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Lignicolous freshwater fungi from karst landscapes in Yunnan Province, China**Wang WP¹, Hyde KD^{2,3}, Bao DF⁴, Wanasinghe DN^{5,11}, Lin CG⁶, Shen HW^{1,2,7}, Lu YZ⁸, Zhang ZQ¹, Su XJ¹, Li YX¹, Al-Otibi F³, Yang LQ^{1,9}, and Luo ZL^{1,10*}**¹ College of Agriculture and Biological Science, Dali University, Dali 671003, Yunnan, P.R. China² Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand³ Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 2455, Riyadh 11451, Saudi Arabia⁴ Engineering and Research Center for Southwest Biopharmaceutical Resource of National Education Ministry of China, Guizhou University, Guiyang, 550025, Guizhou, P.R. China⁵ Department of Soil Science, College of Food and Agriculture Sciences, King Saud University, P.O. Box 145111, Riyadh 11362, Saudi Arabia⁶ School of Life Sciences, Guizhou Normal University, Guiyang, 550025, Guizhou, P.R. China⁷ School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand⁸ School of Food and Pharmaceutical Engineering, Guizhou Institute of Technology, Guiyang 550025, Guizhou, P.R. China⁹ Co-Innovation Center for Cangshan Mountain and Erhai Lake Integrated Protection and Green Development of Yunnan Province, Dali University, Dali 671003, Yunnan, P.R. China¹⁰ Cangshan Forest Ecosystem Observation and Research Station of Yunnan Province, Dali University, Dali 671003, Yunnan, P.R. China¹¹ Center for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Sciences, Honghe 654400, Yunnan, P.R. China

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Abstract

Lignicolous freshwater fungi are an important ecological group that are involved in the material cycle and energy flow in freshwater ecosystems. They break down lignocellulose and soften submerged decaying wood, while their mycelium provides food for aquatic animals. This study explores the diversity of lignicolous freshwater fungi in the karst landscapes of Yunnan Province, focusing on Bamei Town, Wenshan Zhuang and Miao Autonomous Prefecture. Using both morphological examination and multi-gene analysis, this research identifies 14 new species, viz., *Ascolacicola minispora*, *Dictyocheiropsora appendiculata*, *Faiciphoriella hyalina*, *Kirschsteiniothelia distoseptata*, *K. longiconidiophora*, *Occultibambusa clavata*, *Ophioceras aseptatum*, *O. cylindrosporum*, *Pseudorobillarda multiguttulata*, *Sporidesmium filiforme*, *S. guttulatam*, *Tetraploa longiappendiculata*, *Thysanorea fusiformis*, and *Wongia flava* alongside introducing four new combinations, viz., *Ascolacicola coffeae* ($\equiv$ *Ascotaiwania coffeae*), *Ascol. mitriformis* ($\equiv$ *Ascot. mitriformis*), *Ascol. sawadae* ($\equiv$ *Ascot. sawadae*), and *Ascol. uniseptata* ($\equiv$ *Triadelphia uniseptata*). The sexual morph characteristics of *Faiciphoriella* are also provided. Furthermore, the study reports on eight new geographical records for China and identifies four species encountered in freshwater habitats for the first time. This study through detailed morphological and DNA analyses to investigate the species diversity of lignicolous freshwater fungi in karst regions, which will help us understand the microfungal diversity and carry out conservation efforts in these unique ecosystems.

Keywords – 14 new taxa – aquatic mycology – *Ascomycota* – morphology – phylogeny – submerged wood – taxonomy

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INTRODUCTION

Lignicolous freshwater fungi growing on submerged woody substrates in freshwater ponds, lakes, rivers, and streams (Shearer 1993a, 2004, 2009, Thomas 1996, Ho et al. 2001, 2002, Grossart et al. 2019). Presently, freshwater fungi are distributed in 13 phyla, viz., *Ascomycota*, *Aphelidiomycota*, *Basidiomycota*, *Blastocladiomycota*, *Chytridiomycota*, *Entomophthoromycota*, *Monoblepharomycota*, *Mortierellomycota*, *Mucoromycota*, *Olpidiomycota*, *Rozellomycota*, *Sanchytriomycota* and *Zoopagomycota*, with most taxa belonging to *Dothideomycetes* and *Sordariomycetes* in *Ascomycota* (Calabon et al. 2022, 2023a). Lignicolous freshwater fungi play an important role in freshwater ecosystems as they participate in nutrient and carbon cycling by decomposition of wood, facilitating the release of organic matter and supporting diverse aquatic life forms (Wong et al. 1998, Bucher et al. 2004, Wurzbacher et al. 2011, 2014, Hyde et al. 2016a). Moreover, several studies showed that the natural antibacterial substances isolated from lignicolous freshwater fungi may be more effective than the synthetic antibiotics (Wright et al. 2014). However, research on the secondary metabolites with biological activities produced by freshwater fungi requires taxonomic study (Calabon et al. 2023a). Despite their ecological importance, the biodiversity of lignicolous freshwater fungi in karst landscapes, especially in regions such as Yunnan Province, China, remains underexplored. These areas are hotspots for biodiversity, yet the specific fungal communities within them have not been extensively documented.

Karst landforms are formed by the effects of groundwater and surface water on the dissolution and precipitation of soluble rocks (such as limestone, dolomite, and gypsum) erosion and sedimentation (de Waele et al. 2009). The rich natural underground drainage systems, cave with stalactites and stalagmites, enclosed depressions, fluted rocks, and sinkholes are typical features of karst landforms (Ford & Williams 2007). Due to the special geological and climatic conditions, karst areas form a special ecosystem that differ from non-karst areas in terms of terrain and landforms (Zhou et al. 2010, Zheng et al. 2016). In China, karst landforms are mainly distributed in the southwest, especially Guangxi Zhuang Autonomous Region, Guizhou and Yunnan Provinces (Huang & Cai 2009). Yunnan Province, a region with extensive karst formations, has become a hotspot for lignicolous freshwater fungi research in China, but most research has focused on the rivers and lakes outside of the karst regions (Yang & Ding 1986, Cai et al. 2002, Luo et al. 2004, Shen et al. 2022a). Hence, this gap in knowledge highlights the need for comprehensive studies to document the diversity of lignicolous freshwater fungi from karst landscapes, understand their ecological roles and assess their contribution to freshwater ecosystems health and sustainability.

The present study aims to explore the diversity of lignicolous freshwater fungi within karst landscapes of Yunnan Province, specifically focusing on the ecologically rich area of Bamei Town in the Wenshan Zhuang and Miao Autonomous Prefecture. Through the identification of both new and existing fungal species and the documentation of their distribution and ecological roles, our research endeavors to contribute significantly to the enrichment of global fungal diversity records. This investigation employing approach that encompasses morphological and molecular data to uncover the diversity of freshwater fungi (Chethana et al. 2021), such a research method can help us

to better understand these organisms and underlines their important value in biodiversity research. Our findings, documenting 44 species across 25 genera, 21 families, 11 orders and three classes within the *Ascomycota*, mark the first comprehensive study of lignicolous freshwater fungi in the karst formations of Yunnan Province. This research also enhances our understanding of the Fungi in karst landscapes, emphasizing the importance of these fungi in freshwater ecosystems and advocating for their conservation. By drawing attention to the fungal diversity within the karst regions of Yunnan Province, this study seeks to inspire further research and conservation initiatives in these ecologically significant, yet frequently underestimated, ecosystems.

MATERIALS AND METHODS

Sample collecting

Specimens of submerged decaying wood were collected from freshwater streams in karst landscapes in Bamei Town (Fig. 1), Wenshan Zhuang and Miao Autonomous Prefecture, Yunnan Province, China, during the dry season (February). Bamei Town ($24^{\circ}09'28''$ – $24^{\circ}22'24''$ N; $104^{\circ}55'18''$ – $105^{\circ}14'28''$ E) is located in Wenshan Zhuang and Miao Autonomous Prefecture, Yunnan Province, directly connected to Guangxi Zhuang Autonomous Region, and there a large area of karst landforms in this town (Fig. 1). To preserve their integrity, the specimens were transported to the laboratory in plastic bags. The specimens were incubated in plastic boxes lined with moistened tissue at room temperature for ten days.

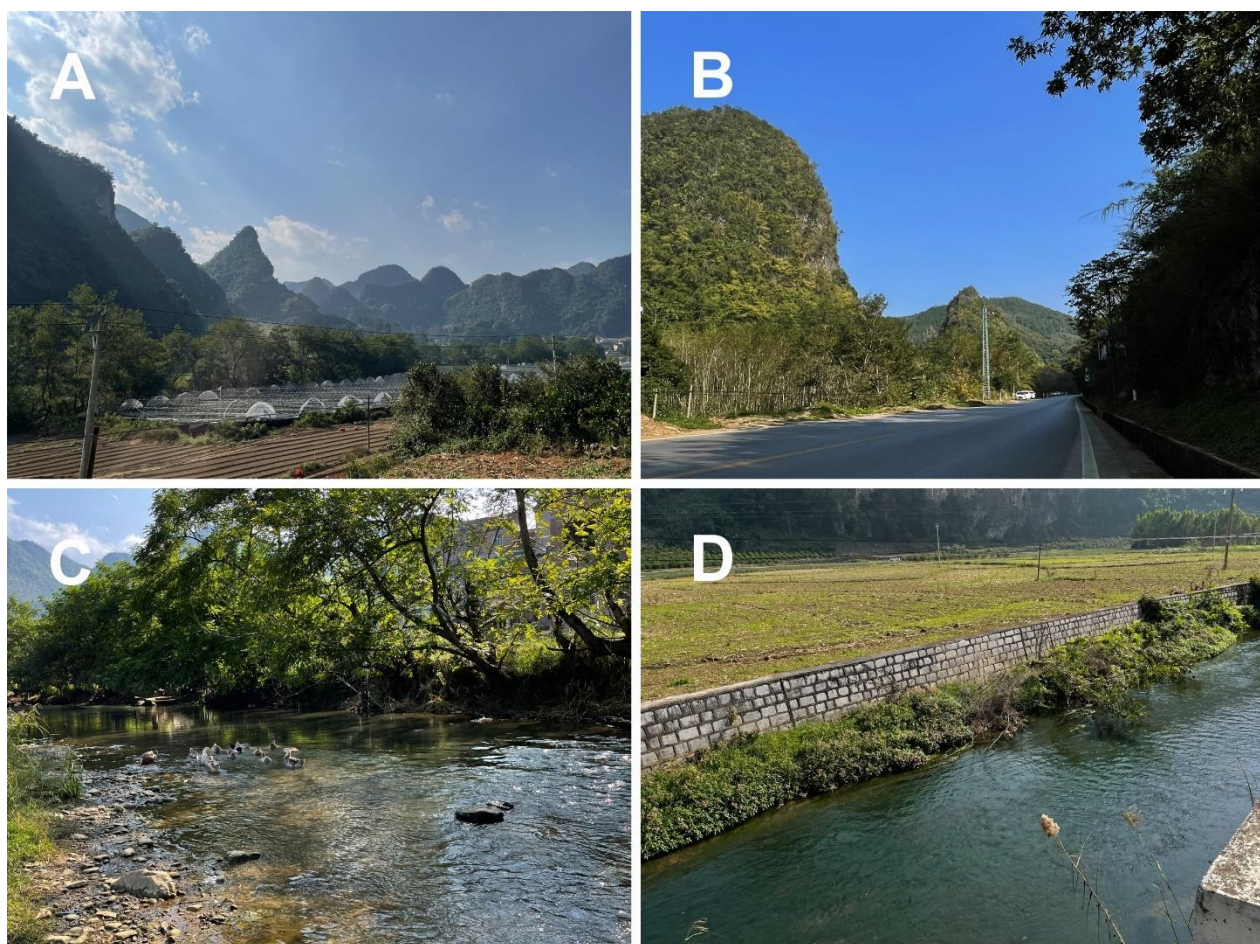


Figure 1 – A, B Karst landforms of Bamei Town. C, D Some of the sample collection locations.

Isolation and morphological examination

The morphology of external and internal macro/micro-structures were observed as described in Luo et al. (2018a). Images were photographed by a Nikon ECLIPSE Ni-U compound microscope

fitted with a Nikon DS-Ri2 digital camera as per the guidelines provided in Senanayake et al. (2020). Measurements were made with the Tarosoft (R) Image Frame Work program, and photo plates representing fungal structures were processed in Adobe Photoshop CS5 software (Adobe Systems Inc., San Jose, CA, USA). Herbarium specimens (dry woody branches with fungal material) were deposited in the herbarium of Cryptogams, Kunming Institute of Botany Academia Sinica (HKAS), Kunming, China. The isolates obtained in this study were deposited in China General Microbiological Culture Collection Center (CGMCC), Beijing, China and the Kunming Institute of Botany Culture Collection Center (KUNCC), Kunming, China. Facesoffungi and Index Fungorum numbers were registered as outlined in Jayasiri et al. (2015) and Index Fungorum (2024). Data of the fungi discovered are lodged in the Greater Mekong Subregion fungal database (Chaiwan et al. 2021).

DNA extraction, PCR amplification and sequencing

A Trelief™ Hi-Pure Plant Genomic DNA Kit (Beijing TsingKe Biotech Co., Ltd., Beijing, China) was used to extract total genomic DNA from fungal mycelia. DNA amplification was performed by a polymerase chain reaction (PCR). Five partial gene regions, the large subunit of nuclear ribosomal RNA gene (LSU), the nuclear ribosomal internal transcribed spacer (ITS: ITS1-5.8S-ITS2), the small subunit of nuclear ribosomal RNA gene (SSU), the translation elongation factor 1- α (*tef1- α*), and the second-largest subunit of RNA polymerase II (*rpb2*) were used in this study. Sequences of LSU, ITS, SSU, *tef1- α* , and *rpb2* were amplified using primer pairs of is LR0R/LR5, ITS5/ITS4, NS1/NS4, EF1-983F/EF1-2218R, and fRPB2-5F/fRPB2-7cR (Vilgalys & Hester 1990, White et al. 1990, Liu et al. 1999, Rehner 2001). The amplification was performed in a 25 μ L reaction volume containing 9.5 μ L deionized water, 12.5 μ L 2 $\times$ Taq PCR Master Mix with blue dye (Sangon Biotech, China), 1 μ L of DNA template and 1 μ L of each primer (10 μ M). Adjusted thermal cycles for the amplification of each locus are given in Table 1. PCR products were checked on 1% agarose electrophoresis gels stained with Gel Red (Beijing TsingKe Biotech Co., Ltd., Beijing, China). The sequencing reactions were carried out with primers mentioned above by Tsingke Biological Engineering Technology and Services Company, Kunming, China.

Table 1 Adjusted thermal cyclers conditions used in PCR amplification (all denaturation, annealing and elongation procedures were carried out with 35 cycles) (Vilgalys & Hester 1990, White et al. 1990, Liu et al. 1999, Rehner 2001).

Locus	PCR thermal cycle protocol				
	Initial denaturation	Denaturation	Annealing	Elongation	Final extension
ITS/SSU	94°C for 3 min	94°C for 30 s	56°C for 50 s	72°C for 1 min	72°C for 10 min
LSU/ <i>tef1-α</i>	94°C for 3 min	94°C for 30 s	55°C for 50 s	72°C for 1 min	72°C for 10 min
<i>rpb2</i>	95°C for 5 min	95°C for 1 min	52°C for 2 min	72°C for 90 s	72°C for 10 min

Note: ‘s’ represents seconds, and ‘min’ represents minutes.

Phylogenetic analyses

The BLAST searches in National Center of Biotechnology Information (NCBI) were performed for finding similar sequences that match our data. The sequences were aligned by using the online multiple alignment program MAFFT version 7 (Kato et al. 2019), and the alignment was manually optimized in BioEdit v.7.0.5.3 (Hall 1999). The single gene dataset was concatenated by SquenceMatrix v.1.7.8 for multi-gene phylogenetic analyses (Vaidya et al. 2011). The alignment formats were changed to PHYLIP and NEXUS formats by AliView (Larsson 2014) and ALignment Transformation EnviRonment (ALTER) website (<http://sing.ei.uvigo.es/ALTER/>).

Maximum likelihood (ML) analysis was conducted using the RAxML-HPC2 on XSEDE (8.2.12) (Stamatakis 2006, Stamatakis et al. 2008) of CIPRES Science Gateway website (Miller et al. 2010: <http://www.phylo.org/portal2>) and the estimated proportion of invariant sites are (GTRGAMMA+I) model. Bayesian analyses were performed in MrBayes 3.2.6 (Ronquist et al. 2012) and the best-fit model of sequences evolution was estimated via MrModeltest 2.2 (Guindon & Gascuel 2003, Nylander 2004, Darriba et al. 2012). The Markov Chain Monte Carlo (MCMC) sampling approach was used to calculate posterior probabilities (PP) (Rannala & Yang 1996). We have obtained similar results using different analytical methods (Zeng et al. 2023).

Phylogenetic trees were visualized using FigTree v. 1.4.0 (<http://tree.bio.ed.ac.uk/software/figtree/>), edited in Microsoft Office PowerPoint. Sequences generated in this study were deposited in GenBank and listed in Table 2.

Table 2 In the sequences generated in this study, the ex-type strains are indicated in bold.

Taxon	Source	GenBank accession number				
		LSU	ITS	SSU	<i>tef1-α</i>	<i>rpb2</i>
<i>Acrocalymma medicaginis</i>	KUNCC 23–13717	OR600928	OR589280	OR743190	–	–
<i>Ascolacicola minispora</i>	KUNCC 23–14565	OR600931	OR589283	OR743193	OR739157	OR820903
<i>Canalisporium jinghongense</i>	KUNCC 23–14579	OR600932	OR589284	OR743194	OR739158	OR820904
<i>Dendryphion hydei</i>	HKAS 130440	OR600933	OR589285	OR743195	OR739159	–
<i>Dictyocheiropsora appendiculata</i>	KUNCC 23–13714	OR600934	OR589286	–	OR739160	–
<i>Dictyocheiropsora rotunda</i>	KUNCC 23–13709	OR600935	OR589287	–	–	–
<i>Dictyocheiropsora rotunda</i>	KUNCC 23–13711	OR600936	OR589288	–	–	–
<i>Dictyocheiropsora rotunda</i>	KUNCC 23–13721	OR600937	OR589289	–	–	–
<i>Dictyocheiropsora rotunda</i>	KUNCC 23–13726	OR600938	OR589290	–	–	–
<i>Dictyocheiropsora rotunda</i>	KUNCC 23–13731	OR600939	OR589291	–	–	–
<i>Dictyocheiropsora rotunda</i>	KUNCC 23–13744	OR600940	OR589292	–	–	–
<i>Dictyocheiropsora rotunda</i>	KUNCC 23–14561	OR600941	OR589293	–	–	–
<i>Dictyocheiropsora taiwanense</i>	KUNCC 23–13720	OR600942	OR589294	–	OR739161	–
<i>Distoseptispora rostrata</i>	KUNCC 23–13736	OR600943	OR589295	OR743196	OR739162	–
<i>Distoseptispora tectonae</i>	KUNCC 23–14563	OR600944	OR589296	OR743197	OR739163	–
<i>Distoseptispora tectonae</i>	KUNCC 23–14572	OR600945	OR589297	OR743198	OR739164	–
<i>Faiciphoriella hyalina</i>	KUNCC 23–13740	OR600946	OR589298	–	–	OR820905
<i>Helminthosporium velutinum</i>	KUNCC 23–13704	OR600947	OR589299	–	–	–
<i>Helminthosporium velutinum</i>	KUNCC 23–13758	OR600948	OR589300	–	–	–

Table 2 Continued.

Taxon	Source	GenBank accession number				
		LSU	ITS	SSU	<i>tef1-a</i>	<i>rpb2</i>
<i>Kirschsteiniothelia distoseptata</i>	KUNCC 23–14619	OR600950	OR714747	OR743200	–	–
<i>Kirschsteiniothelia longiconidiophora</i>	KUNCC 23–14559	OR600951	OR589302	–	–	–
<i>Kirschsteiniothelia longiconidiophora</i>	KUNCC 23–13756	OR600952	OR589303	OR743201	–	–
<i>Kirschsteiniothelia pini</i>	KUNCC 23–13755	OR600949	OR589301	OR743199	–	–
<i>Myrmecridium thailandicum</i>	KUNCC 23–13739	OR600953	OR589304	–	–	–
<i>Neohelicasus elaterascus</i>	KUNCC 23–14566	OR600954	OR589306	OR743202	OR739165	–
<i>Neohelicasus elaterascus</i>	HKAS 131387	OR600955	OR589307	OR743203	OR739166	–
<i>Neohelicasus gallicus</i>	KUNCC 23–13757	OR600956	OR589308	OR743204	OR739167	–
<i>Neohelicasus submersus</i>	KUNCC 23–13741	OR600957	OR589309	OR743205	OR739168	–
<i>Neohelicasus uniseptatus</i>	KUNCC 23–13703	OR600958	OR589310	OR743206	OR739169	–
<i>Neohelicasus uniseptatus</i>	KUNCC 23–13742	OR600959	OR589311	OR743207	OR739170	–
<i>Occultibambusa clavata</i>	KUNCC 23–14577	OR600960	–	OR743208	OR739171	OR820906
<i>Ophioceras aseptatum</i>	KUNCC 23–14570	OR600961	OR589313	OR743209	OR739172	OR820907
<i>Ophioceras cylindrosporum</i>	KUNCC 23–13706	OR600962	OR589314	–	OR739173	–
<i>Pararamichloridium caricicola</i>	HKAS 130439	OR600963	OR589315	–	–	–
<i>Parasympodiella lauri</i>	HKAS 130438	OR600964	OR589316	–	–	–
<i>Periconia thysanolaenae</i>	KUNCC 23–13708	OR600966	OR589318	OR743211	OR739175	–
<i>Phaeoisaria filiformis</i>	KUNCC 23–13723	OR600967	OR589319	OR743212	–	OR820908
<i>Phaeoisaria pseudoclematidis</i>	KUNCC 23–13718	OR600968	OR589320	–	–	–
<i>Pleurotheciella uniseptata</i>	KUNCC 23–14569	OR600970	OR589322	OR743213	–	–
<i>Pseudorobillarda multiguttulata</i>	HKAS 130437	OR600971	OR589323	OR743214	–	OR820909
<i>Sporidesmium aquaticivaginum</i>	KUNCC 23–13373	OR600972	OR589324	OR743215	OR739176	OR820910
<i>Sporidesmium filiforme</i>	HKAS 130435	OR600973	OR589325	OR743216	OR739177	OR820911
<i>Sporidesmium guttulatum</i>	KUNCC 23–13374	PP994882	OR589326	OR743217	PQ007633	OR820912
<i>Tetraploa longiappendiculata</i>	KUNCC 23–13397	OR600975	OR589327	OR743218	OR739179	–

Table 2 Continued.

Taxon	Source	GenBank accession number				
		LSU	ITS	SSU	<i>tef1-a</i>	<i>rpb2</i>
<i>Thysanorea aquatica</i>	KUNCC 23–13737	OR600976	OR589328	OR743219	–	–
<i>Thysanorea fusiformis</i>	KUNCC 23–13729	OR600977	OR589329	OR743220	–	–
<i>Thysanorea lotorum</i>	KUNCC 23–13725	OR600978	OR589330	OR743221	–	–
<i>Thysanorea nonramosa</i>	KUNCC 23–13754	OR600979	PQ559836	OR743222	–	–
<i>Torula chinensis</i>	HKAS 130434	OR600985	OR589337	PP657618	OR739183	–
<i>Torula fici</i>	KUNCC 23–13710	OR600980	OR589332	–	–	–
<i>Torula fici</i>	KUNCC 23–13716	OR600981	OR589333	OR743223	–	–
<i>Torula gaodangensis</i>	KUNCC 23–13705	OR600982	OR589334	OR743224	OR739180	OR820913
<i>Torula gaodangensis</i>	KUNCC 23–13728	OR600983	OR589335	OR743225	OR739181	OR820914
<i>Torula mackenziei</i>	KUNCC 23–13738	OR600984	OR589336	–	OR739182	–
<i>Torula submersa</i>	KUNCC 23–13730	OR600986	OR589338	OR743226	OR739184	–
<i>Vikalpa dujuanhuensis</i>	KUNCC 23–13707	OR600987	OR589339	OR743227	OR739185	–
<i>Vikalpa dujuanhuensis</i>	KUNCC 23–13398	OR600988	OR589340	OR743228	OR739186	–
<i>Wongia flava</i>	KUNCC 23–13715	OR769700	OR589341	OR743229	OR739187	OR820915
<i>Wongia fusiformis</i>	KUNCC 23–13727	OR600989	OR589342	–	–	–
<i>Wongia fusiformis</i>	KUNCC 23–13713	OR600990	OR589343	–	–	–

RESULTS

Dothideomycetes O.E. Erikss & Winka

Kirschsteiniotheliales Hern.-Restr., R.F. Castañeda, Gené & Crous

Kirschsteiniotheliaceae Boonmee & K.D. Hyde

The monotypic family *Kirschsteiniotheliaceae*, was introduced by Boonmee et al. (2012) to accommodate taxa that group with *Kirschsteiniothelia aethiops* based on the phylogenetic analysis. The sexual morph of *Kirschsteiniotheliaceae* is characterized by subglobose to globose ascomata, cylindrical-clavate, bitunicate asci, and brown to dark brown, ellipsoidal, septate ascospores with or without a mucilaginous sheath. And erect, branched or unbranched conidiophores, terminal conidiogenous cells, and obclavate or cylindrical, septate conidia in asexual morph. Currently, only the type genus *Kirschsteiniothelia* is accepted in this family (Boonmee et al. 2012, de Farias et al. 2024).

Kirschsteiniothelia D. Hawksw.

Kirschsteiniothelia was established by Hawksworth (1985) and typified by *K. atra*. Based on

morphological characteristics and phylogenetic analysis, Boonmee et al. (2012) established a new family *Kirschsteinioteliaceae* to accommodate *Kirschsteiniotelia* in the class *Dothideomycetes*. The sexual morph of this genus is characterized by superficial, erumpent, papillate ascomata, 8-spored or rarely 4-spored, pedicellate asci with an ocular chamber, and ellipsoidal, verrucose or smooth-walled, septate ascospores with or without a mucilaginous sheath. The asexual morph of this genus is characterized by erect, septate, cylindrical, apically branched or unbranched conidiophores and integrated, terminal conidiogenous cells, with broadly obovoid or fusiform to obclavate, euseptate or distoseptate conidia with or without a gelatinous sheath at the apex. Freshwater *Kirschsteiniotelia* species all reported as asexual morphs, which are similar to *Sporidesmium* (Su et al. 2016, Bao et al. 2018, Sun et al. 2021, Jayawardena et al. 2022, Hyde et al. 2023, Yang et al. 2023, Zhang et al. 2023a, de Farias et al. 2024). Currently, forty-eight species have been accepted in this genus, and are frequently saprobic on dead wood and mostly found in terrestrial except that eight species are known from freshwater habitats (Su et al. 2016, Bao et al. 2018, Yang et al. 2023, Zhang et al. 2023a, Jin et al. 2024). In this study, four sporidesmium-like taxa were collected and identified as two novel species, namely *Kirschsteiniotelia distoseptata* and *K. longiconidiophora*, and a new habitat record of *K. pini* based on morphological characters and phylogenetic analysis.

Kirschsteiniotelia distoseptata W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 3

Index Fungorum number: IF902421; Facesoffungi number: FoF16094

Etymology – Referring to the distoseptate conidia of the species.

Holotype – HKAS 131382

Saprobic on submerged decaying wood. Asexual morph: *Colonies* effuse, hairy, scattered or gathered, dark brown. *Mycelium* mostly immersed, composed of pale brown, septate, unbranched hyphae. *Conidiophores* 60–140 (–250) × 2.9–3.9 µm ($\bar{x}$ = 119 × 3.5 µm, n = 20), macronematous, mononematous, erect, smooth, pale brown to brown, septate, unbranched, subcylindrical, straight or flexuous at the base, truncate at the apex, darker at the apex connect to conidia. *Conidiogenous cells* 11–23 (–30) × (1.9–) 3.3–4.5 µm ($\bar{x}$ = 18 × 3.8 µm, n = 20), monoblastic, terminal, integrated, subcylindrical, pale brown to brown, with a black thickened scar at the connection with the conidia, percurrent proliferating. *Conidia* 24–35 × 4.9–6.7 µm ($\bar{x}$ = 28.7 × 5.9 µm, n = 10), acrogenous, solitary or occasionally catenate, dry, obclavate, tapering to the apex, 3–4-distoseptate when mature, smooth, straight or slightly curved, pale brown to brown or olive green, rounded apical sometimes with a rounded, gelatinous sheath, thickened scar and truncate at the base. *Conidial secession* schizolytic. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on the potato dextrose agar (PDA) within 12 h, and germ tubes produced from the apex. Colonies on PDA reaching 25 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, flat surface, velvety, brown to dark green, the lower layer is dark green. Reverse dark green, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4436 (HKAS 131382, holotype), ex-type living cultures CGMCC 3.25402 = KUNCC 23–14619.

Notes – *Kirschsteiniotelia distoseptata* resembles *K. submersa* in having solitary or occasionally catenate, obclavate, apically rounded, distoseptate conidia with thickened scars and truncate base (Su et al. 2016). However, the phylogenetic analysis showed that *K. distoseptata* is closely related to *K. sichuanensis* (Fig. 2). *Kirschsteiniotelia distoseptata* is different from *K. sichuanensis* in having distoseptate conidia with a rounded, gelatinous sheath at the apex, and sometimes occasionally catenate. Furthermore, conidia of *K. distoseptata* are comparatively smaller than *K. sichuanensis* (24–35 × 4.9–6.7 vs. 34–54 × 8–14 µm) (Jin et al. 2024). The LSU and ITS sequences data of *K. distoseptata* (CGMCC 3.25402) differ from *K. sichuanensis* (MFLU 21–0130) by 0.54% (4/738 bp) and 14.24% (85/597 bp, 13 gaps), respectively.

Kirschsteiniothelia longiconidiophora W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.

Fig. 4

Index Fungorum number: IF902422; Facesoffungi number: FoF16095

Etymology – Referring to the longer conidiophores of the species in *Kirschsteiniothelia*.

Holotype – HKAS 131379

Saprobic on submerged decaying wood. Asexual morph: *Colonies* effuse, hairy, scattered, brown to dark brown. *Mycelium* immersed, composed of pale brown, septate, unbranched hyphae. *Conidiophores* 150–560 × 2.2–4.3 µm ($\bar{x}$ = 288.4 × 3.3 µm, n = 20), macronematous, mononematous, erect, smooth, pale brown to brown, septate, unbranched, cylindrical, straight or slightly flexuous, slightly inflated at the apex. *Conidiogenous cells* (15–) 23–36 × (2.1–) 2.9–4.9 (–5.5) µm ($\bar{x}$ = 26.1 × 3.9 µm, n = 20), monoblastic, terminal, integrated, determinate, subcylindrical, brown. *Conidia* 19–32 (–44) × 4.2–7.2 µm ($\bar{x}$ = 27.6 × 5.9 µm, n = 15), acrogenous, solitary, dry, obclavate, 3–4-distoseptate when mature, smooth, straight or slightly curved, pale brown to brown or olive green, rounded apical sometimes with a rounded, gelatinous sheath, truncate and with thickened scar at the base. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from both ends. Colonies on PDA reaching 10 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, protrusion, with regular edges, pale brown to dark brown, the lower layer is dark green, velvety. Reverse dark green, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3771 (HKAS 131379, holotype), ex-type living cultures CGMCC 3.25432 = KUNCC 23–14559; *ibid.*, S-3508 (HKAS 131378, paratype), ex-paratype living culture KUNCC 23–13756.

Notes – Phylogenetic analysis showed that *Kirschsteiniothelia longiconidiophora* (CGMCC 3.25432 and KUNCC 23–13756) clustered with *K. cangshanensis* with 96% ML/1.00 PP support (Fig. 2). *Kirschsteiniothelia longiconidiophora* resembles *K. cangshanensis* in having unbranched, cylindrical conidiophores, solitary, obclavate conidia with a gelatinous sheath at the apex. However, *K. longiconidiophora* can easily be distinguished from *K. cangshanensis* in having much longer conidiophores which are slightly inflated at the apex (150–560 × 2.2–4.3 vs. 105.5–135.5 × 6–8 µm) (Bao et al. 2018). A comparison of ITS and LSU sequence data indicated that the type strain of *K. longiconidiophora* (CGMCC 3.25432) differ from *K. cangshanensis* in 4.24% (20/472 bp) and 0.13% (1/767 bp), respectively.

Kirschsteiniothelia pini Y. Jin, W.H. Tian & Maharachch., Phytotaxa 664(2), 103 (2024)

Fig. 5

Index Fungorum number: IF854777; Facesoffungi number: FoF16758

Saprobic on submerged decaying wood. Asexual morph: *Colonies* effuse, hairy, scattered, dark brown, shining. *Mycelium* mostly immersed, composed of pale brown, septate, unbranched hyphae. *Conidiophores* 50–230 (–330) × 3.5–5.5 (–7.6) µm ($\bar{x}$ = 135.3 × 4.7 µm, n = 20), macronematous, mononematous, erect, smooth, brown to dark brown, paler towards the apex, septate, unbranched, subcylindrical to cylindrical, sometimes swollen at the base, slightly flexuous. *Conidiogenous cells* 12–25 (–60) × 3.6–5.9 µm ($\bar{x}$ = 27.1 × 4.8 µm, n = 20), monoblastic, terminal, cylindrical, pale brown to brown, percurrent proliferating. *Conidia* 13–60 × 3.6–10.9 µm ($\bar{x}$ = 29.2 × 7.2 µm, n = 25), acrogenous, solitary, dry, obclavate, 3–4-distoseptate when mature, smooth, straight or slightly curved, pale brown to brown, rounded apical with a rounded, gelatinous sheath, truncate basal with a thickened scar. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the apex. Colonies on PDA reaching 15 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, protrusion, with regular edges, grey to brown, the lower layer is dark green, velvety. Reverse dark green, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3278 (HKAS 131373), living cultures CGMCC 3.25426 = KUNCC 23–13755.

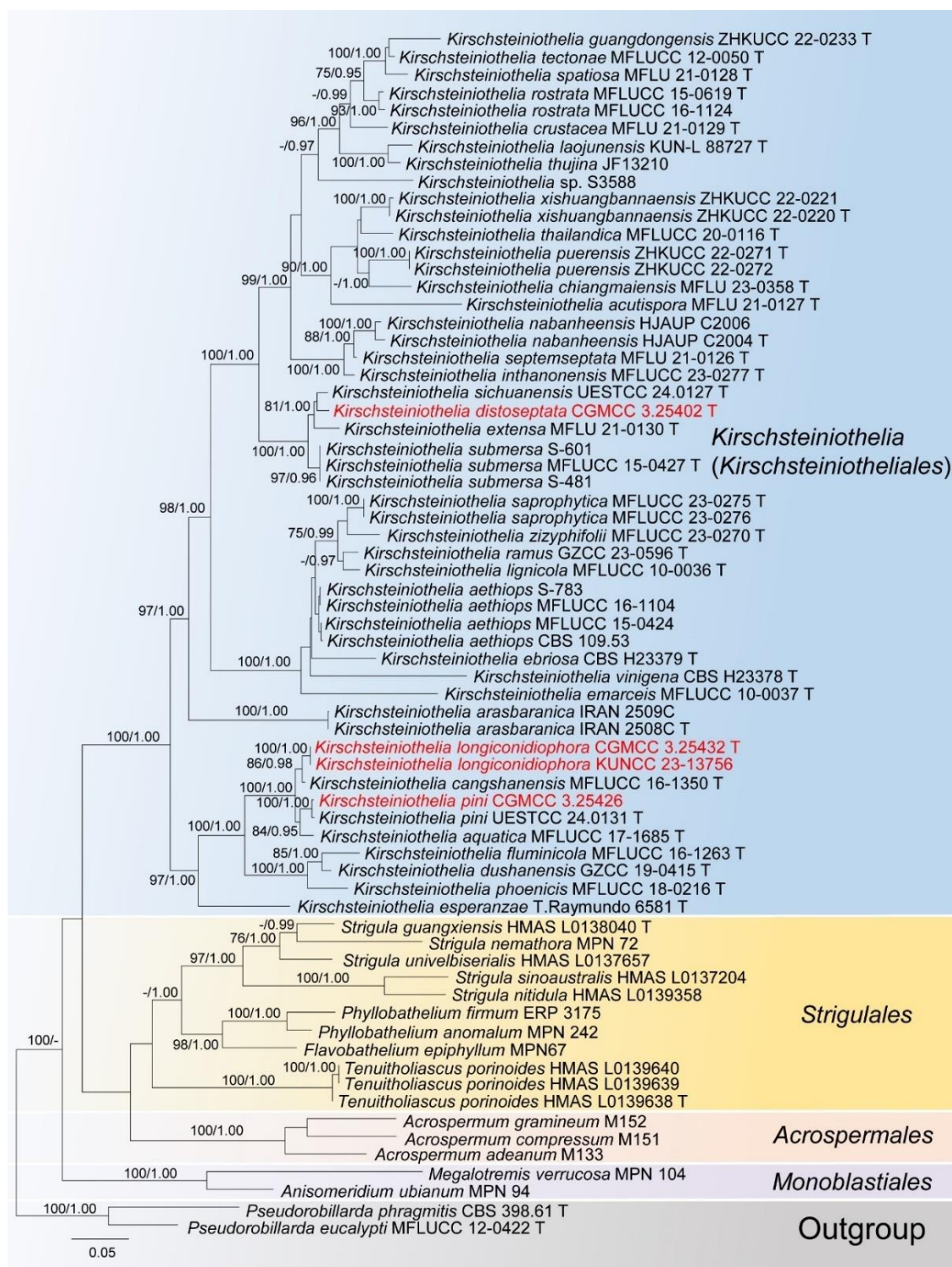


Figure 2 – RAxML tree based on analysis of *Kirschsteinietheliaceae* that combined LSU, ITS, and SSU dataset. The combined analyses include 68 strains with 2133 characters including gaps (LSU: 803 bp, ITS: 491 bp, and SSU: 839 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Pseudorobillarda eucalypti* (MFLUCC 12-0417) and *P. phragmitis* (CBS 398.61). The new collections are indicated in red. Ex-type strains are indicated with "T" after the strain number.

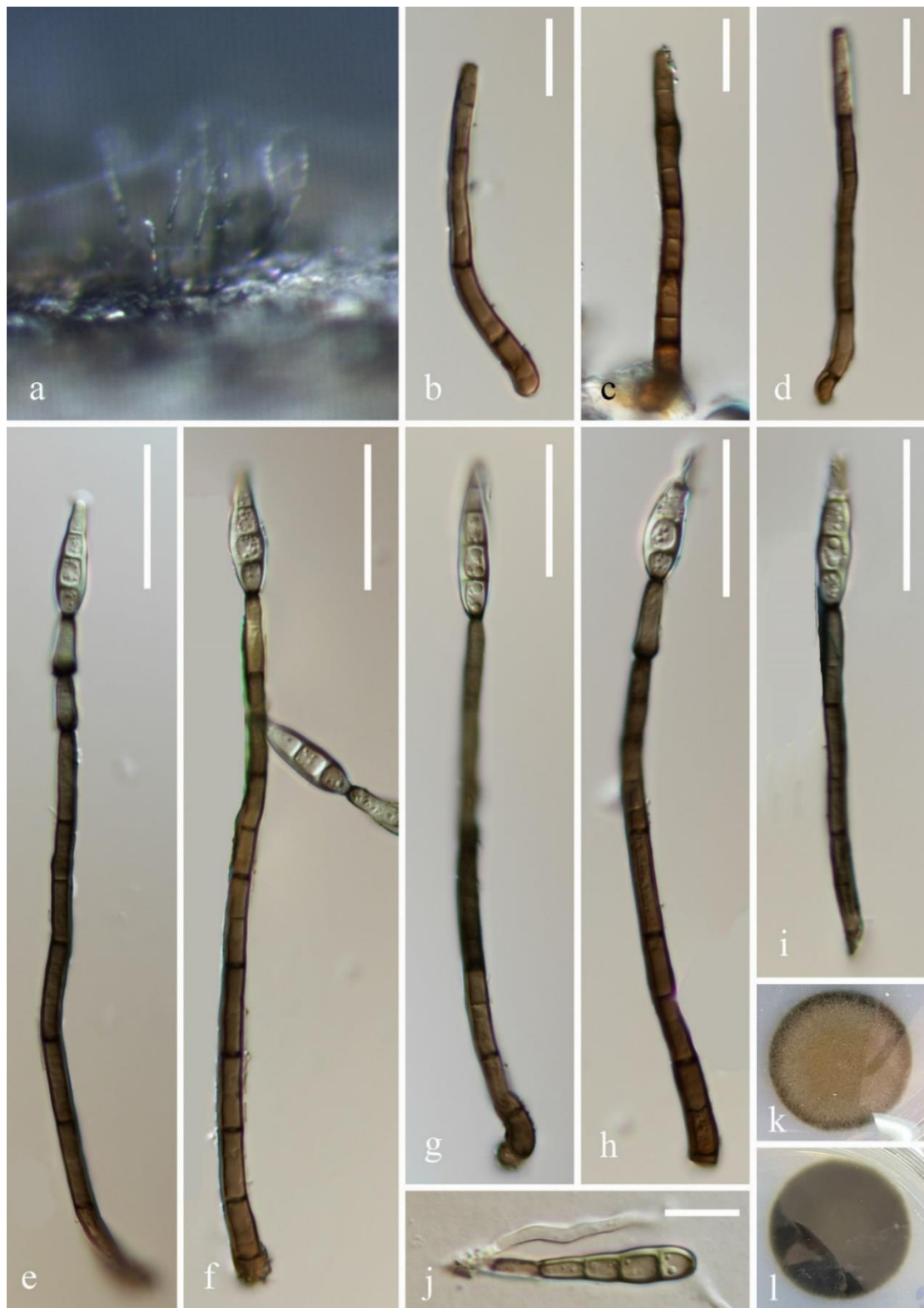


Figure 3 – *Kirschsteiniothelia distoseptata* (HKAS 131382, holotype). a Colonies on the substratum. b–d Conidiophores. e–i Conidiophores with conidia. j Germinating conidium. k, l Colony on PDA from surface and reverse. Scale bars: b–d, j = 15 μ m, e–i = 30 μ m.

Notes – Phylogenetic analysis showed that our new collection clustered with the ex-type strain of *Kirschsteiniothelia pini* (UESTCC 24.0131) with 100% ML/1.00 PP support (Fig. 2). The LSU, ITS, and SSU sequences of our new collection (CGMCC 3.25426) and the type strain (UESTCC 24.0131) showed 99.74% (763/765 bp), 98.88% (440/445 bp), and 100.00% (988/988 bp) similarities, respectively. Our new collection is similar to *K. pini* in having cylindrical, unbranched

conidiophores, terminal, monoblastic conidiogenous cells with percurrent proliferating, and obclavate conidia with truncate base. We therefore identify our new collection as *K. pini*, a species introduced by Jin et al. (2024) from terrestrial habitat in China, and it is the first time to report this species from freshwater habitat.



Figure 4 – *Kirschsteiniothelia longiconidiophora* (HKAS 131379, holotype). a Colonies on the substratum. b Conidiophores. c–f Conidiophores with conidia. g–i Conidiogenous cells with conidia. j, k Conidia. l Germinating conidium. m, n Colonies on PDA from surface and reverse. Scale bars: b–d = 40 μ m, e = 60 μ m, f = 100 μ m, g–i = 15 μ m, j–l = 10 μ m.



Figure 5 – *Kirschsteiniothelia pini* (HKAS 131373). a, b Colonies on the substratum. c, d Conidiophores e–g Conidiophores with conidia. h–j Conidia. k Germinating conidium. l, m Colony on PDA from surface and reverse. Scale bars: c–g = 20 μ m, h–j = 15 μ m, k = 10 μ m.

Pleosporales Luttr. ex M.E. Barr

Acrocalymmaceae Crous & Trakunyingcharoen

Trakunyingcharoen et al. (2014) established *Acrocalymmaceae* to accommodate *Acrocalymma* species, with *Acrocalymma* as the type genus. Currently, only the type genus is accepted in this family. Both sexual and asexual morphs have been reported for this family, and the asexual morphs

of this family are known as coelomycetes, which are characterized by globose to subglobose, unilocular conidiomata, reduced conidiophores, enteroblastic conidiogenous cells, with hyaline, cylindrical or fusiform conidia. The sexual morph of *Acrocalymma* is characterized by erumpent to superficial, globose to subglobose ascomata, numerous hamathecium, cylindric-clavate asci, and fusiform ascospores with narrowly rounded ends. Species of this family have often been reported on dead wood of various plants, and most from terrestrial habitats (Trakunyingcharoen et al. 2014, Dong et al. 2020, Boonmee et al. 2021, Mortimer et al. 2021, Shao et al. 2022, de Silva et al. 2022, Calabon et al. 2023b, Li et al. 2023).

***Acrocalymma* Alcorn & J.A.G. Irwin**

Acrocalymma was established by Alcorn & Irwin (1987), with *A. medicaginis* as the type. Eighteen species are listed in Index Fungorum (2024), and most species were collected from terrestrial habitats, with only four species, *A. aquaticum*, *A. bilobatum*, *A. bipolare*, and *A. fici* were collected from freshwater habitats in Egypt and Thailand (Zhang et al. 2012, Dong et al. 2020, Boonmee et al. 2021, Mortimer et al. 2021, de Silva et al. 2022, Calabon et al. 2023b).

***Acrocalymma medicaginis* Alcorn & J.A.G. Irwin, Trans. Br. mycol. Soc. 88(2), 163 (1987)** Fig. 7

Index Fungorum number: IF130085; Facesoffungi number: FoF07099

Saprobic on submerged decaying wood. Asexual morph: Undetermined. Sexual morph: *Ascomata* 130–170 µm diam, 90–210 µm high ($\bar{x}$ = 146.7 × 126.8 µm, n = 5), semi-immersed to immersed, coriaceous, solitary or scattered, obpyriform or flat subglobose, black. *Ostiole* mostly with neck, 100–130 µm long, 60–100 µm diam, black, flat cylindrical, standing upright in the substrate, sometimes with white, hair-like appendages on the surface. *Peridium* 7.3–33 µm thick, coriaceous, comprising 5–7 layers of pale brown to black cells of *textura angularis*. *Hamathecium* comprising 1.6–2.4 µm wide, numerous, filamentous, branched, septate pseudoparaphyses. *Asci* 80–110 × 6.8–9.7 µm ($\bar{x}$ = 92.2 × 8.4 µm, n = 15), 8-spored, bitunicate, cylindric-clavate, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 16–22 × 4.1–6.2 µm ($\bar{x}$ = 19.8 × 5.2 µm, n = 30), overlapping, 1–2-seriate, fusiform with obtuse to slightly obtuse ends, straight or slightly curved, smooth, mostly 3-septate, constricted at the second septum, hyaline, and becoming pale brown, separation is darker at maturity, guttulate.

Culture characteristics – Ascospores germinating on PDA within 12 h, and germ tubes produced from both ends. Colonies on PDA reaching 30 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, flat surface, has a subglobose protrusion in the center, white. Reverse brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3499 (HKAS 131366), living culture KUNCC 23–13717.

Notes – Multi-gene phylogenetic analysis showed that the new collection (KUNCC 23–13717) grouped with *Acrocalymma medicaginis* (Fig. 6). Our new collection fits well with the description of *A. medicaginis* in having obpyriform or flat subglobose ascomata, cylindric-clavate asci with a short pedicel, and fusiform ascospores with obtuse to slightly obtuse ends (Mapook et al. 2020, Zhang et al. 2023b). We therefore identify our new collection as *A. medicaginis*. The asexual morph of this fungus was introduced by Alcorn & Irwin (1987) on root and crown rotting of *Medicago sativa* (*Fabaceae*) in Australia. Mapook et al. (2020) and Zhang et al. (2023b) reported the sexual morph of this species from terrestrial habitats in Thailand and China, respectively. In this study, *A. medicaginis* was collected on submerged decaying wood in China, and the new collection is introduced here as a new freshwater habitat record.

***Dictyosporiaceae* Boonmee & K.D. Hyde**

Dictyosporiaceae was introduced by Boonmee et al. (2016), with *Dictyosporium* as the type genus. This family comprises 21 genera (Shen et al. 2022b, Tennakoon et al. 2023, Shu et al. 2024,

Tian et al. 2024a). Both coelomycetous and hyphomycetous asexual morphs have been reported in this family, the coelomycetous morph are characterized by phialidic conidiogenous cells, doliiform to lageniform, and cylindrical, hyaline conidia (Tanaka et al. 2015, Tennakoon et al. 2023), and the hyphomycetes morph has cheiroid dictyosporous or phragmosporous conidia. The sexual morphs of this family are characterized by superficial, subglobose, dark brown ascomata, bitunicate, cylindrical, pedicellate asci, and septate, hyaline, sheathed ascospores (Tanaka et al. 2015, Boonmee et al. 2016, Atienza et al. 2021, Shen et al. 2022b).

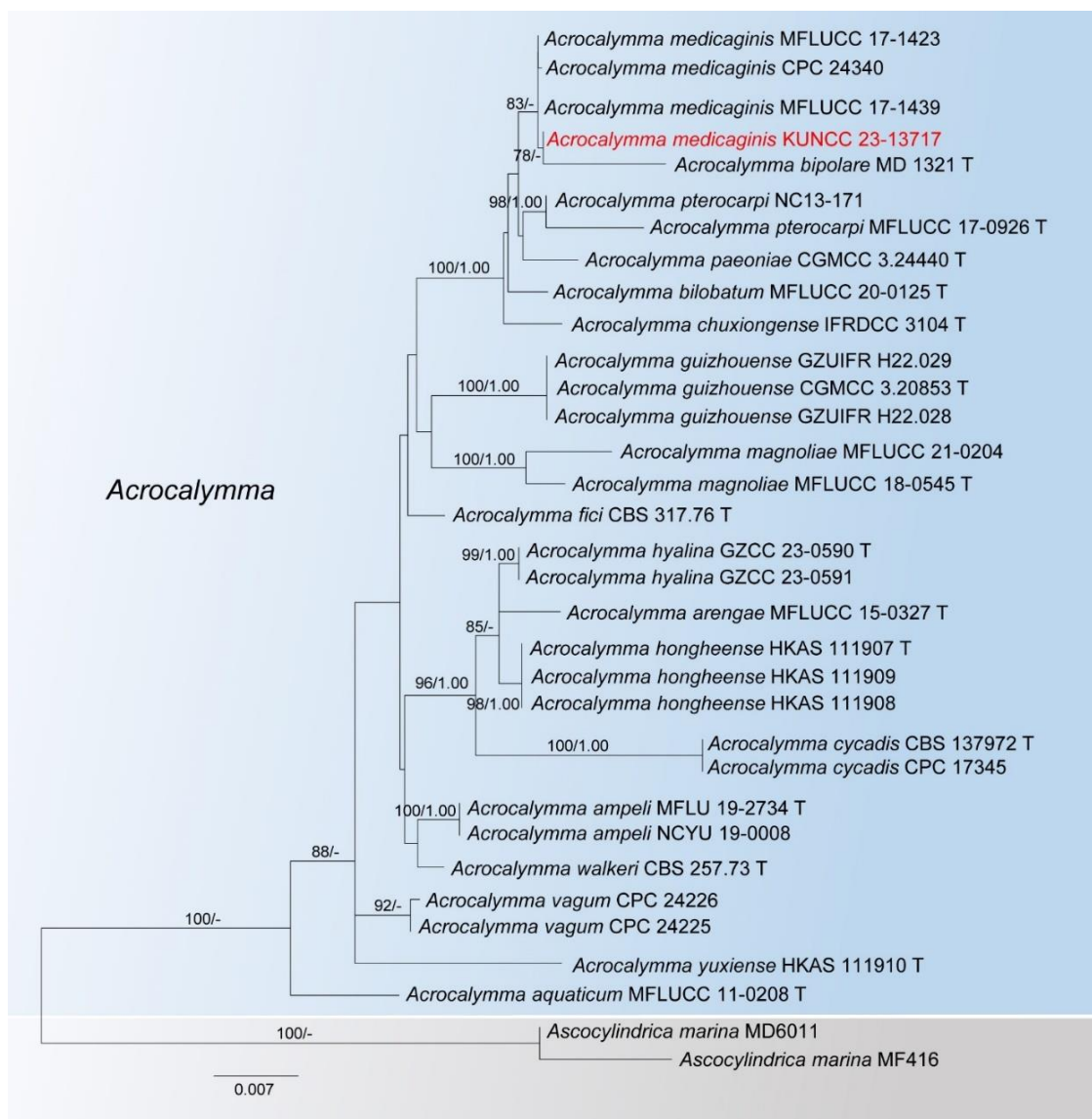


Figure 6 – RAxML tree based on analysis of *Acrocalymma* that combined LSU, ITS, and SSU dataset. The combined analyses include 33 strains with 2783 characters including gaps (LSU: 1330 bp, ITS: 467 bp, and SSU: 986 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Ascocylindrica marina* (MF416) and *A. marina* (MD6011). The new collection is indicated in red. Ex-type strains are indicated with “T” after the strain number.

***Dictyocheirospora* D’souza, Boonmee & K.D. Hyde**

Based on morphological and phylogenetic analysis, Boonmee et al. (2016) introduced *Dictyocheirospora*, with *D. rotunda* as the type species. *Dictyocheirospora* is similar to *Dictyosporium* in having micronematous, mononematous conidiophores and solitary conidia consisting of several arms arising from a basal cell. But the difference between the two genera is that

Dictyocheiropora has cheiroid, aplanate conidia, and mostly with conidial arms closely gathered together at the apex (Boonmee et al. 2016, Wang et al. 2016, Hyde et al. 2017, Li et al. 2017, Yang et al. 2018a, Shen et al. 2022b). Currently, there are 29 epithets listed within *Dictyocheiropora* in Index Fungorum (2024) with 25 species have DNA sequence in the GenBank (Shu et al. 2024). In this study, a new species (*D. appendiculata*), a new record for freshwater habitat (*D. taiwanense*), and a new collection (*D. rotunda*) are reported.

Dictyocheiropora appendiculata W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.
Fig. 9

Index Fungorum number: IF902423; Facesoffungi number: FoF16096

Etymology – Referring to the conidia with appendages of this fungus.

Holotype – HKAS 131353

Saprobic on submerged decaying wood. Asexual morph: Hyphomycetous. *Colonies* superficial, punctiform, dark brown. *Mycelium* mostly immersed, composed of subhyaline, smooth, thin-walled, septate hyphae. *Conidiophores* micronematous, mononematous, subhyaline, smooth, thin-walled. *Conidiogenous cells* 6.1–14 × 3.4–6.5 µm ($\bar{x}$ = 9.8 × 4.6 µm, n = 15), holoblastic, integrated, terminal, determinate, subhyaline to pale brown, smooth, thin-walled. *Conidia* 50–80 × 17–30 µm ($\bar{x}$ = 66.6 × 22.6 µm, n = 40), solitary, cheiroid, fusiform to cylindrical, subhyaline to pale brown, sometimes olive green, not aplanate, composed of 4–7 rows of cells, rows digitate, cylindrical, slightly inwardly curved or straight at the tip, arising from a basal cell, each row with 9–11 cells, euseptate, sometime distoseptate (Fig. 9o), constricted at the septum, with or without 1–2 hyaline, thin-walled, easy to rupture and shrink, globose to subglobose appendages at the apex to middle, 10.3–18 × 7.1–12 µm wide. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the base. Colonies on PDA reaching 45 mm diameter after 4 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, it is a round pie-like projection, with irregular edges, flat surface, grey to brown, and the edges are orange. Reverse orange, with dark brown in the center, smooth, circular, split in the center.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4356 (HKAS 131353, holotype), ex-type living culture KUNCC 23–13714.

Notes – Phylogenetic analysis showed that *Dictyocheiropora appendiculata* (KUNCC 23–13714), *D. multiappendiculata*, and *D. suae* grouped in the same clade (Fig. 8). The three species share similar characteristics in having cheiroid, cylindrical, aplanate, euseptate conidia with hyaline, globose to subglobose subapical appendages. However, *D. appendiculata* differs from *D. multiappendiculata* in having larger conidia (50–80 × 17–30 vs. (50–)55–62(–68) × (–16)19–22(–24) µm) with fewer appendages (Shen et al. 2022b). *Dictyocheiropora appendiculata* differs from *D. suae* in that the appendages of conidia are located in the apex to middle, and each conidial row with less cells (9–11 vs. 12–15) (Shen et al. 2022b).

Dictyocheiropora rotunda M.J. D'souza, Bhat & K.D. Hyde, Fungal Divers. 80, 465 (2016)
Fig. 10

Index Fungorum number: IF551581; Facesoffungi number: FoF01262

Saprobic on submerged decaying wood. Asexual morph: Hyphomycetous. *Colonies* superficial, punctiform, dark brown. *Mycelium* immersed, composed of subhyaline, smooth, thin-walled, septate hyphae. *Conidiophores* 7.2–23 × 1.9–5.7 µm ($\bar{x}$ = 15.2 × 4.1 µm, n = 10), micronematous, mononematous, cylindrical, smooth and thin-walled, subhyaline to pale brown. *Conidiogenous cells* 4.6–11 × 4.4–7.7 µm ($\bar{x}$ = 7.9 × 6 µm, n = 15), holoblastic, integrated, terminal, determinate, pale brown, smooth, thin-walled. *Conidia* 40–60 × (12–) 18–30 µm ($\bar{x}$ = 53.8 × 24.7 µm, n = 40), solitary, cheiroid, ellipsoid to cylindrical, not aplanate, pale brown to brown, composed of 5–7 rows of cells, row digitate, cylindrical, inwardly curved at the tip, arising from a

basal cell, each row with 9–11 cells, euseptate, constricted at the septum, unseparated in water. Sexual morph: Undetermined.

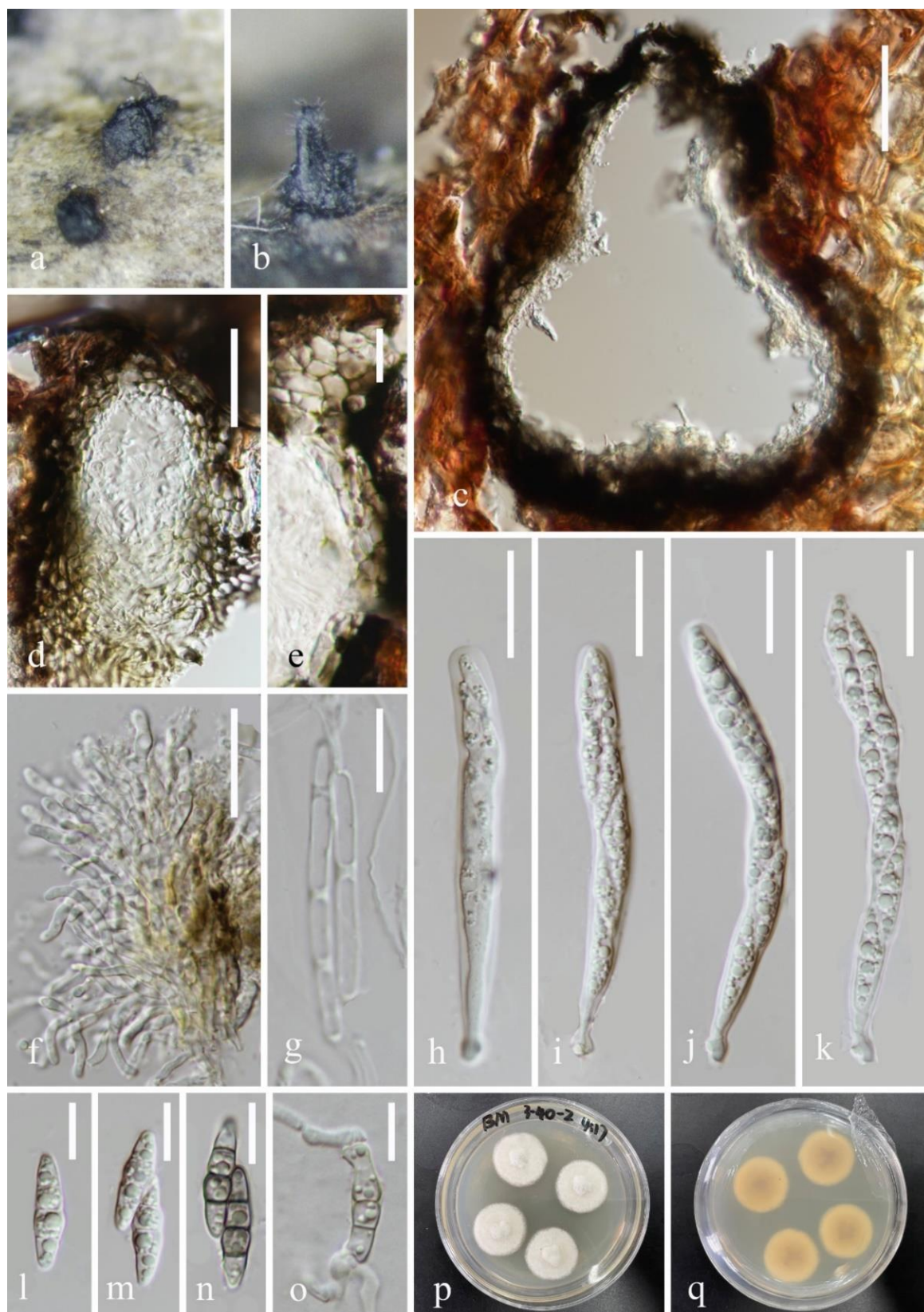


Figure 7 – *Acrocalymma medicaginis* (HKAS 131366). a, b Ascomata on the substratum. c Section of ascoma. d Ostiolar neck. e Peridium. f, g Pseudoparaphyses. h–k Asci. l–n Ascospores. o Germinating ascospore. p, q Colonies on PDA from surface and reverse. Scale bars: c, d = 30 μ m, e, g, l–o = 10 μ m, f, h–k = 20 μ m.

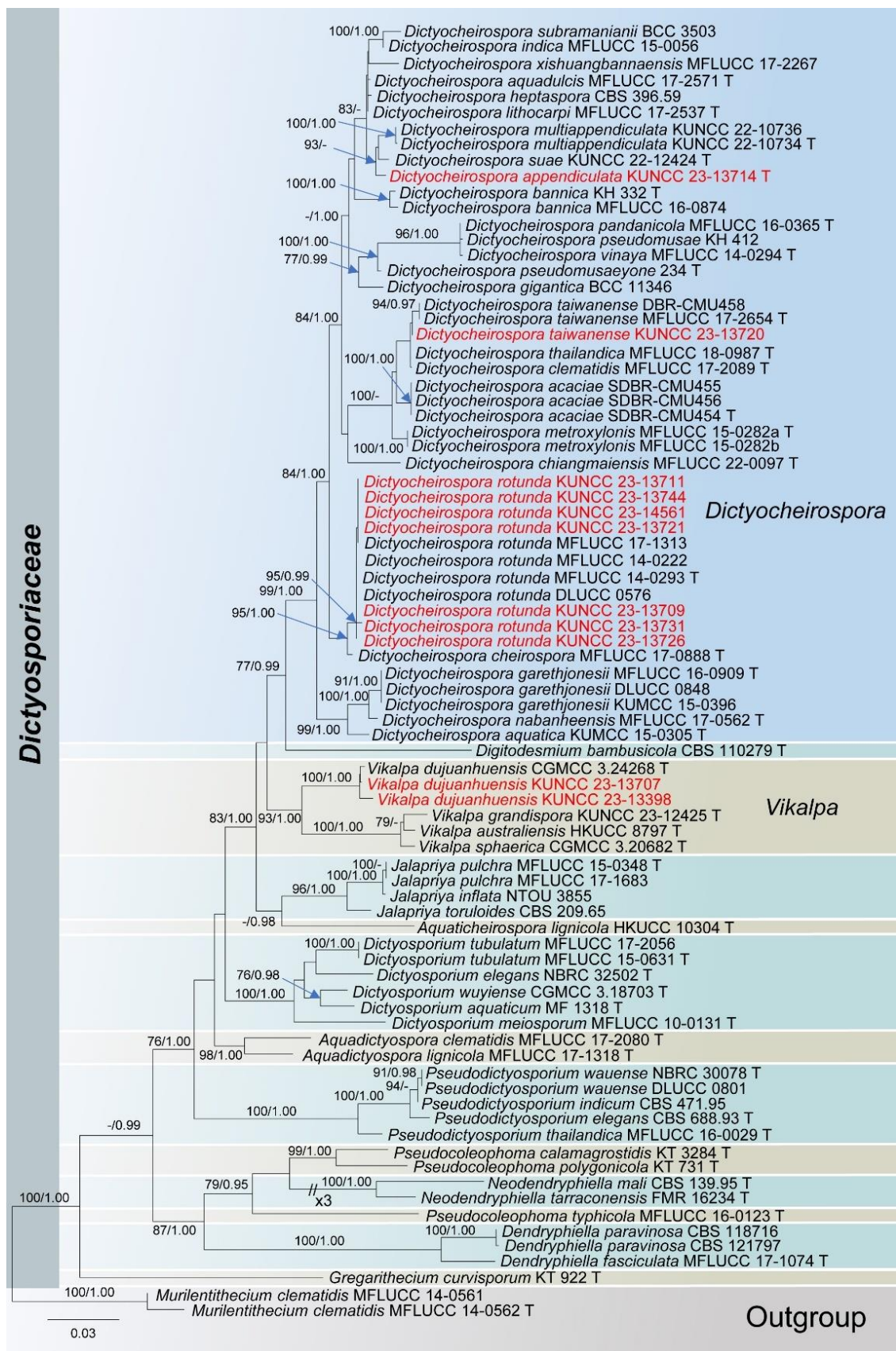


Figure 8 – RAxML tree based on analysis of *Dictyosporiaceae* that combined ITS, LSU, and *tef1-α* dataset. The combined analyses include 81 strains with 2181 characters including gaps (ITS: 498 bp, LSU: 814 bp, and *tef1-α*: 869 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Murilentithecium clematidis* (MFLUCC 14-0561 and MFLUCC 14-

0562). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.

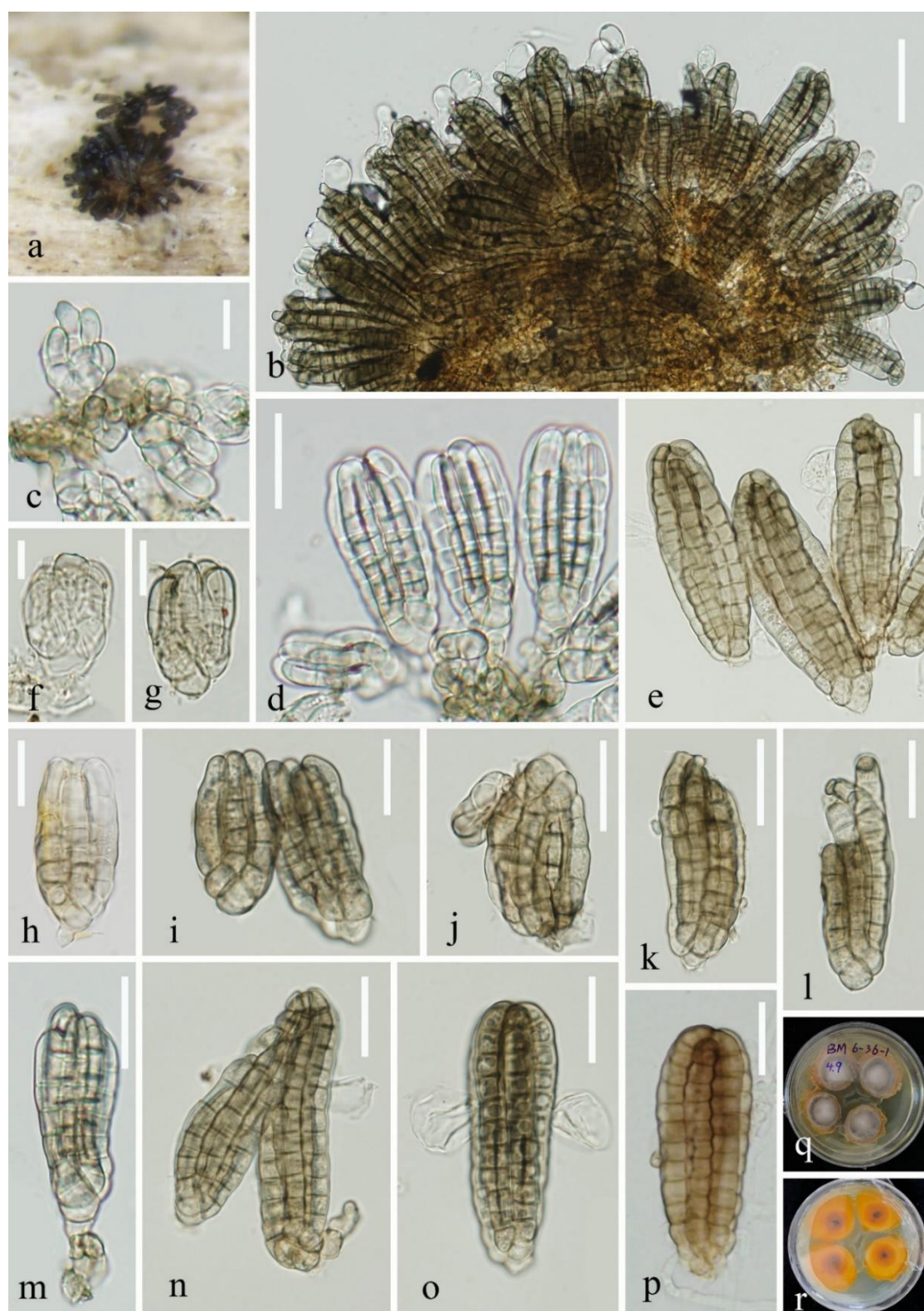


Figure 9 – *Dictyocheiropora appendiculata* (HKAS 131353, holotype). a Colony on the substratum. b Squash mount of conidioma. c, d, m Conidiogenous cells with conidia. e–l, n, o Conidia. p Germinating conidium. q, r Colonies on PDA from surface and reverse. Scale bars: b = 30 μ m, c, f, g = 10 μ m, d, e, j–p = 20 μ m, h, i = 15 μ m.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the base. Colonies on PDA reaching 25 mm diameter after 2 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, has a bulbous protrusion in the center, white to grey. Reverse dark brown in the center, smooth, split from the center.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, H-733 (HKAS 131350), living culture KUNCC 23–13731; *ibid.*, S-3255 (HKAS 131358), living culture KUNCC 23–14561; *ibid.*, S-3266 (HKAS 131354), living culture KUNCC 23–13709; *ibid.*, S-3272 (HKAS 131380), living culture KUNCC 23–13726; *ibid.*, S-3287 (HKAS 131372), living culture KUNCC 23–13711; *ibid.*, S-3494 (HKAS 131384), living culture KUNCC 23–13744; *ibid.*, S-3505 (HKAS 131371), living culture KUNCC 23–13721.

Notes – Phylogenetic analysis showed that our collections nested within *Dictyocheiросpora rotunda* clade, and its morphology fit well with the holotype of *D. rotunda* (Fig. 8). We therefore identified our collections as *D. rotunda*, a species introduced by Boonmee et al. (2016) and collected on submerged decaying wood in Thailand. Afterwards, *D. rotunda* has been repeatedly reported from a variety of habitats and locations in China, making it the most frequently reported species in *Dictyocheiросpora* (Wang et al. 2016, Yang et al. 2018a, Hyde et al. 2019, Dong et al. 2020).

Dictyocheiросpora taiwanense Tennakoon, C.H. Kuo & K.D. Hyde, Fungal Divers. 96, 27 (2019)
Fig. 11

Index Fungorum number: IF556309; Facesoffungi number: FoF05964

Saprobic on submerged decaying wood. Asexual morph: Hyphomycetous. Colonies superficial, punctiform, dark brown. Mycelium immersed, composed of subhyaline, smooth, thin-walled, septate hyphae. Conidiophores 10.2–10.4 × 3.1–3.3 µm, micronematous, mononematous, subhyaline, smooth, thin-walled. Conidiogenous cells 7.5–8.6 × 2.3–3.6 µm, holoblastic, integrated, terminal, determinate, cylindrical, brown, smooth, thin-walled. Conidia 50–80 × 17–26 µm ($\bar{x}$ = 61.3 × 22.9 µm, n = 50), solitary, cheiroid, ellipsoid to clavate, rounded at the apex, not complanate, brown to brownish-red, composed of 6 rows of cells, row digitate, cylindrical, inwardly curved at the tip, arising from a basal cell, each row with 10–12 cells, euseptate, slightly constricted at the septum, unseparated when in water, and the top is tightly clustered together. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the base. Colonies on PDA reaching 30 mm diameter after 3 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, flat surface, white to grey. Reverse orange, with dark brown in the center, smooth, split from the center.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3502 (HKAS 131365), living culture KUNCC 23–13720.

Notes – The phylogenetic analysis showed that our new strain (KUNCC 23–13720) clusters in *Dictyocheiросpora* and sister to *D. taiwanense* (MFLUCC 17–2654 and SDBR-CMU458) with low support (Fig. 8). Our new collection is similar to the holotype of *D. taiwanense* (MFLUCC 17–2654) in having ellipsoid, cheiroid, acomplanate conidia and the conidial rows are cylindrical, arising from a basal cell, constricted at septum with similar number cells of conidial row (10–12 vs. 10–13) and without appendages (Hyde et al. 2019). Comparison of the ITS sequence of our new collection and the ex-type strain of *D. taiwanense* showed that 99.4% (499/502 bp, two gaps) similarity. *Dictyocheiросpora taiwanense* was introduced by Hyde et al. (2019) on decaying wood of *Macaranga tanarius* (*Euphobiaceae*) in Taiwan, China. Tennakoon et al. (2023) reported *D. taiwanense* on decaying stem of *Ficus benjamina* (*Moraceae*) in Thailand. We therefore identified the new collection as *D. taiwanense*, and this is the first report of this species from freshwater habitat.

Vikarpa D'souza, Boonmee, Bhat & K.D. Hyde

Based on morphological and phylogenetic analysis, Boonmee et al. (2016) separated *Vikarpa*

from *Dictyosporium* to accommodate a new species, *V. lignicola*, and three new combinations, *V. australiensis*, *V. freycinetiae* and *V. micronesiaca*. The genus is characterized by acrogenous, solitary, cheiroid, pale brown, euseptate or distoseptate conidia, consisting of a truncate basal cell on which three rows arise parallel and closely compacted, with all three rows in different planes, with or without appendages (Sutton 1985, Boonmee et al. 2016). Recently, Shen et al. (2022b) and Liu et al. (2024a) reported three new species, *V. dujuanhuensis*, *V. grandispora* and *V. sphaerica* from freshwater habitats in China.



Figure 10 – *Dictyocheirospora rotunda* (HKAS 131358). a Colony on the substratum. b Conidiophores with conidiogenous cells. c Squash mount of conidioma. d Conidiophore with

conidia. e–j Conidia. k Germinating conidium. l, m Colonies on PDA from surface and reverse. Scale bars: b = 5 μ m, c = 50 μ m, d–k = 15 μ m.



Figure 11 – *Dictyocheirospora taiwanense* (HKAS 131365). a Colonies on the substratum. b–e, i Conidiogenous cells with conidia. f–h Conidia. j Germinating conidium. k, l Colonies on PDA from surface and reverse. Scale bars: b = 30 μ m, c–j = 20 μ m.

Vikalpa dujuanhuensis H.W. Shen & Z.L. Luo, Mycology, 3 (2024)

Fig. 12

Index Fungorum number: IF571593; Facesoffungi number: FoF15707

Saprobic on submerged decaying wood. Asexual morph: Hyphomycetous. Colonies superficial, punctiform, silver gray. Mycelium mostly immersed, composed of subhyaline, smooth, thin-walled, hyphae. Conidiophores $6.1\text{--}8 \times 1.6\text{--}2.3\ \mu\text{m}$, micronematous, mononematous, septate, subglobose to subcylindrical, unbranched, subhyaline to pale brown, smooth, thin-walled, sometimes reduced to conidiogenous cells. Conidiogenous cells $2.1\text{--}5.8 \times 1.4\text{--}3.4\ \mu\text{m}$ ($\bar{x} = 3.2 \times 2.3\ \mu\text{m}$, $n = 20$), holoblastic, integrated, terminal, determinate, subglobose, subhyaline to pale brown, smooth, thin-walled. Conidia $30.5\text{--}44.2 \times 10.3\text{--}13.5\ \mu\text{m}$ ($\bar{x} = 38.6 \times 11.8\ \mu\text{m}$, $n = 30$), solitary, cheiroid, silver gray or brown, inverted cone, not complanate, composed of 2–3 rows of cells, row digitate, each row with 8–10 cells, arising from a basal cell, arms closely appressed, euseptate, slightly constricted at the septum, guttulate, with or without hyaline or multiple colors mixed together appendages at the apex. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the apex. Colonies on PDA reaching 20 mm diameter after 2 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, has a spherical depression in the center, grey. Reverse brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, 7 February 2022, on submerged decaying wood, W.P. Wang, S-3271 (HKAS 131386), living culture KUNCC 23–13707; *ibid.*, 28 February 2023, S-4349 (HKAS 131362), living culture KUNCC 23–13398.

Notes – Phylogenetic analysis showed that our new collections (KUNCC 23–13398 and KUNCC 23–13707) clustered with the type strain of *Vikalka dujuanhuensis* (CGMCC 3.24268) (Fig. 8). Our new collections fit well with the description of *V. dujuanhuensis* in having septate, unbranched conidiophores or sometimes the conidiophores are reduced to conidiogenous cells and cheiroid, similar in size conidia ($30.5\text{--}44.2 \times 10.3\text{--}13.5$ vs. $30\text{--}41 \times 12\text{--}16\ \mu\text{m}$) consisting of three rows, not complanate, euseptate, with or without appendages at the apex (Liu et al. 2024a). The LSU, ITS, and *tef1- α* sequences of our new collection (KUNCC 23–13398) and the type strain (CGMCC 3.24268) showed 100.00% (1000/1000 bp), 99.46% (368/370 bp), and 99.66% (889/892 bp) similarities, respectively. Thus, our new collections were identified as *V. dujuanhuensis* based on morphology and phylogeny.

Massarinaceae Munk

Massarinaceae was introduced by Munk (1956), with *Massaria* as the type genus. Eleven genera, viz., *Byssothecium*, *Haplohelminthosporium*, *Helminthosporiella*, *Helminthosporium*, *Massarina*, *Mirohelminthosporium*, *Pseudodidymosphaeria*, *Pseudosplanchnonema*, *Semifissispora*, *Stagonospora*, and *Suttonomyces* are accepted in this family (Chethana et al. 2015, Zhang et al. 2020, Konta et al. 2021). The sexual morph of *Massarinaceae* is characterized by flattened or spherical ascomata, cellular pseudoparaphyses, clavate to cylindric-clavate asci, and fusiform to narrowly fusiform, septate ascospores with or without a mucilaginous sheath (Chethana et al. 2015). The hyphomycetes asexual morph of *Massarinaceae* are characterized by erect, cylindrical, septate conidiophores that produce clavate or obclavate, distoseptate conidia, and coelomycetes have phialidic conidiogenous cells with hyaline, aseptate conidia (Zhu et al. 2016, Dong et al. 2020, Konta et al. 2021, Hyde et al. 2023). Species of this family are often saprobic and endophytic in different parts of a variety of plants from terrestrial habitats, and only two genera *Byssothecium* and *Helminthosporium* have been reported from freshwater habitats (Zhu et al. 2016, Dong et al. 2020, Konta et al. 2021, Hyde et al. 2023).

Helminthosporium Link

Helminthosporium was established by Link (1809) and typified by *H. velutinum*. *Helminthosporium* is a species-rich genus, which has a complex taxonomic history. To date, 782 epithets of *Helminthosporium* are listed in Index Fungorum (2024), with most records have been found on dead wood from terrestrial habitats. In the last decade, four species including *H. aquaticum*,

H. lignicolum, *H. submersum*, and *H. velutinum* are known from freshwater habitats (Zhu et al. 2016, Zhao et al. 2018, Dong et al. 2020, Hyde et al. 2023). In this study, we recollected *H. velutinum* from freshwater habitats in karst landscape of Yunnan Province, China.

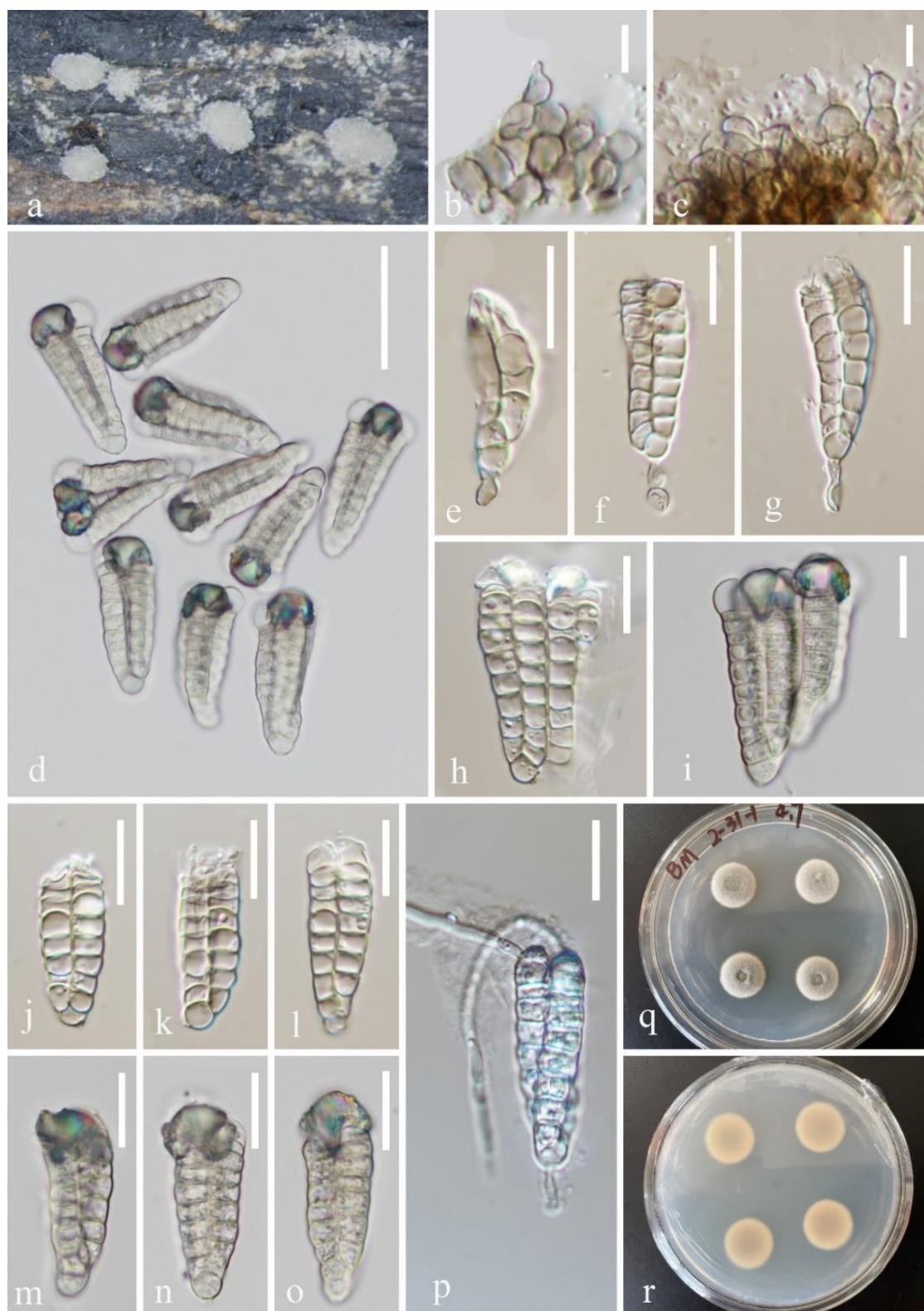


Figure 12 – *Vikalpa dujuanhuensis* (HKAS 131386). a Colonies on the substratum. b, c Conidiophores with conidiogenous cells. d, h–o conidia. e–g Conidiogenous cells with conidia. p Germinating conidium. q, r Colonies on PDA from surface and reverse. Scale bars: b, c = 5 μ m, d = 30 μ m, e–p = 15 μ m.

Helminthosporium velutinum Link, Mag. Gesell. naturf. Freunde, Berlin 3(1–2), 10, tab. 1, 9 (1809)
Fig. 14

Index Fungorum number: IF250075; Facesoffungi number: FoF01053

Saprobic on submerged decaying wood. Asexual morph: Colonies superficial, scattered, erect, single, hairy, brown to dark brown. Mycelium mostly immersed, partly superficial, composed of branched, septate, smooth-walled, pale brown hyphae. Conidiophores $290\text{--}730 \times 7.9\text{--}19 \mu\text{m}$ ($\bar{x} = 430.7 \times 11.3 \mu\text{m}$, $n = 15$), macronematous, mononematous, solitary, erect, mostly unbranched, proliferating, black at the base, paler towards to the apex, septate, straight or slightly flexuous, cylindrical, smooth, thick-walled. Conidiogenous cells polytretic, integrated, intercalary and terminal. Conidia $40\text{--}118 \times 9.7\text{--}18 \mu\text{m}$ ($\bar{x} = 69.3 \times 13.8 \mu\text{m}$, $n = 40$), solitary, obclavate, subhyaline to brown, pale at the apex, 7–12-distoseptate, smooth-walled, straight or slightly curved, thickened scar, truncate at the base and rounded at the apex, multi-guttulate. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the apex. Colonies on PDA reaching 25 mm diameter after 2 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with irregular edges, has a bulbous protrusion in the center, white. Reverse brown in the center, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3270 (HKAS 131393), living culture KUNCC 23–13704; *ibid.*, S-3354 (HKAS 131392), living culture KUNCC 23–13758.

Notes – Phylogenetic analysis showed that our collections clustered within *Helminthosporium velutinum* clade (Fig. 13), and since our collections fit well with the conception of *H. velutinum*, we therefore identify our collections as *H. velutinum*. *Helminthosporium velutinum* was introduced by Link (1809) on a wide range of dead plant material from terrestrial habitats. Zhu et al. (2016) reported *H. velutinum* from freshwater habitat in Yunnan Province, China, and they suspected that this fungus might have grown on the neighboring riparian in terrestrial environment, then migrated to the freshwater when plants invaded the freshwater habitat. Our new collections also isolated from freshwater habitats, which suggests that the species may have fully adapted to the freshwater environment.

Morosphaeriaceae Suetrong, Sakayaroj, E.B.G. Jones & C.L. Schoch

Morosphaeriaceae was established by Suetrong et al. (2009) to accommodate *Helicascus* and *Morosphaeria*, and is typified by *Morosphaeria*. Knapp et al. (2015) introduced a new genus *Aquilomyces* to accommodate *A. patris* but without description. Tanaka et al. (2015) introduced a new genus *Clypeolocus* and provided corresponding morphological information for *Aquilomyces*. Dong et al. (2020) introduced *Aquihelicascus* and *Neohelicascus*, and transferred eight *Helicascus* species to these two genera. Currently, six genera, viz., *Aquihelicascus*, *Aquilomyces*, *Clypeolocus*, *Helicascus*, *Morosphaeria*, and *Neohelicascus* are accepted in this family (Dong et al. 2020, Yang et al. 2023).

Neohelicascus W. Dong, H. Zhang, K.D. Hyde & Doilom

Based on morphology and phylogeny, Dong et al. (2020) introduced *Neohelicascus* to accommodate a new species *N. submersus* and seven species previously placed in *Helicascus*. The asexual morph of *Neohelicascus* is coelomycetous, which is characterized by uniloculate, globose to subglobose, brown pycnidia, reduced conidiophores, holoblastic, determinate, cylindrical to subcylindrical conidiogenous cells, and ellipsoidal to obovoidal, hyaline, aseptate conidia. The sexual morph of *Neohelicascus* is characterized by uni- or multi-loculate ascomata, numerous, cellular, hypha-like pseudoparaphyses, embedded in a gelatinous matrix, bitunicate, clavate, long pedicellate asci, and ellipsoidal to broadly fusiform, brown ascospores with or without a deliquescing sheath (Dong et al. 2020, Yang et al. 2023). *Neohelicascus* comprises nine species, and all of them have been reported from freshwater habitats (Zhang et al. 2014a, Luo et al. 2016, Yang et al. 2023).

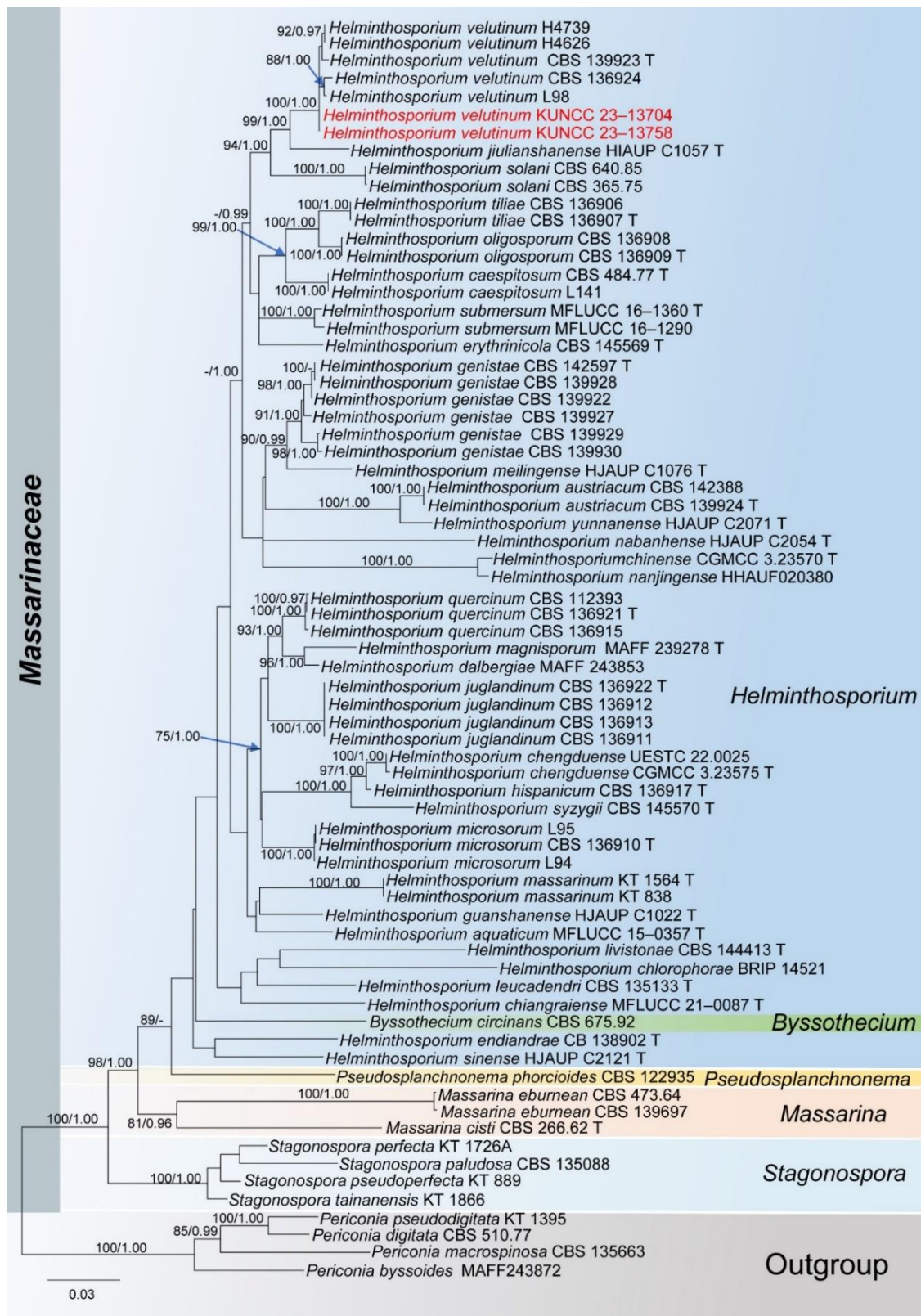


Figure 13 – RAxML tree based on analysis of *Massarinaceae* that combined ITS, LSU, *tef1-α*, *rpb2* and SSU dataset. The combined analyses include 71 strains with 4235 characters including gaps (ITS: 538 bp, LSU: 848 bp, *tef1-α*: 746 bp, *rpb2*: 1111 bp, and SSU: 992 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Periconia byssoides* (MAFF243872), *P. digitata* (CBS 510.77), *P. macrospinosa* (CBS 135663), and *P. pseudodigitata* (KT 1395). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.



Figure 14 – *Helminthosporium velutinum* (HKAS 131393). a, b Colonies on the substratum. c Conidiophore with conidia. d, f, g Apex of conidiophores with conidia. e Apex of conidiophore. h–m Conidia. n Germinating conidium. o, p Colonies on PDA from surface and reverse. Scale bars: c = 100 µm, d = 50 µm, e–g = 40 µm, h–n = 20 µm.

Neohelicascus elaterascus (Shearer) W. Dong, K.D. Hyde & H. Zhang, Fungal Divers. 105, 467 (2020)

Fig. 16

Index Fungorum number: IF557925; Facesoffungi number: FoF09267

Saprobic on submerged decaying wood. Asexual morph: Undetermined. Sexual morph: *Ascomata* 170–610 µm diam, 190–350 µm high., scattered or gregarious, immersed, unilocular or bilocular, fattened at the basal region, lenticular, coriaceous, with ostiolate papilla, perpendicular to substratum. *Peridium* 15–40 µm thick, thickened around the ostiole, cortex of host, coriaceous, consisting of 2–7-layered cells of *textura angularis*, outer layers with pale brown, angular to polygonal, thick-walled cells, inner layers with subhyaline, polygonal, thin-walled cells. *Pseudoparaphyses* up to 3.1 µm wide, abundant, cellular, cylindrical, hyaline, sparsely septate, embedded in a gel matrix. *Asci* (70–) 90–160 (–180) × 13–22 µm ($\bar{x}$ = 114.2 × 17.2 µm, n = 35), 8-spored, bitunicate, clavate, slightly curved, rounded at the apex, partly with an ocular chamber, mostly long, narrow at the base. *Ascospores* 24–34 × 7.2–10.6 µm ($\bar{x}$ = 26.2 × 9.1 µm, n = 50), overlapping, uniseriate or obliquely biseriate, fusiform to ellipsoidal, slightly curved, subhyaline when young, becoming dark yellowish brown when mature, uniseptate, constricted at the septum, guttulate, asymmetrical, apical cell slightly longer than the basal cell, smooth, thin-walled, surrounded by a gelatinous sheath.

Culture characteristics – Ascospores germinating on PDA within 12 h, and germ tubes produced from the base. Colonies on PDA reaching 20 mm diameter after 4 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, flat surface, has a punctate protrusion in the center, white to pale brown. Reverse brown to dark brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3264 (HKAS 131401), living culture KUNCC 23–14566; *ibid.*, S-3291 (HKAS 131387).

Notes – In the phylogenetic analysis, our new collections (KUNCC 23–14566 and HKAS 131387) clustered with *Neohelicascus elaterascus* (Fig. 15). Our new collections share similar characters with *N. elaterascus* in having clavate asci with elongated base, and uniseriate or obliquely biseriate, ellipsoidal, uniseptate ascospores with similar sized (24–34 × 7.2–10.6 vs. 23.5–31 × 8.5–11.5 µm) (Zhang et al. 2013). We therefore identified the new collections as *N. elaterascus*, a species which was introduced by Shearer et al. (1993b) that is associated with on dead wood from a thermal stream in Chile. Thereafter, Dong et al. (2020) reported this fungus on submerged wood in Thailand. In this study, we collected this species from submerged decaying wood in Yunnan Province, and it is the first time to report this species from China.

Neohelicascus gallicus (Y. Zhang & J. Fourn) W. Dong, K.D. Hyde & H. Zhang, *Fungal Divers.* 105, 468 (2020) Fig. 17

Index Fungorum number: IF557926; Facesoffungi number: FoF09268

Saprobic on submerged decaying wood. Asexual morph: Undetermined. Sexual morph: *Ascomata* 180–320 µm diam, 190–330 µm high., scattered, unilocular, immersed, black, comprising dark brown to black fungal tissues growing in cortex of host, with short, perpendicular to substratum ostiole, visible as ellipsoid, prominent, black neck. *Peridium* 12–50 µm thick, thickened around the ostiole, mostly immersed, cortex of host, coriaceous, consisting of 3–7-layered cells of *textura angularis*, outer layers with brown to black, thick-walled cells, inner layers with subhyaline to pale brown, ovoid, thin-walled cells. *Pseudoparaphyses* 1.9–3.1 µm wide, numerous, elongated, cylindrical, hyaline, septate. *Asci* 70–120 × 12–23 µm ($\bar{x}$ = 92.5 × 16.3 µm, n = 30), 8-spored, bitunicate, fissitunicate, clavate, straight or slightly curved, rounded at the apex, with an ocular chamber, sometimes with a long, narrow and straight pedicel. *Ascospores* 20–28 × 7.7–10.5 µm ($\bar{x}$ = 24.8 × 8.8 µm, n = 40), overlapping, mostly obliquely biseriate, fusiform to lunate, slightly curved, subhyaline when young, becoming dark yellowish brown when mature, uniseptate, slightly constricted at the septum, smooth, thin-walled, guttulate, apical cell slightly longer than the basal cell.

Culture characteristic – Colonies on PDA reaching 20 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, white surface, dark brown bottom layer, velvety. Reverse white to dark brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3512 (HKAS 131390), living culture KUNCC 23–13757.

Notes – Phylogenetic analysis showed that our new collection (KUNCC23–13757) clustered with *Neohelicasus gallicus* (BJFUCC 200224, BJFUCC 200228, and CBS 123118) with 96% ML/1.00 PP support (Fig. 15). Our new collection is similar to *N. gallicus* in having immersed ascomata with short ostioles, a peridium thickened around the ostiole, clavate asci with a long pedicel and similar sized ($70\text{--}120 \times 12\text{--}23$ vs. $112\text{--}128 \times 18\text{--}22 \mu\text{m}$), and fusiform to lunate ascospores with similar sized ($20\text{--}28 \times 7.7\text{--}10.5$ vs. $25.1\text{--}31.3 \times 9.3\text{--}12.1 \mu\text{m}$) (Zhang et al. 2014a, Yang et al. 2023). Thus, we identified the new collection as *N. gallicus*. *Neohelicasus gallicus* has been collected from freshwater habitats in China (Guizhou Province), France, and Thailand (Zhang et al. 2014a, Yang et al. 2023). This is the first time to report this species from Yunnan Province, China.

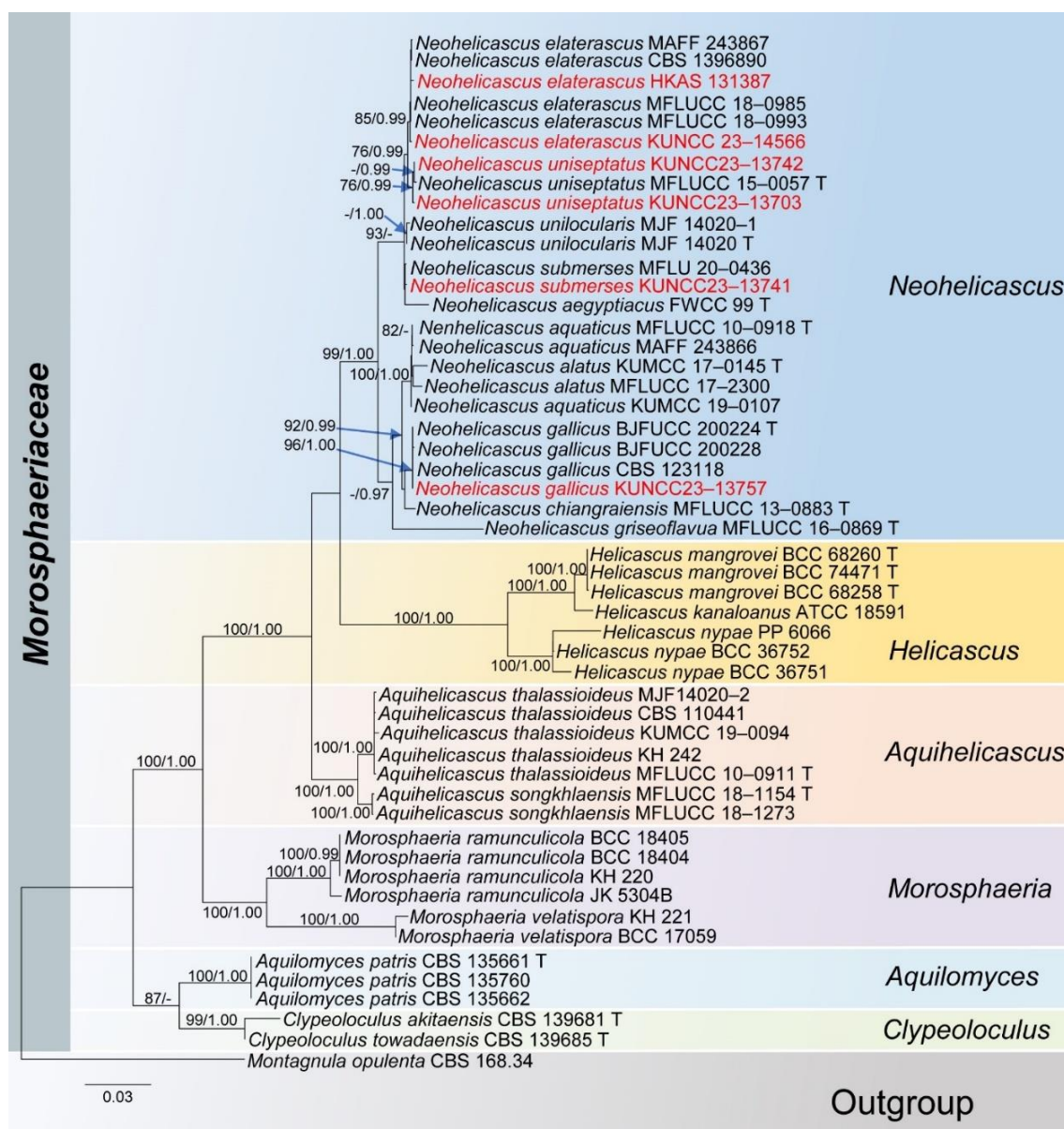


Figure 15 – RAxML tree based on analysis of *Morosphaeriaceae* that combined LSU, ITS, SSU, and *tef1-α* dataset. The combined analyses include 51 strains with 3273 characters including gaps (LSU: 850 bp, ITS: 576 bp, SSU: 946 bp, and *tef1-α*: 901 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Montagnula opulenta* (CBS 168.34). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.

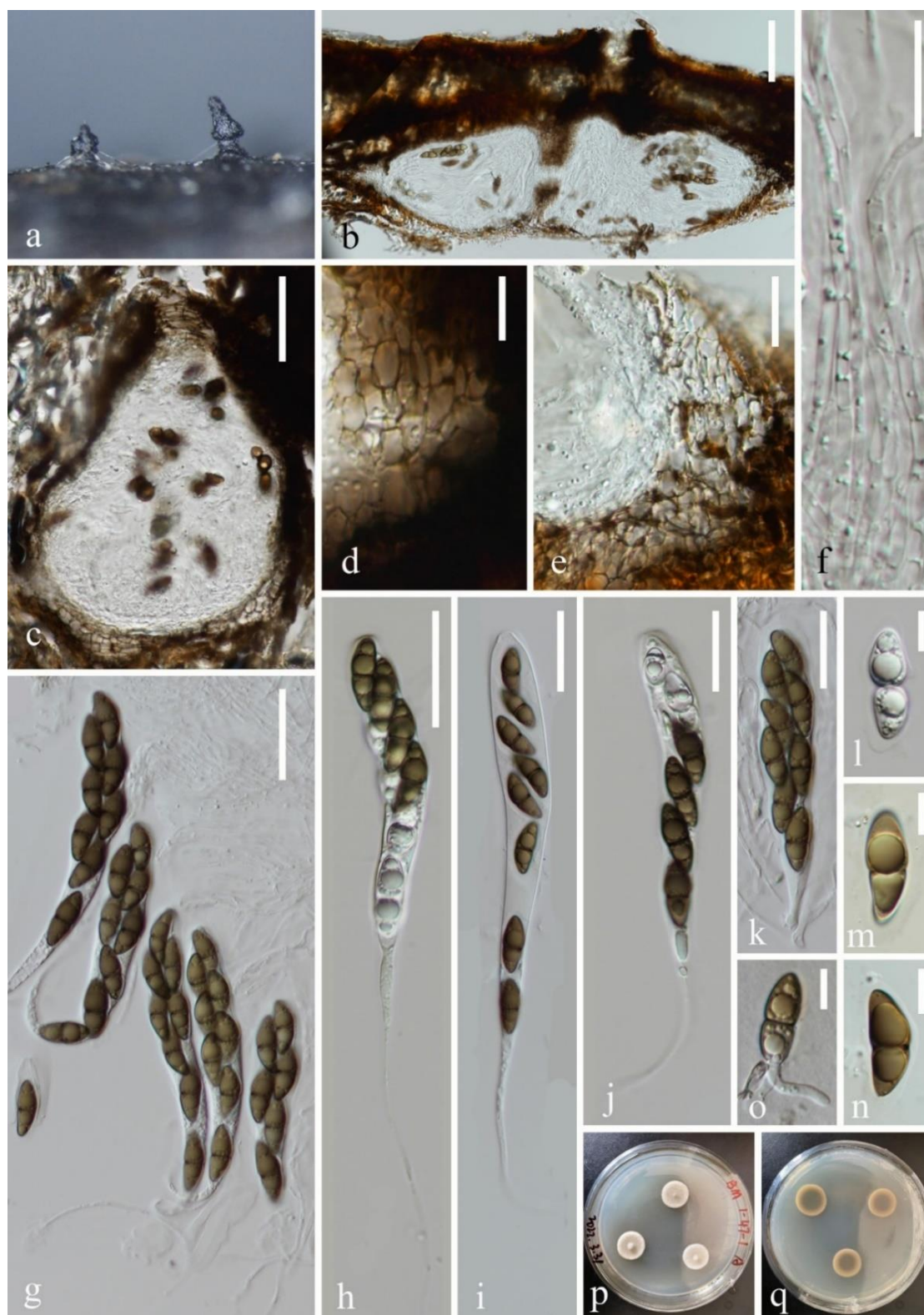


Figure 16 – *Neohelicascus elaterascus* (HKAS 131401). a Ascomata on the substratum. b, c Vertical section of ascomata. d, e Structure of peridium. f Pseudoparaphyses. g–k Asci. l–n Ascospores. o Germinating ascospore. p, q Colonies on PDA from surface and reverse. Scale bars: b = 90 μ m, c = 50 μ m, d, l–o = 10 μ m, e, f = 20 μ m, g–i = 40 μ m, j, k = 30 μ m.

Neohelicascus submersus W. Dong, K.D. Hyde & H. Zhang, Fungal Divers. 105, 468 (2020)

Fig. 18

Index Fungorum number: IF557927; Facesoffungi number: FoF09269

Saprobic on submerged decaying wood. Asexual morph: Undetermined. Sexual morph: *Ascomata* 230–330 µm diam, 170–340 µm high., scattered, comprising dark brown to black fungal tissues growing in cortex of host, immersed, unilocular, lenticular, black, with perpendicular to substratum ostiole, visible as short, prominent, black ostiole dots. *Peridium* 16–48 µm thick, thickened around the ostiole, cortex of host, coriaceous, consisting of 3–6-layered cells of *textura angularis*, outer layers with brown to black, polygonal, thick-walled cells, inner layers with subhyaline, polygonal, thin-walled cells. *Pseudoparaphyses* 2.1–3.4 µm wide, numerous, elongated, cylindrical, hyaline, less separation. *Asci* (60–) 90–160 (–220) × 14–27 µm ($\bar{x}$ = 103.6 × 20 µm, n = 40), 8-spored, bitunicate, clavate, straight or slightly curved, rounded at the apex, with an ocular chamber, base of endoascus long, narrow and coiled within ectoascus. *Ascospores* 25–31 × 6.9–13 µm ($\bar{x}$ = 27.4 × 9.7 µm, n = 40), obliquely arranged, overlapping uniseriate or occasionally biseriate, ellipsoid to fusiform, straight or slightly curved, subhyaline when young, becoming dark olivaceous brown when mature, uniseptate, slightly constricted at the septum, smooth, thin-walled, guttulate, apical cell slightly larger than the basal cell, surrounded by a gelatinous sheath.

Culture characteristics – Ascospores germinating on PDA within 12 h, and germ tubes produced from the base. Colonies on PDA reaching 15 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, protrusions, surface is uneven, grey to pale brown, velvety. Reverse brown to dark brown, smooth, edges is subhyaline gelatinous substance.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3504 (HKAS 131349), living culture KUNCC 23–13741.

Notes – The characteristics of our new collection (HKAS 131349) are indistinguishable from the holotype of *Neohelicascus submersus* (MFLU 20–0436), including unilocular, lenticular ascomata, indistinctly septate pseudoparaphyses, clavate, similar in size (90–160 × 14–27 vs. 120–165 × 17.5–21 µm) asci with long, narrow pedicels, and ellipsoid to fusiform ascospores with a gelatinous sheath (Dong et al. 2020). In addition, phylogenetic analysis also supports our new collection as *N. submersus* (Fig. 15), and this species was recollected from freshwater habitats in Yunnan Province, China.

Neohelicascus uniseptatus (J. Yang, J.K. Liu & K.D. Hyde) W. Dong, K.D. Hyde & H. Zhang, Fungal Divers. 105, 471 (2020) Fig. 19

Index Fungorum number: IF557929; Facesoffungi number: FoF09271

Saprobic on submerged decaying wood. Asexual morph: Undetermined. Sexual morph: *Ascomata* 320–600 µm diam., 310–380 µm high, scattered or gregarious, comprising dark brown to black fungal tissues growing in cortex of host, immersed, unilocular, mammiform, black, with perpendicular to substratum ostiole, visible as short cylindrical, prominent, black neck. *Peridium* 14–44 µm thick, thickened around the ostiole, mostly immersed, cortex of host, coriaceous, consisting of several layered cells of *textura angularis*, outer layers with brown to black, thick-walled cells, inner layers with subhyaline to brown, rectangle to elongated, thin-walled cells. *Pseudoparaphyses* 1.8–4.1 µm wide, numerous, elongated, cylindrical, hyaline, septate, sometimes branched. *Asci* 76–130 × 18–24 µm ($\bar{x}$ = 96.7 × 20.8 µm, n = 15), 8-spored, bitunicate, clavate, straight or slightly curved, rounded at the apex, sometimes base of endoascus long, narrow and coiled within ectoascus. *Ascospores* 25–34 × 8.6–10.9 µm ($\bar{x}$ = 27.9 × 9.8 µm, n = 40), overlapping, mostly obliquely biseriate, fusiform, olivaceous brown, uniseptate, slightly constricted at the septum, smooth, thin-walled, guttulate, apical cell slightly larger than the basal cell.

Culture characteristics – Ascospores germinating on PDA within 12 h, and germ tubes produced from the base. Colonies on PDA reaching 15 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, surface flat, has an obviously punctate protrusion, grey to brown, velvety. Reverse brown to dark brown, smooth, edges with subhyaline gelatinous substance.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3273 (HKAS 131356), living culture KUNCC 23–13703; *ibid.*, S-3503 (HKAS 131394), living culture KUNCC 23–13742.

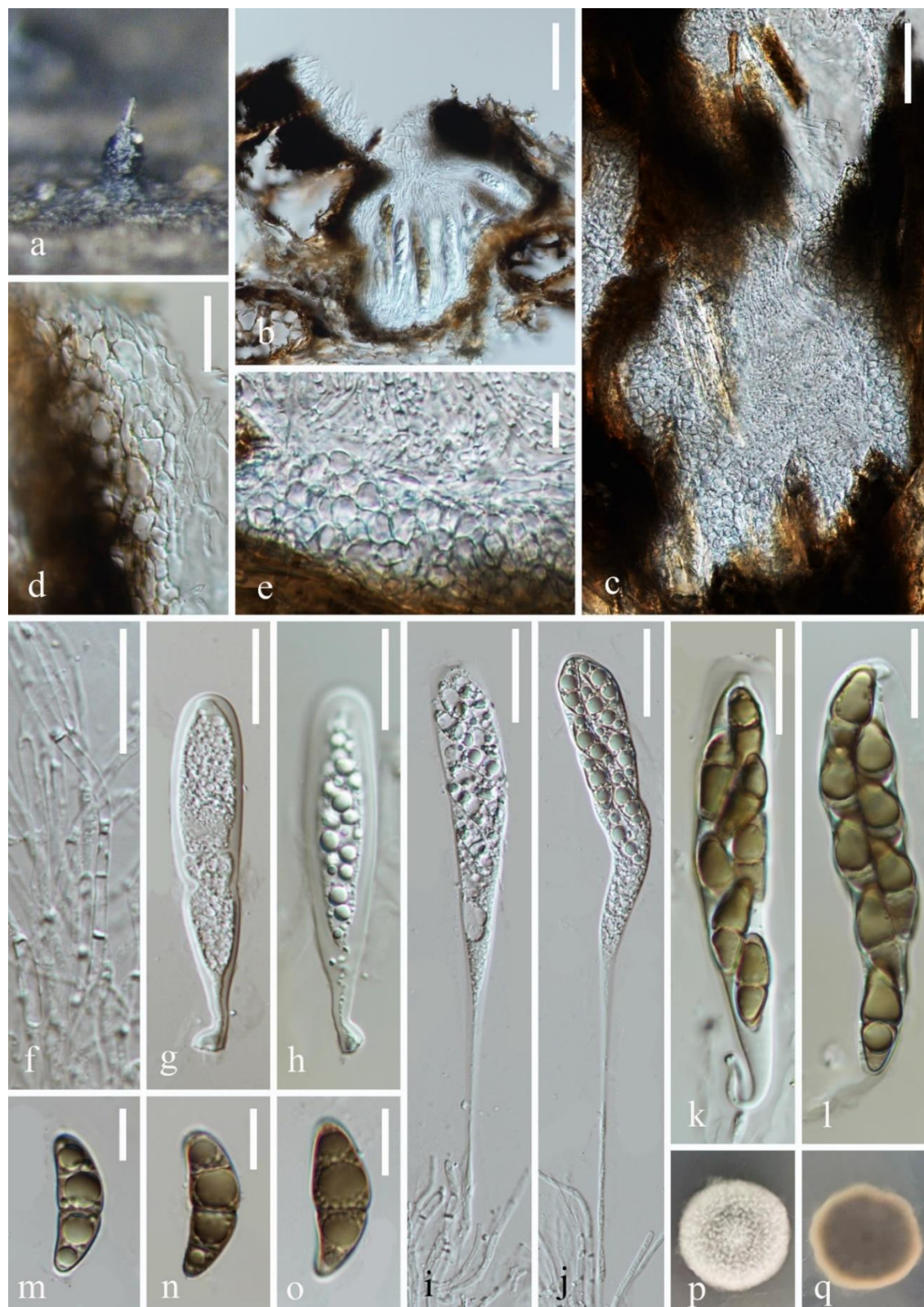


Figure 17 – *Neohelicascus gallicus* (HKAS 131390). a Ascoma on the substratum. b, c Vertical section of ascomata. d, e Structure of peridium. f Pseudoparaphyses. g–l Asci. m–o Ascospores.

p, q Colony on PDA from surface and reverse. Scale bars: b, c = 50 μ m, d, f–h, k, l = 20 μ m, e = 15 μ m, i, j = 30 μ m, m–o = 10 μ m.

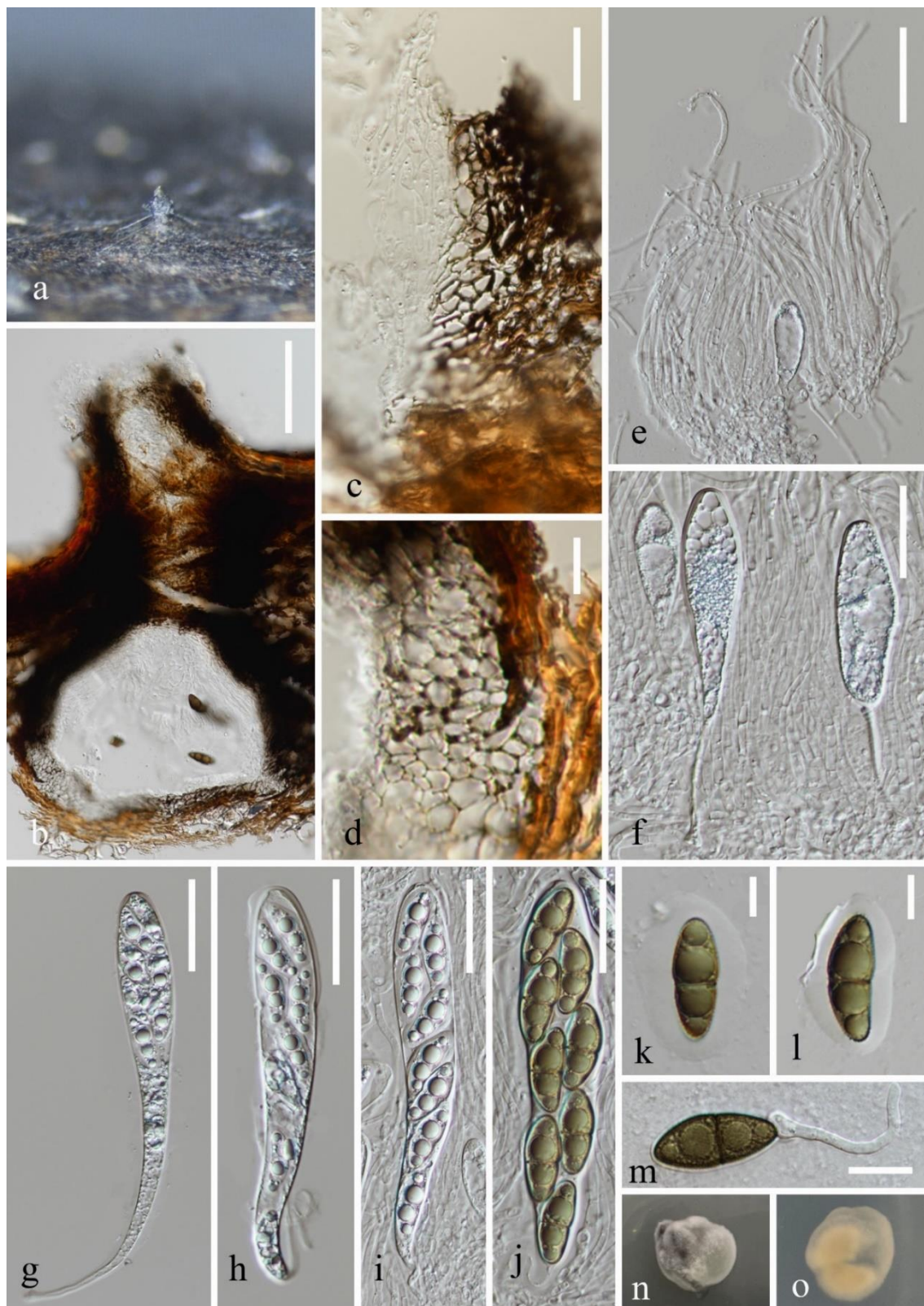


Figure 18 – *Neohelicascus submersus* (HKAS 131349). a Ascoma on the substratum. b Vertical section of ascoma. c, d Structure of peridium. e Pseudoparaphyses. f–j Asci. k, l Ascospores. m Germinating ascospore. n, o Colony on PDA from surface and reverse. Scale bars: b = 80 μ m, c = 20 μ m, d, k–m = 10 μ m, e = 50 μ m, f, j = 30 μ m, g–i = 40 μ m.

Notes – In the phylogenetic analysis (Fig. 15), our new collections (KUNCC23–13703 and KUNCC23–13742) clustered with the type strain of *Neohelicascus uniseptatus* (MFLUCC 15–0057). Moreover, our new collections match well with the description of *N. uniseptatus*. We therefore identified our new collections as *N. uniseptatus*, a species which was introduced by Luo et al. (2016) on submerged wood in Chiang Rai Province, Thailand. In this study, the fungus was collected from China for the first time.

Occultibambusaceae D.Q. Dai & K.D. Hyde

Dai et al. (2017) established *Occultibambusaceae* to accommodate two new genera *Occultibambusa* and *Seriascoma*, as well as two known genera *Versicolorisporium* and *Neooccultibambusa* (Hatakeyama et al. 2008, Doilom et al. 2017), based on morphological and phylogenetic analysis. Then, Phookamsak et al. (2019) added a new genus *Brunneofusispora* to this family. And all above five genera were accepted in *Occultibambusaceae* in recent study (Yu et al. 2021).

Occultibambusa D.Q. Dai & K.D. Hyde

Occultibambusa was introduced by Dai et al. (2017) to accommodate three new species that associated on decaying bamboo culms, with *O. bambusae* as the type. Ten species are accepted in this genus, and all species were isolated from *Bambusoideae* (Hyde et al. 2016b, Zhang et al. 2017a, Jiang et al. 2021a, Yu et al. 2021).

Occultibambusa clavata W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.

Fig. 21

Index Fungorum number: IF902424; Facesoffungi number: FoF16097

Etymology – Referring to the clavate asci of this fungus.

Holotype – HKAS 131377

Saprobic on submerged stem of *Bambusoideae*. Asexual morph: Undetermined. Sexual morph: *Ascomata* 210–350 µm diam, 190–260 µm high., scattered, semi-immersed, visible as black ellipsoidal on host surface, uniloculate, flat spheroids. *Ostiole* papillate, central, cylindrical, periphysate. *Peridium* 9.3–50 µm thick, thinning around the ostiole, cortex of host, coriaceous, consisting of several layered pale brown to brown, irregular or nearly oval cells of *textura angularis*. *Hamathecium* composed of dense, 1.8–4 µm wide, subcylindrical, hyaline to brown, transversely septate, branched pseudoparaphyses. *Asci* 60–130 × 17–21 µm ($\bar{x}$ = 86.1 × 19.1 µm, n = 15), 8-spored, bitunicate, fissitunicate, clavate, slightly curved, mostly with a short pedicel or elongates after discharge (up to 60 µm long), broadly rounded apical with an ocular chamber. *Ascospores* 25–31 × 6.4–8.7 µm ($\bar{x}$ = 28.1 × 7.5 µm, n = 30), overlapping, biseriate, hyaline when young, pale olive when mature, fusiform with acute ends, straight or slightly curved, apical cell slightly larger than the basal cell, mostly uniseptate, septate central, slightly constricted at the septum, guttulate, smooth-walled.

Culture characteristic – Ascospores germinating on PDA within 12 h, and germ tubes produced from the both ends. Colonies on the malt extract agar (MEA) reaching 25 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of MEA, with regular edges, velvety, white. Reverse circular, brown to dark brown, with white edges, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged dead stem of *Bambusoideae* species, 7 February 2022, W.P. Wang, S-3263 (HKAS 131377, holotype), ex-type living cultures CGMCC 3.25424 = KUNCC 23–14577.

Notes – In the phylogenetic analysis, *Occultibambusa clavata* (CGMCC 3.25424) constitutes an independent lineage that is basal to *O. aquatica*, *O. bambusae*, *O. chiangraiensis*, *O. jonesii*, *O. kunmingensis* and *O. pustula* with 100% ML/1.00 PP support (Fig. 20). *Occultibambusa clavata* has larger ascospores than *O. aquatica*, *O. bambusae*, *O. chiangraiensis* and *O. pustula* (Dai et al. 2017, Hyde et al. 2016b, Jiang et al. 2021a). *Occultibambusa clavata* differs from *O. jonesii* in having thinning peridium around the ostiole, shorter, but broader ascospores (25–31 × 6.4–8.7 vs. 27–33.5

$\times 5.5\text{--}6.5\mu\text{m}$) (Zhang et al. 2017a). *Occultibambusa clavata* has dense hamathecium and shorter asci ($60\text{--}130 \times 110\text{--}140\text{--}160\ \mu\text{m}$) with broad rounded apical, which is different from *O. kunmingensis* (Dong et al. 2020). We therefore identify *O. clavata* as a new species.



Figure 19 – *Neohelicasus uniseptatus* (HKAS 131394). a Ascomata on the substratum. b Vertical section of ascoma. c, d Structure of peridium. e Pseudoparaphyses. f–i Asci. j–m Ascospores. n Germinating ascospore. o, p Colonies on PDA from surface and reverse. Scale bars: b = 100 μm , c, j–n = 10 μm , d = 15 μm , e, f = 20 μm , g–i = 30 μm .

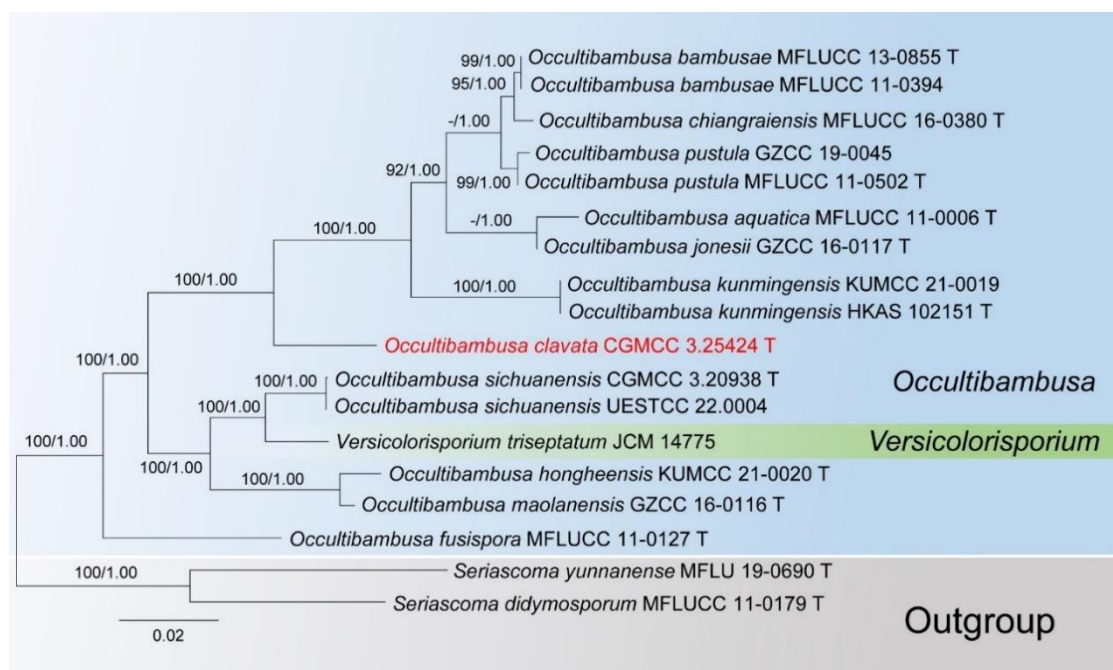


Figure 20 – RAxML tree based on analysis of *Occultibambusa* that combined LSU, SSU, *tef1-α*, ITS, and *rpb2* dataset. The combined analyses include 18 strains with 4302 characters including gaps (LSU: 853 bp, SSU: 986 bp, *tef1-α*: 930 bp, ITS: 566 bp, and *rpb2*: 967 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Seriascoma didymosporum* (MFLUCC 11–0179) and *S. yunnanense* (MFLU 19–0690). The new collection is indicated in red. Ex-type strains are indicated with “T” after the strain number.

***Periconiaceae* Nann**

Periconiaceae was introduced by Nannizzi (1934), and typified by *Periconia*, which is the largest genus of *Periconiaceae*. Originally this family consisted of four genera, viz., *Bambusistroma*, *Flavomyces*, *Noosia*, and *Periconia*, and phylogenetic analysis showed that *Bambusistroma*, *Flavomyces* and *Noosia* clustered within *Periconia* species (Liu et al. 2017, Thambugala et al. 2017, Hyde et al. 2018, Jayasiri et al. 2019, Phookamsak et al. 2019). Yang et al. (2022) treated *Bambusistroma* and *Noosia* as synonyms of *Periconia* based on characteristics and phylogenetic analyses. *Flavomyces* was introduced by Knapp et al. (2015) in root of *Festuca vaginata*, which no corresponding morphological characteristics are provided, and in phylogenetic study, *Flavomyces* species always clustered with *Periconia* species. Therefore, it is difficult to explain that *Flavomyces* and *Periconia* belong to different genera.

***Periconia* Tode**

Periconia was introduced by Tode (1791) and typified by *P. lichenoides*. Most species in the genus are known by the asexual morphs that characterized by reduced or macronematous, mononematous, septate, apically branched or unbranched conidiophores, monoblastic to polyblastic, integrated or discrete conidiogenous cells, and catenate or solitary, aseptate, globose to subglobose, or fusoid-ellipsoidal conidia (Jayawardena et al. 2022, Yang et al. 2022). While, five species, viz., *P. didymosporum*, *P. homothallica*, *P. igniaria*, *P. prolifica*, and *P. pseudodigitata* have been documented with sexual morphs, which are characterized by scattered or grouped, globose ascomata with a central ostiole, oblong to cylindrical, short-pedicellate asci, and hyaline, fusiform, septate ascospores with an entire sheath (Adamčík et al. 2015, Tanaka et al. 2015, Hongsanant et al. 2020). *Periconia* species are commonly saprobic on plant substrates from terrestrial habitats, with only a few species known from freshwater habitats (Tanaka et al. 2015, Dong et al. 2020, Yang et al. 2022).

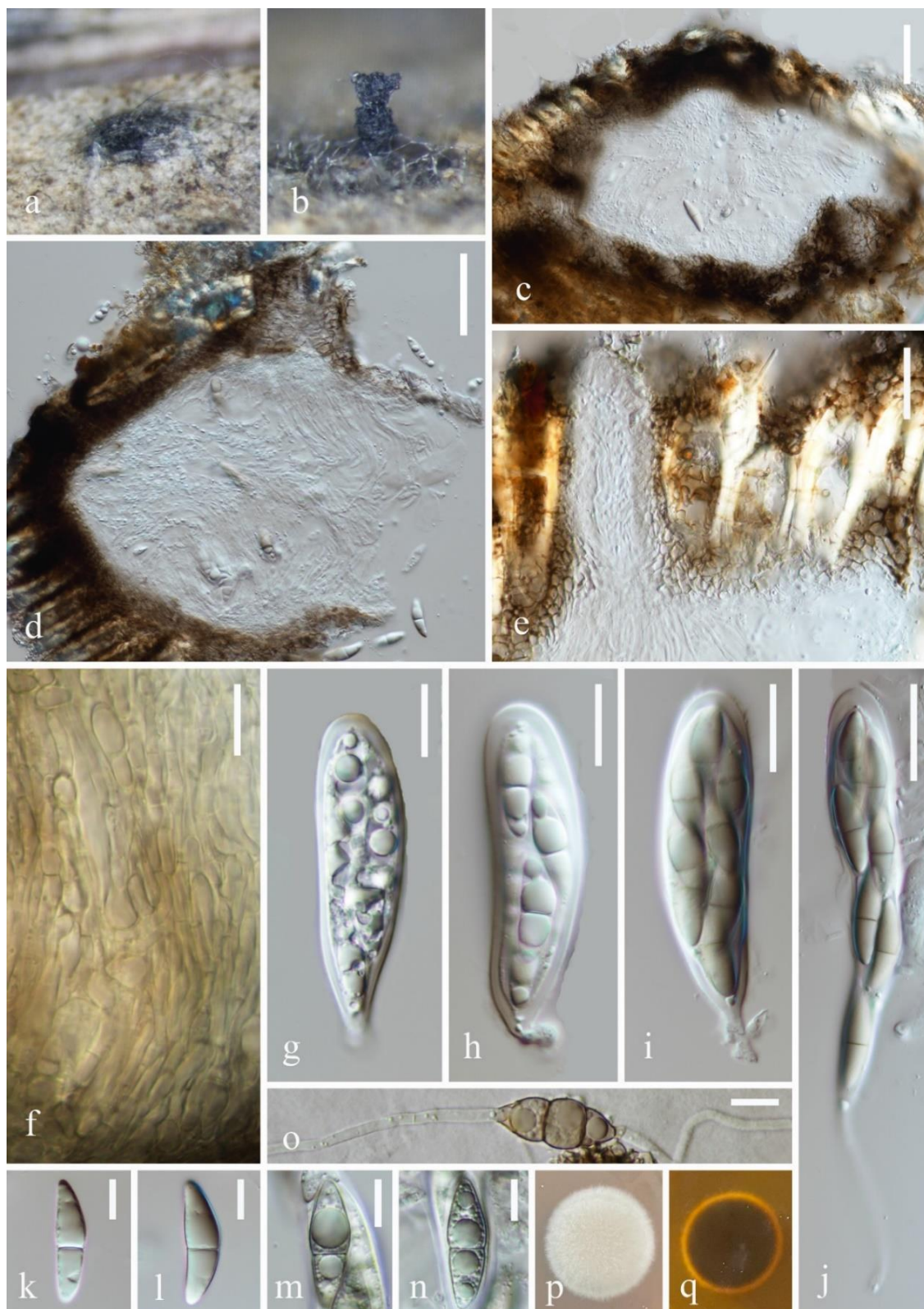


Figure 21 – *Occultibambusa clavata* (HKAS 131377, holotype). a, b Ascomata on the substratum. c, d Vertical section of ascomata. e Structure of ostiole and peridium. f Hamathecium. g–j Asci. k–n Ascospores. o Germinating ascospore. p, q Colony on MEA from surface and reverse. Scale bars: c, d = 50 μ m, e = 30 μ m, f–i = 15 μ m, j = 20 μ m, k–o = 10 μ m.

Periconia thysanolaenae E.F. Yang, H.B. Jiang and Phookamsak, J. Fungi 8, 243, 24 (2022)

Fig. 23

Index Fungorum number: IF559499; Facesoffungi number: FoF16122

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, scattered, effuse, hairy, brown, with loose conidia clump in the apex of conidiophores. *Mycelium* partly superficial, partly immersed, composed of branched, septate, smooth, brown hyphae. *Conidiophores* 130–240 × 3.5–6.4 µm ($\bar{x}$ = 179.7 × 4.8 µm, n = 10), macronematous, mononematous, solitary, straight or slightly flexuous, septate, brown to dark brown, smooth to minutely verrucose, thick-walled, occasionally branched at the apex. *Conidiogenous cells* 4.2–5.9 × 3.4–5.4 µm ($\bar{x}$ = 5 × 4.1 µm, n = 10), polyblastic, integrated, terminal, ovoid to subglobose, brown, proliferating. *Conidia* 4–6 × 3.9–5.7 µm ($\bar{x}$ = 4.9 × 4.6 µm, n = 40), catenate or solitary, globose, pale brown to dark brown, aseptate, slightly verrucose, thin-walled. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the surface. Colonies on PDA reaching 25 mm diameter after 2 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, fluffy, white, velvet. Reverse brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3277 (HKAS 131352), living culture KUNCC 23–13708.

Notes – Phylogenetic analysis showed that our new collection (KUNCC23–13708) clustered with the type strain of *Periconia thysanolaenae* (KUMCC 20–0262) with 97% ML/1.00 PP support (Fig. 22). Our new collection fits well with the description of *P. thysanolaenae* in having conidiophores that are branched at the apex, polyblastic, terminal, ovoidal to subglobose conidiogenous cells and small (4–6 × 3.9–5.7 vs. 4.5–6 × 4–6 µm), catenate or solitary, globose, aseptate, rough-walled conidia. Comparison of the LSU, ITS, SSU, and *tef1-α* sequences of our new collection and the holotype of *P. thysanolaenae* showed 99.49% (785/789 bp, two gaps), 99.81% (512/513 bp, one gaps), 100% (1002/1002 bp) and 99.89% (896/897 bp) similarity, respectively. *Periconia thysanolaenae* was introduced by Yang et al. (2022) on dead culms of *Thysanolaena latifolia* (*Poaceae*) in Yunnan Province, China. This is the first report of this species from a freshwater habitat.

***Tetraplosphaeriaceae* Kaz. Tanaka & K. Hiray.**

Tetraplosphaeriaceae was established by Tanaka et al. (2009) to accommodate *Polyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Tetraplosphaeria* (anamorphs of *Tetraploa*), and *Triplosphaeria*, with *Tetraplosphaeria* as the type genus. Later, Hyde et al. (2013) treated *Tetraplosphaeria* as a synonym of *Tetraploa*. Currently, nine genera are accepted in this family, and species of this family are widely distributed in terrestrial and freshwater habitats (Tanaka et al. 2009, Dong et al. 2020, Hongsanan et al. 2020, Bao et al. 2021, Li et al. 2021a, Tang et al. 2023, Liao et al. 2024).

***Tetraploa* Berk. & Broome**

Tetraploa was introduced by Berkeley & Broome (1850), with *T. aristata* as the type species. Species of this genus are characterized by small globose to subglobose ascomata, cylindrical to clavate asci, narrowly fusiform, uniseptate ascospores with an appendage-like sheath in sexual morph; absent conidiophores, monoblastic conidiogenous cells, and short-cylindrical, brown, verrucose, euseptate, composed of 2–4 columns conidia with setose appendages at the apex in asexual morph (Tanaka et al. 2009, Dong et al. 2020, Jayawardena et al. 2022). Most *Tetraploa* species were reported as asexual morph and showing little morphological differences, which are mainly identified by the size and appendages of conidia and multi-gene phylogenetic analysis.

***Tetraploa longiappendiculata* W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.**
Fig. 25

Index Fungorum number: IF902426; Facesoffungi number: FoF16098

Etymology – Referring to the conidia with longer appendages of this fungus.

Holotype – HKAS 131398

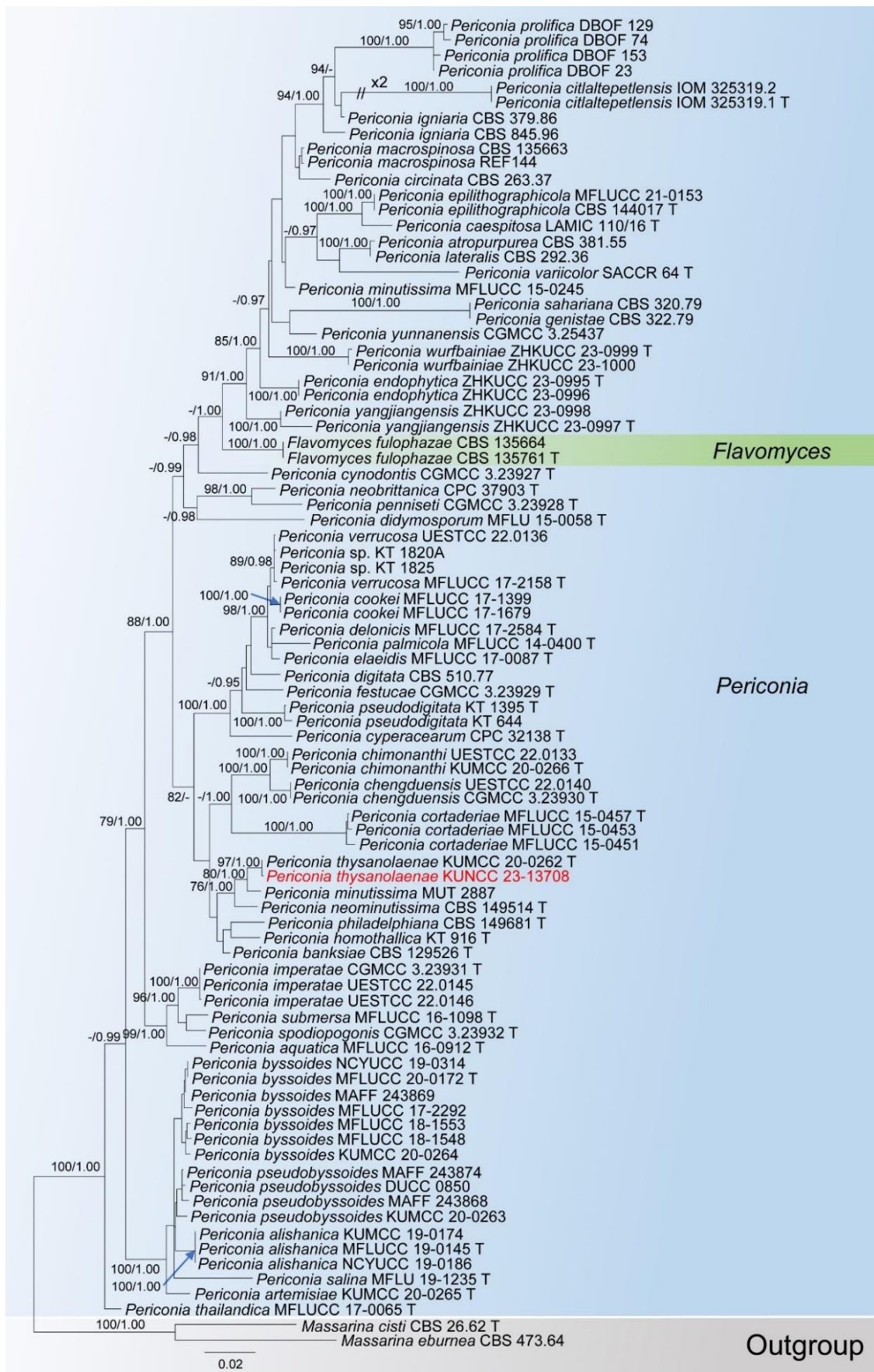


Figure 22 – RAxML tree based on analysis of *Periconia* that combined LSU, ITS, *tef1-α*, and SSU dataset. The combined analyses include 86 strains with 3216 characters including gaps (LSU: 830 bp, ITS: 502 bp, *tef1-α*: 874 bp, and SSU: 1010 bp). Bootstrap support values for maximum

likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Massarina cisti* (CBS 266.62) and *M. eburnea* (CBS 473.64). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.



Figure 23 – *Periconia thysanolaenae* (HKAS 131352). a Colony on the substratum. b Conidiophore. c–e Conidiophores with conidia. f–h Conidiogenous cells and conidia. i Conidia. j Germinating conidium. k, l Colonies on PDA from surface and reverse. Scale bars: b–d = 50 μ m, e = 30 μ m, f, g, j = 10 μ m, h = 15 μ m, i = 5 μ m.

Saprobic on submerged decaying wood. Asexual morph: *Colonies* effuse, dark brown, messy. *Mycelium* superficial, composed of branched, septate, smooth, subhyaline hyphae. *Conidiophores* absent. *Conidiogenous cells* indistinct. *Conidia* $26\text{--}39 \times 16\text{--}32\ \mu\text{m}$ ($\bar{x} = 33.7 \times 24.3\ \mu\text{m}$, $n = 30$), nearly short cylindrical, narrow at the base, solitary, straight, inconspicuous euseptate, verrucose, brown to dark brown, rarely guttulate, composed of 3–4 columns when mature, 3–4-septate in each column, with 3–4 appendages. *Appendage* $110\text{--}180\ \mu\text{m}$ long ($\bar{x} = 140.4\ \mu\text{m}$, $n = 20$), $4.6\text{--}8.4\ \mu\text{m}$ wide at the base, $1.2\text{--}3.1\ \mu\text{m}$ wide at the apex, green to brown, euseptate, smooth, straight, rigid, guttulate. Sexual morph: Undetermined.

Culture characteristics – *Conidia* germinating on PDA within 12 h, and germ tubes produced from the apex of appendage. Colonies on PDA reaching 15 mm diameter after 2 weeks of incubation at room temperature. *Mycelium* dry, dense, colonies on the surface of PDA, with regular edges, circular, with protuberance, grey to brown. Reverse circular, edges are grey and the center is brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4338 (HKAS 131398, holotype), ex-type living cultures CGMCC 3.25433 = KUNCC 23–13397.

Notes – The phylogenetic analysis showed that *Tetraploa longiappendiculata* (CGMCC 3.25433) is sister to *Tetraploa* sp. (KT 2578) with 100 ML/1.00 PP support (Fig. 24). *Tetraploa* sp. (KT 2578) was introduced by Tanaka et al. (2009). This specimen has a similar morphology to *T. ellisii* and *T. sasicola* (basionym: *Tetraplosphaeria sasicola*), but Tanaka et al. (2009) did not give a definitive identification of this specimen. *Tetraploa longiappendiculata* is different from *Tetraploa* sp. (KT 2578) in having smaller conidia ($26\text{--}39 \times 16\text{--}32$ vs. $38\text{--}50 \times 22\text{--}33\ \mu\text{m}$), and shorter ($110\text{--}180$ vs. $142\text{--}330\ \mu\text{m}$) appendages (Tanaka et al. 2009). *Tetraploa longiappendiculata* can be distinguished from *T. ellisii* by the number of conidial columns (3–4 vs. 4) and shorter conidia ($26\text{--}39$ vs. $30\text{--}51\ \mu\text{m}$).

***Torulaceae* Corda**

Torulaceae was introduced by Sturm (1829), and typified by *Torula*. Crous et al. (2015a) provided phylogenetic analysis for the first time to resolve the classification of *Torulaceae*, and accepted two genera, *Dendryphion* and *Torula* in this family. Later, five other genera, *Cylindrotorula*, *Neotorula*, *Rostriconidium*, *Rutola*, and *Sporidesmioides* were added to *Torulaceae* (Li et al. 2016, Su et al. 2016, 2018, Crous et al. 2020, Boonmee et al. 2021). Qiu et al. (2022) combined *Rostriconidium* and *Sporidesmioides* as synonyms of *Neopodoconis* based on morphology and phylogeny. The family currently comprises six genera, viz., *Cylindrotorula*, *Dendryphion*, *Neopodoconis*, *Neotorula*, *Rutola*, and *Torula*. There is no sexual morph reported for this family.

***Dendryphion* Wallr.**

Dendryphion was introduced by Wallroth (1833), with *D. comosum* as the type species. The genus is characterized by erect, polytretic, apically branched, septate, pigmented, thick-walled conidiophores with finely roughened stipe and a distinct conidiogenous apparatus, and catenate, septate conidia formed in simple or branched chains (Su et al. 2016, Li et al. 2020a, Boonmee et al. 2021). Species of *Dendryphion* are saprobic on dead stems and leaves from terrestrial and freshwater habitats (Crous et al. 2014, Su et al. 2016, Li et al. 2020a). There are 85 epithets of *Dendryphion* listed in Index Fungorum (2024), but only 36 species are accepted in *Dendryphion* (Species Fungorum 2024), with only seven species having DNA sequence data (Li et al. 2020a, Boonmee et al. 2021).

Dendryphion hydei J.F. Li, Phookamsak & Jeewon, PLoS One 15(2), 6 (2020)

Fig. 27

Index Fungorum number: IF556746; Facesoffungi number: FoF04574

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, hairy, brown to dark brown. *Mycelium* mostly immersed, composed of branched, septate, pale brown to brown hyphae. *Conidiophores* $330\text{--}415 \times 9.1\text{--}13\ \mu\text{m}$ ($\bar{x} = 380.6 \times 10.2\ \mu\text{m}$, $n = 10$), macronematous,

mononematous, septate, straight or slightly flexuous, cylindrical, thick-walled, with several branches near the apex, brown to dark brown. *Conidiogenous cells* 6.3–11 × 4.2–6.6 µm ($\bar{x}$ = 8.3 × 5.1 µm, n = 20), polytretic, terminal, integrated, doliiform, pale brown. *Conidia* 19–67 × 6.3–9.1 µm ($\bar{x}$ = 44.3 × 7.2 µm, n = 30), acrogenous, solitary or occasionally catenate, monilioid composed subglobose cells, pale brown to brown, slightly paler at the basal cells, dry, verrucose, 8–16-septate, constricted at the septum. *Conidial secession* schizolytic. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from both ends. Colonies on PDA reaching 30 mm diameter after 2 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edge, with protuberance at the center, circular, white to grey. Reverse circular, edges white and the center is dark brown, smooth.

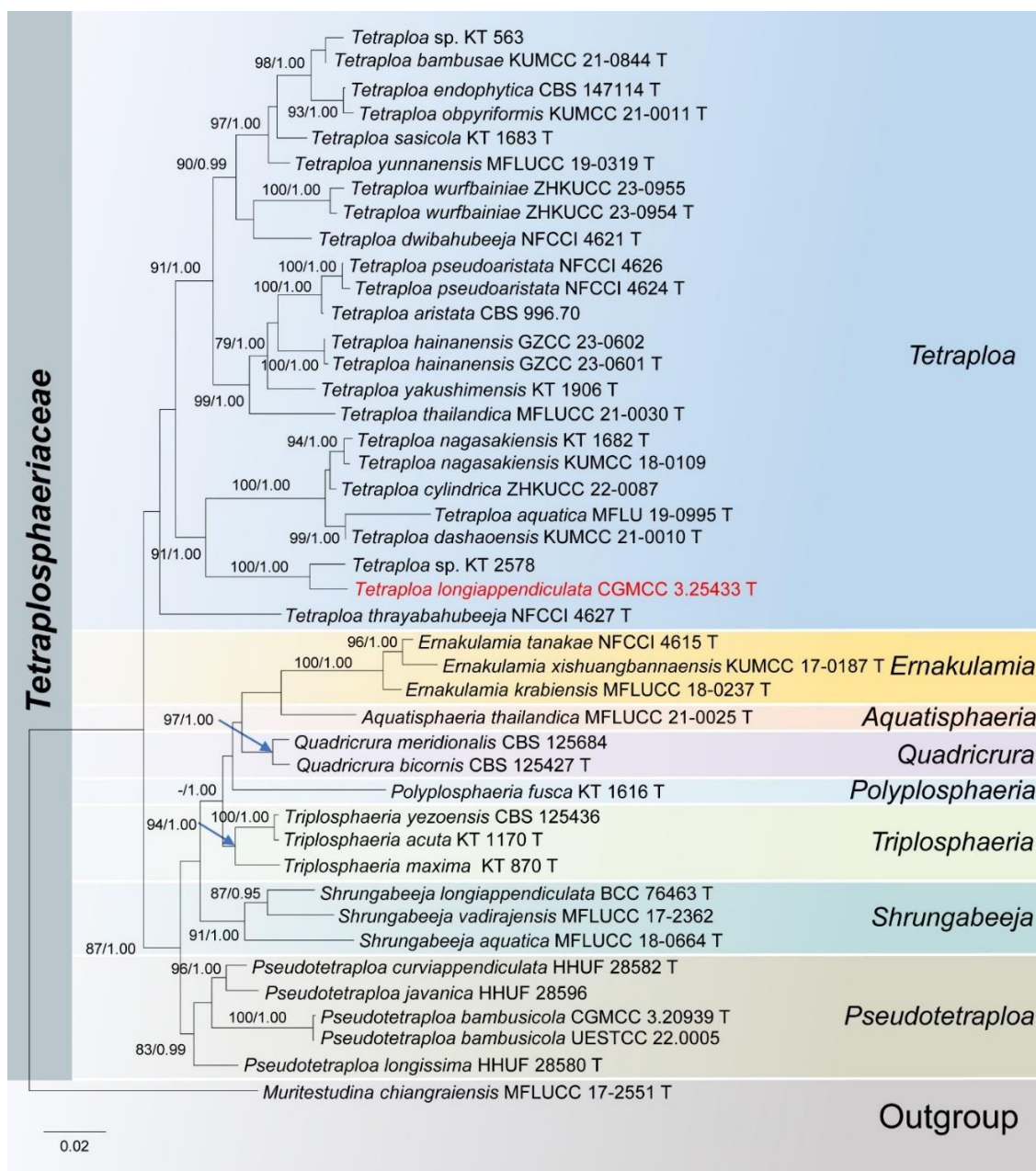


Figure 24 – RAxML tree based on analysis of *Tetraplosphaeriaceae* that combined LSU, ITS, and SSU dataset. The combined analyses include 43 strains with 2358 characters including gaps (LSU: 844 bp, ITS: 523 bp, and SSU: 991 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Muritestudina chiangraiensis* (MFLUCC 17-2551). The new collection is indicated in red. Ex-type strains are indicated with “T” after the strain number.



Figure 25 – *Tetraploa longiappendiculata* (HKAS 131398, holotype). a Colonies on the substratum. b–f conidia. g Germinating conidium. h, i Colonies on PDA from surface and reverse. Scale bars: b, c = 15 µm, d–g = 30 µm.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, H-705 (HKAS 130440).

Notes – Our new collection is indistinguishable from *Dendryphion hydei*, and phylogenetic analysis showed that our new collection (HKAS 130440) clustered with two strains of *D. hydei* (Fig. 26). We therefore identified our collection as *D. hydei*. *Dendryphion hydei* was introduced by Li et al. (2020a) and collected from a branch litter of *Bidens pilosa* in Chiang Mai Province, Thailand. Boonmee et al. (2021) reported this fungus from freshwater habitat in China.

***Torula* Pers.**

Persoon (1794) established *Torula*, with *T. herbarum* as the type. Species of this genus are only known by the hyphomycetous asexual morphs, which are characterized by reduced or micronematous or semi-macronematous, mononematous conidiophores, terminal or lateral, monoblastic or polyblastic conidiogenous cells, and monilioid conidia (Crous et al. 2015a, Crane & Miller 2016, Su et al. 2018, Hyde et al. 2017, 2019). Currently, over 500 species epithets of this genus are listed in Index Fungorum (2024), but most species have been transferred to other genera, and less than 30 species have corresponding molecular data (Wang et al. 2023).

Torula chinensis W.H. Tian, Y.P. Chen & Maharachch. J. Fungi 9, 150, 6 (2023) Fig. 28
Index Fungorum number: IF847014; Facesoffungi number: FoF16099

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, dense, velvety, brown to black. *Mycelium* mostly immersed, composed of septate, branched, smooth, subhyaline hyphae. *Conidiophores* 13–25 (–47) × 1.8–2.8 µm ($\bar{x}$ = 22.8 × 2.3 µm, n = 10), semi-macronematous, mononematous, erect, straight or slightly flexuous, smooth, cylindrical, pale brown to brown, septate, partly reduced to conidiogenous cells, doliiform at the apex. *Conidiogenous cells* 5.2–7.3 × 4.1–6.9 µm ($\bar{x}$ = 6.5 × 5.9 µm, n = 20), monoblastic, terminal, brown to dark brown, dry, minutely verrucose, doliiform to subglobose or cupulate. *Conidia* 15–50 (–90) × 4.3–7.9 µm ($\bar{x}$ = 32.6 × 6.3 µm, n = 50), mostly solitary, and sometimes catenate, straight or slightly curved, brown to dark brown, verrucose, dry, rounded at both ends, monilioid composed of subglobose cells, 6–17-septate, constricted at septum, guttulate. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from both ends. Colonies on PDA reaching 20 mm diameter after 2 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edge, basal layer is light brown gelatinous, and covered with white, velvety hyphae. Reverse circular, pale brown to brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, H-697 (HKAS 130434).

Notes – Phylogenetic analysis showed that our new collection clustered with *Torula chinensis* with 79% ML/0.98 PP support (Fig. 26). The LSU and ITS sequences of our new collections showed 99.88% (803/804 bp) and 99.8% (490/491 bp) similarity with the holotype of *T. chinensis*. Our new collection (HKAS 130434) resembles *T. chinensis* in having straight or slightly flexuous conidiophores with doliiform conidiogenous cells at the apex, and solitary or catenate, monilioid conidia. We therefore recognize our new collections as *T. chinensis*.

Torula fici P.W. Crous, IMA Fungus 6 (1), 192 (2015) Fig. 29
Index Fungorum number: IF816154; Facesoffungi number: FoF02712

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, powdery, dark brown to black. *Mycelium* mostly immersed, composed of branched, smooth-walled, hyaline, septate hyphae. *Conidiophores* 4–7.8 × 2.8–4.1 µm ($\bar{x}$ = 5.5 × 3.3 µm, n = 15), micronematous, with hyaline to pale brown supporting cells. *Conidiogenous cells* 3.9–5.6 × 3.7–4.3 µm ($\bar{x}$ = 4.5 × 4 µm, n = 20), mono- to polyblastic, doliiform to subglobose, brown to dark brown, paler at the base. *Conidia* 9.1–17 × 4.7–5.8 µm ($\bar{x}$ = 12.3 × 5.3 µm, n = 40), phragmosporous, acrogenous, in long branched chains, monilioid composed of subglobose cells, 2–3-septate, with dark bands at the

septum, constricted at septum, verrucose, dry, rounded at both ends, brown to dark brown. *Conidial secession* schizolytic. Sexual morph: Undetermined.

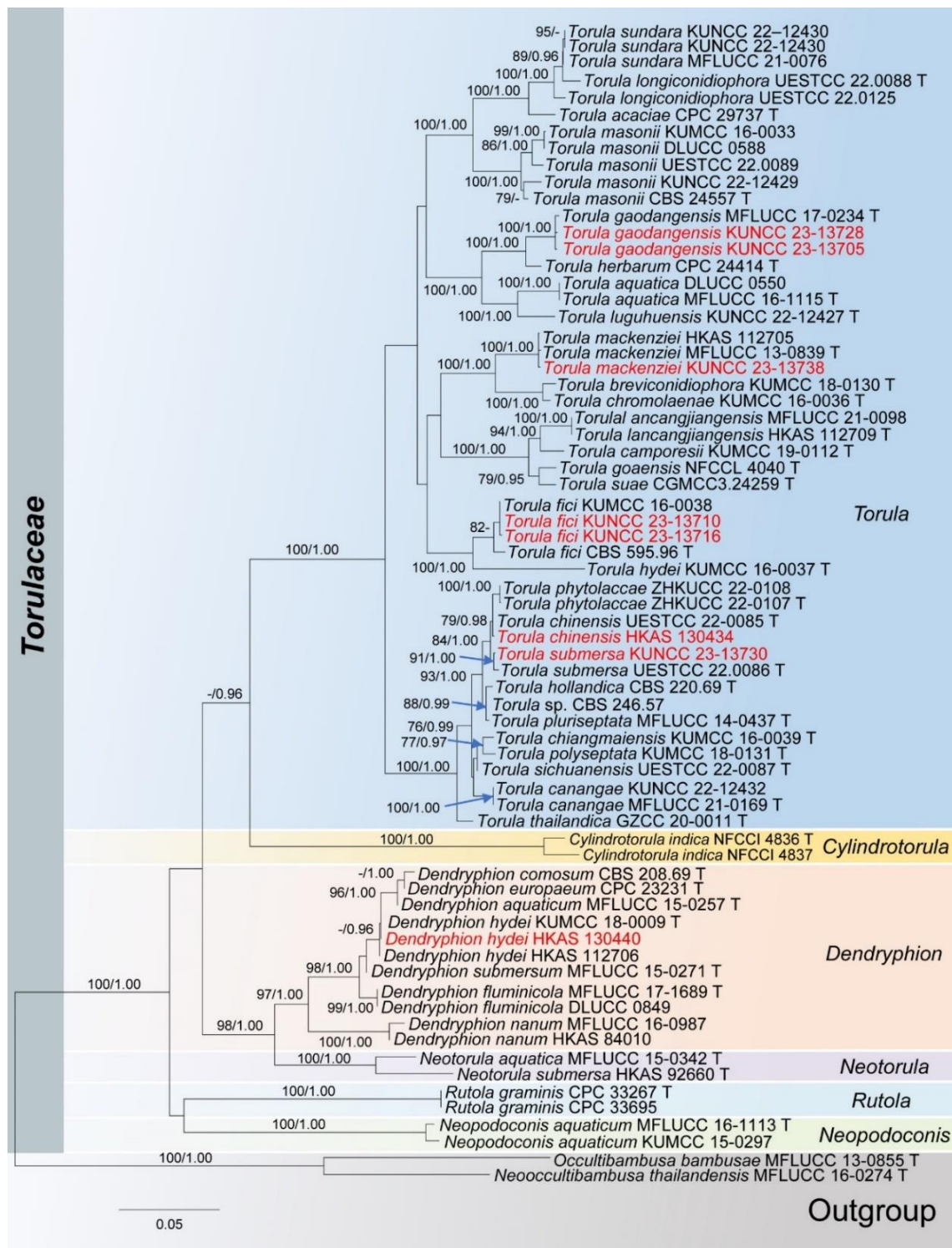


Figure 26 – RAxML tree based on analysis of *Torulaceae* that combined ITS, LSU, *tef1-α*, SSU, and *rpb2* dataset. The combined analyses include 69 strains with 4166 characters including gaps (ITS: 554 bp, LSU: 806 bp, *tef1-α*: 812 bp, SSU: 979 bp, and *rpb2*: 1015 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Neooccultibambusa thailandensis* (MFLUCC 16-0274) and *Occultibambusa bambusae* (MFLUCC 13-0855). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.



Figure 27 – *Dendryphion hydei* (HKAS 130440). a Colonies on the substratum. b Conidiophore. c Conidiophore with conidia. d Apex of conidiophore. e–i Conidia. j Germinating conidium. k, l Colonies on PDA from surface and reverse. Scale bars: b, c = 50 μ m, d = 20 μ m, e–j = 15 μ m.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the end. Colonies on PDA reaching 30 mm diameter after 2 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edge, with protuberance at the center, edges brown, gelatinous, and the center is white, velvety. Reverse brown, dark brown in central, smooth, splitting from the center.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3274 (HKAS 131367), living culture KUNCC 23–13710; *ibid.*, S-3282 (HKAS 131376), living culture KUNCC 23–13716.

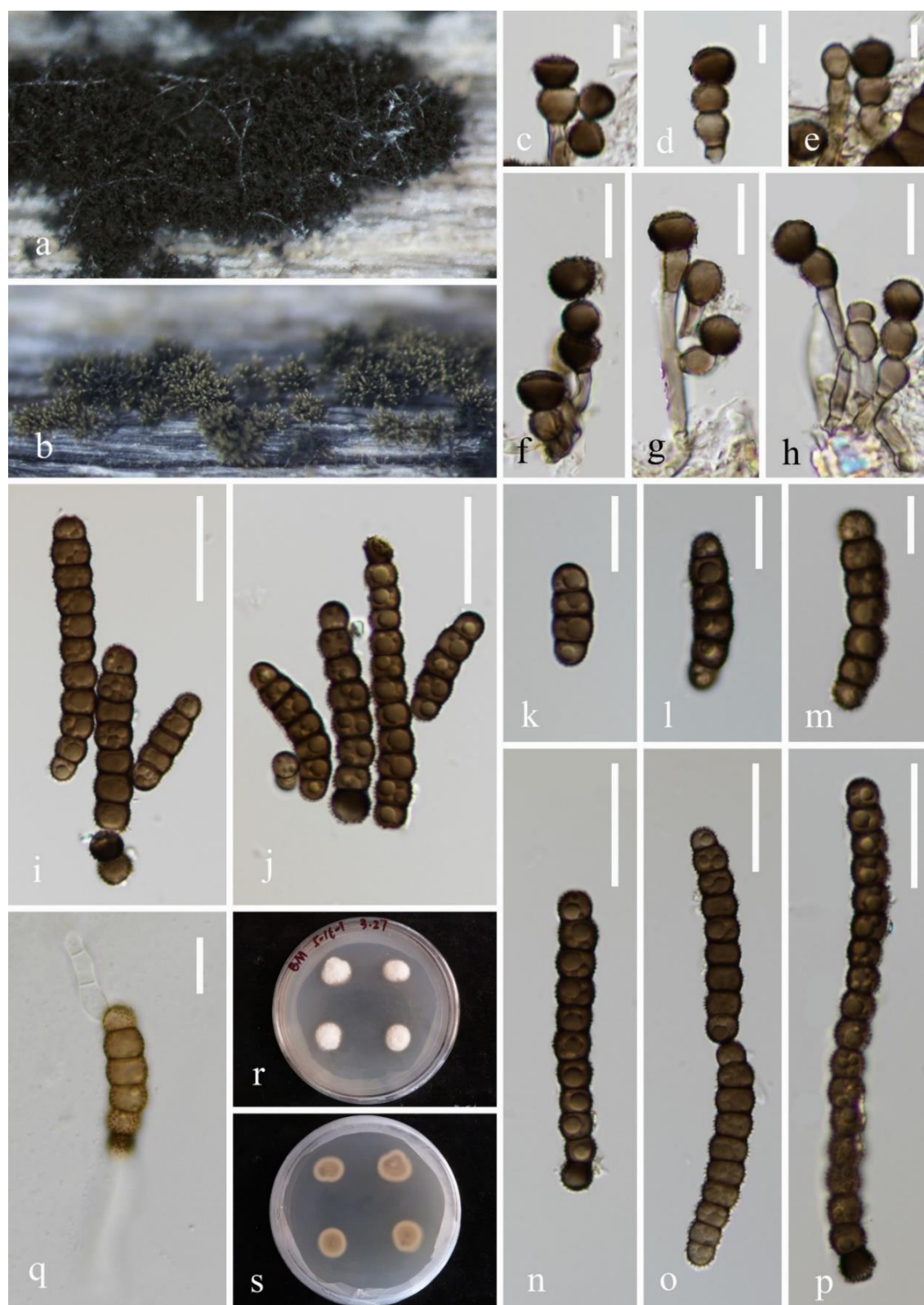


Figure 28 – *Torula chinensis* (HKAS 130434). a, b Colonies on the substratum. c–h Conidiophores with conidiogenous cells. i–p conidia. q Germinating conidium. r, s Colonies on PDA from surface and reverse. Scale bars: c–e = 5 µm, f–h, k–m, q = 10 µm, i, j, n–p = 20 µm.

Notes – In this study, two new collections of *Torula fici* were obtained from freshwater habitats in Yunnan Province, China. Morphological characteristics, such as mono-to polyblastic, doliiform conidiogenous cells and 2–3-septate conidia with dark bands at the septum match well with the concept of *T. fici* (Li et al. 2017, Su et al. 2018), and we therefore identified our isolates as *T. fici*. *Torula fici* was introduced by Crous et al. (2015a) and collected from a branch litter of *Ficus religiosa* in Cuba. Afterwards, several studies have reported this species from terrestrial and freshwater habitats in Asia (Li et al. 2017, Su et al. 2018, Tibpromma et al. 2018, Jayawardena et al. 2022).

Torula gaodangensis J. Yang & K.D. Hyde, Fungal Divers. 87, 113 (2017)

Fig. 30

Index Fungorum number: IF553199; Facesoffungi number: FoF03288

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, sparse, erect, brown to dark brown. *Mycelium* mostly immersed, composed branched, smooth-walled, hyaline to pale brown hyphae. *Conidiophores* 12–70 × 2.5–4.3 µm ($\bar{x}$ = 25.2 × 3.3 µm, n = 10), macronematous, micronematous, erect, straight or flexuous, pale brown to brown, cylindrical, septate, unbranched, thin, smooth-walled. *Conidiogenous cells* 7.2–8.2 × 5.4–7 µm ($\bar{x}$ = 7.8 × 6.1 µm, n = 30), monoblastic, integrated, terminal and intercalary, inflated, subglobose to oblate-sphaeroid, with flattened base, dark brown to black, verrucose. *Conidia* 22–31 × 7–9.1 µm ($\bar{x}$ = 27.6 × 8.2 µm, n = 30), acrogenous, solitary, brown to dark brown, subcylindrical, slightly wider at the middle cell, narrower towards the both ends cells, straight or slightly curved, 6–8-septate, constricted at the septum, apically rounded, truncate at the base, with a darkened scar connect to conidiogenous cell, verrucose, guttulate. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from both ends. Colonies on PDA reaching 40 mm diameter after 4 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edge, edges brown and the center grey, with a ring-shaped depression in the center. Reverse dark brown, smooth, splitting from the center.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3258 (HKAS 131389), living culture KUNCC 23–13705; *ibid.*, S-3285 (HKAS 131391), living culture KUNCC 23–13728.

Notes – Phylogenetic analysis showed that our new collections clustered with the ex-type strain of *Torula gaodangensis* with 99% ML/1.00 PP support (Fig. 26). Our new collections resemble *T. gaodangensis* in having monoblastic-acropetal conidiogenous cells with flattened base, and acrogenous, up to 8-septate conidia with a darkened scar connected to conidiogenous cells. Therefore, we identified our collections as *T. gaodangensis*, a species which was known from freshwater and terrestrial habitats in China (Hyde et al. 2017, 2020a).

Torula mackenziei J.F. Li, Phookamsak & K.D. Hyde, Mycol. Prog. 16, 455 (2017)

Fig. 31

Index Fungorum number: IF819537; Facesoffungi number: FoF02714

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, powdery, dark brown to black. *Mycelium* mostly immersed, partly superficial, composed of septate, branched, smooth, pale brown hyphae. *Conidiophores* 19–44 × 3–4.4 µm ($\bar{x}$ = 28 × 3.5 µm, n = 10), macronematous, mononematous, solitary, erect, minutely verrucose, brown, branched, septate, ellipsoidal to subglobose cells at the apex. *Conidiogenous cells* 5.3–7.1 × 4.3–6.4 µm ($\bar{x}$ = 6.4 × 5.3 µm, n = 10), polyblastic or monoblastic, terminal and intercalary, brown to dark brown, paler at apex, dry, ellipsoidal to subglobose. *Conidia* 11–21 × 5.1–7.2 µm ($\bar{x}$ = 16.5 × 6.1 µm, n = 40), acrogenous, catenate, formed in branched chains, monilioid composed of subglobose cells, rounded at both ends, brown to dark brown, sometimes paler at the apex, minutely verrucose, 3–4-septate, constricted at septum. *Conidial secession* schizolytic. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from one end and the second cell. Colonies on PDA reaching 20 mm diameter after 2 weeks at room

temperature. Mycelium dry, colonies on the surface of PDA, with regular edges, base layer light brown, gelatinous, and covered with white, velvety hyphae. Reverse brown, smooth, crack.

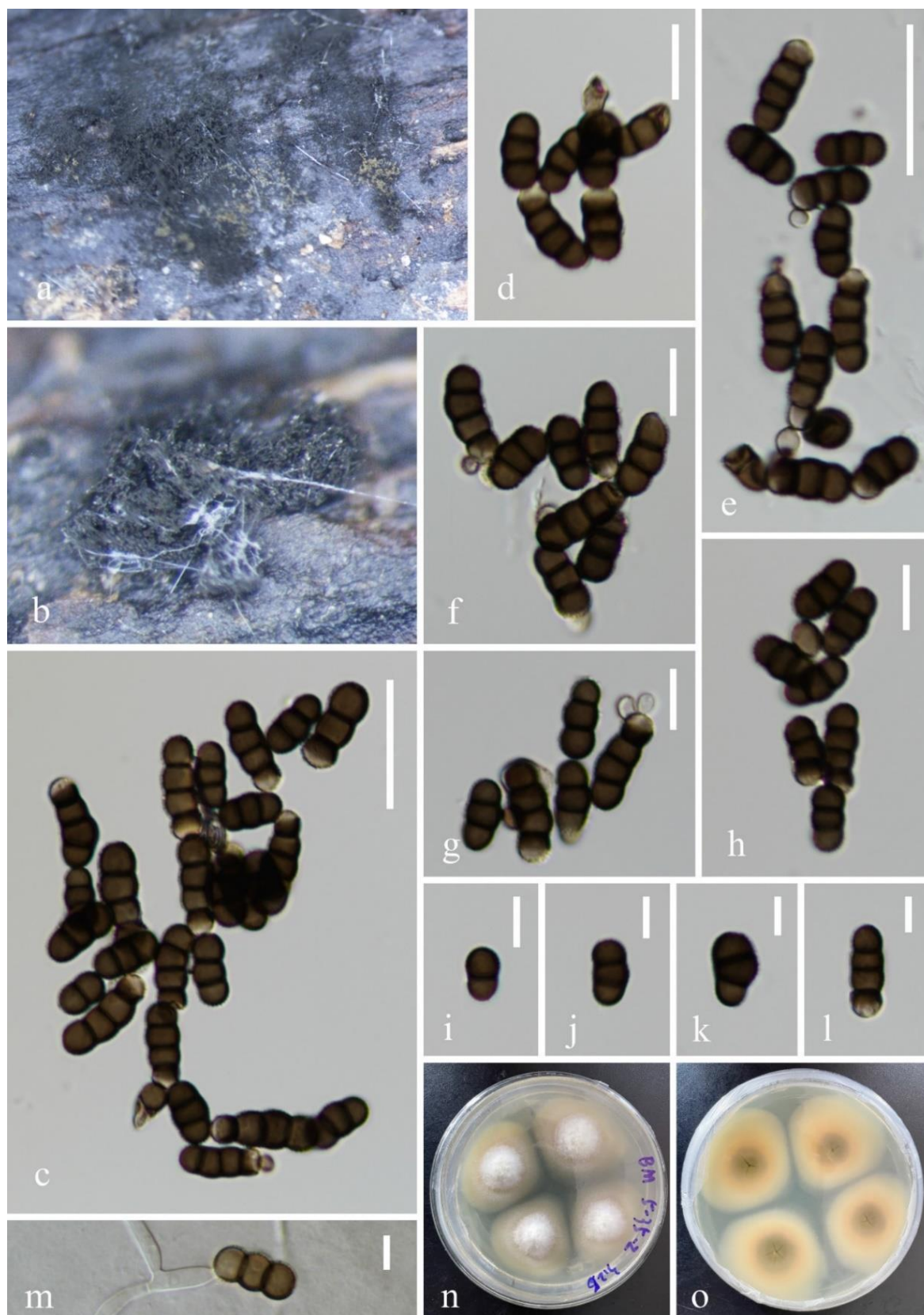


Figure 29 – *Torula fici* (HKAS 131376). a, b Colonies on the substratum. c–l Conidia. m Germinating conidium. n, o Colonies on PDA from surface and reverse. Scale bars: c, e = 20 μ m, d, f–h = 10 μ m, i–m = 5 μ m.

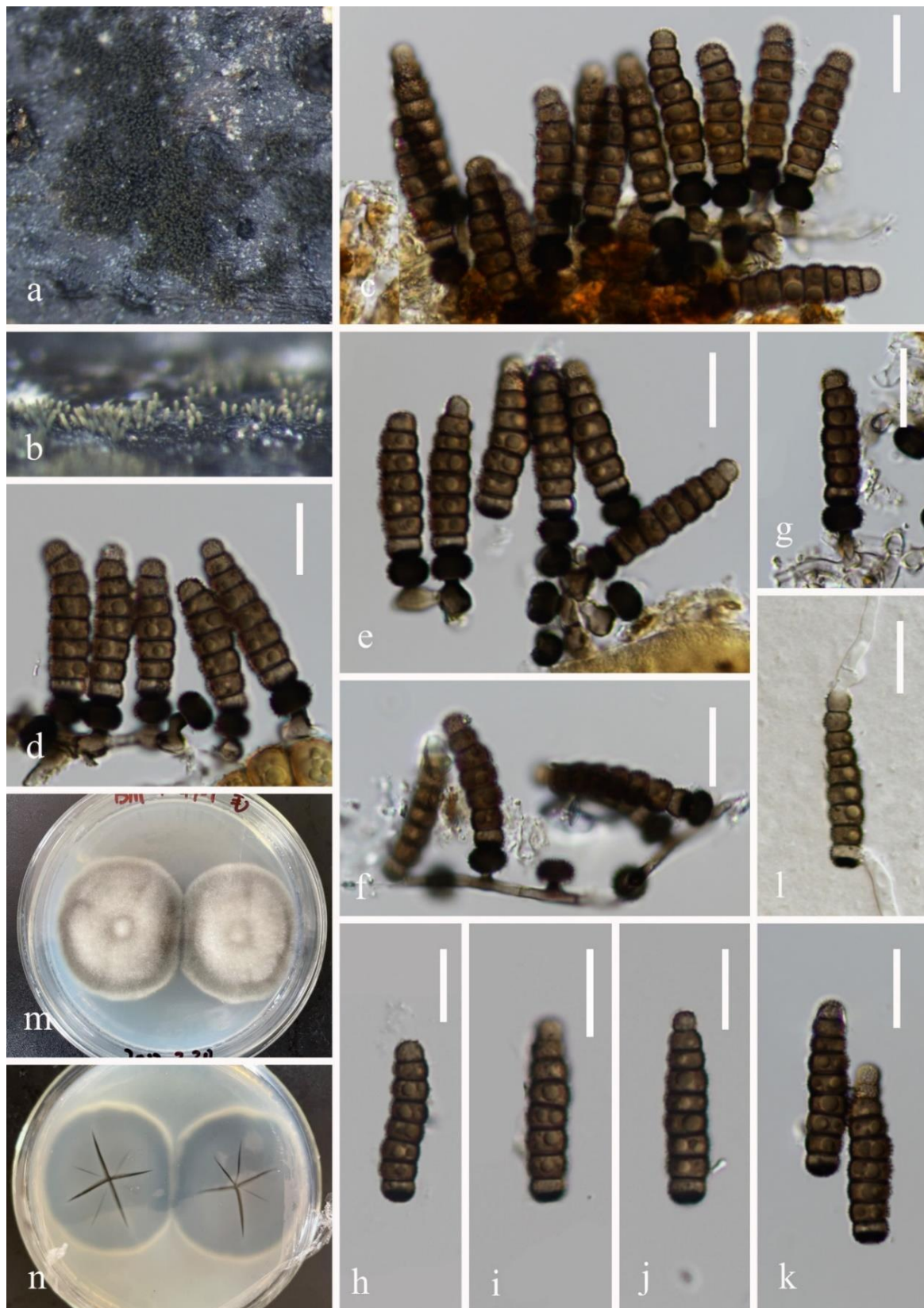


Figure 30 – *Torula gaodangensis* (HKAS 131389). a, b Colonies on the substratum. c–g Conidiophores, Conidiogenous cells with conidia. h–k Conidia. l Germinating conidium. m, n Colonies on PDA from surface and reverse. Scale bars: c–l = 15 μ m.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3488 (HKAS 131385), living culture KUNCC 23–13738.

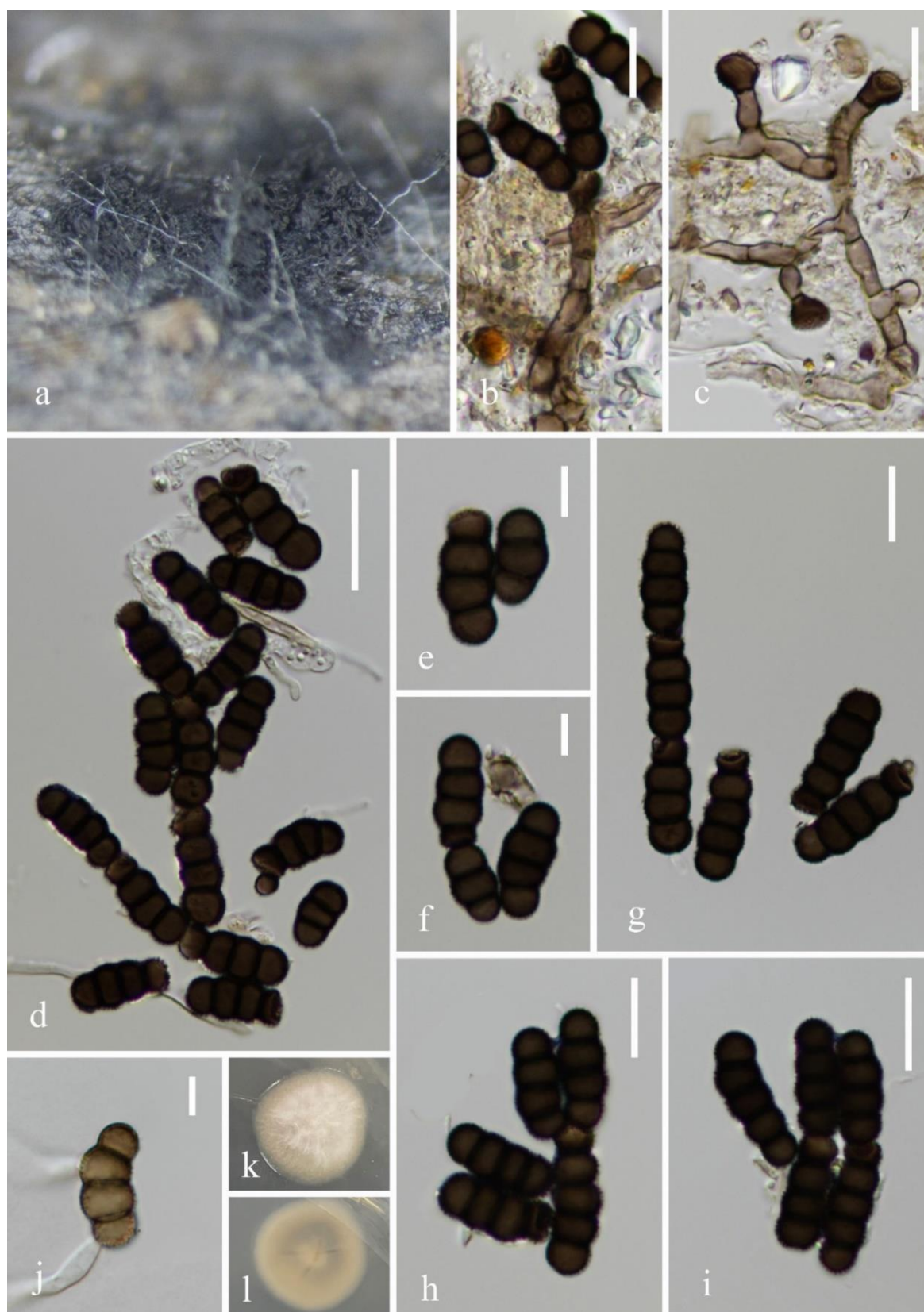


Figure 31 – *Torula mackenziei* (HKAS 131385). a Colonies on the substratum. b Conidiophore with conidia. c Conidiophore. d–i conidia. j Germinating conidium. k, l Colony on PDA from surface and reverse. Scale bars: b, c, g–i = 10 μ m, d = 20 μ m, e, f, j = 5 μ m.

Notes – In the present phylogenetic analysis, our new collection clustered with *Torula mackenziei* (MFLUCC 13–0839 and HKAS 112705) with 100% ML/1.00 PP support (Fig. 26).

Morphologically, it resembles *T. mackenziei* in having polyblastic conidiogenous cells, formed in branched chains, minutely verrucose, similar sized ($11\text{--}21 \times 5.1\text{--}7.2$ vs. $9.4\text{--}18.5 \times 4.4\text{--}4.7$ μm), monilioid conidia composed of subglobose cells (Li et al. 2017, Boonmee et al. 2021). Thus, we identified our new collection as *T. mackenziei*, a species which was introduced by Li et al. (2017) and has been reported from Thailand and China in terrestrial and freshwater habitat (Boonmee et al. 2021).

Torula submersa W.H. Tian, Y.P. Chen & Maharachch. J. Fungi 9, 150, 10 (2023) Fig. 32
Index Fungorum number: IF847013; Facesoffungi number: FoF16100

Saprobic on submerged decaying wood. Asexual morph: Colonies superficial, effuse, velvety, dark brown. Mycelium mostly immersed, composed of septate, branched, smooth-walled, hyaline hyphae. Conidiophores $4.7\text{--}8.8$ (-25) $\times$ $3.2\text{--}5.1$ μm ($\bar{x} = 9.2 \times 4.4$ μm , $n = 10$), macronematous to semi-macronematous, solitary, erect, smooth, thick-walled, brown, without apical branches, septate, ellipsoidal cells at the apex. Conidiogenous cells $6.2\text{--}7 \times 5\text{--}7$ μm ($\bar{x} = 6.8 \times 6$ μm , $n = 10$), polyblastic or monoblastic, terminal and intercalary, brown to dark brown, paler at the apex, dry, doliiform to globose, minutely verrucose. Conidia $9.7\text{--}23 \times 4.8\text{--}6.8$ μm ($\bar{x} = 17.9 \times 5.9$ μm , $n = 40$), acrogenous, phragmosporous, catenate, formed in branched chains, monilioid composed of subglobose cells, brown to dark brown, often paler at the apex, minutely verrucose, 2–5-septate, slightly constricted at septum, Conidial secession schizolytic. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from both ends. Colonies on PDA reaching 25 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edge, white to grey. Reverse circular, pale brown to brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3268 (HKAS 131364), living culture KUNCC 23–13730.

Notes – Phylogenetic analysis showed that our new collection (KUNCC 23–13730) clustered with the ex-type strain of *Torula submersa* with 92% ML/1.00 PP support (Fig. 26). Our new collection resembles *T. submersa* in having macronematous to semi-macronematous, erect conidiophores, terminal, doliiform conidiogenous cells, and catenated, acrogenous, paler at the apex and similar sized conidia ($9.7\text{--}23.1 \times 4.8\text{--}6.8$ vs. $6\text{--}20 \times 4\text{--}8$) (Tian et al. 2023). Hence, we identify our new collection (KUNCC23–13730) as *T. submersa*, which has been introduced by Tian et al. (2023) from freshwater habitat in Sichuan Province, China.

Dothideomycetes families incertae sedis

Pseudorobillardaceae Crous

Crous et al. (2014b, 2018) showed that *Pseudorobillarda* taxa are related to *Pleosporales*. Crous et al. (2019) validated *Pseudorobillardaceae* to accommodate members of *Pseudorobillarda* and placed it in *Dothideomycetes*. The taxonomic placement of *Pseudorobillardaceae* is currently unclear, phylogenetic analysis of LSU sequence data showed that *Pseudorobillarda* is distinct from *Pleosporales*. Therefore, the family is placed in *Dothideomycetes* family *incertae sedis* (Li et al. 2020b).

Pseudorobillarda M. Morelet

Morelet (1968) established the genus *Pseudorobillarda* to accommodate *P. phragmitis* (= *Robillarda phragmitis*) and *P. muhlenbergiae* (= *R. muhlenbergiae*). All species within this genus are coelomycetes, which are characterized by immersed to semi-immersed, globose to subglobose conidiomata, absence or presence hyaline, filiform paraphyses, phialidic or annellidic, cylindrical to ampulliform conidiogenous cells and subcylindrical to fusiform, aseptate or septate conidia with appendages at the one end (Tangthirasunun et al. 2014, Li et al. 2020b, Song et al. 2022). Up to date, twenty-one species are accepted in *Pseudorobillarda*, with ten species have molecular data (Li et al. 2020b, Song et al. 2022).

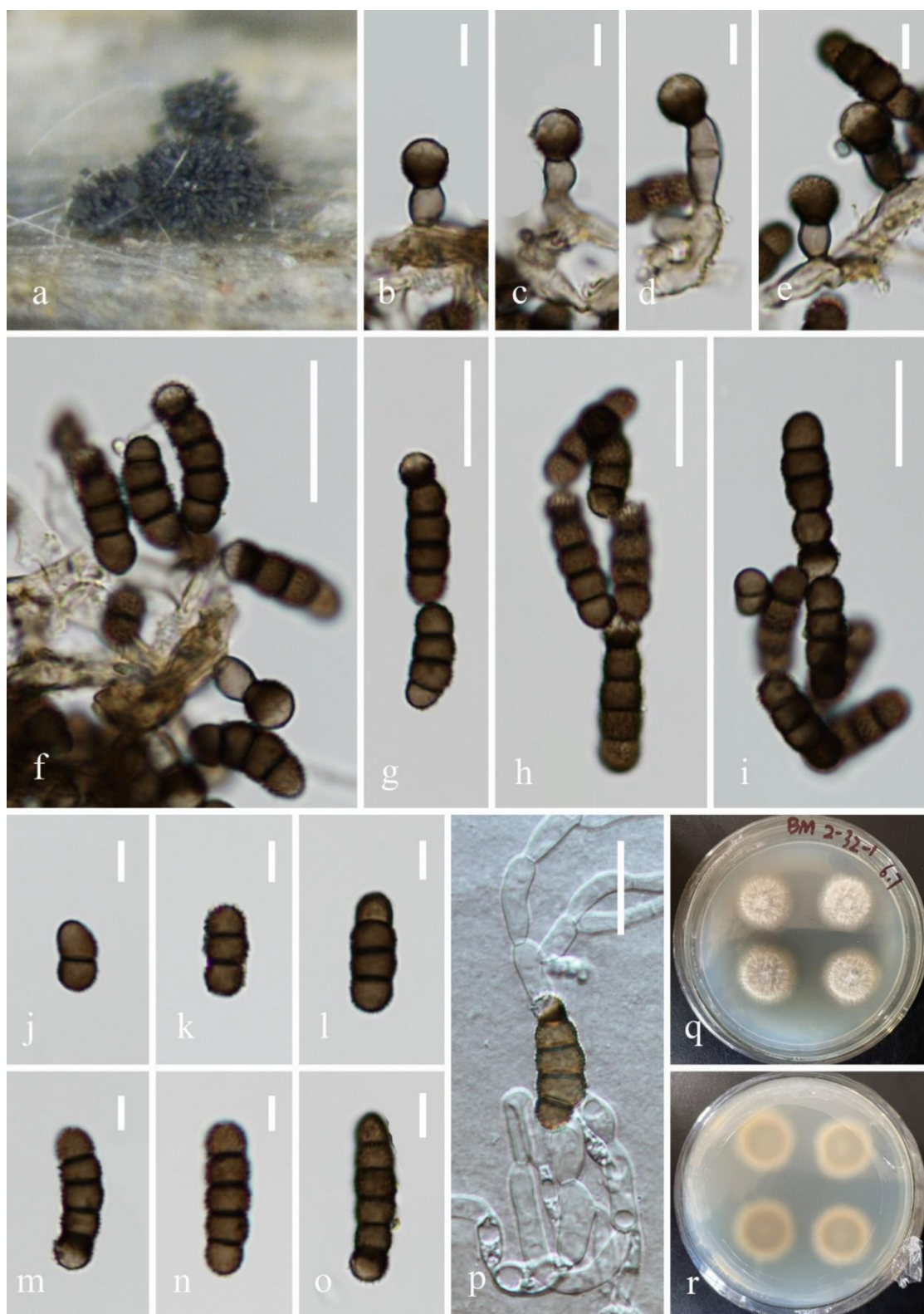


Figure 32 – *Torula submersa* (HKAS 131364). a Colonies on the substratum. b–e Conidiophores with conidiogenous cells. f Conidiophores with conidia. g–o conidia. p Germinating conidium. q, r Colonies on PDA from surface and reverse. Scale bars: b–e, j–o = 5 μ m, f = 20 μ m, g–i, p = 15 μ m.

Pseudorobillarda multiguttulata W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.

Fig. 34

Index Fungorum number: IF902427; Facesoffungi number: FoF16101

Etymology – Referring to the conidia with multiple guttulates in spores of this taxon.

Holotype – HKAS 130437

Saprobic on submerged decaying wood. Asexual morph: *Conidiomata* 170–180 µm diam, 120–140 µm high., scattered, semi-immersed, unilocular, coriaceous, subcylindrical, black, without ostiole. *Conidiomatal wall* 9.9–30 µm thick, consisting of 3–5-layered cells of *textura angularis*, outer layers with brown to black, oblong, thin-walled cells, inner layers with subhyaline to brown, ovoid, thin-walled cells. *Conidiophores* arising all around the cavity of the conidiomata, subcylindrical, aseptate, hyaline, smooth, or reduced to conidiogenous cells, embedded in a mucilaginous matrix. *Paraphyses* 18.8–49.2 × 1.2–2.9 µm ($\bar{x}$ = 28 × 2.1 µm, n = 10), hyaline, unbranched, narrowly cylindrical, aseptate, smooth-walled, rounded at the apex. *Conidiogenous cells* 9.5–15 × 1.8–3.6 µm ($\bar{x}$ = 12 × 2.8 µm, n = 10), enteroblastic, monophialidic, integrated, cylindrical, hyaline, straight, smooth-walled. *Conidia* 25–31 × 4.2–5.6 µm ($\bar{x}$ = 28.8 × 4.9 µm, n = 30), subcylindrical, hyaline, rounded or sharp at the apex, straight or slightly curved, aseptate, multi-guttulate, smooth-walled, with 2–4 unbranched, filiform, flexuous, attenuated, supple apical appendages (25–31 µm long). Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the base. Colonies on PDA reaching 20 mm diameter after 2 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, flat surface, has a punctate protrusion in the center, white to pale brown, velvety. Reverse pale yellow, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3261 (HKAS 130437, holotype).

Notes – The multi-loci phylogenetic analysis showed that *Pseudorobillarda multiguttulata* is sister to *P. texana* with 81% ML/0.96 PP support (Fig. 33). *Pseudorobillarda multiguttulata* resembles *P. texana* in having narrowly cylindrical paraphyses, hyaline, guttulate, smooth conidia with flexuous appendages at the end. However, it differs from *P. texana* in having subcylindrical conidiomata without ostiole, aseptate paraphyses, larger conidia (25–31 × 4.2–5.6 vs. 12.5–18.5 × 2.5–3.5 µm), and longer conidial appendages (25–31 vs. 12.5–20.5) (Plaingam et al. 2005). The LSU and SSU sequences of *P. multiguttulata* revealed 2.64% (22/834 bp, four gaps) and 0.91% (9/988 bp) different from *P. texana*, respectively. Therefore, *P. multiguttulata* (HKAS 130437) is identified as a new species based on both phylogenetic analysis and characteristics.

Eurotiomycetes O.E. Erikss. & Winka

Chaetothyriales M.E. Barr

Herpotrichiellaceae Munk

Herpotrichiellaceae was introduced by Munk (1953), with *Herpotrichiella* as the type genus. The sexual morphs of this family are characterized by ascomata with typical setae and ostioles, bitunicate, saccate to ovoidal asci with a thickened apex, and pale grey to brown ascospores. The asexual morphs are various dematiaceous hyphomycetes (Munk 1953, Dong et al. 2018). A total of 17 genera are currently being accepted in this family (Wijayawardene et al. 2022).

Thysanorea Arzanlou, W. Gams & Crous

Thysanorea was introduced by Arzanlou et al. (2007), with *T. papuana* (= *Periconiella papuana*) as the type. The genus is characterized by micro- or macronematous, erect, septate, simple or apically branched conidiophores, terminal or intercalary, polyblastic conidiogenous cells, and solitary, subglobose to obovate or broadly fusiform, septate conidia with a narrowly truncate base. Phylogenetic studies showed that *Thysanorea* nested within *Minimelanolocus*, but the type species of *Minimelanolocus* lacks sequence data in the GenBank (Dong et al. 2018, Wang et al. 2019). Based on morphological and phylogenetic evidence, most species of *Minimelanolocus* have been transferred to *Thysanorea* (Hernández-Restrepo et al. 2020, Wan et al. 2021, Barreto et al. 2024).

Thysanorea fusiformis W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.

Fig. 36

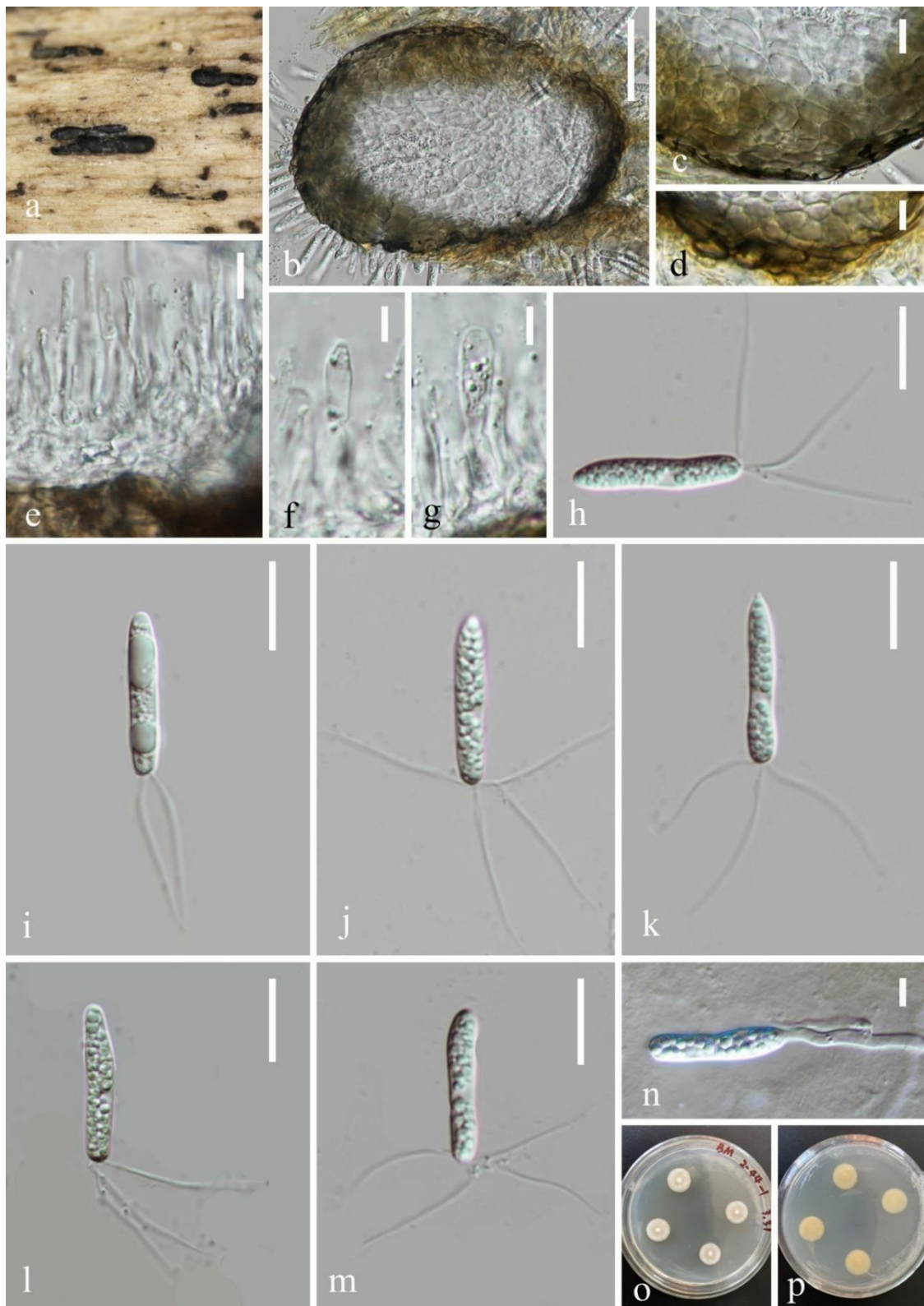


Figure 34 – *Pseudorobillarda multiguttulata* (HKAS 130437, holotype). a Conidiomata on the substratum. b Vertical section of conidioma. c, d Structure of conidiomatal wall. e Paraphyses. f, g Conidiogenous cells with developing conidia. h–m Conidia with appendages. n Germinating conidium. o, p Colonies on PDA from surface and reverse. Scale bars: b = 50 μ m, c, e = 10 μ m, d, f, g, n = 5 μ m, h–m = 15 μ m.

Notes – In the phylogenetic analysis, *Thysanorea fusiformis* is sister to *T. amniculi* (Fig. 35). *Thysanorea fusiformis* and *T. amniculi* can be clearly distinguished from each other by the

conidiophores and conidia. *Thysanorea fusiformis* has unbranched, shorter (180–300 vs. 190–465 μm) conidiophores, but larger ($20\text{--}37 \times 5.1\text{--}9.2$ vs. $(13\text{--}) 15\text{--}23 \times 2.5\text{--}5$ μm) and fusiform conidia (Yang et al. 2023). The comparison nucleotides of ITS and LSU sequences data indicated that *T. fusiformis* (CGMCC 3.25425) differs from *T. amniculi* (GZCC 20–0465) in 2.8% (16/572 bp) and 0.24% (2/826 bp), which strongly support *T. fusiformis* as a new species.

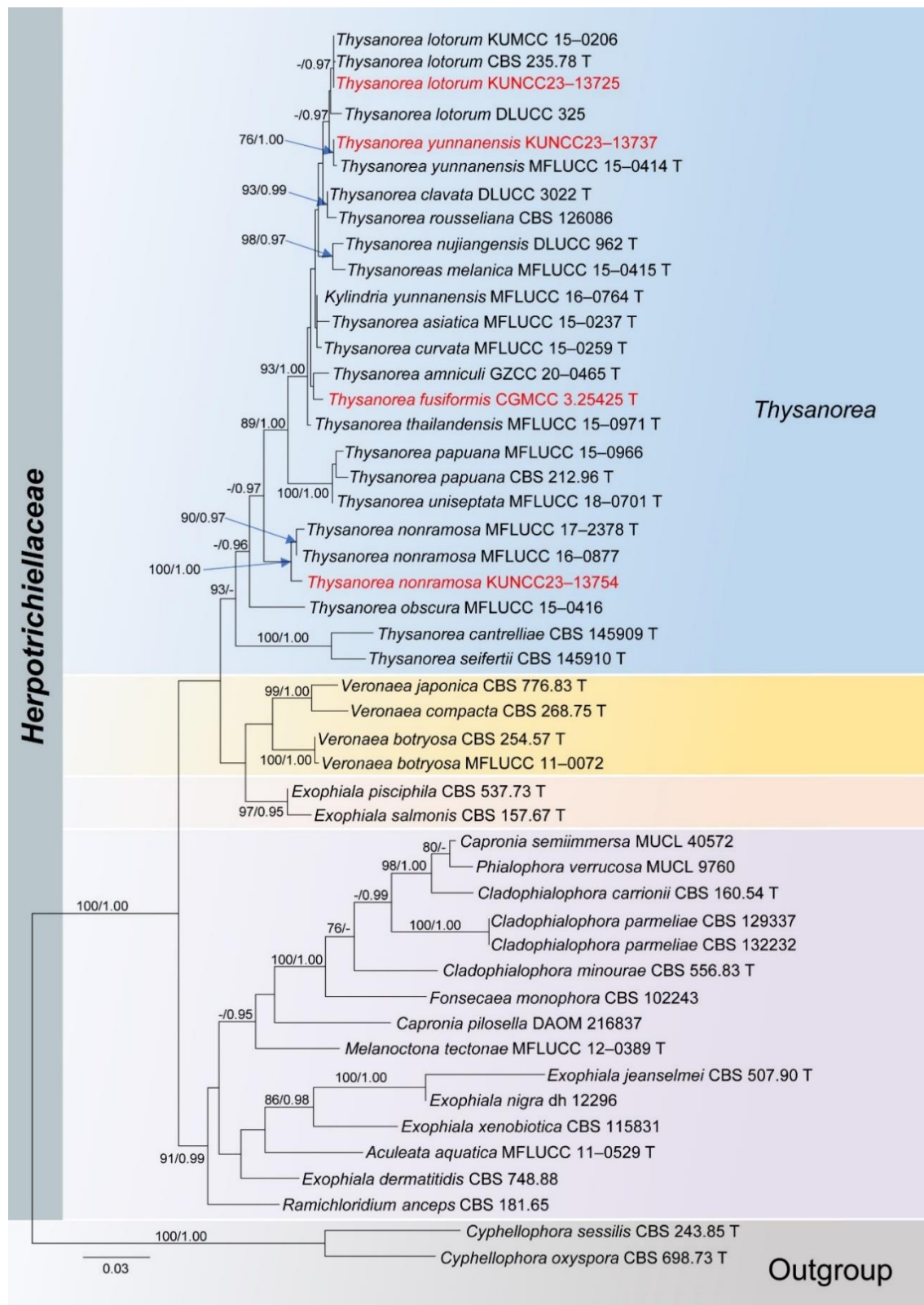


Figure 35 – RAxML tree based on analysis of *Herpotrichiellaceae* that combined LSU, ITS, and SSU dataset. The combined analyses include 48 strains with 2355 characters including gaps (LSU:

857 bp, ITS: 556 bp, and SSU: 942 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Cyphellophora oxyspora* (CBS 698.73) and *C. sessilis* (CBS 243.85). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.

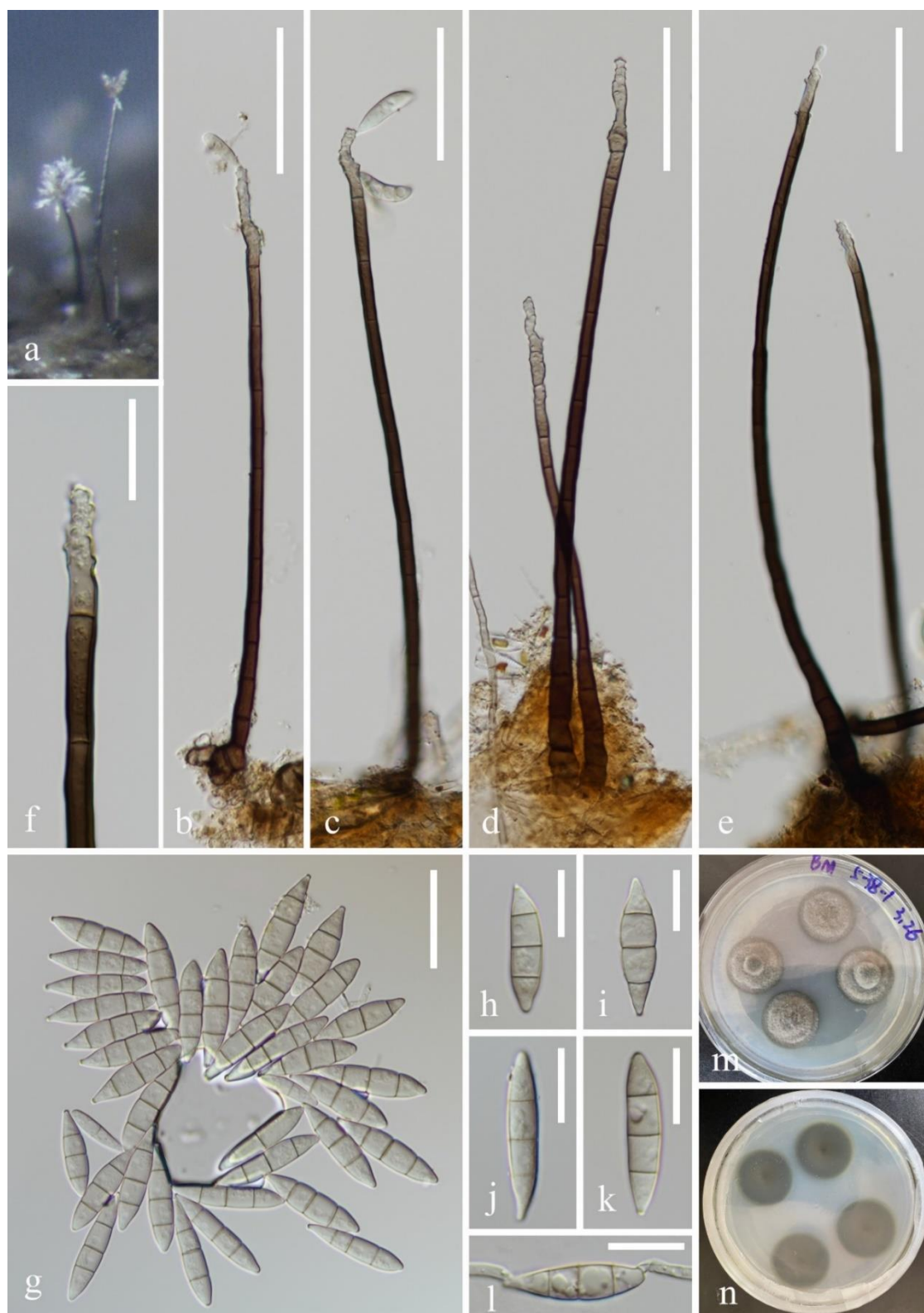


Figure 36 – *Thysanorea fusiformis* (HKAS 131396, holotype). a Colonies on the substratum. b, c, e Conidiophores with conidia. d Conidiophores. f Conidiogenous cell. g–k conidia. m, n Colonies on agar.

l Germinating conidium. m, n Colonies on PDA from surface and reverse. Scale bars: b–e = 50 μ m, f = 20 μ m, g = 30 μ m, h–l = 15 μ m.

Thysanorea litorum (Morgan-Jones) Hern.-Restr. & Crous, Fungal Syst Evol 6, 18 (2020) Fig. 37

Index Fungorum number: IF833922; Facesoffungi number: FoF16105

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, hairy, scattered, dark brown, with subhyaline, fusiform conidia on the apex of conidiophores. *Mycelium* mostly immersed, composed of septate, pale brown, smooth hyphae. *Conidiophores* (70–) 130–230 $\times$ 3.2–8.4 μ m ($\bar{x}$ = 153.4 $\times$ 4.9 μ m, n = 15), mononematous, macronematous, erect, unbranched, cylindrical, straight or slightly flexuous, septate, smooth, thick-walled, dark brown at the base, and gradually paler towards the apex. *Conidiogenous cells* polyblastic, integrated, terminal, sympodially proliferating, subhyaline to pale brown. *Conidia* (10–) 25–50 $\times$ 3–8.5 μ m ($\bar{x}$ = 38.5 $\times$ 5.6 μ m, n = 40), acrogenous, mostly fusiform, sometimes clavate, solitary, straight or slightly curved, 7–8-septate when mature, septum darker, sometimes slightly constricted at the septum, smooth, subhyaline to pale brown, with a hilum at the base. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the both ends and middle. Colonies on PDA reaching 20 mm diameter after 2 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edge, has a bulbous protrusion in the center, celadon. Reverse dark green, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3487 (HKAS 131400), living culture KUNCC 23–13725.

Notes – *Pseudospiropes litorum* (*Leotiomyces*) was introduced by Morgan-Jones (1977), but there is no corresponding molecular data for this fungus. Castañeda et al. (2001) transferred *P. litorum* to *Nigrolentilocus* (*Dothideomycetes*). However, phylogenetic analysis showed that *P. litorum* (CBS 235.78) nested within *Thysanorea* and clustered with *Minimelanolocus submersus* (KUMCC 15–0206). Therefore, Hernández-Restrepo et al. (2020) synonymized *P. litorum* and *M. submersus* under *Thysanorea litorum*. In the phylogenetic analysis, our collection clustered with *T. litorum* clade (Fig. 36), and our collection resembles *T. litorum* in having unbranched, straight or slightly flexuous conidiophores that are gradually paler towards the apex, integrated, sympodially proliferating, terminal conidiogenous cells, and clavate or fusiform, subhyaline to pale brown conidia (Hyde et al. 2016b). We therefore, identified our new collection as *T. litorum*.

Thysanorea nonramosa (X.D. Yu, G.N. Wang & H. Zhang) Hern.-Restr. & Crous, Fungal Syst Evol 6, 18 (2020) Fig. 38

Index Fungorum number: IF833924; Facesoffungi number: FoF12800

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, hairy, scattered or in small groups, dark brown, with silvery, fusiform conidia on the apex of conidiophores. *Mycelium* partly immersed, partly superficial, composed of septate, pale brown, smooth hyphae. *Conidiophores* 100.9–163.2 $\times$ 3.1–5.1 μ m ($\bar{x}$ = 126.8 $\times$ 3.9 μ m, n = 20), mononematous, macronematous, solitary or in small groups, erect, rarely branched, cylindrical, straight or slightly flexuous, septate, smooth, thick-walled, dark brown at the base, and gradually paler towards the apex. *Conidiogenous cells* polyblastic, integrated, terminal, sympodially proliferating, subhyaline to pale brown. *Conidia* 9.1–21.2 $\times$ 2.2–4.4 μ m ($\bar{x}$ = 16.7 $\times$ 3.3 μ m, n = 40), acrogenous, clavate, solitary, straight or slightly curved, mostly 3-septate when mature, sometimes slightly constricted at the septum, smooth, thin-walled, subhyaline to pale brown, rounded at the apex, with a hilum at the base. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the both ends. Colonies on PDA reaching 25 mm diameter after 3 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edge, green, and brown on the surface layer. Reverse dark green, crack in the center, smooth.

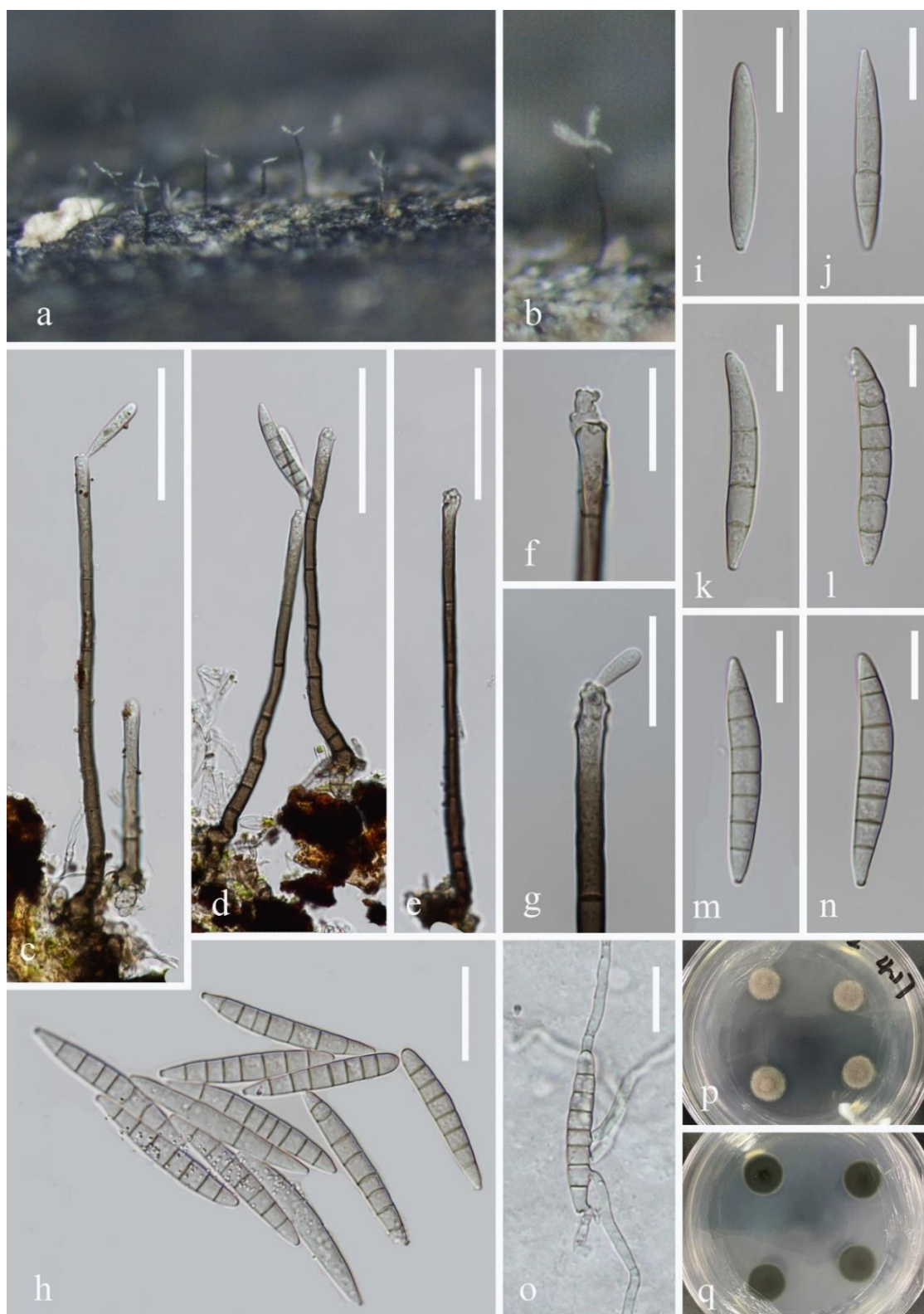


Figure 37 – *Thysanorea litorum* (HKAS 131400). a, b Colonies on the substratum. c, d Conidiophores with conidia. e Conidiophore. f Conidiogenous cell. g Conidiogenous cell with conidium. h–n Conidia. o Germinating conidium. p, q Colonies on PDA from surface and reverse. Scale bars: c–e = 50 μ m, f, g = 20 μ m, h = 25 μ m, i–o = 15 μ m.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4346 (HKAS 131363), living culture KUNCC 23–13754.

Notes – Phylogenetic analysis showed that our new collection (KUNCC 23–13754) clustered with two strains of *Thysanorea nonramosa* (MFLUCC 17–2378 and MFLUCC 16–0877) with 100% ML/1.00 PP support (Fig. 36). Our new collection matches with the description of *T. nonramosa*, except the branched conidiophores. We therefore identified our new collection as *T. nonramosa*, a species which was collected on submerged decaying wood in Thailand (Wang et al. 2019, Yang et al. 2023), and this is the first time to report this species from China.



Figure 38 – *Thysanorea nonramosa* (HKAS 131363). a, b Colonies on the substratum. c, e Conidiophores. d Conidiophore with conidium. f–j Conidia. k Germinating conidium. l, m Cross-sections of the substratum.

l, m Colony on PDA from surface and reverse. Scale bars: c = 30 μ m, d, e = 20 μ m, f, k = 10 μ m, g–j = 5 μ m.

Thysanorea yunnanensis Hern.-Restr. & Crous, Fungal Syst Evol 6, 21 (2020)

Fig. 39

Index Fungorum number: IF833928; Facesoffungi number: FoF16124

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, hairy, scattered, dark brown. *Conidiophores* (90–) 120–250 $\times$ (2.6–) 4.3–8 μ m ($\bar{x}$ = 159.3 $\times$ 5.6 μ m, n = 20), mononematous, macronematous, erect, unbranched, cylindrical, straight or flexuous, septate, smooth, thick-walled, dark brown at the base, and gradually paler towards the apex, swollen into a subglobose at the base. *Conidiogenous cells* integrated, terminal, sympodially proliferating, subhyaline to pale brown. *Conidia* 22–38 $\times$ 3.4–7.2 μ m ($\bar{x}$ = 32.3 $\times$ 5.5 μ m, n = 40), acrogenous, clavate to fusiform, solitary, straight or slightly curved, 5–9-septate when mature, septum darker, smooth, subhyaline to pale brown, with a hilum at the base. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the both ends and middle. Colonies on PDA reaching 50 mm diameter after 4 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, circular, with regular edge, with a small bulbous protrusion in the center, dark brown, the outermost part has a loose layer of hyphae, velvety. Reverse dark green to black, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4355 (HKAS 131402), living culture KUNCC 23–13737.

Notes – *Minimelanolocus aquaticus* was introduced by Liu et al. (2015a) from freshwater habitat in Yunnan Province, China. Hernández-Restrepo et al. (2020) transferred *M. aquaticus* to *Thysanorea* as *T. yunnanensis*. Phylogenetic analysis showed that our new collection (KUNCC23–13737) clustered with the type strain of *T. yunnanensis* (MFLUCC 15–0414) with 76% ML/1.00 PP support (Fig. 35). Our new collection is similar to *T. yunnanensis* (MFLUCC 15–0414) in having unbranched, straight or flexuous conidiophores that are gradually paler towards the apex, and clavate to fusiform and similar-sized conidia, but our new collection has more septa when mature (5–9 vs. 3–7) (Liu et al. (2015a). Comparison of the ITS sequence of our new collection and the ex-type strain of *T. yunnanensis* showed that 99.11% (557/562 bp, two gaps) similarity.

Sordariomycetes O.E. Erikss. & Winka

Coronophorales Hern.-Restr., Gené, Guarro & Crous

Parasymphodiellaceae Hern.-Restr., Gené, Guarro & Crous

The monotypic family *Parasymphodiellaceae* was introduced by Hernández-Restrepo et al. (2017), with *Parasymphodiella* as the type genus. The family is known only by the asexual morph, which are characterized by micro- to macronematous, mononematous, unbranched conidiophores, thallic, sympodial conidiogenous cells, thallic-arthric, aseptate or septate, cylindrical, hyaline, often catenate conidia with schizolytic secession (Hernández-Restrepo et al. 2017, Bundhun et al. 2021). *Parasymphodiellaceae* is previously placed in *Parasymphodiellales*, but was transferred to *Coronophorales* by Bundhun et al. (2021) based on phylogenetic analysis.

Parasymphodiella Ponnappa

Parasymphodiella was established by Ponnappa (1975), with *P. laxa* as the type. Based on phylogenetic analysis, Hernández-Restrepo et al. (2017) accepted four species, viz., *Parasymphodiella elongata*, *P. eucalypti*, *P. laxa*, and *P. lauri* in this genus. Currently, 12 species are accepted in this genus, and these species are often occurred on leaves and twigs from terrestrial habitats, with the exception of *P. minima* which is the only species collected from a freshwater habitat (Sigler et al. 1982, Cheewangkoon et al. 2009, Hernández-Restrepo et al. 2017, Tian et al. 2024a).

Parasymphodiella lauri Hern.-Restr., Gené & Guarro, Stud. Mycol. 86, 87 (2017)

Fig. 41

Index Fungorum number: IF820299; Facesoffungi number: FoF16107



Figure 39 – *Thysanorea yunnanensis* (HKAS 131402). a Colonies on the substratum. b–f Conidiophores. g–i Conidia. j Germinating conidium. k, l Colonies on PDA from surface and reverse. Scale bars: b–d = 30 μ m, e, f = 40 μ m, g–j = 10 μ m.

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, scattered or gathered, hairy, with white flocculent conidia on the apex of conidiophores. *Mycelium* immersed in the natural substratum, composed of brown, smooth hyphae. *Conidiophores* 70–150 (–290) $\times$ 6.1–8.8 μ m ($\bar{x}$ = 149.5 $\times$ 7.3 μ m, n = 10), macronematous, mononematous, erect, unbranched, septate,

straight or slightly flexuous, sometimes obviously flexuous at the base, subcylindrical, sterile part with slightly thickened walls, brown, fertile part with thinner walls, pale brown, becoming paler toward the apex. *Conidiogenous cells* 13–27 × 5.4–8.8 µm ($\bar{x}$ = 20.9 × 7.2 µm, n = 10), holothallic, terminal, integrated, smooth, pale brown, becoming hyaline toward the apex. *Conidia* 42–56 × 6–9 µm ($\bar{x}$ = 48.1 × 8 µm, n = 30), thallic-arthric, dry, smooth, catenate, uniseptate or aseptate, cylindrical, both ends of intercalary conidia truncate, with a septal plug at each end, apically conidia with obtuse or rounded apical, hyaline, smooth, thin-walled. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the end. Colonies on PDA reaching 50 mm diameter after 2 weeks of incubation at room temperature. Mycelium loose, dark green, colonies immersed on PDA, with flat surface, irregular edges, white spots are distributed among them. Reverse dark green.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3254 (HKAS 130438).

Notes – Current phylogenetic analysis showed that our new collection clustered with the ex-type strain of *Parasymphodiella lauri* (FMR 13132) with 99% ML/0.99 PP support (Fig. 40). Morphologically, our collection resembles *P. lauri* in having unbranched conidiophores, proliferating sympodially conidiogenous cells, and thallic-arthric, catenate, cylindrical conidia. Thus, we identified our new collection as *P. lauri*, a species which has been reported from Spain that associated with fallen leaves of *Laurus* sp. (Hernández-Restrepo et al. 2017), and it is the first time to report in China.

Distoseptisporales Z.L. Luo, H.Y. Su & K.D. Hyde

Distoseptisporaceae K.D. Hyde & McKenzie

Distoseptisporaceae was introduced by Su et al. (2016), with *Distoseptispora* as the type genus. Species of the family are generally saprobic on decaying wood and leaves from terrestrial and freshwater habitats, and most taxa are reported to be asexual morphs, with only two species *D. hyalina* and *D. licualae* introduced as asexual morphs. (Su et al. 2016, Hyde et al. 2016b, 2019, 2020b, Luo et al. 2018a, 2019, Song et al. 2020, Dong et al. 2021a, Li et al. 2021b, Shen et al. 2021, Zhang et al. 2022, Jayawardena et al. 2022, Konta et al. 2023).

Distoseptispora K.D. Hyde, McKenzie & Maharachch.

Distoseptispora, the single genus in *Distoseptisporaceae*, was introduced by Su et al. (2016), with *D. fluminicola* as the type species. The asexual morph of *Distoseptispora* is characterized by macronematous, mononematous, erect, cylindrical conidiophores, monoblastic or polyblastic, integrated, terminal, cylindrical conidiogenous cells, and acrogenous, obclavate, distoseptate or euseptate conidia (Su et al. 2016, Shen et al. 2021, Yang et al. 2021). Only two sexual species, *D. hyalina* and *D. licualae* is accepted in the genus, which are characterized by immersed to semi-immersed, perithecial, subglobose to ellipsoidal ascomata with a short neck through host surface, cylindrical, short pedicellate asci obtuse at the apex, with an apical ring, and fusiform, aseptate ascospores with a mucilaginous sheath. Currently, more than eighty species are accepted in this genus, and most species are collected from freshwater habitats (Jayawardena et al. 2022, Konta et al. 2023, Index Fungorum 2024, Shen et al. 2024). Phylogenetic study showed that this genus comprises four clades, but the lack of common features distinguished them (Zhang et al. 2022, Shen et al. 2024).

Distoseptispora rostrata Z.L. Luo, K.D. Hyde & H.Y. Su, Mycosphere 9(3), 453 (2018) Fig. 43

Index Fungorum number: IF554291; Facesoffungi number: FoF04195

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, single or gathered, velvety, olivaceous. *Mycelium* mostly immersed, partly superficial, composed of branched, septate, smooth-walled, pale brown to brown hyphae. *Conidiophores* 29–72 × 3.6–6.1 µm ($\bar{x}$ = 54.8 × 4.7 µm, n = 20), macronematous, mononematous, erect, cylindrical, rounded at the apex, unbranched, 2–4-septate, straight or slightly flexuous, smooth, pale brown to brown. *Conidiogenous*

cells $8.8\text{--}26 \times 3.6\text{--}6.1 \mu\text{m}$ ($\bar{x} = 19.3 \times 4.7 \mu\text{m}$, $n = 20$), monoblastic, integrated, terminal, cylindrical, brown. *Conidia* $36\text{--}180 \times 4\text{--}10.2 \mu\text{m}$ ($\bar{x} = 124.6 \times 7.2 \mu\text{m}$, $n = 40$), acrogenous, solitary, obclavate or lanceolate, rostrate, slightly tapering towards the apex, straight or slightly curved, smooth-walled, multi-distoseptate, olivaceous to pale brown, rounded at the apex, truncate basal with a thickened. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 24 h, and germ tubes produced from apex. Colonies on PDA reaching 30 mm diameter after 3 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edge, circular, a bulbous protrusion in the center, brown. Reverse dark brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4341 (HKAS 131381), living culture KUNCC 23–13736.

Notes – *Distoseptispora rostrata* was introduced by Luo et al. (2018a), was found on submerged decaying wood in China. Our phylogenetic analysis showed that our new isolate (KUNCC23–13736) clustered with the ex-type strain of *D. rostrata* (MFLUCC 16–0969) with 100% ML/1.00 PP support (Fig. 42). The new collection resembles *D. rostrata* in having cylindrical, unbranched conidiophores, obclavate, rostrate, distoseptate conidia with truncate base. Therefore, we identified the new collection as *D. rostrata*.

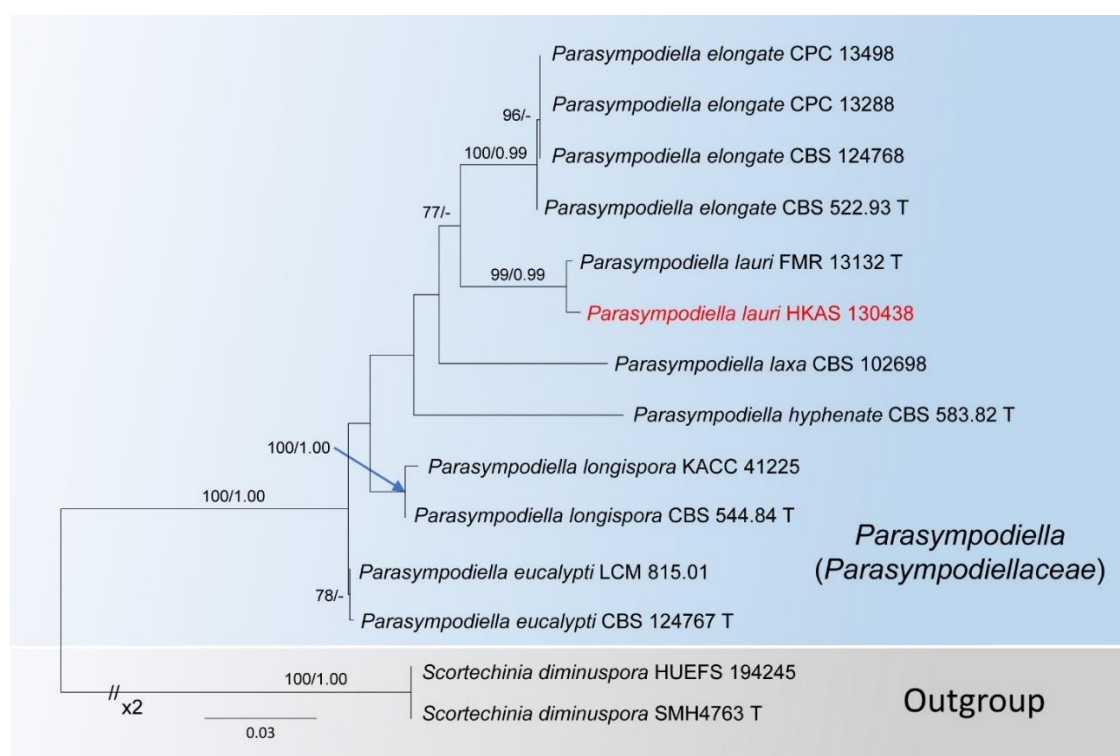


Figure 40 – RAxML tree based on analysis of *Parasympodiella* that combined LSU and ITS dataset. The combined analyses include 14 strains with 1404 characters including gaps (LSU: 868 bp and ITS: 536 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Scortechinia diminuspura* (HUEFS 194245, SMH4763). The new collection is indicated in red. Ex-type strains are indicated with “T” after the strain number.

Distoseptispora tectonae Doilom & K.D. Hyde, Fungal Divers. 80, 222 (2016)

Fig. 44

Index Fungorum number: IF552223; Facesoffungi number: FoF01877

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, single, hairy, dark brown to black. *Mycelium* mostly superficial, composed of branched, septate, smooth-walled, pale brown to brown hyphae. *Conidiophores* $24\text{--}78 \times 4.5\text{--}7.3 \mu\text{m}$ ($\bar{x} = 55.7 \times 6.1 \mu\text{m}$, $n =$

15), macronematous, mononematous, erect, unbranched, 1–5-septate, cylindrical, straight or slightly flexuous, thick, smooth-walled, olivaceous to brown, truncate at the apex. *Conidiogenous cells* 4.7–11 × 4.1–5.9 µm ($\bar{x}$ = 9.2 × 5.1 µm, n = 15), monoblastic, integrated, terminal, cylindrical, brown. *Conidia* 100–220 × 12–20 µm ($\bar{x}$ = 152.6 × 15.4 µm, n = 30), acrogenous, solitary, obclavate, smooth-walled, multi-distoseptate, olivaceous to pale brown, straight or curved at the apex, rounded apical, with truncate base and a 3.4–5.8 µm wide wedge-shaped base. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 24 h, and germ tubes produced from the apex. Colonies on PDA reaching 30 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with regular edges, a bulbous protrusion in the center, green, brown layer covered the surface. Reverse circular, dark green and brown edges, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3964 (HKAS 131360), living culture KUNCC 23–14563; *ibid.*, H-734 (HKAS 131355), living culture KUNCC 23–14572.

Notes – Phylogenetic analysis showed that our new collections (KUNCC 23–14563 and KUNCC 23–14572) clustered with *Distoseptispora tectonae* (Fig. 42). There is no significant difference between our new collections and the holotype of *D. tectonae*, except conidia of our collections are curved at the apex. Thus, we identified our new collections as *D. tectonae*. *Distoseptispora tectonae* was initially introduced by Hyde et al. (2016b) collected from a dead twig of *Tectona grandis*, thereafter, this species has been reported from freshwater habitats in China and Thailand (Luo et al. 2018a, Sun et al. 2020, Dong et al. 2021a, Zhang et al. 2022).

Magnaporthales Thongk., Vijaykr. & K.D. Hyde

Magnaporthaceae P.F. Cannon

Magnaporthaceae was introduced by Cannon (1994), with *Magnaporthe* as the type. The family is characterized by immersed, globose to subglobose ascomata with a long neck, hyaline paraphyses tapering towards the apex, cylindrical to clavate asci with an apical ring, and fusoid to filiform ascospores; reduced or erect, branched conidiophores, phialidic conidiogenous cells, and fusiform or lunate conidia (Luo & Zhang 2013, Hernández-Restrepo et al. 2016, Luo et al. 2019). Based on multi-loci phylogenetic analysis, 19 genera are accepted in *Magnaporthaceae* (Feng et al. 2021). *Magnaporthaceae* species have been reported on various plants from diverse habitats (Luo & Zhang 2013, Hernández-Restrepo et al. 2016, Luo et al. 2019, Feng et al. 2021).

Falciphoriella M. Hern.-Restr. & Crous

Falciphoriella was introduced by Hernández-Restrepo et al. (2016), with *F. solaniterrestris* as the type species. Currently, only the type species is accepted in the genus. The genus is characterized by indeterminate, branched conidiophores, phialidic, solitary or grouped, cylindrical conidiogenous cells with a cylindrical to funnel-shaped collarette, and obovoid or fusiform conidia with pointed base and slightly curved ends. This study introduces the second species in this genus, collected from Yunnan Province, China. Previously, this genus was recognized solely by its asexual morphology. In this study, we introduce an additional species to the genus. Given that the new species exhibits sexual characteristics, we have amended the generic description accordingly.

Falciphoriella M. Hern.-Restr. & Crous, amend

Saprobic on soil and submerged decaying wood. Asexual morph: See Hernández-Restrepo et al. (2016). Sexual morph: *Ascomata* semi-immersed, unilocular, black, subglobose, with a subcylindrical ostiolar. *Peridium* brown, coriaceous, composed of thick-walled, polyhedron cells. *Paraphyses* hyaline, septate, constricted at septum, unbranched, tapering toward the tip. *Asci* 8-spored, unitunicate, fusiform to clavate or inverted clavate, rounded at the apex, hyaline, curved, sessile, with an apical ring. *Ascospores* hyaline, nearly filiform, rounded at both ends, slightly curved, smooth, thin-walled, aseptate.



Figure 41 – *Parasympodiella lauri* (HKAS 130438). a Colonies on the substratum. b–f Conidiophores, Conidiophores with conidia. g–j Conidia. k Germinating conidium. l, m Colonies on PDA from surface and reverse. Scale bars: b, c, h = 25 μ m, d–g = 50 μ m, i–k = 10 μ m.

Falciphoriella hyalina W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.

Fig. 46

Index Fungorum number: IF902443; Facesoffungi number: FoF16123

Etymology – Referring to the hyaline ascospores of this fungus.

Holotype – HKAS 131395

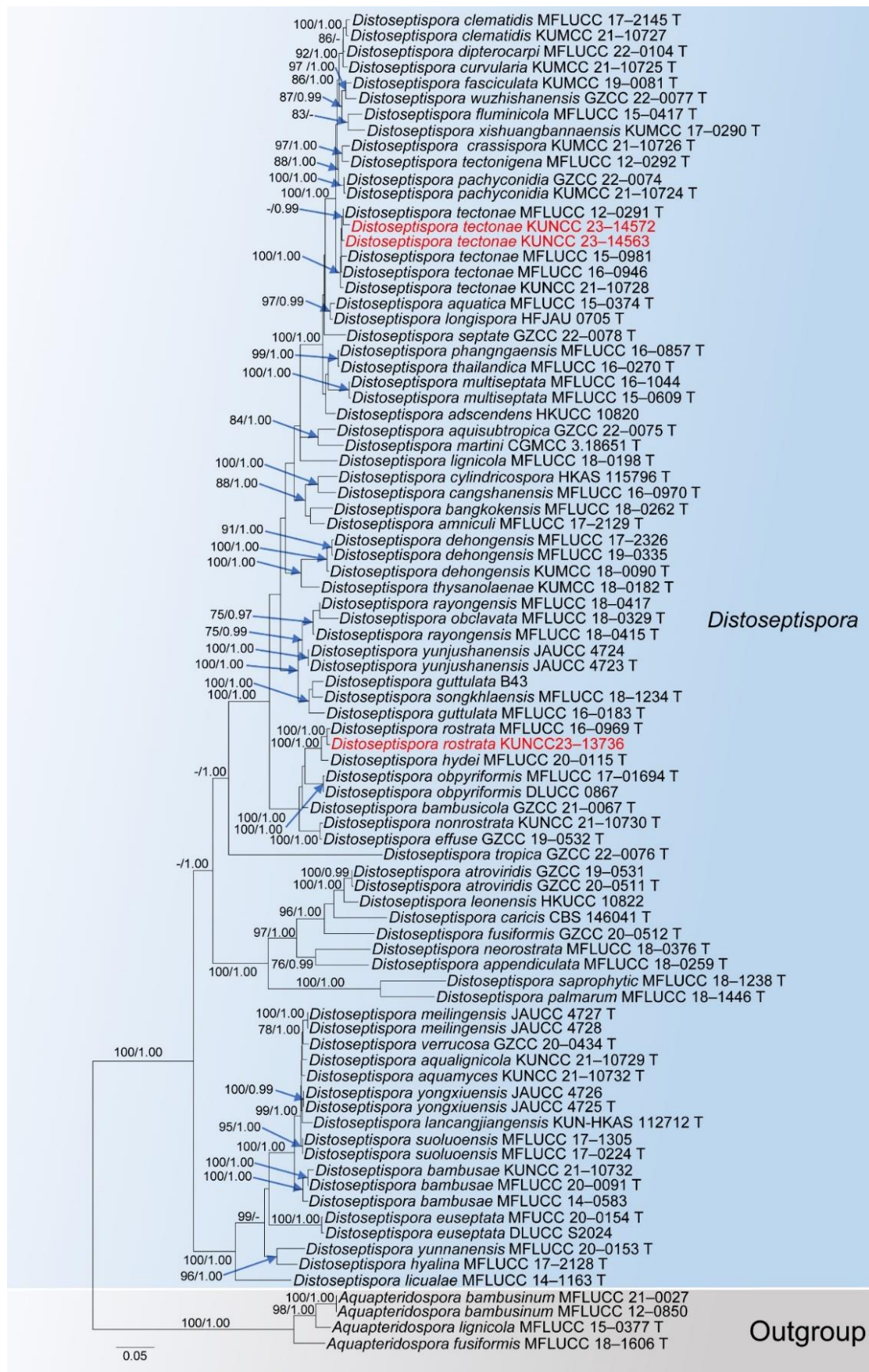


Figure 42 – RAxML tree based on analysis of *Distoseptispora* that combined LSU, ITS, *tef1-α*, and *rpb2* dataset. The combined analyses include 85 strains with 3217 characters including gaps (LSU: 834 bp, ITS: 522 bp, *tef1-α*: 851 bp, and *rpb2*: 1010 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated

above branches as ML/PP. The tree is rooted with *Aquapteridospora bambusinum* (MFLUCC 12–0850 and MFLUCC 21–0027), *A. fusiformis* (MFLUCC 18–1606) and *A. lignicola* (MFLUCC 15–0377). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.

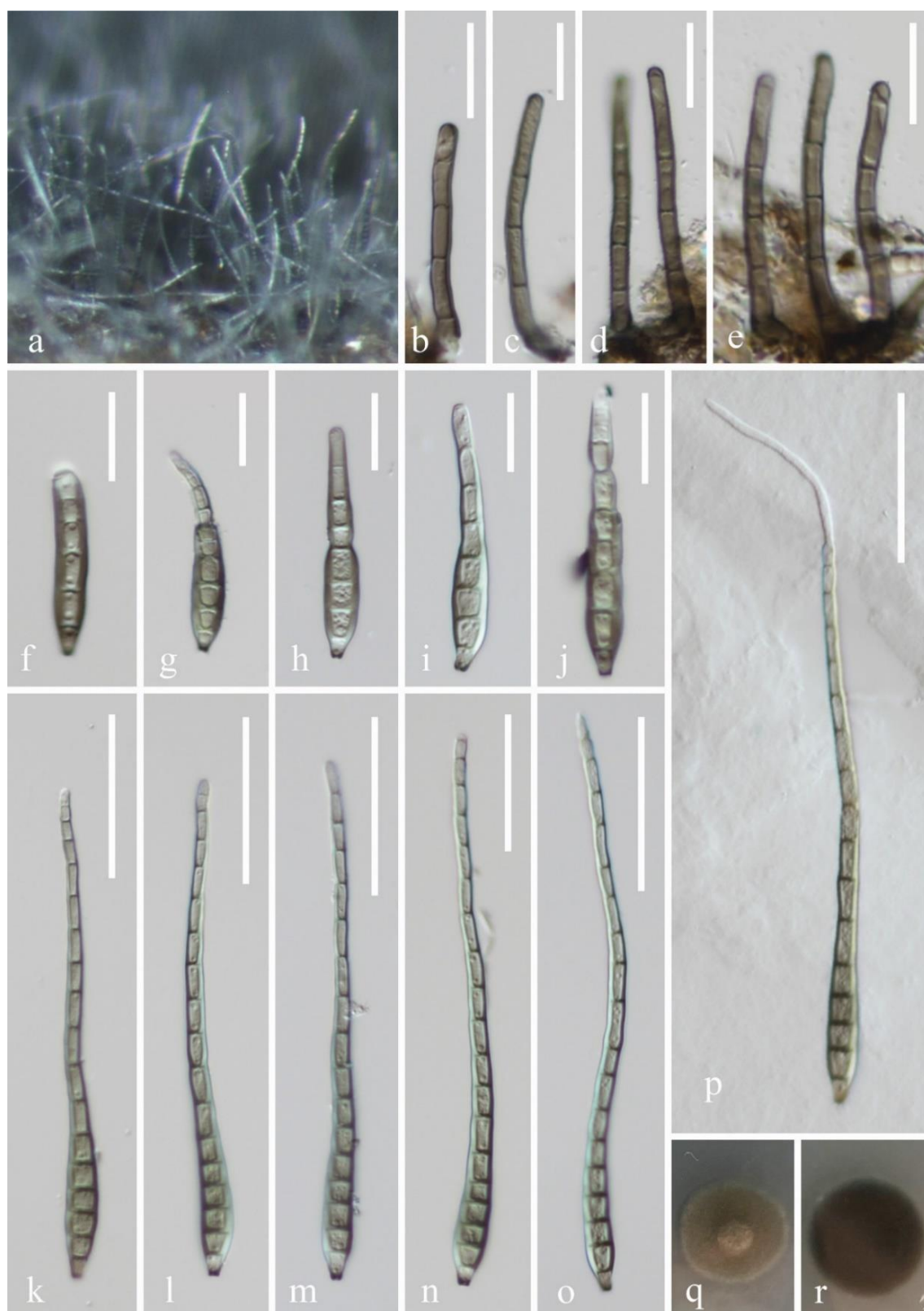


Figure 43 – *Distoseptispora rostrata* (HKAS 131381). a Colonies on the substratum. b–e Conidiophores. f–o Conidia. p Germinating conidium. q, r Colony on PDA from surface and reverse. Scale bars: b–j = 20 μ m, k–p = 50 μ m.



Figure 44 – *Distoseptispora tectonae* (HKAS 131360). a, b Colonies on the substratum. c, d Conidiophores with conidia. e–g Conidiophores. h–l Conidia. m Germinating conidium. n, o Colony on PDA from surface and reverse. Scale bars: c, d = 50 μ m, e–g = 10 μ m, h–m = 40 μ m.

Saprobic on submerged decaying wood. Asexual morph: Undetermined. Sexual morph: *Ascomata* 200–270 μ m diam, 200–210 μ m high., scattered or gathered, semi-immersed, unilocular, black, subglobose, with a short, subcylindrical ostiolar. *Peridium* 9.4–40 μ m thick, coriaceous,

composed 2–6 layers of brown, thick-walled, polyhedron cells of *textura angularis*. *Paraphyses* 5.1–9.4 μm wide, hyaline, septate, constricted at septum, unbranched, broad at the base, tapering toward the tip. *Asci* 90–190 $\times$ 13–19 μm ($\bar{x}$ = 139.1 $\times$ 15 μm , n = 10), 8-spored, unitunicate, fusiform to clavate or inverted clavate, rounded at the apex, hyaline, curved, sessile, with an apical ring. *Ascospores* 80–120 $\times$ 3.3–5 μm ($\bar{x}$ = 108.5 $\times$ 3.9 μm , n = 30), parallel, hyaline, nearly filiform, rounded at both ends, slightly curved, smooth, thin-walled, aseptate.

Culture characteristics – Ascospores germinating on PDA within 12 h, and germ tubes produced from the both ends. Colonies on PDA reaching 55 mm diameter after 3 weeks of incubation at room temperature. Mycelium dry, dense, colonies semi-immersed of PDA, with flat surface, pale brown to brown. Reverse brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3259 (HKAS 131395, holotype), ex-type living cultures CGMCC 3.25423 = KUNCC 23–13740.

Notes – Phylogenetic analysis showed that our new collection clusters with the type species *Falciphoriella solaniterrestris* (CBS 117.83) with 99% ML/0.98 PP support (Fig. 45). However, since no sexual morph has been reported for *F. solaniterrestris*, we are unable to compare the characteristics between our new collection and the holotype of *F. solaniterrestris*. Comparison of the ITS sequence data of *F. hyalina* (CGMCC 3.25423) differs from *F. solaniterrestris* (CBS 117.83) by 1.61% (8/496 bp, eight gaps). We follow the guidelines of Jeewon & Hyde (2016), included i) Region of the ITS sequence analyzed more than 450 bp, and the nucleotide differences >1.5%; ii) Phylogenetic support *F. hyalina* distinct from *F. solaniterrestris* with reliable statistical support. Therefore, we introduce *F. hyalina* as a new species, and it is the first species to be reported with sexual morph in *Falciphoriella*.

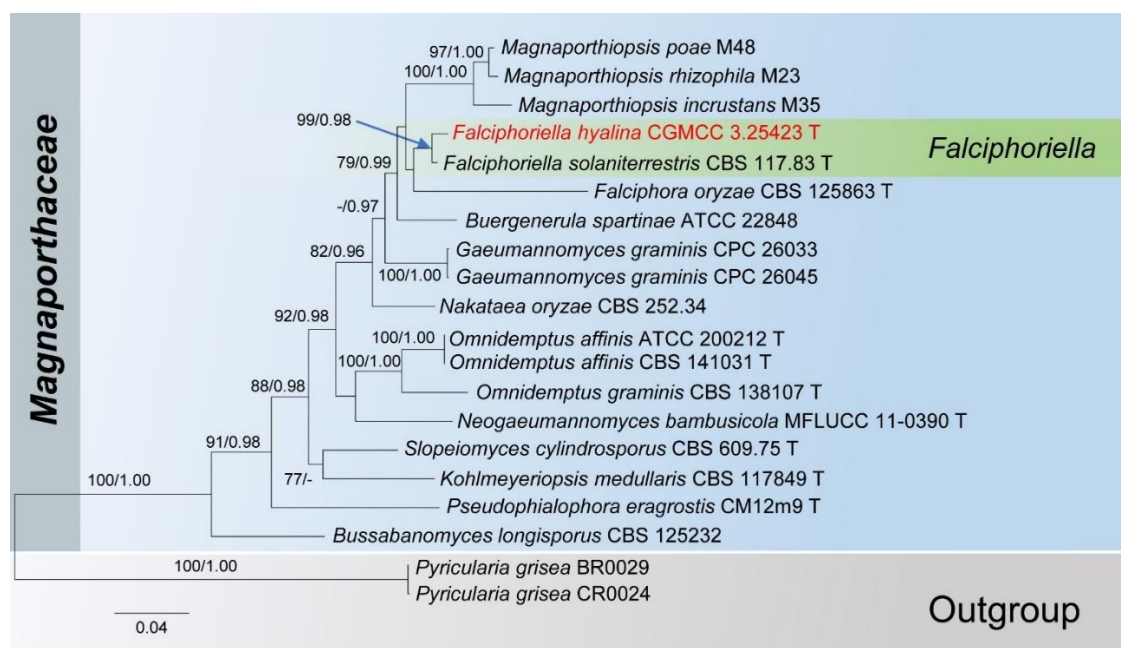


Figure 45 – RAxML tree based on analysis of *Magnaporthaceae* that combined ITS, LSU, *rpb1* and *tef1- α* dataset. The combined analyses include 20 strains with 3181 characters including gaps (ITS: 459 bp, LSU: 830 bp, *rpb1*: 968 bp, and *tef1- α* : 924 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Pyricularia grisea* (BR0029 and CR0024). The new collection is indicated in red. Ex-type strains are indicated with “T” after the strain number.

Ophioceraceae Klaubauf, E.G. LeBrun & Crous

Klaubauf et al. (2014) separated *Ophioceraceae* from *Magnaporthaceae*, with *Ophioceras* as the type. Based on combined morphology and phylogenetic analysis, Jiang et al. (2021b) proposed

that *Ceratosphaerella* is a synonym of *Ophioceras*. All species in this monotypic family are reported with sexual morph, and are characterized by black, immersed to superficial ascomata with a long, periphysate neck, septate, unbranched paraphyses tapering towards the apex, unitunicate, subcylindrical asci, and filiform, hyaline ascospores (Klaubauf et al. 2014, Jiang et al. 2021b, Yang et al. 2023).

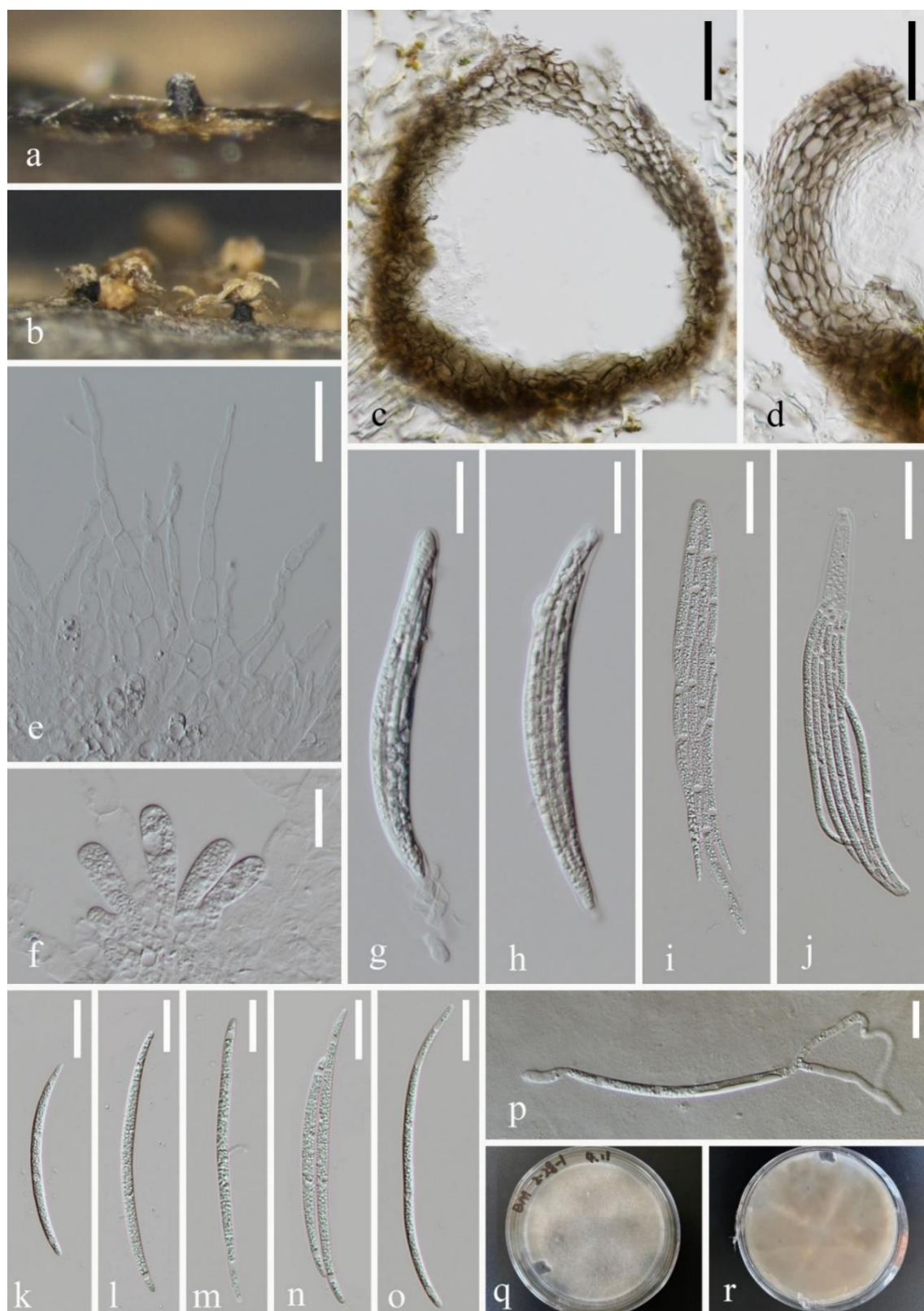


Figure 46 – *Faiciphoriella hyalina* (HKAS 131395, holotype). a, b Ascomata on the substratum. c Vertical section of ascoma. d Structure of peridium. e Paraphyses. f Immature asci. g–j Asci.

k–o Ascospores. p Germinating ascospore. q, r Colonies on PDA from surface and reverse. Scale bars: c = 50 μm , d, e, g–j = 30 μm , f = 15 μm , k–o = 20 μm , p = 10 μm .

***Ophioceras* Sacc.**

Ophioceras was introduced by Saccardo (1883) with *O. dolichostomum* as the type species. Most species of *Ophioceras* are known from decaying wood in terrestrial and freshwater habitats, but a few species isolated from decaying leaves and healthy plants (Thongkantha et al. 2009, Luo et al. 2019, Feng et al. 2021, Jiang et al. 2021b). Index Fungorum (2024) lists 46 species epithets under this genus, but only 18 species have DNA sequence data (Jiang et al. 2021b, Yang et al. 2023, Zhang et al. 2023b).

***Ophioceras aseptatum* W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.**

Fig. 48

Index Fungorum number: IF902432; Facesoffungi number: FoF16108

Etymology – Referring to the aseptate ascospores of this species.

Holotype – HKAS 131369

Saprobic on submerged decaying wood. Asexual morph: Undetermined. Sexual morph: *Ascomata* 380–430 μm diam, 380–430 μm high., scattered, solitary, semi-immersed in the natural substratum, globose to subglobose, black, ostiolate, with a long neck. *Necks* long, black, cylindrical, slightly tapering towards the tip, straight or slightly flexuous, mostly stand upright in the substratum. *Peridium* 35–63 μm thick, coriaceous, consisting of two layered, inner layers composed of hyaline, thin-walled cells of *textura angularis*, becoming pale brown to black, no obvious cellular structure at outer layers. *Paraphyses* 8.7–12 μm wide, at the base, loose, tapering towards the apex, hyaline, unbranched, septate, slightly constricted at the septum. *Asci* 140–200 $\times$ 8.8–15 μm ($\bar{x}$ = 168.8 $\times$ 11.2 μm , n = 20), 8-spored, unitunicate, cylindrical to fusiform, straight or slightly flexuous, short pedicellate to sessile, rounded at the apex, with an apical ring. *Ascospores* 62–79 $\times$ 3.3–4.6 μm ($\bar{x}$ = 71.5 $\times$ 3.9 μm , n = 15), parallel, filiform to cylindrical, slightly curved, hyaline, smooth, thin-walled, aseptate, multi-guttulate.

Culture characteristics – Ascospores germinating on PDA within 12 h, and germ tubes produced from the end. Colonies on PDA reaching 30 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with a bulbous protrusion in the center, regular edges, circular, white to brown. Reverse brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3490 (HKAS 131369, holotype), ex-type living culture KUNCC 23–14570.

Notes – In the phylogenetic analysis, the new collection (KUNCC 23–14570) is sister to *Ophioceras hongkongense* (HKUCC 3624) with 78% ML/0.96 PP support (Fig. 47). Our new collection resembles *O. hongkongense* in having globose to subglobose ascomata with a long neck, cylindrical, short pedicellate asci, and cylindrical, guttulate, hyaline ascospores. However, it differs from *O. hongkongense* in having smaller ascomata (380–430 vs. 700–800 μm in diam, 380–430 vs. 500–640 μm in high), thicker peridium (35–63 vs. 20–40 μm), longer asci (140–200 vs. 100–125 μm), and aseptate, shorter ascospores (62–79 vs. 72–101 μm) (Tsui et al. 2001). *Ophioceras aseptatum* is therefore introduced as a new species based on morphological and phylogenetic analysis.

***Ophioceras cylindrosporum* W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo**

Fig. 49

Index Fungorum number: IF902433; Facesoffungi number: FoF16109

Etymology – Referring to the cylindrical ascospores of this fungus.

Holotype – HKAS 131351

Saprobic on submerged decaying wood. Asexual morph: Undetermined. Sexual morph: *Ascomata* 420–570 μm diam, 120–150 μm high., scattered, solitary, immersed, flat ellipsoidal, black, ostiolate, with a long neck. *Necks* long, black, cylindrical, flexuous, mostly standing upright in the substratum. *Peridium* 4.8–26 μm thick, coriaceous, comprising 4–7 layers of brown to black, mostly

thin-walled, polyhedral cells of *textura angularis*. *Paraphyses* 4.6–9.1 μm wide, at the base, dense, tapering towards the apex, hyaline, unbranched, septate, slightly constricted at the septum. *Asci* 77–110 $\times$ 7.2–15 μm ($\bar{x}$ = 96.7 $\times$ 10 μm , n = 20), 8-spored, unitunicate, cylindrical to fusiform, slightly flexuous, sessile, rounded at the apex, with an apical ring. *Ascospores* 40–86 $\times$ 2–3.3 μm ($\bar{x}$ = 70.3 $\times$ 2.6 μm , n = 20), parallel, cylindrical to filiform, slightly curved to sigmoidal, hyaline, smooth, thin-walled, aseptate, multi-guttulate.

Culture characteristics – Ascospores germinating on PDA within 12 h, and germ tubes produced from the end. Colonies on PDA reaching 30 mm diameter after 3 weeks of incubation at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with flat surface, regular edges, green, and white in the center. Reverse dark brown.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3507 (HKAS 131351, holotype), ex-type living cultures CGMCC 3.25431 = KUNCC 23–13706.

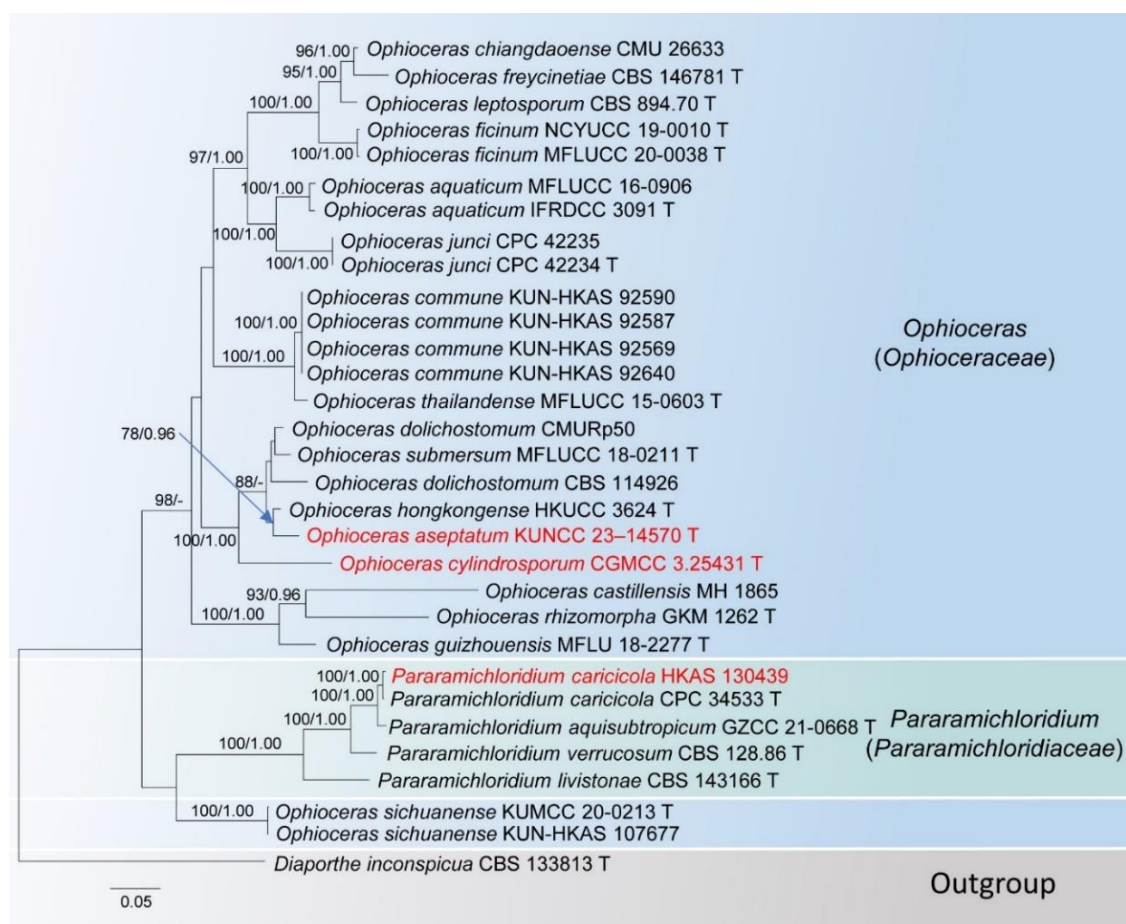


Figure 47 – RAxML tree based on analysis of *Ophioceraaceae* and *Pararamichloridiaceae* that combined LSU and ITS dataset. The combined analyses include 31 strains with 1370 characters including gaps (LSU: 839 bp and ITS: 531 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Diaporthe inconspicua* (CBS 133813). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.

Notes – Morphologically, *Ophioceras cylindrosporum* resembles *O. guttulatum* in having immersed ascomata with a long, cylindrical neck, cylindrical asci with an apical ring, and cylindrical, guttulate, hyaline ascospores. However, *O. cylindrosporum* has comparatively smaller, flat ellipsoidal ascomata (420–570 vs. 1200–1800 μm in diam, 120–150 vs. 400–600 μm in high), sessile asci, and aseptate, smaller ascospores (40–86 $\times$ 2–3.3 vs. 100–128 $\times$ 4–5 μm) distinguishing from

O. guttulatam. Phylogenetic analysis showed that *O. cylindrosporum* constitutes a strongly supported (100% ML/1.00 PP) independent lineage basal to *O. aseptatum* (KUNCC 23–14570), *O. dolichostomum* (CMURp50, CBS 114926), *O. hongkongense* (HKUCC 3624 and KUNCC 23–14570), and *O. submersum* (MFLUCC 18–0211) (Fig. 47). *Ophioceras cylindrosporum* differs from *O. dolichostomum* and *O. submersum* in having aseptate, shorter ascospores (40–86 vs. 94–110 vs. 87–109 μm). *Ophioceras cylindrosporum* has thinner peridium (4.8–26 vs. 20–40 μm), sessile asci, and multi-guttulate ascospores which clearly distinguish it from *O. hongkongense* (Tsui et al. 2001, Luo et al. 2019).

Myrmecridiales Crous

Myrmecridiaceae Crous

Myrmecridiaceae, a monotypic family in *Myrmecridiales*, was introduced by Crous et al. (2015b), with *Myrmecridium* as the type genus. Crous et al. (2018) introduced a new genus *Neomyrmecridium* in this family based on morphological characteristics and phylogenetic analysis.

Myrmecridium Arzanlou

Myrmecridium, typified by *M. schulzeri*, was established to accommodate two ramichloridium-like taxa (*M. schulzeri* and *M. flexuosum*) (Arzanlou et al. 2007). Members of *Myrmecridium* are widely distributed in Asia, Europe, Oceania, and Americas (Crous et al. 2012, 2021, Peintner et al. 2016, Tibpromma et al. 2017, Xu et al. 2023, Yang et al. 2023). Twenty-four species are accepted in this genus (Xu et al. 2023, Index Fungorum 2024), and sexual morph is only known for *M. montsecurinum* (Réblová et al. 2016a).

Myrmecridium thailandicum Crous & Cheew., Persoonia 31, 251 (2013)

Fig. 51

Index Fungorum number: IF805854; Facesoffungi number: FoF16110

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, scattered or aggregated, hairy, dark brown. *Mycelium* partly immersed, partly superficial, composed of aseptate, smooth-walled, hyaline to pale brown hyphae. *Conidiophores* (70–) 83–160 $\times$ 2.7–3.8 μm ($\bar{x}$ = 116.8 $\times$ 3.1 μm , n = 25), macronematous, mononematous, erect, solitary, straight or slightly flexuous, cylindrical, septate, pale brown to reddish brown, paler towards the apex, unbranched. *Conidiogenous cells* polyblastic, integrated, terminal and intercalary, sympodial, obscure denticulate, subhyaline to brown. *Conidia* 4.1–6.9 $\times$ 2.3–3.6 μm ($\bar{x}$ = 5.7 $\times$ 3 μm , n = 40), acropleurogenous, solitary, obovoidal, pale brown, aseptate, smooth or finely verrucose, thin-walled, rounded apical and slightly truncate at the base. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 40 mm diameter after 4 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with irregular edges, circular, wrinkled, has a protrusion in the center, yellow to brick red. Reverse circular, crack, yellow to reddish brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4354 (HKAS 131399), living culture KUNCC 23–13739.

Notes – Our new collection is indistinguishable from the holotype of *Myrmecridium thailandicum*. Phylogenetic analysis showed that our new collection clustered with the ex-type strain of *M. thailandicum* (CPC 21694) with 100 ML/1.00 PP support (Fig. 50). We therefore identified our new collection as *M. thailandicum*. *Myrmecridium thailandicum* was introduced by Crous et al. (2013) on reed litter next to pond in Thailand. While our collection, found on submerged wood in freshwater habitat in China, represents a new record for the country.

Pararamichloridiales Crous

Pararamichloridiaceae Crous

Pararamichloridiaceae was introduced by Crous et al. (2017) to accommodate two genera, *Pararamichloridium* and *Woswasia*, with the former as the type genus. *Woswasia* was subsequently

transferred to the family *Woswasiaceae* by Zhang et al. (2017b). Therefore, currently *Pararamichloridiaceae* is a monotypic family in *Pararamichloridiales* (Hyde et al. 2021, Jayawardena et al. 2022).

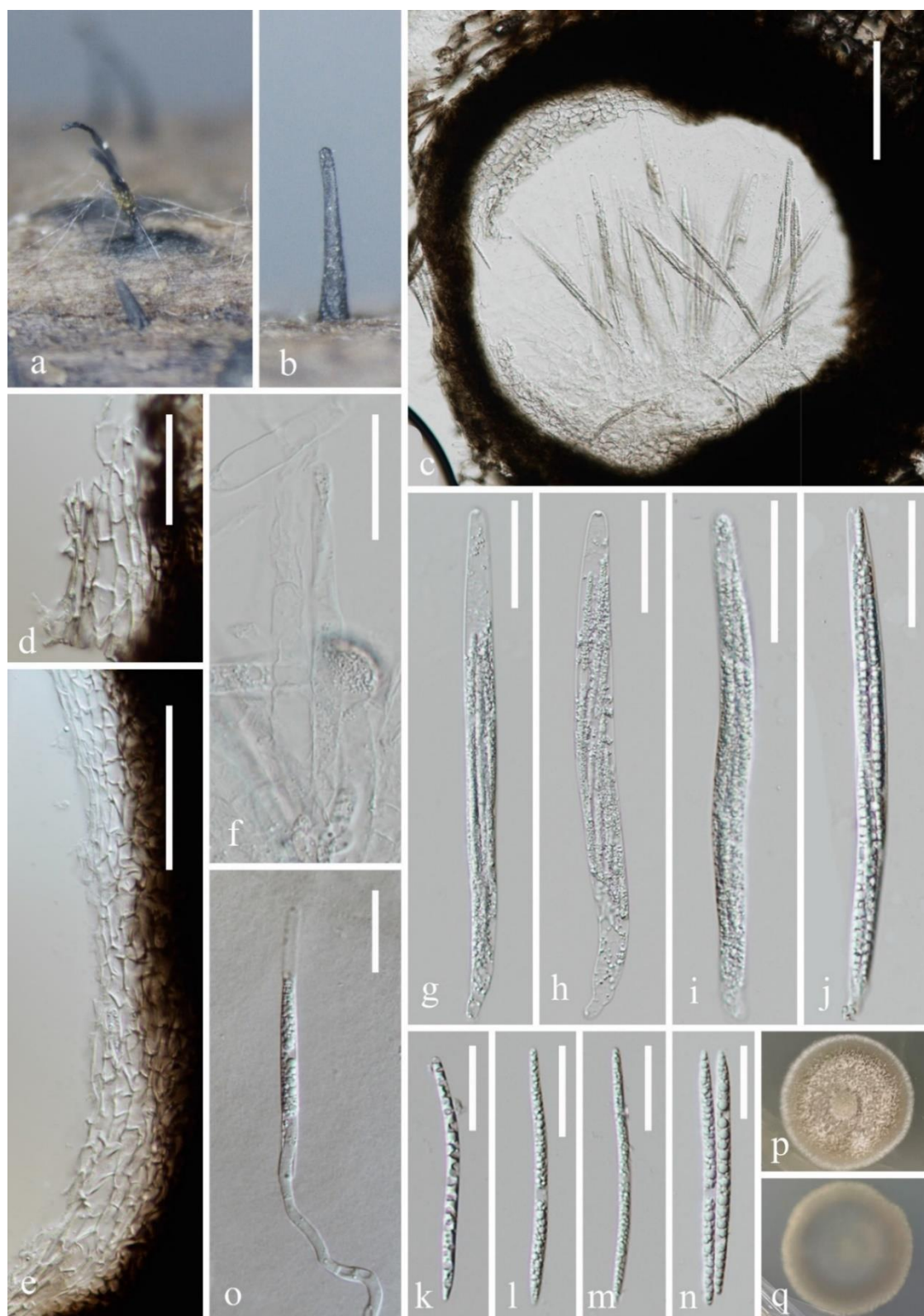


Figure 48 – *Ophioceras aseptatum* (HKAS 131369, holotype). a, b Ascomata on the substratum. c Vertical section of ascoma. d, e Structure of peridium. f Paraphyses. g–j Asci. k–n Ascospores. o Germinating ascospore. p, q Colony on PDA from surface and reverse. Scale bars: c = 100 μ m, d = 30 μ m, e = 50 μ m, f–j = 40 μ m, k–o = 20 μ m.



Figure 49 – *Ophioceras cylindrosporum* (HKAS 131351, holotype). a Ascomata on the substratum. b Vertical section of ascoma. c–e Structure of peridium. f, i–l Asci. g, h Paraphyses. m–o Ascospores. p Germinating ascospore. q, r Colonies on PDA from surface and reverse. Scale bars: b = 60 μ m, c, d, f–l = 20 μ m, e, m–p = 10 μ m.

***Pararamichloridium* Crous**

Pararamichloridium was established by Crous et al. (2017) to accommodate two new species *P. livistonae* (type species) and *P. verrucosum*. *Pararamichloridium* is characterized by

macronematous, mononematous, subcylindrical, unbranched conidiophores, pimple-like denticles, polyblastic conidiogenous cells, and aseptate, ellipsoid or globose to subglobose conidia (Crous et al. 2017, 2018, Jayawardena et al. 2022) Four species currently are accepted in *Pararamichloridium*, with only *P. aquisubtropicum* collected from a freshwater habitat (Crous et al. 2017, 2018, Jayawardena et al. 2022).

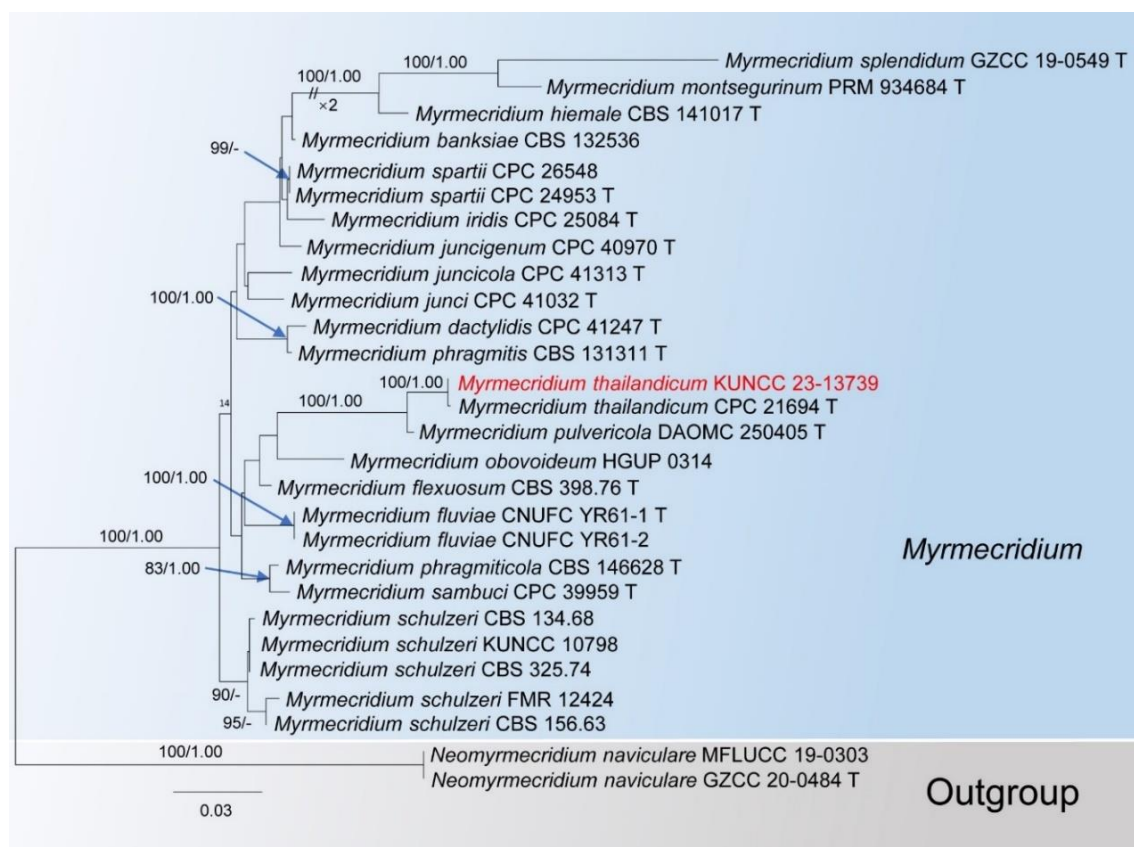


Figure 50 – RAxML tree based on analysis of *Myrmecridium* that combined LSU and ITS dataset. The combined analyses include 28 strains with 1338 characters including gaps (LSU: 799 bp and ITS: 539 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Neomyrmecridium naviculare* (GZCC 20-0484 and MFLUCC 19-0303). The new collection is indicated in red. Ex-type strains are indicated with “T” after the strain number.

Pararamichloridium caricicola Crous, Persoonia 41, 281 (2018)

Fig. 52

Index Fungorum number: IF828187; Facesoffungi number: FoF16111

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, scattered, hairy, brown. *Mycelium* mostly immersed, composed of branched, septate, smooth, pale brown hyphae. *Conidiophores* 120–200 × 2.9–3.9 µm ($\bar{x}$ = 161.4 × 3.6 µm, n = 25), macronematous, mononematous, subcylindrical, straight or flexuous, unbranched, brown at the base, paler towards the apex, septate, verrucose. *Conidiogenous cells* polyblastic, integrated, terminal and intercalary, sympodial, forming a rachis with numerous pimple-like denticles, subhyaline to pale brown. *Conidia* 5.7–8.1 × 2.6–3.5 µm ($\bar{x}$ = 7 × 3.1 µm, n = 40), solitary, aseptate, pale brown, ellipsoid or elongated oval, smooth to finely verrucose, thin-walled, rounded at the apex. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from the base. Colonies on PDA reaching 30 mm diameter after 3 weeks at room temperature. Mycelium dense, dry, colonies on the surface of PDA, slightly crease, with regular edges, flat surface, brown. Reverse brown to reddish brown, circular, smooth.



Figure 51 – *Myrmecridium thailandicum* (HKAS 131399). a Colonies on the substratum. b, e, f Conidiophores. c, d, g, h Conidiophores with conidia. i–k Apex of conidiophores with conidia. l–p Conidia. q, r Colonies on PDA from surface and reverse. Scale bars: b–h = 20 μ m, i–k = 10 μ m, l, m = 5 μ m, n–p = 2 μ m.

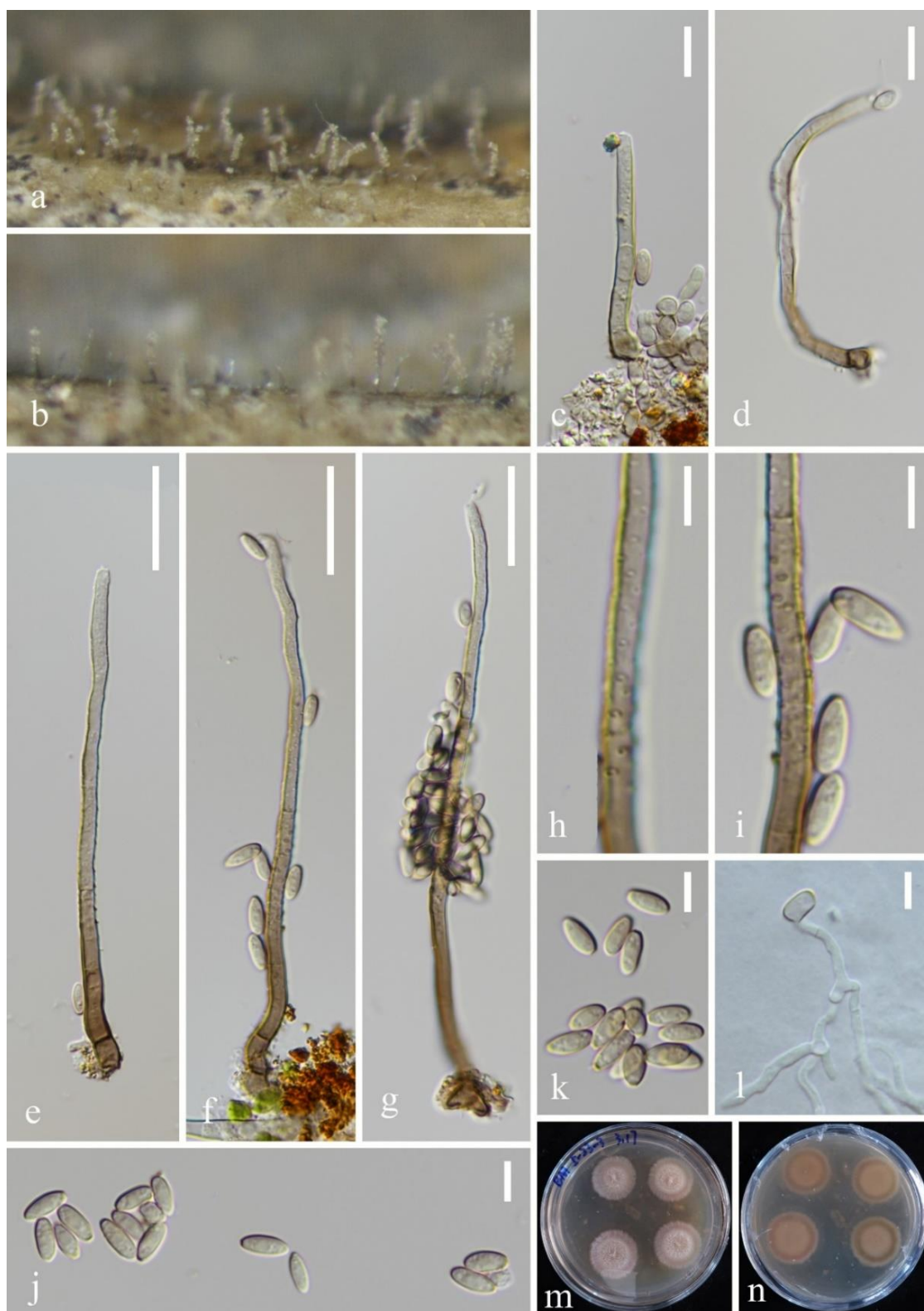


Figure 52 – *Pararamichloridium caricicola* (HKAS 130439). a, b Colonies on the substratum. c–g Conidiophores and conidia. h Conidiogenous cells. i Conidiogenous cells and conidia. j, k Conidia. l Germinating conidium. m, n Colonies on PDA from surface and reverse. Scale bars: c, d = 10 μ m, e–g = 20 μ m, h–l = 5 μ m.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, H-706 (HKAS 130439).

Notes – *Pararamichloridium caricicola* was introduced by Crous et al. (2018), and collected from Thailand on a leaf of *Carex* sp. (*Cyperaceae*). In the phylogenetic analysis, our new collection (HKAS 130439) clustered with *P. caricicola* (CPC 34533) with 100 ML/1.00 PP support (Fig. 47). In addition, our new collection fits well with the original description of *P. caricicola*. Therefore, we identify our new collection as *P. caricicola*, and it was collected from China for the first time.

***Pleurotheciales* Réblová & Seifert**

***Pleurotheciaceae* Réblová & Seifert**

Pleurotheciaceae was introduced by Réblová et al. (2016b), which is the only family in *Pleurotheciales*. The sexual morph of *Pleurotheciaceae* is characterized by perithecial, immersed to superficial, papillate ascomata, with a carbonaceous, brown ascomata wall, branched, cylindrical paraphyses, unitunicate asci with a non-amyloid apical ring, and hyaline or versicolored, one median septate or transversely multi-septate ascospores. The asexual morphs of *Pleurotheciaceae* are represented by hyphomycetes with diverse morphologies, comprising acrodictys-like, helicoon-like, monodictys-like, dactylaria-like taxa, and several genera with muriform conidia (Réblová et al. 2016b, Luo et al. 2018b, Dong et al. 2021b, Jayawardena et al. 2022). 17 genera are accepted in *Pleurotheciaceae*, and *Pleurotheciaceae* species have been found from freshwater, marine, and terrestrial habitats (Réblová et al. 2016b, Boonmee et al. 2021, Bao et al. 2022, Tian et al. 2024b, Wang et al. 2024).

***Phaeoisaria* Höhn.**

Phaeoisaria was established by Höhnelt (1909), with *P. bambusae* as the type species. The asexual morph of *Phaeoisaria* is characterized by indeterminate synnemata, parallel adpressed conidiophores with numerous sympodially extending denticulate conidiogenous cells, and aseptate or septate, mostly ellipsoidal to obovoidal, hyaline conidia (Réblová et al. 2016b, Hyde et al. 2019, Liu et al. 2022). Luo et al. (2019) reported the first species with sexual morph in *Phaeoisaria* (*P. filiformis*), which is characterized by immersed, globose to elongate globose ascomata with a long neck, branched, septate paraphyses, unitunicate, cylindrical asci with a small refractive apical apparatus, and filiform, multi-septate, hyaline ascospores.

***Phaeoisaria pseudoclematidis* D.Q. Dai & K.D. Hyde, Fungal Divers. 72, 24 (2015) Fig. 54**
Index Fungorum number: IF550942; Facesoffungi number: FoF00452

Saprobic on submerged decaying wood. Asexual morph: Colonies effuse, scattered, hairy, dark brown to black, covered by white conidial mass. Mycelium mostly immersed, partly superficial, composed of branched, septate, hyaline to pale brown, smooth hyphae. Synnemata 310–1330 × 14–38 µm ($\bar{x}$ = 743.5 × 24.8 µm, n = 10), erect, straight or slightly flexuous, rigid, dark brown to black, velvety, composed of compactly and parallel adpressed conidiophores, with flared conidiogenous cells in the above half. Conidiophores macronematous, synnematos, cylindrical, brown to dark brown, septate, rarely branched, smooth-walled. Conidiogenous cells 5.3–22 × 1.3–2.9 µm ($\bar{x}$ = 15.2 × 2.3 µm, n = 10), polyblastic, terminal, integrated or discrete, curved, hyaline to pale brown, smooth-walled, sympodial, with several denticulate conidiogenous loci. Conidia 5.1–7.4 × 2.3–3.6 µm ($\bar{x}$ = 6.3 × 2.8 µm, n = 30), ellipsoidal to obovoid, straight, rounded at the apex, aseptate, hyaline, smooth-walled, guttulate. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 10 mm diameter after 3 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, protuberance, hard, with regular edge, brown to dark green. Reverse circular, white to dark brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3479 (HKAS 131361), living culture KUNCC 23–13718.

Notes – Our new collection fits well with *Phaeoisaria pseudoclematidis*, and the phylogenetic analysis showed that our new collection clustered with the ex-type strain of *P. pseudoclematidis*, which support them to be the same species (Fig. 53). Thus, we identified our new collection as

P. pseudoclematidis, a species originally isolated from dead culm of bamboo (*Bambusae*) in Chiang Rai, Thailand (Liu et al. 2015b), and it is the first time to report this species from China.

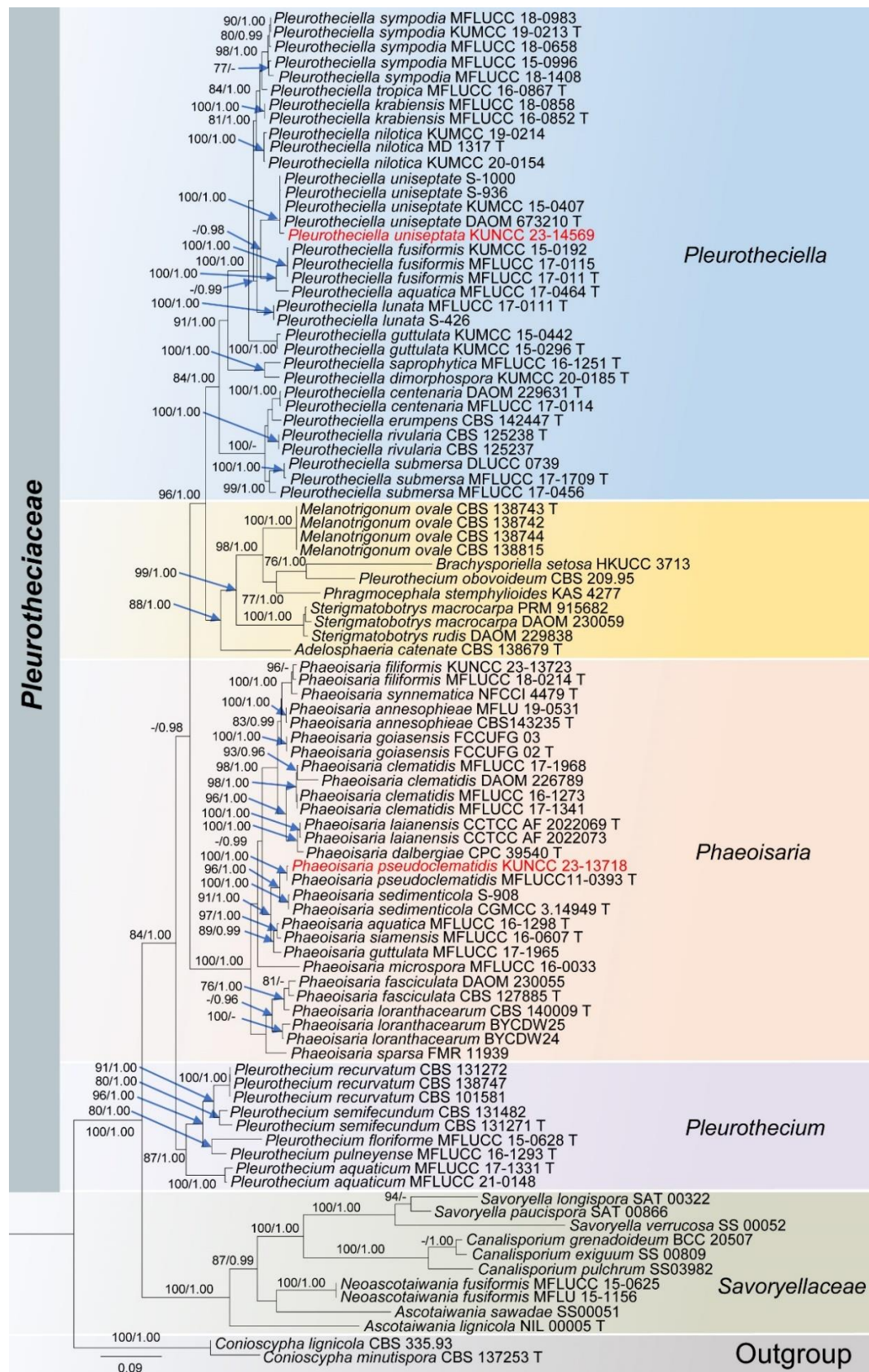


Figure 53 – RAxML tree based on analysis of *Pleurotheciaceae* that combined LSU, ITS, SSU, and *rpb2* dataset. The combined analyses include 94 strains with 3292 characters including gaps (LSU: 810 bp, ITS: 517 bp, SSU: 936 bp, and *rpb2*: 1029 bp). Bootstrap support values for maximum

likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Coniioscypha lignicola* (CBS 335.93) and *C. minutispora* (CBS 137253). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.

***Pleurotheciella* Réblová, Seifert & J. Fourn.**

Pleurotheciella was introduced by Réblová et al. (2012), with *P. rivularia* as the type. The genus is known by both sexual and asexual morphs, which are characterized by subglobose, semi-immersed to superficial ascomata, unitunicate, cylindrical-clavate asci, and ellipsoidal-fusiform, septate ascospores; reduced or unbranched or branched, synnematosus or solitary conidiophores, integrated, conidiogenous cells with denticles, and ellipsoidal to obovoidal to subcylindrical, aseptate or septate conidia (Réblová et al. 2012, Boonmee et al. 2021, Shi et al. 2021). *Pleurotheciella* is distributed worldwide, with 23 accepted species, and most species are known from freshwater habitats, only *P. acericola*, *P. dimorphospora* and *P. hyalospora* are known from terrestrial habitats (Abdel-Aziz et al. 2020, Boonmee et al. 2021, He et al. 2024, Liu et al. 2024b, Wang et al. 2024).

***Pleurotheciella uniseptata* (Matsush.) Seifert, Persoonia, 37, 74 (2016)**

Fig. 55

Index Fungorum number: IF813238; Facesoffungi number: FoF03418

Saprobic on submerged decaying wood. Asexual morph: Colonies superficial, effuse, scattered or gathered, hairy, with dry, whitish to greyish conidia at the apex of conidiophores. Mycelium partly immersed, partly superficial, composed of septate, smooth, unbranched, brown hyphae. Conidiophores 100–160 × (2.7–) 3.3–5.2 µm ($\bar{x}$ = 130.7 × 4 µm, n = 15), macronematous, mononematous, cylindrical, straight or slightly flexuous, unbranched, septate, subhyaline to dark brown, paler towards the apex, smooth-walled, usually with a terminal node of denticles, but rarely extending through the original node with a new extension of the conidiophore. Conidiogenous cells polyblastic, integrated, terminal, cylindrical, subhyaline, smooth-walled, forming conidia sympodially on conspicuous, 1–2 µm long denticles. Conidia 12–17 × 3.2–5.2 µm ($\bar{x}$ = 14.3 × 4.3 µm, n = 20), acrogenous, solitary, subhyaline, guttulate, fusiform or clavate, straight or slightly curved, smooth-walled, uniseptate, slightly constricted at the septum. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced from both ends. Colonies on PDA reaching 15 mm diameter after 3 weeks at room temperature. Mycelium dense, dry, colonies semi-immersed on PDA, surface rough, irregular edges, dry, brownish yellow to dark brown, has a small protrusion in the center. Reverse brownish yellow to brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W. P. Wang, S-4361 (HKAS 131370), living culture KUNCC 23–14569.

Notes – Based on phylogenetic analysis and morphological characteristics, Réblová et al. (2016b) synonymized *Dactylaria uniseptata* as *Pleurotheciella uniseptata*. This species was recollected on submerged decaying wood in Yunnan Province, China (Luo et al. 2018b). Phylogenetic analysis showed that our new collection nested within *P. uniseptata* clade, and our new collection (KUNCC 23–14569) resembles *P. uniseptata* in having unbranched, cylindrical conidiophores, denticulate conidiogenous cells, and fusiform or clavate, straight or slightly curved, uniseptate conidia (Réblová et al. 2016b, Luo et al. 2018b). Thus, we identify our new collection as *P. uniseptata*.

***Savoryellales* Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones**

***Savoryellaceae* Jaklitsch & Réblová**

Savoryellaceae was introduced by Jaklitsch (2015), with *Savoryella* as the type. It is characterized by immersed or superficial, perithecial, globose to pyriform ascomata with periphysate ostioles, coriaceous peridium composed of thick-walled cells, unitunicate, clavate to cylindrical asci with an inamyloid apical ring, and 2-spored or 8-spored, ellipsoidal, fusiform, several-septate

ascospores with or without a polar mucilaginous pads or appendages. Asexual morphs of *Savoryellaceae* are hyphomycetes, characterized by sporodochial conidiomata or effuse colonies, reduced or short conidiophores, and subglobose or obovate to oval conidia with transverse or muriform septa (Dayarathne et al. 2019, Zhang et al. 2019, Yang et al. 2023, Yu et al. 2023). Seven genera including *Aquabispora*, *Ascotaiwania*, *Bactrodesmium*, *Canalisporium*, *Dematiosporium*, *Neoscotaiwania*, and *Savoryella* are accepted in this family (Wijayawardene et al. 2020, Boonmee et al. 2021, Yang et al. 2023).



Figure 54 – *Phaeoisaria pseudoclematidis* (HKAS 131361). a Colonies on the substratum. b–d Synnemata. e Middle to apex of synnema. f Apex of synnema. g Conidiogenous cells.

h Conidiogenous cells with conidia. i, j Conidia. k, l Colonies on PDA from surface and reverse. Scale bars: b, e = 100 µm, c, d = 150 µm, f = 20 µm, g, h = 10 µm, i, j = 5 µm.

Ascolacicola Ranghoo & K. D. Hyde

Ascolacicola was established by Ranghoo & Hyde (1998), with *A. aquatica* as the type species, and currently only the type is accepted in this genus. *Ascolacicola* is characterized by superficial, subglobose, ostiolate, coriaceous ascomata with periphysate, black neck, peridium comprises of several layers of brown, flattened cells, filamentous, flexuous paraphyses, unitunicate, 8-spored, cylindrical, short pedicellate asci with an apical ring, and ellipsoidal or fusiform, septate, brown ascospores with hyaline to pale brown end cells in sexual morph; monotosporella-like asexual morph with broadly obovoidal or pyriform, 1–3-septate conidia with broadly rounded at the apex (Ranghoo & Hyde 1998).

In the phylogenetic analysis, *Ascotaiwania* is polyphyletic and divided into two clades within *Savoryellaceae*, *Ascotaiwania lignicola* and *A. latericola* are sister to *Dematiosporium*. While another clade (including, *Ascot. coffeae*, *Ascot. mitriformis*, *Ascot. sawadae*, *Ascolacicola minispora*, and *Triadelphia uniseptata*) formed a distinct clade basal to the four genera *Ascotaiwania*, *Bactrodesmium*, *Dematiosporium*, and *Neoascotaiwania* (Fig. 56), and these species have broadly obovoidal or pyriform with broadly rounded apical, septate, the upper cells are significantly larger than the basal cells in asexual morph, and are similar to *Ascolacicola* (Ranghoo & Hyde 1998, Dayarathne et al. 2019, Liu et al. 2024a). Therefore, based on morphological characteristics and phylogenetic analysis, we incorporated *Ascolacicola* into *Savoryellaceae*, introduced a new species named *Ascol. minispora*, and transferred *Ascot. coffeae*, *Ascot. mitriformis*, *Ascot. sawadae*, and *Triadelphia uniseptata* to *Ascolacicola*.

Ascolacicola coffeae (L. Lu & Karun.) W.P. Wang, H.W. Shen & Z.L. Luo, comb. nov.

Index Fungorum number: IF902898; Facesoffungi number: FoF16783

Basionym – *Ascotaiwania coffeae* L. Lu & Karun., Mycology, 9 (2024)

Holotype – China. Yunnan Province, Dali City, on a decaying branch of *Coffea arabica*, (101°91'E, 26°09' N, 1,416.46 m), 25 July 2022, DLC19 (ZHKU 23–0083, holotype), living culture ZHKUCC 23–0676 (ex-type) and ZHKUCC 23–0677.

Notes – *Ascotaiwania coffeae* was introduced by Liu et al. (2024a) on decaying branch of *Coffea arabica* in Yunnan Province, China. In our phylogenetic analysis, *Ascotaiwania coffeae* clustered within *Ascolacicola* (Fig. 56). Therefore, we transfer *Ascot. coffeae* to *Ascolacicola* as *Ascol. coffeae* comb. nov.

Ascolacicola minispora W.P. Wang, H.W. Shen, K. D. Hyde & Z.L. Luo, sp. nov.

Fig. 57

Index Fungorum number: IF902897; Facesoffungi number: FoF16784

Etymology – Referring to the smaller conidia in this genus.

Holotype – HKAS 131368

Saprobic on submerged decaying wood. Asexual morph: Colonies superficial, effuse, scattered or gathered, dark brown, glistening. Mycelium immersed, composed of unbranched, aseptate, subhyaline hyphae. Conidiophores reduced to conidiogenous cells. Conidiogenous cells indistinct. Conidia 8.4–12 × 4.1–6.7 (–8.1) µm ($\bar{x}$ = 9.9 × 5.7 µm, n = 40), solitary, obovoidal to pyriform, rounded at the apex, smooth-walled, uniseptate near the base, brown, darkened and thickly banded at the septum, the upper cells are significantly larger than the basal cells, guttulate. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 12 h, and germ tubes produced in the base. Colonies on PDA reaching 15 mm diameter after 5 weeks at room temperature. Mycelium dense, dry, colonies on the surface of PDA, surface rough, dry, irregular edges, initially is dark brown and later covered with a layer of white hyphae. Reverse white to black, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4591 (HKAS 131368, holotype), ex-type living cultures CGMCC 3.25436 = KUNCC 23–14565.



Figure 55 – *Pleurotheciella uniseptata* (HKAS 131370). a, b Colonies on the substratum. c–f Conidiophores. g Apex of conidiophores, conidiogenous cell with conidia. h Conidia. i Germinating conidium. j, k Colony on PDA from surface and reverse. Scale bars: c, d = 20 μ m, e, f = 30 μ m, h = 15 μ m, i = 5 μ m.

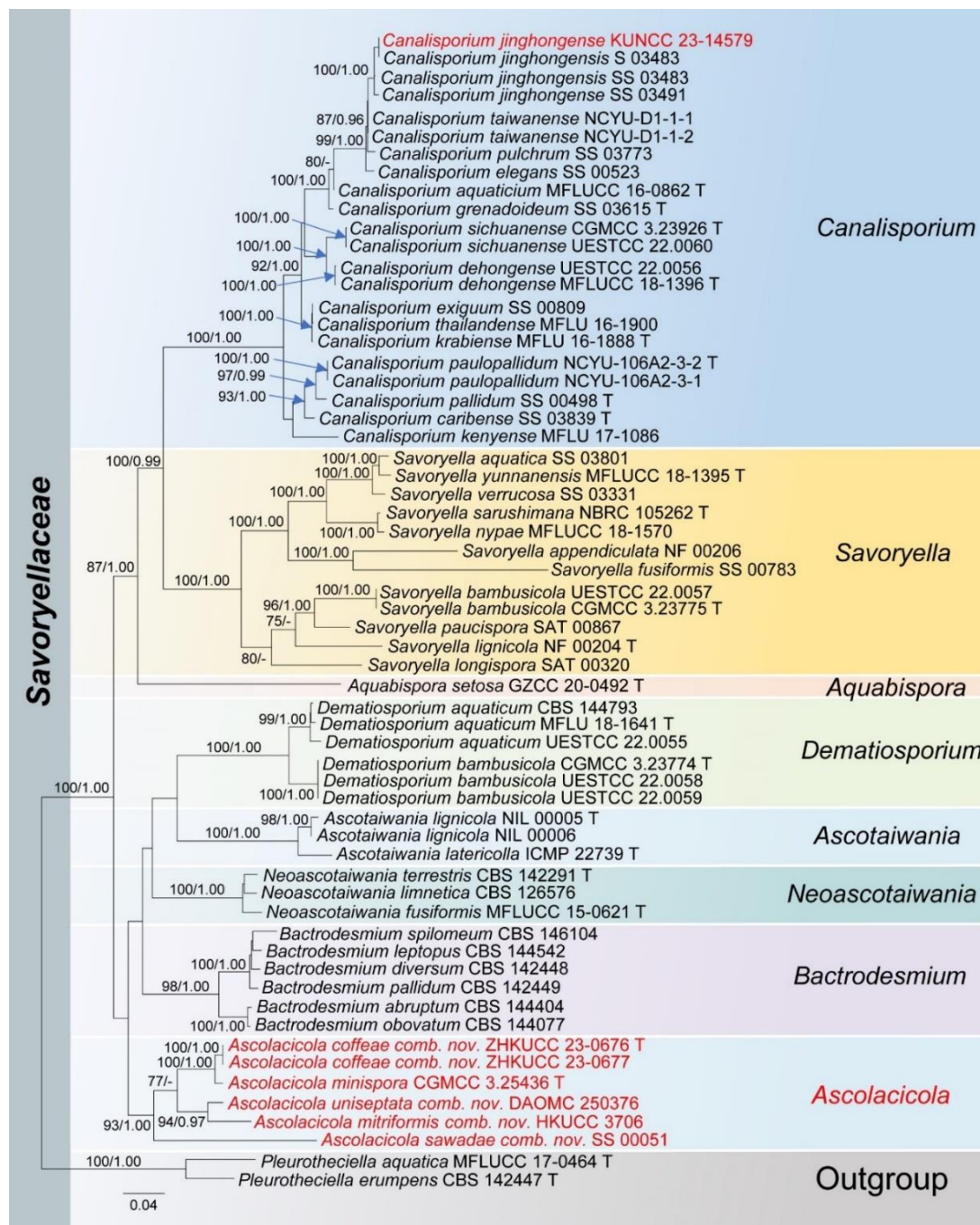


Figure 56 – RAxML tree based on analysis of *Savoryellaceae* that combined LSU, ITS, SSU, *rpb2*, and *tef1-α* dataset. The combined analyses include 61 strains with 4194 characters including gaps (LSU: 798 bp, ITS: 520 bp, SSU: 944 bp, *rpb2*: 1061 bp, and *tef1-α*: 871 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Pleurotheciella aquatica* (MFLUCC 17-0464) and *P. erumpens* (CBS 142447). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.

Notes – Phylogenetic analysis showed that *Ascolacicola coffeae*, *A. minispora*, *A. mitriformis*, *A. sawadae*, and *A. uniseptata* clustered within the genus *Ascolacicola*, with the new species *A. minispora* sister to *A. coffeae* with 100% ML/1.00 PP support (Fig. 56). Comparisons of the ITS, LSU, SSU, *tef1-α*, and *rpb2* sequences of *A. minispora* and the ex-type strain of *A. coffeae* showed 2.24% (12/536 bp, six gaps), 0.24% (2/837 bp), 0.2% (2/992 bp), and 0.87% (8/902 bp), and 3.08% (27/877 bp, three gaps) difference, respectively. *Ascolacicola coffeae* has micronematous,

mononematous conidiophores and terminal becoming intercalary, subglobose or ampulliform conidiogenous cells, while the conidiophores of *A. minispora* are usually reduced to conidiogenous cells and conidiogenous cells are inconspicuous (Liu et al. 2024a). Limited by the small morphological differences between several *Ascolacicola* asexual species, we recognize *A. minispora* as a distinct species based on molecular data.

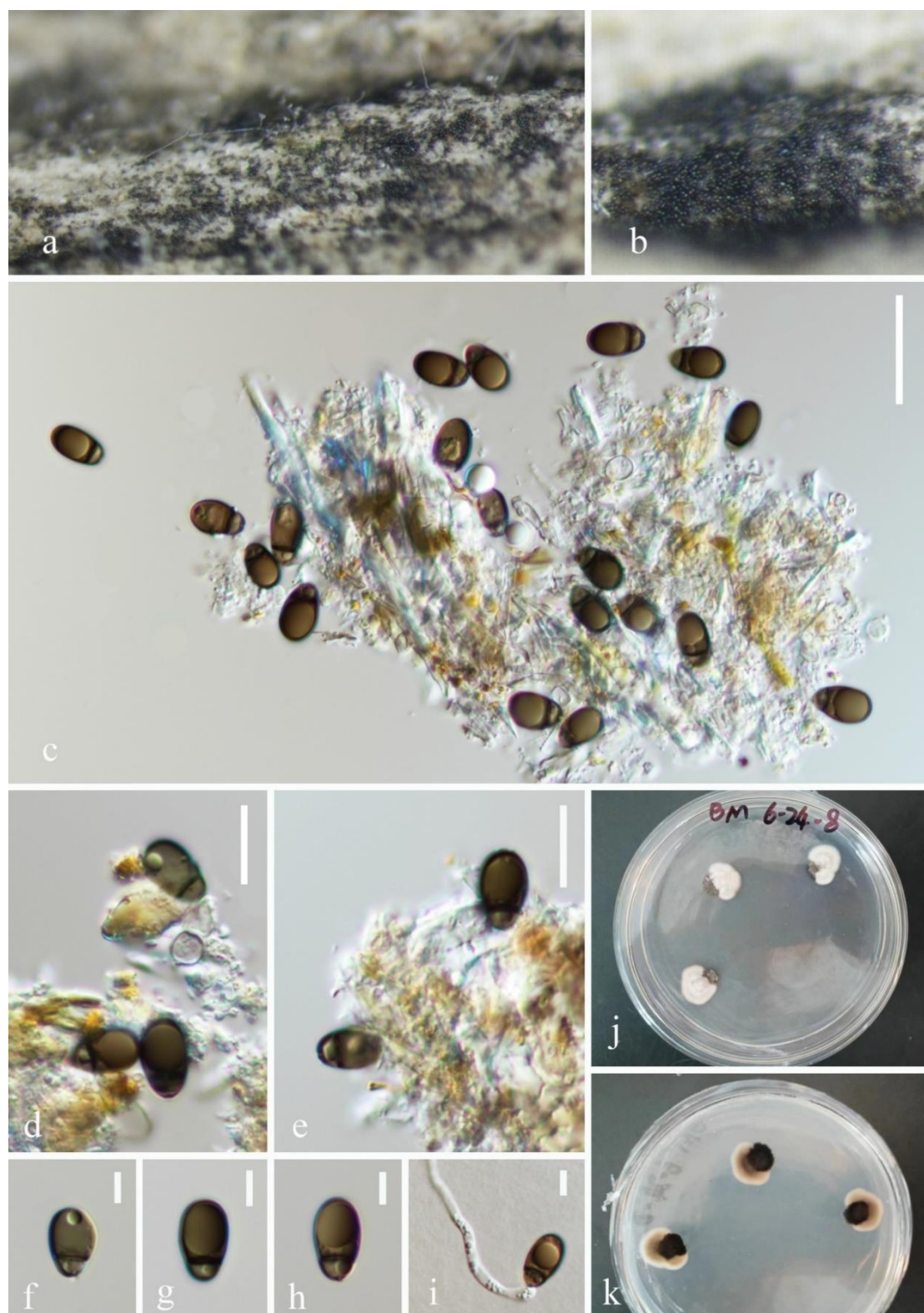


Figure 57 – *Ascolacicola minispora* (HKAS 131368, holotype) a, b Colonies on the substratum. c–e Conidia on the substratum. f–h conidia. i Germinating conidium. j, k Colonies on PDA from surface and reverse. Scale bars: c = 20 μ m, d, e = 10 μ m, f–i = 5 μ m.

Ascolacicola mitriformis (Ranghoo & K.D. Hyde) W.P. Wang, H.W. Shen & Z.L. Luo, comb. nov.
Index Fungorum number: IF902899; Facesoffungi number: FoF16785
Basionym – *Ascotaiwania mitriformis* Ranghoo & K.D. Hyde, Mycologia 90(6), 1059 (1998)
Holotype – China, Hongkong SAR, on submerged wood, 26 Jan. 1997 (HKU(M) 5224).

Notes – *Ascotaiwania mitriformis* was introduced by Ranghoo et al. (1998) from a freshwater habitat in Hong Kong, China. In our phylogenetic analysis, *Ascot. mitriformis* is sister to *Ascol. uniseptata* with 94% ML/0.97 PP support (Fig. 56). We Therefore transfer *Ascot. mitriformis* to *Ascolacicola* as *Ascol. mitriformis* comb. nov.

Ascolacicola sawadae (H. S. Chang & S.-Y. Hsieh) W.P. Wang, H.W. Shen & Z.L. Luo, comb. nov.
Index Fungorum number: IF902900; Facesoffungi number: FoF16117

Basionym – *Ascotaiwania sawadae* H.S. Chang & S.-Y. Hsieh, Mycol. Res. 102 (6), 713 (1998)

Holotype – China, Taiwan, Taipei, Hsoutoupu, 25 Mar. 1992, H.S. Chang, HTP 0329- A0-2, holotype.

Notes – *Ascotaiwania sawadae* was introduced by Chang et al. (1998) from a freshwater habitat in Taiwan, China. Phylogenetic analysis showed that *Ascot. sawadae* clustered within *Ascolacicola* (Fig. 56). We therefore transfer *Ascot. sawadae* to *Ascolacicola* as *Ascol. sawadae* comb. nov.

Ascolacicola uniseptata (H. S. Chang & S.-Y. Hsieh) W.P. Wang, H.W. Shen & Z.L. Luo, comb. nov.

Index Fungorum number: IF902901; Facesoffungi number: FoF16786

Basionym – *Triadelphia uniseptata* P.M. Kirk, Trans. Br. mycol. Soc. 80(3), 464 (1983)

Trichocladium uniseptatum S. Hughes & Piroz. (1973)

Sporidesmium uniseptatum Berk. & Broome (1859)

Holotype – Great Britain, on *Clematis vitalba*, Jan. 1859.

Note – *Triadelphia uniseptata* has been placed within *Ascotaiwania* in previous phylogenetic studies (Réblová et al. 2016b, Yang et al. 2016, Hernández-Restrepo et al. 2017, Dayarathne et al. 2019, Yu et al. 2023). However, it is sister to *Ascolacicola mitriformis* with 94% ML/0.97 PP support in the present study (Fig. 56). Therefore, we transfer *T. uniseptata* to *Ascolacicola* as *Ascol. uniseptata* comb. nov. based on phylogenetic studies results.

Canalisporium Nawawi & Kuthub.

Canalisporium, typified by *C. caribense*, was introduced by Sri-indrasutdhi et al. (2010) to accommodate ten species. The genus is characterized by septate, branched or unbranched conidiophores, consisting of subglobose cells, monoblastic, terminal conidiogenous cells, and dark brown, muriform conidia with thick and darkened septa (Ho & Hyde 2004, Goh & Kuo 2021, Yu et al. 2023). Members of *Canalisporium* are commonly distributed in pantropic, and grow on dead wood from terrestrial and freshwater habitats (Goh et al. 1998, Ferrer & Shearer 2005, Zhang et al. 2014b, Hyde et al. 2019, 2020a). Recently, Worobiec et al. (2021) introduced a new species, *C. lignitum*, on lignite from middle Miocene in Poland. Currently, a total of 23 species are accepted in this genus (Yu et al. 2023, Index Fungorum 2024).

Canalisporium jinghongense L. Cai, K.D. Hyde & McKenzie, Cryptog. Mycol. 24(1), 4 (2003)

Fig. 58

Index Fungorum number: IF550942; Facesoffungi number: FoF16112

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, punctiform, pulvinate, square granular, dark brown. *Mycelium* immersed, composed of unbranched, septate, subhyaline to pale brown hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.4–7.6 × 2.3–4 µm ($\bar{x}$ = 4.7 × 3.2 µm, n = 15), monoblastic, cuneiform, integrated, terminal, determinate, hyaline, sharp at the base. *Conidia* 22–35 × 18–30 µm ($\bar{x}$ = 28.1 × 24 µm, n = 40), solitary, acrogenous, obovoid to irregularly subglobose, brown, smooth, thick-walled, usually

composed of (2–) 3 (–4) rows of transverse septa, and 3–5 columns, starting at the base of the cells, strongly constricted at the septum, darkened and thickly banded at the septa, basal cell cuneiform, guttulate, flat, and on the same plane. Sexual morph: Undetermined.

Culture characteristics – Colonies on the surface of PDA, slow-growing, reaching 10 mm diam in 1 month at room temperature, dry, surface rough, dry, irregular edges, reddish brown to dark brown. Reverse dark brown to black, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4593 (HKAS 131357), living culture KUNCC 23–14579.

Notes – Phylogenetic analysis showed that our new collection (KUNCC 23–14579) clustered with two strains of *Canalisporium jinghongense* (SS 03483 and SS 03491) (Fig. 56). Conidia of our new collection are irregularly subglobose with (2–) 3 (–4) transverse and 2–4 vertically thickly banded septum, and strongly constricted at the septum, which are similar to those of *C. jinghongense*. Therefore, we identify our new collection as *C. jinghongense*. This species has been collected from freshwater habitats in China and Thailand (Boonyuen et al. 2011, Goh & Kuo 2021).

***Sporidesmiales* Crous**

***Sporidesmiaceae* Fr.**

Sporidesmiaceae, a species rich family, was introduced by Fries (1849) with only the type genus *Sporidesmium* accepted. Most species accepted in this family are introduced based mainly on morphological characteristics (Koukol & Delgado 2021, Hyde et al. 2020b). With the application of molecular data, several species have been transferred to other families of *Dothideomycetes* and *Sordariomycetes* (Hyde et al. 2020b). At present, less than 200 species are accepted in this family, with about 30 species having DNA sequences in the GenBank (Hyde et al. 2020b, Bao et al. 2021, Dong et al. 2021a, Yang et al. 2023). In addition, recent phylogenetic analysis showed that *Sporidesmiaceae* are polyphyletic (Yang et al. 2018b, Liu et al. 2019, Bao et al. 2021, Hyde et al. 2021), therefore, a comprehensive and systematic study for *Sporidesmiaceae* is expected to be carried out in future.

***Sporidesmium* Link**

Sporidesmium was established by Link (1809), with *S. atrum* as the type species. Most species of this genus are reported by the asexual morphs, which are characterized by solitary conidiophores or sometimes aggregated in groups, cylindrical, erect or somewhat repent and septate, monoblastic, terminal, cylindrical conidiogenous cells, and acrogenous, distoseptate or euseptate conidia (Su et al. 2016). Currently, only two species (*S. thailandense* and *S. lignicola*) are reported with sexual morph, and they are characterized by 8-spored, unitunicate, cylindrical asci with a distinct, relatively small, refractive, wedge-shaped apical ring, and fusiform, hyaline, septate ascospores (Zhang et al. 2017, Luo et al. 2019).

The current classification system considers that *Sporidesmium* is polyphyletic (Yang et al. 2018b, Liu et al. 2019, Bao et al. 2021, Hyde et al. 2021), and more than 500 species epithets are listed under this genus in Index Fungorum (2024), which are largely due to the acceptance of the species with a broad concept, such as erect, cylindrical conidiophores, monoblastic, terminal conidiogenous cells, and acrogenous, obclavate, septate conidia with or without mucilaginous sheath. However, several genera such as *Ellisembia*, *Kirschsteiniothelia*, and *Neopodoconis* share similar characteristics with *Sporidesmium*, but they are distributed in different families and classes based on phylogenetic analysis (Yang et al. 2023). Therefore, there are still some difficult problems in sporidesmium-like taxa, and further phylogenetic studies are required to clarify the existing problems.

***Sporidesmium aquaticivaginatatum* J. Yang & K.D. Hyde, Fungal Divers. 80, 217 (2016)**

Fig. 60

Index Fungorum number: IF552229; Facesoffungi number: FoF02369

Saprobia on submerged decaying wood. Asexual morph: *Colonies* effuse, scattered or in small groups, hairy, brown to dark brown. *Mycelium* mostly immersed, composed of branched, septate, hyaline to pale brown, smooth-walled hyphae. *Conidiophores* 30–75 × 3.5–5.9 µm ($\bar{x}$ = 53 × 4.9 µm, n = 20), macronematous, mononematous, solitary, cylindrical, straight or slightly flexuous, 1–4-septate, thick-walled, dark brown, truncate at the apex, ellipsoidal or globose at the base. *Conidiogenous cells* 12–19 × 4–5.8 µm ($\bar{x}$ = 14.5 × 4.8 µm, n = 20), monoblastic, integrated, terminal, determinate, cylindrical, smooth-walled, dark brown. *Conidia* (24–) 38–68 × 8.6–12.1 µm ($\bar{x}$ = 53.2 × 11.2 µm, n = 20), acrogenous, solitary, dry, olivaceous to pale brown, paler at the apex, obclavate, tapering gradually towards the apex, smooth-walled, straight or slightly curved, 6–12-distoseptate, most with a mucilaginous sheath over the apex, truncate basal with a 3–4.5 µm wide conspicuous darkened scar. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 24 h, and germ tubes produced at the apex. Colonies on PDA reaching 10 mm diameter after 4 weeks at room temperature. Mycelium damp, dense, colonies on the surface of PDA, dry, with rough surface, irregular edges, protrusion in the center, brown to dark brown. Reverse brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3827 (HKAS 131383), living culture KUNCC 23–13373.

Notes – *Sporidesmium aquaticivaginatum* was introduced by Hyde et al. (2016b) and collected from a freshwater habitat in Thailand. In the phylogenetic analysis, our isolate clustered with the holotype of *S. aquaticivaginatum* (MFLU 15–1159) with 100% ML/1.00 PP support (Fig. 59). Our new collection fits with the concept of *S. aquaticivaginatum* in having cylindrical conidiophores with triangular or globose bases, and solitary, distoseptate conidia with a mucilaginous sheath and truncate base with a 3–4.5 µm wide conspicuous darkened scar. We therefore identified our new collection as *S. aquaticivaginatum*, and it is the first time to report this species from China.

Sporidesmium guttulatum W.P. Wang, H.W. Shen, K. D. Hyde & Z.L. Luo, sp. nov. Fig. 61

Index Fungorum number: IF902435; Facesoffungi number: FoF16119

Etymology – Referring to guttulate conidia of this fungus.

Holotype – HKAS 131397

Saprobia on submerged decaying wood. Asexual morph: *Colonies* effuse, hairy, scattered or in small groups, olivaceous to brown. *Mycelium* mostly immersed, composed of branched, septate, hyaline to pale brown, smooth hyphae. *Conidiophores* 26–55 × 3.4–5 µm ($\bar{x}$ = 40 × 4 µm, n = 20), macronematous, mononematous, solitary, cylindrical, straight or slightly flexuous, 1–3-septate, smooth-walled, olivaceous to brown, truncate at apex, swollen at the base. *Conidiogenous cells* 12–20 × 3–4.8 µm ($\bar{x}$ = 15.4 × 3.9 µm, n = 20), monoblastic, integrated, terminal, determinate, cylindrical, smooth-walled, olivaceous to brown. *Conidia* 44–84 × 8.7–12 µm ($\bar{x}$ = 64 × 10.1 µm, n = 20), acrogenous, solitary, dry, olivaceous to pale brown, paler at the apex, obclavate, tapering gradually towards the apex, smooth-walled, straight or slightly curved, 6–14-distoseptate, guttulate, most with a mucilaginous sheath over the apex to middle, truncate basal with a 2–3.1 µm wide conspicuous darkened scar. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 24 h, and germ tubes produced at the apex and middle. Colonies on PDA reaching 5 mm diameter after 4 weeks at room temperature. Mycelium damp, dense, colonies on the surface of PDA, surface smooth, dry, irregular edges, accumulate in the middle, brown to dark brown. Reverse smooth, brown.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3481 (HKAS 131397, holotype), ex-type living cultures CGMCC 3.27021 = KUNCC 23–13374.

Notes – In the phylogenetic analysis, *Sporidesmium guttulatum* is sister to *S. nujiangense* with 89% ML/ 1.00 PP support (Fig. 59). *Sporidesmium guttulatum* shares the similar sized, septate conidiophores with *S. nujiangense*, however, it differs from *S. nujiangense* in having guttulate and longer (44–84 vs. 54–69 µm) conidia (Bao et al. 2021). Comparison of ITS and LSU nucleotides

sequences between *S. guttulatum* (CGMCC 3.27021) and *S. nujiangense* (DLUCC 983) indicates that 3.74% (17/454 bp, four gaps) and 2.25% (18/801 bp) difference, respectively.

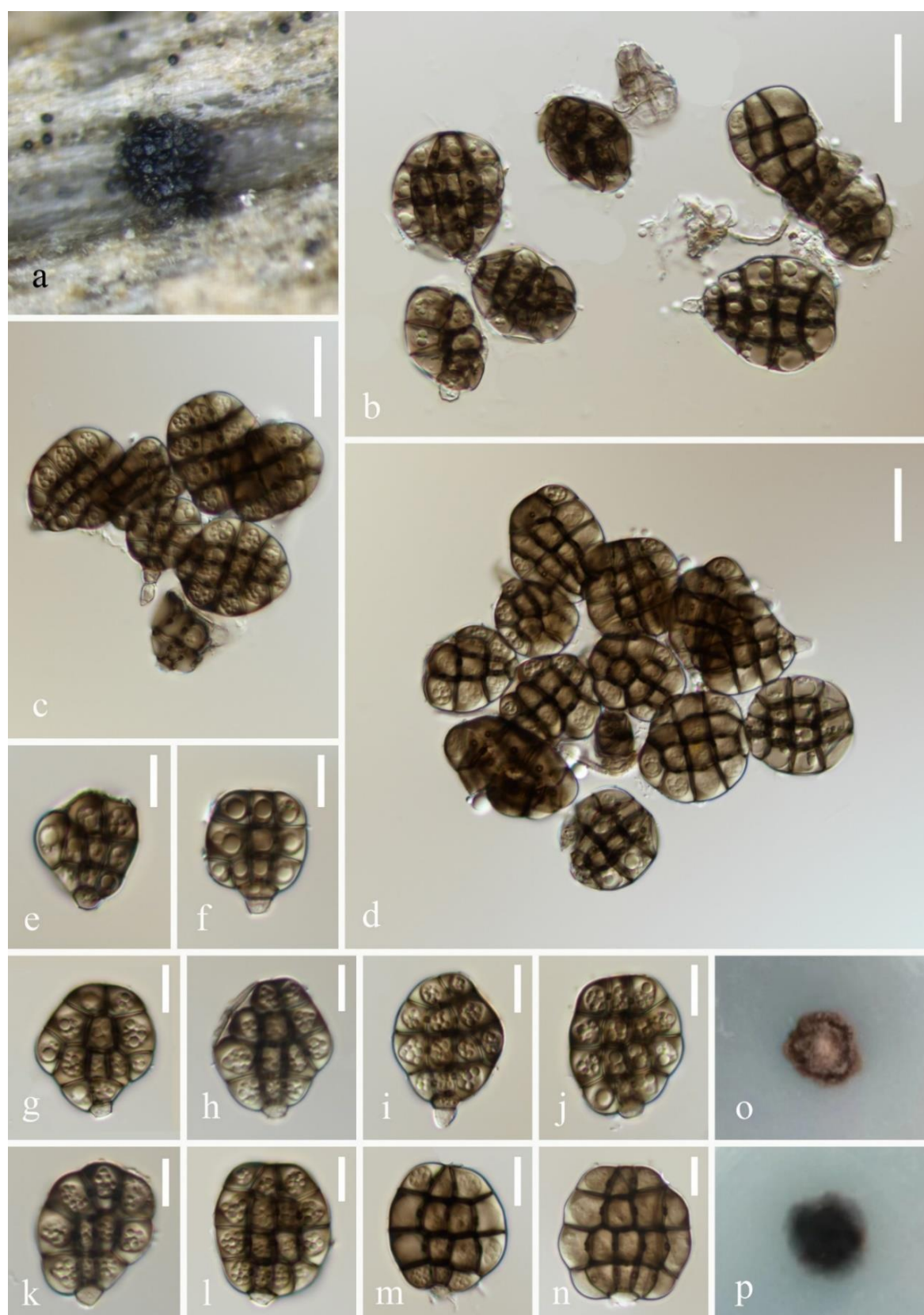


Figure 58 – *Canalisporium jinghongense* (HKAS 131357). a Colony on the substratum. b–d, i Conidiogenous cells and conidia. e–h, j–n conidia. o, p Colony on PDA from surface and reverse. Scale bars: b–d = 20 μ m, e–n = 10 μ m.

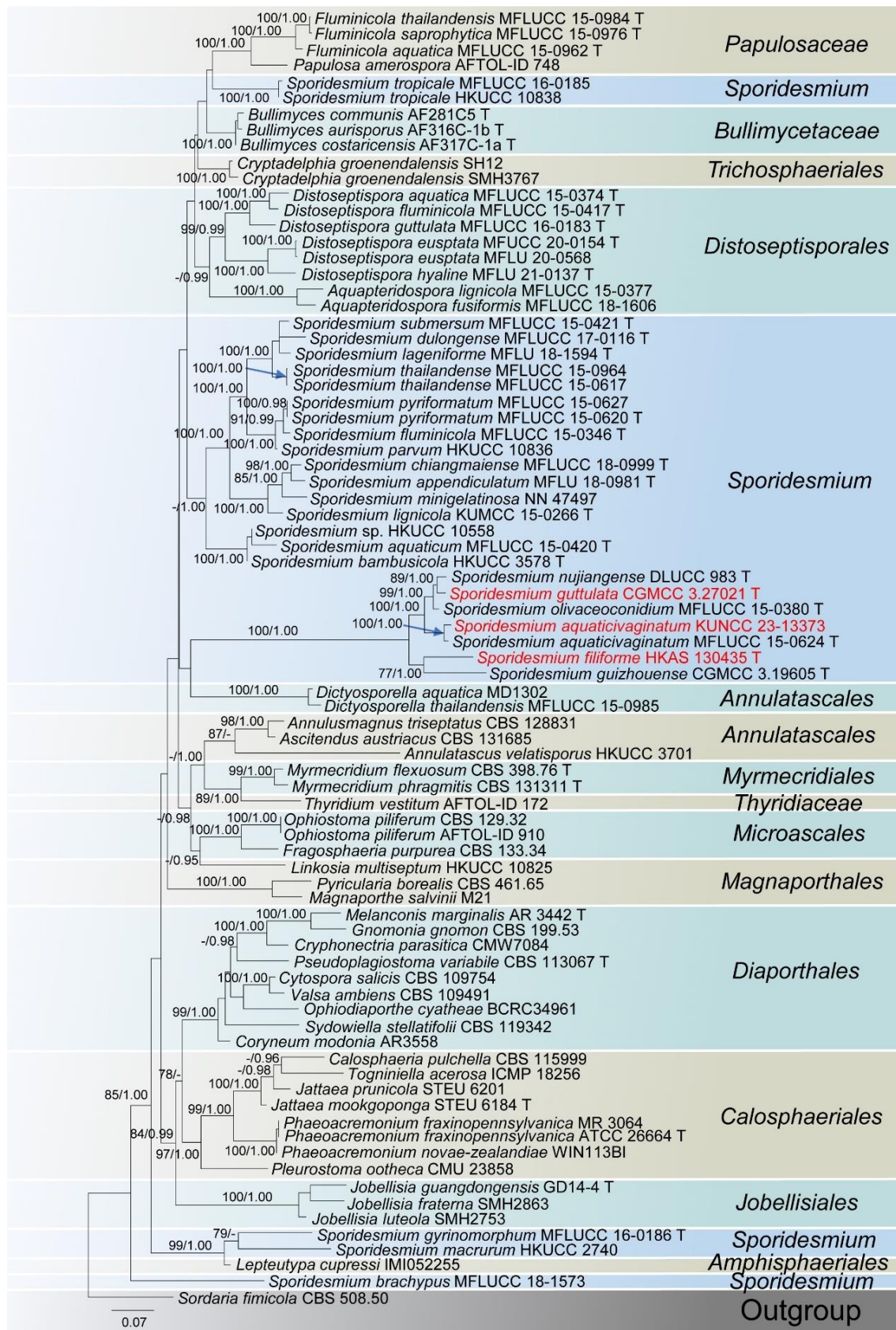


Figure 59 – RAxML tree based on analysis of *Sporidesmium* that combined LSU, ITS, SSU, *rpb2*, and *tef1-α* dataset. The combined analyses include 81 strains with 4172 characters including gaps (LSU: 822 bp, ITS: 525 bp, SSU: 916 bp, *rpb2*: 974 bp and *tef1-α*: 888 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Sordaria fimicola* (CBS 508.50).

The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.



Figure 60 – *Sporidesmium aquaticivaginatatum* (HKAS 131383). a Colonies on the substratum. b Conidiophores. c–e Conidiophores with conidia. f–k Conidia. l Germinating conidium. m, n Colonies on PDA from surface and reverse. Scale bars: b–e = 25 μ m, f–h = 15 μ m, i–l = 20 μ m.

Sporidesmium filiforme W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.
Index Fungorum number: IF902436; Facesoffungi number: FoF16120

Fig. 62



Figure 61 – *Sporidesmium guttulatum* (HKAS 131397, holotype). a Colonies on the substratum. b–e Conidiophores. f Conidiophore with conidium. g–l Conidia. m Germinating conidium. n, o Colonies on PDA from surface and reverse. Scale bars: b–m = 15 μ m.

Etymology – Referring to the filiform conidial appendages of this species.

Holotype – HKAS 130435

Saprobic on submerged decaying wood. Asexual morph: *Colonies* effuse, hairy, scattered, sparkling. *Mycelium* mostly immersed, composed of branched, septate, hyaline to pale brown,

smooth hyphae. *Conidiophores* 22–54 × 3.5–4.9 µm ($\bar{x}$ = 33.8 × 4.2 µm, n = 10), macronematous, mononematous, solitary, cylindrical, straight, 1–3-septate, smooth-walled, brown, truncate at the apex. *Conidiogenous cells* 12–16 × 3.6–4.9 µm ($\bar{x}$ = 14 × 4.1 µm, n = 10), monoblastic, integrated, terminal, determinate, cylindrical, smooth-walled, brown. *Conidia* (33–) 53–100 × 5.8–9.5 µm ($\bar{x}$ = 78 × 7.7 µm, n = 20), acrogenous, solitary or occasionally catenate, dry, pale brown to olivaceous, obclavate, smooth-walled, straight, mostly 10-distoseptate, with a up to 140 µm long, filiform, hyaline to subhyaline apical appendage, truncate base with a conspicuous darkened scar. *Conidial secession* schizolytic. Sexual morph: Undetermined.

Culture characteristics – *Conidia* germinating on PDA within 24 h, and germ tubes produced at the apex and the base. Colonies on PDA reaching 20 mm diameter after 6 weeks at room temperature. Mycelium dry, dense, colonies on the surface of PDA, with rough surface, irregular edges, slightly protuberance in the center, uneven surface, yellow to reddish brown. Reverse yellow to brown. Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3826 (HKAS 130435, holotype).

Notes – Phylogenetic analysis showed that *Sporidesmium filiforme* clustered with *S. guizhouense* with 100% ML/ 1.00 PP support (Fig. 59). However, *S. filiforme* differs from *S. guizhouense* in having elongated and narrow conidia with filiform appendages, but without mucilaginous sheath (Liu et al. 2019). The LSU and ITS sequences data of *S. filiforme* (HKAS 130435) differ from *S. guizhouense* (CGMCC 3.19605) by 4.99% (40/801 bp) and 16.43% (81/493 bp, 42 gaps), respectively. We therefore identified *S. filiforme* as a new species.

Sordariomycetes families incertae sedis

***Papulosaceae* Winka & O.E. Erikss.**

Papulosaceae was introduced by Winka & Eriksson (2000), with *Papulosa* as the type genus. Currently, four genera, viz., *Brunneospora*, *Fluminicola*, *Papulosa*, and *Wongia* are accepted in *Papulosaceae*.

***Wongia* Khemmuk, Geering & R.G. Shivas**

Wongia was established by Khemmuk et al. (2016), with *W. garrettii* as the type species. Seven species are currently accepted in the genus, of which three taxa *W. aquatica*, *W. fusiformis*, and *W. suae* are known from freshwater habitats in China and Thailand, while the other four species, *W. bambusae*, *W. ficherai*, *W. garrettii*, and *W. griffinii* are collected from terrestrial habitats (Luo et al. 2019, Bao et al. 2021, Crous et al. 2022, Zhang et al. 2023c, Yu et al. 2024).

***Wongia flava* W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.**

Fig. 63

Index Fungorum number: IF902437; Facesoffungi number: FoF16121

Etymology – *flava* = yellow, referring to the yellow colonies of this fungus.

Holotype – HKAS 131375

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, hairy, gathered, with yellow conidia located at the apex of the dark brown to black conidiophores. *Mycelium* partly immersed, partly superficial, composed of branched, septate, smooth-walled, pale brown hyphae. *Conidiophores* (67–) 100–160 × 4.7–6.1 µm ($\bar{x}$ = 115.3 × 5.3 µm, n = 15), macronematous, mononematous, solitary, septate, erect, straight, brown to dark brown, paler towards the apex, smooth to slightly verrucose, thick-walled, occasionally branched at the apex or middle. *Conidiogenous cells* polyblastic, sympodially proliferating, finely denticulate, terminal, pale brown to brown. *Conidia* 18–24 × 5.3–7.9 µm, ($\bar{x}$ = 21.5 × 6.9 µm, n = 30), acropleurogenous, solitary, fusiform or clavate, straight, 1–3 inconspicuous septate, slightly constricted in the middle septum, multiple guttulate, pale brown to brown. Sexual morph: Undetermined. Culture characteristics – *Conidia* germinating on PDA within 12 h, and germ tubes produced at the both ends. Colonies on PDA reaching 35 mm diameter after 4 weeks at room temperature. Mycelium dense, dry, colonies on the surface of PDA, rugged

surface, with irregular edges, dark green, and surface is covered with a layer of white hyphae. Reverse dark green, smooth, creak.



Figure 62 – *Sporidesmium filiforme* (HKAS 130435, holotype). a Colonies on the substratum. b, c Conidiophores. d–k conidia. l Germinating conidium. m, n Colonies on PDA from surface and reverse. Scale bars: b = 10 μ m, c 15 μ m, d–f, k, l = 20 μ m, g–j = 30 μ m.



Figure 63 – *Wongia flava* (HKAS 131375, holotype). a Colonies on the substratum. b, d Conidiophores with conidia. c, e, f Conidiophores. g Conidiogenous cells. h Conidiogenous cell with conidium. i–l conidia. m Germinating conidium. n, o Colonies on PDA from surface and reverse. Scale bars: b–f = 20 μ m, g, h, m = 10 μ m, i–l = 5 μ m.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 28 February 2023, W.P. Wang, S-4353 (HKAS 131375, holotype), ex-type living cultures CGMCC 3.25434 = KUNCC 23-13715.

Notes – *Wongia flava* was the fourth species of *Wongia* collected from freshwater habitat, and is clearly distinguishable from *W. aquatica*, *W. fusiformis*, and *W. suae*. *Wongia flava* has longer conidiophores ((67–) 100–160 vs. 70–105 μm) and larger conidia ($18\text{--}24 \times 5.3\text{--}7.9$ vs. $13\text{--}18 \times 4\text{--}5$ μm) than those of *W. fusiformis* (Bao et al. 2021). *Wongia flava* differs from *W. aquatica* by its conidiogenous cells lacking pale brown scars, and the conidia is constricted at the central septum (Luo et al. 2019). Furthermore, *W. flava* has fusiform, larger conidia ($18\text{--}24.2 \times 5.3\text{--}7.9$ vs. $8\text{--}11 \times 3\text{--}4$ μm) than *W. suae*, and the conidia are constricted in the middle septum (Zhang et al. 2023c). Comparison of the ITS sequences of *W. flava* (CGMCC 3.25434) with *W. aquatica* (MFLUCC 18-1607), *W. fusiformis* (MFLUCC 21-0032), and *W. suae* (CGMCC 3.24295) revealed 10.31% (56/543 bp, 28 gaps), 5.96% (32/537 bp, ten gaps), and 5.93% (31/523 bp, eleven gaps) differences, respectively. Therefore, based on morphological characters and phylogenetic analysis, we introduce *W. flava* as a new species.

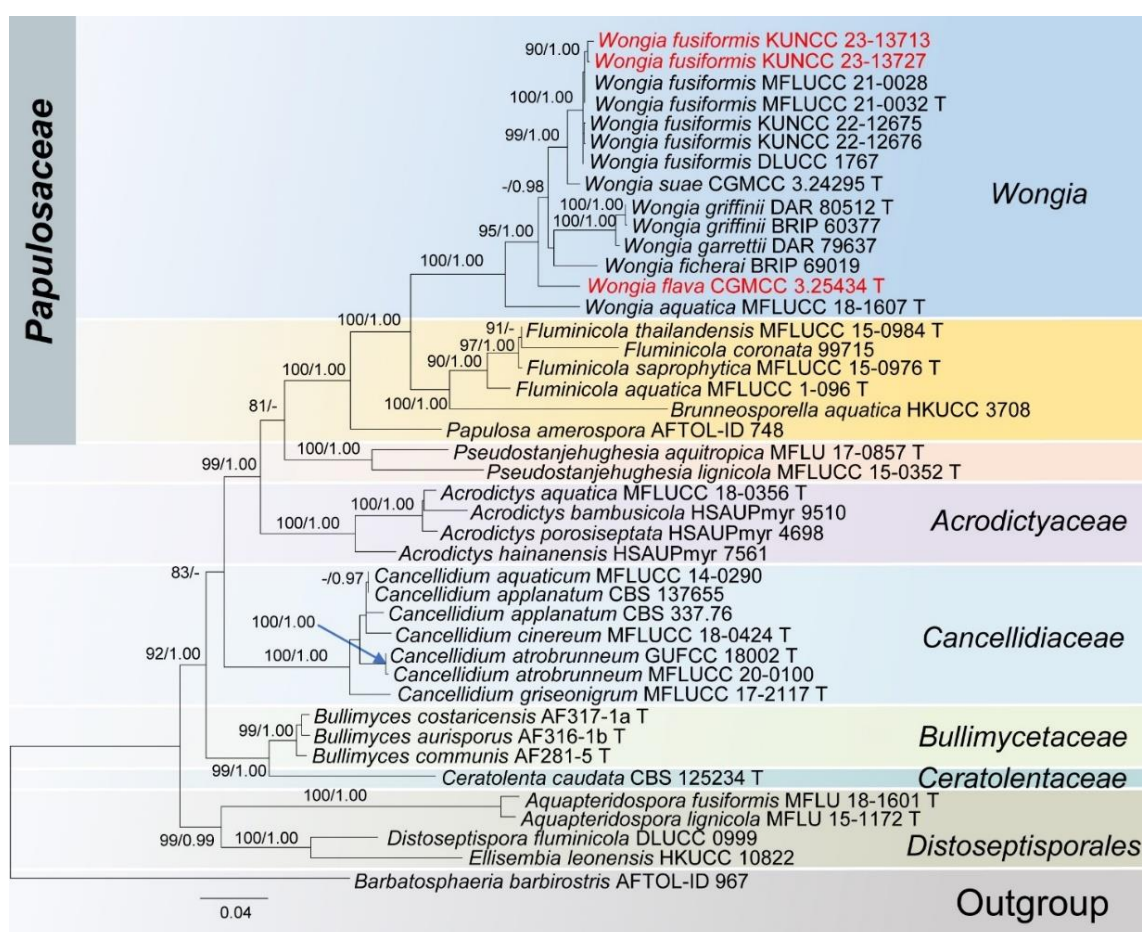


Figure 64 – RAxML tree based on analysis of *Papulosaceae* that combined LSU, ITS, SSU, *tef1-α*, and *rpb2* dataset. The combined analyses include 42 strains with 4024 characters including gaps (LSU: 798 bp, ITS: 524 bp, SSU: 914 bp, *tef1-α*: 850 bp, and *rpb2*: 938 bp). Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML/PP. The tree is rooted with *Barbatosphaeria barbirostris* (AFTOL-ID 967). The new collections are indicated in red. Ex-type strains are indicated with “T” after the strain number.

Wongia fusiformis D.F. Bao, H.Y. Su, K.D. Hyde & Z.L. Luo, J. Fungi 7, 669, 17 (2021) Fig. 65

Index Fungorum number: IF558595; Facesoffungi number: FoF09917

Saprobic on submerged decaying wood. Asexual morph: *Colonies* superficial, effuse, hairy, scattered or gathered, brown to dark brown. *Mycelium* mostly immersed, composed of branched, septate, smooth-walled, pale brown hyphae. *Conidiophores* (16) $34\text{--}110 \times 2.7\text{--}4.7 \mu\text{m}$ ($\bar{x} = 67 \times 3.8 \mu\text{m}$, $n = 25$), macronematous, mononematous, solitary or in small groups, septate, erect, straight or flexuous, brown, paler towards the apex, thick-walled, shrinkage and narrowing at the septa, partly guttulate. *Conidiogenous cells* polyblastic, finely denticulate, terminal, sympodial, subhyaline to pale brown. *Conidia* $13\text{--}25 \times 2.9\text{--}5 \mu\text{m}$ ($\bar{x} = 20.7 \times 4 \mu\text{m}$, $n = 40$), acropleurogenous, solitary, fusiform or clavate, straight, 0–4-septate, pale brown, guttulate, with a hilum at the base. Sexual morph: Undetermined.

Culture characteristics – *Conidia* germinating on PDA within 24 h, and germ tubes produced at the apex. Colonies on PDA reaching 25 mm diameter after 3 weeks at room temperature. Mycelium dense, dry, colonies on the surface of PDA, flat surface and slightly protruding in the center, with regular edges, pale reddish brown to reddish brown. Reverse brown to dark brown, smooth.

Material examined – China, Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3265 (HKAS 131359), living culture KUNCC 23–13727; *ibid.*, S-3283 (HKAS 131345), living culture KUNCC 23–13713.

Notes – *Wongia fusiformis* was introduced by Bao et al. (2021) on submerged decaying wood in Thailand and China. Zhang et al. (2023c) recollected this fungus in Yuanjiang River Basin, Yunnan Province, China. Phylogenetic analysis showed that our new collections clustered with *W. fusiformis* (Fig. 64), and our new collections are indistinguishable from *W. fusiformis* (Bao et al. 2021, Zhang et al. 2023c). We therefore identify our collections as *W. fusiformis*.

DISCUSSION

In this study, we transfer three species of *Ascotaiwania* (*A. coffeae*, *A. mitriformis*, and *A. sawadae*) to *Ascolacicola*. Judging from the current taxonomic status, there are numerous issues in the previous studies of *Ascotaiwania*. Index Fungorum (2024) listed 17 epithets under *Ascotaiwania*. However, based on phylogenetic analysis at present, eight species have been transferred to *Ascolacicola*, *Helicoascotaiwania*, *Neoascotaiwania*, and *Pseudoascotaiwania* (Yang et al. 2016, Hernández-Restrepo et al. 2017, Dayarathne et al. 2019). These genera possess similar sexual morphologies, and the morphological differences are mainly manifested in the asexual morph (Ranghoo & Hyde 1998, Yang et al. 2016, Hernández-Restrepo et al. 2017, Dayarathne et al. 2019, Réblová et al. 2020). Currently, there are nine species accepted in *Ascotaiwania*, and these species are predominantly sexual morphs, and only *A. latericolla* and *A. lignicola* have valuable molecular data. Therefore, the accuracy of the identification of these *Ascotaiwania* species still requires further verification in the future.

The identification of fungal species by combining morphological characteristics and molecular data significantly enhances the accuracy of identification (Luo et al. 2019, Dong et al. 2021b, Yang et al. 2023). In the era dominated by morphology, the taxonomy of fungal species has many subjective elements and limitations. The addition of molecular data has provided a more accurate direction for species identification (Höhnelt 1909, Hyde et al. 2020b, Sushma et al. 2022). However, our research methodology and single morphological identification have yielded some different results, sporidesmium-like taxa are a prime example. It is difficult to explain why species with such similar morphologies are polyphyletic in phylogenetic analyses (Yang et al. 2018b, Liu et al. 2019, Bao et al. 2021, Hyde et al. 2021). These taxonomic groups of ambiguity need a more data to be resolved in future studies, as it is difficult to explain how uncontrollable factors such as habitat and host affect the morphology of different species. In addition, fungal classification that solely relies on morphological identification is unreliable. When identifying some taxa (e.g. *Dictyocheirospora*), we may inadvertently ignore these species without sequences (Sushma et al. 2022, Tennakoon et al. 2023, Shu et al. 2024).



Figure 65 – *Wongia fusiformis* (HKAS 131359). a, b Colonies on the substratum. c, h Conidiophores. d–g, i, j Conidiophores and conidia. k–n conidia. o Germinating conidium. p, q Colonies on PDA from surface and reverse. Scale bars: c, d, k, o = 10 µm, e–j = 20 µm, l–n = 5 µm.

This is the first time that a study has focused specifically on the diversity of lignicolous freshwater fungi in the karst landscapes of Yunnan Province, China. Yang et al. (2023) investigated the diversity of freshwater fungi from karst landscapes areas in Guizhou Province of China and several areas of Thailand. Our study and Yang et al. (2023) documented over 100 species in 54

families, 28 orders and three classes of *Ascomycota*, indicating that the karst landform areas have a high species diversity of lignicolous freshwater fungi. However, both studies showed homogeneity at higher taxonomic levels. All species were classified within *Dothideomycetes*, *Eurotiomycetes*, and *Sordariomycetes* in *Ascomycota*, which is significantly fewer than the 13 phyla mentioned in previous studies (Calabon et al. 2022, 2023a). Furthermore, there was a certain difference in species distribution between our study and Yang et al. (2023). In our study, *Dothideomycetes* (52.3%) accounted for the largest proportion, followed by *Sordariomycetes* (38.6%) and *Eurotiomycetes* (9.1%). Whereas in the study by Yang et al. (2023), *Sordariomycetes* emerged as the dominant class (*Sordariomycetes* accounted for 50%, *Dothideomycetes* for 44.2%, and *Eurotiomycetes* for 5.8%). The small sample size is the main reason for this discrepancy. *Sordariomycetes* should probably be the largest class in freshwater habitat (Shen et al. 2022a, Calabon et al. 2023a, Yang et al. 2023).

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