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ISSN 2077 - 7019 (Electronic)
ISSN 2077 - 7000 (Linking)

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16.525 (2021) Impact factor

Q1 in category "Ecology, Evolution, Behavior and Systematics" and " Plant Science"

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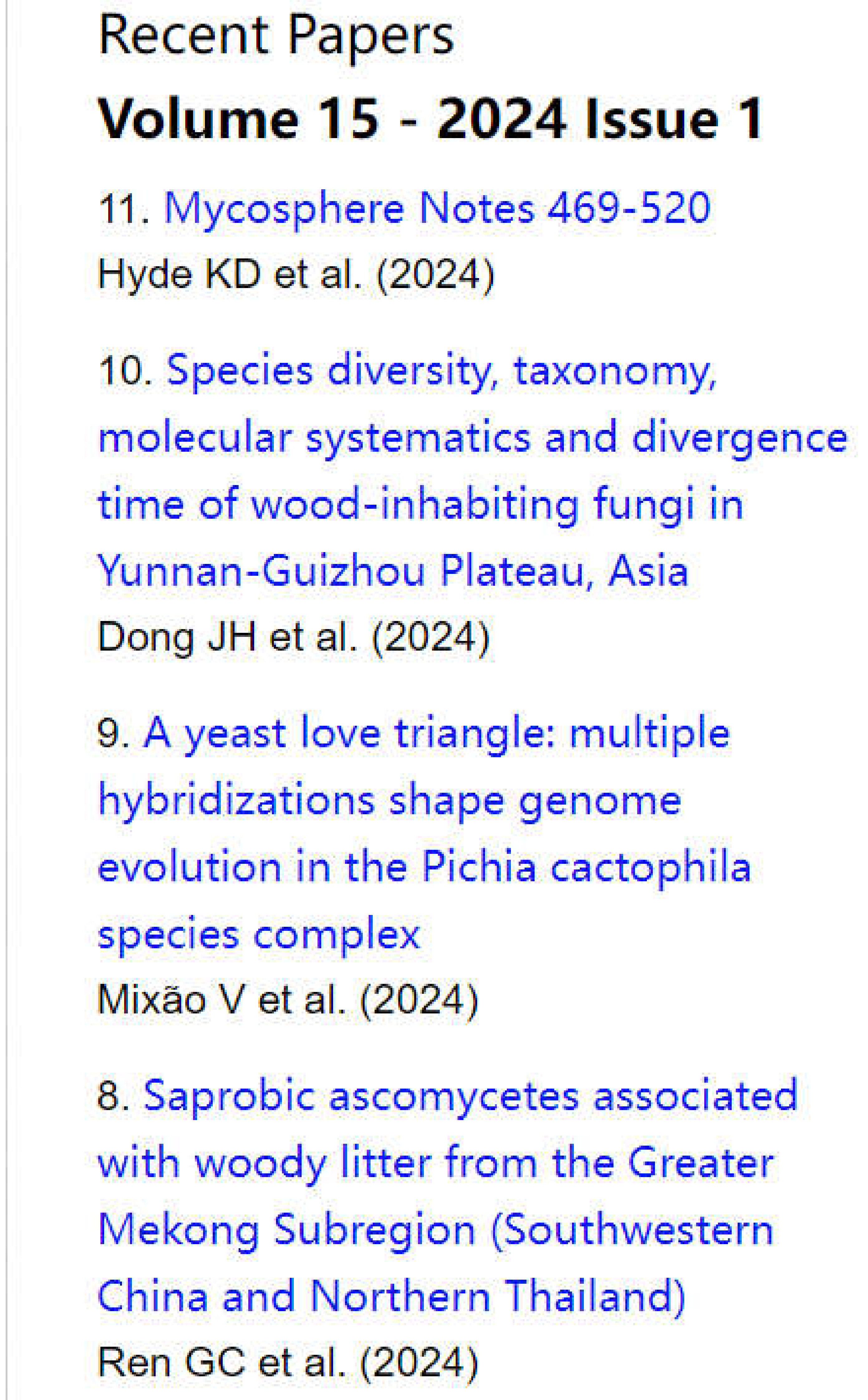

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MYCOSPHERE 15(1): 1110–1293 (2024) www.mycosphere.org ISSN 2077 7019
Doi 10.5943/mycosphere/15/1/10

ARTICLE

Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia

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Citation – Dong JH, Li Q, Yuan Q, Luo YX, Zhang XC, Dai YF, Zhou Q, Liu XF, Deng YL, Zhou HM, Muhammad A, Zhao CL 2024 – Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. Mycosphere 15(1), 1110–1293, Doi 10.5943/mycosphere/15/1/10

Abstract

Wood-inhabiting fungi play a fundamental role in ecosystem processes, particularly in wood degradation and the recycling of organic matter. Recognized as pivotal contributors to the intricate balance of forest ecosystems, these fungi are renowned as “key players” due to their enzymatic prowess, effectively breaking down woody components like lignin, cellulose, and hemicellulose. In the current study, we embarked on an extensive collection expedition spanning various ecological niches. Subsequently, a comprehensive analysis of phylogenetic relationships among fungal wood-inhabiting collections was conducted, based on DNA sequences from multiple loci. These loci 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 (TEF1), RNA polymerase II largest subunit (RPB1), and the second subunit of RNA polymerase II (RPB2). This multi-locus approach allowed for a robust assessment of the evolutionary relationships within the fungal community. Our analyses revealed the new families Hypochniciaceae and Neohypochniciaceae, and a new genus *Donkiella* which are introduced forty-two new species, novel species described in this paper include *Artomyces niveus*, *A. yunnanensis*, *Corticium roseoalbum*, *Dendrothele yunnanensis*, *Donkiella yunnanensis*, *Efibula daweishanensis*, *Etheirodon roseoalbum*, *Fibrodontia bambusicola*, *Hydnoporia pinicola*, *H. yunnanensis*, *Lyomyces daweishanensis*, *L. incanus*, *L. lincangensis*, *L. luteoalbus*, *L. qujingensis*, *L. sinensis*, *Neohypochnicium daweishanense*, *N. farinaceum*, *N. murinum*, *N. velutinum*, *N. yunnanense*, *N. zixishanense*, *Peniophorella daweishanensis*, *P. olivacea*, *Phanerochaete mopanshanensis*, *Phlebiopsis daweishanensis*, *Radulomyces hydnoides*, *R. yunnanensis*, *R. zixishanensis*, *Scytinostroma daweishanense*, *Skeletocutis rhizomorpha*, *Skvortzovia incana*, *Steccherinum lincangense*, *S. longiaculeiferum*, *S. weishanense*, *Subulicystidium yunnanense*, *Tubulicrinis pini*, *Xylodon bamburesupinus*, *X. fissilus*, *X. hydnoidus*, *X. olivaceobubalinus* and *X. pingbianensis*. To enhance accessibility and understanding, the paper includes illustrated descriptions of the newly proposed species and comprehensive notes on the genera under scrutiny.

Submitted: 27 January 2024; **Accepted:** 18 June 2024; **Published:** 27 August 2024
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Accepted by: Ishara Manawasinghe

Keywords – 45 new taxa – Basidiomycota – Hymenochaetales – Molecular systematics – Polyporales – Taxonomy – Wood-decaying fungi

INTRODUCTION

Wood-inhabiting fungi, primarily basidiomycetes, possess industrial, medicinal, edible, and economic value while others contain toxic metabolites (Wu et al. 2019, Zhou et al. 2022, Cheng et al. 2023, Niego et al. 2023) They grow in various kinds of living trees, dead and fallen trunks, fallen branches and stumps (M'Barek et al. 2020, Runnel et al. 2021, Dong et al. 2023a). Wood-inhabiting fungi, with their profound impact on ecosystem processes, stand out as pivotal contributors to the intricate balance and energy flow within forest ecosystems (Dai et al. 2015b, Li et al. 2022a, Xu et al. 2023). They have an ability to degrade plant remains and different environmental contaminants through their extensive capabilities of organic compound degradation (James et al. 2020). Wood-inhabiting fungi produce ligninolytic and cellulolytic enzymes that break down lignins, celluloses, and hemicelluloses, underscores their significance in the recycling of organic matter and nutrient cycling, typically catogerized as the white-rot and brown-rot fungi (Bucher et al. 2004, Liu et al. 2022b). Wood-inhabiting fungi, a large group of Basidiomycota, exhibit diverse morphological features in their basidiomata, and this group include fungi known as poylpores, corticioids, hydnoids within aphyllophoroid fungi, in which the poylpores own poroid hymenopore, and the corticioids have the smooth to tuberculate hymenophore, and the hydnoids have the hydnoid or grandinoid or odontioid hymenophore (Hjortstam et al. 1987). They are cosmopolitan and rich in diversity, growing in tropical, subtropical and temperate regions (Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014, Hyde et al. 2017a, b, Tibpromma et al. 2017, Dai et al. 2021, Jayawardena et al. 2023, Mao et al. 2023, Zhao et al. 2023a). Hence, wood-inhabiting fungi, important strategic biological resources, represent a captivating facet of biodiversity, showcasing a remarkable tapestry of morphological, phylogenetic, and ecological diversity (Park et al. 2020, He & Zhao 2022, Liu et al. 2023c). To enhance resource utilization and minimize the impact of detrimental species, it is essential to systematically identify and thoroughly sample these fungi. The accurate recognition of species diversity also holds a significant role in advancing global conservation initiatives for wood-inhabiting fungi (Krah et al. 2018, Yu et al. 2021a, Zhou & May 2023). The phylogenetic diversity of this group has been extensively investigated recently (Larsson et al. 2004, Justo et al. 2017, Chen et al. 2021, Guan et al. 2023, Zhao et al. 2023a) in various regions worldwide, including Africa (Kinge et al. 2013), Asia (Doğan & Kurt 2016, Cho et al. 2019, Semwal & Bhatt 2019, Gafforov et al. 2020, Yusran et al. 2021, Aman et al. 2022), Europe (Dimou et al. 2016, Fink et al. 2021), and North America (Zhou et al. 2016b). In China, aside from the nationwide records of wood-inhabiting fungi (Dai 2011, 2012), evaluations have been conducted in several provinces (Dai et al. 2011, Bau et al. 2013, 2015, Ma et al. 2022) and renowned reserves (Zhou et al. 2011, Zhou & Dai 2012, Dai et al. 2015b, Yang et al. 2021, Wang et al. 2021c, Tuo et al. 2022).

Yunnan Province is located in the southwest of China, in the Yunnan-Guizhou Plateau. The strategic position of Yunnan Province as an "Ecological Security Barrier in Southwest China" and "Biodiversity Treasure" underscores its crucial role in the over all national ecological safety and conservation of biodiversity (Yan et al. 2021). Northern Yunnan reaches elevations of more than 5000 m.a.s.l, with subalpine environments. Central Yunnan forms part of the Yunnan-Guizhou Plateau, and has an elevation of about 1900 m.a.s.l, and a temperate climate. Southern Yunnan lies in the lower elevations and has sub-tropical to tropical climatic zones (Liu et al. 2023b). The climate in Yunnan offers conducive environments for the speciation and diversification of various life forms (Feng & Yang 2018, Wang et al. 2018a, Mi et al. 2021). This climatic diversity in Yunnan creates varied landscapes with multiple habitats, resulting in a high species diversity index, with over 6000 recorded fungal species (Liu et al. 2023b). The forest coverage rate of the province has reached 65.04%, harboring 19333 higher plant species, which belong to 3084 genera and 440 families, constituting 50.1% of the nation's total (Yan et al. 2021). Forty-three main families (>100 species) account for more than 77% (11,662 species) of all angiosperm species in Yunnan, and nearly half of all angiosperms in Yunnan are represented by three families as Asteraceae Bercht. & J. Presl, Orchidaceae Juss. and Poaceae Barnhart, (Qian et al. 2020). Thirteen main genera comprise over 100 species, including core genera *Rhododendron* L. (349 species, 54% of China) and *Pedicularis* L. (196 species, 59% of China, Qian et al. 2020). Besides, 2 273 species of vertebrates, accounting for 51.4% of the country's total, alongside a network of 166 conservation areas, including 21 designated as National Nature Reserves (Yan et al. 2021, Fig. 1).

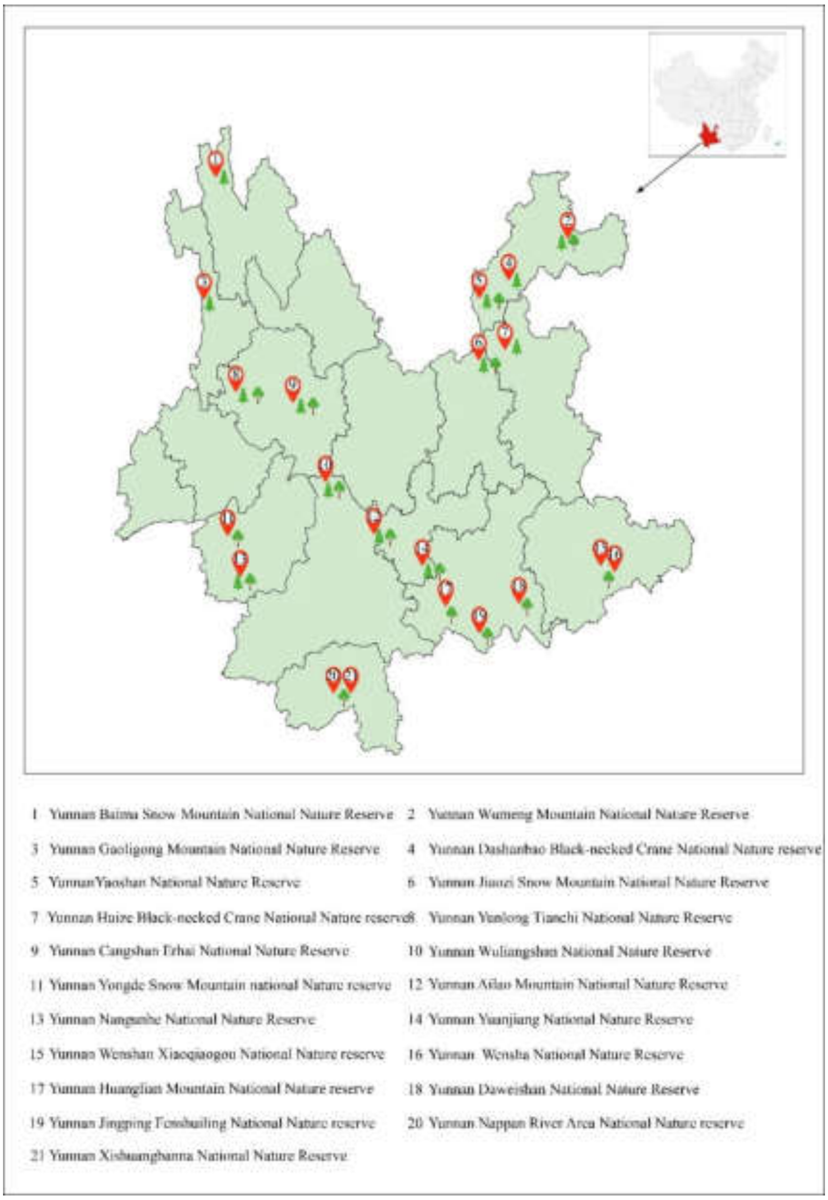

Figure 1 – The number of the National Nature Reserves and vegetation types in Yunnan, Southwest China.

The diversity of seed plants in the Yunnan Province is higher than in other areas in China, and the endemic species of woody plants are rich, and supply substrates for wood-inhabiting fungi (He & Zhao 2022, Dong et al. 2023a). In recent years, several studies conducted on wood-inhabiting fungi in Yunnan Province, China (Luo et al. 2022, Qu et al. 2022, Wu et al. 2022, Zou et al. 2022, Dong et al. 2023a, b, Duan et al. 2023a, b, Guan et al. 2023, Liu et al. 2023c, Yang et al. 2023, Zhang et al. 2023, Yu et al. 2023a, Zhao et al. 2023a, Yang et al. 2024), however, the diversity of wood-inhabiting species has not been thoroughly investigated in Yunnan Province. It is anticipated that numerous wood-inhabiting fungi in the Yunnan Province remain to be identified, harnessed, and conserved. The current study aims to carry out the classification and phylogenetic relationships of the wood-inhabiting fungi within the Basidiomycota. In the present study, extensive morphological examinations, combined with analyses of multi-gene sequences data support the introduction of two families of wood-inhabiting fungi, a new genus, and 42 new species belonging to 22 genera, 17 families and six orders.

MATERIALS AND METHODS

Sample Collection and Herbarium Specimen Preparation

Fresh basidiomata of the fungi growing on angiosperm branches were collected from the Chuxiong, Dali, Dehong, Honghe, Kunming, Lijiang, Lincang, Puer, Qujing, Wenshan and Yuxi of Yunnan Province, China. A total of 131 specimens were studied in this study. 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 Pro 7.7.5 software. Specimens were dried in an electric food dehydrator at 40 ºC, then sealed and stored in an envelope bag and deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphological studies

Macromorphological descriptions are based on field notes and photos captured in the field and laboratory and follow the color terminology of Petersen (1996). Micromorphological data were obtained from the dried specimens following observation under a light microscope (Dai et al. 2015a). The following abbreviations are used for the micro characteristic description: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, CB+ = cyanophilous, IKI = Melzer’s reagent, IKI– = both non-amyloid and non-dextrinoid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens.

Molecular procedures and phylogenetic analyses

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the previous study (Zhao & Wu 2017). The ITS region was amplified with primer pair ITS5 and ITS4 (White et al. 1990). The nuclear LSU region was amplified with primer pair LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi/). The mitochondrial SSU region was amplified with primer pairs MS1 and MS2 (White et al. 1990). TEF1 was amplified with primer pairs EF1-983 F and EF1-2218R (Rehner & Buckley 2005). RPB2 was amplified with primer pairs bRPB2-6F and bRPB2-7.1R (Liu et al. 1999, Matheny et al. 2002, Matheny 2005).

The PCR protocol for ITS and mtSSU was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for ITS and 55 °C for mtSSU for 45 s and 72 °C for 1 min, and a final extension of 72 °C for10 min. The PCR protocol for nLSU and TEF1 was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s,48 °C for nLSU and 59 °C for TEF1 for 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR procedure for RPB1 was 94 °C for 2 min, followed by 10 cycles at 94 °C for 40 s, 60 °C for 40 s and 72 °C for 2 min, then followed by 37 cycles at 94 °C for 45 s, 55 °C for 1.5 min and 72 °C for 2 min, and a final extension of 72 °C for 10 min. The PCR procedure for RPB2 was 95 °C for 2.5 min, followed by 40 cycles at 95 °C for 30 s, 52 °C for 1 min and 72 °C for 1 min, then followed by 40 cycles at 72 °C for 1.5 min, and final extension of 72 °C for 5 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company, Kunming, Yunnan Province, P.R. China. All newly generated sequences were deposited in GenBank (Table 1).

The sequences were aligned in MAFFT version 7 (Katoh et al. 2019) using the G-INS-i strategy. The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). The dataset was initially aligned and later, ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 sequences were combined using Mesquite version 3.51.

Maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI) analyses were applied to the combined three datasets following the methods outlined in a previous study (Zhao & Wu 2017, and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). 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 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. Additionally, the multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 through the Cipres Science Gateway (Miller et al. 2012). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

jModelTest v2 (Darriba et al. 2012) was used to determine the best-fit evolutionary model for each data set for Bayesian inference (BI), which was performed using MrBayes 3.2.7a (Ronquist et al. 2012). The first one-fourth of all generations was discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received maximum likelihood bootstrap value (BS) >70%, maximum parsimony bootstrap value (BT) >70%, or Bayesian posterior probabilities (BPP) >0.95.

Divergence Time Estimation

The divergence times of two new families were estimated with the BEAST v2.6.5 software package (Bouckaert et al. 2014) based on ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 sequence representing all main lineages in Basidiomycota (Table 2). jModelTest (Darriba et al. 2012) with calculation under Akaike information criterion was used to estimate the best-fit evolutionary model for each alignment subjected to phylogenetic analysis. Two time points were selected for calibration: (1) 90 million years ago (Mya) representing the minimum age of Agaricales by *Archaeomarasmius leggetti*, a fossil agaricoid species preserved in a Dominican amber; (2) 125 Mya representing the minimum age of Hymenochaetaceae by *Quatsinoporites cranhamii*, a fossil poroid species collected from Apple Bay on Vancouver Island. According to these time points, the offset age with a gamma distribution prior (scale = 20, shape = 1) for Agaricales was set as 90 Mya, and for Hymenochaetaceae as 125 Mya. After 50 million generations, the first 10% of the sampled trees every 1000th generation were removed as burn-in. The resulting log file was checked for chain convergence using Tracer 1.5.

Sequences of *Schizophyllum fasciatum* Pat. were retrieved from GenBank and used as outgroup taxa in the ITS+nLSU analysis (Fig. 2); *Pterula echo* D.J. McLaughlin & E.G. McLaughlin and *Merulicium fusisporum* (Romell) J. Erikss. & Ryvarden were selected as outgroup taxa in the ITS+nLSU analysis (Fig. 3) as in Zhao et al. (2016a); *Punctularia strigosozonata* (Schwein.) P.H.B. Talbot and *Punctulariopsis obducens* (Hjortstam & Ryvarden) Ghob.-Nejh. were selected as outgroup taxa in the ITS+nLSU analysis (Fig. 4) as in Ghobad-Nejhad et al. (2021); *Resinicium austroasianum* Jia Yu, Xue W. Wang, S.L. Liu & L.W. Zhou and *R. luteosulphureum* (Rick) Baltazar & Rajchenb. were selected as outgroup taxa in the ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 analysis (Fig. 5) as in Wang et al. (2023); *Fomitiporia gabonensis* Amalfi & Decock and *F. rhamnoides* T.Z. Liu & F. Wu were selected as outgroup taxa in the ITS analysis (Fig. 6) following Wang et al. (2023). Sequences of *Basidioradulum radula* (Fr.) Nobles retrieved from GenBank were used as the outgroup in the ITS+nLSU+mtSSU analysis (Fig. 7); *Hymenochaete ochromarginata* P.H.B. Talbot and *H. rubiginosa* (Dicks.) Lév. were selected as an outgroup in the ITS+nLSU analysis (Fig. 8) as in Guan et al. (2023); *Rickenella fibula* (Bull.)

Table 1 List of species, specimens, and GenBank accession number of sequences used in this study. * is shown type material, holotype.

Order/Family	**Species name**	**Sample no.**	**GenBank accessions no.**						**References**
			ITS	**nLSU**	**mtSSU**	**RPB1**	**RPB2**	**TEF1**	
Agaricomycetes									
Agaricales/*Agaricaceae*	*Agaricus campestris*	AFTOL-ID 1492	DQ486682	DQ110871	–	DQ516068	–	–	He et al. (2019)
	Agaricus luteopileus	ZRL 20120589	MK617868	MK617780	–	–	–	MK614377	Cao et al. (2021a)
-/*Incertae sedis*	*Dendrothele acerina*	G0632	–	MK277925	–	–	–	–	Varga et al. (2019)
	Dendrothele alliacea	G0488	–	MK277926	–	–	–	–	Varga et al. (2019)
	Dendrothele americana	FP101995	–	NG071235	–	–	–	–	Binder et al. (2005)
	Dendrothele bisporigera	G0955	–	MK277927	–	–	–	–	Varga et al. (2019)
	Dendrothele candida	HHB-3843	–	AY293177	–	–	–	–	Binder et al. (2005)
	Dendrothele incrustans	HHB-19092	MW740330	–	–	–	–	–	Unpublished
	Dendrothele microspora	FP 101998	OQ694474	OQ694474	–	–	–	–	Unpublished
	Dendrothele griseocana	CBS 340.66	MH858816	MH870455	–	–	–	–	Vu et al. (2019)
	Dendrothele minutissima	G1841	–	MK277929	–	–	–	–	Varga et al. (2019)
	Dendrothele nivosa	CBS 125843	MH863802	MH875264	–	–	–	–	Vu et al. (2019)
	Dendrothele salicicola	G0614	–	MK277932	–	–	–	–	Varga et al. (2019)
	Dendrothele strumosa	G1867	–	MK277936	–	–	–	–	Varga et al. (2019)
	Dendrothele yunnanensis	**CLZhao 17814** *	**OR094484**	**OR449910**	**OR469061**	–	–	–	**Present study**
-/*Pterulaceae*	*Merulicium fusisporum*	Hjm s.n.	EU118647	EU118647	–	–	–	–	Larsson (2007a)
	Pterula echo	AFTOL-ID711	DQ494693	AY629315	–	–	–	–	Wang et al. (2018)
-/*Radulomycetaceae*	*Aphanobasidium pseudotsugae*	HHB-822	GU187509	GU187567	–	–	–	–	Larsson (2007a)
	Aphanobasidium pseudotsugae	UC 2023153	KP814353	AY586696	–	GU187455	GU187781	GU187695	Larsson (2007a)
	Radulomyces confluens	Cui 5977	KU535661	KU535669	–	–	–	–	Wang et al. (2018)
	Radulomyces confluens	He 2224	KU535662	KU535670	–	–	–	–	Wang et al. (2018)
	Radulomyces copelandii	Dai 15061	KU535664	KU535672	–	–	–	–	Wang et al. (2018)
	Radulomyces copelandii	Wu 9606-5	KU535663	KU535671	–	–	–	–	Wang et al. (2018)
	Radulomyces hydnoides	**CLZhao 21337**	**OR096181**	**OR449911**	**OR469062**	**OR687195**	–	OR531378	**Present study**
	Radulomyces hydnoides	**CLZhao 21342**	**OR096182**	**OR449912**	**OR469063**	–	–	–	**Present study**
	Radulomyces hydnoides	**CLZhao 21351**	**OR096183**	**OR449913**	**OR469064**	**OR687196**	**OR729440**	–	**Present study**
	Radulomyces hydnoides	**CLZhao 21632** *	**OR096184**	**OR449914**	**OR469065**	–	**OR729441**	**OR531379**	**Present study**
	Radulomyces hydnoides	**CLZhao 21668**	**OR096185**	**OR449915**	**OR469066**	–	–	**OR531380**	**Present study**
	Radulomyces hydnoides	**CLZhao 21815**	**OR096186**	**OR449916**	**OR469067**	–	–	**OR531381**	**Present study**
	Radulomyces molaris	ARAN-Fungi 2003	–	MT232311	–	MT242320	MT242340	MT242359	Olariaga et al. (2020)
	Radulomyces molaris	ML0499	AY463459	AY586705	–	–	–	–	Larsson et al. (2004)
	Radulomyces paumanokensis	IMG 5985-16	MG050100	MG050110	–	–	–	–	Wang et al. (2018)

Table 1 Contined.

Order/Family	**Species name**	**Sample no.**	**GenBank accessions no.**						**References**
			ITS	**nLSU**	**mtSSU**	**RPB1**	**RPB2**	**TEF1**	
	Radulomyces paumanokensis	LE-BIN 4691	OL764917	–	–	–	–	–	Unpublished
	Radulomyces rickii	JK 951007	–	AY586706	–	–	–	–	Larsson et al. (2004)
	Radulomyces rickii	G1066	–	MK278543	–	–	–	–	Varga et al. (2019)
	Radulomyces yunnanensis	**CLZhao 1262 ***	**OR096191**	**OR449917**	**OR469068**	**OR687197**	**OR729442**	**–**	**Present study**
	Radulomyces yunnanensis	**CLZhao 7364**	**OR096192**	**OR449918**	**OR469069**	**OR687198**	**OR729443**	**–**	**Present study**
	Radulomyces yunnanensis	**CLZhao 24040**	**OR167197**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Radulomyces yunnanensis	**CLZhao 26656**	**OR167198**	**OR449919**	**–**	**–**	**–**	**–**	**Present study**
	Radulomyces yunnanensis	**CLZhao 26685**	**OR167199**	**OR449920**	**–**	**–**	**–**	**–**	**Present study**
	Radulomyces yunnanensis	**CLZhao 27046**	**OR167200**	**OR449921**	**–**	**–**	**–**	**–**	**Present study**
	Radulomyces yunnanensis	**CLZhao 27069**	**OR167201**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Radulomyces zixishanensis	**CLZhao 21127**	**ON033887**	**OR449922**	**OR469070**	**–**	**–**	**OR541903**	**Present study**
	Radulotubus resupinatus	Cui 8383	KU535660	KU535668	–	–	–	–	Zhao et al. (2016a)
	Radulotubus resupinatus	Cui 8462	KU535657	KU535665	–	–	–	–	Zhao et al. (2016a)
-/*Schizophyllaceae*	*Schizophyllum fasciatum*	CBS 267.60	L43385	AF261589	–	–	–	–	Nakasone et al. (1996)
Amylocorticiales/ *Amylocorticiaceae*	*Amylocorticium cebennense*	HHB-2808	GU187505	GU187561	–	GU187439	GU187770	GU187675	He et al. (2019)
	Anomoloma albolutescens	CFMR-L 6088	GU187507	GU187563	–	GU187438	GU187768	GU187671	He et al. (2019)
Atheliales/*Atheliaceae*	*Athelia arachnoidea*	GB 0087426	LR694192	LR694169	–	–	LR694267	LR694213	He et al. (2019)
	Leptosporomyces raunkiaerii	HHB 7268	GU187528	GU187588	–	GU187471	GU187791	GU187719	Binder et al. (2010)
Auriculariales/ *Auriculariaceae*	*Auricularia heimuer*	Dai 13765	KM396793	MH020931	–	MZ753965	KP729317	–	Wu et al. (2014a)
	Heterochaete delicata	TUFC 33717	AB871766	AB871747	–	–	–	–	He et al. (2019)
Boletales/*Boletaceae*	*Boletus edulis*	HMJAU4637	JN563894	KF112455	–	KF112586	KF112704	KF112202	Wu et al. (2014b)
	Royoungia reticulata	HKAS 52253	–	KT990592	–	KT990940	KT990427	KT990786	Wu et al. (2016)
Cantharellales/ *Hydnacea*	*Hydnum albomagnum*	AFTOL-ID 471	DQ218305	AY700199	–	DQ234570	DQ234553	DQ234568	He et al. (2019)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Sistotrema coronilla	AFTOL-ID 618	DQ397337	DQ457641	–	–	–	–	He et al. (2019)
Corticiales/ *Corticiaceae*	*Corticium boreoroseum*	MG42	MW805842	MW805816	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Corticium boreoroseum	MG47	MW805846	HM046920	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Corticium canfieldii	ERC-72-11	MW805850	MW805821	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Corticium erikssonii	MG44	MW805843	MW805818	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Corticium lombardiae	MG147	MW805848	–	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Corticium lombardiae	MG148	MW805849	–	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Corticium malagasoroseum	PC 0094401	MW805856	MW805822	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Corticium roseoalbum	**CLZhao 13525** *	**OR167203**	**OR449923**	–	–	–	–	**Present study**
	Corticium roseum	MG252	MW805872	MW805836	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Corticium silviae	S. Feusi 05.06.2017	MH520061	MH520061	–	–	–	–	Diederich et al. (2018)
	Corticium thailandicum	MG242	MW805868	MW805831	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Erythricium laetum	MG72	GU590875	GU590878	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Erythricium laetum	MG73	GU590874	GU590879	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Laetisaria fuciformis	CBS:182.49	MH856485	MH868023	–	–	–	–	Vu et al. (2019)
	Laetisaria agaves	RLG-10805	MW805851	–	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Lawreymyces palicei	Palice 2509	AY542864	AY542864	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Lawreymyces palicei	Palice 4369	AY542865	AY542865	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Marchandiomyces corallinus	JL128-98	AY583327	AY583331	–	–	–	–	DePriest et al. (2005)
	Marchandiomyces lignicola	MYA 299	AY583328	AY583332	–	–	–	–	DePriest et al. (2005)

Table 1 Contined.

Order/Family	**Species name**	**Sample no.**	**GenBank accessions no.**						**References**
			ITS	**nLSU**	**mtSSU**	**RPB1**	**RPB2**	**TEF1**	
	Mycobernardia incrustans	CBS:172.36	MH855759	MH867272	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Mycobernardia incrustans	CBS:173.36	MH855760	MH867273	–	–	–	–	Ghobad-Nejhad et al. (2021)
	Waitea circinata	CBS:472.82	MH861518	MH873265	–	–	–	–	Vu et al. (2019)
	Waitea circinata	299-G-17	MK817577	MN121346	–	–	–	–	Vojvodic et al. (2023)
-/*Punctulariaceae*	*Punctularia strigosozonata*	CBS:345.34	MH855559	MH867064	–	–	–	–	Vu et al. (2019)
	Punctulariopsis obducens	MG70	HM046918	HM046933	–	–	–	–	Ghobad-Nejhad et al. (2021)
Geastrales/ *Geastraceae*	*Geastrum dolomiticum*	FP 20140223	MT569469	MT569460	–	MT572906	–	MT593361	Finy et al. (2021)
	Sphaerobolus iowensis	ATCC 52850	AY487958	AY439014	AY488008	–	–	AY487984	Geml et al. (2005)
Gloeophyllales/ *Gloeophyllaceae*	*Gloeophyllum sepiarium*	Wilcox-3BB	NR119869	NG060630	–	–	HM536109	–	Garcia-Sandoval et al. (2011)
Gomphales/ *Gomphaceae*	*Gomphus matijun*	HKAS122604	OL673002	OL672986	–	–	–	–	Liu et al. (2022a)
	Gomphus matijun	HKAS122605	OL673001	OL672985	–	–	–	–	Liu et al. (2022a)
Hymenochaetales/ *Chaetoporellaceae*	*Kneiffiella eucalypticola*	LWZ20180515-9	MT319411	MT319143	–	–	–	–	Wang et al. (2021b)
	Kneiffiella subalutacea	GEL2196	DQ340341	DQ340362	–	–	–	–	Yurchenko et al. (2020a)
-/*Hymenochaetaceae*	*Basidioradulum mayi*	LWZ 20180510-18	MN017785	MN017792	ON463756	ON456063	ON456070	–	Wang et al. (2023)
	Basidioradulum radula	LWZ 20201017-62	ON063684	ON063884	ON063747	ON089691	ON100770	ON100713	Wang et al. (2023)
	Coltricia abieticola	Cui 10321	KX364785	KX364804	KY693823	KX364828	KX364876	KY693911	Bian & Dai (2017)
	Coltricia weii	LWZ 20190811-1b	ON063641	ON063840	ON063709	ON100737	ON100684	ON089689	Wang et al. (2023)
	Coniferiporia qilianensis	Dai 13320	MT420707	MT416471	MT386051	MT376013	–	MT470372	Wang et al. (2023)
	Coniferiporia sulphurascens	FP-134848-SP	MT420687	MT416462	MT386065	MT376016	–	MT470375	Wang et al. (2023)
	Cyanotrama gypsea	Cui 10372	KT203290	MT319396	MT326567	–	KT210367	–	Wang et al. (2023)
	Cyanotrama rimosa	MG56	GU566010	GU566003	–	–	–	–	Wang et al. (2023)
	Fomitiporia gabonensis	MUCL 47576	GU461971	GU461990	–	–	JQ087972	GU461923	Wang et al. (2023)
	Fomitiporia rhamnoides	LWZ 20180905-15	ON063643	ON063842	ON063711	ON100739	–	ON089672	Wang et al. (2023)
	Fulvoderma australe	LWZ 20190809-39b	ON063644	ON063843	ON063712	ON100740	ON100686	–	Wang et al. (2023)
	Fulvoderma scaurum	LWZ 20170816-31	ON063645	ON063844	ON063713	–	–	–	Wang et al. (2023)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Fuscoporia ferruginosa	LWZ 20180927-2	–	ON063847	ON063716	ON100743	ON100689	–	Wang et al. (2023)
	Fuscoporia gilva	LWZ 20190814-19b	ON063648	ON063848	ON063717	ON100744	ON100734	ON089686	Wang et al. (2023)
	Hydnoporia corrugata	CLZhao 10344	OM959405	OM967403	–	–	–	–	Unpublished
	Hydnoporia corrugata	HHB-19233	MW740292	–	–	–	–	–	Unpublished
	Hydnoporia diffissa	X3389	MK514611	–	–	–	–	–	Miettinen et al. (2019)
	Hydnoporia diffissa	X2654	MK514598	–	–	–	–	–	Miettinen et al. (2019)
	Hydnoporia gigasetosa	He 1442	KR781016	KR781017	–	–	–	–	Yang et al. (2016)
	Hydnoporia lamellata	Cui 7629	JQ279603	JQ279617	–	–	–	–	He & Dai (2012)
	Hydnoporia lamellata	Dai 10527	JQ279605	–	–	–	–	–	He & Dai (2012)
	Hydnoporia laricicola	Dai 13458	NR166380	NG068765	–	–	–	–	Yang et al. (2016)
	Hydnoporia latesetosa	He 492	JQ716404	JQ716411	–	–	–	–	He & Li (2013)
	Hydnoporia latesetosa	He 502	JQ716405	JQ716410	–	–	–	–	He & Li (2013)
	Hydnoporia lenta	Dai 11046	JQ279616	JQ279628	–	–	–	–	He & Dai (2012)
	Hydnoporia olivacea	FP-102077	OQ539564	–	–	–	–	–	Yu et al. (2023b)
	Hydnoporia pinicola	**CLZhao 22505**	**OR094493**	**OR449924**	**OR469071**	**OR687192**	**OR729444**	**OR541904**	**Present study**
	Hydnoporia pinicola	**CLZhao 27154**	**OR094494**	**OR449925**	**OR469072**	**OR898397**	**OR729445**	**OR541905**	**Present study**
	Hydnoporia pinicola	**CLZhao 27175**	**OR094495**	**OR449926**	**OR469073**	**OR898398**	**OR729446**	**OR541906**	**Present study**
	Hydnoporia pinicola	**CLZhao 27180 ***	**OR094496**	**OR449927**	**OR469074**	**–**	**–**	**OR541907**	**Present study**
	Hydnoporia rhododendri	X2641	MK514593	–	–	–	–	–	Miettinen et al. (2019)
	Hydnoporia rhododendri	X2655	MK514599	–	–	–	–	–	Miettinen et al. (2019)
	Hydnoporia rimosa	X2640	MK514592	–	–	–	–	–	Miettinen et al. (2019)
	Hydnoporia rimosa	X2642	MK514594	–	–	–	–	–	Miettinen et al. (2019)
	Hydnoporia subrigidula	He 1123	JQ716402	JQ716408	–	–	–	–	He & Li (2013)
	Hydnoporia subrigidula	He 1157	JQ716403	JQ716409	–	–	–	–	He &Li (2013)
	Hydnoporia tabacina	LWZ 20210924-26a	ON063651	ON063851	ON063720	ON100747	ON100685	ON089676	Wang et al. (2023)
	Hydnoporia tabacinoides	LWZ 20190814-29b	ON063652	ON063852	ON063721	ON100748	–	–	Wang et al. (2023)
	Hydnoporia tabacinoides	Cui 10428	JQ279604	JQ279618	–	–	–	–	He & Dai (2012)
	Hydnoporia yasudae	Dai 19262	OL470309	OL462824	–	–	–	–	Unpublished
	Hydnoporia yasudae	X2665	MK514609	MK514609	–	–	–	–	Miettinen et al. (2019)
	Hydnoporia yunnanensis	**CLZhao 5942**	**OR094497**	**OR449928**	–	–	–	–	**Present study**
	Hydnoporia yunnanensis	**CLZhao 6123 ***	**OR094498**	**OR449929**	**OR469075**	**–**	**OR729447**	**OR541908**	**Present study**

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Hydnoporia yunnanensis	**CLZhao 6227**	**OR094499**	**OR449930**	**OR469076**	**–**	**OR729448**	**OR541909**	**Present study**
	Hydnoporia yunnanensis	**CLZhao 10896**	**OR094500**	**OR449931**	**OR469077**	**OR687193**	**OR729449**	**–**	**Present study**
	Hymenochaete corrugata	LWZ 20180921-5	ON063653	ON063853	ON063722	ON100749	–	ON089677	Wang et al. (2023)
	Hymenochaete ochromarginata	He 47	KU978861	JQ279666	–	–	–	–	Guan et al. (2023)
	Hymenochaete rubiginosa	He 458	JQ279580	–	–	–	–	–	Guan et al. (2023)
	Hymenochaete rubiginosa	LWZ 20201017-32	ON063655	–	ON063724	ON100751	ON100698	ON089678	Wang et al. (2023)
	Inonotus hispidus	LWZ 20180703-1	ON063659	ON063858	ON063727	ON100753	ON100692	ON089681	Wang et al. (2023)
	Nigrofomes melanoporus	JV 1704/39	MF629835	MF629831	–	–	–	–	Wang et al. (2023)
	Nigrofomes sinomelanoporus	Cui 5277	MF629836	MF629832	–	–	–	–	Wang et al. (2023)
	Nothophellinus andinopatagonicus	MR 10431B	KP347534	KP347529	–	–	–	–	He et al. (2019)
	Ochrosporellus puerensis	Dai 12241	OL583991	OL583985	–	–	–	–	Wang et al. (2023)
	Onnia tomentosa	Cui 10048	MT332141	MT319387	MT326561	–	–	–	Wang et al. (2023)
	Phellinopsis conchata	L-7601	KU139188	KU139257	–	–	KU139315	KU139377	Wang et al. (2023)
	Phellinus piceicola	LWZ 20190921-5	ON063662	ON063862	ON063731	ON100754	ON100695	–	Wang et al. (2023)
	Phylloporia oreophila	LWZ 20190811-27a	ON063665	ON063865	ON063733	–	ON100694	ON089684	Wang et al. (2023)
	Phylloporia radiata	LWZ 20141122-6	ON063666	ON063866	–	–	–	ON089685	Wang et al. (2023)
	Porodaedalea himalayensis	LWZ 20180903-21	ON063667	ON063867	ON063734	ON100755	–	–	Wang et al. (2023)
	Porodaedalea laricis	LWZ 20190724-9	ON063668	ON063868	ON063735	ON100756	ON100693	–	Wang et al. (2023)
	Sanghuangporus quercicola	LWZ 20170821-18	ON063669	ON063869	–	–	–	–	Wang et al. (2023)
	Sanghuangporus weigelae	LWZ 20210623-2a	ON063671	ON063870	ON063736	–	ON100697	ON089687	Wang et al. (2023)
-/*Hyphodontiaceae*	*Hyphodontia arguta*	KHL 11938 (GB)	EU118632	EU118633	–	–	–	–	Larsson (2007a)
	Hyphodontia pallidula	GEL 2097	DQ340317	DQ340372	–	–	–	–	Guan et al. (2023)
-/*Incertae sedis*	*Rigidoporus corticola*	ZRL 20151459	LT716075	KY418899	–	–	KY419038	KY419087	Liu et al. (2022c)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
-/Peniophorellaceae	*Peniophorella aspersa*	TNM F24809	MN062097	MN062142	–	–	–	–	Yurchenko et al. (2020b)
	Peniophorella aspersa	TNM F32708	MN062099	MN062144	–	–	–	–	Yurchenko et al. (2020b)
	Peniophorella capitulata	KHL 8464 (GB)	DQ677491	DQ677491	–	–	–	–	Larsson (2007b)
	Peniophorella cremea	CLZhao 1606	MT955162	–	–	–	–	–	Xu et al. (2020a)
	Peniophorella cremea	CLZhao 1719	MT955163	–	–	–	–	–	Xu et al. (2020a)
	Peniophorella crystallifera	LWZ 20210626-4a	ON063685	ON063885	ON063748	ON100771	–	–	Wang et al. (2023)
	Peniophorella crystallifera	TNM F30331	MN062100	MN062147	–	–	–	–	Yurchenko et al. (2020b)
	Peniophorella daweishanensis	**CLZhao 18600** *	**OR094501**	**OR449932**	**OR469078**	–	–	–	**Present study**
	Peniophorella echinocystis	KHL 6284	DQ677494	DQ681200	–	–	–	–	Larsson (2007b)
	Peniophorella fissurata	CLZhao 9421	MN864260	OM985776	OQ706812	–	–	–	Guan et al. (2020)
	Peniophorella fissurata	CLZhao 5848	MN864262	OM985777	OQ706798	–	–	–	Guan et al. (2020)
	Peniophorella guttulifera	CBS 107303	LT603016	LT603001	–	–	–	LT603027	Kolařík & Vohník (2018)
	Peniophorella guttulifera	NH 12012 (GB)	DQ647501	–	–	–	–	–	Hallenberg et al. (2007)
	Peniophorella odontiiformis	TMI 21347	DQ647496	–	–	–	–	–	Hallenberg et al. (2007)
	Peniophorella odontiiformis	TMI 6824	DQ647500	–	–	–	–	–	Hallenberg et al. (2007)
	Peniophorella olivacea	**CLZhao 25896** *	**OR094502**	**OR449933**	**OR469079**	–	**OR722813**	–	**Present study**
	Peniophorella pallida	UC 2022887	KP814201	–	–	–	–	–	Rosenthal et al (2017)
	Peniophorella pallida	UC 2022844	KP814208	–	–	–	–	–	Rosenthal et al (2017)
	Peniophorella pertenuis	NH 15115 (GB)	DQ647487	–	–	–	–	–	Hallenberg et al. (2007)
	Peniophorella pertenuis	NH 12429 (GB)	DQ647486	–	–	–	–	–	Hallenberg et al. (2007)
	Peniophorella praetermissa	NH 11192 (GB)	DQ647461	–	–	–	–	–	Hallenberg et al. (2007)
	Peniophorella praetermissa	NH 10986 (GB)	DQ647462	–	–	–	–	–	Hallenberg et al. (2007)
	Peniophorella pubera	LWZ 20210624-16b	ON063687	ON063887	ON063750	ON100772	ON100715	–	Wang et al. (2023)
	Peniophorella pubera	CBS:464.86	MH861988	MH873680	–	–	–	–	Vu et al. (2019)
	Peniophorella reticulata	TNM F22559	MN062103	MN062151	–	–	–	–	Yurchenko et al. (2020b)
	Peniophorella reticulata	CLZhao 17066	OM985746	OM985783	OQ706822	–	–	–	Unpublished

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Peniophorella rude	LWZ 20171026-7	ON063688	ON063888	ON063751	ON100773	ON100716	ON089692	Wang et al. (2023)
	Peniophorella subpraetermissa	LWZ 20190816-3b	ON063689	ON063889	ON063752	ON100774	ON100717	–	Wang et al. (2023)
	Peniophorella subpraetermissa	Wu 950627	DQ647493	–	–	–	–	–	Hallenberg et al. (2007)
	Peniophorella yunnanensis	CLZhao 4810	MN864263	OM985788	OQ706796	–	–	–	Guan et al. (2020)
	Peniophorella yunnanensis	CLZhao 6137	MN864266	–	OQ706801	–	–	–	Guan et al. (2020)
-/*Resiniciaceae*	*Resinicium austroasianum*	LWZ 20191208-11	ON063691	ON063891	ON063753	ON100776	ON100720	ON089694	Wang et al. (2023)
	Resinicium luteosulphureum	LWZ 20210923-23a	ON063692	ON427362	ON063754	ON100777	ON100719	ON089695	Wang et al. (2023)
-/*Schizoporaceae*	*Basidioradulum radula*	NH 9453	AF347105	AF347105	–	–	–	–	Larsson et al. (2004)
	Basidioradulum radula	KUC 10671	MW575872	MW570869	–	–	–	–	Ryu et al. (2021)
	Fasciodontia brasiliensis	MSK-F 7245a	MK575201	MK598734	–	–	–	–	Yurchenko et al. (2020a)
	Fasciodontia bugellensis	KAS-FD 10705a	MK575203	MK598735	–	–	–	–	Yurchenko et al. (2020a)
	Fasciodontia yunnanensis	CLZhao 6280	MK811275	MZ146327	–	–	–	–	Luo & Zhao (2021)
	Lyomyces albopulverulentus	CLZhao 21478	OP730712	OP730724	–	–	–	–	Guan et al. (2023)
	Lyomyces allantosporus	KAS-GEL4933	KY800401	–	–	–	–	–	Yurchenko et al. (2017)
	Lyomyces bambusinus	CLZhao 4831	MN945968	–	–	–	–	–	Chen & Zhao (2020)
	Lyomyces daweishanensis	**CLZhao 18344** *	**OR094474**	**OR449934**	**OR469080**	**OR898399**	**OR731372**	–	**Present study**
	Lyomyces elaeidicola	LWZ20180411-20	MT319458	–	–	–	–	–	Wang et al. (2021b)
	Lyomyces fimbriatus	Wu910620-7	MK575209	–	–	–	–	–	Yurchenko et al. (2020a)
	Lyomyces gatesiae	LWZ20180515-3	MT319447	–	–	–	–	–	Wang et al. (2021b)
	Lyomyces griseliniae	KHL 12971 (GB)	DQ873651	–	–	–	–	–	Larsson et al. (2006)
	Lyomyces incanus	**CLZhao 22813**	**OR094480**	**OR449935**	**OR469081**	–	**OR731375**	–	**Present study**
	Lyomyces incanus	**CLZhao 22900** *	**OR094481**	**OR449936**	**OR469082**	–	**OR898400**	–	**Present study**
	Lyomyces juniperi	FR-0261086	KY081799	–	–	–	–	–	Riebesehl & Langer (2017)
	Lyomyces lincangensis	**CLZhao 22966** *	**OR094487**	**OR449937**	**OR469083**	–	–	–	**Present study**
	Lyomyces luteoalbus	**CLZhao 18211**	**OR094485**	**OR449938**	**OR469084**	–	–	–	**Present study**
	Lyomyces luteoalbus	**CLZhao 18347** *	**OR094486**	**OR449939**	**OR469085**	**OR687199**	**OR731373**	**OR541910**	**Present study**

Table 1 Contined.

Order/Family	**Species name**	**Sample no.**	**GenBank accessions no.**						**References**
			ITS	**nLSU**	**mtSSU**	**RPB1**	**RPB2**	**TEF1**	
	Lyomyces macrosporus	CLZhao 4516	MN945977	–	–	–	–	–	Chen & Zhao (2020)
	Lyomyces mascarensis	KAS-GEL4833	KY800399	–	–	–	–	–	Yurchenko et al. (2020a)
	Lyomyces niveus	CLZhao 6442	MZ262542	MZ262527	–	–	–	–	Luo et al. (2021c)
	Lyomyces ochraceoalbus	CLZhao 4385	MZ262535	MZ262521	–	–	–	–	Luo et al. (2021c)
	Lyomyces orientalis	GEL3376	DQ340325	–	–	–	–	–	Yurchenko et al. (2017)
	Lyomyces qujingensis	**CLZhao 27462** *	**OR167768**	**OR449940**	–	–	–	–	**Present study**
	Lyomyces sambuci	KAS-JR7	KY800402	KY795966	–	–	–	–	Yurchenko et al. (2017)
	Lyomyces sinensis	**CLZhao 27391** *	**OR167769**	**OR449941**	–	–	**OR722810**	–	**Present study**
	Lyomyces sinensis	**CLZhao 27464**	**OR167770**	**OR449942**	–	–	**OR722811**	–	**Present study**
	Lyomyces vietnamensis	TNM F9073	JX175044	–	–	–	–	–	Yurchenko et al. (2013)
	Lyomyces yunnanensis	CLZhao 2463	OP730711	OP730723	–	–	–	–	Guan et al. (2023)
	Xylodon acystidiatus	LWZ20180514-9	MT319474	–	–	–	–	–	Wang et al. (2021b)
	Xylodon astrocystidiata	Wu 9211-71	JN129972	–	–	–	–	–	Yurchenko & Wu (2014)
	Xylodon attenuatus	Spirin 8775	MH324476	–	–	–	–	–	Viner et al. (2018)
	Xylodon brevisetus	JS17863	AY463428	–	–	–	–	–	Larsson et al. (2004)
	Xylodon bamburesupinus	**CLZhao 23088** *	**OR167773**	**OR449943**	–	–	–	–	**Present study**
	Xylodon bamburesupinus	**CLZhao 23123**	**OR167774**	**OR449944**	–	–	–	–	**Present study**
	Xylodon cystidiatus	FR-0249200	MH880195	MH884896	–	–	–	–	Riebesehl et al. (2019)
	Xylodon daweishanensis	CLZhao 18446	OP730717	OP730725	–	–	–	–	Guan et al. (2023)
	Xylodon filicinus	MSK-F 12869	MH880199	NG067836	–	–	–	–	Riebesehl et al. (2019)
	Xylodon fissilius	**CLZhao 18740** *	**OR096211**	**OR449945**	**OR469086**	–	**OR722809**	–	**Present study**
	Xylodon fissilius	**CLZhao 18750**	**OR096212**	–	–	–	–	–	**Present study**
	Xylodon gossypinus	CLZhao 8375	MZ663804	MZ663813	–	–	–	–	Luo et al. (2021a)
	Xylodon heterocystidiatus	Wei 17-314	MT731753	–	–	–	–	–	Guan et al. (2023)
	Xylodon hydnoidus	**CLZhao 17991** *	**OR096203**	–	**OR469087**	–	–	–	**Present study**
	Xylodon hydnoidus	**CLZhao 18105**	**OR096206**	–	–	–	–	–	**Present study**
	Xylodon hydnoidus	**CLZhao 18238**	**OR096204**	**OR449946**	–	–	–	–	**Present study**
	Xylodon hydnoidus	**CLZhao 18239**	**OR096205**	–	–	–	–	–	**Present study**
	Xylodon hyphodontinus	KAS-GEL9222	MH880205	MH884903	–	–	–	–	Riebesehl et al. (2019)
	Xylodon kunmingensis	TUB-FO 42565	MH880198	–	–	–	–	–	Riebesehl et al. (2019)
	Xylodon lenis	Wu890714-3	KY081802	–	–	–	–	–	Riebesehl & Langer (2017)
	Xylodon macrosporus	CLZhao 10226	MZ663809	MZ663817	–	–	–	–	Luo et al. (2021a)
	Xylodon nesporii	LWZ20180921-35	MT319655	MT319238	–	–	–	–	Wang et al. (2021b)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Xylodon nothofagi	ICMP 13842	AF145583	–	–	–	–	–	Paulus et al. (2000)
	Xylodon olivaceobubalinus	**CLZhao 25164**	**OR167771**	**OR449947**	**OR469088**	–	–	–	**Present study**
	Xylodon olivaceobubalinus	**CLZhao 25174** *	**OR167772**	**OR449948**	**OR469089**	**OR687194**	**OR722812**	–	**Present study**
	Xylodon pingbianensis	**CLZhao 19029** *	**OR096208**	**OR449949**	**OR469090**	–	–	–	**Present study**
	Xylodon pseudolanatus	CFMR FP-150922	MH880220	–	–	–	–	–	Viner et al. (2018)
	Xylodon puerensis	CLZhao 8142	OP730720	OP730728	–	–	–	–	Guan et al. (2023)
	Xylodon taiwanianus	CBS:125875	MH864080	–	–	–	–	–	Vu et al. (2019)
	Xylodon tropicus	CLZhao 3351	OL619261	OL619269	–	–	–	–	Qu et al. (2022)
	Xylodon wenshanensis	CLZhao 15729	OM338097	OM338104	–	–	–	–	Luo et al. (2022)
	Xylodon xinpingensis	CLZhao 11224	MW394662	MW394654	–	–	–	–	Luo et al. (2022)
	Xylodon yarraensis	LWZ20180510-5	MT319639	–	–	–	–	–	Wang et al. (2021b)
-/*Skvortzoviaceae*	*Skvortzovia dabieshanensis*	LWZ 20210918-15b	ON063694	ON063894	ON063757	ON100779	ON100723	ON089696	Wang et al. (2023)
	Skvortzovia dabieshanensis	LWZ 20201017-55	MW414514	MW414460	–	–	–	–	Yu et al. (2021)
	Skvortzovia furfuracea	KHL 11738 (GB)	DQ873648	DQ873648	–	–	–	–	Larsson et al. (2006)
	Skvortzovia furfuracea	UC 2023081	KP814421	–	–	–	–	–	Dong et al. (2021)
	Skvortzovia furfurella	KHL 10180	DQ873649	DQ873649	–	–	–	–	Yu et al. (2021)
	Skvortzovia furfurella	MAR 12-286	MH248259	–	–	–	–	–	Dong et al. (2021)
	Skvortzovia georgica	KHL 12019 (GB)	DQ873645	DQ873645	–	–	–	–	Larsson et al. (2006)
	Skvortzovia incana	**CLZhao 16338** *	**OR096179**	**OR449950**	**OR469091**	–	**OR731374**	–	**Present study**
	Skvortzovia incana	**CLZhao 16474**	**OR096180**	–	–	–	–	–	**Present study**
	Skvortzovia meridionalis	CFMR 4210	KX065952	–	–	–	–	–	Dong et al. (2021)
	Skvortzovia pinicola	LWZ 20210623-18b	ON063695	ON063695	ON063758	ON100780	ON100724	–	Wang et al. (2023)
	Skvortzovia qilianensis	LWZ 20180904-20	ON063693	ON063693	ON063756	ON100778	ON100722	–	Wang et al. (2023)
	Skvortzovia qilianensis	LWZ 20180904-18	MW414519	MW414465	–	–	–	–	Yu et al. (2021)
	Skvortzovia yunnanensis	CLZhao 16084	MW472754	MW473473	ON063759	–	ON100725	ON089697	Wang et al. (2023)
	Skvortzovia yunnanensis	CLZhao 16181	MW472755	MW473474	–	–	–	–	Dong et al. (2021)
-/*Tubulicrinaceae*	*Tubulicrinis accedens*	ACD0414	OL756001	OL742444	–	–	–	–	Unpublished
	Tubulicrinis australis	MA Fungi:88838	KX017591	KX017594	–	–	–	–	Crous et al. (2016)
	Tubulicrinis borealis	DK14_93	OL436811	–	–	–	–	–	Unpublished
	Tubulicrinis calothrix	LWZ 20210919-1b	ON063704	ON063904	ON063766	–	ON100733	–	Wang et al. (2023)
	Tubulicrinis chaetophorus	Spirin 12616 (H)	ON188814	ON188814	ON228495	–	–	–	Unpublished

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Tubulicrinis glebulosus	LWZ 20180903-13	ON063705	–	–	ON100785	–	ON089698	Wang et al. (2023)
	Tubulicrinis globisporus	KHL 12133 (GB)	DQ873655	DQ873655	–	–	–	–	Larsson et al. (2006)
	Tubulicrinis gracillimus	PDD 95851	HQ533047		–	–	–	–	Unpublished
	Tubulicrinis hirtellus	KHL 11717 (GB)	DQ873657	DQ873657	–	–	–	–	Larsson et al. (2006)
	Tubulicrinis inornatus	KHL 11763 (GB)	DQ873659	DQ873659	–	–	–	–	Larsson et al. (2006)
	Tubulicrinis martinicensis	GG-MAR12-206	KU659609	–	–	–	–	–	Gruhn et al. (2016)
	Tubulicrinis pini	**CLZhao 3679**	**–**	**OR449951**	**OR469092**	**–**	**–**	**–**	**Present study**
	Tubulicrinis pini	**CLZhao 6881** *	**OR096210**	**OR449952**	**–**	**–**	**–**	**OR541911**	**Present study**
	Tubulicrinis subulatus	LWZ 20190914-7	ON063706	ON063906	ON063767	–	–	–	Wang et al. (2023)
	Tubulicrinis xantha	CLZhao 2868	MT153874	MT153881	–	–	–	–	He et al. (2020)
	Tubulicrinis xantha	CLZhao 2869	MT153875	MT153882	–	–	–	–	He et al. (2020)
	Tubulicrinis yunnanensis	CLZhao 3418	MT153879	MT153886	–	–	–	–	He et al. (2020)
	Tubulicrinis yunnanensis	CLZhao 9717	MT153880	MT153887	–	–	–	–	He et al. (2020)
Hysterangiales/ *Hysterangiaceae*	*Aroramyces gelatinosporus*	H4010	–	DQ218524	–	–	DQ218941	DQ219118	Liu et al. (2022c)
-/ *Mesophelliaceae*	*Chondrogaster pachysporus*	OSC49298	–	DQ218538	–	–	DQ218958	DQ219136	Liu et al. (2022c)
Jaapiales/ *Jaapiaceae*	*Jaapia argillacea*	CBS 252.74	GU187524	GU187581	–	–	GU187788	GU187711	Liu et al. (2022c)
Lepidostromatales/ *Lepidostromataceae*	*Lepidostroma vilgalysii*	RV-MX16	JN698907	JN698908	–	–	–	–	Liu et al. (2022c)
	Sulzbacheromyces caatingae	Sulzbacher 1479	KC170320	KC170318	–	–	–	–	Liu et al. (2022c)
Phallales/ *Phallaceae*	*Lysurus mokusin*	MB02012	–	–	–	–	DQ219101	DQ219277	He et al. (2019)
	Phallus hadriani	AFTOL-ID 683	DQ404385	AY885165	–	–	DQ408114	DQ435792	Matheny et al. (2007)
Polyporales/ *Adustoporiaceae*	*Austroporia stratosa*	FF 461	KY948806	KY948881	–	KY949014	–	–	Justo et al. (2017)
	Austroporia stratosa	Cui 16619	MW377266	MW377346	–	MW337163	MW337032	MW337095	Liu et al. (2022b)
	Rhodonia placenta	Wei 1406	KF699129	KT893750	–	ON424739	KT893746	KT893748	Liu et al. (2022b)
	Rhodonia subrancida	Cui 16462	MW377322	ON417243	–	MW337202	MW337075	ON424877	Liu et al. (2022b)
-/ *Auriporiaceae*	*Auriporia aurea*	Cui 10665	KX966182	KX966183	–	–	–	KX966184	Shen et al. (2019)
	Auriporia aurulenta	Dai 6922	MW377261	MW377342	MW382053	–	–	–	Liu et al. (2022b)
-/ *Cerrenaceae*	*Cerrena unicolor*	He 6082	OM100740	OM083972	ON417068	ON424672	ON424756	ON424825	Liu et al. (2022b)
	Cerrena zonata	Cui 18502	ON417154	ON417204	ON417070	ON424674	ON424758	ON424827	Liu et al. (2022b)
	Radulodon casearius	Cui 17979	ON417185	ON417236	ON417093	ON424727	–	ON424868	Liu et al. (2022b)
-/ *Climacocystaceae*	*Climacocystis borealis*	Dai 4014	KJ566627	KJ566637	–	ON688463	–	KJ566644	Liu et al. (2023a)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Climacocystis borealis	FD 31	KP135308	KP135210	–	KP134882	KP134895	–	Liu et al. (2023a)
	Climacocystis borealis	KHL 13318	JN710527	JN710527	–	–	–	–	Cao et al. (2021b)
	Climacocystis montana	Cui 17122	ON682359	ON680811	–	ON688466	ON688485	ON688505	Liu et al. (2023a)
	Climacocystis montana	Cui 17123	ON682360	ON680812	–	ON688467	ON688486	ON688506	Liu et al. (2023a)
-/*Dacryobolaceae*	*Dacryobolus gracilis*	He 5995	ON417156	ON417206	ON417075	–	ON424760	ON424831	Liu et al. (2022b)
	Dacryobolus karstenii	Miettinen-18685	KY948743	KY948900		KY948955			Justo et al. (2017)
	Dacryobolus montanus	He 6314	ON417157	ON417207	ON417076	–	ON424761	ON424832	Liu et al. (2022b)
	Dacryobolus sudans	FP 101996	KC585332	KC585157	–	–	–	–	Ortiz-Santana et al. (2013)
-/*Fibroporiaceae*	*Fibroporia ceracea*	Cui 16300	MW377294	MW377373	MW382080	MW337187	MW337055	MW337121	Liu et al. (2022b)
	Fibroporia vaillantii	Dai 23467	ON417158	ON417208	ON417077	ON424680	ON424763	ON424833	Liu et al. (2022b)
	Pseudofibroporia citrinella	He 20120721	KU550477	KU550500	KU550520		KU550555	KU550574	Chen et al. (2017)
	Pseudofibroporia citrinella	Yuan 6181	KU550478	KU550501	KU550521		KU550556	KU550575	Chen et al. (2017)
-/*Fomitopsidaceae*	*Antrodia serpens*	Dai 7465	KR605813	KR605752	KR606013	ON424666	KR610832	KR610742	Han et al. (2016)
	Antrodia subserpens	Cui 16285	ON417152	ON417201	ON417067	ON424669	ON424755	ON424824	Liu et al. (2022b)
	Brunneoporus malicola	Cui 16272	OK045505	OK045511	OK045499	OK076903	OK076931	OK076959	Liu et al. (2022b)
	Daedalea dickinsii	Yuan 2707	KP171202	KP171224	KR605983	–	KR610804	KR610713	Han et al. (2016)
	Daedalea quercina	Dai 12659	KP171208	KP171230	KR605990	ON424676	KR610810	KR610719	Liu et al. (2022b)
	Fomitopsis ostreiformis	Cui 18217	OL621855	OL621244	OL621755	ON424689	OL588970	OL588984	Liu et al. (2022b)
	Fomitopsis subtropica	Dai 18566	OL621854	OL621243	OL621754	ON424691	ON424768	OL588983	Liu et al. (2022b)
-/*Fragiliporiaceae*	*Fragiliporia fragilis*	Dai 13080	KJ734260	KJ734264	KJ734268	–	KJ790248	KJ790245	Zhao et al. (2015)
	Fragiliporia fragilis	Dai 13559	KJ734261	KJ734265	KJ734269	–	KJ790249	KJ790246	Zhao et al. (2015)
-/*Gelatoporiaceae*	*Cinereomyces lindbladii*	H 19911	FN907909	FN907909	–	–	–	–	Fan et al. (2017)
	Cinereomyces lindbladii	CBS:290.71	MH860129	MH871902	–	–	–	–	Vu et al. (2019)
	Gelatoporia subvermispora	Cui 17120	ON417159	ON417209	–	ON424694	ON424772	ON424835	Liu et al. (2022b)
	Gelatoporia subvermispora	Dai 22847	ON417160	ON417210	–	ON424695	ON424773	ON424836	Liu et al. (2022b)
	Obba rivulosa	Cui 16483	ON417171	ON417221	–	ON424711	ON424787	ON424849	Liu et al. (2022b)
	Obba rivulosa	Cui 16482	ON417172	ON417222	–	ON424712	ON424788	ON424850	Liu et al. (2022b)
-/*Gloeoporellaceae*	*Gloeoporellus merulinus*	Dai 18735	MW377299	MW377378	–	MW337192	ON688490	MW337126	Liu et al. (2023a)
	Gloeoporellus merulinus	Dai 18782	MW377300	MW377379	–	MW337193	ON688491	MW337127	Liu et al. (2023a)
	Gloeoporellus merulinus	Cui 16629	ON682364	ON680816	–	ON688471	ON688492	ON688512	Liu et al. (2023a)
	Gloeoporellus merulinus	Cui 16650	ON682365	ON680817	–	ON688472	ON688493	ON688513	Liu et al. (2023a)
-/*Grifolaceae*	*Grifola frondosa*	AFTOL 701	AY854084	AY629318	–	AY864876	–	AY885153	Lutzoni et al. (2004)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Grifola frondosa	Dai 19172	ON417161	ON417211	–	ON424696	ON424774	ON424837	Liu et al. (2022b)
-/*Hyphodermataceae*	*Hyphoderma cremeoalbum*	NH 11538 (GB)	DQ677492	DQ677492	–	–	–	–	Larsson (2007b)
	Hyphoderma cremeoalbum	**CLZhao 17007**	**OM955862**	**OM955862**	**OQ706819**	**–**	**–**	**–**	**Present study**
	Hyphoderma litschaueri	FP 101740	KP135295	KP135219	–	KP134868	KP134965	–	Floudas & Hibbett (2015)
	Hyphoderma medioburiense	FD 335	KP135298	KP135220	–	KP134869	KP134966	–	Floudas & Hibbett (2015)
	Hyphoderma mutatum	HHB 15479	KP135296	KP135221	–	KP134870	KP134967	–	Floudas & Hibbett (2015)
	Hyphoderma setigerum	FD 312	KP135297	KP135222	–	KP134871	–	–	Floudas & Hibbett (2015)
	Hyphoderma setigerum	FCUG 1688	AJ534272	–	–	–	–	–	Nilsson et al. (2003)
	Hyphoderma setigerum	NH 6748	AJ534259	–	–	–	–	–	Paulus et al. (2007)
	Hyphoderma transiens	NH 12304 (GB)	DQ677504	DQ677504	–	–	–	–	Larsson (2007b)
	Hyphoderma transiens	**CLZhao 1493**	**MT955164**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Hyphoderma transiens	**CLZhao 1606**	**MT955162**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Hyphoderma transiens	**CLZhao 1667**	**MT955166**	**–**	**OQ706787**	**–**	**–**	**–**	**Present study**
	Hyphoderma transiens	**CLZhao 1719**	**MT955163**	**OM985767**	**–**	**–**	**–**	**–**	**Present study**
	Hyphoderma transiens	**CLZhao 1768**	**MT955165**	**–**	**–**	**–**	**–**	**–**	**Present study**
-/*Hypochniciaceae* **fam. nov.**	*Hypochnicium bombycinum*	Otto Miettinen 9441 (H)	**KY415959**	**KY415959**	–	–	–	–	Maekawa et al. (2023)
	Hypochnicium bombycinum	HHB 12631	KY948801	KY415959	–	KY948930	–	–	Justo et al. (2017)
	Hypochnicium karstenii	NH 10924	DQ677510	DQ677510	–	–	–	–	Larsson (2007b)
	Hypochnicium lyndoniae	NL 041031	JX124704	JX124704	–	–	JX109876	JX109905	Unpublished
	Hypochnicium multiforme	TUMH: 64581	LC663674	LC663693	–	–	–	–	Maekawa et al. (2023)
-/*Incrustoporiaceae*	*Skeletocutis albomarginata*	Cui 8844	JN048764	JN048783	–	–	–	–	Zhao et al. (2016b)
	Skeletocutis albomarginata	Cui 8838	JN048765	JN048784	–	–	–	–	Zhao et al. (2016b)
	Skeletocutis amorpha	83252	JQ518277	–	–	–	–	–	Carlsson et al. (2012)
	Skeletocutis bambusicola	Dai 16613	MN908950	MN908952	–	–	–	–	Unpublished
	Skeletocutis bambusicola	Dai 16597	MN908949	MN908951	–	–	–	–	Unpublished
	Skeletocutis calida	X3459	KY953065	–	–	–	–	–	Korhonen et al. (2018)

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			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Skeletocutis calida	X3457	KY953086	–	–	–	–	–	Korhonen et al. (2018)
	Skeletocutis cangshanensis	Cui 17990	MZ327280	MZ348536	–	–	–	–	Jayawardena et al. (2023)
	Skeletocutis cangshanensis	Cui 17994	MZ327281	MZ348537	–	–	–	–	Jayawardena et al. (2023)
	Skeletocutis coprosmae	Cui 16623	ON417193	ON417245	ON417100	ON424741	ON424813	ON424879	Liu et al. (2022b)
	Skeletocutis coprosmae	X518	KY953057	KY953057	–	–	–	KY953115	Korhonen et al. (2018)
	Skeletocutis cummata	X2328	KY953040	KY953040	–	–	–	KY953122	Korhonen et al. (2018)
	Skeletocutis cummata	X465	KY953055	KY953055	–	–	–	KY953113	Korhonen et al. (2018)
	Skeletocutis delicata	X321	MF685349	–	–	–	–	–	Miettinen & Niemela (2018)
	Skeletocutis delicata	X397	MF685350	–	–	–	–	–	Miettinen & Niemela (2018)
	Skeletocutis exilis	X395	MF685356	–	–	–	–	–	Miettinen & Niemela (2018)
	Skeletocutis exilis	X1637	MF685357	–	–	–	–	–	Miettinen & Niemela (2018)
	Skeletocutis kuehneri	X3324	MF685361	–	–	–	–	–	Miettinen & Niemela (2018)
	Skeletocutis lepida	X2990	MF075130	MF075130	–	–	–	KY953133	Korhonen et al. (2018)
	Skeletocutis lepida	X2333	KY953063	KY953063	–	–	–	KY953126	Korhonen et al. (2018)
	Skeletocutis lilacina	HHB10522 sp	KY948834	KY948894	–	KY948967	–	–	Justo et al. (2017)
	Skeletocutis mopanshanensis	CLZhao 1152	MF924720	MF924722	–	–	–	–	Wu et al. (2018b)
	Skeletocutis mopanshanensis	CLZhao 1184	MF924721	MF924723	–	–	–	–	Wu et al. (2018b)
	Skeletocutis nemoralis	X2323	KY953035	KY953035	–	–	–	KY953121	Korhonen et al. (2018)
	Skeletocutis nemoralis	X2342	KY953091	–	–	–	–	–	Korhonen et al. (2018)
	Skeletocutis nivea	Cui 16752	ON682369	ON680821	–	ON688477	ON688497	ON688517	Liu et al. (2023a)
	Skeletocutis ochroalba	X3371	KY953070	KY953070	–	–	–	KY953137	Korhonen et al. (2018)
	Skeletocutis ochroalba	X3372	KY953071	–	–	–	–	KY953138	Korhonen et al. (2018)
	Skeletocutis pseudo-odora	Dai 16528	KY245962	–	–	–	–	–	Fan et al. (2017)
	Skeletocutis pseudo-odora	Dai 16525	KY245960	–	–	–	–	–	Fan et al. (2017)
	Skeletocutis rhizomorpha	**CLZhao 3455**	**OR167775**	**OR449953**	**OR469093**	**OR683148**	**–**	**–**	**Present study**

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Skeletocutis rhizomorpha	**CLZhao 3516**	**OR167776**	**OR449954**	**OR469094**	–	–	–	**Present study**
	Skeletocutis rhizomorpha	**CLZhao 3552** *	**OR167777**	**OR449955**	**OR469095**	**OR683149**	–	–	**Present study**
	Skeletocutis rhizomorpha	**CLZhao 3583**	**OR167778**	**OR449956**	**OR469096**	–	–	–	**Present study**
	Skeletocutis rhizomorpha	**CLZhao 3667**	**OR167779**	**OR449957**	**OR469097**	**OR683150**	–	–	**Present study**
	Skeletocutis semipileata	X2347	KY953108	KY953108	–	–	–	–	Korhonen et al. (2018)
	Skeletocutis semipileata	X2355	KY953102	KY953102	–	–	–	–	Korhonen et al. (2018)
	Skeletocutis subalbomarginata	Dai 19593	MN908953	MN905044	–	–	–	–	Du & Dai (2020)
	Skeletocutis subalbomarginata	Dai 19599	MN908954	MN905045	–	–	–	–	Du & Dai (2020)
	Skeletocutis subchrysella	Cui 17748	MZ327278	MZ348534	–	–	–	–	Jayawardena et al. (2023)
	Skeletocutis vietnamensis	Dai 18374	MG893204	MN905061	–	–	–	–	Du & Ji (2019)
	Skeletocutis vietnamensis	Dai 18378	MG893205	MN905062	–	–	–	–	Du & Ji (2019)
	Skeletocutis yunnanensis	Dai 15709	KU950434	KU950436	MW424990	MW526263	–	MW427605	Bian et al. (2016)
	Skeletocutis yunnanensis	Dai 15712	KU950435	KU950437	–	–	–	–	Bian et al. (2016)
	Tyromyces chioneus	FD 4	KP135311	KP135291	–	KP134891	KP134977	–	Floudas & Hibbett (2015)
	Tyromyces sp.	Cui 16652	ON417196	ON417248	–	ON424749	ON424820	ON424885	Liu et al. (2022b)
-/*Irpicaceae*	*Byssomerulius corium*	FP-102382	KP135007	KP135230	–	KP134802	KP134921	–	Floudas & Hibbett (2015)
	Efibula americana	FP-102165	KP135016	KP135256	–	KP134808	KP134916	MZ913669	Floudas & Hibbett (2015)
	Efibula americana	HHB-8468	KP135012	–	–	–	–	–	Floudas & Hibbett (2015)
	Efibula bubalina	MA-Fungi 86614	KF483005	KF528096	–	–	–	–	Li et al. (2022)
	Efibula clarkii	FD-228	KP135019	–	–	KP134803	–	–	Floudas & Hibbett (2015)
	Efibula daweishanensis	**CLZhao 18946** *	**OR094488**	–	**OR469098**	–	–	**OR541912**	**Present study**
	Efibula daweishanensis	**CLZhao 19002**	**OR094489**	**OR449958**	**OR469099**	–	–	–	**Present study**
	Efibula daweishanensis	**CLZhao 25072**	**OR094490**	**OR449959**	**OR469100**	–	**OR733284**	**OR541913**	**Present study**

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Efibula gracilis	FD-455	KP135027	MZ637116	–	KP134804	OK136077	MZ913679	Chen et al. (2021)
	Efibula gracilis	FP-102052	KP135028	–	–	–	–	–	Floudas & Hibbett (2015)
	Efibula grandinosa	He 6312	MZ422509	MZ422480	–	–	–	–	Li et al. (2022)
	Efibula hainanensis	He 6004	MW580949	MW580939	–	–	–	–	Li et al. (2022)
	Efibula hainanensis	Chen 1284	ON117184	–	–	–	–	–	Li et al. (2022)
	Efibula intertexta	Wu 1707-93	MZ636953	MZ637117	–	MZ748416	OK136085	–	Chen et al. (2021)
	Efibula intertexta	Wu 1707-96	MZ636954	MZ637118	–	MZ748417	OK136086	–	Chen et al. (2021)
	Efibula matsuensis	Wu 1011-18	MZ636956	MZ637119	–	MZ748418	OK136078	MZ913680	Chen et al. (2021)
	Efibula matsuensis	Wu 1011-19	MZ636957	MZ637120	–	–	–	–	Chen et al. (2021)
	Efibula shenghuae	He 3384	MZ422508	MZ422479	–	–	–	–	Li et al. (2022)
	Efibula subglobispora	Chen 1716	MZ636962	MZ637124	–	MZ748427	OK136075	MZ913673	Chen et al. (2021)
	Efibula subglobispora	GC 1604-13	MZ636963	MZ637125	–	MZ748428	OK136076	MZ913674	Chen et al. (2021)
	Efibula taiwanensis	He 4582	MZ422507	MZ422478	–	–	–	–	Li et al. (2022)
	Efibula tropica	WEI 18-149	MZ636967	MZ637129	–	MZ748419	OK136079	MZ913681	Chen et al. (2021)
	Efibula tropica	Wu 0809-8	MZ636968	MZ637130	–	–	–	–	Chen et al. (2021)
	Efibula tuberculata	Wu 1005-55	MZ636970	MZ637132	–	MZ748426	OK136074	MZ913672	Chen et al. (2021)
	Efibula tuberculata	Wu 0711-148	MZ636969	MZ637131	–	–	–	MZ913671	Chen et al. (2021)
	Efibula turgida	Wu 0910-86	MZ636972	MZ637134	–	MZ748439	OK136091	MZ913716	Chen et al. (2021)
	Efibula turgida	Wu 0910-99	MZ636973	MZ637135	–	MZ748440	OK136092	MZ913717	Chen et al. (2021)
	Efibula yunnanensis	Wu 880515-1	MZ636977	GQ470672	–	MZ748420	OK136080	MZ913682	Chen et al. (2021)
	Efibula yunnanensis	CLZhao 11641	MT611529	–	–	–	–	–	Ma et al. (2020)
	Irpex flavus	Wu 0705-1	MZ636988	MZ637149	–	MZ748432	OK136087	MZ913683	Liu et al. (2022b)
	Irpex lacteus	FD-9	KP135026	KP135224	–	KP134806	–	–	Floudas & Hibbett (2015)
	Irpex latemarginatus	FP-55521-T	KP135024	KP135202	–	KP134805	KP134915	–	Floudas & Hibbett (2015)
	Leptoporus mollis	TJV-93-174-T	KY948795	EU402510	–	KY948957	OK136102	MZ913694	Chen et al. (2021)
	Leptoporus mollis	RLG 7163	KY948794	MZ637155	–	KY948956	OK136101	MZ913693	Liu et al. (2023a)
	Phanerochaetella angustocystidiata	Wu 9606-39	MZ637020	GQ470638	–	MZ748422	OK136082	MZ913687	Liu et al. (2023a)
	Phanerochaetella leptoderma	Chen 1362	MZ637025	GQ470646	–	MZ748423	OK136083	MZ913689	Liu et al. (2023a)
-/Ischnodermataceae	*Ischnoderma benzoinum*	Cui 17058	ON417164	ON417214	ON417080	ON424699	ON424777	ON424839	Liu et al. (2022b)
	Ischnoderma benzoinum	Cui 17700	ON417165	ON417215	ON417081	ON424700	ON424778	ON424840	Liu et al. (2022b)
	Ischnoderma resinosum	FD 328	KP135303	KP135225	–	KP134884	KP134972	–	Floudas & Hibbett (2015)

Table 1 Contined.

Order/Family	**Species name**	**Sample no.**	**GenBank accessions no.**						**References**
			ITS	**nLSU**	**mtSSU**	**RPB1**	**RPB2**	**TEF1**	
-/*Laetiporaceae*	*Laetiporus montanus*	Cui 10011	KF951274	KF951315	KX354570	MG867670	KT894790	KX354617	Song et al. (2018)
	Laetiporus sulphureus	Cui 12389	KR187106	KX354487	KX354561	ON424702	KX354653	KX354608	Song et al. (2018)
-/*Laricifomitaceae*	*Gilbertsonia angulopora*	FP 133019	KC585354	KC585182	–	–	–	–	Ortiz-Santana et al. (2013)
	Laricifomes officinalis	JV 0309/49-J	KR605821	KR605764	–	–	KR610846	KR610757	Han et al. (2016)
	Laricifomes officinalis	JV 9010/14	KR605822	KR605765	–	–	KR610847	KR610758	Han et al. (2016)
	Ryvardenia campyla	Cui 16674	MW377323	MW377400	–	MW337203	MW337076	MW337143	Liu et al. (2022b)
	Ryvardenia cretacea	Cui 16731	MW377324	MW377401	MW382102	MW337204	MW337077	MW337144	Liu et al. (2022b)
-/*Meripilaceae*	*Meripilus giganteus*	FP 135344	KP135307	KP135228	–	KP134873	–	–	Floudas & Hibbett (2015)
	Physisporinus longicystidius	Cui 16630	ON417177	ON417227	–	ON424717	ON424795	ON424856	Liu et al. (2022b)
	Physisporinus longicystidius	Cui 16725	ON417178	ON417228	–	ON424718	ON424796	ON424857	Liu et al. (2022b)
	Rigidoporus undatus	Miettinen 13591	KY948731	KY948870	–	KY948945	–	–	Justo et al. (2017)
-/*Meruliaceae*	*Luteoporia albomarginata*	GC 1702-1	LC379003	LC379155	–	LC379160	LC387358	LC387377	Chen et al. (2021)
	Luteoporia lutea	GC 1409-1	MZ636998	MZ637158	–	MZ748467	OK136050	MZ913656	Chen et al. (2021)
	Mycoacia fuscoatra	OMC1380	KY948754	–	–	–	–	–	Justo et al. (2017)
	Mycoacia fuscoatra	**CLZhao 18423**	**MW732423**	**MW732461**	**MW732745**	**–**	**–**	**–**	**Present study**
	Phlebia nantahaliensis	HHB 2816	KY948777	KY948852	–	KY948920	OK136063	MZ913701	Liu et al. (2023a)
	Phlebia tomentopileata	GC 1602-67	MZ637040	MZ637244	–	MZ748457	OK136064	MZ913702	Chen et al. (2021)
	Scopuloides allantoidea	Wei 16-060	MZ637081	MZ637279	–	MZ748463	OK136047	MZ913664	Chen et al. (2021)
-/*Neohypochniciaceae* **fam. nov.**	*Bulbillomyces farinosus*	FP 100488T	KY948802	–	–	KY948929	–	–	Liu et al. (2023a)
	Bulbillomyces farinosus	NH 9933 (GB)	DQ681201	DQ681201	–	–	–	–	Larsson (2007b)
	Gyrophanopsis japonica	TUMH:61400	LC663668	LC663688	–	–	–	–	Maekawa et al. (2023)
	Gyrophanopsis polonense	NH 11337 (GB)	DQ677511	DQ677511	–	–	–	–	Larsson (2007b)
	Gyrophanopsis zealandica	NH 15340	DQ309068	–	–	–	–	–	Paulus et al. (2007)
	Neohypochnicium albostramineum	NH 3688	AF429422	–	–	–	–	–	Paulus et al. (2007)
	Neohypochnicium albostramineum	NH 9637	AF429423	–	–	–	–	–	Paulus et al. (2007)
	Neohypochnicium aotearoae	NH 15862	GQ906536	–	–	–	–	–	Telleria et al. (2010a)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Neohypochnicium asiaticum	TUMH:61220	LC663669	LC663689	–	–	–	–	Maekawa et al. (2023)
	Neohypochnicium asiaticum	TUMH:61227	LC663672	–	–	–	–	–	Maekawa et al. (2023)
	Neohypochnicium cremicolor	CBS:208.54	MH857294	MH868826	–	–	–	–	Vu et al. (2019)
	Neohypochnicium cremicolor	NH 3406	AF429425	–	–	–	–	–	Paulus et al. (2007)
	Neohypochnicium cystidiatum	MUCL 32103	DQ658163	–	–	–	–	–	Paulus et al. (2007)
	Neohypochnicium cystidiatum	MUCL 32104	DQ658164	–	–	–	–	–	Paulus et al. (2007)
	Neohypochnicium daweishanense	**CLZhao 17726 ***	**OQ789010**	–	–	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18089**	**OQ789012**	–	**OR469101**	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18764**	**OQ789013**	**OQ788992**	–	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18771**	**OQ789014**	**OQ788993**	**OR469102**	–	–	**OR541914**	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18787**	**OQ789015**	**OQ788994**	–	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18792**	**OQ789016**	**OQ788995**	**OR469103**	**OR683151**	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18798**	**OQ789017**	–	–	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18820 ***	**OQ789018**	**OQ788996**	**OR469104**	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18844**	**OQ789019**	**OQ788997**	–	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18850**	**OQ789020**	**OQ788998**	**OR469105**	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18856**	**OQ789021**	–	–	–	–	–	**Present study**
	Neohypochnicium farinaceum	**CLZhao 18867**	**OQ789022**	–	**OR469106**	**OR683152**	–	**OR541915**	**Present study**

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Neohypochnicium farinaceum	**CLZhao 18881**	**OQ789023**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Neohypochnicium farinaceum	**CLZhao 19022**	**OQ789024**	**–**	**OR469107**	**–**	**–**	**–**	**Present study**
	Neohypochnicium geogenium	**FCUG 2052**	**AF429426**	–	–	–	–	–	Telleria et al. (2010a)
	Neohypochnicium geogenium	MA-Fungi 48308	FN552534	–	–	–	–	–	Telleria et al. (2010a)
	Neohypochnicium guineense	MA-Fungi 79156	FN552536	–	–	–	–	–	Telleria et al. (2010a)
	Neohypochnicium huinayense	19598Tell	HG000303	–	–	–	–	–	Maekawa et al. (2023)
	Neohypochnicium huinayense	MA-Fungi:13980	HG326616	–	–	–	–	–	Maekawa et al. (2023)
	Neohypochnicium michelii	MA-Fungi 79155	FN552535	JN939579	–	–	–	–	Telleria et al. (2010a)
	Neohypochnicium microsporum	GG-GUY13-100	KY019170	–	–	–	–	–	Gruhn et al. (2017)
	Neohypochnicium microsporum	GG-GUY12-101	KY019171	–	–	–	–	–	Gruhn et al. (2017)
	Neohypochnicium murinum	**CLZhao 6855**	**OQ788983**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Neohypochnicium murinum	**CLZhao 19012** *	**OQ788984**	**OQ789004**	**OR469108**	**–**	**–**	**OR541916**	**Present study**
	Neohypochnicium murinum	**CLZhao 19017**	**OQ788985**	**OQ789005**	**OR469109**	**–**	**–**	**OR541917**	**Present study**
	Neohypochnicium murinum	**CLZhao 19020**	**OQ788986**	**OQ789006**	**–**	**–**	**–**	**–**	**Present study**
	Neohypochnicium murinum	**CLZhao 19031**	**OQ788987**	**OQ789007**	**OR469110**	**–**	**–**	**OR541918**	**Present study**
	Neohypochnicium murinum	**CLZhao 19067**	**OQ788988**	**OQ789008**	**OR469111**	**–**	**–**	**–**	**Present study**
	Neohypochnicium murinum	**CLZhao 19125**	**OQ788989**	**–**	**OR469112**	**–**	**–**	**OR541919**	**Present study**
	Neohypochnicium murinum	**CLZhao 19129**	**OQ788990**	**–**	**OR469113**	**–**	**–**	**OR541920**	**Present study**

Table 1 Contined.

Order/Family	**Species name**	**Sample no.**	**GenBank accessions no.**						**References**
			ITS	**nLSU**	**mtSSU**	**RPB1**	**RPB2**	**TEF1**	
	Neohypochnicium patagonicum	GB:0129149	HG000304	–	–	–	–	–	Maekawa et al. (2023)
	Neohypochnicium perlongicystidiosum	TUMH:40397	LC663679	LC663690	–	–	–	–	Maekawa et al. (2023)
	Neohypochnicium perlongicystidiosum	TUMH:63618	LC663675	–	–	–	–	–	Maekawa et al. (2023)
	Neoheohypochnicium pini	TUMH:61221	LC663680	LC663691	–	–	–	–	Maekawa et al. (2023)
	Neoheohypochnicium pini	F0023763	KC282471	–	–	–	–	–	Jang et al. (2013)
	Neohypochnicium punctulatum	FP 101698	KY948827	KY948860	–	KY948932	–	–	Justo et al. (2017)
	Neohypochnicium punctulatum	NH 7815	AF429408	–	–	–	–	–	Paulus et al. (2007)
	Neohypochnicium subrigescens	KHL 11968	JN710546	–	–	–	–	–	Maekawa et al. (2023)
	Neohypochnicium subrigescens	NH 10421	AF429427	–	–	–	–	–	Telleria et al. (2010a)
	Neohypochnicium velutinum	**CLZhao 18084**	**OQ789999**	**OQ788980**	**OR469114**	**–**	**–**	**OR541921**	**Present study**
	Neohypochnicium velutinum	**CLZhao 18085**	**OQ789000**	**–**	**OR469115**	**–**	**–**	**–**	**Present study**
	Neohypochnicium velutinum	**CLZhao 18101**	**OQ789001**	**–**	**OR469116**	**–**	**–**	**OR541922**	**Present study**
	Neohypochnicium velutinum	**CLZhao 18144** *	**OQ789002**	**OQ788981**	**OR469117**	**–**	**–**	**OR541923**	**Present study**
	Neohypochnicium wakefieldiae	KJM 271	**KY948828**	**DQ677512**	–	**KY948933**	–	–	Justo et al. (2017)
	Neohypochnicium wakefieldiae	NH 12107	AF429416	–	–	–	–	–	Paulus et al. (2007)
	Neohypochnicium yunnanense	**CLZhao 18525** *	**OQ789011**	**OQ789003**	**OR469118**	**–**	**–**	**–**	**Present study**
	Neohypochnicium zixishanense	**CLZhao 7270** *	**OQ789009**	**OQ788991**	**OR469119**	**–**	**–**	**OR541924**	**Present study**
-/*Panaceae*	*Cymatoderma elegans*	Dai 17511	ON417155	ON417205	–	–	–	–	Liu et al. (2022b)
	Cymatoderma sp.	OMC 1427	KY948826	KY948872	–	KY948971	–	–	Justo et al. (2017)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Panus conchatus	Dai 23421	ON417176	ON417226	ON417088	ON424716	ON424794	ON424855	Liu et al. (2022b)
	Panus fragilis	HHB 11042	KP135328	KP135233	–	KP134877	–	–	Floudas & Hibbett (2015)
-/*Phanerochaetaceae*	*Bjerkandera adusta*	HHB-12826-Sp	KP134983	KP135198	–	KP134784	KP134913	KT305938	Floudas & Hibbett (2015)
	Bjerkandera centroamericana	L-13104-sp	KY948791	KY948855	–	KY948936	–	–	Justo et al. (2017)
	Donkia pulcherrima	GC 1707-11	LC378994	LC379152	–	LC379157	LC387351	LC387371	Chen et al. (2018)
	Donkia pulcherrima	Gothenburg-2022	KX752591	KX752591	–	–	–	–	Miettinen et al. (2016)
	Donkiella yunnanensis	**CLZhao 3931 ***	**OR094482**	**OR461467**	**OR548142**	**OR531377**	**OR733285**	**OR541925**	**Present study**
	Donkiella yunnanensis	**CLZhao 18292**	**OR094483**	**OR461468**	**OR548143**	**–**	**OR733286**	**OR541926**	**Present study**
	Geliporus exilisporus	GC 1702-15	LC378995	LC379153	–	LC379158	LC387352	LC387372	Chen et al. (2018)
	Hapalopilus rutilans	FP-102473-Sp	MZ636981	MZ637142	–	MZ748407	OK136004	MZ913723	Chen et al. (2021)
	Hyphodermella corrugata	MA-Fungi 24238	FN600378	JN939586	–	–	–	–	Telleria et al. (2010b)
	Hyphodermella laevigata	He 5427	ON964013	ON963996	–	–	–	–	Li et al. (2023a)
	Hyphodermella tropica	He 3993	ON964011	ON963994	–	–	–	–	Li et al. (2023a)
	Odontoefibula orientalis	Wu 0910-57	LC363490	LC363495	–	LC363501	LC387362	LC387381	Chen et al. (2018)
	Odontoefibula orientalis	GC 1703-76	LC379004	LC379156	–	LC379161	LC387360	LC387379	Chen et al. (2018)
	Oxychaete cervinogilva	Dmitry Schigel 5216	KX752596	KX752596	–	KX752626	–	–	Miettinen et al. (2016)
	Oxychaete cervinogilva	GC 1501-16	MZ422783	MZ637173	–	–	–	MZ913613	Chen et al. (2021)
	Phaeophlebiopsis caribbeana	HHB-6990	KP135415	KP135243	–	KP134810	KP134931	MZ913643	Chen et al. (2021)
	Phaeophlebiopsis himalayensis	Chen 3143	MZ637013	MZ637174	–	MZ748359	OK135992	MZ913633	Chen et al. (2021)
	Phaeophlebiopsis ravenelii	FCUG 2126	MZ637015	GQ470675	–	MZ748361	OK135993	MZ913634	Liu et al. (2023a)
	Phanerina mellea	WEI 17-224	LC387333	LC387340	–	LC387345	LC387363	LC387382	Chen et al. (2018)
	Phanerina mellea	Wu 1010-34	MZ422784	MZ637176	–	–	–	–	Chen et al. (2021)
	Phanerochaete aculeata	Wu 880701-2	MZ422787	GQ470636	–	MZ748380	OK136008	MZ913593	Chen et al. (2021)
	Phanerochaete albida	GC 1407-14	MZ422788	MZ637179	–	MZ748384	OK136013	MZ913704	Chen et al. (2021)
	Phanerochaete alnea	FP 151125	KP135177	MZ637181	–	MZ748385	OK136014	MZ913641	Liu et al. (2023a)
	Phanerochaete alpina	Wu 1308–61	MZ422790	MZ637182	–	MZ748394	OK136022	MZ913598	Chen et al. (2021)
	Phanerochaete arizonica	RLG-10248-Sp	KP135170	KP135239	–	KP134830	KP134949	–	Floudas & Hibbett (2015)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Phanerochaete australis	GC 1505-15	MZ422792	MZ637184	–	MZ748381	OK136010	MZ913595	Chen et al. (2021)
	Phanerochaete bambusicola	Wu 0707-2	MF399404	MF399395	–	LC314324	OK136009	MZ913594	Chen et al. (2021)
	Phanerochaete canolutea	Wu 9211-105	MZ422795	GQ470641	–	MZ748387	OK136018	MZ913640	Chen et al. (2021)
	Phanerochaete chrysosporium	PC139	MZ422797	MZ637186	–	MZ748405	OK136036	MZ913606	Chen et al. (2021)
	Phanerochaete citrinosanguinea	FP-105385	KP135100	KP135234	–	KP134824	KP134941	MZ913602	Chen et al. (2021)
	Phanerochaete concrescens	Wu 1107-53	MZ422799	MZ637187	–	MZ748382	OK136011	MZ913596	Chen et al. (2021)
	Phanerochaete crystallina	GC 1409-7	MZ422803	MZ637189	–	MZ748404	OK136033	MZ913607	Chen et al. (2021)
	Phanerochaete cystidiata	GC 1708-358	LC412096	LC412101	–	LC412107	OK136025	MZ913599	Chen et al. (2021)
	Phanerochaete ericina	HHB-2288	KP135167	KP135247	–	KP134834	KP134950	–	Floudas & Hibbett (2015)
	Phanerochaete fusca	Wu 1409-161	LC412098	LC412105	–	LC412109	OK136028	–	Chen et al. (2021)
	Phanerochaete fuscomarginata	RLG-10834-Sp	MZ422806	MZ637192	–	MZ748396	OK136029	MZ913603	Chen et al. (2021)
	Phanerochaete granulata	Wu 9210-57	MZ422810	MZ637196	–	MZ748406	OK136035	–	Chen et al. (2021)
	Phanerochaete laevis	Wu 0309-40	MZ422818	GQ470655	–	MZ748397	OK136026	MZ913605	Chen et al. (2021)
	Phanerochaete livescens	GC 1612-11	MZ422819	MZ637204	–	MZ748383	OK136012	MZ913597	Chen et al. (2021)
	Phanerochaete mopanshanensis	**CLZhao 2357 ***	**OR096190**	**OR461450**	**OR469120**	**OR683153**	**OR733287**	**OR541927**	**Present study**
	Phanerochaete parmastoi	Wu 880313-6	MZ422823	GQ470654	–	MZ748395	OK136027	MZ913612	Chen et al. (2021)
	Phanerochaete rhizomorpha	Wu 1707-112	MZ422827	MZ637211	–	MZ748391	OK136019	MZ913636	Chen et al. (2021)
	Phanerochaete sanguineocarnosa	FD-359	KP135122	KP135245	–	KP134828	KP134944	–	Floudas & Hibbett (2015)
	Phanerochaete sanguineocarnosa	**CLZhao 4447**	**MK343613**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Phanerochaete sanguineocarnosa	**CLZhao 4634**	**MK343614**	**–**	**–**	**–**	**–**	**–**	**Present study**

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Phanerochaete sanguineocarnosa	**CLZhao 4639**	**MK343615**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Phanerochaete sanguineocarnosa	**CLZhao 4691**	**MK795174**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Phanerochaete sordida	GC 1708-162	MZ422828	MZ637212	–	MZ748388	OK136016	MZ913637	Chen et al. (2021)
	Phanerochaete sordida	Wu 1109-55	MZ422829	MZ637213	–	MZ748389	OK136017	MZ913638	Chen et al. (2021)
	Phanerochaete stereoides	Lin 523	MZ422838	MZ637220	–	MZ748400	OK136032	MZ913600	Chen et al. (2021)
	Phanerochaete subcarnosa	Wu 9310-3	MZ422841	GQ470642	–	MZ748399	OK136024	MZ913604	Chen et al. (2021)
	Phanerochaete taiwaniana	Wu 880824-17	MZ422842	GQ470666	–	MZ748393	OK136021	MZ913610	Chen et al. (2021)
	Phanerochaete thailandica	Wu 1710-3	MZ422843	MZ637223	–	MZ748401	OK136031	MZ913601	Chen et al. (2021)
	Phanerochaete velutina	GC 1604-56	MZ422844	MZ637224	–	MZ748386	OK136015	MZ913642	Chen et al. (2021)
	Phlebiopsis alba	GC 1508-110	MZ637042	MZ637246	–	MZ748368	OK135994	MZ913620	Chen et al. (2021)
	Phlebiopsis brunneocystidiata	Chen 666	MT561707	GQ470640	–	MZ748372	OK135998	MZ913625	Chen et al. (2021)
	Phlebiopsis castanea	GC 1612-6	KY688208	MZ637250	–	MZ748375	OK136001	MZ913618	Chen et al. (2021)
	Phlebiopsis crassa	GC 1602-45	MZ637049	MZ637251	–	MZ748373	OK135999	MZ913626	Chen et al. (2021)
	Phlebiopsis daweishanensis	**CLZhao 17984** *	**OR096193**	**OR461451**	**–**	**–**	**OR733288**	**OR541928**	**Present study**
	Phlebiopsis flavidoalba	GC 1807-47	MZ637050	MZ637254	–	MZ748378	OK136038		Chen et al. (2021)
	Phlebiopsis galochroa	FP-102937-Sp	KP135391	KP135270	–	KP134822	KP134929	MZ913621	Chen et al. (2021)
	Phlebiopsis gigantea	FCUG 1417	MZ637051	AF141634	–	MZ748370	OK135996	MZ913623	Liu et al. (2023a)
	Phlebiopsis laxa	Wu 9311-17	MT561710	GQ470649	–	MZ748374	OK136000	MZ913627	Chen et al. (2021)
	Phlebiopsis odontoidea	GC 1708-181	MZ637054	MZ637255	–	MZ748371	OK135997	MZ913624	Chen et al. (2021)
	Phlebiopsis pilatii	Wu 1707-18	MZ637056	MZ637257	–	MZ748376	OK136002	MZ913617	Chen et al. (2021)
	Phlebiopsis yushaniae	Chen 2358	MZ637047	MZ637261	–	MZ748377	OK136003	MZ913644	Chen et al. (2021)
	Pirex concentricus	OSC-41587	KP134984	KP135275	–	KP134843	KP134940	–	Floudas & Hibbett (2015)
	Porostereum fulvum	LY:18491	MG649452	MG649454	–	–	–	–	Chen et al. (2018)
	Porostereum spadiceum	Wu 9508-139	MZ637062	MZ637263	–	MZ748445	OK136067	MZ913697	Chen et al. (2018)
	Rhizochaete chinensis	Wu 0910-45	LC387335	MF110294	–	LC387348	LC387370	LC270925	Chen et al. (2021)
	Riopa metamorphosa	Spirin 2395	KX752601	KX752601	–	KX752628	–	–	Miettinen et al. (2016)
	Riopa pudens	Cui 3238	JX623931	JX644060	–	–	–	–	Jia et al. (2014)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Roseograndinia zixishanensis	CLZhao 7718	MZ305285	MZ305293	–	–	–	–	Wang et al. (2021a)
	Roseograndinia aurantiaca	CLZhao 10487	MW209023	MW209012	–	–	–	–	Wang & Zhao (2021b)
	Roseograndinia jilinensis	Wu 1307-132	MZ637076	MZ637274	–	MZ748412	OK135984	MZ913631	Shen et al. (2023)
	Roseograndinia jilinensis	Wu 1307-137	MZ637077	MZ637275	–	MZ748413	OK135985	MZ913632	Shen et al. (2023)
	Terana caerulea	FP-104073	KP134980	KP135276	–	KP134865	KP134960	–	Floudas & Hibbett (2015)
	Terana caerulea	GC 1507-2	MZ637090	MZ637287	–	MZ748414	OK136037	MZ913654	Chen et al. (2021)
-/*Podoscyphaceae*	*Abortiporus biennis*	Cui 17845	ON417149	ON417197	ON417064	ON424663	ON424750	ON424821	Liu et al. (2022b)
	Abortiporus biennis	Cui 16986	ON417150	ON417198	ON417065	ON424664	ON424751	ON424822	Liu et al. (2022b)
	Podoscypha tropica	140719–19	OQ305834	OQ305830	–	–	–	–	Si et al. (2023)
	Podoscypha venustula	Cui 16923	ON417181	ON417231	ON417089	ON424722	ON424799	ON424860	Liu et al. (2022b)
-/*Polyporaceae*	*Polyporus squamosus*	Cui 10595	KU189778	KU189809	KU189960	KU189892	KU189988	KU189925	Zhou et al. (2016)
	Polyporus varius	Cui 12249	KU507581	KU507583	KU507585	KU507589	KU507592	KU507591	Zhou et al. (2016)
	Trametes cinnabarina	Dai 14386	KX880629	KX880667	KX880712	KX880818	KX880854	KX880885	Cui et al. (2019)
	Trametes sanguinea	Cui 7091	KX880628	KX880666	KX880711	KX880817	MG867689	KX880884	Cui et al. (2019)
-/*Postiaceae*	*Amaropostia hainanensis*	Cui 13739	KX900909	KX900979	KX901053	KX901171	KX901223	–	Shen et al. (2019)
	Amaropostia stiptica	Cui 17037	OK045504	OK045510	OK045498	OK076902	OK076930	OK076958	Liu et al. (2022b)
	Calcipostia guttulata	Cui 10028	KF727433	KJ684979	KX901066	KX901182	KX901237	KX901277	Shen et al. (2019)
	Calcipostia guttulata	Cui 16281	OM039275	OM039175	OM039210	OM037747	OM037773	OM037797	Liu et al. (2022b)
	Cystidiopostia hibernica	Cui 17624	MW377277	MW377357	MW382064	MW337173	–	MW337105	Liu et al. (2022b)
	Cystidiopostia subhibernica	Cui 17095	MW377278	MW377358	MW382065	MW337174	MW337042	MW337106	Liu et al. (2022b)
	Postia lactea	Cui 17334	OM039287	OM039187	OM039222	OM037753	OM037782	OM037810	Liu et al. (2022b)
	Postia lactea	Cui 17790	OM039288	OM039188	OM039223	OM037754	OM037783	OM037811	Liu et al. (2022b)
-/*Sarcoporiaceae*	*Sarcoporia polyspora*	Cui 16977	MW377326	MW377403	–	MW337206	MW337079	MW337146	Liu et al. (2022b)
	Sarcoporia polyspora	Cui 16995	OM039299	OM039199	–	OM037761	ON424811	OM037817	Liu et al. (2022b)
-/*Sparassidaceae*	*Sparassis crispa*	AFTOL ID 703	DQ250597	AY629321	–	–	DQ408122	DQ056289	Lutzoni et al. (2004)
	Sparassis crispa	MBUH-DORISL ABER/ss25	AY218442	AY218404	–	–	–	–	Wang et al. (2004)
	Sparassis radicata	TENN 52558	AY218450	AY218411	–	–	AY218547	–	Wang et al. (2004)
	Sparassis radicata	OKM 4756	KC987580	KF053407	–	KY949023	–	–	Justo et al. (2017)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
-/*Steccherinaceae*	*Antella americana*	KHL 11949	JN710509	JN710509	JN710656	–	–	JN710711	Miettinen et al. (2012)
	Antella niemelaei	Renvall 3218	AF126876	–	–	–	–	–	Johannesson et al. 2000
	Antrodiella faginea	KHL 11977	JN710514	JN710514	JN710658	–	–	JN710712	Miettinen et al. (2012)
	Antrodiella semisupina	Labrecque & Labbe´ 372	JN710521	JN710521	–	–	–	–	Miettinen et al. (2012)
	Atraporiella neotropica	Ryvarden 44447	HQ659221	HQ659221	–	–	–	–	Miettinen et al. (2012)
	Atraporiella yunnanensis	CLZhao 604	MF962482	MF962485	MZ958849	–	OK000939	OK000966	Wu et al. (2017)
	Butyrea luteoalba	isolate 5403	JN710558	JN710558	JN710682	–	–	JN710719	Cao et al. (2021b)
	Butyrea japonica	isolate 10202	JN710556	JN710556	JN710680	–	–	JN710718	Cao et al. (2021b)
	Cabalodontia albofibrillosa	Sanyal 6903	KP401770	KP401770	–	–	–	–	Westphalen et al. (2021)
	Cabalodontia albofibrillosa	**CLZhao 6394**	**MK838859**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Cabalodontia albofibrillosa	**CLZhao 8722**	**MZ713669**	**MZ713811**	**–**	**–**	**–**	**–**	**Present study**
	Cabalodontia delicata	MCW 564/17	MT849295	MT849295	–	MT833947	–	MT833934	Westphalen et al. (2021)
	Elaphroporia ailaoshanensis	CLZhao 595	MG231568	MG748854	–	–	–	–	Wu et al. (2018b)
	Elaphroporia ailaoshanensis	CLZhao 596	MG231572	MG748855	–	–	–	–	Wu et al. (2018b)
	Etheirodon fimbriatum	KHL 11905	JN710530	JN710530	JN710667	–	–	–	Miettinen et al. (2012)
	Etheirodon fimbriatum	HR98811	MT849300	–	–	MT833955	–	MT833938	Westphalen et al. (2021)
	Etheirodon fimbriatum	**CLZhao 8399**	**MK404503**	**MK404503**	**–**	**–**	**OK000953**	**–**	**Present study**
	Etheirodon fimbriatum	**CLZhao 10069**	**MZ713672**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Etheirodon fimbriatum	**CLZhao 10114**	**MZ713671**	**MZ713841**	**MZ958870**	**–**	**–**	**OK000972**	**Present study**
	Etheirodon fimbriatum	**CLZhao 13977**	**MZ713673**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Etheirodon purpureum	MCW 642/18	MT849301	MT849301	–	–	–	MT833939	Westphalen et al. (2021)
	Etheirodon roseoalbum	**CLZhao 24770** *	**OR096187**	**OR461452**	**OR469121**	**OR683155**	**OR701872**	**OR541929**	**Present study**
	Etheirodon roseoalbum	**CLZhao 24903**	**OR096188**	**OR461453**	**OR469122**	**OR683156**	**OR701873**	**–**	**Present study**
	Flaviporus brownii	Gates 22.V. 2007	JN710538	JN710538	JN710670	–	–	JN710715	Miettinen et al. (2012)
	Flaviporus liebmannii	Ryvarden 44553	JN710540	JN710540	–	–	–	–	Miettinen et al. (2012)
	Frantisekia mentschulensis	BRNM 710170	FJ496670	FJ496728	FJ496748	–	–	–	Tomšovský et al. (2010)
	Frantisekia fissiliformis	CBS 436.72	MH860521	MH872232	AF087446	–	–	–	Vu et al. (2019)
	Junghuhnia crustacea	Miettinen 13852,1	JN710553	JN710553	JN710678	–	–	–	Miettinen et al. (2012)
	Junghuhnia pseudocrustacea	Yuan 6160	MF139551	–	–	–	–	–	Yuan et al. (2019)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Loweomyces fractipes	Setliff 19.8.2007	JN710569	JN710569	JN710689	–	–	–	Miettinen et al. (2012)
	Loweomyces tomentosus	MCW 366/12	KX378870	KX378870	–	–	–	–	Westphalen et al. (2016)
	Metuloidea murashkinsky	X449	JN710588	JN710588	–	–	–	–	Westphalen et al. (2019)
	Metuloidea reniforme	MCW 542/17	MT849303	MT849303	–	MT833950	–	MT833940	Westphalen et al. (2021)
	Metuloidea rhinocephala	X460	JN710562	JN710562	–	–	–	–	Westphalen et al. (2019)
	Mycorrhaphium adustum	KHL 12255	JN710573	JN710573	JN710692	–	–	JN710727	Miettinen et al. (2012)
	Mycorrhaphium hispidum	MCW 429/13	MH475307	MH475307	–	–	MH475313	MH475318	Westphalen et al. (2019)
	Nigroporus vinosus	Yuan12916	MT681923	MT675108	–	–	MT793116	MT793113	Cao et al. (2021b)
	Nigroporus vinosus	Seitzman 2008-100	JN710575	JN710575	JN710693	–	–	JN710728	Miettinen et al. (2012)
	Nigroporus sp.	**CLZhao 4067**	**OR167780**	**–**	**OR469123**	**–**	**OR701865**	**–**	**Present study**
	Nigroporus sp.	**CLZhao 4767**	**OR167781**	**–**	**OR469124**	**–**	**–**	**–**	**Present study**
	Nigroporus sp.	**CLZhao 4768**	**–**	**OR461454**	**OR469125**	**–**	**–**	**–**	**Present study**
	Steccherinum bourdotii	HR102002	MT849310	–	–	MT833953	–	MT833946	Westphalen et al. (2021)
	Steccherinum confragosum	**CLZhao 4247**	**MK343649**	**–**	**–**	**–**	**–**	**–**	**Present study**
	Steccherinum larssonii	MCW 593/17	MT849306	MT849306	–	MT833956	–	MT833941	Westphalen et al. (2021)
	Steccherinum lincangense	**CLZhao 24988** *	**OR096196**	**OR461455**	**OR469126**	**OR683157**	**OR701866**	**OR541930**	**Present study**
	Steccherinum longiaculeiferum	**CLZhao 26243** *	**OR096195**	**–**	**OR469127**	**OR683158**	**OR701867**	**OR541931**	**Present study**
	Steccherinum longiaculeiferum	**CLZhao 26290**	**OR167202**	**–**	**OR469128**	**OR683154**	**OR701868**	**OR541932**	**Present study**
	Steccherinum meridionale	Cui 16691	ON417195	ON417247	–	ON424743	ON424817	ON424882	Liu et al. (2022b)
	Steccherinum ochraceum	KHL 11902	JN710590	JN710590	JN710700	–	JN710738	JN710730	Miettinen et al. (2012)
	Steccherinum ochraceum	isolate 2060	JN710589	JN710589	–	–	–	–	Miettinen et al. (2012)
	Steccherinum subtropicum	CLZhao 11059	OP799390	OP799377	–	–	–	–	Dong et al. (2023b)
	Steccherinum tenue	KHL 12316	JN710598	JN710598	JN710705	–	JN710739	JN710733	Miettinen et al. (2012)
	Steccherinum tenuissimum	CLZhao 3153	MW204582	MW204571	MZ958881	OK000932	–	–	Wu et al. (2021b)
	Steccherinum weishanense	**CLZhao 24911** *	**OR096207**	**OR461456**	**OR469129**	**–**	**OR701869**	**OR541933**	**Present study**

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Steccherinum xanthum	CLZhao 4479	MW204586	MW204575	–	–	–	–	Wu et al. (2021b)
	Steccherinum yunnanense	CLZhao 1445	MW290042	MW290056	MZ958889	–	–	OK000984	Dong et al. (2022)
	Trullella conifericola	Yuan 12657	MT269761	MT259327	–	–	–	MT793110	Cao et al. (2021b)
	Trullella dentipora	Ryvarden 40822	JN710512	JN710512	–	–	–	–	Miettinen et al. (2012)
	Xanthoporus syringae	X339	JN710606	JN710606	–	–	–	–	Miettinen et al. (2012)
	Xanthoporus syringae	Jeppson 2264	JN710607	JN710607	–	–	–	–	Miettinen et al. (2012)
-/*Taiwanofungaceae*	*Taiwanofungus camphoratus*	Cui 17234	MW377327	MW377404	MW382104	ON424747	–	MW337147	Liu et al. (2022b)
	Taiwanofungus salmoneus	B 147	EU232202	EU232278	–	–	–	–	Ortiz-Santana et al. (2013)
Russulales/ *Auriscalpiaceae*	*Artomyces adrienneae*	TFB 8291	KY352645	–	–	–	MF978329	–	Unpublished
	Artomyces adrienneae	7387	AF454418	–	–	–	–	–	Lickey et al. (2003)
	Artomyces austropiperatus	7153	AF454408	–	–	–	–	–	Lickey et al. (2003)
	Artomyces austropiperatus	8335	AF454407	–	–	–	–	–	Lickey et al. (2003)
	Artomyces candelabrus	ICMP: 16999	GQ411509	–	–	–	–	–	Fukami et al. (2010)
	Artomyces candelabrus	3922	AF454420	–	–	–	–	–	Lickey et al. (2003)
	Artomyces carolinensis	1615	AF454409	–	–	–	–	–	Lickey et al. (2003)
	Artomyces colensoi	2807	AF454424	–	–	–	–	–	Lickey et al. (2003)
	Artomyces colensoi	2679	AF454423	–	–	–	–	–	Lickey et al. (2003)
	Artomyces costaricensis	7900	AF454411	–	–	–	–	–	Lickey et al. (2003)
	Artomyces costaricensis	9670	AF454410	–	–	–	–	–	Lickey et al. (2003)
	Artomyces cristatus	GB1701	AF454421	–	–	–	–	–	Lickey et al. (2003)
	Artomyces cristatus	DL8974	AF454422	–	–	–	–	–	Lickey et al. (2003)
	Artomyces dichotomus	DED722	AF454406	–	–	–	–	–	Lickey et al. (2003)
	Artomyces microsporus	ZRL2015014	LT716081	KY418906	–	KY418986	KY419042	–	Unpublished
	Artomyces microsporus	2349	AF336138	–	–	–	–	–	Lickey et al. (2003)
	Artomyces niveus	**CLZhao 18346**	**OR094477**	**OR461457**	**OR469130**	–	–	–	**Present study**
	Artomyces niveus	**CLZhao 18996**	**OR094478**	**OR461458**	**OR469131**	**OR703806**	**OR700201**	–	**Present study**
	Artomyces niveus	**CLZhao 19094** *	**OR094479**	**OR461459**	**OR469132**	–	–	–	**Present study**
	Artomyces nothofagi	MES559	KP025706	–	–	–	–	–	Kneal & Smith (2015)
	Artomyces novae-zelandiae	7024	AF454416	–	–	–	–	–	Lickey et al. (2003)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Artomyces novae-zelandiae	2672	AF454417	–	–	–	–	–	Lickey et al. (2003)
	Artomyces piperatus	5770	AF454404	–	–	–	–	–	Lickey et al. (2003)
	Artomyces piperatus	8221	AF454405	–	–	–	–	–	Lickey et al. (2003)
	Artomyces pyxidatus	KA12-0342	KR673419	–	–	–	–	–	Kim et al. (2015)
	Artomyces pyxidatus	KA12-1374	KR673584	–	–	–	–	–	Kim et al. (2015)
	Artomyces stephenii	9433	AF454425	–	–	–	–	–	Lickey et al. (2003)
	Artomyces stephenii	11022	AF454426	–	–	–	–	–	Lickey et al. (2003)
	Artomyces tasmaniensis	3979	AF454412	–	–	–	–	–	Lickey et al. (2003)
	Artomyces tasmaniensis	3905	AF454413	–	–	–	–	–	Lickey et al. (2003)
	Artomyces turgidus	2682	AF454401	–	–	–	–	–	Lickey et al. (2003)
	Artomyces turgidus	2651	AF454402	–	–	–	–	–	Lickey et al. (2003)
	Artomyces yunnanensis	**CLZhao 7052**	**OR094475**	**OR461460**	**OR469133**	**OR703807**	**OR700202**	**–**	**Present study**
	Artomyces yunnanensis	**CLZhao 7118** *	**OR094476**	**OR461461**	**OR469134**	**OR703808**	**OR700203**	**–**	**Present study**
	Lentinellus sublineolatus	TENN 059307	NR119505	–	–	–	–	–	Schoch et al. (2014)
	Lentinellus vulpinus	7267	AY513230	–	–	–	–	–	Kneal & Smith (2015)
-/*Bondarzewiaceae*	*Heterobasidion annosum*	Dai 20962	ON417163	ON417213	ON417079	ON424698	ON424776	ON529284	Liu et al. (2022b)
-/*Echinodontiaceae*	*Amylostereum chailletii*	NH 8031	AF506406	AF506406	–	–	–	–	Larsson & Larsson (2003)
	Amylostereum laevigatum	NH 12863	AF506407	AF506407	–	–	–	–	Larsson & Larsson (2003)
-/*Peniophoraceae*	*Asterostroma laxum*	EL33-99	AF506410	AF506410	–	–	–	–	Larsson & Larsson (2003)
	Asterostroma muscicola	KHL9537	AF506409	AF506409	–	–	–	–	Larsson & Larsson (2003)
	Baltazaria galactina	CBS 752.86	MH862034	MH873721	–	–	–	–	Vu et al. (2019)
	Baltazaria neogalactina	CBS 755.86	MH862037	MH873724	–	–	–	–	Vu et al. (2019)
	Dichostereum durum	CBS 707.81	MH861450	MH873192	–	–	–	–	Vu et al. (2019)
	Gloiothele lactescens	EL8-98	AF506453	AF506453	–	–	–	–	Larsson & Larsson (2003)
	Gloiothele lamellosa	KHL11031	AF506454	AF506454	–	–	–	–	Larsson & Larsson (2003)
	Lachnocladium schweinfurthianum	KM49740	MH260033	MH260051	–	–	–	–	Leal-Dutra et al. (2018)
	Lachnocladium sp.	KHL10556	AF506461	AF506461	–	–	–	–	Larsson & Larsson (2003)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Peniophora quercina	CBS 407.50	MH856687	MH868204	–	–	–	–	Vu et al. (2019)
	Peniophora tristicula	He 4775	MH669235	MH669239	–	–	–	–	Liu & He (2018)
	Peniophora versiformis	He 3029	MK588756	MK588796	–	–	–	–	Xu et al. (2023)
	Scytinostroma alutum	CBS:766.81	MH861486	MH873225	–	–	–	–	Vu et al. (2019)
	Scytinostroma alutum	CBS 762.81	NR170738	MH873221	AF393150	–	DQ408130	–	Vu et al. (2019)
	Scytinostroma artocreas	GHL-2016-Oct	MH204688	MH204691	–	–	–	–	Liu et al. (2018)
	Scytinostroma beijingense	He 7768	OQ731943	OQ729731	–	–	–	–	Li et al. (2023b)
	Scytinostroma boidinii	He 5138	MK625572	MK625497	–	–	–	–	Li et al. (2023b)
	Scytinostroma boidinii	He 6911	OQ731934	OQ729724	–	–	–	–	Li et al. (2023b)
	Scytinostroma caudisporum	CBS 746.86	MH862030	NG073580	AY293270	–	–	–	Binder et al. (2005)
	Scytinostroma daweishanense	**CLZhao 17926 ***	**OR096194**	**OR461462**	**OR469135**	–	–	**OR541934**	**Present study**
	Scytinostroma duriusculum	He 3590	MK625571	MK625499	MN030923	–	–	MN030970	Unpublished
	Scytinostroma incrustatum	He 2841	MH142906	MH142910	MN030929	–	–	MN030976	Liu et al. (2018)
	Scytinostroma incrustatum	He 5368	MH204689	MH204690	–	–	–	–	Liu et al. (2018)
	Scytinostroma portentosum	EL11-99	AF506470	AF506470	–	–	–	–	Larsson & Larsson (2003)
	Scytinostroma portentosum	CBS 503.48	MH856447	–	AF334890	–	–	–	Vu et al. (2019)
	Scytinostroma renisporum	CBS:770.86	MH862050	MH873737	–	–	–	–	Vu et al. (2019)
	Scytinostroma renisporum	CBS:771.86	MH862051	MH873738	–	–	–	–	Vu et al. (2019)
	Scytinostroma subduriusculum	He 7657	OQ731941	OQ729727	–	–	–	–	Li et al. (2023b)
	Scytinostroma subrenisporum	He 4792	MK625566	MK625493	–	–	–	–	Li et al. (2023b)
	Scytinostroma subrenisporum	He 4384	MK625567	MK625495	–	–	–	–	Li et al. (2023b)
	Scytinostroma yunnanense	CLZhao 10802	MT611446	–	–	–	–	–	Wang et al. (2020)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Scytinostroma yunnanense	CLZhao 11010	MT611447	–	–	–	–	–	Wang et al. (2020)
-/*Russulaceae*	*Russula cyanoxantha*	HMAS 253220	KX441050	KX441297	–	KX441791	KX442038	–	He et al. (2019)
-/*Stereaceae*	*Stereum hirsutum*	AFTOL ID 492	AY854063	–	–	AY864885	AY218520	AY885159	Lutzoni et al. (2004)
Sebacinales/ *Sebacinaceae*	*Sebacina incrustans*	AFTOL-ID 1626	DQ917652	DQ521406	–	–	–	–	He et al. (2019)
	Tremellodendron pallidum	AFTOL-ID 699	DQ411526	AY745701	–	–	DQ408132	DQ029196	He et al. (2019)
Sistotremastrales/ *Sistotremastraceae*	*Sertulicium guttuliferum*	He 3338	MK204540	MK204552	–	–	–	–	Liu et al. (2022c)
	Sistotremastrum suecicum	KHL-11849	MN937571	MN937571	–	–	–	–	Liu et al. (2022c)
Stereopsidales/ *Stereopsidaceae*	*Stereopsis radicans*	OLR45395	KC203496	KC203496	–	–	KC203502	KC203516	Liu et al. (2022c)
	Stereopsis globose	KHL 12592	KC203495	KC203495	–	–	KC203501	KC203515	Liu et al. (2022c)
Thelephorales/ *Bankeraceae*	*Boletopsis leucomelaena*	PBM2678	DQ484064	DQ154112	–	–	GU187820	GU187763	Liu et al. (2022c)
-/*Thelephoraceae*	*Thelephora ganbajun*	ZRL 20151295	LT716082	KY418908	–	–	KY419043	KY419093	Liu et al. (2022c)
Trechisporales/ *Hydnodontaceae*	*Allotrechispora gatesiae*	LWZ 20180515-18	OM523378	OM339206	–	–	OM416817	–	Liu et al. (2022c)
	Allotrechispora gatesiae	LWZ 20180515-20	OM523379	OM339207	–	–	–	OM416797	Liu et al. (2022c)
	Brevicellicium atlanticum	LISU 178566	HE963773	HE963774	–	–	–	–	Telleria et al. (2013)
	Brevicellicium exile	MA-Fungi 26554	HE963777	HE963778	–	–	–	–	He et al. (2019)
	Dextrinocystis calamicola	He 5693	MK204533	MK204546	–	–	–	OM416800	Liu et al. (2019)
	Dextrinocystis calamicola	He 5701	MK204534	MK204547	–	–	OM416819	OM416801	Liu et al. (2019)
	Fibrodontia alba	LWZ 20170820-34	MT802102	MT802108	OM422802	–	MW478706	MW478698	Liu et al. (2022c)
	Fibrodontia austrosinensis	He 6283	MT802104	MT802110	–	–	MW478710	MW478699	Liu et al. (2022c)
	Fibrodontia bambusicola	**CLZhao 11201**	**OR094491**	**OR461463**	**OR469136**	**–**	**OR710284**	**–**	**Present study**
	Fibrodontia bambusicola	**CLZhao 11261 ***	**OR094492**	**OR461464**	**OR469137**	**–**	**OR710285**	**OR541935**	**Present study**
	Fibrodontia brevidens	Wu 9807-16	KC928276	KC928277	–	–	–	–	Liu et al. (2022c)

Table 1 Contined.

Order/Family	Species name	Sample no.	GenBank accessions no.						References
			ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
	Fibrodontia subalba	Dai 15931	MT802100	MT802106	–	–	–	–	Liu et al. (2022c)
	Fibrodontia subaustrosinensis	He 6033	OM523397	OM339222	–	–	–	–	Liu et al. (2022c)
	Luellia cystidiata	JHP-09.455	MW371211	MW371211	–	–	–	–	Liu et al. (2022c)
	Porpomyces submucidus	Cui 5183	KT152143	KT152145	–	–	–	–	Wu et al. (2015)
	Porpomyces submucidus	Dai 13708	KT152144	KT152146	–	–	–	MW478702	Wu et al. (2015)
	Pteridomyces galzinii	Bernicchia 8122	MN937559	MN937559	–	–	–	–	Liu et al. (2022c)
	Pteridomyces galzinii	GB0150230	LR694210	LR694188	–	–	LR694282	LR694226	Liu et al. (2022c)
	Scytinopogon sp.	MEL:2382675	KP013038	KP013038	–	–	–	–	Liu et al. (2022c)
	Scytinopogon sp.	MEL:2382987	KP012842	KP012842	–	–	–	–	Liu et al. (2022c)
	Subulicystidium acerosum	He 3804	MK204539	MK204543	–	–	–	–	Liu et al. (2019)
	Subulicystidium boidinii	L 1584a	MH041527	–	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium brachysporum	He 2207	MK204532	MK204549	–	–	–	–	Liu et al. (2019)
	Subulicystidium brachysporum	KHL16100	MH000599	MH000599	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium cochleum	KHL 14355	MN207034	MN207026	–	–	–	–	Ordynets et al. (2020)
	Subulicystidium cochleum	KHL 11200	MN207036	MN207024	–	–	–	–	Ordynets et al. (2020)
	Subulicystidium daii	LWZ 20170820-35	OM523399	OM339224	OM422786	–	–	–	Liu et al. (2022c)
	Subulicystidium daii	Xiong 221	OM523400	–	–	–	–	–	Liu et al. (2022c)
	Subulicystidium fusisporum	KHL 10360	MH041535	MH041567	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium fusisporum	KHL 12761	MH041536	MH041568	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium grandisporum	F 506781	MH041547	MH041592	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium harpagum	L 1726a	MH041532	MH041588	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium harpagum	LR 15736	MH041531	MH041586	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium inornatum	KHL 10444	MH041558	MH041569	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium longisporum	KHL14229	MH000601	MH000601	–	–	–	–	Ordynets et al. (2018)

Table 1 Contined.

Order/Family	**Species name**	**Sample no.**	**GenBank accessions no.**						**References**
			ITS	**nLSU**	**mtSSU**	**RPB1**	**RPB2**	**TEF1**	
	Subulicystidium longisporum	Ordynets 00146	MN207039	MN207032	–	–	–	–	Ordynets et al. (2020)
	Subulicystidium meridense	LR 19581	MH041551	MH041578	–	–	–	–	Ordynets et al. (2020)
	Subulicystidium nikau	L 1296	MH041513	MH041565	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium obtusisporum	KHL 10622	MH041559	MH041606	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium parvisporum	L 0140	MH041529	MH041590	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium parvisporum	L 1226	MH041528	MH041587	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium perlongisporum	KHL16062	MH000600	MH000600	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium rarocrystallinum	F 918488	MH041512	MH041564	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium robustius	KHL 10813	MH041514	MH041608	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium robustius	KHL 10272	MH041516	MH041607	–	–	–	–	Ordynets et al. (2018)
	Subulicystidium tropicum	He 3968	MK204531	MK204544	OM422787	–	MW478711	–	Liu et al. (2022c)
	Subulicystidium yunnanense	**CLZhao 18950** *	**OR096209**	**OR461465**	–	–	**OR710286**	–	**Present study**
	Subulicystidium yunnanense	**CLZhao 23687**	**OR167195**	**OR461466**	–	–	–	–	**Present study**
	Subulicystidium yunnanense	**CLZhao 23944**	**OR167196**	–	–	–	–	–	**Present study**
	Tubulicium bambusicola	He 4776	MK204536	MK204551	OM422789	–	–	–	Liu et al. (2019)
	Tubulicium raphidisporum	He 3191	OM523534	OM339334	OM422801	–	–	–	Liu et al. (2019)
-/*Sistotremastraceae*	*Sertulicium niveocremeum*	Larsson 13727	MN937563	MN937563	–	–	–	–	Liu et al. (2022c)
	Sistotremastrum mendax	Larsson 12022	MN937570	MN937570	–	–	–	–	Liu et al. (2022c)
Tremellomycetes									
Tremellales*/*Bulleraceae	*Bullera alba*	CBS 501	AF444368	AF075500	–	–	KF036745	KF037016	Liu et al. (2022c)
-/*Cryptococcaceae*	*Dioszegia antarctica*	CBS 10920	DQ402529	FJ640575	–	–	KF036858	KF037129	Liu et al. (2022c)

Table 2 Information of taxa used in molecular clock analysis.

Species name	Sample no.	GenBank accessions no.						References
		ITS	nLSU	mtSSU	RPB1	RPB2	TEF1	
Bulbillomyces farinosus	FP 100488T	KY948802	–	–	KY948929	–	–	Liu et al. (2023a)
Cabalodontia delicata	MCW 564/17	MT849295	MT849295	–	MT833947	–	MT833934	Westphalen et al. (2021)
Calocera cornea	AFTOL 438	AY789083	AY701526	–	AY857980	AY536286	AY881019	Matheny et al. (2007)
Cerrena unicolor	He 6082	OM100740	OM083972	ON417068	ON424672	ON424756	ON424825	Liu et al. (2022a)
Climacocystis borealis	Dai 4014	KJ566627	KJ566637	–	ON688463	–	KJ566644	Liu et al. (2023a)
Climacocystis borealis	FD-31	KP135308	KP135210	–	KP134882	KP134895	–	Floudas & Hibbett (2015)
Cymatoderma elegans	Dai 17511	ON417155	ON417205	–	–	–	–	Liu et al. (2022b)
Dacryopinax spathularia	AFTOL 454	AY854070	AY701525	–	AY857981	AY786054	AY881020	Matheny et al. (2007)
Fomitiporia mediterranea	AFTOL-ID 688	AY854080	AY684157	–	AY864869	AY803748	AY885149	Matheny et al. (2007)
Gyrophanopsis japonica	TUMH:61400	LC663668	LC663688	–	–	–	–	Maekawa et al. (2023)
Gyrophanopsis polonense	NH 11337 (GB)	DQ677511	DQ677511	–	–	–	–	Larsson et al. (2007a)
Gyrophanopsis zealandica	NH 15340	DQ309068	–	–	–	–	–	Paulus et al. (2007)
Heterobasidion annosum	Dai 20962	ON417163	ON417213	ON417079	ON424698	ON424776	ON529284	Liu et al. (2022b)
Hyphoderma mutatum	HHB 15479	KP135296	KP135221	–	KP134870	KP134967	–	Floudas & Hibbett (2015)
Hypochnicium bombycinum	HHB 12631	KY948801	KY415959	–	KY948930	–	–	Justo et al. (2017)
Hypochnicium bombycinum	Otto Miettinen 9441 (H)	KY415959	KY415959	–	–	–	–	Maekawa et al. (2023)
Leptoporus mollis	TJV-93-174-T	KY948795	EU402510	–	KY948957	OK136102	MZ913694	Justo et al. (2017)
Mycena amabilissima	AFTOL 1686	DQ490644	DQ457691	–	DQ447926	DQ474121	GU187727	Matheny et al. (2007)
Mycena aurantiidisca	AFTOL 1685	DQ490646	DQ470811	–	DQ447927	DQ474122	GU187728	Matheny et al. (2007)
Marasmius rotula	AFTOL 1505	DQ182506	DQ457686	–	DQ447922	DQ474118	GU187723	Matheny et al. (2007)
Neohypochnicium cystidiatum	MUCL 32103	DQ658163	–	–	–	–	–	Paulus et al. (2007)
Neohypochnicium michelii	MA-Fungi 79155	FN552535	JN939579	–	–	–	–	Telleria et al. (2010a)
Neohypochnicium murinum	CLZhao 19017	OQ788985	OQ789005	OR469109	–	–	OR541917	Present study
Neohypochnicium perlongicystidiosum	TUMH:40397	LC663679	LC663690	–	–	–	–	Maekawa et al. (2023)
Neohypochnicium velutinum	CLZhao 18084	OQ789999	OQ788980	OR469114	–	–	OR541921	Present study
Panus fragilis	HHB 11042	KP135328	KP135233	–	KP134877	–	–	Floudas & Hibbett (2015)
Phellinus hartigii	Dai 11766	KT203287	KT203308	KT203329	KJ651628	KJ651721	–	Liu et al. (2022a)
Phlebia nantahaliensis	HHB 2816	KY948777	KY948852	–	KY948920	OK136063	MZ913701	Liu et al. (2023a)
Phlebiopsis gigantea	FCUG 1417	MZ637051	AF141634	–	MZ748370	OK135996	MZ913623	Liu et al. (2023a)
Physisporinus longicystidius	Cui 16630	ON417177	ON417227	–	ON424717	ON424795	ON424856	Liu et al. (2022a)
Polyporus squamosus	Cui 10595	KU189778	KU189809	KU189960	KU189892	KU189988	KU189925	Zhou et al. (2016)
Schizosaccharomyces pombe	972h-	Z19578	Z19136	–	NM_001021568	NM_001018498	NM_001021161	Matheny et al. (2007)
Steccherinum meridionale	Cui 16691	ON417195	ON417247	–	ON424743	ON424817	ON424882	Liu et al. (2022b)
Stereum hirsutum	AFTOL ID 492	AY854063	–	–	AY864885	AY218520	AY885159	Lutzoni et al. (2004)
Trametes cinnabarina	Dai 14386	KX880629	KX880667	KX880712	KX880818	KX880854	KX880885	Cui et al. (2019)

Raithelh. was selected as outgroup taxa in the ITS+nLSU+mtSSU+RPB2 analysis (Fig. 9) as in Dong et al. (2021); *Gyroporus castaneus* (Bull.) Quél. was selected as outgroup taxa in the ITS+nLSU+mtSSU analysis (Fig. 10) as in He et al. (2020); *Cinereomyces lindbladii* (Berk.) Jülich was selected as outgroup taxa in the ITS analysis (Fig. 11) as in Fan et al (2017); *Byssomerulius corium* (Pers.) Parmasto was selected as outgroup taxa in the ITS+nLSU+TEF1 analysis (Fig. 12) as in Chen et al. (2021); *Heterobasidion annosum* (Fr.) Bref. and *Stereum hirsutum* (Willd.) Pers. were selected as outgroup taxa in the ITS+nLSU+mtSSU+RPB1+TEF1 analysis (Fig. 13) as in Liu et al. (2022b); *Hyphoderma setigerum* (Fr.) Donk was selected as outgroup taxa in the ITS analysis (Fig. 14) as in Telleria et al. (2010a); Sequences of *Schizosaccharomyces pombe* Lindner were retrieved from GenBank and used as outgroup taxa in the ITS analysis (Fig. 15); *Irpex lacteus* (Fr.) Fr. and *I. latemarginatus* (Durieu & Mont.) C.C. Chen & Sheng H. Wu were selected as outgroup taxa in the ITS+nLSU+RPB1+RPB2+TEF1 analysis (Fig. 16) as in Chen et al. (2021); *Climacocystis borealis* (Fr.) Kotl. & Pouzar was selected as outgroup taxa in the ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 analysis (Fig. 17) as in Dong et al. (2023b); *Lentinellus vulpinus* (Sowerby) Kühner & Maire and *L. sublineolatus* R.H. Petersen were selected as outgroup taxa in the ITS analysis (Fig. 18) as in Kneal & Smith (2015); *Amylostereum chailletii* (Pers.) Boidin and *A. laevigatum* (Fr.) Boidin were selected as outgroup taxa in the ITS+nLSU analysis (Fig. 19) as in Li et al. (2023b); *Sertulicium niveocremeum* (Höhn. & Litsch.) Spirin & K.H. Larss. and *Sistotremastrum mendax* Spirin & Volobuev were selected as outgroup taxa in the ITS+nLSU+mtSSU+RPB2+TEF1 analysis (Fig. 20) as in Liu et al. (2022c); *Heterobasidion annosum* (Fr.) Bref. and *Stereum hirsutum* (Willd.) Pers. were selected as outgroup taxa in the ITS+nLSU analysis (Fig. 21) as in Liu et al. (2022b).

RESULTS

Molecular phylogeny

Dendrothele phylogeny based on combined ITS+nLSU sequence data (Fig. 2)

The aligned dataset comprised 12 specimens representing 12 species. Four Markov chains were run for 2 runs from random starting trees, each for 0.3 million generations for the combined ITS+nLSU (Fig. 2) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2007 characters, of which 1297 characters are constant, 445 are variable and parsimony uninformative, and 265 are parsimony informative. Maximum parsimony analysis yielded 1 equally parsimonious trees (TL = 1106, CI = 0.8083, HI = 0.1917, RI = 0.6455, and RC = 0.5218). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was SYM+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.001885 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 913.5.

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

The aligned dataset comprised 27 specimens representing 12 species. Four Markov chains were run for 2 runs from random starting trees, each for 1.5 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 2120 characters, of which 1718 characters are constant, 115 are variable and parsimony uninformative, and 257 are parsimony informative. Maximum parsimony analysis yielded 18 equally parsimonious trees (TL = 640, CI = 0.7312, HI = 0.2688, RI = 0.8030, and RC = 0.5872). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was SYM+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.008710 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 463.

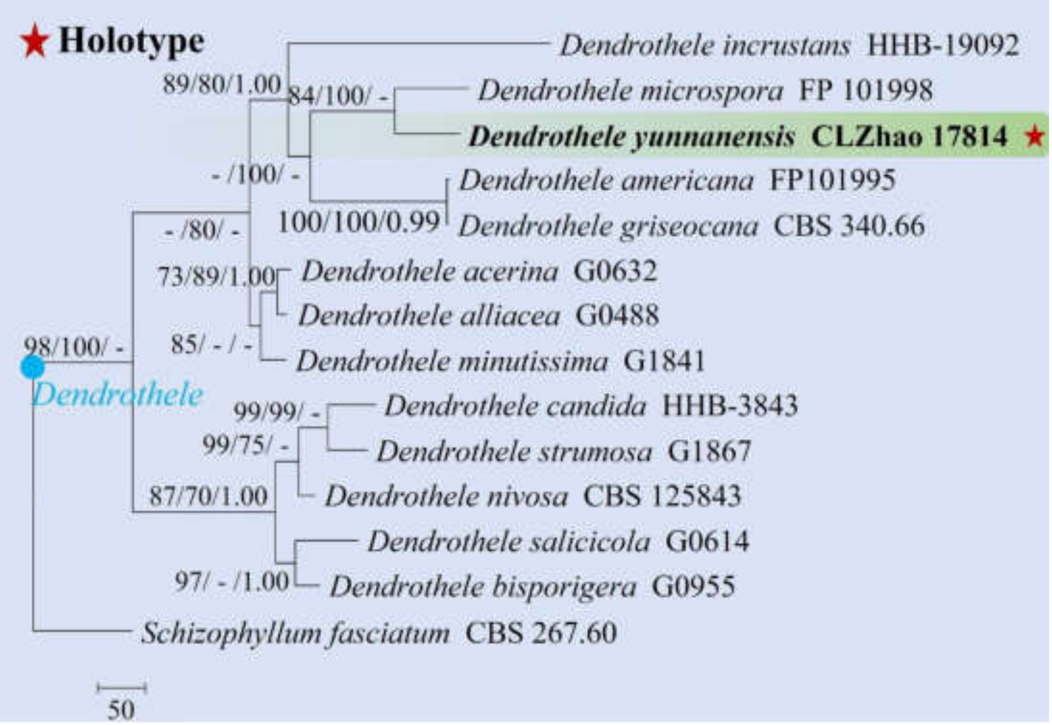

Figure 2 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Dendrothele yunnanensis* and related species in *Dendrothele* based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

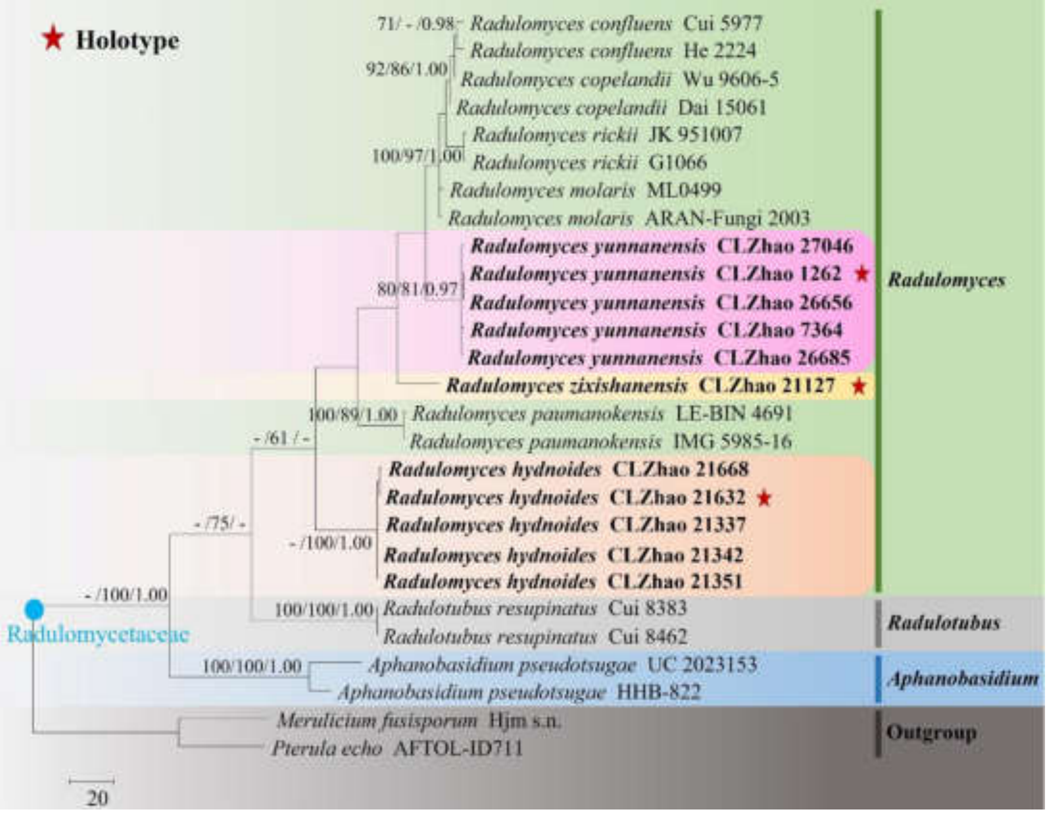

Figure 3 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Radulomyces* and related genera in Radulomycetaceae based on ITS+nLSU sequences. Branches are labeled with

maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

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

The aligned dataset comprised 25 specimens representing 19 species. 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 2173 characters, of which 1471 characters are constant, 214 are variable and parsimony uninformative, and 488 are parsimony informative. Maximum parsimony analysis yielded 8 equally parsimonious trees (TL = 1603, CI = 0.6182, HI = 0.3818, RI = 0.6762, and RC = 0.4180). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.004148 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 703.5.

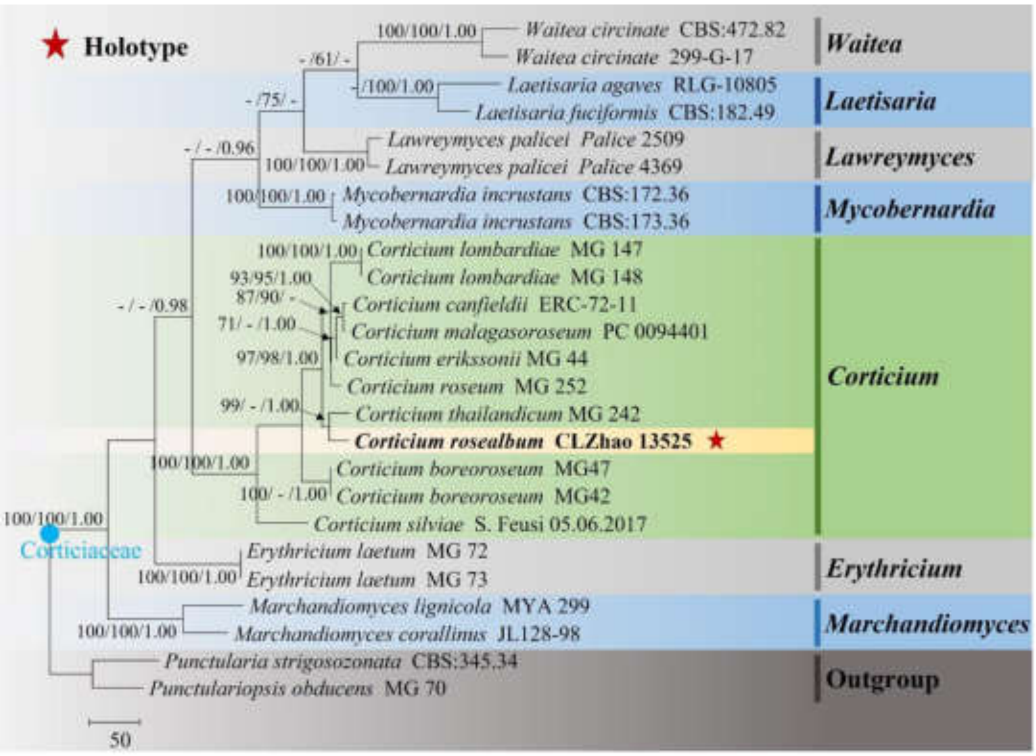

Figure 4 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Corticium* and related genera in Corticiaceae based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

***Hydnoporia* phylogeny based on combined ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 sequence data** (Fig. 5) **and ITS sequence data** (Fig. 6)

The aligned dataset comprised 45 specimens representing 43 species. Four Markov chains were run for 2 runs from random starting trees, each for 1.5 million generations for the combined ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 (Fig. 5) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 7543 characters, of which 4005 characters are constant, 870 are variable and parsimony uninformative, and 2668 are parsimony informative. Maximum parsimony analysis yielded 1 equally parsimonious trees (TL = 13866, CI = 0.4518, HI = 0.5482, RI = 0.4911, and RC = 0.2219). The best model for the ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.007014 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 422.

The aligned dataset comprised 33 specimens representing 18 species. Four Markov chains were run for 2 runs from random starting trees, each for 0.5 million generations for the ITS (Fig. 6) with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 755 characters, of which 502 characters are constant, 70 are variable and parsimony uninformative, and 183 are parsimony informative. Maximum parsimony analysis yielded 23 equally parsimonious trees (TL = 454, CI = 0.7181, HI = 0.2819, RI = 0.8164, and RC = 0.5862). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was HKY+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.007958 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 201.

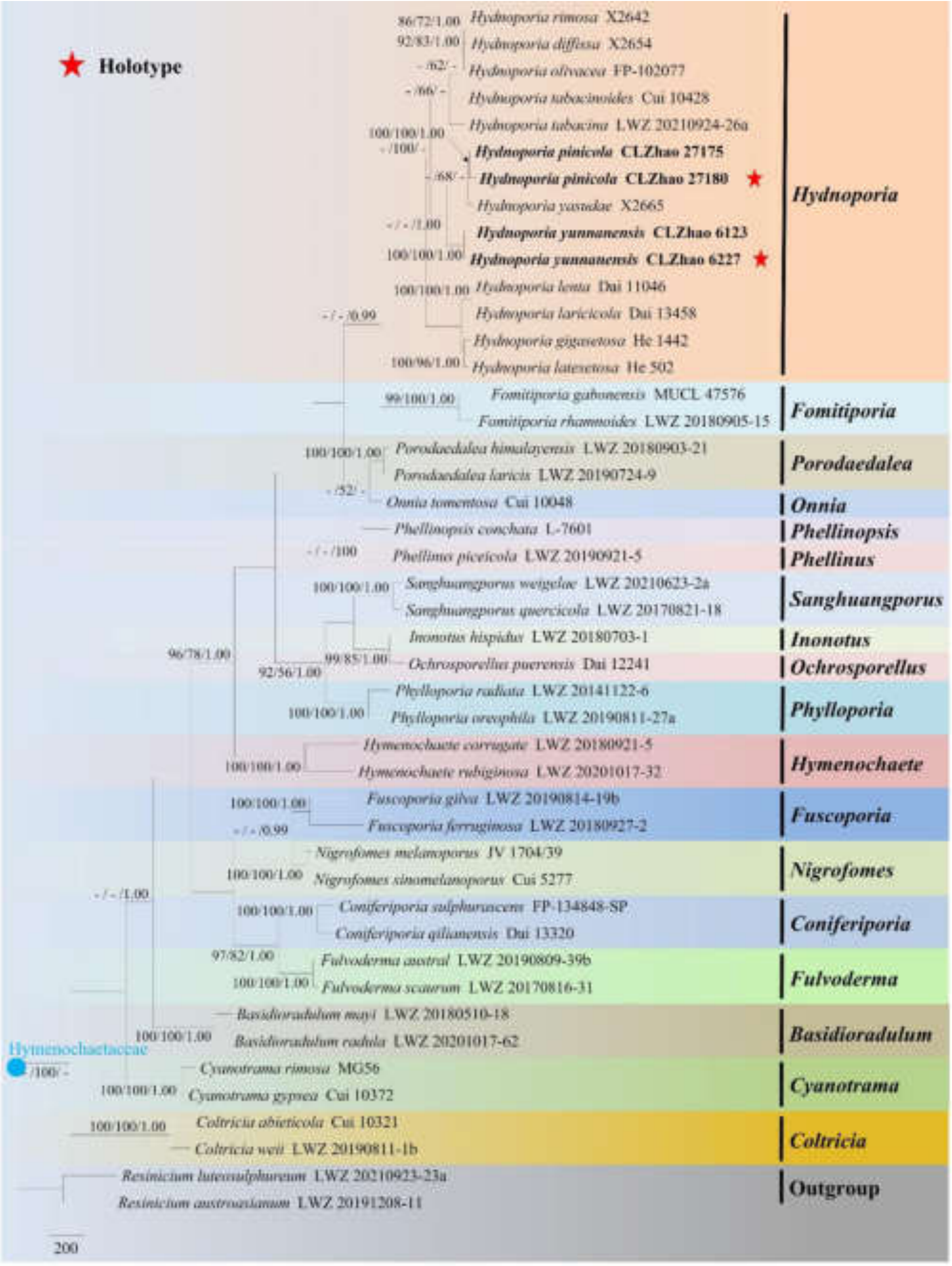

Figure 5 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Hydnoporia* and related genera in Hymenochaetaceae based on ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 sequences.

Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

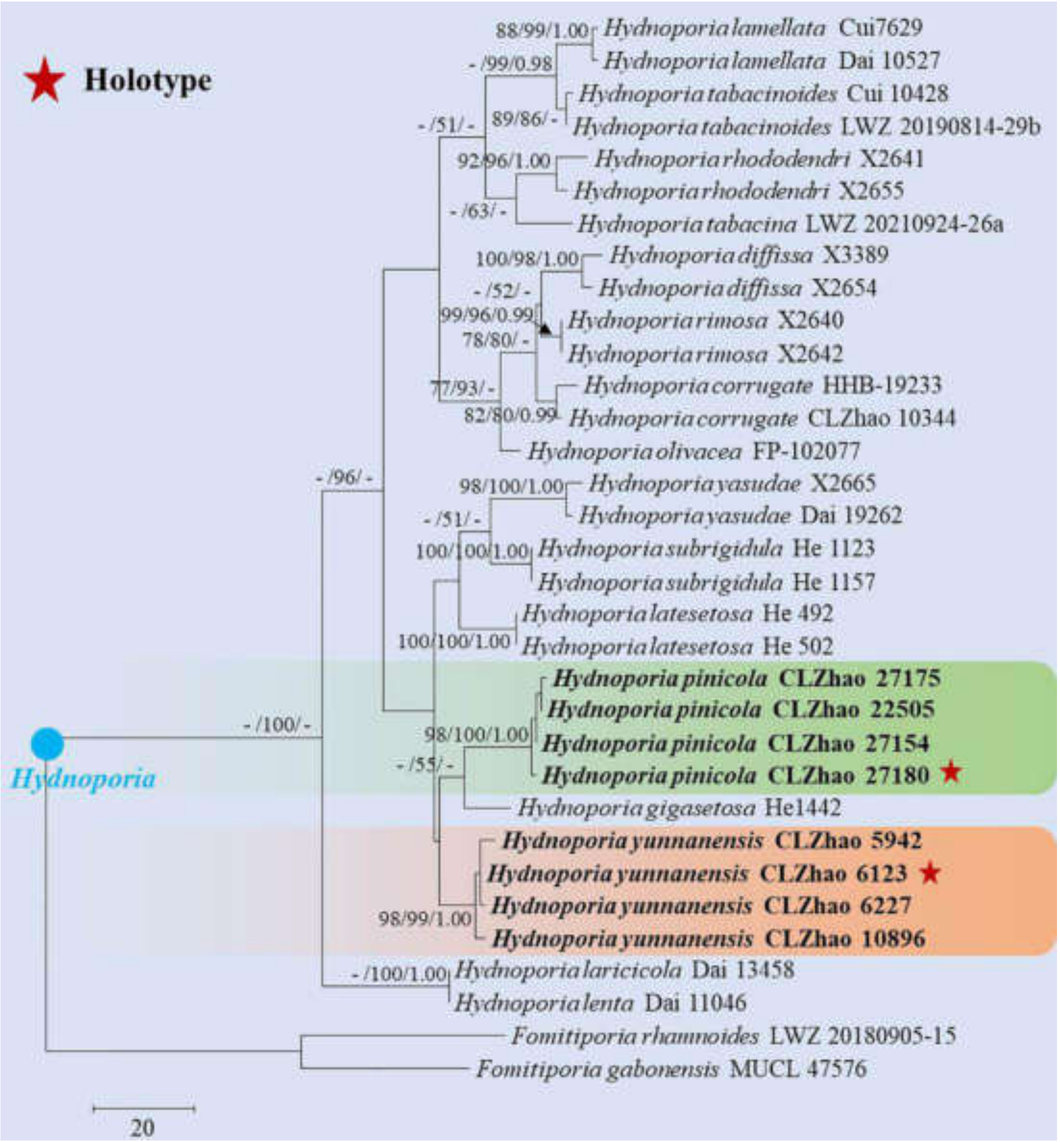

Figure 6 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Hydnoporia pinicola*, *H. yunnanensis* and related species in *Hydnoporia* based on ITS sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

***Peniophorella* phylogeny based on combined ITS, nLSU and mtSSU sequence data** (Fig. 7)

The aligned dataset comprised 33 specimens representing 19 species. Four Markov chains were run for two runs from random starting trees, each for one million generations the combined for ITS+nLSU+mtSSU (Fig. 7) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 3295 characters, of which 2473 characters are constant, 259 are variable and parsimony uninformative, and 563 are parsimony informative. Maximum parsimony analysis yielded 6 equally parsimonious trees (TL = 1723, CI = 0.6541, HI = 0.3459, RI = 0.7325, and RC = 0.4791). The best model for the ITS+nLSU+mtSSU dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.006507 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 454.

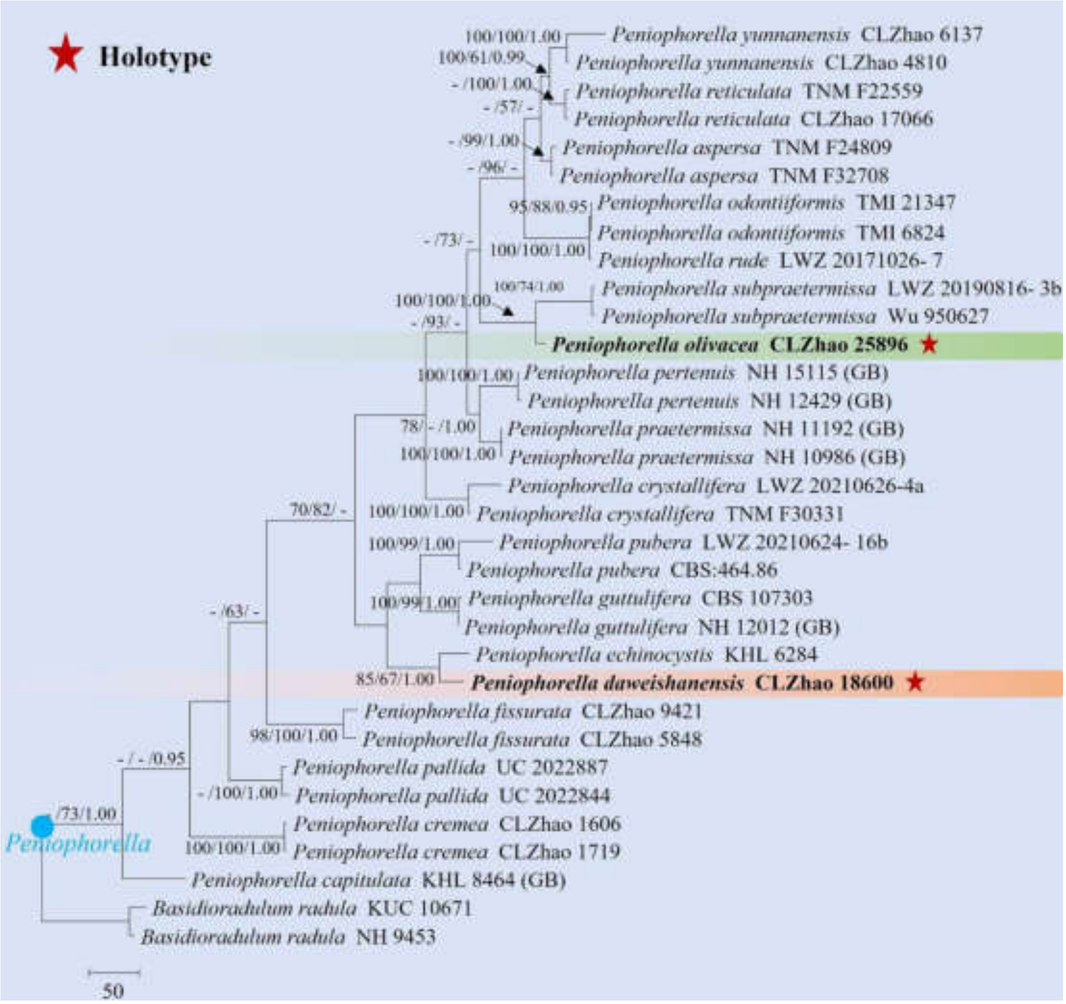

Figure 7 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Peniophorella daweishanensis*, *P. olivacea* and related species in *Peniophorella* based on ITS+nLSU+mtSSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

***Lyomyces* and *Xylodon* phylogeny based on combined ITS+nLSU sequence data** (Fig. 8)

The aligned dataset comprised 66 specimens representing 57 species. Four Markov chains were run for 2 runs from random starting trees, each for 2.5 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 2260 characters, of which 1229 characters are constant, 389 are variable and parsimony uninformative, and 642 are parsimony informative. Maximum parsimony analysis yielded 1 equally parsimonious trees (TL = 4736, CI = 0.3571, HI = 0.6429, RI = 0.5230, and RC = 0.1867). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.013716 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 674.

***Skvortzovia* phylogeny based on combined ITS, nLSU, mtSSU and RPB2 sequence data** (Fig. 9)

The aligned dataset comprised 16 specimens representing 10 species. Four Markov chains were run for 2 runs from random starting trees, each for 1 million generations for the combined ITS+nLSU+mtSSU+RPB2 (Fig. 9) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 3391 characters, of which 2339 characters are constant, 476 are variable and parsimony uninformative, and 576 are parsimony informative. Maximum parsimony analysis yielded one equally parsimonious trees (TL = 1874, CI = 0.7796, HI = 0.2204, RI = 0.6570, and RC = 0.5122). The best model for the ITS+nLSU+mtSSU+RPB2 dataset, estimated and applied in the Bayesian analysis, was GTR+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.004675 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 966.

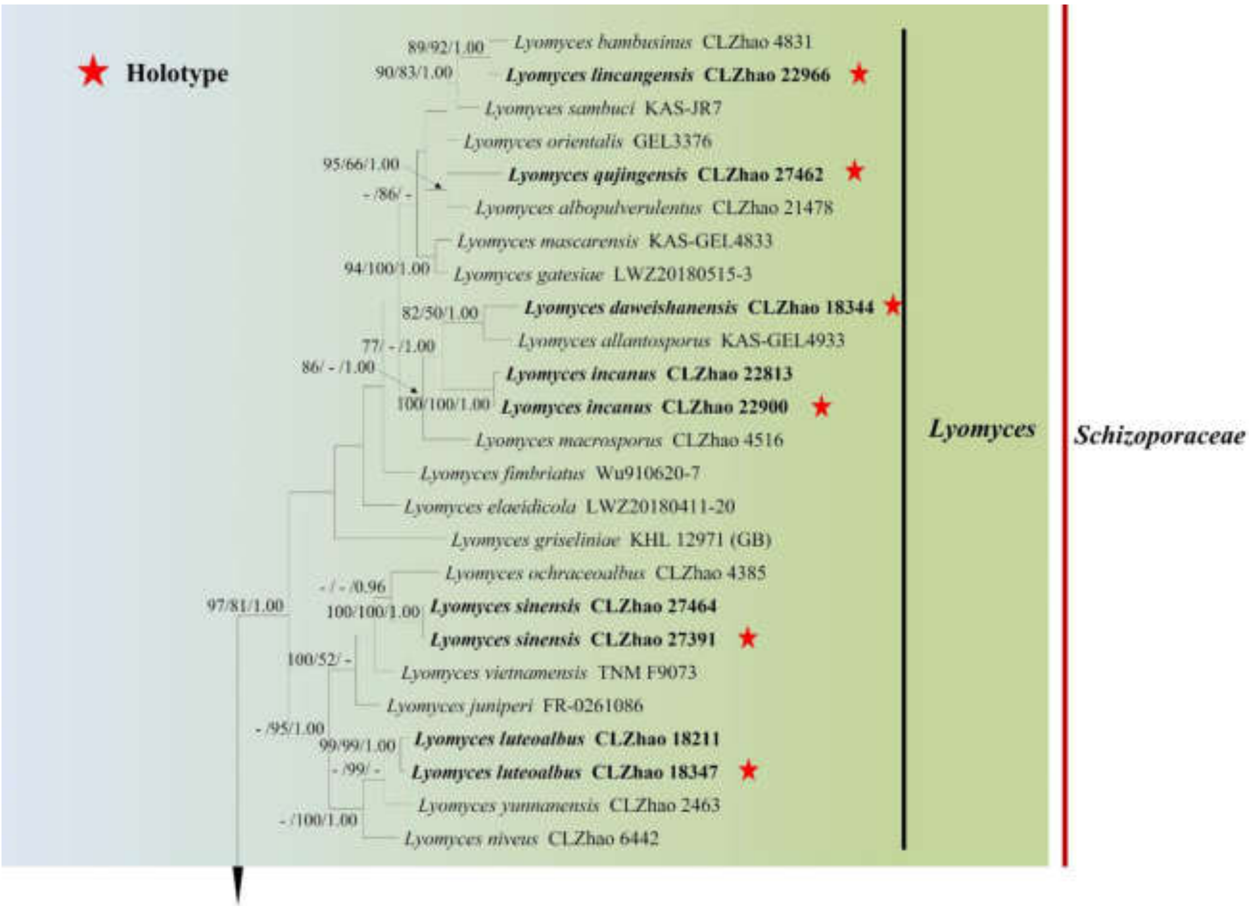

Figure 8 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Lyomyces*, *Xylodon* and related genera in Schizoporaceae based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

***Tubulicrinis* phylogeny based on combined ITS, nLSU and mtSSU sequence data** (Fig. 10)

The aligned dataset comprised 19 specimens representing 16 species. Four Markov chains were run for two runs from random starting trees, each for 0.8 million generations for the combined ITS+nLSU+mtSSU (Fig. 10) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2856 characters, of which 1598 characters are constant, 643 are variable and parsimony uninformative, and 615 are parsimony informative. Maximum parsimony analysis yielded 1 equally parsimonious trees (TL = 2300, CI = 0.7243, HI = 0.2757, RI = 0.2757, and RC = 0.4212). The best model for the ITS+nLSU+mtSSU dataset, estimated and applied in the Bayesian analysis, was GTR+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.008968 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 909.5.

***Skeletocutis* phylogeny based on combined ITS sequence data** (Fig. 11)

The aligned dataset comprised 45 specimens representing 23 species. Four Markov chains were run for 2 runs from random starting trees, each for 1.1 million generations for the ITS (Fig. 11) with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 704 characters, of which 361 characters are constant, 34 are variable and parsimony uninformative, and 309 are parsimony informative. Maximum parsimony analysis yielded 3 equally parsimonious trees (TL = 852, CI = 0.6103, HI = 0.6103, RI = 0.8524, and RC = 0.5202). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was HKY+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.009860 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 145.

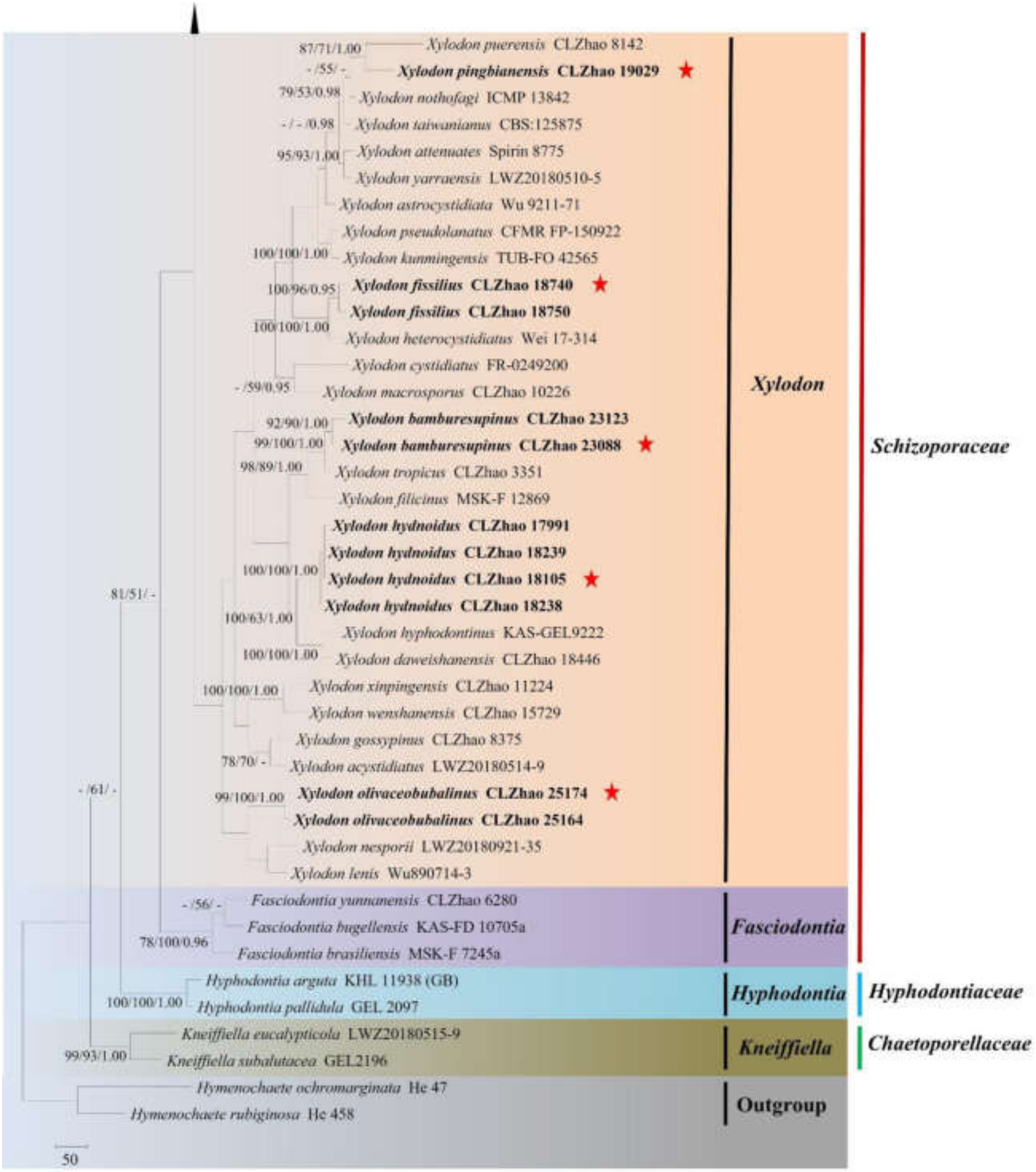

Figure 8 – Continued.

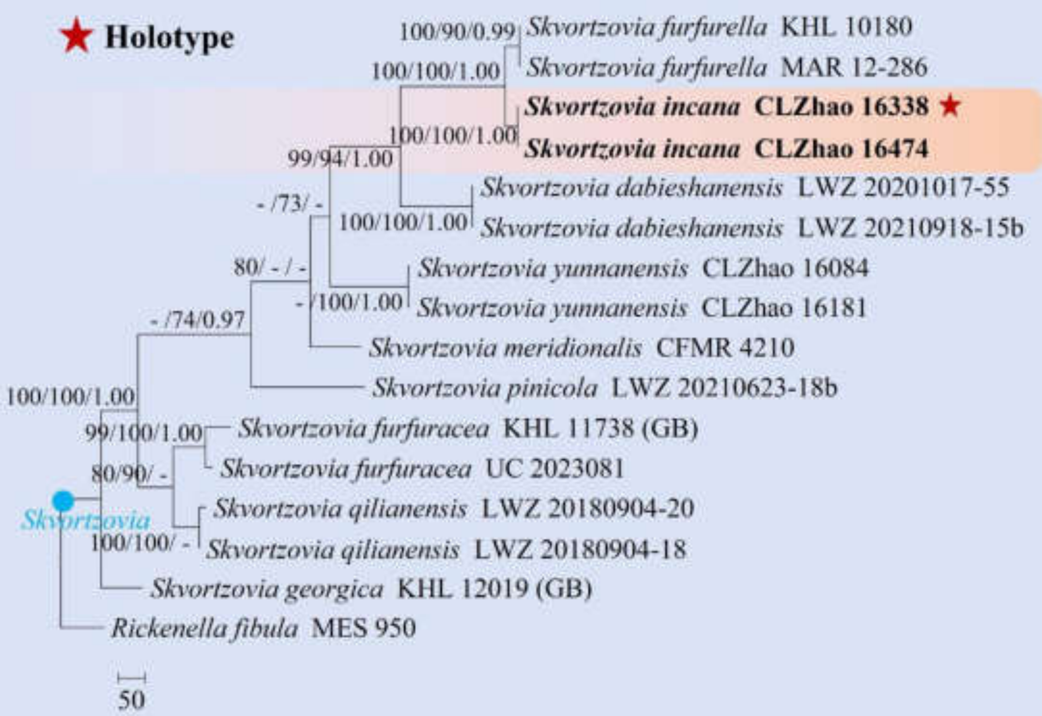

Figure 9 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Skvortzovia incana* and related species in *Skvortzovia* based on ITS+nLSU+mtSSU+RPB2 sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

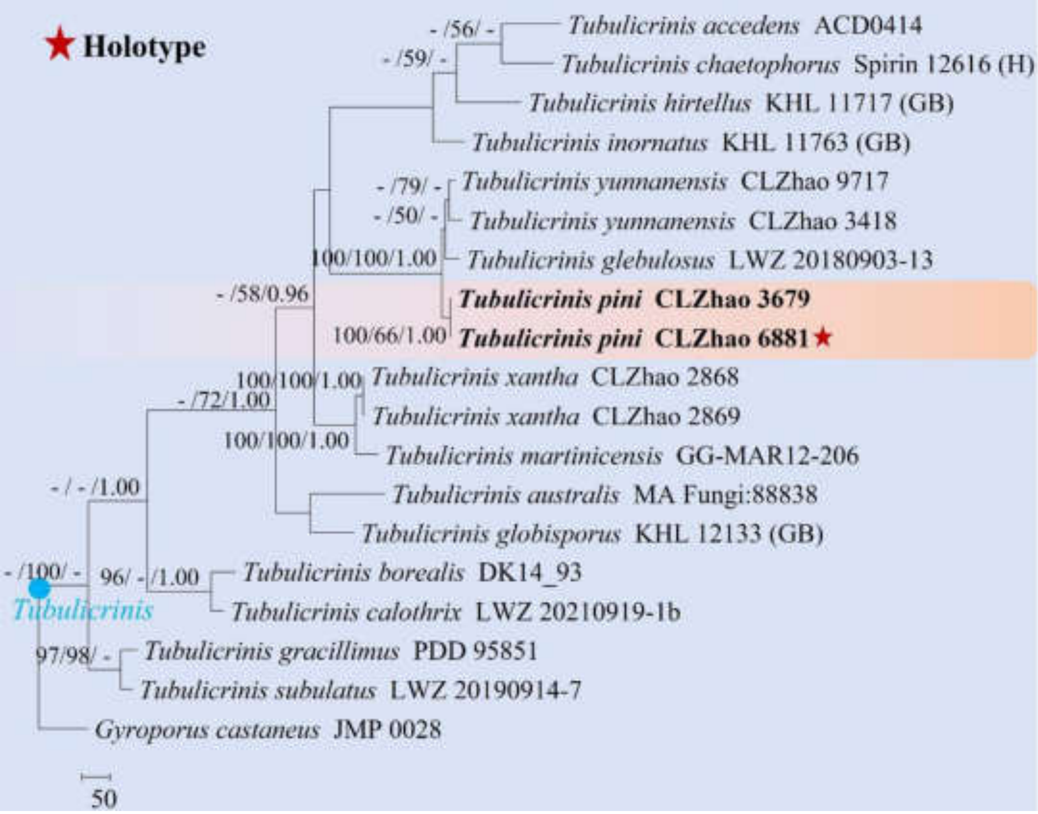

Figure 10 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Tubulicrinis pini* and related species in *Tubulicrinis* based on ITS+nLSU+mtSSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

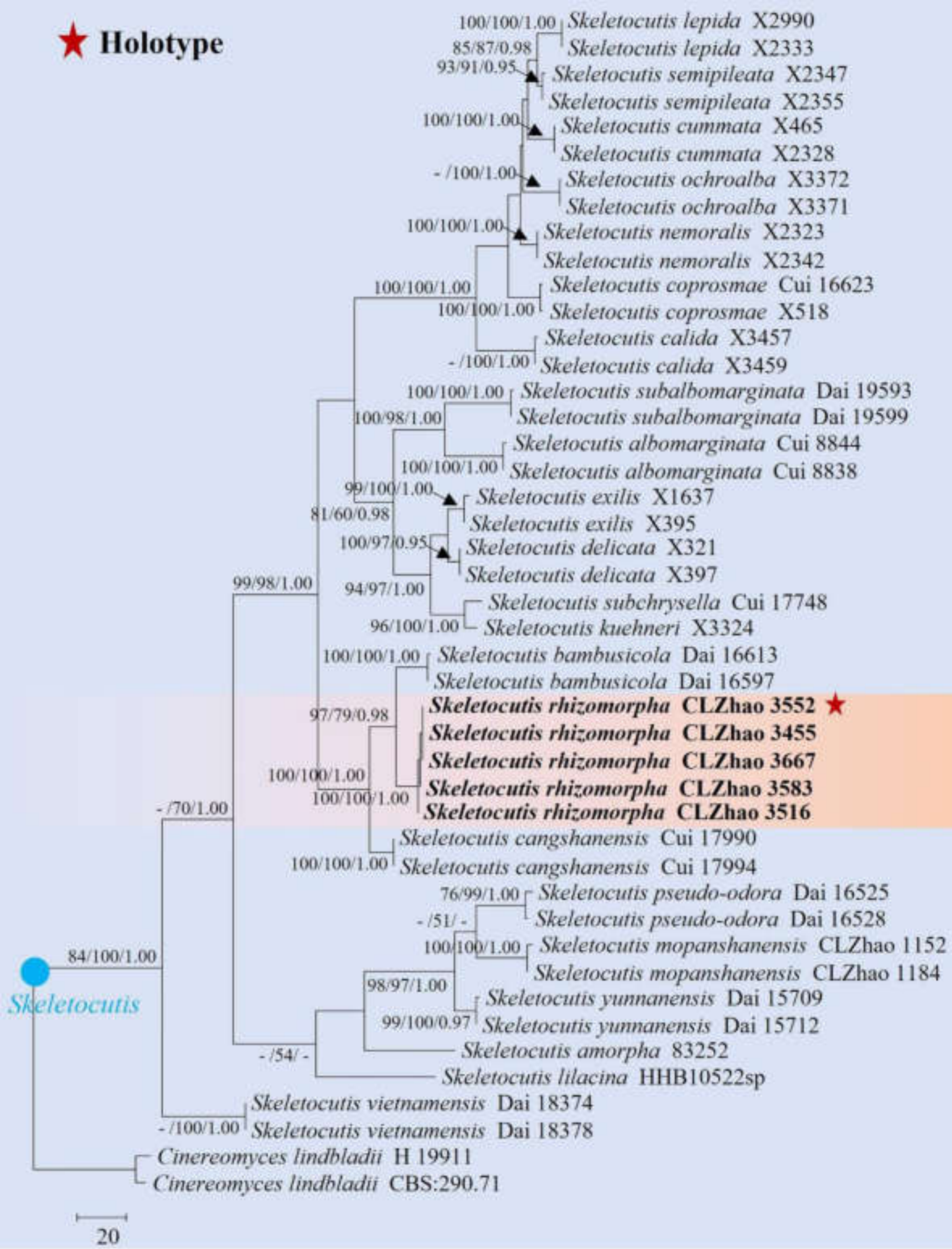

Figure 11 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Skeletocutis rhizomorpha* and related species in *Skeletocutis* based on ITS sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

***Efibula* phylogeny based on combined ITS, nLSU and TEF1 sequence data** (Fig. 12)

The aligned dataset comprised 29 specimens representing 17 species. Four Markov chains were run for two runs from random starting trees, each for one million generations for the combined ITS+nLSU+TEF1 (Fig. 12) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2968 characters, of which 2229 characters are constant, 153 are variable and parsimony uninformative, and 586 are parsimony informative.

Maximum parsimony analysis yielded 1 equally parsimonious trees (TL = 1535, CI = 0.6508, HI = 0.3492, RI = 0.7387, and RC = 0.4807). The best model for the ITS+nLSU+TEF1 dataset, estimated and applied in the Bayesian analysis, was SYM+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.003396 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 345.5.

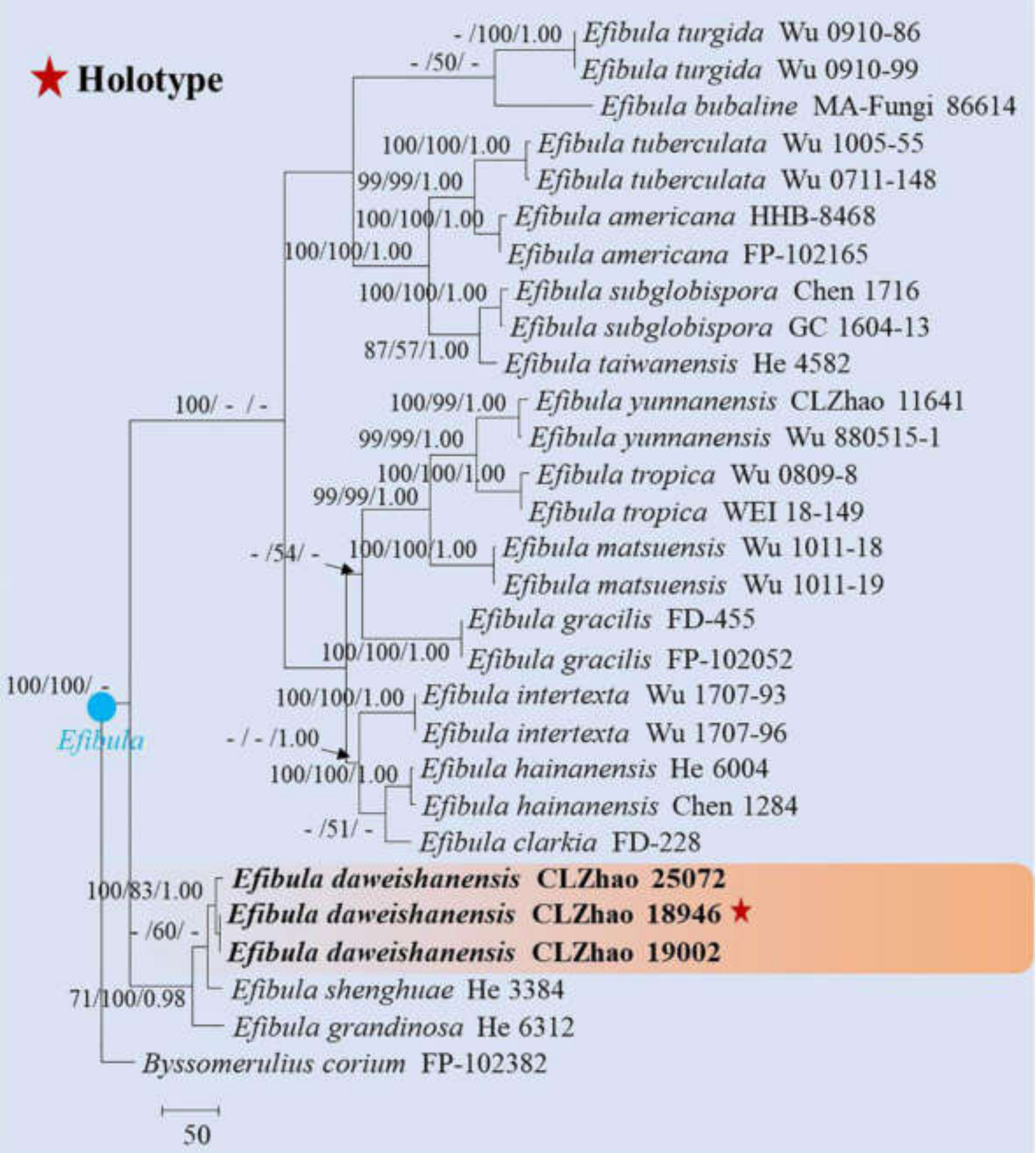

Figure 12 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Efibula daweishanensis* and related species in *Efibula* based on ITS+nLSU+TEF1 sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

***Neohypochnicium* phylogeny based on combined ITS, nLSU, mtSSU, RPB1 and TEF1 sequence data** (Fig. 13) **and ITS sequence data** (Fig. 14)

The aligned dataset comprised 142 specimens representing 115 species. Four Markov chains were run for two runs from random starting trees, each for seven million generations for the combined ITS+nLSU+mtSSU+RPB1+TEF1 (Fig. 13) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 5510 characters, of which 1854 characters are constant, 921 are variable and parsimony uninformative, and 2735 are parsimony informative. Maximum parsimony analysis yielded 100 equally parsimonious trees (TL = 33957, CI = 0.2059, HI = 0.7941, RI = 0.5116, and RC = 0.1053). The best model for the ITS+nLSU+mtSSU+RPB1+TEF1 dataset estimated and applied in the Bayesian analysis was GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with

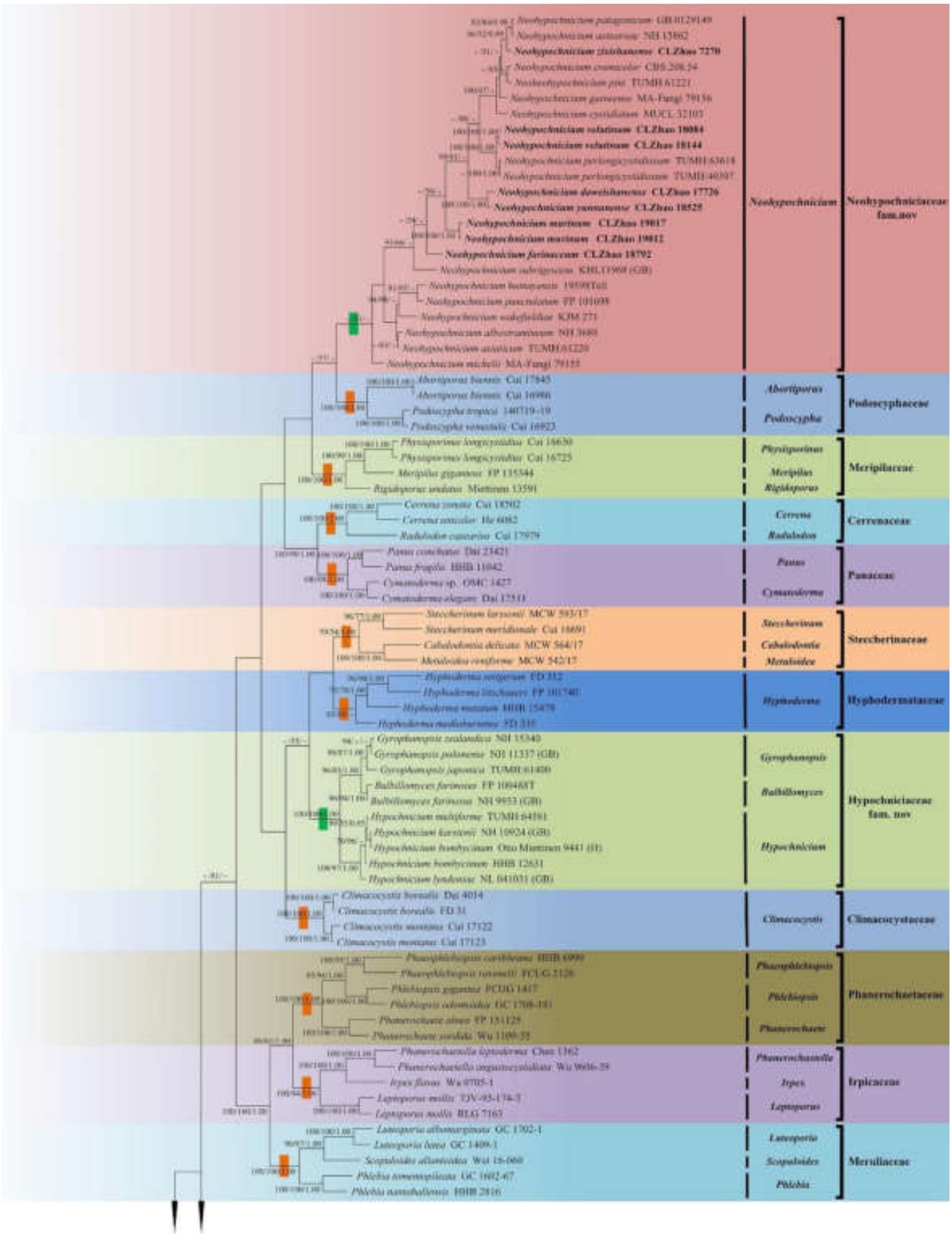

Figure 13 – Maximum parsimony strict consensus tree illustrating the phylogeny of Neohypochniciaceae, Hypochniciaceae and related families in Polyporales based on ITS+nLSU+mtSSU+RPB1+TEF1 sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

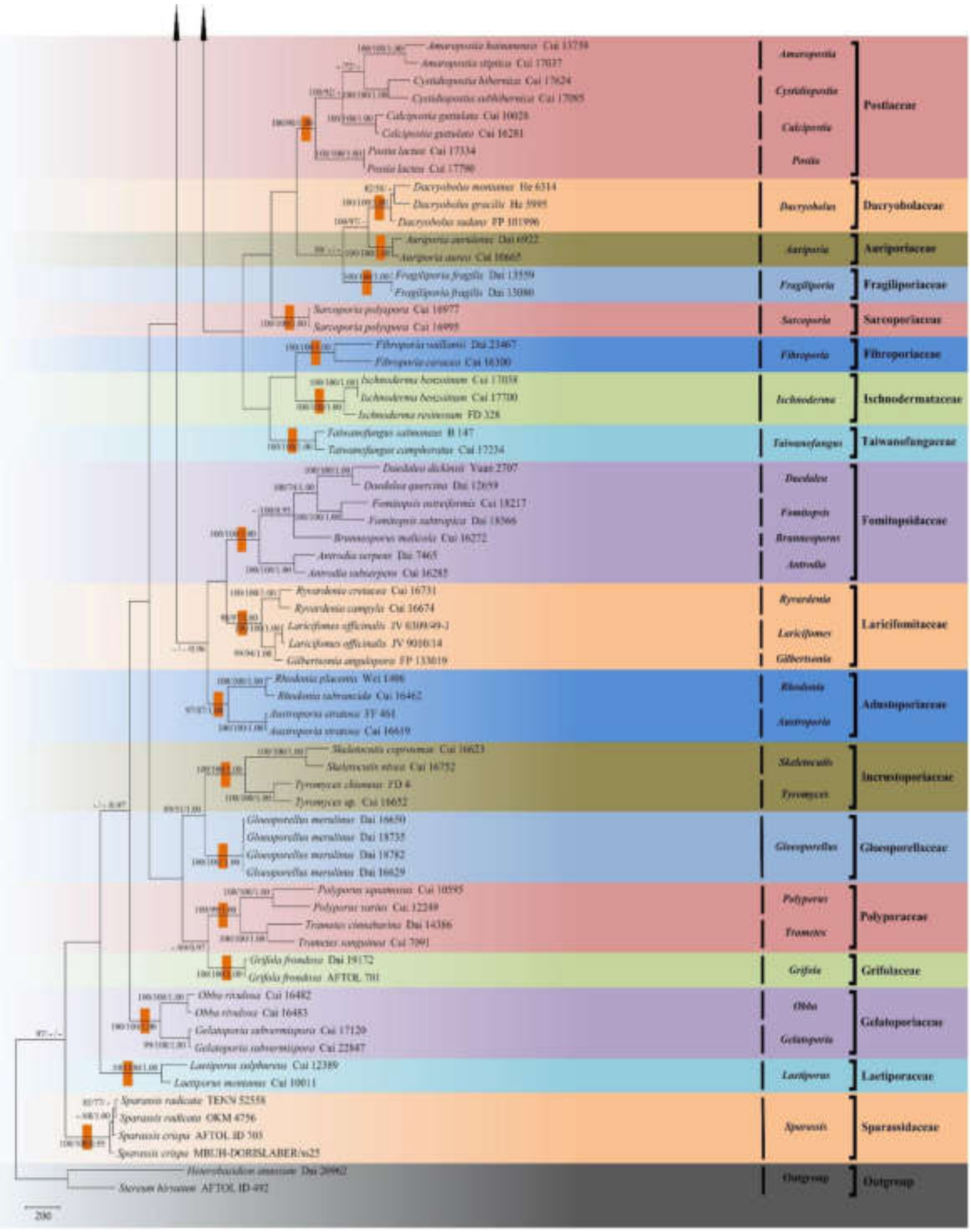

Figure 13 – Continued.

an average standard deviation of split frequencies = 0.107171 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 382.5.

The aligned dataset comprised 58 specimens representing 22 species. Four Markov chains were run for 2 runs from random starting trees, each for 1.3 million generations for the ITS (Fig. 14) with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 661 characters, of which 291 characters are constant, 50 are variable and parsimony uninformative, and 320 are parsimony informative. Maximum parsimony analysis yielded one equally parsimonious trees (TL = 1333, CI = 0.4554, HI = 0.4554, RI = 0.7551, and RC = 0.7551). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.008032 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 100.5.

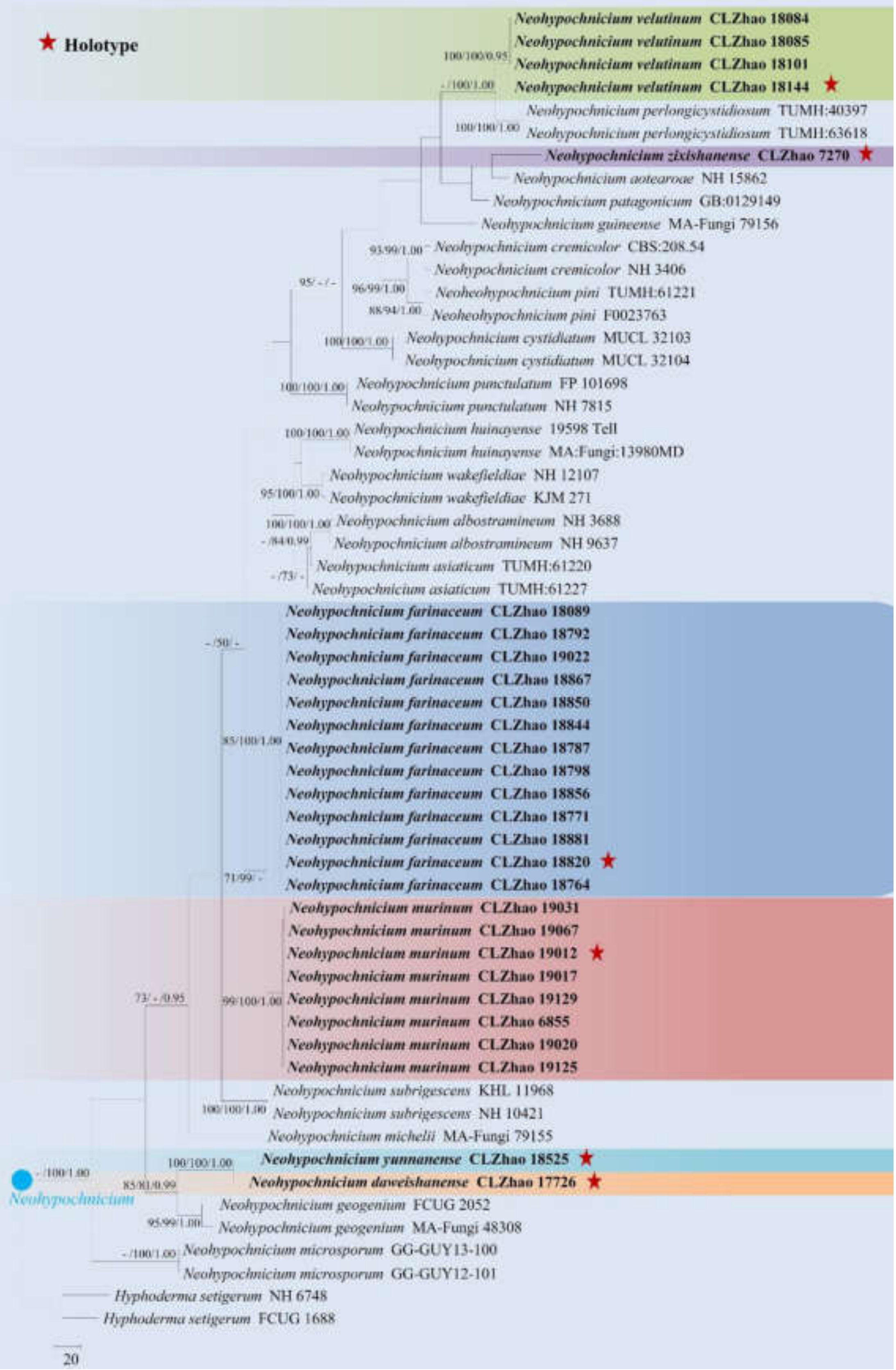

Figure 14 – Maximum parsimony strict consensus tree illustrating the phylogeny of six new species and related species in *Neohypochnicium* based on ITS sequences. Branches are labeled with

maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

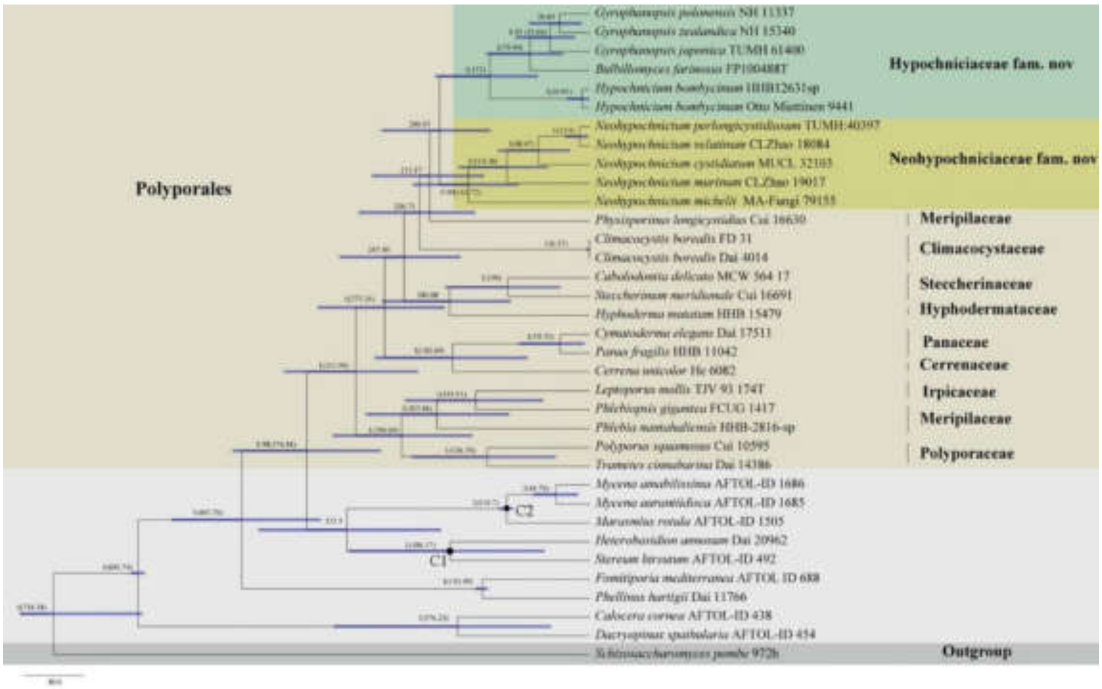

Figure 15 – Chronogram and estimated divergence times of Neohypochniciaceae and Hypochniciaceae generated by molecular clock analysis using the ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 dataset. The chronogram was obtained using the Ascomycota–Basidiomycota divergence time of 582 Mya as the calibration point. The calibration points and objects of this study are marked in the chronogram. The geological time scale is in millions years ago (Mya).

The divergence time of Hypochniciaceae and Neohypochniciaceae based on ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 (Fig. 15)

The ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 dataset included 35 collections, of which 25 belonged to Polyporales. This dataset resulted in a concatenated alignment of 5466 characters with GTR+I+G as the best-fit evolutionary model. Chain convergence was indicated by the ESSs. In Polyporales, the family Neohypochniciaceae occurred in a mean crown age of 161.72 Mya with a 95% highest posterior density (HPD) of 95.71–235.28 Mya, followed by Hypochniciaceae with a mean crown age of 133 Mya and a 95% HPD of 69.58–205.77 Mya (Table 3).

Table 3 Inferred divergence time of Hypochniciaceae and Neohypochniciaceae.

Family	**means of stem age (Mya) time/95%HPD (Mya) Posterior probabilities**	**means of crown age (Mya) time/95%HPD (Mya) Posterior probabilities**
Hypochniciaceae	200.03/132.24–276.85/–	133/69.58–205.77/1
Neohypochniciaceae	200.03/132.24–276.85/–	161.72/95.71–235.28/1
C1: Hymenochaetales	–	143.09/135.79–151.67/1
C2: Agaricales	–	110.7/102.26–120.35/1

***Donkiella* gen. nov., *Phanerochaete* and *Phlebiopsis* phylogeny based on combined ITS, nLSU, RPB1, RPB2 and TEF1 sequence data** (Fig. 16)

The aligned dataset comprised 72 specimens representing 65 species. Four Markov chains were run for two runs from random starting trees, each for five million generations for the combined ITS+nLSU+RPB1+RPB2+TEF1 (Fig. 16) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 5870 characters, of which 3395 characters are constant, 506 are variable and parsimony uninformative, and 1969 are parsimony informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 15633, CI = 0.2785, HI = 0.7215, RI = 0.4691, and RC = 0.4691). The best model for the ITS+nLSU+RPB1+RPB2+TEF1 dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.0081392 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 730.5.

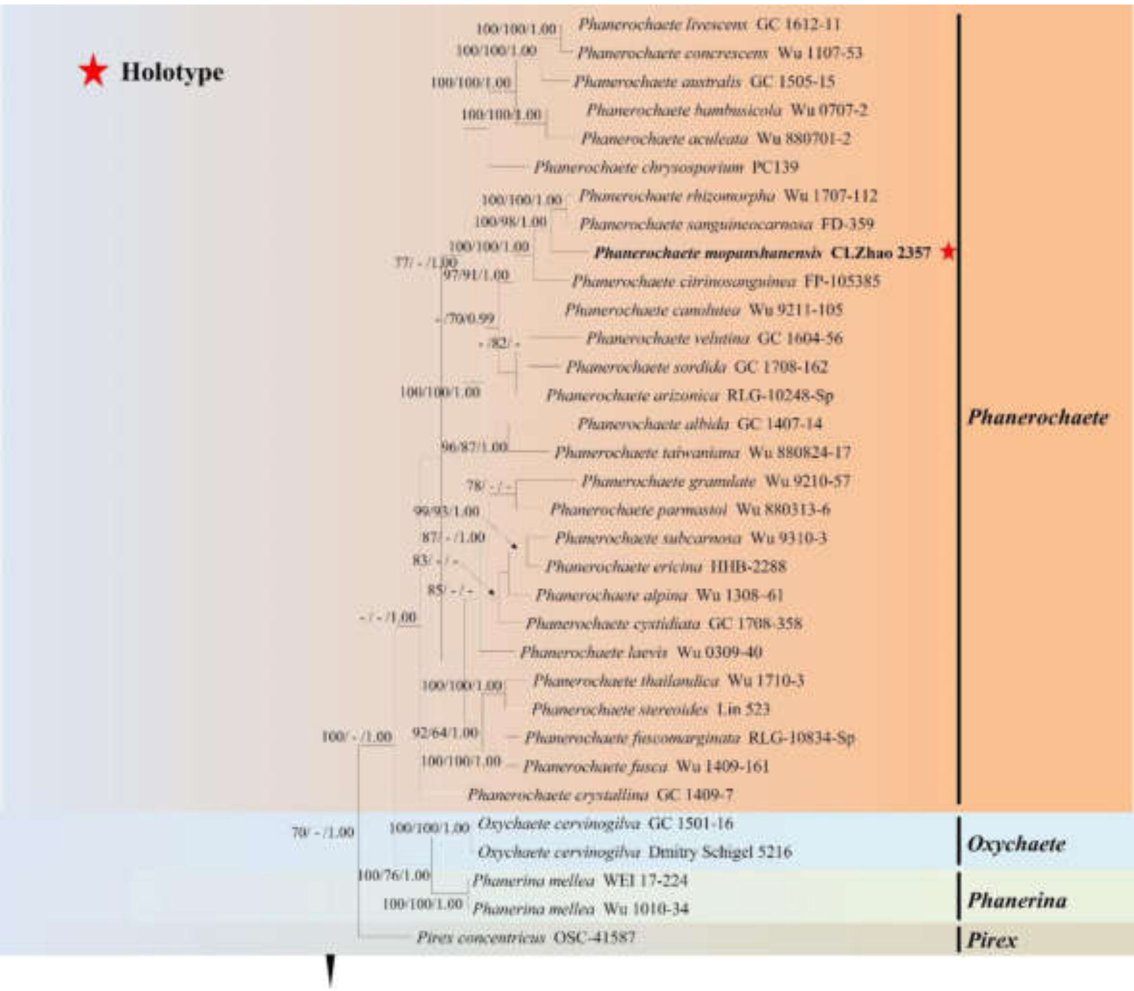

Figure 16 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Donkiella*, *Phanerochaete*, *Phlebiopsis* and related genera in Phanerochaetaceae based on ITS+nLSU+RPB1+RPB2+TEF1 sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

***Etheirodon*, *Nigroporus* and *Steccherinum* phylogeny based on combined ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 sequence data** (Fig. 17)

The aligned dataset comprised 47 specimens representing 41 species. Four Markov chains were run for two runs from random starting trees, each for 1.5 million generations for the combined ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 (Fig. 17) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 7214 characters, of which 3884 characters are constant, 1299 are variable and parsimony uninformative, and 2031 are parsimony informative. Maximum parsimony analysis yielded one equally parsimonious trees (TL = 8510, CI = 0.5707, HI = 0.4293, RI = 0.5186, and RC = 0.5186). The best model for the ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 dataset, estimated and applied in the Bayesian analysis, was GTR+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.012861 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 421.5.

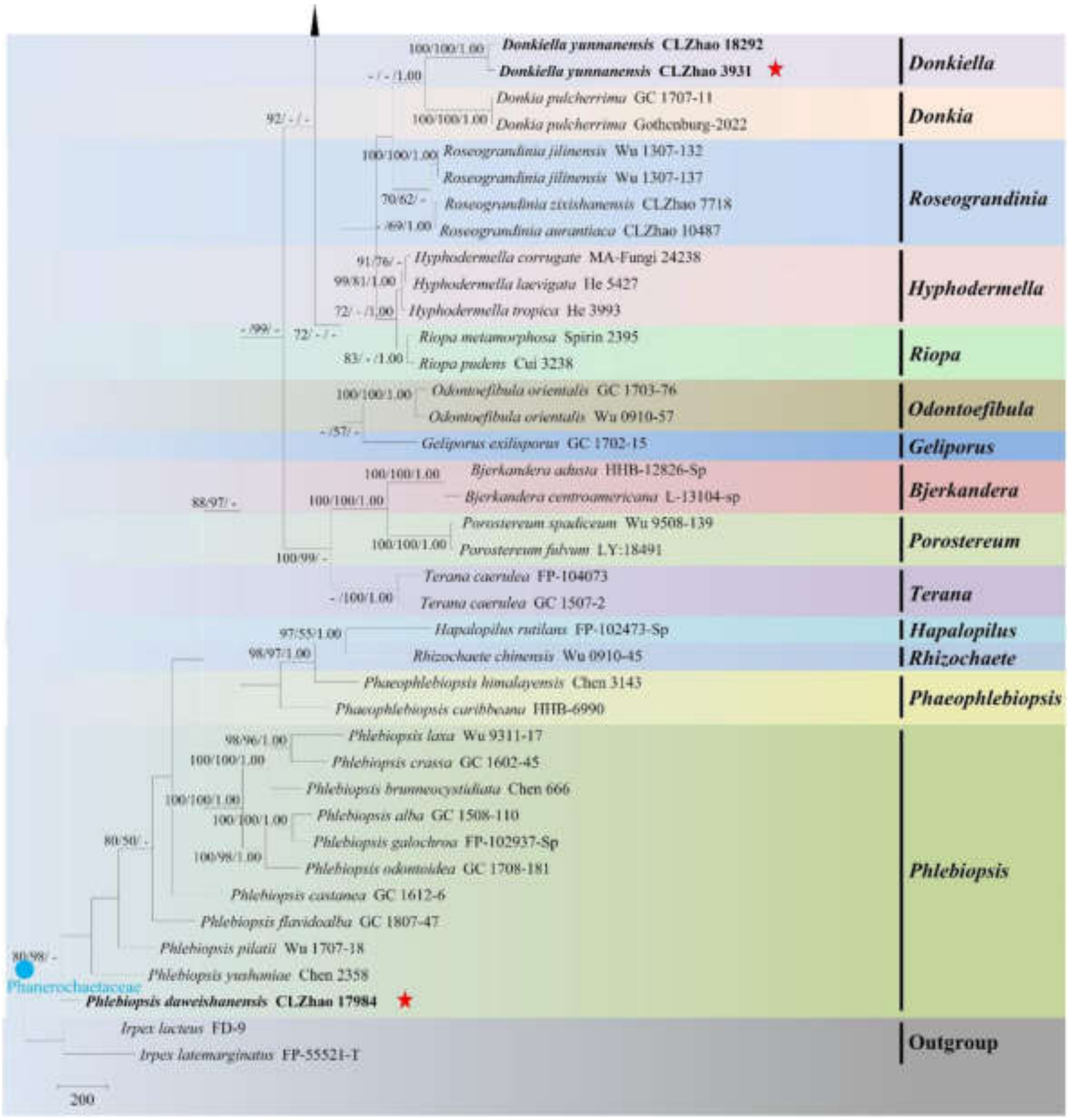

Figure 16 – Continued.

***Artomyces* phylogeny based on combined ITS sequence data** (Fig. 18)

The aligned dataset comprised 36 specimens representing 20 species. Four Markov chains were run for 2 runs from random starting trees, each for 1.5 million generations for the ITS (Fig. 18) with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 703 characters, of which 420 characters are constant, 32 are variable and parsimony uninformative, and 251 are parsimony informative. Maximum parsimony analysis yielded 10 equally parsimonious trees (TL = 926, CI = 0.4795, HI = 0.5205, RI = 0.6785, and RC = 0.3253). The best model for the ITS dataset, estimated and applied in the Bayesian analysis, was HKY+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.006800 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 182.

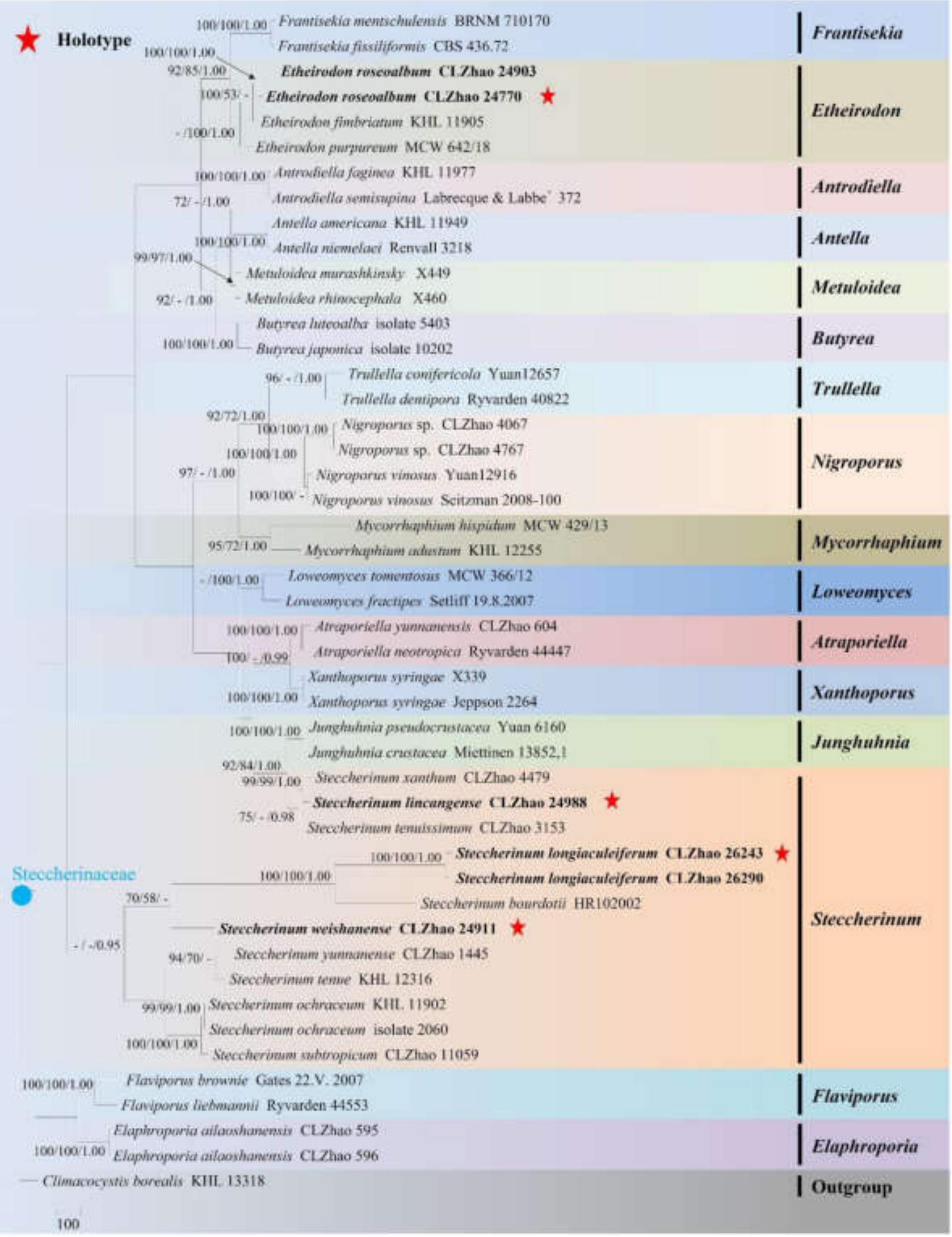

Figure 17 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Etheirodon*, *Nigroporus*, *Steccherinum* and related genera in Steccherinaceae based on ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

Scytinostroma phylogeny based on combined ITS+nLSU sequence data (Fig. 19)

The aligned dataset comprised 34 fungal specimens representing 26 species. Four Markov chains were run for 2 runs from random starting trees, each for 1 million generations for the combined ITS+nLSU (Fig. 19) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 2597 characters, of which 1516 characters are constant, 329 are variable and parsimony uninformative, and 752 are parsimony informative. Maximum parsimony analysis yielded 1 equally parsimonious trees (TL = 3661, CI = 0.4990, HI = 0.5010, RI = 0.5955, and RC = 0.2972). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was SYM+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.004818 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 632.5.

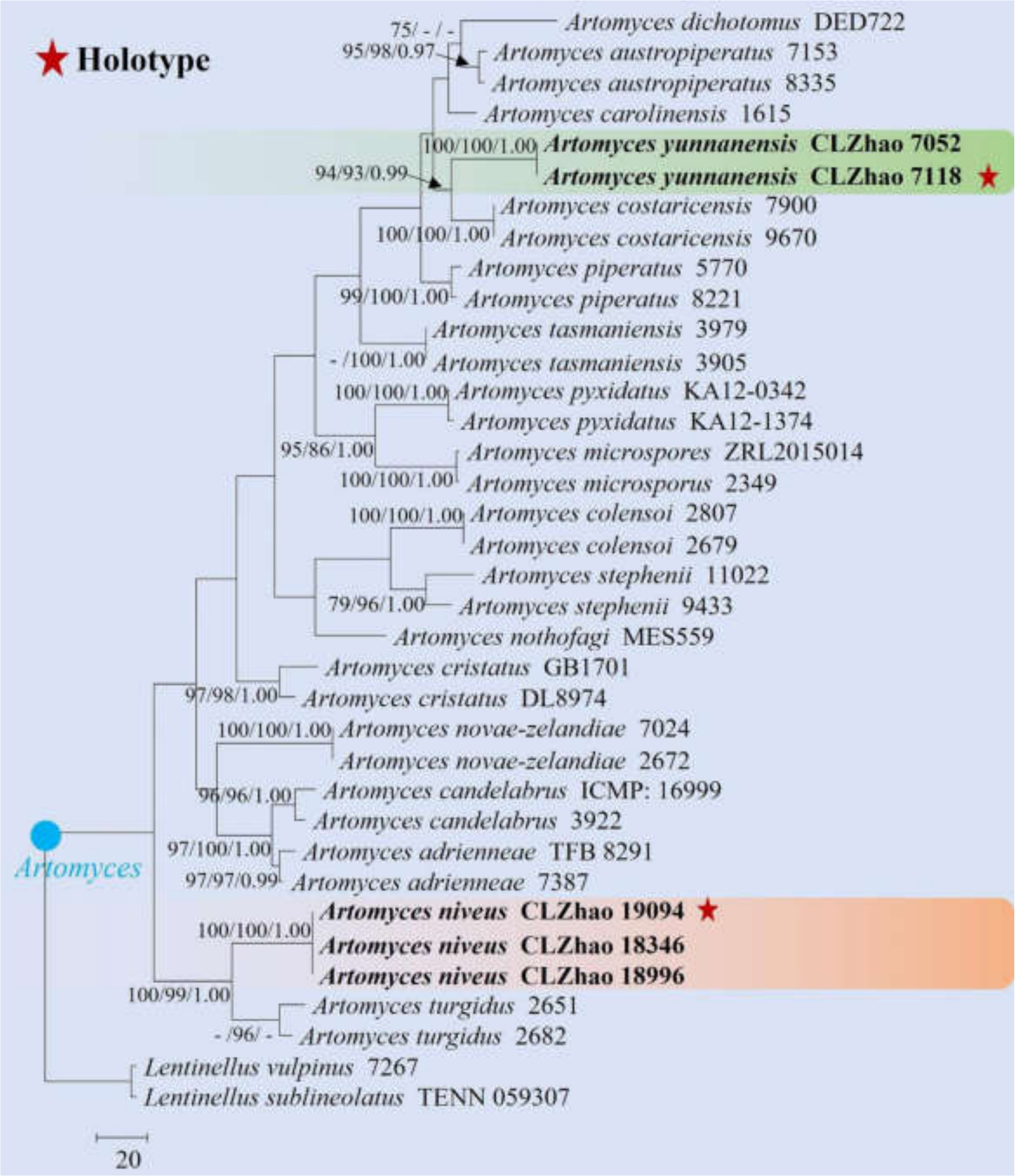

Figure 18 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Artomyces niveus*, *A. yunnanensis* and related species in *Artomyces* based on ITS sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

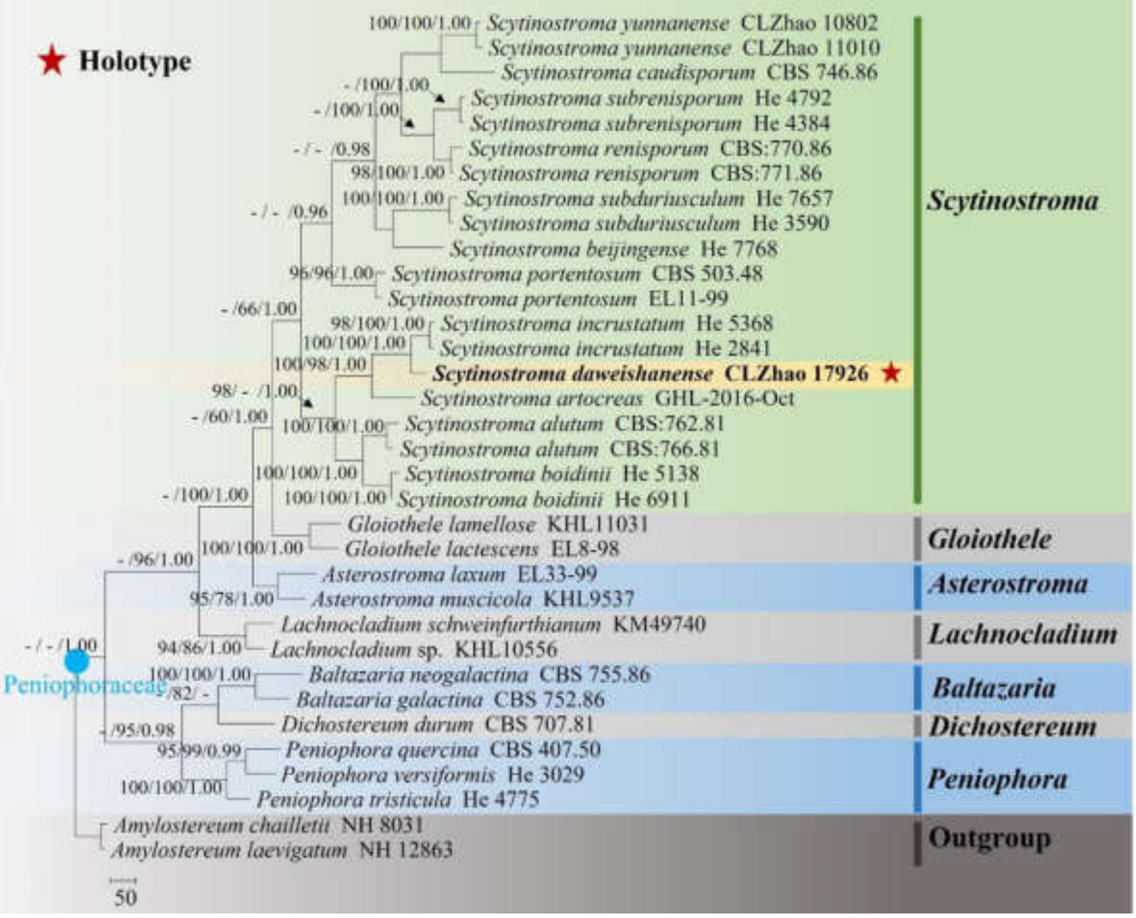

Figure 19 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Scytinostroma* and related genera in Peniophoraceae based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

Fibrodontia and _Subulicystidium_ phylogeny based on combined ITS, nLSU, mtSSU, RPB2 and TEF1 sequence data (Fig. 20)

The aligned dataset comprised 52 fungal specimens representing 37 species. Four Markov chains were run for 2 runs from random starting trees, each for 4 million generations for the combined ITS+nLSU+mtSSU+RPB2+TEF1 (Fig. 20) data set with trees and parameters sampled every 1000 generations. The dataset had an aligned length of 4218 characters, of which 2116 characters are constant, 897 are variable and parsimony uninformative, and 1205 are parsimony informative. Maximum parsimony analysis yielded 2 equally parsimonious trees (TL = 6273, CI = 0.5218, HI = 0.4782, RI = 0.4782, and RC = 0.2606). The best model for the ITS+nLSU+mtSSU+RPB2+TEF1 dataset, estimated and applied in the Bayesian analysis, was SYM+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.010846 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 861.5.

The seven species new to China phylogeny based on combined ITS+nLSU sequence data (Fig. 21)

The aligned dataset comprised 110 specimens representing 84 species. Four Markov chains were run for 4 runs from random starting trees, each for three million generations for the combined ITS+nLSU (Fig. 21) data set with trees and parameters sampled every 1000 generations.

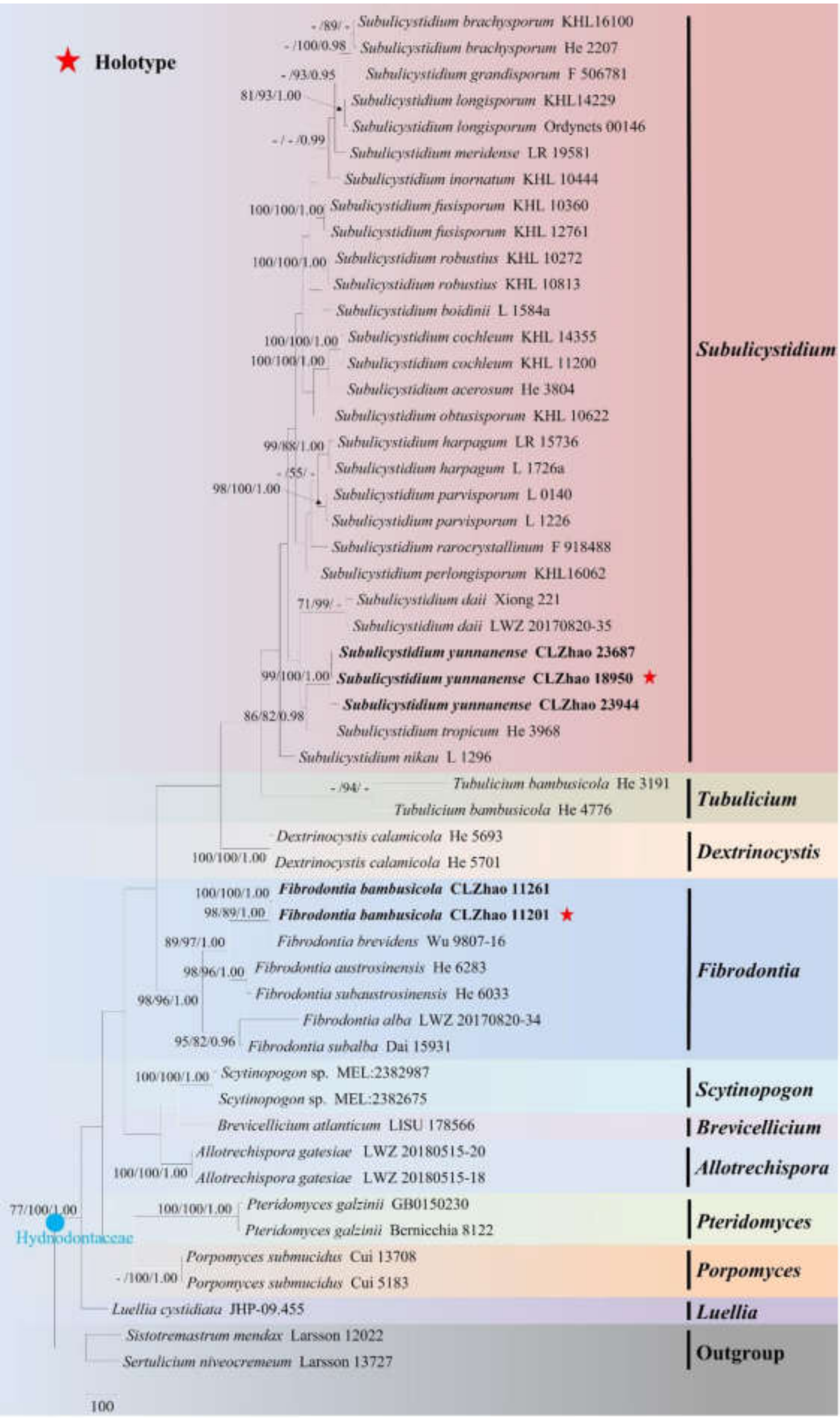

Figure 20 – Maximum parsimony strict consensus tree illustrating the phylogeny of *Fibrodontia*, *Subulicystidium* and related genera in Hydnodontaceae based on ITS+nLSU+RPB2+TEF1

sequences. Branches are labeled with maximum likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

The dataset had an aligned length of 2251 characters, of which 1172 characters are constant, 178 are variable and parsimony uninformative, and 901 are parsimony informative. Maximum parsimony analysis yielded 1 equally parsimonious trees (TL = 9402, CI = 0.2145, HI = 0.7855, RI = 0.5258, and RC = 0.1128). The best model for the ITS+nLSU dataset, estimated and applied in the Bayesian analysis, was GTR+I+G. Both Bayesian analysis and ML analysis resulted in a similar topology to MP analysis with an average standard deviation of split frequencies = 0.012025 (BI), and the effective sample size (ESS) for Bayesian analysis across the two runs is the double of the average ESS (avg ESS) = 605.5.

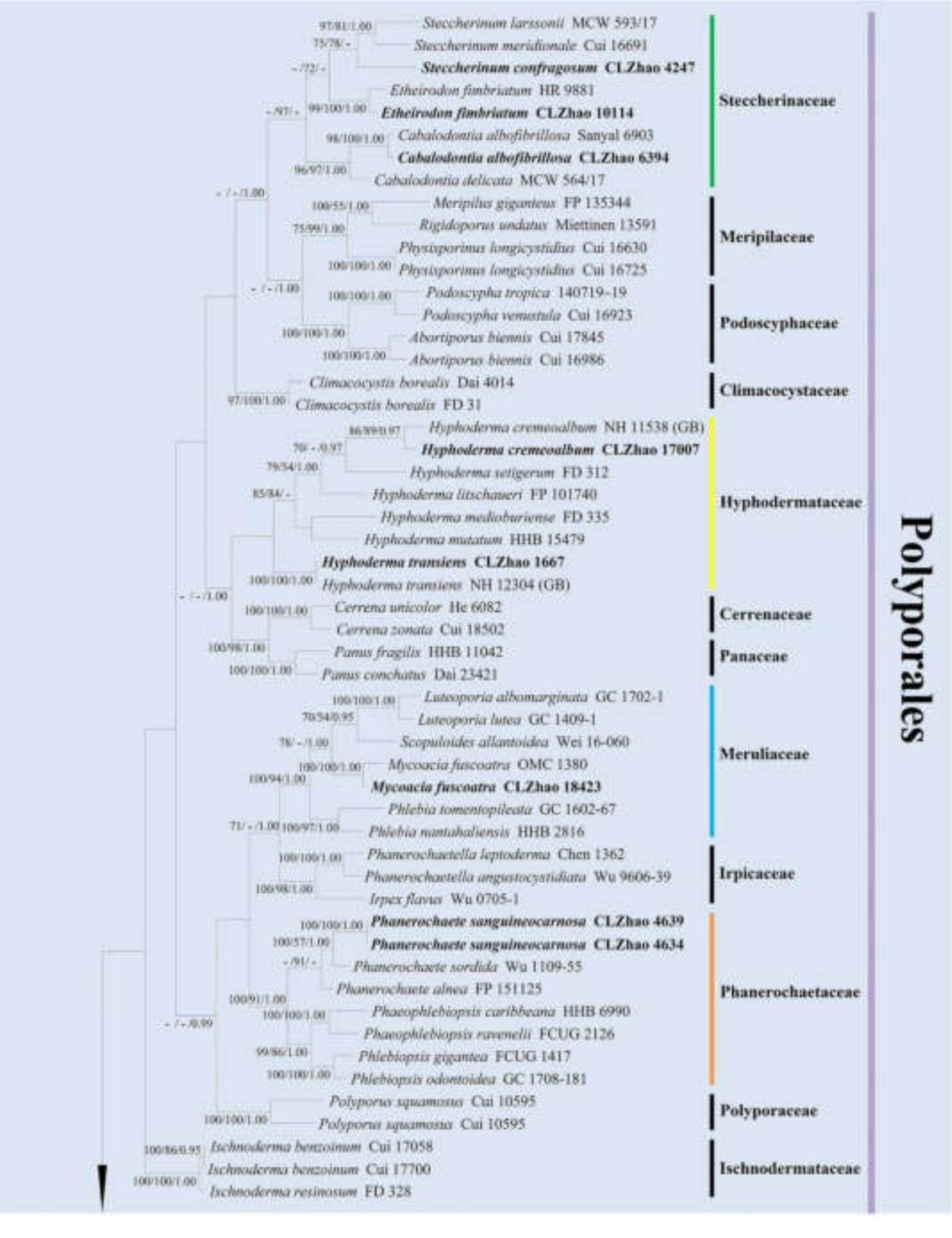

Figure 21 – Maximum parsimony strict consensus tree illustrating the phylogeny of seven new record species in China based on ITS+nLSU sequences. Branches are labeled with maximum

likelihood bootstrap values higher than 70%, parsimony bootstrap values higher than 50% and Bayesian posterior probabilities more than 0.95 respectively.

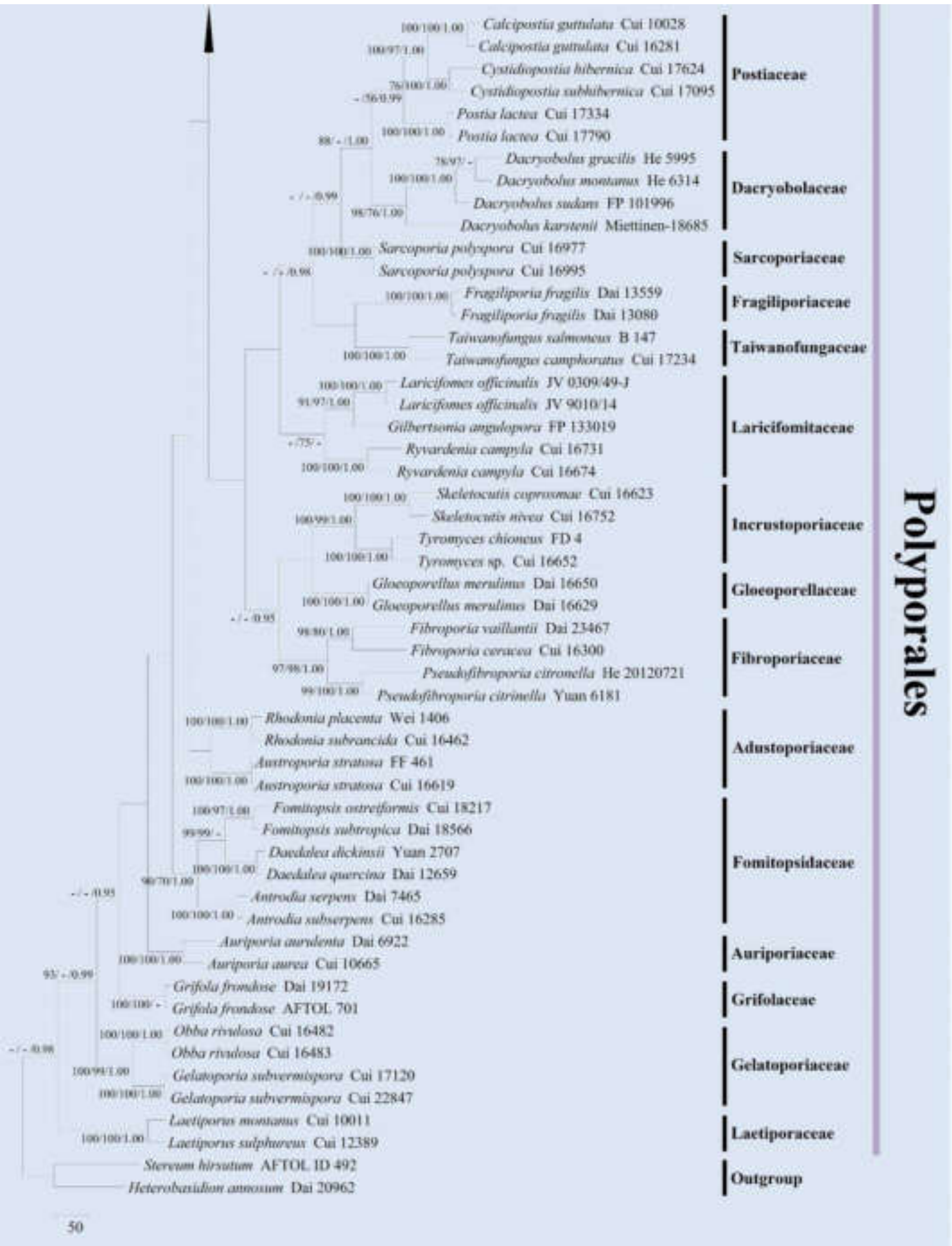

Figure 21 – Continued.

Taxonomy

Agaricales Underw.

Dendrothele Höhn. & Litsch.

Index Fungorum number: IF17484; Facesoffungi number: FoF15390

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

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

Dendrothele yunnanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 22, 23

Index Fungorum number: IF850313; Facesoffungi number: FoF15391

Diagnosis – Differs from other *Dendrothele* species by the ceraceous basidiomata with white to cream, smooth hymenial surface with numerous crevices, monomitic hyphal system with clamped generative hyphae and subglobose to globose basidiospores measuring 7.5–9 × 6–7.8 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 1 August 2019, CLZhao 17814 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, coriaceous, without odor or taste when fresh, becoming hard ceraceous upon drying, up to 15 cm long, 100–200 µm thick. Hymenial surface smooth, cracked with numerous crevices, white when fresh, white to cream upon drying. Sterile margin cream, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, difficult to discern, colorless, thin-walled, rarely branched, 2–3 µm in diameter; IKI–, CB–, tissues unchanged in KOH; dendrohyphidia numerous, 1–2.5 µm in diameter; subhymenial hyphae densely covered by larger crystals. Cystidia and cystidioles absent. Basidia subclavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, 31–40 × 6–8 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose to globose, thin-walled, colorless, smooth, IKI–, CB–, (7–)7.5–9(–9.2) × (5.7–)6–7.8 µm, L = 8.34 µm, W = 6.82 µm, Q = 1.22 (n = 30/1).

Notes – Based on the ITS+nLSU data (Fig. 2), the new species *Dendrothele yunnanensis* is grouped into *Dendrothele*, and is clustered with *D. americana* Nakasone and *D. griseocana* (Bres.) Bourdot & Galzin. However, *D. americana* can be delimited from *D. yunnanensis* by its greyish yellow to yellowish grey hymenial surface, and its obclavate to vesiculose basidia (25–55 × 7–12 µm, Nakasone 2006). *Dendrothele griseocana* can be delimited from *D. yunnanensis* by its greyish or ochraceous hymenial surface, shorter basidia (20–30 × 6–8 µm) and longer basidiospores (9–11 × 7–8 µm, Bernicchia & Gorjón 2010).

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

Index Fungorum number: IF831047; Facesoffungi number: FoF15392

Type genus – *Radulomyces* M.P. Christ.

Radulomyces M.P. Christ.

Index Fungorum number: IF18442; Facesoffungi number: FoF15393

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

Notes – *Radulomyces* M.P. Christ. was introduced by Christiansen (1960) and is typified by *R. confluens* (Fr.) M.P. Christ. Larsson et al. (2004) showed that *Coronicium alboglaucum* (Bourdot & Galzin) Jülich, *R. confluens*, *R. molaris* (Chaillet ex Fr.) M.P. Christ. and *R. rickii*

(Bres.) M.P. Christ. nested within the euagarics clade. The placement of two genera *Aphanobasidium* Jülich and *Radulomyces* were previously located in the family Pterulaceae by the phylogenetic reconstructions of corticioid taxa (Larsson et al. 2004, Larsson 2007a). Phylogenetically, *Radulomyces* belonged in the Pterulaceae (Agaricales) and was most closely related to *Radulotubus* Y.C. Dai, S.H. He & C.L. Zhao and *Aphanobasidium* (Zhao et al. 2016a). These three genera form a strongly supported clade sister to the *Pterula-Deflexula-Pterulicium-Merulicium-Coronicium* clade based on sequence analyses of ITS+nLSU (Zhao et al. 2016a, Wang et al. 2018b). Based on the phylogenetical and morphological analysis, Leal-Dutra et al. (2020) reveailed that no members of the three genera within this superclade were pteruloid (i.e. coralloid basidiomes with dimitic hyphal system) in their morphology and then consequently they proposed the new family Radulomycetaceae to accommodate them. In the present study, based on the ITS+nLSU data (Fig. 3) and morphological characteristics, three new species *R. hydnoides*, *R. yunnanensis* and *R. zixishanensis* spp. nov. are introduced.

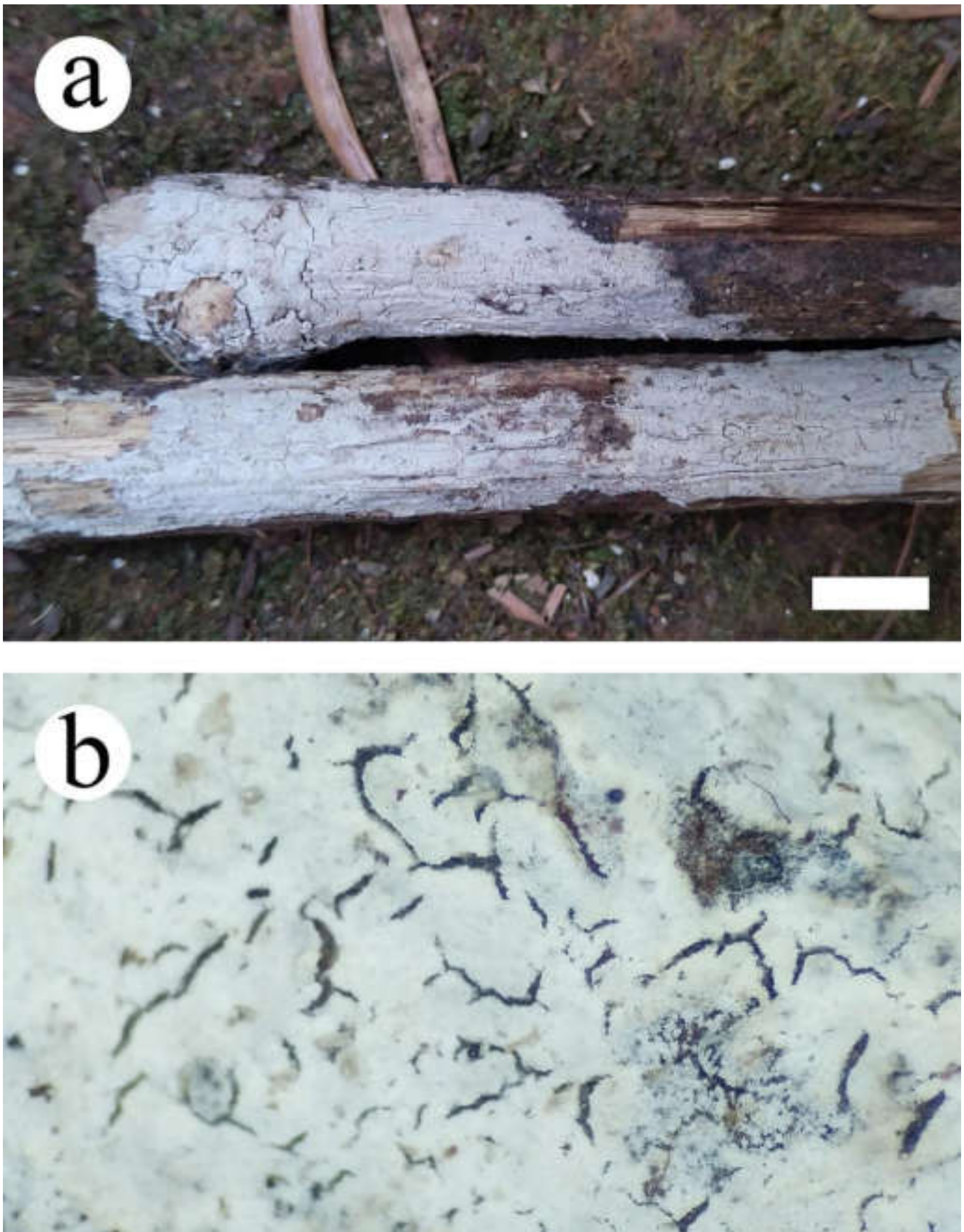

Figure 22 – Basidiomata of *Dendrothele yunnanensis* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

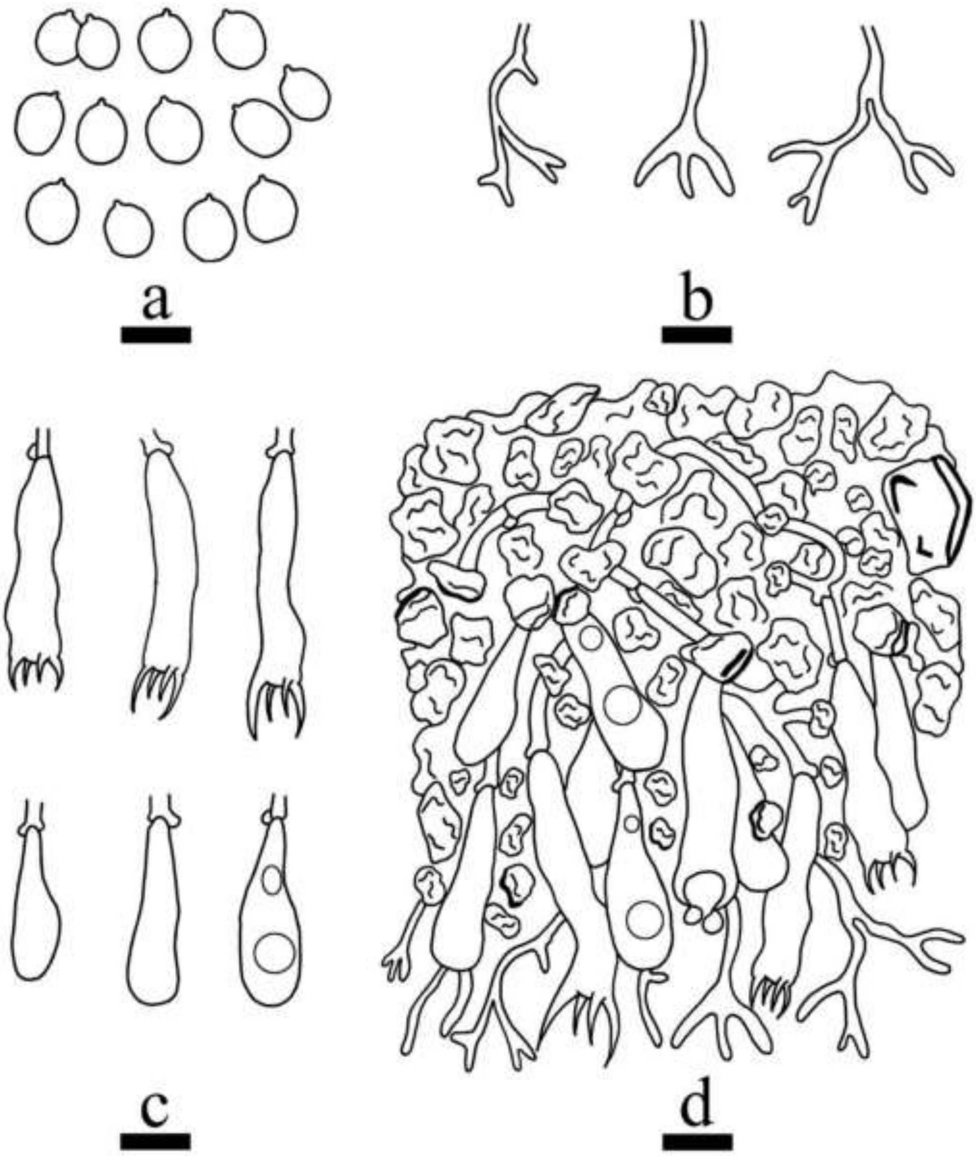

Figure 23 – Microscopic structures of *Dendrothele yunnanensis* (drawn from the holotype). a Basidiospores. b Dendrohyphidia. c Basidia and basidioles. d A section of hymenium. Scale bars: a–d = 10 µm.

Radulomyces hydnoides J.H. Dong & C.L. Zhao, sp. nov. Figs 24, 25

Index Fungorum number: IF850315; Facesoffungi number: FoF15394

Diagnosis – Differs from other *Radulomyces* species by the corneous basidiomata with orange to ochraceous, hydnoid hymenial surface, monomitic hyphal system with clamped generative hyphae and subglobose to globose basidiospores measuring 7.5–9 × 6–7–8.7 µm.

Etymology – *hydnoides* (Lat.): referring to the hydnoid hymenophore of the type specimen.

Type – China, Yunnan Province, Lijiang, Heilongtan Park, Xiangshan, GPS coordinates 26°53' N, 100°14' E, altitude 2500 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 21 July 2021, CLZhao 21632 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, corneous, without odor or taste, becoming hard coriaceous upon drying, up to 10 cm long, 3 cm wide, 50–200 µm thick. Hymenial surface hydnoid, slightly orange when fresh, turning to orange to ochraceous upon drying. Sterile margin cream to slightly orange, abrupt, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to thick-walled, arranged in a parallel structure, 2–4 µm in diameter; IKI–, CB–, tissues unchanged in

KOH. Hyphal ends frequently present in the basidial layer; cystidia and cystidioles absent. Basidia subclavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, with abundant oil droplets, 21–34 × 8.5–12.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose to globose, colorless, thin to slightly thick-walled, smooth, with abundant oil contents, IKI–, CB+, (7.2–)7.5–9(–9.5) × (–6.8)7–8.7(–9.5) µm, L = 8.14 µm, W = 7.81 µm, Q = 1.04–1.07 (n = 120/4).

Material examined (paratypes) – China, Yunnan Province, Lijiang, Lashihai Nature Reserve, Meiquan Village, GPS coordinates 26°53' N, 100°9' E, altitude 2450 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 19 July 2021, CLZhao 21337; on the trunk of angiosperm, leg. C.L. Zhao, 19 July 2021, CLZhao 21342, CLZhao 21351; Lijiang, Heilongtan Park, Xiangshan, GPS coordinates 26°53' N, 100°14' E, altitude 2500 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 21 July 2021, CLZhao 21668, CLZhao 21815 (SWFC).

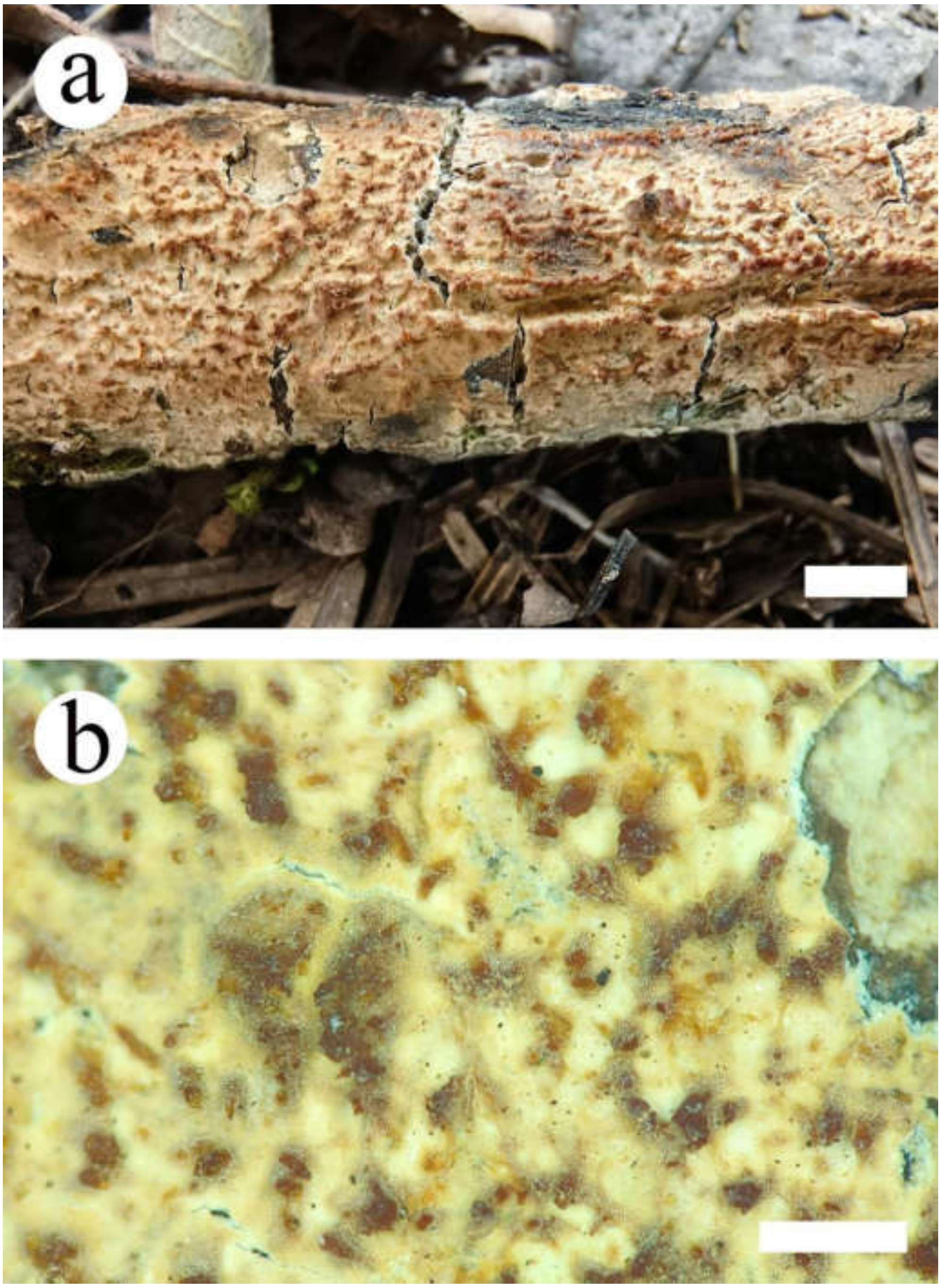

Figure 24 – Basidiomata of *Radulomyces hydnoides* (holotype). Scale bars: a = 1 cm, b = 1 mm.

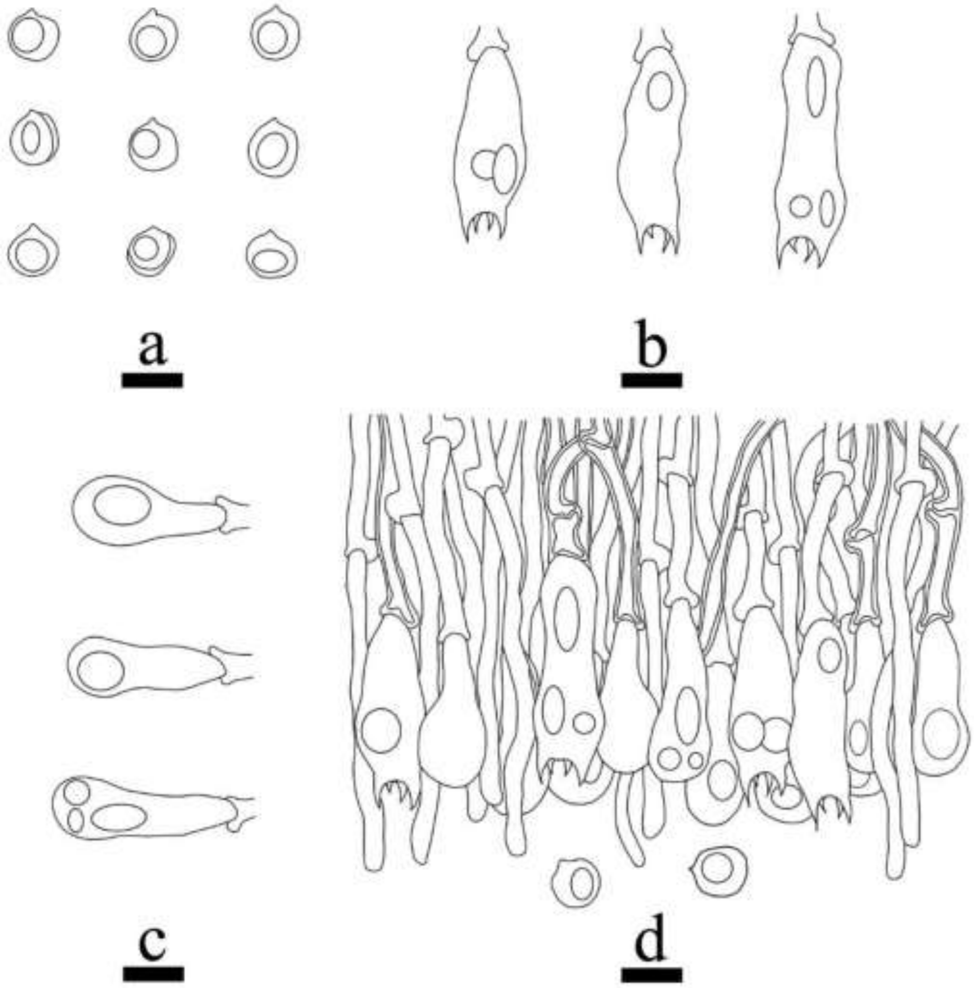

Figure 25 – Microscopic structures of *Radulomyces hydnoides* (drawn from the holotype). a Basidiospores. b Basidia. c Basidioles. d A section of hymenium. Scale bars: a–d = 10 µm.

Notes – Based on the ITS+nLSU data (Fig. 3), the new species *Radulomyces hydnoides* grouped with *Radulomyces* species, and forming a monophyletic lineage.

Radulomyces hydnoides resembles *R. copelandii* (Pat.) Hjortstam & Spooner and *R. paumanokensis* J. Horman, Nakasone & B. Ortiz in sharing subglobose to globose basidiospores. However, *R. copelandii* differs from *R. hydnoides* due to its white hymenial surface, its narrower basidia (29–35 × 6–7 µm) and smaller basidiospores (6.4–7 × 5.4–6.2 µm, Ginns & Millman 2011); *R. paumanokensis* can be distinguished from *R. hydnoides* by its orange white to pale orange hymenial surface, its narrower basidia (25–31 × 5–7.5 µm) and smaller basidiospores (5.8–6.9 × 5.2–6.4 µm, Wang et al. 2018b).

Radulomyces yunnanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 26, 27

Index Fungorum number: IF850316; Facesoffungi number: FoF15395

Diagnosis – Differs from other *Radulomyces* species by the coriaceous basidiomata with cream, smooth hymenial surface with deep ravine, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 8.2–9.5 × 5.5–7 µm.

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

Type – China, Yunnan Province, Kunming, Xishan District, Haikou Forestry Park, GPS coordinates 24°48' N, 102°36' E, altitude 2300 m asl., on the fallen branch of *Quercus*, leg. C.L. Zhao, 22 April 2017, CLZhao 1262 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, coriaceous, without odor or taste, becoming hard coriaceous upon drying, up to 15 cm long, 5 cm wide, 100–250 µm thick. Hymenial surface smooth, cracked with deep ravine, slightly cream when fresh, turning cream upon drying. Sterile margin narrow, slightly cream, abrupt, up to 0.5 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, arranged in a parallel structure, 2.5–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Hyphal ends frequently present in the basidial layer; cystidia and cystidioles absent. Basidia subclavate, slightly sinuous, some with a few guttulae, with 4 sterigmata and a basal clamp connection, with abundant oil content 24–35 × 7–11 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, with oily granular content, IKI–, CB–, (7.5–)8.2–9.5(–10) × (5–)5.5–7(–7.5) µm, L = 8.89 µm, W = 6.26 µm, Q = 1.42–1.51 (n = 150/5).

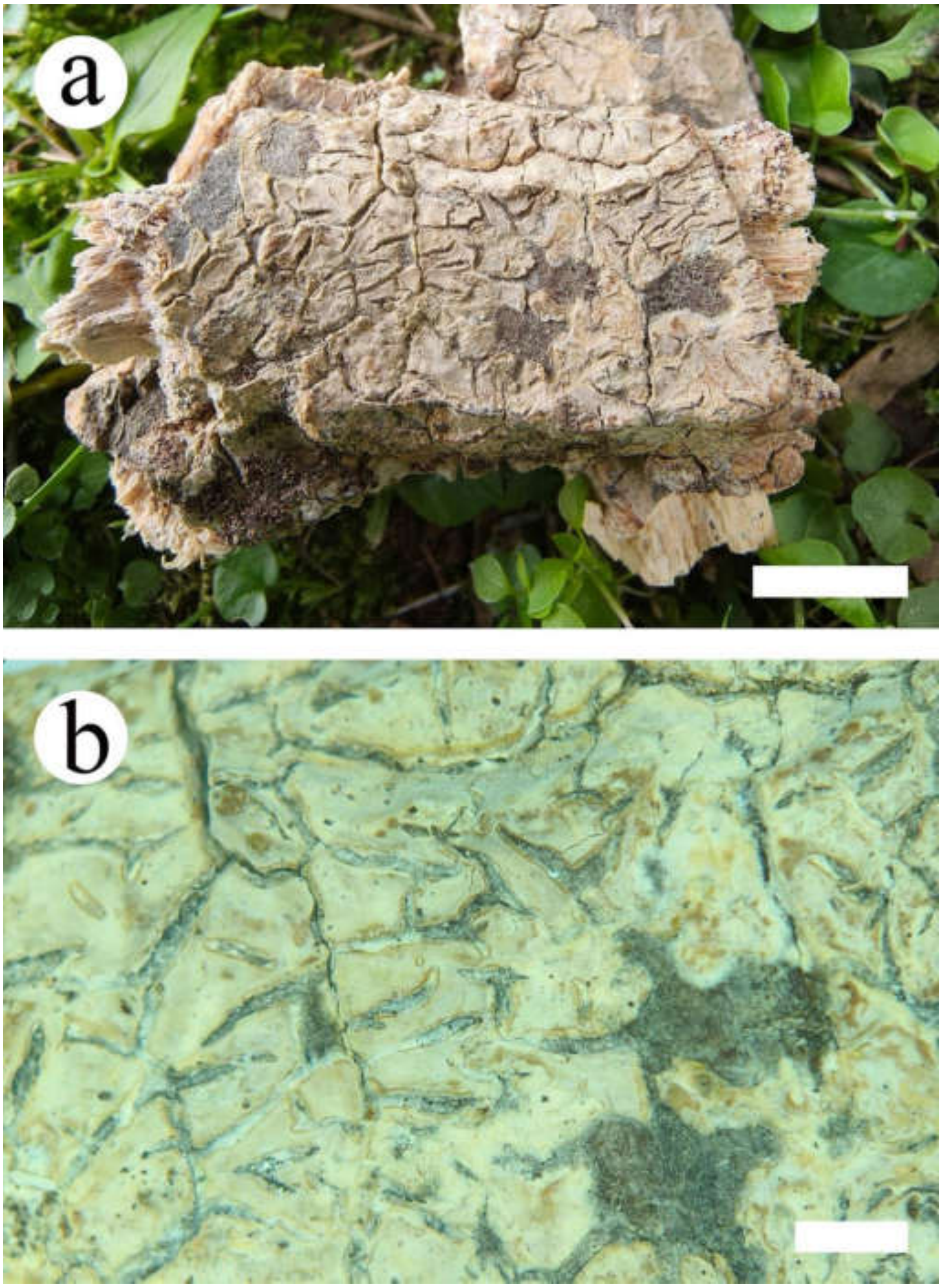

Figure 26 – Basidiomata of *Radulomyces yunnanensis* (holotype). Scale bars: a = 1 cm, b = 2 mm.

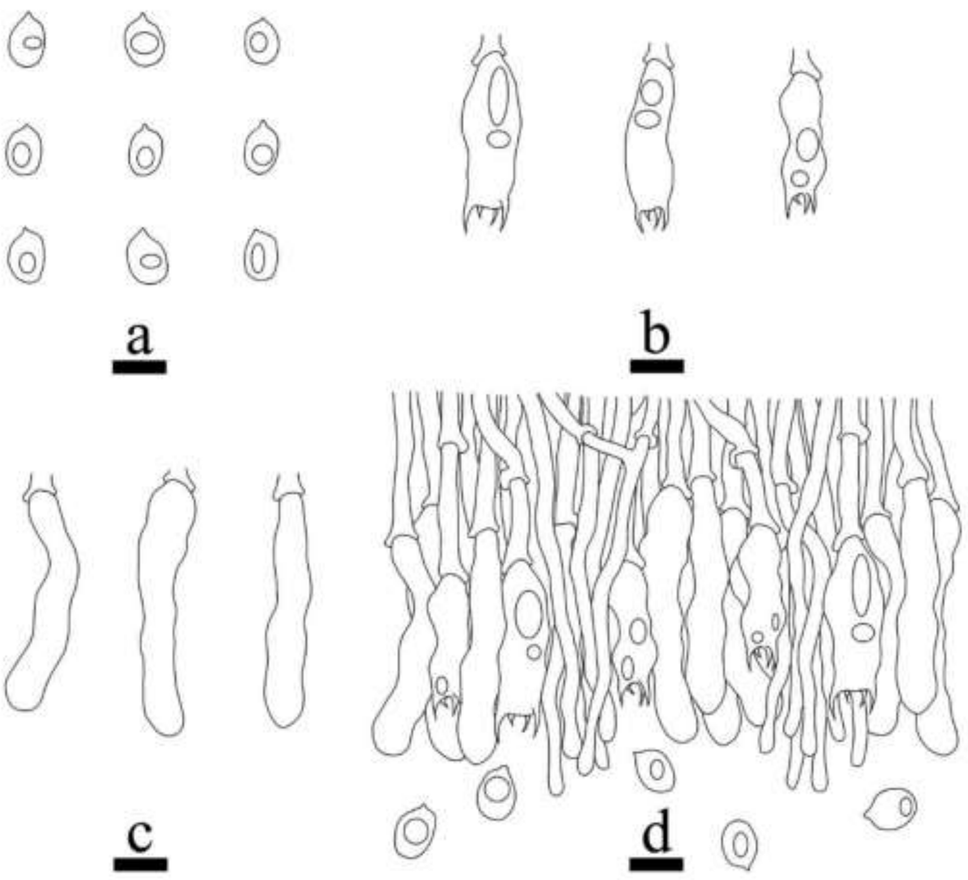

Figure 27 – Microscopic structures of *Radulomyces yunnanensis* (drawn from the holotype). a Basidiospores. b Basidia. **c** Basidioles. d A section of hymenium. Scale bars: a–d = 10 µm.

Material examined (paratypes) – China, Yunnan Province, Chuxiong, Zixishan Forestry Park, GPS coordinates 25°01' N, 101°24' E, altitude 2500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 2 July 2018, CLZhao 7364; Qujing, Liaokuo Park, GPS coordinates 25°01' N, 101°24' E, altitude 2000 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 26 August 2022, CLZhao 24040; Qujing, Qilin District, Cuishan Forest Park, GPS coordinates 25°32' N, 103°42' E, altitude 2250 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 5 November 2022, CLZhao 26656; 6 November 2022, CLZhao 26685, CLZhao 27046, CLZhao 27069 (SWFC).

Notes – Based on ITS+nLSU data (Fig. 3), *Radulomyces yunnanensis* grouped with *Radulomyces* species, where it formed a monophyletic lineage.

Radulomyces yunnanensis resembles *R. fuscus* (W.B. Cooke) Ginns and *R. tantalusensis* Gilb. & Nakasone in having the smooth hymenial surface. However, *R. fuscus* differs from *R. yunnanensis* due to its pale orange-brown to orange-yellow hymenial surface, and its longer basidia (35–65 × 8–10 µm, Ginns 1976). *Radulomyces tantalusensis* can be distinguished from *R. yunnanensis* by its yellow-ocherous hymenial surface, and its longer basidiospores (10–12 × 4–5 µm, Gilbertson et al. 2003).

Radulomyces zixishanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 28, 29

Index Fungorum number: IF850317; Facesoffungi number: FoF15396

Diagnosis – Differs from other *Radulomyces* species by the hard coriaceous basidiomata with cream to slightly brown, smooth hymenial surface with numerous deep ravines, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 7–8.8 × 5.5–6.8 µm.

Etymology – *zixishanensis* (Lat.): referring to the locality (Zixishan) of the type specimen.

Type – China, Yunnan Province, Chuxiong, Zixishan National Forestry Park, GPS coordinates 25°01' N, 101°24' E, altitude 2500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 2 July 2021, CLZhao 21127 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, coriaceous, without odor or taste, becoming hard coriaceous upon drying, up to 15 cm long, 5 cm wide, 150–250 µm thick. Hymenial surface smooth, cracked with numerous deep ravines, cream when fresh, turning cream to slightly brown upon drying. Sterile margin narrow, cream, abrupt, up to 1 mm wide.

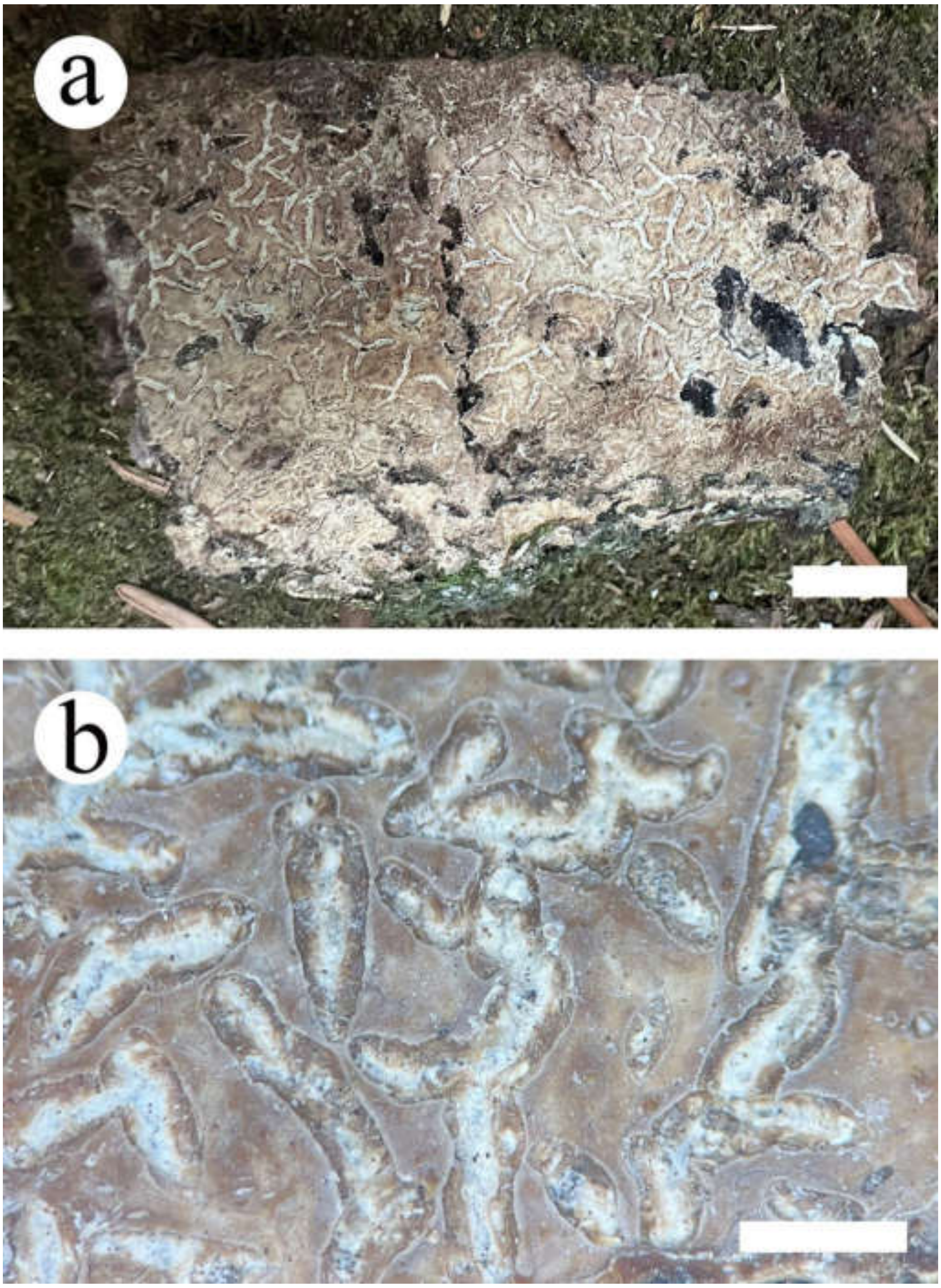

Figure 28 – Basidiomata of *Radulomyces zixishanensis* (holotype). Scale bars: a = 1 cm, b = 2 mm.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, interwoven, 3–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia and cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 28–43 × 6.5–8.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, with an oildrop, IKI–, CB–, 7–8.8(–9) × 5.5–6.8(–7) µm, L = 8.08 µm, W = 6.26 µm, Q = 1.29 (n = 30/1).

Notes – *Radulomyces zixishanensis* grouped with *Radulomyces* species based on the ITS+nLSU data (Fig. 3), and formed a monophyletic lineage.

Radulomyces zixishanensis resembles *R. arborifer* Malysheva & Zmitr. and *R. molaris* (Chaillet ex Fr.) M.P. Christ. in sharing ellipsoid basidiospores. However, *R. arborifer* differs from *R. zixishanensis* due to its dendroid or coralloid hymenial surface, and its slightly thick-walled basidiospores (7–10 × 5–6.5 µm, Malysheva 2006); *R. molaris* can be distinguished from *R. zixishanensis* by its hydnoid hymenial surface, and its slightly thick-walled basidiospores (8–12 × 6–8 µm, Bernicchia & Gorjón 2010).

Type genus – *Corticium* Pers.

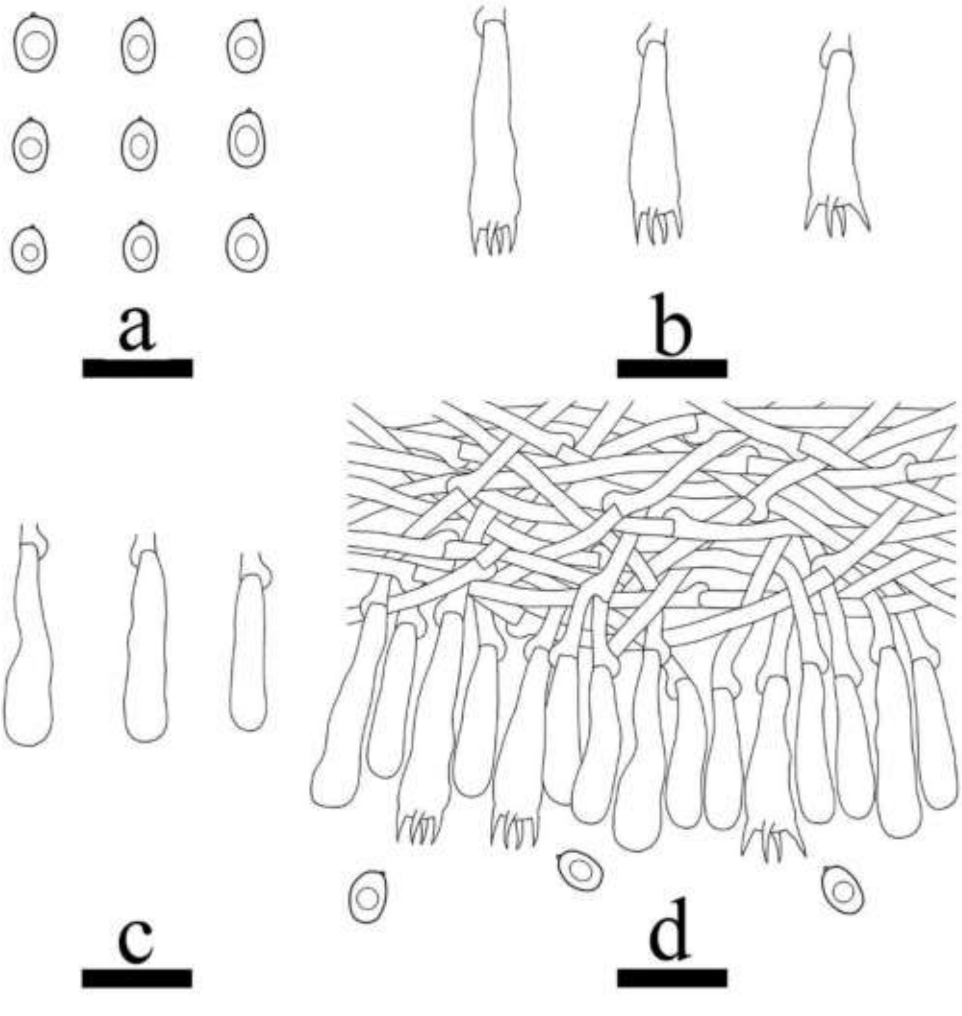

Figure 29 – Microscopic structures of *Radulomyces zixishanensis* (drawn from the holotype). a Basidiospores. b Basidia. c Basidioles. d A section of hymenium. Scale bars: a–d = 10 µm.

Corticiales K.H. Larss.

Corticiaceae Herter

Index Fungorum number: IF80648; Facesoffungi number: FoF15397

Corticium Pers.

Index Fungorum number: IF17387; Facesoffungi number: FoF15398

Type species – *Corticium roseum* Pers.

Notes – *Corticium* Pers. was erected by Persoon (1794) and is typified by *C. roseum* Pers. With the emergence of the molecular data, the genus has become more narrowly defined as many species were transferred to other genera, families and orders (Ghobad-Nejhad et al. 2021). The taxonomic studies for the genus *Corticium* contributed to the definition of *Corticium* in its strict sense (Boidin et al. 1968, Boidin & Lanquetin 1984, Boidin & Gilles 1998), and later, mycologists revealed the concept of *Laeticorticium* Donk based on further research (Larsen & Gilbertson 1974, 1978, Larsen & Nakasone 1984, Duhem & Michel 2006, 2009). Ghobad-Nejhad et al. (2021) confirmed that the genus *Corticium* was monophyletic. In the present study, one new species of *Corticium* is described from China based on morphological characteristics and phylogenetic analyses inferred from ITS+nLSU sequences (Fig. 4).

Corticium roseoalbum J.H. Dong & C.L. Zhao, sp. nov. Figs 30, 31

Index Fungorum number: IF850318; Facesoffungi number: FoF15399

Diagnosis – Differs from other *Corticium* species by the leathery basidiomata with white to slightly pinkish, tuberculate hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 11.5–16.5 × 8–11 µm.

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

Type – China, Yunnan Province, Kunming, Southwest Forestry University, GPS coordinates 25°06' N, 102°57' E, altitude 1950 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 17 January 2019, CLZhao 13525 (SWFC, holotype).

Description – Basidiomata annual, resupinate, soft coriaceous, without odor or taste, becoming leathery upon drying, up to 6.5 cm long, 4 cm wide, 0.1–0.5 mm thick. Hymenial surface tuberculate, white to slightly pinkish when fresh, turning pinkish upon drying. Sterile margin narrow, white to slightly pinkish, thinning out, up to 0.5 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 3.5–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia and cystidioles absent. Basidia clavate, with 4 long and short sterigmata and a basal clamp connection, 49–65 × 9.5–14 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (11–)11.5–16.5(–17) × 8–11(–11.5) µm, L = 14.06 µm, W = 9.65 µm, Q = 1.45 (n = 30/1).

Notes – *Corticium roseoalbum* grouped with *Corticium* species based on the ITS+nLSU data (Fig. 4) where *C. roseoalbum* is sister to *C. thailandicum* Ghobad-Nejhad. However, *C. thailandicum* can be delimited from *C. roseoalbum* by its smooth hymenial surface, and its subglobose basidiospores (10–13 × 7–9 µm, Ghobad-Nejhad et al. 2021).

Hymenochaetales Oberw.

Hymenochaetaceae Donk

Index Fungorum number: IF536196; Facesoffungi number: FoF15400

Type genus – *Hymenochaete* Lév.

Hydnoporia Murrill

Index Fungorum number: IF17793; Facesoffungi number: FoF15401

Type species – *Hydnoporia fuscescens* (Schwein.) Murrill

Notes – *Hydnoporia* Murrill was introduced by Murrill (1907) and is typified by *H. fuscescens* (Schwein.) Murrill. *Hydnoporia* can morphologically be divided into two groups, the effused-reflexed species and resupinate species; however, phylogenetic analyses showed that this is not supported (Miettinen et al. 2019). Miettinen et al. (2019) used morphology and phylogenetic analyses to discuss 13 *Hydnoporia* species, including one new species and 12 combined species. In the present study, based on the ITS, nLSU, mtSSU, RPB1, RPB2, TEF1 and ITS data (Figs 5, 6), the genus *Hydnoporia* nested in Hymenochaetaceae, in which two new species *H. pinicola* and *H. yunnanensis* are reported.

Hydnoporia pinicola J.H. Dong & C.L. Zhao, sp. nov. Figs 32, 33

Index Fungorum number: IF850319; Facesoffungi number: FoF15402

Diagnosis – Differs from other *Hydnoporia* species by the leathery basidiomata with greyish-brown, labyrinthine hymenial surface with numerous crevices, monomitic hyphal system with septate generative hyphae and cylindrical basidiospores measuring 3.7–5.2 × 2–2.7 µm.

Etymology – *pinicola* (Lat.): referring to grow on the *Pinus yunnanensis* of the type specimen.

Type – China, Yunnan Province, Qujing, Zhanyi District, Lingjiao Town, Xiajia Village, GPS coordinates 25°58′ N, 103°47′ E, altitude 2000 m asl., on the fallen branch of *Pinus yunnanensis*, leg. C.L. Zhao, 6 March 2023, CLZhao 27180 (SWFC, holotype).

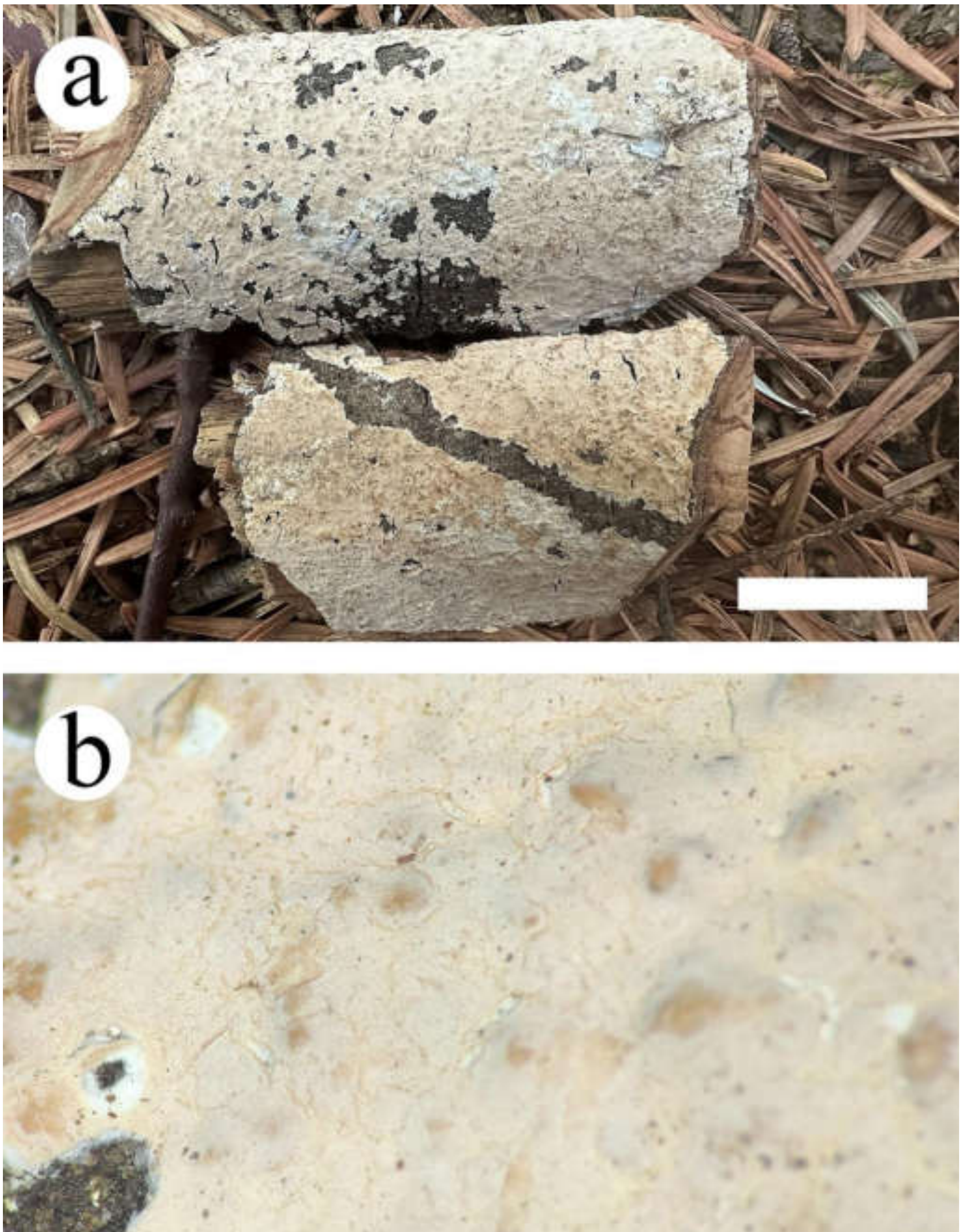

Figure 30 – Basidiomata of *Corticium roseoalbum* (holotype). Scale bars: a = 2 cm, b = 2 mm.

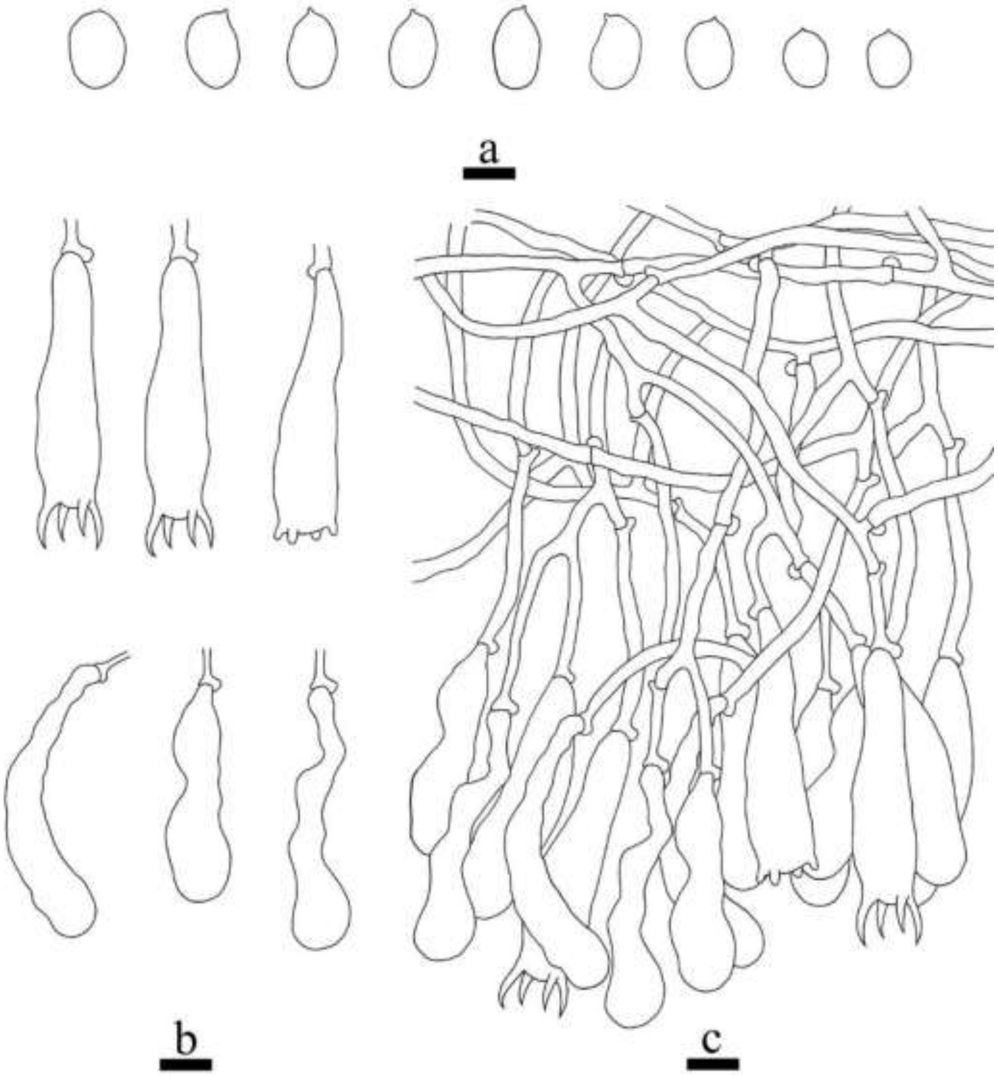

Figure 31 – Microscopic structures of *Corticium roseoalbum* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c A section of hymenium. Scale bars: a–c = 10 µm.

Description – Basidiomata annual, resupinate, without odor or taste, soft leathery when fresh, becoming leathery upon drying, up to 10 cm long, 1.5 cm wide, 50–100 µm thick. Hymenial surface labyrinthine, with numerous crevices, slightly brown when fresh, turning to greyish-brown upon drying. Sterile margin grey, abrupt, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with simple septa, yellowish, thick-walled, frequently branched, interwoven, 3.5–5.5 µm in diameter; IKI–, CB–, tissues darkening in KOH. Cystidia and cystidioles absent. Hymenial setae abundant, subulate, reddish-brown, thick-walled, smooth with obtuse tip, 55–112 × 9–18 µm, projecting above the hymenium. Basidia clavate, constricted, with 4 sterigmata and a basal simple septum, 15–27 × 3.5–5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores cylindrical, colorless, thin-walled, smooth, IKI–, CB–, (3.3–)3.7–5.2 × (1.8–)2–2.7(–2.9) µm, L = 4.29 µm, W = 2.31 µm, Q =1.75–1.86 (n = 120/4).

Material examined (paratypes) – China, Yunnan Province, Dali, Weishan County, Qinghua Town, Green peacock Reserve (Jiangzui Village), GPS coordinates 25°01' N, 100°11' E, altitude 1500 m asl., on the fallen branch of *Pinus yunnanensis*, leg. C.L. Zhao, 18 July 2022, CLZhao 22505; Qujing, Zhanyi District, Lingjiao Town, Xiajia Village, GPS coordinates 25°58′ N, 103°47′ E, altitude 2000 m asl., on the fallen branch of *Pinus yunnanensis*, leg. C.L. Zhao, 6 March 2023, CLZhao 27154, CLZhao 27175(SWFC).

Notes – *Hydnoporia pinicola* grouped in *Hydnoporia* based on the ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 data (Fig. 5), within the family Hymenochaetaceae. Based on ITS data (Fig. 6), *H. pinicola* is sister to *H. gigasetosa* (Parmasto) Miettinen & K.H. Larss. *Hydnoporia gigasetosa* can be delimited from *H. pinicola* by its smooth and fimbriate hymenial surfac, and its longer basidiospores (6–8 × 1.5–2 µm, Yang et al. 2016).

Hydnoporia pinicola shares similarities with *H. corrugata* (Fr.) K.H. Larss. & Spirin in sharing cylindrical basidiospores. However, *H. corrugata* differs from *H. pinicola* due to its granulose hymenial surface, and its narrower basidiospores (4.5–5 × 1.5–2 µm, Bernicchia & Gorjón 2010).

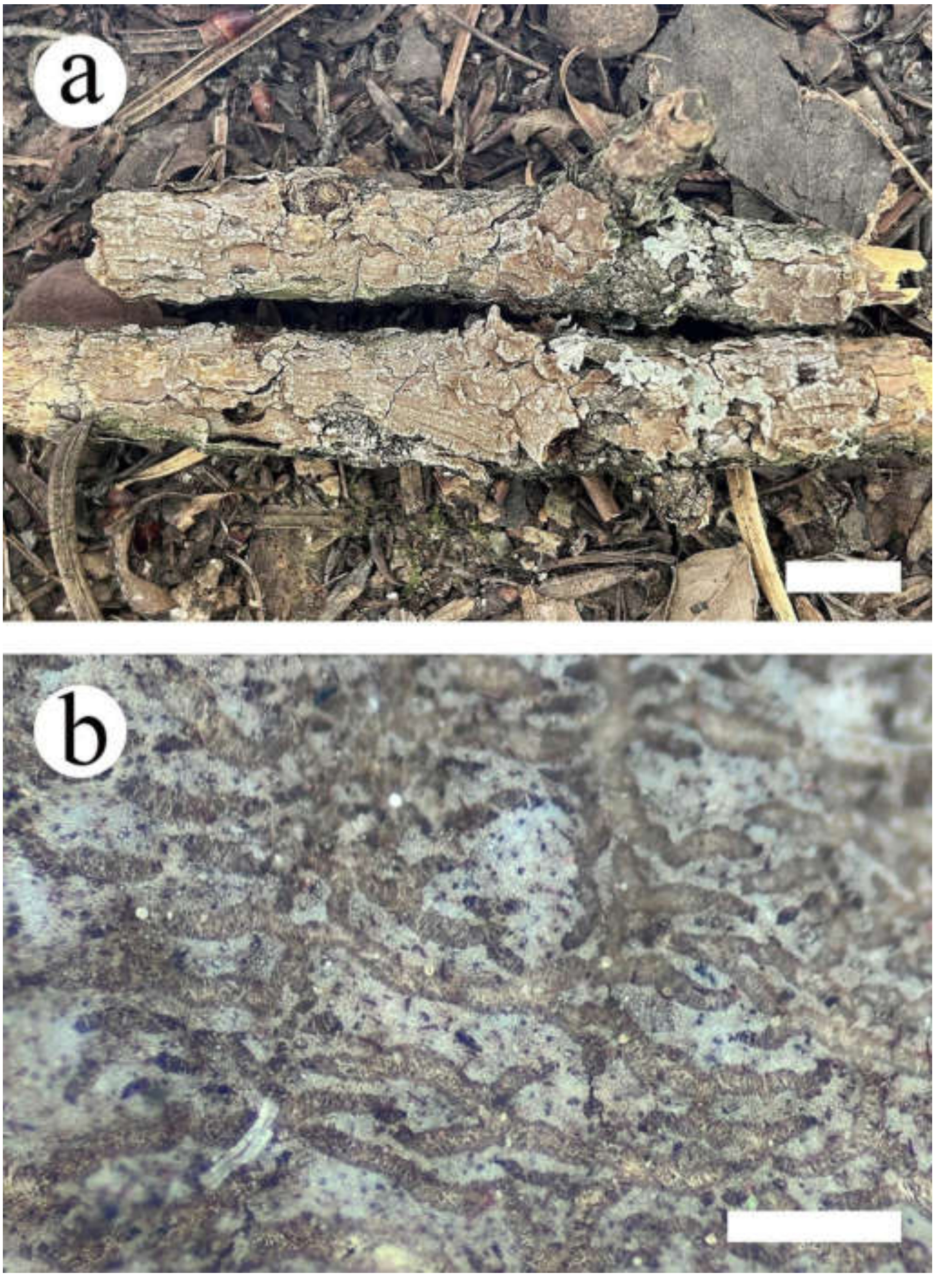

Figure 32 – Basidiomata of *Hydnoporia pinicola* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

Hydnoporia yunnanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 34, 35

Index Fungorum number: IF850320; Facesoffungi number: FoF15403

Diagnosis – Differs from other *Hydnoporia* species by the soft coriaceous to leathery basidiomata with dark brown, smooth hymenial surface, monomitic hyphal system with septate generative hyphae and allantoid basidiospores measuring 6–8.5 × 1.8–2.8 µm.

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

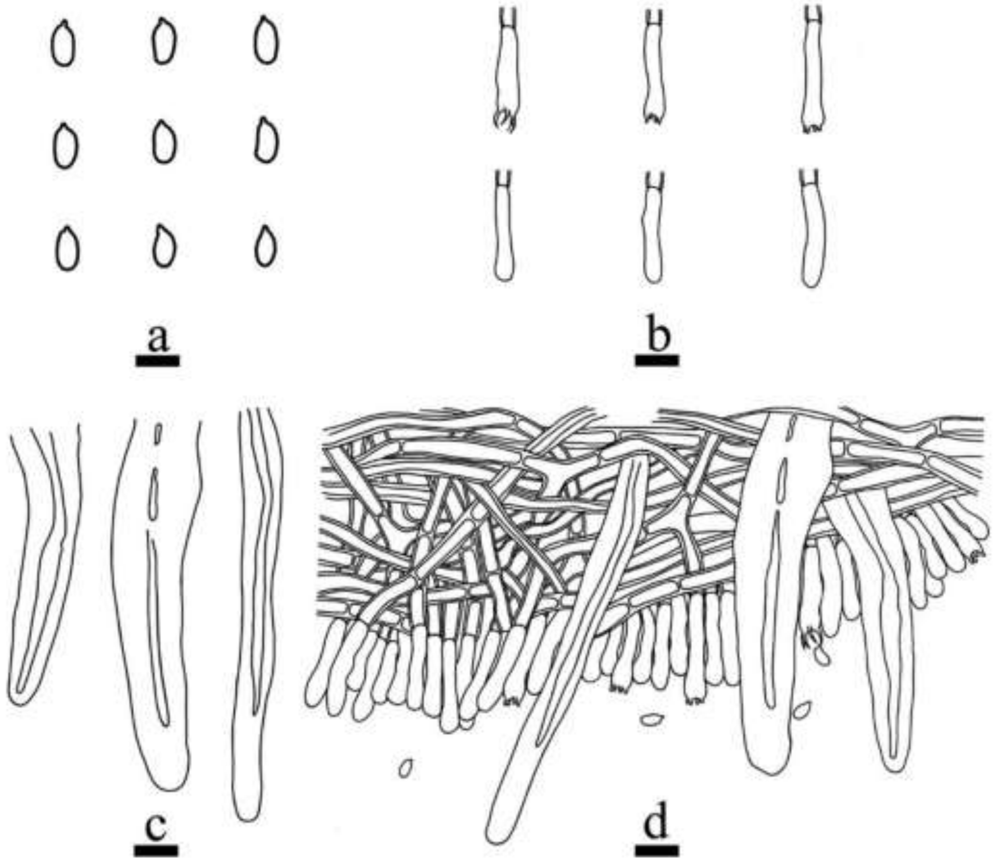

Figure 33 – Microscopic structures of *Hydnoporia pinicola* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Setae. d A section of hymenium. Scale bars: a = 5 µm, b–d = 10 µm.

Type – China, Yunnan Province, Puer, Zhenyuan County, Heping Town, Damoshan, GPS coordinates 23°07' N, 101°03' E, altitude 2150 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 16 January 2018, CLZhao 6123 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft coriaceous when fresh, becoming leathery upon drying, up to 15 cm long, 5 cm wide, 100–200 µm thick. Hymenial surface smooth, usually densely cracked with age, cinnamon to clay-buff when fresh, turning to dark brown upon drying. Sterile margin slightly brown, abrupt, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with simple septa, yellowish brown, thick-walled, occasionally branched, interwoven, 4–7.5 µm in diameter; IKI–, CB–, tissues darkening in KOH. Cystidia and cystidioles absent. Hymenial setae abundant, subulate, reddish brown, thick-walled, smooth with obtuse tip, 50–125 × 8–19 µm, projecting above the hymenium. Basidia subclavate, constricted, with 4 sterigmata and a basal simple septum, 20–24 × 3.5–5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores allantoid, colorless, thin-walled, smooth, IKI–, CB–, (5.5–)6–8.5(–9) × 1.8–2.8 µm, L = 7.13 µm, W = 2.34 µm, Q = 2.72–3.43 (n = 120/4).

Material examined (paratypes) – China, Yunnan Province, Puer, Zhenyuan County, Heping Town, Liangzizhai Village, GPS coordinates 25°01' N, 101°24' E, altitude 2500 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 15 January 2018, CLZhao 5942; Yuxi, Xinping County, Mopanshan National Forestry Park, GPS coordinates 23°51' N, 101°16' E, altitude 1700 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 18 January 2018, CLZhao 6227; Wenshan, Xichou County, Xiaoqiaogou, National Nature Reserve, GPS coordinates 23°22' N, 104°45' E, altitude 2500 m asl., 15 January 2019, CLZhao 10896 (SWFC).

Notes – *Hydnoporia yunnanensis* grouped in *Hydnoporia* (Hymenochaetaceae) based on the ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 data (Fig. 5). Based on ITS data (Fig. 6), *H. yunnanensis* forming a monophyletic lineage.

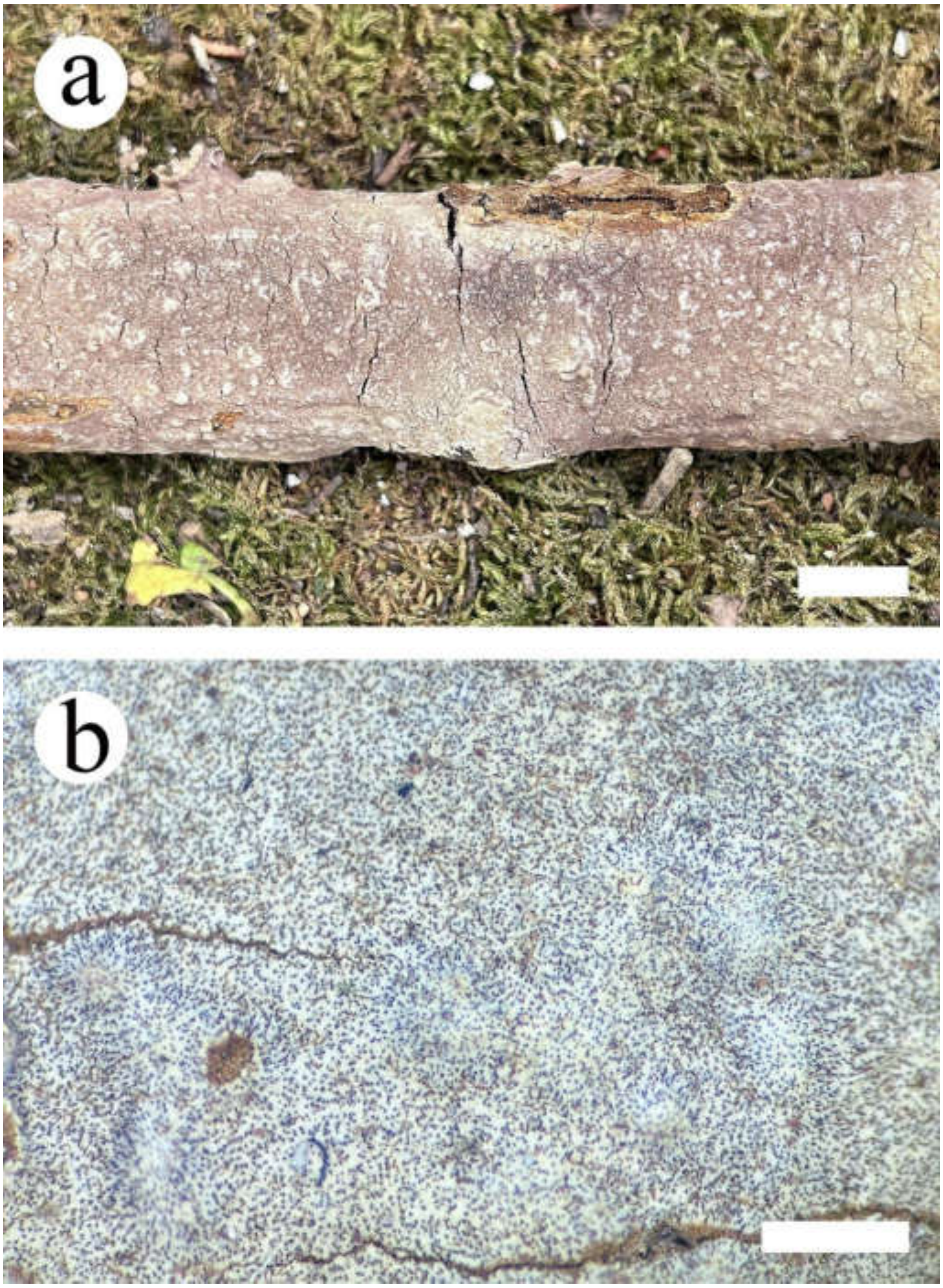

Figure 34 – Basidiomata of *Hydnoporia yunnanensis* (holotype). Scale bars: a = 1 cm, b = 1 mm.

Hydnoporia yunnanensis shares similarities with *H. latesetosa* (S.H. He & Hai J. Li) Miettinen & K.H. Larss., *H. rhododendri* (Corfixen & Parmasto) Spirin & Miettinen and *H. subrigidula* (S.H. He & Hai J. Li) Miettinen & K.H. Larss. in sharing allantoid basidiospores. However, *H. latesetosa* differs from *H. yunnanensis* by its pale mouse gray, ash-gray to fawn hymenial surface, and shorter basidia (15–20 × 3.5–4 µm, He & Li 2013); *H. rhododendri* differs from *H. yunnanensis* by its pale brown hymenial surface, and smaller basidiospores (3.9–5.2 × 1.2–1.6 µm, Miettinen et al. 2019); *H. subrigidula* differs from *H. yunnanensis* by its slightly tuberculate hymenial surface, and shorter basidia (10–20 × 2.8–4 µm, He & Li 2013).

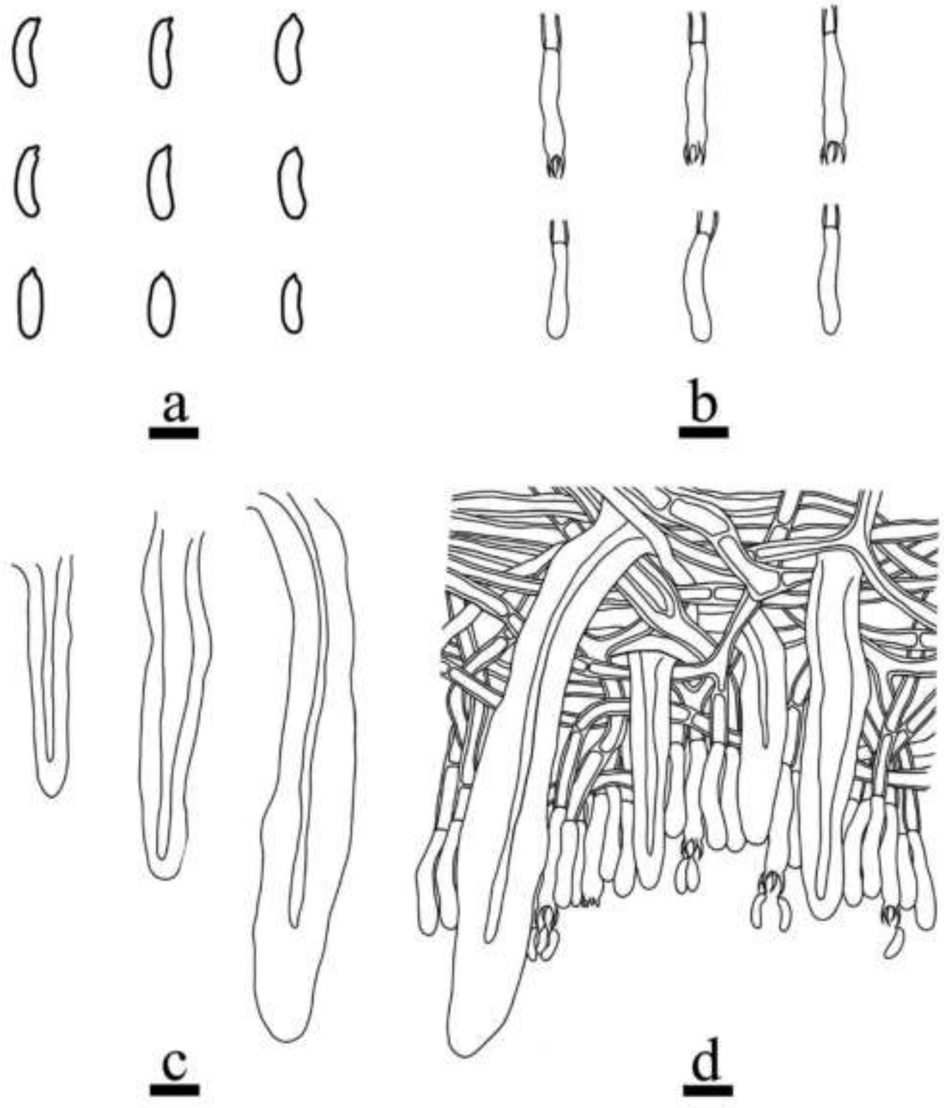

Figure 35 – Microscopic structures of *Hydnoporia yunnanensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Setae. d A section of hymenium. Scale bars: a–d = 10 µm.

Peniophorellaceae L.W. Zhou, Xue W. Wang & S.L. Liu

Index Fungorum number: IF900252; Facesoffungi number: FoF14026

Type genus – *Peniophorella* P. Karst.

Peniophorella P. Karst.

Index Fungorum number: IF18202; Facesoffungi number: FoF15404

Type species – *Peniophorella pubera* (Fr.) P. Karst.

Notes – *Peniophorella* was introduced as a monotypic genus typified by *P. pubera* (Karsten 1889). Molecular studies of *Hyphoderma* Wallr. revealed that the reinstatement of *Peniophorella* resulted in 19 new combinations in *Peniophorella* and all species nested into the hymenochaetoid clade (Larsson 2007b). Miettinen & Larsson (2011) revealed that *P. praetermissa* (P. Karst.) K.H.

Larss. and *P. tsugae* (Burt) K.H. Larss. grouped together and clustered into Hymenochaetales. Telleria et al. (2012) studied *Hyphoderma* and its discrimination from closely related taxa and revealed that eight *Peniophorella* species were closely grouped and were distinct from *Hyphoderma* s.s. Justo et al. (2017) revised the family-level classification of the order Polyporales (Basidiomycota) and proposed that 20 species were classified in *Peniophorella* located in the family Hyphodermataceae (Hymenochaetales). Morphological studies and phylogenetic analyses showed six new taxa of *Peniophorella* and displayed the taxonomic status for the new taxa within the genus (Guan et al. 2020, Xu et al. 2020a, Yurchenko et al. 2020b). Wang et al. (2023) proposed that the genus *Peniophorella* should be transferred to a new family Peniophorellaceae. In the present study, based on the ITS, nLSU and mtSSU data (Fig. 7), two new species *P. daweishanensis* and *P. olivacea* are introduced.

Peniophorella daweishanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 36, 37

Index Fungorum number: IF850322; Facesoffungi number: FoF15405

Diagnosis – Differs from other *Peniophorella* species by the soft coriaceous basidiomata with buff to slightly yellowish, reticulate hymenial surface, monomitic hyphal system with clamped generative hyphae and cylindrical to ellipsoid basidiospores measuring 8.5–10 × 4–5 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 6 June 2020, CLZhao 18600 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft coriaceous when fresh, becoming coriaceous upon drying, up to 10 cm long, 2 cm wide, 50–150 µm thick. Hymenial surface reticulate, cream when fresh, turning buff to slightly yellowish upon drying. Sterile margin cream, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, 4–5.5µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) capitate, thin-walled, smooth, tapered and obtuse apex, 52–63 × 6.5–7.5 µm, projecting above the hymenium; (2) clavate, thin-walled, smooth, 26–36 × 12.5–17 µm; cystidioles absent. Basidia subclavate, slightly constricted, with 4 sterigmata and a basal clamp connection, 31.5–38 × 7–9 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores cylindrical to ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (8–)8.5–10(–10.5) × (3.5–)4–5(–5.5) µm, L = 9.19 µm, W = 4.49 µm, Q = 2.05 (n = 30/1).

Notes – *Peniophorella daweishanensis* is grouped into *Peniophorella* based on the ITS, nLSU and mtSSU data (Fig. 7), and is revealed as a sister to *P. echinocystis* (J. Erikss. & Å. Strid) K.H. Larss. *Peniophorella echinocystis* can be delimited from *P. daweishanensis* by its odontioid hymenial surface, smaller basidia (25–30 × 6–7 µm) and wider basidiospores (9–11 × 5–6 µm, Bernicchia & Gorjón 2010).

Peniophorella daweishanensis resembles *P. pallida* (Bres.) K.H. Larss. in having a smooth hymenial surface. However, *P. pallida* differs from *P. daweishanensis* due to its pale brownish to reddish brown hymenial surface, smaller basidia (20–25 × 5–6 µm) and narrower basidiospores (7–10 × 2.5–3.5 µm, Bernicchia & Gorjón 2010).

Peniophorella olivacea J.H. Dong & C.L. Zhao, sp. nov. Figs 38, 39

Index Fungorum number: IF850323; Facesoffungi number: FoF15406

Diagnosis – Differs from other *Peniophorella* species by the farinaceous basidiomata with greyish olivaceous, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 6.5–7.5 × 3.2–4.5 µm.

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

Type – China, Yunnan Province, Qujing, Qilin District, Cuishan Forest Park, GPS coordinates 25°32' N, 103°42' E, altitude 2250 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 27 October 2022, CLZhao 25896 (SWFC).

Description – Basidiomata annual, resupinate, adnate, without odor or taste, ceraceous when fresh, becoming farinaceous upon drying, up to 10 cm long, 2.5 cm wide, 50–100 µm thick. Hymenial surface smooth, grey when fresh, turning to greyish olivaceous upon drying. Sterile margin grey, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, 3.5–4.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) fusiform, thin to thick-walled, smooth, 28.5–39 × 8.5–11 µm; (2) halocystidia, thin-walled, smooth, 42–50 × 8–9 µm, projecting above the hymenium; cystidioles absent.

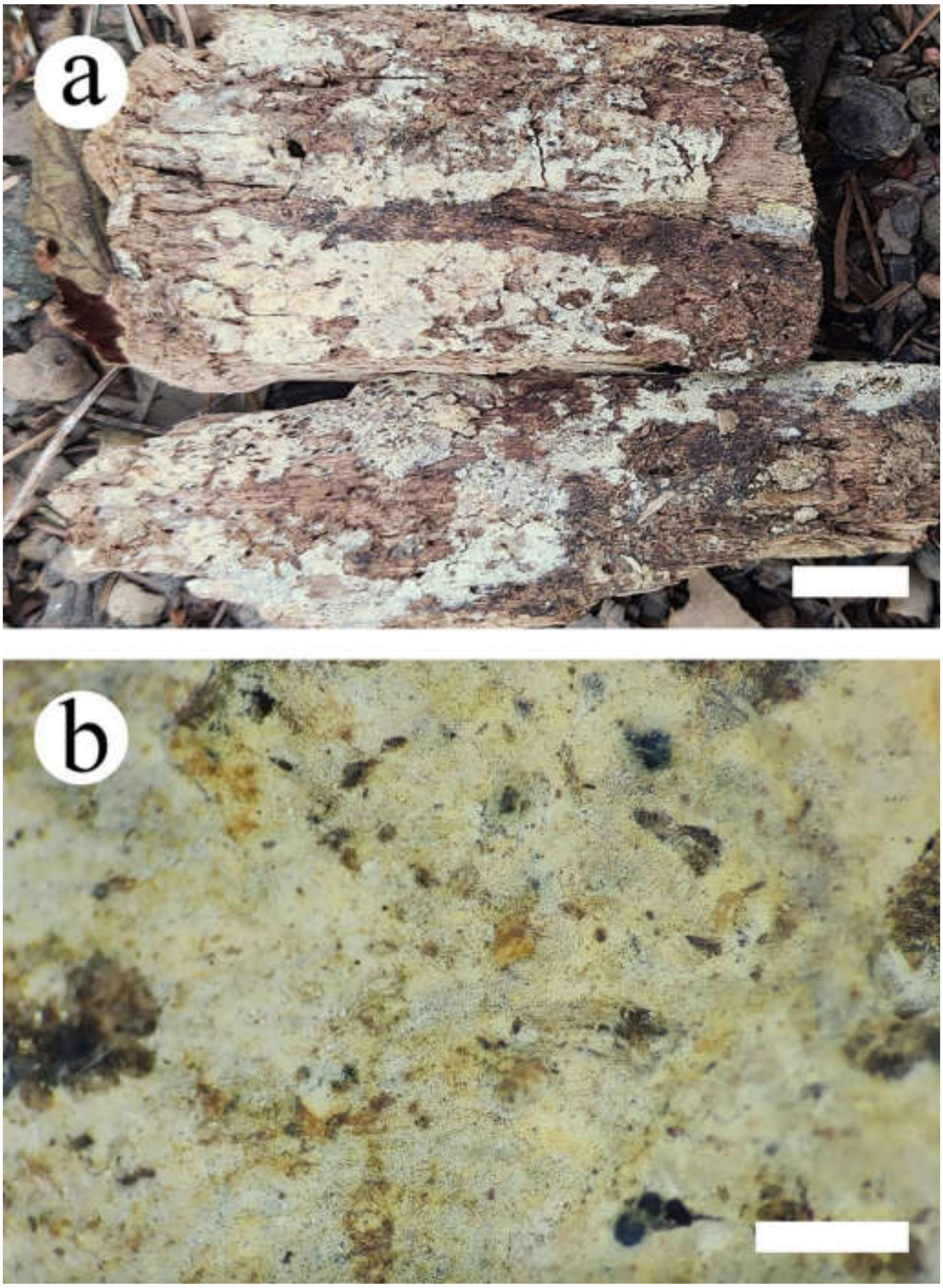

Figure 36 – Basidiomata of *Peniophorella daweishanensis* (holotype). Scale bars: a = 1 cm, b = 1 mm.

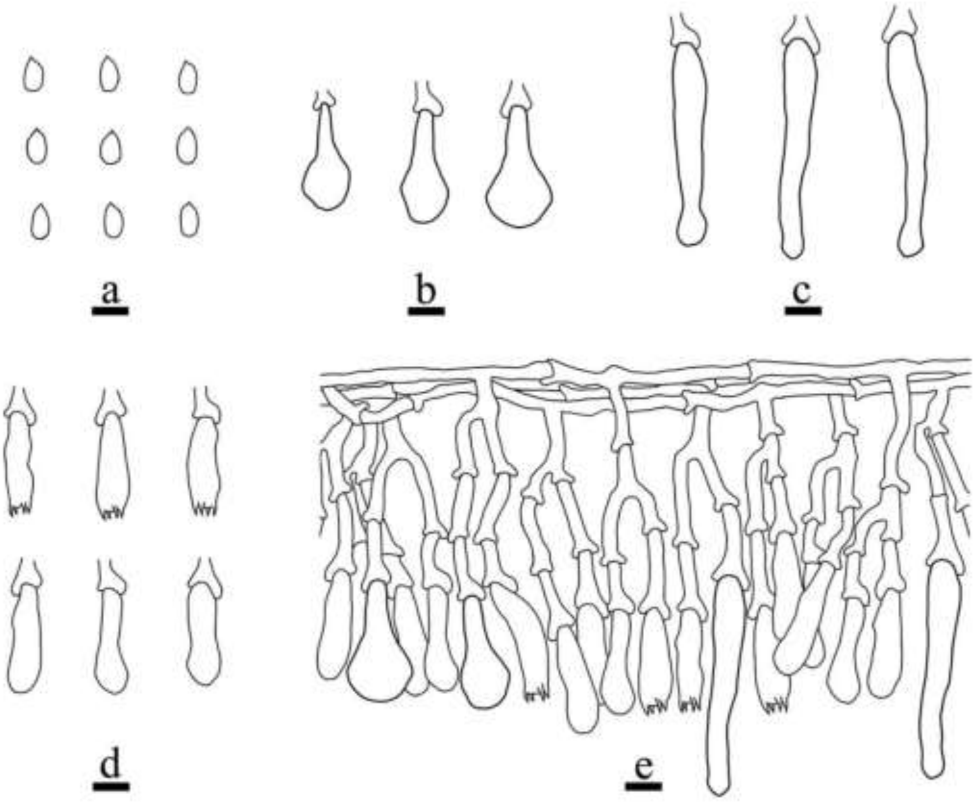

Figure 37 – Microscopic structures of *Peniophorella daweishanensis* (drawn from the holotype). a Basidiospores. b Clavate cystidia. c Capitate cystidia. d Basidia and basidioles. e A section of hymenium. Scale bars: a–e = 10 µm.

Basidia clavate, some with guttula, with 4 sterigmata and a basal clamp connection, 17.5–20 × 6–7 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, sometimes with one guttula, IKI–, CB–, (6–)6.5–7.5(–8) × 3.2–4.5(–5) µm, L = 6.94 µm, W = 3.84 µm, Q = 1.81 (n = 30/1).

Material examined (paratype) – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 25°52' N, 97°38' E, altitude 1000 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 19 July 2023, CLZhao 30245 (SWFC).

Notes – Based on the ITS, nLSU and mtSSU data (Fig. 7), the new species *Peniophorella olivacea* is grouped with *Peniophorella* species and is revealed as a sister to *P. subpraetermissa* (Sheng H. Wu) K.H. Larss. *Peniophorella subpraetermissa* can be delimited from *P. olivacea* by its cream-colored to slightly purplish hymenial surface, and longer basidia (20–35 × 6–8 µm, Wu 1997).

Peniophorella olivacea resembles *P. yunnanensis* C.L. Zhao in having ellipsoid basidiospores. However, *P. yunnanensis* differs from *P. olivacea* due to its grandinioid hymenial surface, and larger basidiospores (8–9 × 4.5–5.5 µm, Guan et al. 2020).

Schizoporaceae Jülich

Index Fungorum number: IF80038; Facesoffungi number: FoF15407

Type genus – *Schizopora* Velen.

Lyomyces P. Karst.

Index Fungorum number: IF18000; Facesoffungi number: FoF15408

Type species – *Lyomyces sambuci* (Pers.) P. Karst.

Notes – The genus *Lyomyces* P. Karst. was introduced by Karsten (1881) and is typified by *L. sambuci* (Pers.) P. Karst. Six well-distinguished clades viz the *Lagarobasidium* clade, *Kneiffiella*-*Alutaceodontia* clade, *Hyphodontia* clade, *Hastodontia* clade, *Xylodon*-*Lyomyces*, *Rogersella* clade, and *Xylodon*-*Schizopora*-*Palifer* clade, were included based on the phylogenetical studies of *Hyphodontia* s.l., in which the genera *Xylodon* and *Lyomyces* nested within the *Xylodon*-*Lyomyces*-*Rogersella* clade and *Xylodon*-*Schizopora*-*Palifer* clade, respectively (Yurchenko & Wu 2016). Riebesehl & Langer (2017) revealed that *Hyphodontia* s.l. was divided into six genera, viz., *Hastodontia* (Parmasto) Hjortstam & Ryvarden, *Hyphodontia* J. Erikss, *Kneiffiella* P. Karst, *Lagarobasidium* Jülich, *Lyomyces*, and *Xylodon*, in which 35 new combinations were proposed, including 14 *Lyomyces* species. Yurchenko et al. (2017) clarified the *Lyomyces sambuci* complex based on analysis of ITS+nLSU sequences, and described four new species. Riebesehl et al. (2019) clarified the generic concept and their phylogenetic reconstruction of *Lyomyces*, in which *L. sambuci* was sister to *L. crustosus* (Pers.) P. Karst. Chen & Zhao (2020) utilized morphological and molecular evidence and indicated that four new resupinate species clustered into the genus *Lyomyces*. Based on a combination of morphological and molecular

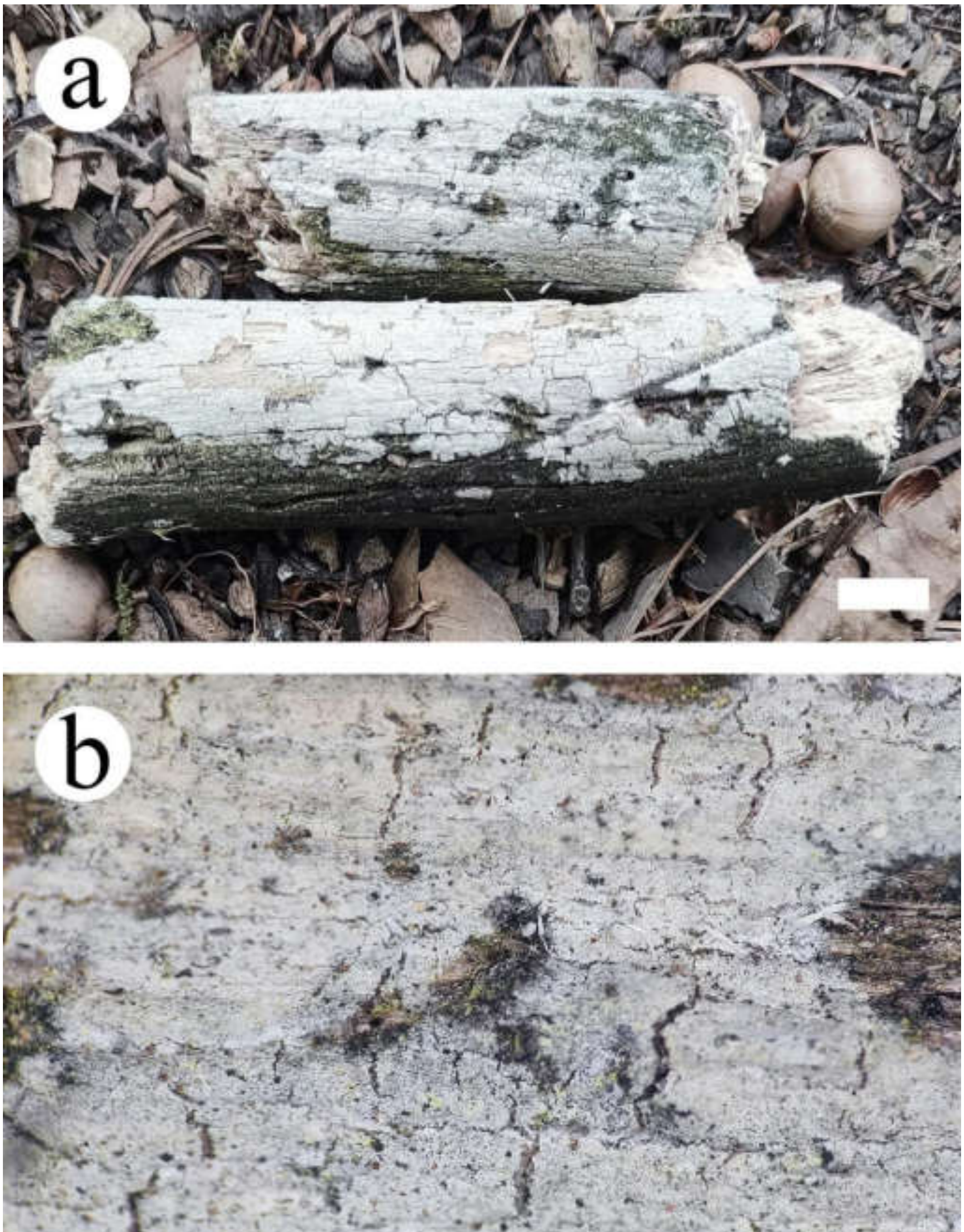

Figure 38 – Basidiomata of *Peniophorella olivacea* (holotype). Scale bars: a = 1 cm, b = 1 mm.

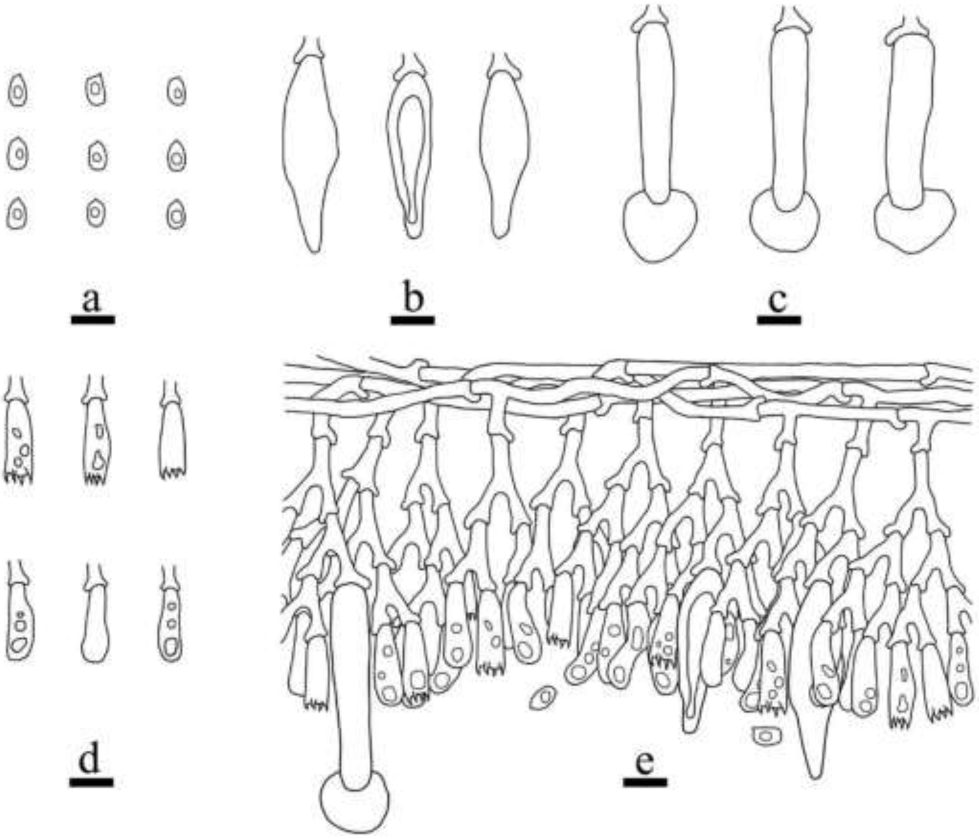

Figure 39 – Microscopic structures of *Peniophorella olivacea* (drawn from the holotype). a Basidiospores. b Fusiform cystidia. c Halocystidia cystidia. d Basidia and basidioles. e A section of hymenium. Scale bars: a–e = 10 µm.

evidence, the wood-inhabiting Fungal Diversity within the family Schizoporaceae of the order Hymenochaetales were analyzed, including *Lyomyces fissuratus* C.L. Zhao, *L. fumosus* C.L. Zhao, *L. niveus* C.L. Zhao and *L. ochraceoalbus* C.L. Zhao (Luo et al. 2021b, c). The morphological and molecular studies of Schizoporaceae, in which five new species were described, including *L. albopulverulentus* C.L. Zhao and *L. yunnanensis* C.L. Zhao (Guan et al. 2023). In the present study, based on the ITS+nLSU data (Fig. 8), *Loymyces* were grouped with several genera as *Fasciodontia*, *Hyphodontia*, *Kneiffielle* and *Xylodon*, in which six new species *L. daweishanensis*, *L. incanus*, *L. lincangensis*, *L. luteoalbus*, *L. qujingensis* and *L. sinensis* spp. nov. are grouped into the genus *Lyomyces*.

Lyomyces daweishanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 40, 41

Index Fungorum number: IF850324; Facesoffungi number: FoF15409

Diagnosis – Differs from other *Lyomyces* species by the farinaceous basidiomata with white to cream, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid to subglobose basidiospores measuring 9–11.5 × 6–7.5 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 3 August 2019, CLZhao 18344 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, farinaceous when fresh and drying, without odor or taste when fresh, up to 5 cm long, 1.5 cm wide, 50–150 µm thick. Hymenial surface smooth, pruinose, white when fresh, turning white to cream upon drying. Sterile margin thin, white, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 2.5–4.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH, subhymenial hyphae densely covered by the crystals. Cystidia of two types: (1) clavate, colorless, thin-walled, 11–18 × 7–8.5 µm; (2) capitate, colorless, thin-walled, smooth, slightly constricted at the neck, with a globose tip, 19–22.5 × 4–6.5 µm; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 21.5–36.5 × 6.5–8.5 µm. Numerous crystals present among hymenium. Basidiospores ellipsoid to subglobose, colorless, thin-walled, smooth, IKI–, CB–, (8.5–)9–11.5(–11.8) × 6–7.5 µm, L = 10.48 µm, W = 6.64 µm, Q = 1.57 (n = 30/1).

Material examined (paratypes) – China, Yunnan Province, Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 25°52' N, 97°38' E, altitude 1000 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 19 July 2023, CLZhao 30846 (SWFC).

Figure 40 – Basidiomata of *Lyomyces daweishanensis* (holotype). Scale bars: a = 2 cm, b = 2 mm.

Notes – Based on the ITS+nLSU data (Fig. 8), the new species *Lyomyces daweishanensis* is grouped with *Lyomyces* species, and is revealed as a sister to *L. allantosporus* Riebesehl, Yurch. & Langer. *Lyomyces allantosporus* can be distinguished from *L. daweishanensis* by its grandinioid hymenial surface, smaller basidia (12.5–15.5 × 5–5.5 µm) and smaller basidiospores (7–9 × 3–3.8 µm, Yurchenko et al. 2017).

Lyomyces daweishanensis resembles *L. albopulverulentus*, *L. fumosus*, *L. niveus*, *L. ochraceoalbus* and *L. denudatus* Viner in having a smooth hymenial surface. However, *L. albopulverulentus* differs from *L. daweishanensis* due to its brittle basidiomata, and its longer capitate cystidia (37–54 × 5–9 µm, Guan et al. 2023); *L. denudatus* differs from *L. daweishanensis* by its effuse-reflexed basidiomata, both smaller basidia (15–21.1 × 3.8–5.5 µm) and basidiospores (4.8–7 × 2.8–4.2 µm, Viner & Miettinen 2022); *L. fumosus* differs from *L. daweishanensis* due to its smoky grey hymenial surface, both smaller basidia (11.5–17.5 × 3–5 µm) and basidiospores (3.8–6.2 × 3.3–5.4 µm, Luo et al. 2021b); *L. niveus* distinguish from *L. daweishanensis* in its subcoriaceous basidiomata, both smaller basidia (9.5–15 × 3.5–5.5 µm) and basidiospores (3.5–5 × 3–4 µm, Luo et al. 2021c). *Lyomyces ochraceoalbus* differs from *L. daweishanensis* by its pale ochraceous hymenial surface, both smaller basidia (11–16.5 × 3.5–5 µm) and basidiospores (4–5 × 2.5–3.5 µm, Luo et al. 2021c).

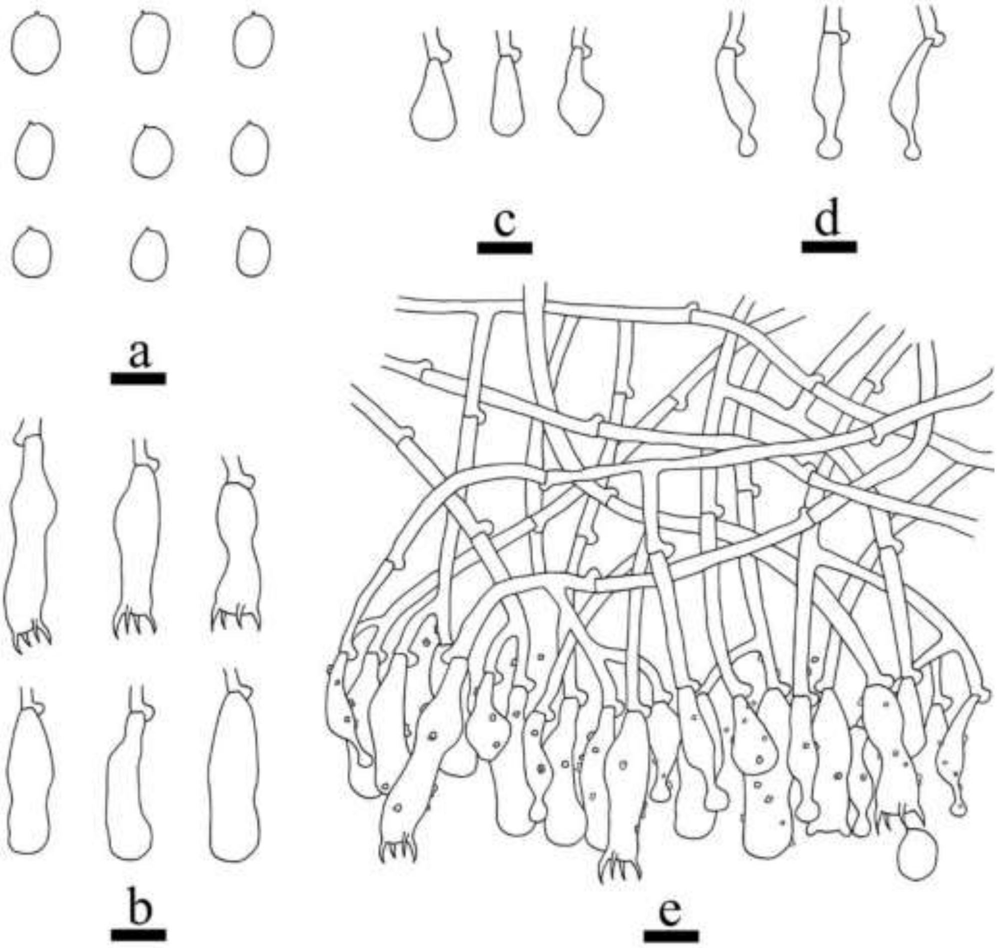

Figure 41 – Microscopic structures of *Lyomyces daweishanensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Clavate cystidia. d Capitate cystidia. e A section of hymenium. Scale bars: a–e = 10 µm.

Lyomyces incanus J.H. Dong & C.L. Zhao, sp. nov. Figs 42, 43

Index Fungorum number: IF850325; Facesoffungi number: FoF15410

Diagnosis – Differs from other *Lyomyces* species by the furfuraceous basidiomata with incanus, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 5–6.5 × 4–5 µm.

Etymology – *incanus* (Lat.): referring to the incanus hymenophore surface of the type specimen.

Type – China, Yunnan Province, Lincang, Fengqing County, Yaojie Town, Xingyuan Village, GPS coordinates 24°58' N, 99°92' E, altitude 1600 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 20 July 2022, CLZhao 22900 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, pruinose when fresh, becoming furfuraceous upon drying, without odor or taste when fresh, up to 4 cm long, 0.6 cm wide, 50–100 µm thick. Hymenial surface smooth, white to incanus when fresh, turning incanus upon drying. Sterile margin indistinct, slightly incanus, thinning out, up to 0.5 mm wide.

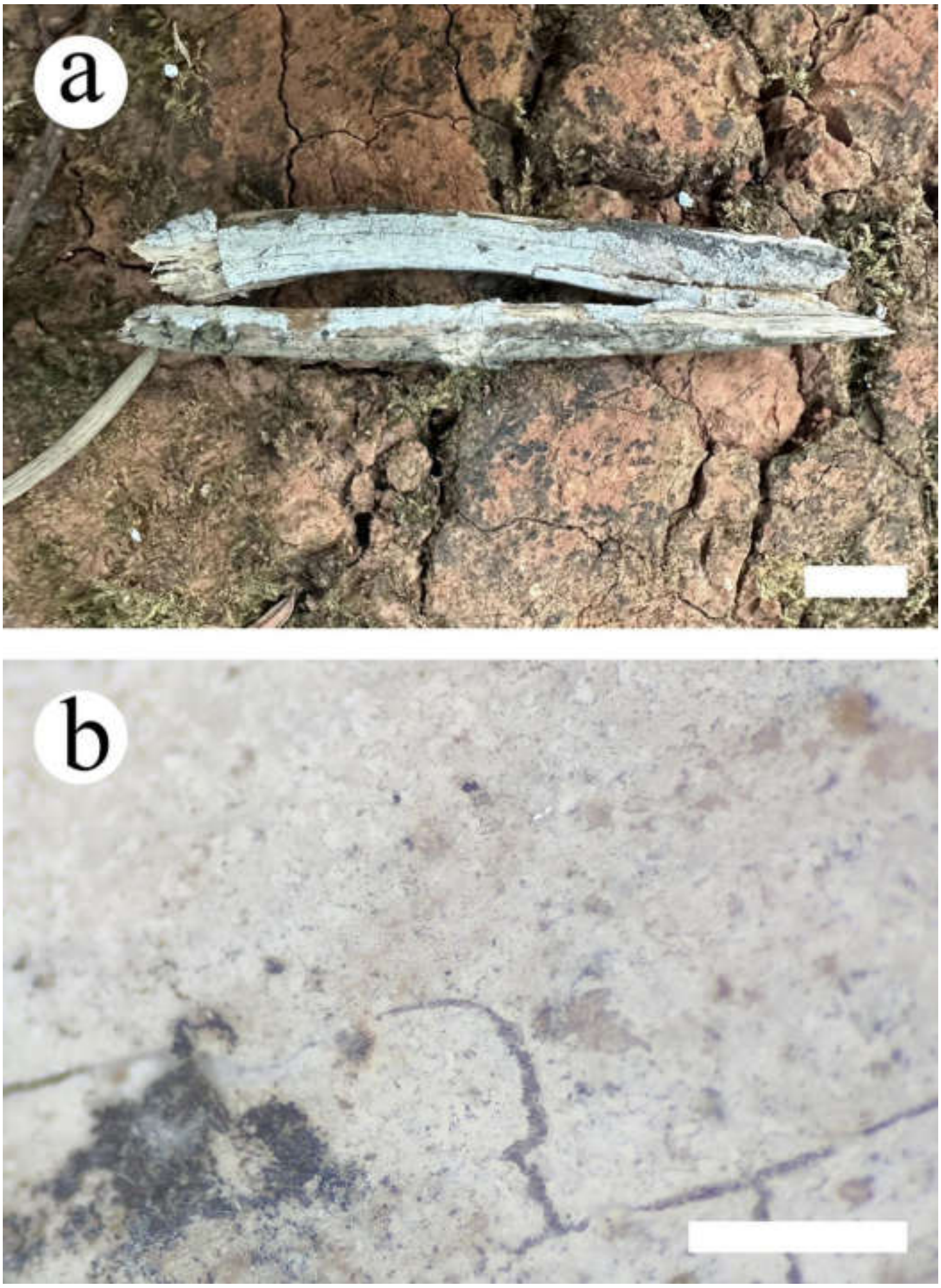

Figure 42 – Basidiomata of *Lyomyces incanus* (holotype). Scale bars: a = 1 cm, b = 1 mm.

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 of two types: (1) Subcylindrical, colorless, thin-walled, 14–26 × 2–3 µm; (2) subclavate, colorless, thin-walled, smooth, 17–22 × 4.5–7 µm; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 12–20.5 × 4–5 µm. Subhymenial hyphae densely covered by crystals. Basidiospores ellipsoid, colorless, thin-walled, smooth, with drop, IKI–, CB–, 5–6.5(–7) × 4–5 µm, L = 5.89 µm, W = 4.45 µm, Q = 1.18–1.32 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Lincang, Fengqing County, Yaojie Town, Xingyuan Village, GPS coordinates 24°58' N, 99°92' E, altitude 1600 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 20 July 2022, CLZhao 22813 (SWFC).

Notes – Based on ITS+nLSU data (Fig. 8), *Lyomyces incanus* grouped with *Lyomyces* species, where it formed a monophyletic lineage.

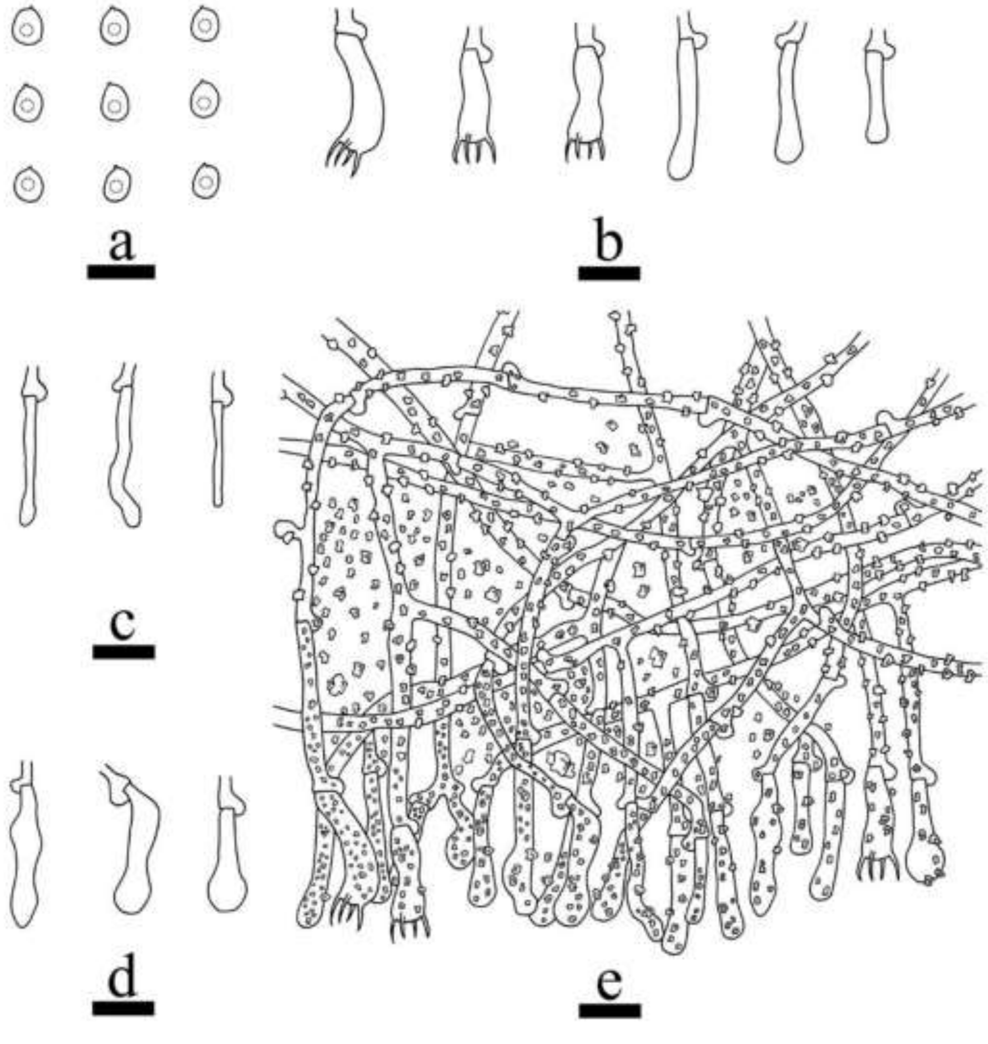

Figure 43 – Microscopic structures of *Lyomyces incanus* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Subcylindrical cystidia. d Subclavate cystidia. e A section of hymenium. Scale bars: a–e = 10 µm.

Lyomyces incanus resembles *L. capitatocystidiatus* (H.X. Xiong, Y.C. Dai & Sheng H. Wu) Riebesehl & Langer, *L. fimbriatus* (Sheng H. Wu) Riebesehl & Yurchenko, *L. mascarensis* Riebesehl, Yurchenko & E. Langer, *L. organensis* Yurchenko & Riebesehl and *L. sambuci* in having ellipsoid basidiospores. However, *L. capitatocystidiatus* differs from *L. incanus* due to its grandinioid hymenial surface, and suburniform basidia (14–23 × 4–5 µm, Xiong et al. 2009); *L. fimbriatus* differs from *L. incanus* by its grandinioid hymenial surface, and utriform to subutriform basidia (16–22 × 3.8–4.5 µm, Wu 1990); *L. mascarensis* can be distinguished from *L. incanus* in its tuberculate hymenial surface, and narrower basidiospores (4.5–6 × 3.3–4 µm, Yurchenko et al. 2017); *L. organensis* differs from *L. incanus* by its warted hymenial surface, smaller basidia (11–12.5 × 3.5–4 µm) and narrower basidiospores (5–6 × 2.5–3.5 µm, Yurchenko et al. 2017); *L. sambuci* differs from *L. incanus* in its tuberculate hymenial surface, and narrower basidiospores (4.5–6 × 3.5–4 µm, Bernicchia & Gorjón 2010).

Lyomyces lincangensis J.H. Dong & C.L. Zhao, sp. nov. Figs 44, 45

Index Fungorum number: IF850326; Facesoffungi number: FoF15411

Diagnosis – Differs from other *Lyomyces* species by the coriaceous basidiomata with cream to buff, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 4.5–6.5 × 3.5–5 µm.

Etymology – *lincangensis* (Lat.): referring to the locality (Lincang) of the type specimen.

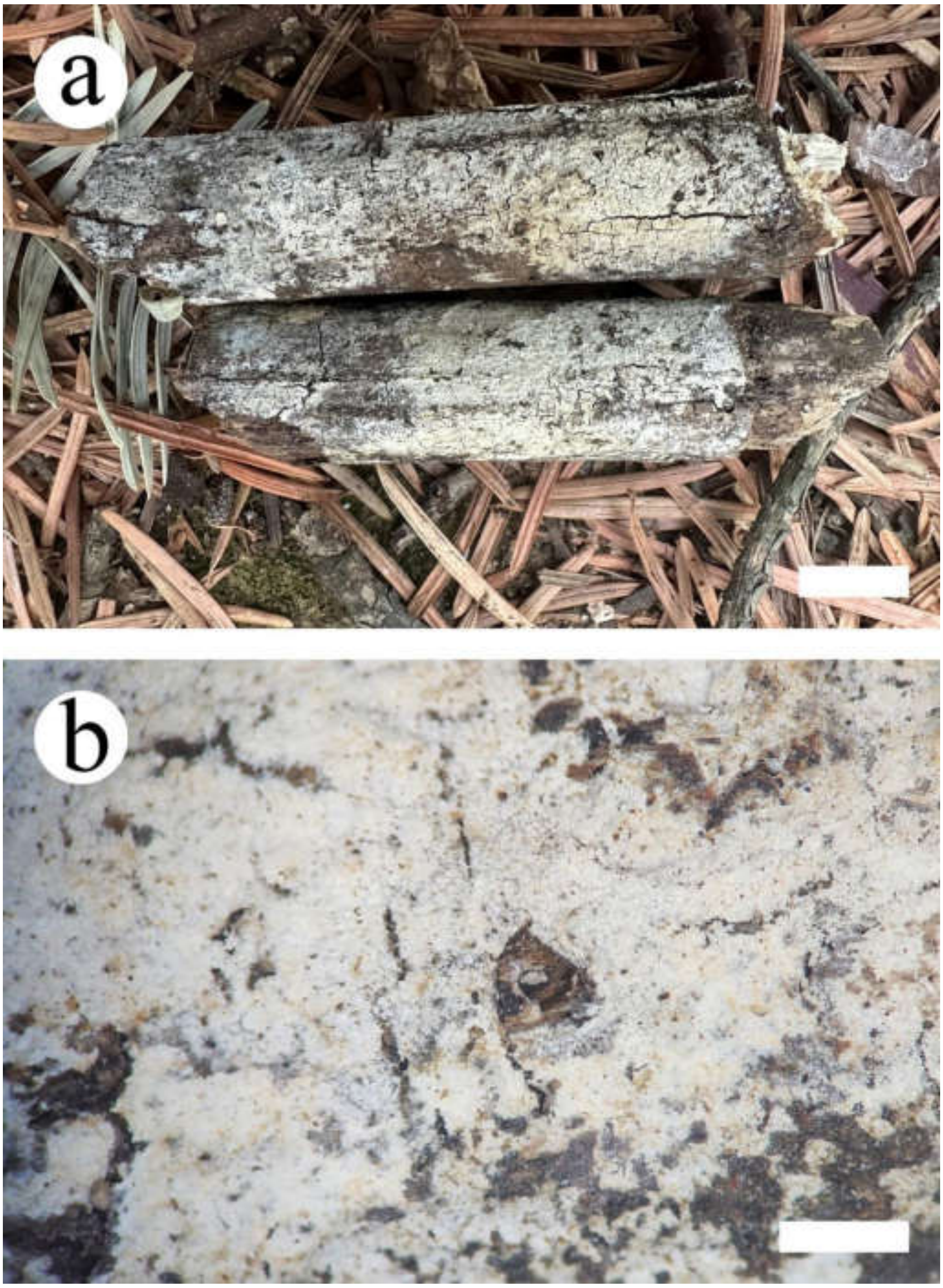

Figure 44 – Basidiomata of *Lyomyces lincangensis* (holotype). Scale bars: a = 1 cm, b = 2 mm.

Type – China, Yunnan Province, Lingcang, Lancangjiang Forestry Region, GPS coordinates 23°48' N, 100°05' E, altitude 2900 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 21 July 2022, CLZhao 22966 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, coriaceous when fresh, becoming hard coriaceous upon drying, without odor or taste when fresh, up to 7.5 cm long, 3cm wide, 100–150 µm thick. Hymenial surface smooth, cream when fresh, tunning cream to buff when drying. Sterile margin indistinct, white, thinning out, up to 3 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 1.5–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) capitate, colorless, thin-walled, smooth, slightly constricted at the neck, 25.5–32.5 × 4.5–6 µm; (2) fusiform, colorless, thin-walled, smooth, 26–35 × 2–3 µm; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 18–20 × 4.5–6.5 µm. Numerous crystals present among hymenium. Basidiospores ellipsoid, colorless, thin-walled, smooth, with a droplet inside, IKI–, CB–, 4.5–6.5(–7) × 3.5–5 µm, L = 5.74 µm, W = 4.43 µm, Q = 1.29 (n = 30/1).

Notes – The new species *Lyomyces lincangensis* is grouped within *Lyomyces* based on the ITS+nLSU data (Fig. 8), and is identified as a sister to *L. bambusinus*. *Lyomyces bambusinus* differs from *L. lincangensis* by its colliculose to tuberculate hymenial surface, and its longer capitate cystidia (35–55 × 4–7 µm, Chen & Zhao 2020).

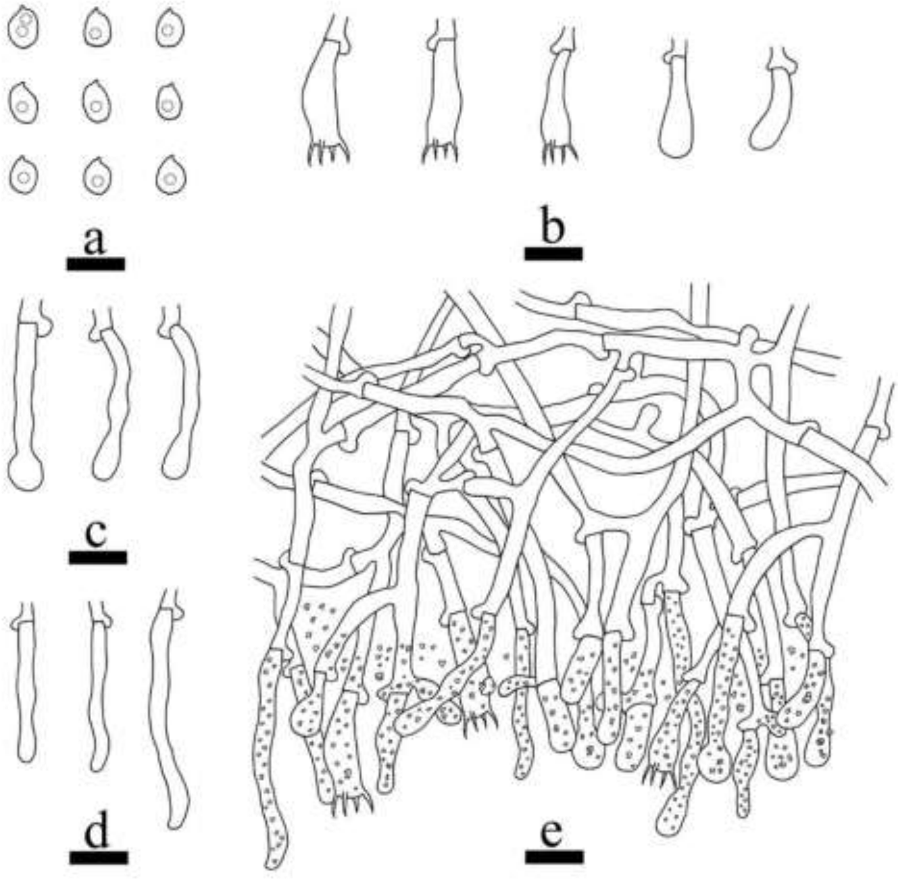

Figure 45 – Microscopic structures of *Lyomyces lincangensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Capitate cystidia. d Fusiform cystidia. e A section of hymenium. Scale bars: a–e = 10 µm.

Lyomyces lincangensis resembles, *L. albopulverulentus*, *L. cremeus* C.L. Zhao, *L. mascarensis*, *L. orientalis* Riebesehl, Yurch. & Langer, and *L. wuliangshanensis* C.L. Zhao have capitate cystidia and ellipsoid basidiospores. However, *L. albopulverulentus* differs from

L. lincangensis due to its white hymenial surface, larger basidia (24.5–28.5 × 7–9 µm) and basidiospores (8–10.5 × 5.5–7 µm, Guan et al. 2023); *L. cremeus* differs from *L. lincangensis* by its pale cream hymenial surface, and shorter basidia (9–18.5 × 3–6 µm, Chen & Zhao 2020); *L. mascarensis* differs from *L. lincangensis* by its tuberculate hymenial surface, and smaller basidia (16–17.5 × 3.5–4.5 µm, Yurchenko et al. 2017); *L. orientalis* differs from *L. lincangensis* by its tuberculate hymenial surface, shorter capitate cystidia (13–20 × 3–5 µm) and narrower basidia (13–20 × 3.5–4.5 µm, Yurchenko et al. 2017); *L. wuliangshanensis* can be distinguished from *L. lincangensis* by its tuberculate hymenial surface, narrower basidia (12–20 × 3–4.3 µm) and thick-walled basidiospores (3.5–5.3 × 2.8–4 µm, Chen & Zhao 2020).

Lyomyces luteoalbus J.H. Dong & C.L. Zhao, sp. nov. Figs 46, 47

Index Fungorum number: IF850327; Facesoffungi number: FoF15412

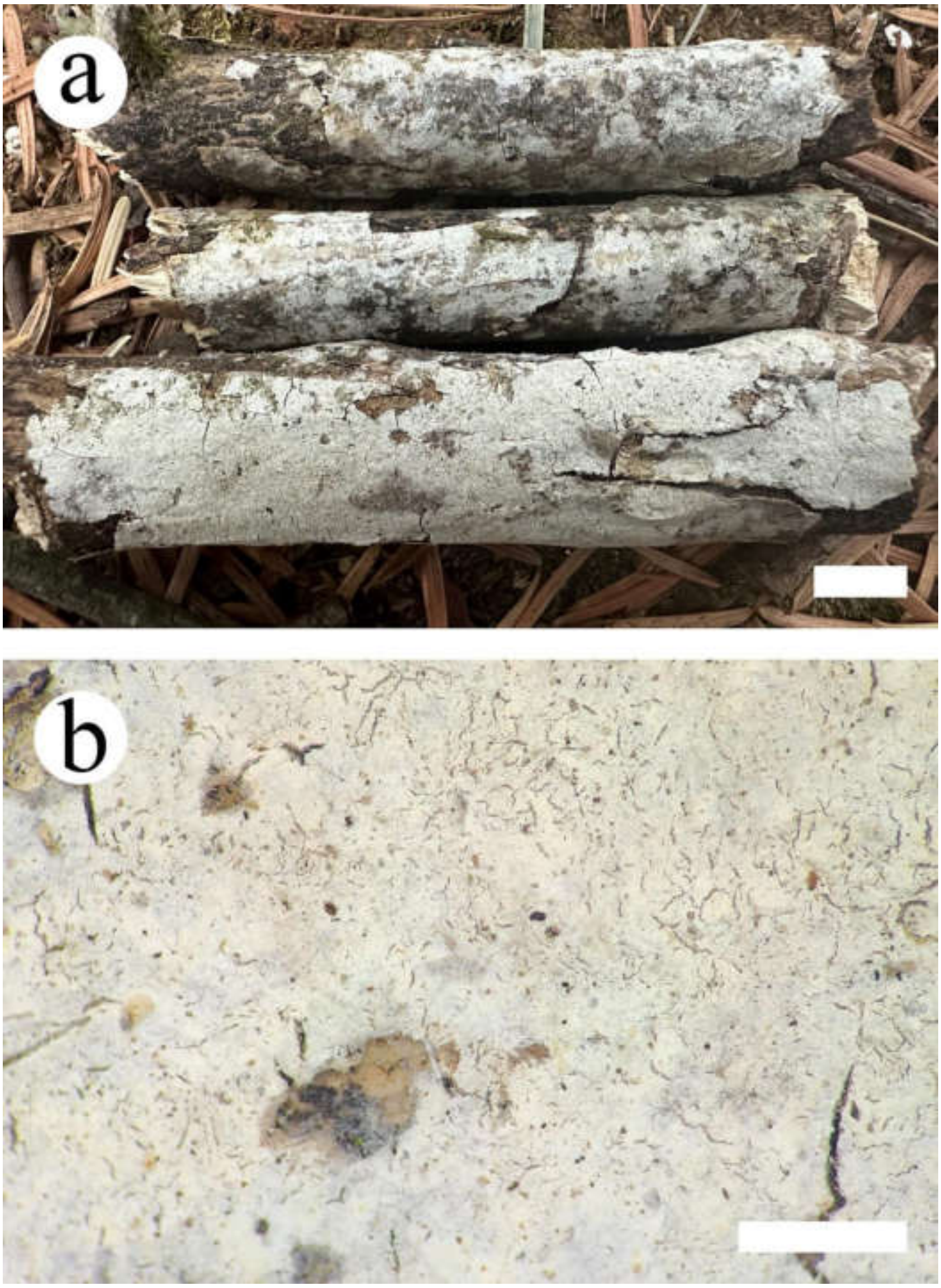

Figure 46 – Basidiomata of *Lyomyces luteoalbus* (holotype). Scale bars: a = 2 cm, b = 2 mm.

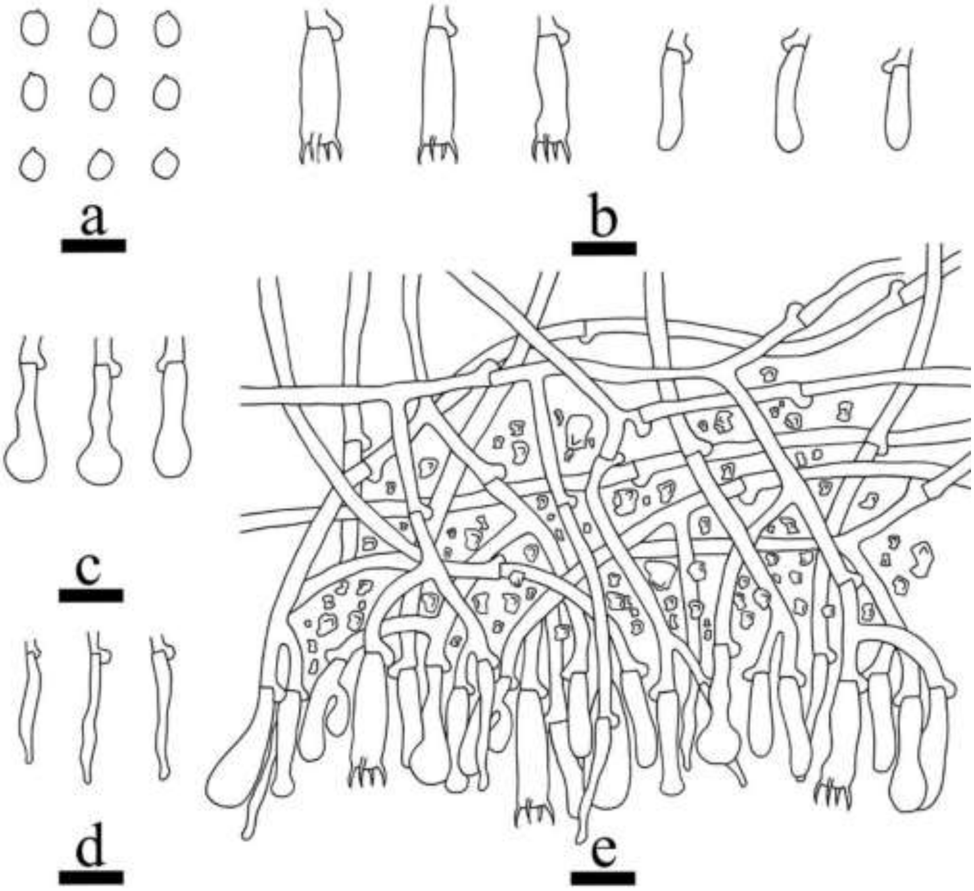

Figure 47 – Microscopic structures of *Lyomyces luteoalbus* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Capitate cystidia. d Tapering cystidia. e A section of hymenium. Scale bars: a–e = 10 µm.

Diagnosis – Differs from other *Lyomyces* species by the membranaceous basidiomata with white to buff, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 4.5–6.5 × 3–4.5 µm.

Etymology – *luteoalbus* (Lat.): referring to the white to buff hymenophore of the type specimen.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 3 August 2019, CLZhao 18347 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, soft membranaceous when fresh, becoming membranaceous upon drying, without odor or taste when fresh, up to 9 cm long, 3 cm wide, 100–150 µm thick. Hymenial surface smooth, cracked, white when fresh, turning white to buff when drying. Sterile margin indistinct, white, abrupt, up to 1 mm wide.

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 of two types: (1) capitate, colorless, thin-walled, smooth, slightly constricted at the neck, 17–21.5 × 4–7.5 µm; (2) tapering, colorless, thin-walled, 12–17 × 2–3.5 µm; cystidioles absent. Subhymenial hyphae densely covered by crystals. Basidia cylindrical to clavate, with 4 sterigmata and a basal clamp connection, 15–18.5 × 3.5–6 µm. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, 4.5–6.5(–7.4) × 3–4.5 µm, L = 5.46 µm, W = 3.81 µm, Q = 1.26–1.43 (n = 60/2).

Material examined (paratypes) – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 3 August 2019, CLZhao 18211 (SWFC).

Notes – Based on the ITS+nLSU data (Fig. 8), the new species *Lyomyces luteoalbus* is grouped into *Lyomyces* species, revealing it is clustered with *L. niveus* and *L. yunnanensis*. However, *Lyomyces niveus* can be delimited from *L. luteoalbus* by its niveous hymenial surface, and its shorter basidia (9.5–15 × 3.5–5.5 µm, Luo et al. 2021c); *L. yunnanensis* be delimited from *L. luteoalbus* by its grandinioid hymenial surface, and its larger tapering cystidia (18–39 × 4–6 µm, Guan et al. 2023).

Lyomyces luteoalbus resembles five species as *L. bambusinus*, *L. fumosus*, *L. macrosporus*, *L. mascarensis*, *L. wuliangshanensis*, in sharing the morphological characters of the capitate cystidia and tapering cystidia. However, *L. bambusinus* differs from *L. luteoalbus* due to its colliculose to tuberculate hymenial surface, both larger capitate cystidia (35–55 × 4–7 µm) and tapering cystidia (40–65 × 4–5.5 µm, Chen & Zhao 2020); *L. fumosus* differs from *L. luteoalbus* by its smoky grey hymenial surface, and its larger tapering cystidia (18.2–50.6 × 3.8–4.5 µm, Luo et al. 2021b); *L. macrosporus* differs from *L. luteoalbus* in its reticulate hymenial surface, its longer basidia (22.2–38 × 4.5–7 µm) and larger basidiospores (6.7–8.9 × 4.4–5.4 µm, Chen & Zhao 2020); *L. mascarensis* distinguish from *L. luteoalbus* in its tuberculate hymenial surface, larger tapering cystidia (25–30 × 3.5–4.5 µm) and subcylindrical basidia (16–17.5 × 3.5–4.5 µm, Yurchenko et al. 2017); *L. wuliangshanensis* differs from *L. luteoalbus* by its tuberculate hymenial surface, longer capitate cystidia (22–37 × 3–6 µm) and larger tapering cystidia (21–35 × 4–6.5 µm, Chen & Zhao 2020).

Lyomyces qujingensis J.H. Dong & C.L. Zhao, sp. nov. Figs 48, 49

Index Fungorum number: IF850328; Facesoffungi number: FoF15413

Diagnosis – Differs from other *Lyomyces* species by the pruinose basidiomata with white, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 6.5–8.5 × 5.5–7 µm.

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

Type – China, Yunnan Province, Qujing, Zhanyi District, Dapo Town, Tuole Village, GPS coordinates 25°57' N, 103°56' E, altitude 1740 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 7 March 2023, CLZhao 27462 (SWFC, holotype).

Description – Basidiomata annual, resupinate, pruinose, without odor or taste when fresh, up to 6.8 cm long, 0.6 cm wide, 50–100 µm thick. Hymenial surface smooth, white when fresh and upon drying. Sterile margin thin, white to buff, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 2.5–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) clavate, colorless, thin-walled, smooth, 16.5–18 × 7.5–8.5 µm; (2) capitate, colorless, thin-walled, smooth, slightly constricted at the neck, with a globose tip, 40–60 × 4–7.5 µm; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 19–20.5 × 7.5–10 µm. Numerous crystals present among hymenium. Basidiospores ellipsoid, colorless, thin-walled, smooth, with drop, IKI–, CB–, (6.3–)6.5–8.5 × 5.5–7 µm, L = 7.78 µm, W = 6.31 µm, Q = 1.27 (n = 30/1).

Notes – Based on the ITS+nLSU data (Fig. 8), the new species *Lyomyces qujingensis* is grouped into *Lyomyces* species, revealing it as a sister to *L. albopulverulentus*. However, *L. albopulverulentus* can be distinguished from *L. qujingensis* by its brittle basidiomata, and longer basidia (24.5–28.5 × 7–9 µm, Guan et al. 2023).

Lyomyces qujingensis resembles *L. capitatocystidiatus*, *L. fimbriatus*, *L. mascarensis*, *L. organensis* and *L. sambuci* in sharing the ellipsoid basidiospores. However, *L. capitatocystidiatus* differs from *L. qujingensis* due to its grandinioid hymenial surface, narrower basidia (14–23 × 4–5 µm) and smaller basidiospores (4.1–5.6 × 3.5–4.3 µm, Xiong et al. 2009); *L. fimbriatus* differentiates from *L. qujingensis* by its grandinioid hymenial surface, both narrower basidia (16–22 × 3.8–4.5 µm) and basidiospores (5.7–6.7 × 3.5–4.2 µm, Wu 1990); *L. mascarensis* can be distinguished from *L. qujingensis* in its tuberculate hymenial surface, both smaller basidia (16–17.5 × 3.5–4.5 µm) and basidiospores (4.5–6 × 3.3–4 µm, Yurchenko et al. 2017);

L. organensis differs from *L. qujingensis* by its warted hymenial surface, smaller basidia (11–12.5 × 3.5–4 µm) and basidiospores (5–6 × 2.5–3.5 µm, Yurchenko et al. 2017); *L. sambuci* differentiates from *L. qujingensis* in its tuberculate hymenial surface, narrower basidia (20–30 × 4–5 µm) and smaller basidiospores (4.5–6 × 3.5–4 µm, Bernicchia & Gorjón 2010).

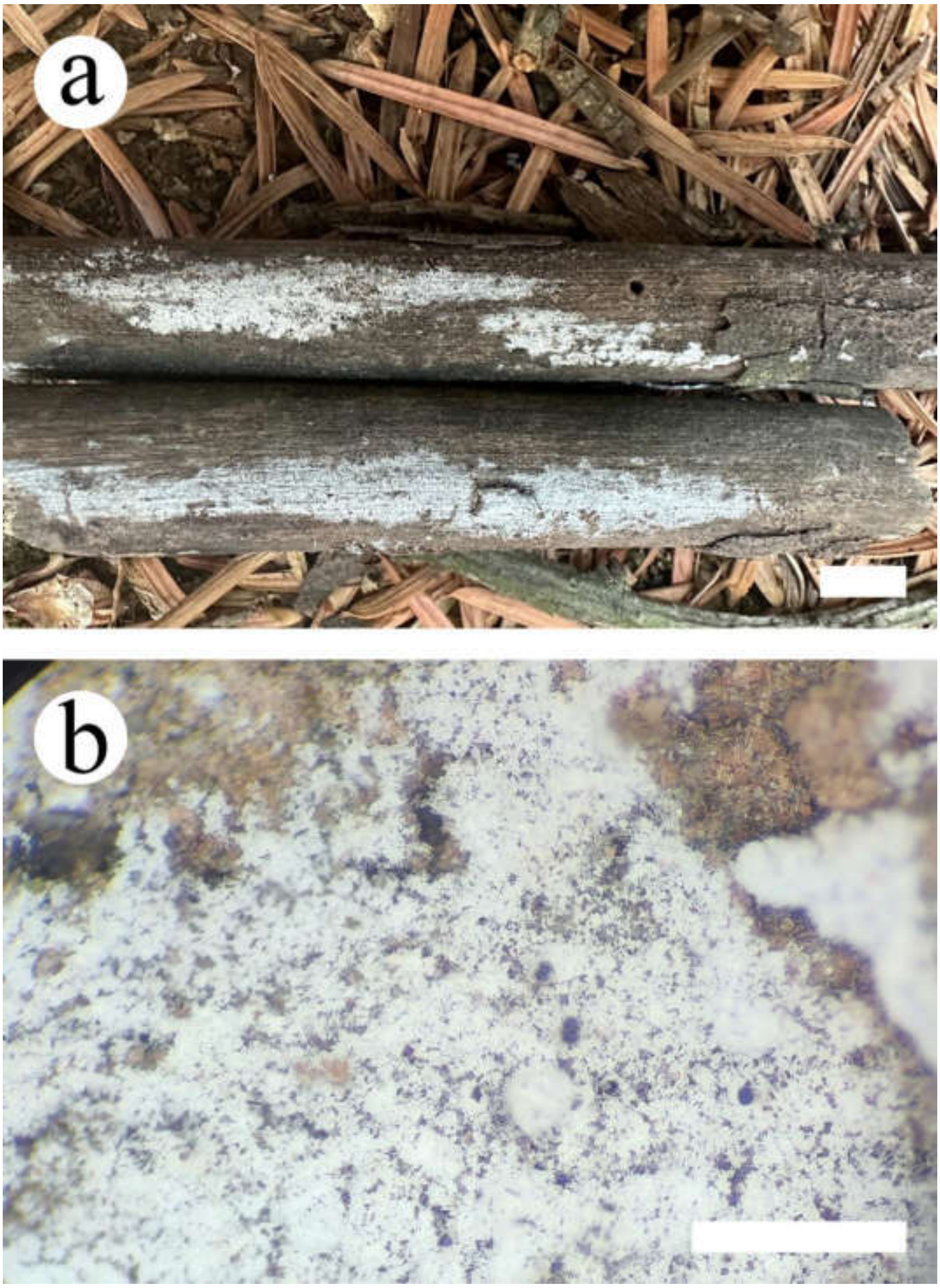

Figure 48 – Basidiomata of *Lyomyces qujingensis* (holotype). Scale bars: a = 1 cm, b = 1 mm.

Lyomyces sinensis J.H. Dong & C.L. Zhao, sp. nov. Figs 50, 51

Index Fungorum number: IF850329; Facesoffungi number: FoF15414

Diagnosis – Differs from other *Lyomyces* species by the coriaceous basidiomata with cream, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and broadly ellipsoid to ellipsoid basidiospores measuring 4.5–6 × 3.5–4.5 µm.

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

Type – China, Yunnan Province, Qujing, Zhanyi District, Yanzhu Village, GPS coordinates 25°50' N, 103°46' E, altitude 1740 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 7 March 2023, CLZhao 27391 (SWFC, holotype).

Description – Basidiomata annual, resupinate, coriaceous when fresh, becoming hard coriaceous upon drying, without odor or taste when fresh, up to 4.5 cm long, 1cm wide, 50–150 µm thick. Hymenial surface smooth, cracked, slightly cream when fresh, turning cream upon drying. Sterile margin indistinct, white to cream, slightly fimbriate, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 2–4.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) clavate, colorless, thin-walled, smooth, 17–24.5 × 4.5–6.5 µm; (2) tapering, colorless, thin-walled, 26–32 × 3.5–4.5 µm; cystidioles absent. Basidia subclavate, with 4 sterigmata and a basal clamp connection, 18.5–24.5 × 4–5.5 µm. Subhymenial hyphae densely covered by crystals. Basidiospores broadly ellipsoid to ellipsoid, colorless, thin-walled, smooth, with drop, IKI–, CB–, 4.5–6(–6.5) × 3.5–4.5(–4.8) µm, L = 5.71 µm, W = 4.23 µm, Q = 1.28–1.37 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Qujing, Zhanyi District, Dapo Town, Tuole Village, GPS coordinates25°57' N, 103°56' E, altitude 1590 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 7 March 2023, CLZhao 27464 (SWFC).

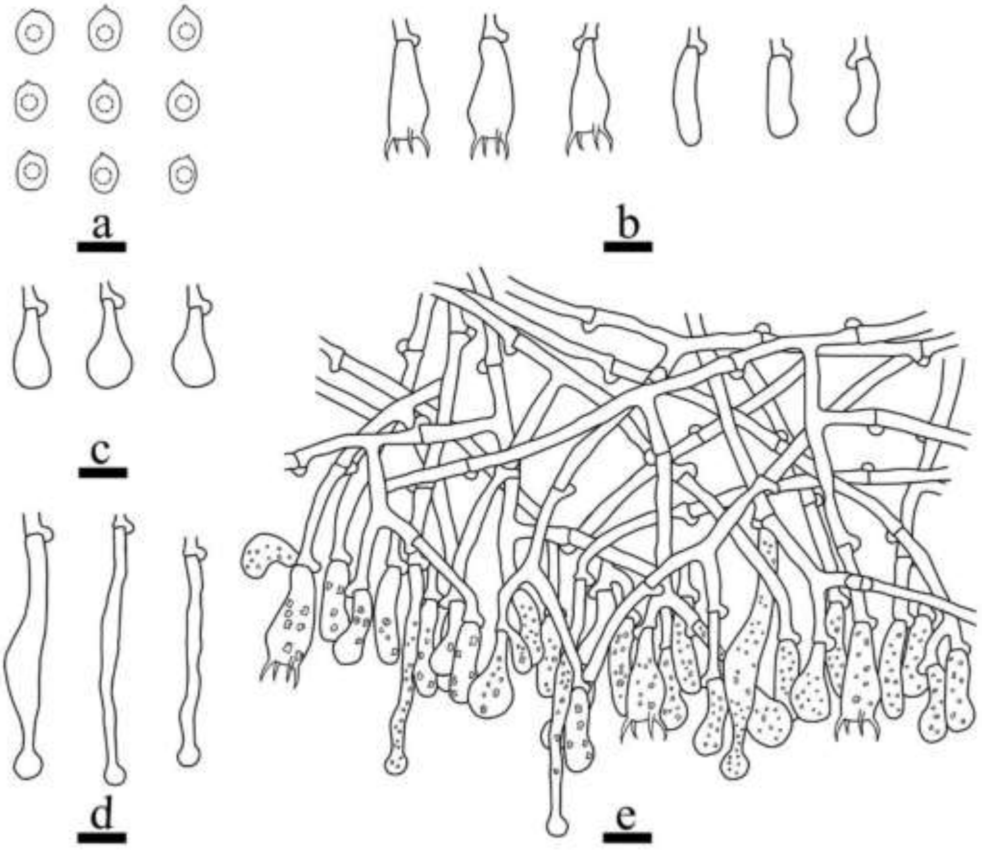

Figure 49 – Microscopic structures of *Lyomyces qujingensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Clavate cystidia. d Capitate cystidia. e A section of hymenium. Scale bars: a–e = 10 µm.

Notes – With reference to the ITS+nLSU data (Fig. 8), the new species *Lyomyces sinensis* is grouped into *Lyomyces*, and is clustered with *L. juniperi* (Bourdot & Galzin) Riebesehl & Langer, *L. ochraceoalbus* and *L. vietnamensis* (Yurchenko & Sheng H. Wu) Riebesehl & Langer. However, *L. juniperi* can be distinguished from *L. sinensis* by its grandinioid hymenial surface, and narrower basidiospores (4.5–5 × 3–3.5 µm, Hjortstam & Ryvarden 2004); *L. ochraceoalbus* can be delineated from *L. sinensis* by its pale ochraceous hymenial surface, shorter basidia (11–16.5 × 3.5–5 µm) and narrower basidiospores (4–5 × 2.5–3.5 µm, Luo et al. 2021c); *L. vietnamensis* can be distinguished from *L. sinensis* by its grandinioid hymenial surface, utriform to suburniform basidia (17–20 × 3.5–4.5 µm) and longer basidiospores (6–6.5 × 2.5–3 µm, Yurchenko et al. 2013).

Lyomyces sinensis shares similarities with *L. cremeus*, *L. fumosus*, *L. macrosporus* and *L. mascarensis* showing tapering cystidia and ellipsoid basidiospores. However, *L. cremeus* differs from *L. sinensis* by its pale cream hymenial surface, and shorter basidia (9–18.5 × 3–6 µm, Chen & Zhao 2020); *L. fumosus* differentiates from *L. sinensis* by its smoky grey hymenial surface, and shorter basidia (11.5–17.5 × 3–5 µm, Luo et al. 2021b); *L. macrosporus* can be distinguished from *L. sinensis* in its reticulate hymenial surface, and larger basidiospores (6.7–8.9 × 4.4–5.4 µm, Chen & Zhao 2020); *L. mascarensis* differs from *L. sinensis* by its tuberculate hymenial surface, and shorter basidia (16–17.5 × 3.5–4.5 µm, Yurchenko et al. 2017).

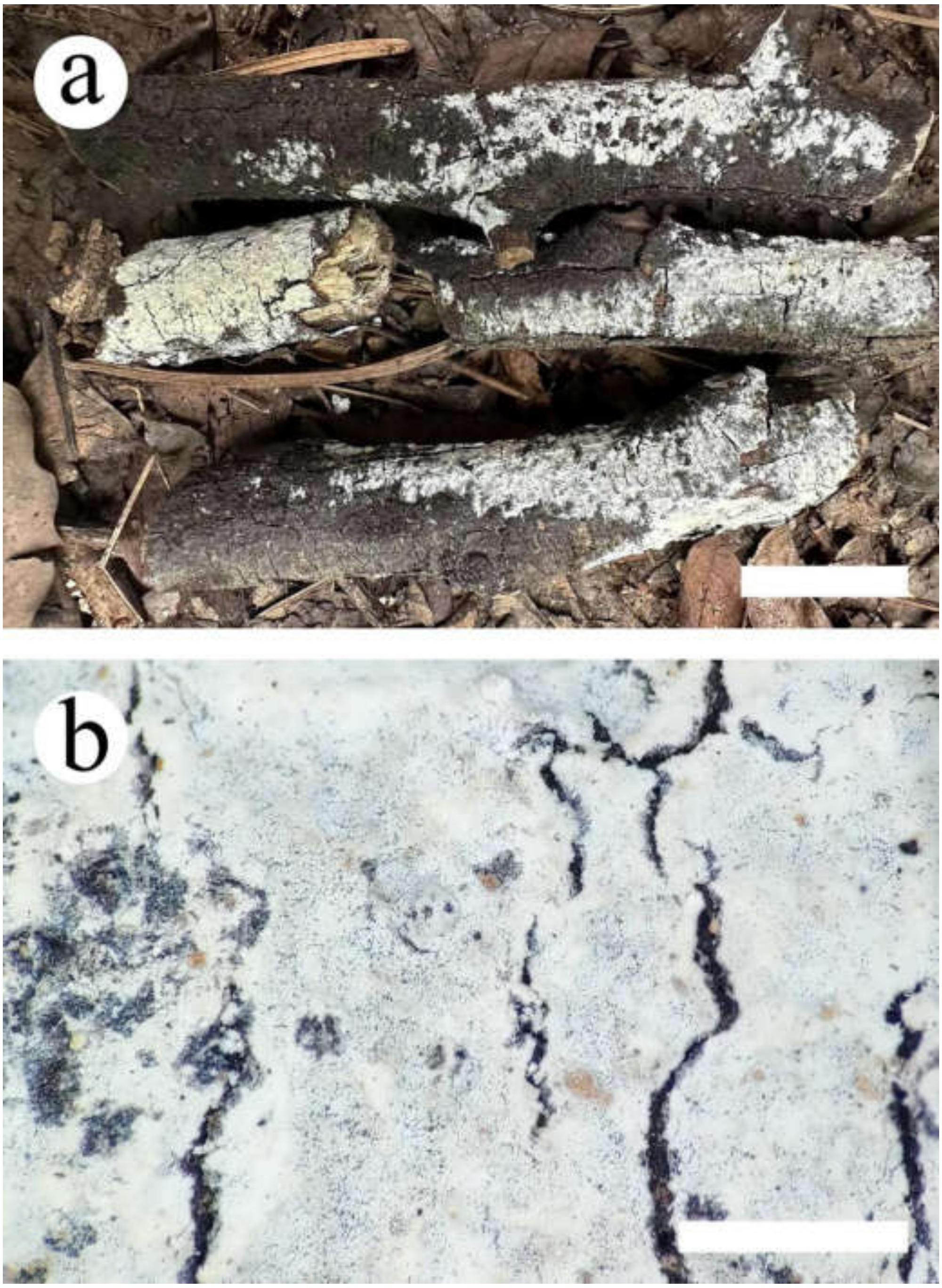

Figure 50 – Basidiomata of *Lyomyces sinensis* (holotype). Scale bars: a = 2 cm, b = 2 mm.

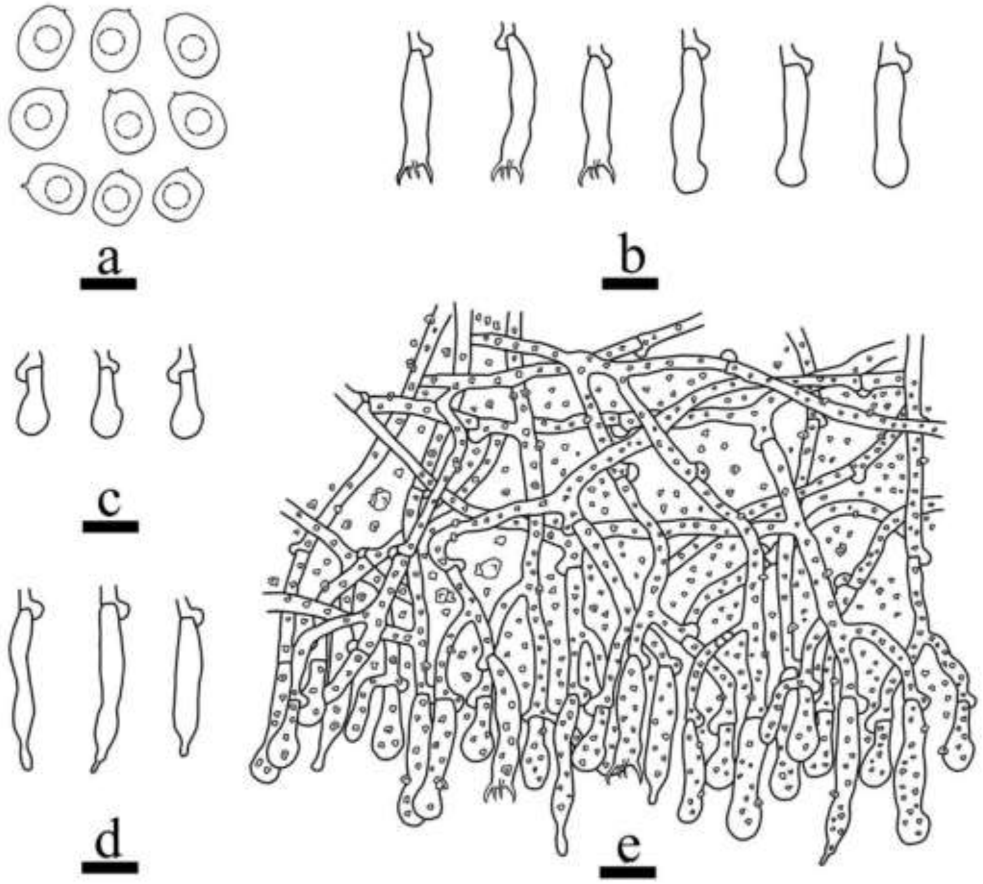

Figure 51 – Microscopic structures of *Lyomyces sinensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Clavate cystidia. d Tapering cystidia. e A section of hymenium. Scale bars: a = 5 µm, b–e = 10 µm.

Xylodon (Pers.) Gray

Index Fungorum number: IF18771; Facesoffungi number: FoF15415

Type species – *Xylodon quercinus* (Pers.) Gray

Notes – The genus *Xylodon* (Pers.) Gray was introduced by Gray (1821) and typifies by *X. quercinus* (Pers.) Gray. Due to a lack of rDNA sequences for many taxa, the molecular data were insufficient to clearly distinguish many genera; hence, a broader concept of *Hyphodontia* s.l. was employed by mycologists (Hjortstam & Ryvarden 2009, Yurchenko & Wu 2016, Riebesehl & Langer 2017, Riebesehl et al. 2019). Moreover, *Hyphodontia* s.l. was shown to be a polyphyletic genus, with *Xylodon* and *Kneiffiella* being the most species rich (Yurchenko & Wu 2016, Riebesehl & Langer 2017, Riebesehl et al. 2019). Yurchenko & Wu (2016) described two clades: the *Xylodon*-*Lyomyces*-*Rogersella* clade and the *Xylodon*-*Schizopora*-*Palifer* clade, and they proposed the inclusion of species from *Xylodon*, *Schizopora* Velen., *Palifer* Stalpers & P.K. Buchanan, *Lyomyces* P. Karst. and *Rogersella* Liberta & A.J. Nava within both clades. The research comprised the representative sequences and taxa of *Hyphodontia* s.l., including *Xylodon*, *Schizopora*, *Palifer*, *Lyomyces*, and *Rogersella*. The results demonstrated the difficulty of distinguishing the two genera *Xylodon* and *Schizopora* based on morphological and phylogenetic information; hence, the authors proposed that *Xylodon* and *Schizopora* should be united under *Xylodon* (Riebesehl & Langer 2017). It was confirmed that the two genera *Lagarobasidium* Jülich and *Xylodon* should be synonymous based on molecular data from the ITS+nLSU regions, and in which the three species were combined into *Xylodon* (Viner et al. 2018). In this study, based on the ITS+nLSU data (Fig. 8), *Xylodon* is grouped with *Loymyces*, *Fasciodontia* Yurchenko & Riebesehl, *Hyphodontia* and *Kneiffielle*, with five new species *X. bamburesupinus*, *X. fissilis*, *X. hydnoides*, *X. olivaceobubalinus* and *X. pingbianensis* spp. nov., included in *Xylodon*.

Xylodon bamburesupinus J.H. Dong & C.L. Zhao, sp. nov. Figs 52, 53

Index Fungorum number: IF850330; Facesoffungi number: FoF15416

Diagnosis – Differs from other *Xylodon* species by the farinaceous basidiomata with white to cream, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid to broadly ellipsoid basidiospores measuring 4–5.5 × 3.5–5 µm.

Etymology – *bamburesupinus* (Lat.): referring to resupinate to grow on bamboo of the type specimen.

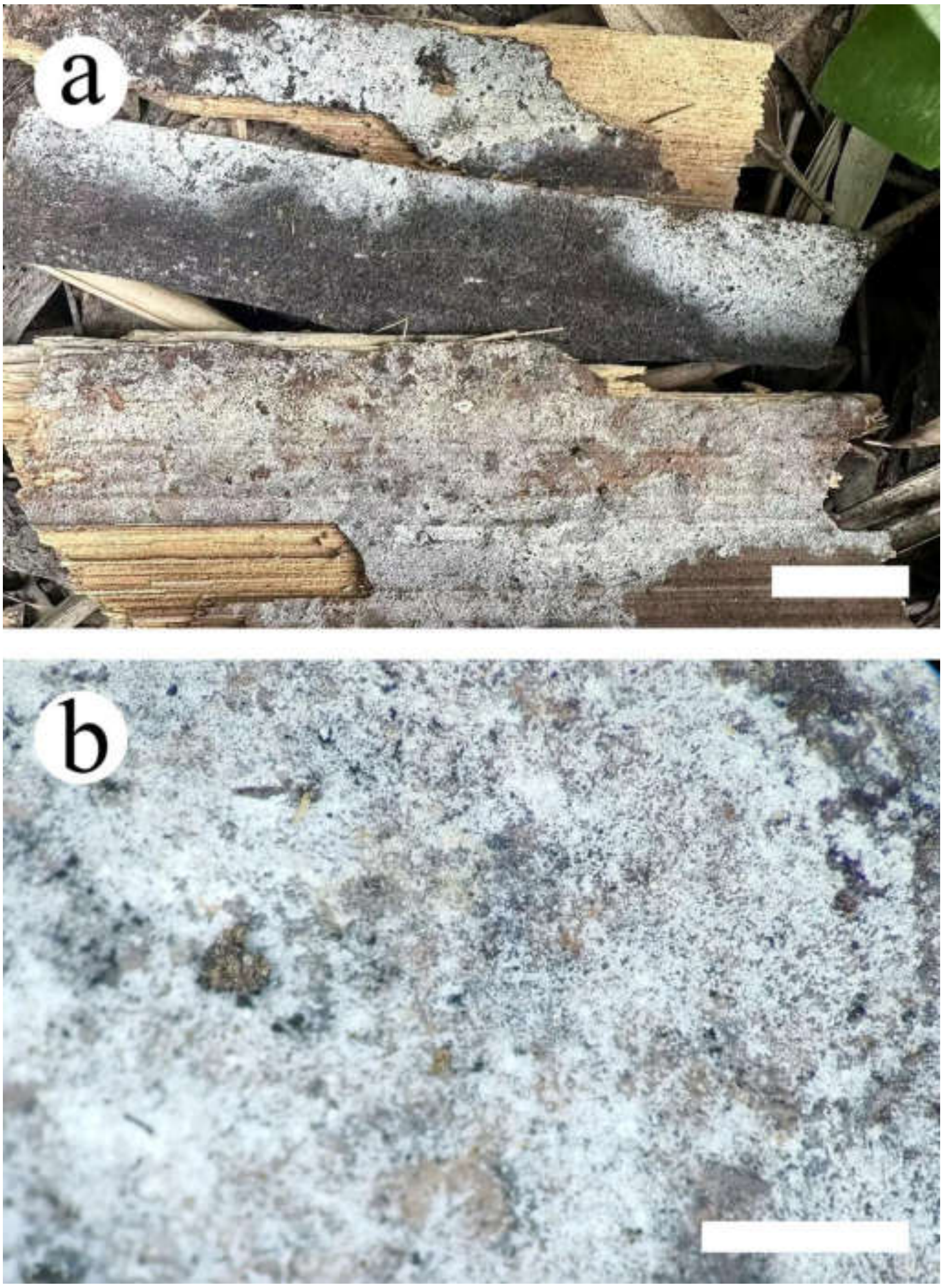

Figure 52 – Basidiomata of *Xylodon bamburesupinus* (holotype). Scale bars: a = 1 cm, b = 2 mm.

Type – China, Yunnan Province, Qujing, Zhanyi District, Lingjiao Village, GPS coordinates 25°89' N, 103°67' E, altitude 1930 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 22 August 2022, CLZhao 23088 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, farinaceous, without odor or taste when fresh, up to 7.5 cm long, 3 cm wide, 100–150 µm thick. Hymenial surface smooth, pruinose, white when fresh, turning white to cream upon drying. Sterile margin thin, white, thinning out, up to 0.5 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 2–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) capitate, colorless, thin-walled, smooth, 34.5–53.5 × 3.5–6 µm; (2) tapering, colorless, thin-walled, 30–43 × 3.5–5.5 µm; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 14–16.5 × 3.5–4 µm. Basidiospores ellipsoid to broadly ellipsoid, colorless, thin-walled, smooth, with drop, IKI–, CB–, 4–5.5(–6) × 3.5–5 µm, L = 4.99 µm, W = 4.16 µm, Q = 1.15–1.25 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Qujing, Zhanyi District, Lingjiao Village, GPS coordinates 25°89' N, 103°67' E, altitude 1930 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 22 August 2022, CLZhao 23123 (SWFC).

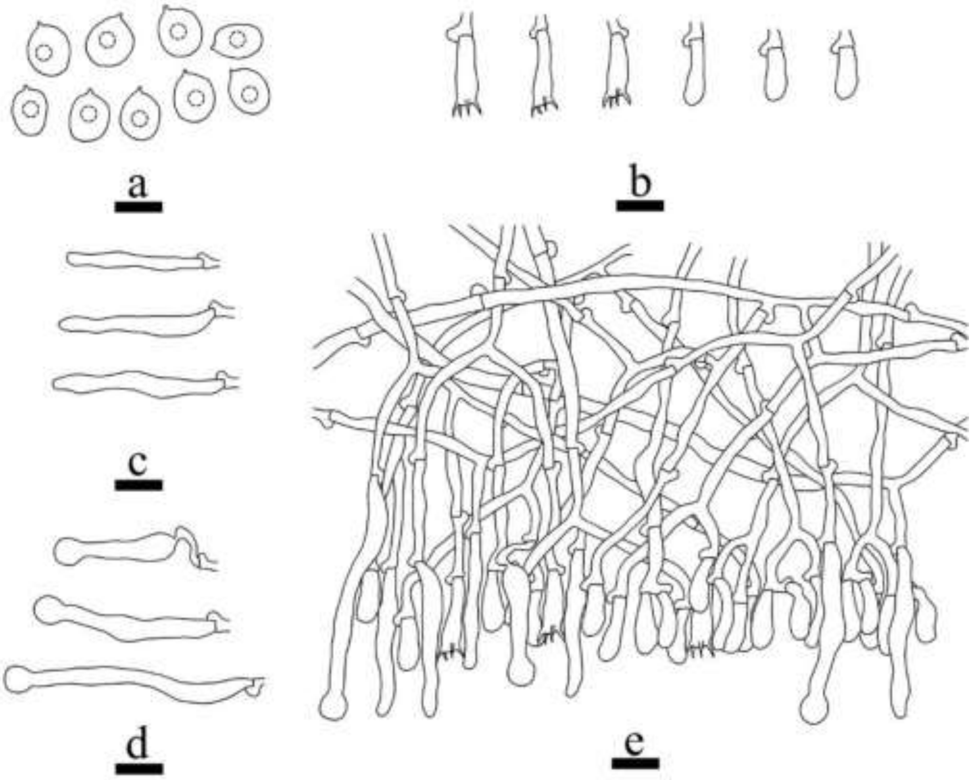

Figure 53 – Microscopic structures of *Xylodon bamburesupinus* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Tapering cystidia. d Capitate cystidia. e A section of hymenium. Scale bars: a = 5 µm, b–e = 10 µm.

Notes – In this study, the new species *Xylodon bamburesupinus* is classified within *Xylodon* based on the ITS+nLSU data (Fig. 8), and is clustered with *X. filicinus* and *X. tropicus* C.L. Zhao. However, *X. filicinus* can be distinguished from *X. bamburesupinus* by its odontioid hymenial surface, and larger basidia (16–20 × 4.5–5.5 µm, Riebesehl et al. 2019); *X. tropicus* can be delimited from *X. bamburesupinus* by its grandinioid hymenial surface, shorter basidia (7.1–13.5 × 2.3–4 µm) and smaller basidiospores (2–4.8 × 1.6–4 µm, Qu et al. 2022).

Xylodon bamburesupinus resembles *X. attenuatus* Spirin & Viner, *X. dimiticus* (Jia J. Chen & L.W. Zhou) Riebesehl & E. Langer, *X. fissuratus* C.L. Zhao, *X. grandineus* and *X. vesiculosus* Y Yurchenko, Nakasone & Riebesehl in its shared characteristic of ellipsoid basidiospores. However, *X. attenuatus* differs from *X. bamburesupinus* by its odontoid hymenial surface, and shorter capitate cystidia (14.2–27.2 × 3.3–4.5 µm, Viner et al. 2018); *X. dimiticus* differentiates from *X. bamburesupinus* by its poroid hymenial surface, and narrower basidiospores (3.8–4.6 × 2.8–3.5

µm, Chen et al. 2016); *X. fissuratus* can be distiniguished from *X. bamburesupinus* by its grandinioid hymenial surface, and shorter capitate cystidia (11.5–16.5 × 3–4.5 µm, Guan et al. 2023); *X. grandineus* differs from X. *bamburesupinus* in its grandinioid hymenial surface, and smaller basidiospores (3–4.5 × 2–3 µm, Luo et al. 2022); *X. vesiculosus* can be distinguished from X. *bamburesupinus* by its odontioid hymenial surface, and longer basidiospores (5.3–6.3 × 3–4 µm, Riebesehl et al. 2019)

Xylodon fissilis J.H. Dong & C.L. Zhao, sp. nov. Figs 54, 55

Index Fungorum number: IF850331; Facesoffungi number: FoF15417

Diagnosis – Differs from other *Xylodon* species by the coriaceous to furfuraceous basidiomata with buff, grandinoid hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 5.5–6 × 4–4.5 µm.

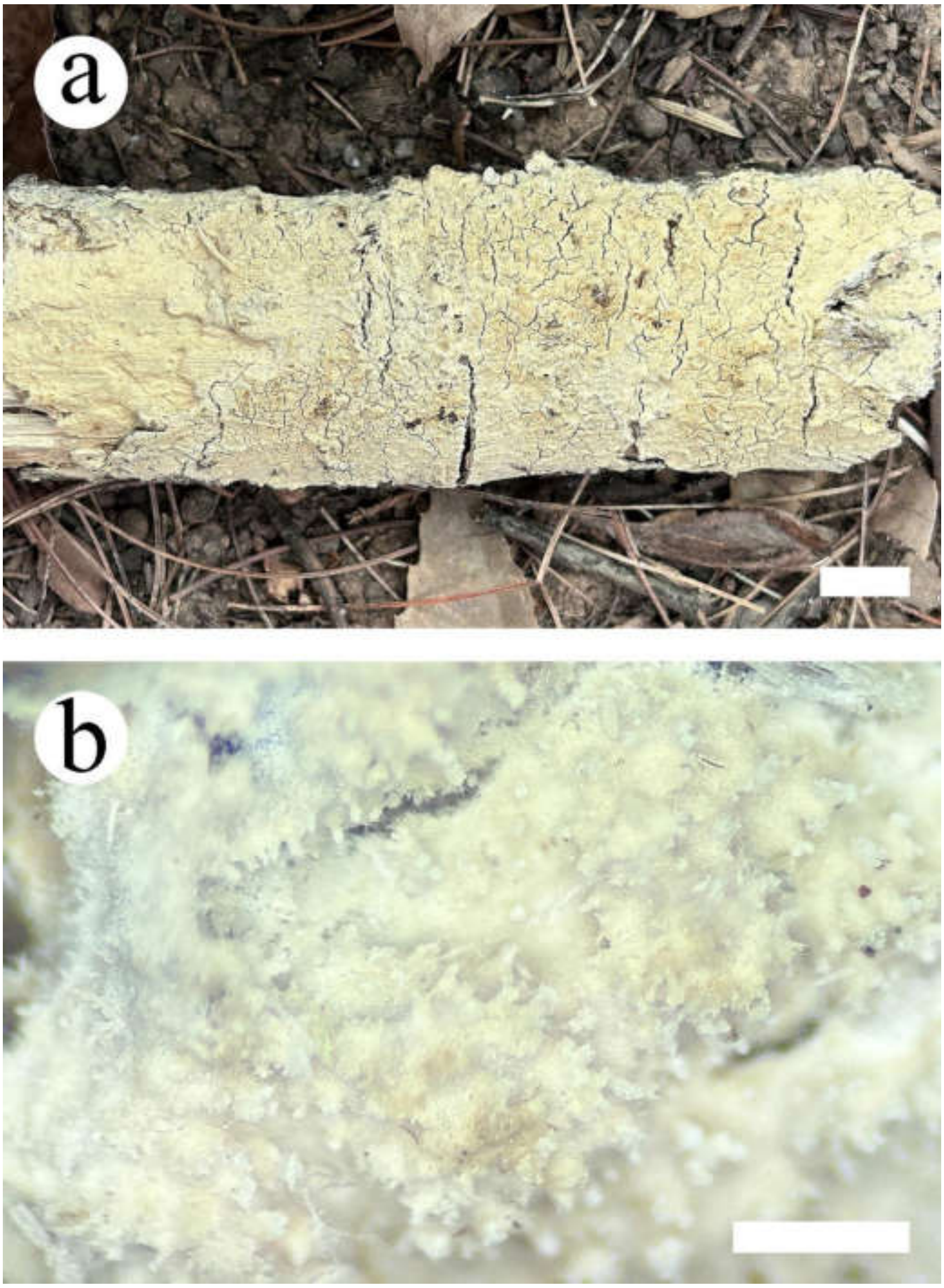

Figure 54 – Basidiomata of *Xylodon fissilius* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 7 June 2020, CLZhao 18740 (SWFC, holotype).

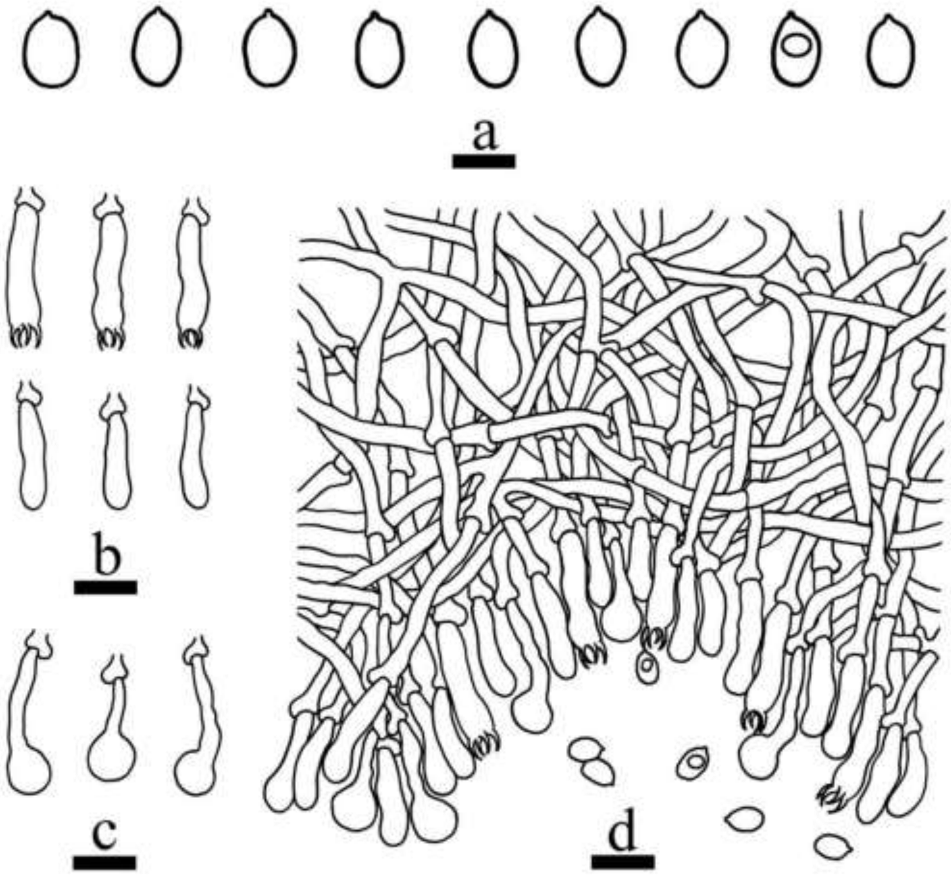

Figure 55 – Microscopic structures of *Xylodon fissilius* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Capitate cystidia. d A section of hymenium. Scale bars: a =5 µm, b–d = 10 µm.

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft coriaceous when fresh, becoming furfuraceous upon drying, up to 12 cm long, 5 cm wide, 100–200 µm thick. Hymenial surface grandinoid, cracked, slightly buff when fresh, turning to buff upon drying. Sterile margin narrow, slightly buff, abrupt, up to 1–2 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, with a lot of crystals, 2–4.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia numerous, capitate, thin-walled, constricted at the neck, with a globose tip, 15–25 × 5.5–8.5 µm; cystidioles absent. Basidia cylindrical, with a median constriction, with 4 sterigmata and a basal clamp connection, 14.5–22 × 4.5–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, sometimes with a guttula, IKI–, CB–, 5.5–6(–6.3) × (3.8–)4–4.5 µm, L = 5.85 µm, W = 4.15µm, Q = 1.40–1.42 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 7 June 2020, CLZhao 18750 (SWFC).

Notes – The new species *Xylodon fissilis* is placed within *Xylodon* based on the ITS+nLSU data (Fig. 8), and is identified as a sister taxon to *X. heterocystidiatus* (H.X. Xiong, Y.C. Dai &

Sheng H. Wu) Riebesehl, Yurch. & Langer. However, *X. heterocystidiatus* can be delimited from *X. fissilis* by its cream hymenial surface, fimbriate sterile margin, and smaller basidiospores (4.4–5.3× 2.8–3.3 µm, Xiong et al. 2009)

Xylodon fissilis shares similarities with *X. fissuratus* C.L. Zhao, *X. laceratus* C.L. Zhao, *X. lenis* Hjortstam & Ryvarden, *X. macrosporus* C.L. Zhao & K.Y. Luo and *X. punctus* K.Y. Luo & C.L. Zhao, all of which are characterized by a cracked hymenial surface and ellipsoid basidiospores. However, *X. fissuratus* can be distinguished from *X. fissilis* by its white hymenial surface, narrower basidia (10.5–16.5 × 2–4 µm) and smaller basidiospores (4–5 × 3–4 µm, Guan et al. 2023); *X. laceratus* differs from *X. fissilis* by its cream hymenial surface, narrower capitate cystidia (15.4–24.7 × 3.8–4.7 µm) and smaller basidiospores (3.9–5.3 × 2.6–4.1 µm, Qu et al. 2022); *X. lenis* Hjortstam & Ryvarden differentiates from *X. fissilis* in its odontioid to hydnoid hymenial surface, narrower basidia (16–21 × 3.5–4 µm) and smaller basidiospores (4.2–5 × 3–3.5 µm, Wu 1990); *X. macrosporus* differs from *X. fissilis* by its brittle basidiomata, wider basidia (11.5–36 × 5–11 µm) and larger basidiospores (8–10.5 × 7.5–9 µm, Luo et al. 2021a); *X. punctus* can be distinguished from *X. fissilis* by its white hymenial surface, and smaller basidiospores (2–4 × 1.5–2.5 µm, Luo et al. 2022).

Xylodon hydnoides J.H. Dong & C.L. Zhao, sp. nov. Figs 56, 57

Index Fungorum number: IF850332; Facesoffungi number: FoF15418

Diagnosis – Differs from other *Xylodon* species by the coriaceous basidiomata with cream to slightly brown, hydnoid hymenial surface, monomitic hyphal system with clamped generative hyphae and subglobose to globose basidiospores measuring 3.8–4.6 ×3.2–4 µm.

Etymology – *hydnoides* (Lat.): referring to the hydnoid hymenophore surface of the type specimen.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 2 August 2020, CLZhao 17991 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, without odor or taste, coriaceous when fresh, becoming hard coriaceous upon drying, up to 8 cm long, 3.5 cm wide, 100–200 µm thick. Hymenial surface hydnoid, cream when fresh, turning to cream to slightly brown upon drying. Sterile margin narrow, cream, abrupt, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thick-walled, frequently branched, interwoven, 2–3.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Asterocystidia, clavate, thin-walled, with the apical part encrusted, 29.5–38.5 × 3.5–4.5 µm; cystidioles absent. Basidia cylindrical, with 4 sterigmata and a basal clamp connection, 12.5–16.5 × 3–5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose to globose, colorless, thin-walled, smooth, sometimes with a guttula, IKI–, CB–, (3.6–)3.8–4.6(–5) × (2.9–)3.2–4(–4.3) µm, L = 4.25 µm, W = 3.64 µm, Q = 1.13–1.17 (n = 120/4).

Material examined (paratypes) – China, Yunnan Province, Honghe City, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 2 August 2020, CLZhao 18105, CLZhao 18238, CLZhao 18239 (SWFC).

Notes – Based on the ITS+nLSU data, the new species *Xylodon hydnoides* is classified within *Xylodon* (Fig. 8) and forms a cluster with *X. daweishanensis* C.L. Zhao and *X. hyphodontinus* (Hjortstam & Ryvarden) Riebesehl, Yurchenko & G. Gruhn. However, *X. daweishanensis* can be distinguished from *X. hydnoides* by its buff hymenial surface, and shorter asterocystidia (11–26.5 × 2.5–4.5 µm, Guan et al. 2023); *X. hyphodontinus* can be delineated from *X. hydnoides* by its light ochraceous hymenial surface, and larger basidiospores (5 × 4.5 µm, Riebesehl et al. 2019).

Xylodon hydnoides resembles *X. flocculosus* C.L. Zhao, sharing similar asterocystidia. However, *X. flocculosus* differs from *X. hydnoides* byits grandinoid hymenial surface, and ellipsoid and thick-walled basidiospores (4.2–5.7 × 3.1–4.4 µm, Qu & Zhao 2022).

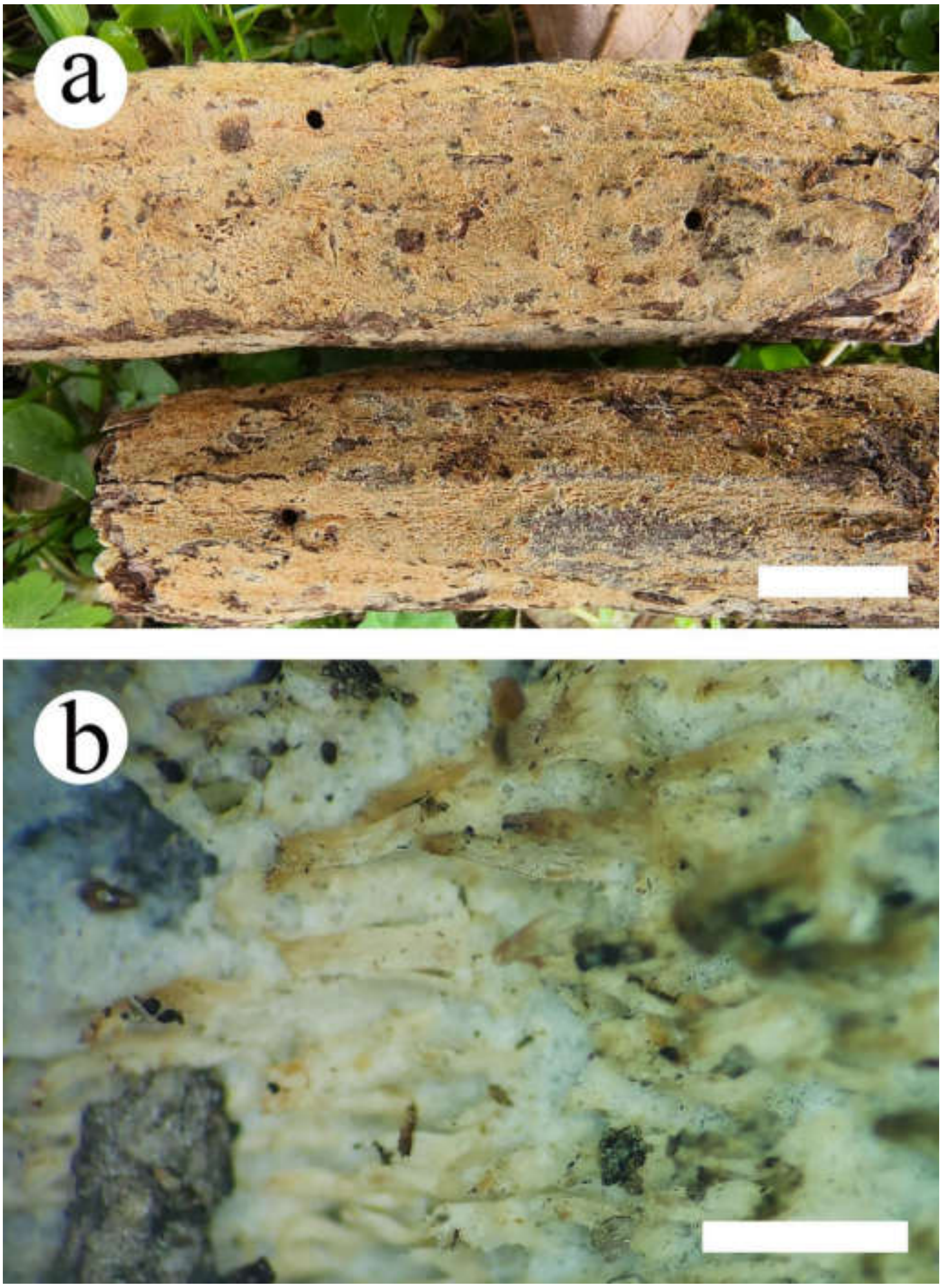

Figure 56 – Basidiomata of *Xylodon hydnoides* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

Xylodon hydnoides is similar to *X. lenis* Hjortstam & Ryvarden by the presence of hydnoid hymenial surface. However, *X. lenis* can be distinguished from *X. hydnoides* by its pinkish buff hymenial surface, longer basidia (16–21 × 3.5–4 µm) and broadly ellipsoid basidiospores (4.2–5 × 3–3.5 µm, Wu 1990).

Xylodon hydnoides shows similarities with *X. crustosoglobosus* (Hallenb. & Hjortstam) Hjortstam & Ryvarden, *X. poroideoefibulatus* (Sheng H. Wu) Hjortstam & Ryvarden and *X. xinpingensis* C.L. Zhao & X. Ma, characterized by the presence ofsubglobose to globose basidiospores. However, *X. crustosoglobosus* differs from *X. hydnoides* by its smooth hymenial surface, andlonger basidia (17–25 × 4.5–5 µm, Hallenberg & Hjortstam 1996); *X. poroideoefibulatus* differentiates from *X. hydnoides* by its poroid hymenial surface, wider basidia (12–23 × 5.5–6.5 µm) and larger basidiospores (5–5.7 × 4–4.5 µm, Wu 2001); *X. xinpingensis* differs from *X. hydnoides* in its reticulate hymenial surface, longer basidia (18.5–33 × 3–6.5 µm) and basidiospores (4.5–6 × 3.5–5 µm, Ma & Zhao 2021).

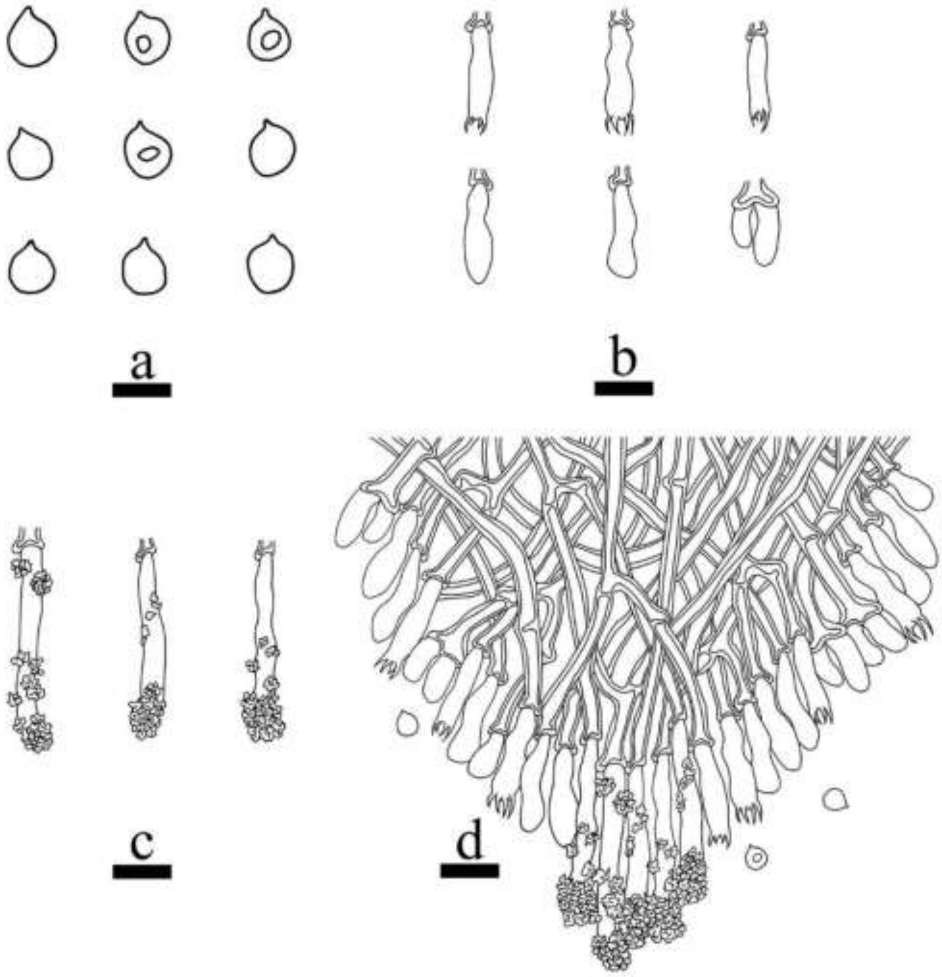

Figure 57 – Microscopic structures of *Xylodon hydnoides* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Asterocystidia. d A section of hymenium. Scale bars: a = 5 µm, b–d = 10 µm.

Xylodon olivaceobubalinus J.H. Dong & C.L. Zhao, sp. nov. Figs 58, 59

Index Fungorum number: IF850333; Facesoffungi number: FoF15419

Diagnosis – Differs from other *Xylodon* species by the subceraceous basidiomata with buff to flavescent, grandinoid hymenial surface, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 6–8 × 4–6.5 µm.

Etymology – *olivaceobubalinus* (Lat.): referring to the olivaceous to buff hymenophore of the type specimen.

Type – China, Yunnan Province, Lincang, Yun County, Dumu Village, GPS coordinates 24°44' N, 100°12' E, altitude 1590 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 20 October 2022, CLZhao 25174 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, thin, very hard to separate from substrate, soft membranaceous when fresh, becoming subceraceous upon drying, up to 2.7 cm long, 1.6 cm wide, 50–100 µm thick. Hymenial surface grandinoid, olivaceous when fresh, turning to buff to flavescent upon drying. Sterile margin indistinct, buff, thinning out, up to 0.5 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven 3–5.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Capitate cystidia, smooth, colorless, thin-walled, slightly constricted at the neck, with a globose head, 24.5–29 × 4–6 µm; cystidioles absent. Basidia subclavate, with 4 sterigmata and a basal clamp connection, 26.5–29.5 × 6–7 µm. Basidiospores ellipsoid, colorless, thin-walled, smooth, with one oil drop inside, IKI–, CB–, (5.8–)6–8(–9.2) × 4–6.5 µm, L = 6.8 µm, W = 5.76 µm, Q = 1.16–1.19 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Lincang City, Yun County, Dumu Village, GPS coordinates 24°44' N, 100°12' E, altitude 1590 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 20 October 2022, CLZhao 25164 (SWFC).

Notes – In this study, the new species *Xylodon olivaceobubalinus* is placed within *Xylodon* based on the ITS+nLSU data (Fig. 8), and it forms a cluster with *X. lenis* Hjortstam & Ryvarden and *X. nesporii* (Bres.) Hjortstam & Ryvarden. However, *X. lenis*can be distinguished from *X. olivaceobubalinus* by its odontioid to hydnoid hymenial surface, smaller basidia (16–21 × 3.5–4 µm) and basidiospores (4.2–5 × 3–3.5 µm, Wu 1990); *X. nesporii* be delineated from *X. olivaceobubalinus* by its odontioid hymenial surface, smaller basidia (15–25 × 4–5 µm) and basidiospores (4.5–6 × 2–2.5 µm, Bernicchia & Gorjón 2010).

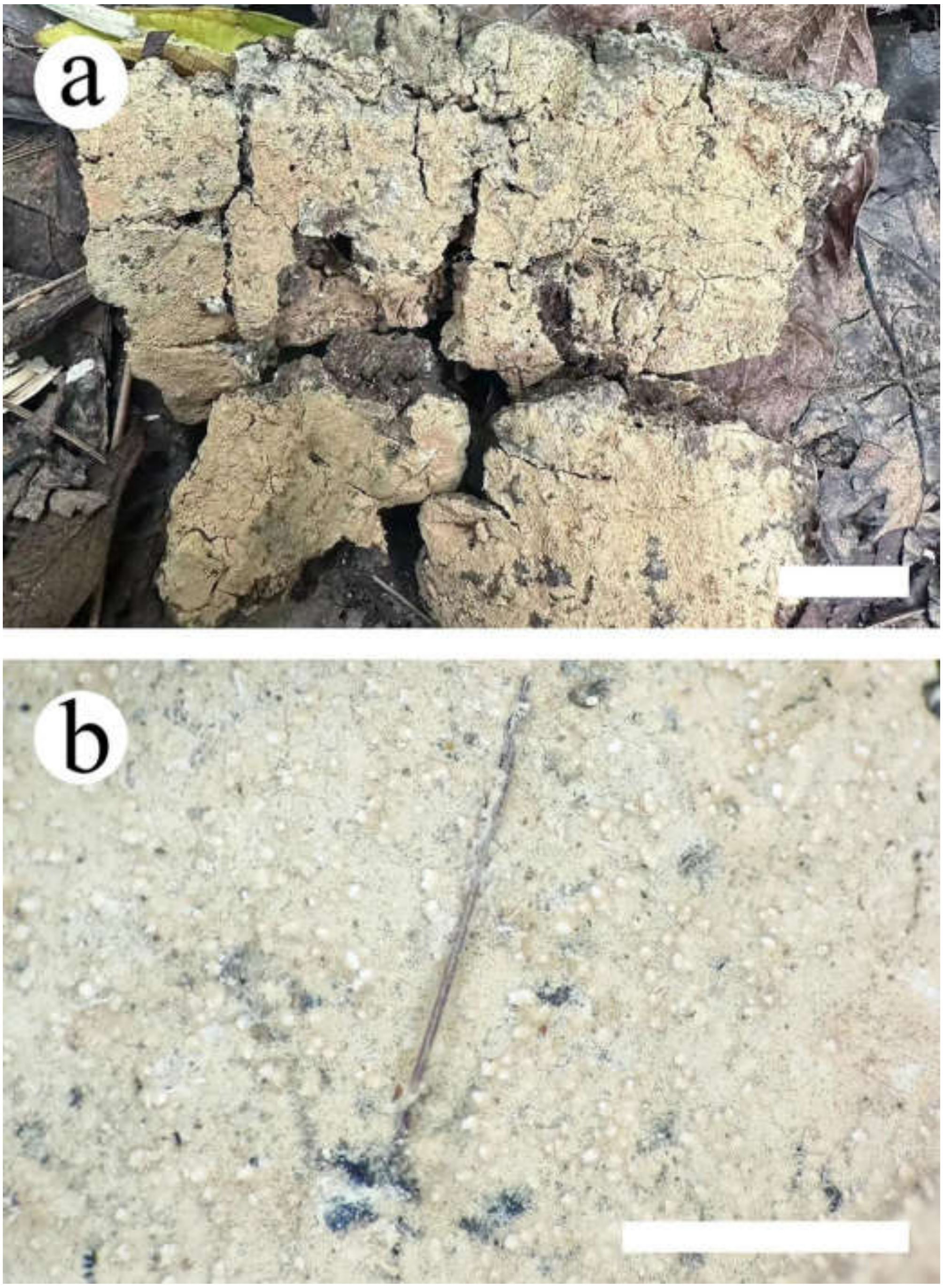

Figure 58 – Basidiomata of *Xylodon olivaceobubalinus* (holotype). Scale bars: a = 1 cm, b = 2 mm.

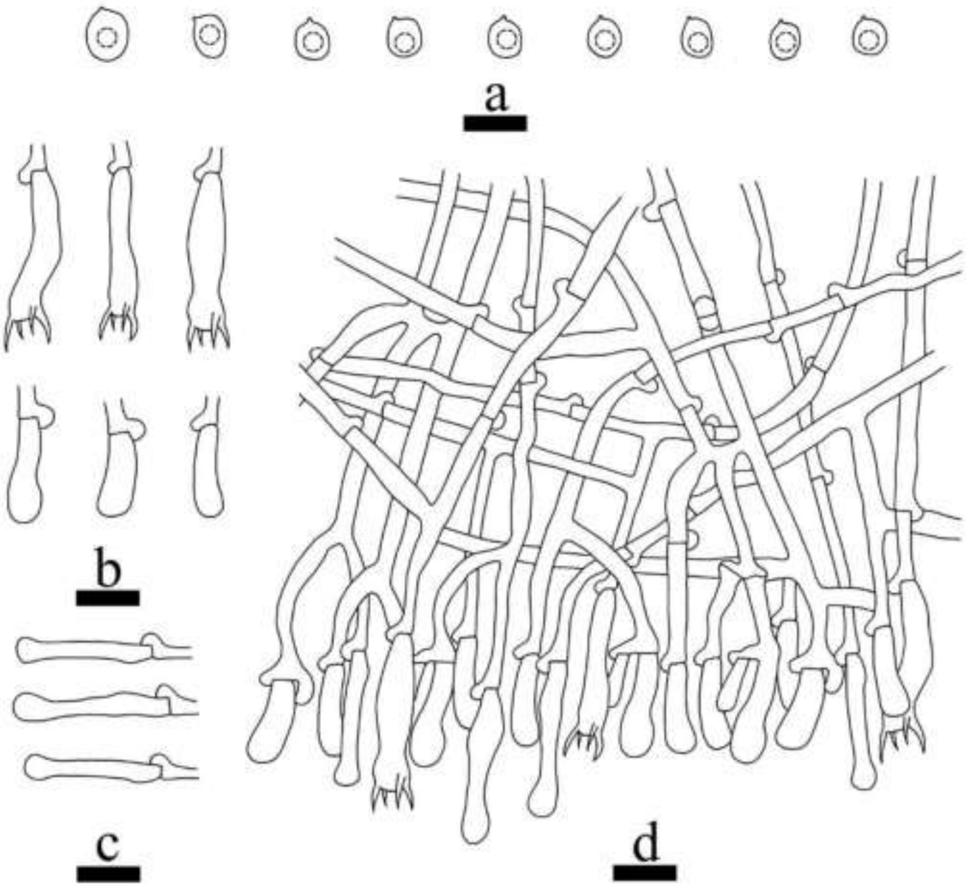

Figure 59 – Microscopic structures of *Xylodon olivaceobubalinus* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Capitate cystidia. d A section of hymenium. Scale bars: a–d = 10 µm.

Xylodon olivaceobubalinus resembles *X. bambusinus* C.L. Zhao & X. Ma, *X. laceratus* C.L. Zhao, *X. macrosporus*, *X. tropicus*, and *X. ussuriensis* Viner by the presence of grandinioid hymenial surface. However, *X. bambusinus* differs from *X. olivaceobubalinus* by its white basidiomata, narrower basidia (15–28 × 3.5–4.5 µm) and smaller basidiospores (4–5.5 × 3–4 µm, Ma & Zhao 2021); *X. laceratus* differentiates from *X. olivaceobubalinus* by its cream hymenial surface, smaller basidia (11–17.5 × 3.2–5.5 µm) and basidiospores (3.9–5.3 × 2.6–4.1 µm, Qu et al. 2022); *X. macrosporus* can be distinguishesd from *X. olivaceobubalinus* in its brittle basidiomata, and larger basidiospores (8–10.5 × 7.5–9 µm, Luo et al. 2021a); *X. tropicus* differs from *X. olivaceobubalinus* by its cream to pale hymenial surface, smaller basidia (7.1–13.5 × 2.3–4 µm) and basidiospores (2–4.8 × 1.6–4 µm, Qu et al. 2022); *X. ussuriensis* differentites from *X. olivaceobubalinus* by its white hymenial surface, smaller basidia (14.7–22.8 × 3.4–4.9 µm) and shorter basidiospores (5.1–6 × 3.8–4.6 µm, Viner et al. 2018).

Xylodon pingbianensis J.H. Dong & C.L. Zhao, sp. nov. Figs 60, 61

Index Fungorum number: IF850334; Facesoffungi number: FoF15420

Diagnosis – Differs from other *Xylodon* species by the membranaceous basidiomata with pale-orange, grandinoid hymenial surface, monomitic hyphal system with clamped generative hyphae and subglobose to globose basidiospores measuring 7–8 × 6.5–7.6 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 19029 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft membranaceous when fresh, becoming hard membranaceous upon drying, up to 5 cm long, 2 cm wide, 50–150 µm thick. Hymenial surface grandinoid, slightly cinnamon-buff when fresh, turning to pale-orange upon drying. Sterile margin narrow, slightly white, slightly fimbriate, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to slightly thick-walled, frequently branched, interwoven, 4–7 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia numerous, tubular, slightly thick-walled, 100–165 × 10–14 µm; cystidioles absent. Basidia clavate, constricted, with 4 sterigmata and a basal clamp connection, 25–34 × 7.5–10.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose to globose, colorless, thick-walled, smooth, IKI–, CB+, 7–8(–8.5) × 6.5–7.6(–8) µm, L = 7.69 µm, W = 7.16µm, Q = 1.07 (n = 30/1).

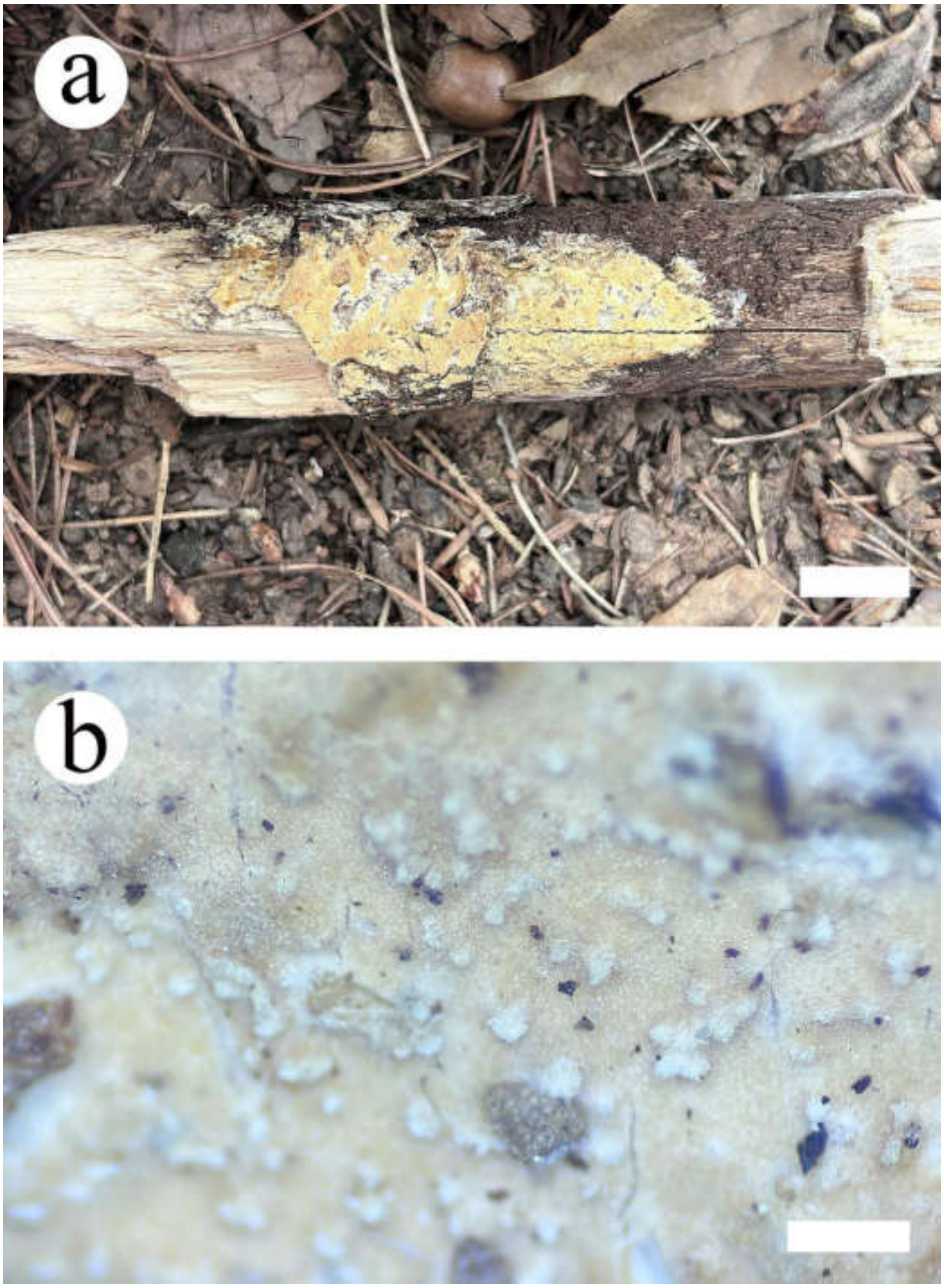

Figure 60 – Basidiomata of *Xylodon pingbianensis* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

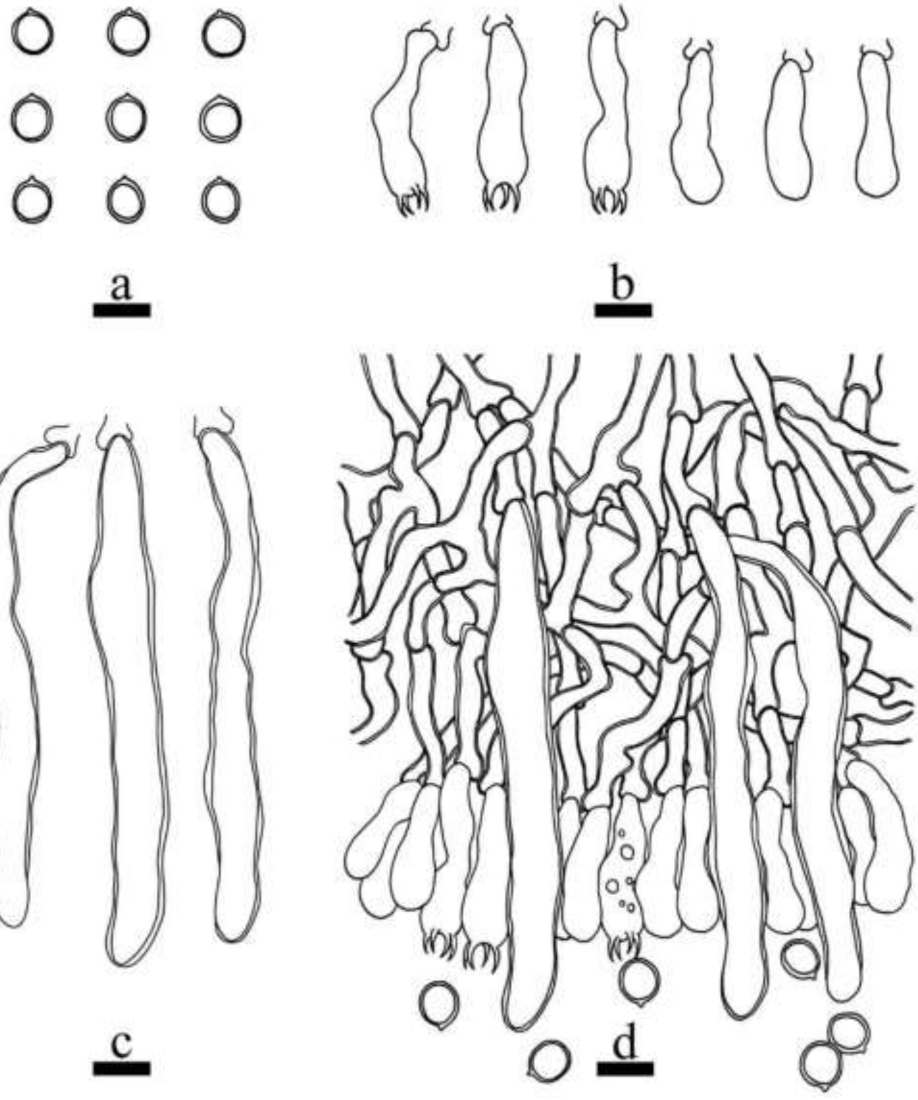

Figure 61 – Microscopic structures of *Xylodon pingbianensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Tubular cystidia. d A section of hymenium. Scale bars: a–d = 10 µm.

Notes – Based on the ITS+nLSU data (Fig. 8), the new species *Xylodon pingbianensis* is grouped into *Xylodon*, and is clustered with *X. nothofagi* (G. Cunn.) Hjortstam & Ryvarden, *X. puerensis* C.L. Zhao and *X. taiwanianus* (Sheng H. Wu) Hjortstam & Ryvarden. However, *X. nothofagi* can be delimited from *X. pingbianensis* by its poroid hymenial surface, smaller basidia (12–14 × 3–4 µm) and basidiospores (5–6.5 × 1.5–2 µm, Hjortstam & Ryvarden 2009); *X. puerensis* can be distinguished from *X. pingbianensis* by its poroid hymenial surface, smaller basidia (14.5–20 × 5–7 µm) and basidiospores (6–7 × 4.5–5.5 µm, Guan et al. 2023); *X. taiwanianus* can be delimited from *X. pingbianensis* by its poroid hymenial surface, smaller basidia (14–20 × 4–5 µm) and basidiospores (4.5–5.5 × 2.6–3 µm, Wu 2001).

Xylodon pingbianensis shares similaraties with *X. xinpingensis* C.L. Zhao & X. Ma, *X. crustosoglobosus* (Hallenb. & Hjortstam) Hjortstam & Ryvarden, *X. poroideoefibulatus* (Sheng H. Wu) Hjortstam & Ryvarden, *X. rudis* (Hjortstam & Ryvarden) Hjortstam & Ryvarden, *X. sinensis* C.L. Zhao & K.Y. Luo and *X. subglobosus* Samita, Sanyal & Dhingra ex L.W. Zhou & T.W. May, all characterized by having subglobose to globose basidiospores. However, *X. crustosoglobosus* differs from *X. pingbianensis* by its smooth and greyish white to pale yellowish hymenial surface, smaller basidia (17–25 × 4.5–5 µm) and basidiospores (4.5–5 × 3.8–4 µm, Hallenberg & Hjortstam 1996); *X. poroideoefibulatus* differentiates from *X. pingbianensis* by its poroid hymenial surface, smaller basidia (12–23 × 5.5–6.5 µm) and basidiospores (5–5.7 × 4–4.5 µm, Wu 2001); *X. rudis* can be distinguished from *X. pingbianensis* in its odontoid and pale ochraceous hymenial surface, narrower basidia (25–30 × 4.5–5 µm) and smaller basidiospores (5 × 4 µm, Hjortstam & Ryvarden 1997); *X. sinensis* differs from *X. pingbianensis* by its cream to buff hymenial surface, smaller basidia (9.5–17.5 × 2.5–4.5 µm) and basidiospores (3–5 × 2.5–4 µm, Luo et al. 2021a); *X. subglobosus* differentiates from *X. pingbianensis* by its odontoid and pale orange hymenial surface, smaller basidia (20–26 × 4.7–5.3 µm) and basidiospores (4.2–5.2 × 3–5 µm, Wang et al. 2021b)

Skvortzoviaceae L.W. Zhou & Xue W. Wang

Index Fungorum number: IF900259; Facesoffungi number: FoF14030

Type genus – *Skvortzovia* Bononi & Hjortstam

Skvortzovia Bononi & Hjortstam

Index Fungorum number: IF14446; Facesoffungi number: FoF14030

Type species – *Skvortzovia furfurella* (Bres.) Bononi & Hjortstam

Notes – The genus *Skvortzovia* Bononi & Hjortstam was established by Hjortstam & Bononi (1987) and typified by *S. furfurella* (Bres.) Hjortstam & Bononi. A molecular phylogeny, inferred from 5.8S and nLSU rDNA sequences for the hymenochaetoid clade showed that *Skvortzovia* nested into the *Rickenella* clade and then grouped with *Resinicium* Parmasto (Larsson et al. 2006). Morphological and molecular studies on *Resinicium* revealed that three species of *Skvortzovia* closely formed a group, subsequently clustering with a clade comprising *Cyphellostereum* D.A. Reid, *Resinicium* and *Rickenella* Raithelh. (Nakasone 2007). When revising the taxonomy of *Resinicium*, Nakasone (2007) excluded *R. furfurellum* from *Resinicium* sensu stricto, treating this species as a member of *Resinicium* sensu lato. Recently, four species *Resinicium furfuraceum* (Bres.) Parmasto, *R. meridionale* (Burds. & Nakasone) Nakasone, *R. pinicola* (J. Erikss.) J. Erikss. & Hjortstam and *Phlebia georgica* Parmasto were formally transferred to *Skvortzovia* (Gruhn & Hallenberg 2018). The research, supported by morphological studies and the phylogenetic analyses, revealed the three new taxa of *Skvortzovia* the new taxa within *Skvortzovia* (Dong et al. 2021, Yu et al. 2021b). In this, based on the ITS, nLSU, mtSSU and RPB2 data (Fig. 9), a new species *S. incana* is introduced.

Skvortzovia incana J.H. Dong & C.L. Zhao, sp. nov. Fig 62, 63

Index Fungorum number: IF850335; Facesoffungi number: FoF15421

Diagnosis – Differs from other *Skvortzovia* species by the membranaceous basidiomata with incanus, odontioid hymenial surface, monomitic hyphal system with clamped generative hyphae and allantoid basidiospores measuring 5.2–5.7 × 1.1–1.3 µm.

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

Type – China, Yunnan Province, Wenshan, Pinba Town, Wenshan National Nature Reserve, GPS coordinates 23°22' N, 104°43' E, altitude 1500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 25 July 2019, CLZhao 16338 (SWFC, holotype).

Description – Basidiomata annual, resupinate, very thin, adnate, soft membranaceous, without odour or taste when fresh, becoming membranaceous upon drying, up to 12 cm long, 3.5 cm wide, 50–100 µm thick. Hymenial surface odontioid, white when fresh, turning incanus upon drying. Sterile margin white to incanus, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to thick-walled, frequently branched, interwoven, 2.5–3.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia numerous, capitate, colorless, thin-walled, smooth, 28–32 × 2–2.5 µm, projecting above the hymenium; cystidioles absent. Basidia subclavate, thin-walled, with 4 long sterigmata and a basal clamp connection, 11–15 × 2.5–4 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores allantoid, colorless, thin-walled, smooth, CB–, IKI–, (5–)5.2–5.7(–6) × 1.1–1.3 µm, L = 5.45 µm, W = 1.15 µm, Q = 4.70–4.74 (n = 60/2).

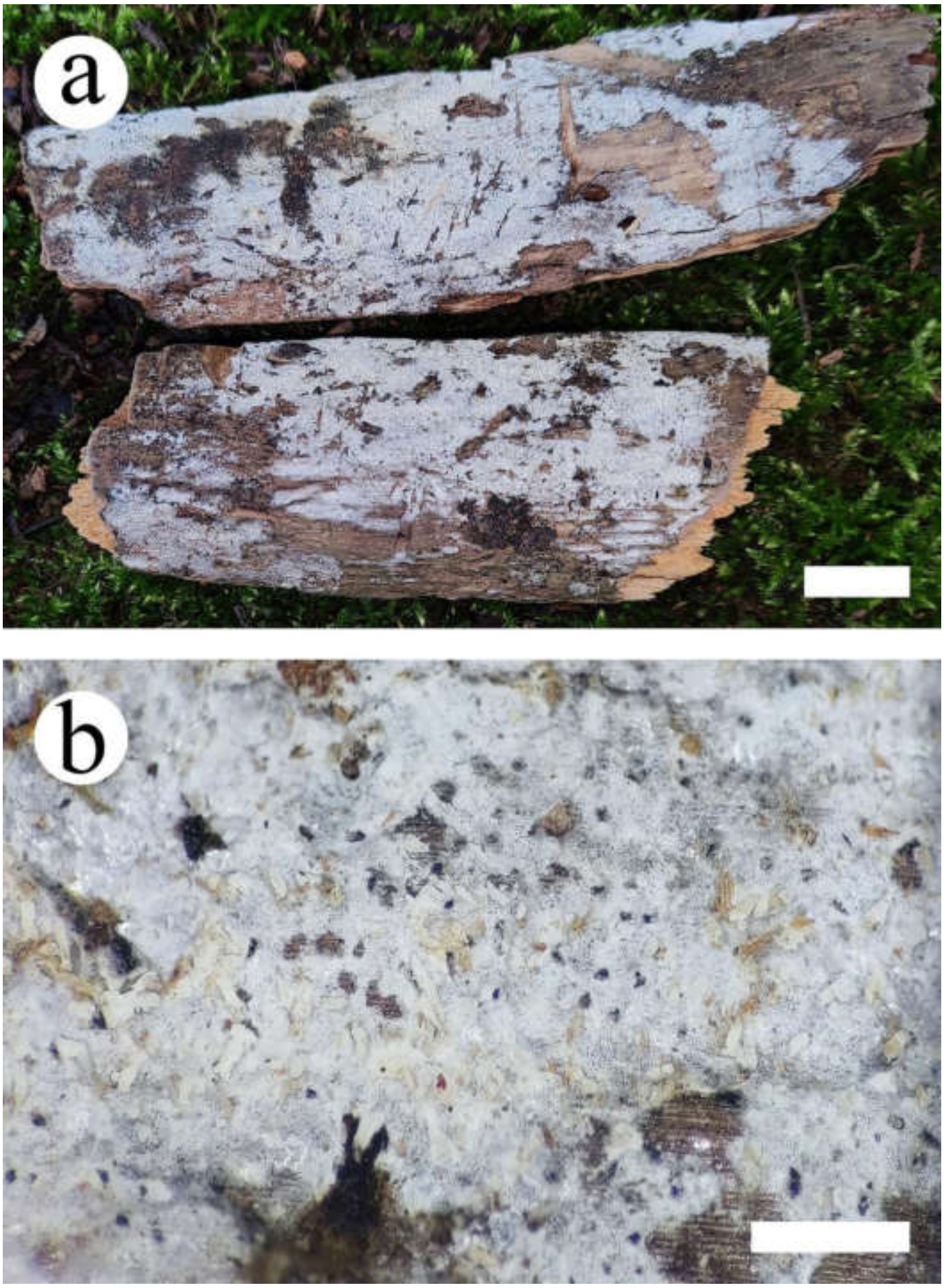

Figure 62 – Basidiomata of *Skvortzovia incana* (holotype). Scale bars: a = 1 cm, b = 1 mm.

Material examined (paratype) – China, Yunnan Province, Wenshan, Pinba Town, Wenshan National Nature Reserve, GPS coordinates GPS coordinates 23°22' N, 104°43' E, altitude 1500 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 26 July 2019, CLZhao 16474 (SWFC).

Notes – Based on the ITS, nLSU, mtSSU and RPB2 data (Fig. 9), the new species *Skvortzovia incana* is grouped into *Skvortzovia*, and is revealed as a sister to *S. furfurella* (Bres.) Bononi & Hjortstam. However, *S. furfurella* can be delimited from *S. incana* by its darkening and pale ochraceous hymenial surface, and smaller basidiospores (4–5 × 1 µm, Hjortstam & Bononi 1987).

Skvortzovia incana resembles *S. georgica* (Parmasto) G. Gruhn & Hallenb. in sharing the allantoid basidiospores. However, *S. georgica* differs from *S. incana* due to its smooth hymenial surface, and wider basidiospores (4.5–5 × 2–2.5 µm, Bernicchia & Gorjón 2010).

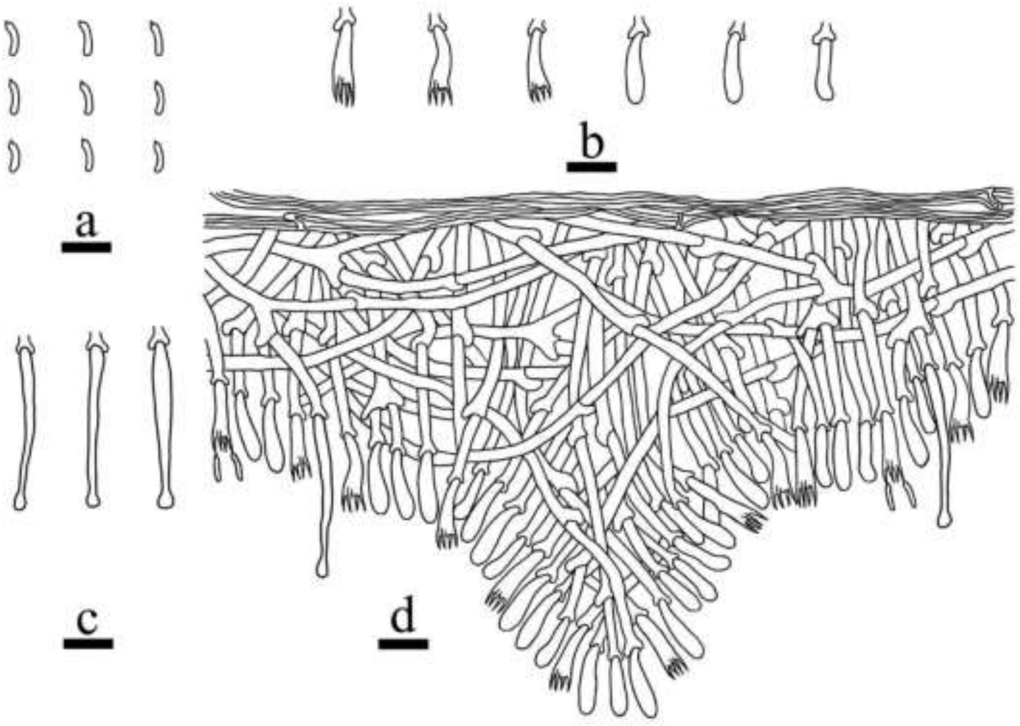

Figure 63 – Microscopic structures of *Skvortzovia incana* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Capitate cystidia. d A section of hymenium. Scale bars: a = 5 µm, b–d = 10 µm.

Tubulicrinaceae Jülich

Index Fungorum number: IF80048; Facesoffungi number: FoF15422

Type genus – *Tubulicrinis* Donk

Tubulicrinis Donk

Index Fungorum number: IF18693; Facesoffungi number: FoF15423

Type species – *Tubulicrinis glebulosus* (Fr.) Donk

Notes – The genus *Tubulicrinis* Donk, typified by *T. glebulosus* (Fr.) Donk (Donk 1956), was a member of the corticioid fungi. *Tubulicrinis* has undergone molecular studies, examining its genetic makeup and molecular features to gain insights into its taxonomy and functional genomics (Larsson et al. 2006, Dai 2011, Crous et al. 2016, He et al. 2020). The research on the molecular phylogeny of the hymenochaetoid clade revealed two *Tubulicrinis* species, *T. gracillimus* (Ellis & Everh. ex D.P. Rogers& H.S. Jacks.) G. Cunn. and *T. subulatus* (Bourdot & Galzin) Donk, formed a monophyletic lineage and were subsequently grouped with the *Coltricia* and Hymenochaetaceae clades (Larsson et al. 2006). A revised checklist of corticioid and hydnoid fungi in China revealed six recorded *Tubulicrinis* species (Dai 2011). Six new *Tubulicrinis* species were nested into the Tubulicrinaceae clade, belonging to Hymenochaetales (Crous et al. 2016). He et al. (2020), based on morphological and molecular analysis of *Tubulicrinis*, described two new species; *T. xantha* C.L. Zhao and *T. yunnanensis* C.L. Zhao. In this study, we describe one additional species of *Tubulicrinis* from China, based on morphological characteristics and phylogenetic analyses inferred from ITS, nLSU and mtSSU sequences (Fig. 10).

Tubulicrinis pini J.H. Dong & C.L. Zhao, sp. nov. Figs 64, 65

Index Fungorum number: IF850336; Facesoffungi number: FoF15424

Diagnosis – Differs from other *Tubulicrinis* species by the coriaceous basidiomata with slightly buff, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and cylindrical to allantoid basidiospores measuring 5–6 × 1.8–2.3 µm.

Etymology – *pini* (Lat.): referring to growing on the pines (*Pinus yunnanensis*) of the type specimen.

Type – China, Yunnan Province, Chuxiong, Zixishan National Forestry Park, GPS coordinates 25°01' N, 101°24' E, altitude 2500 m asl., on the fallen branch of *Pinus yunnanensis*, leg. C.L. Zhao, 30 June 2018, CLZhao 6881 (SWFC, holotype).

Description – Basidiomata annual, resupinate, thin, adnate, coriaceous, without odor or taste when fresh, becoming hard coriaceous upon drying, up to 10–15 cm long, 5 cm wide, 100–200 µm thick. Hymenial surface smooth, white when fresh, turn to slightly buff upon drying. Sterile margin white to buff, abrupt, up to 1 mm wide.

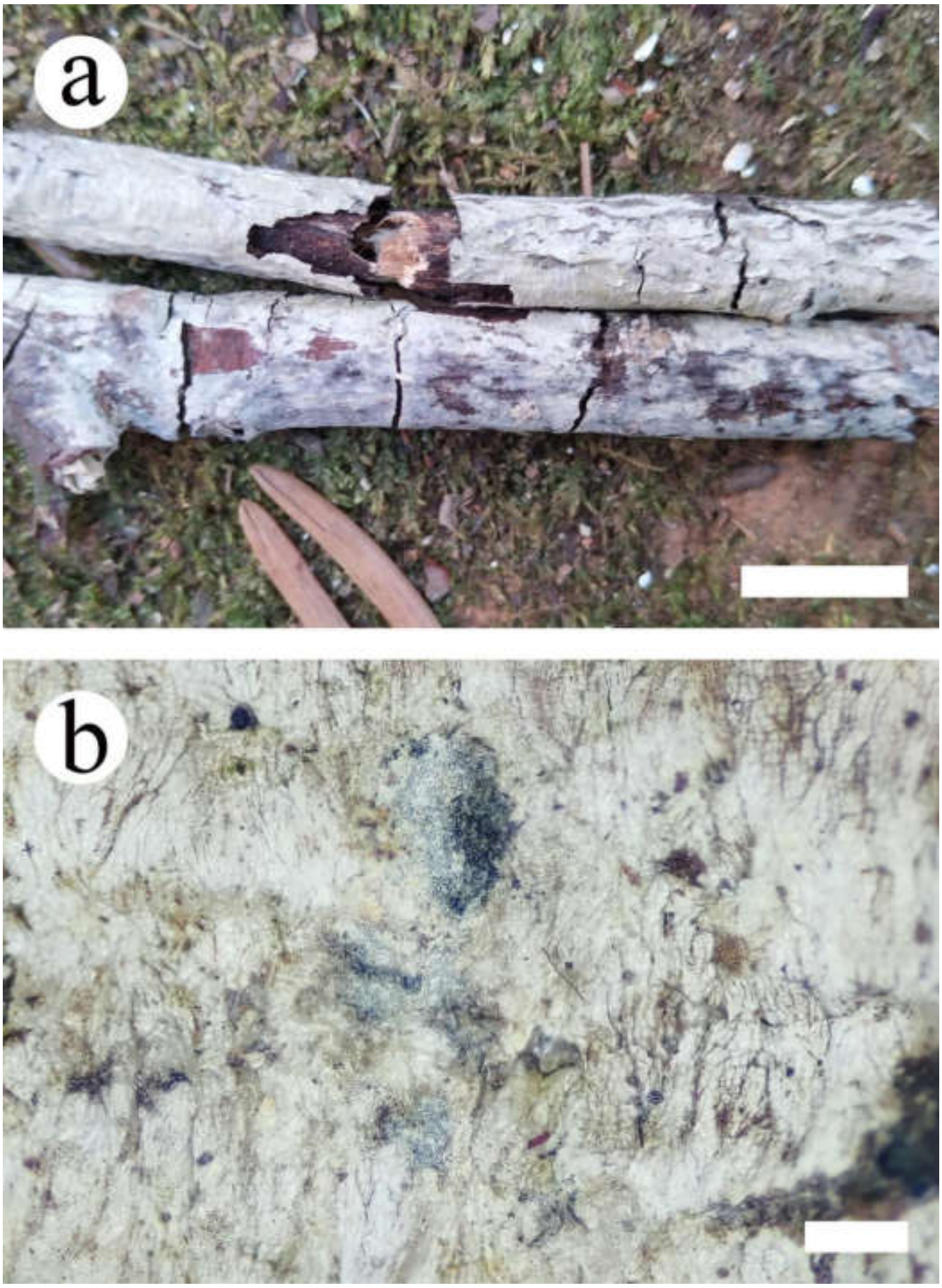

Figure 64 – Basidiomata of *Tubulicrinis pini* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, 2–3.5 µm in diameter, subhymenial hyphae immersed in a resinous matter; IKI–, CB–, tissues unchanged in KOH. Lyocystidia numerous, projecting, cylindrical to slightly sinuous, bi-rooted, 55–75 × 8.5–10 µm, projecting above the hymenium; cystidioles absent. Basidia clavate, with 4 sterigmata and a basal clamp connection, 11–14.5 × 4.5–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores cylindrical to allantoid, colorless, thin-walled, smooth, IKI–, CB–, (4.8–)5–6(–6.4) × 1.8(–2)–2.3 µm, L = 5.52 µm, W = 2.20 µm, Q = 2.43–2.51 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Puer, Jingdong County, Ailaoshan National Nature Reserve, GPS coordinates 24°36' N, 10°32' E, altitude 2500 m asl., on the fallen branch of *Pinus*, leg. C.L. Zhao, 3 October 2017, CLZhao 3679 (SWFC).

Notes – Based on the ITS, nLSU and mtSSU data (Fig. 10), the new species *Tubulicrinis pini* is grouped within *Tubulicrinis*, forming a monophyletic lineage, and is closely associated with *T. glebulosus* (Fr.) Donk and *T. yunnanensis* C.L. Zhao. However, *T. glebulosus* can be delimited from *T. pini* by its whitish to pale ochraceous hymenial surface, longer basidia (20–25 × 4–5 µm) and basidiospores (6–9 × 1.5–2.25 µm, Bernicchia & Gorjón 2010); *T. yunnanensis* can be distinguished from *T. pini* by its primrose to olivaceous buff hymenial surface, and narrower basidia (8.5–20.5 × 2.5–4.5 µm, He et al. 2020).

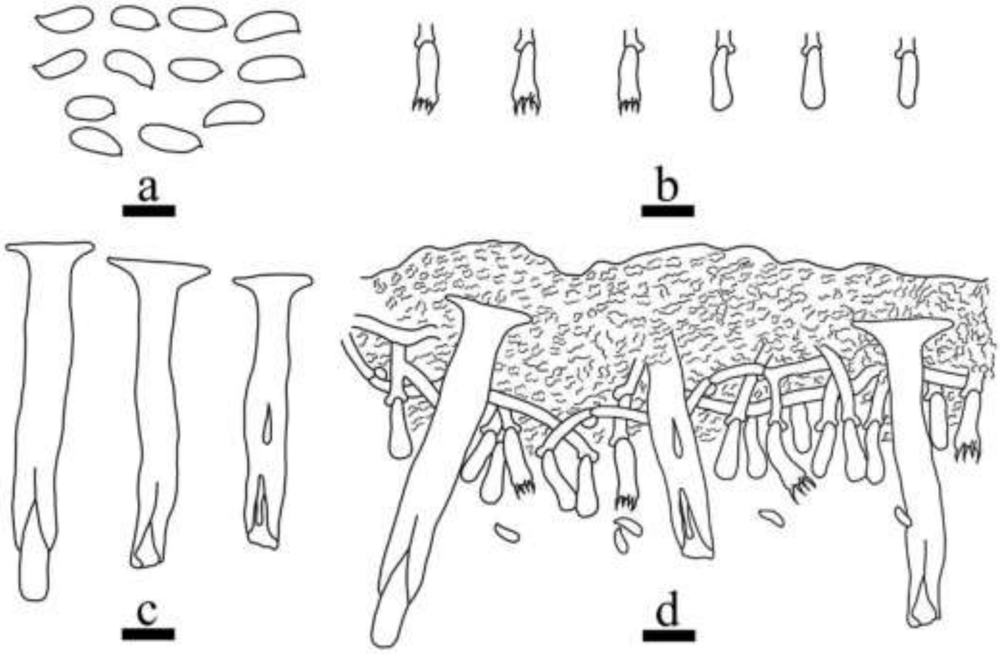

Figure 65 – Microscopic structures of *Tubulicrinis pini* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Lyocystidia. d A section of hymenium. Scale bars: a = 5 µm, b–d = 10 µm.

Polyporales Gäum.

Hypochniciaceae J.H. Dong & C.L. Zhao, fam. nov.

Index Fungorum number: IF848334; Facesoffungi number: FoF15425

Etymology – *Hypochniciaceae* (Lat.): referring to the type genus *Hypochnicium*.

Type genus – *Hypochnicium* J. Erikss.

Description – Basidiomata resupinate. Hymenial surface smooth, hypochnoid, tuberculate to odontioid. Hyphal system monomitic; generative hyphae with clamp connections. Cystidia present. Basidia clavate to suburniform, usually constricted, with 4 sterigmata and a basal clamp connection. Basidiospores ellipsoid, subglobose to globose, distinctly thick-walled, smooth, IKI–, cyanophilous.

Notes – Justo et al. (2017) and He et al. (2019) indicated that *Hypochnicium* could not be assigned to any recognized family of Polyporales, and its classification at the family level was treated as incertae sedis. Maekawa et al. (2023), based on the morphological and phylogenetic studies of *Hypochnicium* sensu lato, supported a monophyletic lineage of *Hypochnicium* s. str. In this study, the new family Hypochniciaceae formed a single lineage (100% BS, 100% BP and 1.00 BPP) and then grouped with Hyphodermataceae Jülich and Steccherinaceae Parmasto, using combined ITS, nLSU, mtSSU, RPB1 and TEF1 sequence data (Fig. 13). Hence, based on morphology and molecular evidence, Hypochniciaceae is established for *Hypochnicium*, and three genera are accepted in Hypochniciaceae viz., *Bulbillomyces* Jülich, *Gyrophanopsis* Jülich and *Hypochnicium*.

Hypochnicium J. Erikss.

Index Fungorum number: IF17832; Facesoffungi number: FoF15426

Type species – *Hypochnicium bombycinum* (Sommerf.) J. Erikss.

Notes – The genus *Hypochnicium* J. Erikss. was introduced by Eriksson (1958) and typified by *H. bombycinum* (Sommerf.) J. Erikss. *Hypochnicium* has been continually studied based on both morphology and phylogeny (Nilsson & Hallenberg 2003, Paulus et al. 2007, Telleria et al. 2010a, Justo et al. 2017, Maekawa et al. 2023). Nilsson & Hallenberg (2003) clarified the phylogeny of the *H. punctulatum* complex through parsimony analysis based on ITS sequence, in which the new combination *H. cremicolor* Bres. was synonymized with *H. punctulatum* (Cooke) J. Erikss. and *H. caucasicum* Parmasto was demonstrated to be a synonym to *H. wakefieldiae* (Bres.) J. Erikss. Phylogenetic analyses based on the ITS region of rDNA suggested that the species of *Hypochnicium* formed a monophyletic group, and the synonymy of *Gyrophanopsis* with *Hypochnicium* was validated and *Nodotia* Hjortstam was re-evaluated as a synonym of *Hypochnicium* (Paulus et al. 2007). *Hypochnicium* was reevaluated based on morphological and molecular data, revealing six clades, with one containing taxa with smooth spores, and three with ornamented spores, and proposing two new species *H. guineense* Tellería, M. Dueñas, Melo & M.P. Martín, *H. michelii* Tellería, M. Dueñas, Melo & M.P. Martín (Telleria et al. 2010a). Justo et al. (2017) studied the phylogenetic relationships within *Hypochnicium* and proposed several species grouped in Podoscyphaceae, although they did not appear closely related to the type species *H. bombycinum*. The study of *Hypochnicium* sensu lato included 14 species of *Hypochnicium* in *Neohypochnicium* N. Maek. & R. Sugaw. supporting a monophyletic lineage of *Hypochnicium* s. str. (Maekawa et al. 2023).

Incrustoporiaceae Jülich

Index Fungorum number: IF81733; Facesoffungi number: FoF15427

Type genus – *Incrustoporia* Domański

Skeletocutis Kotl. & Pouzar

Index Fungorum number: IF18554; Facesoffungi number: FoF15428

Type species – *Skeletocutis amorpha* (Fr.) Kotl. & Pouzar

Notes – The genus *Skeletocutis* Kotl. & Pouzar was established by Kotlába & Pouzar (1958) and typified by *S. amorpha* (Fr.) Kotl. & Pouzar. Based on multi-gene analyses, Binder et al. (2013) demonstrated that the type species of *Skeletocutis* (*S. amorpha*) belongs to the tyromyces clade, and appearing to be grouped with *Tyromyces chioneus* (Fr.) P. Karst., and *Piloporia sajanensis* (Parmasto) Niemelä by using ribosomal DNA sequences. Bian et al. (2016) described a new poroid species in *Skeletocutis* based on its morphological characters and rDNA sequences, which also belonged to the tyromyces clade, and was related to *S. amorpha* and *S. portcrosensis* A. David. Extensive taxonomic and phylogenetic studies have been conducted on polypores in China, with limited emphasis on *Skeletocutis* within Incrustoporiaceae (Jayawardena et al. 2023). In this study, one new species of *Skeletocutis* is introduced from China based on morphological characteristics and phylogenetic analyses inferred from ITS sequences.

Skeletocutis rhizomorpha J.H. Dong & C.L. Zhao, sp. nov. Figs 66, 67

Index Fungorum number: IF850337; Facesoffungi number: FoF15429

Diagnosis – Differs from other *Skeletocutis* species by the soft corky basidiomata with cream to buff, poroid hymenial surface, rhizomporphic margin, dimitic hyphal system with clamped generative hyphae and allantoid basidiospores measuring 2–2.7 × 1–1.5 µm.

Etymology – *rhizomorpha* (Lat.): referring to growing the rhizomorphic hymenophore of the type specimen.

Type – China, Yunnan Province, Puer, Jingdong County, Wuliangshan National Nature Reserve, GPS coordinates 23°57' N, 100°22' E, altitude 3380 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 2 October 2017, CLZhao 3552 (SWFC, holotype).

Description – Basidiomata annual, resupinate, soft corky, without odor or taste when fresh, becoming coriaceous upon drying, up to 5 cm long, 3cm wide, 1 mm thick. Poroid surface cream when fresh, turning to cream to buff upon drying, pores angular, 4–8 per mm, up to 1.5 mm deep, 0.2 mm in diameter; dissepiments thin; tubes concolorous with poroid surface. Context cream, flocculence, up to 1 mm thick. Margin distinct when juvenile, white to cream, rhizomporphic, up to 2 mm wide.

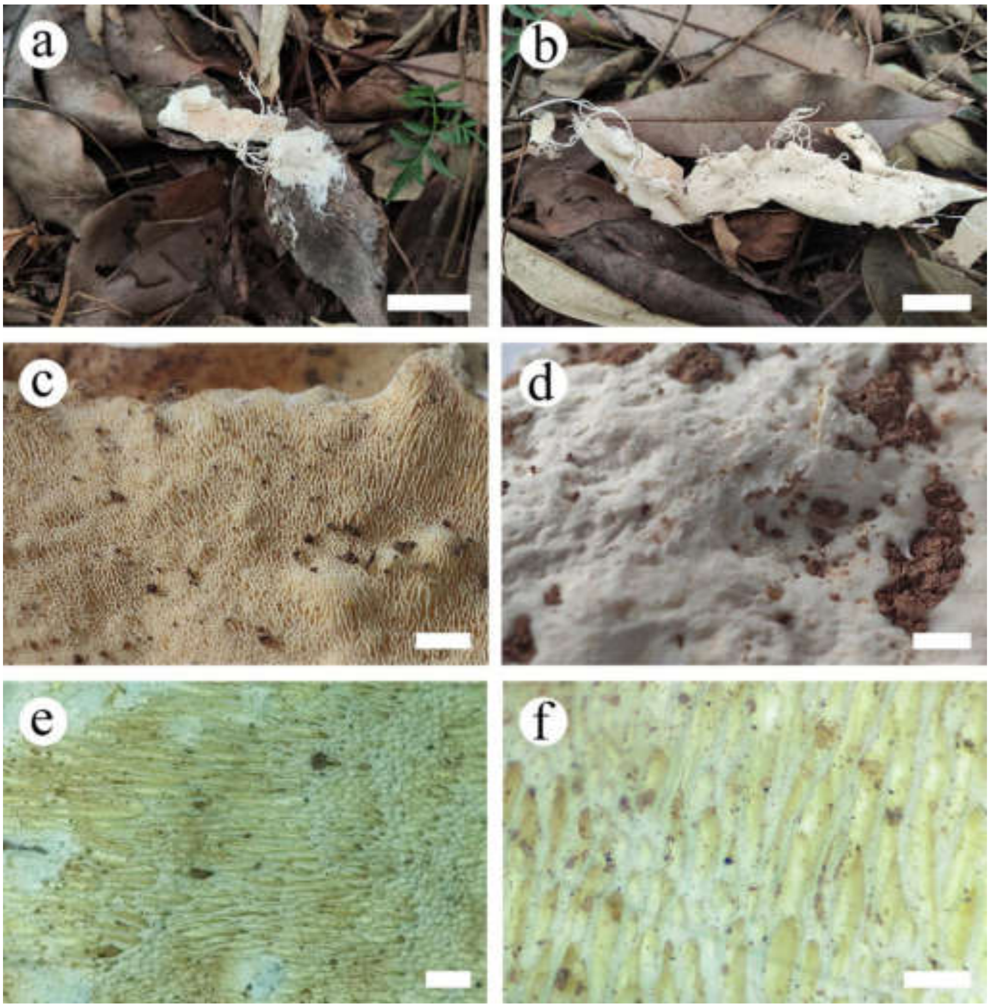

Figure 66 – Basidiomata of *Skeletocutis rhizomorpha* (holotype). Scale bars: a–b = 2 cm, c–e = 1 mm, f = 0.5 mm.

Hyphal system dimitic, generative hyphae with clamp connections; skeletal hyphae dominant, IKI–, CB–, tissues unchanged in KOH. Subiculum: generative hyphae, colorless, thin-walled, occasionally branched and bearing crystals, 2.5–3.5 µm in diameter; skeletal hyphae dominant, thick-walled, flexuous, unbranched, interwoven, 3–5 µm in diameter. Tubes: generative hyphae, thin-walled, usually covered by crystals, sharp-pointed encrustations, especially at dissepiment edge, 2–3 µm in diameter; skeletal hyphae dominant, thick-walled with a narrow lumen to subsolid, unbranched, subparallel along the tubes, 3–4.5 µm in diameter. Dissepiment edge with abundant smooth skeletal hyphae, fairly straight, encrusted generative hyphae. Cystidia absent, cystidioles abundant, bottle-shaped, with a conical apex, almost as size as basidia, 5.5–9 × 2.5–4 µm. Basidia barrelled, with 4 sterigmata and a basal clamp connection, 5.5–9 × 3–4 µm; basidioles infrequent, in shape similar to basidia, but slightly smaller. Basidiospores allantoid, colorless, thin-walled, smooth, usually bearing one to two small guttulae, CB–, IKI–, (1.8–)2–2.7(–3) × 1–1.5 µm, L = 2.34 µm, W = 1.29 µm, Q = 1.71–1.96 (n = 120/4).

Material examined (paratypes) – China, Yunnan Province, Puer, Jingdong County, Wuliangshan National Nature Reserve, GPS coordinates 23°57' N, 100°22' E, altitude 3380 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 2 October 2017, CLZhao 3516; on the trunk of angiosperm, leg. C.L. Zhao, 2 October 2017, CLZhao 3455, CLZhao 3583, CLZhao 3667 (SWFC).

Notes – In this study, the new species *Skeletocutis rhizomorpha* is grouped into *Skeletocutis*, based on the ITS data (Fig. 11), and is found to be sister to the species *S. bambusicola* L.W. Zhou & W.M. Qin. However, *S. bambusicola* can be delimited from *S. rhizomorpha* by its both larger basidia (12–20 × 4–5 µm) and basidiospores (2.7–3.1 × 1.5–1.9 µm, Zhou & Qin 2012).

Skeletocutis rhizomorpha resembles *S. subchrysella* B.K. Cui & Shun Liu by sharing allantoid basidiospores. However, *S. subchrysella* differs from *S. rhizomorpha* by its both longer basidia (10.3–15.6 × 3.2–4.5 µm) and basidiospores (2.7–3.2 × 0.7–1 µm, Jayawardena et al. 2023).

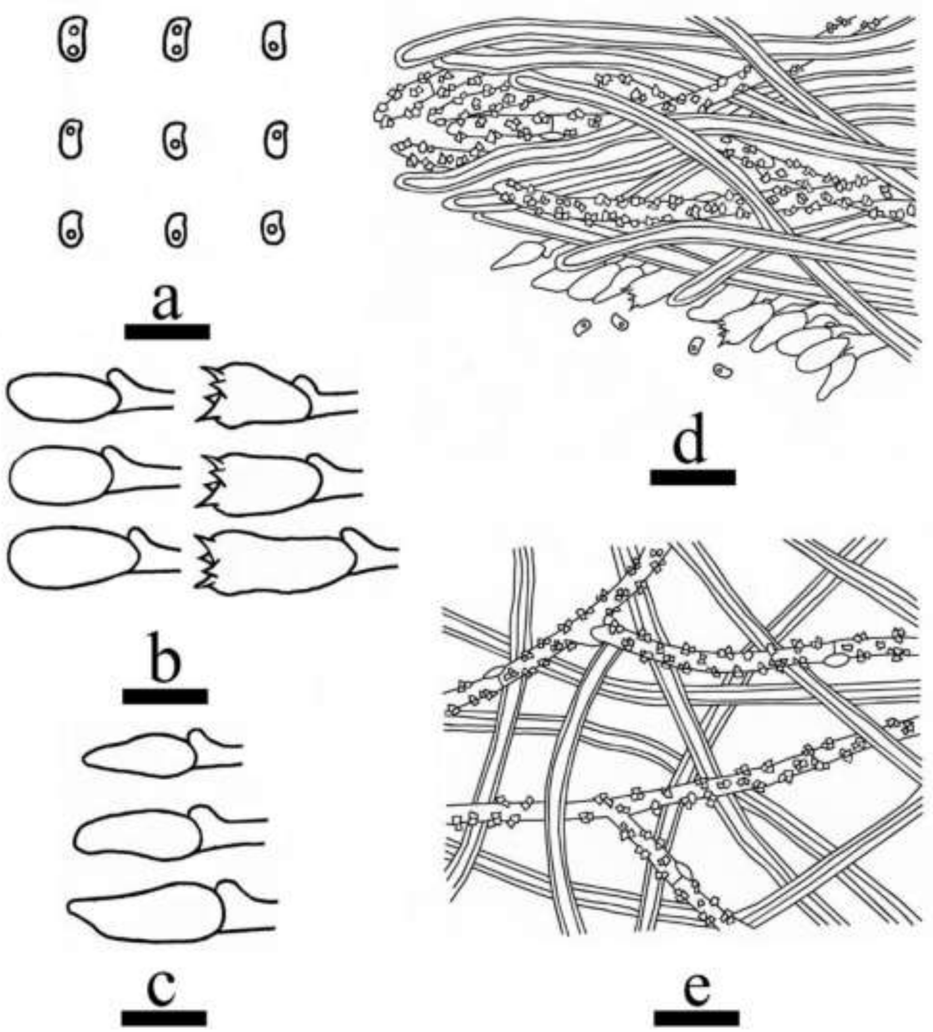

Figure 67 – Microscopic structures of *Skeletocutis rhizomorpha* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Cystidioles. d A section of hymenium. e Hyphal from context. Scale bars: a–c = 5 µm, d–e = 10 µm.

Irpicaceae Spirin & Zmitr.

Index Fungorum number: IF82147; Facesoffungi number: FoF15430

Type genus – *Irpex* Fr.

Efibula Sheng H. Wu

Index Fungorum number: IF25473; Facesoffungi number: FoF15431

Type species – *Efibula tropica* Sheng H. Wu

Notes – The genus *Efibula* Sheng H. Wu was introduced by Wu (1990) and typified by *E. tropica* Sheng H. Wu. Revisiting the taxonomy of *Phanerochaete* P. Karst. using a four gene dataset, revealed that four *Efibula* species clustered together and then grouped with *Byssomerulius* corium (Pers.) Parmasto (Floudas & Hibbett 2015). A phylogenetic study revising the family-level classification of the Polyporales showed that *E. clarkia* Floudas & Hibbett and *E. gracilis* Floudas & Hibbett grouped, with *Efibula* species nested within Irpicaceae (Justo et al. 2017). Chen et al. (2021) demonstrated through phylogenetic analyses of multiple genes that the *Efibula* was paraphyletic in the phylogenetic tree, however, there was insufficient morphological evidence to support the recognition of separate genera. In this study, a new *Efibula* species is introduced from China, characterized by morphological traits and analyzed phylogenetically using ITS, nLSU and TEF1 sequences.

Efibula daweishanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 68, 69

Index Fungorum number: IF850338; Facesoffungi number: FoF15432

Diagnosis – Differs from other *Efibula* species by the coriaceous basidiomata with cream to slightly buff, grandinoid hymenial surface, monomitic hyphal system with septate generative hyphae and elliposoid basidiospores measuring 6–7.5 × 3.5–4.8 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 18946 (SWFC).

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft coriaceous when fresh, becoming coriaceous upon drying, up to 5 cm long, 3 cm wide, 50–100 µm thick. Hymenial surface grandinoid, white to cream when fresh, turning to cream to slightly buff upon drying. Sterile margin narrow, slightly cream, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with simple septa, colorless, thin-walled, frequently interwoven, subhymenial hyphae more or less covered by the crystals, 2.5–4 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia and cystidioles absent. Basidia clavate, slightly sinuous, with 4 sterigmata and a basal simple septum, 14–19 × 5–6.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores elliposoid, colorless, thin-walled, smooth, IKI–, CB–, (5.8–)6–7.5 × 3.5–4.8(–5) µm, L = 6.67 µm, W = 4.12 µm, Q = 1.55–1.66 (n = 90/3).

Material examined (paratypes) – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 19002; Lincang, Yun County, Dumu Village, GPS coordinates 24°44' N, 100°12' E, altitude 1590 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 20 October 2022, CLZhao 25072 (SWFC).

Notes – Based on the ITS, nLSU and TEF1 data (Fig. 12), the new species *Efibula daweishanensis* is classified within *Efibula*, and clusters with *E. grandinosa* Yue Li & S.H. H and *E. shenghuae* Yue Li & S.H. He. However, *E. grandinosa* can be delimited from *E. daweishanensis* by its pale orange to grayish orange hymenial surface, and longer basidia (36–43 × 5–7 µm, Li et al. 2022b); *E. shenghuae* can be distinguished from *E. daweishanensis* by its orange white to pale orange hymenial surface, longer basidia (23–38 × 4.5–7 µm) and narrower basidiospores (6–6.5 × 3–3.5 µm, Li et al. 2022b).

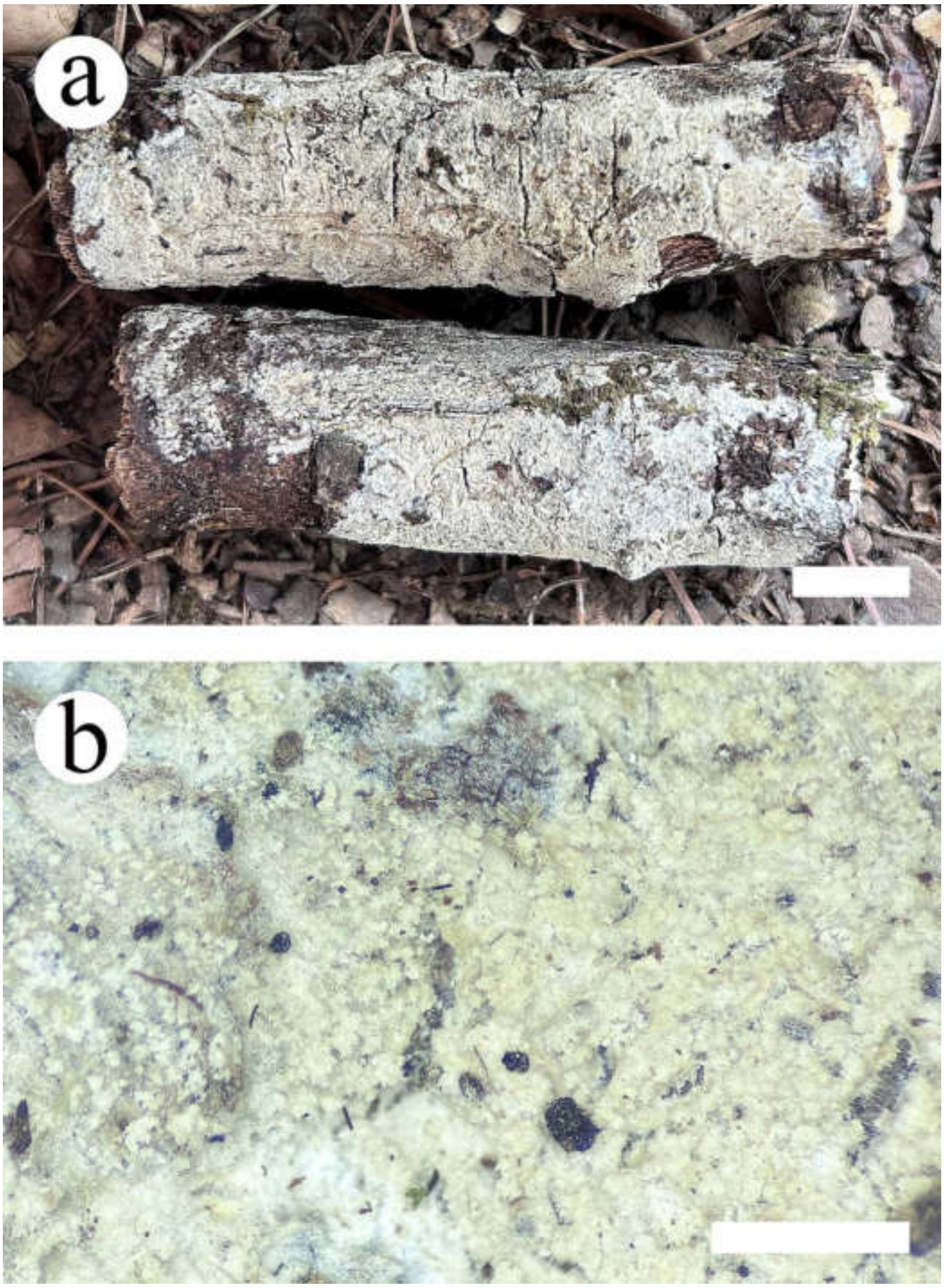

Figure 68 – Basidiomata of *Efibula daweishanensis* (holotype). Scale bars: a = 1 cm, b = 1 mm.

Neohypochniciaceae J.H. Dong & C.L. Zhao, fam. nov.

Index Fungorum number: IF850339; Facesoffungi number: FoF15433

Etymology – *Neohypochniciaceae* (Lat.): referring to the type genus *Neohypochnicium*.

Type genus – *Neohypochnicium* N. Maek. & R. Sugaw.

Description – Basidiomata resupinate. Hymenial surface smooth to odontoid. Hyphal system monomitic; generative hyphae with clamp connections. Cystidia present. Basidia subclavate to suburniform, with 4 sterigmata and a basal clamp connection. Basidiospores ellipsoid, subglobose to globose, smooth, finely verrucose or finely echinulate, thick-walled, IKI–, cyanophilous.

Notes – *Neohypochnicium* could not be assigned to any recognized family of Polyporales, and its classification at the family level was treated as incertae sedis (Maekawa et al. 2023). In this study, based on combined ITS, nLSU, mtSSU, RPB1 and TEF1 sequence data, the new family Neohypochniciaceae formed a single lineage and then placed within Podoscyphaceae D.A. Reid

(Fig. 13). Hence, based on morphological characters and molecular evidence, Neohypochniciaceae fam. nov. is proposed for *Neohypochnicium*. Up to date, only *Neohypochnicium* taxa are accepted within Neohypochniciaceae.

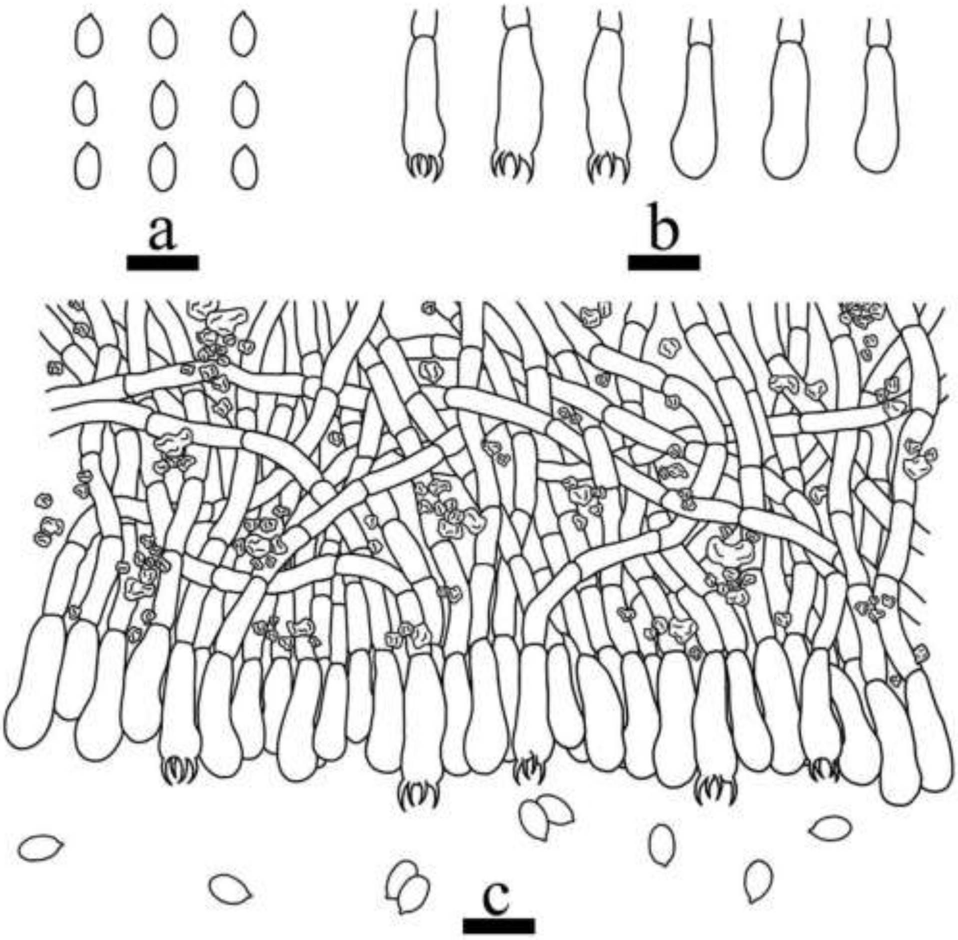

Figure 69 – Microscopic structures of *Efibula daweishanensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c A section of hymenium. Scale bars: a–d = 10 µm.

Neohypochnicium N. Maek. & R. Sugaw.

Index Fungorum number: IF842573; Facesoffungi number: FoF15434

Type species – *Neohypochnicium perlongicystidiosum* N. Maek., Kogi & Norikura

Notes – The genus *Neohypochnicium* N. Maek. & R. Sugaw. was established by Maekawa et al. (2023) and typified by *N. perlongicystidiosum* N. Maek., Kogi & Norikura. Maekawa et al. (2023), based on the morphological and phylogenetic studies of *Hypochnicium* sensu lato, supported a monophyletic lineage of *Hypochnicium* s. str., in which 14 species of *Hypochnicium* were included in "*Neohypochnicium*" clade, namely, *Hypochnicium albostramineum*, *H. aotearoae* B.C. Paulus, H. Nilsson & Hallenb., *H. cremicolor* (Bres.) H. Nilsson & Hallenb., *H. cystidiatum* Boidin & Gilles, *H. geogenium*, *H. guineense* Tellería, M. Dueñas, Melo & M.P. Martín, *H. huinayense* Tellería, M. Dueñas & M.P. Martín, *H. michelii*, *H. microsporum* G. Gruhn, Schimann & M. Roy, *H. patagonicum* Gorjón & Hallenb., *H. pini*, *H. punctulatum*, *H. subrigescens*, and *H. wakefieldiae* (Maekawa et al. 2023). In this study, six new species, *N. daweishanense*, *N. farinaceum*, *N. murinum*, *N. velutinum*, *N. yunnanense* and *N. zixishanense* are described from China based on morphology and phylogeny.

Neohypochnicium daweishanense J.H. Dong & C.L. Zhao, sp. nov. Figs 70, 71

Index Fungorum number: IF850340; Facesoffungi number: FoF15435

Diagnosis – Differs from other *Neohypochnicium* species by the membranaceous basidiomata with slightly yellowish to yellowish brown, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and globose basidiospores measuring 7.8–9.5 × 7.7–9 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 17726 (SWFC).

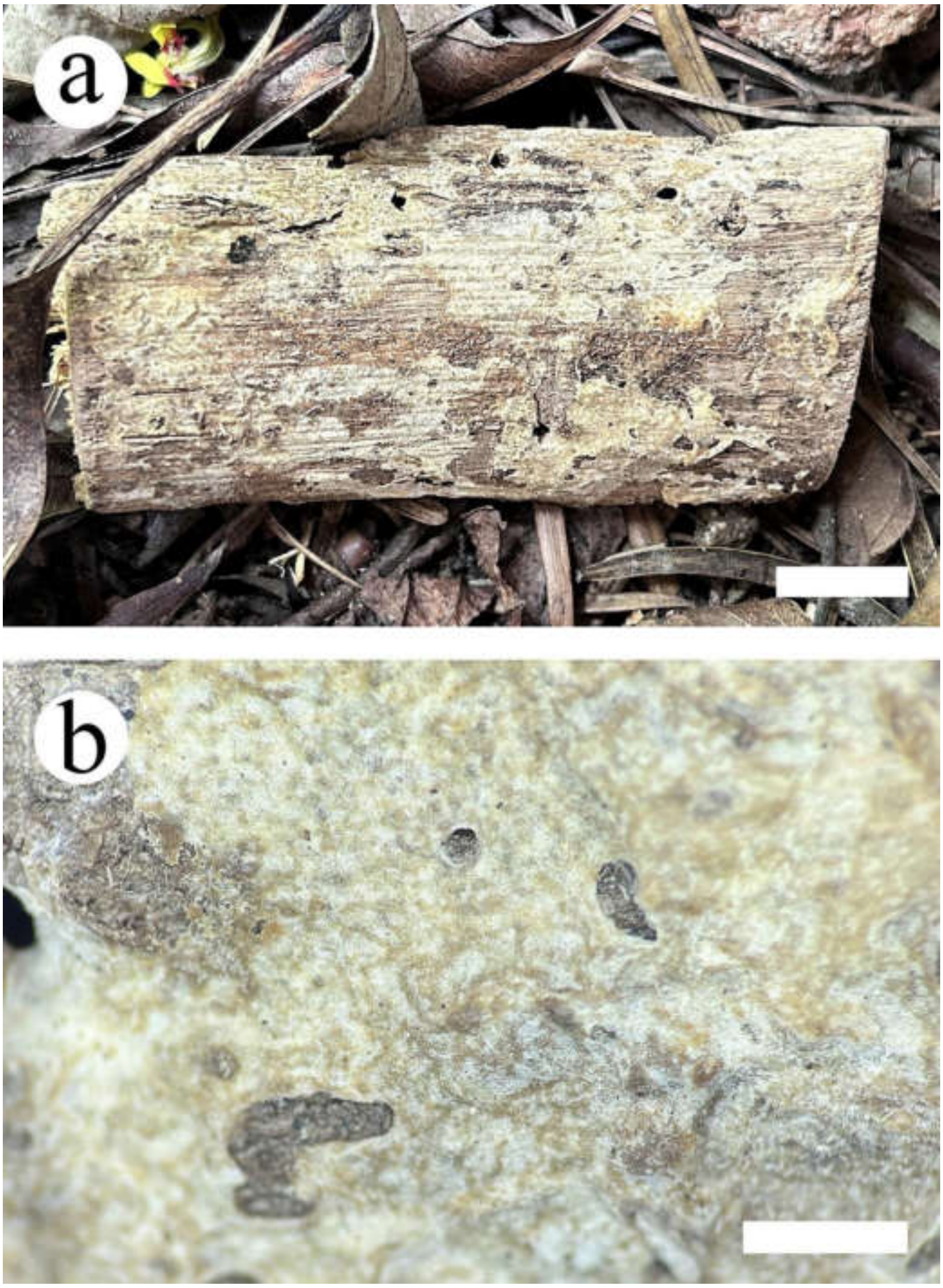

Figure 70 – Basidiomata of *Newhypochnicium daweishanense* (holotype). Scale bars: a = 1 cm, b = 1 mm.

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft membranaceous when fresh, becoming hard membranaceous upon drying, up to 10 cm long, 5 cm wide, 50–100 µm thick. Hymenial surface smooth, hypochnoid, cream to slightly yellowish when fresh, turning to slightly yellowish to yellowish brown upon drying. Sterile margin narrow, slightly cream, abrupt, up to 1 mm wide.

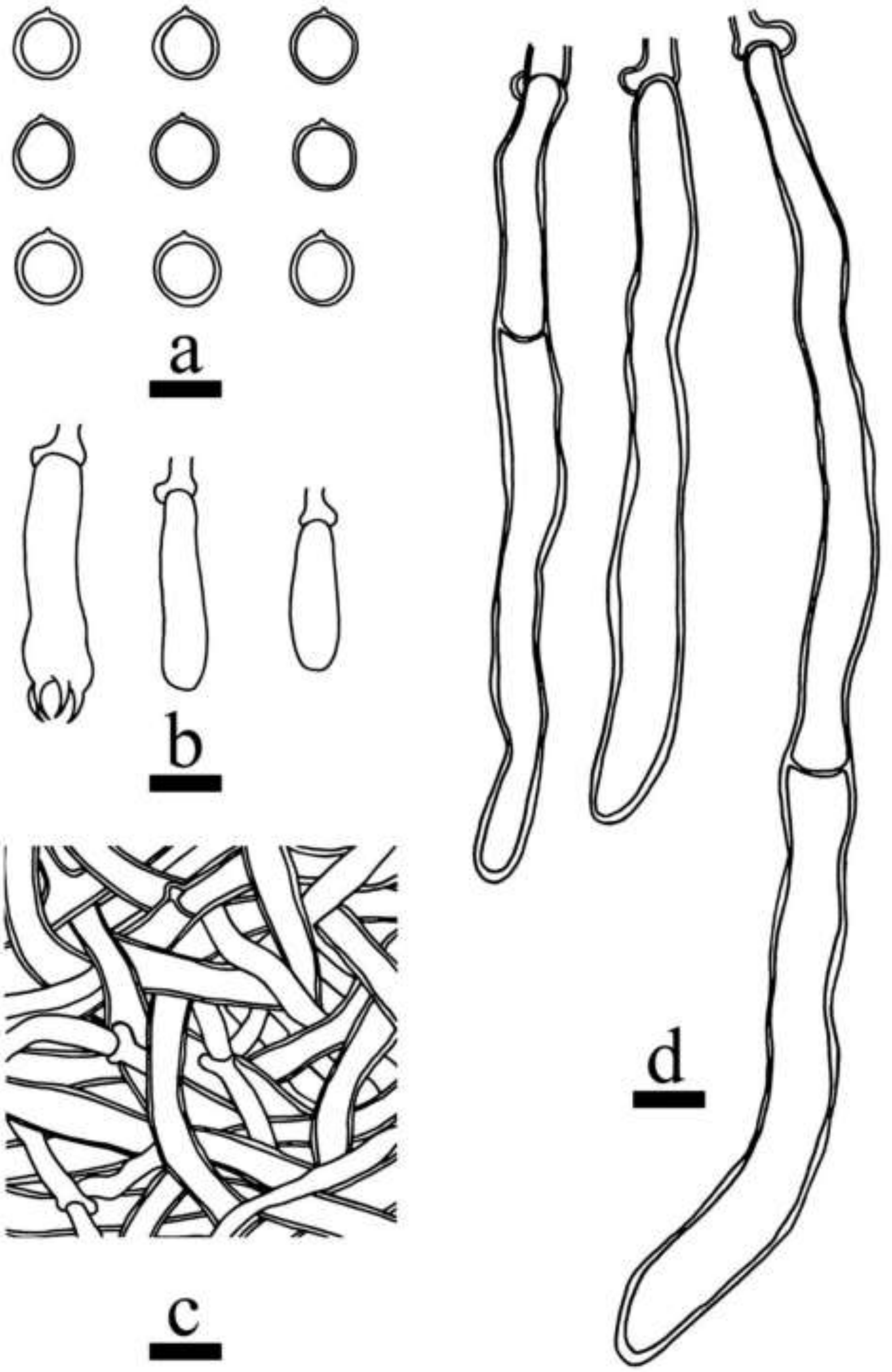

Figure 71 – Microscopic structures of *Newhypochnicium daweishanense* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c A section of hymenium. d Tubular cystidia. Scale bars: a–d = 10 µm.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to thick-walled, branched, interwoven, 4–7 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia numerous, tubular, slightly thick-walled, with one or several adventitious septa, with tapered apex, 80–180 × 6–10 µm; cystidioles absent. Basidia subclavate, with 4 sterigmata and a basal clamp connection, 30–35 × 8–12 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores globose, colorless, thick-walled, smooth, IKI–, CB+, (7.5–)7.8–9.5 × (7.5–)7.7–9 µm, L =8.57 µm, W = 8.46 µm, Q = 1.01 (n = 30/1).

Notes – Based on the ITS, nLSU, mtSSU, RPB1 and TEF1 data (Fig. 13), the new species *Neohypochnicium daweishanense* is grouped within *Neohypochnicium*, and clustered with *N. geogenium* (Bres.) N. Maek. and *N. yunnanense*. However, *N. geogenium* can be delimited from *N. daweishanense* by its tuberculate hymenial surface, smaller basidia (20–30 × 5–6 µm) and smaller basidiospores (6–7.5 × 4–4.5 µm, Eriksson & Ryvarden 1976); *N. yunnanense* can be differentiated from *N. daweishanens* by its cream hymenial surface and corticous basidiomata.

Neohypochnicium daweishanense resembles *N. aotearoae* (B.C. Paulus, H. Nilsson & Hallenb.) N. Maek. and *N. asiaticum* N. Maek. & Kogi in having the smooth hymenial surface. However, *N. aotearoae* differs from *N. daweishanense* by its white to cream hymenial surface, verrucose and narrower basidiospores (5.6–8.7 × 4.8–7.3 µm, Paulus et al. 2007); *N. asiaticum* differentiates from *N. daweishanense* by its white hymenial surface, verrucose and narrower basidiospores (7–8 × 5.5–6.5 µm, Maekawa et al. 2023).

Neohypochnicium daweishanense is similar to *N. michelii* (Tellería, M. Dueñas, Melo & M.P. Martín) N. Maek., *N. microsporum* (G. Gruhn, Schimann & M. Roy) N. Maek. and *N. subrigescens* (Boidin) N. Maek. in having the smooth basidiospores. The species *N. michelii* differs from *N. daweishanense* by its porulose hymenial surface, smaller basidia (20–30 × 6–7.5 µm) and narrower basidiospores (9–11 × 7–7.5 µm, Telleria et al. 2010a); *N. microsporum* differentiates from *N. daweishanense* by its smaller basidiospores (3.9–5 × 3.8–5 µm, Gruhn et al. 2017); *N. subrigescens* differs from *N. daweishanense* by its both smaller basidia (20–25 × 5–6 µm) and basidiospores (4.2–6 × 3.6–5 µm, Kotiranta & Saarenoksa 1990).

Neohypochnicium farinaceum J.H. Dong & C.L. Zhao, sp. nov. Figs 72, 73

Index Fungorum number: IF848329; Facesoffungi number: FoF15436

Diagnosis – Differs from other *Neohypochnicium* species by the farinaceous basidiomata with slightly buff to buff, hypochnoid hymenial surface, monomitic hyphal system with clamped generative hyphae and subglobose to globose basidiospores measuring 7–8.5 × 6.5–7.5 µm.

Etymology – *farinaceum* (Lat.): referring to the farinaceous hymenophore of the type specimens.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 8 June 2020, CLZhao 18820 (SWFC, holotype).

Description – Basidiomata annual, resupinate, thin, without odor or taste, farinaceous when fresh, becoming brittle upon drying, up to 15 cm long, 3 cm wide, 50–200 µm thick. Hymenial surface hypochnoid, slightly buff when fresh, turning to buff upon drying. Sterile margin narrow, slightly buff, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven, 3–6 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) tubular, slightly thick-walled, obtuse apex, 93–120 × 4–6.5 µm; (2) clavate to subcylindrical, 50–90 ×5–8.5 µm; cystidioles absent. Basidia clavate, slightly constricted in the middle, with 4 sterigmata and a basal clamp connection, 20–32.5 × 6.5–8.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose to globose, colorless, thick-walled, smooth, cyanophilous, IKI–, (6.8–)7–8.5 × 6.5–7.5(–7.7) µm, L = 7.68 µm, W = 7.08 µm, Q = 1.05–1.15 (n = 300/10).

Material examined (paratypes) – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 2 August 2019, CLZhao 18089; 8 June 2020, CLZhao 18792, CLZhao 18856; 8 June 2020, CLZhao 19022; on the trunk of angiosperm, leg. C.L. Zhao, 8 June 2020, CLZhao 18764, CLZhao 18771, CLZhao 18787, CLZhao 18798, CLZhao 18844, CLZhao 18850, CLZhao 18867, CLZhao 18881 (SWFC).

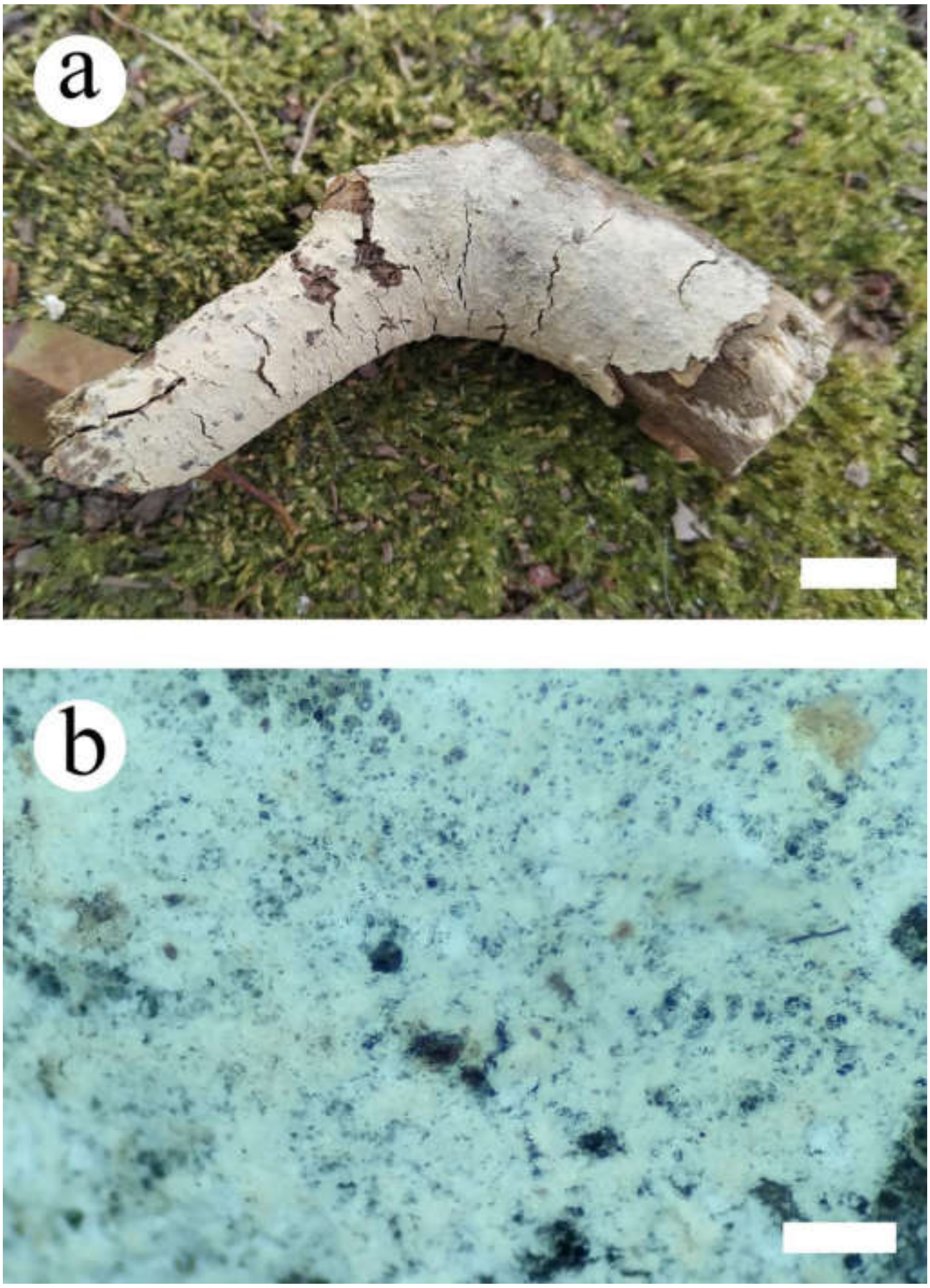

Figure 72 – Basidiomata of *Neohypochnicium farinaceum* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

Notes – In this study, using ITS, nLSU, mtSSU, RPB1 and TEF1 data (Fig. 13), the new species *Neohypochnicium farinaceum* is classified within *Neohypochnicium*, forming a monophyletic lineage and emerging as a sister to *N. murinum*. However, *N. murinum* can be delimited from *N. farinaceum* by its grey hymenial surface, and smaller basidiospores (5.5–6.5 × 5–6.3 µm).

Neohypochnicium farinaceum shares similarities with *N. cremicolor* (Bres.) N. Maek., *N. geogenium*, *N. perlongicystidiosum*, *N. punctulatum* (Cooke) N. Maek. and *N. wakefieldiae* (Bres.) N. Maek. in sharing the tubular cystidia. However, *N. cremicolor* differs from *N. farinaceum* by its porulose hymenial surface, smaller basidiospores (6–6.5 × 5–5.5 µm, Bernicchia & Gorjón 2010); *N. geogenium* differentiates from *N. farinaceum* in its tuberculate hymenial surface, narrower basidia (20–30 × 5–6 µm) and basidiospores (6–7.5 × 4–4.5 µm, Eriksson & Ryvarden 1976); *N. perlongicystidiosum* can be distinguished from *N. farinaceum* by its grandinioid to odontoid hymenial surface, larger basidia (46–70 × 9–12 µm) and basidiospores (10–12 × 9–11 µm, Maekawa et al 2023); *N. punctulatum* differs from *N. farinaceum* by its tuberculate hymenial surface, and smaller basidiospores (5.5–6.6 × 4.5–5 µm, Eriksson & Ryvarden 1976); *N. wakefieldiae* can be distiniguished from *N. farinaceum* by its porulose hymenial surface, and narrower basidiospores (6.5–8× 5.5–6 µm, Bernicchia & Gorjón 2010).

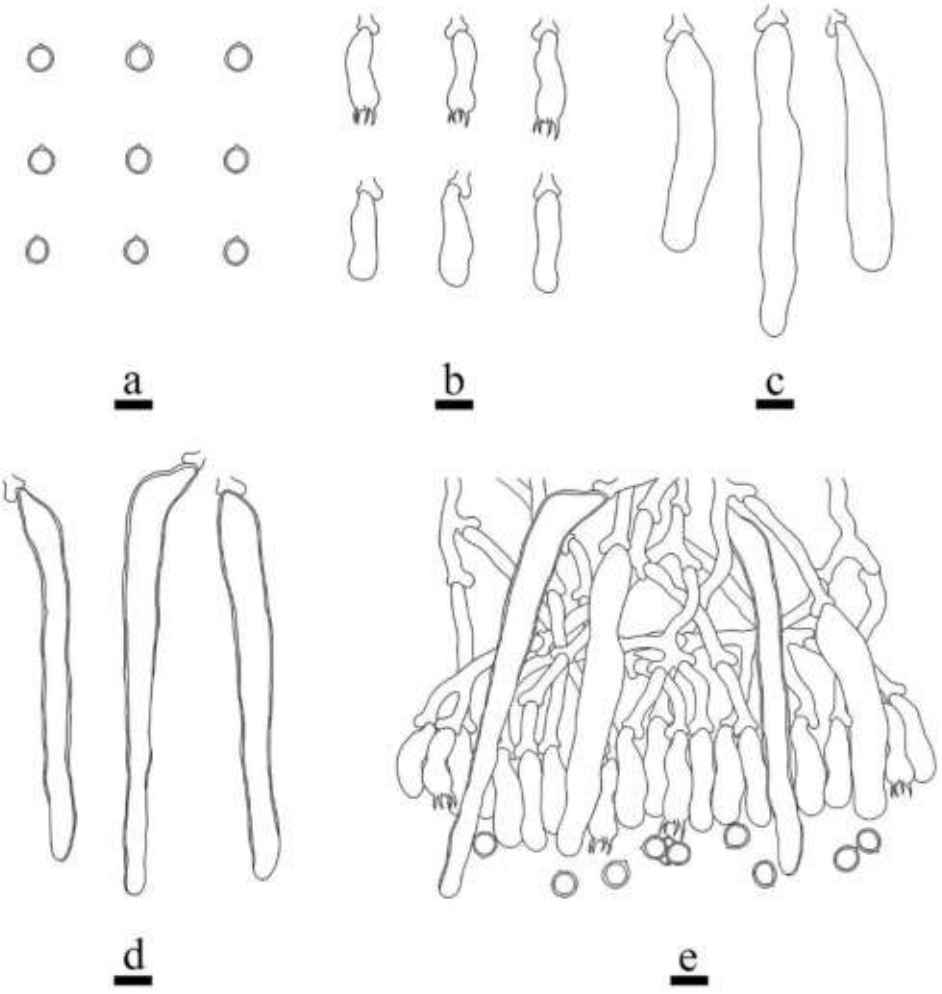

Figure 73 – Microscopic structures of *Neohypochnicium farinaceum* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Clavate to subcylindrical cystidia. d Tubular cystidia. e A section of hymenium. Scale bars: a–e = 10 µm.

Neohypochnicium murinum J.H. Dong & C.L. Zhao, sp. nov. Figs 74, 75

Index Fungorum number: IF848330; Facesoffungi number: FoF15437

Diagnosis – Differs from other *Neohypochnicium* species by the farinaceous basidiomata with grey, hypochnoid hymenial surface, monomitic hyphal system with clamped generative hyphae and subglobose basidiospores measuring 5.5–6.5 × 5–6.3 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 19012 (SWFC, holotype).

Description – Basidiomata annual, resupinate, without odor or taste, soft membranaceous when fresh, becoming furfuraceous upon drying, up to 10 cm long, 3.5 cm wide, 50–100 µm thick. Hymenial surface hypochnoid, white to slightly grey when fresh, turning to grey upon drying. Sterile margin narrow, slightly grey, thinning out, up to 1 mm wide.

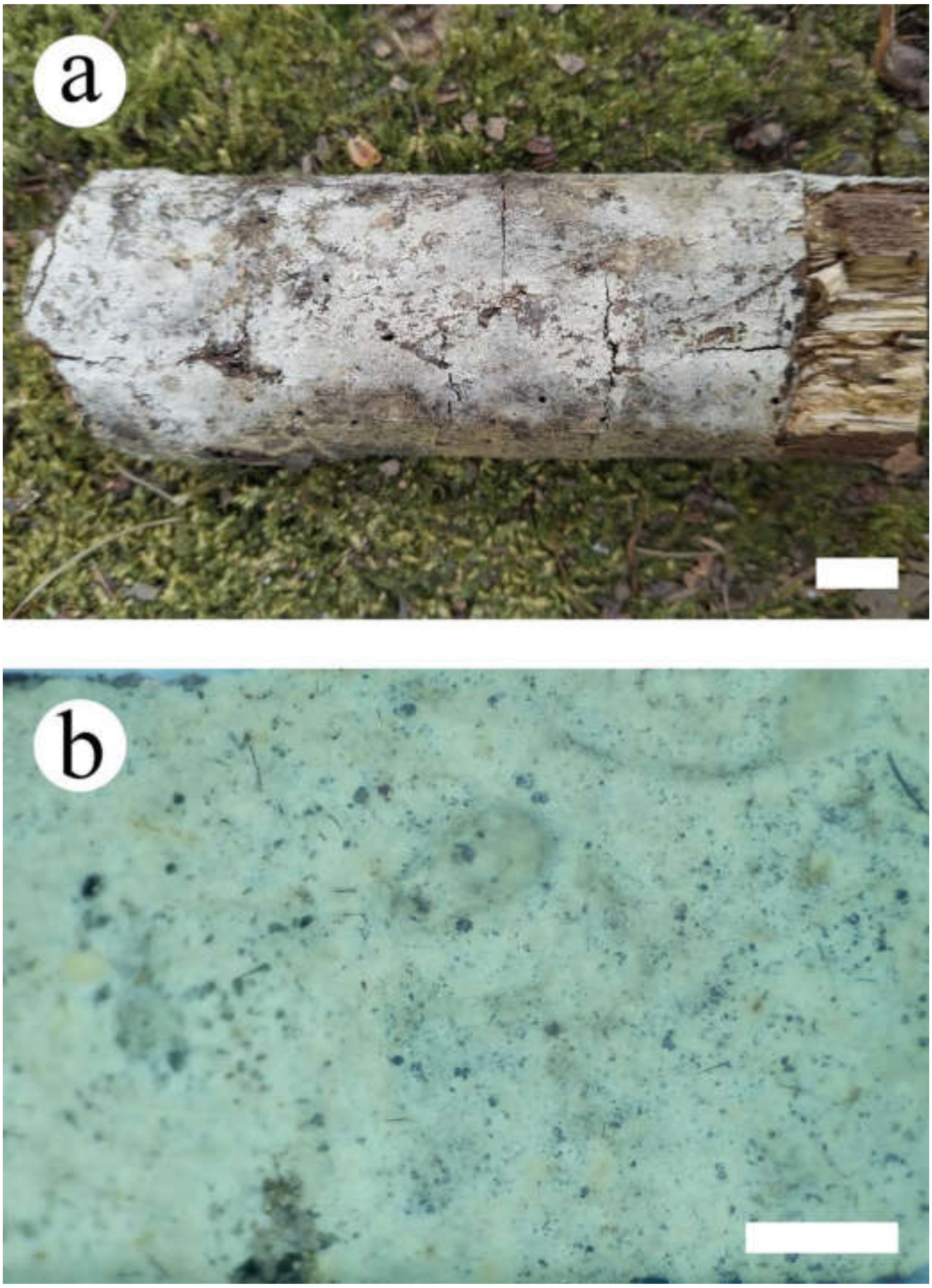

Figure 74 – Basidiomata of *Neohypochnicium murinum* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thick-walled, frequently branched, interwoven, 3.5–5.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia numerous, thick-walled, tubular, tapered and obtuse apex, 90–150 × 8.5–12 µm; cystidioles absent. Basidia clavate, constricted, some with a few guttulae, with 4 sterigmata and a basal clamp connection, 18–29 × 5.5–8 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose, colorless, thick-walled, smooth, sometimes with a few guttula, cyanophilous, IKI–, (5.3–)5.5–6.5(–6.8) × 5–6.3(–6.5) µm, L = 6.25 µm, W = 5.68 µm, Q = 1.08–1.11 (n = 210/7).

Material examined (paratypes) – China, Yunnan Province, Chuxiong, Zixishan National Forestry Park, GPS coordinates 25°01' N, 101°24' E, altitude 2500 m asl., on the trunk of *Pinus yunnanensis*, leg. C.L. Zhao, 30 June 2018, CLZhao 6855; Honghe, Pingbian County, Daweishan

National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 19017, CLZhao 19020, CLZhao 19031, CLZhao 19125, CLZhao 19129; on the trunk of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 19067 (SWFC).

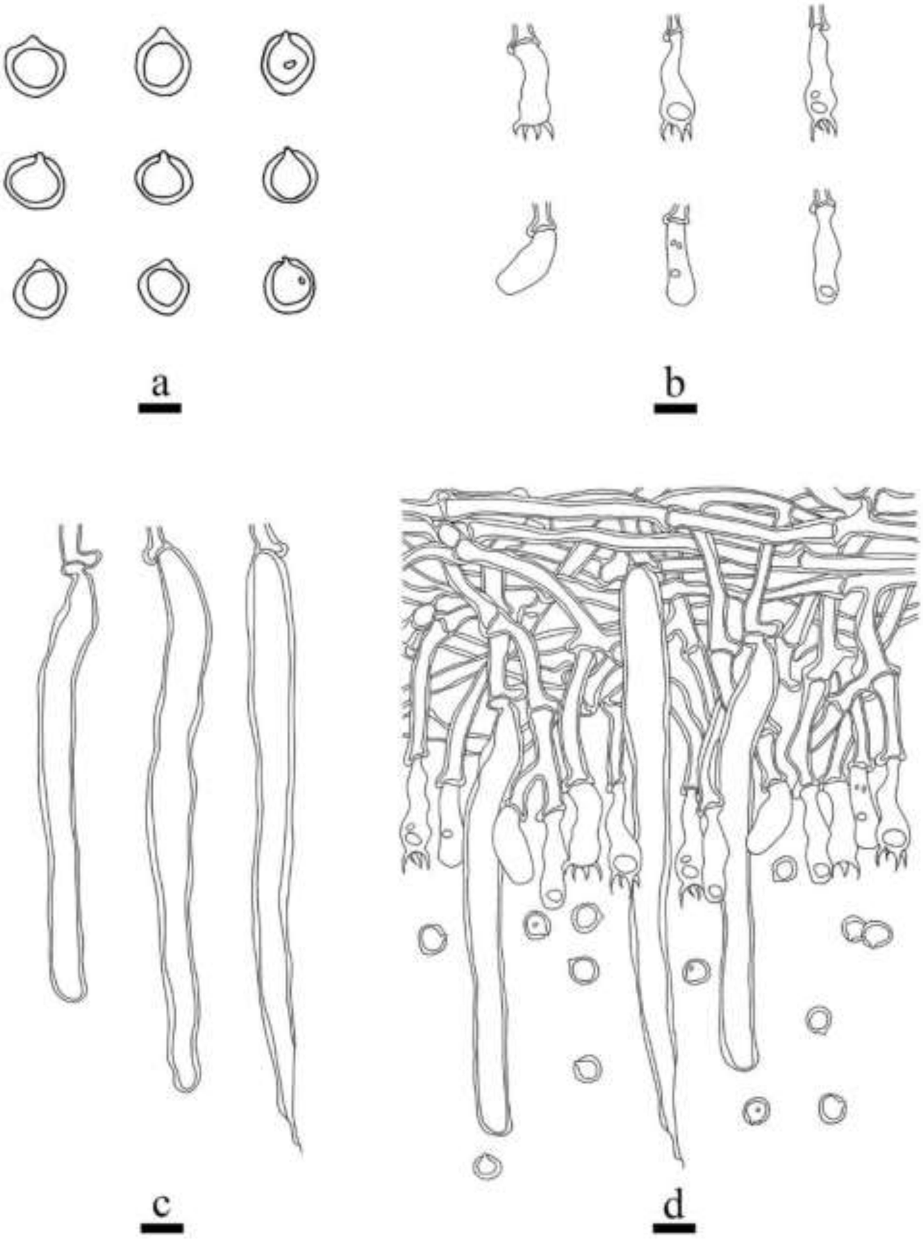

Figure 75 – Microscopic structures of *Neohypochnicium murinum* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Cystidia. d A section of hymenium. Scale bars: a–d = 10 µm.

Notes – Based on the ITS, nLSU, mtSSU, RPB1 and TEF1 data (Fig. 13), the new species *Neohypochnicium murinum* is grouped into *Neohypochnicium* forming a monophyletic lineage, and it is identified as a sister to *N. farinaceum*. However, *N. farinaceum* can be delimited from *N. murinum* by its buff hymenial surface, and larger basidiospores (7–8.5 × 6.5–7.5 µm).

Neohypochnicium murinum shares similarities with *N. albostramineum* (Bres.) N. Maek, *N. perlongicystidiosum* and *N. punctulatum* by having tubular cystidia. However, *N. albostramineum* differs from *N. murinum* by its porulose hymenial surface, longer basidia (30–40 × 6–8 µm) and larger basidiospores (8–10 × 6.5–7 µm, Bernicchia & Gorjón 2010);

N. perlongicystidiosum differentiates from *N. murinum* by its grandinioid to odontoid hymenial surface, larger basidia (46–70 × 9–12 µm) and basidiospores (10–12 × 9–11 µm, Maekawa et al. 2023); *N. punctulatum* differs from *N. murinum* in its tuberculate hymenial surface, longer basidia (30–40 × 6–7 µm) and narrower basidiospores (5.5–6.6 × 4.5–5 µm, Eriksson & Ryvarden 1976).

Neohypochnicium murinum is similar to *N. geogenium* and *N. michelii* in having the smooth basidiospores. However, *N. geogenium* differs from *N. murinum* due to its tuberculate hymenial surface, and narrower basidiospores (6–7.5 × 4–4.5 µm, Eriksson & Ryvarden 1976); *N. michelii* differentiates from *N. murinum* in its porulose hymenial surface, and larger basidiospores (9–11 × 7–7.5 µm, Telleria et al. 2010a).

Neohypochnicium velutinum J.H. Dong & C.L. Zhao, sp. nov. Figs 76, 77

Index Fungorum number: IF848331; Facesoffungi number: FoF15438

Diagnosis – Differs from other *Neohypochnicium* species by the panniform basidiomata with cream to slightly ochreous, velutinous hymenial surface, monomitic hyphal system with clamped generative hyphae and subglobose to globose basidiospores measuring 8.5–11.2 × 7.5–10.5 µm.

Etymology – *velutinum* (Lat.): referring to velutinous hymenophore of the type specimens.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 2 August 2019, CLZhao 18144 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft when fresh, becoming panniform upon drying, up to 7 cm long, 2.5 cm wide, 100–200 µm thick. Hymenial surface velutinous, cream when fresh, turning to cream to slightly ochreous upon drying. Sterile margin narrow, slightly gery, abrupt, up to 1.5 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thick-walled, frequently branched, interwoven, 4–6 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) tubular, slightly thick-walled, 92–120 × 8–9.5 µm; (2) capitate or subclavate, with three to four adventitious septa, 30–41 × 6–9 µm; cystidioles absent. Basidia clavate, slightly constricted, with 4 sterigmata and a basal clamp connection, 30–50 × 8.5–12 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose to globose, colorless, smooth and verrucose, thick-walled, some with a few guttulae, cyanophilous IKI–, 8.5–11.2(–11.5) × (7–)7.5–10.5(–10.8) µm, L = 9.96 µm, W = 9.09 µm, Q = 1.07–1.12 (n = 90/3).

Material examined (paratypes) – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 2 August 2019, CLZhao 18084, CLZhao 18085, CLZhao 18101; Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates 25°52' N, 97°38' E, altitude 1000 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 19 July 2023, CLZhao 30807, CLZhao 30839 (SWFC).

Notes – In this study, based on the ITS, nLSU, mtSSU, RPB1 and TEF1 data (Fig. 13), the new species *Neohypochnicium velutinum* is classified within *Neohypochnicium* and identified as a sister to *N. perlongicystidiosum*. However, *N. perlongicystidiosum* can be delimited from *N. velutinum* by its grandinioid to odontoid hymenial surface, and suburniform basidia (46–70 × 9–12 µm, Maekawa et al. 2023).

Neohypochnicium velutinum resembles *N. albostramineum* (Bres.) N. Maek., *N. cremicolor*, *N. huinayense* (Tellería, M. Dueñas & M.P. Martín) N. Maek., *N. punctulatum* and *N. wakefieldiae* in having the verrucose basidiospores. However, *N. albostramineum* differs from *N. velutinum* by its porulose hymenial surface,narrower basidia (30–40 × 6–8 µm) and smaller basidiospores (8–10 × 6.5–7 µm, Bernicchia & Gorjón 2010); *N. cremicolor* can be distinguished from *N. velutinum* in its porulose hymenial surface,narrower basidia (30–40 × 6–8 µm) and smaller basidiospores (6–6.5 × 5–5.5 µm, Bernicchia & Gorjón 2010); *N. huinayense* differs from *N. velutinum* by its porulose hymenial surface, shorter basidia (25–30 × 7–9 µm) and basidiospores (6.5–8 × 6.5–8 µm, Crous et al. 2013); *N. punctulatum* can be distinguished from *N. velutinum* in its tuberculate hymenial surface, narrower basidia (30–40 × 6–7 µm) and smaller basidiospores (5.5–6.6 × 4.5–5 µm, Eriksson & Ryvarden 1976); *N. wakefieldiae* differs from *N. velutinum* due to its porulose hymenial surface, narrower basidia (30–40 × 6–8 µm) and smaller basidiospores (6.5–8× 5.5–6 µm, Bernicchia & Gorjón 2010).

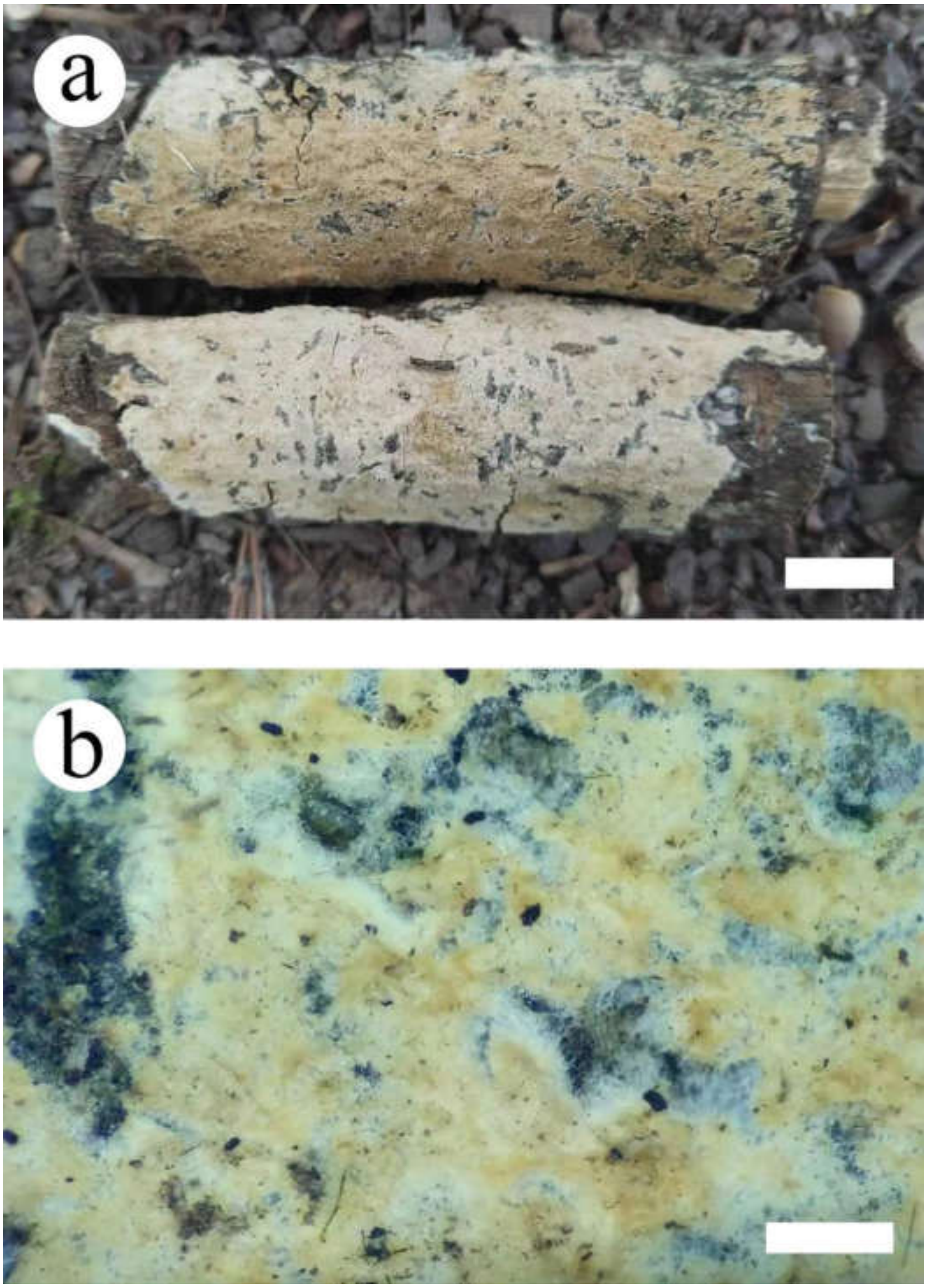

Figure 76 – Basidiomata of *Neohypochnicium velutinum* (holotype). Scale bars: a = 1 cm, b = 1 mm.

Neohypochnicium yunnanense J.H. Dong & C.L. Zhao, sp. nov. Figs 78, 79

Index Fungorum number: IF848332; Facesoffungi number: FoF15439

Diagnosis – Differs from other *Neohypochnicium* species by the corticous basidiomata with cream, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae and subglobose to globose basidiospores measuring 7–9.3 × 6.5–8.7 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 3 August 2019, CLZhao 18525 (SWFC, holotype).

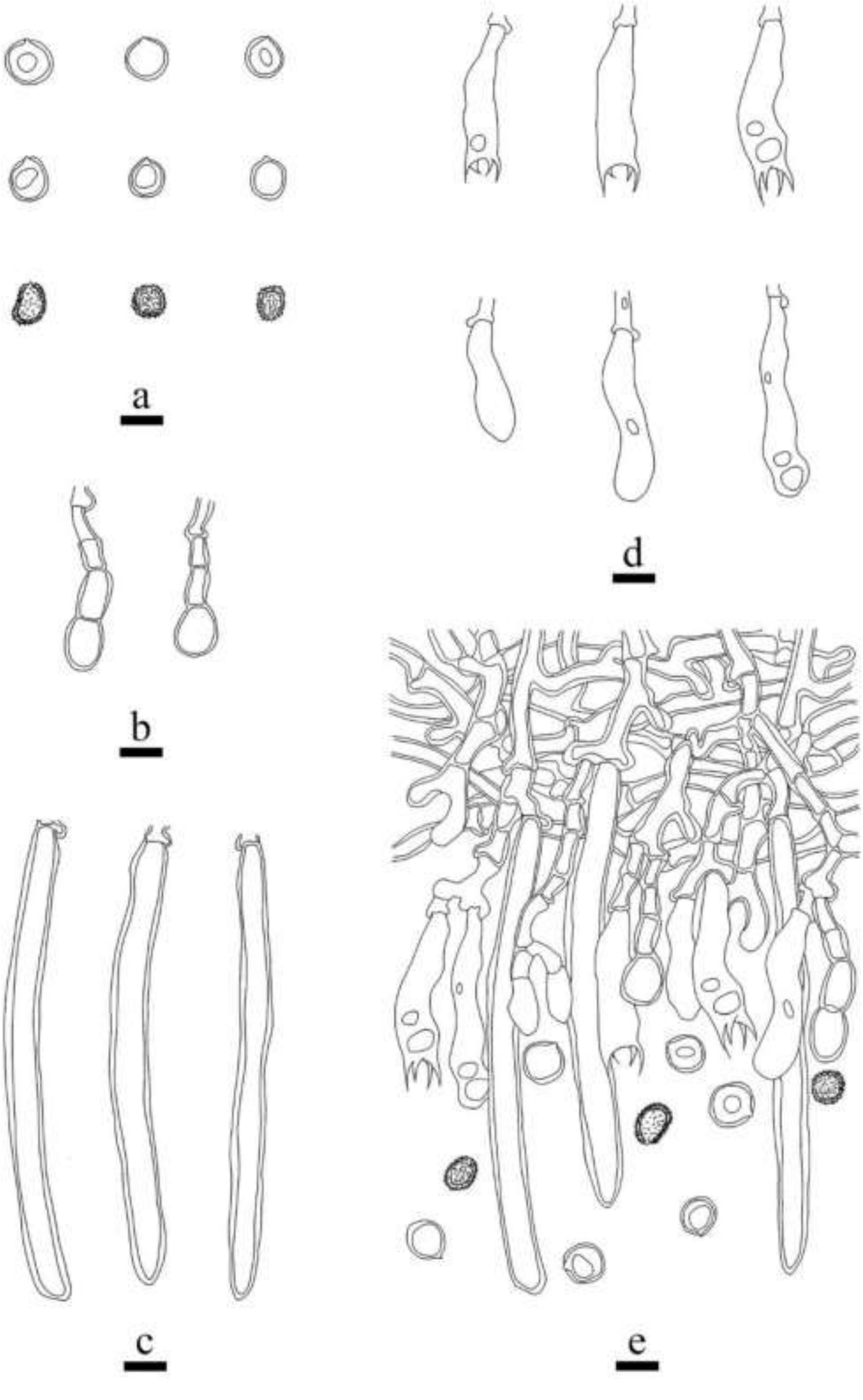

Figure 77 – Microscopic structures of *Neohypochnicium velutinum* (drawn from the holotype). a Basidiospores. b Subclavate cystidia. c Tubular cystidia. d Basidia and basidioles. e A section of hymenium. Scale bars: a–e = 10 µm.

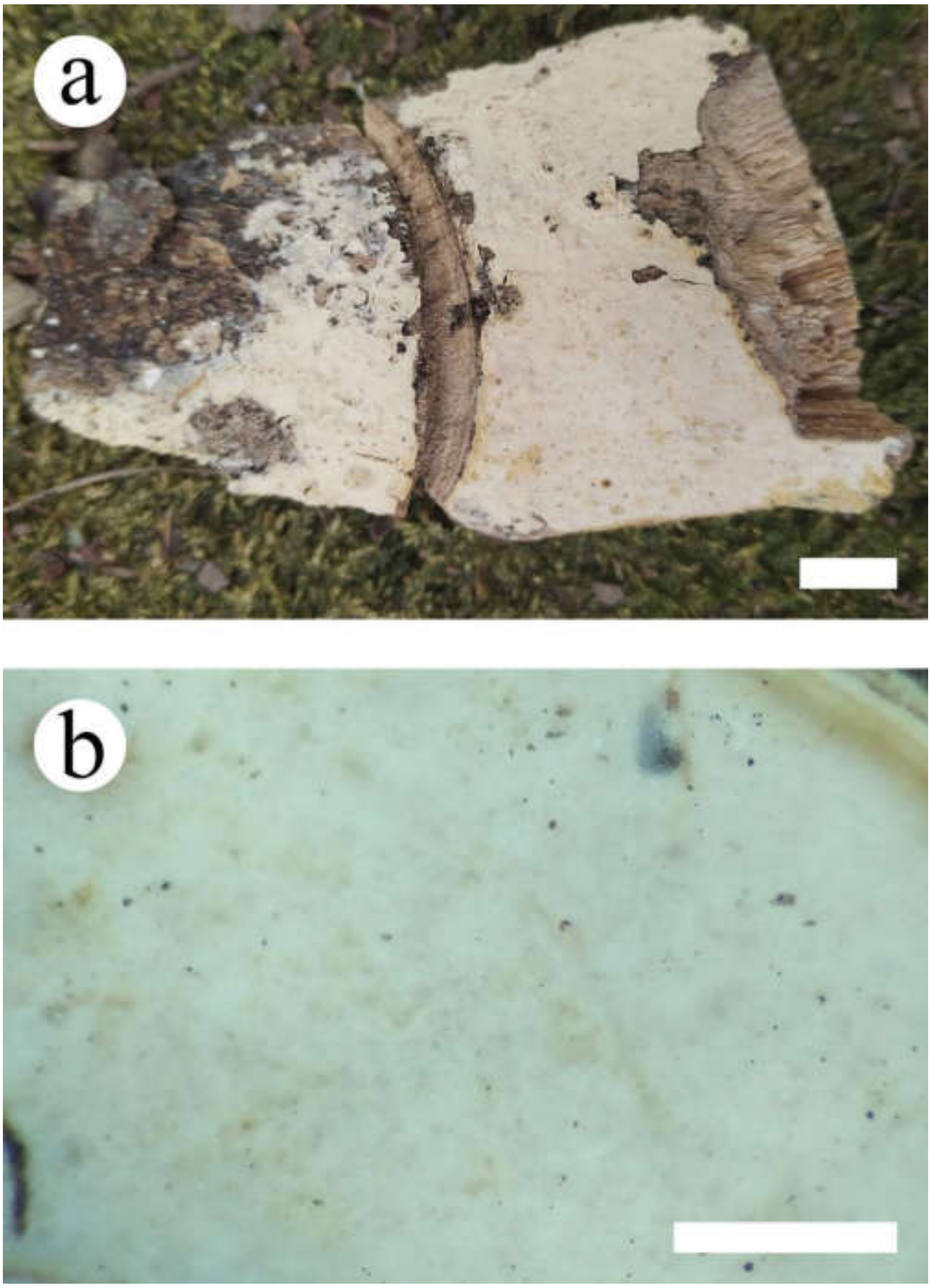

Figure 78 – Basidiomata of *Neohypochnicium yunnanense* (holotype). Scale bars: a = 1 cm, b = 1 mm.

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft corticous when fresh, becoming hard corticous upon drying, up to 10 cm long, 4.5 cm wide, 200–250 µm thick. Hymenial surface smooth, white to slightly cream when fresh, turning to cream upon drying. Sterile margin narrow, slightly cream, abrupt, up to 2 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to thick-walled, branched, more or less interwoven, 2.5–4.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) tubular, slightly thick-walled, with two or three adventitious septa, 72–109 × 6.5–10 µm; (2) cylindrical, slightly sinuous, 40–70 × 7–11 µm; cystidioles absent. Basidia clavate, slightly constricted, with 4 sterigmata and a basal clamp connection, 30–42 × 7.5–9 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose to globose, colorless, thick-walled, smooth, cyanophilous, IKI–, (6.8–)7–9.3(–9.5) × (6.2–)6.5–8.7(–9) µm, L = 8.18 µm, W = 7.70 µm, Q = 1.06 (n = 30/1).

Notes – In this study, based on the ITS, nLSU, mtSSU, RPB1 and TEF1 data (Fig. 13), the new species *Neohypochnicium yunnanense* is classified within *Neohypochnicium*. And is clustered with *N. daweishanense* and *N. geogenium*. However, *N. daweishanense* can be delimited from *N. yunnanense* by its slightly yellowish hymenial surface and membranaceous basidiomata. *N. geogenium* can be distinguished from *N. yunnanense* by its tuberculate hymenial surface, smaller basidia (20–30 × 5–6 µm) and narrower basidiospores (6–7.5 × 4–4.5 µm, Eriksson & Ryvarden 1976).

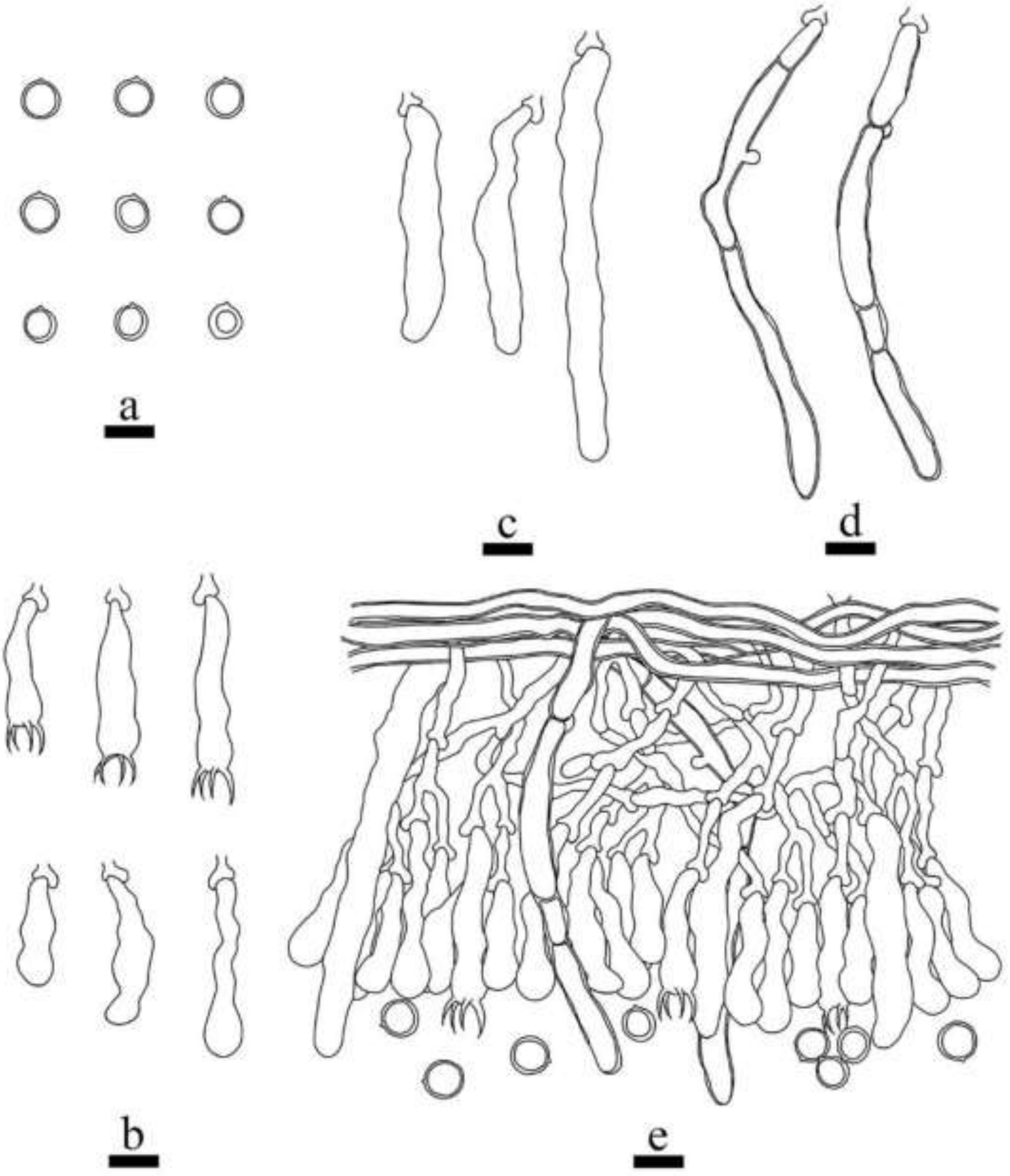

Figure 79 – Microscopic structures of *Neohypochnicium yunnanens* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Subcylindrical cystidia. d Tubular cystidia. e A section of hymenium. Scale bars: a–e = 10 µm.

Neohypochnicium yunnanense resembles *N. aotearoae* and *N. asiaticum*, characterized by the presence of smooth hymenial surface. However, *N. aotearoae* differs can be distinguished by *N. yunnanense* by its membranaceous basidiomata, and verrucose basidiospores (5.6–8.7 × 4.8–7.3 µm, Paulus et al. 2007); *N. asiaticum* can be differentiated *N. yunnanense* by its verrucose and narrower basidiospores (7–8 × 5.5–6.5 µm, Maekawa et al. 2023).

Neohypochnicium yunnanense shares similarities with *N. michelii*, *N. microsporum* and *N. subrigescens*, all of which exhibit smooth basidiospores. The species *N. michelii* can be distinguished from *N. yunnanense* by its porulose hymenial surface, and smaller basidia (20–30 × 6–7.5 µm, Telleria et al. 2010a); *N. microsporum* can be differentiated from *N. yunnanense* by its smaller basidiospores (3.9–5 × 3.8–5 µm, Gruhn et al. 2017); *N. subrigescens* can be distinguished from *N. yunnanense* in its both smaller basidia (20–25 × 5–6 µm) and basidiospores (4.2–6 × 3.6–5 µm, Kotiranta & Saarenoksa 1990).

Neohypochnicium zixishanense J.H. Dong & C.L. Zhao, sp. nov. Figs 80, 81

Index Fungorum number: IF848333; Facesoffungi number: FoF15440

Diagnosis – Differs from other *Neohypochnicium* species by the farinaceous basidiomata with slightly buff, hypochnoid hymenial surface, monomitic hyphal system with clamped generative hyphae and subglobose basidiospores measuring 6–7.7 × 5–6.5 µm.

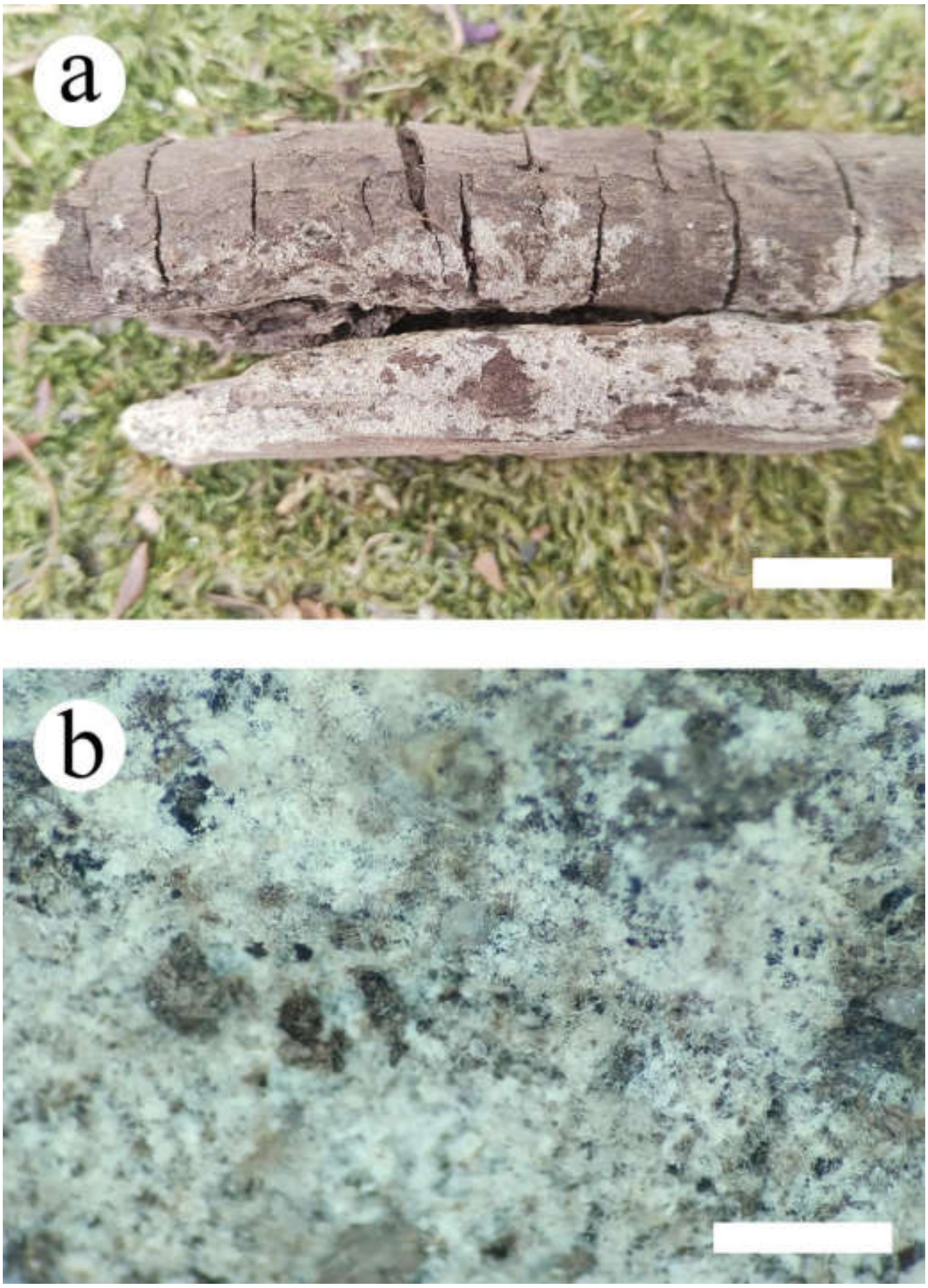

Figure 80 – Basidiomata of *Neohypochnicium zixishanense* (holotype). Scale bars: a = 1 cm, b = 1 mm.

Etymology – *zixishanense* (Lat.): referring to the provenance (Zixishan) of the type specimen.

Type – China, Yunnan Province, Chuxiong, Zixishan National Forestry Park, GPS coordinates 25°01' N, 101°24' E, altitude 2500 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 1 July 2018, CLZhao 7270 (SWFC, holotype).

Description – Basidiomata annual, resupinate, loosely adnate, thin, without odor or taste, farinaceous when fresh, becoming fragile upon drying, up to 6 cm long, 1.5 cm wide, 100–150 µm thick. Hymenial surface hypochnoid, white when fresh, turning to slightly buff upon drying. Sterile margin narrow, white to slightly buff, slightly fimbriate, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, more or less interwoven, 4–5.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia numerous, tubular, slightly thick-walled, with three adventitious septa or not, 112–130 × 10–14 µm; cystidioles absent. Basidia clavate, slightly constricted in the middle to somewhat sinuous, some with several adventitious septa, with 4 sterigmata and a basal clamp connection, 30–40 × 5.5–7 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose, colorless, thick-walled, smooth, cyanophilous, IKI–, 6–7.7(–8) × 5–6.5(–6.8) µm, L = 6.97 µm, W = 5.90 µm, Q = 1.18 (n = 30/1).

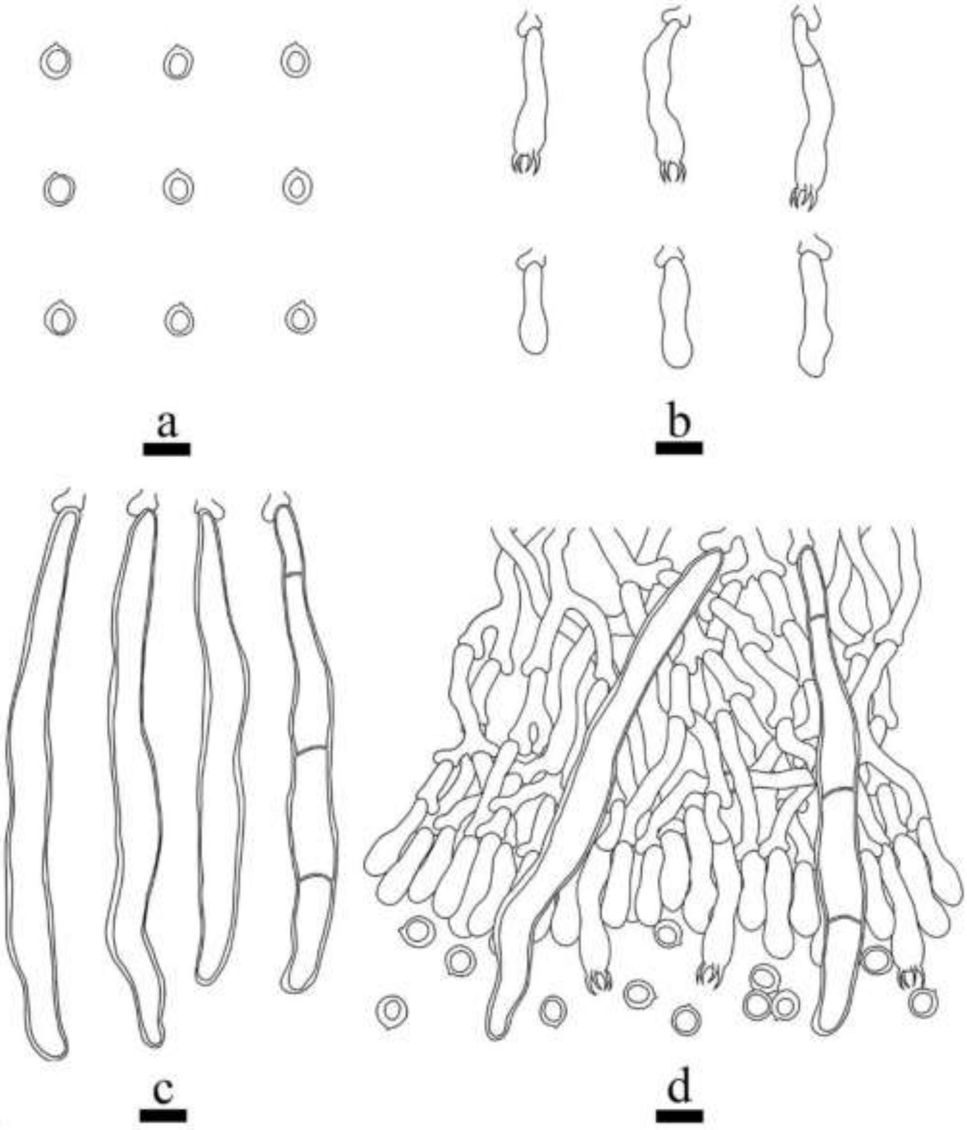

Figure 81 – Microscopic structures of *Neohypochnicium zixishanense* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Tubular cystidia. d A section of hymenium. Scale bars: a–d = 10 µm.

Notes – Based on the ITS, nLSU, mtSSU, RPB1 and TEF1 data (Fig. 13), the new species *Neohypochnicium zixishanense* is grouped into *Neohypochnicium*, (Fig. 14), forming a monophyletic lineage closely associated with *N. aotearoae* and *N. patagonicum* (Gorjón & Hallenb.) N. Maek. However, *N. aotearoae* can be delimited from *N. zixishanense* by its membranaceous basidiomata, and verrucose basidiospores (5.6–8.7 × 4.8–7.3 µm, Paulus et al. 2007); *N. patagonicum* can be distinguished from *N. zixishanense* by its grandinioid hymenial surface, longer basidia (40–60 × 6–8 µm) and larger basidiospores (8–10 × 7.5–8.5 µm, Gorjón & Hallenberg 2013).

Neohypochnicium zixishanense shares similarities with *N. michelii*, *N. microsporum* and *N. subrigescens* characterized by the presence of smooth basidiospores. However, *N. michelii* can be distiniguished from *N. zixishanense* by its porulose hymenial surface, shorter basidia (20–30 × 6–7.5 µm) and larger basidiospores (9–11 × 7–7.5 µm, Telleria et al. 2010a); *N. microsporum* differentiates from *N. zixishanense* in its smaller basidiospores (3.9–5 × 3.8–5 µm, Gruhn et al. 2017); *N. subrigescens* is characterized by its shorter basidia (20–25 × 5–6 µm) and smaller basidiospores in contrast to *N. zixishanense* (4.2–6 × 3.6–5 µm, Kotiranta & Saarenoksa 1990).

Phanerochaetaceae Jülich

Index Fungorum number: IF80024; Facesoffungi number: FoF15441

Type genus – *Phanerochaete* P. Karst.

Donkiella J.H. Dong & C.L. Zhao, gen. nov.

Index Fungorum number: IF850341; Facesoffungi number: FoF15442

Etymology – *Donkiella* (Lat.): referring to the related genus *Donkia*.

Type species – *Donkiella yunnanensis* J.H. Dong & C.L. Zhao.

Description – Basidiomata annual, resupinate, adnate, membranaceous. Hymenial surface smooth, cream to slightly grey. Hyphal system monomitic; generative hyphae with simple septa, colorless, slightly thick-walled, subhymenial hyphae usually covered by the crystals. Cystidia and cystidioles absent. Basidia subclavate to cylindrical, with 4 sterigmata and a basal simple septum. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–.

Notes – In our phylogenetical analyses (Fig. 16), *Donkiella* was identified as a monophyletic group, typified by *D. yunnanensis.* The new genus *Donkiella* falls within Phanerochaetaceae (Polyporales) and is closely related to *Donkia* Pilát. However, *Donkia* is distinguished from *Donkiella* by its pileate basidiomata with white to cream context (Chen et al. 2021), and pale fawn tan, cinnamon to orange-brown hymenial surface having odontoid to hydnoid hymenophore (Pilát 1936, Maas Geesteranus 1971, Nakasone 1990, Moreno et al. 2007).

Donkiella resembles *Hyphodermella* J. Erikss. & Ryvarden in sharing resupinate basidiomata, simple-septate generative hyphae, ellipsoid, thin-walled basidiospores. However, *Hyphodermella* differs from *Donkiella* by its grandinioid to odontioid or hydnoid hymenial surface with small aculei and a fibrillose apex, and clavate to suburniform basidia (Eriksson & Ryvarden 1976, Bernicchia & Gorjon 2010). *Donkiella* seemingly can been included in *Efibula* or *Phanerochaete* because of its monomitic hyphal system with primarily simple-septate, mostly ellipsoid basidiospores. *Efibula* can be distinguished from *Donkiella* mainly by its effused, subceraceous or ceraceous basidiomata and clavate basidia (Wu 1990); *Phanerochaete* can be distinguished from *Donkiella* mainly by its smooth, tuberculate, hydnaceous or velutinous hymenial surface, with the projecting cystidia (Bernicchia & Gorjon 2010). In this study, *Donkiella*, originating from the subtropical regions, suggests the possibility of discovering new corticioid taxa through further investigations and molecular analyses.

Donkiella yunnanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 82, 83

Index Fungorum number: IF850342; Facesoffungi number: FoF15443

Diagnosis – Differs from other *Donkiella* species by the membranaceous basidiomata with cream to slightly grey, smooth hymenial surface, monomitic hyphal system with septate generative hyphae and ellipsoid basidiospores measuring 4.2–6 × 2.5–3.2 µm.

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

Type – China, Yunnan Province, Puer, Jingdong County, Taizhong Town, Ailaoshan National Nature Reserve, GPS coordinates 24°49' N, 100°54' E, altitude 1550 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 4 October 2017, CLZhao 3931 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, very difficult to separate from substrate, without odor or taste, membranaceous when fresh, becoming coriaceous upon drying, up to 10 cm long, 2 cm wide, 50–100 µm thick. Hymenial surface smooth, white to cream when fresh, turning to cream to slightly grey upon drying. Sterile margin narrow, cream, abrupt, up to 0.5 mm wide.

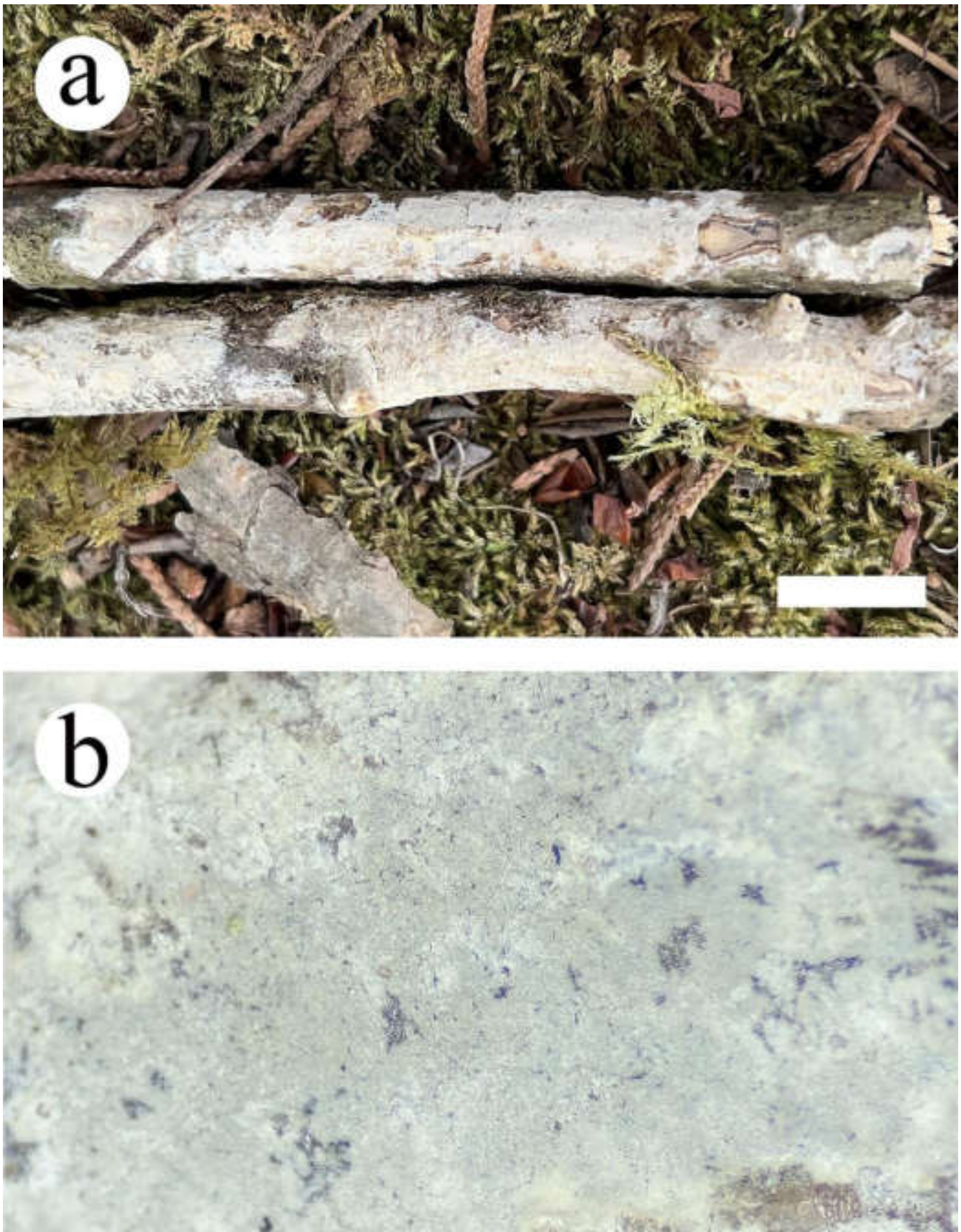

Figure 82 – Basidiomata of *Donkiella yunnanensis* (holotype). Scale bars: a = 1 cm, b = 1 mm.

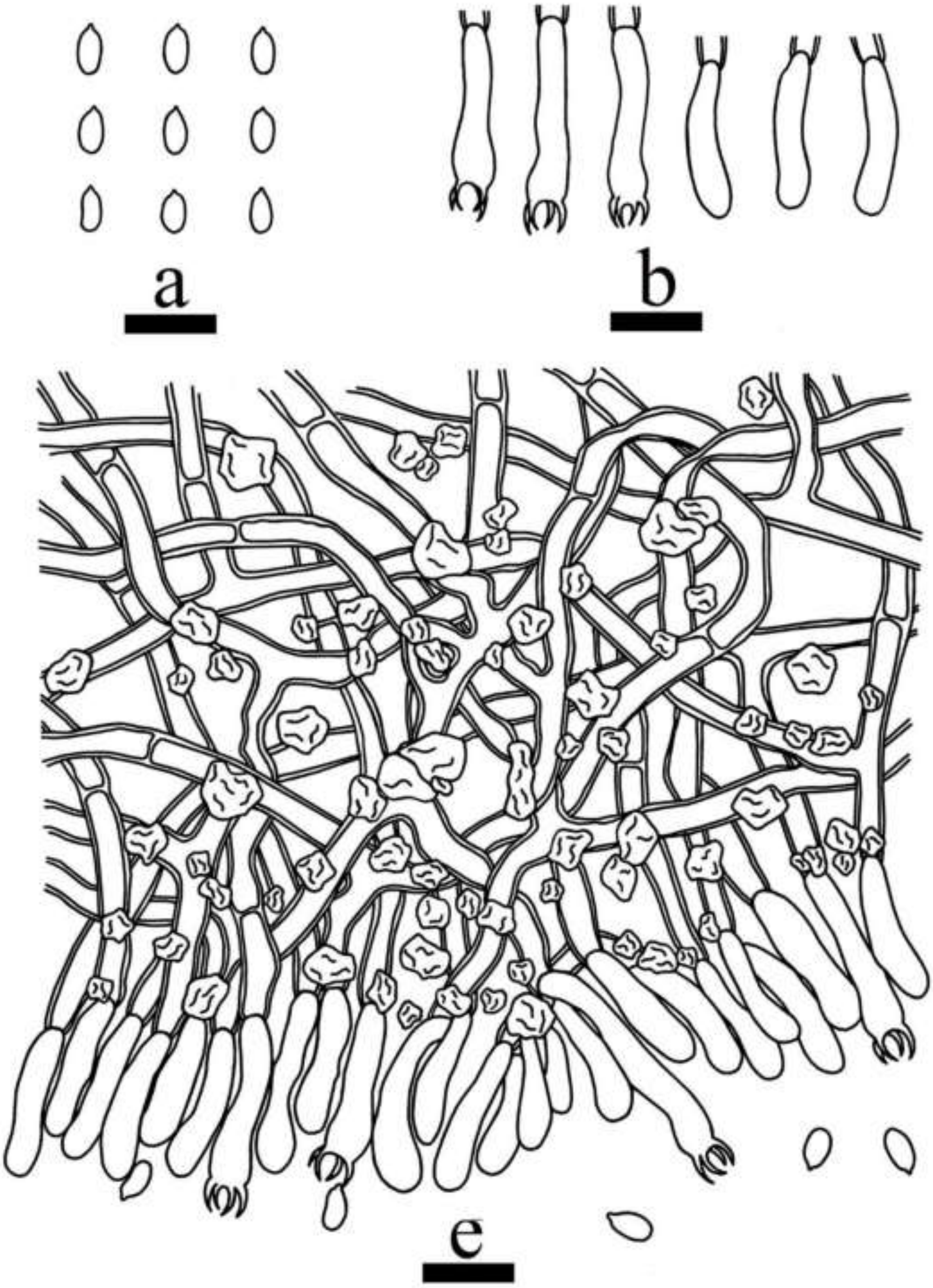

Figure 83 – Microscopic structures of *Donkiella yunnanensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c A section of hymenium. Scale bars: a–d = 10 µm.

Hyphal system monomitic, generative hyphae with simple septa, colorless, thick-walled, frequently branched, interwoven, subhymenial hyphae usually covered by the crystals, 3–6 µm in diameter, IKI–, CB–, tissues unchanged in KOH. Cystidia and cystidioles absent. Basidia subclavate to cylindrical, slightly sinuous, with 4 sterigmata and a basal simple septum, 16.5–25 × 4–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (4–)4.2–6 × 2.5–3.2(–3.5) µm, L = 5.14 µm, W = 2.87 µm, Q = 1.81–1.92 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 3 August 2019, CLZhao 18292 (SWFC).

Notes – Based on the ITS, nLSU, RPB1, RPB2 and TEF1 data (Fig. 16), the newly proposed genus *Donkiella* is identified as a monophyletic group within Phanerochaetaceae. *Donkiella yunnanensis* exhibits similarities with *H. poroides* Y.C. Dai & C.L. Zhao and *H. rosae* (Bres.) Nakasone particularly in the shared ellipsoid shape of basidiospores. However, *H. poroides* differs from *D. yunnanensis* by its poroid hymenial surface, and shorter basidiospores (3–3.5 × 2.5–3 µm, Zhao et al. 2017a); *H. rosae* can be distinguished from *D. yunnanensis* in its odontoid hymenial surface, larger basidia (25–35 × 5.5–7.5 µm) and basidiospores (7–8.5 × 4.5–5.5 µm, Bernicchia & Gorjón 2010).

Phanerochaete P. Karst

Index Fungorum number: IF18245; Facesoffungi number: FoF15445

Type species – *Phanerochaete alnea* (Fr.) P. Karst.

Notes – *Phanerochaete* P. Karst. is a member of the wood-inhabiting fungi, which is typified by *P. alnea* (Fr.) P. Karst (Karsten 1889). A molecular study involving *Phanerochaete* based on the ribosomal DNA (rDNA) sequences, revealed the phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi, in which *P. chrysosporium* Burds. nested into phlebioid clade in Polyporales (Binder et al. 2005). A reassessment of the taxonomy of *Phanerochaete*, using a four gene dataset and extensive ITS sampling, indicated that *Phanerochaete* sensu lato was polyphyletic, distributed across nine lineages in the phlebioid clade, in which six lineages were associated with described genera (Floudas & Hibbett 2015). Miettinen et al. (2016) explored the DNA-phylogeny-based and morphology-based approaches to reconcile the polypores and genus concepts in Phanerochaetaceae, which the macromorphology of fruiting bodies and hymenophore construction did not accurately reflect monophyletic groups and *Ceriporia inflata* B.S. Jiaand B.K. Cui was combined into *Phanerochaete*. Amplifying nrITS, nrLSU and RPB1 genesacross the Polyporales revealed that 11 genera formed a cluster within Phanerochaetaceae, while Hapalopilaceae and Bjerkanderaceae, were placed as synonyms of Phanerochaetaceae (Justo et al. 2017). Recent research, supported by morphology and phylogenetic analyses, has shown that many new taxa of *Phanerochaete* s.s., elucidating the taxonomic status of these additions (Wu et al. 2018a, Xu et al. 2020c, Chen et al. 2021, Wang & Zhao 2021a, Yu et al. 2023a). In this study, we describe one new species of *Phanerochaete* from China, based on the morphological characteristics and phylogenetic analyses inferred from ITS, nLSU, RPB1, RPB2 and TEF1 sequences.

Phanerochaete mopanshanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 84, 85

Index Fungorum number: IF850343; Facesoffungi number: FoF15444

Diagnosis – Differs from other *Phanerochaete* species by the coriaceous basidiomata with buff to slightly yellowish, smooth hymenial surface, monomitic hyphal system with septate generative hyphae and ellipsoid basidiospores measuring 4.2–5.3 × 2.8–3.5 µm.

Etymology – *mopanshanensis* (Lat.): referring to the locality (Mopanshan) of the type specimen.

Type – China, Yunnan Province, Yuxi, Xinping County, Mopanshan National Forestry Park, GPS coordinates 23°51' N, 101°16' E, altitude 1790 m asl., on the fallen branch of *Quercus semecarpifolia*, leg. C.L. Zhao, 19 August 2017, CLZhao 2357 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, without odor or taste, soft membranaceous when fresh, becoming coriaceous upon drying, up to 3 cm long, 1.5 cm wide, 50–150 µm thick. Hymenial surface smooth, hypochnoid, cream to buff when fresh, turning to buff to slightly yellowish upon drying. Sterile margin narrow, cream to buff, fimbriate, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with simple septa, colorless, thick-walled, branched, interwoven, encrusted with small hyaline crystals, 4–7 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia and cystidioles absent. Basidia subclavate, slightly sinuous, with 4 sterigmata and a basal simple septum, 20–28.5 × 5–6.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (4–)4.2–5.3(–5.5) × 2.8–3.5 µm, L = 4.75 µm, W = 3.19 µm, Q = 1.46 (n = 30/1).

Notes – In this study, based on the ITS, nLSU, RPB1, RPB2 and TEF1 data, the new species *Phanerochaete mopanshanensis* is placed within *Phanerochaete* (Fig. 16), forming a monophyletic lineage closely associated with *P. rhizomorpha* C.C. Chen, Sheng H. Wu & S.H. H and *P. sanguineocarnosa* Floudas & Hibbett. However, *P. rhizomorpha* can be delimited from *P. mopanshanensis* by its buff to pale ochraceous hymenial surface, and narrower basidia (25–28 × 4–5 µm, Chen et al. 2021); *P. sanguineocarnosa* is distinguished from *P. mopanshanensis* by its pale yellow to brown hymenial surface, and cylindrical basidia (24–30 × 4–5.5 µm, Floudas & Hibbett 2015).

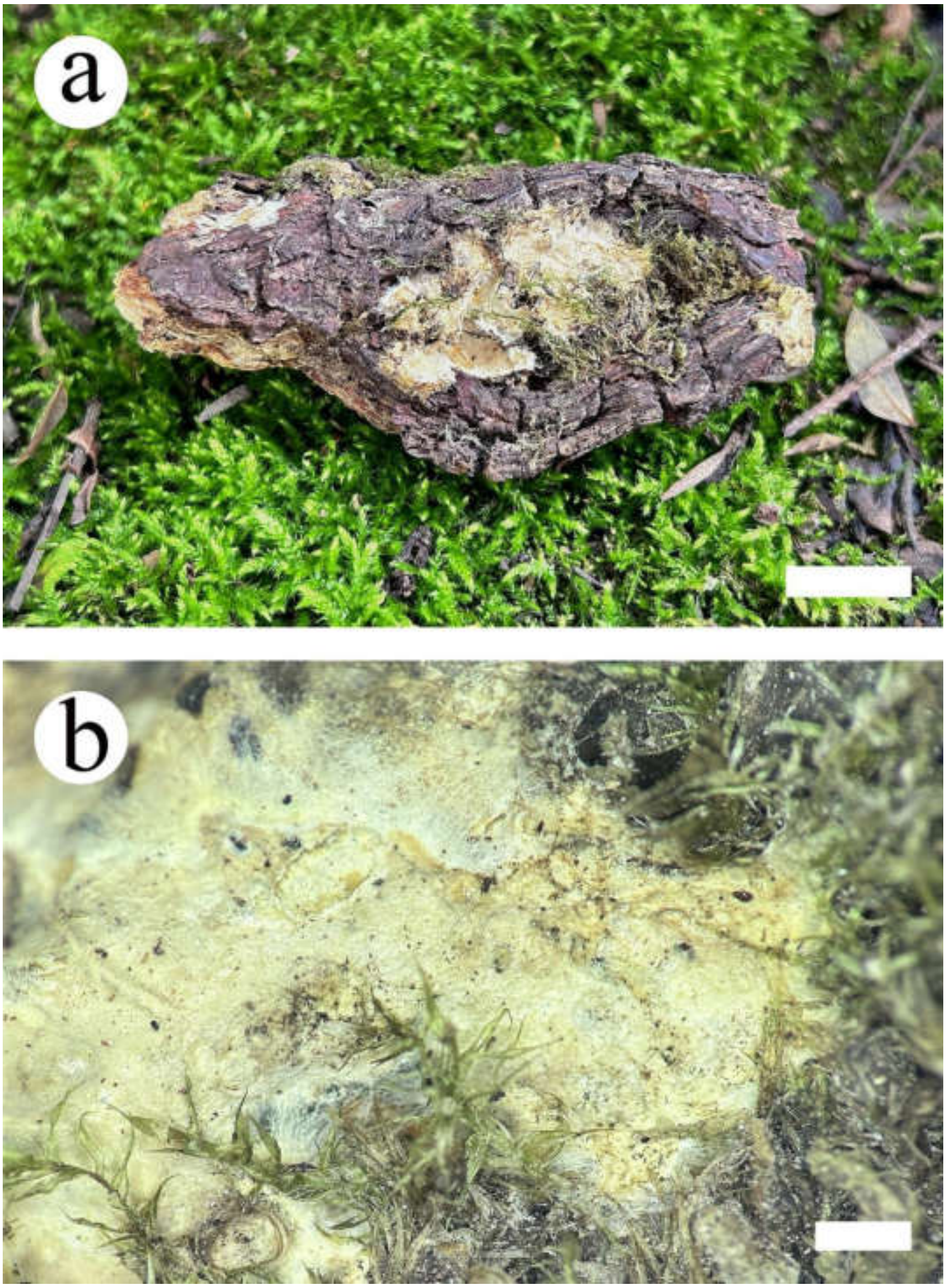

Figure 84 – Basidiomata of *Phanerochaete mopanshanensis* (holotype). Scale bars: a = 1 cm, b = 1 mm.

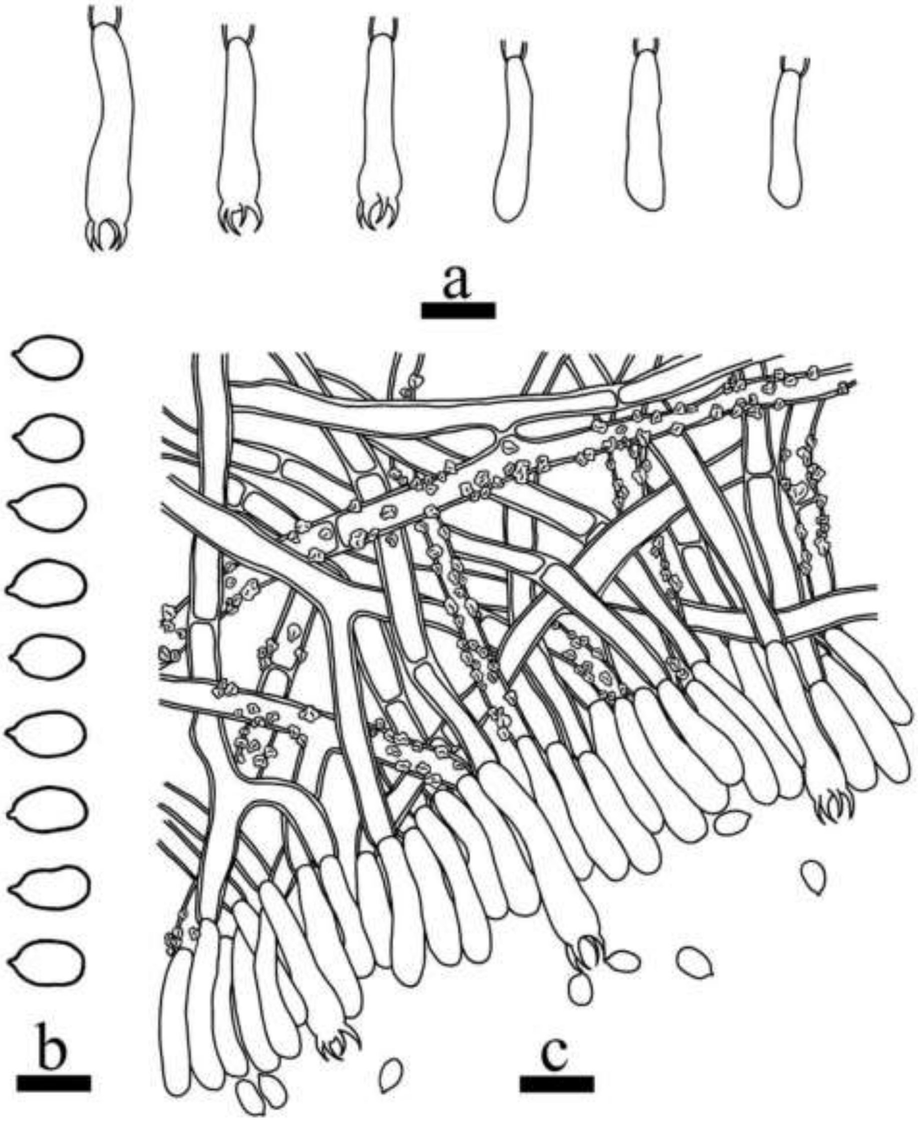

Figure 85 – Microscopic structures of *Phanerochaete mopanshanensis* (drawn from the holotype). A Basidia and basidioles. b Basidiospores. c A section of hymenium. Scale bars: a = 5 µm, b–c = 10 µm.

Phanerochaete mopanshanensis shares similarities with *P. brunnea* S.H. Wu, *P. pruinosa* C.L. Zhao and D.Q. Wang and *P. spadicea* C.C. Chen & Sheng H. Wu characterized by the lack of cystidia. However, *P. brunnea* distiniguished from *P. mopanshanensis* by its cinnamon-pink to cartridge buff hymenial surface, narrower basidia (18–25 × 4.2–5 µm, Wu 1990); *P. pruinose* distinguished from *P. mopanshanensis* by its white to slightly cream, pruinose hymenial surface, narrower basidia (13–24 × 3.5–4.5 µm) and basidiospores (3.5–6.7 × 1.5–2.7 µm, Wang & Zhao 2021a); *P. spadicea* differentiates from *P. mopanshanensis* in its buff to pale brown hymenial surface, narrower basidia (23–24 × 3.6–4.3 µm) and basidiospores (4.2–5.2 × 1.8–2.2 µm, Chen et al. 2021).

Phlebiopsis Jülich

Index Fungorum number: IF25478; Facesoffungi number: FoF15446

Type species – *Phlebiopsis gigantea* (Fr.) Jülich

Notes – *Phlebiopsis* Jülich is a member of the corticioid fungi, typified by *P. gigantea* (Fr.) Jülich. (Jülich 1978). The systematics of *Phlebiopsis* has benefited from numerous molecular studies (Larsson 2007a, Binder et al. 2013, Floudas & Hibbett 2015, Miettinen et al. 2016, Justo et al. 2017, Zhao et al. 2019). Larsson (2007a) presented the classification of corticioid fungi proposing that *Phlebiopsis flavidoalba* (Cooke) Hjortstam was nested within Phanerochaetaceae. Nevertheless, Binder et al. (2013) showed that *Phlebiopsis flavidoalba* belongs to the phlebioid clade and appears to be grouped with *Phanerochaete lamprocystidiata* Sheng H. Wu. A study of *Phanerochaete* P. Karst. by Floudas & Hibbett (2015) using a four gene dataset, suggested that *Phlebiopsis* s.s. clustered into the phlebioid clade and group with *Phaeophlebiopsis* Floudas & Hibbett and *Rhizochaete* Gresl., Nakasone & Rajchenb. Furthermore, Miettinen et al. (2016) demonstrated that the generic type species *Phlebiopsis gigantea* is associated with *Phaeophlebiopsis* and *Rhizochaete*. Using a multi-gene dataset, Justo et al. (2017) proposed a revised family-level classification of Polyporales and confirmed that *P. gigantea* belongs to Phanerochaetaceae and clustered with *P. crassa* (Lév.) Floudas & Hibbett and *P. galochroa* (Bres.) Hjortstam & Ryvarden. Zhao et al. (2019) introduced a new species *Phlebiopsis yunnanensis* C.L. Zhao, based on morphological characters and rDNA sequences, in which this species was found to be related to *P. gigantea* and *P. lamprocystidiata*. Recent research, supported by both morphology and phylogeny has revealed many new taxa within *Phlebiopsis* and elucidated their taxonomic status (Xu et al. 2020b, Chen et al. 2021, Li et al. 2021, Zhao et al. 2021, Li et al. 2023a). In this study, one new species of *Phlebiopsis* is introduced from China, distinguished through an examination of both morphological characteristics and phylogenetic analyses inferred from ITS, nLSU, RPB1, RPB2 and TEF1 sequences.

Phlebiopsis daweishanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 86, 87

Index Fungorum number: IF 850344; Facesoffungi number: FoF15447

Diagnosis – Differs from other *Phlebiopsis* species by the membranaceous basidiomata with cream to slightly brown, smooth hymenial surface, monomitic hyphal system with septate generative hyphae and broadly ellipsoid to ellipsoid basidiospores measuring 4.5–5.2 × 4–4.6 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 2 August 2019, CLZhao 17984 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, very difficult to separate from substrate, without odor or taste, membranaceous when fresh, becoming hard membranaceous upon drying, up to 10 cm long, 2 cm wide, 50–100 µm thick. Hymenial surface smooth, cream when fresh, turning to cream to slightly brown upon drying. Sterile margin cream, thinning out, up to 0.5 mm wide.

Hyphal system monomitic, generative hyphae with simple septa, colorless, slightly thick-walled, branched, interwoven, 3–5.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia numerous, conical, thick-walled, heavily encrusted with crystalline crystals, 30–55 × 6.5–12 µm; cystidioles absent. Basidia subclavate, slightly sinuous, with 4 sterigmata and a basal simple septum, 15–25 × 5–7.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid to ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (4.3–)4.5–5.2(–5.5) × (3.5–)4–4.6(–5) µm, L = 4.93 µm, W = 4.15 µm, Q = 1.19 (n = 30/1).

Notes – In this analysis, based on the ITS, nLSU, RPB1, RPB2 and TEF1 data (Fig. 16), the new species *Phlebiopsis daweishanensis* is placed within *Phlebiopsis*, forming a monophyletic lineage.

Phlebiopsis daweishanensis resembles *P. lacerata* C.L. Zhao, *P. odontoidea* C.C. Chen & Sheng H. Wu and *P. yunnanensis* C.L. Zhao in sharing the ellipsoid basidiospores. However, *P. lacerata* differs from *P. daweishanensis* by its poroid hymenial surface, and narrower basidiospores (4–5.5 × 3–3.5 µm, Xu et al. 2020b); *P. odontoidea* differentiates from *P. daweishanensis* in its odontioid hymenial surface, narrower basidia (22–25 × 4–5 µm) and longer basidiospores (5.2–5.9 × 3.2–3.7 µm, Chen et al. 2021); *P. yunnanensis* differs from *P. daweishanensis* due to its odontioid hymenial surface, narrower basidia (10–21 × 3.5–4.5 µm) and smaller basidiospores (3.5–4.5 × 2.5–3.5 µm, Zhao et al. 2019).

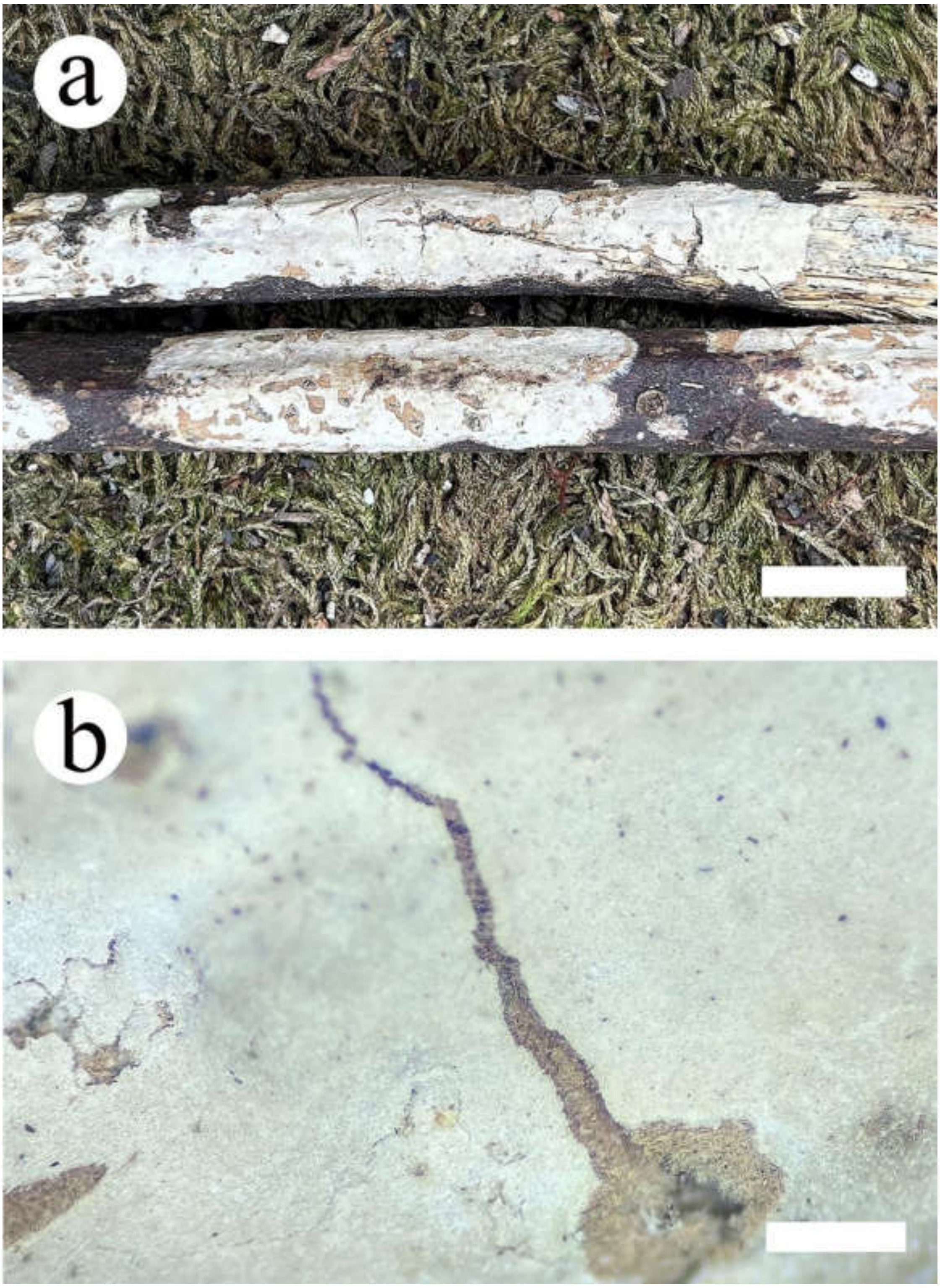

Figure 86 – Basidiomata of *Phlebiopsis daweishanensis* (holotype). Scale bars: a = 1 cm, b = 0.5 mm.

Steccherinaceae Parmasto

Index Fungorum number: IF81420; Facesoffungi number: FoF15448

Type genus – *Steccherinum* Gray

Etheirodon Banker

Index Fungorum number: IF17571; Facesoffungi number: FoF15449

Type species – *Etheirodon fimbriatum* (Pers.) Banker

Notes – The genus *Etheirodon* was established by Banker (1902) and typified by *E. fimbriatum* (Pers.) Banker. Banker (1902) proposed the genus name as *Etheirodon* after a thorugh study of its type species. Eriksson (1958) suggested the combined species *Steccherinum fimbriatum* (Pers.) J. Erikss, focusing on the study of Heterobasidiomycetes and Homobasidiomycetes-aphyllophorales in muddus National Park in North Sweden. The systematic study of Polyporaceae was presented within the overview of Polyporales, reaffirming the established placement of *Etheirodon* (Zmitrovich 2018). Westphalen et al. (2021) provided comprehensive morphological and phylogenetic analyses on the hydnoid specimens of Steccherinaceae, identifying four genera as *Cabalodontia* Piatek, *Etheirodon*, *Metuloidea* G. Cunn., and *Steccherinum* Gray. In this study, a novel species *E. roseoalbum* is proposed based on morphological characteristics and phylogenetic analyses inferred from ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 sequences.

Etheirodon roseoalbum J.H. Dong & C.L. Zhao, sp. nov. Figs 88, 89

Index Fungorum number: IF850345; Facesoffungi number: FoF15450

Diagnosis – Differs from other *Etheirodon* species by the ceraceous basidiomata with purplish to rose, grandinoid hymenial surface, monomitic hyphal system with septate generative hyphae and ellipsoid basidiospores measuring 3.5–4.2 × 2.5–3.2 µm.

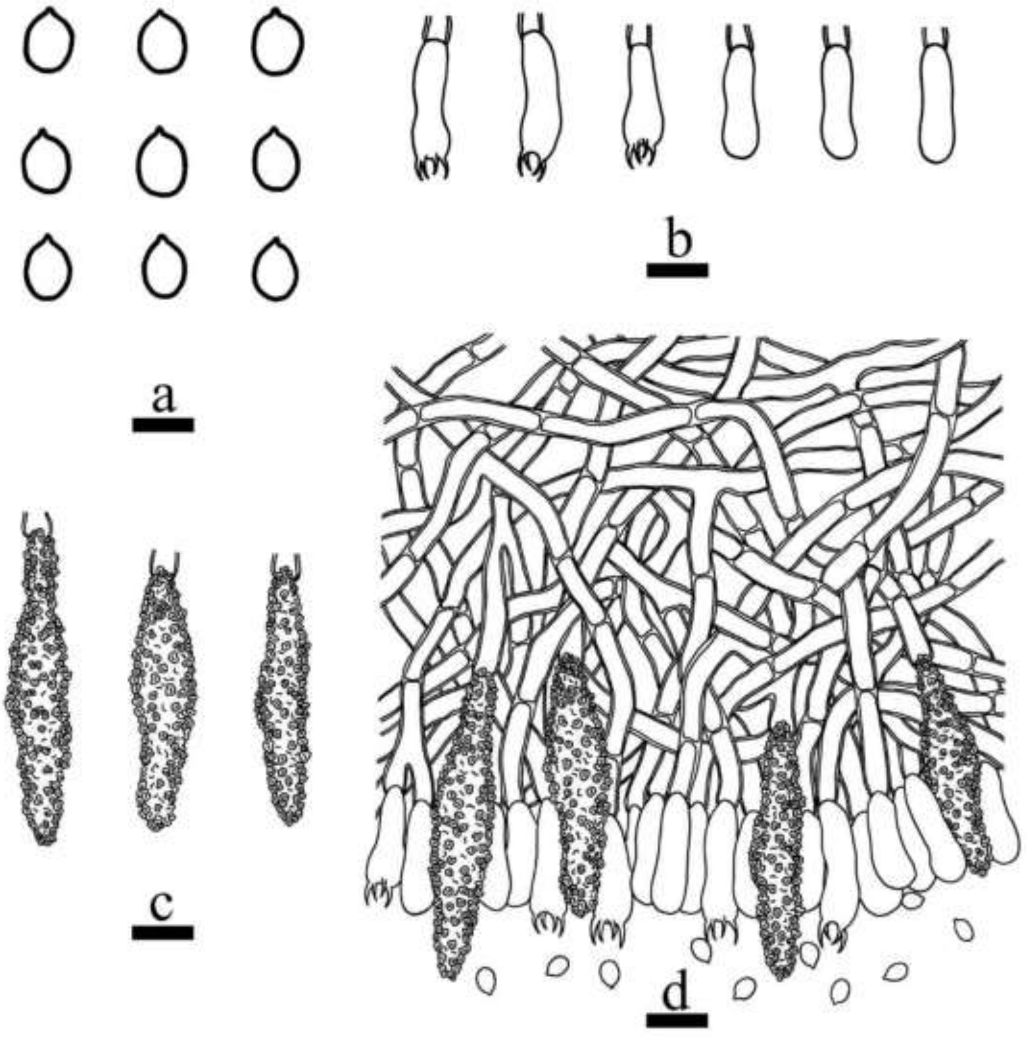

Figure 87 – Microscopic structures of *Phlebiopsis daweishanensis* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Conical cystidia. d A section of hymenium. Scale bars: a = 5 µm, b–d = 10 µm.

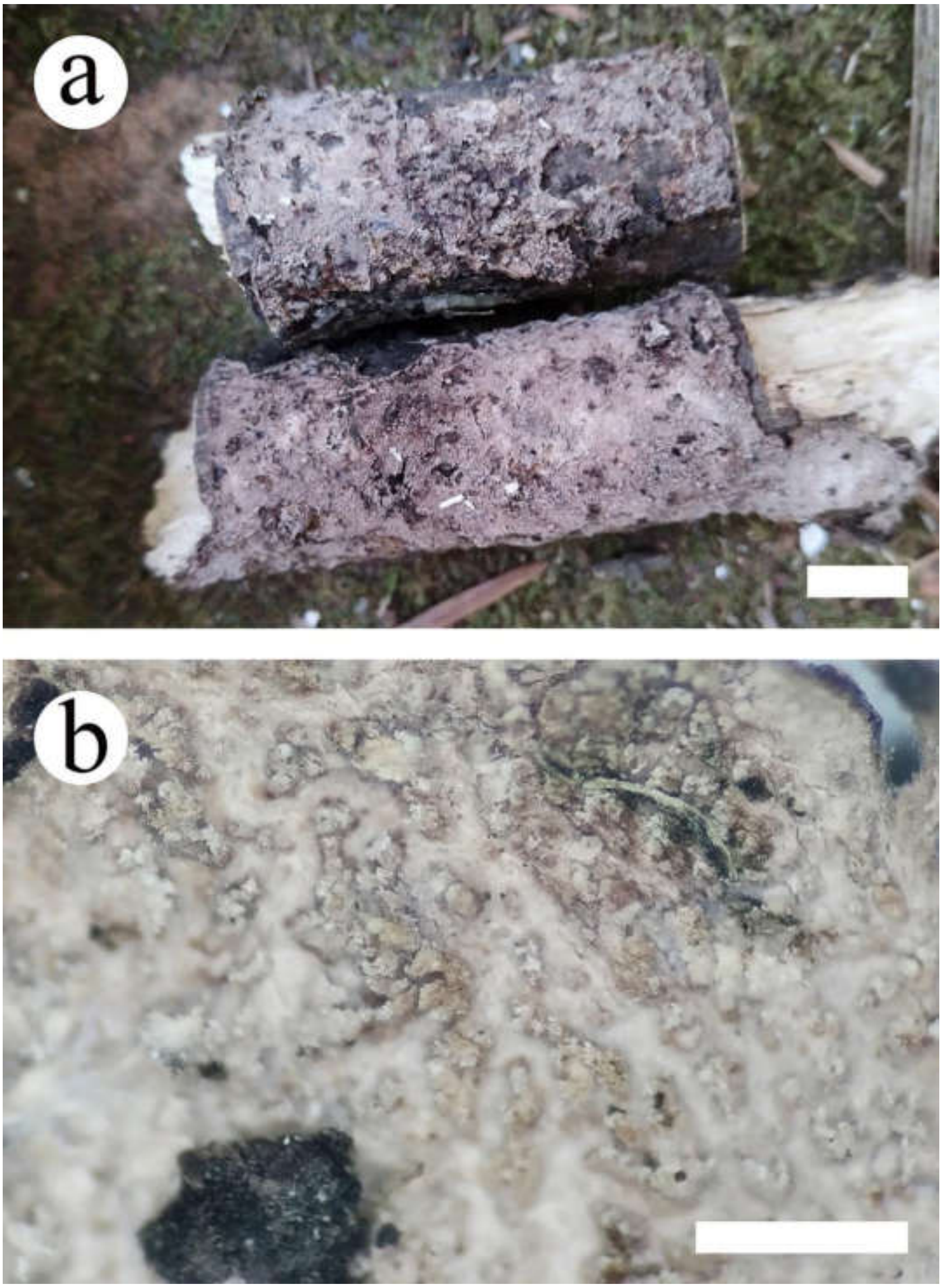

Figure 88 – Basidiomata of *Etheirodon roseoalbum* (holotype). Scale bars: a = 1 cm, b = 1 mm.

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

Type – China, Yunnan Province, Dali, Weishan County, Qinghua Town, GPS coordinates 25°08' N, 100°10' E, altitude 2000 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 18 October 2022, CLZhao 24770 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, soft ceraceous, without odor or taste when fresh, becoming hard ceraceous upon drying, up to 15 cm long, 3 cm wide, 100–150 µm thick. Hymenial surface grandinoid, white to slightly purplish when fresh, turning to purplish to rose upon drying. Sterile margin distinct, white to slightly purplish, fimbriate, up to 0.5–1 mm wide.

Hyphal system dimitic, generative hyphae with simple septa, colorless, thin to slightly thick-walled, branched, more or less interwoven, 3–5 µm in diameter; skeletal hyphae yellowish to pale brown, thick-walled to solid, 4–5.5 µm diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia and cystidioles absent. Basidia clavate, slightly constricted, with 4 sterigmata and a basal simple septum, 20–28 × 4.5–6 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, thin-walled, colorless, smooth, IKI–, CB–, 3.5–4.2(–4.5) × 2.5–3.2(–3.5) µm, L = 3.89 µm, W = 2.85 µm, Q = 1.37–1.45 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Dali, Weishan County, Qinghua Town, GPS coordinates 25°08' N, 100°10' E, altitude 2000 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 18 October 2022, CLZhao 24903 (SWFC).

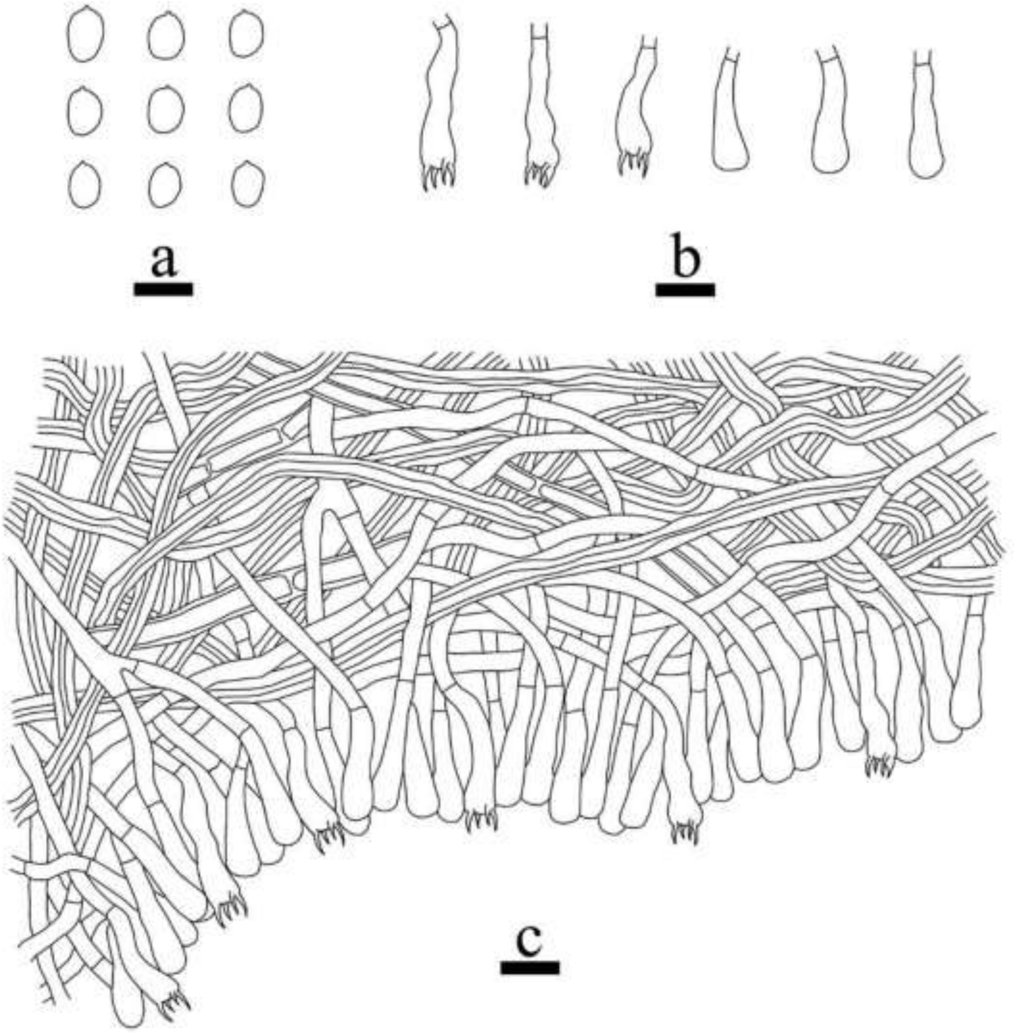

Figure 89 – Microscopic structures of *Etheirodon roseoalbum* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c A section of hymenium. Scale bars: a = 5 µm, b–c = 10 µm.

Notes – In this study, the new species *Etheirodon roseoalbum* is classified within *Etheirodon* based on ITS, nLSU, mtSSU, RPB1, RPB2, and TEF1 data (Fig. 17), and it is identified *E. fimbriatum* (Pers.) Banker. However, *E. fimbriatum* can be distinguished from *E. roseoalbum* by its odontioid hymenial surface, smaller basidia (18–20 × 4–4.5 µm) and narrower basidiospores (3.25–4 × 2.25–2.5 µm, Hjortstam & Ryvarden 2007). In this study, the new species *E. roseoalbum* doesn't contain cystidia, however, the description of the genus has encrusted cystidia, and perhaps both species are postmature or the lacking of nutrition or energy or other environmental conditions or some nucleotide base deletion.

Etheirodon roseoalbum shares similarities with *E. purpureum* Westphalen, in having a fimbriate margin and ellipsoid basidiospores. However, *E. purpureum* differs itself from

E. roseoalbum in its shorter basidia (10–15 × 4–5.5 µm) and narrower basidiospores (4–4.5 × 2–2.5 µm, Westphalen et al. 2021).

Steccherinum Gray

Index Fungorum number: IF18582; Facesoffungi number: FoF15453

Type species – *Steccherinum ochraceum* (Pers. ex J.F. Gmel.) Gray

Notes – The genus *Steccherinum* Gray was established by Gray (1821) and typified by *S. ochraceum* (Pers. ex J.F. Gmel.) Gray. Molecular phylogenies have increased the knowledge concerning the evolution of *Steccherinum* (Miettinen et al. 2012, Binder et al. 2013, Justo et al. 2017, Westphalen et al. 2018, Westphalen et al. 2021, Wu et al. 2021a, b, Dong et al. 2022, 2023b). Based on sequences of the gene regions ITS, nLSU, mtSSU, atp6, rpb2, and tef1, Miettinen et al. (2012) demonstrated that the phylogeny of the poroid and hydnoid taxa, including *Antrodiella* Ryvarden and I. Johans., *Junghuhnia* Corda and *Steccherinum* (Polyporales, Basidiomycota) clusters together, revealing that *Steccherinum* contains both hydnoid and poroid species. Using whole genome sequence data in comparison to extensively sampled multigene datasets, Binder et al. (2013), indicated that *Steccherinum* species belonged to the residual polyporoid clade, and the generic type (*S. ochraceum*) was grouped with *Junghuhnia nitida* (Pers.) Ryvarden Justo et al. (2017) clarified the family level classification of 18 families within Polyporales (Basidiomycota), indicating that *Steccherinum* belonged to Steccherinaceae Parmasto. Westphalen et al. (2018) conducted morphological and multigene analyses of *Junghuhnia* s.lat., in which a new species *Steccherinum neonitidum* Westphalen & Tomšovský and three new combinations, *S. meridionale* (Rajchenb.) Westphalen, Tomšovský & Rajchenberg, *S. polycystidiferum* (Rick) Westphalen, Tomšovský & Rajchenb. and *S. undigerum* (Berk. & M.A. Curtis) Westphalen & Tomšovský were reported. Westphalen et al. (2021) conducted morphological and phylogenetic analyses on hydnoid specimens of Steccherinaceae, unveiling four genera as *Cabalodontia*, *Etheirodon*, *Metuloidea*, and *Steccherinum*, and describing three new neotropical species, including *S. larssonii* Westphalen & Motato-Vásq.

In recent, phylogenetic analyses on *Steccherinum* from China, based on ITS+nLSU sequences and morphology, several new *Steccherinum* species were described; *Steccherinum fissurutum* J.H. Dong & C.L. Zhao, *S. fragile* Z.B. Liu & Y.C. Dai, *S. hirsutum* Y.X. Wu & C.L. Zhao, *S. incrustans* Z.B. Liu, Y.C. Dai & Jing Si, *S. juniperi* Z.B. Liu, Y.C. Dai & Jing Si, *S. puerense* Y.X. Wu, J.H. Dong & C.L. Zhao, *S. punctatum* J.H. Dong & C.L. Zhao, *S. rubigimaculatum* Y.X.Wu, J.H. Dong & C.L. Zhao, *S. subtropicum* J.H. Dong & C.L. Zhao, *S. tenuissimum* C.L. Zhao & Y.X. Wu, *S. xanthum* C.L. Zhao & Y.X. Wu, and *S. yunnanense* Y.X. Wu & C.L. Zhao (Liu & Dai 2021, Wu et al. 2021a, b, Dong et al. 2022, 2023b, Liu et al. 2023d). Hence, based on morphological and molecular systematics evidence, we propose three new species: *S. lincangense*, *S. longiaculeiferum* and *S. weishanense*.

Steccherinum lincangense J.H. Dong & C.L. Zhao, sp. nov. Figs 90, 91

Index Fungorum number: IF850347; Facesoffungi number: FoF15454

Diagnosis – Differs from other *Steccherinum* species by the coriaceous basidiomata with slightly buff, odontioid hymenial surface with subulate aculei, 2–4 per mm, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 3.8–4.2 × 2.5–2.8 µm.

Etymology – *lincangense* (Lat.): referring to the locality (Lincang) of the type specimen.

Type – China, Yunnan Province, Lincang, Yun County, Maolan Town, Shiyan Village, GPS coordinates 24°33' N, 100°22' E, altitude 2000 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 19 October 2022, CLZhao 24988 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, soft coriaceous, without odor or taste when fresh, becoming coriaceous upon drying, up to 15 cm long, 2 cm wide, 50–150 µm thick. Hymenial surface odontioid, with subulate aculei, 2–4 per mm, up to 1–1.5 mm long, cream when fresh, turning to slightly buff upon drying. Sterile margin white to cream, slightly fimbriate, up to 2 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to thick-walled, branched, interwoven, 3–4 µm in diameter, IKI–, CB–, tissues unchanged in KOH. Skeletocystidia numerous, thick-walled, strongly encrusted in the obtuse apex, sometimes with several dissepiments, 45–90 × 6.5–9 µm; cystidioles absent. Basidia clavate, sometimes slightly sinuous, with 4 sterigmata and a basal clamp connection, 9–13.5 × 3.5–5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, thin-walled, colorless, smooth, IKI–, CB–, (3.5–)3.8–4.2(–4.5) × (2.3–)2.5–2.8 µm, L = 3.96 µm, W = 2.65 µm, Q = 1.55 (n = 30/1).

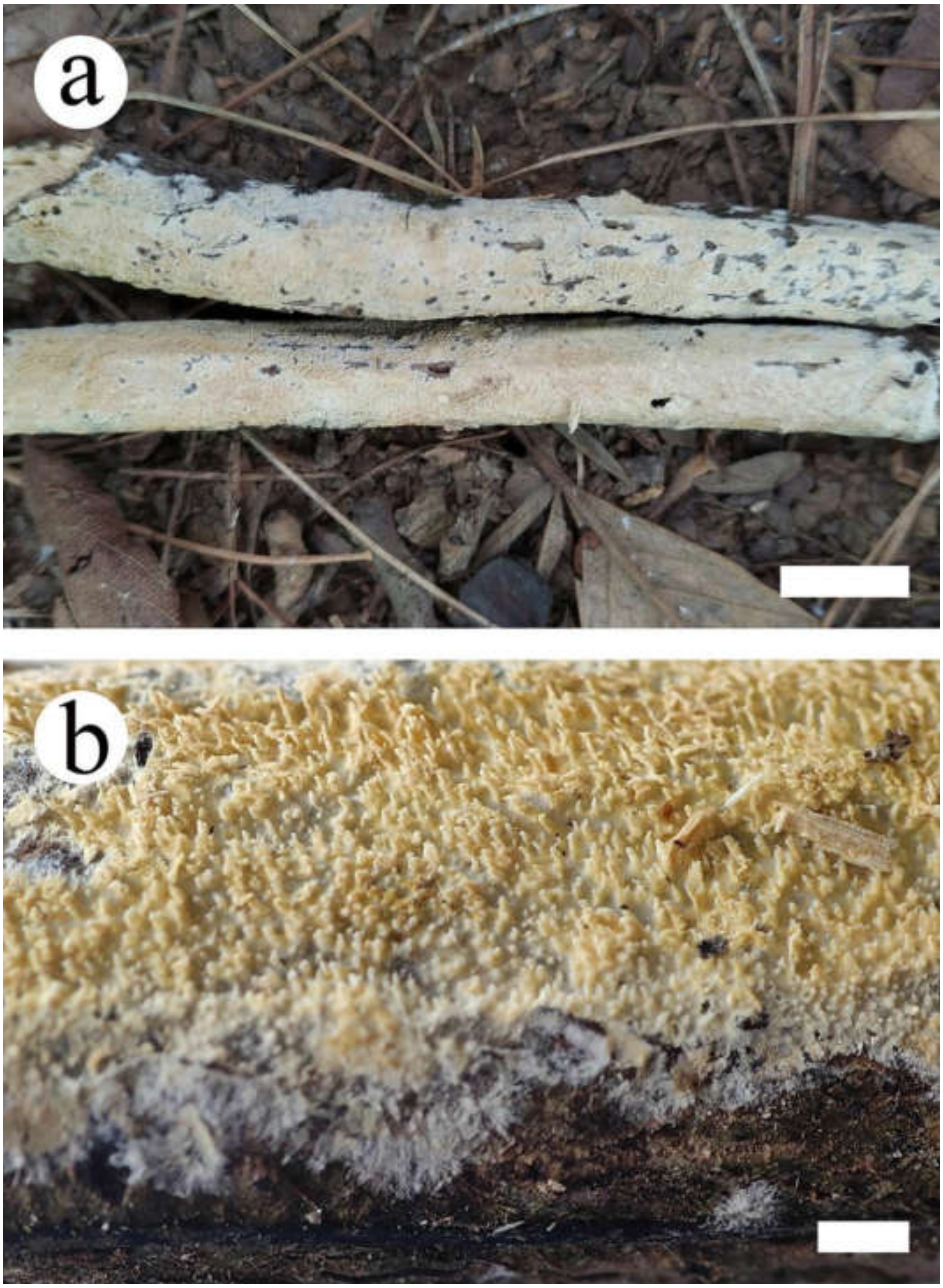

Figure 90 – Basidiomata of *Steccherinum lincangense* (holotype). Scale bars: a = 1 cm, b = 2 mm.

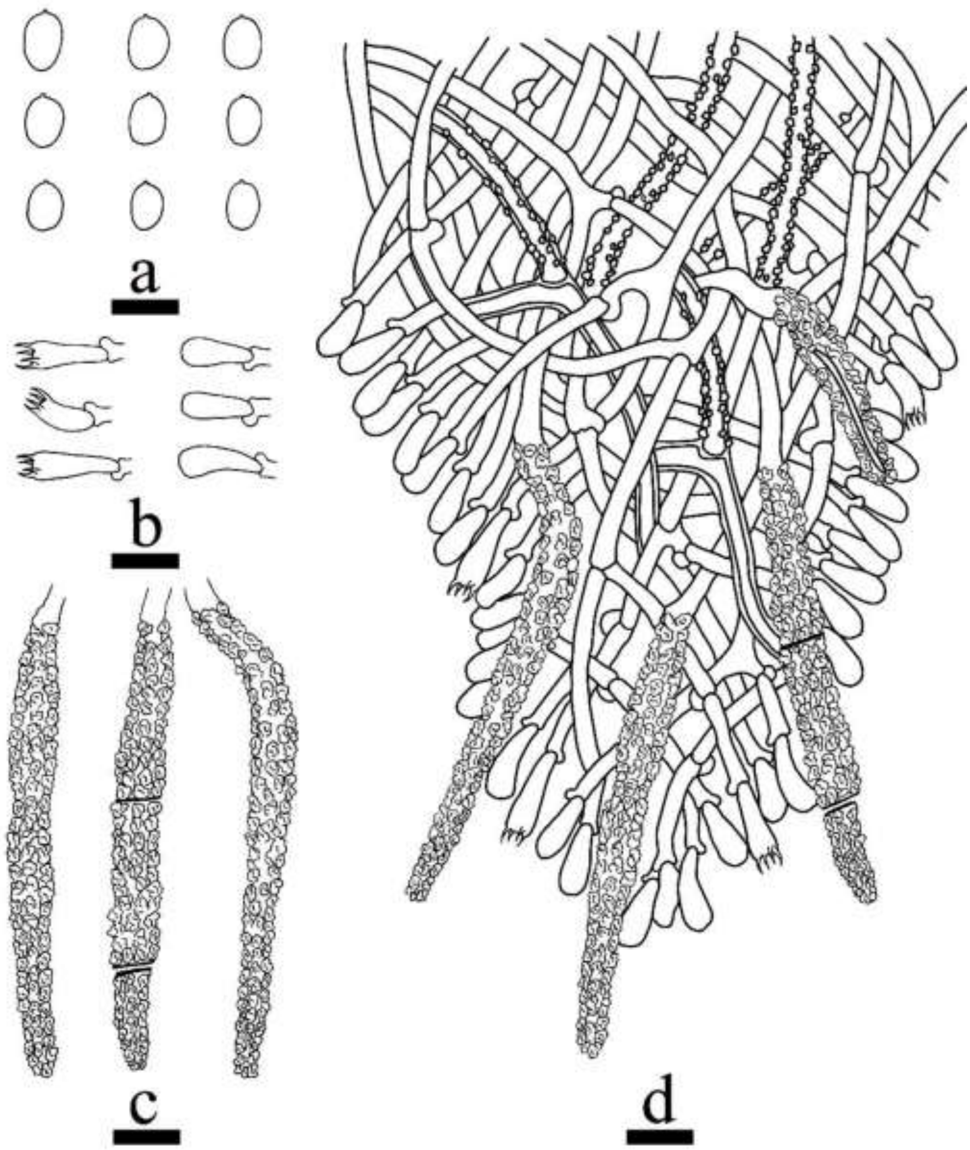

Figure 91 – Microscopic structures of *Steccherinum lincangense* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Skeletocystidia. d A section of hymenium. Scale bars: a = 5 µm, b–d = 10 µm.

Notes – In the present study, based on the ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 data (Fig. 17), the new species *Steccherinum lincangense* is grouped within *Steccherinum*, and clusters with *S. tenuissimum* and *S. xanthum*. However, *S. tenuissimum* can be delimited from *S. lincangense* by its shorter aculei (0.2–0.5 mm), and smaller skeletocystidia (22–39 × 4.5–6 µm, Wu et al. 2021b); *S. xanthum* differs from *S. lincangense* by its buff hymenial surface and shorter aculei (0.1–0.3 mm, Wu et al. 2021b).

Steccherinum lincangense resembles *S. fissurutum*, *S. fragile* and *S. punctatum* in having the monomitic hyphal system. However, *S. fissurutum* differs from *S. lincangense* by its grandinoid and cracked hymenial surface, shorter skeletocystidia (26.5–36 × 6.5–9.5 µm) and longer basidiospores (4.5–6 × 2.5–3 µm, Dong et al. 2023b); *S. fragile* differentiates from *S. lincangense* in its poroid hymenial surface, and smaller basidiospores (2.8–3.1 × 2.1–2.2 µm, Liu & Dai 2021); *S. punctatum* differs from *S. lincangense* by its grandinoid hymenial surface, and larger basidia (23–27 × 5.5–7.5 µm, Dong et al. 2023b).

Steccherinum longiaculeiferum J.H. Dong & C.L. Zhao, sp. nov. Figs 92, 93

Index Fungorum number: IF850348; Facesoffungi number: FoF15455

Diagnosis – Differs from other *Steccherinum* species by the coriaceous basidiomata with cream, hydnoid hymenial surface with long aculei, 2–5 per mm, monomitic hyphal system with clamped generative hyphae and broadly ellipsoid to ellipsoid basidiospores measuring 4–4.3 × 2.5–3 µm.

Etymology – *longiaculeiferum* (Lat.): referring to the hymenophore with long aculei of the type specimen.

Type – China, Yunnan Province, Qujing, Qilin District, Cuishan Forest Park, GPS coordinates 25°32' N, 103°42' E, altitude 2250 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 5 November 2022, CLZhao 26243 (SWFC, holotype).

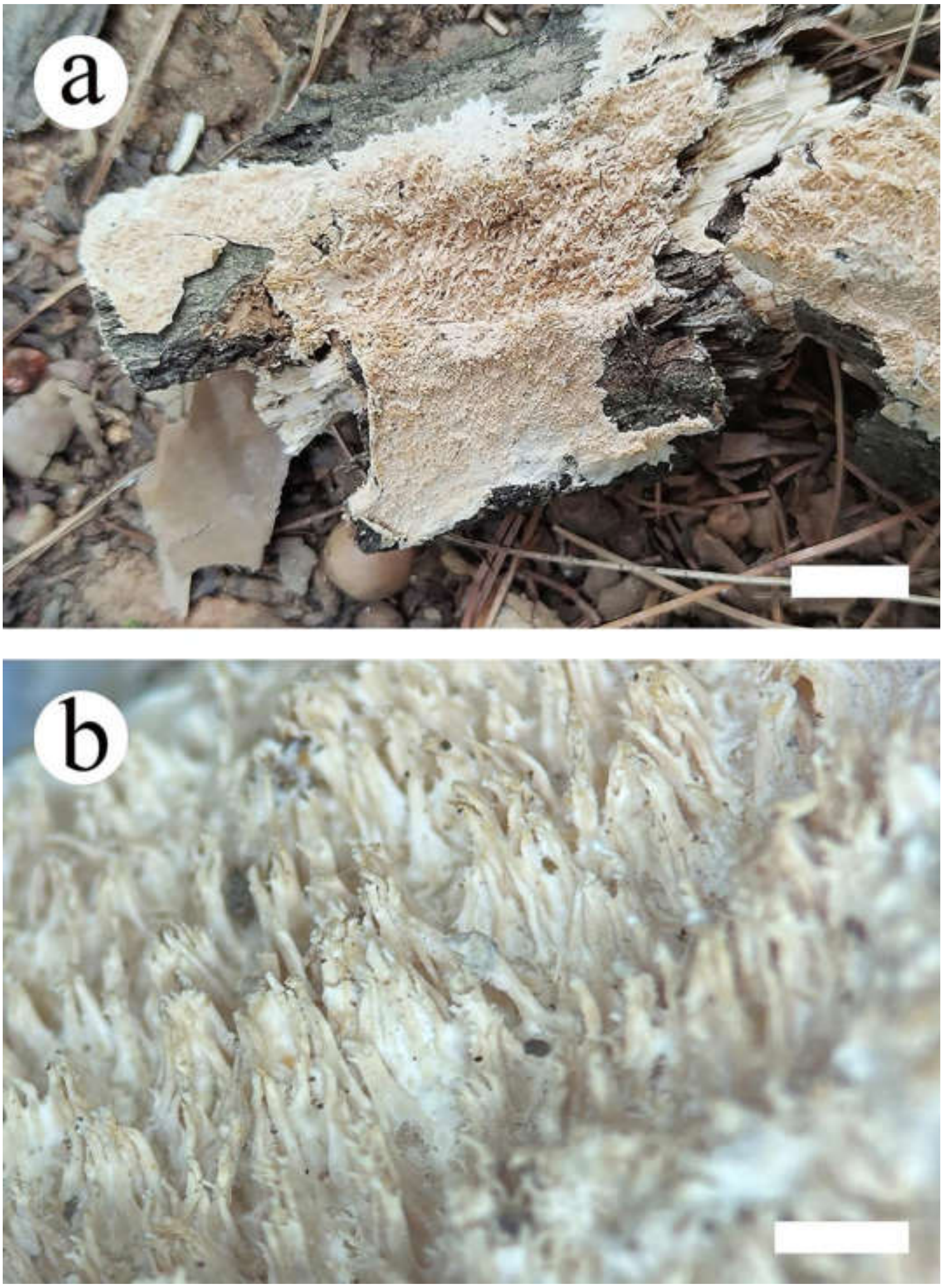

Figure 92 – Basidiomata of *Steccherinum longiaculeiferum* (holotype). Scale bars: a = 1 cm, b = 2 mm.

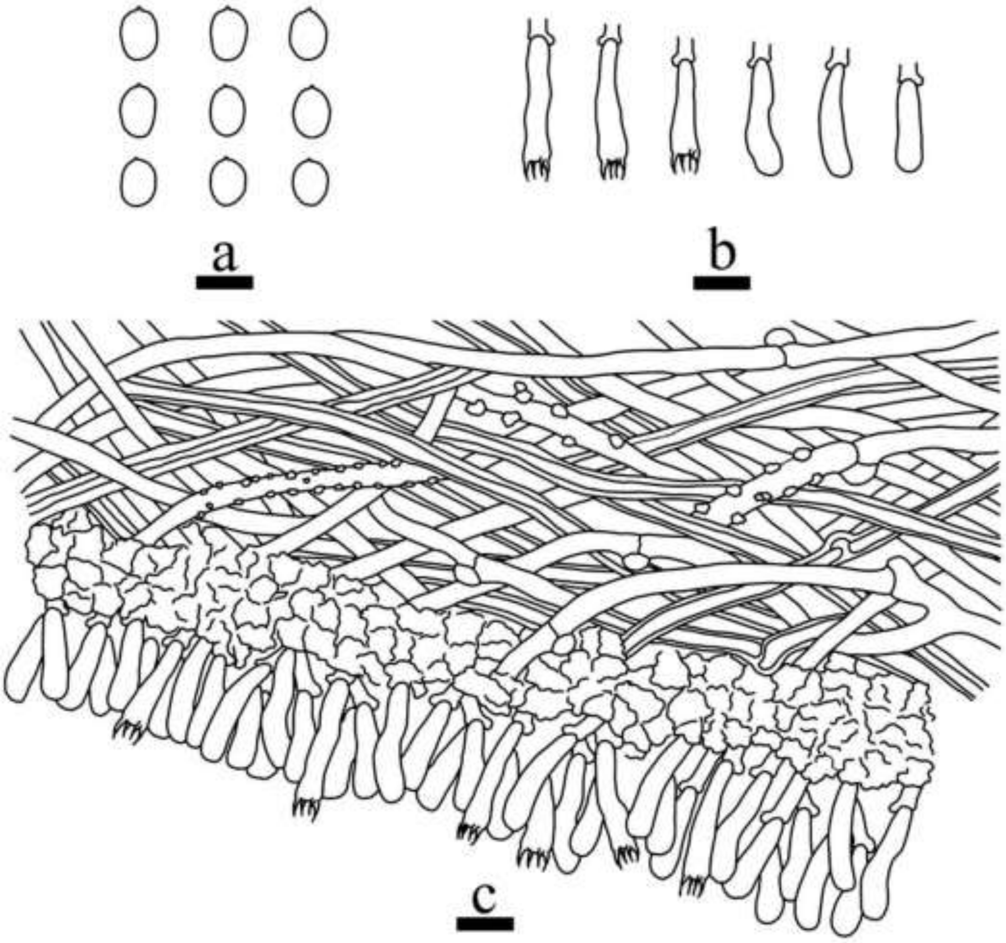

Figure 93 – Microscopic structures of *Steccherinum longiaculeiferum* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c A section of hymenium. Scale bars: a = 5 µm, b–c = 10 µm.

Description – Basidiomata annual, resupinate, adnate, coriaceous, without odor or taste when fresh, becoming hard coriaceous upon drying, up to 5 cm long, 3 cm wide, up to 2 mm thick. Hymenial surface hydnoid, with long aculei, 2–5 per mm, up to 2.5 mm long, slightly cream when fresh, turning to cream upon drying. Sterile margin white, thinning out, up to 2 mm wide.

Hyphal system dimitic, generative hyphae with clamp connections, colorless, thin to thick-walled, branched, interwoven, more or less loosely covered by numerous crystals, 3–5 µm in diameter; Skeletal hyphae colorless, thick-walled, 4–5.5 µm diameter; all hyphae IKI–, CB–, tissues unchanged in KOH. Subhymenium indistinct, densely covered by numerous crystals. Cystidia and cystidioles absent. Basidia clavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, 16.5–23.5 × 4.5–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid to ellipsoid, thin-walled, colorless, smooth, IKI–, CB–, (3.8–)4–4.3(–4.5) × 2.5–3 µm, L = 4.16 µm, W = 2.83 µm, Q = 1.45–1.51 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Qujing, Qilin District, Cuishan Forest Park, GPS coordinates 25°32' N, 103°42' E, altitude 2250 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 5 November 2022, CLZhao 26290 (SWFC).

Notes – The new species *Steccherinum longiaculeiferum* is grouped within *Steccherinum* based on the ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 data (Fig. 17) and is identified as a sister to *S. bourdotii* Saliba & A. David. However, *S. bourdotii* can be distinguished from *S. longiaculeiferum* by its effuse-reflexed basidiomata with the pale ochraceous hymenial surface, larger basidiospores (4.5–5.5 × 3–4.5 µm) and presence encrusted cystidia (Bernicchia & Gorjón 2010).

Steccherinum longiaculeiferum shares a hydnoid hymenial surface with *S. oreophilum* Lindsey & Gilb. and *S. subcrinale* (Peck) Ryvarden. However, *S. oreophilum* differs from *S. longiaculeiferum* by its effuse-reflexed basidiomata and white hymenial surface, along with larger basidiospores (5–6.5 × 3–3.2 µm) and presence encrusted cystidia (Bernicchia & Gorjón 2010); *S. subcrinale* can be distinguished from *S. longiaculeiferum* with its ochraceous to isabelline hymenial surface, generative hyphae with simple septa, and smaller basidiospores (3–3.5 × 2–2.5 µm, Bernicchia & Gorjón 2010).

Steccherinum longiaculeiferum is similar to *S. fragile*, *S. ochraceum* and *S. subtropicum*, sharing ellipsoid basidiospores. However, *S. fragile* differs from *S. longiaculeiferum* by its poroid hymenial surface, and smaller basidiospores (2.8–3.1 × 2.1–2.2 µm, Liu & Dai 2021); *S. ochraceum* differentiates from *S. longiaculeiferum* by its ochraceous hymenial surface, smaller basidiospores (3–3.5 × 2–2.5 µm) and presence encrusted cystidia (Bernicchia & Gorjón 2010); *S. subtropicum* can be distinguished from *S. longiaculeiferum* in its effuse-reflexed basidiomata and pink hymenial surface, shorter basidiospores (2.8–3.4 × 2–2.7 µm) and presence encrusted cystidia (Dong et al. 2023b).

Steccherinum weishanense J.H. Dong & C.L. Zhao, sp. nov. Figs 94, 95

Index Fungorum number: IF850349; Facesoffungi number: FoF15456

Diagnosis – Differs from other *Steccherinum* species by the coriaceous basidiomata with cream, odontioid hymenial surface with subulate aculei, 7–10 per mm, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 4–4.8 × 2.5–3.3 µm.

Etymology – *weishanense* (Lat.): referring to the locality (weishan) of the type specimen.

Type – China, Yunnan Province, Dali, Weishan County, Qinghua Town, Green Peacock Reserve, GPS coordinates 25°01' N, 100°11' E, altitude 1500m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 18 October 2022, CLZhao 24911 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, coriaceous, without odor or taste when fresh, becoming hard coriaceous upon drying, up to 10 cm long, 2 cm wide, up to 1 mm thick. Hymenial surface odontioid, with subulate aculei, 7–10 per mm, up to 0.3 mm long, white to cream when fresh, turning to cream to buff upon drying. Sterile margin cream, thinning out, up to 1 mm wide.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin to thick-walled, branched, interwoven, 3–5 µm in diameter, IKI–, CB–, tissues unchanged in KOH. Cystidia of two types: (1) clavate, colorless, thin-walled, smooth, 26.5–66 × 5–8.5 µm; (2) encrusted, colorless, thick-walled, strongly encrusted in the obtuse apex, 28.5–55 × 9.5–14 µm; cystidioles absent. Basidia subclavate, slightly sinuous, with 4 sterigmata and a basal clamp connection, 11–15 × 4–6 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, thin-walled, colorless, smooth, IKI–, CB–, (3.8–)4–4.8(–5) × (2.3–)2.5–3.3(–3.5) µm, L = 4.29 µm, W = 2.92 µm, Q = 1.47 (n = 30/1).

Notes – In this study, the new species *Steccherinum weishanense* is classified within *Steccherinum* based on the ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 data (Fig. 17) forming a monophyletic lineage.

Steccherinum weishanense shares similarities with *S. fragile*, *S. juniperi*, *S. ochraceum*, and *S. robustius* (J. Erikss. & S. Lundell) J. Erikss. However, *S. fragile* differs from *S. weishanense* by its poroid hymenial surface, and smaller basidiospores (2.8–3.1 × 2.1–2.2 µm, Liu & Dai 2021); *S. juniperi* can be distinguished from *S. weishanense* by its poroid hymenial surface, dimitic hyphal system, narrower basidia (10–15 × 3–4 µm) and shorter basidiospores (3–4 × 2–3 µm, Liu et al. 2023d); *S. ochraceum* differentiates from *S. weishanense* in its ochraceous hymenial surface, dimitic hyphal system and smaller basidiospores (3–3.5 × 2–2.5 µm, Bernicchia & Gorjón 2010); *S. robustius* differs from *S. weishanense* by its fimbriate sterile margin, dimitic hyphal system, and longer basidia (20–30 × 4–5 µm, Bernicchia & Gorjón 2010).

Steccherinum weishanense is similar to *S. subtropicum* in sharing the ellipsoid basidiospores. *Steccherinum subtropicum* is distinguished from *S. weishanense* by its effuse-reflexed basidiomata and pink hymenial surface, dimitic hyphal system and shorter basidiospores (2.8–3.4 × 2–2.7 µm, Dong et al. 2023b).

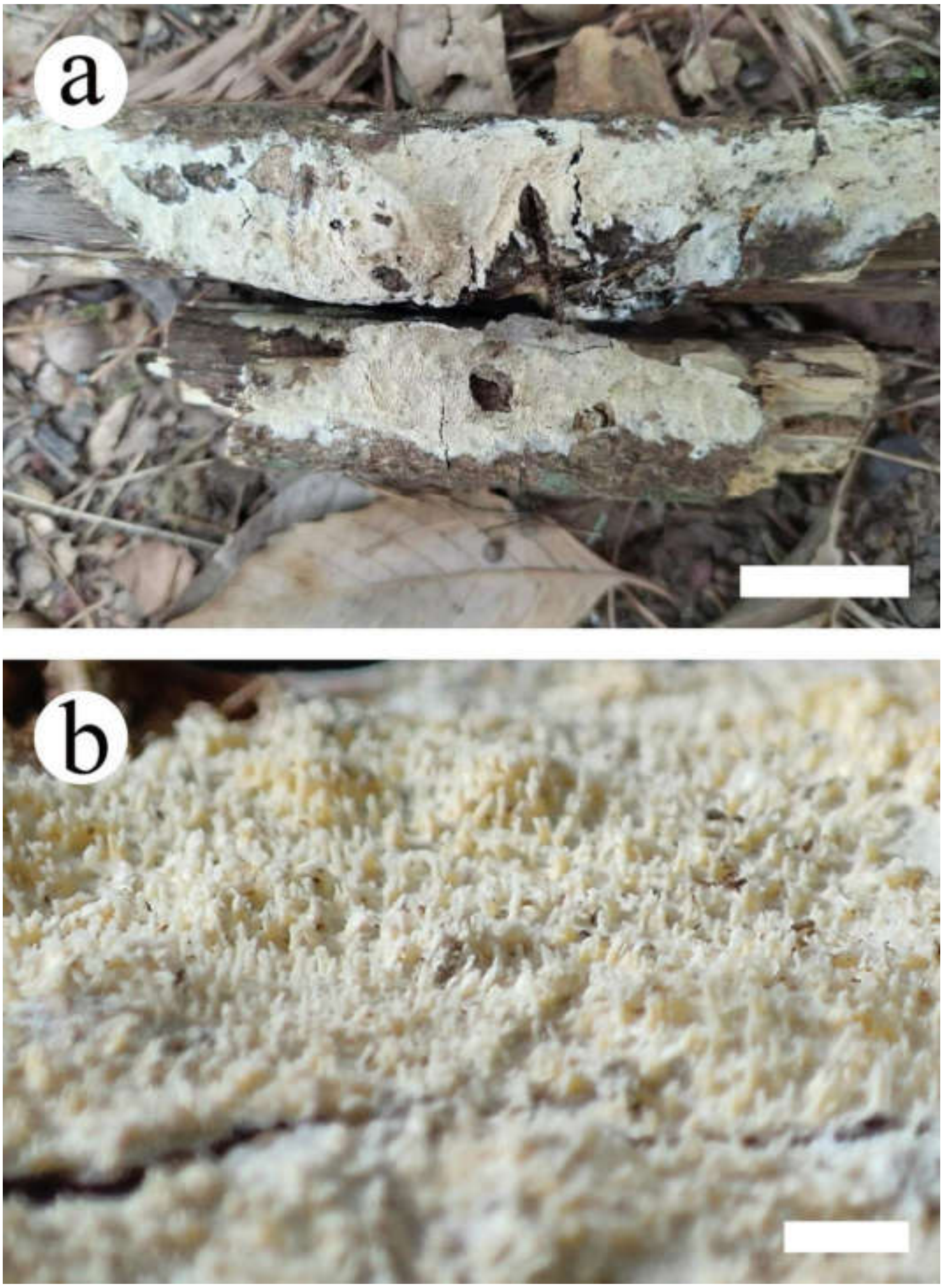

Figure 94 – Basidiomata of *Steccherinum weishanense* (holotype). Scale bars: a = 1 cm, b = 1 mm.

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

Auriscalpiaceae Maas Geest.

Index Fungorum number: IF80506; Facesoffungi number: FoF15457

Type genus – *Auriscalpium* Gray

Artomyces Jülich

Index Fungorum number: IF17104; Facesoffungi number: FoF15458

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

Notes – Jülich (1982) introduced the genus *Artomyces* and typified it with *A. pyxidatus* (Pers.) Jülich, proposing *Artomyces* as a distinct genus separate from *Clavicorona* Doty. Lickey et al. (2003) conducted a comprehensive phylogenetic and taxonomic study of *Artomyces*, accepting 15 species within the genus based on a combination of morphology, nuclear ribosomal internal transcribed spacer DNA (nrITS DNA) sequences, and mating studies. In addition, they described seven new species. Furthermore, Kneal & Smith (2015) described a new species *A. nothofagi* R.J. Kneal & M.E. Sm., based on morphology and phylogeny. In this study, we propose two new species, *A. niveus* and *A. yunnanensis*, based on morphological and molecular systematics evidence.

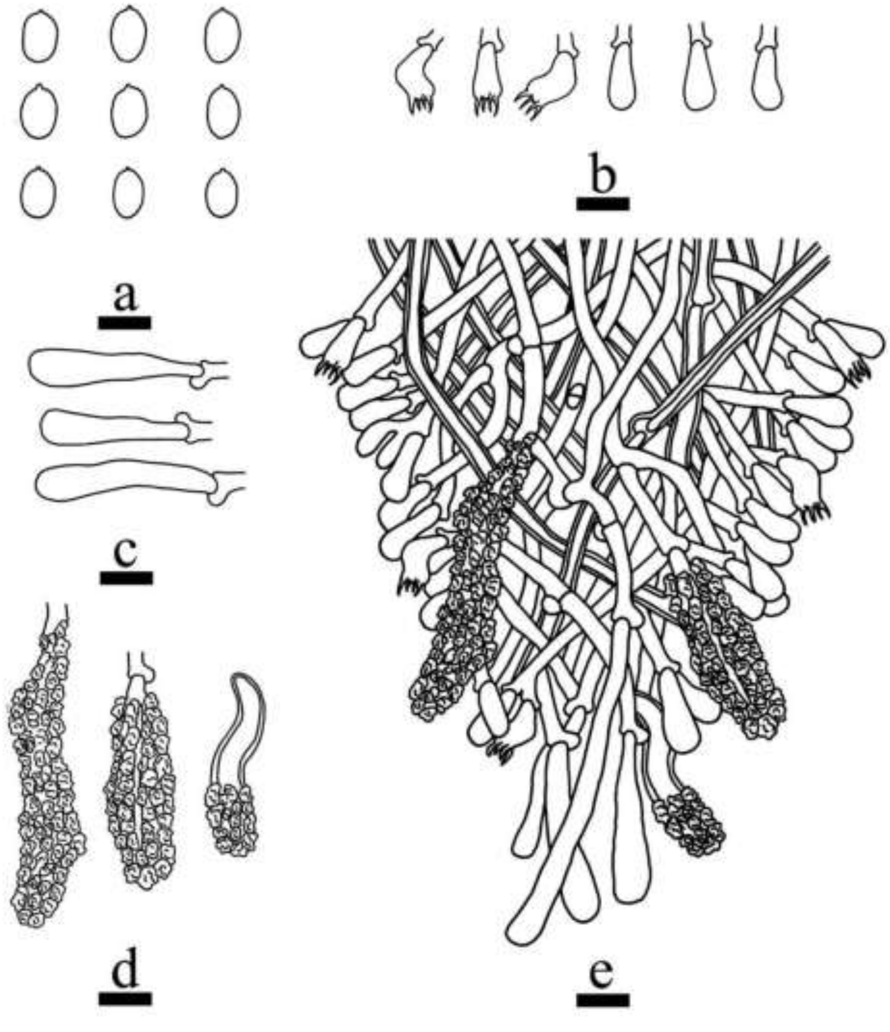

Figure 95 – Microscopic structures of *Steccherinum weishanense* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Clavate cystidia. d Encrusted cystidia. e A section of hymenium. Scale bars: a = 5 µm, b–e = 10 µm.

Artomyces niveus J.H. Dong & C.L. Zhao, sp. nov. Figs 96, 97

Index Fungorum number: IF850350; Facesoffungi number: FoF15459

Diagnosis – Differs from other *Artomyces* species by the gregarious basidiomata with niveous, coronate-cristate to cuspidate apices, monomitic hyphal system with clamped generative hyphae and broadly ellipsoid basidiospores measuring 3–3.8 × 2.5–3.3 µm.

Etymology – *niveus* (Lat.): referring to the niveous hymenophore of the type specimen.

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 19094 (SWFC).

Description – Basidiomata lignicolous, gregarious, 30–45 mm tall × 15–30 mm wide, frequently branched and coronate, forming cristate branches at the apices; apices coronate-cristate to cuspidate; without odor or taste, soft when fresh, becoming brittle upon drying, usually lacking obvious basal mycelium. Niveous when fresh, turning to caramel brown upon drying.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, 2.5–4 µm diameter; IKI–, CB–, tissues unchanged in KOH. Gloeoplerous hyphae, common in the trama, aseptate, colorless, thin-walled, 2.5–9.5 µm diameter, terminating in the hymenium as gloeocystidia. Gloeocystidia common, clavate, flexuous, 31.5−60 × 6−11.5 µm; cystidioles absent. Basidia clavate, slightly sinuous, thin-walled, with 4 sterigmata and a basal clamp connection, 13–17.5 × 3–5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores broadly ellipsoid, thin-walled, colorless, smooth, amyloid, CB–, 3–3.8(–4) × 2.5–3.3(–3.5) µm, L = 3.38 µm, W = 2.90 µm, Q = 1.15–1.21 (n = 90/3).

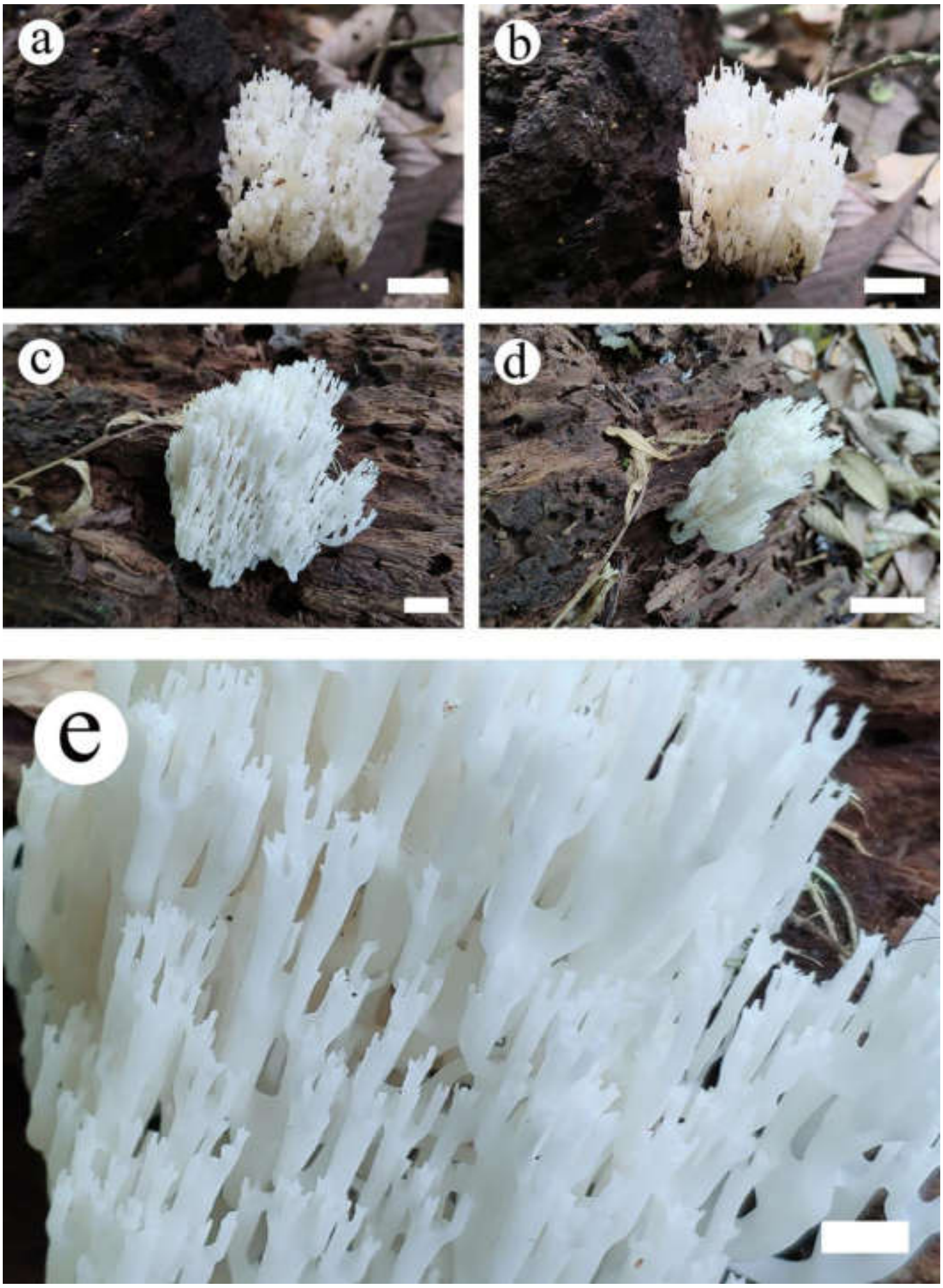

Figure 96 – Basidiomata of *Artomyces niveus* (holotype). Scale bars: a–d = 1 cm, e = 2 mm.

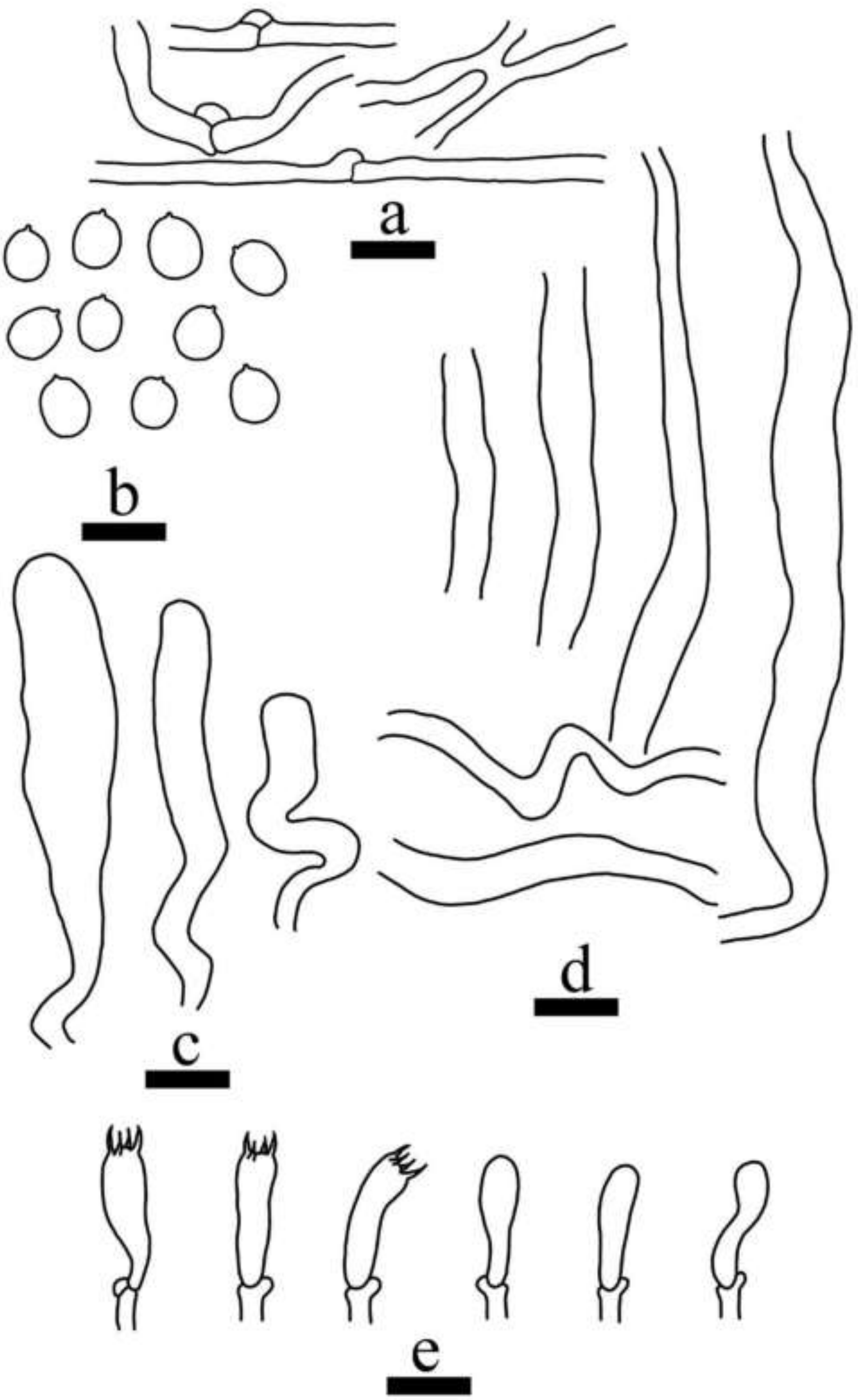

Figure 97 – Microscopic structures of *Artomyces niveus* (drawn from the holotype). a Generative hypha. b Basidiospores. c Gloeocystidia. d Gloeoplerous hyphae. e Basidia and basidioles. Scale bars: a, c–e = 10 µm, b = 5 µm.

Material examined (paratypes) – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 3 August 2019, CLZhao 18346; 9 June 2020, CLZhao 18996 (SWFC).

Notes – Based on the ITS data (Fig. 18), the new species *Artomyces niveus* is placed within *Artomyces*. and identified as the sister species to *A. turgidus* (Lév.) Jülich. However, *A. turgidus* can be distinguished from *A. niveus* by its longer basidiospores (4–5 × 3–3.5 µm, Lickey et al. 2003).

Artomyces niveus resembles *A. novae-zelandiae* Lickey and *A. tasmaniensis* Lickey in having the broadly ellipsoid basidiospores. However, *A. novae-zelandiae* differs from *A. niveus* by its larger basidiospores (4.6–6 × 3.6–4.8 µm, Lickey et al. 2003); *A. tasmaniensis* differentiates from *A. niveus* in its longer basidia (22–32 × 4–5.2 µm, Lickey et al. 2003).

Artomyces yunnanensis J.H. Dong & C.L. Zhao, sp. nov. Figs 98, 99

Index Fungorum number: IF850351; Facesoffungi number: FoF15460

Diagnosis – Differs from other *Artomyces* species by the scattered to gregarious basidiomata with greyish brown to dark brown, coronate-cristate to cuspidate apices, monomitic hyphal system with clamped generative hyphae and ellipsoid basidiospores measuring 5–6 × 3.7–4.7 µm.

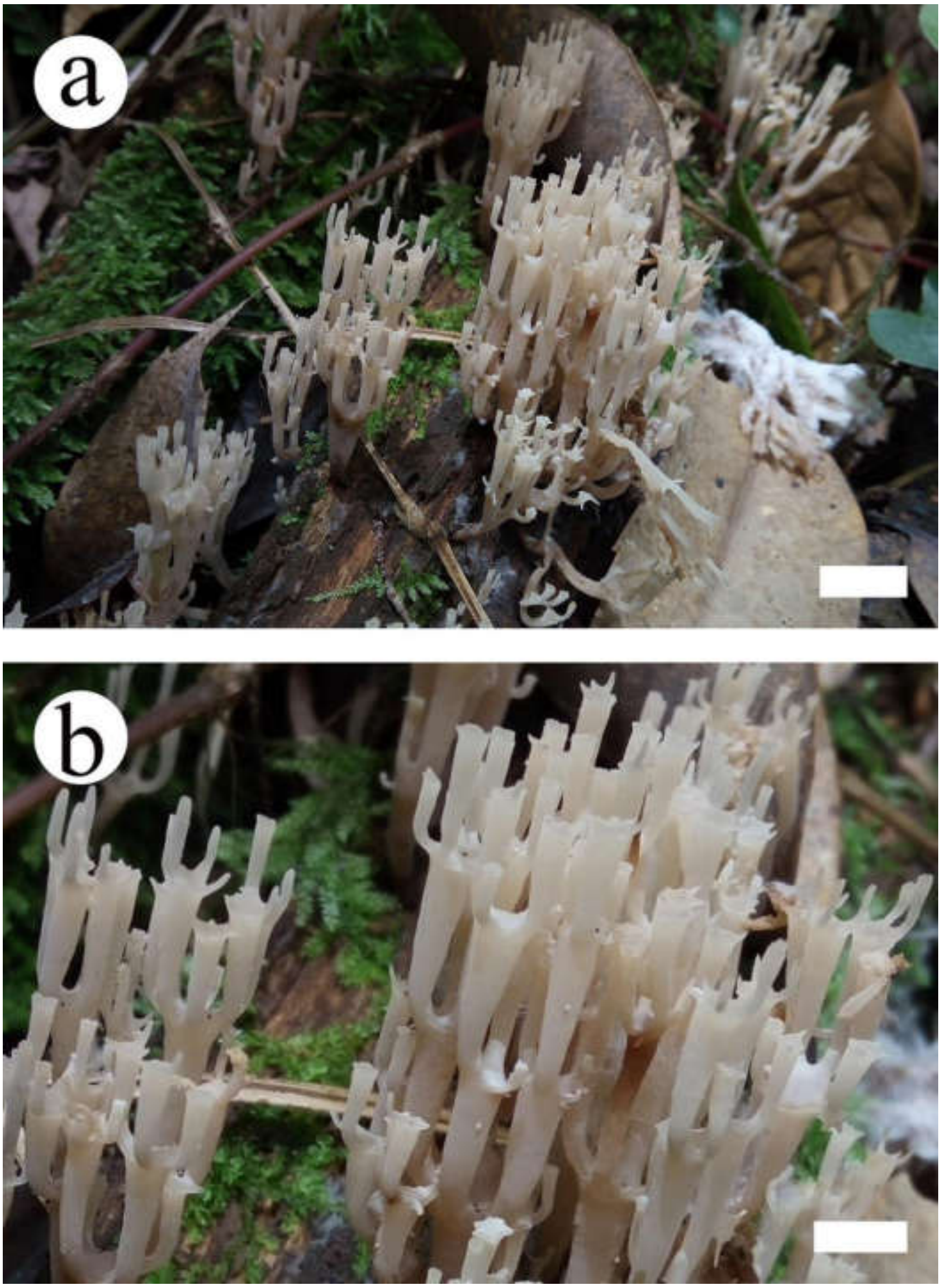

Figure 98 – Basidiomata of *Artomyces yunnanensis* (holotype). Scale bars: a = 1 cm, b = 5 mm.

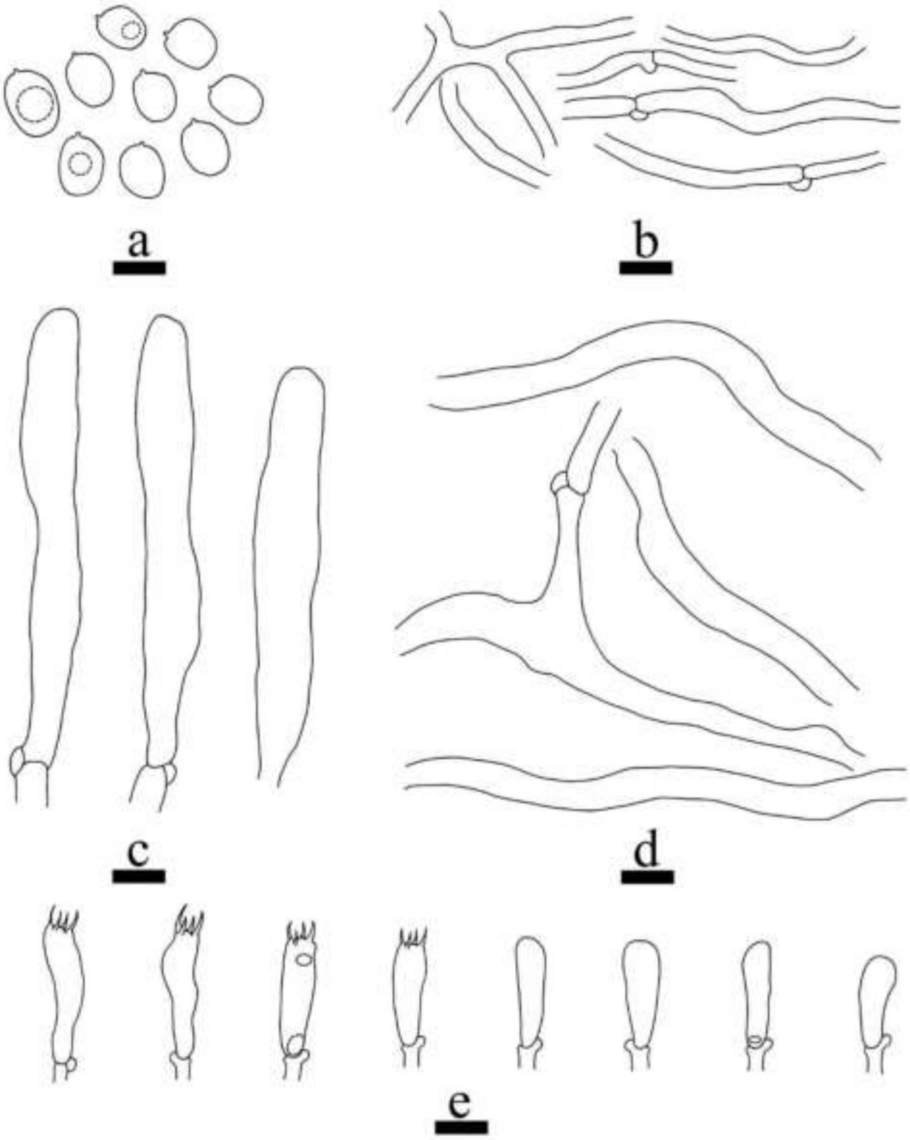

Figure 99 – Microscopic structures of *Artomyces yunnanensis* (drawn from the holotype). a Basidiospores. b Generative hyphae. c Gloeocystidia. d Gloeoplerous hyphae. e Basidia and basidioles. Scale bars: a = 5 µm, b–e = 10 µm.

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

Type – China, Yunnan Province, Chuxiong, Zixishan National Forestry Park, GPS coordinates 25°01' N, 101°24' E, altitude 2500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 1 July 2018, CLZhao 7118 (SWFC, holotype).

Description – Basidiomata lignicolous, scattered to gregarious, 20–35 mm tall × 10–20 mm wide, frequently branched and coronate, forming cristate branches at the apices; apices coronate-cristate to cuspidate; without odor or taste, soft when fresh, becoming brittle upon drying, usually lacking obvious basal mycelium. Slightly cream when fresh, turning to greyish brown to dark brown upon drying.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, branched, 2.5–4.5 µm diameter; IKI–, CB–, tissues unchanged in KOH. Gloeoplerous hyphae, common in the trama, aseptate, colorless, thin-walled, 4.5–13 µm diameter, terminating in the hymenium as gloeocystidia. Gloeocystidia common, mostly cylindrical to clavate, flexuous, 70−85.5 × 10−17 µm; cystidioles absent. Basidia clavate, slightly sinuous, thin-walled, with 4 sterigmata and a basal clamp connection, sometimes with a guttula, 20.5–26.5 × 5.7–7 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, thin-walled, colorless, smooth, sometimes with a guttula, amyloid, CB–, 5–6(–6.5) × 3.7–4.7(–5) µm, L = 5.43 µm, W = 4.26 µm, Q = 1.27–1.31 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Chuxiong, Zixishan National Forestry Park, GPS coordinates 25°01' N, 101°24' E, altitude 2500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 1 July 2018, CLZhao 7052 (SWFC).

Notes – In this study, based on the ITS data (Fig. 18), the new species *Artomyces yunnanensis* is classified within *Artomyces*, and found to be the sister species to *A. carolinensis* Lickey. However, *A. carolinensis* can be distinguished from *A. yunnanensis* by its narrower basidia (14–20 × 4–4.8 µm) and smaller basidiospores (3.6–4.4 × 2.8–3.4 µm, Lickey et al. 2003).

Artomyces yunnanensis shares similarities with *A. adrienneae* Lickey and *A. colensoi* (Berk.) Jülich in sharing the ellipsoid basidiospores. However, *A. adrienneae* differs from *A. yunnanensis* by its narrower basidiospores (4.2–5.2 × 2.8–3.6 µm, Lickey et al. 2003); *A. colensoi* can be distinguished from *A. yunnanensis* by its narrower basidia (20–28 × 3.6–5.2 µm) and smaller basidiospores (3.6–4.4 × 2.4–3 µm, Lickey et al. 2003).

Peniophoraceae Lotsy

Index Fungorum number: IF81123; Facesoffungi number: FoF15461

Type genus – *Peniophora* Cooke

Scytinostroma Donk

Index Fungorum number: IF18530; Facesoffungi number: FoF15462

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

Notes – The genus *Scytinostroma* Donk was established by Donk (1956) and typified by *S. portentosum* (Berk. & M.A. Curtis) Donk. Phylogenetic research on this genus revealed that five species of *Scytinostroma*; *S. galactinum* (Fr.) Donk, *S. jacksonii* Boidin, *S. ochroleucum* Donk, *S. odoratum* (Fr.) Donk and *S. portentosum* (type species), occurred on five distinct branches that were distantly separated in Peniophoraceae (Larsson & Larsson 2003, Miller et al. 2006). Leal-Dutra et al. (2018) constructed a phylogenetic tree to focus on the relationships among the species of *Scytinostroma* and proposed the new genus *Baltazaria* Leal-Dutra, Dentinger & G.W. Griff. To accommodate four species: *S. galactinum*, *S. neogalactinum* Boidin & Lanq., *S. eurasiaticogalactinum* Boidin & Lanq. and *Parapterulicium octopodites* Corner. Based on a morphology study, Stalpers et al. (2021) transferred two species of *Michenera* Berk. & M.A. to *Scytinostroma* and treated the former genus as a synonym of the latter. Li et al. (2023b) conducted phylogenetic analyses of Peniophoraceae based on concatenating ITS1-5.8S-ITS2-nrLSU sequence data, with a focus on samples of *Scytinostroma* s.s. worldwide, and introduced four new species *S. beijingensis*, *S. boidinii*, *S. subduriusculum* and *S. subrenisporum*. In this study, one new species of *Scytinostroma* is described from China based on morphological characteristics and phylogenetic analyses inferred from ITS+nLSU sequences.

Scytinostroma daweishanense J.H. Dong & C.L. Zhao, sp. nov. Figs 100–102

Index Fungorum number: IF850352; Facesoffungi number: FoF15463

Diagnosis – Differs from other *Scytinostroma* species by the effused-reflexed, coriaceous basidiomata with slightly orange-yellow, smooth hymenial surface, dimitic hyphal system with septate generative hyphae and subglobose to globose basidiospores measuring 14.5–17 × 13.5–17 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 1 August 2019, CLZhao 17926 (SWFC, holotype).

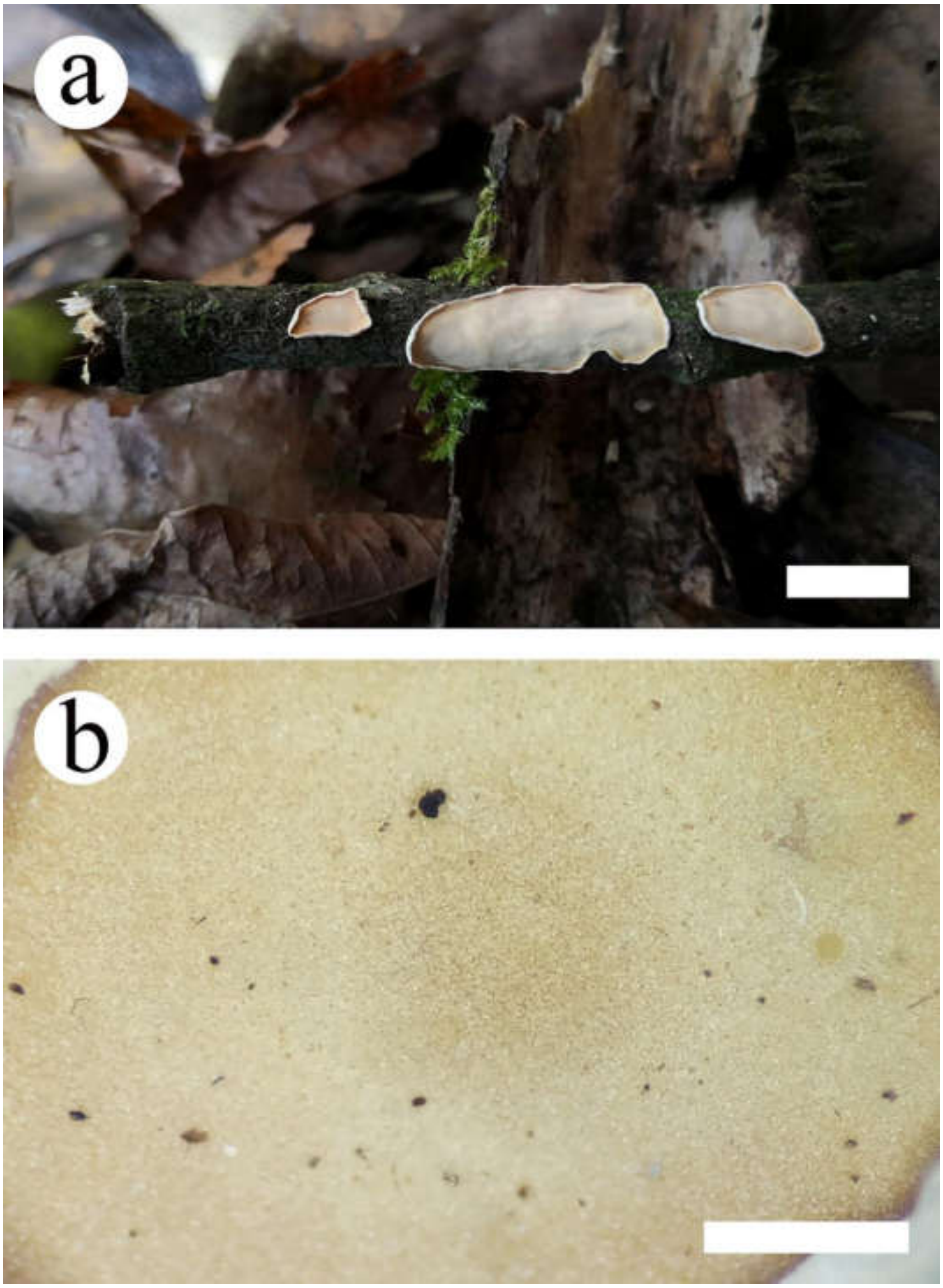

Figure 100 – Basidiomata of *Scytinostroma daweishanense* (holotype). Scale bars: a = 1 cm, b = 2 mm.

Description – Basidiomata annual, resupinate, discoid, effused-reflexed, adnate with slightly detached margins, without odor or taste, soft coriaceous when fresh, becoming coriaceous upon drying, to 1–2.5 cm long, up to 1 mm thick. Hymenial surface smooth, cuticolor to cream to lightly orange when fresh, turning to slightly orange-yellow upon drying. Sterile margin cream to lightly orange, abrupt, up to 0.5 mm wide.

Hyphal system dimitic, generative hyphae with simple septa, colorless, thin-walled, moderately branched, composed of loosely interwoven, 2–3 µm in diameter, IKI–, CB–; skeletal hyphae dominant, aseptate, colorless, thick-walled, frequently branched, interwoven, 2.5–4 µm diameter, IKI+, CB+; tissues unchanged in KOH. Gloeocystidia numerous, embedded, cylindrical to subclavate, with a rounded apex, simple septum at base, thick-walled, empty or contents concentrated in upper part, usually with several adventitious septa, 150–200 × 12–16 µm; cystidioles absent. Basidia clavate, elongate, somewhat sinuous, sometimes with a few guttulae, thin-walled, with 4 sterigmata and a basal simple septum, 100–110 × 17–20 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores subglobose to globose with a distinct apiculus, thin to slightly thick-walled, colorless, smooth, sometimes with a guttula, IKI–, CB+, (13.5–)14.5–17(–18) × (12.5–)13.5–17(–17.5) µm, L = 15.87 µm, W = 15.53 µm, Q = 1.02 (n = 30/1).

Notes – Based on the ITS+nLSU data (Fig. 19), the new species *Scytinostroma daweishanense* is grouped into *Scytinostroma*, and forms a cluster with *S. artocreas* (Berk. & M.A. Curtis) K.H. Larss. and *S. incrustatum* (S.H. He, S.L. Liu & Nakasone) K.H. Larss. However, *S. artocreas* can be differentiated from *S. daweishanense* by its smaller basidia (70–100 × 13–15 µm, Lemke 1964); *S. incrustatum* can be distinguished from *S. daweishanense* by its tuberculate or undulating hymenial surface, along with both longer basidia (170–230 × 18–26 µm) and larger basidiospores (17–22 × 16–21 µm, Liu et al. 2018).

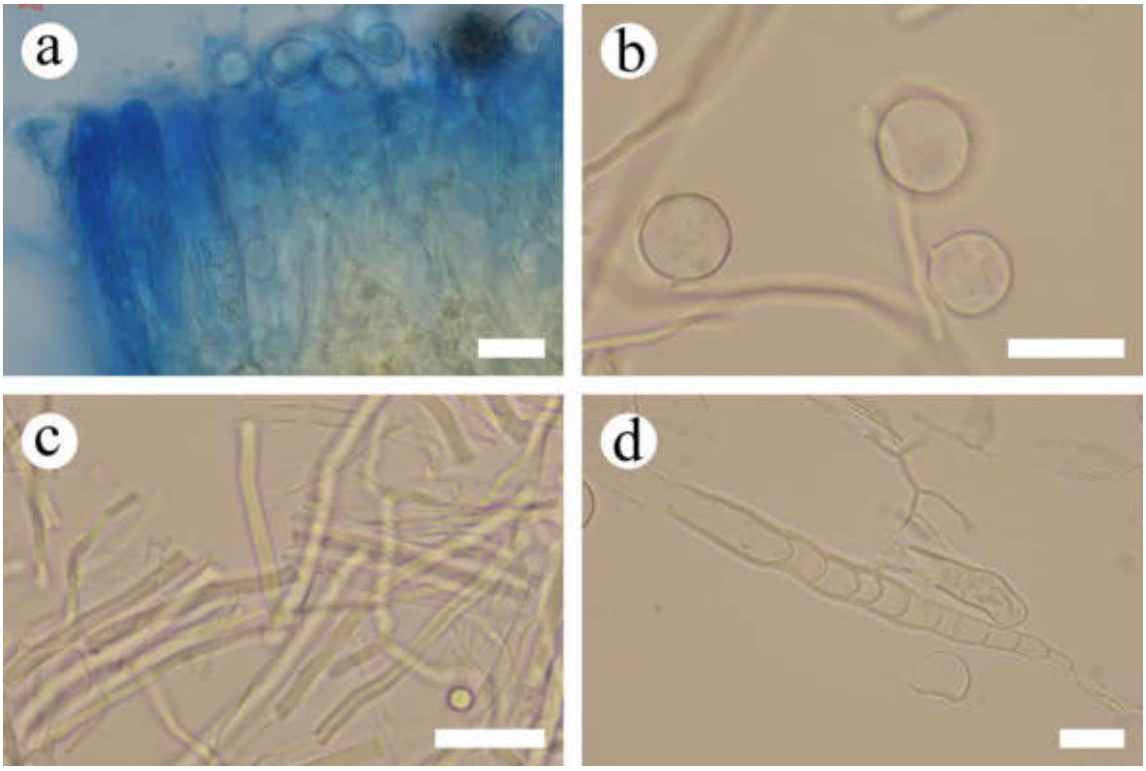

Figure 101 – Microscopic structures of *Scytinostroma daweishanense* (holotype) a Basidia and basidioles. b Basidiospores. c Hyphae. d Gloeocystidia. Scale bars: a–d = 20 µm, 10 × 100 Oil.

Trechisporales K.H. Larss.

Hydnodontaceae Jülich

Index Fungorum number: IF81729; Facesoffungi number: FoF15464

Type genus – *Hydnodon* Banker

Fibrodontia Parmasto

Index Fungorum number: IF17584; Facesoffungi number: FoF15465

Type species – *Fibrodontia gossypina* Parmasto

Notes – The genus *Fibrodontia* Parmasto was established by Parmasto (1968) and designated with *F. gossypina* Parmasto as its type species. To date, eight species are accepted in *Fibrodontia* (Liu et al. 2022c). Here, we describe, one additional species of *Fibrodontia* from China based on morphological characteristics and phylogenetic analyses inferred from ITS, nLSU, mtSSU, RPB2 and TEF1 DNA sequences.

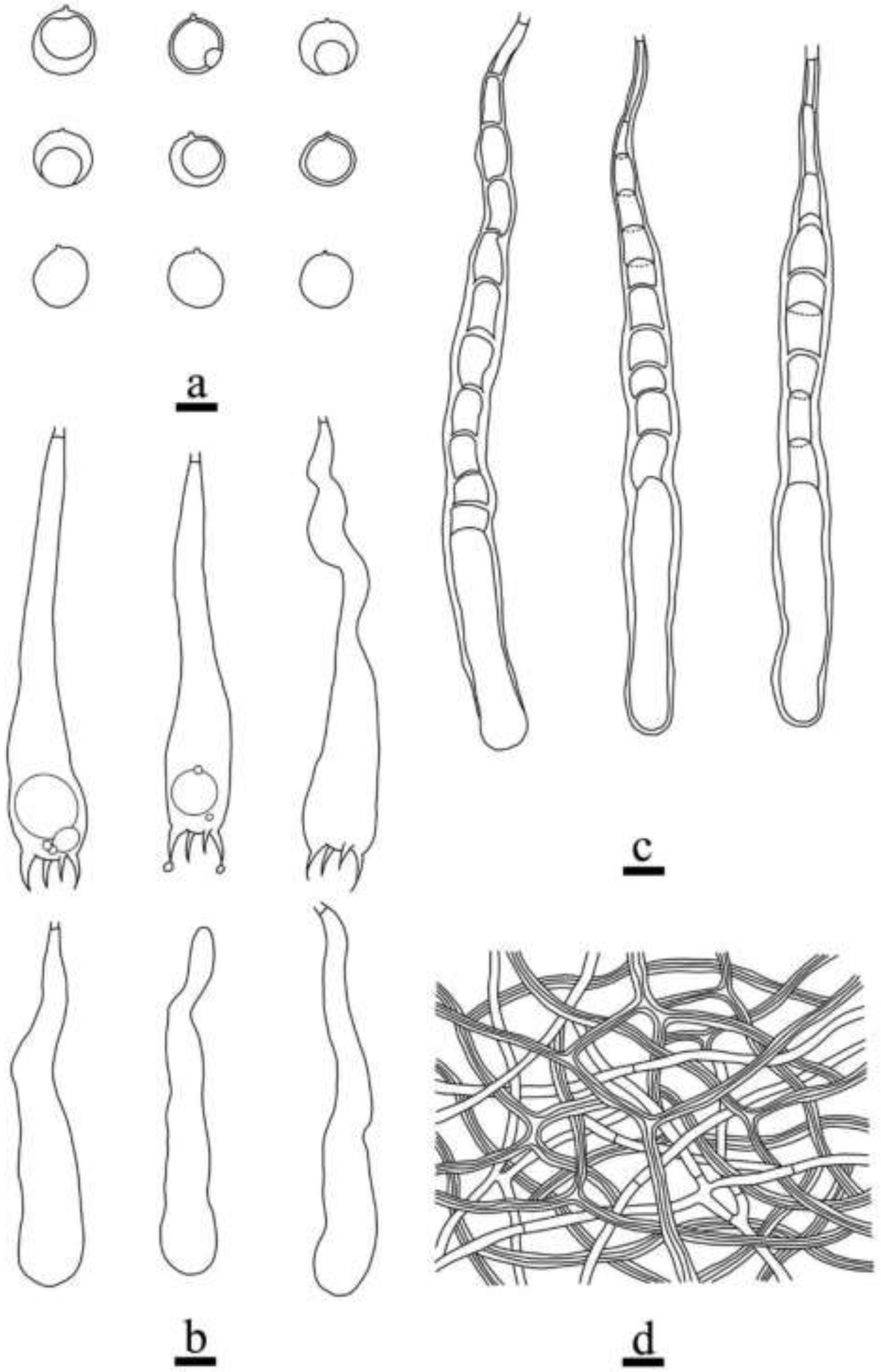

Figure 102 – Microscopic structures of *Scytinostroma daweishanense* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Gloeocystidia. d A section of hymenium. Scale bars: a–d = 10 µm.

Fibrodontia bambusicola J.H. Dong & C.L. Zhao, sp. nov. Figs 103, 104

Index Fungorum number: IF850353; Facesoffungi number: FoF15466

Diagnosis – Differs from other *Fibrodontia* species by the pruinose basidiomata with pinkish buff to olivaceous buff, smooth hymenial surface, dimitic hyphal system with clamped generative hyphae and broadly ellipsoid to subglobose basidiospores measuring 5.3–6.7 × 4–6 µm.

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

Type – China, Yunnan Province, Wenshan, Xichou County, Xiaoqiaogou National Nature Reserve, GPS coordinates 23°21' N, 104°4' E, altitude 2990 m asl., on the dead bamboo, leg. C.L. Zhao, 16 January 2019, CLZhao 11261 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, very hard to separate from substrate, without odor or taste, soft pruinose when fresh, becoming pruinose upon drying, up to 4.5 cm long, 2.5 cm wide, 20–50 µm thick. Hymenial surface smooth, slightly buff when fresh, turning to pinkish buff to olivaceous buff upon drying. Sterile margin narrow, slightly buff, thinning out, up to 0.5 mm wide.

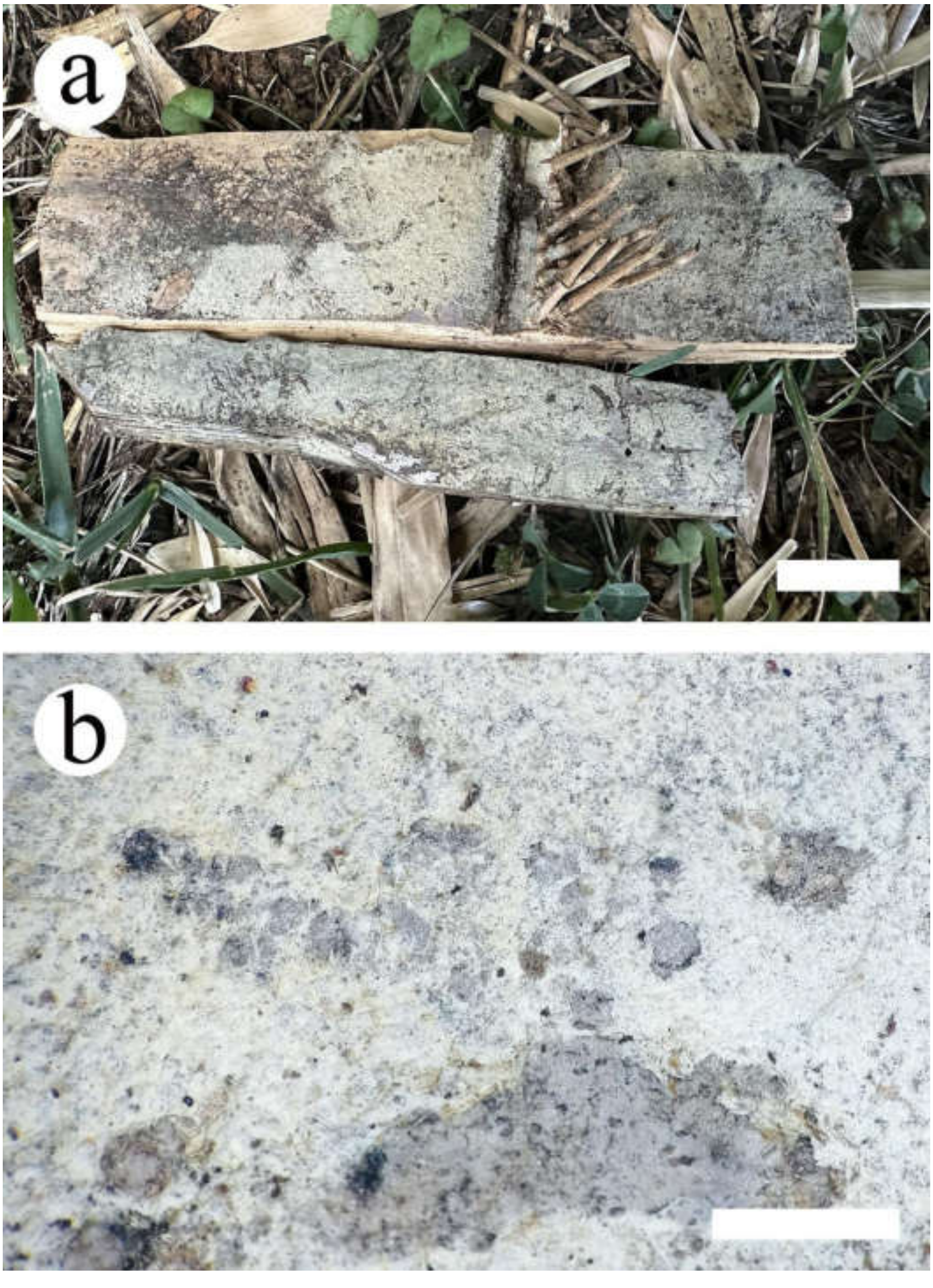

Figure 103 – Basidiomata of *Fibrodontia bambusicola* (holotype). Scale bars: a = 2 cm, b = 2 mm.

Hyphal system dimitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, interwoven 2–3 µm in diameter; skeletal hyphae, thick-walled, colorless, 2.5–

4 µm diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia and cystidioles absent. Basidia cylindrical, slightly sinuous, with 4 sterigmata and a basal clamp connection, 24–29 × 4–6 µm. Basidiospores broadly ellipsoid to subglobose, colorless, thin-walled, smooth, cyanophilous, IKI–, (5–)5.3–6.7(–7) × 4–6 µm, L = 6.13 µm, W = 4.93 µm, Q = 1.21–1.25 (n = 60/2).

Material examined (paratype) – China, Yunnan Province, Wenshan, Xichou County, Xiaoqiaogou, National Nature Reserve, GPS coordinates 23°21' N, 104°4' E, altitude 2990 m asl., on the dead bamboo, leg. C.L. Zhao, 16 January 2019, CLZhao 11201 (SWFC).

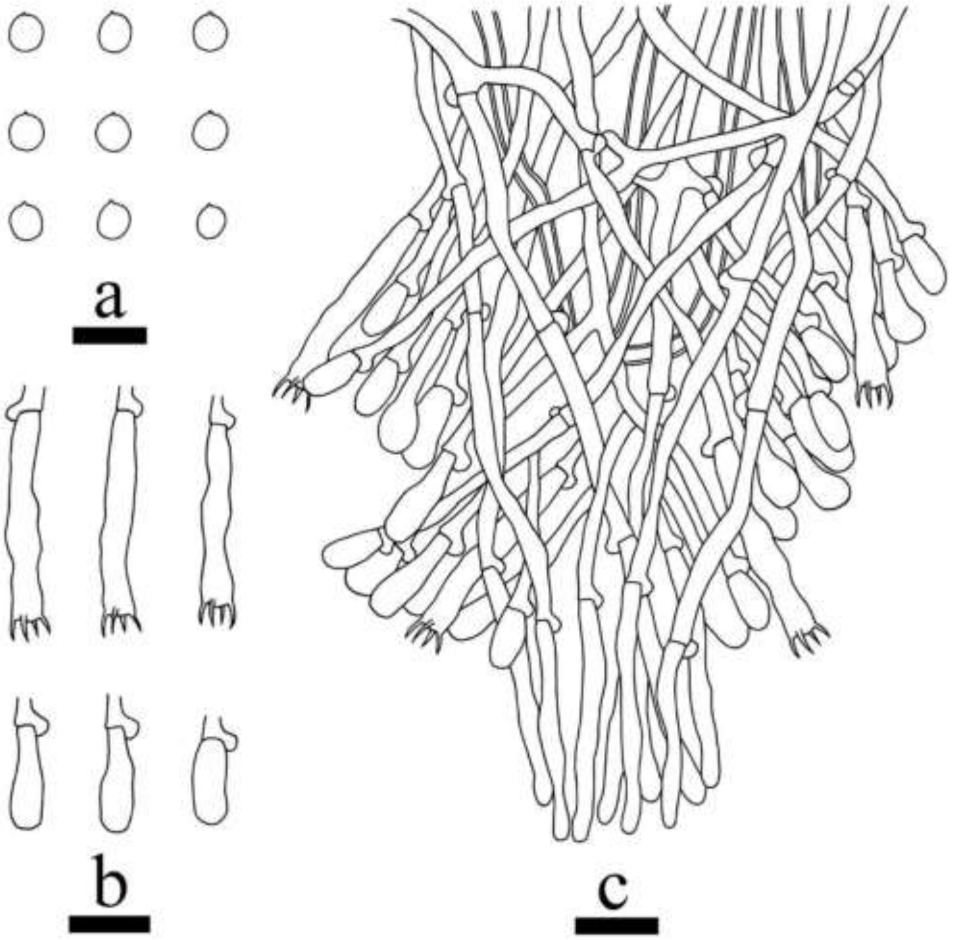

Figure 104 – Microscopic structures of *Fibrodontia bambusicola* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c A section of hymenium. Scale bars: a–c = 10 µm.

Notes – Based on the ITS, nLSU, mtSSU, RPB2 and TEF1 data (Fig. 20), the new species *Fibrodontia bambusicola* is classified within *Fibrodontia*, forming a sister relationship with *F. brevidens* (Pat.) Hjortstam & Ryvarden, and clustering with *F. austrosinensis* S.L. Liu, S.H. He & L.W. Zhou, *F. brevidens* and *F. subaustrosinensis* S.L. Liu, S.H. He & L.W. Zhou. However, *F. austrosinensis* can be distinguished from *F. bambusicola* by its grandinioid to odontioid hymenial surface, both shorter basidia (13–16 × 4.5–5.5 µm) and smaller basidiospores (4.2–5.2 × 3.5–4.5 µm, Liu et al. 2021); *F. brevidens* can be differentiated from *F. bambusicola* by its grandinioid to odontioid hymenial surface, and shorter basidiospores (4.5–5 × 3.5–4.5 µm, Ryvarden et al. 2005); *F. subaustrosinensis* can be distinguished from *F. bambusicola* by its grandinioid hymenial surface, and ellipsoid to ovoid basidiospores (4.8–6 × 4–5 µm, Liu et al. 2022c).

Subulicystidium Parmasto

Index Fungorum number: IF18619; Facesoffungi number: FoF15467

Type species – *Subulicystidium longisporum* (Pat.) Parmasto

Notes – The genus *Subulicystidium* Parmasto was established by Parmasto (1968) and typified by *S. longisporum* Parmasto. Molecular studies by Hibbett & Binder (2002) and Larsson et al. (2004) revealed that *Subulicystidium* was closely related to *Tubulicium vermiferum* (Bourdot) Oberw. and both were placed within the trechisporoid clade, next to other *Trechispora* species. In this study, one new species, *S. yunnanense* is reported based on morphological and phylogenetic evidence, using ITS, nLSU, mtSSU, RPB2 and TEF1 data (Fig. 20), bringing the total number of described *Subulicystidium* species to 13 (Ordynets et al. 2018, Liu et al. 2019).

Subulicystidium yunnanense J.H. Dong & C.L. Zhao, sp. nov. Figs 105, 106

Index Fungorum number: IF850354; Facesoffungi number: FoF15468

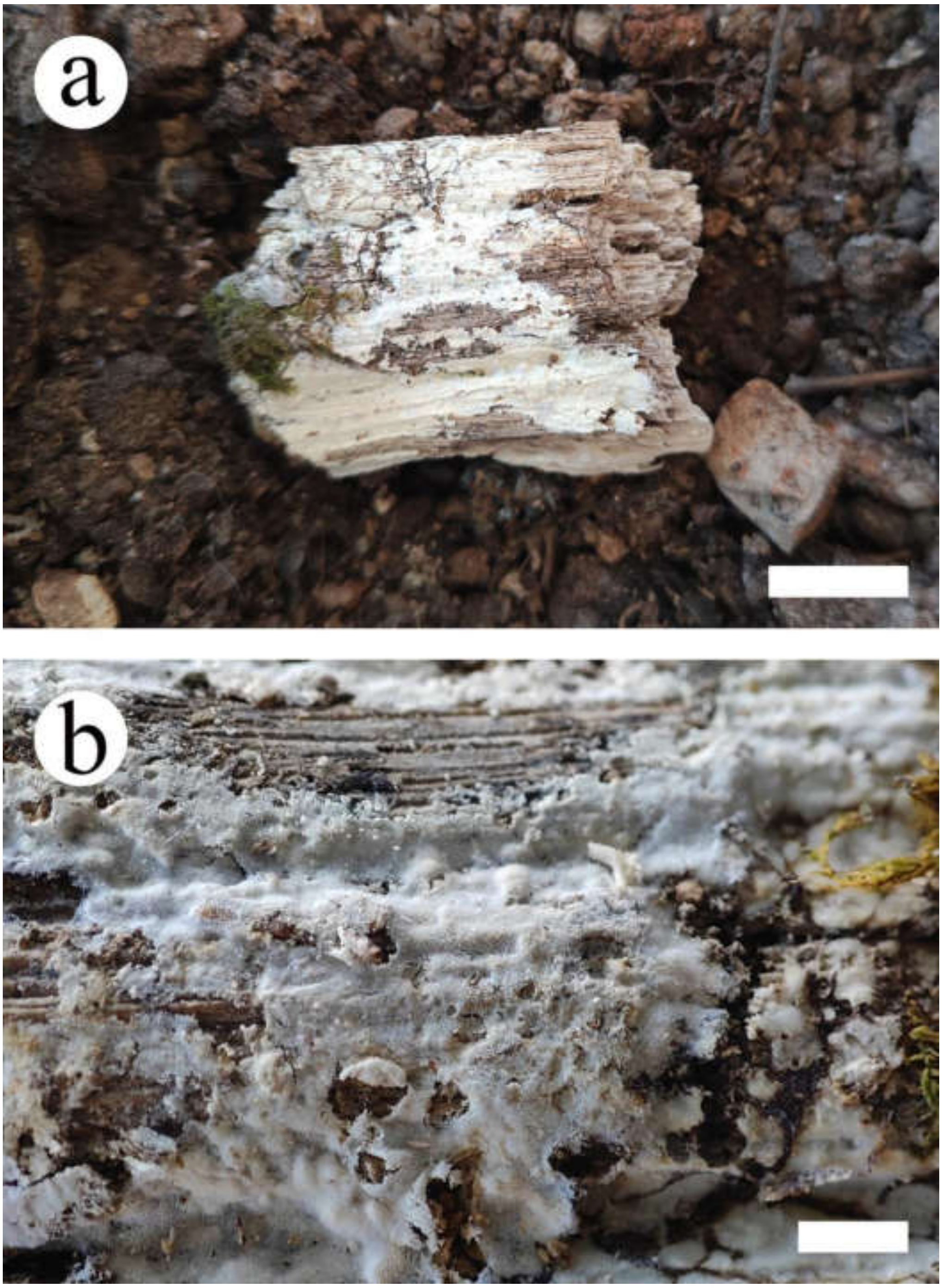

Figure 105 – Basidiomata of *Subulicystidium yunnanense* (holotype). Scale bars: a = 1 cm, b = 2 mm.

Diagnosis – Differs from other *Subulicystidium* species by the membranous basidiomata with white to cream, smooth hymenial surface, monomitic hyphal system with clamped generative hyphae, numerous protruding cystidia and vermicular to sigmoid basidiospores measuring 13.5–16 × 2–2.5 µm.

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

Type – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 22°51' N, 103°41' E, altitude 2360 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 9 June 2020, CLZhao 18950 (SWFC, holotype).

Description – Basidiomata annual, resupinate, adnate, very thin, loosely attached to the substrates, without odor or taste, membranous when fresh, becoming coriaceous upon drying, up to 5 cm long, 50–150 µm thick. Hymenial surface smooth, white when fresh, turning to white to cream upon drying. Sterile margin white to cream, abrupt, up to 0.5 mm wide.

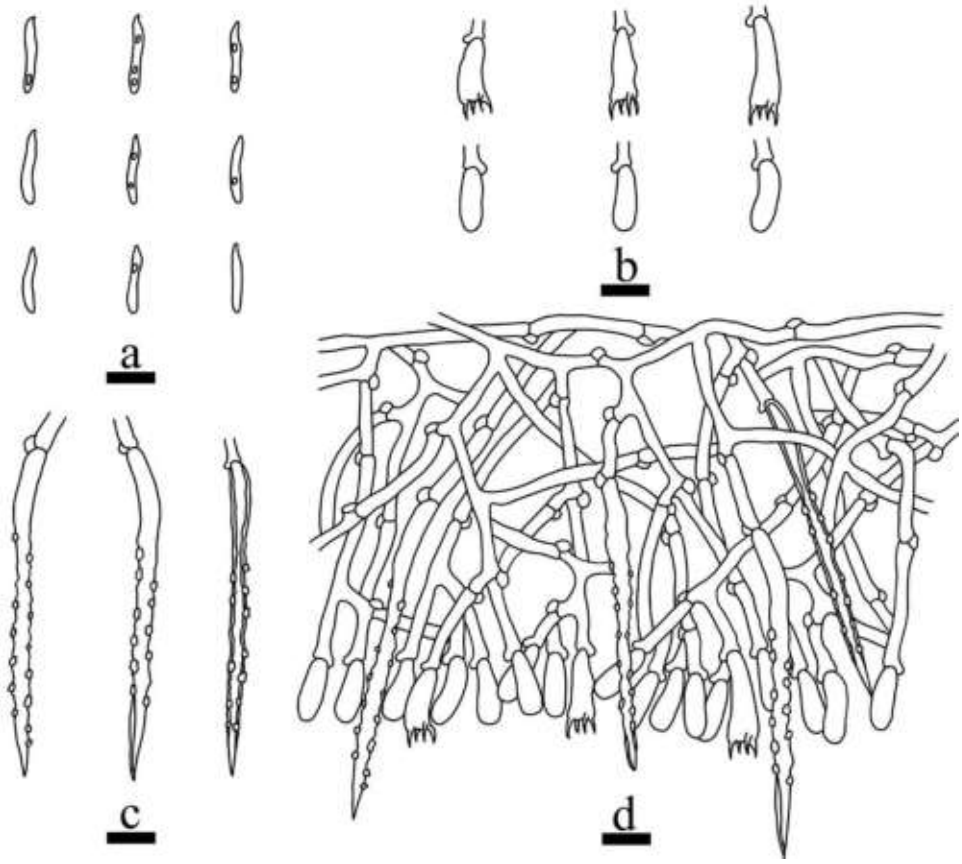

Figure 106 – Microscopic structures of *Subulicystidium yunnanense* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Subulate cystidia. d A section of hymenium. Scale bars: a–d = 10 µm.

Hyphal system monomitic, generative hyphae with clamp connections, colorless, thin-walled, frequently branched, loosely interwoven, 2–3.5 µm in diameter; IKI–, CB–, tissues unchanged in KOH. Cystidia abundant, subulate, projecting beyond hymenium, colorless, thin to thick-walled and regularly covered with rectangular crystals except at the apex, 65–73 × 4.5–5.5 µm; cystidioles absent. Basidia subclavate, with 4 sterigmata and a basal clamp connection, 13–20.5 × 5–6.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller. Basidiospores vermicular to sigmoid, colorless, thin-walled, smooth, IKI–, CB–, 13.5–16(–16.5) × 2–2.5(–2.8) µm, L = 14.47 µm, W = 2.30 µm, Q = 6.22–6.28 (n = 90/3).

Material examined (paratypes) – China, Yunnan Province, Zhaotong, Yiliang County, Luozehe Town, Lijiaping Village, GPS coordinates 27°53' N, 104°10' E, altitude 2000 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 25 August 2022, CLZhao 23687, CLZhao 23944 (SWFC).

Notes – In the present study, based on the ITS, nLSU, mtSSU, RPB2 and TEF1 data (Fig. 20), the new species *Subulicystidium yunnanense* is placed within *Subulicystidium*, and was sister to *S. tropicum* S.H. He & S.L. Liu. However, *S. tropicum* can be distinguished from *S. yunnanense* by its orange grey to greyish-orange hymenial surface, narrower basidia (12–17 × 4–5 µm) and shorter basidiospores (11–12.5 × 1.8–2.2 µm, Liu et al. 2019).

Subulicystidium yunnanense shares similarities with *S. boidinii* Ordynets, M.M. Striegel & Langer, *S. fusisporum* Ordynets & K.H. Larss. and *S. grandisporum* Ordynets & K.H. Larss. in sharing the white hymenial surface. However, *S. boidinii* differs from *S. yunnanense* by its shorter basidia (10–12 × 4–5.5 µm) and basidiospores (5.9–7.2 × 2.8–3.3 µm, Ordynets et al. 2018); *S. fusisporum* differs from *S. yunnanense* by its shorter basidiospores (10.7–12.8 × 2.4–3.4 µm, Ordynets et al. 2018); *S. grandisporum* differs from *S. yunnanense* by its wider basidiospores (10.5–14.5 × 3.3–3.9 µm, Ordynets et al. 2018).

Species new to China

Along with these new species, we found the following 7 species belonging to Basidiomycota for the first time in China (Fig. 21).

Cabalodontia albofibrillosa (Hjortstam & Ryvarden) Westphalen

Basionym – *Phlebia albofibrillosa* Hjortstam & Ryvarden, Mycotaxon 20(1): 139 (1984)

Index Fungorum number: IF836502; Facesoffungi number: FoF15469

Material examined – China, Yunnan Province, Yuxi, Xinping County, Mopanshan National Forestry Park, GPS coordinates 23°56' N, 101°29' E, altitude 2200 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 18 January 2018, CLZhao 6394; Puer, Ailaoshan National Nature Reserve, GPS coordinates 24°29' N, 100°56' E, altitude 2450 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 25 Aguest 2018, CLZhao 8722 (SWFC).

Etheirodon fimbriatum (Pers.) Banker

Basionym – *Odontia fimbriata* Pers., Observ. mycol. (Lipsiae) 1: 88 (1796)

Index Fungorum number: IF632166; Facesoffungi number: FoF15470

Material examined – China, China, Yunnan Province, Puer, Jingdong County, Ailaoshan Ecological Station, GPS coordinates 24°50' N, 100°94' E, altitude 2000 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 23 August 2018, CLZhao 8399; Dali, Nanjian County, Lingbaoshan, GPS coordinates 24°76' N, 100°50' E, altitude 2500 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 9 January 2019, CLZhao 10069, CLZhao 10114; Kunming, Yeyahu Forest Park, on the fallen branch of angiosperm, leg. C.L. Zhao, 30 September 2019, CLZhao 13977 (SWFC).

Hyphoderma cremeoalbum (Höhn. & Litsch.) Jülich

Basionym – *Corticium cremeoalbum* Höhn. & Litsch., Wiesner Festschrift (Wien): 63 (1908)

Index Fungorum number: IF315511; Facesoffungi number: FoF15471

Material examined – China, Yunnan Province, Wenshan, Pingba Town Natoinal Reserve, GPS coordinates 23°24' N, 104°11' E, altitude 1657 m asl., on the fallen branch of angiosperm, leg. C.L. Zhao, 28 July 2019, CLZhao 17007 (SWFC).

Hyphoderma transiens (Bres.) Parmasto

Basionym – *Odontia transiens* Bres., in Torrend, Brotéria, sér. bot. 11(1): 72 (1913)

Index Fungorum number: IF836887; Facesoffungi number: FoF15472

Material examined – China, Yunnan Province, Kunming, Xishan District, Haikou Forestry Park, on the fallen branch of angiosperm, 22 April 2017, CLZhao 1261, on the fallen branch of *Populus yunnanensis*, CLZhao 1365; 23 April 2017, CLZhao 1493; Kunming, Yeyahu Forestry Park, on the fallen branch of an angiosperm, 23 June 2017, CLZhao 1606, CLZhao 1667, CLZhao

1719, CLZhao 1768; Wuliangshan Nature Reserve, on the fallen branch of an angiosperm, 6 January 2019, CLZhao 9628 (SWFC).

Mycoacia fuscoatra (Fr.) Donk

Basionym – *Hydnum fuscoatrum* Fr. [as 'fusco-atrum'], Novit. fl. svec. 2: 39 (1814)

Index Fungorum number: IF252296; Facesoffungi number: FoF15473

Material examined – China, Yunnan Province, Honghe, Pingbian County, Daweishan National Nature Reserve, GPS coordinates 103°30' N, 23°42' E, altitude 1500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 3 August 2019, CLZhao 18423 (SWFC).

Phanerochaete sanguineocarnosa Floudas & Hibbett

Index Fungorum number: IF811925; Facesoffungi number: FoF15474

Material examined – China, Yunnan Province, Puer, Jingdong County, Wuliangshan National Nature Reserve, GPS coordinates 24°46' N, 100°58' E, altitude 2500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 6 September 2017, CLZhao 4447, CLZhao 4634, CLZhao 4639, CLZhao 4691 (SWFC)

Steccherinum confragosum Maas Geest. & Lanq.

Index Fungorum number: IF324023; Facesoffungi number: FoF15475

China, Yunnan Province, Puer, Jingdong County, Wuliangshan National Nature Reserve, GPS coordinates 24°46' N, 100°58' E, altitude 2500 m asl., on the trunk of angiosperm, leg. C.L. Zhao, 5 October 2017, CLZhao 4247; 17 October 2017, CLZhao 4297 (SWFC).

DISCUSSION

In recent years, many taxa of wood-inhabiting fungi have been continuously reported and recorded all over the world (Cui et al. 2019, Wijayawardene et al. 2020, Chen et al. 2021, Liu et al. 2022a, b, c, Jayawardena et al. 2023). 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 2012, Hyde et al. 2017a, b, Tibpromma et al. 2017, Hibbett 2016, He et al. 2022, Wijayawardene et al. 2020, Jayawardena et al. 2023). In addition, the diversity of wood-inhabiting fungi in the Yunnan-Guizhou Plateau of China holds great significance. Hence, the present study focuses on the species diversity, taxonomy, molecular systematics, and divergence times of wood-inhabiting fungi in the Yunnan-Guizhou Plateau, Asia.

A great step has been made for the phylogenetic relationships within wood-inhabiting fungi based on the morphology, multi-locus and genomic phylogeny (Hyde et al. 2017a, b, 2018, 2021, Cui et al. 2019, Chen et al. 2021, Liu et al. 2022b, c, Jayawardena et al 2023, Liu et al. 2023a). Molecular studies in Basidiomycota revealed that 599 genera lacked sequence data in public repositories, which implies nearly one third of the genera in Basidiomycota were not included in the molecular systematic studies (He et al. 2019), consequently, there is a need for more multilocus sequences in the future for wood-inhabiting fungi. Thus, in the present study, we have compiled sequence data for wood-inhabiting fungi, containing 128 ITS, 91 nLSU, 83 mtSSU, 27 RPB1, 39 RPB2 and 40 TEF1, which belong to the taxa as six orders, 17 families, 22 genera. Our focus has been intensified on exploring the molecular systematics and divergence times of wood-inhabiting fungi in the Yunnan-Guizhou Plateau. Additionally, we have delved into their topological relationships through the analysis of phylogenetic trees.

The placement of two genera, *Aphanobasidium* Jülich and *Radulomyces*, was previously located in Pterulaceae based on phylogenetic reconstructions of corticioid taxa (Larsson et al. 2004, Larsson 2007a). *Radulomyces* belonged to the Pterulaceae (Agaricales) and was most closely related to *Radulotubus* Y.C. Dai, S.H. He & C.L. Zhao and *Aphanobasidium* (Zhao et al. 2016a). These three genera formed a strongly supported clade and were sisters to the *Pterula-Deflexula-Pterulicium-Merulicium-Coronicium* clade based on the demonstrated sequence analyses of the ITS+nLSU data (Zhao et al. 2016a, Wang et al. 2018b). Radulomycetaceae was characterized by the combination of resupinate basidiomes, a monomitic hyphal system, and the absence of cystidia, in which the phylogenetic analyses strongly support the segregation of Radulomycetaceae from Pterulaceae (Leal-Dutra et al. 2020). Thus, Leal-Dutra et al. (2020) proposed the introduction of a new family for these three genera (i.e. *Aphanobasidium* and *Radulomyces*, *Radulotubus*) instead of placing them in Pterulaceae, as they were distinct from nearly all the other members of Pterulaceae clearly by morphology and phylogeny. In this study, based on the ITS+nLSU data (Fig. 3) and morphological characteristics, three new species *Radulomyces hydnoides*, *R. yunnanensis* and *R. zixishanensis* are nested within *Radulomyces*. In addition, these three genera (i.e. *Aphanobasidium* and *Radulomyces*, *Radulotubus*) are clustered together within Radulomycetaceae, and this finding is consistent with the results of previous studies (Leal-Dutra et al. 2020).

Corticium is the type genus of Corticiaceae and has a checkered past as a dumping ground for basidiomycetes with simple corticioid basidiomata (Donk 1963). With the emergence of molecular data, the genus has become more narrowly defined, with many species transferred to other genera, families, and orders. This study confirms that *Corticium* constitutes a monophyletic genus for species characterized by conspicuous wall thickening at the bases of basidia and basidioles, flexuous basidia developing from bladder-like basidioles, and constantly bearing dendrohyphidia and clamped hyphae (Ghobad-Nejhad et al. 2021). Besides, the mycologists recognized 14 species in *Corticium*, of which seven species were confirmed phylogenetically. In this study, based on ITS+nLSU phylogenetic analysis (Fig. 4), we confirm that *Corticium* is a monophyletic genus nested within the family Corticiaceae, which is similar to the work of Ghobad-Nejhad et al. (2021).

Due to the lack of sequences for a part of the fungal taxa, clear differentiation among many genera in this group using molecular data was challenging, hence, a broad concept of some wood-inhabiting fungal genera were accepted, such as *Hyphodontia* s.l. (Yurchenko & Wu 2016, Riebesehl & Langer 2017, Riebesehl et al. 2019). Three genera, formerly belonged to *Hyphodontia* sensu lato, viz. *Fasciodontia*, *Lyomyces* and *Xylodon*, formed a strongly supported clade, which occupied an independent position at the family level in Hymenochaetales (Wang et al. 2021b). *Xylodon* was previously synonymous with *Schizopora*, and the former family name Schizoporaceae, typified by *Schizopora*, was adopted to accommodate *Fasciodontia*, *Lyomyces* and *Xylodon* (Wang et al. 2021b). In the present study, this phylogenetic arrangement is confirmed by the current phylogenies (Fig. 8) and remains consistent with previous studies (Wang et al. 2021b, 2023, Guan et al. 2023).

Delineating wood-inhabiting fungal species often requires the application of genealogical concordance and phylogenetic species recognition methods (Taylor et al. 2000, Hibbett & Taylor 2013, Hyde et al. 2017b, Cui et al. 2019, Chen et al. 2021, Hyde et al. 2021, Liu et al. 2022b). Justo et al. (2017) performed a revised family level classification of Polyporales. In their phylogenetic analysis, the families Dacryobolaceae Jülich, Fomitopsidaceae Jülich, Laetiporaceae Jülich and Sparassidaceae Herter were assigned, with Phanerochaetaceae Jülich was regarded as a synonym of Laetiporaceae, however, the Laetiporaceae clade did not receive significant support in the phylogenetic analysis (Justo et al. 2017). In this study, based on phylogenetic analysis (Fig. 16), the classification of Fomitopsidaceae and Sparassidaceae is consistent with previous studies (Justo et al. 2017, Liu et al. 2022b).

Hypochnicium could not be assigned to any recognized family of the Polyporales, and its classification at the family level was treated as incertae sedis (Justo et al. 2017, He et al. 2019, Wijayawardene et al. 2020). Based on the analysis of the ITS region of rDNA, Paulus et al. (2007) proposed that *Hypochnicium* forms a monophyletic group, and *Gyrophanopsis* is a synonymy of *Hypochnicium.* Subsequently, Telleria et al. (2010a) detected two major clades within *Hypochnicium* through phylogenetic analysis in which the morphological character of basidiospores played a crucial role in this classification, with one clade containing taxa with smooth basidiospores, and another one with ornamented basidiospores. Justo et al. (2017) demonstrated *Hypochnicium* constituted a polyphyletic lineage within the "residual clade" of Polyporales. Based on molecular phylogenetic analyses using ITS, nLSU and rpb1 genes, the genus was divided into two distinct clades. The "hypochnicium clade", comprises the type species *H. bombycinum* and

H. karstenii, producing the smooth basidiospores. In contrast another clade contains *H. punctulatum* and *H. wakefieldiae* characterized by ornamented basidiospores, and is situated in Podoscyphaceae. Maekawa et al. (2023) conducted molecular phylogenetic analyses, revealing that *Hypochnicium* s. lat. was clearly polyphyletic. In this study, phylogenetic analysis based on ITS, LSU, mtSSU, RPB1 and TEF1 data (Fig. 13), clearly demonstrates the polyphyletic nature of *Hypochnicium*. These findings are consistent with latest research by Justo et al. (2017) and Maekawa et al. (2023), but contradict the concept of "a monophyletic group" proposed by Paulus et al. (2007).

Hypochnicium s. str. comprised a limited set of species characterized by smooth basidiospores, whereas *Neohypochnicium* encompassed both species with smooth basidiospores and those with ornamented basidiospores (Maekawa et al. 2023). Supported by molecular systematics, it was possible to identify the genus to which a hypochnicioid species with smooth basidiospores belongs within the framework of *Hypochnicium* (Maekawa et al. 2023). Hence, 14 native species of *Hypochnicium* were transferred to *Neohypochnicium,* while hypochnicioid species with smooth basidiospores lacking molecular data were retained in *Hypochnicium* (Maekawa et al. 2023). In our present study, based on ITS, LSU, mtSSU, RPB1 and TEF1 phylogenetic analysis (Fig. 16), we proposed that *Hypochnicium* s. str. closely groups together with the genera *Bulbillomyces* and *Gyrophanopsis*, forming a well-supported lineage. Moreover, this clade is closely related to Hyphodermataceae and Steccherinaceae. Morphologically the three genera share the resupinate basidiomata, smooth, tuberculate to odontioid hymenial surface, monomitic hyphal system, clavate to suburniform basidia, ellipsoid, subglobose to globose basidiospores. In addition, the phylogenetic analysis (Fig. 16) revealed that *Neohypochnicium* groups with the family Podoscyphaceae, forming a monophyletic lineage. Morphologically, Podoscyphaceae can be distinguished from *Neohypochnicium* by its poroid hymenial surface (Patouillard 1900). Hence, based on both morphological characteristics and phylogenetic evidence, two new families Hypochniciaceae and Neohypochniciaceae, are proposed.

Divergence time is estimated with ITS+nLSU+mtSSU+RPB1+RPB2+TEF1 sequences representing all main lineages in Polyporales (Fig. 15). The time ranges for Basidiomycota, with the phylum originating ca. 530 Mya, the subphyla 406–490 Mya, most classes 245–393 Mya and orders 120–290 Mya were inferred by Zhao et al. (2017b). However, the time range of most families in Polyporales was 62–138 Mya. In our study, the divergence time of two new families was 200.03 Mya (PP = 1) which supports a recent study of ranking a family with divergence time estimates (He et al. 2019, Wu et al. 2020).

Binder et al. (2005) showed that *Climacocystis* Kotl. and Pouzar nested inside the antrodia clade, however, other analyses indicated that *Climacocystis* within the residual polyporoid clade (Miettinen et al. 2012, Binder et al. 2013, Justo et al. 2017). Justo et al. (2017) indicated that *Climacocystis* and *Diplomitoporus* Domanski grouped with high support within the residual clade and could not be assigned to any recognized family in the Polyporales. Previous studies may have lacked sufficient morphological features and molecular data to determine the family affiliation of *Climacocystis* and *Diplomitoporus*. Consequently, their classifications at the family level were treated as incertae sedis (He et al. 2019). However, based on the multiple genes phylogenetic analysis, it was revealed that *Climacocystis* and *Diplomitoporus* grouped together with high support within the residual clade, which has unique morphological characters and forms a well-supported clade (Liu et al. 2023a). Phylogenetically, the family Climacocystaceae B.K. Cui, Shun Liu & Y.C. Dai was closely related to Hyphodermataceae, Meripilaceae, Podoscyphaceae, and Steccherinaceae. In our current study, phylogenetic analysis based on ITS, LSU, mtSSU, RPB1 and TEF1 data (Fig. 16), reveals that Climacocystaceae is closely related to Hypochniciaceae, Hyphodermataceae, and Steccherinaceae, in which the topology is different from the previous study (Liu et al. 2023a). This different results between both studies may be due to the composition of datasets, samples, supported values and gene fragments used in the two studies. Hence, it is necessary to carry out more in-depth phylogenetic analysis for wood-inhabiting fungi with more samples and sequences worldwide.

Justo et al. (2017) revealed that *Tyromyces merulinus* was a sister to Incrustoporiaceae, and this species could not be assigned to any family within Polyporales. Subsequently, *Gloeoporellus* was proposed to accommodate *Tyromyces merulinus* (Zmitrovich 2018) and was placed in the Incrustoporiaceae (Zmitrovich 2018, He et al. 2019), though without confirming the phylogenetic analysis. Liu et al. (2023a), based on phylogenetic analysis of multiple genes, showed that specimens of *Gloeoporellus merulinus* were grouped together, forming a monophyletic lineage (viz. Gloeoporellaceae B.K. Cui, Shun Liu & Y.C. Dai), and was closely related Fragiliporiaceae and Incrustoporiaceae without statistical support. In this study, the phylogenetic analysis based on ITS, LSU, mtSSU, RPB1 and TEF1 data (Fig. 13) reveals that Gloeoporellaceae is the sister taxon to Incrustoporiaceae and is not closely related to Fragiliporiaceae. This finding contrasts with the results of the previous study (Liu et al. 2023a), and the discrepancy may be due to the unstable topology and lower support values. Hence, using more gene segments and scientific methods to study wood-inhabiting fungi is a current trend.

The *Phanerochaete* lineage contains a large corticoid genus *Phanerochaete* s.s. and three small polyporoid genera: *Oxychaete* Miettinen, *Phanerina* Miettinen and *Riopa* D.A. Reid, where these four genera were typically characterized by having the resupinate basidiocarps, and a monomitic hyphal system with simple septate generative hyphae (Chen et al. 2021). The boundaries of the genera in the lineage were determined through morphological and molecular analyses by various researchers (Floudas & Hibbett 2015, Miettinen et al. 2016). Hence, numerous additional taxa, with a particular focus on *Phanerochaete* s.s., have been described based on morphological and molecular characteristics in recent years (Xu et al. 2020c, Chen et al. 2021, Wang & Zhao 2021a, Yu et al. 2023a). Nevertheless, the whole *Phanerochaete* s.l. remains a polyphyletic group, as certain species of *Phanerochaete* s.l. were clustered together with other genera in the Irpicaceae according to fungal research works (Floudas & Hibbett 2015, Justo et al. 2017, Chen et al. 2021). In our study, phylogenetic analysis based on ITS, nLSU, RPB1, RPB2 and TEF1 data (Fig. 16), *Phanerochaete* s.s. is closely related to the fungal genera *Oxychaete*, *Phanerina* and *Pirex* Hjortstam & Ryvarden, in which the topology among several species differs slightly from the previous study (Chen et al. 2021). Hence, the taxonomy and phylogeny of *Phanerochaete* s.l. need to go further exploration, based on additional specimens and sequences worldwide.

Traditionally, the genus *Steccherinum* has been distinguished from other genera by the hymenophore configuration, with a poroid structure in *Junghuhnia* and a hydnoid in *Steccherinum*, however, microscopically, both genera exhibit almost identical characters (Westphalen et al. 2021). *Antrodiella* was also related to *Steccherinum*, yet, distinguished by the lack of cystidia (Ryvarden 1991). Despite recent studies, including molecular data (Miettinen et al. 2012), showed that the morphological segregation of *Junghuhnia* and *Steccherinum* was not supported by molecular phylogeny. Although *Steccherinum* was well-supported within the residual polyporoid clade (Miettinen et al. 2012, Binder et. al 2013), the clade remained unresolved. Many species were treated as *Junghuhnia* group within the *Steccherinum* clade, separated from *J. crustacea*, the type of *Junghuhnia* and is distinguished by the morphological character of the hydnoid hymenophore (Westphalen et al. 2021). The phylogenetic analysis, based on molecular data of ITS+nLSU sequences, indicated that two newly identified *Steccherinum* species, i.e. *S. tenuissimum* and *S. xanthum*, formed a cluster within the residual polyporoid clade (Wu et al. 2021b). Nevertheless, the phylogenetic analysis based on ITS+nLSU sequences of *Steccherinum* and related genera in Steccherinaceae, showed that the two species *S. tenuissimum* and *S. xanthum* were not clustered with the core group (Dong et al. 2023b). However, these two species shared the distinctly hydnoid hymenophore, in which they were placed within *Steccherinum* instead of the *Junghuhnia* (Wu et al. 2021b). In our study, the phylogenetic analysis based on ITS, nLSU, mtSSU, RPB1, RPB2 and TEF1 data (Fig. 17), we confirm that the two species *S. tenuissimum* and *S. xanthum*, do not cluster with the core group. Besides, we report a new species, *S. lincangense*, closely related to two other species, *S. tenuissimum* and *S. xanthum. Steccherinum lincangense* shares similarities with the hydnoid hymenophore observed in *S. tenuissimum* and *S. xanthum*. Additionally, a peculiar phenomenon occurs in *Steccherinum* where it becomes challenging to identify morphologically different characteristics to coincide with the results of the phylogeny, making it difficult to delineate distinct phylogenetic species. Consequently, this difficulty may result in the recognition of 'new taxa' within *Steccherinum*. Hence, we choose not to treat many lineages as separate genera of *Steccherinum*, until we have sufficient evidence from morphology and phylogeny, including available samples and sequences worldwide in future studies.

Previous studies have shown that *Scytinostroma* is polyphyletic (Larsson & Larsson 2003). Based on ITS1-5.8S-ITS2-nrLSU sequences of samples of *Scytinostroma* s.s. and representative taxa of other related genera, the phylogenetic analyses of Peniophoraceae revealed that this clade was treated as a monophyletic group. The two *Scytinostroma* species *S. artocreas* (Berk. & M.A. Curtis) K.-H. Larss. and *S. incrustatum* (S.H. He et al.) K.H. Larss. were transferred from *Michenera* by Stalpers et al. (2021) based on morphological evidence. Subsequently, from phylogenetic analyses, it was inferred that *S. artocreas* and *S. incrustatum* grouped together and were nested within *Scytinostroma* s.s. (Li et al. 2023b). In our current study, based on phylogenetic analysis using ITS+nLSU data (Fig. 19), the two species are confirmed to be grouped together and clustered into the genus *Scytinostroma*, in consistent with previous research (Li et al. 2023b). Moreover, the new species *S. daweishanense* is closely related to both *S. artocreas* and *S. incrustatum*.

Molecular studies have shown that *Subulicystidium* is closely related to *Tubulicium vermiferum* (Bourdot) Oberw. (Hibbett & Binder 2002, Larsson et al. 2004). Later, molecular evidence supported *Subulicystidium* as a member of Hydnodontaceae (Trechisporales), despite a lack of clear morphological affinity (Larsson 2007a). The monotypic genus *Aegeritina* comprises *A. tortuosa* (Bourdot & Galzin) Jülich, accepted as the asexual stage of *Subulicystidium longisporum* (Eriksson et al. 1984). Stalpers et al. (2021) recommended retention of the earlier generic name *Subulicystidium* over *Aegeritina*, and then *Subulicystidium* was morphologically distinct from other genera in Trechisporales in the presence of a crystalline sheath on the cystidia (Liu et al. 2022c). In our current study, based on ITS, nLSU, mtSSU, RPB2 and TEF1 data phylogenetic analysis (Fig. 20), *Subulicystidium* is closely grouped with the genus *Tubulicium* Oberw. Morphologically, *Tubulicium* is distinguished from *Subulicystidium* by its multi-rooted lyocystidia covered by dendroid hyphae and sigmoid smooth basidiospores (Bernicchia & Gorjón 2010).

Yunnan Province is situated in the Yunnan-Guizhou Plateau, which includes the Hengduan Mountain Range. Yunnan’s climate is dominated by a large elevational range and the seasonal alternation of the southwest and southeast monsoons (Qian et al. 2020). The climate of Yunnan Province belongs to the subtropical monsoon climate, and a small part of the southern region has a tropical monsoon climate. Yunnan Province is rich in biodiversity due to its diverse topography and climate, harboring the most plant species in the country. This includes various types such as tropical, subtropical, warm temperate, middle temperate and cold temperate zones (Liu et al. 1959, Zhu 2022). Up to now, Yunnan has established over 150 nature reserves (Yan et al. 2021), including 21 national nature reserves (Fig. 1). The number continues to increase, with northern Yunnan being characterized by mixed forest, while the southern part of the province is predominantly broad-leaved forest (Fig. 1). These distinctions are influenced by terrain, elevation, climate and other factors in Yunnan-Guizhou Plateau (Wu 1980, 1987, Zhu 2022). The Yunnan Province, recognized as the “Ecological Security Barrier in Southwest China” and “Biodiversity Treasure”, plays a crucial role in the national ecological safety and biodiversity conservation structure (Yan et al. 2021). The Yunnan-Guizhou Plateau is rich in woody plant species, providing excellent substrates for wood-inhabiting fungi. 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 enrich the species diversity of fungi worldwide but also contribute to the branches of the fungal tree of life.

Despite the discovery of high species diversity among wood-inhabiting fungi in recent years (Wijayawardene et al. 2020, Chen et al. 2021, He et al. 2022, Liu et al. 2022b, c, Jayawardena et al. 2023, Zhao et al. 2023a), systematic studies still need to be conducted for many groups. The present study aims to fill the knowledge gap regarding wood-inhabiting fungi by reporting new species, and providing the detailed morphological descriptions and phylogenetic analyses of these fungal species, while also contributing to the enrichment of fungal diversity in East Asia.

ACKNOWLEDGEMENTS

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

Author contributions

Conceptualization, C-LZ; methodology, C-LZ, AM and J-HD; software, C-LZ, H-MZ, and J-HD; validation, C-LZ and J-HD; formal analysis, C-LZ and J-HD; investigation, C-LZ, J-HD, Y-LD and X-FL; resources C-LZ; writing–original draft preparation, AM, C-LZ, H-MZ, J-HD, QL, QY, QZ, X-CZ, Y-FD, Y-LD and Y-XL; writing–review and editing, AM, C-LZ and J-HD; visualization, C-LZ, H-MZ and J-HD; supervision, C-LZ, and H-MZ; project administration, C-LZ; funding acquisition, C-LZ. All authors have read and agreed to the published version of the manuscript.

Conflict of interest

The authors declare that there is no conflict of interest.

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