow determinately and follow a genetically encoded developmental program that orchestrates their growth, tissue differentiation and sexual sporulation. Despite more than a century of research, our understanding of the molecular details of fruiting body morphogenesis is still limited and a general synthesis of the genetics of this complex process is lacking (Virágh et al. 2022, Nagy et al. 2023). Recent research on *Agaricomycete* fruiting body morphogenesis has largely relied on comparative-omics techniques, which provided insights into the gene repertoire and the regulation of gene expression during fruiting body development (Royse et al. 2017). An emerging driving force in the study of fruiting body morphogenesis was the mushroom industry, which used sexual fruiting bodies as food or as a source of bioactive compounds (Ma et al. 2018).

Previous studies on wood-inhabiting fungal molecular systematics showed that species within the same family or the same genus have different macroscopic characteristics but similar microscopic characteristics (Shi et al. 2019, Guan et al. 2021b, Guan & Zhao 2021, Zhao & Zhao 2021, Luo et al. 2022, Luo & Zhao 2022, Guan et al. 2023, Yang et al. 2023b, Luo et al. 2024).

The objectives of the present study are exploring more new fungal taxa in *Basidiomycota* and revealing the phylogenetic relationships of wood-inhabiting fungi. Herein we provide present morphological and molecular phylogenetic evidence that supports the thirteen new species and a new genus in their taxa, based on the multiple gene sequences.

MATERIALS AND METHODS

Morphological Studies

The collection process was thorough, resulting in the discovery of 19 specimens of *Kneiffiella*, *Merismodes*, *Peniophora*, *Punctulariopsis*, and *Sertulicium* in spring, 10 specimens of *Gloiothele*, *Gracilihypha*, *Hyphodontia*, *Hyphoderma*, and *Merismodes* in autumn, and four specimens of *Coniophoropsis*, *Gloeopeniophorella*, *Hyphoderma*, and *Peniophora* in winter. These findings, including 10 specimens in the rainy season and 23 in the dry season, provide a comprehensive understanding of the seasonal distribution of these species. They were dried in an electric food dehydrator at 40 °C (Hu et al. 2022), then sealed and stored in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. The samples were photographed in situ and fresh macroscopic details were recorded. Photographs were taken by a Jianeng 80D camera (Tokyo, Japan). All of the photos were focus stacked and merged using Helicon Focus software. Macromorphological descriptions are based on field notes and photos captured in the field and laboratory and follow the color terminology of Petersen (1996). Micromorphology was studied at magnifications 1000×, using a Nikon Eclipse 80i microscope with phase contrast illumination. The following abbreviations were used: KOH = 5% potassium hydroxide water solution, CB = Cotton Blue, CB– = acyanophilous, CB+ = cyanophilous, IKI = Melzer's reagent, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n=a/b (number of spores (a) measured from a given number (b) of specimens, in general the number of spores (a) are 30).

DNA Extraction, PCR and Sequencing

Genomic DNA was extracted from dried specimens using the EZNA HP Fungal DNA Kit (Omega Biotechnologies Co., Ltd., Kunming, China) according to the manufacturer's instructions. The ITS, nLSU, *tef*1-α, mt-SSU, *rpb1* and *rpb2* regions were amplified with the ITS5/ITS4 (White et al. 1990), LR0R/LR7 (Vilgalys & Hester 1990), EF1-983F/EF1-2218R (Rehner & Samuels 1994), MS1/MS2 (White et al. 1990), RPB1-Af/RPB1-Cf (Matheny et al. 2002) and bRPB2-6F/bRPB2-7.1R (Matheny 2005) primer pairs respectively. The polymerase chain reaction (PCR) procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. 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 *tef*1-α was as follows: (1) initial denaturation at 94 °C for 2.5 min, (2) denaturation at 94 °C for 45 s, (3) annealing at 60 °C for 50 s (minus 1 °C per cycle), (4) extension at 72 °C for 2 min, (5) repeat for 6 cycles starting at step 2, (6) denaturation at 94 °C for 30 s, (7) annealing at 55 °C for 50 s, (8) extension at 72 °C for 1.5 min, (9) repeat for 34 cycles starting at step 6, (10) leave at 72 °C for 5 min. The PCR procedure for mt-SSU was as follows: initial denaturation at 94 °C for 2 min, followed by 36 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 *rpb1* was as follows: (1) initial denaturation at 94 °C for 2 min, (2) denaturation at 94 °C for 40 s, (3) annealing at 60 °C for 40 s, (4) extension at 72 °C for 2 min, (5) repeat for 10 cycles starting at step 2, (6) denaturation at 94 °C for 45 s, (7) annealing at 55 °C for 1.5 min, (8) extension at 72 °C for 2 min, (9) repeat for 37 cycles starting at step 6, (10) leave at 72 °C for 10 min. The PCR procedure for *rpb2* was as follows: (1) initial denaturation at 95 °C for 2.5 min, (2) denaturation at 95 °C for 30 s, (3) annealing at 52 °C for 1 min, (4) extension at 72 °C for 1 min (add 1 °C per cycle), (5) repeat for 40 cycles starting at step 2, (6) extension at 72 °C for 1.5 min, (7) repeat for 40 cycles starting at step 6, (8) leave at 72 °C for 5 min. The PCR products were purified and directly sequenced with the genetic analyzer Applied Biosystems ABI 3730XL, and method of Sanger sequencing, Kunming Tsingke Biological Technology Limited Company, Yunnan Province, China. All newly generated sequences were deposited in GenBank (Table 1).

Phylogenetic Analyses

The DNA sequences were aligned in MAFFT version 7 using the G-INS-i strategy (Katoh et al. 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). Later, ITS, nLSU, mt-SSU, *rpb1*, *rpb2*, and *tef*1-α sequences were combined using Mesquite version 3.51. The initial BLAST search based on the DNA barcoding within the NCBI dataset was carried out, in which the type specimen or authoritative sequences were referred to (Dong et al. 2024).

Maximum parsimony (MP), Maximum likelihood (ML), and Bayesian inference (BI) analyses were applied to the combined datasets following the methods outlined in a previous study (Zhao & Wu 2017). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum parsimonious Tree generated in PAUP* version 4.0b10 (Swofford 2002). Sequences were also analyzed using Maximum likelihood (ML) with RAxML-HPC2 through the CIPRES Science Gateway (Miller et al. 2012). Branch support (BS) for ML analysis was determined by 1,000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian Inference (BI), which was calculated with MrBayes 3.2.7a with a general time reversible model of DNA substitution and a gamma distribution rate variation across sites (Ronquist et al. 2012). Two independent runs were employed each including four chains and starting from random trees. Trees were sampled every 1,000th generation, and the first one-fourth generations were discarded as burn-in, ensuring the average standard deviation of split frequencies had reached < 0.01 for all datasets. At the same time, the other 75% were retained for constructing a 50% majority consensus tree and calculating Bayesian posterior probabilities (BPP). A majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received Maximum likelihood bootstrap (BS) ≥ 75%, Maximum parsimony bootstrap (BT) ≥ 75%, or Bayesian posterior probabilities (BPP) ≥ 0.95.

TABLE 1 Names, samples numbers, references and corresponding GenBank accession numbers of the taxa used in this study.

Species Name	Sample No.	GenBank Accession No.						References
		ITS	nLSU	mt-SSU	*rpb1*	*rpb2*	*tef1-α*	
Acanthocorticium brueggemannii	JMB2122	KT275193	KT275195	–	–	–	–	Silva-Filho et al. (2023)
Amylostereum chailletii	NH8031	AF506406	AF506406	–	–	–	–	Xu et al. (2023)
Asterostroma laxum	EL33-99	AF506410	AF506410	–	–	–	–	Xu et al. (2023)
Asterostroma muscicola	KHL9537	AF506409	AF506409	–	–	–	–	Xu et al. (2023)
Auricularia cornea	LWZ 20190421-1	MT319406	MT319135	MT326526	–	–	–	Wang et al. (2021)
Baltazaria eurasiaticogalactina	CBS 666.84	–	AY293211	–	–	–	–	Xu et al. (2023)
Baltazaria octopodites	FLOR 56449	MH260025	MH260047	–	–	–	–	Xu et al. (2023)
Boidinia aculeata	Dai 16175	KY860398	KY860456	–	–	–	–	Zhao & Zhao (2023)
Boidinia aculeata	Wu 890714-52	AF506433	AF506433	–	–	–	–	Zhao & Zhao (2023)
Boidinia furfuracea	JS 16717	AF506376	AF506376	–	–	–	–	Zhao & Zhao (2023)
Bridgeoporus sinensis	Cui 10013	KY131832	KY131891	–	–	–	–	Wang et al. (2021)
Confertobasidium olivaceoalbum	FP90196	AF511648	AF511648	–	–	–	–	Xu et al. (2023)
Coniophora arida	FP-104367	GU187510	GU187573	–	–	–	–	Yang et al. (2023a)
Coniophora arida	He 4658	MG763875	MH476322	–	–	–	–	Yang et al. (2023a)
Coniophora beijingensis	He 6635	MW192496	–	–	–	–	–	Yang et al. (2023a)
Coniophora beijingensis	He 6920	MW192497	–	–	–	–	–	Yang et al. (2023a)
Coniophora cerebella	HK 8	GU187513	GU187569	–	–	–	–	Yang et al. (2023a)
Coniophora cystidiophora	CBS 153.33	MH855390	MH866840	–	–	–	–	Yang et al. (2023a)
Coniophora eremophila	MA-Fungi 86371	HG326617	–	–	–	–	–	Yang et al. (2023a)
Coniophora eremophila	MA-Fungi 86372	HG326618	–	–	–	–	–	Yang et al. (2023a)
Coniophora fusispora	MA-Fungi 57734	HF921467	–	–	–	–	–	Yang et al. (2023a)
Coniophora fusispora	He 6777	MW192495	–	–	–	–	–	Yang et al. (2023a)
Coniophora hanoiensis	He 5197	MG763873	–	–	–	–	–	Yang et al. (2023a)
Coniophora hanoiensis	He 5202	MG763874	MH476323	–	–	–	–	Yang et al. (2023a)
Coniophora marmorata	MUCL:31667	GU187515	GU187571	–	–	–	–	Yang et al. (2023a)
Coniophora marmorata	P 158	AJ518879	–	–	–	–	–	Yang et al. (2023a)
Coniophora merulioides	CBS 152.35	MH855612	–	–	–	–	–	Yang et al. (2023a)
Coniophora mollis	Prem 36877	HF921469	–	–	–	–	–	Yang et al. (2023a)
Coniophora olivacea	He 6100	OM100743	–	–	–	–	–	Yang et al. (2023a)
Coniophora olivacea	He 6111	OM100744	–	–	–	–	–	Yang et al. (2023a)
Coniophora opuntiae	AH 31855	FJ790314	–	–	–	–	–	Yang et al. (2023a)
Coniophora prasinoides	FP-105969	GU187519	GU187576	–	–	–	–	Yang et al. (2023a)
Coniophora puteana	MUCL1000	AM293076	–	–	–	–	–	Yang et al. (2023a)
Coniophora puteana	CBS 148.32	MH855248	–	–	–	–	–	Yang et al. (2023a)
Coniophora yunnanensis	CLZhao 3517	OP901836	OP904195	–	–	–	–	Yang et al. (2023a)
Coniophora yunnanensis	CLZhao 3594	OP901837	OP904196	–	–	–	–	Yang et al. (2023a)
Coniophoropsis bambusicola	He 5208	MG763877	MH476325	–	–	–	–	Yang et al. (2023a)
Coniophoropsis bambusicola	He 5210	MG763878	MH476326	–	–	–	–	Yang et al. (2023a)
Coniophoropsis sinensis	**CLZhao 17797**	**OR149909**	–	–	–	–	–	**Present study**
Coltricia perennis	Cui 10319	KU360687	KU360653	–	KX364848	KX364894	–	Wang et al. (2021)
Coltriciella dependens	Dai 10944	KY693737	KY693757	–	–	KY693908	–	Wang et al. (2021)

Species Name	Sample No.	GenBank Accession No.						References
		ITS	nLSU	mt-SSU	*rpb1*	*rpb2*	*tef1-α*	
Dentocorticium bicolor	He2772	MF626354	MF626378	–	–	–	–	Liu et al. (2018)
Dentocorticium bicolor	He2757	MF626355	MF626379	–	–	–	–	Liu et al. (2018)
Dentocorticium portoricense	He2202	MF626357	MF626381	–	–	–	–	Liu et al. (2018)
Dentocorticium portoricense	He2161	MF626356	MF626380	–	–	–	–	Liu et al. (2018)
Dentocorticium sulphurellum	DLL2011-016	KJ140542	–	–	–	–	–	Liu et al. (2018)
Dentocorticium sulphurellum	FP11801	JN165018	–	–	–	–	–	Liu et al. (2018)
Dentocorticium taiwanianum	He4615	MF626362	MF626386	–	–	–	–	Liu et al. (2018)
Dentocorticium taiwanianum	He3777	–	MF626388	–	–	–	–	Liu et al. (2018)
Dentocorticium ussuricum	CLZhao 16063	MW582752	–	–	–	–	–	Liu et al. (2018)
Dentocorticium ussuricum	He3278	MF626358	MF626382	–	–	–	–	Liu et al. (2018)
Dichostereum effuscatum	GG930915	AF506390	AF506390	–	–	–	–	Xu et al. (2023)
Dichostereum pallescens	NH7046/673	AF506392	AF506392	–	–	–	–	Xu et al. (2023)
Digitatispora marina	3027C	KM272371	KM272362	–	–	–	–	Silva-Filho et al. (2023)
Diplomitoporus crustulinus	FD-137	KP135299	KP135211	–	KP134883	–	–	Yang et al. (2023b)
Duportella kuehneri	CBS 721.91	MH862309	MH873982	–	–	–	–	Xu et al. (2023)
Duportella kuehneroides	CBS 732.91	MH862318	MH873990	–	–	–	–	Xu et al. (2023)
Duportella rhoica	CBS 943.96	MH862625	MH874246	–	–	–	–	Xu et al. (2023)
Entomocorticium belizense	18050	MZ098132	MZ098117	–	–	–	–	Xu et al. (2023)
Entomocorticium cobbii	B720	MT741707	MT741692	–	–	–	–	Xu et al. (2023)
Entomocorticium portiae	B1039	MT741710	MT741695	–	–	–	–	Xu et al. (2023)
Entomocorticium sullivanii	B1252	MT741715	MT741700	–	–	–	–	Xu et al. (2023)
Fasciodontia brasiliensis	MSKF 7245a	MK575201	MK598734	–	–	–	–	Wang et al. (2021)
Fasciodontia bugellensis	KAS-FD 10705a	MK575203	MK598735	–	–	–	–	Wang et al. (2021)
Fasciodontia yunnanensis	CLZhao 6280	MK811275	MZ146327	–	–	–	–	Wang et al. (2021)
Flagelloscypha austrofilicis	PDD 105591	KM975436	KM975368	–	–	–	–	Silva-Filho et al. (2023)
Flagelloscypha eruciformis	MH-2018-0187	MK434305	–	–	–	–	–	Silva-Filho et al. (2023)
Flagelloscypha eruciformis	MH-2018-0190	MK434306	–	–	–	–	–	Silva-Filho et al. (2023)
Flagelloscypha japonica	NBRC 101830	LC146734	AB455964	–	–	–	–	Silva-Filho et al. (2023)
Flagelloscypha minutissima	CBS 823.88	AY571040	AY571006	–	–	–	–	Silva-Filho et al. (2023)
Fulvoderma scaurum	LWZ 20170816-31	MT332135	MT319395	MT326509	–	–	–	Wang et al. (2021)
Gloeocystidiellum aspellum	LIN625	AF506432	AF506432	–	–	–	–	Zhao & Zhao (2023)
Gloeocystidiellum compactum	Wu 880615-21	AF506434	AF506434	–	–	–	–	Zhao & Zhao (2023)
Gloeocystidiellum formosanum	Wu 9404-19	AF506439	AF506439	–	–	–	–	Zhao & Zhao (2023)
Gloeocystidiellum porosum	EB990923	AY048881	AY048881	–	–	–	–	Zhao & Zhao (2023)
Gloeocystidiellum porosum	FP101749	AF310091	AF310091	–	–	–	–	Zhao & Zhao (2023)
Gloeopeniophorella bambusicola	**CLZhao 35561**	**PP819702**	–	–	–	–	–	**Present study**
Gloeopeniophorella convolvens	KHL10103	AF506435	AF506435	–	–	–	–	Zhao & Zhao (2023)
Gloeopeniophorella laxa	He4176	KY860413	KY860472	–	–	–	–	Zhao & Zhao (2023)
Gloeopeniophorella laxa	Wu 911010-8	AF506440	AF506440	–	–	–	–	Zhao & Zhao (2023)
Gloeopeniophorella sacrata	ICMP 10158	MZ325952	–	–	–	–	–	Zhao & Zhao (2023)
Gloeopeniophorella sacrata	PDD:121290	OR607674	–	–	–	–	–	Zhao & Zhao (2023)
Gloeophyllum abietinum	P254	–	AJ583431	–	–	–	–	Guan et al. (2021b)
Gloeophyllum sepiarium	FP 125002-T	–	AY333806	–	–	–	–	Guan et al. (2021b)

Species Name	Sample No.	GenBank Accession No.						References
		ITS	nLSU	mt-SSU	*rpb1*	*rpb2*	*tef1-α*	
Gloiothele citrina	LE-BIN 2968	OL840636	–	–	–	–	–	Unpublished
Gloiothele globosa	NLB 1109	MT536993	MT524528	–	–	–	–	Unpublished
Gloiothele lactescens	He 4321	KY860374	–	–	–	–	–	Unpublished
Gloiothele lactescens	He 3939	KY860373	–	–	–	–	–	Unpublished
Gloiothele lactescens	xc 2 1	OP803103	–	–	–	–	–	Unpublished
Gloiothele lamellosa	KHL11031	AF506454	AF506454	–	–	–	–	Lasson et al. (2003)
Gloiothele lamellosa	LR35533	AF506452	AF506452	–	–	–	–	Lasson et al. (2003)
Gloiothele lamellosa	CBS404.83	AF506487	AF506487	–	–	–	–	Lasson et al. (2003)
Gloiothele olearia	BIO-Fungi11969	MT240525	–	–	–	–	–	Unpublished
Gloiothele sp.	KUC11069	KJ713991	–	–	–	–	–	Unpublished
Gloiothele sp.	HAY-F-005141	OR859419	–	–	–	–	–	Unpublished
Gloiothele sp.	IN01	OM972318	–	–	–	–	–	Unpublished
Gloiothele torrendii	JB18615	AF506455	AF506455	–	–	–	–	Lasson et al. (2003)
Gloiothele yunnanensis	**CLZhao 17663**	**PP819703**	–	–	–	–	–	**Present study**
Gracilihypha abeliae	**CLZhao 21356**	**PP819704**	**PP826256**	–	–	**PP843025**	–	**Present study**
Gracilihypha abeliae	**CLZhao 21445**	**PP819705**	**PP826257**	–	–	**PP843026**	**PP843032**	**Present study**
Gracilihypha abeliae	**CLZhao 21485**	**PP819706**	**PP826258**	**PP824643**	**PP843021**	–	–	**Present study**
Gracilihypha abeliae	**CLZhao 21487**	**PP819707**	**PP826259**	–	–	–	**PP843033**	**Present study**
Gracilihypha abeliae	**CLZhao 21489**	**PP819708**	**PP826260**	–	–	**PP843027**	–	**Present study**
Gracilihypha abeliae	**CLZhao 21492**	**PP819709**	**PP826261**	–	–	–	**PP843034**	**Present study**
Gyrodontium sacchari	He 4157	MG763879	MH476327	–	–	–	–	Yang et al. (2023a)
Halocyphina villosa	IFO32088	AY571042	–	–	–	–	–	Silva-Filho et al. (2023)
Hastodontia halonata	Finn Oldervik	ON188810	ON188810	ON228482	–	–	–	Wang et al. (2021)
Hastodontia halonata	HHB-17058	MK575207	MK598738	–	–	–	–	Wang et al. (2021)
Hastodontia hastata	KHL 14646	MH638232	MH638232	–	–	–	–	Wang et al. (2021)
Hymenochaete rubiginosa	He 1049	JQ716407	JQ279667	–	–	–	–	Wang et al. (2021)
Hyphoderma amoenum	USO 286622	HE577030	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma asianum	**CLZhao 18091**	**OR141726**	**PP826262**	**PP824644**	**PP843022**	**PP843028**	–	**Present study**
Hyphoderma assimile	CBS:125852	MH863808	MH875272	–	–	–	–	Yang et al. (2023b)
Hyphoderma cremeoalbum	NH 11538 (GB)	DQ677492	DQ677492	–	–	–	–	Yang et al. (2023b)
Hyphoderma cremeoalbum	CLZhao 17007	OM985716	OM985753	OQ706819	–	–	–	Yang et al. (2023b)
Hyphoderma crystallinum	CLZhao 9338	MW917161	MW913414	–	–	–	–	Yang et al. (2023b)
Hyphoderma crystallinum	CLZhao 9374	MW917162	MW913415	–	–	–	–	Yang et al. (2023b)
Hyphoderma definitum	NH 12266 (GB)	DQ677493	DQ677493	–	–	–	–	Yang et al. (2023b)
Hyphoderma fissuratum	CLZhao 6731	MT791331	MT791335	OQ706806	–	–	–	Yang et al. (2023b)
Hyphoderma fissuratum	CLZhao 6726	MT791330	MT791334	OQ706805	–	–	–	Yang et al. (2023b)
Hyphoderma floccosum	CLZhao 17129	MW301683	MW293733	OQ706826	–	–	–	Yang et al. (2023b)
Hyphoderma floccosum	CLZhao 17215	MW301687	MW293735	OQ706829	–	–	–	Yang et al. (2023b)
Hyphoderma granuliferum	5273	JN710545	JN710545	JN710673	–	–	–	Yang et al. (2023b)
Hyphoderma incrustatum	KHL6685	–	AY586668	–	–	–	–	Yang et al. (2023b)
Hyphoderma litschaueri	NH 7603 (GB)	DQ677496	DQ677496	–	–	–	–	Yang et al. (2023b)
Hyphoderma litschaueri	FP-101740-Sp	KP135295	KP135219	–	KP134868	KP134965	–	Yang et al. (2023b)
Hyphoderma macaronesicum	MA:Fungi 90388	KC984327	–	–	–	KF181122	–	Yang et al. (2023b)

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		ITS	nLSU	mt-SSU	*rpb1*	*rpb2*	*tef1-α*	
Hyphoderma macaronesicum	TFC:Mic 15115	HE577011	–	–	–	KF181118	–	Yang et al. (2023b)
Hyphoderma marginatum	CLZhao 3404	OM985717	OM985754	–	–	–	–	Yang et al. (2023b)
Hyphoderma medioburiense	FD-335	KP135298	KP135220	–	KP134869	KP134966	–	Yang et al. (2023b)
Hyphoderma membranaceum	CLZhao 5844	MW917167	MW913420	OQ706797	–	–	–	Yang et al. (2023b)
Hyphoderma membranaceum	CLZhao 6971	MW917168	MW913421	OQ706807	–	–	–	Yang et al. (2023b)
Hyphoderma microporoides	CLZhao 6857	MW917169	MW913422	–	–	–	–	Yang et al. (2023b)
Hyphoderma microporoides	CLZhao 8695	MW917170	MW913423	–	–	–	–	Yang et al. (2023b)
Hyphoderma moniliforme	Wu 0211-42	KC928282	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma moniliforme	Wu 0211-46	KC928284	KC928285	–	–	–	–	Yang et al. (2023b)
Hyphoderma mopanshanense	CLZhao 6498	MT791329	MT791333	–	–	–	–	Yang et al. (2023b)
Hyphoderma mopanshanense	CLZhao 6449	OM985720	OM985759	OQ706803	–	–	–	Yang et al. (2023b)
Hyphoderma nemorale	TNM F3931	KJ885183	KJ885184	–	–	–	–	Yang et al. (2023b)
Hyphoderma nemorale	Wu 9508-14	KC928280	KC928281	–	–	–	–	Yang et al. (2023b)
Hyphoderma niveomarginatum	CLZhao 25078	OR141728	OR506179	–	–	OR543992	–	Yang et al. (2023b)
Hyphoderma nudicephalum	Wu9307_29	AJ534269	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma nudicephalum	CLZhao 17839	OM985721	OM985760	OQ706835	–	–	–	Yang et al. (2023b)
Hyphoderma obtusiforme	KHL1464	JN572909	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma obtusiforme	KHL11105	JN572910	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma obtusum	JS17804	–	AY586670	–	–	–	–	Yang et al. (2023b)
Hyphoderma occidentale	KHL 8477 (GB)	DQ677499	DQ677499	–	–	–	–	Yang et al. (2023b)
Hyphoderma paramacaronesicum	MA:Fungi 87736	KC984399	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma paramacaronesicum	MA:Fungi 87737	KC984405	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma pinicola	TNM F13637	KJ885181	KJ885182	–	–	–	–	Yang et al. (2023b)
Hyphoderma pinicola	Wu 0108-36	KC928278	KC928279	–	–	–	–	Yang et al. (2023b)
Hyphoderma prosopidis	ARIZ HHB 8479	HE577029	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma puerense	CLZhao 9476	MW443045	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma puerense	CLZhao 9583	MW443046	MW443051	–	–	–	–	Yang et al. (2023b)
Hyphoderma qujingense	**CLZhao 26018**	**OR141729**	**PP826263**	**PP824645**	**PP843023**	**PP843029**	–	**Present study**
Hyphoderma roseocremeum	NH10545	–	AY586672	–	–	–	–	Yang et al. (2023b)
Hyphoderma setigerum	FCUG 1200	AJ534273	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma setigerum	FCUG 1688	AJ534272	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma sinense	CLZhao 7963	MW301679	MW293730	–	–	–	–	Yang et al. (2023b)
Hyphoderma sinense	CLZhao 17811	MW301682	MW293732	–	–	–	–	Yang et al. (2023b)
Hyphoderma sordidum	CLZhao 27379	OR141731	–	OR507165	–	–	–	Yang et al. (2023b)
Hyphoderma sordidum	CLZhao 27390	OR141732	OR506180	OR507166	OR520149	–	–	Yang et al. (2023b)
Hyphoderma subtestaceum	CBS:125877	MH864081	MH875539	–	–	–	–	Yang et al. (2023b)
Hyphoderma subsetigerum	HHB11620	GQ409521	–	–	–	–	–	Yang et al. (2023b)
Hyphoderma tenuissimum	CLZhao 7221	MW443049	MW443054	OQ706809	–	–	–	Yang et al. (2023b)
Hyphoderma tenuissimum	CLZhao 16210	MW443050	MW443055	–	–	–	–	Yang et al. (2023b)
Hyphoderma transiens	NH 12304 (GB)	DQ677504	DQ677504	–	–	–	–	Yang et al. (2023b)
Hyphoderma tropicum	CLZhao 17308	OM985727	OM985768	–	–	–	–	Yang et al. (2023b)
Hyphoderma variolosum	CBS:734.91	MH862320	MH873992	–	–	–	–	Yang et al. (2023b)
Hyphoderma variolosum	CBS:735.91	MH862321	MH873993	–	–	–	–	Yang et al. (2023b)

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		ITS	nLSU	mt-SSU	*rpb1*	*rpb2*	*tef1-α*	
Hyphoderma weishanense	CLZhao 22403	OR141727	OR506181	–	–	–	–	Yang et al. (2023b)
Hyphoderma yunnanense	CLZhao 8845	OM985728	OM985769	OQ706811	–	–	–	Yang et al. (2023b)
Hyphodontia alutaria	KHL 11889	DQ873603	DQ873603	–	–	–	–	Wang et al. (2021)
Hyphodontia alutaria	KHL 11978	EU118631	EU118631	–	–	–	–	Wang et al. (2021)
Hyphodontia arguta	FR-0219450	KR349242	–	–	–	–	–	Wang et al. (2021)
Hyphodontia arguta	FR-0219451	KR349243	–	–	–	–	–	Wang et al. (2021)
Hyphodontia borbonica	FR-0219441	KR349240	–	–	–	–	–	Wang et al. (2021)
Hyphodontia borbonica	FR-0219444	KR349241	–	–	–	–	–	Wang et al. (2021)
Hyphodontia daweishanensis	**CLZhao 18444**	**PP819710**	**PP826264**	–	–	**PP843030**	–	**Present study**
Hyphodontia daweishanensis	**CLZhao 18536**	**PP819711**	**PP826265**	–	–	–	–	**Present study**
Hyphodontia pachyspora	LWZ 20170908-5	MT319426	MT319160	MT326431	MT326350	MT326261	–	Wang et al. (2021)
Hyphodontia pachyspora	LWZ 20180905-6	MT319425	MT319159	MT326430	–	–	–	Wang et al. (2021)
Hyphodontia pallidula	Kotiranta 18839	OP620785	OP620785	OP620779	–	–	–	Wang et al. (2021)
Hyphodontia pallidula	He 6087	OM100749	OM083983	–	–	–	–	Wang et al. (2021)
Hyphodontia setulosa	HHB-6891-Sp	KP135382	KP135267	–	KP134864	KP134901	–	Wang et al. (2021)
Hyphodontia setulosa	P170	MT821164	–	–	–	–	–	Wang et al. (2021)
Hyphodontia subdetritica	FR-0261085	KY081793	–	–	–	–	–	Wang et al. (2021)
Hyphodontia subdetritica	FR-0261087	KY081794	–	–	–	–	–	Wang et al. (2021)
Hyphodontia wongiae	LWZ 20180414-16	MT319414	MT319146	–	–	–	–	Wang et al. (2021)
Hyphodontia wongiae	LWZ 20180417-16	MT319416	MT319147	–	–	–	–	Wang et al. (2021)
Hyphodontia zhixiangii	LWZ 20160909-4	KY440396	MT319154	MT326426	–	–	–	Wang et al. (2021)
Hyphodontia zhixiangii	LWZ 20160909-8	KY440397	MT319155	MT326427	–	–	–	Wang et al. (2021)
Inonotus hispidus	LWZ 20180703-1	MT332137	MT319383	MT326506	–	–	–	Wang et al. (2021)
Kneiffiella abdita	Dai 15045	MW209700	–	MW221940	–	–	–	Wang et al. (2021)
Kneiffiella abdita	Miettinen 22165	ON188809	ON188809	ON228493	–	–	–	Wang et al. (2021)
Kneiffiella abieticola	GEL 2924	DQ340331	–	–	–	–	–	Wang et al. (2021)
Kneiffiella abieticola	KHL 12498	DQ873601	DQ873601	–	–	–	–	Wang et al. (2021)
Kneiffiella alienata	CBS 127219	MH864327	MH875772	–	–	–	–	Wang et al. (2021)
Kneiffiella alienata	EL 14-98	AY466401	AY586727	–	–	–	–	Wang et al. (2021)
Kneiffiella altaica	PRM 956489	OM971676	OM971690	–	–	–	–	Wang et al. (2021)
Kneiffiella altaica	PRM 956491	OM971678	OM971692	–	–	–	–	Wang et al. (2021)
Kneiffiella alutacea	GEL 2284	DQ340340	–	–	–	–	–	Wang et al. (2021)
Kneiffiella alutacea	GEL 2937	DQ340338	–	–	–	–	–	Wang et al. (2021)
Kneiffiella barba-jovis	KHL 11730	DQ873609	DQ873610	–	–	–	–	Wang et al. (2021)
Kneiffiella cineracea	GEL 4875	DQ340335	–	–	–	–	–	Wang et al. (2021)
Kneiffiella cineracea	GEL 4958	DQ340336	–	–	–	–	–	Wang et al. (2021)
Kneiffiella curvispora	KHL 1591	DQ873615	DQ873616	–	–	–	–	Wang et al. (2021)
Kneiffiella curvispora	Pennanen 4040	OP620787	OP620787	OP620781	–	–	–	Wang et al. (2021)
Kneiffiella decorticans	SP 415980	KY081795	–	–	–	–	–	Wang et al. (2021)
Kneiffiella efibulata	GB-0151167	KY081796	–	–	–	–	–	Wang et al. (2021)
Kneiffiella eucalypticola	LWZ 20180509-11	MT319410	MT319142	MT326421	–	–	–	Wang et al. (2021)
Kneiffiella eucalypticola	LWZ 20180512-7	MT319409	MT319141	MT326420	–	–	–	Wang et al. (2021)
Kneiffiella floccosa	Berglund 150-02	DQ873618	DQ873618	–	–	–	–	Wang et al. (2021)

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		ITS	nLSU	mt-SSU	*rpb1*	*rpb2*	*tef1-α*	
Kneiffiella floccosa	UC2022896	KP814440	–	–	–	–	–	Wang et al. (2021)
Kneiffiella microspora	Hjortstam 18578	KY081792	–	–	–	–	–	Wang et al. (2021)
Kneiffiella palmae	DI21-18	OK353607	–	–	–	–	–	Wang et al. (2021)
Kneiffiella pilaecystidiata	Cui 13239	KY290984	–	–	–	–	–	Wang et al. (2021)
Kneiffiella pilaecystidiata	MSK-F 4723	MK575208	MK598739	–	–	–	–	Wang et al. (2021)
Kneiffiella pseudoabdita	LWZ 20210624-6b	OQ540894	OQ540852	–	–	–	–	Wang et al. (2021)
Kneiffiella pseudoalutacea	LWZ 20210625-5b	OQ540895	OQ540853	–	–	–	–	Wang et al. (2021)
Kneiffiella qujingensis	**CLZhao 27466**	**OR149910**	**PP826266**	**PP824646**	–	–	–	**Present study**
Kneiffiella stereicola	Blackwell 2141	KY081797	–	–	–	–	–	Wang et al. (2021)
Kneiffiella subaltaica	HHB-20039	OM971679	OM971693	–	–	–	–	Wang et al. (2021)
Kneiffiella subalutacea	GEL 2142	DQ340334	–	–	–	–	–	Wang et al. (2021)
Kneiffiella subalutacea	GEL 2196	DQ340341	–	–	–	–	–	Wang et al. (2021)
Kneiffiella subefibulata	Dai 10526	KT989970	–	–	–	–	–	Wang et al. (2021)
Kneiffiella subefibulata	Dai 10803	KT989971	–	–	–	–	–	Wang et al. (2021)
Kneiffiella subglobosa	LWZ 20180416-6	MT319413	MT319145	MT326422	–	–	–	Wang et al. (2021)
Lachnella alboviolascens	PB332	AY571048	AY571012	–	–	–	–	Silva-Filho et al. (2023)
Lachnella alboviolascens	Wu724	OR990018	–	–	–	–	–	Silva-Filho et al. (2023)
Lachnella tiliae	G0887	–	MK277903	–	–	–	–	Silva-Filho et al. (2023)
Lachnella villosa	PB321	AY571049	AY571013	–	–	–	–	Silva-Filho et al. (2023)
Lachnella villosa	PB322	AY571050	AY571014	–	–	–	–	Silva-Filho et al. (2023)
Lachnocladium schweinfurthianum	KM 49740	MH260033	MH260051	–	–	–	–	Xu et al. (2023)
Lachnocladium sp.	KHL10556	AF506461	AF506461	–	–	–	–	Xu et al. (2023)
Lactarius leonis	SJ 91016	AF506411	AF506411	–	–	–	–	Zhao & Zhao (2023)
Lactarius torminosus	CBS 197.72	MH860447	MH872175	–	–	–	–	Zhao & Zhao (2023)
Lactifluus taibaiensis	HKAS 122860	OL423562	OL423575	–	–	–	–	Zhao & Zhao (2023)
Lactifluus volemus	LE 254509	JQ753937	JQ348388	–	–	–	–	Zhao & Zhao (2023)
Licrostroma subgiganteum	MG230	KX358901	KX358903	–	–	–	–	Xu et al. (2023)
Licrostroma subgiganteum	MG231	KX358902	KX358904	–	–	–	–	Xu et al. (2023)
Lyomyces albopulverulentus	CLZhao 21478	OP730712	OP730724	–	–	–	–	Guan et al. (2023)
Lyomyces bambusinus	CLZhao 4831	MN945968	MW264919	–	–	–	–	Guan et al. (2023)
Lyomyces sambuci	KASJR 7	KY800402	KY795966	–	–	–	–	Guan et al. (2023)
Lyomyces yunnanensis	CLZhao 2463	OP730711	OP730723	–	–	–	–	Guan et al. (2023)
Maireina filipendula	TL14226	KX772745	KX772745	–	–	–	–	Silva-Filho et al. (2023)
Maireina filipendula	TL2015-724890	KX772746	KX772746	–	–	–	–	Silva-Filho et al. (2023)
Maireina monacha	AM2106285	OP099548	OR197581	–	–	–	–	Silva-Filho et al. (2023)
Maireina subsphaerospora	AM2012151	OR234754	OR197582	–	–	–	–	Silva-Filho et al. (2023)
Maireina subsphaerospora	AM2004282	OP099549	OR234751	–	–	–	–	Silva-Filho et al. (2023)
Mensularia radiata	Yuan 6589	MT332140	–	–	–	–	–	Wang et al. (2021)
Merismodes anomala	PB318	AY571035	AY570998	–	–	–	–	Silva-Filho et al. (2023)
Merismodes anomala	PB323	AY571036	AY570999	–	–	–	–	Silva-Filho et al. (2023)
Merismodes fasciculata	HHB-11894	AY571051	AY571015	–	–	–	–	Silva-Filho et al. (2023)
Merismodes fasciculata	PB342	AY571052	AY571016	–	–	–	–	Silva-Filho et al. (2023)
Merismodes wumengshanensis	**CLZhao 33643**	**PP819712**	**PP826267**	–	–	–	–	**Present study**

Species Name	Sample No.	GenBank Accession No.						References
		ITS	nLSU	mt-SSU	*rpb1*	*rpb2*	*tef1-α*	
Merismodes yunnanensis	**CLZhao 27351**	**OR149911**	**PP826268**	**PP824647**	**PP843024**	**PP843031**	**PP843035**	**Present study**
Merismodes yunnanensis	**CLZhao 32261**	**PP819713**	**PP826269**	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33037**	**PP819714**	–	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33444**	**PP819715**	**PP826270**	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33497**	**PP819716**	**PP826271**	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33554**	**PP819717**	–	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33612**	**PP819718**	**PP826272**	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33618**	**PP819719**	–	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33629**	**PP819720**	**PP826273**	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33660**	**PP819721**	**PP826274**	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33711**	**PP819722**	–	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33719**	**PP819723**	**PP826275**	–	–	–	–	**Present study**
Merismodes yunnanensis	**CLZhao 33722**	**PP819724**	–	–	–	–	–	**Present study**
Metulodontia nivea	NH13108/2712	AF506423	AF506423	–	–	–	–	Lasson et al. (2003)
Multifurca ochricompacta	JJ2010.08	MH063879	MH063844	–	–	–	–	Zhao & Zhao (2023)
Multifurca orientalis	XHW3034	MH063856	MH063825	–	–	–	–	Zhao & Zhao (2023)
Multifurca pseudofurcata	XHW3205	MH063849	MH063819	–	–	–	–	Zhao & Zhao (2023)
Neoantrodiella gypsea	Cui 10372	KT203290	MT319396	MT326567	–	–	–	Wang et al. (2021)
Neoantrodiella thujae	Dai 5065	KT203293	MT319397	MT326568	–	–	–	Wang et al. (2021)
Nia furcatipilosa	AH20191108-1	LC769762	LC769818	–	–	–	–	Nakagiri et al. (2024)
Nia furcatipilosa	AH20190926-1	LC769760	LC769816	–	–	–	–	Nakagiri et al. (2024)
Nia furcatipilosa	AN-1850	LC769753	LC769809	–	–	–	–	Nakagiri et al. (2024)
Nia lenicarpa	CBS-H-23851	OQ555325	MK491336	–	–	–	–	Nakagiri et al. (2024)
Nia singaporensis	AN-1023	LC769779	–	–	–	–	–	Nakagiri et al. (2024)
Nia singaporensis	AN-1026	LC769780	LC769835	–	–	–	–	Nakagiri et al. (2024)
Nia sphaerocystis	AN-1851	LC769799	LC769854	–	–	–	–	Nakagiri et al. (2024)
Nia sphaerocystis	AH20191004-1	LC769802	LC769857	–	–	–	–	Nakagiri et al. (2024)
Nia vibrissa	AN-1825	LC769781	LC769836	–	–	–	–	Nakagiri et al. (2024)
Nia vibrissa	AH20190527-3	LC769783	LC769838	–	–	–	–	Nakagiri et al. (2024)
Nigrofomes melanoporus	JV 1704/39	MF629835	MF629831	–	–	–	–	Wang et al. (2021)
Nigrofomes sinomelanoporus	Cui 5277	MF629836	MT319398	–	–	–	–	Wang et al. (2021)
Onnia tomentosa	Cui 10048	MT332141	MT319387	MT326561	–	–	–	Wang et al. (2021)
Oxyporus corticola	Dai 12632	KF111018	KF111020	KT203334	–	–	–	Wang et al. (2021)
Oxyporus cuneatus	Dai 7339	KT203294	KT203315	KT203335	–	–	–	Wang et al. (2021)
Oxyporus piceicola	Dai 5033	KT203301	KT203322	KT203341	–	–	–	Wang et al. (2021)
Peniophora albobadia	CBS 329.66	MH858809	MH870448	–	–	–	–	Vu et al. (2019)
Peniophora albobadia	He2159	MK588755	MK588795	–	–	–	–	Xu et al. (2023)
Peniophora aurantiaca	UBCF:19732	HQ604854	HQ604854	–	–	–	–	Xu et al. (2023)
Peniophora aurantiaca	CBS 396.50	MH856678	MH868195	–	–	–	–	Vu et al. (2019)
Peniophora bicornis	He3609	MK588763	MK588803	–	–	–	–	Xu et al. (2023)
Peniophora bicornis	He4767	MK588764	MK588804	–	–	–	–	Xu et al. (2023)
Peniophora borbonica	He4606	MK588765	MK588805	–	–	–	–	Xu et al. (2023)
Peniophora borbonica	He4597	MK588766	MK588806	–	–	–	–	Xu et al. (2023)

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		ITS	nLSU	mt-SSU	*rpb1*	*rpb2*	*tef1-α*	
Peniophora cinerea	CBS 261.37	MH855905	MH867412	–	–	–	–	Vu et al. (2019)
Peniophora cinerea	He3725	MK588769	MK588809	–	–	–	–	Xu et al. (2023)
Peniophora crassitunicata	CBS663.91	MH862292	MH873972	–	–	–	–	Vu et al. (2019)
Peniophora crassitunicata	He3814	MK588770	MK588810	–	–	–	–	Xu et al. (2023)
Peniophora cremicolor	He5385	MK588791	MK588831	–	–	–	–	Xu et al. (2023)
Peniophora crustosa	CBS 125882	MH864084	MH875542	–	–	–	–	Vu et al. (2019)
Peniophora duplex	B1022	MN475153	MN475820	–	–	–	–	Zou et al. (2022)
Peniophora duplex	CBS286.58	MH857787	MH869321	–	–	–	–	Vu et al. (2019)
Peniophora erikssonii	CBS287.58	MH857788	MH869322	–	–	–	–	Vu et al. (2019)
Peniophora erikssonii	Cui11871	MK588771	MK588811	–	–	–	–	Xu et al. (2023)
Peniophora exima	B 1011	MN475155	MN475821	–	–	–	–	Zou et al. (2022)
Peniophora exima	T 523	MK588772	MK588812	–	–	–	–	Zou et al. (2022)
Peniophora fasticata	CBS 942.96	MH862624	–	–	–	–	–	Vu et al. (2019)
Peniophora fissilis	CBS 681.91	MH862298	MH873975	–	–	–	–	Vu et al. (2019)
Peniophora fissilis	CBS 684.91	MH862299	MH873976	–	–	–	–	Vu et al. (2019)
Peniophora fissurata	**CLZhao 25689**	**PP819725**	**PP826276**	–	–	–	–	**Present study**
Peniophora fissurata	**CLZhao 27436**	**OR149912**	**PP826277**	–	–	–	–	**Present study**
Peniophora gabonensis	CBS 673.91	MH862293	–	–	–	–	–	Vu et al. (2019)
Peniophora gilbertsonii	CBS 357.95	MH862528	MH874164	–	–	–	–	Vu et al. (2019)
Peniophora gilbertsonii	CBS 360.95	MH862530	MH874165	–	–	–	–	Vu et al. (2019)
Peniophora guadelupensis	CBS 715.91	MH862304	MH873977	–	–	–	–	Vu et al. (2019)
Peniophora halimi	CBS 863.84	MH861844	MH873532	–	–	–	–	Vu et al. (2019)
Peniophora halimi	CBS 864.84	MH861845	MH873533	–	–	–	–	Vu et al. (2019)
Peniophora incarnata	CBS 430.72	MH860518	MH872230	–	–	–	–	Vu et al. (2019)
Peniophora incarnata	NH10271	AF506425	AF506425	–	–	–	–	Lasson et al. (2003)
Peniophora junipericola	CBS 349.54	MH857354	–	–	–	–	–	Vu et al. (2019)
Peniophora junipericola	He2462	MK588773	MK588813	–	–	–	–	Xu et al. (2023)
Peniophora laeta	CBS 255.56	MH857616	MH869164	–	–	–	–	Vu et al. (2019)
Peniophora laeta	CBS 256.56	MH857617	MH869165	–	–	–	–	Vu et al. (2019)
Peniophora lassa	Dai 17081A	MK588759	MK588799	–	–	–	–	Xu et al. (2023)
Peniophora lassa	He3052	MK588758	MK588798	–	–	–	–	Xu et al. (2023)
Peniophora laurentii	CBS 325.73	–	MH872397	–	–	–	–	Vu et al. (2019)
Peniophora laxitexta	BAFC 3309	FJ882040	–	–	–	–	–	Xu et al. (2023)
Peniophora laxitexta	LGMF1159	JX559580	–	–	–	–	–	Xu et al. (2023)
Peniophora lilacea	CBS 337.66	MH858813	MH870452	–	–	–	–	Vu et al. (2019)
Peniophora limitata	olrim963	AY787678	–	–	–	–	–	Xu et al. (2023)
Peniophora lycii	Boid-437	MK588774	MK588814	–	–	–	–	Vu et al. (2019)
Peniophora lycii	CBS 264.56	MH857624	MH869169	–	–	–	–	Xu et al. (2023)
Peniophora major	He5528	MK588792	MK588832	–	–	–	–	Xu et al. (2023)
Peniophora malaiensis	CBS 679.91	MH862297	MH873974	–	–	–	–	Vu et al. (2019)
Peniophora manshurica	He2956	MK588776	MK588816	–	–	–	–	Xu et al. (2023)
Peniophora manshurica	He3729	MK588777	MK588817	–	–	–	–	Xu et al. (2023)
Peniophora meridionalis	CBS 289.58	MH857789	MH869323	–	–	–	–	Vu et al. (2019)

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Peniophora molesta	CBS 676.91	MH862294	MH873973	–	–	–	–	Vu et al. (2019)
Peniophora molesta	CBS 677.91	MH862295	–	–	–	–	–	Vu et al. (2019)
Peniophora monticola	CBS 649.91	MH862289	MH873970	–	–	–	–	Vu et al. (2019)
Peniophora nuda	He5280	MK588778	MK588818	–	–	–	–	Xu et al. (2023)
Peniophora nuda	HHB-4916-Sp	MK588779	MK588819	–	–	–	–	Xu et al. (2023)
Peniophora ovalispora	CBS 653.91	MH862290	MH873971	–	–	–	–	Vu et al. (2019)
Peniophora parvocystidiata	CBS 716.91	MH862305	MH873978	–	–	–	–	Vu et al. (2019)
Peniophora parvocystidiata	CBS 717.91	MH862306	MH873979	–	–	–	–	Vu et al. (2019)
Peniophora piceae	olrim10	AY781264	–	–	–	–	–	Xu et al. (2023)
Peniophora piceae	209	JX507718	–	–	–	–	–	Xu et al. (2023)
Peniophora pilatiana	CBS 265.56	MH857625	MH869170	–	–	–	–	Vu et al. (2019)
Peniophora pilatiana	CBS-A1/A2	MK588780	MK588820	–	–	–	–	Xu et al. (2023)
Peniophora pini	Hjm 18143	EU118651	EU118651	–	–	–	–	Zou et al. (2022)
Peniophora pini	CBS 274.56	MH857632	MH869177	–	–	–	–	Vu et al. (2019)
Peniophora pithya	CBS 277.56	MH857635	MH869180	–	–	–	–	Vu et al. (2019)
Peniophora pithya	He3107	MK588781	MK588821	–	–	–	–	Xu et al. (2023)
Peniophora polygonia	CBS 404.50	MH856684	MH868201	–	–	–	–	Vu et al. (2019)
Peniophora polygonia	He4651	MK588782	MK588822	–	–	–	–	Xu et al. (2023)
Peniophora proxima	CBS 405.50	MH856685	MH868202	–	–	–	–	Vu et al. (2019)
Peniophora proxima	He5498	MK588783	MK588823	–	–	–	–	Xu et al. (2023)
Peniophora pseudonuda	FCUG 2384	GU322866	–	–	–	–	–	Zou et al. (2022)
Peniophora pseudonuda	FCUG 2390	GU322865	–	–	–	–	–	Zou et al. (2022)
Peniophora pseudopini	DAOM-30124-Sp	MK588784	MK588824	–	–	–	–	Xu et al. (2023)
Peniophora pseudoversicolor	CBS 338.66	MH858814	MH870453	–	–	–	–	Vu et al. (2019)
Peniophora pseudoversicolor	He5132	MK588785	MK588825	–	–	–	–	Xu et al. (2023)
Peniophora quercina	CBS 407.50	MH856687	MH868204	–	–	–	–	Vu et al. (2019)
Peniophora quercina	CBS:410.50	MH856688	MH868205	–	–	–	–	Vu et al. (2019)
Peniophora reidii	CBS 397.83	MH861616	MH873334	–	–	–	–	Vu et al. (2019)
Peniophora rhoica	CBS 943.96	MH862625	MH874246	–	–	–	–	Vu et al. (2019)
Peniophora roseoalba	CLZhao 3513	ON786559	OP380690	–	–	–	–	Zou et al. (2022)
Peniophora roseoalba	CLZhao 9401	ON786560	–	–	–	–	–	Zou et al. (2022)
Peniophora rufa	CBS 351.59	MH857891	MH869432	–	–	–	–	Vu et al. (2019)
Peniophora rufa	He2788	MK588786	MK588826	–	–	–	–	Xu et al. (2023)
Peniophora rufomarginata	CBS 281.56	MH857639	MH869183	–	–	–	–	Vu et al. (2019)
Peniophora rufomarginata	CBS 282.56	MH857640	MH869184	–	–	–	–	Vu et al. (2019)
Peniophora septentrionalis	CBS 294.58	MH857791	MH869325	–	–	–	–	Vu et al. (2019)
Peniophora shenghuae	He3507	MK588788	MK588828	–	–	–	–	Xu et al. (2023)
Peniophora shenghuae	He3535	MK588789	MK588829	–	–	–	–	Xu et al. (2023)
Peniophora simulans	CBS 874.84	MH861849	MH873537	–	–	–	–	Vu et al. (2019)
Peniophora sordida	CBS 875.84	MH861850	MH873538	–	–	–	–	Vu et al. (2019)
Peniophora sphaerocystidiata	HHB-8827-Sp	MK588787	MK588827	–	–	–	–	Xu et al. (2023)
Peniophora subsalmonea	CBS 696.91	MH862302	–	–	–	–	–	Vu et al. (2019)
Peniophora subsalmonea	CBS 697.91	MH862303	–	–	–	–	–	Vu et al. (2019)

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Peniophora taiwanensis	He4870	MK588775	MK588815	–	–	–	–	Xu et al. (2023)
Peniophora taiwanensis	Wu 9206-28	MK588793	MK588833	–	–	–	–	Xu et al. (2023)
Peniophora tamaricicola	CBS 438.62	MH858203	MH869802	–	–	–	–	Vu et al. (2019)
Peniophora tamaricicola	CBS 439.62	MH858204	MH869803	–	–	–	–	Vu et al. (2019)
Peniophora trigonosperma	CBS 402.83	MH861618	MH873335	–	–	–	–	Vu et al. (2019)
Peniophora trigonosperma	He3602	MK588762	MK588802	–	–	–	–	Xu et al. (2023)
Peniophora versicolor	CBS 358.61	MH858082	MH869651	–	–	–	–	Vu et al. (2019)
Peniophora versiformis	CBS 358.54	MH857360	MH868902	–	–	–	–	Vu et al. (2019)
Peniophora versiformis	He3029	MK588756	MK588796	–	–	–	–	Xu et al. (2023)
Peniophora vietnamensis	He5242	MK588760	MK588800	–	–	–	–	Xu et al. (2023)
Peniophora vietnamensis	He5252	MK588761	MK588801	–	–	–	–	Xu et al. (2023)
Peniophora violaceolivida	CBS 348.52	MH857077	MH868613	–	–	–	–	Vu et al. (2019)
Peniophora yunnanensis	CLZhao 3978	OP380617	OP380689	–	–	–	–	Zou et al. (2022)
Peniophora yunnanensis	CLZhao 7347	OP380616	–	–	–	–	–	Zou et al. (2022)
Peyronelina glomerulata	NBRC 32867	–	AB455963	–	–	–	–	Silva-Filho et al. (2023)
Peyronelina glomerulata	NBRC 104522	–	AB455961	–	–	–	–	Silva-Filho et al. (2023)
Phellinus piceicola	Cui 10440	JQ828908	MT319389	MT326563	–	–	–	Wang et al. (2021)
Polyporus squamosus	Cui 10595	KU189778	KU189809	KU189960	–	KU189988	KU189925	Liu et al. (2022)
Porodaedalea pini	Dai 7624	MT332142	MT319391	MT326565	–	–	–	Wang et al. (2021)
Pseudoxenasma verrucisporum	EL34-95	AF506426	AF506426	–	–	–	–	Zhao & Zhao (2023)
Punctularia bambusicola	CLZhao 4133	MW559982	MW559984	–	–	–	–	Guan et al. (2021b)
Punctularia strigosozonata	CBS 345.34	MH855559	MH867064	–	–	–	–	Guan et al. (2021b)
Punctularia strigosozonata	BHI-F586b	MH558554	–	–	–	–	–	Guan et al. (2021b)
Punctularia subhepatica	He 5695	MW507075	MW507015	–	–	–	–	Guan et al. (2021b)
Punctularia subhepatica	He 4436	MW507074	MW507014	–	–	–	–	Guan et al. (2021b)
Punctulariopsis asiana	**CLZhao 27375**	**PP819726**	–	–	–	–	–	**Present study**
Punctulariopsis asiana	**CLZhao 27479**	**PP819727**	–	–	–	–	–	**Present study**
Punctulariopsis cremeoalbida	Burdsall 9616	KR494275	–	–	–	–	–	Ariyawansa et al. (2015)
Punctulariopsis efibulata	Burdsall 8824	KR494276	–	–	–	–	–	Ariyawansa et al. (2015)
Punctulariopsis efibulata	He 2027	MW507077	–	–	–	–	–	Ariyawansa et al. (2015)
Punctulariopsis obducens	MG70	HM046918	–	–	–	–	–	Ariyawansa et al. (2015)
Punctulariopsis subglobispora	GB: Hallenberg 12761	NR_119827	–	–	–	–	–	Ariyawansa et al. (2015)
Punctulariopsis subglobispora	FCUG 2535	HM046917	HM046932	–	–	–	–	Ariyawansa et al. (2015)
Punctulariopsis yunnanensis	CLZhao 21443	PP425905	PP572972	–	–	–	–	Muhammad et al. (2024)
Punctulariopsis yunnanensis	CLZhao 21561	PP425906	PP572970	–	–	–	–	Muhammad et al. (2024)
Russula aurantiaca	SJ93006	AF506427	AF506427	–	–	–	–	Zhao & Zhao (2023)
Russula emetica	517IS76	AY061673	AY061673	–	–	–	–	Zhao & Zhao (2023)
Russula nauseosa	SJ97015	AF506462	AF506462	–	–	–	–	Zhao & Zhao (2023)
Russula persicina	SJ98044	AF506463	AF506463	–	–	–	–	Zhao & Zhao (2023)
Scytinostroma acystidiatum	Dai 24608	OQ689127	OQ629351	–	–	–	–	Zhang et al. (2023)
Scytinostroma renisporum	CBS 770.86	MH862050	MH873737	–	–	–	–	Zhang et al. (2023)
Sertulicium chilense	19610Tell	HG315521	–	–	–	–	–	Liu et al. (2022)
Sertulicium granuliferum	LE314054	MT002315	MT002342	–	–	–	–	Liu et al. (2022)

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Sertulicium granuliferum	LE314056	MT002316	MT002343	–	–	–	–	Liu et al. (2022)
Sertulicium jacksonii	Miettinen 17141	MN987944	–	–	–	–	–	Liu et al. (2022)
Sertulicium jacksonii	Svantesson 699	MN937562	MN937562	–	–	–	–	Liu et al. (2022)
Sertulicium lateclavigerum	LY 13467	MG913225	–	–	–	–	–	Liu et al. (2022)
Sertulicium lateclavigerum	Spirin 13457	MW049161	–	–	–	–	–	Liu et al. (2022)
Sertulicium limonadense	He 6276	OK298489	OK298947	–	–	–	–	Liu et al. (2022)
Sertulicium limonadense	GUY13-092	MT180982	MT180979	–	–	–	–	Liu et al. (2022)
Sertulicium niveocremeum	Larsson 13727	MN937563	MN937563	–	–	–	–	Liu et al. (2022)
Sertulicium vernale	Söderholm 3886	MT002311	MT664174	–	–	–	–	Liu et al. (2022)
Sertulicium yunnanense	**CLZhao 27295**	**PP819728**	–	–	–	–	–	**Present study**
Sistotrema muscicola	KHL 8791	AF506474	AF506474	–	–	–	–	Zhao & Zhao (2023)
Sistotremastrum aculeatum	Miettinen 10380.1	MN991176	MW045423	–	–	–	–	Liu et al. (2022)
Sistotremastrum aculeatum	Miettinen 13799.1	MN988623	–	–	–	–	–	Liu et al. (2022)
Sistotremastrum aculeicrepitans	GG MAR15-010	MG913218	MG913207	–	–	–	–	Liu et al. (2022)
Sistotremastrum aculeicrepitans	KHL16097	MN937564	MN937564	–	–	–	–	Liu et al. (2022)
Sistotremastrum confusum	KHL160004	MN937567	MN937567	–	–	–	–	Liu et al. (2022)
Sistotremastrum confusum	KHL16023	MN937566	–	–	–	–	–	Liu et al. (2022)
Sistotremastrum denticulatum	MV894	MN954694	MW045424	–	–	–	–	Liu et al. (2022)
Sistotremastrum fibrillosum	GG GUY12-180	MG913222	MG913208	–	–	–	–	Liu et al. (2022)
Sistotremastrum fibrillosum	GG GUY12-191	MG913223	MG913209	–	–	–	–	Liu et al. (2022)
Sistotremastrum geminum	Miettinen 14333	MN991177	MN991177	–	–	–	–	Liu et al. (2022)
Sistotremastrum induratum	Spirin 8598	MT002324	MT664173	–	–	–	–	Liu et al. (2022)
Sistotremastrum induratum	Spirin 8804	MT002318	–	–	–	–	–	Liu et al. (2022)
Sistotremastrum mendax	JN9579	MN937569	–	–	–	–	–	Liu et al. (2022)
Sistotremastrum mendax	KHL12022	MN937570	MN937570	–	–	–	–	Liu et al. (2022)
Sistotremastrum rigidum	MV833	MN954693	MW045435	–	–	–	–	Liu et al. (2022)
Sistotremastrum suecicum	KHL11849	MN937571	MN937571	–	–	–	–	Liu et al. (2022)
Sistotremastrum vigilans	Fonneland 2011-78	MN937572	MN937572	–	–	–	–	Liu et al. (2022)
Sistotremastrum vigilans	Spirin 8778	MN991182	MN991182	–	–	–	–	Liu et al. (2022)
Sistotremastrum sp.	LWZ 20171015-32	OM523376	OM339204	–	–	–	–	Liu et al. (2022)
Sistotremastrum sp.	LWZ 20191107-25	MW477771	MW474864	OM422784	–	MW478712	MW478703	Liu et al. (2022)
Sistotremastrum sp.	LWZ 20191207-26	OM523377	OM339205	OM422785	–	OM416816	OM416796	Liu et al. (2022)
Tropicoporus boehmeriae	LWZ 20140729-10	KT223640	MT319393	–	–	–	–	Wang et al. (2021)
Vararia yingjiangensis	CLZhao 30284	OR917879	OR921225	–	–	–	–	Deng et al. (2024b)
Vararia investiens	TAA164122	AF506484	AF506484	–	–	–	–	Xu et al. (2023)
Xylodon asiaticu	CLZhao 10368	OM959479	OM967417	–	–	–	–	Zhang et al. (2024)
Xylodon bambusinus	CLZhao 9174	MW394657	MW394650	–	–	–	–	Zhang et al. (2024)
Xylodon montanus	CLZhao 8179	OL619260	OL619268	–	–	–	–	Zhang et al. (2024)
Xylodon quercinus	KHL 11076	KT361633	AY586678	–	–	–	–	Zhang et al. (2024)

*ITS: internal transcribed spacer regions, nLSU: large subunit nuclear ribosomal RNA, mt-SSU: small subunit mitochondrial RNA, *rpb1*: RNA polymerase largest subunit I, *rpb2*: RNA polymerase largest subunit II, and *tef1-α*: translation elongation factor 1-alpha. The new species are shown in bold black, – which refers to sequence unavailability.

RESULTS

During the investigations on the wood-inhabiting fungi, nine species of *Hyphoderma*, *Trechispora* and *Xylodon* have different basidiomata (Fig. 1), the latitude, altitude, forest type, temperature and humidity of habitat are in connection with this phenomenon. In addition, we collected 33 specimens that showed thirteen new species and a new genus of *Basidiomycota* with different basidiomata morphologies from China that could not be assigned to any described species. In total, 13 species were identified belonging to *Coniophoropsis*, *Gloeopeniophorella*, *Gloiothele*, *Gracilihypha*, *Hyphoderma*, *Hyphodontia*, *Kneiffiella*, *Merismodes*, *Peniophora*, *Punctulariopsis*, *Sertulicium* and *Coniophoraceae*, *Hyphodermataceae*, *Hyphodontiaceae*, *Niaceae*, *Peniophoraceae*, *Punctulariaceae*, *Russulaceae*, *Sistotremastraceae*.

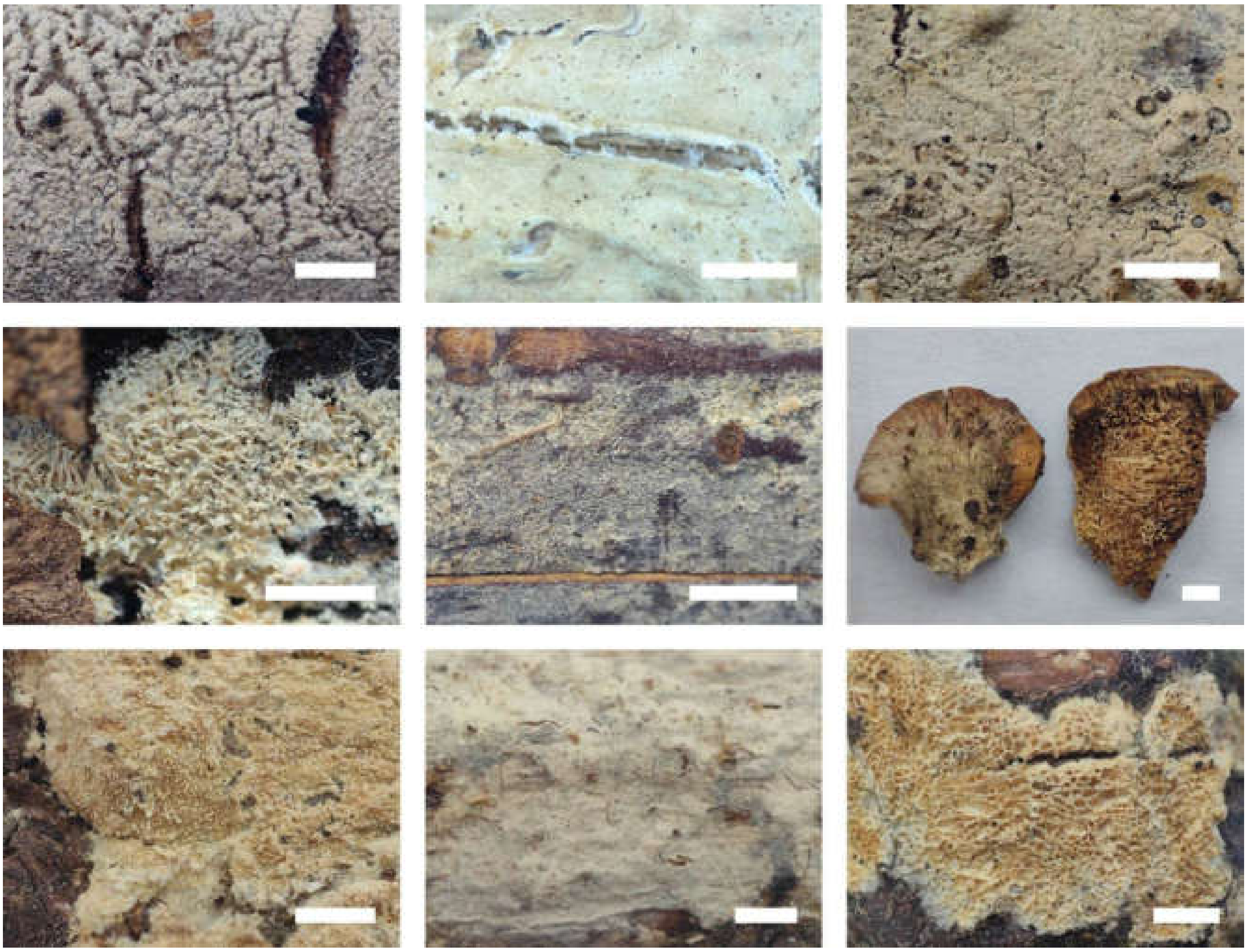

Figure 1 – Morphologically different basidiomata within the same genus. Top row left to right: *Hyphoderma floccosum*, *H. niveomarginatum*, *H. tenuissimum*; Middle row: *Trechispora fimbriata*, *T. olivacea*, *T. pileata*; Bottom row: *Xylodon kunmingensis*, *X. punctus*, *X. puerensis*. Scale bars = 2 mm.

Molecular phylogeny

***Niaceae* phylogeny based on combined ITS+nLSU+mtSSU+*rpb1*+*rpb2*+*tef*1-α sequence data** (Fig. 2)

The aligned dataset comprised 54 specimens representing 24 species. Sequences of *Acanthocorticium brueggemannii* Baltazar, Gorjón & Rajchenb. were retrieved from GenBank and used as an outgroup as in Silva-Filho et al. (2023). Four Markov chains were run for 2 runs from random starting trees, each for 4 million generations for the combined ITS+nLSU+mtSSU+*rpb1*+*rpb2*+*tef*1-α (Fig. 2) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 6099 characters, of which 4399 characters were constant, 495 were variable and parsimony-uninformative, and 1165 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 3433, CI = 0.6493, HI = 0.3507, RI = 0.7965, RC = 0.5172). The best model for the ITS+nLSU+mtSSU+*rpb1*+*rpb2*+*tef*1-α dataset estimated and applied in the Bayesian analysis was GTR+G. Bayesian analysis and MP analysis resulted in a similar topology as ML analysis, with an average standard deviation of split frequencies = 0.003969 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 453.5.

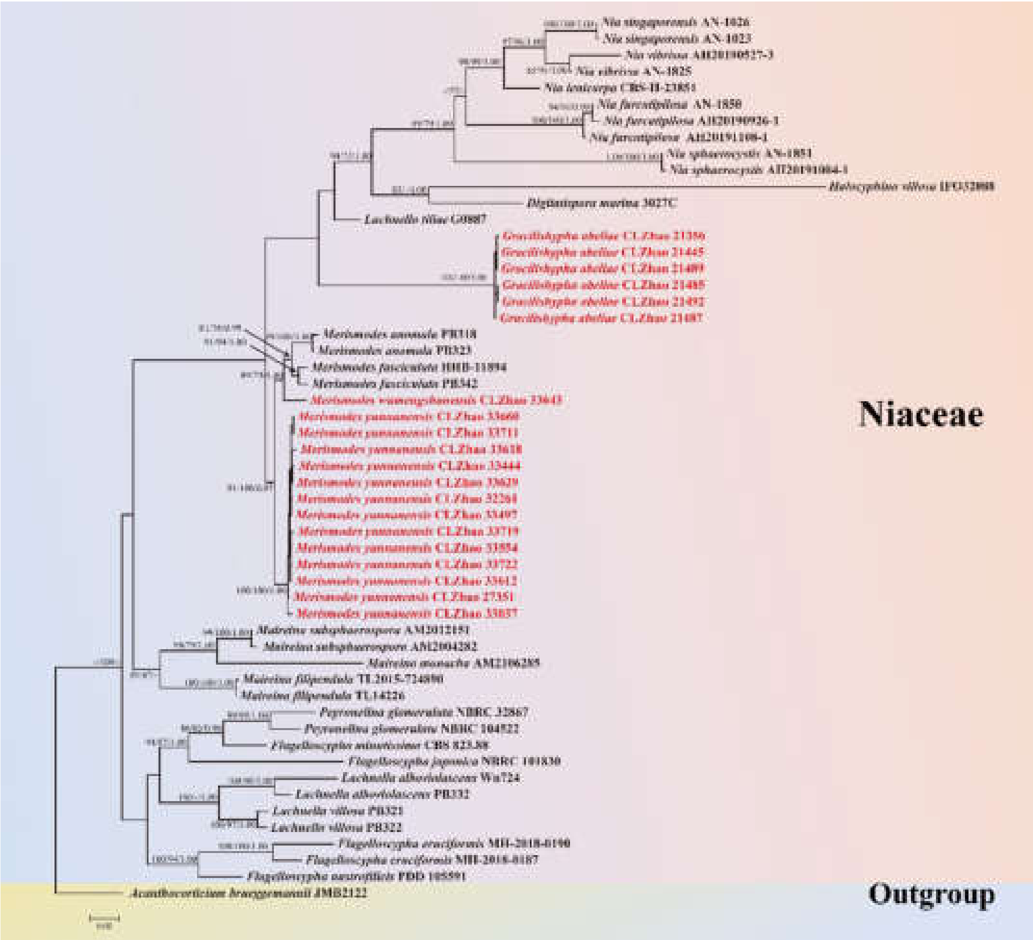

Figure 2 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Gracilihypha*, *Merismodes* and related genera in *Niaceae* based on ITS+nLSU+mtSSU+*rpb1*+*rpb2*+*tef*1-α sequences, *Acanthocorticium brueggemannii* used as an outgroup. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Coniophoropsis* phylogeny based on combined ITS+nLSU sequence data** (Fig. 3)

The aligned dataset comprised 28 specimens representing 18 species. *Gyrodontium sacchari* (Spreng.) Hjortstam was selected as an outgroup as in Yang et al. (2023a). Four Markov chains were run for 2 runs from random starting trees, each for 1 million generations for the combined ITS+nLSU (Fig. 3) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 715 characters, of which 422 characters were constant, 88 were variable and parsimony-uninformative, and 205 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 636, CI = 0.6352, HI = 0.3648, RI = 0.7245, RC = 0.4602). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was HKY+G. Bayesian analysis and MP analysis resulted in a similar topology as ML analysis, with an average standard deviation of split frequencies = 0.009997 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 362.

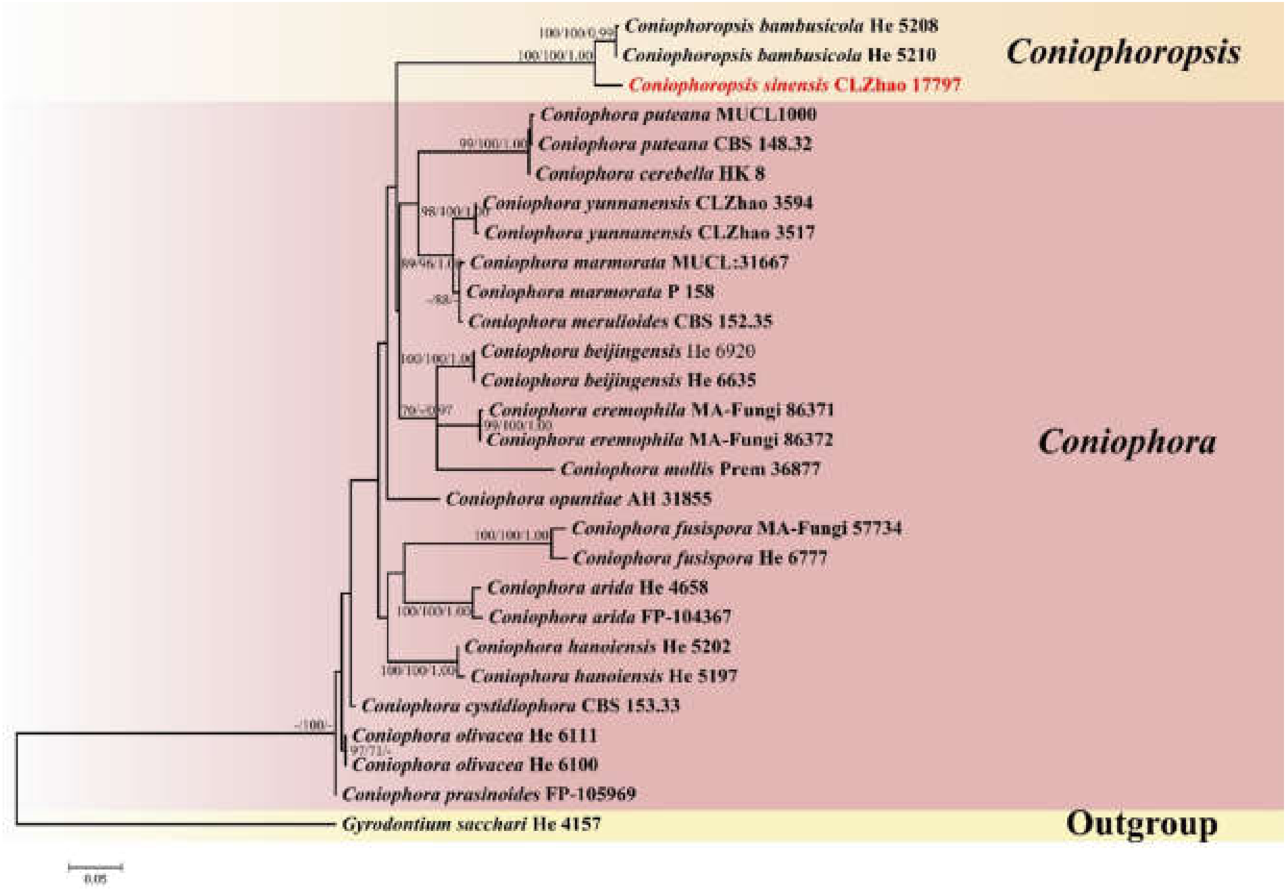

Figure 3 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Coniophoropsis sinensis* and related species based on ITS+nLSU sequences, *Gyrodontium sacchari* used as an outgroup. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Punctulariopsis* phylogeny based on combined ITS+nLSU sequence data** (Fig. 4)

The aligned dataset comprised 27 specimens representing 16 species. *Gloeophyllum abietinum* (Bull.) P. Karst. and *G. sepiarium* (Wulfen) P. Karst. was selected as outgroup taxa as in Ghobad-Nejhad et al. (2010). Four Markov chains were run for 2 runs from random starting trees, each for 1 million generations for the combined ITS+nLSU (Fig. 4) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 1962 characters, of which 1564 characters were constant, 37 were variable and parsimony-uninformative, and 361 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 707, CI = 0.7440, HI = 0.2560, RI = 0.8883, RC = 0.6609). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.003504 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 634.

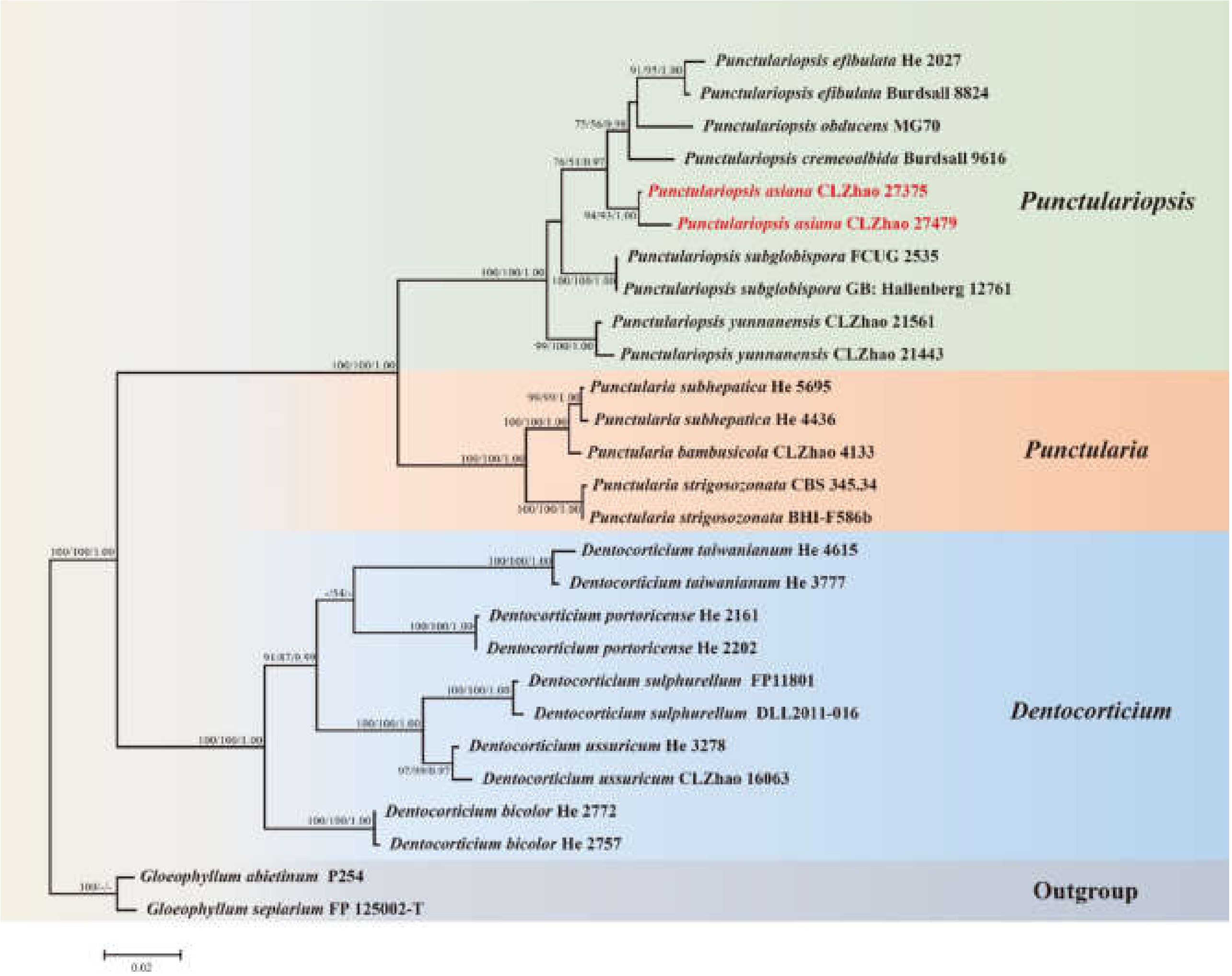

Figure 4 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Punctulariopsis asiana* and related species based on ITS+nLSU sequences, *Gloeophyllum abietinum* used as outgroup taxa. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Hymenochaetales* phylogeny based on combined ITS+nLSU+mtSSU+*rpb1*+*rpb2* sequence data** (Fig. 5)

The aligned dataset comprised 89 specimens representing 65 species. *Auricularia cornea* Ehrenb. was selected as outgroup taxa as in Wang et al. (2021). Four Markov chains were run for 2 runs from random starting trees, each for 12 million generations for the combined ITS+nLSU+mtSSU+*rpb1*+*rpb2* (Fig. 5) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 5603 characters, of which 2908 characters were constant, 1121 were variable and parsimony-uninformative, and 1574 were parsimony-informative. Maximum parsimony analysis yielded 3 equally parsimonious trees (TL = 11628, CI = 0.3671, HI = 0.6329, RI = 0.4790, RC = 0.1759). The best model for the ITS+nLSU+mtSSU+*rpb1*+*rpb2* dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.066150 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 261.

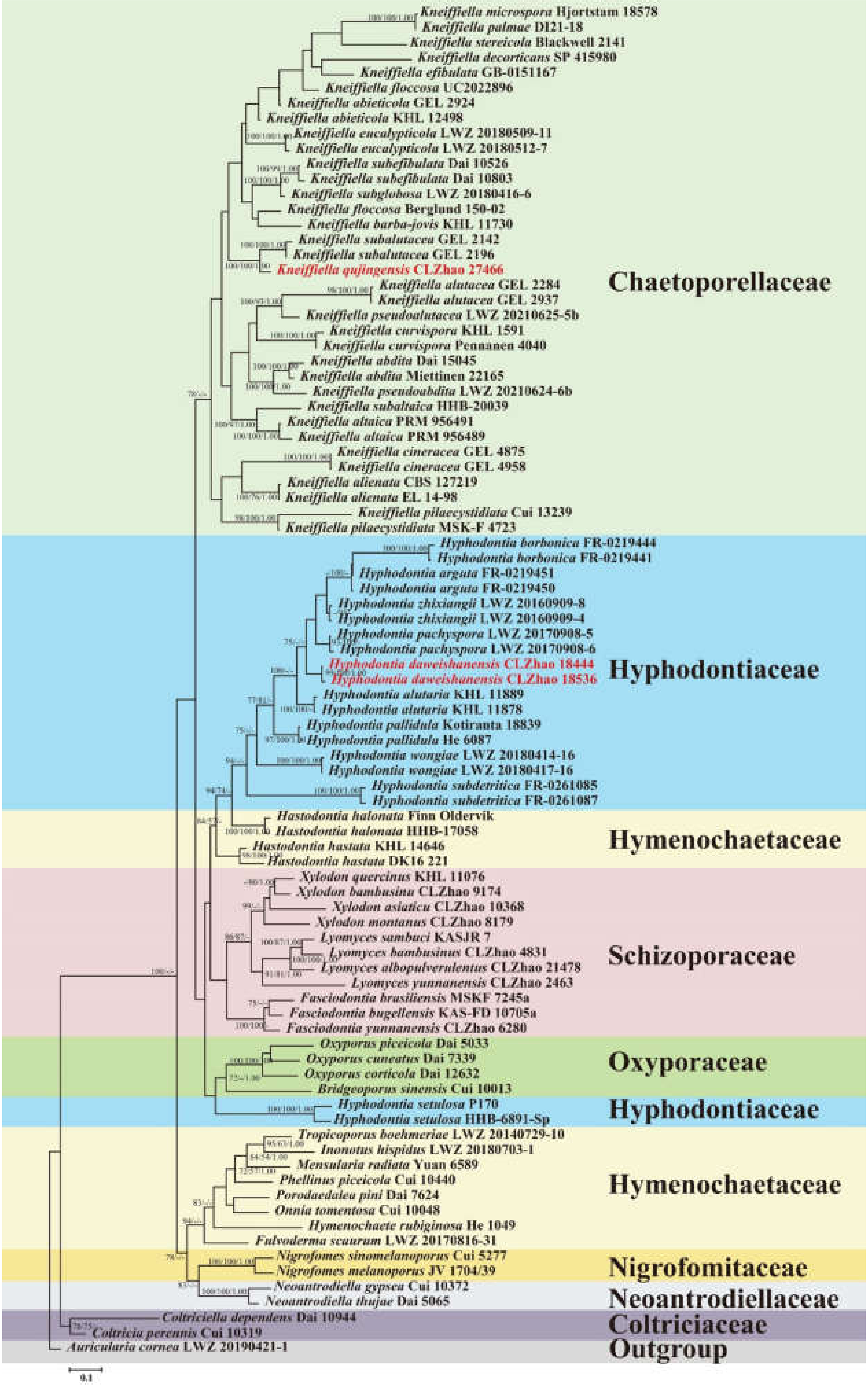
Kneiffiella microspora Hjortstam 18578
Kneiffiella palmae DI21-18
Kneiffiella stereicola Blackwell 2141
Kneiffiella decorticans SP 415980
Kneiffiella efibulata GB-0151167
Kneiffiella floccosa UC2022896
Kneiffiella abieticola GEL 2924
Kneiffiella abieticola KHL 12498
Kneiffiella eucalypticola LWZ 20180509-11
Kneiffiella eucalypticola LWZ 20180512-7
Kneiffiella subefibulata Dai 10526
Kneiffiella subefibulata Dai 10803
Kneiffiella subglobosa LWZ 20180416-6
Kneiffiella floccosa Berglund 150-02
Kneiffiella barba-jovis KHL 11730
Kneiffiella subalutacea GEL 2142
Kneiffiella subalutacea GEL 2196
Kneiffiella qujingensis CLZhao 27466
Kneiffiella alutacea GEL 2284
Kneiffiella alutacea GEL 2937
Kneiffiella pseudoalutacea LWZ 20210625-5b
Kneiffiella curvispora KHL 1591
Kneiffiella curvispora Pennanen 4040
Kneiffiella abdita Dai 15045
Kneiffiella abdita Miettinen 22165
Kneiffiella pseudoabdita LWZ 20210624-6b
Kneiffiella subaltaica HHB-20039
Kneiffiella altaica PRM 956491
Kneiffiella altaica PRM 956489
Kneiffiella cineracea GEL 4875
Kneiffiella cineracea GEL 4958
Kneiffiella alienata CBS 127219
Kneiffiella alienata EL 14-98
Kneiffiella pilaecystidiata Cui 13239
Kneiffiella pilaecystidiata MSK-F 4723
Chaetoporellaceae
Hyphodontia borbonica FR-0219444
Hyphodontia borbonica FR-0219441
Hyphodontia arguta FR-0219451
Hyphodontia arguta FR-0219450
Hyphodontia zhixiangii LWZ 20160909-8
Hyphodontia zhixiangii LWZ 20160909-4
Hyphodontia pachyspora LWZ 20170908-5
Hyphodontia pachyspora LWZ 20170908-6
Hyphodontia daweishanensis CLZhao 18444
Hyphodontia daweishanensis CLZhao 18536
Hyphodontia alutaria KHL 11889
Hyphodontia alutaria KHL 11878
Hyphodontia pallidula Kotiranta 18839
Hyphodontia pallidula He 6087
Hyphodontia wongiae LWZ 20180414-16
Hyphodontia wongiae LWZ 20180417-16
Hyphodontia subdetritica FR-0261085
Hyphodontia subdetritica FR-0261087
Hyphodontiaceae
Hastodontia halonata Finn Oldervik
Hastodontia halonata HHB-17058
Hastodontia hastata KHL 14646
Hastodontia hastata DK16 221
Hymenochaetaceae
Xylodon quercinus KHL 11076
Xylodon bambusinu CLZhao 9174
Xylodon asiaticu CLZhao 10368
Xylodon montanus CLZhao 8179
Lyomyces sambuci KASJR 7
Lyomyces bambusinus CLZhao 4831
Lyomyces albopulverulentus CLZhao 21478
Lyomyces yunnanensis CLZhao 2463
Fasciodontia brasiliensis MSKF 7245a
Fasciodontia bugellensis KAS-FD 10705a
Fasciodontia yunnanensis CLZhao 6280
Schizoporaceae
Oxyporus piceicola Dai 5033
Oxyporus cuneatus Dai 7339
Oxyporus corticola Dai 12632
Bridgeoporus sinensis Cui 10013
Oxyporaceae
Hyphodontia setulosa P170
Hyphodontia setulosa HHB-6891-Sp
Hyphodontiaceae
Tropicoporus boehmeriae LWZ 20140729-10
Inonotus hispidus LWZ 20180703-1
Mensularia radiata Yuan 6589
Phellinus piceicola Cui 10440
Porodaedalea pini Dai 7624
Onnia tomentosa Cui 10048
Hymenochaete rubiginosa He 1049
Fulvoderma scaurum LWZ 20170816-31
Hymenochaetaceae
Nigrofomes sinomelanoporus Cui 5277
Nigrofomes melanoporus JV 1704/39
Nigrofomitaceae
Neoantrodiella gypsea Cui 10372
Neoantrodiella thujae Dai 5065
Neoantrodiellaceae
Coltriciella dependens Dai 10944
Coltricia perennis Cui 10319
Coltriciaceae
Auricularia cornea LWZ 20190421-1
Outgroup
0.1

Figure 5 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Hyphodontia* sensu lato within *Hymenochaetales* based on ITS+nLSU+mtSSU+*rpb1*+*rpb2* sequences, *Auricularia cornea* used as outgroup. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Hyphoderma* phylogeny based on combined ITS+nLSU+mtSSU+*rpb1*+*rpb2* sequence data** (Fig. 6)

The aligned dataset comprised 63 specimens representing 41 species. *Diplomitoporus crustulinus* (Bres.) Domański was selected as outgroup taxa as in Yang et al. (2023b). Four Markov chains were run for 2 runs from random starting trees, each for 4 million generations for the combined ITS+nLSU+mtSSU+*rpb1*+*rpb2* (Fig. 6) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 4378 characters, of which 2951 characters were constant, 530 were variable and parsimony-uninformative, and 897 were parsimony-informative. Maximum parsimony analysis yielded 24 equally parsimonious trees (TL = 4734, CI = 0.4413, HI = 0.5587, RI = 0.5560, RC = 0.2453). The best model for the ITS+nLSU+mtSSU+*rpb1*+*rpb2* dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.008882 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 531.

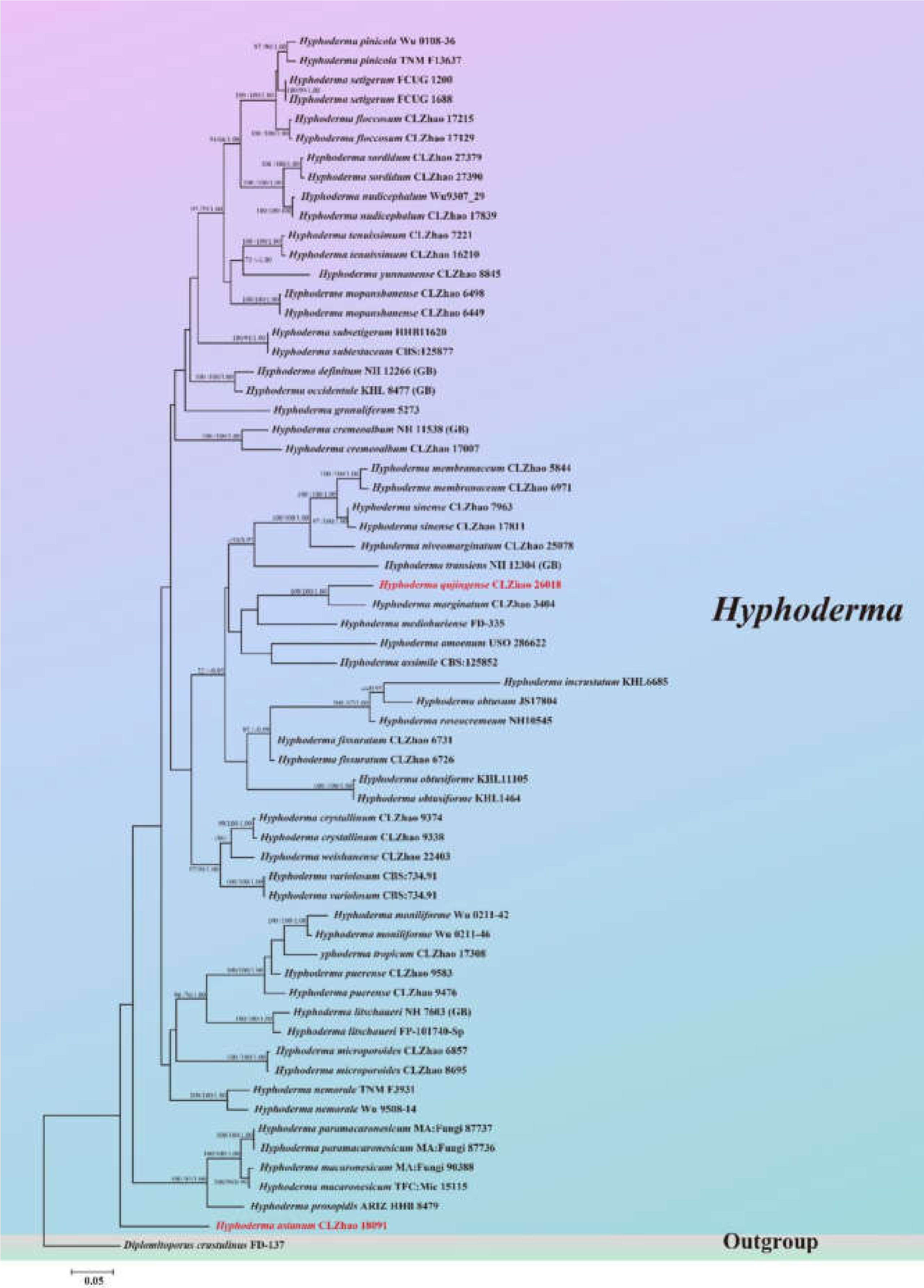

Figure 6 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Hyphoderma* based on ITS+nLSU+mtSSU+*rpb1*+*rpb2* sequences, *Diplomitoporus crustulinus* used as outgroup. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%,

Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Peniophoraceae* phylogeny based on combined ITS+nLSU sequence data** (Fig. 7)

The aligned dataset comprised 42 specimens representing 36 species. Sequences of *Amylostereum chailletii* (Pers.) Boidin was used as the outgroup as in Xu et al. (2023). Four Markov chains were run for 2 runs from random starting trees, each for 2 million generations for the combined ITS+nLSU (Fig. 7) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2275 characters, of which 1174 characters were constant, 333 were variable and parsimony-uninformative, and 768 were parsimony-informative. Maximum parsimony analysis yielded 48 equally parsimonious trees (TL = 3047, CI = 0.5816, HI = 0.4184, RI = 0.7124, RC = 0.4143). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.009109 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 1055.

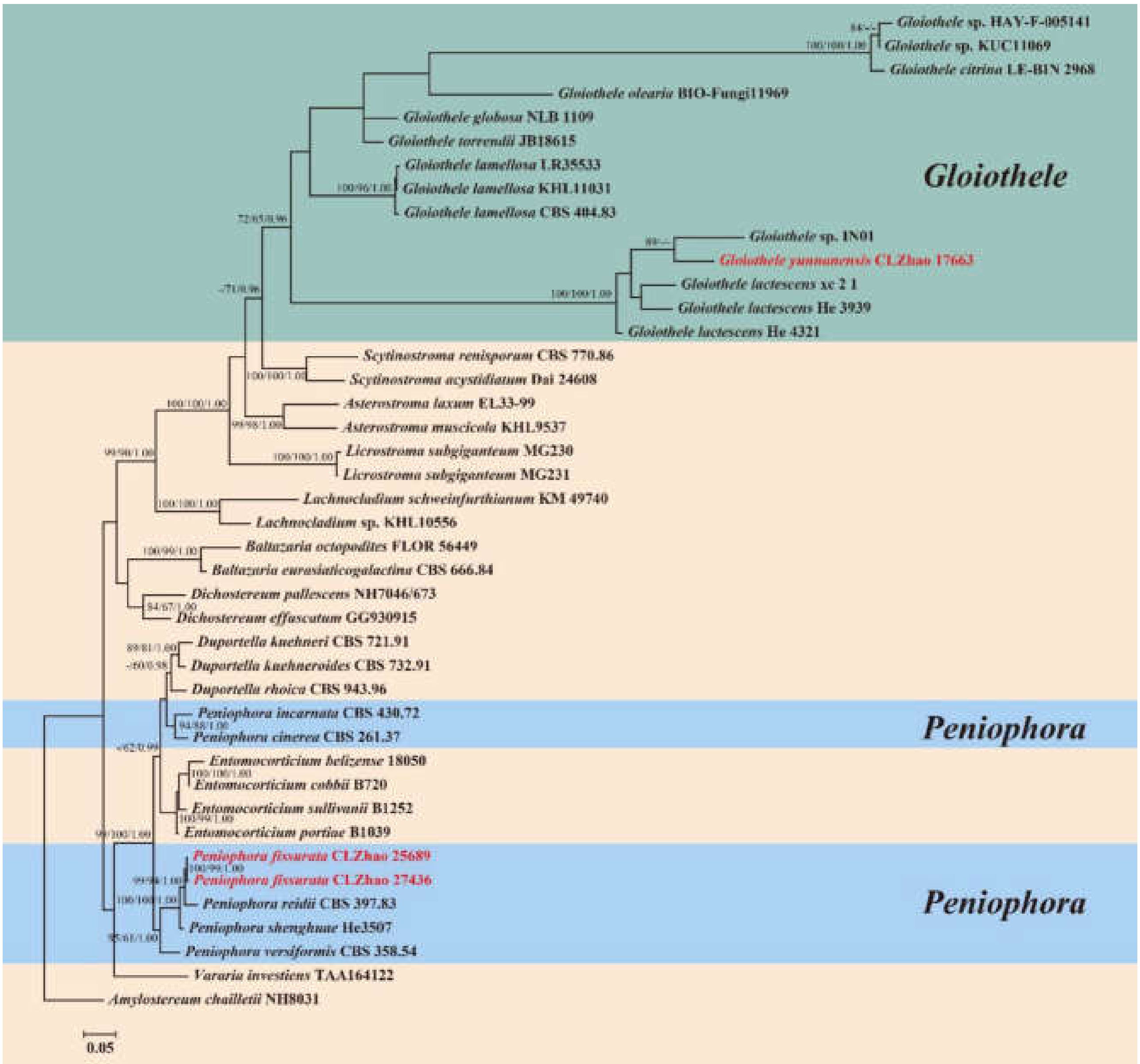

Figure 7 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Peniophoraceae* based on ITS+nLSU sequences, *Amylostereum chailletii* used as the outgroup. Branches are labeled

with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Gloiothele* phylogeny based on combined ITS+nLSU sequence data** (Fig. 8)

The aligned dataset comprised 15 specimens representing 11 species. *Vararia yingjiangensis* Y.L. Deng & C.L. Zhao was selected as the outgroup. Four Markov chains were run for 2 runs from random starting trees, each for 1 million generations for the combined ITS+nLSU (Fig. 8) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2059 characters, of which 1399 characters were constant, 269 were variable and parsimony-uninformative, and 391 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 1060, CI = 0.8292, HI = 0.1708, RI = 0.8250, RC = 0.6841). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.002364 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 3290.5.

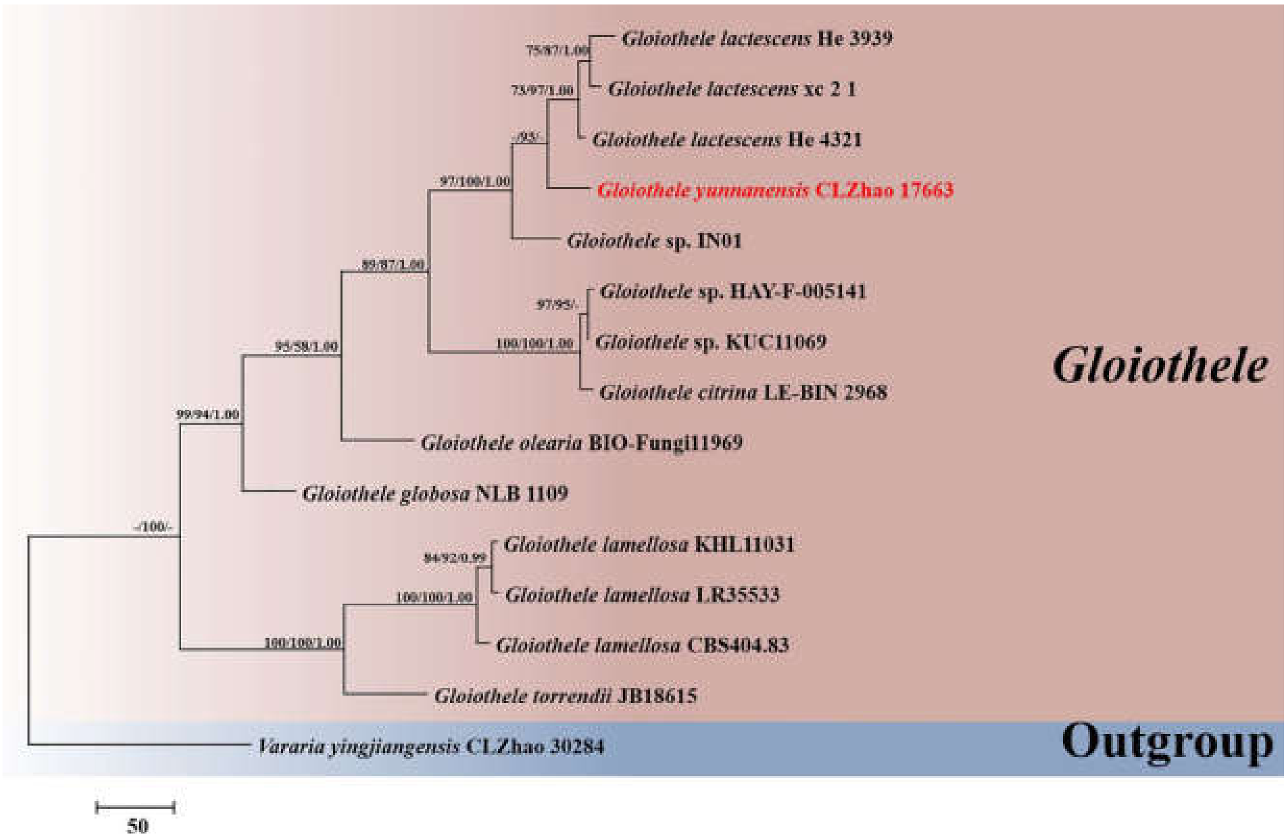

Figure 8 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Gloiothele yunnanensis* and related species in *Gloiothele* based on ITS+nLSU sequences, *Vararia yingjiangensis* used as the outgroup. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Peniophora* phylogeny based on combined ITS+nLSU sequence data** (Fig. 9)

The aligned dataset comprised 110 specimens representing 66 species. *Confertobasidium olivaceoalbum* (Bourdot & Galzin) Jülich and *Metulodontia nivea* (P. Karst.) Parmasto were selected as outgroups as in Xu et al. (2023). Four Markov chains were run for 2 runs from random starting trees, each for 16 million generations for the combined ITS+nLSU (Fig. 9) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2034 characters, of which 1413 characters were constant, 247 were variable and parsimony-uninformative, and 374 were parsimony-informative. Maximum parsimony analysis yielded 100 equally parsimonious trees (TL = 2517, CI = 0.3417, HI = 0.6583, RI = 0.6015, RC = 0.2055). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was SYM+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.046509 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 218.

Figure 9 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Peniophora fissurata* and related species in *Peniophora* based on ITS+nLSU sequences, *Confertobasidium olivaceoalbum* and *Metulodontia nivea* were selected as outgroups. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Gloeopeniophorella* phylogeny based on combined ITS+nLSU sequence data** (Fig. 10)

The aligned dataset comprised 27 specimens representing 23 species. *Sistotrema muscicola* (Pers.) S. Lundell was selected as outgroup taxa as in Zhao & Zhao (2023). Four Markov chains were run for 2 runs from random starting trees, each for 2 million generations for the combined ITS+nLSU (Fig. 10) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2226 characters, of which 1365 characters were constant, 304 were variable and parsimony-uninformative, and 557 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 2188, CI = 0.5864, HI = 0.4136, RI = 0.5668, RC = 0.3323). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.004094 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 1633.5.

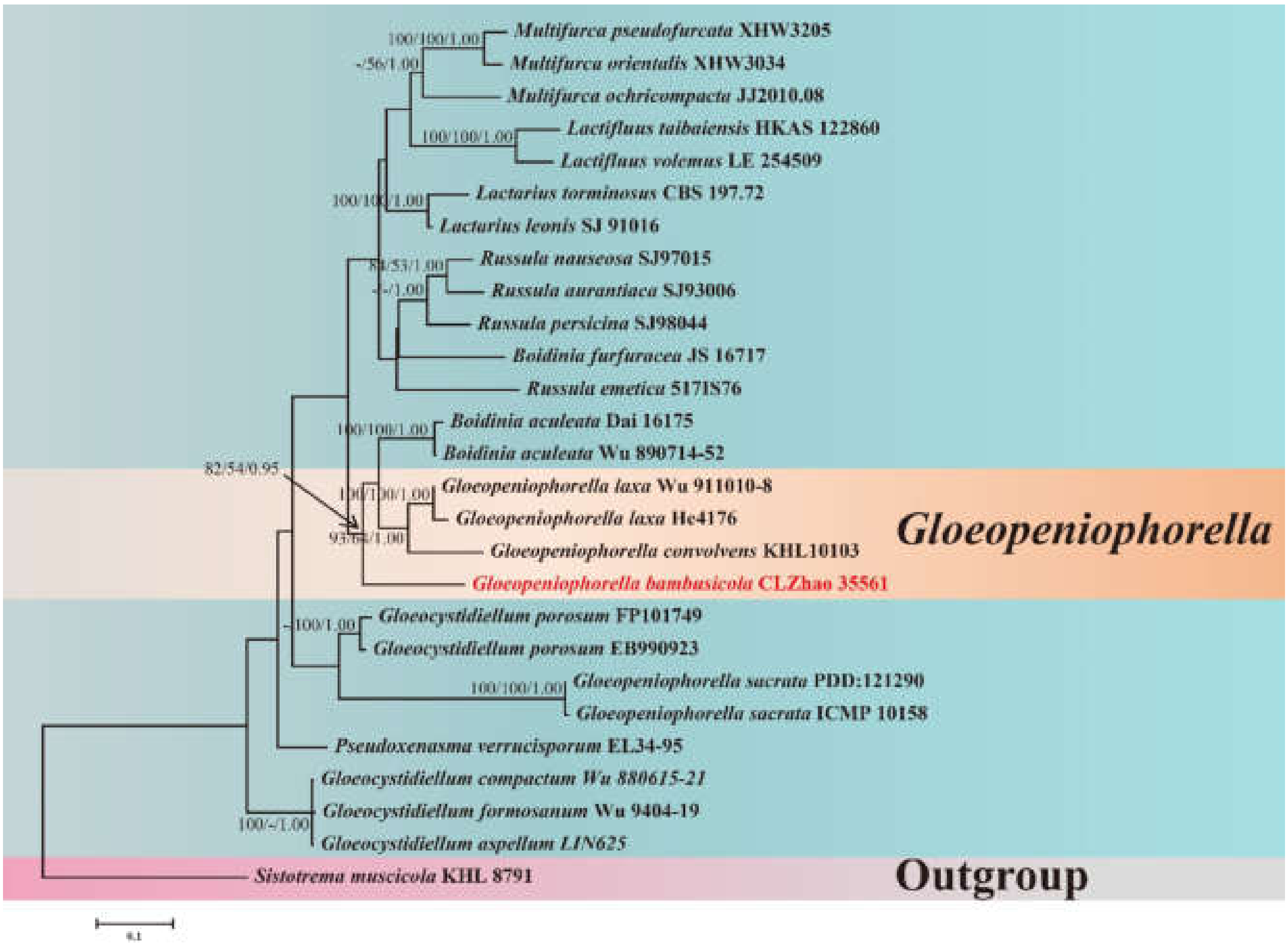

Figure 10 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Gloeopeniophorella bambusicola* and related species based on ITS+nLSU sequences, *Sistotrema muscicola* used as outgroup. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

***Sistotremastrales* phylogeny based on combined ITS+nLSU sequence data** (Fig. 11)

The aligned dataset comprised 34 specimens representing 22 species. *Polyporus squamosus* (Huds.) Fr. was selected as outgroup taxa as in Liu et al. (2022). Four Markov chains were run for 2 runs from random starting trees, each for 10 million generations for the combined ITS+nLSU (Fig. 11) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 3820 characters, of which 2154 characters were constant, 1039 were variable and parsimony-uninformative, and 627 were parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 2726, CI = 0.7946, HI = 0.2054, RI = 0.8240, RC =

0.6547). The best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis was GTR+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.007131 (BI), and the effective sample size (ESS) across the two runs is double that of the average ESS (avg ESS) = 4168.

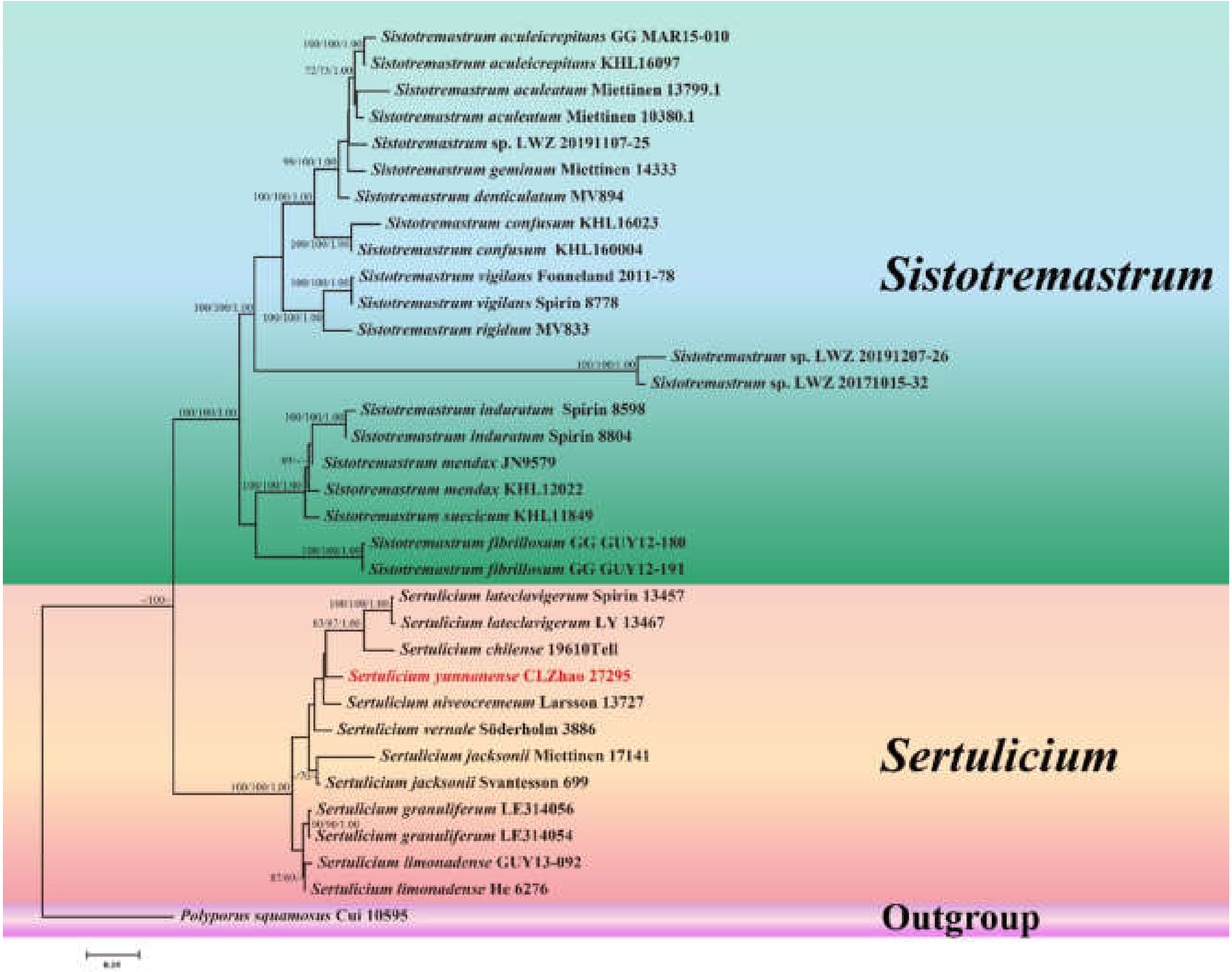

Figure 11 – Maximum likelihood strict consensus tree illustrating the phylogeny of *Sertulicium yunnanense* and related species in *Sistotremastrales* based on ITS+nLSU sequences, *Polyporus squamosus* used as outgroup. Branches are labeled with Maximum likelihood bootstrap values equal to or higher than 70%, Maximum parsimony bootstrap values equal to or higher than 50% and Bayesian posterior probabilities equal to or higher than 0.95.

Taxonomy

Agaricales Underw.

Index Fungorum number: IF17030

Type family – *Agaricaceae* Chevall.

Niaceae Jülich

Index Fungorum number: IF80014

Type genus – *Nia* Jülich

Gracilihypha Y. Yang & C.L. Zhao, gen. nov.

Index Fungorum number: IF854077; Facesoffungi number: FoF16598

Etymology – *Gracilihypha* (Lat.): referring to the gracile generative hyphae.

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

Diagnosis – Characterized by hard coriaceous basidiomata with cracked hymenophore surface, a monomitic hyphal system with clamp connections and the gracile generative hyphae, and broadly ellipsoid to subglobose basidiospores.

Description – Basidiomata annual, resupinate, adnate, soft coriaceous to hard coriaceous. Hymenophore surface white slightly cream, cracked. Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, very thin. Cystidia fusiform, thin-walled. Basidia clavate, with 4 sterigmata and a basal clamp connection, basidioles in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid to subglobose, colorless, thin-walled, smooth, with irregular oil droplets inside occasionally, IKI–, CB–.

Notes – Based on ITS+nLSU+mtSSU+*rpb1*+*rpb2*+*tef*1-α sequence data (Fig. 2), six wood-inhabiting fungal specimens from Southwest China form a distinct lineage with strong support within the family *Niaceae* in phylogenetic analysis. Morphologically, these six specimens have coriaceous and cracked hymenophore, a monomitic hyphal system with very thin generative hyphae, fusiform cystidia, ellipsoid to subglobose and thin-walled basidiospores that are distinguished from known genera in *Merismodes* (Silva-Filho et al. 2023). Therefore, a new genus *Gracilihypha* is described on the basis of these six specimens.

Gracilihypha abeliae Y. Yang & C.L. Zhao, sp. nov. Fig. 12

Index Fungorum number: IF854078; Facesoffungi number: FoF16599

Etymology – *Abeliae* (Lat.): referring to the host tree genus (*Abelia*) of the type specimen.

Type – China, Yunnan Province, Lijiang, Lashihai Wetland Park, Meiquan Village, 26°51′39″ N, 100°8′22″ E; 2450 m, on the fallen *Abelia* branches, 19 July 2021, CLZhao 21356 (SWFC, holotype).

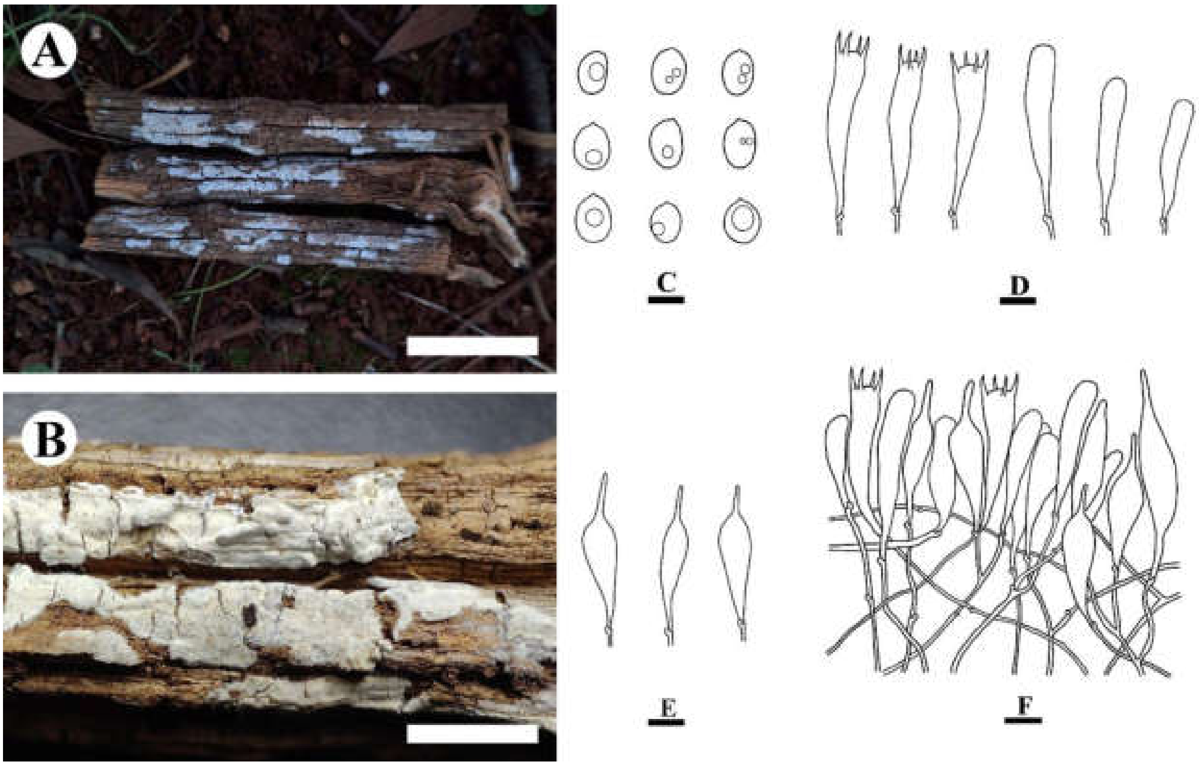

Figure 12 – Basidiomata and microscopic structures of *Gracilihypha abeliae* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Cystidia. F A section of hymenium. Bars: A = 3 cm, B = 5 mm, C–F = 10 µm.

Diagnosis – Characterized by coriaceous basidiomata with cracked hymenophore surface, a monomitic hyphal system with clamp connections and thin generative hyphae, and broadly ellipsoid to subglobose basidiospores.

Description – Basidiomata annual, resupinate, adnate, without odor or taste when fresh, soft coriaceous when fresh, hard coriaceous upon drying, up to 6 cm long and 2 cm wide, 200–500 µm thick. Hymenophore surface white when fresh, white to slightly cream upon drying, cracked. Sterile margin white, up to 0.5 mm.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, very thin, 0.5–2.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Cystidia fusiform, colorless, thin-walled, 24–46.5 × 5–11.5 µm ($\bar{x}$ = 32.75 × 8.72 µm). Basidia clavate, with 4 sterigmata and a basal clamp connection, 29–40 × 6–10 µm ($\bar{x}$ = 33.21 × 8.09 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores broadly ellipsoid to subglobose, colorless, thin-walled, smooth, with irregular oil droplets inside occasionally, IKI–, CB–, (8–)8.5–13(–14) × (6–)7–10(–10.5) µm, L = 11.01 µm, W = 8.39 µm, Q = 1.21–1.31 (n = 180/6).

Material examined (paratypes) – China, Yunnan Province, Lijiang, Lashihai Wetland Park, Meiquan Village, 26°51′39″ N, 100°8′22″ E, 2450 m, on the fallen *Abelia* branches, 19 July 2021, CLZhao 21445; CLZhao 21485; CLZhao 21487; CLZhao 21489; CLZhao 21492 (SWFC).

Notes – *Gracilihypha abeliae* is characterized by the coriaceous basidiomata with the white to slightly cream and cracked hymenophore, a monomitic hyphal system with very thin generative hyphae, and fusiform cystidia, ellipsoid to subglobose and thin-walled basidiospores.

Merismodes Earle

Index Fungorum number: IF18047

Merismodes was established by Earle (1909), with *Merismodes fasciculata* (Schwein.) Earle as the type species, in which *Merismodes* contains 11 accepted species (Silva-Filho et al. 2023). The typical feature of this genus is the structure of cyphelloid receptacle, cupulate to tubular basidiomata, covered with yellow brown to brown hairs, and subglobose, ellipsoid, cylindrical, allantoid or subfusiform basidiospores (Silva-Filho et al. 2023). We describe two new species *viz. Merismodes wumengshanensis* and *M. yunnanensis* in this study.

Merismodes wumengshanensis Y. Yang & C.L. Zhao, sp. nov. Fig. 13

Index Fungorum number: IF854079; Facesoffungi number: FoF16600

Etymology – *Wumengshanensis* (Lat.): referring to the locality (Wumengshan) of the type specimen.

Type – China, Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, 27°47′9″ N, 104°19′51″ E, 1800 m, on the fallen angiosperm branches, 20 September 2023, CLZhao 33643 (SWFC, holotype).

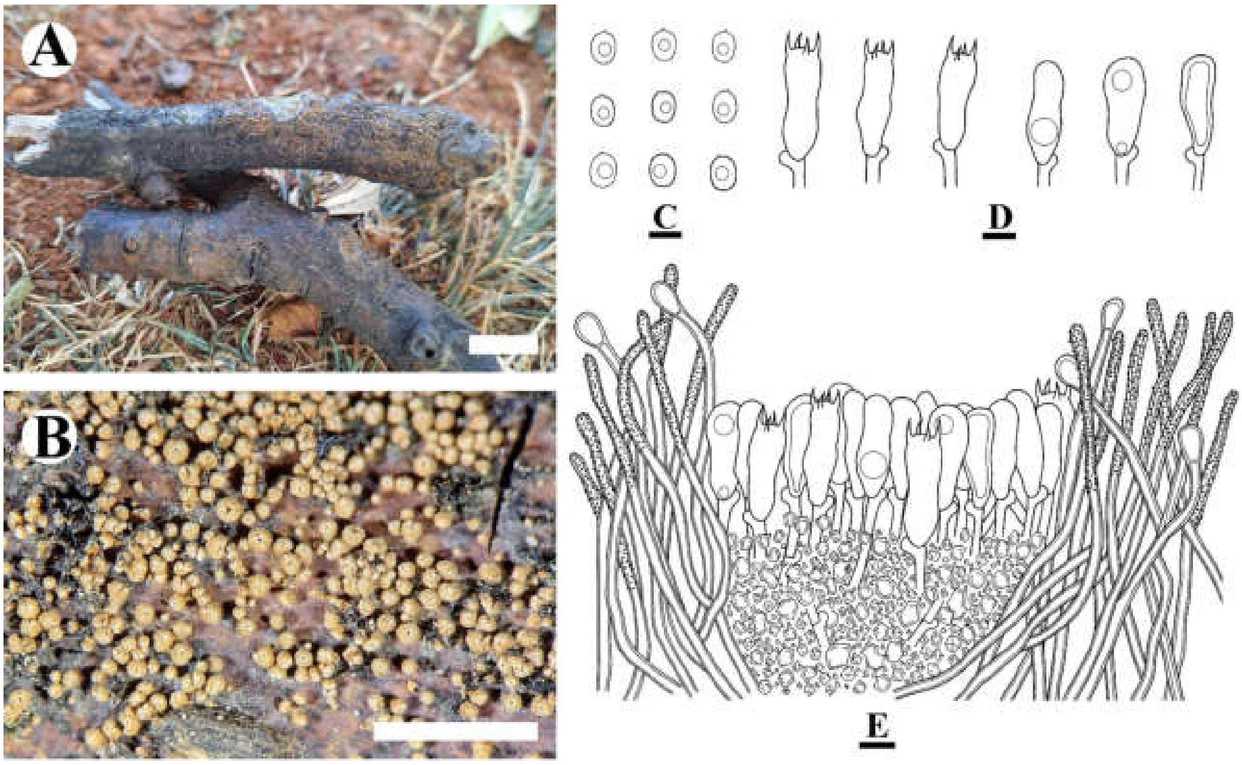

Figure 13 – Basidiomata and microscopic structures of *Merismodes wumengshanensis* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E A section of hymenium. Bars: A = 1 cm, B = 1 mm, C–E = 10 µm.

Diagnosis – Differs from *Merismodes yunnanensis* by covered in a dense mat of cinnamon-buff hairs, cinnamon-buff hymenophore surface, thin-walled generative hyphae, and larger basidiospores (8–9.5 ×5.5–6.5 µm).

Description – Basidiomata annual, resupinate, cupulate when fresh, tubular when dry, dense groups on substrate, covered in a dense mat of cinnamon-buff hairs, up to 6–12 per mm, up to 0.5 mm high and 0.2 mm wide. Hymenophore surface cinnamon-buff when fresh, clay-buff upon drying.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, interwoven, 2.5–3 µm in diameter, covered in abundant crystals; IKI–, CB–, tissues unchanged in KOH. Hairs almost straight to undulating, occasionally constricted, 3–4 µm wide, covered in crystals, often with septate at the slightly inflated (clavate) apex.

Cystidia absent. Basidia barrelled, with 4 sterigmata and a basal clamp connection, 27–34 × 7.5–11 µm ($\bar{x}$ = 29.32 × 8.69 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores ellipsoid to broadly ellipsoid, colorless, thin-walled, smooth, with irregular oil droplets inside occasionally, IKI–, CB–, (7–)8–9.5(–10) × (5–)5.5–6.5 µm, L = 8.69 µm, W = 6.02 µm, Q = 1.44 (n = 30/1).

Notes – Based on the ITS+nLSU+mtSSU+*rpb1*+*rpb2*+*tef*1-α sequence data (Fig. 2), the new species *Merismodes wumengshanensis* is clustered with *M. anomala* (Pers.) Singer and *M. fasciculata*. However, *M. anomala* can be delimited from *M. wumengshanensis* by its brown hymenophore and longer basidia (32–44 × 7–8 µm, Agerer 1978). The species *M. fasciculata* can be delimited from *M. wumengshanensis* by its basidiomata with the white tomentose (Schweinitz 1832).

Merismodes yunnanensis Y. Yang & C.L. Zhao, sp. nov. Fig. 14

Index Fungorum number: IF854080; Facesoffungi number: FoF16601

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

Type – China, Yunnan Province, Qujing, Zhanyi District, Yanzhu Village, 25°47′20″ N, 103°36′11″ E; 1950 m, on the fallen angiosperm branches, 7 March 2023, CLZhao 27351 (SWFC, holotype).

Diagnosis – Differs from *Merismodes wumengshanensis* by covered in a dense mat of whitish to pale brownish hairs, brown hymenophore surface, slightly thick-walled generative hyphae, and smaller basidiospores (4.5–6 × 2.5–4 µm).

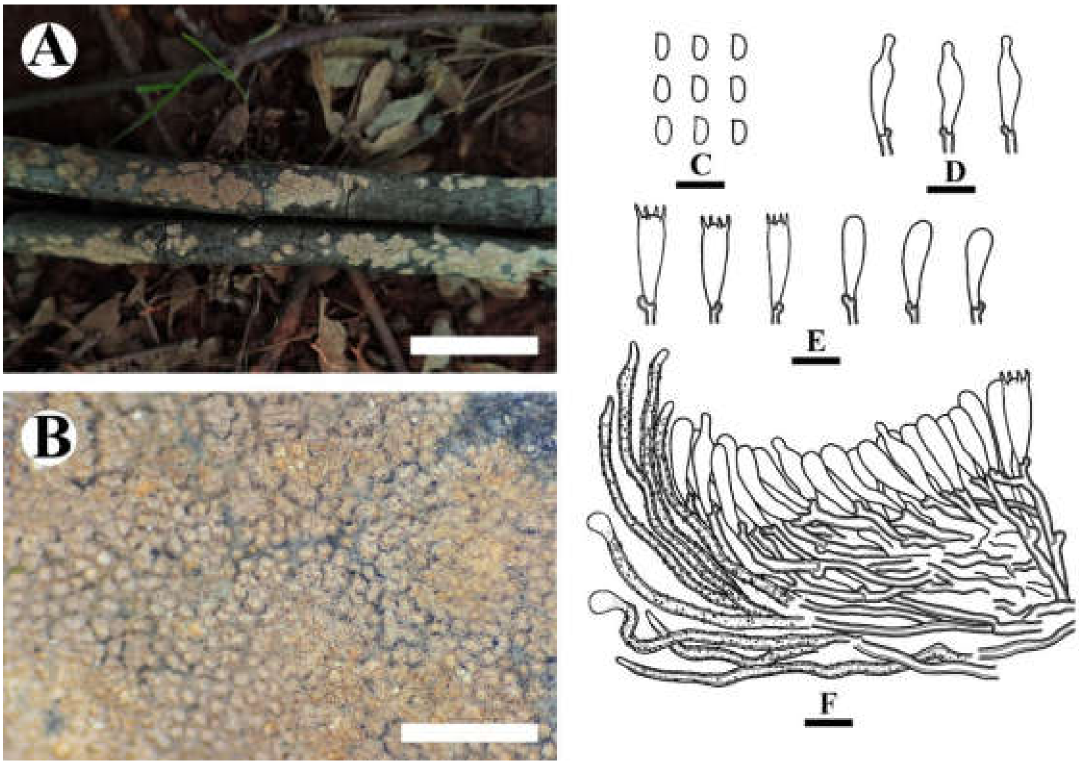

Figure 14 – Basidiomata and microscopic structures of *Merismodes yunnanensis* (holotype). A–B Basidiomata. C Basidiospores. D Cystidia. E Basidia and basidioles. F A section of hymenium. Bars: A = 2 cm, B = 1 mm, C–F = 10 µm.

Description – Basidiomata annual, resupinate, cupulate when fresh, tubular when dry, dense groups on substrate, covered in a dense mat of whitish to pale brownish hairs, up to 7–10 per mm, up to 0.4 mm high and 0.2 mm wide. Hymenophore surface slightly brown when fresh, greyish brown upon drying. Sterile margin slightly brown, up to 1.5 mm.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, slightly thick-walled, frequently branched, interwoven, 2–3 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Hairs almost straight to undulating, occasionally constrict-ed, 2–3.5 µm wide, covered in crystals and often more so at the slightly inflated (clavate) apex.

Cystidia fusiform, colorless, thin-walled, 12–18 × 3–6 µm ($\bar{x}$ = 15.13 × 4.33 µm). Basidia clavate, with 4 sterigmata and a basal clamp connection, 8–14 × 3–5.5 µm ($\bar{x}$ = 11.12 × 3.94 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores ellipsoid, colorless, thin-walled, smooth, with irregular oil droplets inside occasionally, IKI–, CB–, (4–)4.5–6(–6.5) × 2.5–4 µm, L = 5.31 µm, W = 3.22 µm, Q = 1.53–1.66 (n = 150/5).

Material examined (paratypes) – China, Yunnan Province, Zhaotong, Wumengshan National Nature Reserve, 27°47′9″ N, 104°19′51″ E, 1800 m, on the fallen angiosperm branches, 18 September 2023, CLZhao 32261; CLZhao 33037; CLZhao 33444; CLZhao 33497; CLZhao 33550; CLZhao 33554; CLZhao 33612; CLZhao 33618; CLZhao 33629; CLZhao 33660; CLZhao 33711; CLZhao 33719; CLZhao 33722 (SWFC).

Notes – Based on the multiple genes sequence data (Fig. 2), the new species *Merismodes yunnanensis* is grouped into *Merismodes*, in which it is clustered with *M. wumengshanensis*.

However, *M. wumengshanensis* can be distinguished from *M. yunnanensis* by its cinnamon-buff hairs, cinnamon-buff hymenophore, and larger basidiospores (8–9.5 × 5.5–6.5 µm).

Boletales E.-J. Gilbert

Index Fungorum number: IF90529

Type family – *Boletaceae* Chevall.

Coniophoraceae Ulbr.

Index Fungorum number: IF80632

Type genus – *Coniophora* DC.

Coniophoropsis Hjortstam & Ryvarden

Index Fungorum number: IF25755

The genus *Coniophoropsis* Hjortstam & Ryvarden (1986) was erected for *Coniophoropsis obscura* Hjortstam & Ryvarden, in which this genus has been found only 2 species in Argentina and Vietnam (Zhao et al. 2018). The genus is characterized by having brown, resupinate basidiomata with a smooth hymenophore, a monomitic hyphal system, and thick-walled, verrucose and cyanophilous basidiospores. Except for the ornamented basidiospores, *Coniophoropsis* is very similar to *Coniophora* DC. (1815). Larsson (2007) treated *Coniophoropsis* as *incertae sedis* in *Boletales* since the type species had not been (and to date still has not been) sequenced (Zhao et al. 2018). We report a new species of *Coniophoropsis sinensis* in this study.

Coniophoropsis sinensis Y. Yang & C.L. Zhao, sp. nov. Fig. 15

Index Fungorum number: IF854081; Facesoffungi number: FoF16602

Etymology – *Sinensis* (Lat.): referring to the locality (China) of the type specimen.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°56′1″ N, 103°41′31″ E; 1950 m, on the stalks of dead bamboo, 1 August 2019, CLZhao 17797 (SWFC, holotype).

Diagnosis – Differs from *C. bambusicola* S.H. He & Nakasone by collect from China, with the buff to honey-yellow hymenophore, and shorter subclavate basidia (17–22 × 4.5–7 µm).

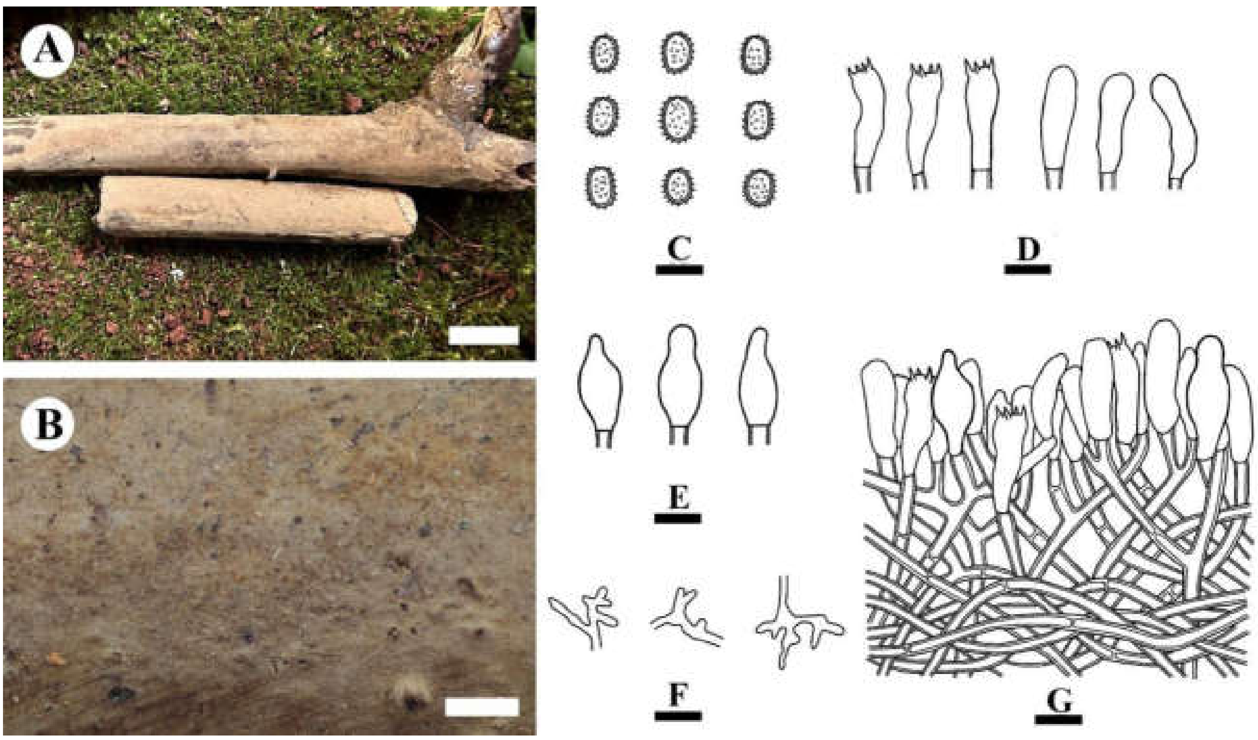

Figure 15 – Basidiomata and microscopic structures of *Coniophoropsis sinensis* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Cystidia. F Dendrohyphidia. G A section of hymenium. Bars: A = 1 cm, B = 1 mm, C–G = 10 µm.

Description – Basidiomata annual, resupinate, closely adnate, inseparable from substrate, membranaceous to crustose, without odor or taste when fresh, up to 12 cm long, 1.5 cm wide, 50–300 µm thick. Hymenophore surface smooth, buff to honey-yellow when fresh, greyish brown to deep olive when drying. Sterile margin greyish brown, up to 1 mm.

Hyphal system monomitic; generative hyphae with simple septa, colorless, thick-walled, frequently branched, interwoven, 2–3.5 µm in diameter; IKI–, CB–, tissues un-changed in KOH.

Gloeocystidia abundant, colorless, thin-walled, 15–22 × 4.5–8 µm ($\bar{x}$ = 18.76 × 6.35 µm). Dendrohyphidia numerous, colorless, thin-walled, usually torulose. Basidia subclavate, thin-walled, with 4 sterigmata and a basal simple septum, 17–22 × 4.5–7 µm ($\bar{x}$ = 19.63 × 5.49 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores ellipsoid, colorless, thick-walled, verrucose, IKI–, CB–, (5.5–)6–8.5(–9) × (4–)4.5–6.5(–7) µm, L = 7.27 µm, W = 5.43 µm, Q = 1.35 (n = 30/1).

Notes – Based on the ITS+nLSU sequence data (Fig. 3), the new species *Coniophoropsis sinensis* is grouped into *Coniophoropsis*, and is clustered with *C. bambusicola*. However, *C. bambusicola* differs from *C. sinensis* by its brown hymenophore, and longer subcylindrical to suburniform basidia (32–40 × 5–8 µm, Zhao et al. 2018).

Corticiales K.H. Larss.

Index Fungorum number: IF501299

Type family – *Corticiaceae* Herter

Punctulariaceae Donk

Index Fungorum number: IF81315

Type genus – *Punctularia* Pat.

Punctulariopsis Ghob.-Nejh.

Index Fungorum number: IF518085

The genus *Punctulariopsis* Ghob.-Nejh. was established in 2010, and was typified by *Punctulariopsis subglobispora* (Hallenb. & Hjortstam) Ghob.-Nejh., in which this genus contains five species currently (Ghobad-Nejhad et al. 2010). The genus is characterized by resupinate basidiomata, reddish-ochraceous, smooth hymenium surface, a monomitic hyphal system, smooth or irregularly encrusted and lightly branched dendrohyphidia and broadly ellipsoid, smooth basidiospores (Ghobad-Nejhad et al. 2010, Muhammad et al. 2024). This study introduces a new species *Punctulariopsis asiana*, from this genus.

Punctulariopsis asiana Y. Yang & C.L. Zhao, sp. nov. Fig. 16

Index Fungorum number: IF854082; Facesoffungi number: FoF16603

Etymology – Asiana (Lat.): referring to the locality (Asia) of the type specimen.

Type – China, Yunnan Province, Qujing, Zhanyi, Dapo Town, Tuole Village, 25°41′30″ N, 103°33′25″ E; 2060 m, on the fallen branches of angiosperm, 7 March 2023, CLZhao 27479 (SWFC, holotype).

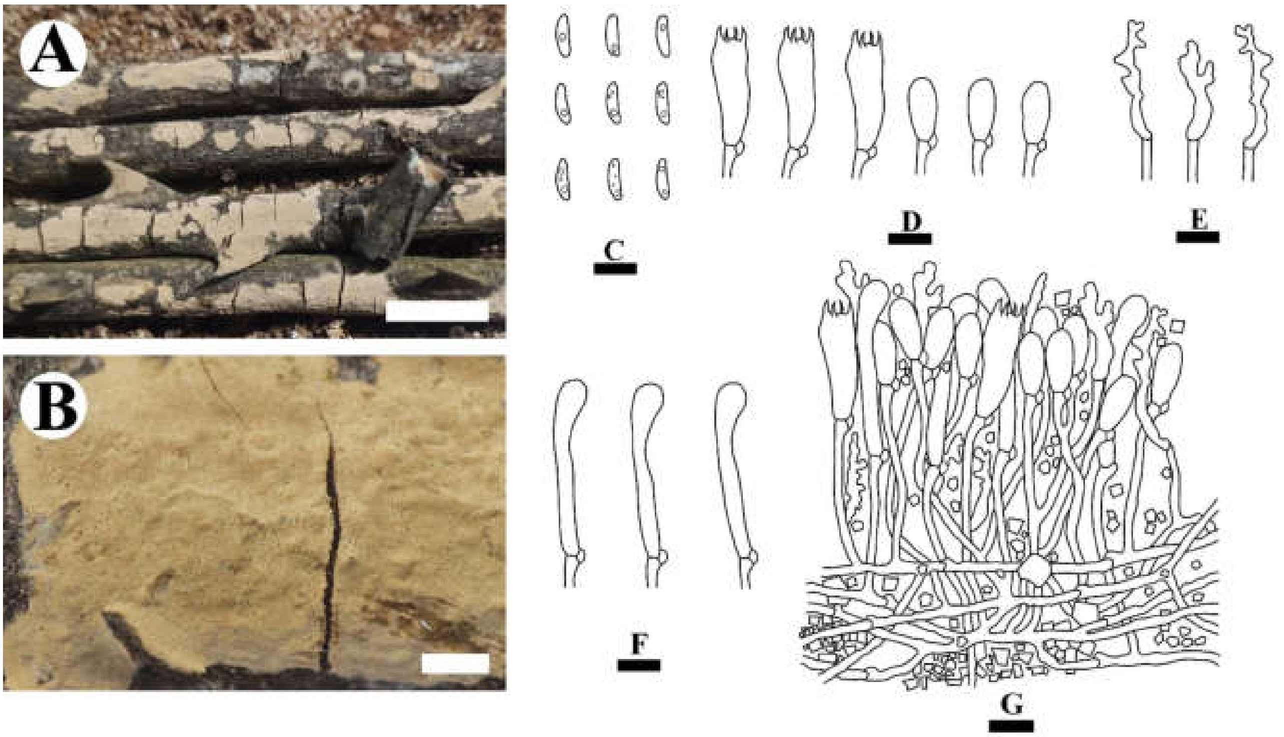

Figure 16 – Basidiomata and microscopic structures of *Punctulariopsis asiana* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Dendrohyphidia. F Cystidia. G A section of hymenium. Bars: A = 1 cm, B = 1 mm, C–G = 10 µm.

Diagnosis – Differs from *Punctulariopsis cremeoalbida* (M.J. Larsen & Nakasone) Ghob.-Nejh by collect from East Asia, with salmon hymenophore, and cylindrical to sub-allantoid basidiospores.

Description – Basidiomata annual, resupinate, adnate but easily separable, membranous when fresh, becoming rigid upon drying, up to 6 cm long, up to 1 cm wide, 100–200 µm thick. Hymenial surface smooth, salmon when fresh, turn to salmon to peach upon drying. Sterile margin white, up to 1 mm.

Hyphal system monomitic; generative hyphae with clamp connections, IKI–, CB+, tissues unchanged in KOH. Subhymenial hyphae colorless, more or less interwoven, thin-walled, rarely branched, 3.5–4.5 µm in diameter.

Cystidia subclavate, colorless, thin-walled, mostly embedded, 28.5–43.5 ×7–9 µm ($\bar{x}$ = 34.66 × 7.86 µm). Dendrohyphidia colorless, thin-walled; Basidia clavate, with four sterigmata and a basal clamp connection, 30–40 × 8–12 µm ($\bar{x}$ = 34.28 × 10.09 µm); basidioles dominant, in shape similar to basidia, but slightly smaller.

Basidiospores cylindrical to sub-allantoid, thin-walled, smooth, IKI–, CB–, 7–12.5 × 2–3 µm, L = 10.16 µm, W = 2.51 µm, Q = 4.04 (n = 90/3).

Material examined (paratypes) – China, Yunnan Province, Qujing, Zhanyi, Dapo Town, Tuole Village, 25°41′30″ N, 103°33′25″ E; 2060 m, on the fallen branches of *Pyrus xerophila*, 7 March 2023, CLZhao 27447 (SWFC); Qujing, Zhanyi, Yanzhu Village, 25°47′20″ N, 103°36′11″ E; 1950 m, on the fallen branches of angiosperm, 7 March 2023, CLZhao 27375 (SWFC).

Notes – Based on the ITS+nLSU sequence data (Fig. 4), *Punctulariopsis asiana* grouped with *Punctulariopsis* species, and is clustered with *P. cremeoalbida*. However, *P. cremeoalbida* differs from *P. asiana* by its cream hymenophore, and broadly ellipsoid basidiospores (11–12 × 6.5–8 µm, Larsen & Nakasone 1984).

Hymenochaetales Oberw.

Index Fungorum number: IF90548

Type family – *Hymenochaetaceae* Donk

Hyphodontiaceae Xue W. Wang & L.W. Zhou

Index Fungorum number: IF557193

Type family – *Hyphodontia* J. Erikss.

Hyphodontia J. Erikss.

Index Fungorum number: IF17826

This genus was proposed by J. Erikss. (1958) with *Hyphodontia pallidula* (Bres.) J. Erikss. as the type species. Species in this widespread genus commonly occur in temperate to tropical areas causing white rot. *Hyphodontia* are characterized by a monomitic hyphal system with clamped generative hyphae, broadly-ellipsoid basidiospores (Wang et al. 2023). In addition, the various shapes of cystidia elements are also important morphological characteristics for the identification of the genus. We describe a new species as *Hyphodontia daweishanensis* in this study.

Hyphodontia daweishanensis Y. Yang & C.L. Zhao, sp. nov. Fig. 17

Index Fungorum number: IF854083; Facesoffungi number: FoF16604

Etymology – *Daweishanensis* (Lat.): referring to the locality (Daweishan) of the type specimen.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°56′1″ N, 103°41′31″ E; 2050 m, on the fallen branches of angiosperm, 3 August 2019, CLZhao 18536 (SWFC, holotype).

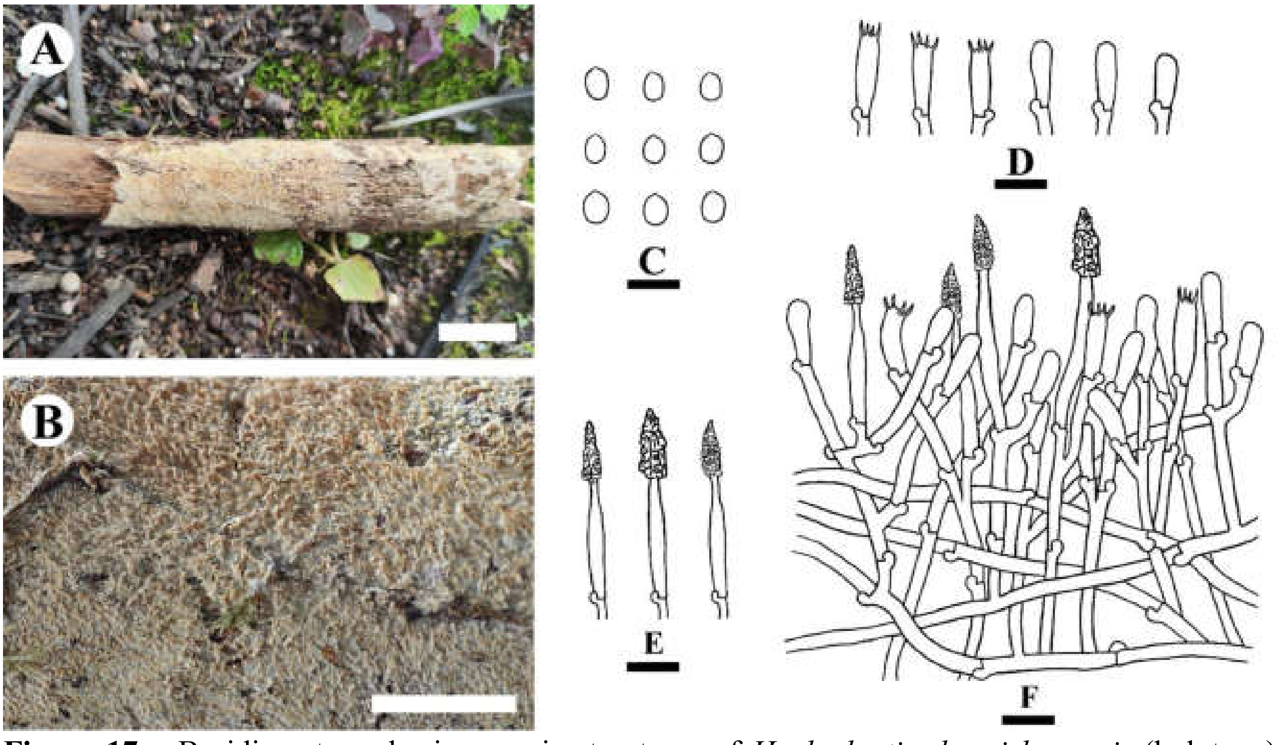

Figure 17 – Basidiomata and microscopic structures of *Hyphodontia daweishanensis* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Lagenocystidia. F A section of hymenium. Bars: A = 2 cm, B = 5 mm, C–F = 10 µm.

Diagnosis – Differs from *Hyphodontia alutaria* (Burt) J. Erikss. by collect from Daweishan, with cream hymenophore, and widder basidiospores (4.5–6.5 × 4–5.5 µm).

Description – Basidiomata annual, resupinate, adnate, without odor or taste when fresh, brittle when dry, up to 10 cm long, 4 cm wide, 50–100 µm thick. Hymenophore surface hydnoid, cream when fresh, peach to apricot-orange upon drying. Sterile margin cream, up to 1 mm.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 3–5 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Lagenocystidia abundant, thin-walled, with broad bases tapering abruptly towards the apices, apically encrusted, 20–40 × 4–6 µm (x̄ = 33.17 × 3.99 µm). Basidia cylindrical, thin-walled, with 4 sterigmata and a basal clamp connection, 15–20 × 4.5–6 µm (x̄ = 18.18 × 5.05 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores broadly ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (4–)4.5–6.5 × (3.5–)4–5.5 µm, L = 5.36 µm, W = 4.71 µm, Q = 1.14–1.2 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°56′1″ N, 103°41′31″ E; 2050 m, on the fallen branches of angiosperm, 3 August 2019, CLZhao 18444 (SWFC).

Notes – Based on the ITS+nLSU+mtSSU+*rpb1*+*rpb2* sequence data (Fig. 5), the new species *Hyphodontia daweishanensis* is grouped into *Hyphodontia*, and is clustered with *H. alutaria* and *H. pachyspora* Xue W. Wang & L.W. Zhou. However, *H. alutaria* can be distinguished from *H. daweishanensis* by its subceraceous basidiomata, pale yellowish hymenophore, and narrower basidiospores (4.5–5 × 3–3.5 µm, Bernicchia & Gorjón 2010). *H. pachyspora* differs from *H. daweishanensis* by its smooth to grandinioid basidiomata, and white hymenophore (Wang et al. 2021).

Kneiffiella P. Karst.

Index Fungorum number: IF17877

Kneiffiella was established by P. Karst. (1889), with *Kneiffiella barba-jovis* (Bull.) P. Karst. as the type species, in which *Kneiffiella* contains 40 accepted species (Viner et al. 2024). The typical feature of this genus is the structure of smooth, floccose, tuberculate, grandinioid, coralloid, odontioid or irpicoid basidiomata, whitish, creamish, yellowish, grey, buff, brown or ochraceous hymenophore surface, monomitic to pseudodimitic hyphal system, and cylindrical, ellipsoid or allantoid basidiospores (Wang et al. 2021). In this study, a new species, *Kneiffiella qujingensis*, is described.

Kneiffiella qujingensis Y. Yang & C.L. Zhao, sp. nov. Fig. 18

Index Fungorum number: IF854084; Facesoffungi number: FoF16605

Etymology – *Qujingensis* (Lat.): referring to the locality (Qujing) of the type specimen.

Type – China, Yunnan Province, Qujing, Zhanyi District, Dapo Town, Tuole Village, 25°41′12″ N, 103°33′2″ E; 1900 m, on the fallen branches of angiosperm, 7 March 2023, CLZhao 27466 (SWFC, holotype).

Diagnosis – Differs from *Kneiffiella subalutacea* (P. Karst.) Jülich & Stalpers by collect from Qujing, with white to cream hymenophore, and ellipsoid basidiospores (6–8 × 1.5–2 µm).

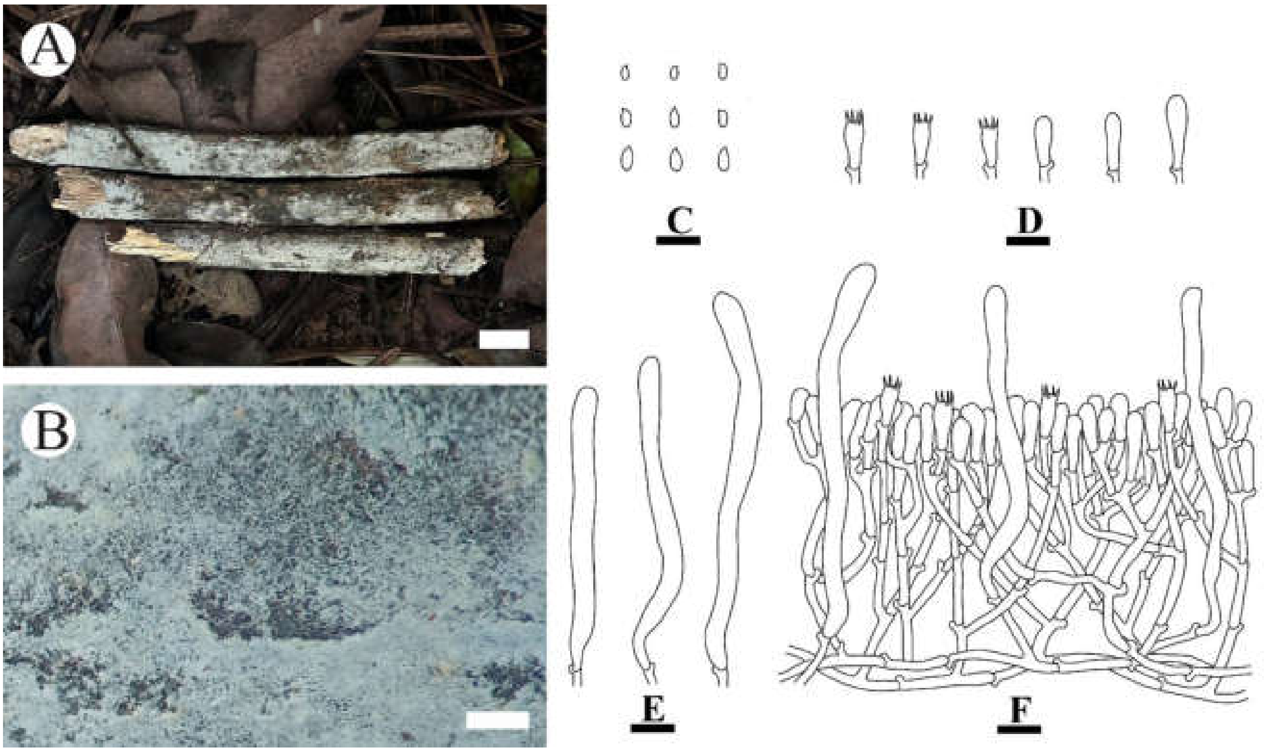

Figure 18 – Basidiomata and microscopic structures of *Kneiffiella qujingensis* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Cystidia. F A section of hymenium. Bars: A = 1 cm, B = 5 mm, C–F = 10 µm.

Description – Basidiomata annual, resupinate, adnate, without odor or taste when fresh, farinaceous when dry, up to 5 cm long, 2 cm wide, 50–100 µm thick. Hymenophore surface smooth, white to cream when fresh, cream upon drying. Sterile margin slightly cream, up to 1 mm.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 2–3.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Cystidia tubular, thin-walled, rising from subiculum with a basal clamp, 35–70 × 4–7 µm ($\bar{x}$ = 49.35 × 5.43 µm). Basidia clavate, thin-walled, with 4 sterigmata and a basal clamp connection, 8–11 × 3–4 µm ($\bar{x}$ = 9.64 × 3.74 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (3–)3.5–7 × 1–2.5 µm, L = 5.04 µm, W = 1.74 µm, Q = 2.89 (n = 30/1).

Notes – Based on the ITS+nLSU+mtSSU+*rpb1*+*rpb2* sequence data (Fig. 5), *Kneiffiella qujingensis* grouped with *Kneiffiella* species, and is clustered with *K. subalutacea*. However, *K. subalutacea* can be delimited from *K. qujingensis* by its yellowish hymenophore, and allantoid basidiospores (6–8 × 1.5–2 µm, Bernicchia & Gorjón 2010).

Polyporales Gäum.

Index Fungorum number: IF90565

Type family – *Polyporaceae* Fr. ex Corda

Hyphodermataceae Jülich

Index Fungorum number: IF81731

Type family – *Hyphoderma* Fr.

Hyphoderma Wallr.

Index Fungorum number: IF17823

The genus *Hyphoderma* Wallr. (1833) typified by *Hyphoderma spiculosum* Wallr., and represented one of the important genera among wood-inhabiting fungi. The genus is characterized by resupinate to effuse-reflexed basidiomata with ceraceous consistency, and smooth to tuberculate, grandinioid or odontioid hymenial surface, a monomitic hyphal system (rarely dimitic) with clamp connections on generative hyphae, presence of cystidia or not, suburniform to subcylindrical and cylindrical basidia, and ellipsoid to subglobose, smooth, thin-walled basidiospores. Currently 117 species have been accepted worldwide (Yang et al. 2023b). This study introduces two new species viz. *Hyphoderma asianum* and *H. qujingense*.

Hyphoderma asianum Y. Yang & C.L. Zhao, sp. nov. Fig. 19

Index Fungorum number: IF854085; Facesoffungi number: FoF16606

Etymology – *Asianum* (Lat.): referring to the locality (Asia) of the type specimen.

Type – China, Yunnan Province, Honghe, Pingbian County, Heping Town, Daweishan National Nature Reserve, 22°56′1″ N, 103°41′31″ E; 1950 m, on the fallen branches of angiosperm, 2 August 2019, CLZhao 18091 (SWFC, holotype).

Diagnosis – Differs from *Hyphoderma prosopidis* (Burds.) Tellería, M. Dueñas & M.P. Martín by collect from East Asia, with cream hymenophore, and smaller barrelled basidia (17.5–22 × 6.5–8 µm).

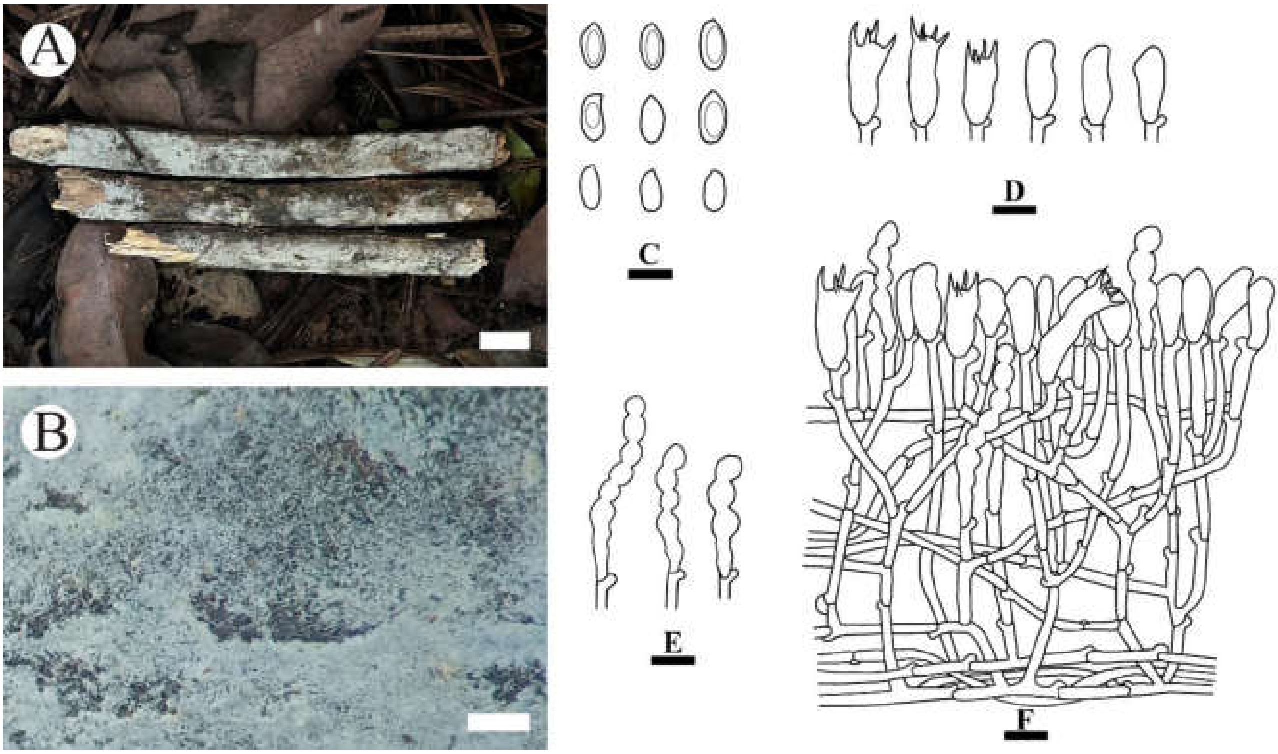

Figure 19 – Basidiomata and microscopic structures of *Hyphoderma asianum* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Cystidia. F A section of hymenium. Bars: A = 1 cm, B = 5 mm, C–F = 10 µm.

Description – Basidiomata annual, resupinate, adnate, ceraceous to membranous, without odor or taste when fresh, up to 11 cm long, 2 cm wide, 50–150 µm thick. Hymenophore surface smooth, floccose, white when fresh, cream upon drying. Sterile margin white, up to 0.5 mm.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 2–3.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Cystidia moniliform, colorless, thin-walled, 20–50 × 4–6 µm ($\bar{x}$ = 30.94 × 5.34 µm). Basidia barrelled, slightly constricted in the median to somewhat sinuous, thin-walled, with 4 sterigmata and a basal clamp connection, 17.5–22 × 6.5–8 µm ($\bar{x}$ = 19.20 × 7.02 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores ellipsoid, colorless, thin-walled, smooth, some with irregular oil droplets inside, IKI–, CB–, (6–)6.5–10 × (3.5–)4–6(–6.5) µm, L = 8.78 µm, W = 4.62 µm, Q = 1.91 (n = 30/1).

Notes – Based on the multiple genes sequence data (Fig. 6), the new species *Hyphoderma asianum* is grouped into *Hyphoderma*, and is clustered with *H. prosopidis*. However, *H. prosopidis* differs from *H. asianum* by its cartridge buff to pinkish buff hymenophore, and larger clavate basidia (40–45 × 8–11 µm, Telleria et al. 2012).

Hyphoderma qujingense Y. Yang & C.L. Zhao, sp. nov. Fig. 20

Index Fungorum number: IF854087; Facesoffungi number: FoF16607

Etymology – *Qujingense* (Lat.): referring to the locality (Qujing) of the type specimen.

Type – China, Yunnan Province, Qujing, Qilin District, Cuishan Forest Park, 25°32′56″ N, 103°42′3″ E; 2050 m, on the fallen branches of *Pinus*, 4 November 2022, CLZhao 26018 (SWFC, holotype).

Diagnosis – Differs from *Hyphoderma marginatum* Z.Y. Duan & C.L. Zhao by collect from Qujing, with capitate halocystidia, and wider barrelled basidia (18–23 × 7–8 µm).

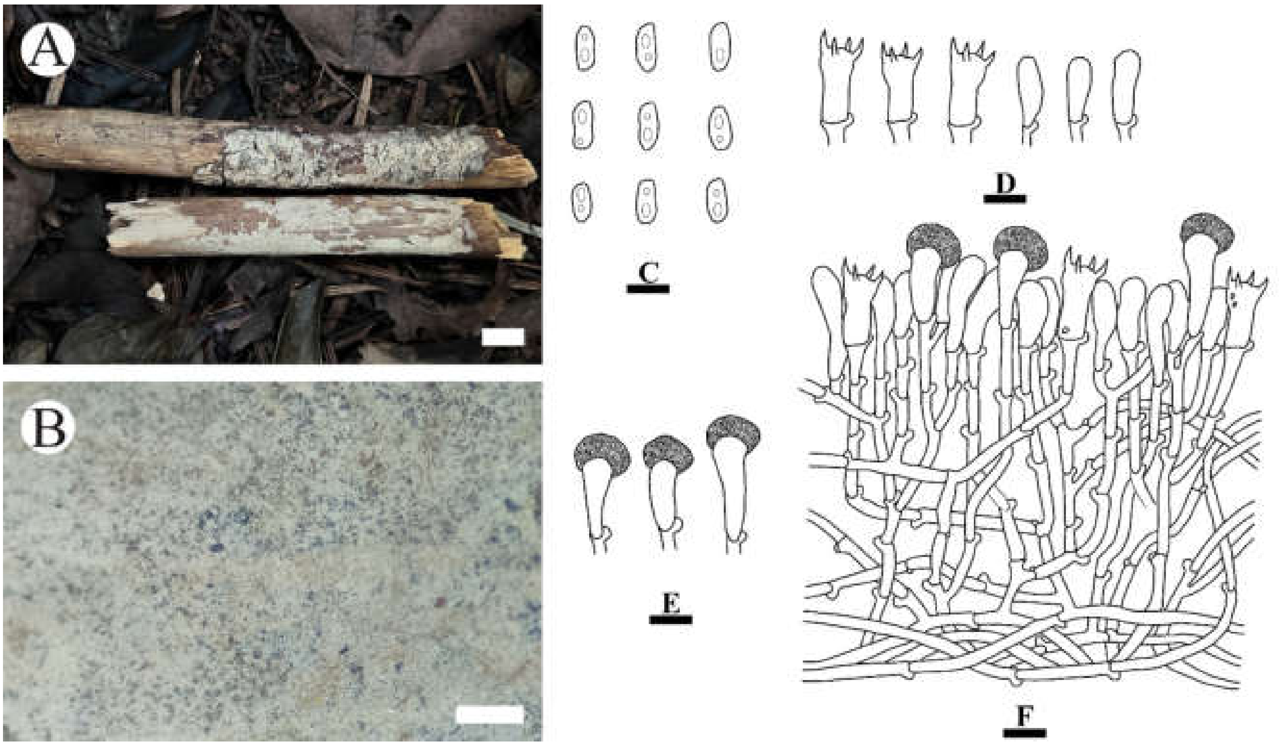

Figure 20 – Basidiomata and microscopic structures of *Hyphoderma qujingense* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Halocystidia. F A section of hymenium. Bars: A = 1 cm, B = 5 mm, C–D = 10 µm.

Description – Basidiomata annual, resupinate, adnate, without odor or taste when fresh, membranous, up to 9 cm long, 2 cm wide, 50–150 µm thick. Hymenophore surface smooth, floccose, cream when fresh, buff to buff-yellow upon drying. Sterile margin cream, up to 1 mm.

Hyphal system monomitic; generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 3–4.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Halocystidia capitate, thin-walled, smooth, 20–40 × 9–13 µm ($\bar{x}$ = 27.89 × 10.59 µm). Basidia barrelled, thin-walled, with 4 sterigmata and a basal clamp connection, 18–23 × 7–8 µm ($\bar{x}$ = 20.78 × 7.29 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores ellipsoid to cylindrical, colorless, thin-walled, smooth, some with irregular oil droplets inside, IKI–, CB–, 7–11.5 × (3–)3.5–5(–5.5) µm, L = 9.39 µm, W = 4.29 µm, Q = 2.21 (n = 30/1).

Notes – Based on the ITS+nLSU+mtSSU+*rpb1*+*rpb2* sequence data (Fig. 6), the new species *Hyphoderma qujingense* is grouped into *Hyphoderma*, and is sister with *H. marginatum*. However, *H. marginatum* can be distinguished from *H. qujingense* by its cylindrical cheilocystidia and slender clavate basidia (21–31.5 × 5–7 µm, Duan et al. 2023).

Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David
Index Fungorum number: IF90569
Type family – *Russulaceae* Lotsy

Peniophoraceae Lotsy
Index Fungorum number: IF81123
Type family – *Peniophora* Cooke

Gloiothele Bres.
Index Fungorum number: IF17678

The genus *Gloiothele* Bres. was established in 1920, and was typified by *Gloiothele lamellosa* (Henn.) Bres., in which this genus contains 13 species currently. The genus is characterized by monomitic hyphal system, clampless corticioid species with sulfopositive gloeocystidia and smooth, amyloid basidiospores (Bernicchia & Gorjón 2010). This study introduces a new species *Gloiothele yunnanensis* from this genus.

Gloiothele yunnanensis Y. Yang & C.L. Zhao, sp. nov. Fig. 21

Index Fungorum number: IF854088; Facesoffungi number: FoF16608

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, 22°56′1″ N, 103°41′31″ E; 1900 m, on the fallen branches of angiosperm, 1 August 2019, CLZhao 17663 (SWFC, holotype).

Diagnosis – Differs from *Gloiothele lactescens* (Berk.) Hjortstam by collect from Yunnan Province, with ceraceous basidiomata, yellowish hymenophore, shorter basidia (13–20 × 6–8.5 µm) and globose to subglobose basidiospores.

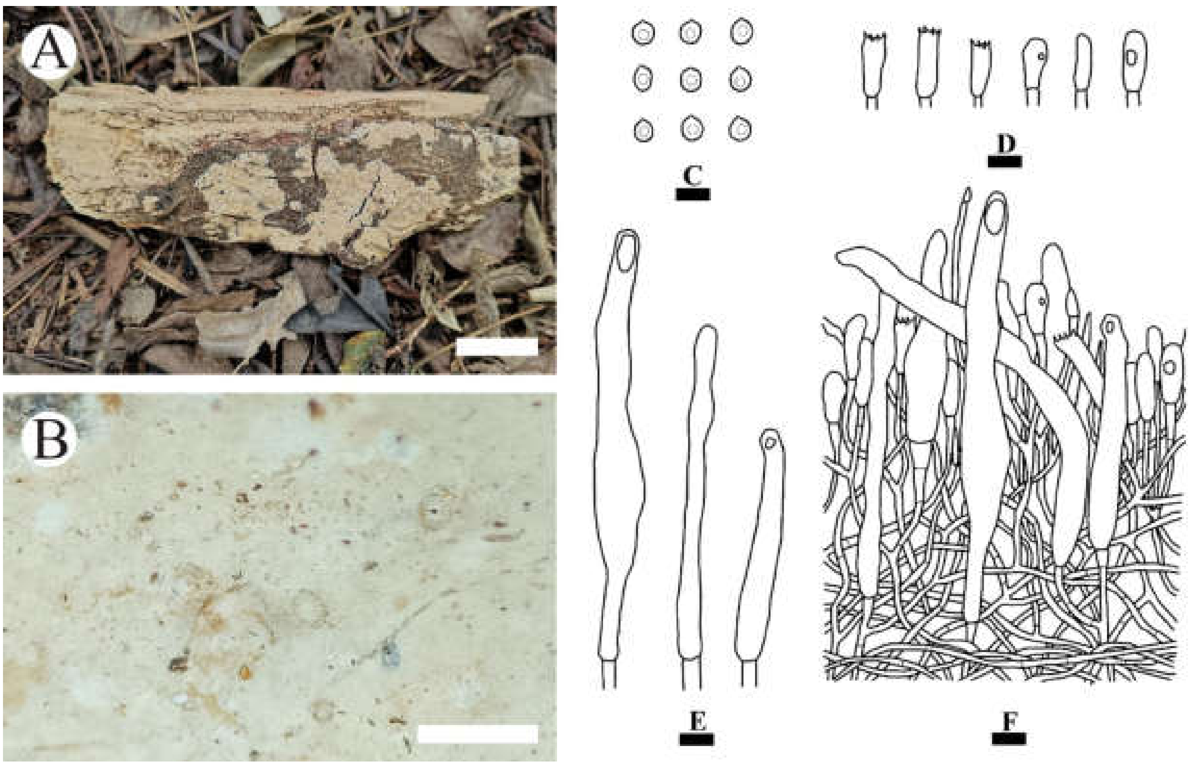

Figure 21 – Basidiomata and microscopic structures of *Gloiothele yunnanensis* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Gloeocystidia. F A section of hymenium. Bars: A = 1 cm, B = 1 mm, C–D = 10 µm.

Description – Basidiomata annual, resupinate, adnate, ceraceous, without odor or taste when fresh, up to 7 cm long, 5 cm wide, 500–1000 µm thick. Hymenophore surface smooth, buff when fresh, salmon to olivaceous buff upon drying. Sterile margin cream to buff, up to 1 mm.

Hyphal system monomitic; generative hyphae with simple septa, colorless, thin-walled, frequently branched, interwoven, 1–2.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Gloeocystidia numerous, cylindrical to fusiform, colorless, thin-walled, 30–150 × 7–10 µm ($\bar{x}$ = 99.58 × 8.23 µm). Basidia clavate to barreled, thin-walled, with 4 short sterigmata and a basal simple septum, 13–20 × 6–8.5 µm ($\bar{x}$ = 16.81 × 7.08 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores globose to subglobose, colorless, thin-walled, smooth, with oil droplets inside, IKI–, CB–, (5–)5.5–7 × (4–)4.5–6.5(–7) µm, L = 6.04 µm, W = 5.64 µm, Q = 1.11 (n = 30/1).

Notes – Based on the ITS+nLSU sequence data (Fig. 8), the new species *Gloiothele yunnanensis* is grouped into *Gloiothele*, and is clustered with *G. lactescens*. However, *G. lactescens* differs from *G. yunnanensis* by its yellowish hymenophore, longer basidia (45–60 × 6–7 µm) and ellipsoid basidiospores (Bernicchia & Gorjón 2010).

Peniophora Cooke

Index Fungorum number: IF18201

The genus *Peniophora* Cooke was introduced in 1879, and typified by *Peniophora quercina* (Pers.) Cooke, is one of the oldest genera of corticioid fungi. 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 basidiomes 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 (Xu et al. 2023). We report a new species of *Peniophora fissurata* in this study.

Peniophora fissurata Y. Yang & C.L. Zhao, sp. nov. Fig. 22

Index Fungorum number: IF854089; Facesoffungi number: FoF16609

Etymology – *Fissurata* (Lat.): referring to the cracking hymenial surface.

Type – China, Yunnan Province, Qujing, Zhanyi District, Dapo Town, Tuole Village, 25°41′12″ N, 103°33′2″ E; 1900 m, on the fallen branches of angiosperm, 7 March 2023, CLZhao 27436 (SWFC, holotype).

Diagnosis – Differs from *Peniophora reidii* Boidin & Lanq by coriaceous basidiomata, cracking hymenophore surface, and cylindrical basidiospores (10–13 × 3.5–5 µm).

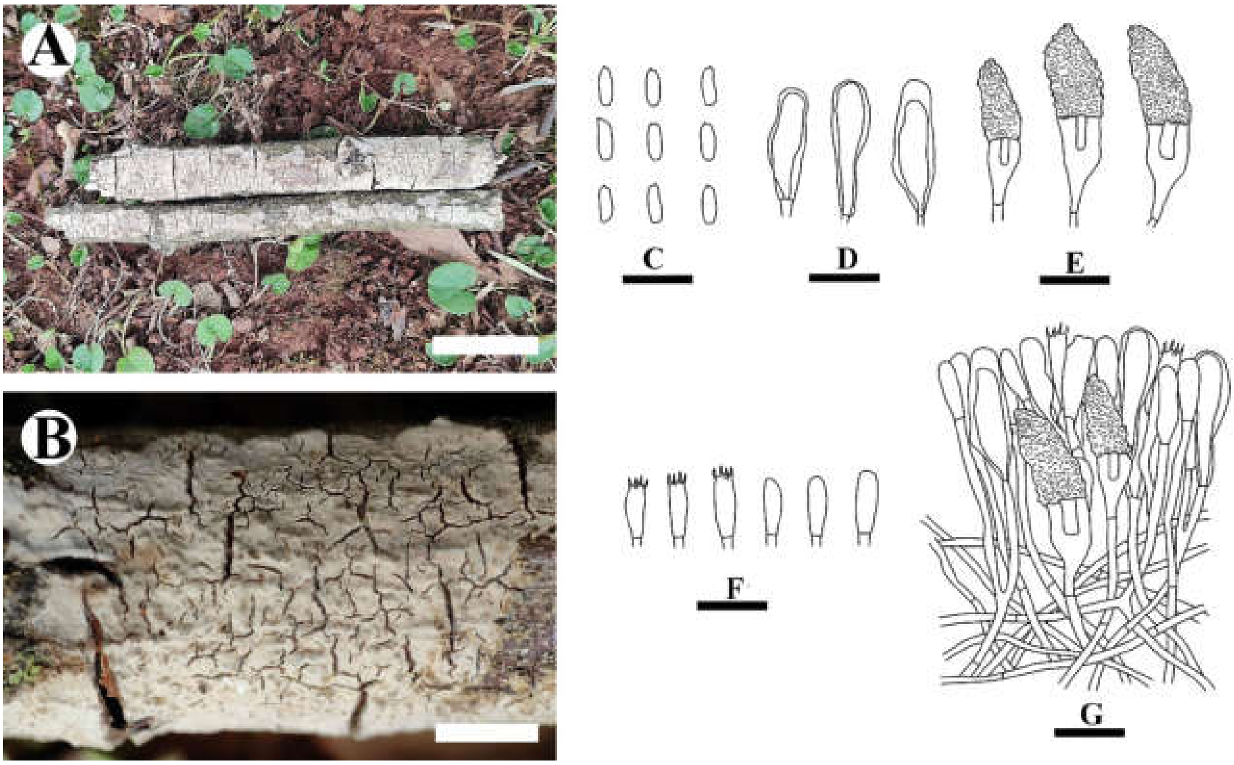

Figure 22 – Basidiomata and microscopic structures of *Peniophora fissurata* (holotype). A–B Basidiomata. C Basidiospores. D Gloeocystidia. E Lamprocystidia. F Basidia and basidioles. G A section of hymenium. Bars: A = 2 cm, B = 3 mm, C–G = 10 µm.

Description – Basidiomata annual, resupinate, adnate, coriaceous, without odor or taste when fresh, brittle when dry, up to 5 cm long, 2 cm wide, 100–300 µm thick. Hymenophore surface smooth, cracked, lightly vinaceous grey when fresh, buff upon drying. Sterile margin light vinaceous grey, up to 1 mm.

Hyphal system monomitic; generactive hyphae with simple septa, colorless, thin-walled, frequently branched, interwoven, 2.5–3.5 µm in diameter; IKI–, CB+, tissues unchanged in KOH.

Cystidia of two types: (1) gloeocystidia subclavate, colorless, slightly thick-walled, with a basal simple septum, 24–52 × 7–14 µm ($\bar{x}$ = 36.43 × 11.29 µm); (2) lamprocystidia numerous, colorless, thick-walled, heavily encrusted with crystals in the middle and upper parts, with a basal simple septum, 34–58 × 7–15 µm ($\bar{x}$ = 48.97 × 11.42 µm). Basidia clavate, thin-walled, with 4 sterigmata and a basal simple septum, 10.5–23 × 5–8 µm ($\bar{x}$ = 15.34 × 6.66 µm); basidioles in shape similar to basidia, but slightly smaller.

Basidiospores cylindrical, colorless, thin-walled, smooth, IKI–, CB+, (9.5–)10–13(–14) × 3.5–5 µm, L = 11.16 µm, W = 4.17 µm, Q = 2.59–2.68 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Lincang, Fengqing County, Yaojie Town, Xingyuan Village, 24°36′24″ N, 100°9′54″ E; 2100 m, on the fallen branches of angiosperm, 22 October 2022, CLZhao 25689 (SWFC).

Notes – Based on the ITS+nLSU sequence data (Fig. 9), *Peniophora fissurata* is grouped into *Peniophora*, and is sister with *P. reidii*. However, *P. reidii* can be distinguished from *P. fissurata* by its membranaceous basidiomata, and the lack of clamps on the hyphae (Boidin & Lanquetin 1983).

Russulaceae Lotsy

Index Fungorum number: IF81358

Type family – *Russula* Pers.

Gloeopeniophorella Rick

Index Fungorum number: IF22169

This genus was proposed by Rick (1934), with *Gloeopeniophorella rubroflava* Rick as the type species. It includes four species. This genus is characterized by resupinate basidiomata, a smooth to tuberculate hymenophore surface, a monomitic hyphal system with simple-septate generative hyphae, and ellipsoid basidiospores (Bernicchia & Gorjón 2010). This study describes a new species, *Gloeopeniophorella bambusicola*.

Gloeopeniophorella bambusicola Y. Yang & C.L. Zhao, sp. nov. Fig. 23

Index Fungorum number: IF854090; Facesoffungi number: FoF16610

Etymology – *Bambusicola* (Lat.): refers to growing on bamboo.

Type – China, Yunnan Province, Zhaotong, Yongshan County, Mugan Town, Wumengshan Nature Reserve, 28°8′10″ N, 103°58′2″ E, 1180 m, on the fallen branches of bamboo, 7 November 2023, CLZhao 35561 (SWFC, holotype).

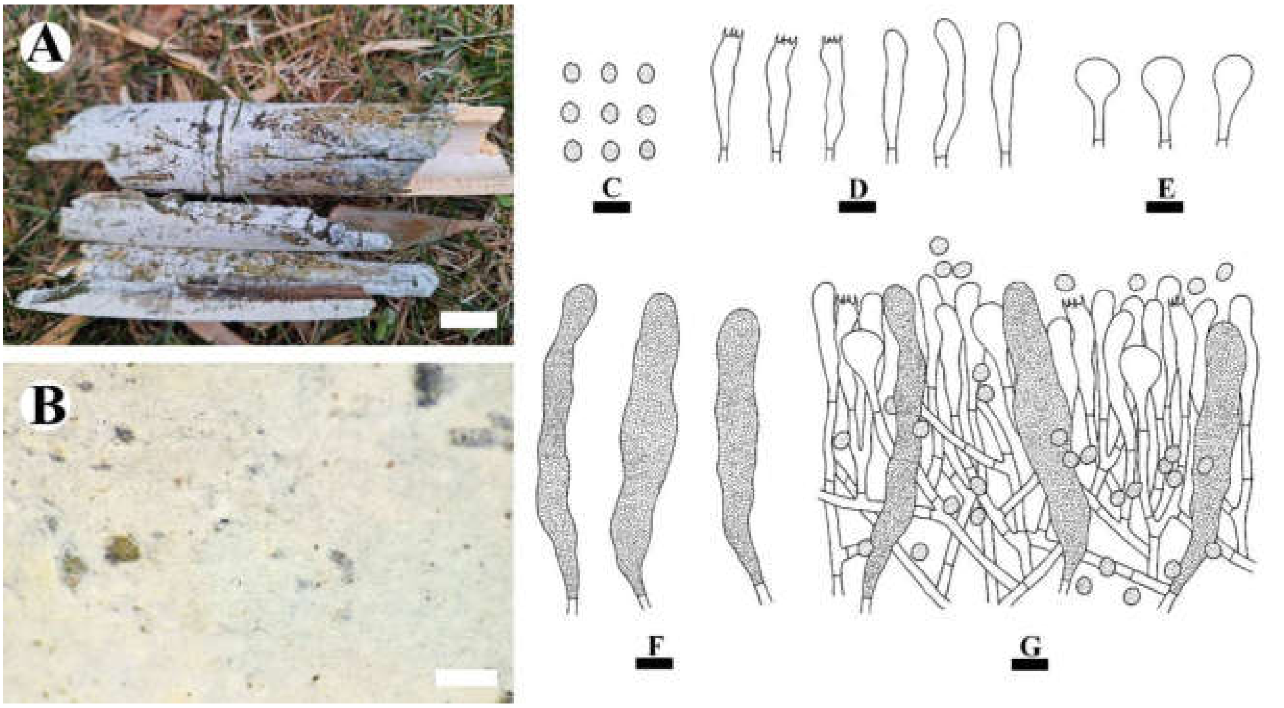

Figure 23 – Basidiomata and microscopic structures of *Gloeopeniophorella bambusicola* (holotype). A–B Basidiomata. C Basidiospores. D Basidia and basidioles. E Cystidia with subglobose apex. F Gloeocystidia. G A section of hymenium. Bars: A = 1 cm, B = 1 mm, C–D = 10 µm.

Diagnosis – Differs from *Gloeopeniophorella convolvens* (P. Karst.) Boidin, Lanq. & Gilles by growing on bamboo, with farinaceous basidiomata, white to cream hymenophore, and wider subglobose to globose basidiospores (4.5–6 × 3.5–5 µm).

Description – Basidiomata annual, resupinate, closely adnate, farinaceous, up to 12 cm long, 8 cm wide and 0.2 mm thick. Hymenophore surface smooth, white when fresh, white to cream when dry. Sterile margin pale cream, up to 1 mm.

Hyphal system monomitic; generative hyphae simple-septate, colorless, thin-walled, frequently branched, interwoven, 3–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Cystidia of two kinds: 1) cystidia with subglobose apex, colorless, thin-walled, mostly embedded, 25.5–32 × 11–12.5 µm ($\bar{x}$ = 28.64 × 11.87 µm); 2) gloeocystidia subcylindrical to subclavate, slightly sinuous, with granular content, colorless, thin-walled, mostly embedded, 70.5–94 × 8.5–15 µm ($\bar{x}$ = 84.16 × 10.56 µm). Basidia clavate, colorless, thin-walled, with a basal simple septum and 4-sterigmata, 27–35 × 5–6.5 µm ($\bar{x}$ = 30.91 × 6.11 µm); basidioles dominant, in shape similar to basidia, but slightly smaller.

Basidiospores subglobose to globose, colorless, thin-walled, verrucose, IKI–, CB–, 4.5–6 × 3.5–5 µm, L = 5.25 µm, W = 4.36 µm, Q = 1.20 (n = 30/1).

Notes – Based on the ITS+nLSU sequence data (Fig. 10), the new species *Gloeopeniophorella bambusicola* is grouped into *Gloeopeniophorella*, and is clustered with *G. convolvens*. However, *G. convolvens* differs from *G. bambusicola* by its tuberculate basidiomata, white to yellowish hymenophore, and narrower ellipsoid basidiospores (4–5.5 × 2.5–3.5 µm, Boidin et al. 1997).

Sistotremastrales L.W. Zhou & S.L. Liu

Index Fungorum number: IF559875

Type family – *Sistotremastraceae* L.W. Zhou & S.L. Liu

Sistotremastraceae L.W. Zhou & S.L. Liu

Index Fungorum number: IF559876

Type family – *Sistotremastrum* J. Erikss.

Sertulicium Spirin, Volobuev & K.H. Larss.

Index Fungorum number: IF833941

This genus was proposed by Spirin, Volobuev & K.H. Larss. (2021) with *Sertulicium niveocremeum* (Höhn. & Litsch.) Spirin & K.H. Larss. as the type species, which includes seven species. This genus is characterized by very thin to rather thin, pruinose or waxy basidiomata, smooth hymenophore surface, a monomitic hyphal system with clamp connections generative hyphae, and narrowly ellipsoid to cylindrical basidiospores (Spirin et al. 2021). We describe a new species *Sertulicium yunnanense*, in this study.

Sertulicium yunnanense Y. Yang & C.L. Zhao, sp. nov. Fig. 24

Index Fungorum number: IF854091; Facesoffungi number: FoF16611

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

Type – China, Yunnan Province, Qujing, Zhanyi District, Lingjiao Town, 25°52′2″ N, 103°40′9″ E; 1850 m, on the fallen branches of *Pinus yunnanensis*, 6 March 2023, CLZhao 27295 (SWFC, holotype).

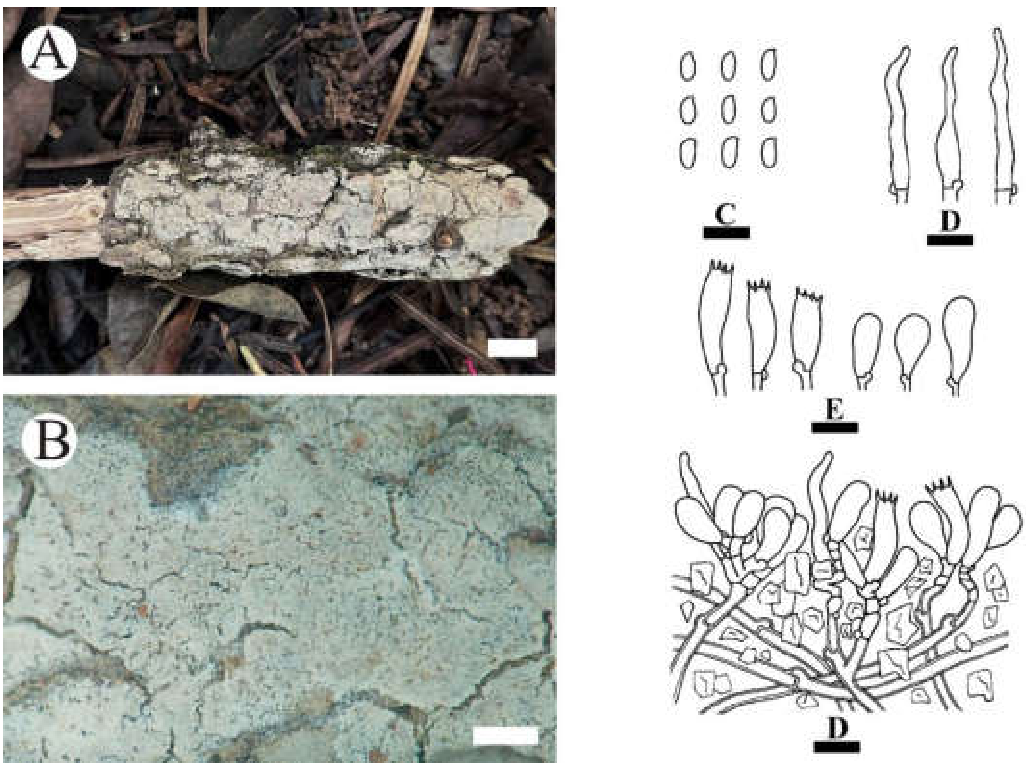

Figure 24 – Basidiomata and microscopic structures of *Sertulicium yunnanense* (holotype). A–B Basidiomata. C Basidiospores. D Hyphidia. E Basidia and basidioles. F A section of hymenium. Bars: A = 1 cm, B = 1 mm, C–F = 10 µm.

Diagnosis – Differs from *Sertulicium vernale* Spirin & Volobuev by collect from Yunnan Province, with cream to pale ochraceous hymenophore, suburniform basidia, and ellipsoid basidiospores (5–6.5 × 2–3 µm).

Description – Basidiomata annual, effused, adnate, farinaceous, without odor or taste when fresh, brittle when dry, up to 10 cm long, 4 cm wide, 50–200 µm thick. Hymenophore surface smooth, pruinose, cream when fresh, pale ochraceous upon drying. Sterile margin cream, up to 0.5 mm.

Hyphal system monomitic; generative hyphae with clamp connections, usually encrusted crystals. Subicular hyphae interwoven, slightly thick-walled, irregularly branched, 3–4.5 µm in diameter. Tramal hyphae thin-walled, rather loosely arranged, interwoven, as a rule short-celled and more or less distinctly inflated, 2–4 µm in diameter. Subhymenial hyphae thin-walled, easily collapsing, often short-celled and slightly inflated or twisted, 2–3.5 µm in diameter.

Cystidia absent. Hyphidia occasionally present, tapering, with constrictions, thin-walled, with a basal clamp connection, 15–35 × 3–5 µm ($\bar{x}$ = 27.33 × 4.62 µm). Basidia suburniform, with 4 sterigmata and a basal clamp connection, 12–20 × 4–7 µm ($\bar{x}$ = 16.90 × 5.43 µm); basidioles bladder-shaped to subglobose, slightly smaller than basidia.

Basidiospores narrowly ellipsoid, colorless, thin-walled, smooth, IKI–, CB+, (4.5–)5–6.5(–7) × 2–3(–3.5) µm, L = 5.78 µm, W = 2.52 µm, Q = 2.29 (n = 30/1).

Notes – Based on the ITS+nLSU sequence data (Fig. 11), *Sertulicium yunnanense* is grouped into *Sertulicium*, and is clustered with *S. vernale*. However, *S. vernale* can be distinguished from *S. yunnanense* by its greyish hymenophore and clavate basidia (Spirin et al. 2021).

DISCUSSION

In recent years, many taxa of wood-inhabiting fungi have been continuously reported and recorded all over the world (Wijayawardene et al. 2020, Yu et al. 2021, Mao et al. 2023, Shen et al. 2023, Zhao et al. 2023, Deng et al. 2024a). Over the past ten years, global studies have explored the diversity, ecology, and systematics of wood-inhabiting fungi, with variations in focus among the taxa studied (Dai et al. 2015, Hibbett 2016, Hyde et al. 2021, Wijayawardene et al. 2020, He et al. 2022, Cho et al. 2023, Zhou et al. 2024). In addition, the diversity of wood-inhabiting fungi in the Yunnan-Guizhou Plateau of China holds great significance.

Based on taxonomy and molecular systematics research recently, the macroscopic and microcosmic characteristics are inconsistent with molecular systematics from wood-inhabiting fungi (Liu et al. 2023, Nagy et al. 2023). In the present study, the analyses find that the different important macroscopic characteristics of species within the family *Hyphodermataceae* cluster together in the phylogenetic tree. The different taxa of the representative genus *Hyphoderma* have different hymenophores as smooth, floccose, and grandinioid, but they also have similar microscopic characteristics. We have listed nine species in three different genera to uncover this phenomenon (Fig. 1). *Hyphoderma floccosum* C.L. Zhao & Q.X. Guan, *H. niveomarginatum* Yang Yang & C.L. Zhao, *H. tenuissimum* C.L. Zhao & Q.X. Guan have the floccose, smooth and grandinioid basidiomata, respectively, however, they are closely related in the ITS+nLSU+mtSSU+*rpb1*+*rpb2* sequences phylogenetic trees, especially *H. floccosum* and *H. tenuissimum* (Fig. 6), and they all have similar microcosmic characteristics as the monomitic hyphal system, generative hyphae with clamps, clavate basidia and ellipsoid basidiospores with similar size (6–10.5 × 3–5 µm) (Guan et al. 2021a, Guan & Zhao 2021, Yang et al. 2023b). *Trechispora fimbriata* C.L. Zhao have hydnoid basidiomata, *T. olivacea* K.Y. Luo & C.L. Zhao have the farinaceous basidiomata, and *T. pileate* K.Y. Luo & C.L. Zhao have pileate basidiomata, in which *T. fimbriata* and *T. olivacea* have a close phylogenetic relationship in the ITS sequences phylogenetic trees (Luo & Zhao 2022), and both have a monomitic hyphal system with the generative hyphae having clamps, and ornamented ellipsoid basidiospores with similar size (2.5–4 × 1.5–3 µm) (Zhao & Zhao 2021, Luo & Zhao 2022), but *T. pileate* formed a single clade in ITS+nLSU phylogenetic trees (Luo et al. 2024). *Xylodon kunmingensis* L.W. Zhou & C.L. Zhao, *X. punctus* K.Y. Luo & C.L. Zhao and *X. puerensis* C.L. Zhao have odontioid, smooth and poroid basidiomata, respectively, in which they are closely related in the ITS+nLSU sequences phylogenetic trees (Zhang et al. 2024), and they also have similar microcosmic characteristics as a monomitic hyphal system, generative hyphae with clamps, ellipsoid and thin-walled basidiospores (Shi et al. 2019, Luo et al. 2022, Guan et al. 2023). There are plenty of taxa having this phenomenon, such as *Lyomyces*, *Peniophorella*, *Phebia*, and so on; in which these species are located in different families and even different orders, and numerous species of wood-inhabiting fungi have inconsistencies in macroscopic and microcosmic characteristics with molecular systematics. We speculate that the macroscopic characteristics of wood-inhabiting fungi have a fast evolutionary process affected by the external environment such as latitude, altitude, forest type, temperature, and humidity, but the microcosmic characteristics are free from disturbing by the external environment, which reveals that the microcosmic characteristics have a close degree of fitting with the phylogenetic topology in the wood-inhabiting fungal group.

In the present study, a new genus *Gracilihypha* and thirteen new species *viz. Coniophoropsis sinensis*, *Gloeopeniophorella bambusicola*, *Gloiothele yunnanensis*, *Gracilihypha abeliae*, *Hyphoderma asianum*, *H. qujingense*, *Hyphodontia daweishanensis*, *Kneiffiella qujingensis*, *Merismodes wumengshanensis*, *M. yunnanensis*, *Peniophora fissurata*, *Punctulariopsis asiana*, and *Sertulicium yunnanense*, are described based on the phylogenetic analyses and morphological characteristics. These thirteen new species belong to eleven genera, eight families, and seven orders.

Despite the discovery of high species diversity among wood-inhabiting fungi in recent years (Cui et al. 2019, Wijayawardene et al. 2020, He et al. 2022, Ji et al. 2022, Zhao et al. 2023, Luo et al. 2024, Wang et al. 2024), the systematic studies still need to be conducted for many groups. The Yunnan-Guizhou Plateau is rich in woody plant species, providing excellent substrates for wood-inhabiting fungi. After noting important information (Rathnayaka et al. 2024), all specimens were meticulously collected from Yunnan Province in China, a region known for its rich biodiversity. Hence, studying the diversity of wood-inhabiting fungi in the Yunnan-Guizhou Plateau of China is of great significance. Based on this study, the results not only discuss the inconsistency of macroscopic and microcosmic characteristics with molecular systematics from wood-inhabiting fungi but also enrich the species diversity of fungi worldwide. It is also necessary for the genomics and transcriptomics techniques to be used to further reveal the environmental adaptation mechanism of their morphological characteristics and ecological functions.

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