

Bambusicolous Fungi from Southwestern China

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Abstract

During an ongoing investigation of bambusicolous ascomycetous fungi in southwestern China, a diverse range of asexual and sexual morphs of saprobic fungi were collected from freshwater and terrestrial habitats. Based on detailed morphological comparisons and multi-gene phylogenetic studies, we introduce one new family, Neodictyosporiaceae, along with seven new genera, viz. *Aculeatosporella*, *Antebambusa*, *Ascosichuania*, *Flavosporella*, *Multiseptoconidium*, *Nigroconidius* and *Sichuanomyces*, and describe 29 new species, viz. *Aculeatosporella bambusae*, *Antebambusa sichuanensis*, *Ascosichuania bambusicola*, *A. fusiformis*, *Bambusicola meishanensis*, *Conioscypha muchuanensis*, *Conlarium bambusae*, *Dictyosporella bambusicola*, *Distoseptispora chengduensis*, *D. muchuanensis*, *Flavosporella bambusae*, *Hongkongmyces sichuanensis*, *Multiseptoconidium fuscosporellum*, *Neodictyosporium bambusae*, *N. cheirosporum*, *N. sexuale*, *N. sichuanense*, *Nigroconidius bambusae*, *N. septatus*, *Pseudosetoseptoria bambusae*, *Periconia muchuanensis*, *P. sichuanensis*, *Roussoella aseptata*, *R. saprophytica*, *R. striata*, *R. terricola*, *Sichuanomyces bambusicola*, *Triplosphaeria bambusicola* and *T. fusiformis*. Furthermore, we report 16 new records, including asexual morph, sexual morph, geographical, habitat and host, they are *Acrodictys pyriformis*, *Distoseptispora aquamyces*, *D. atroviridis*, *D. dehongensis*, *D. euseptata*, *D. meilingensis*, *D. suoluensis*, *D. yongxiuensis*, *Neoaquastroma cylindricum*, *Neodeightonia subglobosa*, *Neoheliosia guizhouensis*, *Nigrograna magnoliae*, *Pleopunctum ellipsoideum*, *P. pseudoellipsoideum*, *Pseudopolyphosphaeria guizhouensis* and *Sporidesmium chiangmaiense*. Detailed, illustrated descriptions and notes for each taxon are provided, along with a brief note for each genus and family.

Keywords – 37 new taxa – Dothideomycetes – multi-gene – Phylogeny – Sordariomycetes – Taxonomy

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INTRODUCTION

The excessive utilization of wood has led to the depletion of forest resources globally, posing significant environmental challenges (Dlamini et al. 2022). Bamboo has a short growth cycle, high yield, and robust regeneration capabilities, making it the most abundant non-wood resource that can be a substitute for wood (Chaowana 2013, Li & He 2019, Dlamini et al. 2022). As a sustainable material, bamboo is extensively used in various applications such as food, construction, fiber and pulp production, furniture, tools, musical instruments, kitchenware, decorations, and interior design (Lobovikov et al. 2007, Shukla et al. 2016, Dlamini et al. 2022, Jiang et al. 2022). Additionally, bamboo forests contribute significantly to forest ecosystems and conservation efforts (Lobovikov et al. 2007, Shukla et al. 2016, Dlamini et al. 2022, Jiang et al. 2022). Therefore, bamboo is not only a crucial agricultural plant but also plays a vital role in climate change mitigation and human adaptation.

China possesses the richest bamboo resources, accounting for about one-third of the world's total bamboo forest area (Dlamini et al. 2022). Sichuan Province, located in southwestern China, is notable for its extensive bamboo forests, covering approximately 592,800 hectares and ranking fifth in the country (Dlamini et al. 2022). This province, a biodiversity hotspot, has complex topography and climatic conditions that significantly influence biodiversity. The highly variable climate and dense bamboo forests must profoundly impact bamboo fungal diversity.

The term “fungorum bambusicolorum” (bambusicolous fungi) was initially used by Hino (1938) without a definition. Hyde et al. (2002) later defined bambusicolous fungi as “fungi that inhabit leaves, culms, branches, rhizomes and roots of bamboo”, a definition that has been widely adopted in later studies. Bambusicolous fungi are globally distributed in bamboo-growing regions and predominantly belong to the phylum Ascomycota (Hatakeyama et al. 2005, 2008, Tanaka & Harada 2005a, b, Tanaka et al. 2005, 2009, Sato et al. 2008, Dai et al. 2017, Yang et al. 2019a, b, c, d, 2024, Zhang et al. 2020b, Dai et al. 2022, Jiang et al. 2021a, b, Phookamsak et al. 2022, Liang et al. 2023, Yu et al. 2022, 2023, 2024). The economic value of fungi has been estimated at USD 54.57 trillion, with bambusicolous fungi contributing significantly to this value (Niego et al. 2023). Bambusicolous Ascomycota comprise a diverse assemblage of saprobes, pathogens, and endophytes (Hyde et al. 2002, Dai et al. 2018, Jiang et al. 2022, Huang et al. 2023). As saprobes, they play a crucial role in decomposing decaying bamboo and recycling nutrients within forest ecosystems (Jiang et al. 2022). As pathogens, they can significantly impact bamboo cultivation, causing severe damage to bamboo forests and plantations (Jiang et al. 2022). As endophytes, they influence bamboo development, growth, and ultimately the quality and quantity of bamboo-derived compounds (Huang et al. 2023).

In China, the number of reported bambusicolous Ascomycota exceeds one-third of the world's total (Jiang et al. 2022). Up to 2022, 174 bambusicolous ascomycetes taxa have been documented in Southwest China, representing approximately 34% of China's total bambusicolous Ascomycota taxa (Jiang et al. 2022). The species richness of bambusicolous Ascomycota in Yunnan province has historically dominated the southwestern region (Jiang et al. 2022). Recently, Yang et al. (2019a, b, c, d, 2024) have investigated the bambusicolous Ascomycota in this region and reported a series of interesting fungi. Our peer investigation (Yu et al. 2024) also suggests that many bamboo fungi remain unexplored and undiscovered in southwestern China.

This study focuses on bambusicolous ascomycetes in southwestern China, aiming to identify these fungi and resolve their systematic placement. Fungi were collected from decaying bamboo in both freshwater and terrestrial habitats. Through morphological and molecular phylogenetic analyses, we have resolved the taxonomy of over 50 taxa, introducing one new family, seven new genera, and 29 new species with detailed descriptions and illustrations. Additionally, 16 new

records, encompassing asexual and sexual morphs, geographical distributions, habitats, and host associations, are reported.

MATERIALS AND METHODS

Isolation and Morphology

Fungal specimens associated with decaying bamboo were collected from 21 sites across Southwestern China between 2021 and 2023. The majority of the specimens were obtained from locations within Sichuan Province, with additional samples collected near the borders of Sichuan and the neighboring provinces of Guizhou and Yunnan. Samples were taken to the laboratory in paper envelopes or plastic bags, and the morphology of associated fungi were examined and fungal spores were isolated following the methods described in Senanayake et al. (2020).

Herbarium specimens were deposited in the Herbarium of Cryptogams, Kunming Institute of Botany Academia Sinica (KUN-HKAS), Kunming, China and the Herbarium of the University of Electronic Science and Technology (HUEST), Chengdu, China. The isolates obtained in this study were deposited in China General Microbiological Culture Collection Center (CGMCC) and the University of Electronic Science and Technology Culture Collection (UESTCC). Facesoffungi and MycoBank numbers were registered as outlined in (Jayasiri et al. 2015) and MycoBank (Crous et al. 2004), respectively.

DNA extraction, PCR amplification and sequencing

A Trelief TM Plant Genomic DNA Kit (Beijing TsingKe Biotech Co., Beijing, China) was used to extract total genomic DNA from fungal mycelia grown on potato dextrose agar (PDA). Seven partial gene regions, viz. the partial nuclear ribosomal small subunit rRNA gene (SSU), the nuclear ribosomal internal transcribed spacer region (ITS: ITS1-5.8S-ITS2), the partial nuclear ribosomal large subunit rRNA gene (LSU), the partial second-largest subunit of RNA polymerase II gene (*rpb2*), the partial translation elongation factor 1- α gene (*tef1- α*), the partial β -tubulin gene (*tub2*) and the partial mitochondrial ribosomal small subunit (mtSSU), were applied for the phylogenetic analysis. The primers and PCR thermal cycle programs are shown in Table 1. PCR products were checked on 1% agarose electrophoresis gels stained with Gel Red. The sequencing reactions were carried out with primers mentioned above by Sangon Biotech Co., Shanghai, China.

Phylogenetic analysis

Sequences generated in this study were deposited in GenBank and listed in Table 2. BLAST searches were used to find similar sequences that match our data. Based on BLAST similarities and relevant publications, closely related reference sequences were downloaded from GenBank (Supplementary material). The sequences were aligned by using the online multiple alignment program MAFFT v.7 (Kazutaka & Standley 2013), and the alignment files were further trimmed using trimAl (Capella-Gutierrez et al. 2009) version 1.2 with the option “-gapthreshold 0.5”, which only allows 50% of taxa with a gap in each site. Each gene dataset was concatenated by Mesquite v. 3.11 for the multi-gene phylogenetic analyses. Maximum likelihood (ML) and Bayesian inference (BI) were carried out as detailed in Dissanayake et al. (2020). Maximum likelihood (ML) analysis was performed using RAxML-HPC v.8 tool via the CIPRES Science Gateway V3.3 (Miller et al. 2010) with rapid bootstrap analysis. The Bayesian inference (BI) analyses were performed by using PAUP v.4.0b10 (Swofford 2003) and MrBayes v. 3.1.2 (Huelsenbeck & Ronquist 2001). The best model for different genes partition in the concatenated dataset was determined by MrModeltest 2.3. (Nylander et al. 2008), and posterior probabilities were determined by Markov chain Monte Carlo sampling (MCMC) in MrBayes v.3.1.2 (Rannala & Yang 1996, Huelsenbeck & Ronquist 2001). The phylogenetic tree was visualized by FigTree v. 1.4.0 (Rambaut 2006) and Treeview v. 1.6.6 (Page 1996).

Table 1 Gene loci amplified in this study with the corresponding PCR thermal cycle programs.

Loci	PCR primers (forward/reverse)	PCR reaction system	PCR thermal cycles	References
SSU	NS1/NS4	Total: 50 µL 2 × Taq Plus MasterMix (Dye): 25 µL	(94 °C: 30 s, 54 °C: 30 s, 72 °C: 30 s) × 35 cycles	White et al. (1990)
ITS	ITS5/ITS4	ddH ₂ O: 20 µL	(94 °C: 30 s, 54 °C: 30 s, 72 °C: 30 s) × 35 cycles	White et al. (1990)
LSU	LR0R/LR5	Each primer (10 µM): 2 µL DNA template: 1 µL	(94 °C: 30 s, 54 °C: 30 s, 72 °C: 30 s) × 35 cycles	Vilgalys & Hester (1990)
<i>rpb2</i>	fRPB2-5F/fRPB2-7cR		(94 °C: 30 s, 56 °C: 30 s, 72 °C: 30 s) × 35 cycles	Liu et al. (1999)
<i>tef1-α</i>	EF1-728F, EF1-986R 983F/2218R		(94 °C: 30 s, 62 °C: 30 s, 72 °C: 30 s) × 35 cycles	Carbone & Kohn (1999), Rehner & Buckley (2005)
<i>tub2</i>	Bt2a/Bt2b		(94 °C: 30 s, 56 °C: 30 s, 72 °C: 30 s) × 35 cycles	Glass & Donaldson (1995)
mtSSU	MS1/MS2		(94 °C: 30 s, 56 °C: 30 s, 72 °C: 30 s) × 35 cycles	White et al. (1990)

Note: 2×Taq Plus MasterMix (mixture of Taq Plus DNA Polymerase, MgCl₂ and dNTP; CoWin Biosciences, Taizhou, China).

Table 2 Sequences generated in this study with their GenBank accession numbers.

Taxon	Source	Status	Family	GenBank accession number				
				SSU	ITS	LSU	<i>tef1-α</i>	<i>rpb2</i>
<i>Neodeighntonia subglobosa</i>	UESTCC 24.0137		Botryosphaeriaceae	PQ066533	PQ067762	PQ067677	N/A	N/A
<i>Neoheliosia guizhouensis</i>	UESTCC 23.0252		Eriomycetaceae	N/A	PQ067764	PQ067679	PQ278544	N/A
<i>Sichuanomyces bambusicola</i>	CGMCC 3.27445	T	Eriomycetaceae	N/A	PQ067765	PQ067680	PQ278543	N/A
<i>Sichuanomyces bambusicola</i>	CGMCC 3.27451		Eriomycetaceae	N/A	PQ067766	PQ067681	PQ278542	N/A
<i>Sichuanomyces bambusicola</i>	UESTCC 23.0251		Eriomycetaceae	N/A	PQ067763	PQ067678	PQ278541	N/A
<i>Antebambusa sichuanensis</i>	CGMCC 3.25592	T	Anteagloniaceae	PQ066537	PQ067770	PQ067685	N/A	N/A
<i>Antebambusa sichuanensis</i>	UESTCC 24.0138		Anteagloniaceae	PQ066534	PQ067767	PQ067682	PQ271589	N/A
<i>Antebambusa sichuanensis</i>	UESTCC 24.0139		Anteagloniaceae	PQ066535	PQ067768	PQ067683	PQ271590	N/A
<i>Antebambusa sichuanensis</i>	UESTCC 24.0140		Anteagloniaceae	PQ066536	PQ067769	PQ067684	PQ271591	PQ212614
<i>Bambusicola meishanensis</i>	CGMCC 3.25594	T	Bambusicolaceae	PQ066540	PQ067775	PQ067690	PQ278548	N/A
<i>Flavosporella bambusae</i>	CGMCC 3.25593	T	Bambusicolaceae	PQ066539	PQ067774	PQ067689	PQ278547	N/A
<i>Flavosporella bambusae</i>	UESTCC 24.0141		Bambusicolaceae	PQ066538	PQ067773	PQ067688	PQ278546	PQ186971
<i>Flavosporella bambusae</i>	UESTCC 24.0142		Bambusicolaceae	N/A	PQ067771	PQ067686	N/A	N/A
<i>Flavosporella bambusae</i>	UESTCC 24.0143		Bambusicolaceae	N/A	PQ067772	PQ067687	PQ278545	N/A
<i>Pseudosetoseptoria bambusae</i>	CGMCC 3.25595	T	Lentitheciaceae	N/A	PQ067776	PQ067691	N/A	N/A
<i>Hongkongomyces sichuanensis</i>	CGMCC 3.25596	T	Lindgomycetaceae	PQ066541	PQ067777	PQ067692	PQ278549	PQ186972

Table 2 Continued.

Taxon	Source	Status	Family	GenBank accession number				
				SSU	ITS	LSU	<i>tef1-a</i>	<i>rpb2</i>
<i>Nigrograna magnoliae</i>	UESTCC 24.0144		Nigrogranaceae	N/A	PQ067778	PQ067693	N/A	N/A
<i>Aculeatosporella bambusae</i>	CGMCC 3.27443	T	Occultibambusaceae	PQ066542	PQ067779	PQ067694	PQ281802	PQ212615
<i>Aculeatosporella bambusae</i>	UESTCC 23.0258		Occultibambusaceae	PQ066543	PQ067780	PQ067695	PQ281803	PQ240854
<i>Neoaquastroma cylindricum</i>	UESTCC 24.0145		Parabambusicolaceae	PQ066544	PQ067781	PQ067696	PQ278550	N/A
<i>Periconia muchuanensis</i>	CGMCC 3.25599	T	Periconiaceae	PQ066546	PQ067783	PQ067698	PQ278553	N/A
<i>Periconia muchuanensis</i>	UESTCC 23.0260	T	Periconiaceae	N/A	PQ067785	PQ067700	N/A	N/A
<i>Periconia sichuanensis</i>	CGMCC 3.25598	T	Periconiaceae	PQ066545	PQ067782	PQ067697	PQ278551	N/A
<i>Periconia sichuanensis</i>	UESTCC 23.0259	T	Periconiaceae	N/A	PQ067784	PQ067699	PQ278552	N/A
<i>Pleopunctum ellipsoideum</i>	UESTCC 24.0146		Phaeoseptaceae	N/A	PQ067787	PQ067702	PQ278554	N/A
<i>Pleopunctum ellipsoideum</i>	UESTCC 24.0147		Phaeoseptaceae	N/A	PQ067786	PQ067701	N/A	PQ186973
<i>Pleopunctum pseudoellipsoideum</i>	UESTCC 24.0148		Phaeoseptaceae	N/A	PQ067788	PQ067703	PQ278555	PQ212616
<i>Roussoella aseptata</i>	CGMCC 3.25604	T	Roussoellaceae	PQ066551	PQ067793	PQ067709	N/A	N/A
<i>Roussoella aseptata</i>	UESTCC 24.0151		Roussoellaceae	PQ066552	PQ067794	PQ067710	PQ278560	N/A
<i>Roussoella saprophytica</i>	CGMCC 3.25601	T	Roussoellaceae	PQ066547	PQ067789	PQ067704	PQ278556	PQ186974
<i>Roussoella saprophytica</i>	UESTCC 24.0149		Roussoellaceae	N/A	PQ067790	PQ067705	PQ278557	N/A
<i>Roussoella saprophytica</i>	UESTCC 24.0150		Roussoellaceae	PQ066548	N/A	PQ067706	N/A	N/A
<i>Roussoella striata</i>	CGMCC 3.25603	T	Roussoellaceae	PQ066550	PQ067792	PQ067708	PQ278559	PQ186975
<i>Roussoella terricola</i>	CGMCC 3.25602	T	Roussoellaceae	PQ066549	PQ067791	PQ067707	PQ278558	N/A
<i>Ascosichuania bambusicola</i>	CGMCC 3.25606	T	Teichosporaceae	PQ066555	PQ067797	PQ067713	PQ271586	N/A
<i>Ascosichuania bambusicola</i>	UESTCC 24.0152		Teichosporaceae	PQ066553	PQ067795	PQ067711	PQ271585	PQ241021
<i>Ascosichuania bambusicola</i>	UESTCC 24.0153		Teichosporaceae	PQ066556	PQ067798	PQ067714	PQ271587	PQ241022
<i>Ascosichuania bambusicola</i>	UESTCC 24.0154		Teichosporaceae	PQ066557	PQ067799	PQ067715	PQ271588	N/A
<i>Ascosichuania fusiformis</i>	CGMCC 3.25605	T	Teichosporaceae	PQ066554	PQ067796	PQ067712	PQ271584	PQ241023
<i>Multiseptoconidium fuscosporellum</i>	CGMCC 3.25607	T	Teichosporaceae	N/A	PQ067800	PQ067716	N/A	N/A
<i>Pseudopolyposphaeria guizhouensis</i>	CGMCC 3.25608		Tetraplosphaeriaceae	PQ066558	PQ067801	PQ067717	PQ325524	N/A
<i>Pseudopolyposphaeria guizhouensis</i>	UESTCC 24.0155		Tetraplosphaeriaceae	N/A	PQ067802	PQ067718	PQ325525	N/A
<i>Triplosphaeria bambusicola</i>	CGMCC 3.25610	T	Tetraplosphaeriaceae	N/A	PQ067805	PQ067721	N/A	N/A
<i>Triplosphaeria fusiformis</i>	CGMCC 3.25609	T	Tetraplosphaeriaceae	PQ066560	PQ067804	PQ067720	N/A	N/A
<i>Triplosphaeria fusiformis</i>	UESTCC 24.0156		Tetraplosphaeriaceae	PQ066559	PQ067803	PQ067719	PQ325526	N/A
<i>Conlarium bambusae</i>	CGMCC 3.27447	T	Conlariaceae	PQ066567	PQ067814	PQ067730	PQ278562	PQ186976
<i>Acrodictys pyriformis</i>	UESTCC 24.0157		Acrodictyceae	PQ066568	PQ067815	PQ067731	PQ278563	N/A
<i>Acrodictys pyriformis</i>	UESTCC 24.0158		Acrodictyceae	PQ066569	PQ067816	PQ067732	PQ278564	N/A
<i>Dictyosporella bambusicola</i>	CGMCC 3.27442	T	Junewangiaceae	N/A	PQ067809	PQ067725	PQ278561	N/A
<i>Neodictyosporium bambusae</i>	CGMCC 3.27440	T	Neodictyosporiaceae	PQ066578	PQ067826	PQ067742	PQ271582	N/A
<i>Neodictyosporium bambusae</i>	UESTCC 24.0111	T	Neodictyosporiaceae	PQ066561	PQ067806	PQ067722	PQ271581	N/A
<i>Neodictyosporium bambusae</i>	UESTCC 24.0159	T	Neodictyosporiaceae	PQ066577	PQ067825	PQ067741	N/A	N/A
<i>Neodictyosporium cheirosorum</i>	CGMCC 3.27450	T	Neodictyosporiaceae	PQ066579	PQ067827	PQ067743	PQ271578	N/A

Table 2 Continued.

Taxon	Source	Status	Family	GenBank accession number				
				SSU	ITS	LSU	<i>tef1-a</i>	<i>rpb2</i>
<i>Neodictyosporium cheirosorum</i>	UESTCC 24.0121	T	Neodictyosporiaceae	PQ066573	PQ067821	PQ067737	PQ271577	PQ241075
<i>Neodictyosporium sexuale</i>	CGMCC 3.27441	T	Neodictyosporiaceae	PQ066563	PQ067808	PQ067724	PQ271583	PQ241074
<i>Neodictyosporium sexuale</i>	UESTCC 24.0112	T	Neodictyosporiaceae	PQ066562	PQ067807	PQ067723	N/A	PQ241073
<i>Neodictyosporium sichuanense</i>	CGMCC3.27593	T	Neodictyosporiaceae	PQ066574	PQ067822	PQ067738	PQ271579	N/A
<i>Neodictyosporium sichuanense</i>	UESTCC 24.0136	T	Neodictyosporiaceae	N/A	PQ067845	N/A	PQ271580	N/A
<i>Nigroconidius bambusae</i>	CGMCC 3.27446	T	Pseudostanjehughesiaceae	PQ066566	PQ067813	PQ067729	PQ280792	PQ247602
<i>Nigroconidius bambusae</i>	UESTCC 24.0160		Pseudostanjehughesiaceae	PQ066575	PQ067823	PQ067739	PQ280793	PQ247603
<i>Nigroconidius bambusae</i>	UESTCC 24.0161		Pseudostanjehughesiaceae	PQ066576	PQ067824	PQ067740	PQ280794	PQ247604
<i>Nigroconidius septatus</i>	CGMCC 3.27449	T	Pseudostanjehughesiaceae	PQ066572	PQ067820	PQ067736	PQ280797	PQ247605
<i>Nigroconidius septatus</i>	UESTCC 24.0162		Pseudostanjehughesiaceae	PQ066570	PQ067817	PQ067733	PQ280795	PQ247606
<i>Nigroconidius septatus</i>	UESTCC 24.0163		Pseudostanjehughesiaceae	PQ066571	PQ067818	PQ067734	N/A	PQ247607
<i>Nigroconidius septatus</i>	UESTCC 24.0164		Pseudostanjehughesiaceae	N/A	PQ067819	PQ067735	PQ280796	PQ247608
<i>Distoseptispora aquamyces</i>	UESTCC 24.0165		Distoseptisporaceae	PQ066590	PQ067842	PQ067758	PQ278579	N/A
<i>Distoseptispora atroviridis</i>	UESTCC 24.0166		Distoseptisporaceae	PQ066586	PQ067835	PQ067751	PQ278572	N/A
<i>Distoseptispora chengduensis</i>	CGMCC 3.27439	T	Distoseptisporaceae	PQ066580	PQ067828	PQ067744	PQ278565	N/A
<i>Distoseptispora dehongensis</i>	UESTCC 24.0167		Distoseptisporaceae	N/A	PQ067836	PQ067752	PQ278573	N/A
<i>Distoseptispora euseptata</i>	UESTCC 24.0168		Distoseptisporaceae	PQ066584	PQ067833	PQ067749	PQ278570	PQ186981
<i>Distoseptispora meilingensis</i>	UESTCC 24.0169		Distoseptisporaceae	PQ066593	PQ067841	PQ067757	PQ278578	N/A
<i>Distoseptispora meilingensis</i>	UESTCC 24.0170		Distoseptisporaceae	PQ066591	PQ067843	PQ067759	PQ278580	N/A
<i>Distoseptispora meilingensis</i>	UESTCC 24.0171		Distoseptisporaceae	N/A	PQ067829	PQ067745	PQ278566	PQ186977
<i>Distoseptispora muchuanensis</i>	CGMCC 3.27444	T	Distoseptisporaceae	PQ066585	PQ067834	PQ067750	PQ278571	N/A
<i>Distoseptispora suoluoensis</i>	UESTCC 24.0172		Distoseptisporaceae	PQ066582	PQ067831	PQ067747	PQ278568	PQ186979
<i>Distoseptispora suoluoensis</i>	UESTCC 24.0173		Distoseptisporaceae	PQ066592	PQ067844	PQ067760	PQ278581	PQ186982
<i>Distoseptispora suoluoensis</i>	UESTCC 24.0174		Distoseptisporaceae	PQ066581	PQ067830	PQ067746	PQ278567	PQ186978
<i>Distoseptispora suoluoensis</i>	UESTCC 24.0175		Distoseptisporaceae	PQ066583	PQ067832	PQ067748	PQ278569	PQ186980
<i>Distoseptispora yongxiuensis</i>	UESTCC 24.0176		Distoseptisporaceae	PQ066587	PQ067837	PQ067753	PQ278574	N/A
<i>Distoseptispora yongxiuensis</i>	UESTCC 24.0177		Distoseptisporaceae	PQ066588	PQ067838	PQ067754	PQ278575	N/A
<i>Distoseptispora yongxiuensis</i>	UESTCC 24.0178		Distoseptisporaceae	N/A	PQ067839	PQ067755	PQ278576	N/A
<i>Distoseptispora yongxiuensis</i>	UESTCC 24.0179		Distoseptisporaceae	PQ066589	PQ067840	PQ067756	PQ278577	N/A
<i>Sporidesmium Chiangmaiense</i>	UESTCC 24.0180		Sporidesmiaceae	PQ066564	PQ067810	PQ067726	PQ261007	PQ241035
<i>Sporidesmium Chiangmaiense</i>	UESTCC 24.0181		Sporidesmiaceae	PQ066565	PQ067811	PQ067727	PQ261008	PQ241036
<i>Sporidesmium Chiangmaiense</i>	UESTCC 24.0182		Sporidesmiaceae	N/A	PQ067812	PQ067728	N/A	N/A
<i>Conioscypha muchuanensis</i>	CGMCC 3.27448	T	Conioscyphaceae	PQ066594	PQ067846	PQ067761	PQ278582	PQ186983

New species are in bold and ex-type strains are denoted as T.

RESULTS

Taxonomy

Dothideomycetes O.E. Erikss. & Winka, Myconet 1: 5 (1997)

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98: 1050 (2007)

Botryosphaeriaceae Theiss. & P. Syd., Annales Mycologici 16: 16 (1918)

MycoBank number: MB80530; Facesoffungi number: FoF00116

Notes – Botryosphaeriaceae, with an estimated divergence crown age of 70 MYA (Rathnayaka et al. 2023), contains common plant pathogens, endophytes, and saprobes on various hosts (Phillips et al. 2013, Manawasinghe et al. 2021, 2022, Wu et al. 2023b). The sexual morphs of Botryosphaeriaceae are characterized by solitary or clustered ascostromata, clavate to cylindro-clavate asci, hyaline to brown, smooth to verrucose, aseptate to septate, fusoid to ellipsoid or ovoid ascospores, and its asexual morphs are coelomycetous, characterized by hyaline, phialidic conidiogenous cells, and hyaline to pigmented conidia (Liu et al. 2012b). The family currently comprises 22 genera: *Alanphillipsia*, *Barriopsis*, *Botryobambusa*, *Botryosphaeria*, *Cophinforma*, *Diplodia*, *Dothiorella*, *Endomelanconiopsis*, *Eutiarosporella*, *Lasiodiplodia*, *Macrophomina*, *Marasasiomyces*, *Mucoharknessia*, *Neodeightonia*, *Neofusicoccum*, *Neoscytalidium*, *Oblongocollomyces*, *Phaeobotryon*, *Sakireeta*, *Sardiniella*, *Sphaeropsis* and *Tiarosporella* (Phillips et al. 2019, Dissanayake et al. 2021, Zhang et al. 2021b).

Neodeightonia C. Booth, Mycological Progress 119: 17 (1970)

MycoBank number: MB3450; Facesoffungi number: FoF07627

Notes – *Neodeightonia* typified by *N. subglobosa*, which is commonly reported as plant pathogens or saprobes (Xiong et al. 2022, Wu et al. 2023b). There are 15 records of *Neodeightonia* listed in Index Fungorum (2024). In this study, a new asexual morph record of *N. subglobosa* from a natural substrate in China is reported based on morphological and phylogenetic analyses, a description and illustration is also provided.

Neodeightonia subglobosa C. Booth, Mycological Papers 119: 19 (1970)

Fig. 1

MycoBank number: MB318601; Facesoffungi number: FoF01966

Saprobic on dead branches of bamboo. Sexual morph: See Liu et al. (2012b). Asexual morph: *Conidiomata* 130–170 µm high, 200–300 µm diam., dark brown to black, solitary, subglobose to obpyriform, semi-immersed, uni-locular, thick-walled. *Conidiomatal wall* 30–60 µm wide, composed of thick-walled, brown cells of *textura angularis*. *Conidiophores* hyaline, cylindrical, unbranched, straight or slightly flexuous, aseptate, or reduced to conidiogenous cells. *Conidiogenous cells* 8–11 × 3–6 µm, holoblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth-walled. *Conidia* 9–13 × 7–10 µm ($\bar{x}$ = 11 × 8 µm; n = 50), hyaline, unicellular, subglobose to oval, rounded at the apex, smooth-walled, guttulate.

Culture characteristics – Colonies on PDA reaching 50–60 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, velvety, brownish-black; reverse black.

Material examined – China, Sichuan Province, Luzhou city, Naxi district, Dawang Bamboo Sea, 28°39'24" N, 105°32'53" E, elevation 700 m, on dead branches of bamboo, 20 April 2023, X.D. Yu, M9 (HUEST 24.0154), living culture UESTCC 24.0137.

Notes – The sexual morph of *Neodeightonia subglobosa* was originally collected from *Bambusa arundinacea* in Africa. Liu et al. (2012b) recollected *N. subglobosa* from bamboo in Thailand, represented by its sexual morph and later, Wu et al. (2022) reported its asexual morph, also on bamboo in Thailand. Morphology of our new collection is almost identical to the asexual morph of *N. subglobosa* described in Wu et al. (2022). Phylogenetically, our new collection (UESTCC 24.0137) clustered with *N. subglobosa* (CBS 448.91 and MFLUCC 22-0005) with 100% ML/1.00 BYPP statistical support (Fig. 2). Therefore, the new collection is identified as *N. subglobosa*. This is the first report of its asexual morph produced on a natural substrate in China.

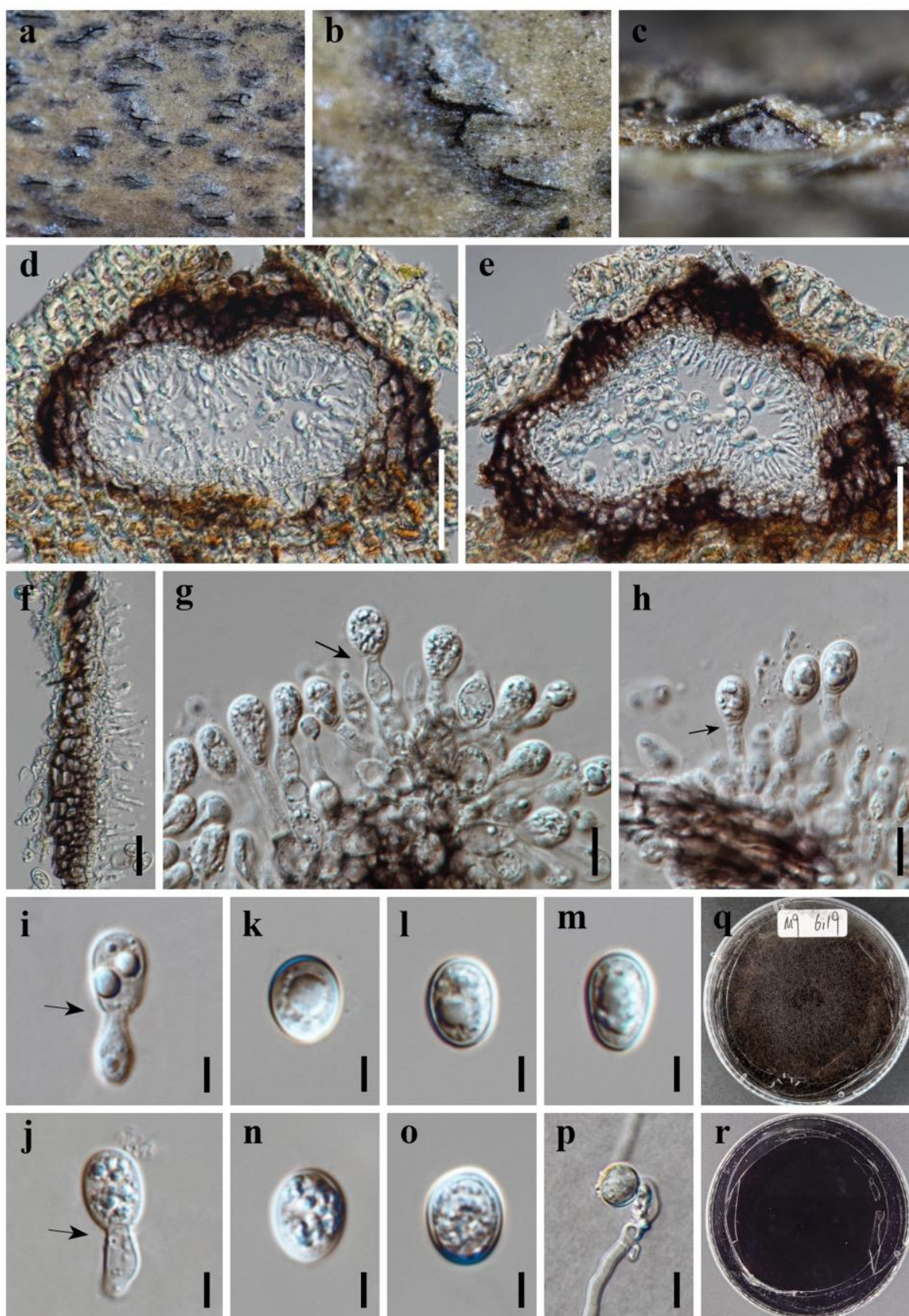


Figure 1 – *Neodeigh-tonia subglobosa* (HUEST 24.0154). a–c Conidiomata on surface of dead bamboo culms. d, e Vertical sections of conidiomata. f Wall of conidioma. g–j Conidiogenous cells bearing conidia (arrows indicate how the conidiogenous cells produce conidia). k–o Conidia. p Germinating conidium. q, r Colony on PDA from above and below. Scale bars: d, e = 50 μ m, f = 20 μ m, g, h, p = 10 μ m, i–o = 5 μ m.

Notes – Eriomycetaceae was established by Hyde et al. (2020) to accommodate *Eriomyces* Huanraluek, Thambugala & K.D. Hyde. The latest taxonomic treatment of the family contains nine non-lichenized genera, viz. *Eriomyces*, *Funbolia*, *Haudseptoria*, *Heleiosa*, *Italiofungus*, *Karstiomyces*, *Neoheliosia*, *Phellinocrescentia* and *Pseudopassalora* (Zhang et al. 2023).

Sichuanomyces X.D. Yu, K.D. Hyde & Jian K. Liu, gen. nov.

MycoBank number: MB854869; Facesoffungi number: FoF16562

Etymology – Refers to Sichuan Province, where the fungus was first discovered.

Type species – *Sichuanomyces bambusicola* X.D. Yu, K.D. Hyde & Jian K. Liu

Saprobic on decaying bamboo. Sexual morph: *Ascostromata* solitary, scattered to gregarious, immersed, globose or subglobose, coriaceous, uni- or multi-loculate. *Peridium* composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* hyphae-like, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, long and furcate pedicellate, rounded at apex, with an ocular chamber. *Ascospores* overlapping uniseriate, fusiform, hyaline, becoming pale brown to brown at maturity, 1-septate, constricted at the septum, guttulate, smooth-walled, surrounded by mucilaginous sheaths. Asexual morph: Undetermined.

Notes – This monotypic genus is introduced to accommodate *Sichuanomyces bambusicola*, which formed a distinct clade sister to *Heleiosa* and *Neoheliosia* within Eriomycetaceae (Fig. 5). *Sichuanomyces* resembles *Heleiosa* and *Neoheliosia* in forming 8-spored, cylindrical asci, and uniseriate, pale brown to brown, 1-septate ascospores (Kohlmeyer et al. 1996, Mortimer et al. 2021). However, *Sichuanomyces* differs in having multi-loculate ascomata, and fusiform ascospores surrounded by a mucilaginous sheath. The new genus is introduced based on the morphology and multi-gene phylogeny.

Sichuanomyces bambusicola X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 3

MycoBank number: MB854870; Facesoffungi number: FoF16569

Etymology – Refers to its bamboo host.

Saprobic on dead branches of bamboo. Sexual morph: *Ascostromata* solitary, scattered to gregarious, immersed, slightly erumpent in host epidermis, visible as yellow area with a small black dot, in vertical section 80–160 μm high, 230–600 μm diam., depressed globose or irregular subglobose, coriaceous, uni- or bi-loculate. *Peridium* 18–22 μm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1–2 μm wide, hyphae-like, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 80–140 $\times$ 7–10 μm ($\bar{x}$ = 120 $\times$ 8.5 μm , n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, long and furcate pedicellate, rounded at apex, with an ocular chamber. *Ascospores* 15–20 $\times$ 5–7 μm ($\bar{x}$ = 18 $\times$ 6 μm , n = 50), overlapping uni-seriate, fusiform, brown, hyaline when immature, 1-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 3 months at 25 °C, irregular, raised to umbonate, dense, edge undulate, white at the inner ring, and yellow at the outer ring; yellow from the reverse.

Material examined – China, Sichuan Province, Leshan City, Muchuan County, Muchuan Bamboo Sea, 28°51'29" N, 103°56'58" E, 525 m elevation, on dead branches of bamboo, 14 November 2022, X.D. Yu, G8 (HKAS 135145, holotype), ex-type living culture CGMCC 3.27451; Meishan City, Danling County, Jiulongshan Forest Park, 29°54'48" N, 103°35'13" E, 460 m elevation, on dead branches of bamboo, 14 July 2022, X.D. Yu, D6 (HUEST 24.0127); living culture CGMCC 3.27445; Chengdu City, Dujiangyan County, Mount Qingcheng, 30°54'29" N, 103°32'36" E, elevation 960 m, on dead branches of bamboo, 2 December 2021, X.D. Yu, B14 (HKAS 135163); living culture UESTCC 23.0251.

Additional mtSSU GenBank numbers – CGMCC 3.27445 = PQ164984; UESTCC 23.0251 = PQ164982.

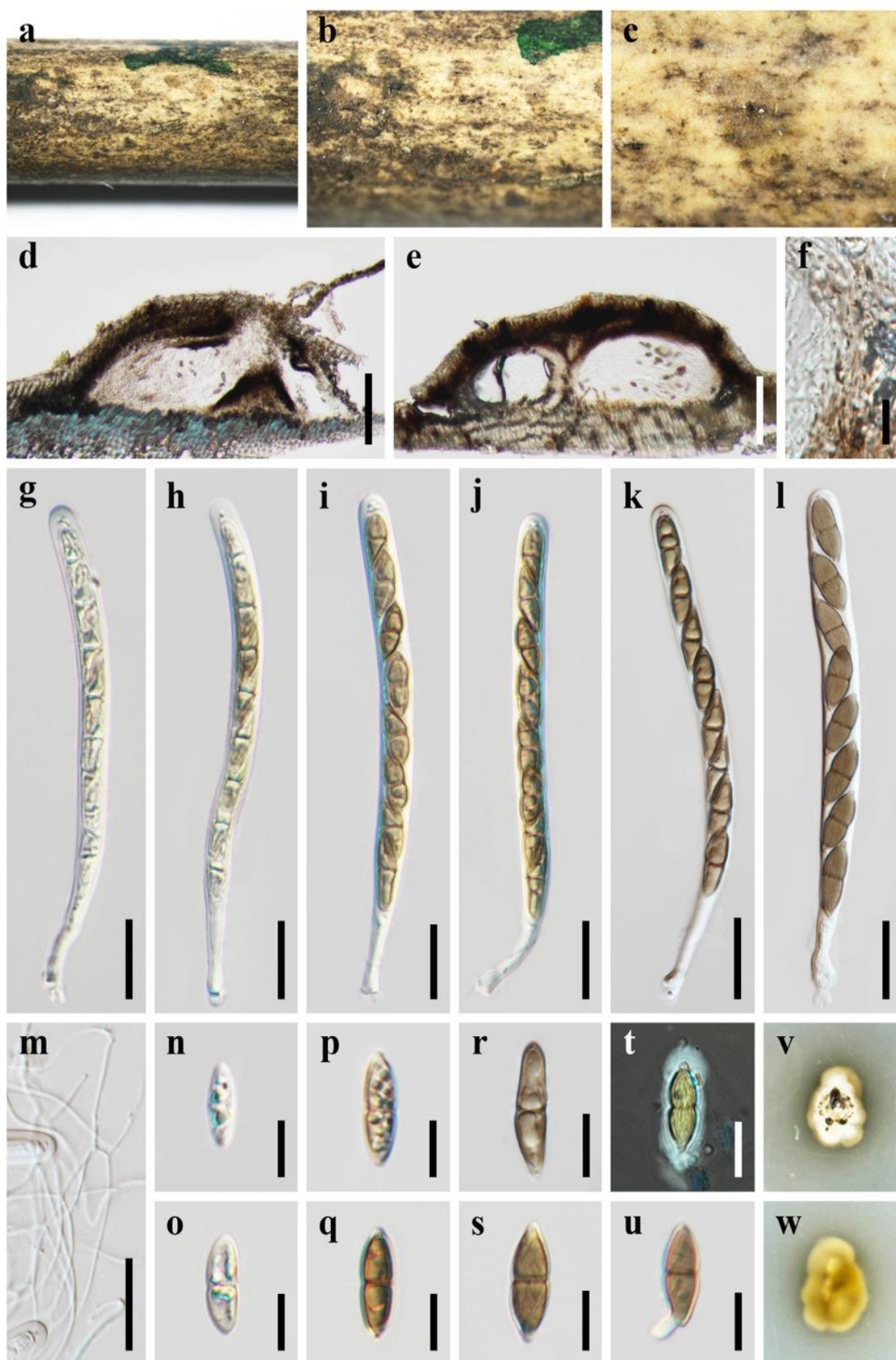


Figure 3 – *Sichuanomyces bambusicola* (HKAS 135145, holotype). a–c Ascomata on host substrate. d, e Vertical sections of ascomata. f Structure of peridium. g–l Asci. m Pseudoparaphyses. n–s Ascospores. t Ascospore with mucilaginous sheath. u Germinated

ascospore. v, w Colony on PDA from above and below. Scale bars: d, e = 100 μ m, g–m = 20 μ m, f, n–u = 10 μ m.

Neoheliosia Mortimer, *Frontiers in Microbiology* 12: 6 (2021)

MycoBank number: MB838517; Facesoffungi number: FoF11959

Notes – *Neoheliosia* was introduced by Mortimer et al. (2021) based on *Neoheliosia lincangensis*. This genus is characterized by immersed to erumpent, globose to subglobose or obpyriform, dark brown to black ascomata, 8-spored, bitunicate, cylindrical asci and uniseriate, narrowly ovoid to clavate, 1-septate ascospores with guttules (Mortimer et al. 2021). Zhang et al. (2023) introduced the second species *N. guizhouensis* based on morphological and phylogenetic analyses. Subsequently, *N. guizhouensis* was rediscovered on decaying rachides of *Trachycarpus fortunei* (Zhang et al. 2024a). Two species are accepted in the genus. In this study, we introduce a new host record for *N. guizhouensis*.

Neoheliosia guizhouensis J.F. Zhang & K.D. Hyde, *Fungal Diversity* 122: 75 (2023) Fig. 4

MycoBank number: MB900722; Facesoffungi number: FoF14575

Saprobic on dead branches of bamboo. Sexual morph: *Ascostromata* solitary to gregarious, immersed to erumpent, visible as black dome-shaped on host surface, in vertical section 90–170 μ m high, 220–340 μ m diam., irregular subglobose, coriaceous, uni- or bi-loculate. *Peridium* 10–20 μ m wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2.5 μ m wide, hyphae-like, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 70–120 $\times$ 9–12 μ m ($\bar{x}$ = 90 $\times$ 10.5 μ m, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short and furcate pedicellate, rounded at apex, with an ocular chamber. *Ascospores* 10–19 $\times$ 5–8 μ m ($\bar{x}$ = 15 $\times$ 6.5 μ m, n = 50), overlapping uniseriate, narrowly ovoid to clavate, pale brown to brown, 1-septate, constricted at the septum, guttulate, smooth-walled, without any appendages or sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 3 months at 25 °C, circular, raised to umbonate, dense, white, reverse brown.

Material examined – China, Sichuan Province, Chengdu City, Jianyang County, Three Forks Lake, 30°17'55" N, 104°17'38" E, elevation 470 m, on dead branches of bamboo, 9 May 2022, X.D. Yu, C3 (HUEST 23.0252), living culture UESTCC 23.0252.

Additional mtSSU GenBank number – UESTCC 23.0252 = PQ164983.

Notes – The morphology and molecular data (Fig. 5) of our isolate (UESTCC 23.0252) are almost identical to the type of *Neoheliosia guizhouensis* (MFLU 18-2268, GZAAS 19-1762), which was found on dead culm of unidentified herbaceous plant in Guizhou, China (Zhang et al. 2023). Therefore, a new host record for *N. guizhouensis* from bamboo is provided in this study.

Pleosporales Luttrell ex M.E. Barr, *Prodromus to class Loculoascomycetes*: 67 (1987)

Anteagloniaceae K.D. Hyde, Jian K. Liu & A. Mapook, *Fungal Diversity* 63: 33 (2013)

MycoBank number: MB804658; Facesoffungi number: FoF06700

Notes – Anteagloniaceae was established by Hyde et al. (2013) to accommodate *Anteaglonium*. Four genera were accepted in this family, viz. *Anteaglonium*, *Flammeascoma*, *Neolophiotrema* and *Purpureofaciens* (Ren et al. 2021). Anteagloniaceae species have a cosmopolitan distribution, most are saprobic or endophytes on woody based substrates in aquatic and terrestrial habitats (De Almeida et al. 2014, Dong et al. 2020, Ren et al. 2021).

Antebambusa X.D. Yu, K.D. Hyde & Jian K. Liu, gen. nov.

MycoBank number: MB854871; Facesoffungi number: FoF16563

Etymology – In reference to a new genus in Anteagloniaceae and its host *Bambusa*.

Type species – *Antebambusa sichuanensis* X.D. Yu & Jian K. Liu

Saprobic on decaying bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, subglobose, coriaceous, uni-loculate. *Peridium* composed of several layers of brown,

thick-walled cells of *textura angularis*. *Hamathecium* hyphae-like, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, with an ocular chamber. *Ascospores* uniseriate or biseriate, fusiform, septate, guttulate, smooth-walled, surrounded by a gelatinous sheath. Asexual morph: Undetermined.

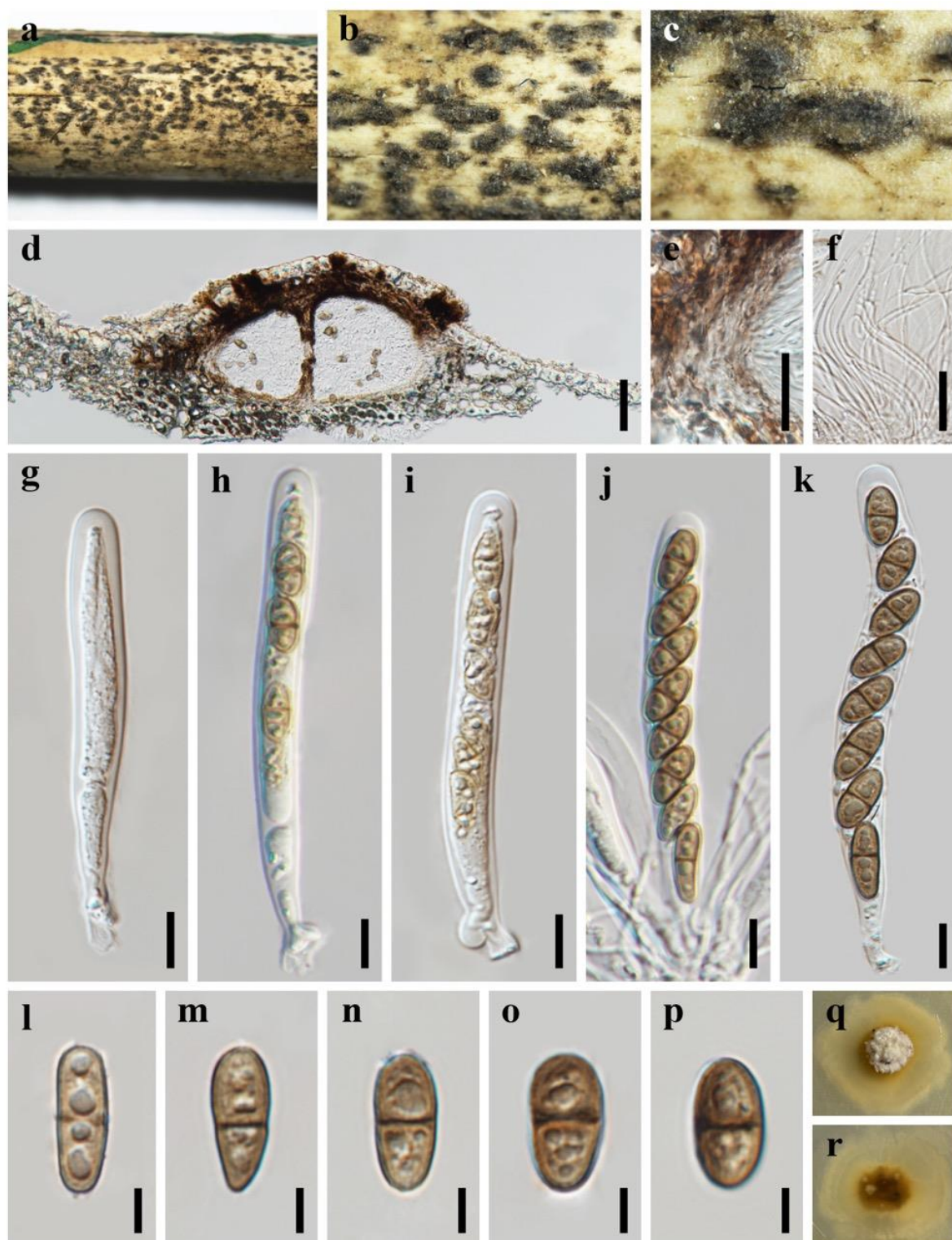


Figure 4 – *Neoheliosia guizhouensis* (HUEST 23.0252). a–c Ascomata on host substrate. d Vertical section of ascoma. e Structure of peridium. f Pseudoparaphyses. g–k Asci. l–p Ascospores. q, r Colony on PDA from above and below. Scale bars: d = 50 μ m, e, f = 20 μ m, g–k = 10 μ m, l–p = 5 μ m.

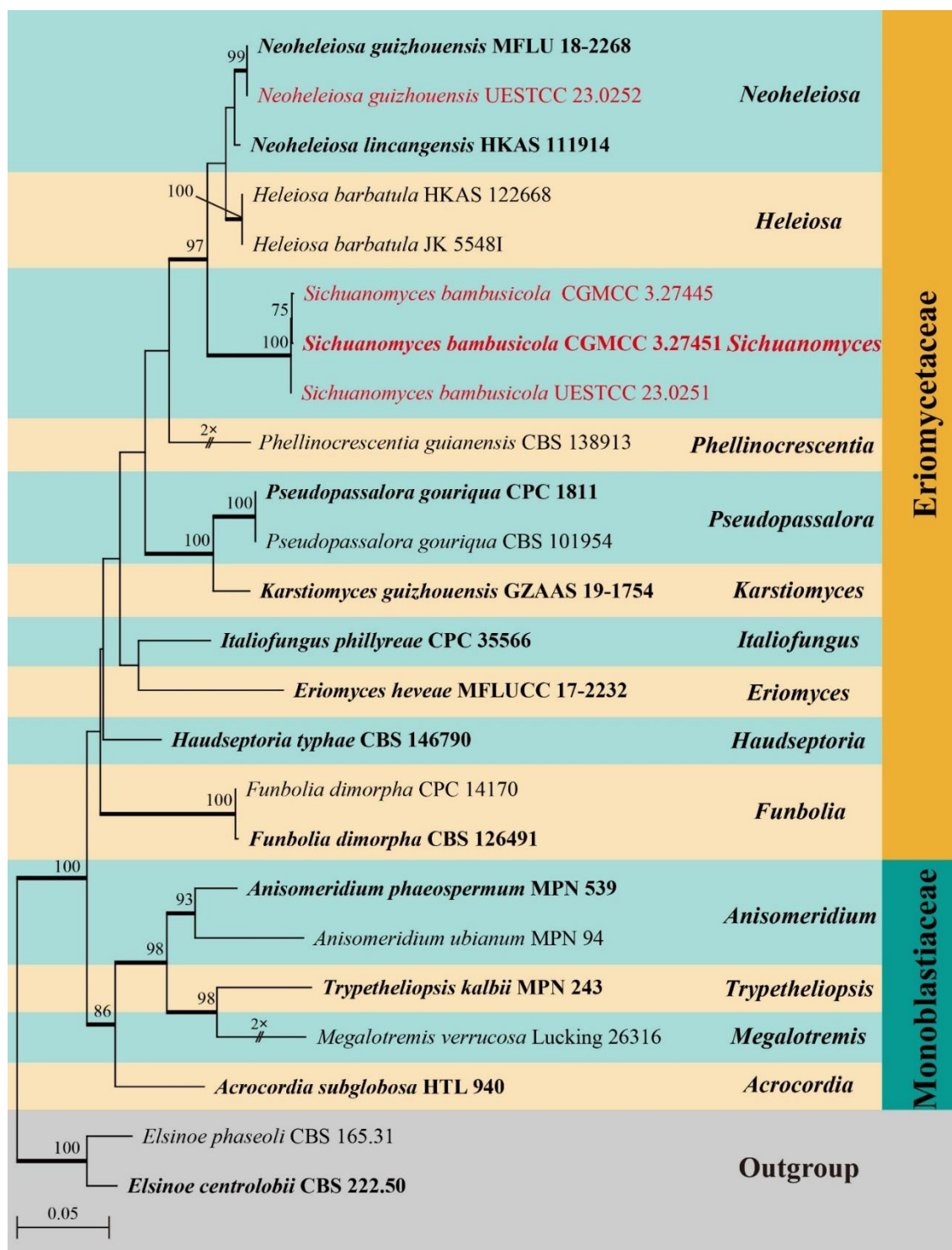


Figure 5 – RAxML tree generated from combined SSU, ITS, LSU, *tef1-α* and mtSSU sequence data of Monoblastiales. The tree was rooted with *Elsinoe centrolobii* (CBS 222.50) and *E. phaseoli* (CBS165.31). Ex-type strains are in bold and newly generated sequences in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 were in bold.

Notes – The phylogenetic analysis showed that four isolates of *Antebambusa* formed a monophyletic clade, sister to the monotypic genus *Neolophiotrema* (type: *N. xiaokongense*) (Fig. 7). *Antebambusa* resembles *Neolophiotrema* in having 8-spored, short pedicellate asci, and hyaline, 1-septate ascospores surrounded by a gelatinous sheath. However, *Antebambusa* has semi-immersed ascomata, cylindrical asci and fusiform ascospores, while *Neolophiotrema* has immersed

ascomata, cylindrical-clavate asci, and broadly fusiform ascospores with rounded ends (Ren et al. 2021). The BLAST search based on SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data of our new collection showed that the similarity of our strain to *N. xiaokongense* (KUMCC 20-0173) is 98% (427/434), 83% (394/477), 97% (754/781), 86% (743/864) and 92% (821/890), respectively. We, hereby, introduce the new genus based on the distinctiveness of morphology and multi-gene phylogeny.

Antebambusa sichuanensis X.D. Yu & Jian K. Liu, sp. nov.

Fig. 6

MycoBank number: MB854872; Facesoffungi number: FoF16570

Etymology – Epithet refers to Sichuan Province where the fungus was collected.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, in vertical section 100–170 μm high, 200–270 μm diam., subglobose, coriaceous, uni-loculate. *Peridium* 15–20 μm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.6–2.0 μm wide, hyphae-like, pseudoparaphyses, branched, embedded in a gelatinous matrix. *Asci* 45–65 × 11–16 μm ($\bar{x}$ = 60 × 14 μm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 17–24 × 4.5–7.5 μm ($\bar{x}$ = 20 × 6 μm, n = 50), overlapping uni-seriate or bi-seriate, fusiform, hyaline, 1-septate, constricted at the septum, upper cell slightly wider than lower cell, guttulate, smooth-walled, surrounded by a gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 50–60 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, white grey at the inner ring, and dark greyish-brown at the outer ring; in reverse black.

Material examined – China, Sichuan Province, Luzhou City, Naxi County, Dawang Bamboo Sea, 28°39'24" N, 105°32'53" E, elevation 700 m, on dead branches of bamboo, 20 April 2023, X.D. Yu, M3 (HKAS 135143, holotype); ex-type living culture CGMCC 3.25592; Shanhuashan Village, 28°36'5" N, 105°28'53" E, 680m elevation, on dead branches of bamboo, 20 April 2023, X.D. Yu, K11 (HUEST 24.0155); living culture UESTCC 24.0138; *ibid.* K13 (HUEST 24.0156); living culture UESTCC 24.0139; *ibid.* K15 (HUEST 24.0157), living culture UESTCC 24.0140.

Bambusicolaceae D.Q. Dai & K.D. Hyde, Fungal Diversity 63: 49 (2013)

MycoBank number: MB804293; Facesoffungi number: FoF00586

Notes – *Bambusicolaceae* was introduced by Hyde et al. (2013) to accommodate the genus *Bambusicola* based on the phylogeny inferred from combined SSU, LSU, *rpb2* and *tef1-α* gene regions. Taxa in the family are widely distributed and commonly saprobic on Arecaceae (palms), Betulaceae (*Corylus*), Fabaceae (*Leucaena*), Moraceae (*Ficus*), and Poaceae (bamboos) in terrestrial habitats (Dai et al. 2015, Jayasiri et al. 2019, Brahmanage et al. 2020, Wijesinghe et al. 2020, Yu et al. 2022).

Bambusicola D.Q. Dai & K.D. Hyde, Cryptogamie Mycologie 33: 367 (2012)

MycoBank number: MB801041; Facesoffungi number: FoF01433

Notes – *Bambusicola* was introduced by Dai et al. (2012) and is typified by *B. massarinia* D.Q. Dai & K.D. Hyde. There are 18 species listed under *Bambusicola* in Species Fungorum (2024). Most species are parasites or saprobes on bamboos (Poaceae) in terrestrial habitats (Dai et al. 2012, 2015, 2017, Thambugala et al. 2017, Yang et al. 2019d, Monkai et al. 2021, Liang et al. 2023), except *B. aquatica* (from a freshwater habitat) and *B. ficuum* (on *Ficus* sp., Moraceae) (Brahmanage et al. 2020, Dong et al. 2020). We introduce a new species of *Bambusicola* which was collected in terrestrial habitats in Sichuan province of China based on comprehensive morphology and phylogeny analyses.

Bambusicola meishanensis X.D. Yu & Jian K. Liu, sp. nov.

Fig. 8

MycoBank number: MB854873; Facesoffungi number: FoF16571

Etymology – Epithet refers to the location, Meishan, Sichuan Province of China, where the species was collected.

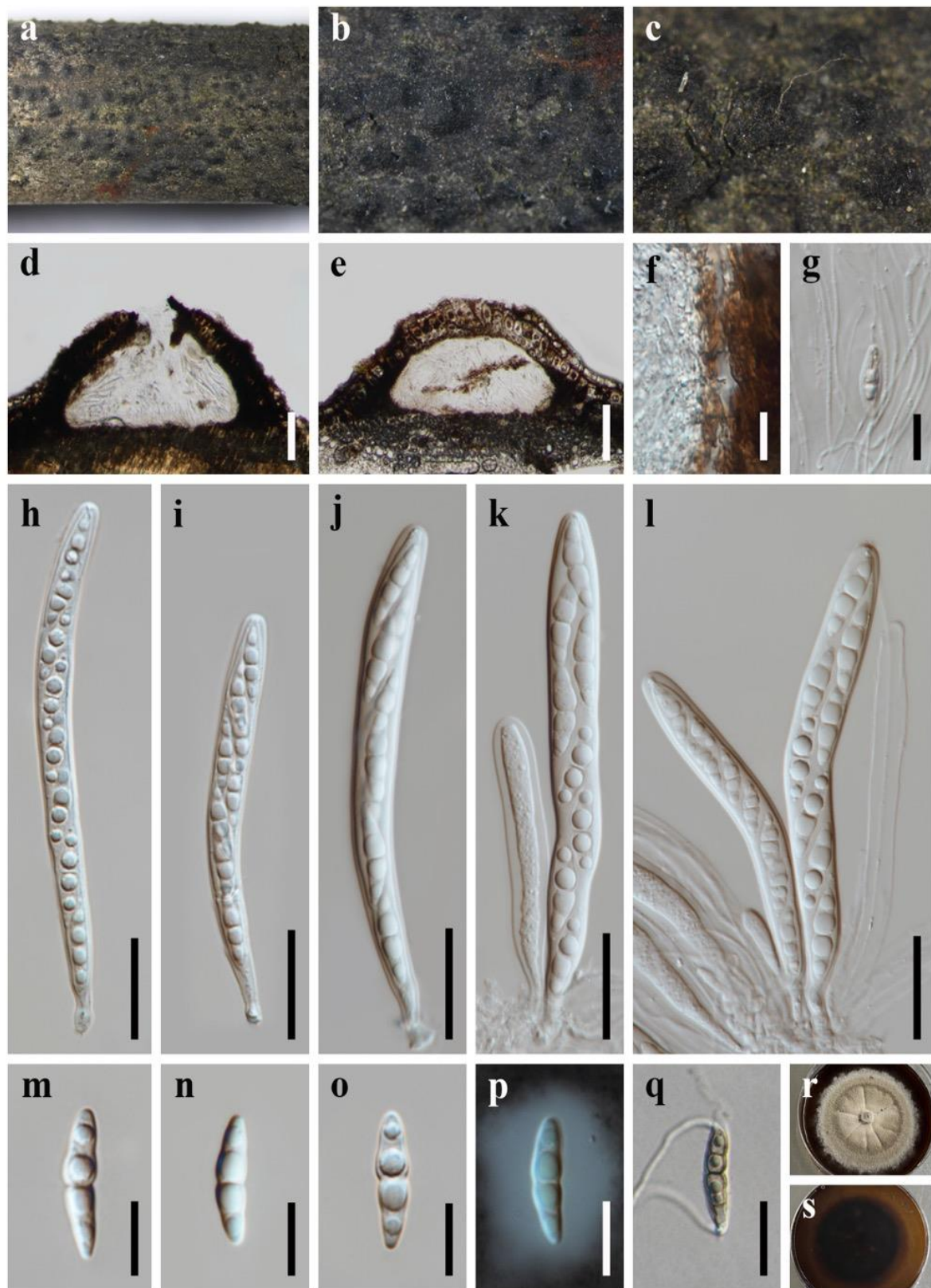


Figure 6 – *Antebambusa sichuanensis* (HKAS 135143, holotype). a–c Ascomata on host substrate. d, e Vertical section of ascomata. f Structure of peridium. g Pseudoparaphyses. h–l Asci. m–o Ascospores. p Ascospores with mucilaginous sheath. q Germinated ascospore. r, s Colony on PDA from above and below. Scale bars: d, e = 100 μ m, h–l, q = 20 μ m, f, g, m–p = 10 μ m.

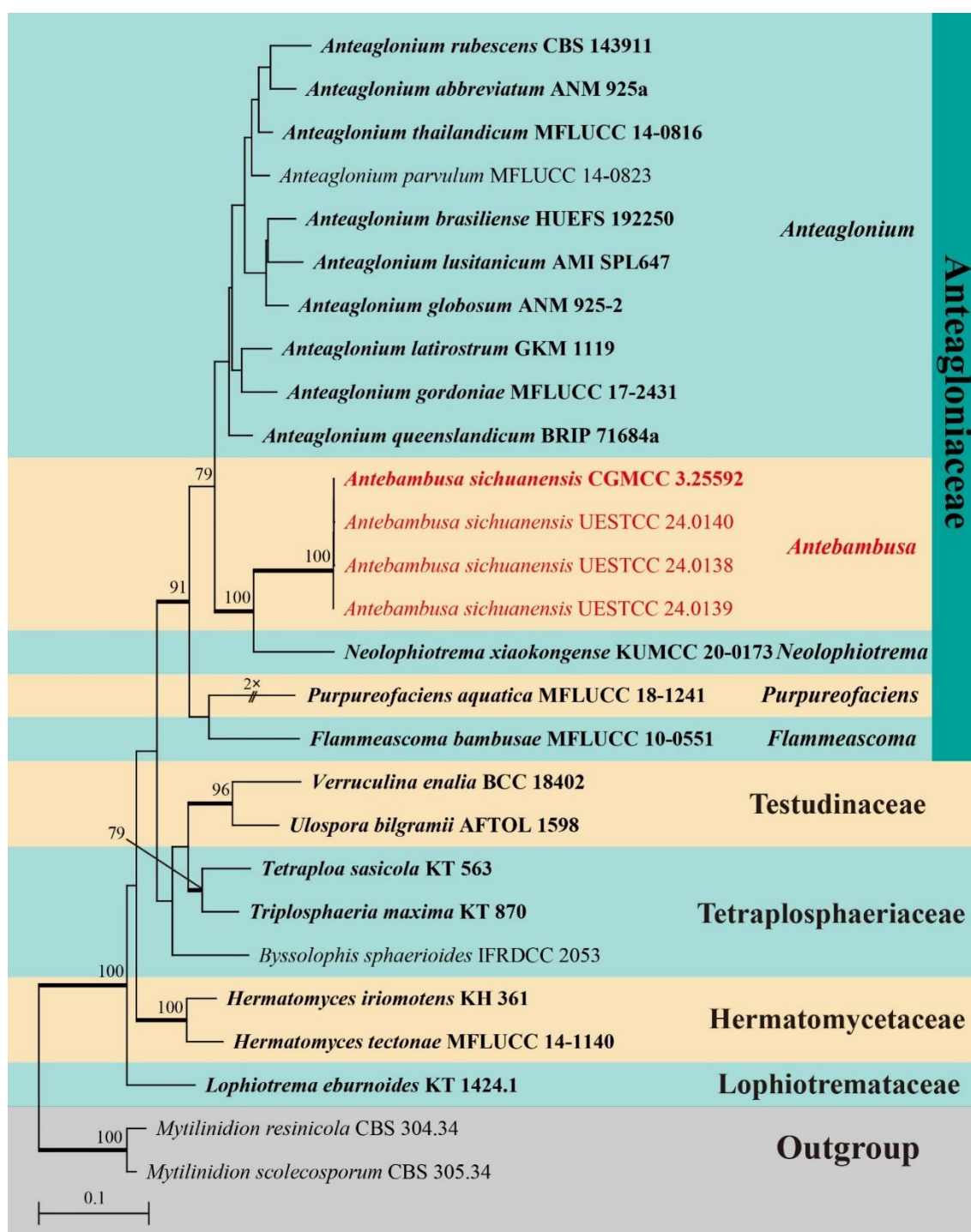


Figure 7 – RAxML tree generated from combined SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data of Anteagloniaceae. The tree was rooted with *Mytilinidion resinicola* (CBS 304.34) and *M. scolecosporem* (CBS 305.34). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, in vertical section 120–190 μm high, 200–360 μm diam., subglobose, coriaceous, uni-loculate. *Peridium* 25–65 μm wide, composed of several layers of pale brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.4–2.4 μm wide, hyphae-like, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 45–70 × 13–15 μm

($\bar{x}$ = 55 × 14 μ m, n = 30), 8-spored, bitunicate, fissitunicate, broad cylindrical to cylindric-clavate, straight or slightly curved, short pedicellate to sessile, rounded at apex, with an ocular chamber. *Ascospores* 18–24 × 6–7.5 μ m ($\bar{x}$ = 21 × 6.5 μ m, n = 50), overlapping biserial or 3-seriate, fusiform, straight to slightly curved, hyaline, 1-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

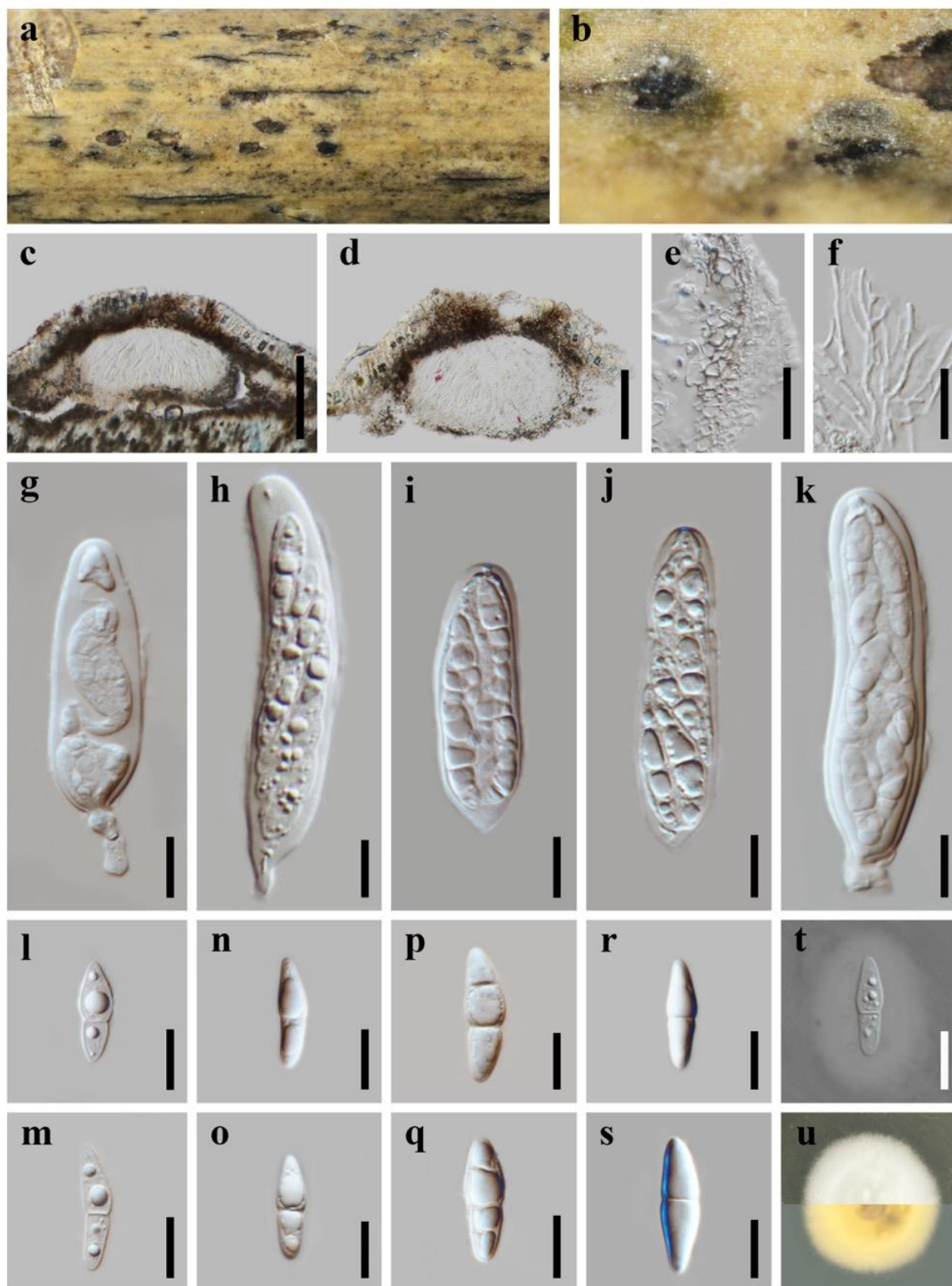


Figure 8 – *Bambusicola meishanensis* (HKAS 135160, holotype). a–b Ascomata on host substrate. c, d Vertical section of ascomata. e Structure of peridium. f Pseudoparaphyses. g–k Asci. l–s Ascospores. t, u Ascospores with mucilaginous sheath.

l–s Ascospores. t Ascospore with mucilaginous sheath. u Colony on PDA from above and below. Scale bars: c, d = 100 μ m, d, e = 20 μ m, g–t = 10 μ m.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 3 months at 25 °C, circular, raised to umbonate, dense, white, reverse yellow.

Material examined – China, Sichuan Province, Meishan City, Qingshen County, Bamboo Forest Wetland Park, 29°48'43" N, 103°49'26" E, elevation 400 m, on dead branches of bamboo, 4 November 2022, X.D. Yu, J32 (HKAS 135160, holotype), ex-type living culture CGMCC 3.25594.

Notes – *Bambusicola meishanensis* shows a close phylogenetic affinity to *B. fusispora* and *B. nanensis* with 100% ML/1.00 BYPP statistical support (Fig. 10). However, we could not compare their morphology as *B. nanensis* is only represented by a coelomycetous asexual morph (Phukhamsakda et al. 2022). *Bambusicola meishanensis* resembles *B. fusispora* in broad cylindrical to cylindric-clavate asci and fusiform ascospores (Monkai et al. 2021). However, *B. meishanensis* has broader asci (45–70 $\times$ 13–15 vs. 47–104 $\times$ 6–12) and ascospores (18–24 $\times$ 6–7.5 vs. 20–30 $\times$ 3–7) (Monkai et al. 2021). In addition, there are 2.15% (10/465) differences in ITS and 0.94% (8/850) differences in LSU gene regions between *B. meishanensis* and *B. fusispora*, which also supports the introduction of *B. meishanensis* as a new species.

Flavosporella X.D. Yu, K.D. Hyde & Jian K. Liu, gen. nov.

Mycobank number: MB854875, Facesoffungi number: FoF16564

Etymology – Latin “*flavum*”, meaning yellowish, referring to the yellow ascospores.

Type species – *Flavosporella bambusae* X.D. Yu & Jian K. Liu

Saprobic on decaying bamboo. Sexual morph: *Ascostromata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, subglobose, coriaceous, uni- or bi-loculate. *Peridium* composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* hyphae-like, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, obovoid to cylindrical, straight or slightly curved, short pedicellate, rounded at apex, with an ocular chamber. *Ascospores* bi-seriate, didymosporous, fusiform, yellow, 1-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Notes – In the phylogenetic analysis four isolates of *Flavosporella* formed a distinct clade within Bambusicolaceae (Fig. 10). *Flavosporella* resembles *Palmiascoma* and *Neopalmiascoma* in forming semi-immersed ascomata, 8-spored and short pedicellate asci, bi-seriate, 1-septate and yellowish ascospores surrounded by a mucilaginous sheath. However, *Flavosporella* differs from the latter in having uni- or two-loculate ascomata, and smooth ascospores (Liu et al. 2015, Zhang et al. 2024b). Therefore, *Flavosporella* is described as a new genus based on phylogeny coupled with morphology.

Flavosporella bambusae X.D. Yu & Jian K. Liu, sp. nov.

Fig. 9

Mycobank number: MB854875; Facesoffungi number: FoF16572

Etymology – *Bambusae* refers to the host.

Saprobic on dead branches of bamboo. Sexual morph: *Ascostromata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, in vertical section 230–280 μ m high, 440–460 μ m diam., subglobose, coriaceous, bi-loculate. *Peridium* 30–80 μ m wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.0–2.0 μ m wide, hyphae-like, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 45–70 $\times$ 8–12 μ m ($\bar{x}$ = 60 $\times$ 9 μ m, n = 30), 8-spored, bitunicate, fissitunicate, obovoid to cylindrical, straight or slightly curved, short pedicellate, rounded at apex, with an ocular chamber. *Ascospores* 10–13 $\times$ 3.5–6 μ m ($\bar{x}$ = 12 $\times$ 4.5 μ m, n = 50), bi-seriate, broad fusiform, hyaline, becoming yellowish at maturity, 1-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 3 months at 25 °C, circular, white to pale white, velvety, hairy, in reverse black.

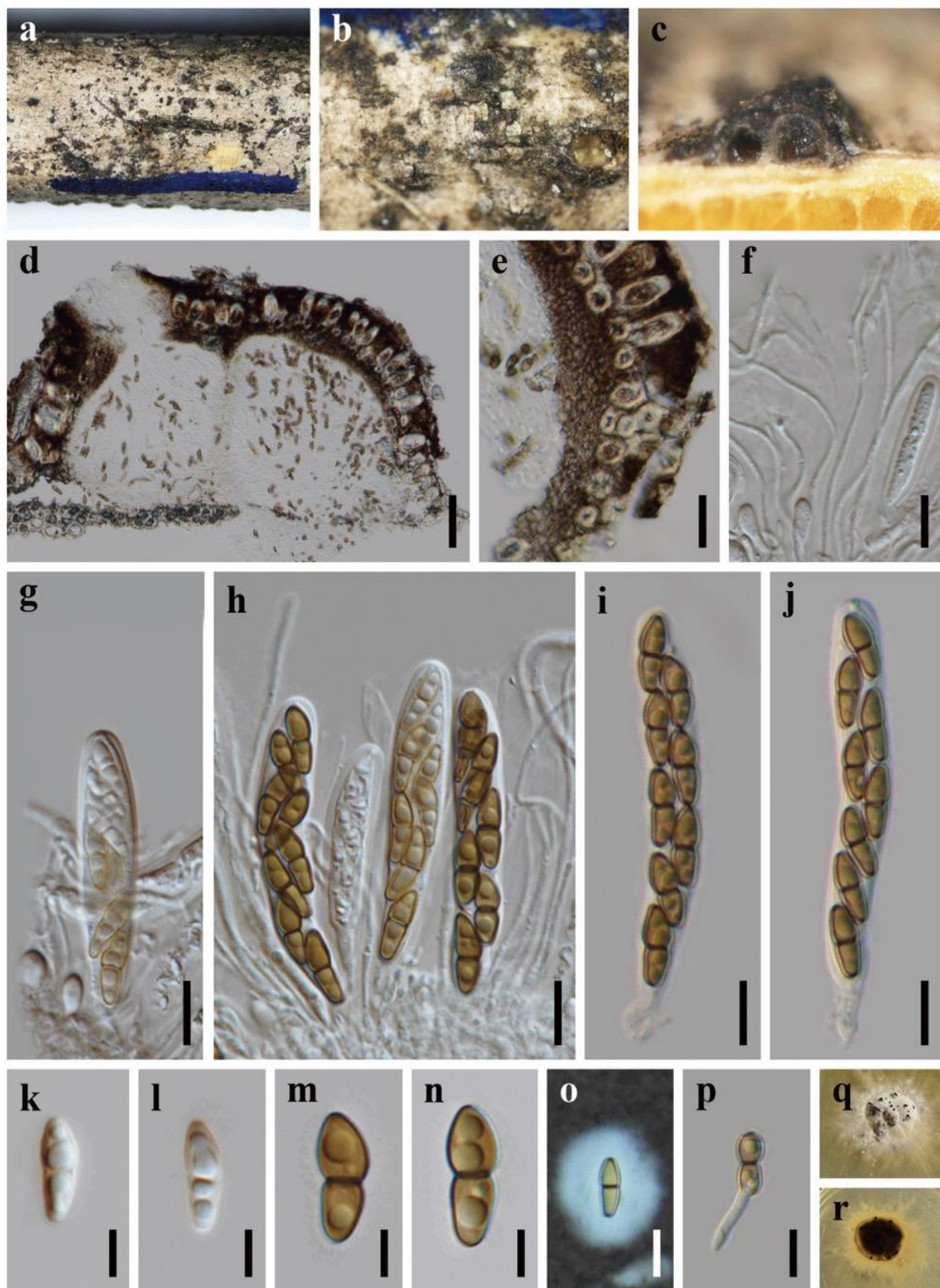


Figure 9 – *Flavosporella bambusae* (HKAS 135159, holotype). a–c Ascomata on host substrate. d Vertical section of ascoma. e Structure of peridium. f Pseudoparaphyses. g–j Asci. k–n Ascospores. o Ascospore with mucilaginous sheath. p Germinated ascospore. q, r Colony on PDA from above and below. Scale bars: d = 50 μ m, e = 20 μ m, f–j, o, p = 10 μ m, k–n = 5 μ m.

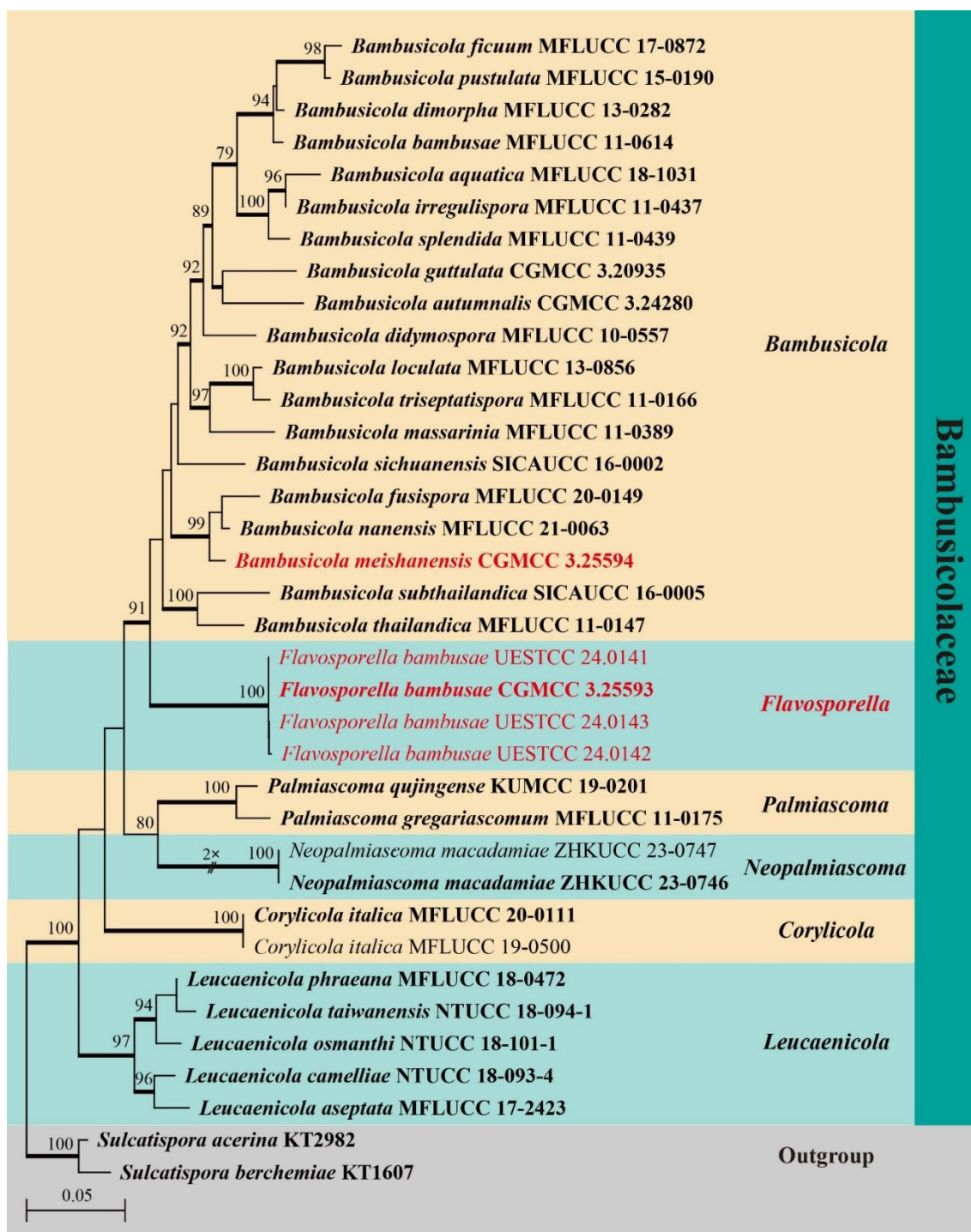


Figure 10 – RAxML tree generated from combined SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data of Bambusicolaceae. The tree was rooted with *Sulcatisspora acerina* (KT 2982) and *S. berchemia* (KT 1607). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Material examined – China, Sichuan Province, Zigong City, Rong County, Hualonggou Bamboo Sea, 29°28'52" N, 104°17'20" E, elevation 625 m, on dead branches of bamboo, 3 November 2022, X.D. Yu, H19 (HKAS 135159, holotype), ex-type living culture CGMCC 3.25593; *ibid.* H15 (HUEST 24.0158); living culture UESTCC 24.0141; Chengdu City, Dujiangyan County, Sea of Bamboo, 31°3'29"N, 103°38'31"E, 810 m elevation, on dead branches of bamboo, 2

December 2021, X.D. Yu, B32 (HUEST 24.0159); living culture UESTCC 24.0142; *ibid.* B32-1 (HUEST 24.0160); living culture UESTCC 24.0143.

Lentithecaceae Y. Zhang *et al.*, C.L. Schoch, J. Fourn., Crous & K.D. Hyde, *Studies in Mycology* 64: 93 (2009)

MycoBank number: MB515470; Facesoffungi number: FoF08256

Notes – Lentithecaceae was established by Zhang *et al.* (2009) and typified by *Lentithecium* K.D. Hyde, J. Fourn. & Yin. Zhang., which is characterized by immersed, lenticular, solitary or scattered ascomata, cylindro-clavate to cylindro-oblong, short pedicellate asci, fusiform or filiform, hyaline to pale yellow, septate ascospores. Most Lentithecaceae species are saprobes and have been found on stems and twigs of herbaceous and woody plants in freshwater, terrestrial, or marine environments (Wanasinghe *et al.* 2014, Wijayawardene *et al.* 2015, Tibpromma *et al.* 2017, Hyde *et al.* 2018, Jiang *et al.* 2019b, Xu *et al.* 2020, Liu *et al.* 2022).

Pseudosetoseptoria X.G. Tian, K.D. Hyde & Tibpromma, *Mycosphere* 15: 46 (2024)

MycoBank number: MB900974; Facesoffungi number: FoF14287

Notes – The coelomycetous genus *Pseudosetoseptoria* was established in Lentithecaceae by Tian *et al.* (2024) to accommodate *Pseudosetoseptoria bambusae*. The genus is characterized by holoblastic, hyaline, subcylindrical to ampulliform conidiogenous cells, hyaline, smooth, 1-septate, ellipsoid to ovoid with both ends rounded, guttulate conidia (Tian *et al.* 2024). In this study, morphological characteristics and multi-gene phylogenetic analysis of a combined SSU, ITS, LSU and *tef1-α* sequence data revealed a new species of *Pseudosetoseptoria* from dead branches of bamboo collected in China.

Pseudosetoseptoria bambusae X.D. Yu & Jian K. Liu, *sp. nov.*

Fig. 11

MycoBank number: MB854876; Facesoffungi number: FoF16573

Etymology – Bambusae referring to the host.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 150–200 µm high, 200–280 µm diam., black, pycnidial, visible as black domes on the substrate, solitary to gregarious, subglobose in section, semi-immersed, uni-locular, thick-walled. *Conidiomatal wall* 35–65 µm wide, composed of thick-walled, subhyaline to brown cells of *textura angularis*. *Conidiophores* hyaline, cylindrical, unbranched, straight or slightly flexuous, aseptate, and occasionally reduced to conidiogenous cells. *Conidiogenous cells* 5.5–7.5 × 2–5 µm, holoblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth walled. *Conidia* 9–15 × 6–9 µm ($\bar{x}$ = 12 × 7.5 µm, n = 50), hyaline, unicellular, occasionally 1-septate, subcylindrical to irregular cylindrical, sometimes with a narrow and truncate base, straight or slightly curved, smooth-walled, guttulate.

Culture characteristics – Colonies growing on PDA, reaching a diameter of 60–70 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, dark grey; in reverse black.

Material examined – China, Sichuan Province, Luzhou City, Naxi County, Dawang Bamboo Sea, 28°39'24" N, 105°32'53" E, elevation 700 m, on dead branches of bamboo, 20 April 2023, X.D. Yu, M14 (HKAS 135126, holotype), ex-type living culture CGMCC 3.25595.

Notes – The phylogenetic analyses based on SSU, ITS, LSU and *tef1-α* sequence data showed that *Pseudosetoseptoria bambusae* nested in *Pseudosetoseptoria* and formed a distinct lineage (Fig. 12). *Pseudosetoseptoria bambusae* resembles *P. oryzae* in having hyaline, septate, guttulate conidia (Tian *et al.* 2024). However, they can be distinguished by the modes of conidiogenous cells (holoblastic vs. annellidic). The establishment of *P. bambusae* is justified by morphological and phylogenetic evidence.

Lindgomycetaceae K. Hiray., Kaz. Tanaka & Shearer, *Mycologia* 102: 733 (2010)

MycoBank number: MB515187; Facesoffungi number: FoF08267

Notes – The fungal family Lindgomycetaceae (Pleosporales, Dothideomycetes) was introduced by Hirayama et al. (2010) to accommodate four new species of *Lindgomyces*. Members of Lindgomycetaceae are characterized by immersed, semi-immersed, erumpent to superficial ascomata papillate or clypeus-like on the host surface, mostly with ocular chamber of asci and cylindrical, fusiform or clavate, hyaline or brown, uni- or multi-septate, straight or slightly curved ascospores with or without a mucilaginous sheath; as well as coelomycetous, which produce dark brown to black or pearl white to dull yellow, ostiolate pycnidia, phialidic or holoblastic conidiogenous cells sometimes with sympodial proliferations and hyaline, cylindrical, ellipsoid, obovoid, globose to subglobose or irregular, 0–1-septate conidia with or without a mucilaginous sheath or appendages (Dong et al. 2020, Yang et al. 2023).

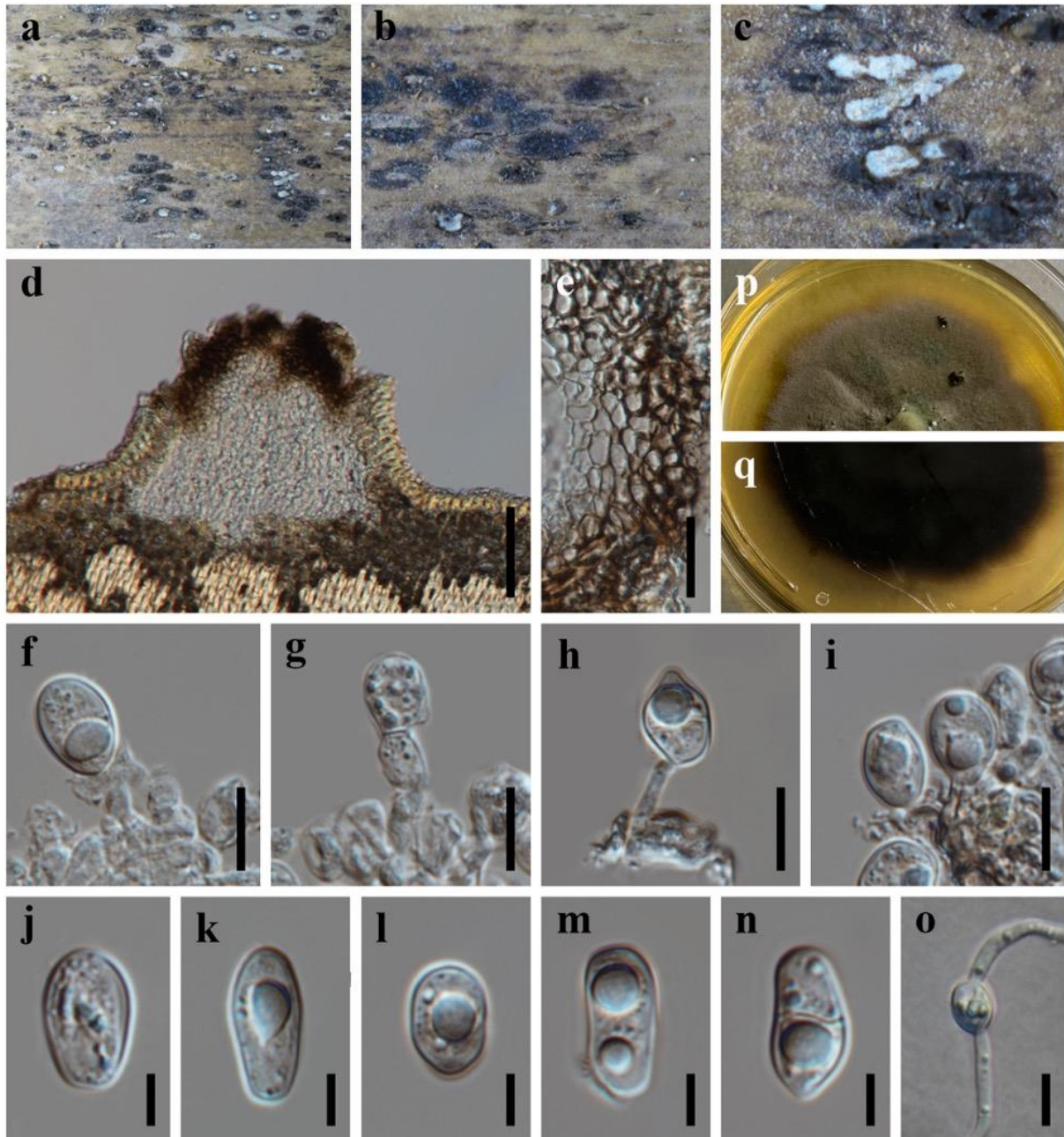


Figure 11 – *Pseudosetoseptoria bambusae* (HKAS 135126, holotype). a–c Conidiomata on surface of dead bamboo culms. d Vertical section of conidioma. e Wall of conidioma. f–i Conidiogenous cells bearing conidia. j–n Conidia. o Germinating conidium. p, q Colony on PDA from above and below. Scale bars: d = 50 μ m, e = 20 μ m, f–i, o = 10 μ m, j–n = 5 μ m.

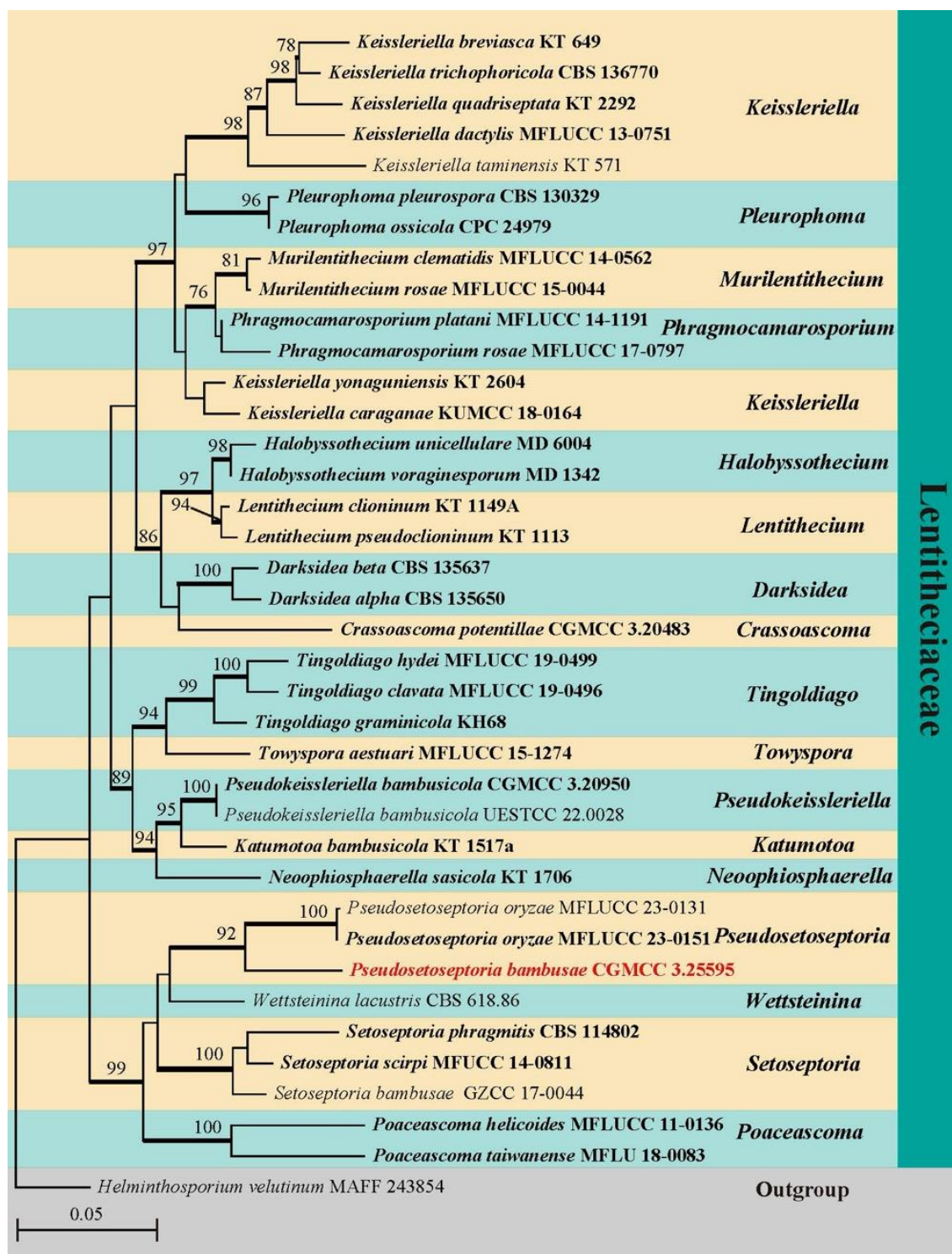


Figure 12 – RAxML tree generated from combined SSU, ITS, LSU and *tef1-α* sequence data of Lentitheciaceae. The tree is rooted with *Helminthosporium velutinum* (MAFF 243854). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Hongkongmyces C.C. Tsang, J.F.W. Chan, N.J. Trendell-Smith, A.H.Y. Ngan, I.W.H. Ling, S.K.P. Lau & P.C.Y. Woo, Medical Mycology 52: 740 (2014)

Mycobank number: MB805515; Facesoffungi number: FoF08269

Notes – *Hongkongmyces* was introduced by Tsang et al. (2014) to accommodate a human pathogen, *H. pedis*. However, most *Hongkongmyces* species are saprobes and have been found in

freshwater habitats (Jayawardena et al. 2023). In this study, a coelomycetous *Hongkongmyces* species is introduced.

Hongkongmyces sichuanensis X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 13

Mycobank number: MB854877; Facesoffungi number: FoF16574

Etymology – The epithet refers to Sichuan Province where the fungus was collected.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 80–120 µm high, 140–190 µm diam., black, pycnidial, visible as black domes on the substrate, solitary to gregarious, subglobose in section, semi-immersed, uni-locular, thick-walled. *Conidiomatal wall* 20–30 µm wide, composed of thick-walled, subhyaline to brown cells of *textura angularis* or brown cells of *textura prismatica*. *Conidiophores* hyaline, cylindrical, unbranched, straight or slightly flexuous, aseptate, occasionally reduced to conidiogenous cells. *Conidiogenous cells* 6–9 × 4.5–6.5 µm, holoblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth-walled. *Conidia* 10–17 × 10–13 µm ($\bar{x}$ = 14 × 11 µm, n = 50), hyaline, unicellular, globose or ellipsoidal, sometimes with a narrow and truncate base, straight or slightly curved, smooth-walled, guttulate.

Culture characteristics – Colonies on PDA reaching 40–50 mm after 3 months at 25 °C, circular, grey, velvety, hairy, in reverse black.

Material examined – China, Sichuan Province, Chengdu City, Xinjin County, Banzhulin, 30°29'48"N, 103°48'47"E, elevation 480 m, on dead branches of bamboo in a freshwater habitat, 9 May 2022, X.D. Yu, C7 (HKAS 135146, holotype), ex-type living culture CGMCC 3.25596.

Notes – *Hongkongmyces sichuanensis* is introduced as new species based on morphological and phylogenetic evidence. In the phylogeny, *H. sichuanensis* (CGMCC 3.25596) clustered with *H. kokensis* with 100% ML and 1.00 PP statistical support (Fig. 14). *Hongkongmyces sichuanensis* is distinguishable from *H. kokensis* by its smaller conidiogenous cells (6–9 × 4.5–6.5 µm vs. 7–21 × 3–12 µm) and conidial shape (globose or ellipsoidal vs. subglobose to obovoid) (Boonmee et al. 2021). In addition, comparison of ITS sequences between *H. sichuanensis* and *H. kokensis* showed 4.96% (39/787 bp, including three gaps) nucleotide differences, which strongly support our isolate as a new species.

Nigrogranaceae Jaklitsch & Voglmayr, Studies in Mycology 85: 54 (2016)

Mycobank number: MB817780; Facesoffungi number: FoF08317

Notes – Nigrogranaceae is a monotypic family with *Nigrograna* as the type genus (Jaklitsch & Voglmayr 2016). Nigrogranaceae (Pleosporales, Dothideomycetes), with an estimated divergence crown age of 72 MYA (Liu et al. 2024), contains saprobic, pathogenic or endophytic species on plant tissues, and occasionally can infect humans (Li et al. 2023).

Nigrograna Gruyter, Verkley & Crous, Studies in Mycology 75: 31 (2012)

Mycobank number: MB564794; Facesoffungi number: FoF08318

Notes – *Nigrograna* was introduced by de Gruyter et al. (2013) with *N. mackinnonii* as the type species. *Nigrograna* is characterized by having black ascomata with clavate, short pedicellate asci and pale to chocolate brown, fusoid to narrowly ellipsoid, septate ascospores (de Silva et al. 2022, Hyde et al. 2023).

Nigrograna magnoliae Wanas., Plos One 15: 19 (2020)

Fig. 15

Mycobank number: MB557331; Facesoffungi number: FoF09092

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, subglobose, coriaceous, uni-loculate. *Hamathecium* 1–2 µm wide, hyphae-like, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 60–80 × 7.5–9.5 µm ($\bar{x}$ = 70 × 8.5 µm, n = 30), 8-spored, bitunicate, fissitunicate, clavate to cylindrical, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 12–16 × 4.5–5.5 µm ($\bar{x}$ = 13.5 × 5 µm, n = 50), uni-seriate or bi-

seriate, ellipsoid, straight to somewhat curved, pale brown and one-septate when young, becoming yellowish brown to brown at maturity, 3-euseptate, constricted at the median septum. Asexual morph: Undetermined.

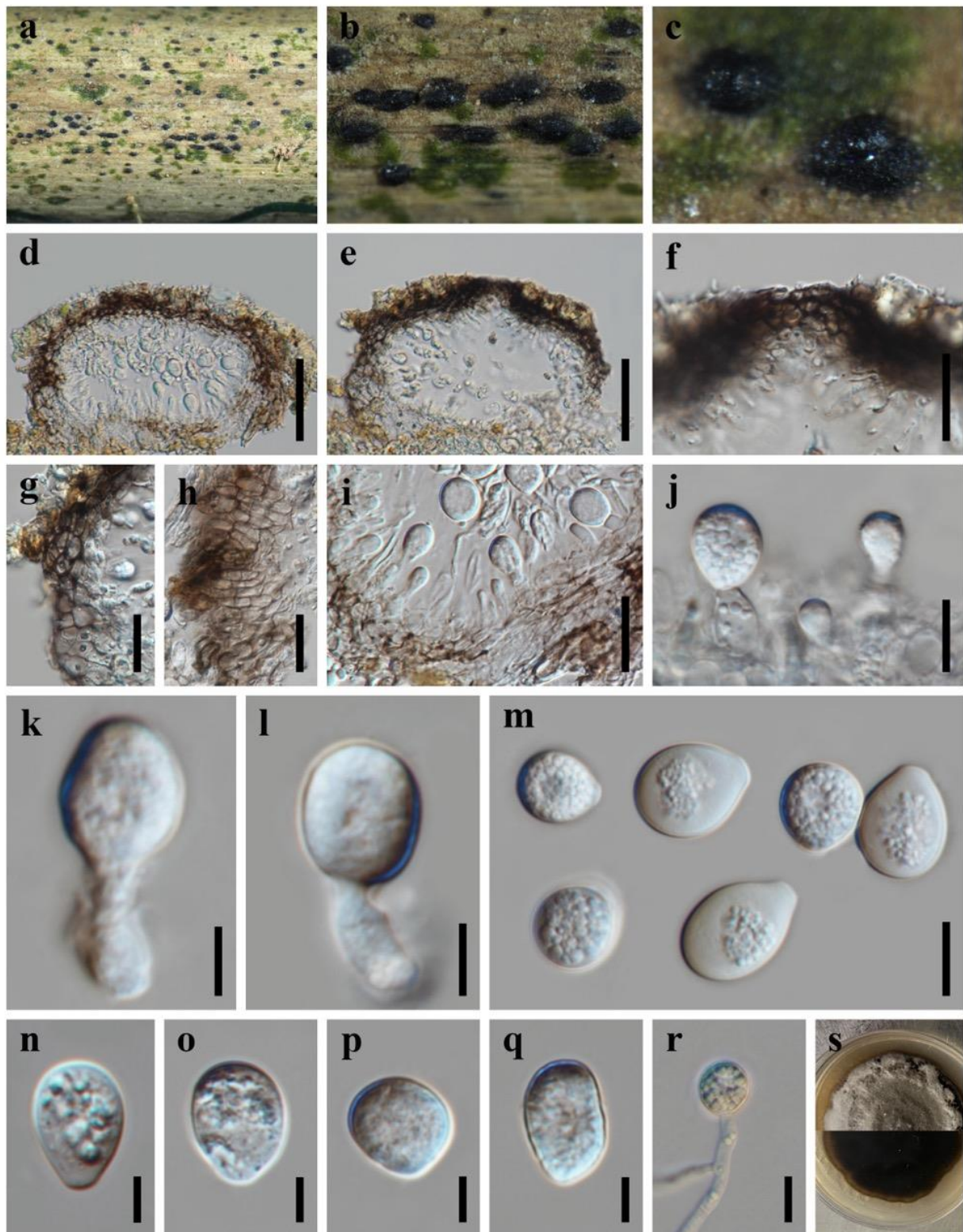


Figure 13 – *Hongkongmyces sichuanensis* (HKAS 135146, holotype). a–c Conidiomata on surface of dead bamboo culms. d, e Vertical sections of conidiomata. f Ostiole. g, h Wall of conidioma. i–l Conidiogenous cells bearing conidia. m–q Conidia. r Germinating conidium. s Colony on PDA from above and below. Scale bars: d, e = 50 µm, f–i = 20 µm, j, m, r = 10 µm, k, l, n–q = 5 µm.

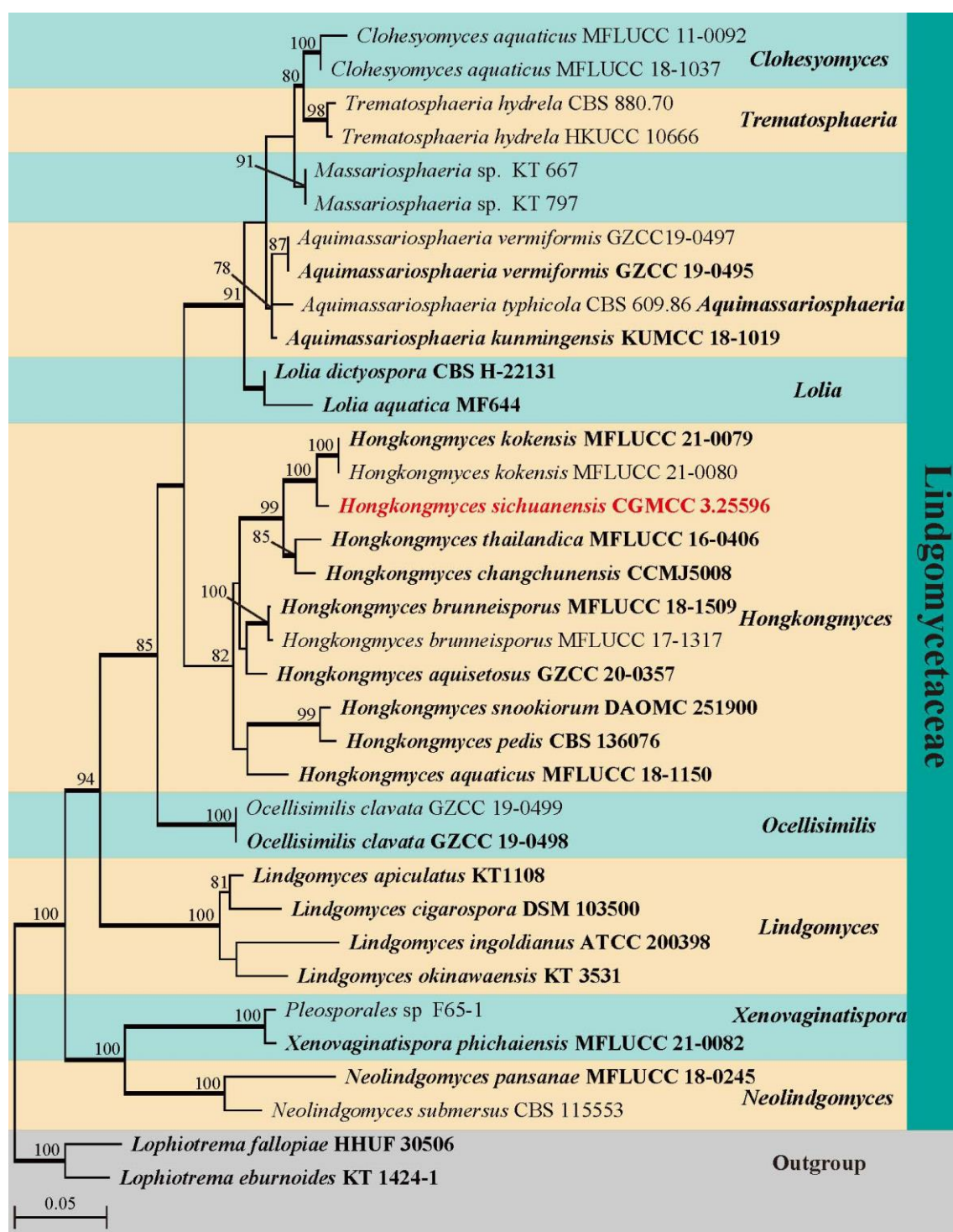


Figure 14 – RAxML tree generated from combined SSU, ITS, LSU and *tef1-α* sequence data of Lindgomycetaceae. The tree was rooted with *Lophiotrema eburnoides* (KT 1424.1) and *L. fallopieae* (HHUF 30506). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 3 months at 25 °C, dense, circular, surface sparsely hairy, white hairy, in reverse dark brown.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan County, Mount Qingcheng, 30°54'29"N, 103°32'36"E, elevation 960 m, on dead branches of bamboo, 2 December 2021, X.D. Yu, B4 (HUEST 24.0161), living culture UESTCC 24.0144.

Notes – Wanasinghe et al. (2020) introduced *Nigrograna magnoliae*, which was collected from *Magnolia denudata* (Magnoliaceae) in Kunming City, Yunnan Province, China. Subsequently, Zhang et al. (2020a) recollected and described it in China and Thailand, where it occurs on decaying submerged wood. Later, Li et al. (2023) reported this species from *Acer truncatum*, *Juglans regia* and *Olea europaea*. Hyde et al. (2024) also reported this species from a dead twig of *Aquilaria* sp. in Menghai City, Xishuangbanna Yunnan Province. Our collection was found from decaying bamboo in terrestrial environments. We identify it as *N. magnoliae* based on the morphological characters and phylogenetic analyses (Fig. 16). This is the first report of *N. magnoliae* from bamboo in a terrestrial habitat.

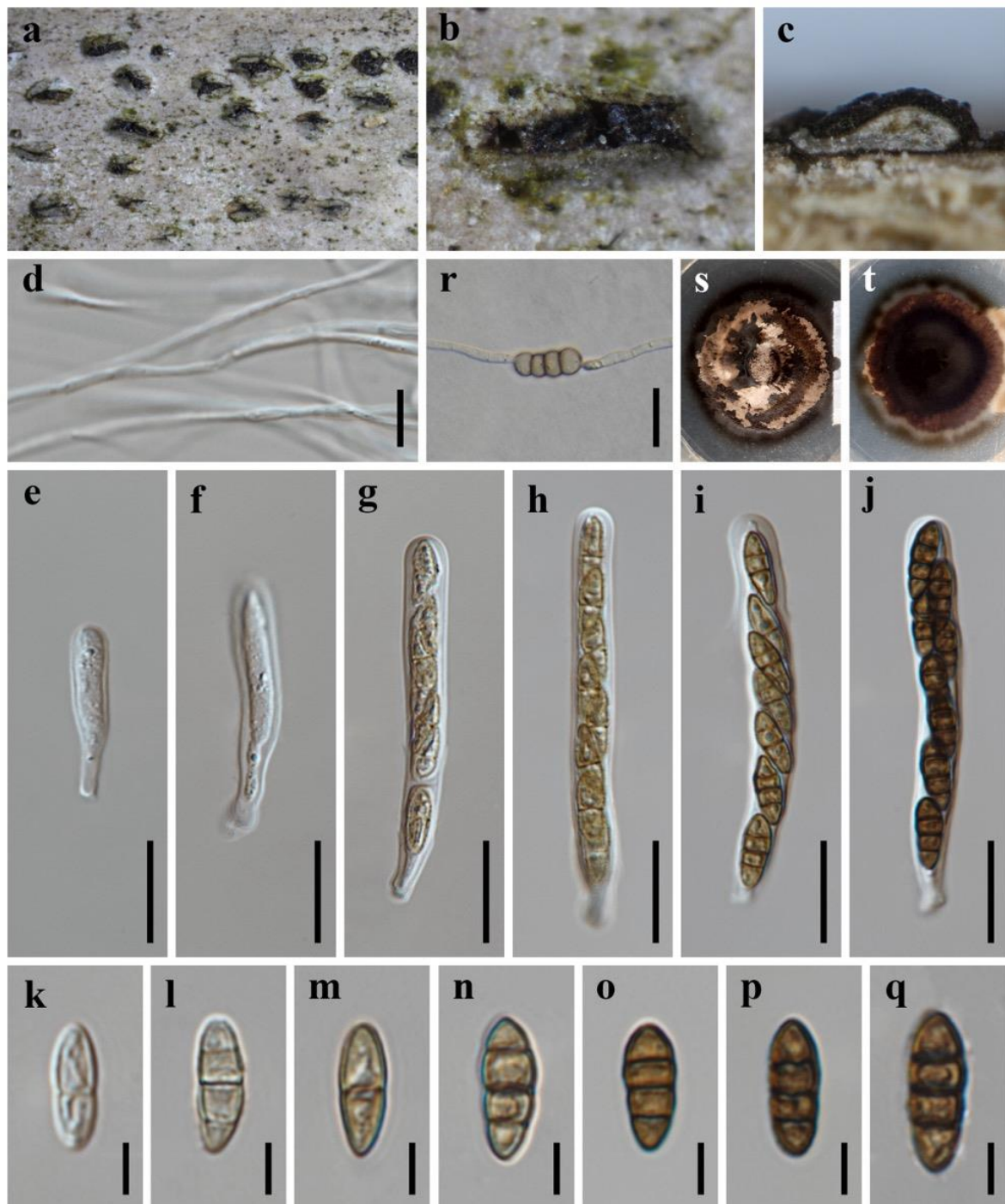


Figure 15 – *Nigrograna magnoliae* (HUEST 24.0161). a–b Ascomata on host substrate. c Vertical section of ascoma. d Pseudoparaphyses. e–j Asci. k–q Ascospores. r Germinated ascospore. s, t Colony on PDA from above and below. Scale bars: e–j, r = 20 μ m, d = 10 μ m, k–q = 5 μ m.

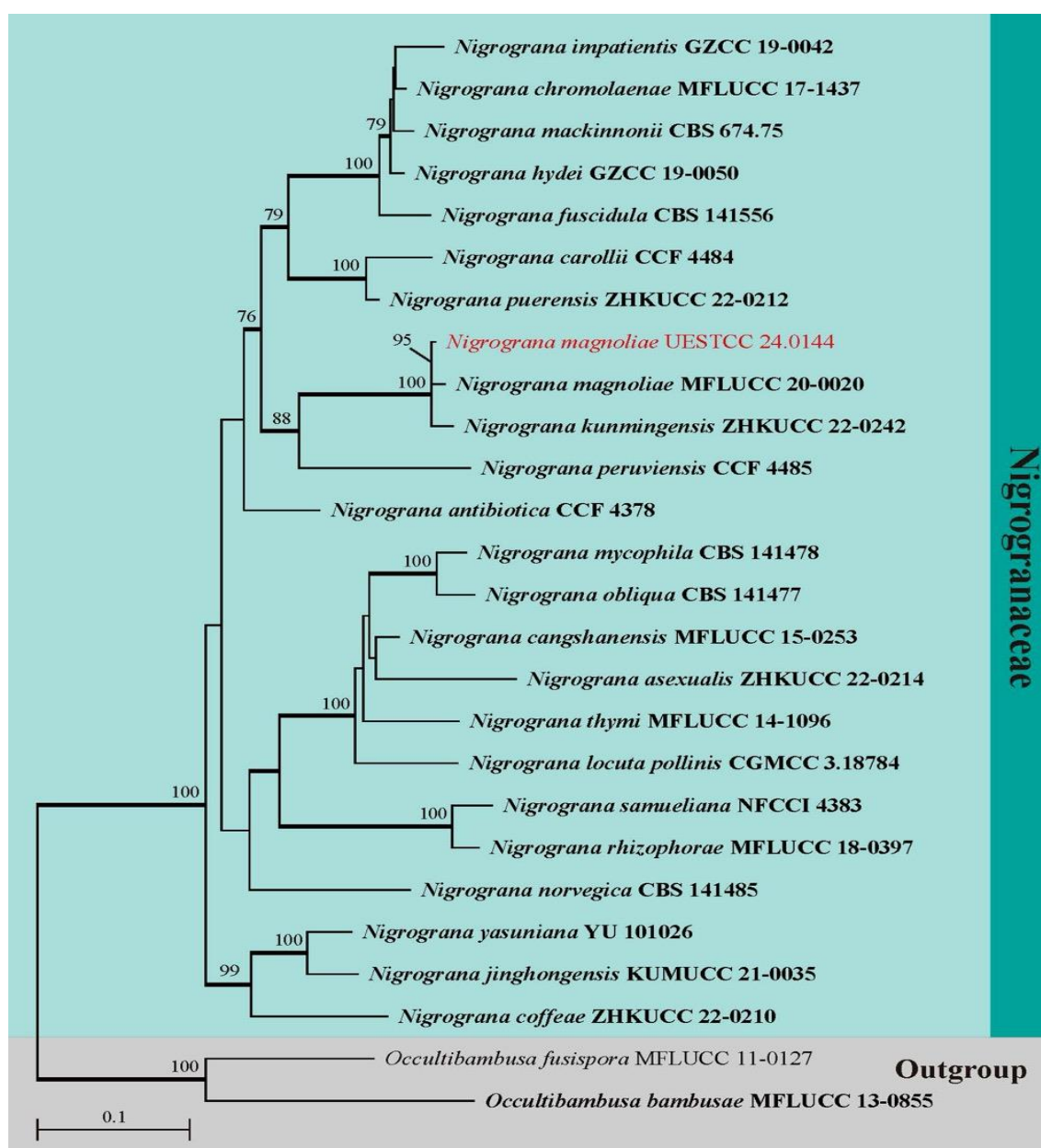


Figure 16 – RAxML tree generated from combined SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data of Nigrogranaceae. The tree was rooted with *Occultibambusa bambusae* (MFLUCC 13-0855) and *O. fusispora* (MFLUCC 11-0127). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Occultibambusaceae D.Q. Dai & K.D. Hyde, Fungal Diversity 82: 25 (2016)

Mycobank number: MB552013; Facesoffungi number: FoF01973

Notes – Occultibambusaceae was introduced by Dai et al. (2017), and typified by *Occultibambusa*. Five genera are accepted in this family, viz. *Brunneofusispora*, *Neooccultibambusa*, *Occultibambusa*, *Seriascoma* and *Versicolorisporium* (Jiang et al. 2021a, Yu et al. 2021). Most Occultibambusaceae species are saprobic and frequently found on monocotyledons or hardwood trees in terrestrial and aquatic habitats (Dai et al. 2017, Doilom et al. 2017).

Aculeatosporella X.D. Yu, K.D. Hyde & Jian K. Liu, gen. nov.

MycoBank number: MB854878; Facesoffungi number: FoF16565

Etymology – In reference to the characteristic of aculeate ascospores.

Type species – *Aculeatosporella bambusae* X.D. Yu, K.D. Hyde & Jian K. Liu

Saprobic on dead wood. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, subglobose, coriaceous, uniloculate. *Peridium* composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* hyphae-like, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, clavate, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* fusiform, hyaline, becoming brown at maturity, 1-septate, aculeate, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Notes – *Aculeatosporella* is typical of *Occultibambusaceae* in having 8-spored, fissitunicate, clavate, short pedicellate asci and fusiform, septate ascospores surrounded by a mucilaginous sheath (Dai et al. 2017). It is distinguished from other genera in *Occultibambusaceae* by brown, 1-septate and aculeate ascospores. The phylogenetic analyses showed (Fig. 18) that two isolates of *Aculeatosporella bambusae* are sister to *Neooccultibambusa thailandensis*, and they formed a monophyletic clade with low bootstrap support in *Occultibambusaceae*. *Aculeatosporella bambusae* resembles *Neooccultibambusa thailandensis* in having 8-spored, fissitunicate, short pedicellate asci, fusiform, brown, 1-septate ascospores. However, *A. bambusae* differs from *N. thailandensis* in having semi-immersed ascomata, broadly clavate asci, and aculeate ascospores with a mucilaginous sheath. In addition, the comparison of nucleotide differences between *A. bambusae* and *N. thailandensis* showed that there are 5.6% (27/479, including 10 gaps) differences in ITS, 0.7% (6/861) in LSU, 7.8% (70/892, including 2 gaps) in *rpb2* and 3.5% (34/970, including 1 gap) in *tef1-α* gene regions. Hence, we establish a new genus to accommodate *Aculeatosporella bambusae* based on the morpho-phylogenetic evidence.

Aculeatosporella bambusae X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 17

MycoBank number: MB854879; Facesoffungi number: FoF16575

Etymology – The epithet refers to the host, on which the holotype was collected.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, in vertical section 80–90 µm high, 110–160 µm diam., subglobose, coriaceous, uniloculate. *Peridium* 15–45 µm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, hyphae-like, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 40–60 × 6–9 µm ($\bar{x}$ = 50 × 7.5 µm, n = 30), 8-spored, bitunicate, fissitunicate, broadly clavate, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 10–13 × 3–4 µm ($\bar{x}$ = 12 × 3.5 µm, n = 50), 3-seriate, fusiform, straight to somewhat curved, hyaline, becoming brown at maturity, 1-septate, constricted at the septum, aculeate, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, dark greyish at the inner ring, and black at the outer ring; in reverse black.

Material examined – China, Sichuan Province, Meishan City, Danling County, JiuLongShan Forest Park, 29°54'48"N, 103°35'13"E, elevation 460 m, on dead branches of bamboo, 14 July 2022, X.D. Yu, D25 (HKAS 135144, holotype), ex-type living culture CGMCC 3.27443; *ibid.* Neijiang City, Shuangqiao Town, Mansiba Village, 29°45'54"N, 105°9'32"E, elevation 350 m, on dead branches of bamboo, 3 May 2023, X.D. Yu, K47 (HUEST 23.0258); living culture UESTCC 23.0258.

Parabambusicolaceae Kaz. Tanaka & K. Hiray., *Studies in Mycology* 82: 115 (2015)

MycoBank number: MB811324; Facesoffungi number: FoF06708

Notes – *Parabambusicolaceae* was established by Tanaka et al. (2015) and typified by *Parabambusicola* Kaz. Tanaka & K. Hiray., which is characterized by scattered to grouped, immersed to erumpent, globose to subglobose ascomata, fissitunicate, clavate to broadly cylindrical

asci, clavate to fusiform, hyaline, multiseptate ascospores and monodictys-like hyphomycetes. Most Parabambusicolaceae species are saprobes and have been found on dicotyledonous plants, monocotyledonous plants, and ferns in aquatic and terrestrial environments (Xie et al. 2022).

Neoaquastroma Wanas., E.B.G. Jones & K.D. Hyde, Phytotaxa 302: 139 (2018)

MycoBank number: MB552499; Facesoffungi number: FoF02609

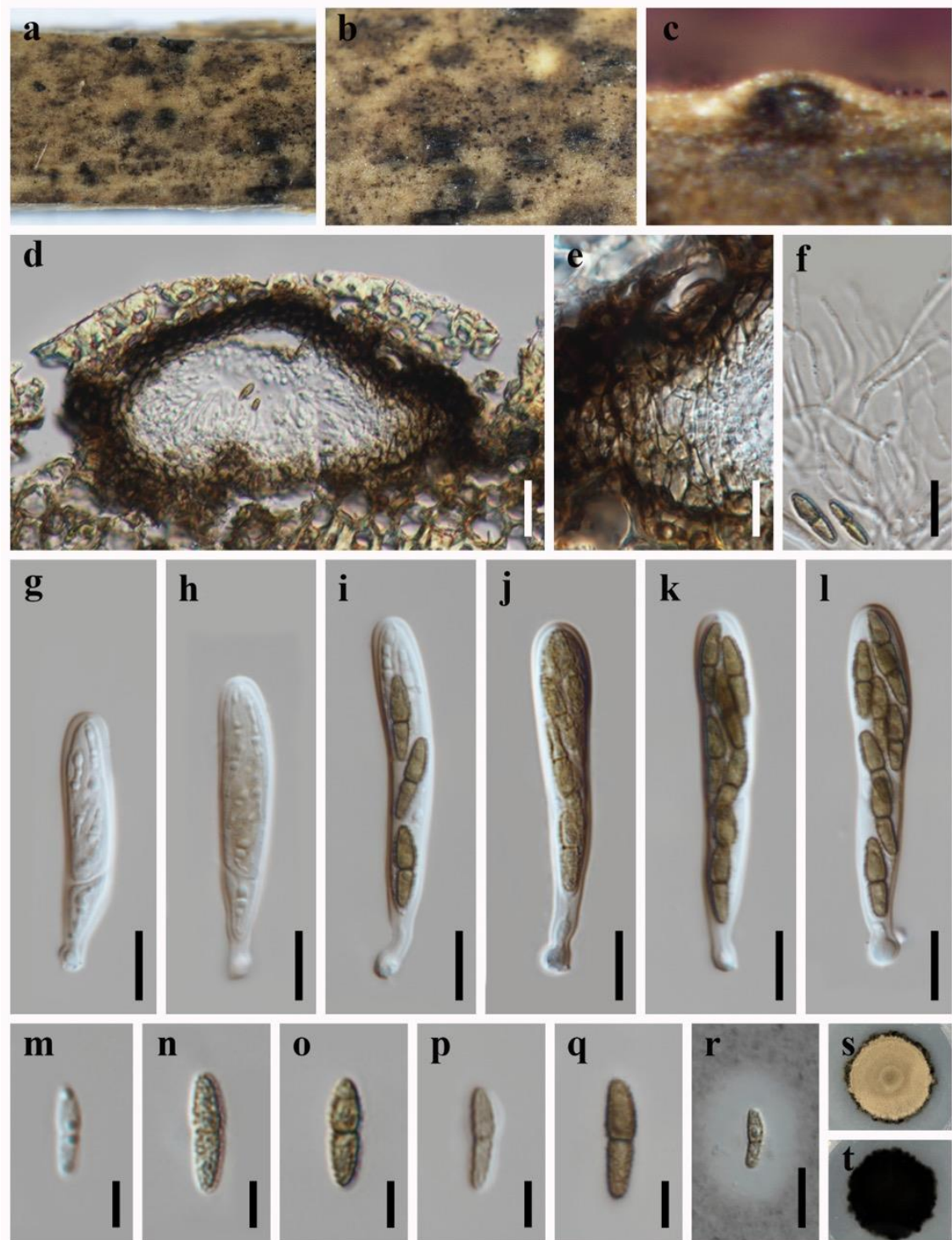


Figure 17 – *Aculeatosporella bambusae* (HKAS 135144, holotype). a–c Ascomata on host substrate. d Vertical section of ascoma. e Structure of peridium. f Pseudoparaphyses. g–l Asci. m–q Ascospores. r Ascospores with mucilaginous sheath. s, t Colony on PDA from above and below. Scale bars: d = 20 μ m, e–l, r = 10 μ m, m–q = 5 μ m.

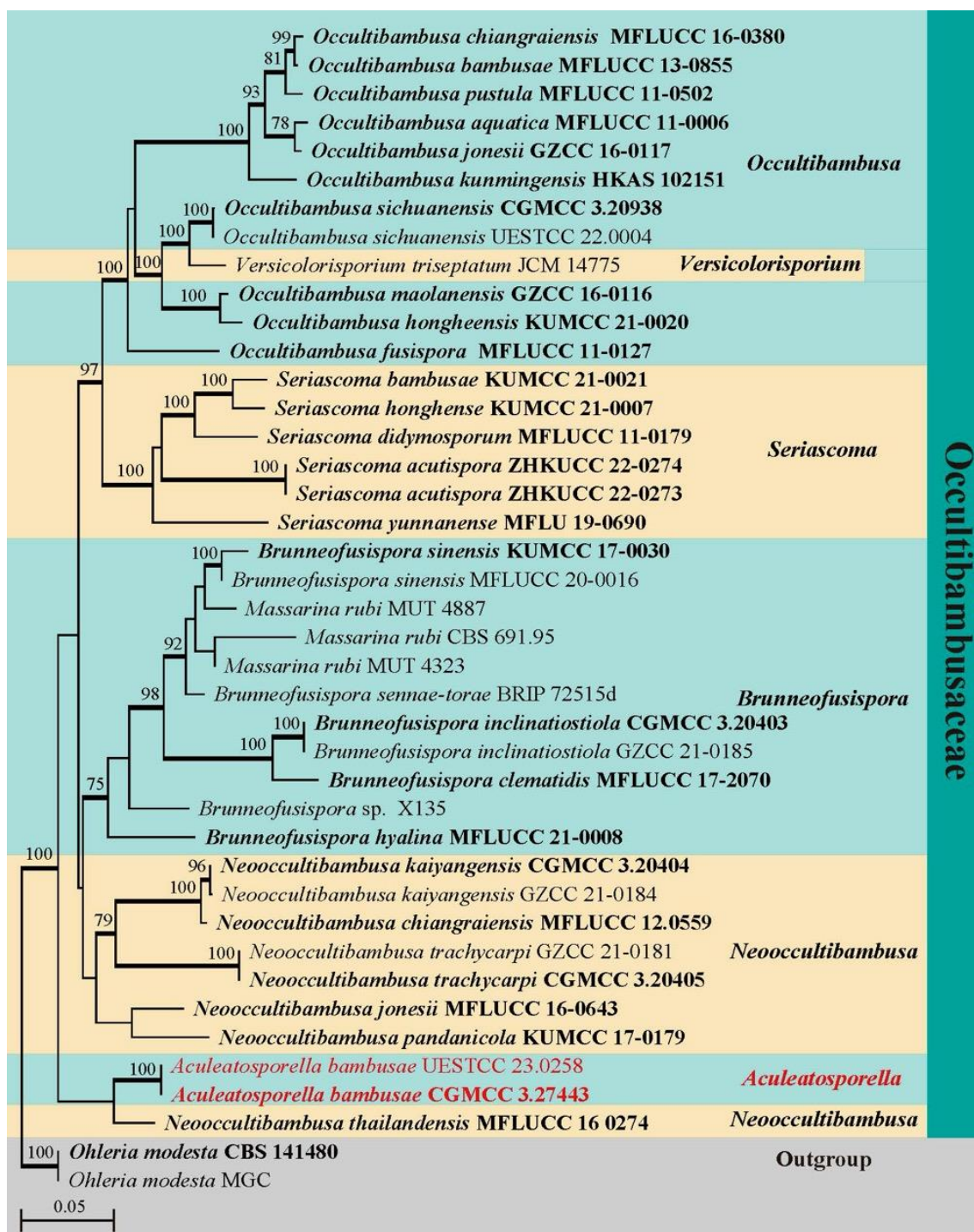


Figure 18 – RAxML tree generated from combined SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data of Occultibambusaceae. The tree was rooted with *Ohleria modesta* (CBS 141480) and *O. modesta* (MGC). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Notes – *Neoaquastroma* was established by Wanasinghe et al. (2017) and typified by *Neoaquastroma guttulatum* Wanas., E.B.G. Jones & K.D. Hyde, which is characterized by 8-spored, bitunicate, fissitunicate, clavate, short pedicel asci, biseriate to triseriate, and ellipsoidal to subfusiform, hyaline, multi-septate ascospores (Wanasinghe et al. 2017). Five species are accepted in the genus, viz. *N. bauhiniae* Phukhams. & K.D. Hyde, *N. cylindricum* Samarak. & K.D. Hyde, *N. guizhouense* J.F. Zhang & Jian K. Liu, *N. guttulatum* Wanas., E.B.G. Jones & K.D. Hyde and

N. krabiense Phukhams. & K.D. Hyde (Wanasinghe et al. 2017, Phukhamsakda et al. 2018, Samarakoon et al. 2019, Zhang et al. 2023).

Neoaquastroma cylindricum Samarak. & K.D. Hyde, Asian Journal of Mycology 2: 240 (2019)

Fig. 19

MycoBank number: MB556820; Facesoffungi number: FoF06520

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, immersed to erumpent, usually forming in a linear series on the host surface, in vertical section 150–250 µm high, 300–350 µm diam., subglobose, coriaceous, uniloculate. *Peridium* 30–50 µm wide, composed of several layers of hyaline to brown cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, hyphae-like, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 130–150 × 40–50 µm ($\bar{x}$ = 140 × 45 µm, n = 30), 8-spored, bitunicate, fissitunicate, broad cylindric-clavate, straight or slightly curved, short pedicellate to subsessile, rounded at the apex, with an ocular chamber. *Ascospores* 50–60 × 12–16 µm ($\bar{x}$ = 55 × 14 µm, n = 50), multi-seriate, sub-cylindrical to fusiform, straight to somewhat curved, hyaline, septate, smooth-walled, surrounded by a mucilaginous sheath when young, disappearing mucilaginous sheath at maturity. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, greyish at the inner ring, and brown at the outer ring; in reverse dark brown.

Material examined – China, Sichuan Province, Meishan City, Danling County, Jiulongshan Forest Park, 29°54'48"N, 103°35'13"E, elevation 460 m, on dead branches of bamboo, 14 July 2022, X.D. Yu, D4 (HUEST 24.0162), living culture UESTCC 24.0145.

Notes – In the multi-loci phylogenetic analyses, our strain *Neoaquastroma cylindricum* (UESTCC 24.0145) clustered with the ex-type strain of *N. cylindricum* (MFLUCC 19-0489) with 100% ML and 1.00 PP support (Fig. 20). Our strain shares similar morphology with the type of *N. cylindricum* in having solitary to gregarious, subglobose ascomata, cylindric-clavate asci, and fusiform ascospores (Samarakoon et al. 2019). The nucleotide comparisons showed that our strain (UESTCC 24.0145) is not significantly different from the type strain of *N. cylindricum* (MFLUCC 19-0489) in SSU, ITS, LSU and *tef1-α*, which indicated that they are the same species (Chethana et al. 2021). Therefore, we identify our collection as *N. cylindricum*, with an additional bamboo host record.

Periconiaceae Nann., Repert. mic. uomo: 482 (1934)

MycoBank number: MB81124; Facesoffungi number: FoF06657

Notes – Nannizzi (1934) initially introduced Periconiaceae based on the type genus *Periconia* Tode. Tanaka et al. (2015) formally established the family Periconiaceae and placed it in the order Pleosporales based on modern fungal systematics. Members of Periconiaceae are characterized by scattered, immersed to erumpent ascomata, pseudoparaphyses, oblong to cylindrical asci, and broadly fusiform, 1-septate, hyaline ascospores; as well as synnemata or noosia-like asexual morphs, which produce macronematous, mononematous conidiomata, monoblastic to polyblastic, discrete and branched conidiogenous cells, and globose to ellipsoidal, aseptate, catenate, brown conidia (Tanaka et al. 2015, Senwanna et al. 2021).

Periconia Tode, Fungi Mecklenburgenses Selecti 2: 2 (1791)

MycoBank number: MB9263; Facesoffungi number: FoF06658

Notes – *Periconia* was introduced by Tode (1791) with *P. lichenoides* as the type species. *Periconia* species have been reported as saprobes, endophytes and plant pathogens (Tian et al. 2024). In this study, two new species (*P. muchuanensis* and *P. sichuanensis*) are described with detailed descriptions and illustrations.

Periconia muchuanensis X.D. Yu & Jian K. Liu, sp. nov.

Fig. 21

MycoBank number: MB854880; Facesoffungi number: FoF16576

Etymology – The specific epithet “*muchuanensis*” refers to the location, Muchuan, Sichuan Province of China, where the new species was collected.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies superficial, effuse, hairy, scattered, dark brown to black. *Conidiophores* 400–600 × 10–18 µm ($\bar{x}$ = 500 × 14 µm, n = 20), macronematous, mononematous, solitary, erect, cylindrical, straight or slightly flexuous, dark brown to black, partly forming obovoid heads and branched at apex, producing 2–3 secondary conidiophores, septate, smooth. *Conidiogenous cells* holoblastic, polyblastic, terminal, integrated or discrete, pale brown to brown, smooth. *Conidia* 7.5–9.5 × 5.5–8.5 µm ($\bar{x}$ = 8.5 × 6.5 µm, n = 50), oval to subglobose, aseptate, solitary, pale brown, verruculose.

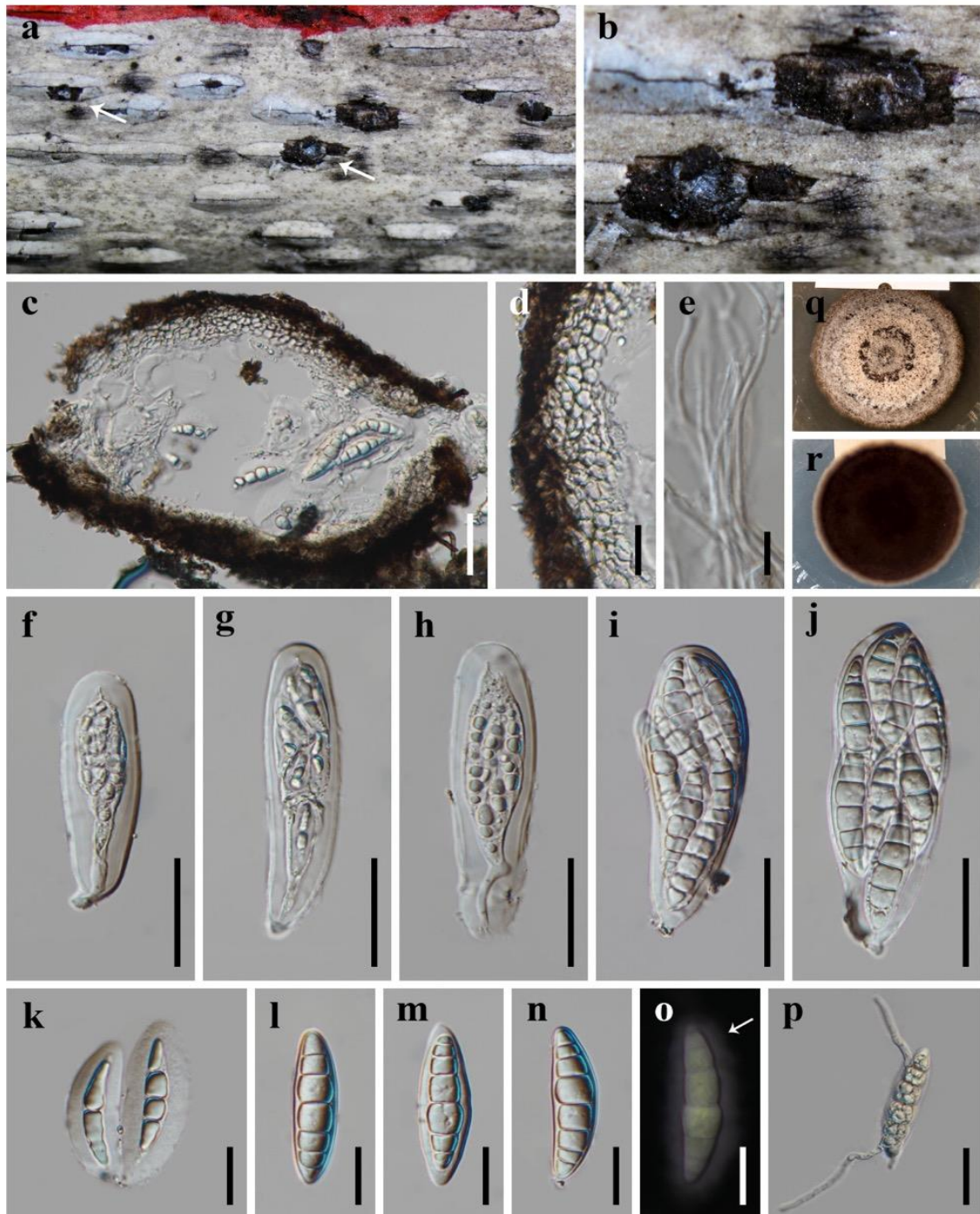


Figure 19 – *Neoaquastroma cylindricum* (HUEST 24.0162). a–b Ascomata on host substrate. c Vertical section of ascoma. d Structure of peridium. e Pseudoparaphyses. f–j Asci. k–n Conidia. o Conidium with a white arrow pointing to a feature. p Conidium with a long, thin appendage.

k–n Ascospores. o Ascospore with mucilaginous sheath. p Germinated ascospore. q, r Colony on PDA from above and below. Scale bars: c, f–j = 50 μ m, d, k–p = 20 μ m, e = 10 μ m.

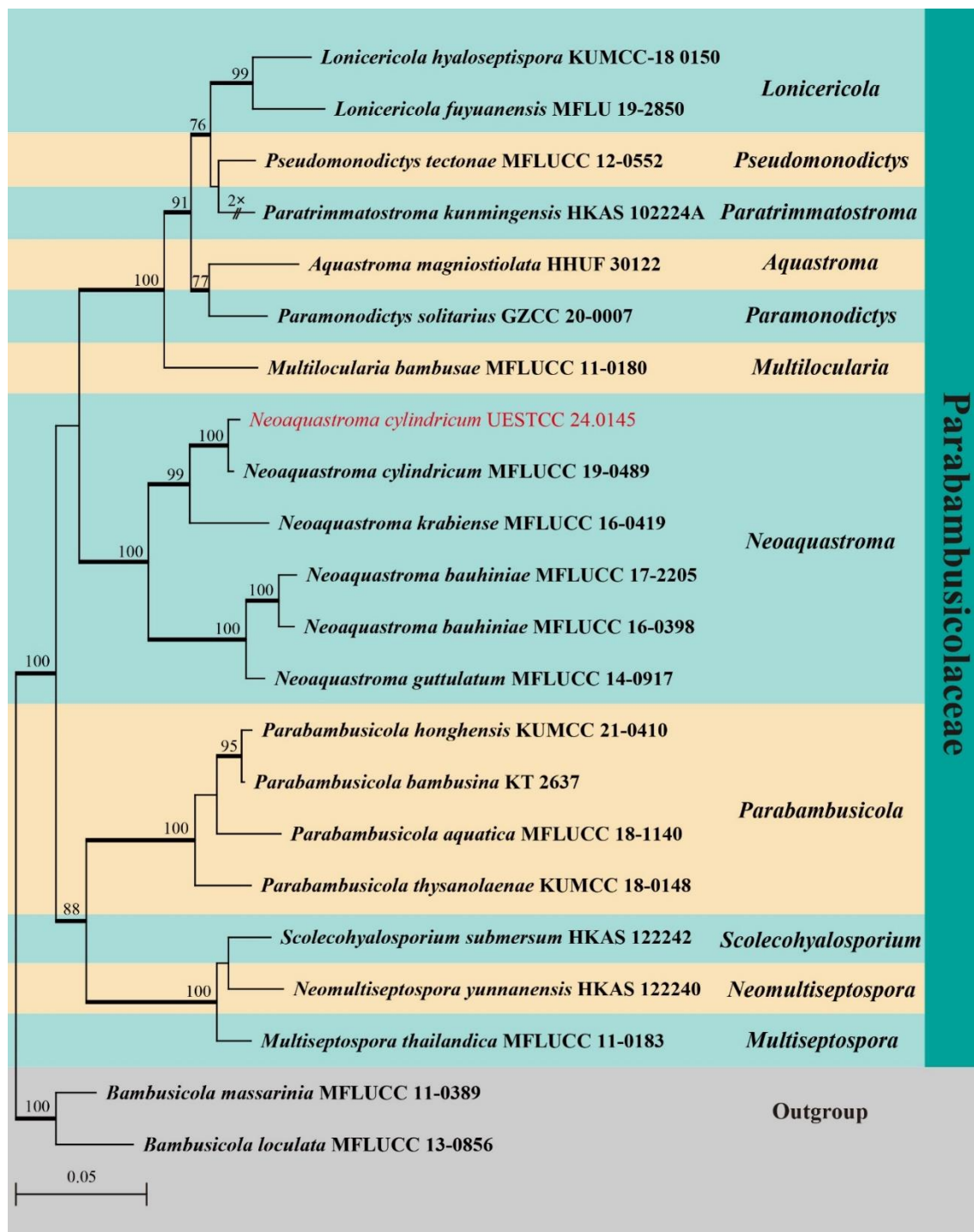


Figure 20 – RAxML tree generated from combined SSU, ITS, LSU and *tef1- α* sequence data of Parabambusicolaceae. The tree was rooted with *Bambusicola loculata* (MFLUCC 13-0856) and *B. massarinia* (MFLUCC 11-0389). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Culture characteristics – Colonies on PDA reaching 50–60 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, white; in reverse brown.

Material examined – China, Sichuan Province, Muchuan City, Taoyuan Mountain House, 28°57'11"N, 103°53'28"E, elevation 403 m, on dead branches of bamboo, 3 November 2022, X.D. Yu, F13 (HKAS 135150, holotype), ex-type living culture CGMCC 3.25599 = UESTCC 23.0260.

Notes – In the SSU-ITS-LSU-*tef1-α* phylogenetic tree, *Periconia muchuanensis* formed a basal branch of the *Periconia* clade (Fig. 23). *Periconia muchuanensis* is most similar to *P. thysanolaenae* in having macronematous, mononematous, branched conidiophores, polyblastic conidiogenous cells and verruculose conidia (Yang et al. 2022). However, *P. muchuanensis* differs in having solitary and larger conidia. The establishment of *P. muchuanensis* is justified by morphological and phylogenetic evidence.

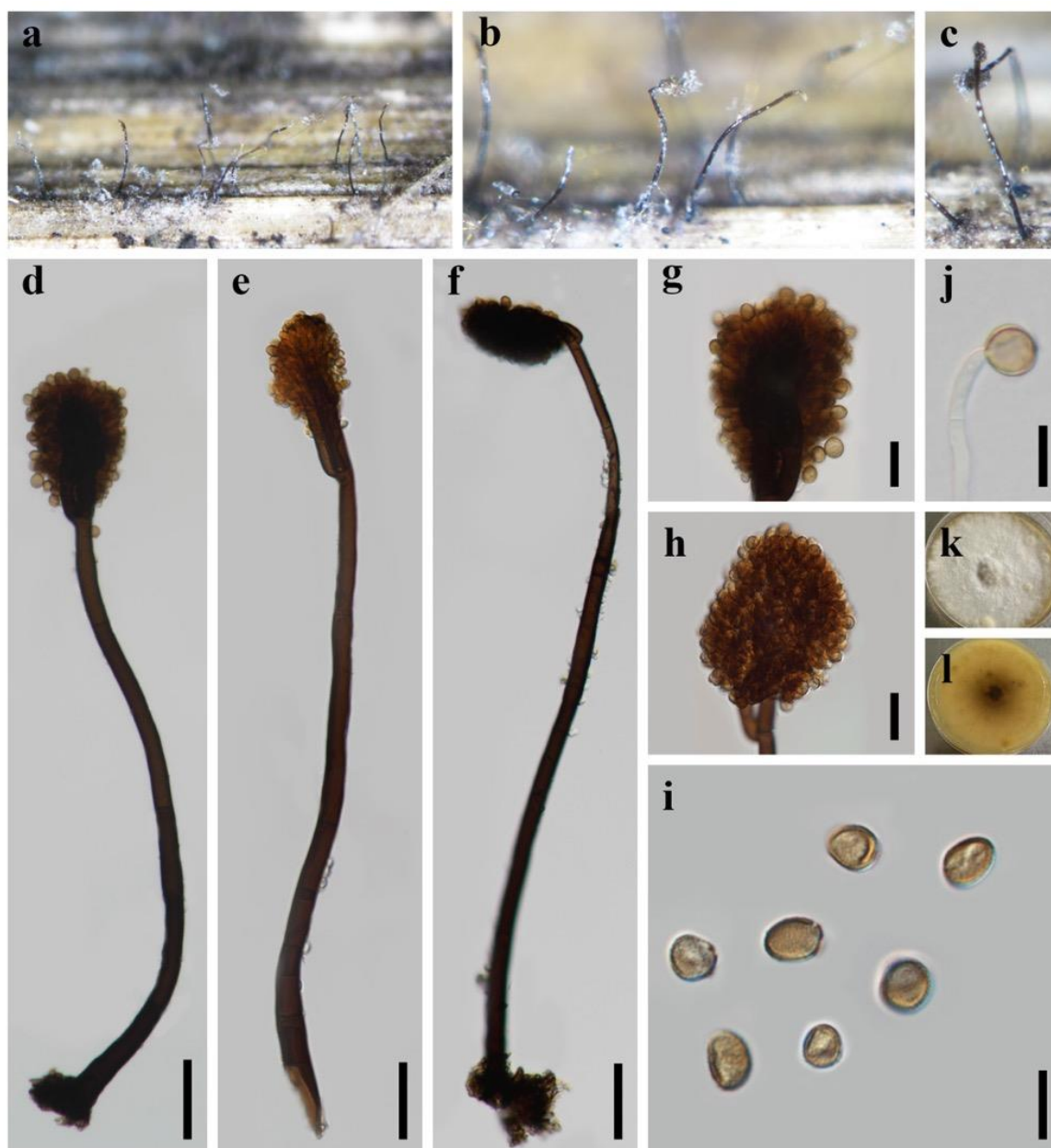


Figure 21 – *Periconia muchuanensis* (HKAS 135150, holotype). a–c Colonies. d–f Conidiophores and conidia. g, h Conidiogenous cells. i Conidia. j Germinating conidium. k, l Colony on PDA from above and below. Scale bars: d–f = 50 μ m, g–h = 20 μ m, i–j = 10 μ m.

Periconia sichuanensis X.D. Yu & Jian K. Liu, sp. nov.

Mycobank number: MB854881; Facesoffungi number: FoF16577

Etymology – The epithet refers to Sichuan Province where the fungus was collected.

Fig. 22

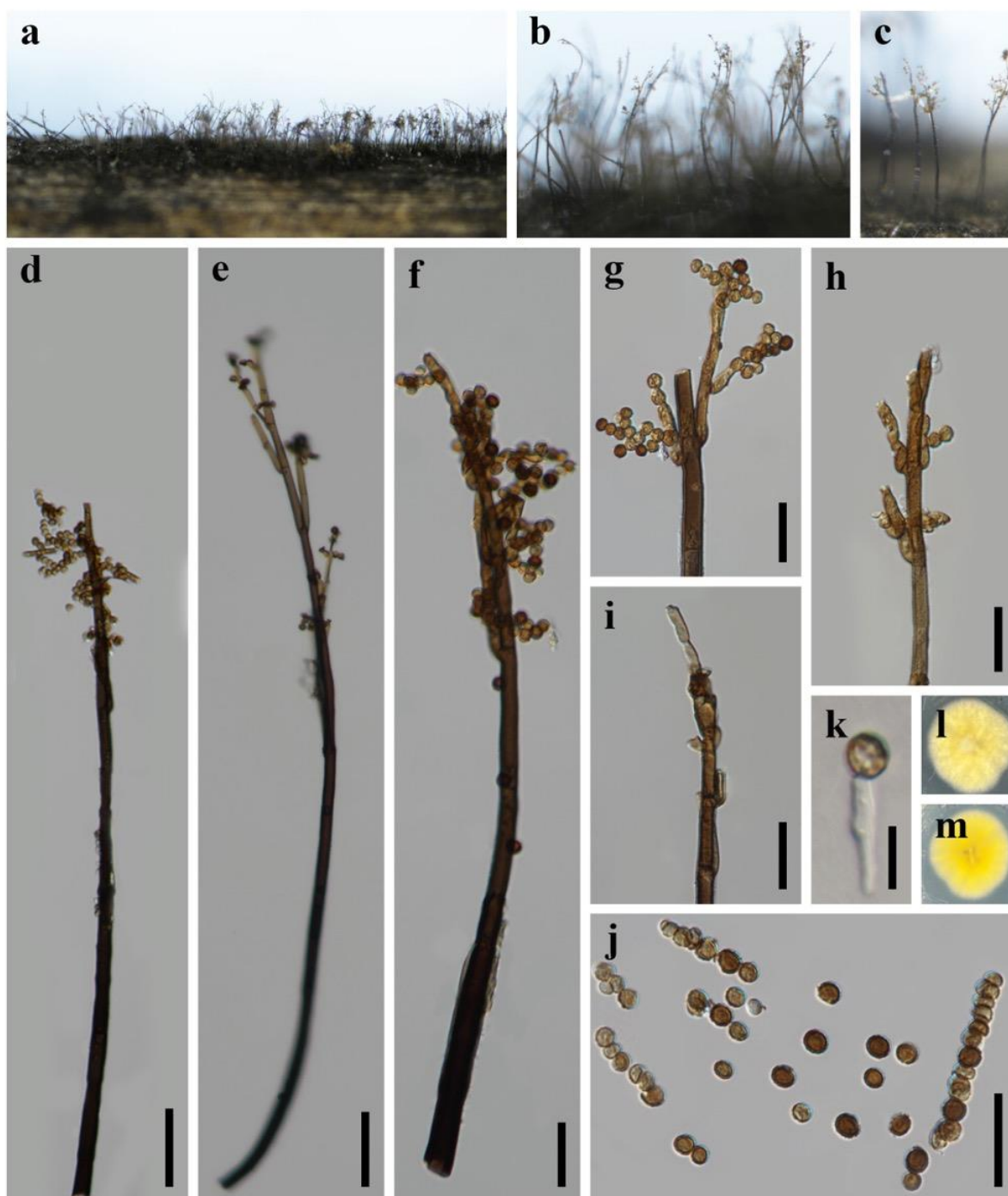


Figure 22 – *Periconia sichuanensis* (HKAS 135157, holotype). a–c Colonies. d–f Conidiophores and conidia. g–i Conidiogenous cells. j Conidia. k Germinating conidium. l, m Colony on PDA from above and below. Scale bars: d–e = 50 μ m, f–j = 20 μ m, k = 10 μ m.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies superficial, effuse, hairy, scattered, dark brown to black. Conidiophores 250–750 $\times$ 6–12 μ m ($\bar{x}$ = 500 $\times$ 8 μ m, n = 20), macronematous, mononematous, solitary, erect, cylindrical, slightly wider at the basal portion, straight or slightly flexuous, brown to dark brown, usually with one or a number of short branches near the apex, septate, smooth. Conidiogenous cells holoblastic, polyblastic, terminal, integrated or discrete, pale brown to brown, smooth. Conidia 4.5–5.5 μ m diam. ($\bar{x}$ = 5.0 μ m, n = 50), acropleurogenous, catenate, globose, aseptate, pale brown to brown.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 3 months at 25 $^{\circ}$ C, circular, with dense mycelium on the surface, pale yellow; in reverse yellow.

Material examined – China, Sichuan Province, Qionglai City, Lugou Bamboo Sea, 30°22'37"N, 103°16'45"E, elevation 730 m, on dead branches of bamboo, 12 October 2021, X.D. Yu, A40 (HKAS 135157, holotype), ex-type living culture CGMCC 3.25598 = UESTCC 23.0259.

Notes – The phylogenetic analyses based on SSU, ITS, LSU and *tef1-α* sequence data showed that the new collection *Periconia sichuanensis* nested in *Periconia* (Fig. 23) and formed a distinct lineage. *P. sichuanensis* resembles *P. digitata*, *P. pseudodigitata* and *P. verrucosa* in having catenate, globose, aseptate conidia (Tanaka et al. 2015, Phukhamsakda et al. 2020, Tian et al. 2024). However, *P. sichuanensis* differs in not having echinulate or verruculose conidia. Therefore, establishment of the new species is justified by morphology and phylogenetic evidence.

Phaeoseptaceae Boonmee, Thambugala & K.D. Hyde, Mycosphere 9: 323 (2018)

MycoBank number: MB554385; Facesoffungi number: FoF04462

Notes – Phaeoseptaceae was introduced by Hyde et al. (2018) to accommodate *Lignosphaeria*, *Neolophiostoma* and *Phaeoseptum* in Pleosporales with *Phaeoseptum* as the type genus. Subsequently, Liu et al. (2019b) introduced a new genus *Pleopunctum* in the family that is represented only by the asexual morph.

Pleopunctum N.G. Liu, K.D. Hyde & J.K. Liu, Mycosphere 10: 767 (2019)

MycoBank number: MB556522; Facesoffungi number: FoF06113

Notes – *Pleopunctum* was introduced by Liu et al. (2019b) to accommodate *P. ellipsoideum* and *P. pseudoellipsoideum* and is typified by *P. ellipsoideum*. Eleven records are listed in Index Fungorum (2024). *Pleopunctum* is characterized by macronematous, mononematous conidiophores, monoblastic conidiogenous cells and muriform, oval to ellipsoidal conidia often with a hyaline, elliptical to globose basal cell.

Pleopunctum ellipsoideum N.G. Liu, K.D. Hyde & Jian K. Liu, Mycosphere 10: 767 (2019)

Fig. 24

MycoBank number: MB556523; Facesoffungi number: FoF06114

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substratum, sporodochial, scattered to gregarious, black, glistening, superficial, punctiform. Mycelium immersed, composed of septate, branched, subhyaline to greyish-brown hyphae. Conidiophores macronematous, mononematous, brown, often reduced to conidiogenous cells. Conidiogenous cells monoblastic, terminal, integrated, medium brown. Conidia 45–70 × 20–30 μm ($\bar{x}$ = 55 × 25 μm, n = 50), acrogenous, solitary, muriform, constricted at septa, oval to ellipsoidal, smooth-walled, dark brown, broadly obtuse at apex, truncate at base, often with a hyaline, elliptical to globose basal cell, 18–22 μm diam. ($\bar{x}$ = 20 μm, n = 50).

Culture characteristics – Colonies on PDA reaching 40–50 mm after 3 months at 25 °C, circular, umbonate, fluffy, velvety edge, a circular raised band, grey white, in reverse grey white to dark grey, black toward the center.

Material examined – China, Sichuan Province, Luzhou City, Naxi District, Dawang Bamboo Sea, 28°39'24"N, 105°32'53"E, elevation 700 m, on dead branches of bamboo, 20 April 2023, X.D. Yu, M13 (HUEST 24.0163), living culture UESTCC 24.0146 = UESTCC 24.0147.

Notes – In the multi loci phylogenetic analyses, our strains UESTCC 24.0146 and UESTCC 24.0147 grouped together with *Pleopunctum ellipsoideum* strains (Fig. 26). Our new isolate is similar to *P. ellipsoideum* except for the size of conidia (45–70 × 20–30 vs. 39–51 × 17–24) (Liu et al. 2019b). Thus, we named our strains as *P. ellipsoideum* and they are reported as a new host record on bamboo.

Pleopunctum pseudoellipsoideum N.G. Liu, K.D. Hyde & Jian K. Liu, Mycosphere 10: 768 (2019)

Fig. 25

MycoBank number: MB556524; Facesoffungi number: FoF06115

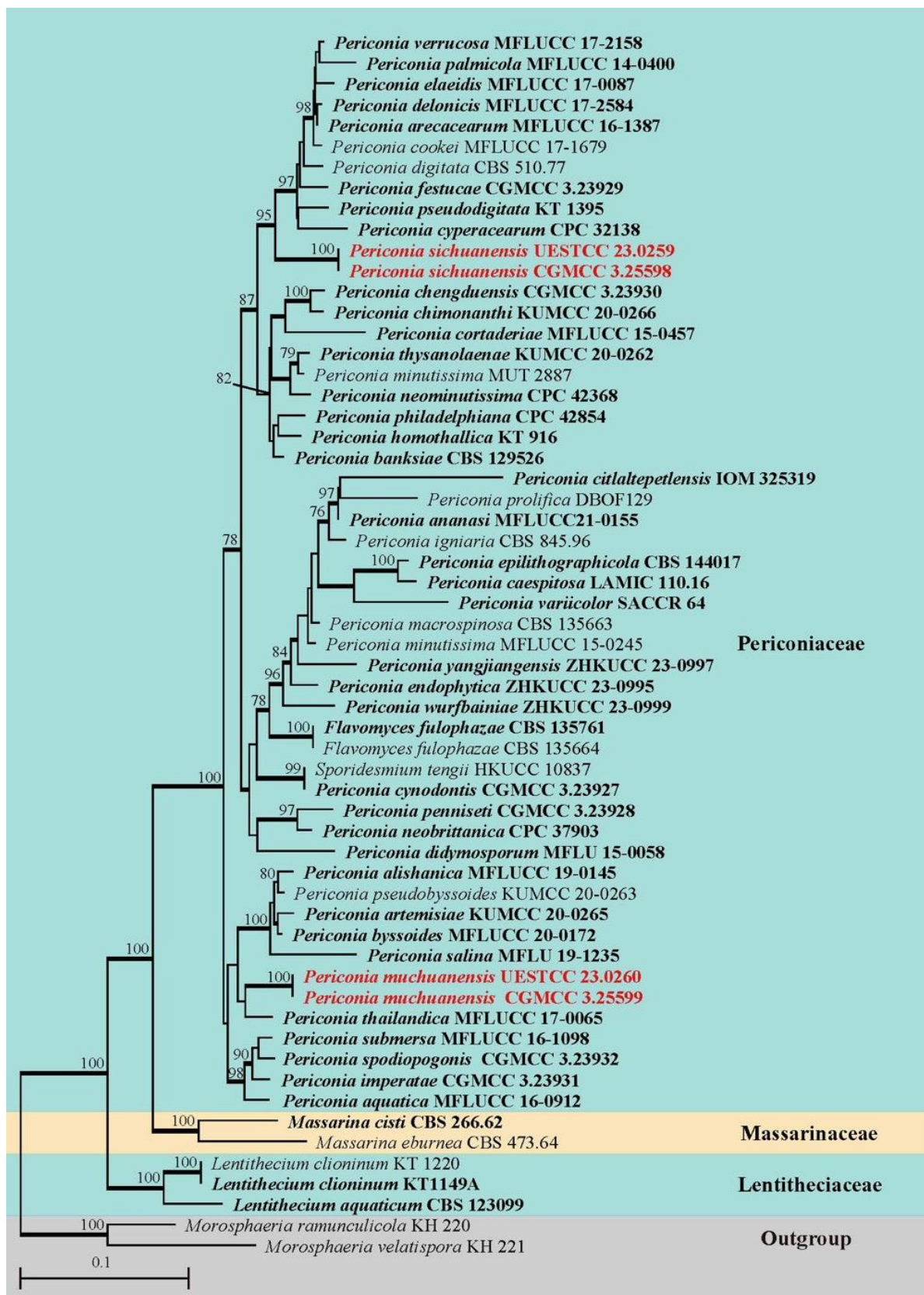


Figure 23 – RAxML tree generated from combined SSU, ITS, LSU and *tef1-α* sequence data of Periconiaceae. The tree was rooted with *Morosphaeria ramunculicola* (KH 220) and *M. velatispora* (KH 221). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

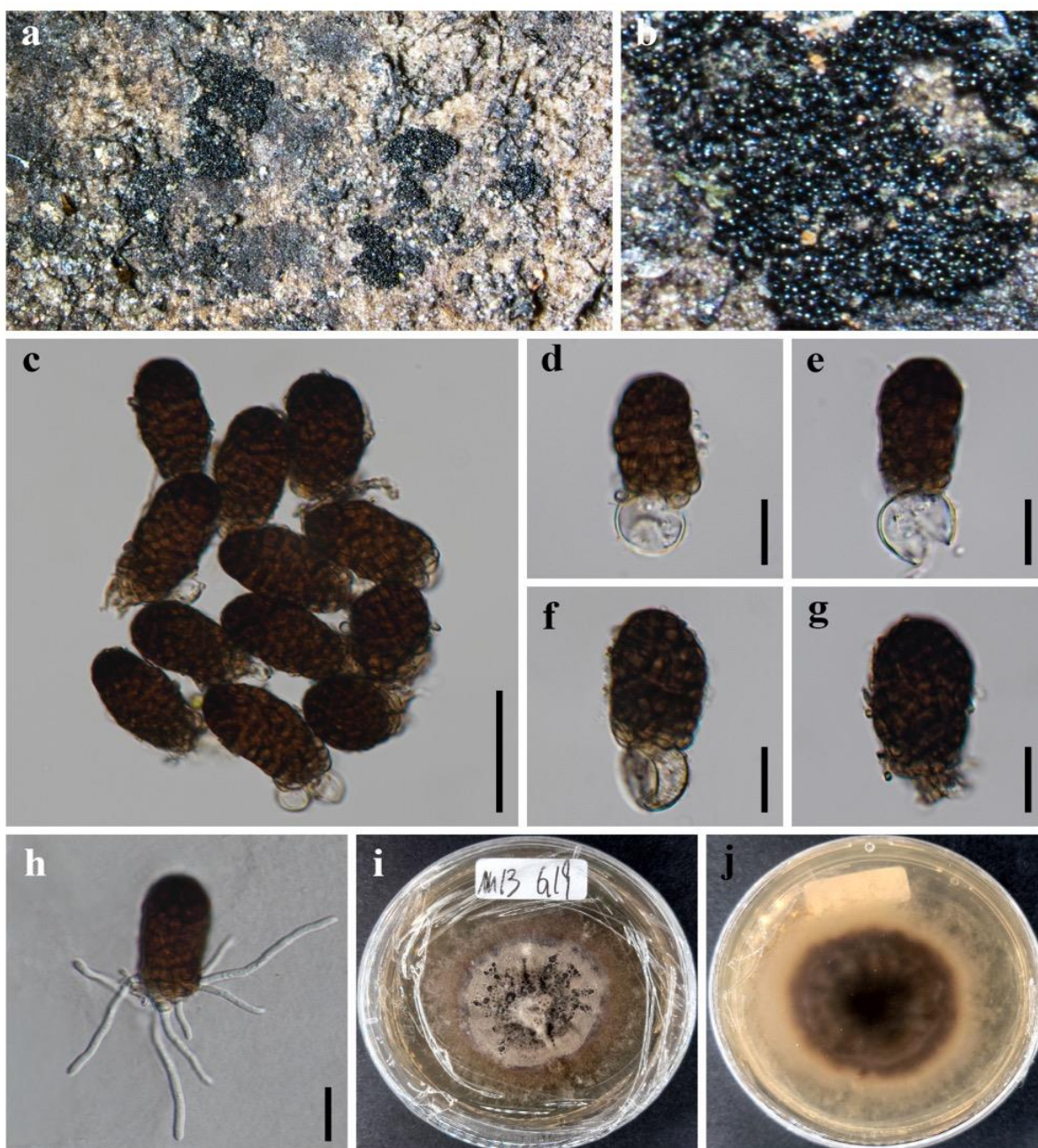


Figure 24 – *Pleopunctum ellipsoideum* (HUEST 24.0163). a–b Colonies. c Conidiophores and conidia. d–f Conidia with basal hyaline cell. g Conidium. h Germinating conidium. i, j Colony on PDA from above and below. Scale bars: c = 50 μ m, d–h = 20 μ m.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substratum, sporodochial, scattered to gregarious, black, glistening, superficial, punctiform. Mycelium immersed, composed of septate, branched, subhyaline to greyish-brown hyphae. Conidiophores macronematous, mononematous, brown, often reduced to conidiogenous cells. Conidiogenous cells monoblastic, terminal, integrated, medium brown. Conidia 35–60 $\times$ 20–30 μ m ($\bar{x}$ = 50 $\times$ 25 μ m, n = 50), acrogenous, solitary, muriform, constricted at septa, oval to ellipsoidal, smooth-walled, dark brown, broadly obtuse at apex, truncate at base, often with a hyaline, elliptical to globose basal cell, 10–15 μ m diam. ($\bar{x}$ = 13 μ m, n = 50).

Culture characteristics – Colonies on PDA reaching 40–50 mm after 3 months at 25 $^{\circ}$ C, circular, umbonate, fluffy, velvety edge, a circular raised band, grey white, in reverse black.

Material examined – China, Sichuan Province, Luzhou City, Na Xi District, Dawang Bamboo Sea, 28°39'24"N, 105°32'53"E, elevation 700 m, on dead branches of bamboo, 20 April 2023, X.D. Yu, M16 (HUEST 24.0165), living culture UESTCC 24.0148.

Notes – In the multi loci phylogenetic analyses, our strain UESTCC 24.0148 grouped together with *Pleopunctum pseudoellipsoideum* strains (Fig. 26). Our collection is similar to *P. pseudoellipsoideum* (MFLUCC 19-0391, holotype) in having muriform, oval to ellipsoidal conidia (Liu et al. 2019b). In addition, the nucleotide comparisons showed that our strain is not significantly different from MFLUCC 19-0391 in SSU, ITS, LSU, *rpb2* and *tef1-α*, indicating that they are the same species. Thus, we identified our strain as *P. pseudoellipsoideum* and it is a new host record on bamboo.

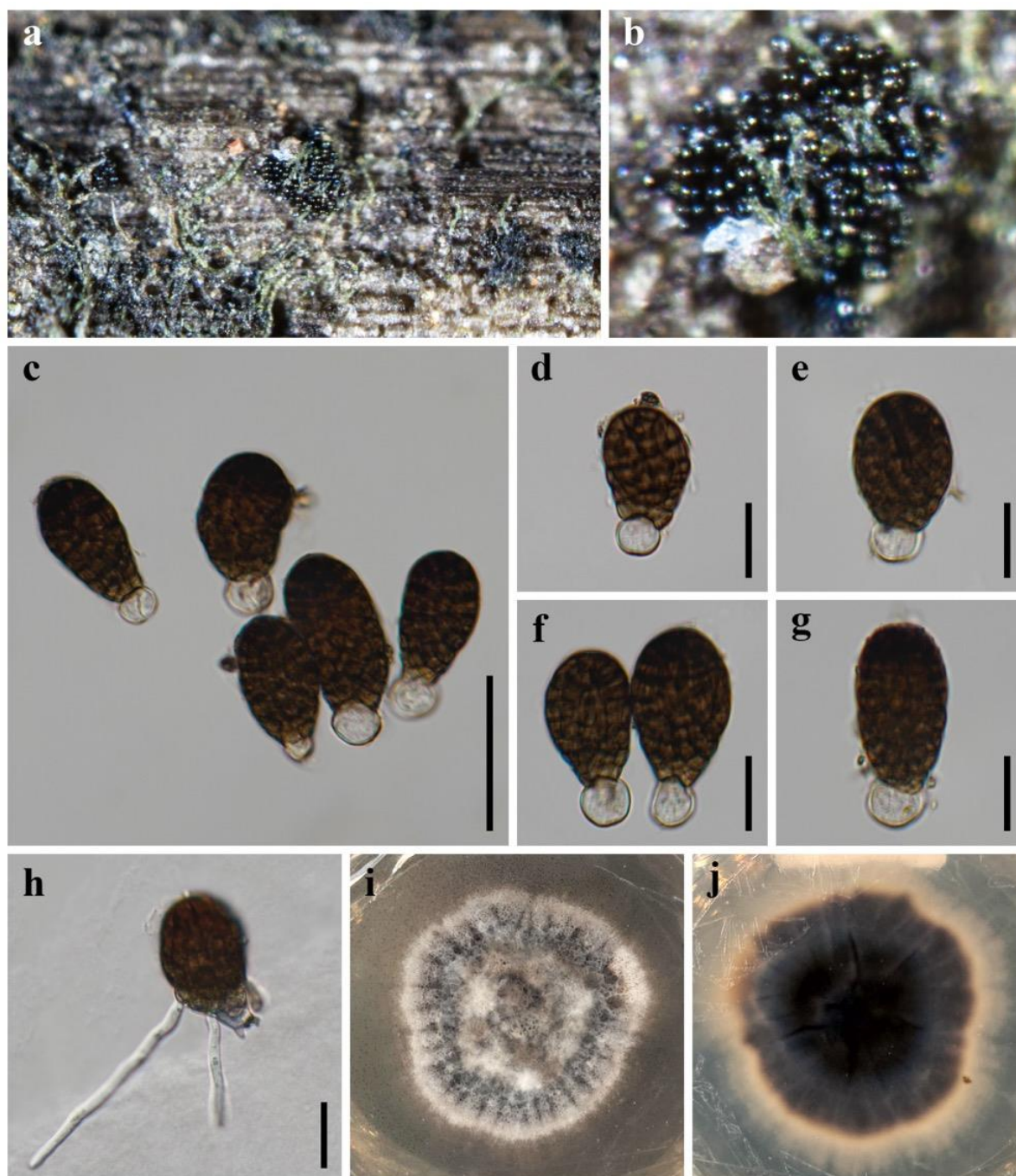


Figure 25 – *Pleopunctum pseudoellipsoideum* (HUEST 24.0165). a–b Colonies. c–g Conidia with basal hyaline cell. h Germinating conidium. i, j Colony on PDA from above and below. Scale bars: c = 50 μ m, d–h = 20 μ m.

Roussoella Sacc., Atti Ist. Veneto Sci. Lett. Arti ser. 6, 6: 410 (1888)

MycoBank number: MB4799; Facesoffungi number: FoF01689

Notes – *Roussoella* was introduced by Saccardo & Malacenses (1888) with *R. nitidula* as the type species recorded from bamboo in Malacca, Malaysia. *Roussoella* contains generally saprobic fungi on gramineous plants (bamboo and palms) in China, Tanzania, Italy, and other countries (Dai et al. 2022, Wu et al. 2023a). We introduce four new species obtained from bamboo in China.

Roussoella aseptata X.D. Yu & Jian K. Liu, sp. nov.

Fig. 27

MycoBank number: MB854882; Facesoffungi number: FoF16578

Etymology – In reference to the aseptate conidia.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 170–230 µm high, 380–480 µm diam., dark brown to black, pycnidial, usually forming in a linear series on the host surface, solitary, closed when young, becoming erumpent, stromatic, conical or hemispherical in section, immersed, uni-locular, thick-walled, with an ostiole opening. *Conidiomatal wall* 30–40 µm wide, composed of thick-walled, subhyaline to brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.5–8.5 × 2–3 µm, enteroblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth-walled. *Conidia* 4–5 × 2–3 µm ($\bar{x}$ = 4.5 × 2.5 µm; n = 50), hyaline, unicellular, aseptate, cylindrical to oblong, straight, smooth-walled, guttulate.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 2 weeks at 25 °C, circular, with dense mycelium on the surface, white; in reverse black.

Material examined – China, Sichuan Province, Yibin City, Shunan Bamboo Sea, 28°28'26"N, 104°58'14"E, elevation 570 m, on dead branches of bamboo, 21 April 2023, X.D. Yu, N8 (HKAS 135155, holotype), ex-type living culture CGMCC 3.25604; *ibid*; N13 (HUEST 24.0168, paratype), living culture UESTCC 24.0151.

Notes – Multi-gene phylogenetic analysis showed that our isolates belong to *Roussoella* and are closely related to *R. yunnanensis* with 90% ML/1.00 BYPP support (Fig. 31). Comparison of the ITS, LSU and *tef1-α* sequences of *R. aseptata* and *R. yunnanensis* showed 96.57% (478/495bp), 99.15% (819/826bp) and 97.54% (793/816bp) sequence similarity, respectively. However, we were unable to compare their morphology as the latter species is only represented by an ascomycetes sexual morph (Jiang et al. 2019a). Based on the available evidence, *R. aseptata* is identified as a new species.

Roussoella saprophytica X.D. Yu & Jian K. Liu, sp. nov.

Fig. 28

MycoBank number: MB854883; Facesoffungi number: FoF16579

Etymology – In reference to saprobic life mode of the fungus.

Saprobic on dead branches of bamboo. Sexual morph: *Ascstromata* solitary to gregarious, immersed under a clypeus or epidermis, visible as black domes on the substrate, in vertical section 200–300 µm high, 900–1400 µm long, 300–700 µm wide, elliptical to ampulliform, coriaceous, uni-to bi-loculate. *Peridium* 15–35 µm wide, composed of several layers of light brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, hyphae-like, branched, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 70–130 × 6–8 µm ($\bar{x}$ = 100 × 7 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 12–20 × 3.5–5.5 µm ($\bar{x}$ = 16 × 4 µm, n = 50), partial overlapping uni-seriate, cylindrical to fusiform, straight to somewhat curved, hyaline to dark brown, 1-septate, constricted at the septum, guttulate, rough-walled, with longitudinal striations and surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, white; in reverse yellow.

Material examined – China, Sichuan Province, Qionglai City, Chuanxi Bamboo Sea, 30°20'32"N, 103°18'26"E, elevation 540 m, on dead branches of bamboo in terrestrial habitat, 12 October 2021, X.D. Yu, A8 (HKAS 135147, holotype), ex-type living culture CGMCC 3.25601;

ibid, Chuanxi Bamboo Sea, 30°20'32"N, 103°18'26"E, elevation 540 m, on dead branches of bamboo in freshwater habitat, 12 October 2021, X.D. Yu, A16 (HUEST 24.0166), living culture UESTCC 24.0149; *ibid*, Lugou Bamboo Sea, 30°22'37"N, 103°16'45"E, elevation 730 m, on dead branches of bamboo in terrestrial habitat, 12 October 2021, X.D. Yu, A35 (HUEST 24.0167), living culture UESTCC 24.0150.

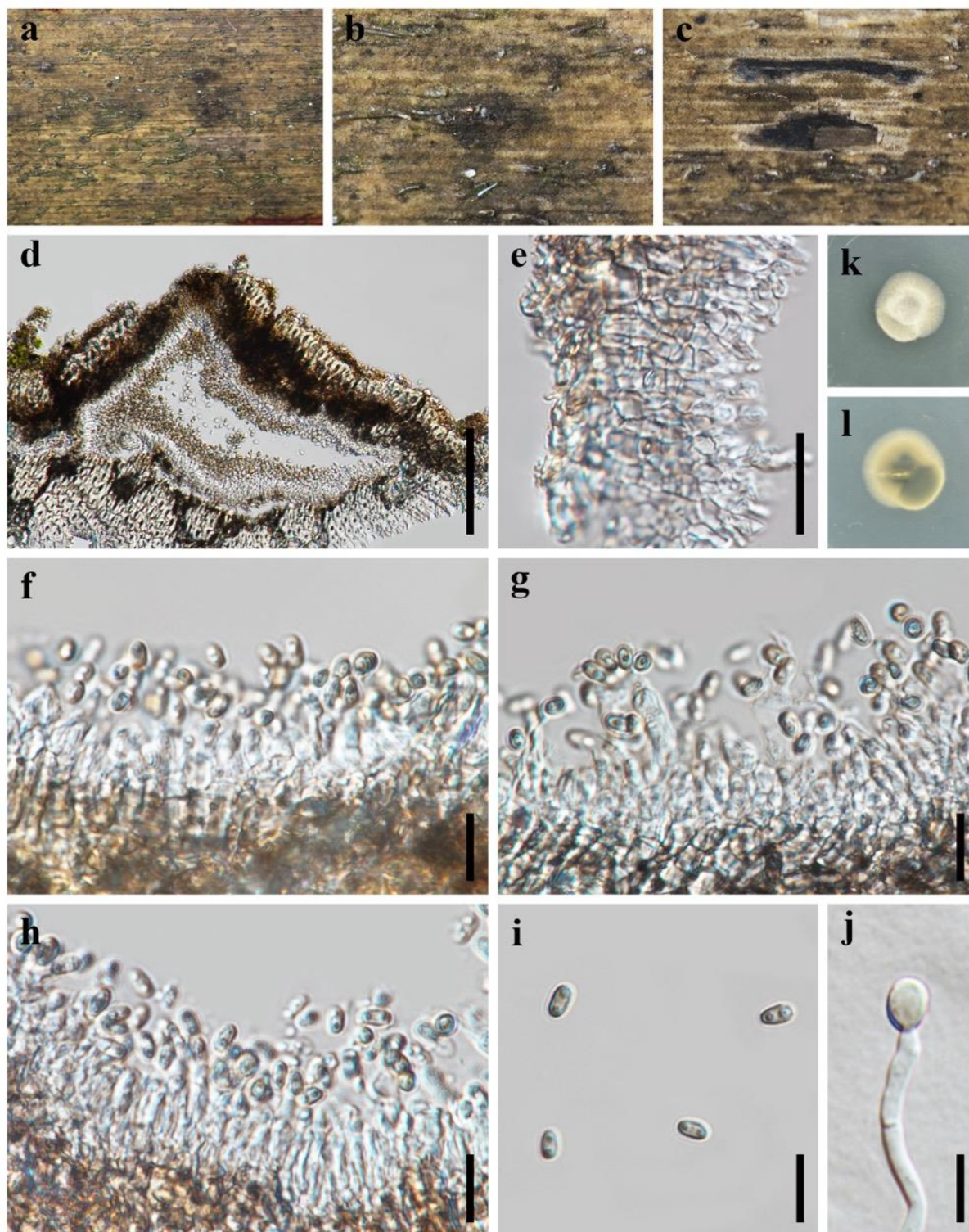


Figure 27 – *Roussioella aseptata* (HKAS 135155, holotype). a–c Conidiomata on surface of dead bamboo culms. d Vertical section of conidioma. e Wall of conidioma. f–h Conidiogenous cells bearing conidia. i Conidia. j Germinating conidium. k, l Colony on PDA from above and below. Scale bars: d = 100 μ m, e = 20 μ m, f–j = 10 μ m.

Notes – *Roussoella saprophytica* forms a distinct clade basal to *R. hysterioides*, *R. japonensis* and *R. papillata* with 94% ML/1.00 BYPP statistical support (Fig. 31). *Roussoella saprophytica* resembles these three species in having 8-spored, cylindrical, short pedicellate asci, uniseriate, septate ascospores with longitudinal striations and being surrounded by a mucilaginous sheath (Hyde et al. 1996, Liu et al. 2014, Dai et al. 2022). However, they can be distinguished by the shape of ascospores (fusiform-ellipsoidal in *R. hysterioides* and *R. japonensis*; ellipsoidal to broad fusiform in *R. papillata*; cylindrical to fusiform in *R. saprophytica*). The establishment of the new species *R. saprophytica* is justified by morphological and phylogenetic evidence.

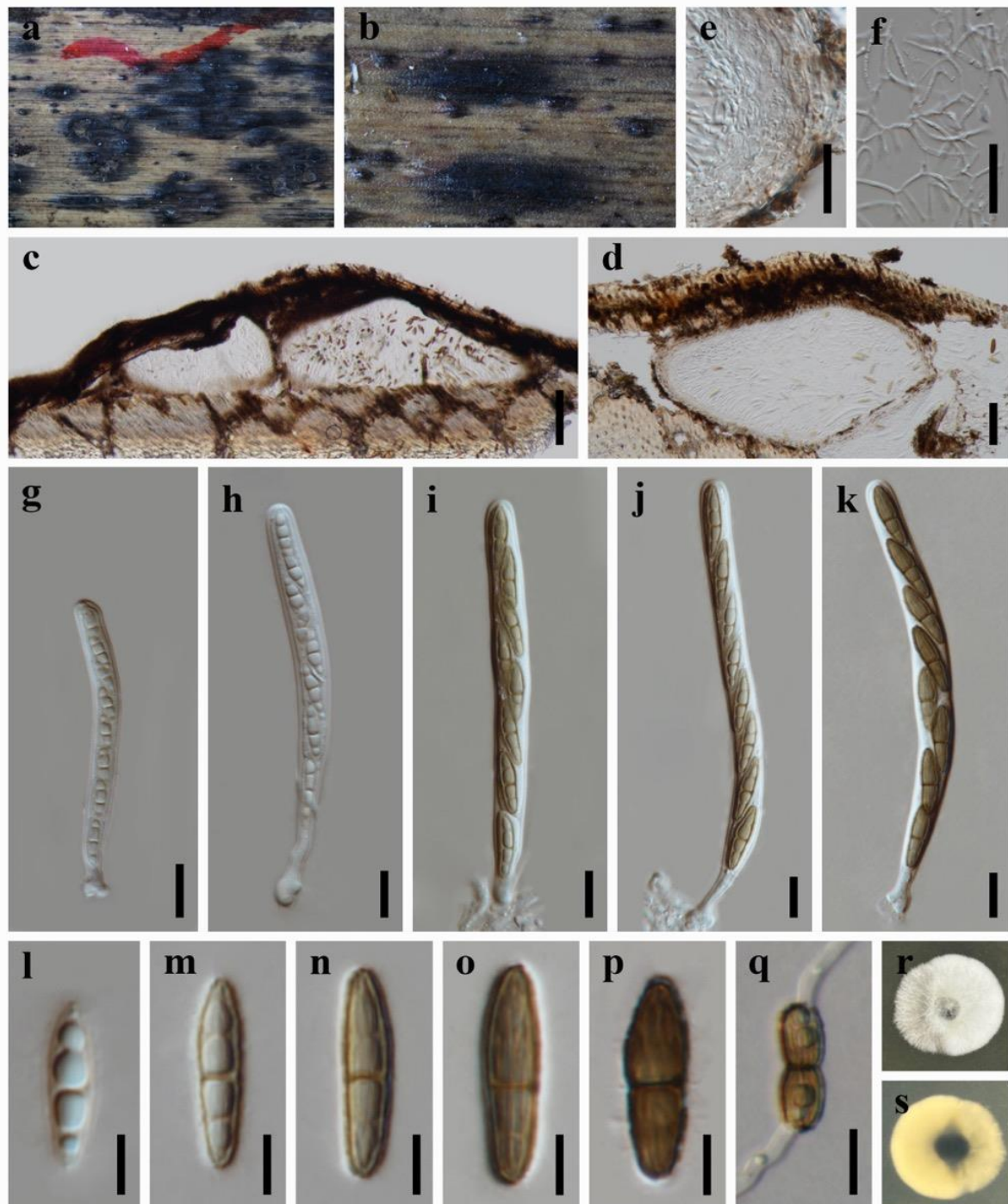


Figure 28 – *Roussoella saprophytica* (HKAS 135147, holotype). a–b Ascostromata on host substrate. c, d Vertical section of ascostromata. e Structure of peridium. f Pseudoparaphyses. g–k Asci. l–p Ascospores. q Germinated ascospore. r, s Colony on PDA from above and below. Scale bars: c = 100 μ m, d = 50 μ m, e, f = 20 μ m, g–k, q = 10 μ m, l–p = 5 μ m.

Roussoella striata X.D. Yu & Jian K. Liu, sp. nov.

Fig. 29

Mycobank number: MB854884; Facesoffungi number: FoF16580

Etymology – In reference to the distinctive striations on the ascospores wall.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, visible as black domes on the substrate, in vertical section 100–200 µm high, 280–480 µm diam., elliptical to ampulliform, coriaceous, uni-loculate, with a central ostiole, with minute papilla. *Peridium* 20–40 µm wide, composed of several layers of light brown, thick-walled cells of *textura angularis*. *Hamathecium* 1–2 µm wide, hyphae-like, branched, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 70–90 × 5.5–6.5 µm ($\bar{x}$ = 80 × 6 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 10–12 × 4–5 µm ($\bar{x}$ = 11 × 4.5 µm, n = 50), uni-seriate, ellipsoidal to fusiform, light brown to brown, 1-septate, constricted at the septum, guttulate, rough-walled, with longitudinal striations and surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 30–40 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, white; in reverse brown.

Material examined – China, Sichuan Province, Yaan City, Yingjing County, Longcanggou Forest Park, 29°37'24"N, 102°53'17"E, elevation 1486 m, on dead branches of bamboo, 28 July 2022, X.D. Yu, E18 (HKAS 135148, holotype), ex-type living culture CGMCC 3.25603.

Notes – *Roussoella striata* resembles *R. kunmingensis* in having 8-spored, cylindrical, short pedicellate asci, uniseriate, ellipsoidal to fusiform, light brown to brown, 1-septate ascospores with longitudinal striations and surrounded by a mucilaginous sheath. However, *R. striata* has longer asci (70–90 × 5.5–6.5 µm vs. 68–78 × 5.5–6.5) and larger ascospores (10–12 × 4–5 µm vs. 9.2–10.6 × 3.5–4.3 µm) than *R. kunmingensis* (Jiang et al. 2019a). The phylogenetic analyses (Fig. 31) indicated that *R. striata* is a phylogenetically distinct species. In addition, comparison of nucleotide differences between *R. striata* and *R. kunmingensis* showed that there are 5.3% (27/505, including 6 gaps) differences in ITS, 6.1% (56/920) in *rpb2* and 2% (17/849) in *tef1-α* gene regions, which also supports the introduction of *R. striata* as a new species.

Roussoella terricola X.D. Yu & Jian K. Liu, sp. nov.

Fig. 30

Mycobank number: MB854885; Facesoffungi number: FoF16581

Etymology – Referring to the terrestrial habitat of this fungus.

Saprobic on dead branches of bamboo. Sexual morph: *Ascostromata* solitary to gregarious, immersed under a clypeus or epidermis, visible as black domes on the substrate, multi-loculate. *Ascomata* solitary, globose, in vertical section 350–400 µm high, 400–450 µm diam., coriaceous. *Peridium* 15–25 µm wide, composed of several layers of brown, thin-walled cells of *textura angularis*. *Hamathecium* 1.0–2.0 µm wide, hyphae-like, branched, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 110–180 × 8–10 µm ($\bar{x}$ = 160 × 9 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 20–27 × 5–8 µm ($\bar{x}$ = 23 × 6.5 µm, n = 50), partial overlapping uni-seriate, cylindrical to fusiform, straight to somewhat curved, hyaline to dark brown, 1-septate, constricted at the septum, guttulate, rough-walled, with longitudinal striations and surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 3 months at 25 °C, circular, with dense mycelium on the surface, white; in reverse white, black at the center.

Material examined – China, Sichuan Province, Yaan City, Yingjing County, Longcanggou Forest Park, 29°37'24"N, 102°53'17"E, elevation 1486 m, on dead branches of bamboo, 28 July 2022, X.D. Yu, E5 (HKAS 135158, holotype), ex-type living culture CGMCC 3.25602.

Notes – *Roussoella terricola* is introduced as a novel species based on morphological distinctions and phylogenetic analyses. In the multi loci phylogenetic analyses, *R. terricola* (CGMCC 3.25602) clustered as a sister lineage to *R. intermedia* (NBRC 106245) and *R. pustulans* (MAFF 239637) (Fig. 31). Morphologically, *R. terricola* resembles *R. intermedia* and *R. pustulans*

in having 8-spored, cylindrical, short pedicellate asci, and uniseriate, septate ascospores with striations. However, *R. terricola* has relatively larger asci ($110\text{--}180 \times 8\text{--}10 \mu\text{m}$ vs. $(86\text{--})92\text{--}117(\text{--}130) \times 6\text{--}8 \mu\text{m}$ vs. $68\text{--}83 \times 6.5\text{--}8.5 \mu\text{m}$) and ascospores ($20\text{--}27 \times 5\text{--}8 \mu\text{m}$ vs. $12\text{--}18 \times 4\text{--}5 \mu\text{m}$ vs. $\times 10\text{--}16 \times 4\text{--}5 \mu\text{m}$) (Liu et al. 2014). Therefore, the new species is justified by morphology and phylogenetic evidence.

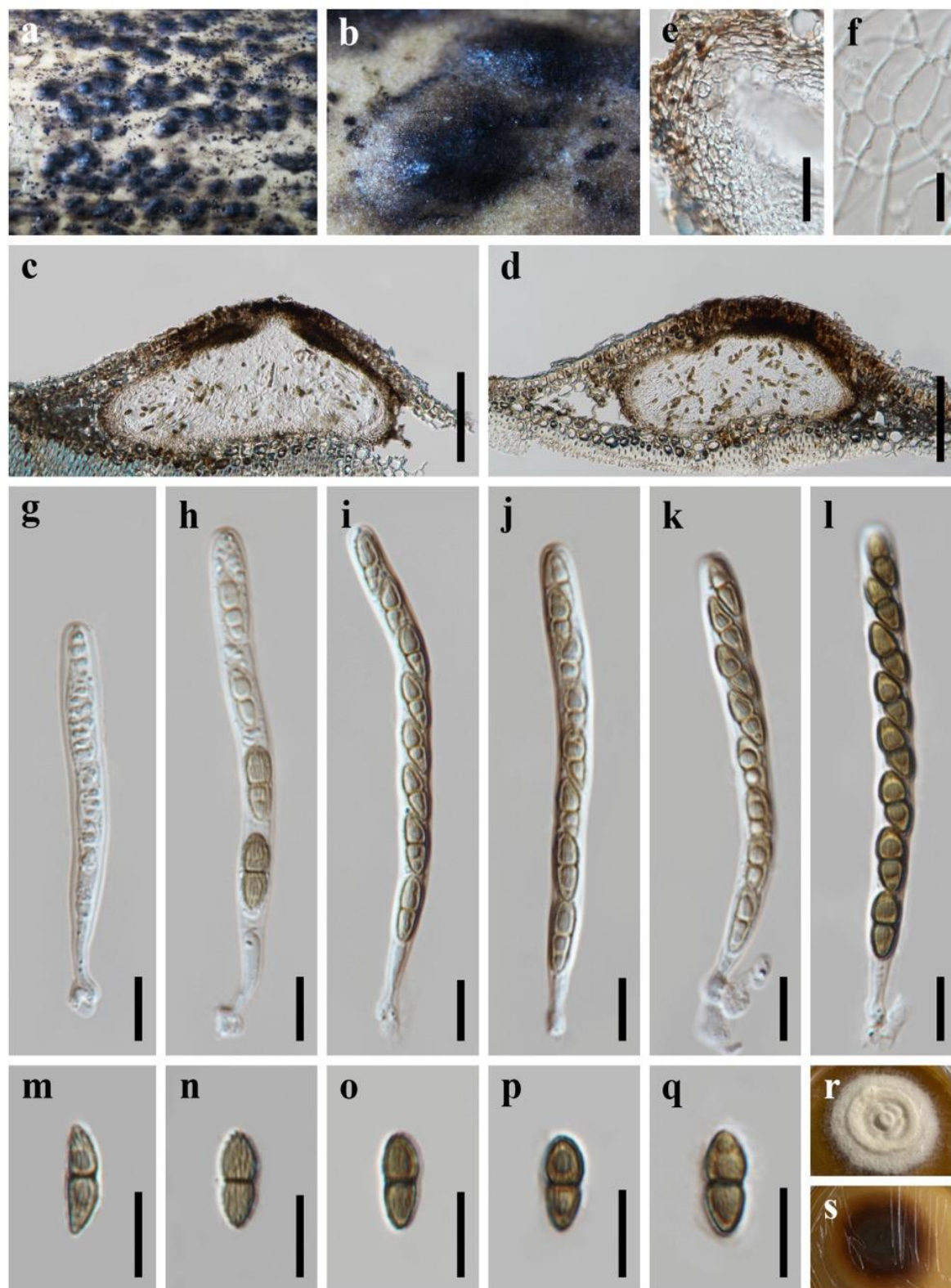


Figure 29 – *Rousoella striata* (HKAS 135148, holotype). a–b Ascomata on host substrate. c–d Vertical sections of ascomata. e Structure of peridium. f Pseudoparaphyses. g–l Asci. m–q Ascospores. r–s Additional structures.

m–q Ascospores. r, s Colony on PDA from above and below. Scale bars: c, d = 100 μ m, e = 20 μ m, f–q = 10 μ m.

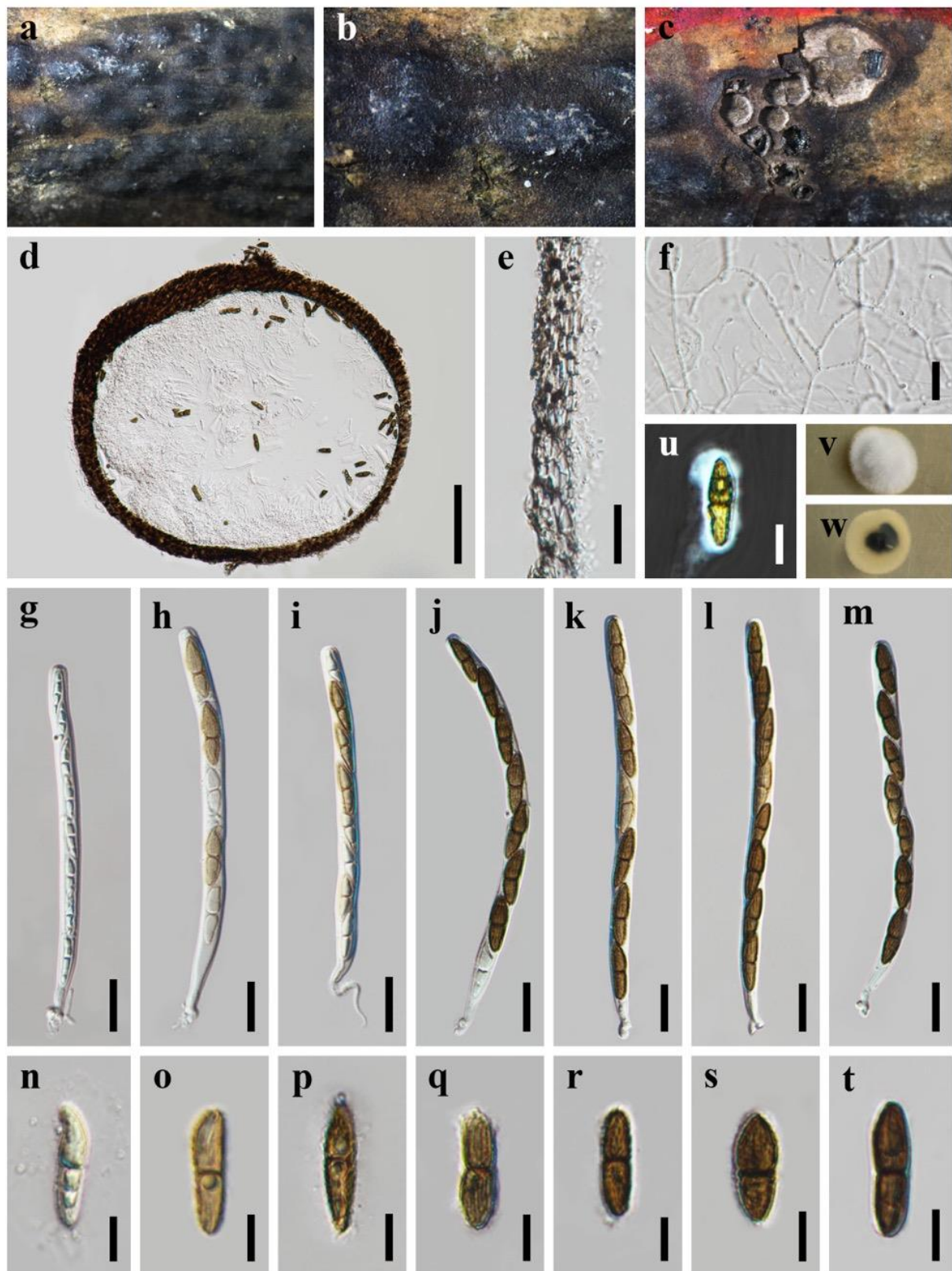


Figure 30 – *Roussioella terricola* (HKAS 135158, holotype). a–c Ascostromata on host substrate. d Vertical section of ascoma. e Structure of peridium. f Pseudoparaphyses. g–m Asci. n–t Ascospores. u Ascospore with mucilaginous sheath. v, w Colony on PDA from above and below. Scale bars: d = 100 μ m, e–f = 20 μ m, n–u = 10 μ m.

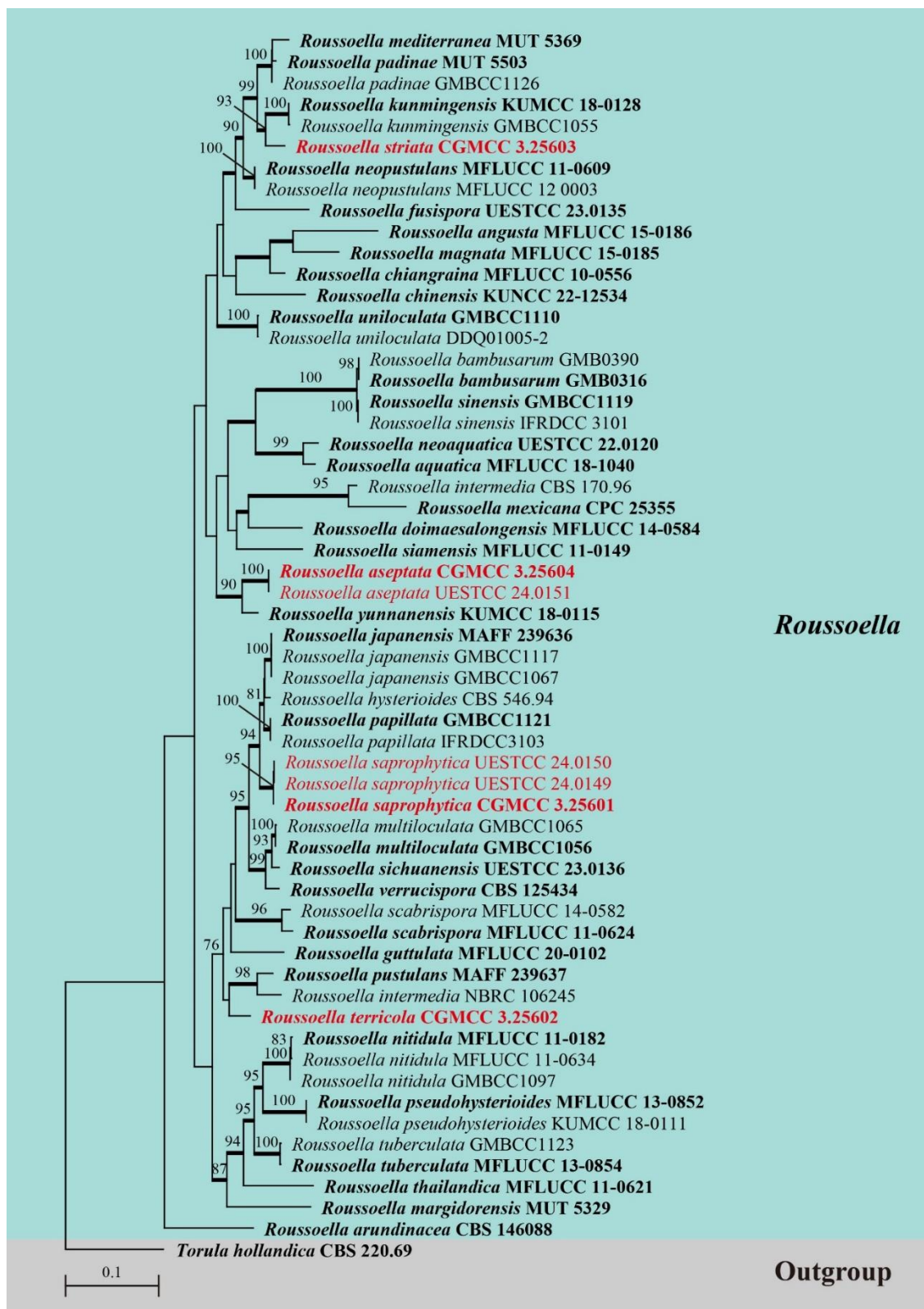


Figure 31 – RAxML tree generated from combined ITS, LSU, *rpb2* and *tef1-α* sequence data of Roussoellaceae. The tree was rooted with *Torula hollandica* (CBS 220.69). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Teichosporaceae M.E. Barr, Mycotaxon 82: 374 (2002)
 MycoBank number: MB82136; Facesoffungi number: FoF00830

Notes – Teichosporaceae was introduced by Barr (2002), and typified by *Teichospora*. The family contains 12 genera, including 3 genera lacking molecular data (Tennakoon et al. 2021a). *Pseudoteichospora*, typified by *Pseudoteichospora thailandensis*, was subsequently introduced to this family by Tian et al. (2024).

Ascosichuania X.D. Yu, K.D. Hyde & Jian K. Liu, gen. nov.

MycoBank number: MB854886; Facesoffungi number: FoF16566

Etymology – “Asco” refers to “Ascomycota” and “sichuania” refers to Sichuan, the country of origin.

Type species – *Ascosichuania bambusicola* X.D. Yu & Jian K. Liu

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, subglobose, coriaceous, uniloculate. *Peridium* composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* uni-seriate, fusiform, straight or slightly curved, hyaline, septate, constricted at the septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Notes – *Ascosichuania* is introduced to accommodate two novel species *A. bambusicola* and *A. fusiformis* and it forms a well-supported lineage clearly representing a new genus. *Ascosichuania* is distinguished from members in Teichosporaceae by its solitary to gregarious, semi-immersed, subglobose ascomata, 8-spored, cylindrical, short pedicellate asci and uni-seriate, fusiform, hyaline, septate, guttulate ascospores surrounded by a mucilaginous sheath (Tennakoon et al. 2021a), and phylogenetic analyses indicated it does not belong to any existing genera.

Ascosichuania bambusicola X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 32

MycoBank number: MB854887; Facesoffungi number: FoF16582

Etymology – Refers to the bamboo host from which the fungus was found.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, in vertical section 100–200 µm high, 250–450 µm diam., subglobose, coriaceous, uniloculate. *Peridium* 30–70 µm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1–2 µm wide, hyphae-like, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 60–90 × 6.5–7.5 µm ($\bar{x}$ = 75 × 7 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 14.5–16.5 × 3–4 µm ($\bar{x}$ = 15.5 × 3.5 µm, n = 50), overlapping uni-seriate, fusiform, straight to slightly curved, hyaline, 3-septate, constricted at the septa, guttulate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 2 weeks at 25 °C, circular, with dense mycelium on the surface, white; reverse yellowish to pale brown.

Material examined – China, Sichuan Province, Qionglai City, Lugou Bamboo Sea, 30°22'37"N, 103°16'45"E, elevation 730 m, on dead branches of bamboo, 12 October 2021, X.D. Yu, A38 (HKAS 135165, holotype), ex-type living culture CGMCC 3.25606; *ibid*; A26 (HUEST 24.0169, paratype), living culture UESTCC 24.0152; *ibid*; Dujiangyan City, Mount Qingcheng, 30°54'29"N, 103°32'36"E, elevation 960 m, on dead branches of bamboo, 2 December 2021, X.D. Yu, B12 (HUEST 24.0170), living culture UESTCC 24.0153; *ibid*; B16 (HUEST 24.0171), living culture UESTCC 24.0154.

Notes – The NCBI BLASTn search of our new collection matched *Teichospora kingiae* (TJU_JAN37) with 89.26% similarity in ITS sequences; the LSU sequences matched *Paulkirkia arundinis* (MFLUCC 12-0328) with 97.07% similarity; the *tef1-α* matched *Misturatosphaeria tennesseensis* (ANM 911) with 95.31% similarity; and the SSU sequences matched *Magnibotryascoma mali* (ZHKUCC 22-0338) with 98.94% similarity.

Our four isolates clustered together and are almost identical in their sequence data, which indicated they can be recognized as a single species. The distinguishing characteristics of *A. bambusicola* are the semi-immersed, subglobose, black ascomata, and fusiform, 3-septate, hyaline ascospores, constricted at the septa and surrounded by a mucilaginous sheath.

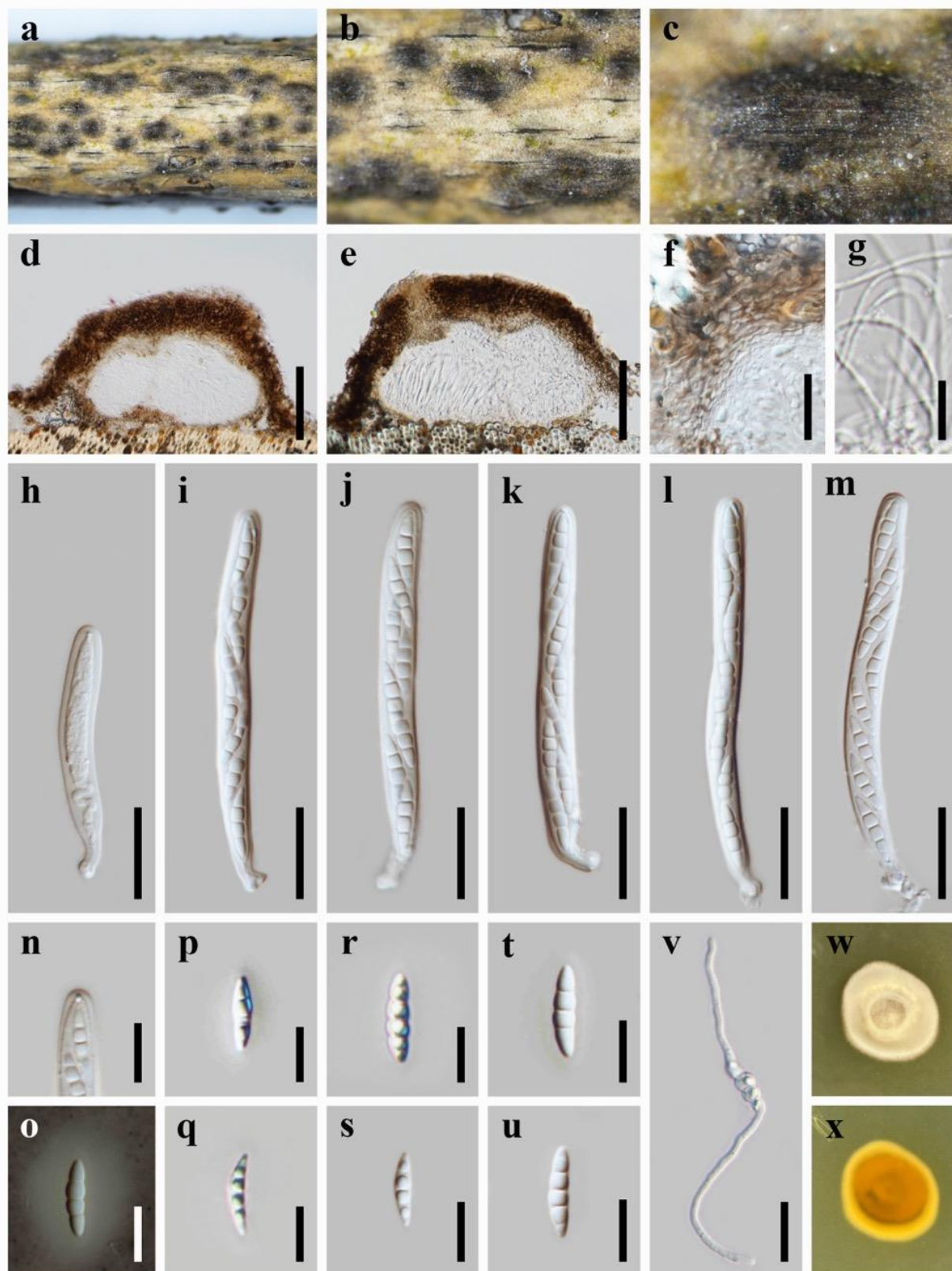


Figure 32 – *Ascosichuania bambusicola* (HKAS 135165, holotype). a–c Ascomata on host substrate. d–e Vertical sections of ascomata. f Structure of peridium. g Pseudoparaphyses.

h–m Asci. n Ascus apex with an ocular chamber. o Ascospore with mucilaginous sheath. p–u Ascospores. v Germinated ascospore. w, x Colony on PDA from above and below. Scale bars: d, e = 100 μ m, f, h–m, v = 20 μ m, g, n–u = 10 μ m.

Ascosichuania fusiformis X.D. Yu & Jian K. Liu, sp. nov.

Fig. 33

MycoBank number: MB854888; Facesoffungi number: FoF16583

Etymology – Refers to the fusiform ascospores.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, in vertical section 150–200 μ m high, 400–600 μ m diam., subglobose, coriaceous, uniloculate. *Peridium* 20–40 μ m wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1–2 μ m wide, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 75–85 $\times$ 5–6 μ m ($\bar{x}$ = 80 $\times$ 5.5 μ m, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 13–15 $\times$ 3.0–3.5 μ m ($\bar{x}$ = 14 $\times$ 3.3 μ m, n = 50), overlapping uni-seriate, fusiform, straight to somewhat curved, hyaline, 3-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 2 weeks at 25 °C, circular, raised to umbonate, with dense mycelium on the surface, grey; in reverse brown.

Material examined – China, Sichuan Province, Qionglai City, Lugou Bamboo Sea, 30°22'37"N, 103°16'45"E, elevation 730 m, on dead branches of bamboo, 12 October 2021, X.D. Yu, A29 (HKAS 135168, holotype), ex-type living culture CGMCC 3.25605.

Notes – *Ascosichuania fusiformis* clustered with the generic type *A. bambusicola* with 100% ML/1.00 BYPP bootstrap support (Fig. 35). However, *A. fusiformis* has relatively narrower asci (75–85 $\times$ 5–6 vs. 60–90 $\times$ 6.5–7.5) and smaller ascospores (13–15 $\times$ 3.0–3.5 vs. 14.5–16.5 $\times$ 3–4) than *A. bambusicola*. The phylogenetic analyses (Fig. 35) indicated that *A. fusiformis* is a phylogenetically distinct species. In addition, the comparison of nucleotide differences between *A. fusiformis* and *A. bambusicola* showed that there are 0.3% (2/773) differences in SSU, 9.3% (38/409) differences in ITS, 3% (22/460, including 6 gaps) in LSU and 2.5% (18/721) in *tef1-a* gene regions, which also supports the introduction of *A. fusiformis* as a new species (Chethana et al. 2021).

Multiseptoconidium X.D. Yu, K.D. Hyde & Jian K. Liu, gen. nov.

MycoBank number: MB854889; Facesoffungi number: FoF16567

Etymology – Referring to the multiseptate, phragmosporous conidia.

Type species – *Multiseptoconidium fuscosporellum* X.D. Yu & Jian K. Liu

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Conidiomata* dark brown to brown, pycnidial, visible as black domes on the substrate, solitary, subglobose in section, semi-immersed, uni-locular, thick-walled. *Conidiomatal wall* composed of thick-walled, subhyaline to brown cells of *textura angularis*. *Conidiophores* hyaline, cylindrical, unbranched, straight or slightly flexuous, aseptate, occasionally reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth-walled. *Conidia* hyaline to brown, unicellular when young, becoming muriform at maturity, ellipsoidal to subcylindrical, sometimes with a narrow and truncate base, straight or slightly curved, smooth-walled.

Notes – *Multiseptoconidium* is introduced as a monotypic genus to accommodate the type species *M. fuscosporellum* based on morphological examination and molecular analysis. In the phylogenetic analyses *Ascosichuania* and *Multiseptoconidium* formed a sister clade with low statistical support in Teichosporaceae. We were unable to compare their morphology as *Multiseptoconidium fuscosporellum* is only represented by a coelomycetous asexual morph. *Multiseptoconidium* is reported from a terrestrial habitat but without a known sexual morph. The phylogenetic placement of *Multiseptoconidium fuscosporellum* is unstable in this study. Fresh

collections of *Multiseptoconidium* are needed to stabilize the placement of this genus in the family Teichosporaceae.

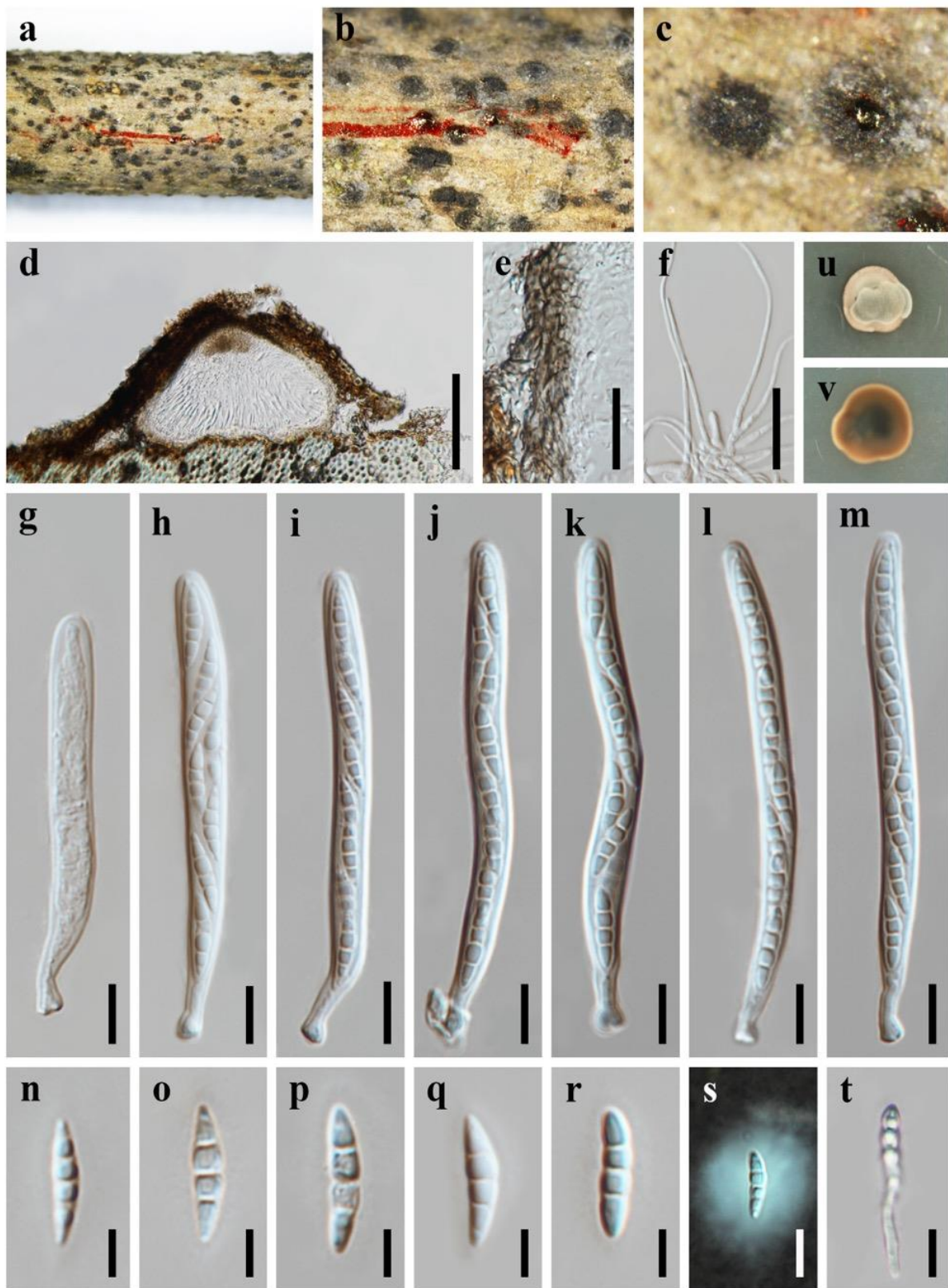


Figure 33 – *Ascospichuania fusiformis* (HKAS 135168, holotype). a–c Ascomata on host substrate. d Vertical section of ascoma. e Structure of peridium. f Pseudoparaphyses. g–m Asci. n–r Ascospores. s Ascospore with mucilaginous sheath. t Germinated ascospore. u, v Colony on PDA from above and below. Scale bars: d = 100 µm, e, f = 20 µm, g–m, s, t = 10 µm, n–r = 5 µm.

Multiseptoconidium fuscosporellum X.D. Yu & Jian K. Liu, sp. nov.
Mycobank number: MB854890; Facesoffungi number: FoF16584
Etymology – “*Fusca*” referring to the dark brown conidia.

Fig. 34

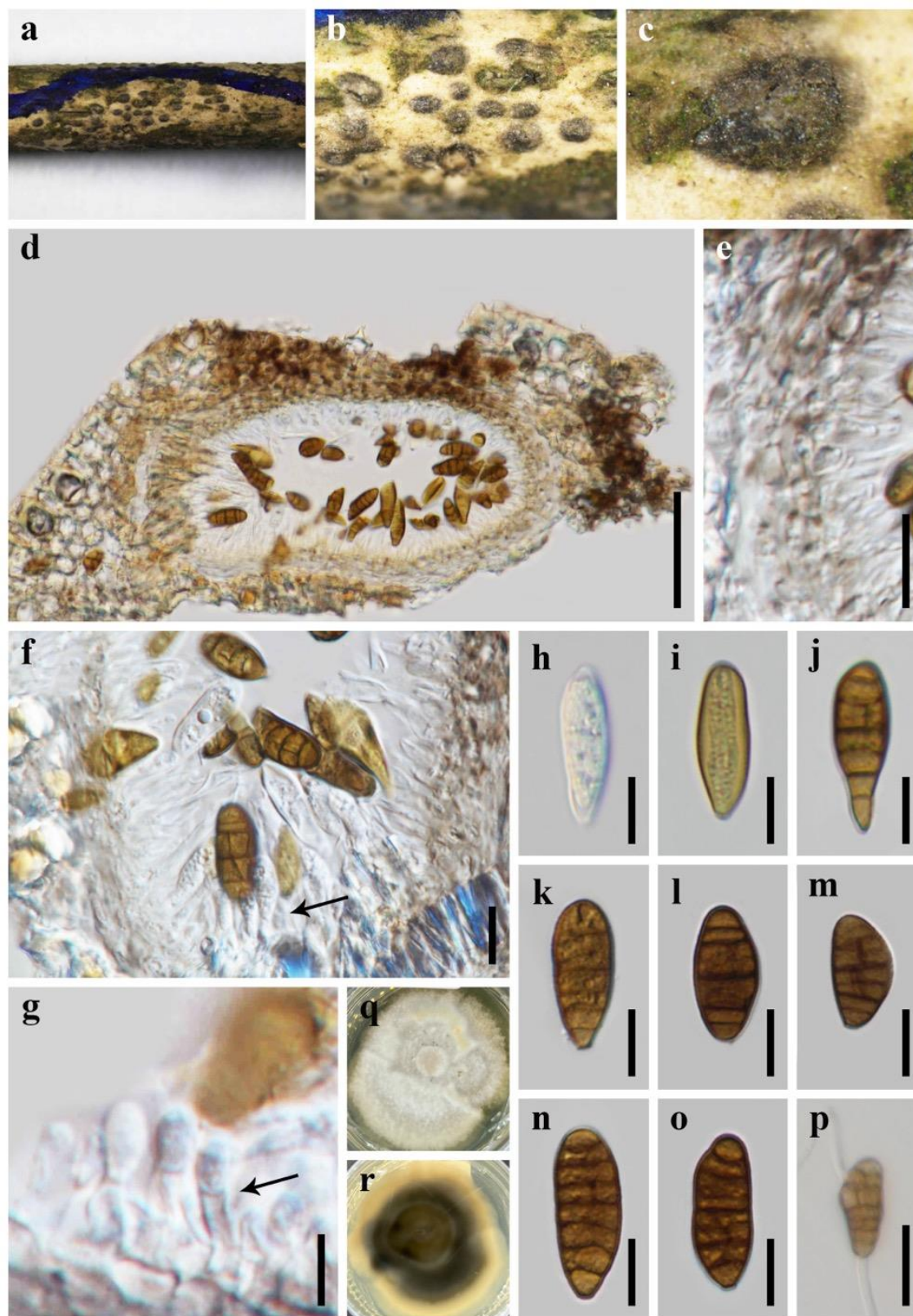


Figure 34 – *Multiseptoconidium fuscosporellum* (HKAS 135167, holotype). a–c Conidiomata on surface of dead bamboo culms. d Vertical section of conidioma. e Wall of conidioma. f, g Conidiogenous cells bearing conidia (arrows indicate how the conidiogenous cells produce

conidia). h–o Conidia. p Germinating conidium. q, r Colony on PDA from above and below. Scale bars: d = 50 µm, p = 20 µm, e, f, h–o = 10 µm, g = 5 µm.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 100–260 µm high, 180–380 µm diam., dark brown to brown, pycnidial, visible as black domes on the substrate, solitary, stromatic, subglobose in section, semi-immersed, unilocular, thick-walled. *Conidiomatal wall* 15–30 µm wide, composed of thick-walled, subhyaline to brown cells of *textura angularis*. *Conidiophores* hyaline, cylindrical, unbranched, straight or slightly flexuous, aseptate, occasionally reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 1.5–2.5 µm, holoblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth-walled. *Conidia* 15–25 × 8–10 µm ($\bar{x}$ = 20 × 9 µm; n = 50), hyaline to brown, unicellular when young, becoming muriform and brown at maturity, ellipsoidal to subcylindrical, sometimes with a narrow and truncate base, straight or slightly curved, smooth-walled.

Material examined – China, Sichuan Province, Meishan City, Qingshen County, Bamboo Forest Wetland Park, 29°48'43"N, 103°49'26"E, elevation 400 m, on dead branches of bamboo, 4 November 2022, X.D. Yu, J13 (HKAS 135167, holotype), ex-type living culture CGMCC 3.25607.

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray., *Studies in Mycology* 64: 177 (2009)

MycoBank number: MB515253; Facesoffungi number: FoF06665

Notes – Tetraplosphaeriaceae was established by Tanaka et al. (2009) and typified by *Tetraplosphaeria sasicola* Kaz. Tanaka & K. Hiray. *Tetraplosphaeria* was treated as a synonym of *Tetraploa* due to nomenclatural priority (Hyde et al. 2013). Sexual morphs in Tetraplosphaeriaceae are massarina-like characterized by hyaline, 1–3-septate ascospores surrounded by a sheath, and asexual morphs are characterized by conidia with setose appendages (Tanaka et al. 2009, Hyde et al. 2013, Tibpromma et al. 2017). Ten genera are accepted in the family, viz. *Aquatisphaeria*, *Byssolophis*, *Ernakulamia*, *Polyplosphaeria*, *Pseudopolyplosphaeria*, *Pseudotetraploa*, *Quadricrura*, *Shrungabeeja*, *Tetraploa* (type genus) and *Triplosphaeria* (Zhang et al. 2023).

Pseudopolyplosphaeria J.F. Zhang, Y.Y. Chen & Jian K. Liu, *Fungal Diversity* 122: 59 (2023)

MycoBank number: MB900766; Facesoffungi number: FoF14570

Notes – *Pseudopolyplosphaeria* was introduced to accommodate *Pseudopolyplosphaeria guizhouensis* which is commonly found on dead bamboo culms in terrestrial habitats (Zhang et al. 2023). *Pseudopolyplosphaeria* is distinguished from other genera in Tetraplosphaeriaceae by ascostromata containing several ascomata (Zhang et al. 2023).

Pseudopolyplosphaeria guizhouensis J.F. Zhang, Y.Y. Chen & Jian K. Liu, *Fungal Diversity* 122: 61 (2023) Fig. 36

MycoBank number: MB900717; Facesoffungi number: FoF14571

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, in vertical section 200–300 µm high, 300–400 µm diam., subglobose, coriaceous, uniloculate. *Peridium* 20–60 µm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, hyphae-like, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 110–140 × 19–25 µm ($\bar{x}$ = 125 × 22 µm, n = 30), 8-spored, bitunicate, fissitunicate, broad clavate to cylindric-clavate, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 35–45 × 8–10 µm ($\bar{x}$ = 40 × 9 µm, n = 50), overlapping bi- to tri-seriate, fusiform, hyaline, 1-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 2 weeks at 25 °C, circular, raised to umbonate, surface rough, dense, edge undulate, black, dry, reverse dark.

Material examined – China, Sichuan Province, Meishan City, Danling County, JiuLongShan Forest Park, 29°54'48"N, 103°35'13"E, elevation 460 m, on dead branches of bamboo in a

freshwater habitat, 14 July 2022, X.D. Yu, D5 (HUEST 23.0269), ex-type living culture CGMCC 3.25608; *ibid.* D31 (HUEST 24.0172); living culture UESTCC 24.0155.

Additional *tub2* GenBank numbers – CGMCC 3.25608 = PQ179744; UESTCC 24.0155 = PQ179745.

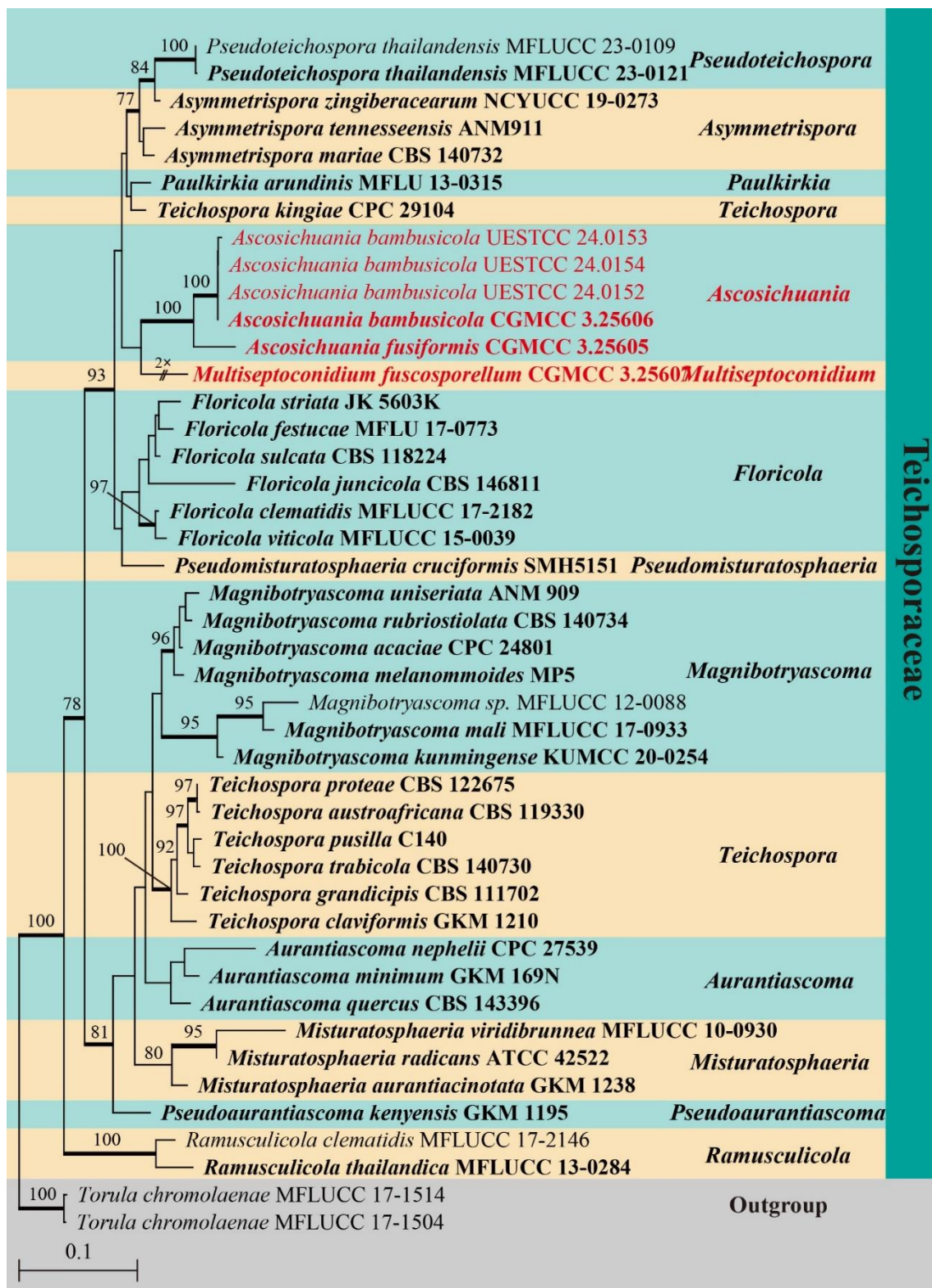


Figure 35 – RAxML tree generated from combined ITS, LSU, SSU, *rpb2* and *tef1-α* sequence data of Teichosporaceae. The tree was rooted with *Torula chromolaenae* (MFLUCC 17-1504) and *T. chromolaenae* (MFLUCC 17-1514). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches.

Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Notes – In the multi-loci phylogenetic analyses, our collections (CGMCC 3.25608 and UESTCC 24.0155) clustered together with the type of *Pseudopolyplosphaeria guizhouensis* (GZCC 19-0247) (Fig. 39). Morphology, as well as the ITS, LSU, SSU, *tub2* and *tef1- α* sequence data of our collections and *P. guizhouensis* are almost identical (Zhang et al. 2023). Thus, we identified our collections as *P. guizhouensis* and it is a new habitat (freshwater) and new host record (bamboo).

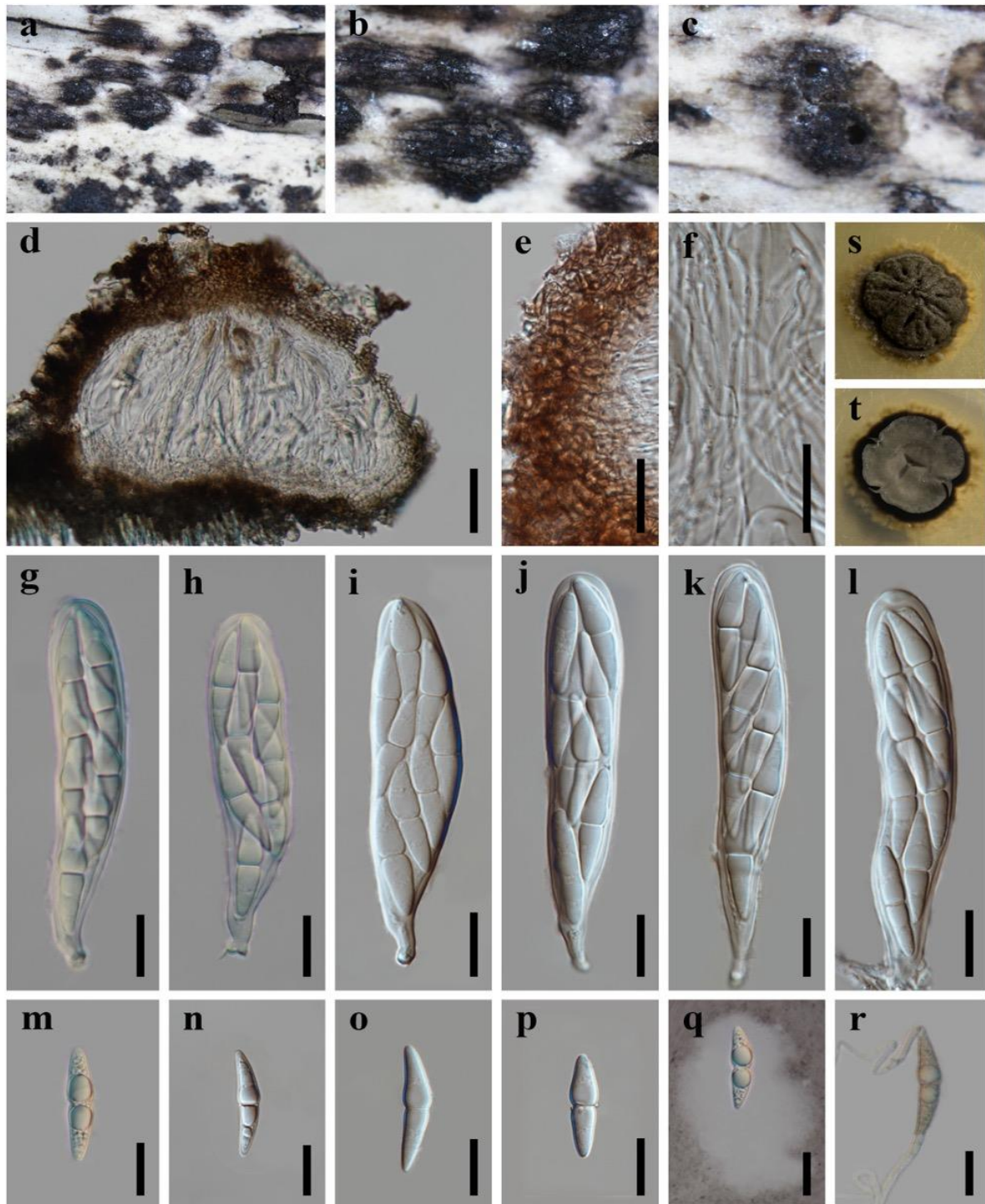


Figure 36 – *Pseudopolyplosphaeria guizhouensis* (HUEST 23.0269). a–c Ascomata on host substrate. d Vertical section of ascoma. e Structure of peridium. f Pseudoparaphyses. g–l Asci.

m–p Ascospores. q Ascospore with mucilaginous sheath. r Germinated ascospore. s, t Colony on PDA from above and below. Scale bars: d = 50 µm, e–r = 20 µm.

Triplosphaeria Kaz. Tanaka & K. Hiray., Studies in Mycology 64: 185 (2009)

MycoBank number: MB515255; Facesoffungi number: FoF06672

Notes – *Triplosphaeria* was introduced by Tanaka et al. (2009) to accommodate *T. acuta*, *T. cylindrica* and *T. yezoensis* and is typified by *T. yezoensis*. *Triplosphaeria guizhouensis* was subsequently introduced to this genus by Liu et al. (2023). Five *Triplosphaeria* species are recorded in Index Fungorum (2024).

Triplosphaeria bambusicola X.D. Yu & Jian K. Liu, sp. nov.

Fig. 37

MycoBank number: MB854891; Facesoffungi number: FoF16585

Etymology – Refers to the bamboo host from which the fungus was found.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, black. Mycelium superficial. Conidiophores absent. Conidiogenous cells monoblastic, integrated, usually indistinguishable from superficial hyphae. Conidia 45–85 × 20–30 µm ($\bar{x}$ = 60 × 25 µm, n = 50), solitary, subglobose, amygdaliform to ovoid, dark brown to black, distoseptate, consisting of 2–6 columns, with 0–6 setose appendages. Appendages 20–40 × 3–5 µm ($\bar{x}$ = 25 × 4 µm, n = 50), 0–2-septate, dark brown, smooth, unbranched, straight or curved.

Culture characteristics – Colonies on PDA reaching 40–50 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, black, reverse dark.

Material examined – China, Sichuan Province, Chengdu City, Dayi County, Xiling Town, Xiling Snow Mountain, 30°41'50"N, 103°9'43" E, elevation 3200 m, on dead branches of bamboo, 2 May 2023, X.D. Yu, K51 (HKAS 135161, holotype), ex-type living culture CGMCC 3.25610.

Notes – In the phylogenetic analyses (Fig. 39) *Triplosphaeria bambusicola* formed a distinct lineage within *Triplosphaeria*. *Triplosphaeria bambusicola* resembles *Triplosphaeria* sp. (HHUF 27481 and KTC 2546) in having monoblastic conidiogenous cells and conidial body size. However, they can be distinguished by the number (0–6 vs 3), size (20–40 × 3–5 vs 51–120(–160)) and septation (0–2 vs 4–12) of the setose appendages (Tanaka et al. 2009).

Triplosphaeria fusiformis X.D. Yu & Jian K. Liu, sp. nov.

Fig. 38

MycoBank number: MB854892; Facesoffungi number: FoF16586

Etymology – Refers to its fusiform ascospores.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, semi-immersed, visible as dark brown to black domes on the substrate, in vertical section 150–250 µm high, 400–500 µm diam., subglobose, coriaceous, uniloculate. *Peridium* 40–70 µm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, hyphae-like, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 110–160 × 16–24 µm ($\bar{x}$ = 130 × 21 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, straight or slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 30–50 × 8.5–11.5 µm ($\bar{x}$ = 40 × 9.5 µm, n = 50), overlapping uni- to bi-seriate, fusiform, straight to somewhat curved, hyaline, 1-septate, constricted at the septum, guttulate, smooth-walled, without a sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 2 weeks at 25 °C, circular, dry, the mycelium sparse at the margin, greyish at the inner ring, and white at the outer ring, reverse greyish-brown.

Material examined – China, Sichuan Province, Zigong City, Rong County, Hualonggou Bamboo Sea, 29°28'52" N, 104°17'20" E, elevation 625 m, on dead branches of bamboo, 3 November 2022, X.D. Yu, H5 (HKAS 135166, holotype), ex-type living culture CGMCC 3.25609; *ibid.* H3 (HUEST 24.0173); living culture UESTCC 24.0156.

Additional *tub2* GenBank numbers – CGMCC 3.25609 = PQ179747; UESTCC 24.0156 = PQ179746.

Notes – Multi-gene phylogenetic analysis showed that our isolates belong to *Triplosphaeria* and are closely related to *T. guizhouensis* (Fig. 39). However, comparison of molecular data of *T. fusiformis* and *T. guizhouensis* showed that there are 5.68% (20/352) nucleotide differences in *tub2* gene regions and our isolate could be recognized as a new species. It fits well with the genus *Triplosphaeria* in having cylindrical to clavate asci and fusiform, hyaline, septate ascospores. However, the dimensions of asci and ascospores distinguish *T. fusiformis* from other species (Table 3).

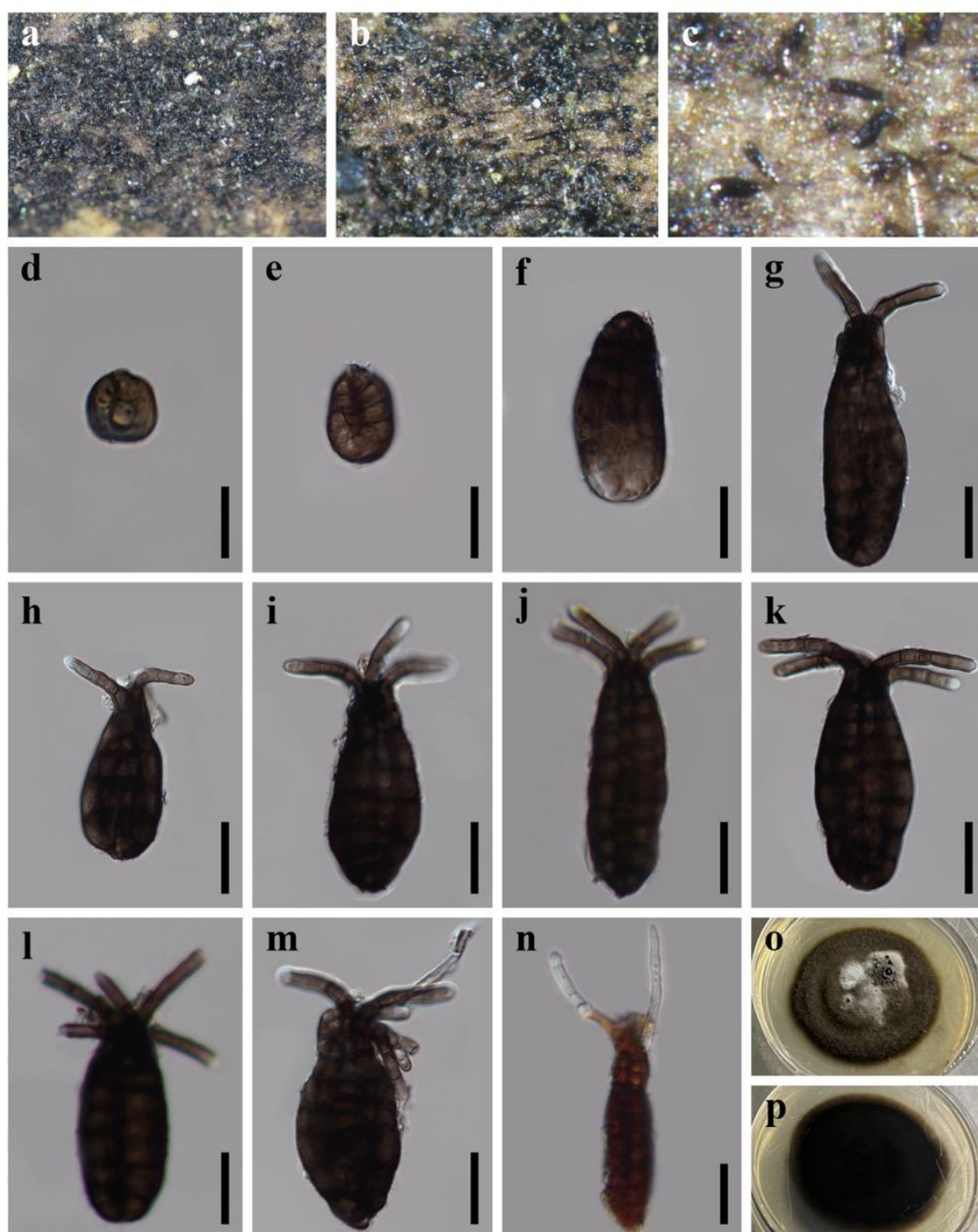


Figure 37 – *Triplosphaeria bambusicola* (HKAS 135161, holotype). a–c Colonies on natural substratum. d–m Conidia. n Germinating conidium. o, p Colony on PDA from above and below. Scale bars: d–n = 20 μ m.

Sordariomycetes O.E. Erikss. & Winka, Myconet 1: 10 (1997)

Diaporthomycetidae Senan., Maharachch. & K.D. Hyde, Fungal Diversity 72: 208 (2015)

Conlariales K.D. Hyde & Hongsanan, Fungal Diversity 107: 94 (2021)

Conlariaceae H. Zhang, K.D. Hyde & Maharachch., Fungal Diversity 85: 90 (2017)

MycoBank number: MB553758; Facesoffungi number: FoF03336

Notes – Conlariaceae was established by Zhang et al. (2017) to accommodate *Conlarium* with *C. duplumascosporum* as the type species. Currently, Conlariaceae comprises two genera (*Conlarium* and *Riomyces*) with twelve species (Yu et al. 2024).

Conlarium F. Liu & L. Cai, Mycologia 104: 1180 (2012)

MycoBank number: MB564382; Facesoffungi number: FoF05074

Notes – *Conlarium* is a holomorphic genus and typified by *C. duplumascosporum* (Liu et al. 2012a). Most *Conlarium* species are saprobes and have been found on bamboo, *Ficus virens* (Moraceae), or dead branches of woody plants in freshwater and terrestrial habitats (Liu et al. 2012a, Phookamsak et al. 2019, Dong et al. 2021, Dubey & Manikpuri 2021, Zhang et al. 2021a, Yang et al. 2023). A few species were reported as endophytes isolated from sugarcane rhizosphere, e.g., *C. baiseense*, *C. nanningense* and *C. sacchari* (Xie et al. 2019).

Table 3 Morphological comparison of sexual morph of *Triplosphaeria* species.

Taxa	Ascomata (μm)	Asci		Ascospores		References
		Morphology	Size (μm)	Morphology	Size (μm)	
<i>T. acuta</i>	135–230 $\times$ 540–750	Cylindrical to clavate	(62–)73–106 $\times$ 11–15	Narrowly fusiform, septate, hyaline, with a sheath	25–35 $\times$ 4– 6(–7)	Tanaka et al. (2009)
<i>T. cylindrica</i>	110–190 $\times$ 450–1180	Cylindrical to clavate	(70–)80–126 $\times$ 14.5–21(– 23.5)	Broadly fusiform to cylindrical, septate, hyaline, with a sheath	(22–)25–31(– 33) $\times$ 6–10	Tanaka et al. (2009)
<i>T. fusiformis</i>	150–250 $\times$ 400–500	Cylindrical to clavate	110–160 $\times$ 16–24	Fusiform, 1- septate, hyaline, without a sheath	30–50 $\times$ 8.5– 11.5	This study
<i>T. maxima</i> ^T	250–300 $\times$ 900–1000	Clavate to cylindrical	95–133 $\times$ 14.5–21	Narrowly fusiform, 1- septate, hyaline, with a sheath	(32.5–)34– 45(–48.5) $\times$ (6–)7–9(–10)	Tanaka et al. (2009)
<i>T. yezoensis</i>	140–160 $\times$ 450–550	Cylindrical to clavate	(60–)72– 119(–141) $\times$ 12–18.5	Narrowly fusiform, 1- septate, hyaline, with a sheath	(22.5–)26– 32(–35) $\times$ 5–8	Tanaka et al. (2009)

Conlarium bambusae X.D. Yu & Jian K. Liu, sp. nov.

Fig. 40

MycoBank number: MB854893; Facesoffungi number: FoF16587

Etymology – Referring to its bamboo host.

Saprobic on dead branches of bamboo in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* sporodochial, broadly punctiform, gregarious, raised, brown to black. *Mycelium* mostly immersed, comprising branched, hyaline to pale brown, smooth and thin-walled hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, holoblastic, integrated, determinate, cylindrical, hyaline to brown, smooth, up to 1.5–4.5 μm wide. *Conidia* 20–30 $\times$ 16–26 μm ($\bar{x}$ = 26 $\times$ 21 μm , n = 50), acrogenous, solitary, dry, mostly subglobose or irregular, brown to dark brown, clathrate, muriform, 2–4-transversely septate, 1–3-longitudinally septate, slightly constricted at the septa, smooth and thin-walled, with a small, sub-rounded, dark brown ornamentation on the surface of each cell. Conidial secession schizolytic.

Culture characteristics – Conidium germinated on PDA within 24 h. Colonies attained a diameter about 6 mm after 2 weeks at 25 °C, irregular, raised to umbonate, dense, the edge slightly undulate and black, black from the reverse.

Material examined – China, Sichuan Province, Leshan City, Muchuan County, Muchuan Bamboo Sea, 28°51'29"N, 103°56'58"E, elevation 525 m, on dead branches of bamboo, 4 November 2022, X.D. Yu, G42 (HKAS 135141, holotype), ex-type living culture CGMCC 3.27447.



Figure 38 – *Triplosphaeria fusiformis* (HKAS 135166, holotype). a–b Ascomata on host substrate. c–d Vertical sections of ascomata. e Structure of peridium. f Pseudoparaphyses. g–k Asci. l–q Ascospores. r Germinated ascospore. s, t Colony on PDA from above and below. Scale bars: c, d = 100 µm, e–k, r = 20 µm, l–q = 10 µm.

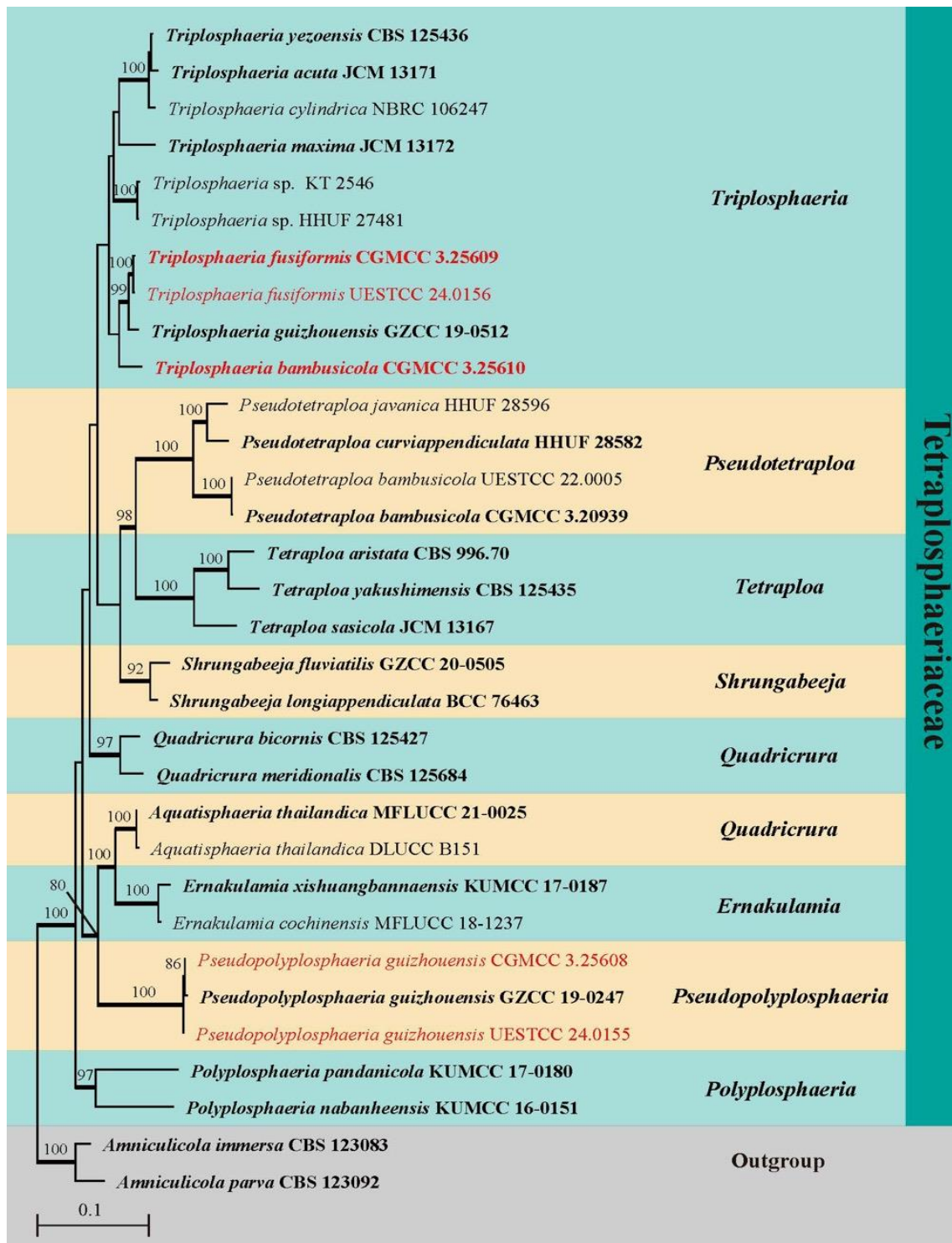


Figure 39 – RAxML tree generated from combined ITS, LSU, SSU, *tub2* and *tef1-α* sequence data of Tetraplosphaeriaceae. The tree was rooted with *Amniculicola parva* (CBS 123092) and *A. immersa* (CBS 123083). Ex-type strains are in bold and newly generated sequences in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

Notes – In the multi-loci phylogenetic analyses, *C. bambusae* (CGMCC 3.27447) clustered as a sister lineage to *C. muriforme* (GZCC 20-0442) (Fig. 60). *Conlarium bambusae* resembles *C. muriforme* in having monoblastic, cylindrical, hyaline to brown conidiogenous cells and subglobose or irregular, brown to dark brown, muriform conidia (Yang et al. 2023). In addition, the

conidia size is also similar ($20\text{--}30 \times 16\text{--}26 \mu\text{m}$ vs. $17\text{--}35 \times 16\text{--}34 \mu\text{m}$). However, ITS comparison between *C. bambusae* and *C. muriforme* showed that there are 10 bp differences (including 3 gaps) in a total of 422 bp, and 23 bp differences in a total of 909 bp for *tef1- α* . Therefore, we identify *C. bambusae* as a novel species following the guidelines for species delineation in Maharachchikumbura et al. (2021).

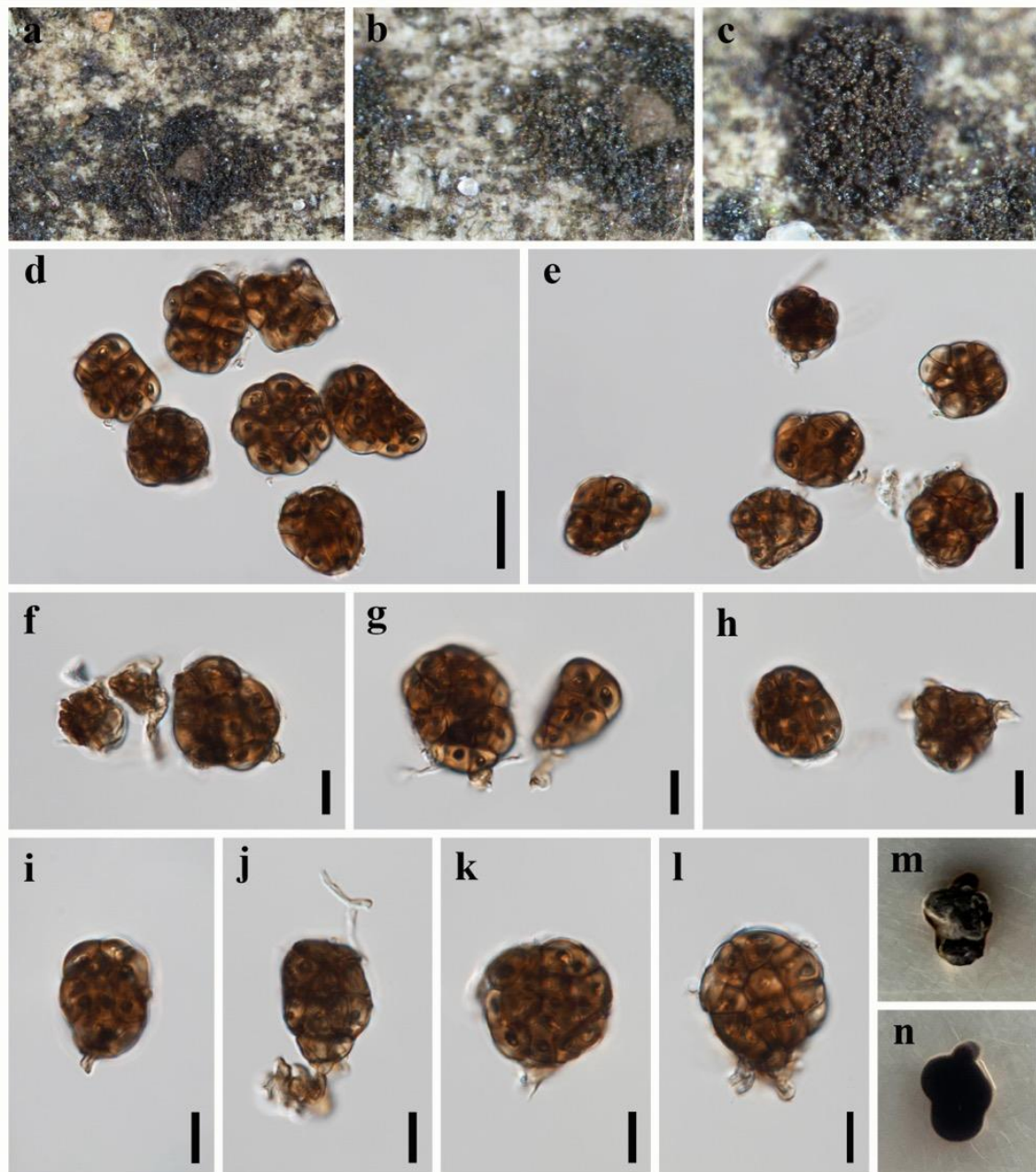


Figure 40 – *Conlarium bambusae* (HKAS 135141; holotype). a–c Colonies. d–l Conidiogenous cells and conidia. m, n Colony on PDA from above and below. Scale bars: d, e = 20 μm , f–l = 10 μm .

Diaporthomycetidae family *incertae sedis*.

Acrodictyaceae J.W. Xia & X.G. Zhang, Scientific Reports 7: 2 (2017)

Mycobank number: MB818894; Facesoffungi number: FoF06600

Notes – Acrodictyaceae was established by Xia et al. (2017) to accommodate *Acrodictys* M.B. Ellis. Members of Acrodictyaceae are saprobic dematiaceous hyphomycetes from terrestrial and freshwater environments (Yang et al. 2023).

Acrodictys M.B. Ellis, Mycological Papers 79: 5 (1961)

MycoBank number: MB7034; Facesoffungi number: FoF06601

Notes – *Acrodictys* was established by Ellis (1961) and typified by *Acrodictys bambusicola* M.B. Ellis, which is characterized by macronematous, mononematous, erect, straight or flexuous conidiophores, monoblastic, integrated, terminal conidiogenous cells, solitary, dry, acrogenous, obovoid to pyriform, muriform conidia (Xia et al. 2017, Hyde et al. 2023).

Acrodictys pyriformis J. Yang, Jian K. Liu & K.D. Hyde, Fungal Diversity 119: 189 (2023)

Fig. 41

MycoBank number: MB559867, Facesoffungi number: FoF12847

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, hairy, dark brown, scattered, glistening. Mycelium mostly immersed. Conidiophores 100–190 × 3–7 µm ($\bar{x}$ = 140 × 5 µm, n = 10), macronematous, mononematous, erect, straight, or slightly curved, cylindrical, septate, smooth-walled, unbranched, dark brown, slightly paler and narrower towards the apex. Conidiogenous cells monoblastic, integrated, terminal, determinate, cylindrical to obclavate, brown, truncate at the apex, sometimes elongating percurrently. Conidia 22–25 × 13.5–14.5 µm ($\bar{x}$ = 23.5 × 14 µm, n = 30), acrogenous, solitary, broadly obovoid to pyriform, muriform, usually with three transverse septa and a longitudinal septum, smooth-walled, pale greyish-green to pale brown, guttulate, slightly constricted at the septa, with conspicuous septal pores, truncate at the base, basal cell obconical, pale brown.

Culture characteristics – Colonies on PDA reaching 20–50 mm after 2 weeks at 25 °C, circular, with dense mycelium on the surface, white; in reverse black at the inner ring, and brown at the outer ring.

Material examined – China, Sichuan Province, Leshan City, Muchuan County, Muchuan Bamboo Sea, 28°51'29"N, 103°56'58"E, elevation 525 m, on dead branches of bamboo, 4 November 2022, X.D. Yu, G47 (HUEST 24.0174), living culture UESTCC 24.0157; *ibid*; G51 (HUEST 24.0175), living culture UESTCC 24.0158.

Notes – In our phylogenetic analyses, our strains *Acrodictys pyriformis* (UESTCC 24.0157 and UESTCC 24.0158) clustered with *A. pyriformis* (GZCC 20-0507) with 100% ML and 1.00 PP statistical support (Fig. 60). Our strains is similar to *A. pyriformis* in having macronematous, mononematous, erect, cylindrical, septate, unbranched conidiophores, acrogenous, solitary, broadly obovoid to pyriform, muriform conidia and the conidial size of our isolates is also similar to *A. pyriformis* (Yang et al. 2023). In addition, the nucleotide comparisons showed that our strains are not significantly different from *A. pyriformis* (GZCC 20-0507) in ITS, SSU, LSU, and *tef1-α*, which indicated that they are the same species. Thus, we identified our strains as *A. pyriformis* and it is a new host and habitat record on bamboo in a terrestrial habitat.

Junewangiaceae J.W. Xia & X.G. Zhang, Scientific Reports 7: 12 (2017)

MycoBank number: MB818897; Facesoffungi number: FoF06602

Notes – Junewangiaceae was established by Xia et al. (2017) and typified by *Junewangia* W.A. Baker & Morgan-Jones, which is characterized by macronematous, cylindrical conidiophores, monoblastic conidiogenous cells with narrow or flaring collarette, and oval, ellipsoidal to spherical conidia. Four genera are accepted in the family, viz. *Dictyosporella* Abdel-Aziz, *Jennwenomyces* Goh & C.H. Kuo, *Junewangia* W.A. Baker & Morgan-Jones and *Sporidesmiella* P.M. Kirk (Goh & Kuo 2020, Hyde et al. 2023).

Dictyosporella Abdel-Aziz, Fungal Diversity 75: 143 (2015)

MycoBank number: MB551480; Facesoffungi number: FoF00973

Notes – *Dictyosporella* was established by Ariyawansa et al. (2015) to accommodate the aquatic hyphomycetous species *D. aquatica* (type species). *Dictyosporella* species are known from China, Egypt and Thailand, most are saprobic on Poaceae in freshwater habitats (Ariyawansa et al.

2015, Zhang et al. 2017, Song et al. 2018, Yuan et al. 2020, Dong et al. 2021, Hyde et al. 2023). We introduce a new terrestrial species to the genus.

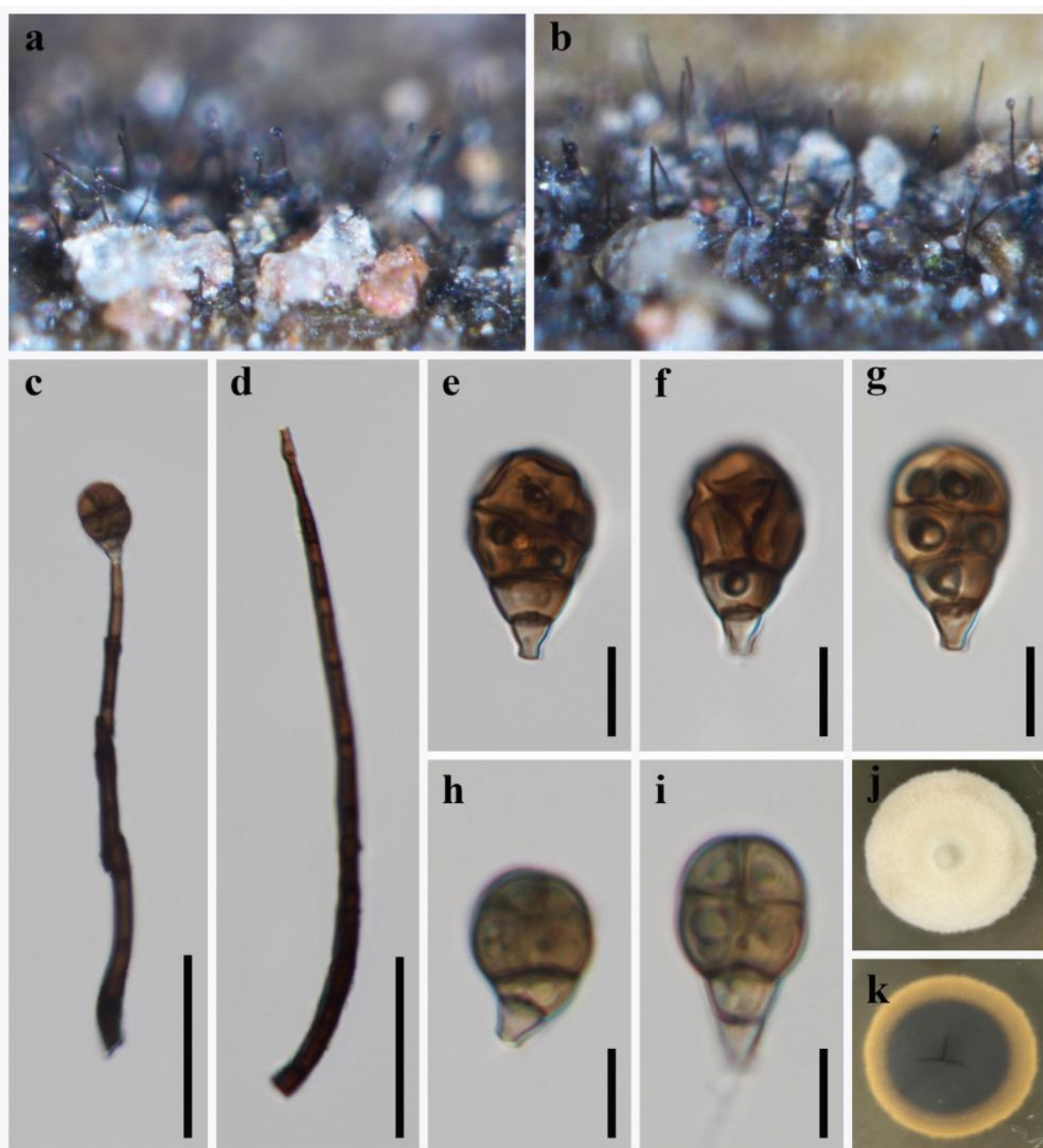


Figure 41 – *Acrodictys pyriformis* (HUEST 24.0174). a–b Colonies. c Conidiophores and conidia. d Conidiophore. e–i Conidia. j, k Colony on PDA from above and below. Scale bars: c–d = 50 μ m, e–i = 10 μ m.

Dictyosporella bambusicola X.D. Yu & Jian K. Liu, sp. nov.

Fig. 42

Mycobank number: MB854894; Facesoffungi number: FoF16588

Etymology – Refers to the bamboo host from which the fungi was found.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate sporodochial, punctiform, raised, gregarious or scattered, black. Mycelium partly immersed, partly superficial, composed of septate, hyaline hyphae. Conidiophores micronematous, mononematous, consisting of subglobose to cylindrical, hyaline to brown cells, smooth, unbranched, septate, constricted at the septa. Conidiogenous cells holoblastic, monoblastic, integrated, determinate, terminal, cylindrical to subglobose, hyaline, smooth, thin-walled. Conidia

14–20 × 10–12 µm ($\bar{x}$ = 17 × 11 µm, n = 50), solitary, acrogenous, ellipsoidal or subglobose, dictyoseptate, smooth, olivaceous to brown, slightly constricted at the septa, with a truncate base, basal cell cuneiform, 2.0–4.0 µm wide, sometimes swollen, hyaline.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 2 weeks at 25 °C, circular, with dense mycelium, raised, entire at the edge, black, reverse grey.

Material examined – China, Sichuan Province, Chengdu City, Tianfu New Area, Dalin Village, 30°16'43"N, 104°6'44"E, elevation 500 m, on dead branches of bamboo, 24 July 2021, X.D. Yu, bamboo4 (HKAS 135152, holotype), ex-type living culture CGMCC 3.27442.

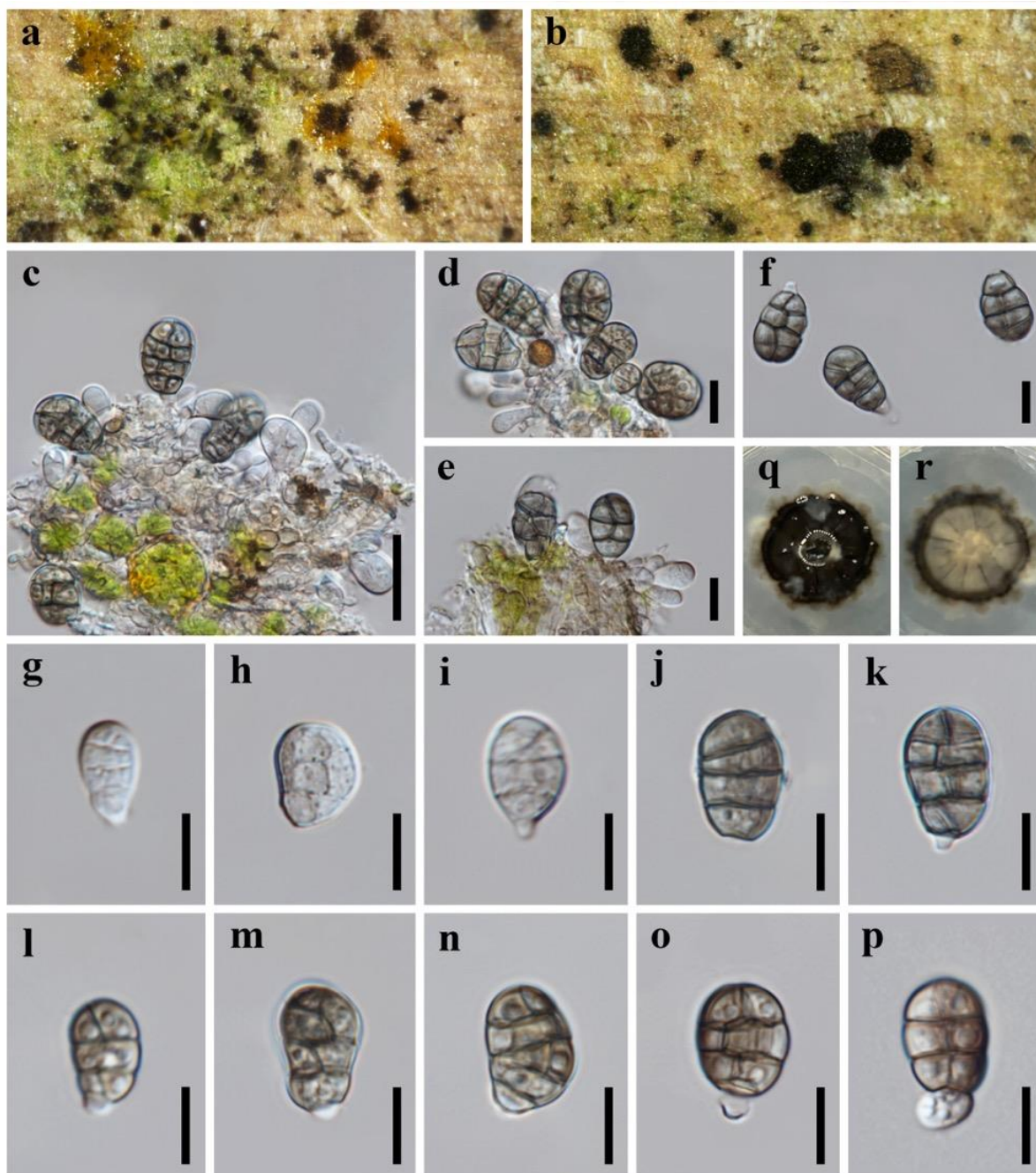


Figure 42 – *Dictyosporiella bambusicola* (HKAS 135152; holotype). a–b Colonies. c–e Conidiophores and conidia. f–o Conidia. p Germinating conidium. q, r Colony on PDA from above and below. Scale bars: c = 20 µm, d–p = 10 µm.

Notes – The phylogenetic analyses based on SSU, ITS, LSU, *rpb2* and *tef1a* sequence data showed that *Dictyosporiella bambusicola* nested in *Dictyosporiella* and formed a distinct lineage

(Fig. 60). *Dictyospora bambusicola* resembles *D. yunnanensis* in having acrogenous, solitary, ellipsoidal or subglobose, dictyoseptate conidia (Hyde et al. 2023). However, they can be easily distinguished by the colour of conidia (olivaceous to brown in *D. bambusicola*, yellow-brown to brown in *D. yunnanensis*). In addition, phylogenetic analysis (Fig. 60) also supports them are distinct species. Establishment of the new species is justified by morphological and phylogenetic evidence.

Neodictyosporiaceae X.D. Yu, K.D. Hyde & Jian K. Liu, fam. nov.

MycoBank number: MB854895; Facesoffungi number: FoF16561

Etymology – Name reflects the type genus.

Type genus – *Neodictyosporium* Tennakoon, C.H. Kuo & K.D. Hyde

Saprobic on dead wood. Sexual morph: *Ascomata* solitary to gregarious, immersed to semi-immersed, subglobose, uni- or multi-loculate. *Peridium* brown, thick-walled. *Paraphyses* hyaline, septate. *Asci* 8-spored, unitunicate, cylindrical, long pedicellate, with an apical ring. *Ascospores* fusiform, septate, with or without a mucilaginous sheath. Asexual morph: Coelomycetes. *Conidiomata* pycnidial, scattered or solitary, superficial, dark brown to black, subglobose. *Conidiomatal* wall thick-walled, brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, cylindrical to subcylindrical, determinate, terminal. *Conidia* two types, Type I: cheirosporous, hyaline to pale brown, consisting of arms, euseptate in each arm, with a basal connecting cell; Type II: clavate to obovoid, hyaline, septate, guttulate, smooth-walled.

Notes – A new family, Neodictyosporiaceae, is introduced to accommodate *Neodictyosporium*. The phylogenetic position (Fig. 60), which is distinct from other families, supports the establishment of the new family within Diaporthomycetidae families *incertae sedis*.

Neodictyosporium Tennakoon, C.H. Kuo & K.D. Hyde, Fungal Diversity 108: 188 (2021)

MycoBank number: MB555756; Facesoffungi number: FoF09377

Type species – *Neodictyosporium macarangae* Tennakoon, C.H. Kuo & K.D. Hyde

Saprobic on dead wood. Sexual morph: *Ascomata* solitary, semi-immersed, visible as black domes on the substrate, subglobose, coriaceous, uni- or multi-loculate. *Peridium* composed of several layers of brown, thick-walled cells of *textura angularis*. *Paraphyses* numerous, hyaline, hyphae-like, septate and unbranched. *Asci* 8-spored, unitunicate, cylindrical, straight or slightly curved, long pedicellate, rounded at the apex, with an apical ring. *Ascospores* ellipsoid-fusiform, hyaline, septate, smooth-walled, with or without a mucilaginous sheath. Asexual morph: See (Tennakoon et al. 2021b).

Notes – The generic type of *Neodictyosporium*, *N. macarangae*, was initially discovered on a dead petiole of *Macaranga tanarius* (Euphorbiaceae) (Tennakoon et al. 2021b). Based on molecular data, the sexual morph of *Neodictyosporium* is reported for the first time in this study, which is characterized by subglobose ascomata, 8-spored, cylindrical, long pedicellate, unitunicate asci and fusiform, septate ascospores. The asexual morph of *Neodictyosporium* resembles *Sirothecium* in forming pycnidoid conidiomata, euseptate and chiroid conidia and consisting of arms (Karsten 1887, Hu et al. 2007). *Sirothecium* species also have been found from bamboo culms (Hu et al. 2007). However, Vijaykrishna et al. (2006) deduced that *Sirothecium* might belong to Pleosporales (Dothideomycetes), while *Neodictyosporium* was placed in a different class based on molecular data (Tennakoon et al. 2021b). For the first time we introduce two new sexual morph species of *Neodictyosporium*, namely, *N. bambusae* and *N. sexuale*, and two new species with asexual morph, introduced based on DNA molecular data.

Neodictyosporium bambusae X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 43

MycoBank number: MB854896; Facesoffungi number: FoF16589

Etymology – Refers to the bamboo host from which the fungi was found.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, immersed, in vertical section 100–200 µm high, 110–190 µm diam., subglobose, coriaceous, multi-

loculate. *Peridium* 15–30 μm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Paraphyses* 2.5–3.5 μm wide, numerous, hyphae-like, unbranched, hyaline, septate, constricted at the septa. *Asci* 100–125 $\times$ 8–10 μm ($\bar{x}$ = 115 $\times$ 9 μm , n = 30), 8-spored, unitunicate, cylindrical, straight or slightly curved, long pedicellate, rounded at the apex, with an apical ring. *Ascospores* 13.5–16.5 $\times$ 4.5–5.5 μm ($\bar{x}$ = 15 $\times$ 5 μm , n = 50), overlapping, uniseriate, ellipsoid-fusiform, hyaline, 0–3-septate, smooth-walled, thin-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

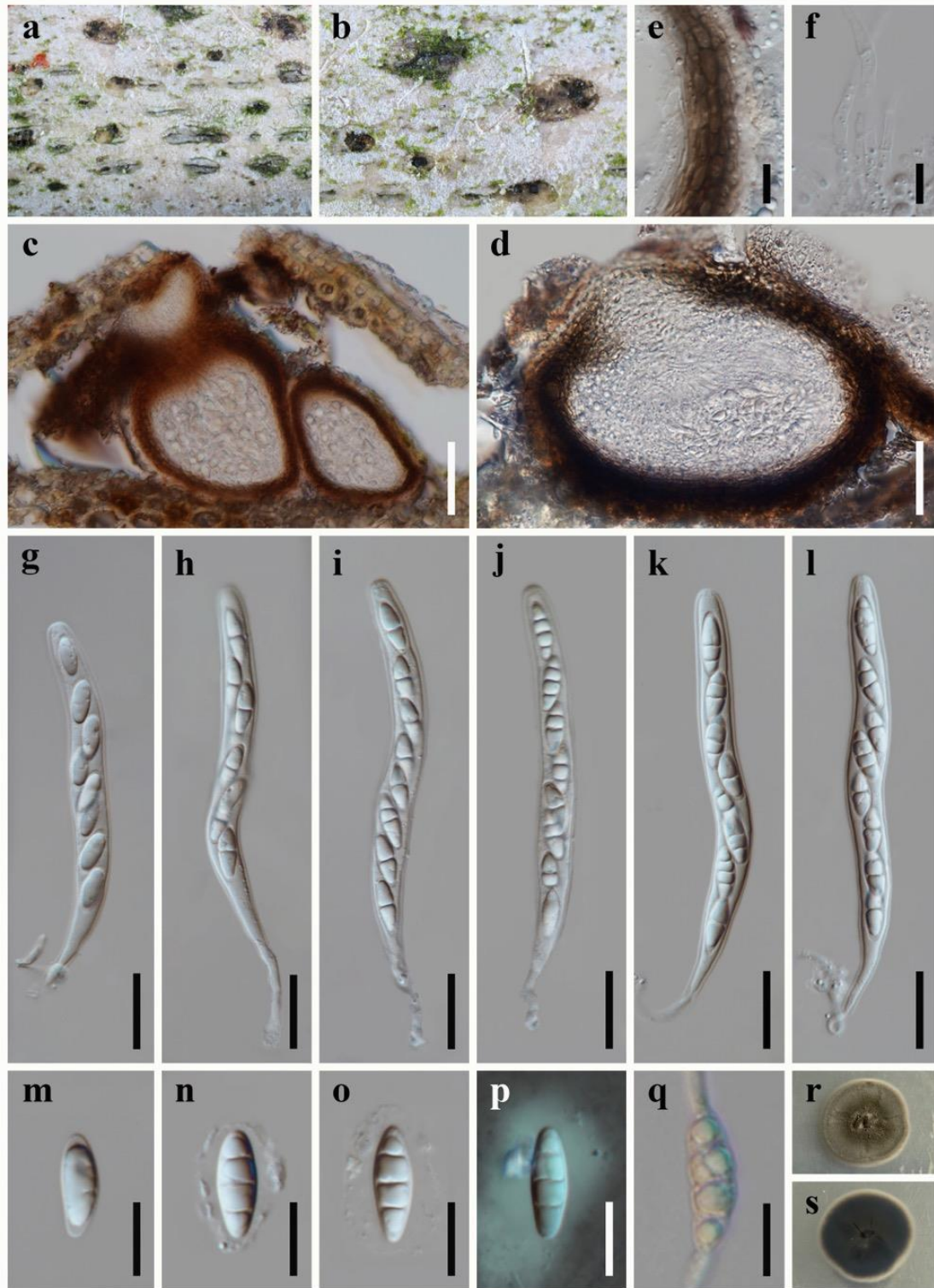


Figure 43 – *Neodictyosporium bambusae* (HKAS 135151; holotype). a–b Ascomata on host substrate. c–d Vertical sections of ascomata. e Peridium. f Paraphyses. g–l Asci. m–o Ascospores.

p Ascospore with mucilaginous sheath. q Germinated ascospore. r, s Colonies on PDA from above and below. Scale bars: c = 50 μ m, d = 30 μ m, e–f, m–q = 10 μ m, g–l = 20 μ m.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, grey, reverse dark.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan County, Qingcheng Mountain, 30°54'29"N, 103°32'36"E, 960 m, on dead branches of bamboo, 2 December 2021, X.D. Yu, B5-new (HKAS 135151, holotype); ex-type living culture CGMCC 3.27440; *ibid*: B5-1 (HUEST 24.0176); living culture UESTCC 24.0159; *ibid*: B5 (HUEST 24.0116); living culture UESTCC 24.0111.

Neodictyosporium cheirosporum X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 44

MycoBank number: MB854898; Facesoffungi number: FoF16590

Etymology – The name refers to the cheiroid conidia.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 70–160 μ m high, 80–140 μ m diam., pycnidial, solitary, scattered, superficial, dark brown to black, uniloculate, thick-walled, lying horizontal to the host surface. *Conidiomatal wall* 20–40 μ m wide, composed of thick-walled, brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth-walled. *Conidia* 23–30 $\times$ 13–25 μ m ($\bar{x}$ = 27 $\times$ 20 μ m; n = 30), solitary, hyaline to pale brown, claw-shaped, cheiroid, smooth-walled, consisting of 3–5 arms, 21–30 $\times$ 4–5.5 μ m ($\bar{x}$ = 25 $\times$ 4.5 μ m; n = 30), 4–6-euseptate in each arm, with a basal connecting cell and two divergent basal cells at both sides, which are obpyriform and hyaline.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, black, reverse dark.

Material examined – China, Sichuan Province, Meishan City, Qingshen County, Bamboo Forest Wetland Park, 29°48'43"N, 103°49'26" E, elevation 400 m, on dead branches of bamboo, 4 November 2022, X.D. Yu, J17-new (HKAS 135128, holotype), ex-type living culture CGMCC 3.27450; *ibid*: J17 (HUEST 24.0126); living culture UESTCC 24.0121.

Notes – The phylogenetic analyses based on SSU, ITS, LSU, *rpb2* and *tef1- α* sequence data showed that the new collection nested in *Neodictyosporium* (Fig. 60) and formed a distinct lineage to *N. macarangae* (type species). *Neodictyosporium cheirosporum* is similar to *N. macarangae* in having pycnidoid conidiomata, holoblastic, integrated, brown conidiogenous cells and euseptate, cheiroid conidia consisting of arms (Tennakoon et al. 2021b). However, the latter has two conidia types that were not observed in *N. cheirosporum*. Therefore, the new species is justified by morphology and phylogenetic evidence.

Neodictyosporium sexuale X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 45

MycoBank number: MB854899; Facesoffungi number: FoF16591

Etymology – ‘*Sexuale*’ referring to it forming a sexual morph.

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary, semi-immersed, visible as black domes on the substrate, in vertical section 100–120 μ m high, 130–160 μ m diam., subglobose, coriaceous, uniloculate. *Peridium* 14–22 μ m wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Paraphyses* 3–4 μ m wide, hyaline, numerous, hyphae-like, septate and unbranched. *Asci* 90–130 $\times$ 9–11 μ m ($\bar{x}$ = 110 $\times$ 10 μ m, n = 30), 8-spored, unitunicate, cylindric, straight or slightly curved, long pedicellate, rounded at the apex, with an apical ring. *Ascospores* 15–18 $\times$ 6–7 μ m ($\bar{x}$ = 16 $\times$ 6.5 μ m, n = 50), overlapping, uniseriate, fusiform to elliptical, straight, rarely slightly curved, hyaline, 0–3-septate, smooth-walled, thin-walled, without mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, grey, reverse dark.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan County, Qingcheng Mountain, 30°54'29"N, 103°32'36"E, 960 m, on dead branches of bamboo in terrestrial habitat, 2 December 2021, X.D. Yu, B11 (HKAS 135154, holotype); ex-type living culture CGMCC 3.27441; *ibid*: B11-new (HUEST 24.0117); living culture UESTCC 24.0112.

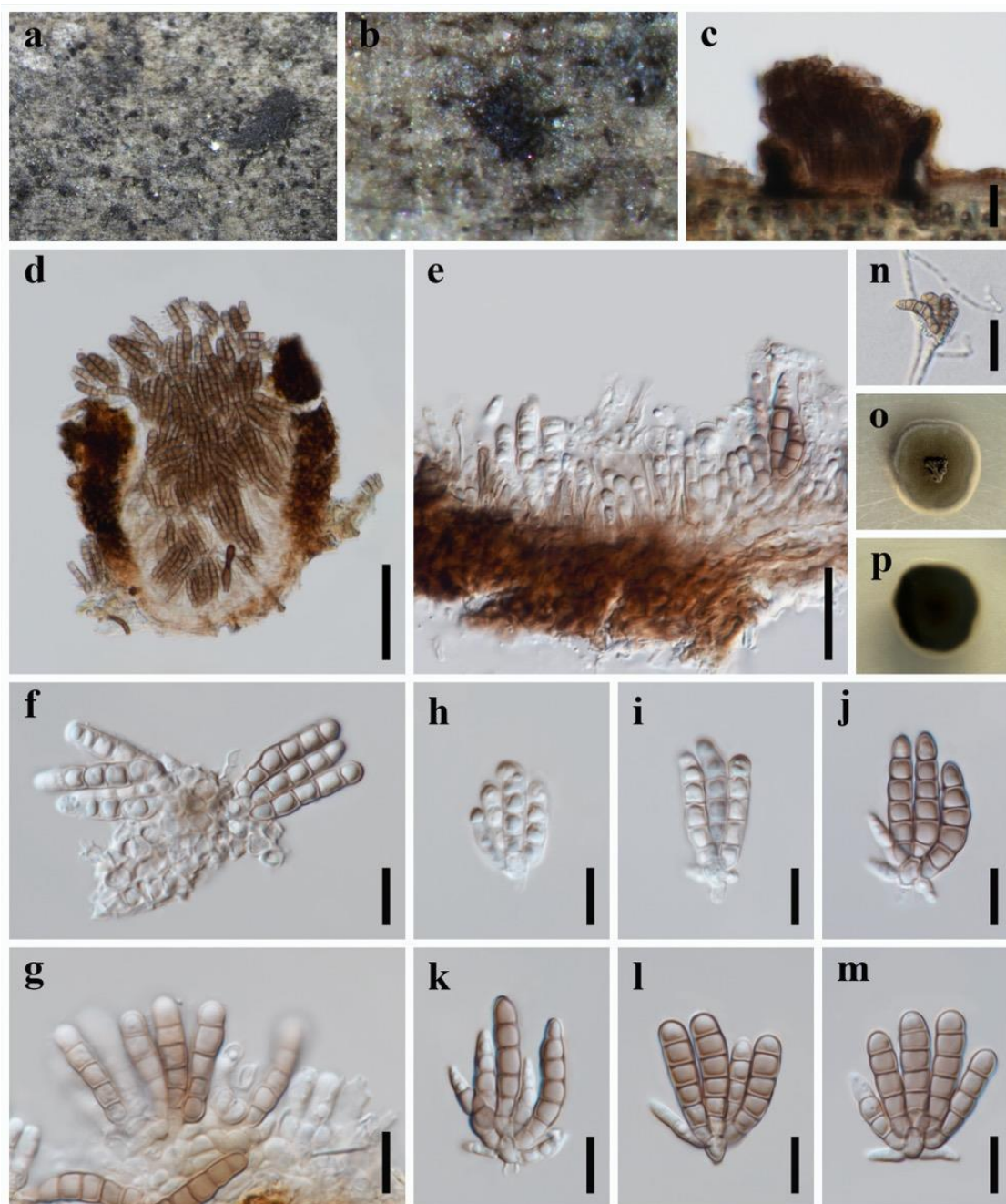


Figure 44 – *Neodictyosporium cheirosporum* (HKAS 135128; holotype). a–b Conidiomata on surface of dead bamboo culms. c–d Vertical section of conidioma. e–g Conidiogenous cells and developing conidia. h–m Conidia. n Germinating conidium. o, p Colony on PDA from above and below. Scale bars: c, e, n = 20 μ m, d = 50 μ m, f–m = 10 μ m.

Notes – Multi-gene phylogenetic analysis showed that our isolates belong to *Neodictyosporium* and are closely related to *N. macarangae* (Fig. 60). However, we were not able to compare their morphology as the latter species is only represented by a coelomycetous asexual morph. Nevertheless, *N. sexuale* differs from *N. macarangae* in their nucleotide sequences, viz. SSU (1/437) and LSU (15/802), respectively. *Neodictyosporium sexuale* resembles *N. bambusae* in

having 8-spored, unitunicate, cylindric, long pedicellate asci, and uniseriate, fusiform to elliptical, hyaline ascospores. However, *N. sexuelle* differs from the latter in having semi-immersed, uniloculate ascomata, and ascospores without a mucilaginous sheath. Moreover, the two species are phylogenetically distinct (Fig. 60).

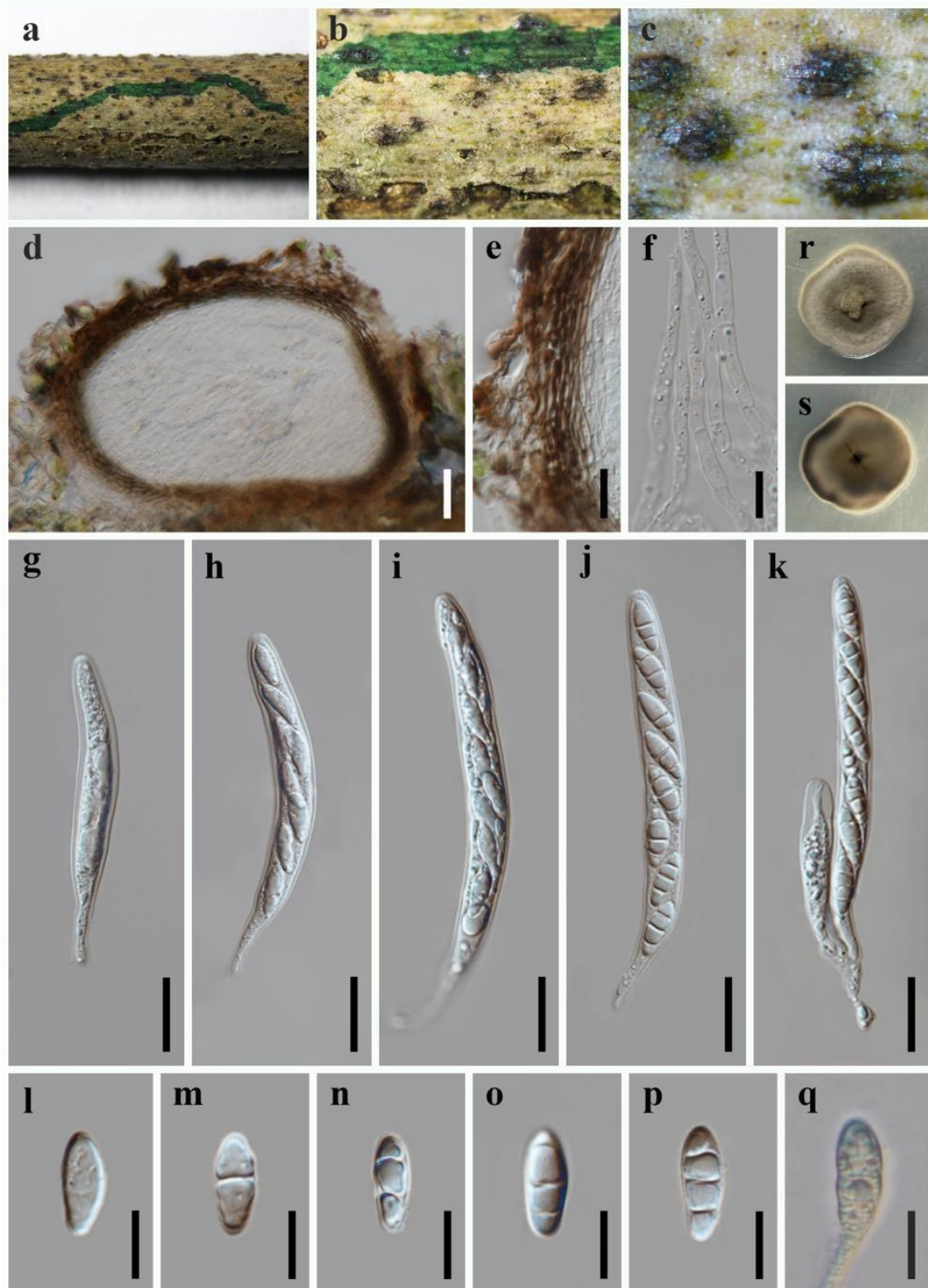


Figure 45 – *Neodictyosporium sexuelle* (HKAS 135154; holotype). a–c Ascomata on host substrate. d Vertical section of ascoma. e Peridium. f Paraphyses. g–k Asci. l–p Ascospores. q Germinated ascospore. r, s Colonies on PDA from above and below. Scale bars: d = 20 µm, e–f, l–q = 10 µm, g–k = 20 µm.

Neodictyosporium sichuanense X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 46

Mycobank number: MB854900; Facesoffungi number: FoF16592

Etymology – The epithet refers to Sichuan Province where the fungus was collected.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 60–100 µm high, 110–180 µm diam., pycnidial, scattered, solitary, superficial, dark brown to black, uniloculate, thick-walled, lying horizontal to the host surface. *Conidiomatal wall* 15–40 µm wide, composed of thick-walled, brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth-walled. *Conidia* 15–25 × 14–20 µm ($\bar{x}$ = 20 × 16.5 µm; n = 30), solitary, hyaline to pale brown, claw-shaped, cheiroid, smooth-walled, consisting of 3–5 arms, 12–21 × 3.5–5.5 µm ($\bar{x}$ = 16 × 4.5 µm; n = 30), 1–4-euseptate in each arm, with a basal connecting cell, and two divergent basal cells at both sides, which are obpyriform and hyaline.

Culture characteristics – Colonies on PDA reaching 10–20 mm after 2 weeks at 25 °C, circular, raised to umbonate, surface rough, dry, dense, greyish-yellow.

Material examined – China, Sichuan Province, Ziyang City, Le Zi County, Jinmasi Village, 30°19'55"N, 105°2'40" E, elevation 540 m, on dead branches of bamboo, 22 April 2023, X.D. Yu, K28 (HKAS 135140, holotype), ex-type living culture CGMCC 3.27593; *ibid*: K28-new (HUEST 24.0152); living culture UESTCC 24.0136.

Notes – *Neodictyosporium sichuanense* clustered with *N. cheirosporum* with 94% ML/1.00 BYPP bootstrap support (Fig. 60). However, they formed separate branches in the multi-gene phylogeny and could be recognized as different species. The comparison of molecular data of *N. sichuanense* and *N. cheirosporum* showed that there are 2% (9/453) nucleotide differences in ITS and 0.3% (3/899) in *tef1-α* gene regions. *Neodictyosporium sichuanense* differs from *N. cheirosporum* in having relatively smaller conidia (15–25 × 14–20 vs. 23–30 × 13–25) and the number of septa in each arm (1–4-euseptate vs. 4–6-euseptate). The morphological and phylogenetic differences support the delineation of *N. sichuanense* as a new species.

Pseudostanjeughesiaceae K.D. Hyde & Hongnan, Fungal Diversity 107: 96 (2017)

Mycobank number: MB557990; Facesoffungi number: FoF09420

Notes – Pseudostanjeughesiaceae was established by Hyde et al. (2021a) and typified by *Pseudostanjeughesia* J. Yang & K.D. Hyde, which is characterized by macronematous, mononematous, solitary, cylindrical conidiophores, monoblastic, integrated, terminal, brown conidiogenous cells, and acrogenous, solitary, fusiform or obclavate, septate, mid to dark brown conidia (Hyde et al. 2021a). Taxonomically, this family belongs to Diaporthomycetidae family *incertae sedis* in Sordariomycetes, and the divergence time of this family has a stem age of 111 MYA (Hyde et al. 2021). Members of this family are generally saprobic fungi on decaying wood submerged in a freshwater stream (Yang et al. 2018, Luo et al. 2019).

Nigroconidius X.D. Yu, K.D. Hyde & Jian K. Liu, gen. nov.

Mycobank number: MB854901; Facesoffungi number: FoF16568

Etymology – Referring to the black conidia.

Type species – *Nigroconidius bambusae* X.D. Yu, K.D. Hyde & Jian K. Liu

Saprobic on dead wood. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, black. *Mycelium* superficial. *Conidiophores* micronematous, mononematous, cylindrical or reduced to conidiogenous cells, aseptate and unbranched. *Conidiogenous cells* holoblastic, monoblastic, cuneiform, integrated, terminal, determinate, hyaline. *Conidia* solitary, acrogenous, septate, pyriform to obovoid, brown to black, broadly rounded at apex, truncate at the base, smooth-walled.

Notes – The phylogenetic analysis showed that seven isolates of *Nigroconidiis* formed a monophyletic clade in Pseudostanjeughesiaceae, closely related to the genus *Pseudostanjeughesia* (*P. aquitropica* and *P. lignicola*) (Fig. 60). *Nigroconidiis* is distinguished from *Pseudostanjeughesia* by its pyriform to obovoid, brown to black, septate conidia (Yang et al.

2018). Thus, *Nigroconidiis* is introduced as a new genus within Pseudostanjehughesiaceae based on morphology and multigene phylogeny.

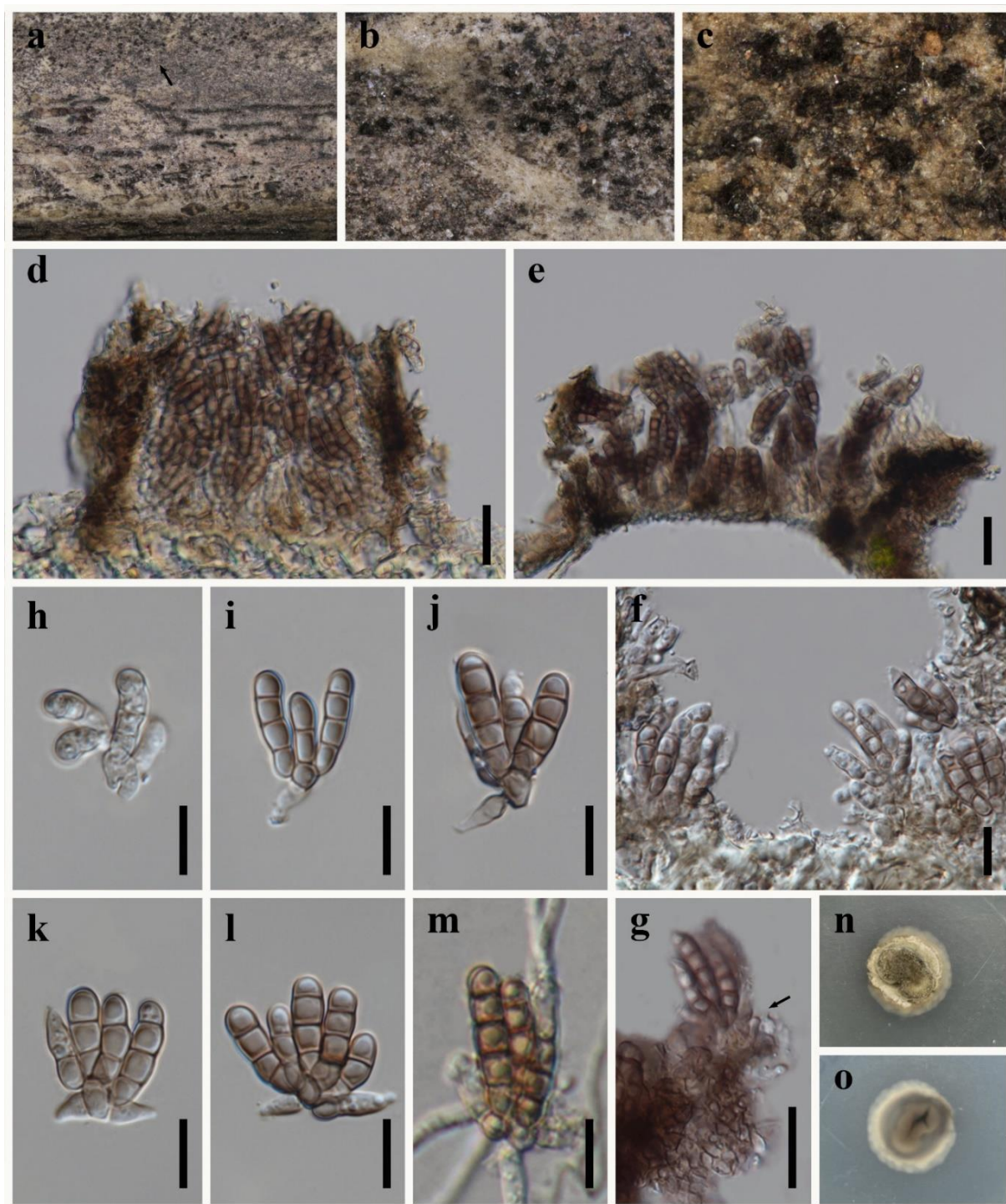


Figure 46 – *Neodictyosporium sichuanense* (HKAS 135140; holotype). a–c Conidiomata on surface of dead bamboo culms. d–e Vertical sections of conidioma. f–g Conidiogenous cells and developing conidia. h–l Conidia. m Germinating conidium. n, o Colony on PDA from above and below. Scale bars: d, e, g = 20 µm, f, h–m = 10 µm.

Nigroconidius bambusae X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Mycobank number: MB854902; Facesoffungi number: FoF16593

Etymology – The epithet “bambusae” from *Bambusa*, refers to the host, on which the holotype was collected.

Fig. 47

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, black. Mycelium superficial. Conidiophores micronematous, mononematous, cylindrical, unbranched, aseptate or reduced to conidiogenous cells. Conidiogenous cells holoblastic, monoblastic, cuneiform, integrated, terminal, determinate, hyaline. Conidia $32\text{--}52 \times 14\text{--}26 \mu\text{m}$ ($\bar{x} = 42 \times 20 \mu\text{m}$, $n = 50$), solitary, acrogenous, septate, pyriform and becoming brown towards the apex and paler towards the base when young, obovoid and black when mature, broadly rounded at apex, truncate at the base, smooth-walled.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, light grey at the inner ring, and olive green at the outer ring; reverse black.

Material examined – China, Sichuan Province, Leshan City, Muchuan County, Muchuan Bamboo Sea, 28°51'29"N, 103°56'58"E, elevation 525 m, on dead branches of *Bambusa* sp., 4 November 2022, X.D. Yu, G37 (HKAS 135142, holotype), ex-type living culture CGMCC 3.27446; China, Sichuan Province, Yibin City, Shunan Bamboo Sea, 28°28'26"N, 104°58'14"E, elevation 570 m, on dead branches of bamboo, 21 April 2023, X.D. Yu, N15 (HUEST 24.0177), living culture UESTCC 24.0160; *ibid*; N18 (HUEST 24.0178), living culture UESTCC 24.0161.

Notes – Three of our *Nigroconidius bambusae* isolates clustered together and were almost identical in their SSU, ITS, LSU, *rpb2* and *tef1a* sequence data, which indicated they can be recognized as a single species. *N. bambusae* was found on dead branches of bamboo in terrestrial habitats.

Nigroconidius septatus X.D. Yu, K.D. Hyde & Jian K. Liu, sp. nov.

Fig. 48

MycoBank number: MB854903; Facesoffungi number: FoF16594

Etymology – ‘*Septatus*’ referring to ‘septate’ conidia.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, black. Mycelium superficial. Conidiophores micronematous, mononematous, cylindrical, unbranched, aseptate or reduced to conidiogenous cells. Conidiogenous cells holoblastic, monoblastic, cuneiform, integrated, terminal, determinate, hyaline. Conidia $25\text{--}50 \times 10\text{--}25 \mu\text{m}$ ($\bar{x} = 35 \times 18 \mu\text{m}$, $n = 50$), solitary, acrogenous, septate, pyriform, brown towards the apex and paler towards the base when young, obovoid and black when mature, broadly rounded at apex, truncate at the base, smooth-walled.

Culture characteristics – Colonies on PDA reaching 40–50 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, black, reverse dark brown to black.

Material examined – China, Sichuan Province, Zigong City, Rong County, Hualonggou Bamboo Sea, 29°28'52" N, 104°17'20" E, elevation 625 m, on dead branches of bamboo, 3 November 2022, X.D. Yu, H32 (HKAS 135149, holotype), ex-type living culture CGMCC 3.27449; *ibid*. H16 (HUEST 24.0179); living culture UESTCC 24.0162; *ibid*. H20 (HUEST 24.0180); living culture UESTCC 24.0163; *ibid*. H27 (HUEST 24.0181); living culture UESTCC 24.0164.

Notes – The phylogenetic analyses showed that four isolates of *Nigroconidius septatus* and *N. bambusae* formed a sister clade with 100% ML/1.00 BYPP statistical support (Fig. 60) in Pseudostanzhughesiaceae. *Nigroconidiis septatus* resembles *N. bambusae* in forming dematiaceous, pyriform to obovoid, brown to black conidia. However, *N. septatus* has relatively smaller conidia than that of *N. bambusae* ($35 \times 18 \mu\text{m}$ vs. $42 \times 20 \mu\text{m}$). We hereby introduce the new species based on the distinctiveness of morphology and multi-gene phylogeny.

Distoseptisporales Z.L. Luo, H.Y. Su & K.D. Hyde, Fungal Diversity 99: 482 (2019)

Distoseptisporaceae K.D. Hyde & McKenzie, Fungal Diversity 80: 402 (2016)

MycoBank number: MB551850; Facesoffungi number: FoF01754

Notes – Distoseptisporaceae was established as a monotypic family to accommodate the type genus *Distoseptispora* based on strong molecular evidence and morphological investigation (Su et al. 2016). Wijayawardene et al. (2018) assigned Distoseptisporaceae in Diaporthomycetidae

families *incertae sedis*. Subsequently, Luo et al. (2019) introduced Distoseptisporales to accommodate Distoseptisporaceae.

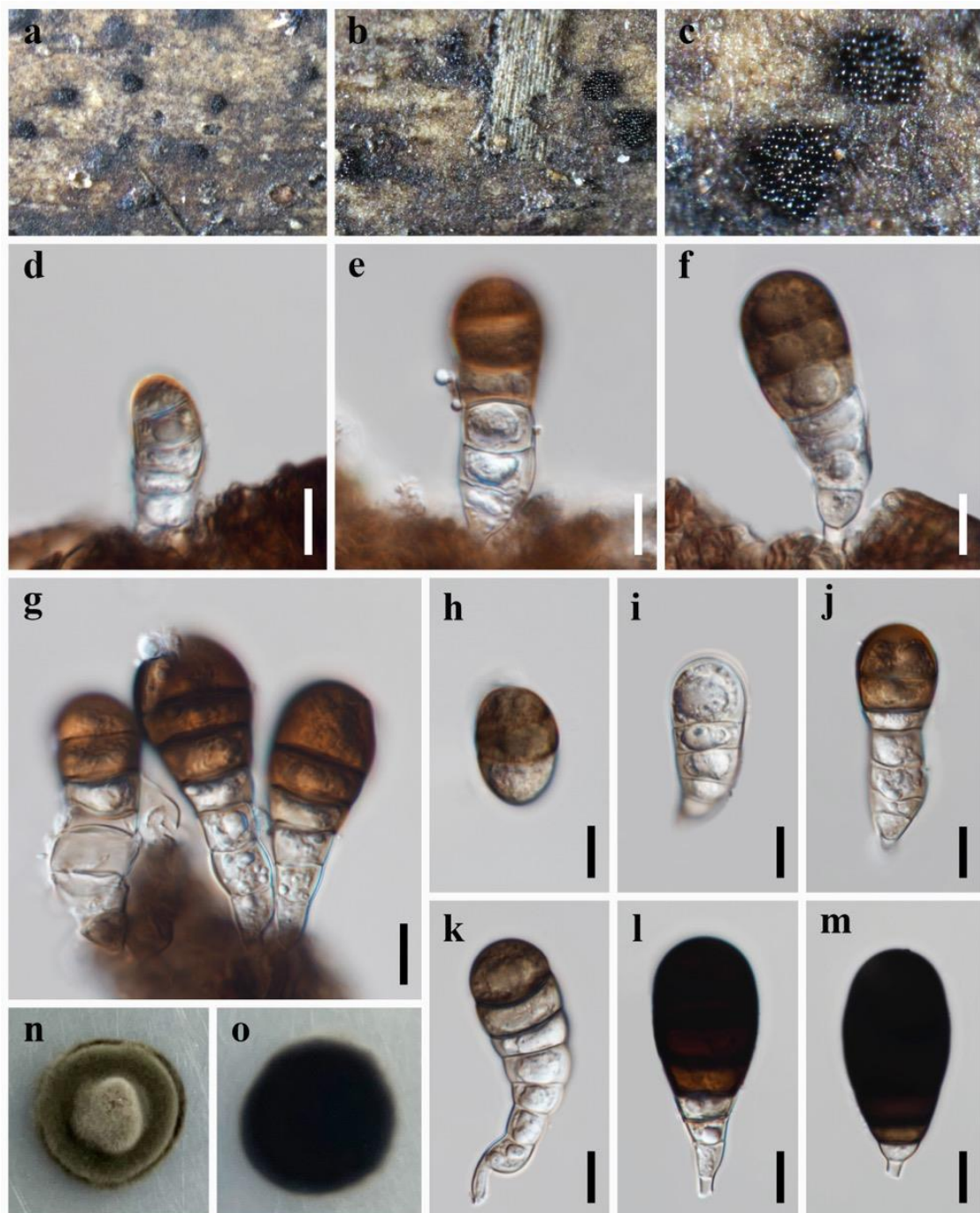


Figure 47 – *Nigroconidius bambusae* (HKAS 135142; holotype). a–c Colonies. d–g Conidiophores and conidia. h–m Conidia. n, o Colony on PDA from above and below. Scale bars: d–m = 10 μ m.

Distoseptispora K.D. Hyde, McKenzie & Maharachch., Fungal Diversity 80: 402 (2016)

Mycobank number: MB551833; Facesoffungi number: FoF01755

Notes – The hyphomycetous genus *Distoseptispora* was introduced by Su et al. (2016) with *D. fluminicola* McKenzie, Hong Y. Su, Z.L. Luo & K.D. Hyde., as the type species. Members of *Distoseptispora* are characterized by solitary or gregarious, immersed to semi-immersed, subglobose to ellipsoidal, dark brown ascomata with a short neck, and hyaline, septate ascospores with a mucilaginous sheath (Yang et al. 2021). In addition, they are dematiaceous hyphomycetes,

which produce macronematous conidiophores, percurrent, elongate conidiogenous cells, olivaceous, brown, yellowish, or reddish-brown, euseptate or distoseptate conidia, and rarely muriform conidia (Su et al. 2016, Hyde et al. 2021b, Jayawardena et al. 2023, Konta et al. 2023). Based on molecular DNA data, Yang et al. (2021) reported *Distoseptispora hyalina* J. Yang and K.D. Hyde, as the first sexual morph species of this genus.

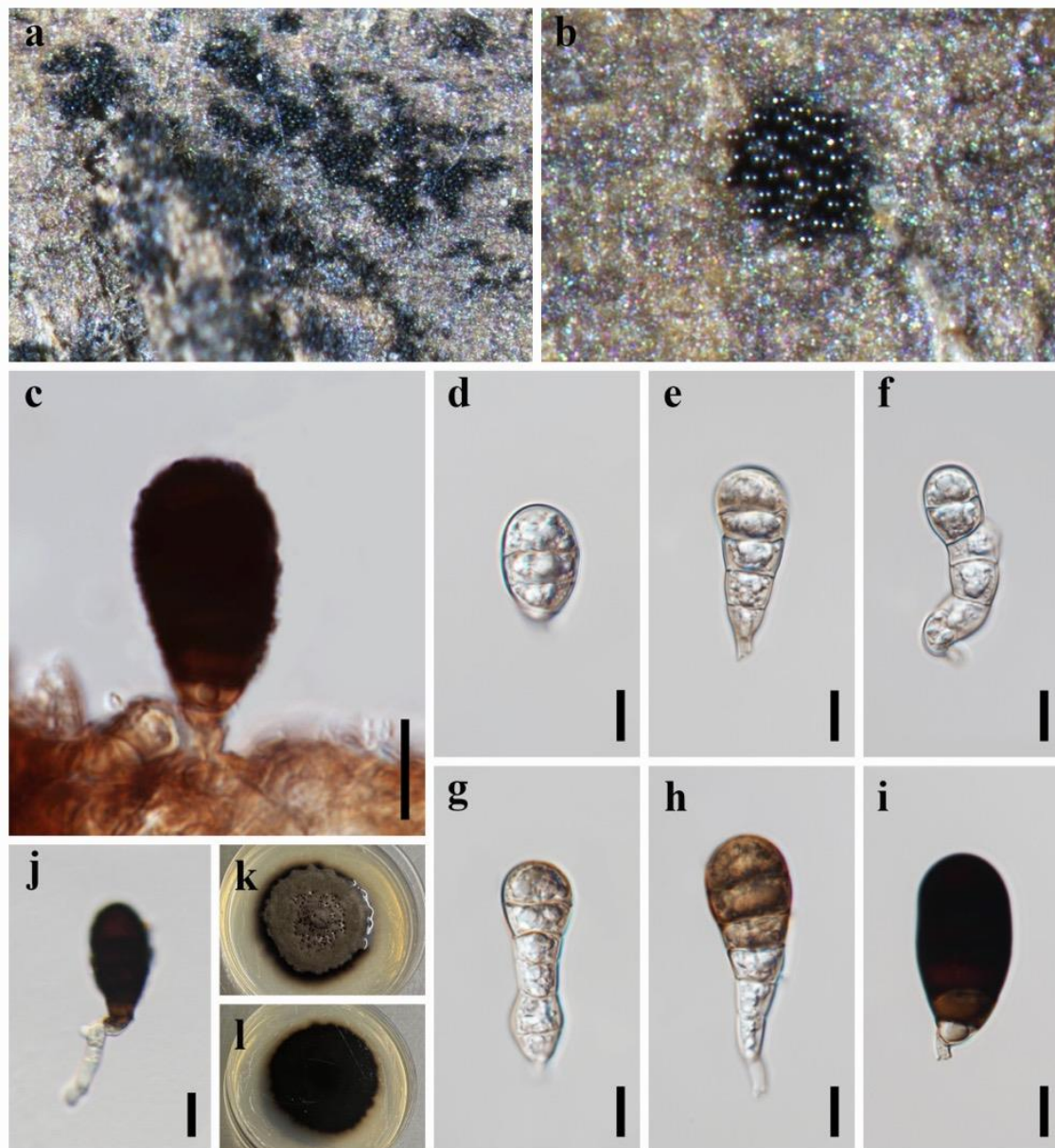


Figure 48 – *Nigroconidiis septatus* (HKAS 135149; holotype). a–b Colonies. c Conidiophore and conidium. d–i Conidia. j Germinating conidium. k, l Colony on PDA from above and below. Scale bars: c–j = 10 μ m.

Distoseptispora aquamyces R. Zhu & Huang Zhang, Journal of Fungi 8: 10 (2022)

Fig. 49

Mycobank number: MB559919; Facesoffungi number: FoF12576

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate superficial, effuse, scattered, hairy, black. Mycelium partly superficial, partly immersed, composed of branched, septate, smooth, hyaline to pale-brown hyphae. Conidiophores 75–240 $\times$ 5–8 μ m ($\bar{x}$ = 150 $\times$ 6.5 μ m, n = 10), macronematous, mononematous, unbranched, septate, cylindrical, straight or slightly flexuous, smooth, dark-brown. Conidiogenous cells monoblastic, integrated, determinate, terminal, cylindrical, brown, smooth.

Conidia 65–130 × 7–14 µm ($\bar{x}$ = 95 × 11 µm, n = 30), acrogenous, dry, obclavate to obpyriform, mostly rostrate, straight or curved, (4–)6–9(–10)-euseptate, tapering towards the rounded apex, thin-walled, brown at the base, subhyaline to pale-brown at the apex, verrucose.

Culture characteristics – Colonies on PDA reaching 50–60 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, white grey, reverse dark.

Material examined – China, Sichuan Province, Yibin City, Gao County, Dawu Village, 28°39'47"N, 104°36'50" E, elevation 610 m, on dead branches of bamboo, 21 April 2023, X.D. Yu, K2 (HUEST 24.0182), living culture UESTCC 24.0165.

Notes – *Distoseptispora aquamyces* was introduced by Zhang et al. (2022) from submerged wood in Sichuan Province, China. The new collection clustered with *D. aquamyces* in the multi-gene phylogeny (Fig. 60), and shares similar conidiogenous cells and conidial morphology. Therefore, we identify our collection as *D. aquamyces* and an additional bamboo host and habitat record is provided.

***Distoseptispora atroviridis* J. Yang & K.D. Hyde, Journal of Fungi 7: 10 (2021)**

Fig. 50

MycoBank number: MB558671; Facesoffungi number: FoF10252

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, dark brown to black, scattered or in small groups, glistening. Mycelium mostly immersed, composed of septate, smooth-walled, hyaline to brown hyphae. Conidiophores 135–150 × 4–7 µm ($\bar{x}$ = 145 × 5.5 µm, n = 10), macronematous, fasciculate, loosely compact, erect, straight or slightly flexuous, cylindrical, wider and truncate at the apex, smooth-walled, septate, unbranched, brown, slightly paler at the apical cell. Conidiogenous cells monoblastic, integrated, terminal, determinate, sometimes elongating percurrently, flared, pale brown. Conidia 35–45 × 18–22 µm ($\bar{x}$ = 40 × 20 µm, n = 30), solitary, ellipsoidal to obovoid, dark green, subhyaline at the basal cell, 6-septate, smooth-walled, guttulate, truncate at the base.

Culture characteristics – Colonies on PDA reaching 50–60 mm after 2 weeks at 25 °C, circular, dry, raised, entire at the edge, white at the inner ring, and grey at the outer ring; reverse dark.

Material examined – China, Sichuan Province, Leshan City, Muchuan County, MuChuan Bamboo Sea, 28°51'29" N, 103°56'58" E, 525 m elevation, on dead branches of bamboo in a terrestrial habitat, 4 November 2022, X.D. Yu, G4 (HUEST 24.0183); living culture UESTCC 24.0166.

Notes – Phylogenetic analyses of combined SSU, ITS, LSU, *rpb2* and *tef1-a* sequence data demonstrated that our strain (UESTCC 24.0166) clustered with the ex-type of *Distoseptispora atroviridis* (GZCC 20-0511) (Fig. 60). It resembles the holotype of *D. atroviridis* in having monoblastic, integrated, pale brown conidiogenous cells and solitary, ellipsoidal to obovoid, dark green conidia (Yang et al. 2021). Based on both phylogeny and morphology, our strain is identified as *D. atroviridis*, a new host and habitat record from bamboo in terrestrial habitat.

***Distoseptispora chengduensis* X.D. Yu & Jian K. Liu, sp. nov.**

Fig. 51

MycoBank number: MB854904; Facesoffungi number: FoF16595

Etymology – Name refers to Chengdu, the city where the fungus was collected.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate superficial, effuse, black, hairy, solitary or gregarious. Mycelium immersed, composed of septate, hyaline to brown hyphae, smooth-walled. Conidiophores 90–130 × 4–6 µm ($\bar{x}$ = 110 × 5 µm, n = 10), macronematous, mononematous, solitary or in groups, erect, straight or slightly flexuous, cylindrical, brown, paler at the apical cell, septate, unbranched, smooth-walled. Conidiogenous cells monoblastic, terminal, determinate, subcylindrical, pale brown, smooth-walled. Conidia 40–80 × 8–12 µm ($\bar{x}$ = 65 × 9.5 µm, n = 30), acrogenous, solitary, obclavate, truncate at base, tapering towards the apex, straight or slightly curved, brown, 1–5-distoseptate, smooth.

Culture characteristics – Colonies on PDA reaching 50–60 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, black at the inner ring, and grey at the outer ring; reverse dark.

Material examined – China, Sichuan Province, Qionglai City, Lugou Bamboo Sea, 30°22'37"N, 103°16'45"E, elevation 730 m, on dead branches of bamboo, 12 October 2021, X.D. Yu, A45 (HKAS 135129, holotype), ex-type living culture CGMCC 3.27439.



Figure 49 – *Distoseptispora aquamyces* (HUEST 24.0182). a–b Colonies. c–d Conidiophores and conidia. e–i Conidia. j Germinating conidium. k, l Colony on PDA from above and below. Scale bars: c–d = 50 μ m, e–j = 20 μ m.

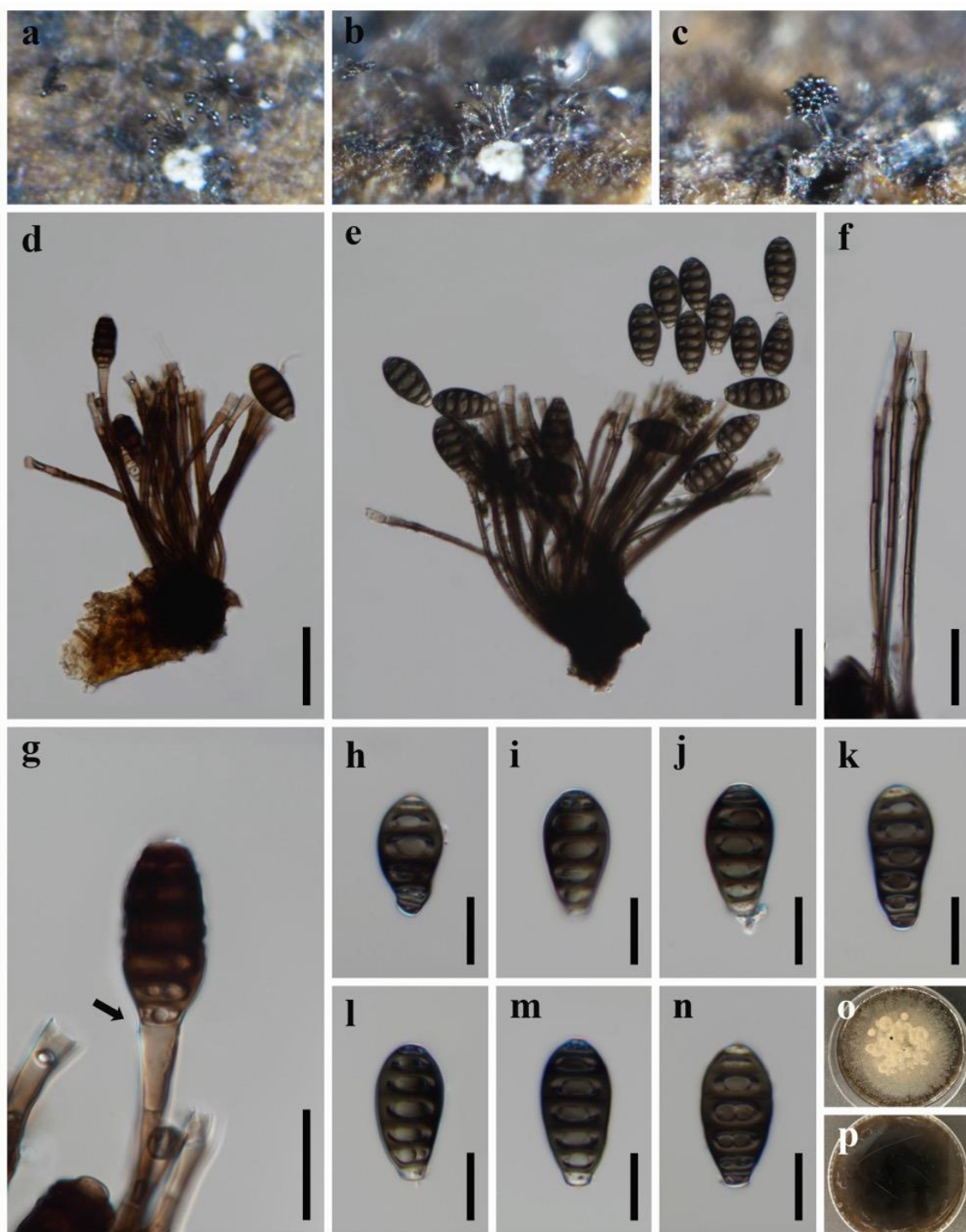


Figure 50 – *Distoseptispora atroviridis* (HUEST 24.0183). a–c Colonies. d–e Conidiophores and conidia. f Conidiophores. g Conidiogenous cells. h–n Conidia. o, p Colony on PDA from above and below. Scale bars: d–e = 50 μ m, f = 30 μ m, g–n = 20 μ m.

Notes – One strain of *Distoseptispora chengduensis* (CGMCC 3.27439) clustered with *D. xinpingensis* (KUNCC 22-12667) with 95% ML/1.00 BYPP statistical support (Fig. 60). *Distoseptispora chengduensis* resembles *D. xinpingensis* in having acrogenous, solitary, obclavate, brown conidia (Shen et al. 2024). However, they can be easily distinguished by the number of septa (1–5-euseptate vs. 8–12-euseptate) and conidial size (40–80 $\times$ 8–12 μ m vs. (95–)107–139(–155) $\times$ (7–)8–9(–10)). Comparison of the ITS and *tef1-a* sequences of *D. chengduensis* and *D. xinpingensis* (KUNCC 22-12667) showed 96.5% (473/490bp, including 4 gaps) and 98.0%

(698/712bp) sequence similarity, respectively. Therefore, the new species *D. chengduensis* is justified by morphology and phylogenetic evidence.

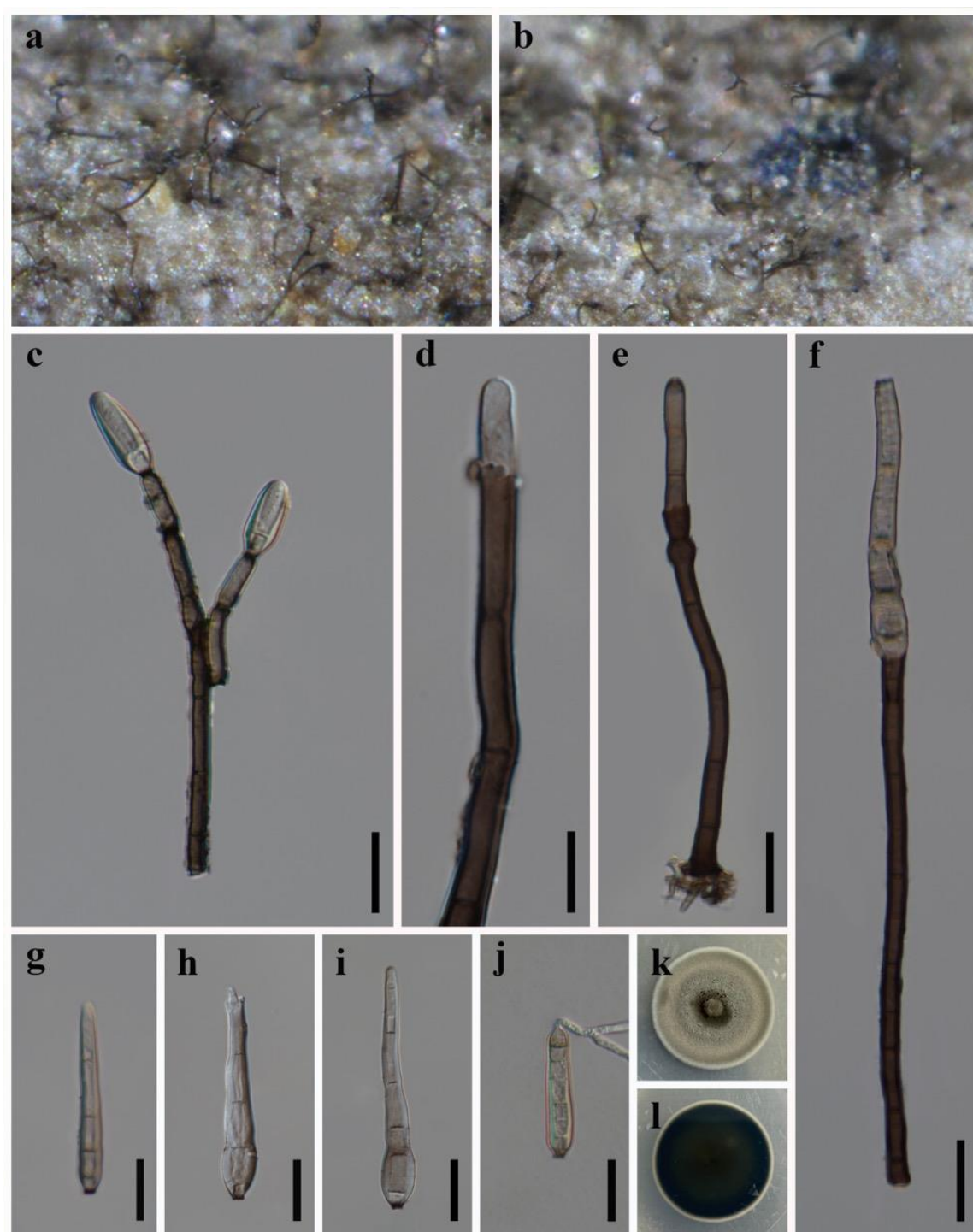


Figure 51 – *Distoseptispora chengduensis* (HKAS 135129, holotype). a–b Colonies. c, f Conidiophores and conidia. d–e Conidiophores. g–i Conidia. j Germinating conidium. k, l Colony on PDA from above and below. Scale bars: c, e, f, g–j = 20 μ m, d = 10 μ m.

Distoseptispora dehongensis W. Dong, H. Zhang & K.D. Hyde, Fungal Diversity 96: 145 (2019)
Fig. 52

Mycobank number: MB555406; Facesoffungi number: FoF05057

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate gregarious or scattered, effuse, hairy, black. *Mycelium* mostly

immersed, consisting of branched, septate, smooth, hyaline hyphae. *Conidiophores* 55–100 × 4–6 µm ($\bar{x}$ = 85 × 5 µm, n = 10), macronematous, mononematous, unbranched, erect, straight or flexuous, cylindrical, brown, septate, smooth-walled. *Conidiogenous cells* monoblastic or polyblastic, terminal, determinate, cylindrical, brown. *Conidia* 25–50 × 9–11 µm ($\bar{x}$ = 35 × 10 µm, n = 30), acrogenous, solitary, broad cylindrical, obpyriform to obclavate, 3–5-distoseptate, brown, thick-walled, smooth, rounded at the apex, truncate at the base, sometimes with percurrent proliferation and forming another conidium from the conidial apex.

Culture characteristics – Colonies on PDA reaching 40–50 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, caramel-colored, reverse dark brown.

Material examined – China, Sichuan Province, Leshan City, Muchuan County, Muchuan Bamboo Sea, 28°51'29"N, 103°56'58"E, elevation 525 m, on dead branches of bamboo, 4 November 2022, X.D. Yu, G43 (HUEST 24.0184), living culture UESTCC 24.0167.

Notes – *Distoseptispora dehongensis* has been reported from decaying submerged wood in a stream, Dehong City, Yunnan Province, China (Hyde et al. 2019), and on decaying submerged wood of unidentified plants in Thailand (Zhang et al. 2022). Our new collection clustered with the holotype of *D. dehongensis* and was found from decaying bamboo in terrestrial environments. This is the first report of *D. dehongensis* from bamboo in a terrestrial habitat.

Distoseptispora euseptata W.L. Li, H.Y. Su & Jian K. Liu, Phytotaxa 520: 80 (2021) Fig. 53

MycoBank number: MB557967; Facesoffungi number: FoF09450

Saprobic on dead branches of bamboo. Sexual morph: *Ascostromata* dark brown to black, immersed to erumpent, usually forming in a linear series on the host surface, solitary, in vertical section 290–310 µm high, 240–320 µm diam., subglobose, unilocular, thick-walled. *Peridium* 30–75 µm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Paraphyses* 4.5–5.5 µm wide, numerous, hyphae-like, hyaline, septate and unbranched. *Asci* 115–205 × 13–17 µm ($\bar{x}$ = 155 × 15 µm, n = 30), 8-spored, unitunicate, cylindric, straight or slightly curved, long pedicellate, rounded at the apex, with an apical ring. *Ascospores* 20–36 × 8–11 µm ($\bar{x}$ = 30 × 9 µm, n = 50), overlapping, biseriate, fusiform, straight, rarely slightly curved, hyaline, aseptate, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: See Li et al. (2021).

Culture characteristics – Colonies on PDA reaching 40–50 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, black, reverse dark.

Material examined – China, Sichuan Province, Meishan City, Danling County, JiuLongShan Forest Park, 29°54'48"N, 103°35'13"E, elevation 460 m, on dead branches of bamboo, 14 July 2022, X.D. Yu, D44 (HUEST 24.0185), living culture UESTCC 24.0168.

Notes – *Distoseptispora euseptata* with its asexual morph was introduced by Li et al. (2021), isolated from submerged wood in Yunnan Province, China. Subsequently, Shen et al. (2024) recollected and described it in Yunnan Province, China, on decaying submerged wood. In the multi-gene phylogeny, our new isolate clustered together with the ex-type of *D. euseptata* with 100% ML/1.00 BYPP support (Fig. 60). A comparison of nucleotide differences between strain UESTCC 24.0168 and MFUCC 20–0154 (from holotype) showed that there are 1% (4/508 bp, including 1 gap) differences in ITS, 0% (0/805) in LSU and 0% (0/884) in *rpb2* gene regions, respectively. Thus, we recognize our collection as the sexual morph of *D. euseptata*, recovered on bamboo in a terrestrial habitat for the first time.

Distoseptispora meilingensis Z.J. Zhai & D.M. Hu, MycoKeys 88: 40 (2022) Fig. 54

MycoBank number: MB842067

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, brown to dark brown, hairy. *Mycelium* mostly immersed. *Conidiophores* 65–200 × 5–6 µm ($\bar{x}$ = 120 × 5.5 µm, n = 10), macronematous, mononematous, erect, cylindrical, straight or slightly flexuous, septate, brown, robust at the base. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, cylindrical, brown. *Conidia* 55–75 × 9.5–14.5

μm ($\bar{x}$ = $65 \times 11 \mu\text{m}$, $n = 30$), acrogenous, solitary, straight or slightly curved, obclavate, brown, 5–9- euseptate, rounded at the apex, truncate at the base, tapering towards apex.

Culture characteristics – Colonies on PDA reaching 40–50 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, grey, reverse dark.

Material examined – China, Sichuan Province, Meishan City, Qingshen County, Bamboo Forest Wetland Park, 29°48'43"N, 103°49'26"E, elevation 400 m, on dead branches of bamboo, 4 November 2022, X.D. Yu, J6 (HUEST 24.0186), living culture UESTCC 24.0169; China, Sichuan Province, Chengdu City, Dujiangyan County, Mount Qingcheng, 30°54'29" N, 103°32'36" E, elevation 960 m, on dead branches of bamboo, 2 December 2021, X.D. Yu, B8 (HUEST 24.0188), living culture UESTCC 24.0171; China, Sichuan Province, Ziyang City, Le Zi County, Jinmasi Village, 30°19'55"N, 105°2'40" E, elevation 540 m, on dead branches of bamboo, 22 April 2023, X.D. Yu, K22 (HUEST 24.0187), living culture UESTCC 24.0170.

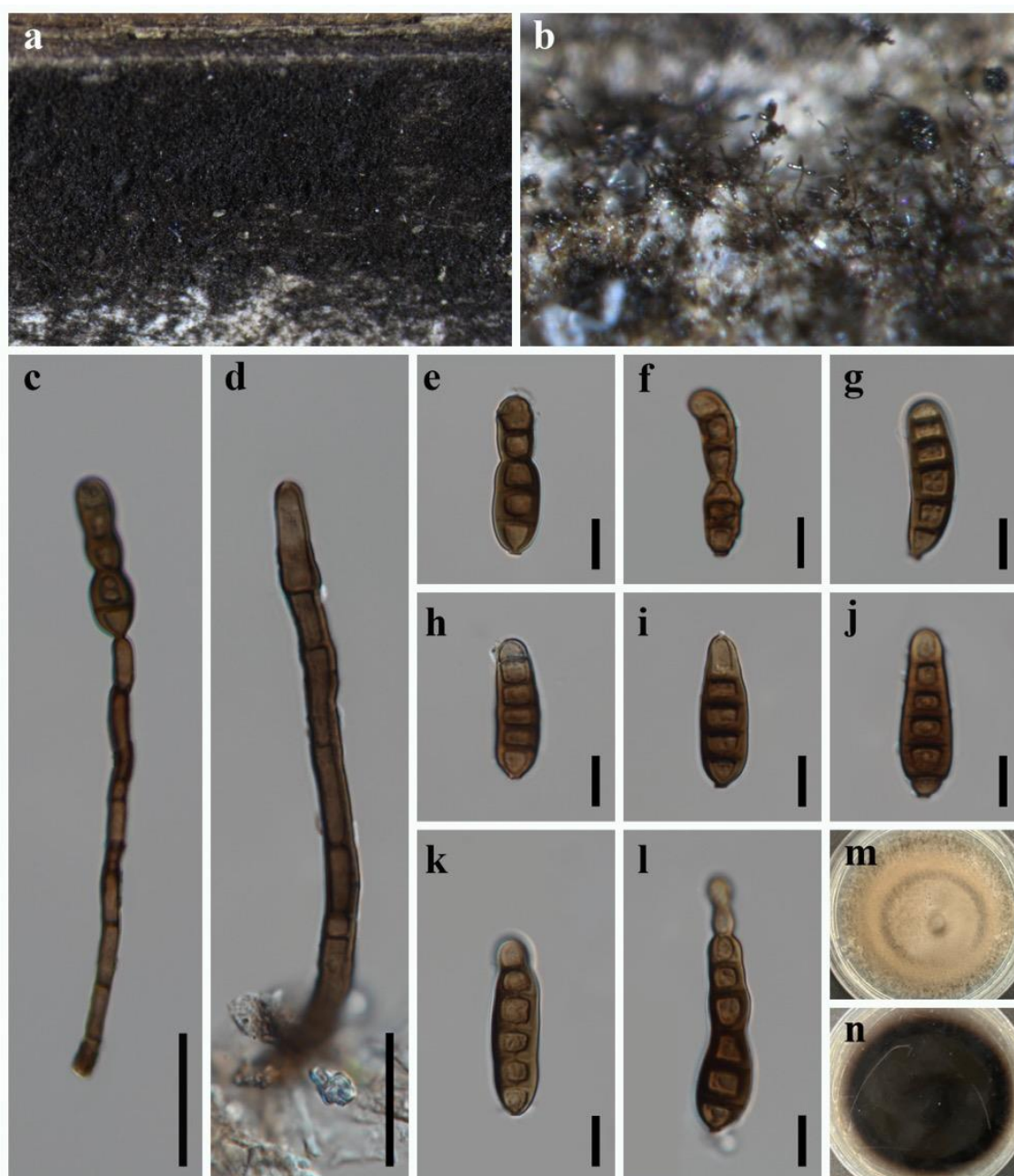


Figure 52 – *Distoseptispora dehongensis* (HUEST 24.0184). a–b Colonies. c Conidiophore and conidium. d Conidiophore. e–l Conidia. m, n Colony on PDA from above and below. Scale bars: c = 30 μm , d = 20 μm , e–l = 10 μm .

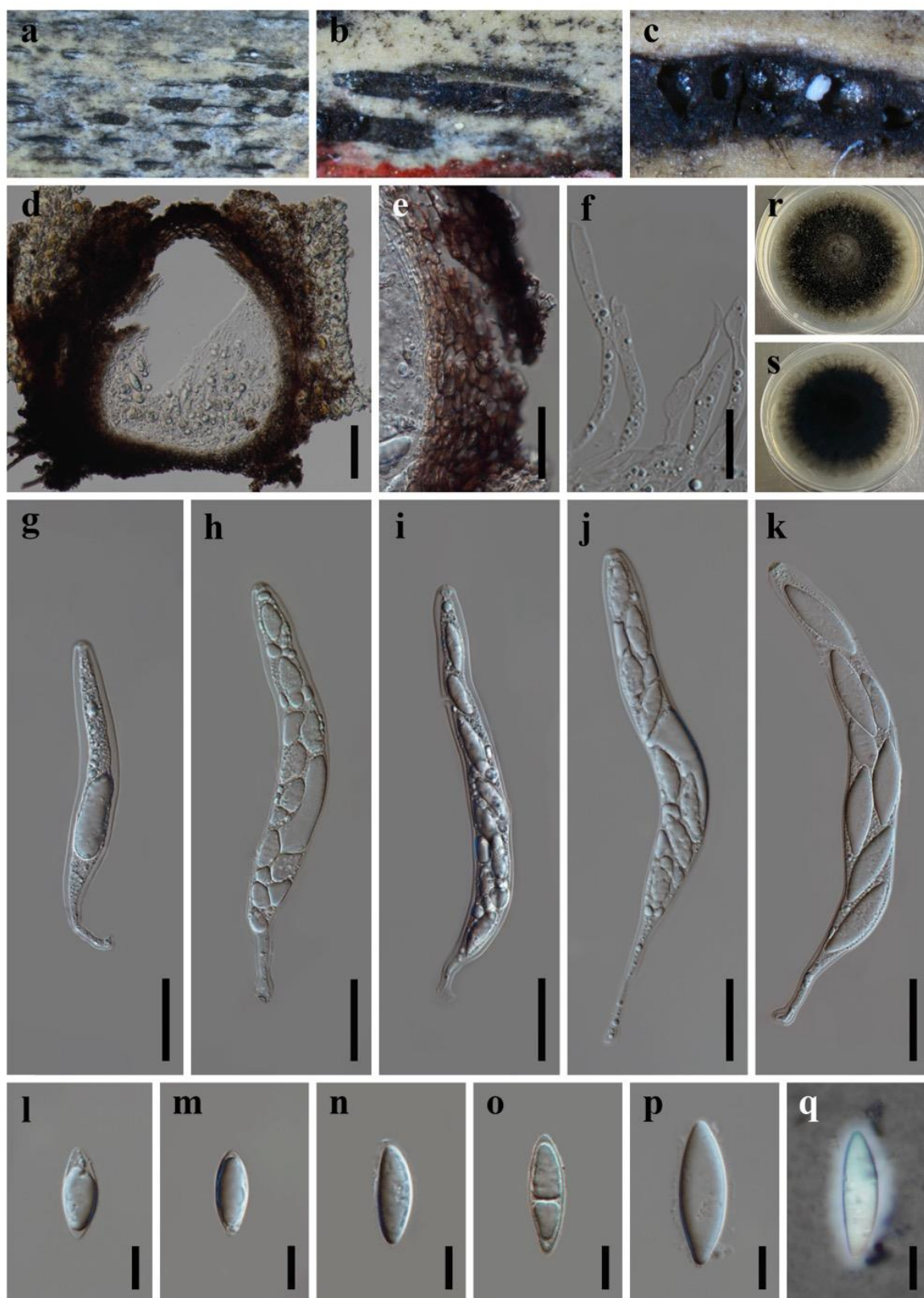


Figure 53 – *Distoseptispora euseptata* (HUEST 24.0185). a–c Ascomata on host substrate. d Vertical section of ascoma. e Peridium. f Paraphyses. g–k Asci. l–p Ascospores. q Ascospore with a mucilaginous sheath. r, s Colonies on PDA from above and below. Scale bars: d = 50 μ m, e–f = 20 μ m, g–k = 20 μ m, l–q = 10 μ m.

Notes – *Distoseptispora meilingensis* is characterized by holoblastic, monoblastic, cylindrical conidiogenous cells, acrogenous, solitary, obclavate, brown conidia (Zhai et al. 2022). Our

collections are similar to the holotype of *D. meilingensis* (JAUCC 4727 = JAUCC 4728). The multilocus phylogeny shows that our isolates clustered with the ex-type strain of *D. meilingensis* with 100% ML/1.00 BYPP support (Fig. 60). Therefore, we identified our isolates as *D. meilingensis*, and this is the first report of *D. meilingensis* in a terrestrial habitat.



Figure 54 – *Distoseptispora meilingensis* (HUEST 24.0186). a–c Colonies. d–g Conidiophores and conidia. h–l Conidia. m Germinating conidium. n, o Colony on PDA from above and below. Scale bars: d = 50 μ m, e–m = 20 μ m.

Distoseptispora muchuanensis X.D. Yu & Jian K. Liu, sp. nov.

Mycobank number: MB854905; Facesoffungi number: FoF16596

Etymology – Name refers to Muchuan, the city where the fungus was collected.

Fig. 55

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate superficial, effuse, scattered, hairy, black. *Mycelium* partly superficial, partly immersed, composed of branched, septate, smooth, hyaline to pale brown hyphae. *Conidiophores* 40–75 × 4.5–5.5 µm ($\bar{x}$ = 65 × 5 µm, n = 10), macronematous, mononematous, unbranched, septate, cylindrical, straight or slightly flexuous, smooth, olivaceous to brown. *Conidiogenous cells* monoblastic, integrated, determinate, terminal, cylindrical, olivaceous to brown, smooth. *Conidia* 40–60 × 10–13 µm ($\bar{x}$ = 50 × 11 µm, n = 30), acrogenous, dry, obclavate, straight or slightly curved, 6–12-distoseptate, tapering towards the rounded apex, olivaceous to brown.

Culture characteristics – Colonies on PDA reaching 20–30 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, olivaceous, reverse dark.

Material examined – China, Sichuan Province, Muchuan City, Taoyuan Mountain House, 28°57'11"N, 103°53'28"E, elevation 403 m, on dead branches of bamboo, 3 November 2022, X.D. Yu, F6 (HKAS 135156, holotype), ex-type living culture CGMCC 3.27444.

Notes – Phylogenetic analysis showed that *Distoseptispora muchuanensis* formed a sister clade to *D. lignicola* (MFLUCC 18-0198) and *D. menghaiensis* (HJAUP C2045) (Fig. 60). *Distoseptispora muchuanensis* resembles *D. lignicola* and *D. menghaiensis* in having macronematous, mononematous, unbranched, septate, cylindrical conidiophores, monoblastic, cylindrical conidiogenous cells, acrogenous, dry, obclavate and septate conidia (Luo et al. 2019, Hu et al. 2023). However, they can be easily distinguished by the number of septa (6–12-distoseptate in *D. muchuanensis*, 5–9-euseptate in *D. lignicola* and 4–8-distoseptate in *D. menghaiensis*) and conidial colour (olivaceous to brown in *D. muchuanensis*, brown in *D. lignicola* and brown in *D. menghaiensis*). The establishment of the new species *Distoseptispora muchuanensis* is justified by morphological and phylogenetic evidence.

Distoseptispora suoluensis J. Yang, Maharachch. & K.D. Hyde, Mycological Progress 17: 609 (2017) Figs 56, 57

MycoBank number: MB821273; Facesoffungi number: FoF03359

Saprobic on dead branches of bamboo. Sexual morph: *Ascostromata* immersed to erumpent, brown, with a black, slit-like opening, solitary, unilocular, subglobose, in vertical section 200–300 µm high, 210–260 µm diam., thick-walled. *Peridium* 15–55 µm wide, composed of several layers of brown, thick-walled cells of *textura angularis*. *Paraphyses* 5.5–8.5 µm wide, numerous, hyaline, hyphae-like, septate and unbranched. *Asci* 140–160 × 14.5–16.5 µm ($\bar{x}$ = 150 × 15.5 µm, n = 30), 8-spored, bitunicate, clavate to cylindrical, straight or slightly curved, long pedicellate, rounded at the apex, with an apical ring. *Ascospores* 25–32 × 8–11 µm ($\bar{x}$ = 28 × 9 µm, n = 50), overlapping, biseriate, ellipsoid-fusiform, hyaline, aseptate, smooth-walled, thin-walled, surrounded by a mucilaginous sheath. Asexual morph: *Colonies* on natural substrate effuse, dark brown to black, scattered or in small groups, hairy, glistening. *Mycelium* partly immersed, composed of branched, septate, smooth, hyaline to pale brown hyphae. *Conidiophores* 44–210 × 5–6 µm ($\bar{x}$ = 120 × 5.5 µm, n = 10), macronematous, mononematous, unbranched, septate, cylindrical, straight or slightly flexuous, smooth, brown. *Conidiogenous cells* monoblastic, integrated, determinate, terminal, cylindrical, brown, smooth. *Conidia* 70–90 × 10–12 µm ($\bar{x}$ = 85 × 11 µm, n = 30), acrogenous, dry, obovoid to obclavate, straight or curved, septate, tapering towards the rounded apex, thin-walled, brown.

Culture characteristics – Colonies on PDA reaching 40–50 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, greyish-brown, reverse black.

Material examined – China, Sichuan Province, Chengdu City, Xinjin County, Banzhulin, 30°29'48"N, 103°48'47"E, elevation 480 m, on dead branches of bamboo, 9 May 2022, X.D. Yu, C13 (HUEST 24.0189), living culture UESTCC 24.0172; China, Sichuan Province, Chengdu City, Tianfu New Area, Dalin Village, 30°16'43"N, 104°6'44"E, elevation 500 m, on dead branches of bamboo, 24 July 2021, X.D. Yu, Bamboo1 (HUEST 24.0191), living culture UESTCC 24.0174. China, Sichuan Province, Chengdu City, Qinglong Lake Wetland Park, 30°38'5"N, 104°10'39"E,

510 m, on dead branches of bamboo, 13 August 2021, X.D. Yu, QLH6 (HUEST 24.0190), living culture UESTCC 24.0173. China, Sichuan Province, Meishan City, Danling County, JiuLongShan Forest Park, 29°54'48"N, 103°35'13"E, elevation 460 m, on dead branches of bamboo, 14 July 2022, X.D. Yu, D27 (HUEST 24.0192); living culture UESTCC 24.0175.

Notes – The asexual morph of *Distoseptispora suoluoensis* was introduced by Yang et al. (2018) from decaying wood submerged in China. In the multi-locus phylogenetic analyses, our collections have a close affinity to *D. suoluoensis* (Fig. 60) and a comparison of SSU, ITS, LSU, *rpb2* and *tef1- α* sequence data has no significant differences. This is the first time that the sexual and asexual morphs of *D. suoluoensis* have been found on bamboo in a terrestrial environment.



Figure 55 – *Distoseptispora muchuanensis* (HKAS 135156, holotype). a–b Colonies. c–f Conidiophores and conidia. g–j Conidia. k Germinating conidium. l, m Colony on PDA from above and below. Scale bars: c–k = 20 μ m.

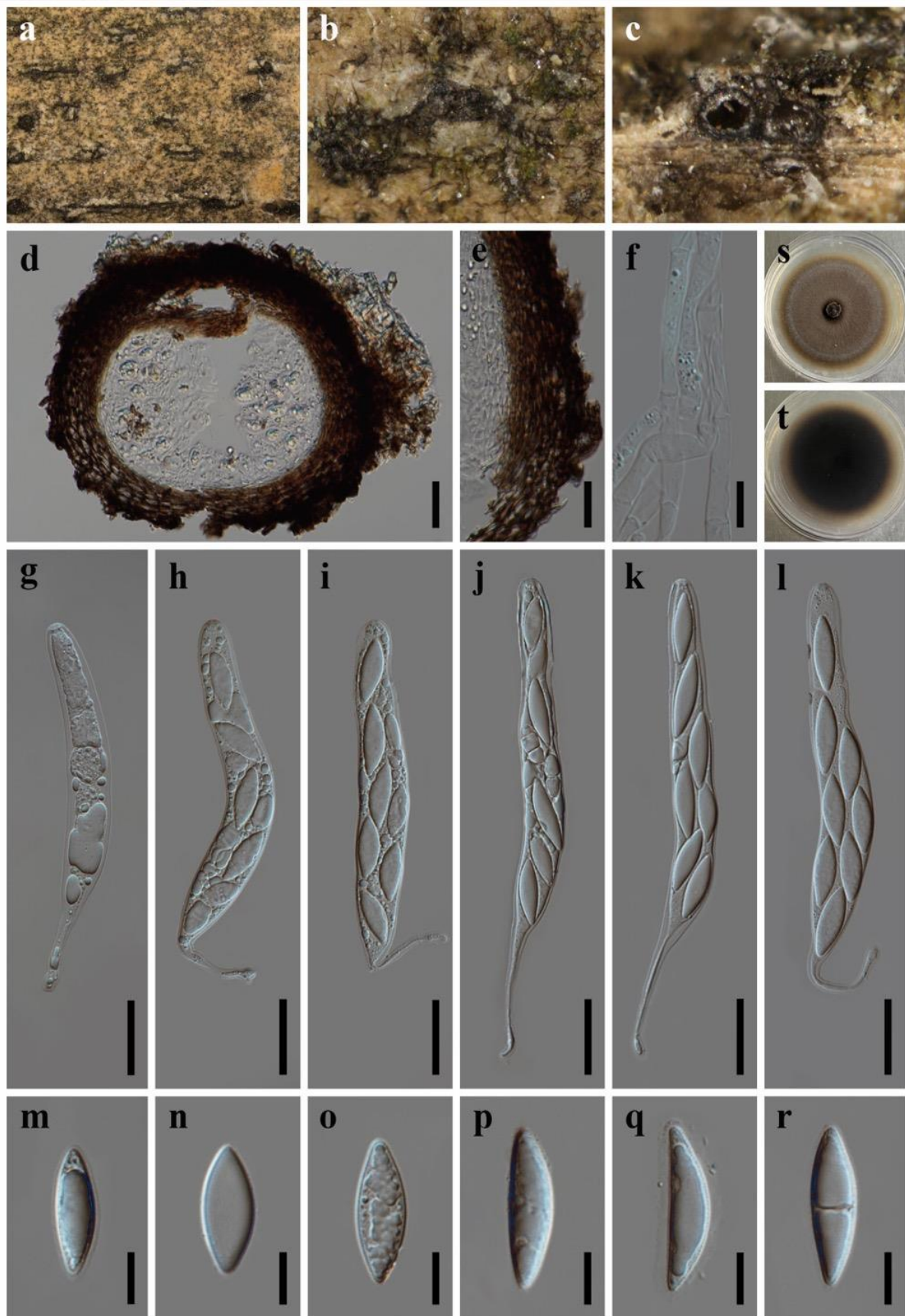


Figure 56 – *Distoseptispora suoluensis* (HUEST 24.0189). a–c Ascomata on host substrate. d Vertical section of ascoma. e Peridium. f Paraphyses. g–l Asci. m–r Ascospores. s, t Colonies on PDA from above and below. Scale bars: d, g–l = 30 μ m, e = 20 μ m, f, m–r = 10 μ m.



Figure 57 – *Distoseptispora suoluoensis* (HUEST 24.0191). a–c Colonies. d–e Conidiophores and conidia. f–h Conidiogenous cells and conidia. i–n Conidia. o Germinating conidium. p, q Colony on PDA from above and below. Scale bars: d–e = 50 μ m, f = 20 μ m, g–h = 10 μ m, i–o = 30 μ m.

Distoseptispora yongxiuensis Z.J. Zhai & D.M. Hu, MycoKeys 88: 42 (2022)

Fig. 58

MycoBank number: MB842066

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate superficial, effuse, scattered, hairy, black. Mycelium partly superficial, partly immersed, composed of branched, septate, smooth, hyaline to pale brown hyphae. Conidiophores 110–250 $\times$ 5–7 μ m ($\bar{x}$ = 160 $\times$ 6 μ m, n = 10), macronematous, mononematous, solitary or aggregated at the base, cylindrical, straight or slightly flexuous, septate,

olivaceous to dark brown, paler at the apical, rounded at the apex. *Conidiogenous cells* monoblastic, integrated, determinate, terminal, cylindrical, olivaceous, smooth. *Conidia* 40–85 × 7–12 µm ($\bar{x}$ = 70 × 10 µm, n = 30), acrogenous, solitary, obclavate, straight or flexuous, rostrate, 3–8-euseptate, olivaceous to yellowish-brown, paler or hyaline towards the apex, guttulate.

Culture characteristics – Colonies on PDA reaching 50–60 mm after 2 weeks at 25 °C, circular, dry, with dense mycelium, raised, entire at the edge, white, reverse dark.

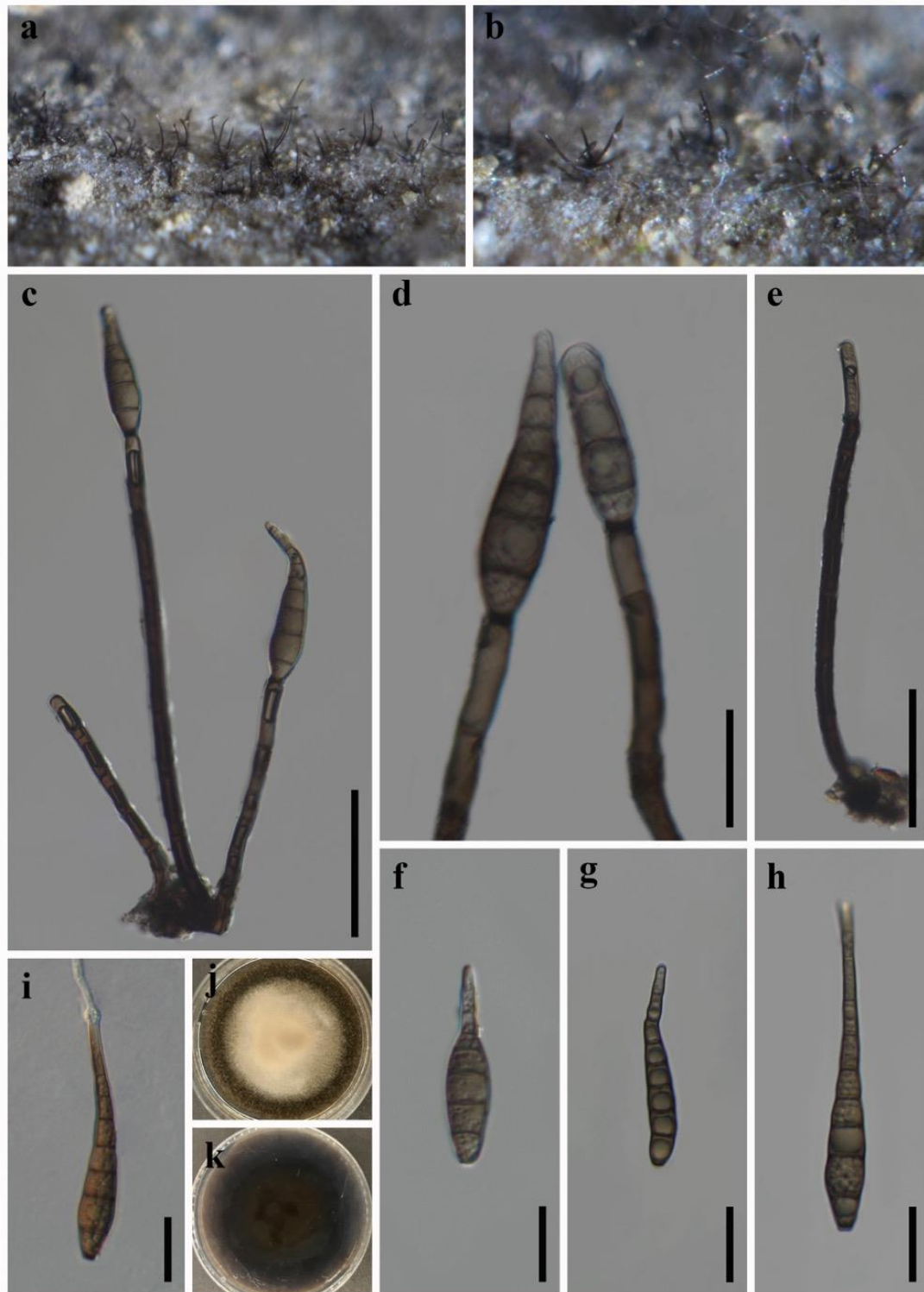


Figure 58 – *Distoseptispora yongxiuensis* (HUEST 24.0193). a–b Colonies. c Conidiophores and conidia. d Conidiogenous cells and conidia. e Conidiophore. f–h Conidia. i Germinating conidium. j, k Colony on PDA from above and below. Scale bars: c, e = 50 µm, d, f–i = 20 µm.

Material examined – China, Sichuan Province, Zigong City, Rong County, Hualonggou Bamboo Sea, 29°28'52" N, 104°17'20" E, elevation 625 m, on dead branches of bamboo, 3 November 2022, X.D. Yu, H10 (HUEST 24.0193), living culture UESTCC 24.0176; *ibid.* H12 (HUEST 24.0194), living culture UESTCC 24.0177; *ibid.* H17 (HUEST 24.0195), living culture UESTCC 24.0178; *ibid.* H34 (HUEST 24.0196), living culture UESTCC 24.0179.

Notes – Based on the morphological traits and molecular evidence (Fig. 60), our strains are identified as *Distoseptispora yongxiuensis*. *Distoseptispora yongxiuensis* was described by Zhai et al. (2022), isolated from decaying submerged bamboo culms in freshwater habitats. We report a new habitat record of *D. yongxiuensis* and extend its habitat from freshwater ecosystem to terrestrial.

Sporidesmiales Crous, Persoonia 40: 377 (2018)

Sporidesmiaceae Fr., Summa veg. Scand., Section Post. (Stockholm): 504 (1849)

MycoBank number: MB81405; Facesoffungi number: FoF01830

Notes – Sporidesmiaceae was introduced by Fries (1849), but it was not widely used. Subsequently, Su et al. (2016) formally resurrected the family name.

Sporidesmium Link, Mag. Ges. Naturf. Freunde Berlin 3: 41 (1809)

MycoBank number: MB10024; Facesoffungi number: FoF01750

Notes – *Sporidesmium* was established by Link (1809) and typified by *S. ehrenbergii* M.B. Ellis, which is characterized by macronematous, mononematous, cylindrical, brown, septate conidiophores, monoblastic, holoblastic conidiogenous cells, ovoid, obpyriform or rostrate, euseptate or distoseptate conidia with or without an appendage or mucilaginous sheath (Yang et al. 2023). Phylogenetic analyses have shown that *Sporidesmium* is polyphyletic (Shenoy et al. 2006, Liu et al. 2019a).

Sporidesmium chiangmaiense X.D. Yu, W. Dong & H. Zhang, Mycosphere 12: 44 (2021)

Fig. 59

MycoBank number: MB558033; Facesoffungi number: FoF09554

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate superficial, effuse, gregarious, hairy, black. *Mycelium* partly immersed, composed of septate, brown, thin-walled hyphae. *Conidiophores* 40–90 × 5.5–7.5 µm ($\bar{x}$ = 60 × 6 µm, n = 10), macronematous, mononematous, fasciculate, erect, cylindrical, straight or flexuous, septate, unbranched, brown, smooth. *Conidiogenous cells* holoblastic, monoblastic, integrated, determinate, terminal, subcylindrical, brown, smooth. *Conidia* 65–80 × 12–17 µm ($\bar{x}$ = 70 × 15 µm, n = 30), acrogenous, solitary, dry, smooth, obclavate, straight or curved, brown, with a truncate base, rostrate, tapering towards apex, 8–10-distoseptate, apex with a conspicuous, gelatinous sheath.

Culture characteristics – Colonies attaining a diameter about 6 mm after 2 weeks at 25 °C, irregular, raised to umbonate, dense, the edge slightly undulate and white, white from the reverse

Material examined – China, Sichuan Province, Meishan City, Danling County, JiuLongShan Forest Park, 29°54'48"N, 103°35'13"E, elevation 460 m, on dead branches of bamboo, 14 July 2022, X.D. Yu, D26 (HUEST 24.0197); living culture UESTCC 24.0180; *ibid.* D30 (HUEST 24.0198); living culture UESTCC 24.0181; *ibid.* D36 (HUEST 24.0199); living culture UESTCC 24.0182.

Notes – A phylogenetic analysis showed that our collections clustered with *Sporidesmium chiangmaiense* with 100% ML/1.00 BYPP bootstrap support (Fig. 60). Morphology of our collections is consistent with *S. chiangmaiense* (Dong et al. 2021), including the measurements of conidiophores and conidia. We therefore, identify our collections as *S. chiangmaiense* and it is a new geographical, habitat and host record from bamboo in terrestrial habitat for China.

Savoryellomycetidae Hongsanan, K.D. Hyde & Maharachch., Fungal Diversity 84: 35 (2017)

Conioscyphales Réblová & Seifert, Persoonia 37: 63 (2015)

Conioscyphaceae Réblová & Seifert, Persoonia 37: 63 (2015)

MycoBank number: MB813227; Facesoffungi number: FoF05190

Notes – Conioscyphaceae was initially placed within Conioscyphales with a single genus *Conioscypha* (Réblová et al. 2016). Subsequently, *Vanakripa* was recognized as a member of Conioscyphaceae based on phylogenetic evidence (Yang et al. 2020, Phukhamsakda et al. 2022). Two genera are currently accepted in this family, *Conioscypha* and *Vanakripa* (Yu et al. 2024).

Conioscypha Höhn., Ann. Mycol. 2: 58 (1904)

MycoBank number: MB7754; Facesoffungi number: FoF05191

Notes – The dematiaceous hyphomycetous genus *Conioscypha*, typified by *C. lignicola*, was introduced by Höhnelt (1904). Réblová & Seifert (2004) introduced *Conioscyphascus* as the sexual morph of *Conioscypha*. Due to nomenclatural priority (Turland 2018), *Conioscyphascus* was synonymized under *Conioscypha*. Members of *Conioscypha* are worldwide and have been reported from Africa, America, Asia and Europe (Liu et al. 2019c), and most are saprobes and have been found on decaying plant tissues in freshwater and terrestrial habitats (Yu et al. 2024).

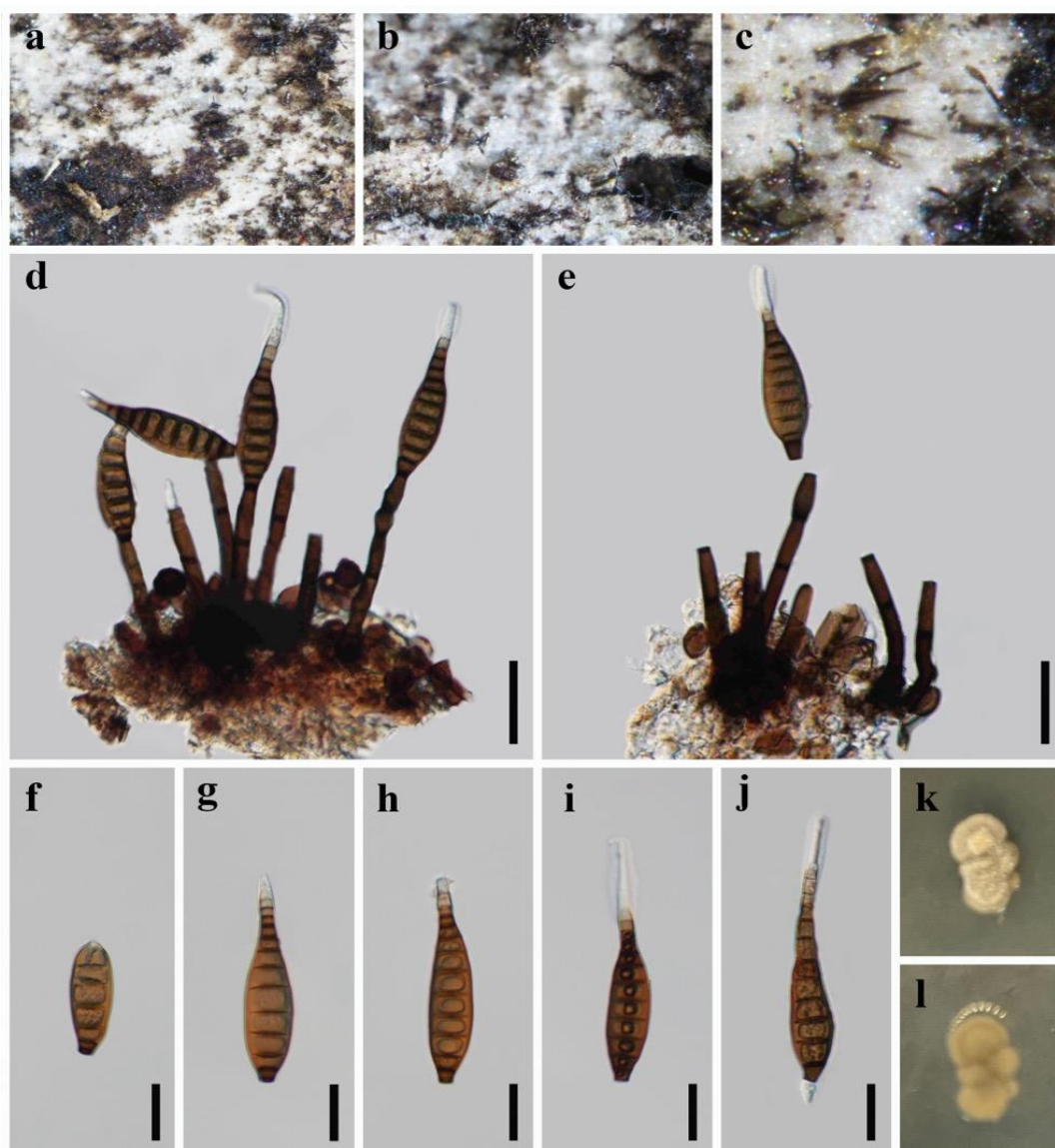


Figure 59 – *Sporidesmium chiangmaiense* (HUEST 24.0198). a–c Colonies. d–e Conidiophores and conidia. f–i Conidia. j Germinating conidium. k, l Colony on PDA from above and below. Scale bars: d–e = 30 µm, f–j = 20 µm.

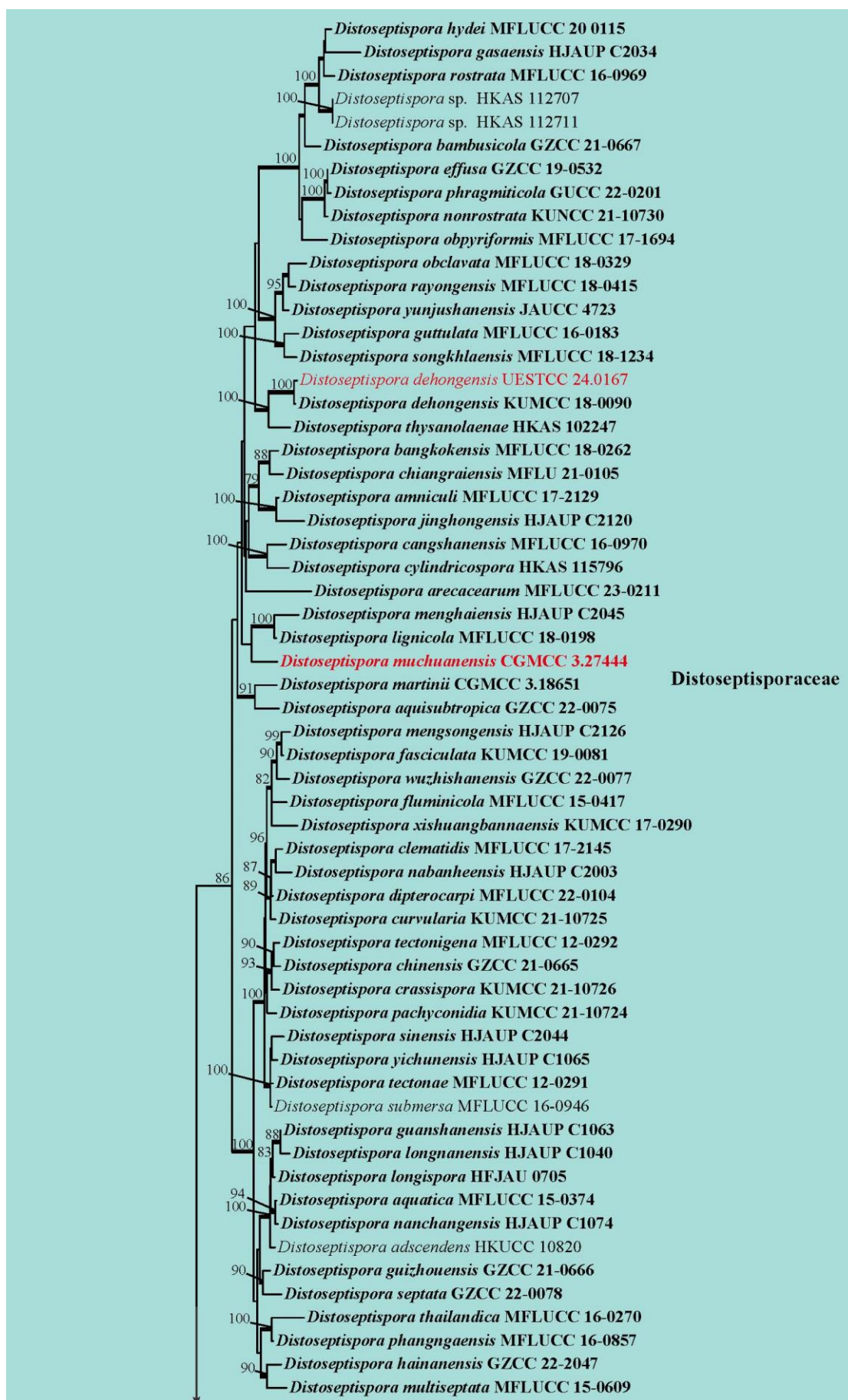


Figure 60 – RAxML tree generated from combined SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data of Diaporthomycetidae. The tree was rooted with *Conioscypha aquatica* (MFLUCC 18-1333) and

Fuscospora guizhouensis (CGMCC 3.20884). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

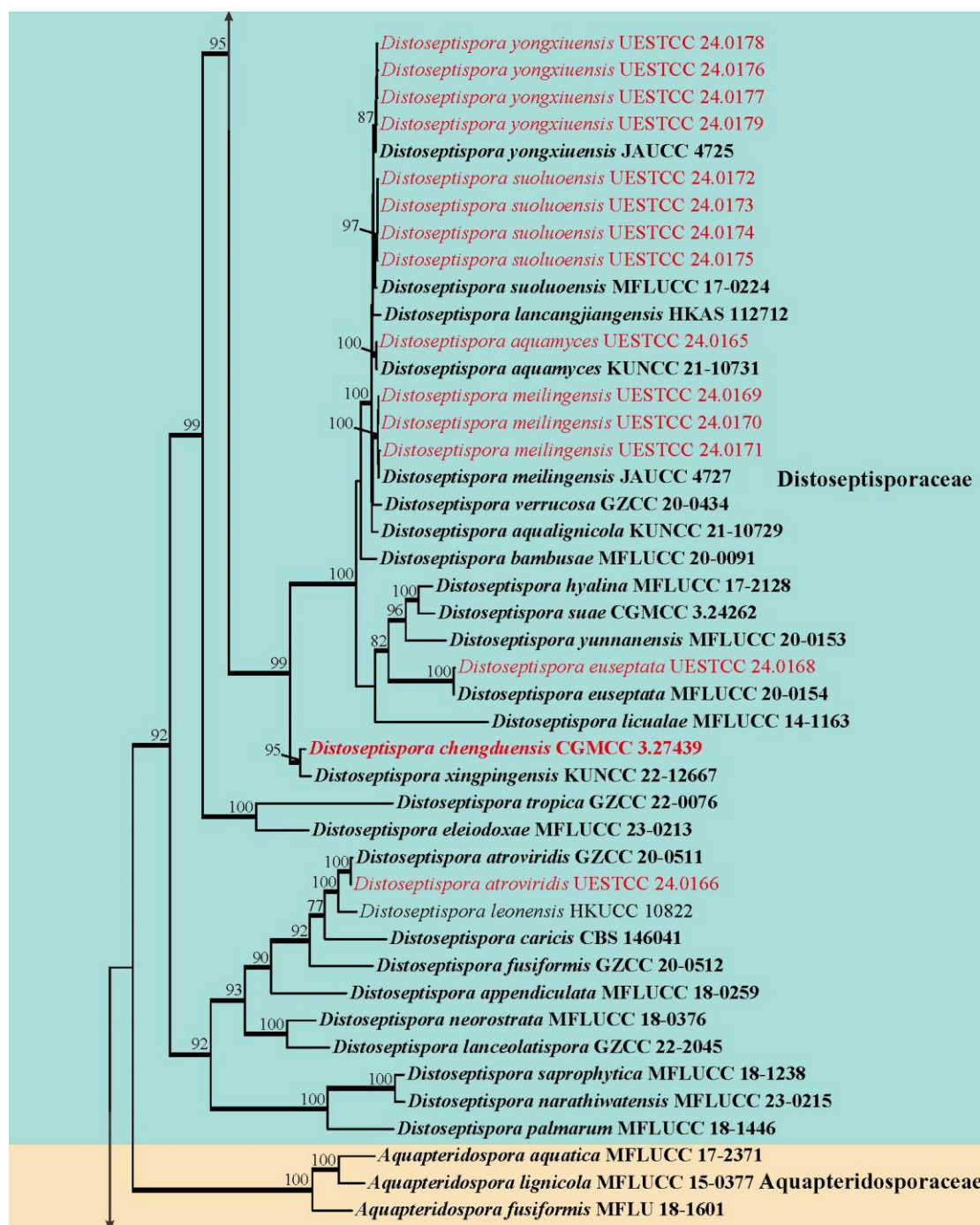


Figure 60 – Continued.

Conioscypha muchuanensis X.D. Yu & Jian K. Liu, sp. nov.

Fig. 61

Mycobank number: MB854906; Facesoffungi number: FoF16597

Etymology – Name refers to Muchuan, the city where the fungus was collected.

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on natural substratum, effuse, scattered to gregarious, black, glistening, superficial. Mycelium immersed, composed of hyaline, septate, branched, smooth hyphae. Conidiophores micronematous, mononematous, arising directly from the hyphae, hyaline, often

reduced to conidiogenous cells. *Conidiogenous cells* phialidic, integrated, sessile or on short conidiophores, subcylindrical, hyaline, percurrently proliferating, with cup-shaped multi-collarette smooth-walled. *Conidia* 11–15 × 9–15 µm ($\bar{x}$ = 13 × 11.5 µm, n = 50), acrogenous, solitary, globose to subglobose, brown when young, dark brown to black when mature, smooth-walled, aseptate, broadly rounded at apex, subtruncate at base.

Culture characteristics – Colonies attaining a diameter about 6 mm after 2 weeks at 25 °C, irregular, raised to umbonate, dense, the edge slightly undulate and white, white from the reverse.

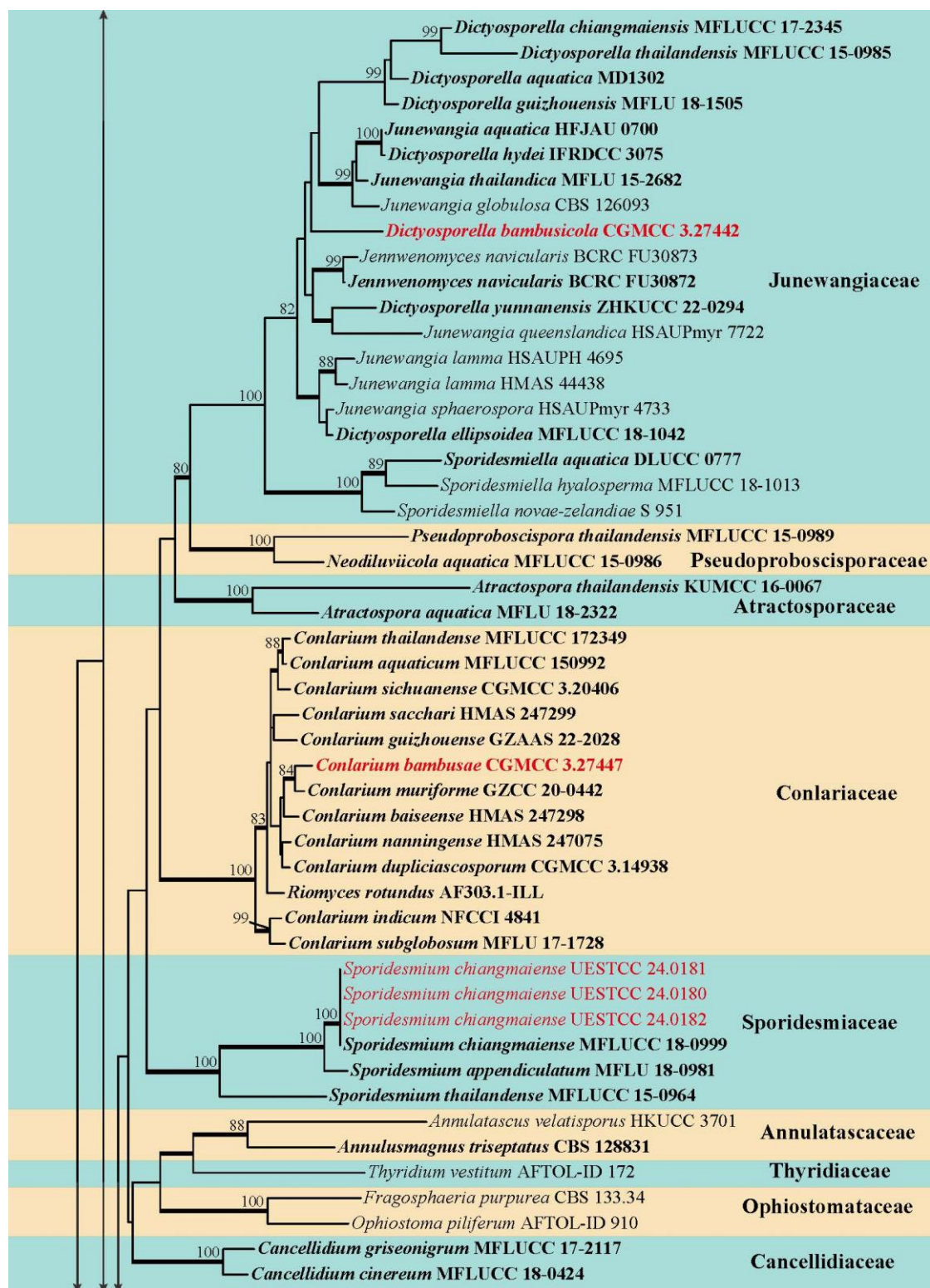


Figure 60 – Continued.

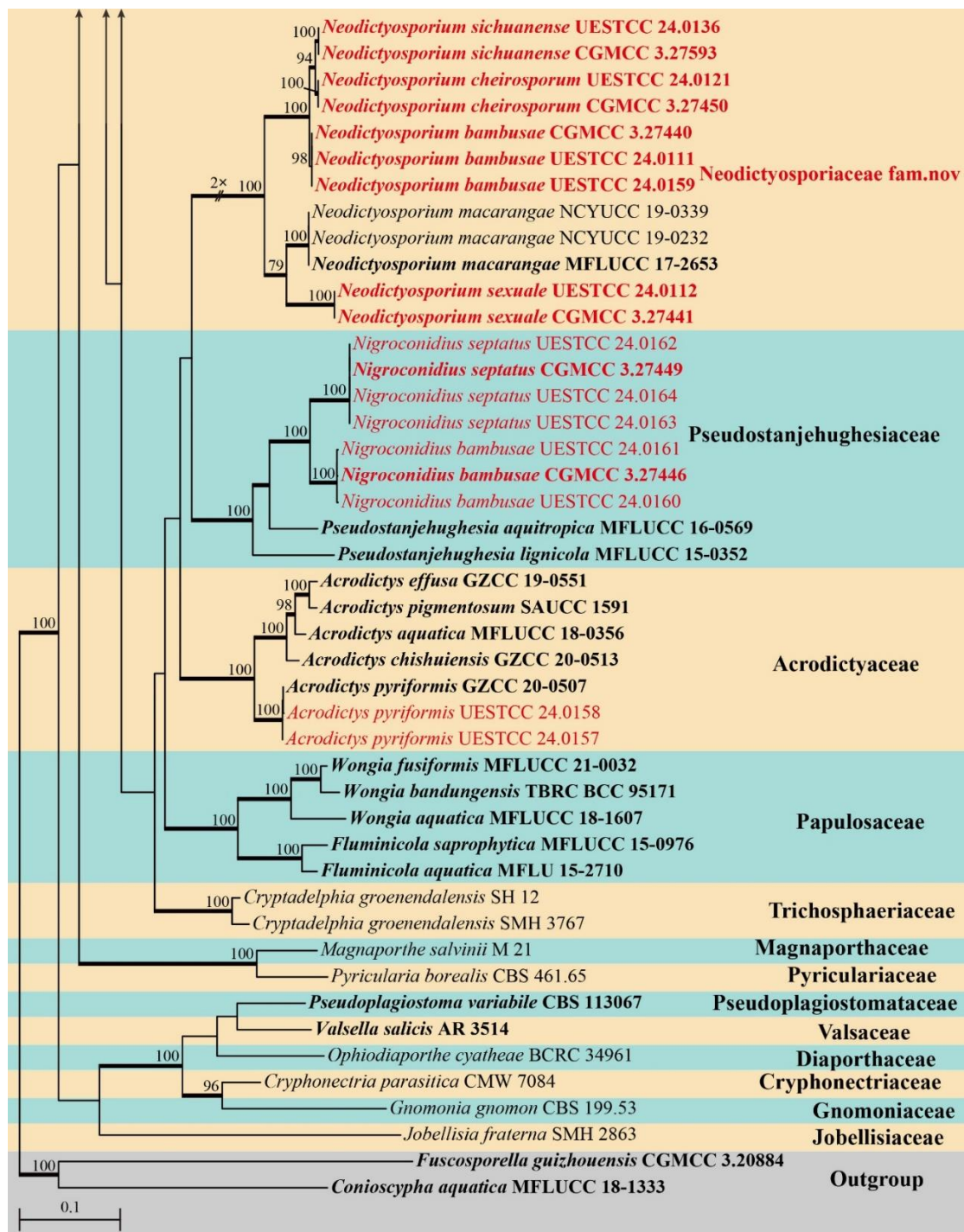


Figure 60 – Continued.

Material examined – China, Sichuan Province, Leshan City, Muchuan County, Muchuan Bamboo Sea, 28°51'29"N, 103°56'58"E, elevation 525 m, on dead branches of bamboo, 4 November 2022, X.D. Yu, G50 (HKAS 135127, holotype), ex-type living culture CGMCC 3.27448.

Notes – The phylogenetic analyses based on SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data showed that *Conioscypha muchuanensis* formed a distinct lineage nested in *Conioscypha* (Fig. 62). *Conioscypha muchuanensis* is similar to *C. sichuanensis* in having phialidic conidiogenous cells, globose to subglobose and dark brown to black conidia (Yu et al. 2024). However, *C. muchuanensis* has broader conidia than those of *C. sichuanensis* (11–15 × 9–15 μm vs. 10.0–12.5 μm diam.). The establishment of the new species *C. muchuanensis* is justified by morphological and phylogenetic evidence.

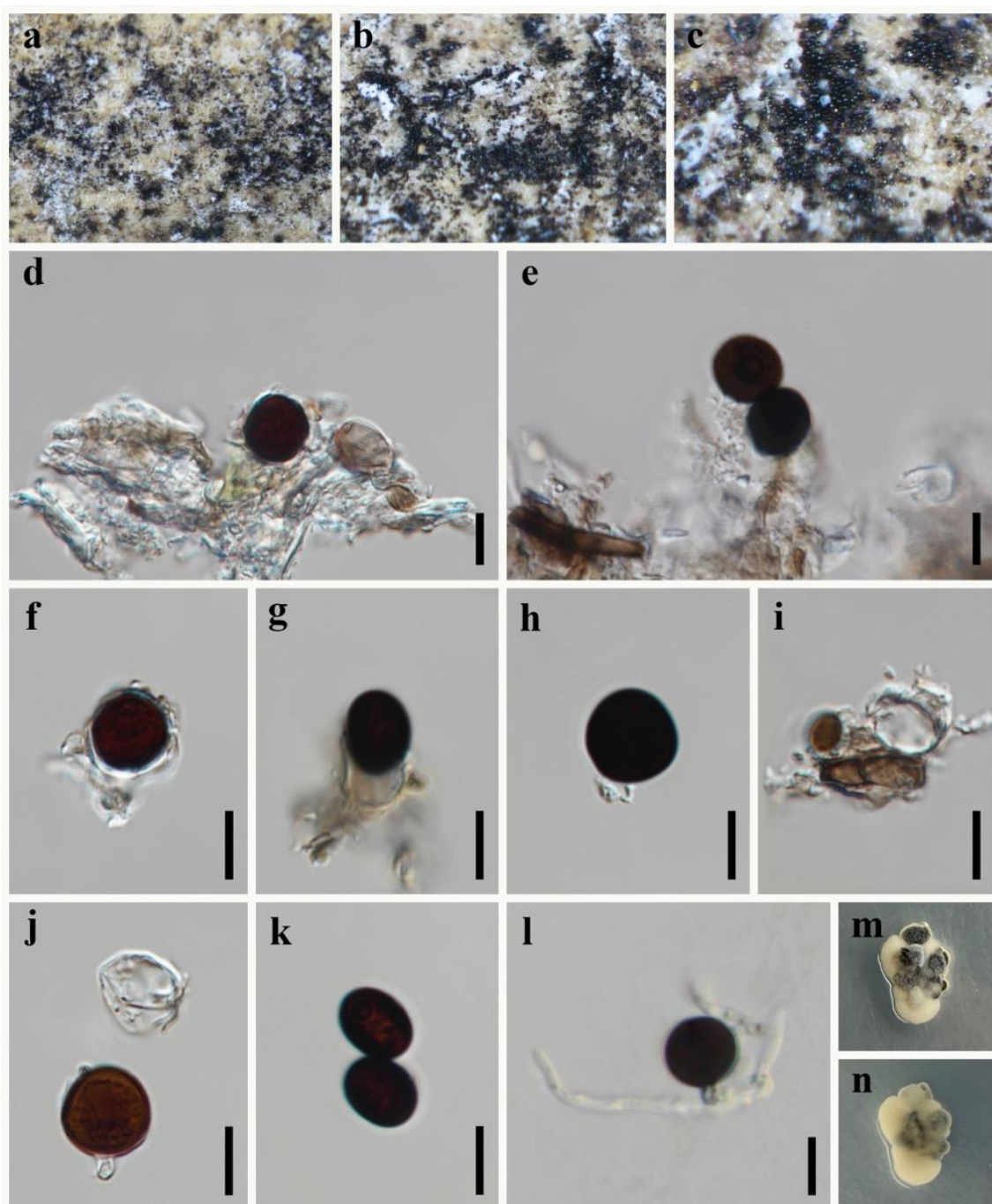


Figure 61 – *Conioscypha muchuanensis* (HKAS 135127, holotype). a–c Colonies. d, f, g, i Conidia and conidiogenous cells with cup-shaped multi-collarete. e, h, j Conidia and conidiogenous cell. k Conidia. l Germinating conidium. m, n Colony on PDA from above and below. Scale bars: d–l = 10 μ m.

Conclusion

This study highlights the remarkable diversity of bambusicolous ascomycetous fungi in southwestern China, a region rich in bamboo ecosystems. Through extensive fieldwork in freshwater and terrestrial habitats, we identified both asexual and sexual morphs of saprobic fungi. Our investigation led to the introduction of one new fungal family, *Neodictyosporiaceae*, and seven new genera, including *Aculeatosporella*, *Antebambusa*, *Ascosichuania*, *Flavosporella*, *Multiseptoconidium*, *Nigroconidius*, and *Sichuanomyces*. We also described 29 new species, significantly expanding the knowledge of fungal biodiversity associated with bamboo. These discoveries are the result of a detailed morphological analysis and multi-gene phylogenetic studies,

which together provided a robust framework for taxonomic revisions and the identification of new taxa.

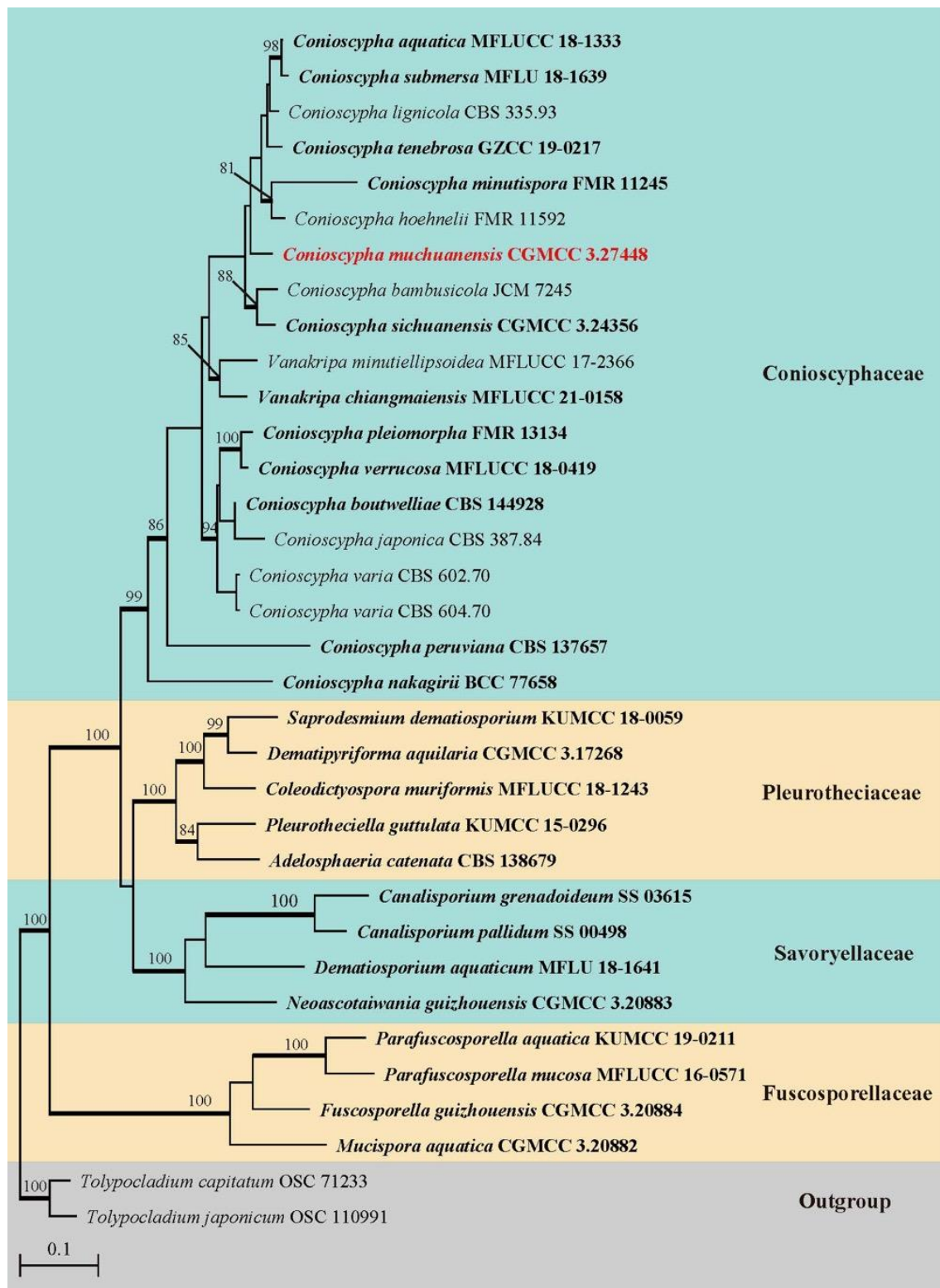


Figure 62 – RAxML tree generated from combined SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data of Savoryellomycetidae. The tree was rooted with *Tolypocladium capitatum* (OSC 71233) and *T. japonicum* (OSC 110991). Ex-type strains are in bold and newly generated sequences are in red. Bootstrap values for ML equal to or greater than 75% are placed above the branches. Branches with Bayesian posterior probabilities (BYPP) from MCMC analysis equal to or greater than 0.95 are in bold.

The introduction of these new taxa underscores the ecological importance of bamboo habitats as reservoirs for fungal diversity. Bamboo is widely distributed across the region and plays a key role in the structure of many ecosystems. The fungi associated with bamboo, particularly those described in this study, contribute to nutrient cycling by decomposing dead bamboo material. The wide range of both asexual and sexual morphs collected suggests that bamboo ecosystems support a complex fungal community with diverse ecological roles. Our findings also reveal the presence of fungi in various habitats, further emphasizing the adaptability of these species in different environmental conditions.

In addition to the new taxa, we reported 16 new records of fungi, including species with novel morphs, new geographical distributions, and new host associations. These records enhance our understanding of fungal distribution and host specificity within bamboo ecosystems. The results of this study contribute significantly to fungal taxonomy and provide a foundation for future research on the ecological roles of bambusicolous fungi. As bamboo continues to be an important ecological and economic resource, understanding its fungal associations will be crucial for biodiversity conservation and sustainable management practices.

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