

Taxonomic and phylogenetic insights to *Dothideomycetes* and *Sordariomycetes* associated with medicinal plants in Southwestern China

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Abstract

This study provides taxonomic and phylogenetic insights into fungal taxa within *Dothideomycetes* and *Sordariomycetes* associated with medicinal plants in Southwestern China. These fungi are of significant interest for investigating their functional potential and for broader studies on medicinal plant-fungal interactions. A total of 90 fungal isolates were obtained from medicinal plants in Yunnan, Guizhou, and Sichuan Provinces, representing 27 genera, 19 families, and six orders. Among these, one species was identified in *Pleurotremataceae* (*Dyfrlomycetales*, *Dothideomycetes*), three in *Eriomycetaceae* (*Monoblastiales*, *Dothideomycetes*), and 30 species across 12 families of *Pleosporales* (*Dothideomycetes*). Additional taxa include three species in *Amphisphaeriaceae* and *Sporocadaceae* (*Amphisphaeriales*, *Sordariomycetes*), ten in *Distoseptisporaceae* (*Distoseptisporales*, *Sordariomycetes*), and two in *Magnaporthaceae* and *Ophiocercaceae* (*Magnaporthales*, *Sordariomycetes*). Species delimitations and new taxa establishments were based on morphological characterization, cultural features, and multi-locus phylogenies. A novel genus, *Testudiniscutum*, is introduced, together with 32 new species: *Acrocallymma kevinii*, *Amphisphaeria davidihuangticiae*, *A. hydeimucosa*, *Brunneofusispora kevinimucosa*, *Chromolaenicola hydei*, *Ch. hydeiwikstroemiae*, *Chromolaenomyces davidii*, *Distoseptispora combreticola*, *D. davidalangii*, *D. heptapleuricola*, *D. keviniligustrina*, *D. uncariicola*, *Gaeumannomyces hydeicoicis*, *Leptoparies hydei*, *Leucaenicola hydeinandinae*, *Lophiotrema hydeirubicola*, *Lo. kevinobpyriforme*, *Melomastia kevinhydei*, *Neoheliosia hydeispora*, *N. hydeiverrucosa*, *N. septata*, *Neokalmusia kevinitetradii*, *Neorousoella kevinii*, *Ophioceras hydeanum*, *Paraconiothyrium kevinhydei*, *Paraphaeosphaeria hydeihelleniae*, *Parathyridariella davidiseptata*, *Periconia hydeiguttulosa*, *Pseudochaetosphaeronema hydeiseptatum*, *Pseudoteichospora hydei*, *Seiridium kevinibouchinicola*, and *Testudiniscutum isodonticola*. Fourteen new host records are reported for *Austropleospora ochracea*, *Distoseptispora aquatica*, *D. longispora*, *D. pachyconidia*, *D. yichunensis*, *Lophiostoma japonicum*, *Lophiotrema hydei*, *Lo. mucilaginosus*, *Lo. neohysterioides*, *Periconia alishanica*, *Pe. byssoides*, *Pe. pseudobyssoides*, *Pe. verrucosa*, and *Pseudothyridariella idesia*. Moreover, three new host and geographical records are provided for *Chromolaenicola lampangensis*, *Distoseptispora tectonigena*, and *Parathyridaria ellipsoidea*. *Chromolaenicola nanensis* is synonymized under *Ch. Lampangensis* based on

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morphological and molecular evidence. Detailed descriptions, illustrations, and taxonomic notes are provided for all new taxa and records. This study represents the first comprehensive account of fungi from medicinal plants in China, significantly enriching knowledge of fungal diversity and their ecological associations in medicinal plant ecosystems.

Keywords – 33 new taxa – 17 new records – *Ascomycota* – Diversity – Multi-locus – Phylogeny – Taxonomy

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INTRODUCTION

Medicinal plants are vital natural resources for disease prevention and treatment and play an irreplaceable role in human life due to their unique pharmacological activities and bioactive compounds (Nalawade et al. 2003, Cole et al. 2007, Sofowora et al. 2013, Schmidt & Cheng 2017, Rahman et al. 2019, Ali et al. 2021, Atanasov et al. 2021). It is estimated that more than 80% of the population in developing countries relies primarily on herbal medicines, while approximately 25% of prescribed drugs in developed countries are derived from wild plants (Hamilton 2004, Ekor 2014, Rasool et al. 2020). Notable examples include artemisinin, an antimalarial compound, and paclitaxel, an anticancer drug (Schwikkard & Van Heerden 2006, Zhu & Chen 2019). In addition, many medicinal plants serve as sources of anti-inflammatory, antibacterial, and antiviral agents (Anand et

al. 2019, Adeleye et al. 2022). The quality of medicinal plants is closely linked to clinical safety and efficacy (Abtahi & Nourani 2017) and is strongly influenced by environmental factors such as climate, soil, geography, and microorganisms. Among these, microfungi are increasingly recognized as key determinants of medicinal plant quality, occurring as endophytes, pathogens, or saprobes (Chen et al. 2021a, Keshri et al. 2021, Du et al. 2022, Medina et al. 2020, Yang et al. 2022b).

Microfungi associated with medicinal plants have been studied mainly as endophytes, with emphasis on their isolation, identification, secondary metabolites, pharmacological activities, and pathogenicity (He et al. 2019, Adeleke & Babalola 2021, Du et al. 2022, Khalil et al. 2021). For example, *Fusarium acuminatum*, *Acrocalymma vagum*, and *Paraboeremia putaminum* isolated from *Glycyrrhiza uralensis* produce glycyrrhizin and glycyrrhizic acid, compounds with osmoprotective activity (He et al. 2019). Pathogenic fungi such as *Colletotrichum* (Niu et al. 2016) and pestalotioid taxa (Sun et al. 2023b) are also frequently reported. In contrast, studies of saprobic fungi on medicinal plants remain limited, although they are mainly distributed in *Dothideomycetes* and *Sordariomycetes* (Abtahi & Nourani 2017, Chen et al. 2021a, b, Khalil et al. 2021, Zhang et al. 2024). A few taxa have also been documented from *Agaricomycetes*, *Eurotiomycetes*, *Leotiomycetes*, and freshwater lineages (Sharma et al. 2017, Tran et al. 2022, Wu et al. 2024). These findings highlight that fungal diversity associated with medicinal plants is only partially known, with saprobic taxa remaining underexplored despite their ecological importance.

China is recognized as one of the world's megadiverse countries (Tang et al. 2006, Huang 2011, Ma et al. 2016), with more than 38,000 higher plant species (Chinese Academy of Sciences 2025), of which approximately 18,000 are medicinal (Huang 2024). Southwestern China, particularly Guizhou, Sichuan, and Yunnan provinces, is a hotspot of medicinal plant diversity owing to its unique karst landscapes and heterogeneous environments (Liu et al. 2018, Qian et al. 2020, Wijayawardene et al. 2021, Dou et al. 2023). These provinces also contribute substantially to the supply of commonly used Chinese herbal medicines (Shan et al. 2022, 2023). Given the wide variety and rich resources (Chen et al. 2016, Rasool et al. 2020), medicinal plants will mostly provide a favorable advantage for discovering fungal diversity. Recent studies have reported novel fungi from medicinal plants in this region (Zhang et al. 2018, 2023a, b, Du et al. 2022, 2024a, Sun et al. 2023a, b, Yang et al. 2023, Wu et al. 2024, Li et al. 2024a), but the number of species and host plants surveyed remains limited. Considering the accelerating threats from deforestation, climate change, and overharvesting (Chi et al. 2017), both fungal and plant diversity are at risk, emphasizing the need for targeted exploration.

During the investigation of microfungi associated with medicinal plants in Southwestern China, this study aimed to explore the diversity of ascomycetous taxa. A total of 90 taxa representing 27 genera, 19 families, and six orders were identified, mainly in *Dothideomycetes* and *Sordariomycetes*. We describe 32 new species, introduce one new genus, and report 17 new records (14 new host records and three new host–geographical records). Taxonomic conclusions were based on detailed morphological studies combined with multi-locus phylogenetic analyses (ITS, LSU, SSU, *rpb2*, *tefl- α* , and *tub2*). Comprehensive descriptions, illustrations, and notes are provided for each taxon. This study contributes the first large-scale assessment of micro-fungi on medicinal plants in China and provides a foundation for further studies on their taxonomy, ecology, and potential applications.

MATERIALS AND METHODS

Collection and Examination of Specimens

Specimens were collected from 35 families of medicinal plants (*Acanthaceae*, *Alangiaceae*, *Apocynaceae*, *Araliaceae*, *Asparagaceae*, *Asteraceae*, *Berberidaceae*, *Buxaceae*, *Caprifoliaceae*, *Caryophyllaceae*, *Costaceae*, *Combretaceae*, *Eucommiaceae*, *Euphorbiaceae*, *Fabaceae*, *Helwingiaceae*, *Lamiaceae*, *Liliaceae*, *Magnoliaceae*, *Melastomataceae*, *Meliaceae*, *Oleaceae*, *Orchidaceae*, *Poaceae*, *Polygonaceae*, *Ranunculaceae*, *Rosaceae*, *Rubiaceae*, *Rutaceae*, *Sapindaceae*, *Smilacaceae*, *Solanaceae*, *Taxaceae*, *Thymelaeaceae*, and *Zingiberaceae*) in Southwestern China from October 2020 to November 2022, viz., Guizhou Province (105°41'23"E–106°54'55"E, 26°22'15"N–27°5'1"N, elevation 1,125–1,633 m); Sichuan Province

(102°40'53"E–105°58'35"E, 29°13'2"N–32°41'32"N, elevation 503–2,068 m); and Yunnan Province (100°47'19"E–103°2'32"E, 21°55'34"N–26°19'20"N, elevation 505–2,348 m). The sampling information such as date, host, location, GPS coordinates, etc. were recorded. The host plants were identified based on morphological characteristics and verified using the Kew Gardens Database (<https://mpns.science.kew.org/>) for taxonomic validation (Fig. 1 to Fig. 4).



Figure 1 – Photos of medicinal plant hosts (I). a *Acacia confusa* (Fabaceae). b *Acer palmatum* (Sapindaceae). c *Alangium chinense* (Alangiaceae). d *Amomum kravanh* (Zingiberaceae). e *Asparagus cochinchinensis* (Asparagaceae). f *Arundina graminifolia* (Orchidaceae). g *Bambusa*

tuldoides (Poaceae). h–j *Bletilla striata* (Orchidaceae), flower (j). k *Buxus sinica* (Buxaceae). l *Cercis chinensis* (Fabaceae). m *Citrus medica* (Rutaceae). n *Clematis florida* (Ranunculaceae). o *Coix lacryma-jobi* (Poaceae). p *Combretum densiflorum* (Combretaceae).



Figure 2 – Photos of medicinal plant hosts (II). a *Dahlia pinnata* (Asteraceae). b *Datura metel* (Solanaceae). c *Dianthus superbus* (Caryophyllaceae). d *Eranthemum pulchellum* (Acanthaceae). e, f *Erythrina corallodendron* (Fabaceae). g *Eucommia ulmoides* (Eucommiaceae). h, i *Hellenia speciosa* (Costaceae). j *Helwingia chinensis* (Helwingiaceae). k *Heptapleurum heptaphyllum* (Araliaceae). l *Huangtcia renifolia* (Fabaceae). m *Isodon coetsa* (Lamiaceae). n *Kopsia arborea* (Apocynaceae). o *Ligustrum quihoui* (Oleaceae). p *Lilium brownii* var. *viridulum* (Liliaceae).

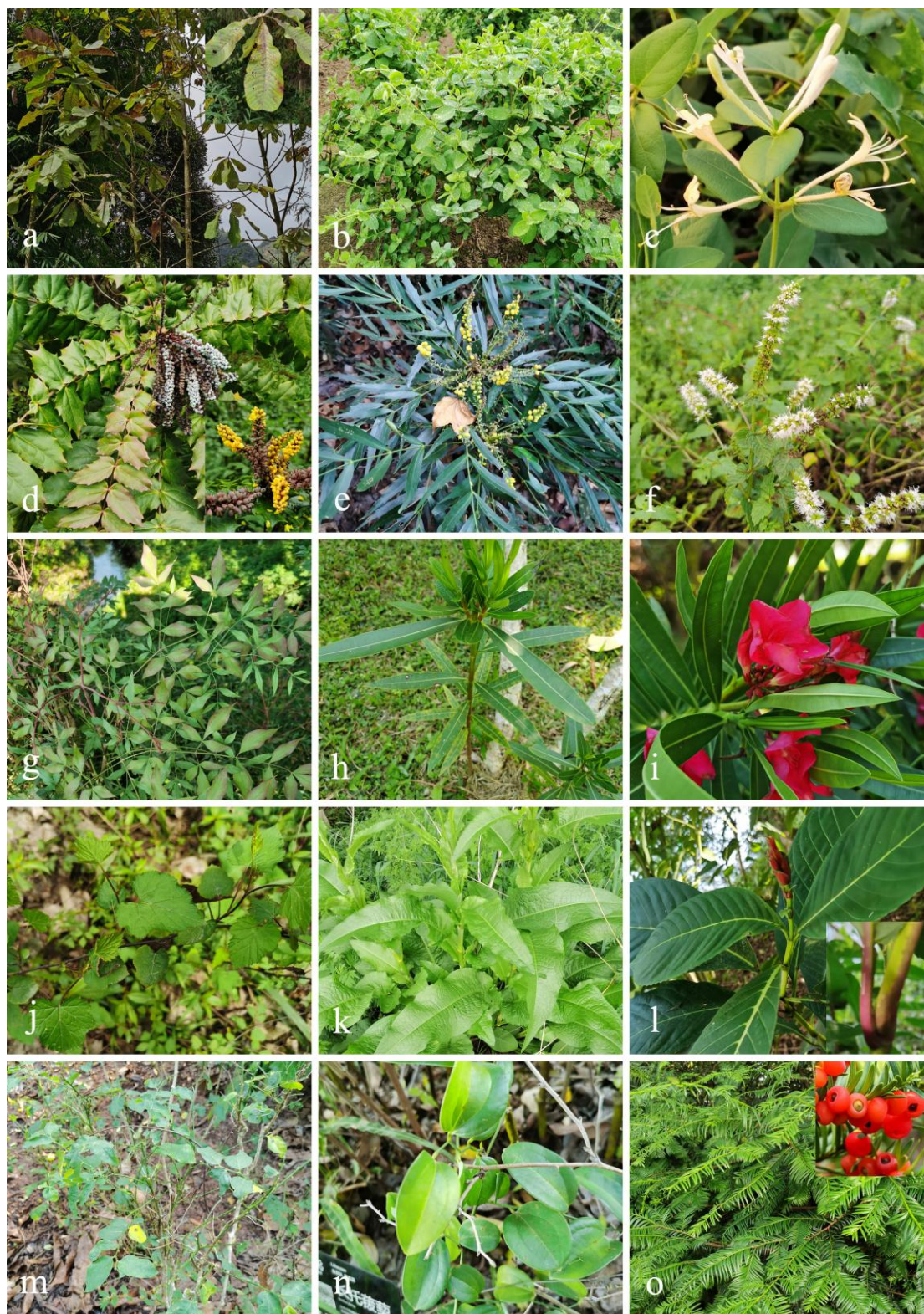


Figure 3 – Photos of medicinal plant hosts (III). a *Magnolia officinalis* var. *biloba* (Magnoliaceae). b, c *Lonicera japonica* (Caprifoliaceae). d *Mahonia bealei* (Berberidaceae). e *Mahonia eurybracteata* (Berberidaceae). f *Mentha canadensis* (Lamiaceae). g *Nandina domestica* (Berberidaceae). h, i *Nerium oleander* (Apocynaceae). j *Rubus corchorifolius* (Rosaceae). k *Rumex acetosa* (Polygonaceae). l *Sanchezia nobilis* (Acanthaceae). m *Sauropus androgynus* (Euphorbiaceae). n *Smilax ferox* (Smilacaceae). o *Taxus wallichiana* var. *chinensis* (Taxaceae).



Figure 4 – Photos of medicinal plant hosts (IV). a *Tetradium ruticarpum* (Rutaceae). b *Toona sinensis* (Meliaceae). c, d *Tibouchina urvilleana* (Melastomataceae). e–h *Uncaria rhynchophylla* (Rubiaceae), flowers (f), single hook (g) and double hooks (h). i *Wikstroemia indica* (Thymelaeaceae). j *Zanthoxylum bungeanum* (Rutaceae).

Specimens, including dead leaves, petioles, stems, twigs, and vines from medicinal plants, were collected and packaged in envelopes, and brought to the laboratory following the method described by Senanayake et al. (2020). Morphological observations were made using a Motic SMZ (Stereoscopic Zoom Microscope) 168 Series dissecting microscope (Motic, Xiamen, China) for fungal structures on natural substrates. The fruiting structures were collected using a syringe needle and transferred to a drop of water on a clean slide. The features were examined and photographed using a Nikon ECLIPSE Ni-U compound microscope fitted with a Nikon DS-Ri2 digital camera. Measurements were carried out by the Tarosoft Image Frame Work v. 0.9.7 software following the procedures outlined by Liu et al. (2010), and images used for photo plates were processed with Adobe Photoshop CC 2018 software (Adobe Systems, San Jose, CA, USA). Single spore isolations were made on potato dextrose agar (PDA, Oxoid) or water agar (WA, Oxoid) and later transferred onto new PDA plates following the methods described by Senanayake et al. (2020). The plates were incubated in an incubator under dark condition at 25 °C, and pure cultures were obtained.

Herbarium specimens were deposited in the Herbarium of Cryptogams, Kunming Institute of Botany Academia Sinica (HKAS), Kunming, China, and in the Herbarium of University of Electronic Science and Technology (HUEST), Chengdu, China. The pure cultures obtained in this study were deposited in the China General Microbiological Culture Collection Center (CGMCC) in Beijing, China and in the University of Electronic Science and Technology Culture Collection (UESTCC), Chengdu, China. The new taxa were registered to the Faces of Fungi database (Jayasiri et al. 2015) and MycoBank (Crous et al. 2004).

DNA extraction, PCR amplification and sequencing

Isolates were grown on PDA media in and incubated in the dark at 25 °C for two to three weeks. Fungal mycelia were scraped off and transferred to 1.5 mL microcentrifuge tubes using a sterilized lancet, for the extraction of genomic DNA. Tsingke Fungus Genomic DNA Extraction Kit (Tsingke Biotech, Shanghai, P.R. China) was used to extract DNA following the manufacturer's instructions. Five gene regions were amplified by Polymerase Chain Reaction (PCR). The internal transcribed spacer region of ribosomal DNA (ITS), nuclear large subunit rDNA (28S, LSU), nuclear small subunit rDNA (18S, SSU), RNA polymerase II second largest subunit (*rpb2*), translation elongation factor 1- α (*tef1- α*) and β -tubulin (*tub2*) were amplified via polymerase chain reaction (PCR). The amplifications were performed in a 25 μ L reaction volume containing 9.5 μ L ddH₂O, 12.5 μ L 2 $\times$ Taq PCR Master Mix with blue dye (Sangon Biotech, Shanghai, P.R. China), 1 μ L of DNA template and 1 μ L of each primer. The PCR product purification was performed using gel extraction technique, followed by Sanger sequencing at Beijing Tsingke Biotechnology (Chengdu) Co., Ltd. in China. The loci, primers and amplification conditions are listed in Table 1.

To better reveal the phylogenetic relationships and taxonomic distinctions of new fungal collections, multi-locus phylogenetic analyses were conducted based on the commonly used loci for different fungal groups (Stielow et al. 2015). The loci and primers used for *Acrocalymma*, *Amphisphaeria*, *Austropleospora*, *Brunneofusispora*, *Chromolaenicola*, *Chromolaenomyces*, *Distoseptispora*, *Gaeumannomyces*, *Leptoparies*, *Leucaenicola*, *Lophiostoma*, *Lophiotrema*, *Melomastia*, *Neoheliosia*, *Neokalmusia*, *Neorousoella*, *Ophioceras*, *Paraconiothyrium*, *Paraphaeosphaeria*, *Parathyridaria*, *Parathyridariella*, *Periconia*, *Pseudochaetosphaeronema*, *Pseudoteichospora*, *Pseudothyridariella*, *Seiridium*, and *Testudiniscutum* are ITS (ITS5/ITS4), LSU (LR0R/LR5), SSU (NS1/NS4), *tef1- α* (TEF1-983F/TEF1-2218R), and *rpb2* (fRPB2-5F/fRPB2-7cR). Additionally, *tub2* (T1/T22) was used for *Amphisphaeria*; *tef1- α* (728F/EF2) was used for *Seiridium*, and *tub2* (T1/Bt2b) was used for both *Paraconiothyrium* and *Paraphaeosphaeria*.

Table 1 Loci, primers and amplification conditions in this study.

Locus	Primers	Optimized PCR Protocols	References
ITS	ITS5	94 °C 3 min; 36 cycles of 94 °C 45 s, 55 °C 55 s,	White et al. (1990)
	ITS4	72 °C 1 min; 10 min at 72 °C; 4 °C on hold	
LSU	LR0R	94 °C 3 min; 36 cycles of 94 °C 45 s, 55 °C 55 s,	Vilgalys & Hester (1990)
	LR5	72 °C 1 min; 10 min at 72 °C; 4 °C on hold	
SSU	NS1	94 °C 3 min; 38 cycles of 94 °C 45 s, 55 °C 50 s,	White et al. (1990)
	NS4	72 °C 1 min; 10 min at 72 °C; 4 °C on hold	
<i>tub2</i>	T1	94 °C 5 min; 38 cycles of 95 °C 40 s, 55 °C 50 s,	Glass & Donaldson (1995)
	Bt2b	72 °C 90 s; 10 min at 72 °C; 4 °C on hold	
	T1	94 °C 5 min; 38 cycles of 95 °C 40 s, 55 °C 50 s,	Glass & Donaldson (1995)
	T22	72 °C 90 s; 10 min at 72 °C; 4 °C on hold	
<i>tef1-α</i>	TEF1-983F	94 °C 3 min; 38 cycles of 94 °C 45 s, 56 °C 55 s,	Rehner & Buckley (2005)
	TEF1-2218R	72 °C 1 min; 10 min at 72 °C; 4 °C on hold	
	EF1-728F	94 °C 3 min; 35 cycles of 94 °C 45 s, 55 °C 55 s,	Carbone & Kohn (1999), O'Donnell et al. (1998)
	EF2	72 °C 1 min; 10 min at 72 °C; 4 °C on hold	
<i>rpb2</i>	fRPB2-5F	95 °C 5 min; 40 cycles of 95 °C 15 s, 56 °C 50 s,	Liu et al. (1999)
	fRPB2-7cR	72 °C 2 min; 10 min at 72 °C; 4 °C on hold	

Abbreviations: ITS: Internal transcribed spacer regions; LSU: Nuclear large subunit rDNA; SSU: Nuclear small subunit rDNA; *tub2*: β -tubulin; *tef1- α* : Translation elongation factor 1- α ; *rpb2*: RNA polymerase II second largest subunit.

Phylogenetic analyses

In this study, the taxa included in the phylogenetic analyses were selected and obtained from relevant previous studies and GenBank. Alignments for each locus were made in MAFFT v. 7 (<http://mafft.cbrc.jp/alignment/server/>) (Katoh & Standley 2013) and checked visually using AliView

(Larsson 2014). The alignments were trimmed using trimAl v 1.2 (Capella-Gutierrez et al. 2009) with minimal coverage (-cons) = 0.8 and gap threshold (-gt) = 0.6. Single locus alignments were combined using Sequence Matrix 1.7.8 (Vaidya et al. 2011). Maximum likelihood (ML) and Bayesian inference (BI) analyses were employed to assess phylogenetic relationships as detailed in Dissanayake et al. (2020a).

ML analyses were performed with RAxML-HPG v.8 on XSEDE (8.2.12) (Stamatakis 2006, Stamatakis et al. 2008) through the CIPRES Science Gateway V. 3.3 (<https://www.phylo.org/portal2/login!input.action>) (Miller et al. 2010). The tree search included 1,000 non-parametric bootstrap replicates and the best scoring tree was selected among suboptimal trees from each run by comparing likelihood scores under the GTRGAMMA substitution model. The resulting replicates were plotted onto the best scoring tree obtained previously. The ML bootstrap values equal to or greater than 75% were marked near each node.

BI analyses were performed in MrBayes 3.2.6 (Ronquist et al. 2012). The program MrModeltest 2 v. 2.3 (Nylander 2008) was used to determine the best nucleotide substitution model for each data partition. Posterior probabilities (PP) (Rannala & Yang 1996) were determined by Markov chain Monte Carlo sampling (MCMC). Six simultaneous Markov chains were run for 10 million generations, and trees were sampled at every 1,000th generation, and ending the run automatically when the standard deviation of split frequencies dropped below 0.01. The first 25% of saved trees, representing the burn-in phase of the analysis, were discarded. The remaining trees were used for calculating posterior probabilities in the majority rule consensus tree (Larget & Simon 1999). The PP values equal to or greater than 0.95 were marked near each node.

Phylogenetic trees were produced with Fig Tree v. 1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>) and the layout was created in Adobe Illustrator CS6 software (Adobe Systems, USA).

RESULTS

Taxonomy

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

MycoBank number: MB501481; Facesoffungi number: FoF14145

Dyfrlolomycetales K.L. Pang, K.D. Hyde & E.B.G. Jones, Fungal Diversity 63: 7 (2013)

MycoBank number: MB805281; Facesoffungi number: FoF07670

Notes – *Dyfrlolomycetales* was regarded as an order of marine fungi within *Dothideomycetes*, which was introduced by Hyde et al. (2013) to accommodate the family *Dyfrlolomycetaceae*. Later, *Dyfrlolomycetaceae* was synonymized under the family *Pleurotremataceae* by Maharachchikumbura et al. (2016). Currently, *Pleurotremataceae*, which is comprising three genera, *Dyfrlolomyces*, *Melomastia*, and *Pleurotrema*, was accepted within this order (Hyde et al. 2024). The divergence time of *Dyfrlolomycetales* is established at approximately 76 (38–125) MYA in crown age and 174 (113–243) MYA in stem age (Liu et al. 2017).

Pleurotremataceae Walt. Watson, New Phytologist 28: 113 (1929)

MycoBank number: MB557099; Facesoffungi number: FoF01911

Notes – *Pleurotremataceae* was proposed by Watson (1929) to accommodate the monotypic genus *Pleurotrema* with *P. polysemum* as the type species. Pang et al. (2013) established the family *Dyfrlolomycetaceae* and was later synonymized under the *Pleurotremataceae* by Maharachchikumbura et al. (2016). *Pleurotremataceae* is characterized by immersed ascomata, with a clypeus on the substrate, bitunicate, cylindrical asci, and hyaline, multi-septate, broadly fusiform ascospores with or without a sheath (Watson 1929, Barr 1994, Pang et al. 2013). Currently, three genera, *Dyfrlolomyces*, *Melomastia*, and *Pleurotrema* were accepted in *Pleurotremataceae* (Wijayawardene et al. 2017, Hongsanan et al. 2020a, Kularathnage et al. 2023, Hyde et al. 2024).

Melomastia Nitschke ex Sacc., Conspectus generum pyrenomycetum italicorum systemate carpologico dispositum: 14 (1875)

MycoBank number: MB3118; Facesoffungi number: FoF07673

Notes – *Melomastia* was introduced by Saccardo (1875) to accommodate *M. mastoidea* (= *M. friesii*) as the type species. Norphanphoun et al. (2017) formally confirmed the taxonomic placement of *Melomastia* in *Pleurotremataceae*. The genera *Melomastia* and *Dyffrolomyces* shared a close relationship. Li et al. (2022) treated *Dyffrolomyces* as a synonym of *Melomastia*. However, Kularathnage et al. (2023) reinstated *Dyffrolomyces* as a distinct genus based on morphological and phylogenetic evidence, accommodating *D. tiomanensis* (= *M. tiomanensis*, the type species) and *D. chromolaenae* (= *M. chromolaenae*). The sexual morph of *Melomastia* is characterized by immersed, ostiolate ascomata, unitunicate, 8-spored, cylindrical asci, and ovoid, hyaline, multi-septate, fusiform to oblong ascospores with or without gelatinous sheath (Norphanphoun et al. 2017, Li et al. 2022, Kularathnage et al. 2023, Xu et al. 2024). However, the asexual morph of *Melomastia* has yet to be discovered or reported (Norphanphoun et al. 2017, Li et al. 2022, Xu et al. 2024).

Melomastia kevinhydei H.Z. Du & Jian K. Liu, sp. nov.

Fig. 5

MycoBank number: MB857555; Facesoffungi number: FoF17825

Etymology – The epithet '*kevinhydei*' named for in honor of Prof. Kevin D. Hyde for his contribution to ascomycetes taxonomy.

Holotype – HKAS 132455

Saprobic on dead twigs of *Nerium oleander* L. (*Apocynaceae*). Visible as black raised dots. Sexual morph: *Ascomata* 542–790 µm diam. × 502–788 µm high ($\bar{x}$ = 718 × 645 µm, n = 20), perithecial, semi-immersed to erumpent, solitary or gregarious, subglobose to obpyriform, carbonaceous, uniloculate to multiloculate, dark brown to black, ostiolate, papillate. *Ostiole* central or eccentric, carbonaceous, blackish brown, opening by a pore, filled with periphyses. *Peridium* 25–31 µm wide ($\bar{x}$ = 28 µm, n = 20), comprising several layers of *textura angularis* cells, brown to dark brown, thick-walled. *Hamathecium* comprising 2–3 µm wide, hyaline, filiform, unbranched, septate, guttulate pseudoparaphyses, embedded in a gelatinous matrix, longer than the asci. *Asci* 99–140 × 7–13.5 µm ($\bar{x}$ = 125 × 10 µm, n = 20), 8-spored, bitunicate, cylindric, straight or flexuous, apically obtuse, short pedicellate, rounded at the apex, smooth-walled. *Ascospores* 14–17 × 4.6–6 µm ($\bar{x}$ = 16 × 5.5 µm, n = 30), uniseriate, hyaline, ellipsoid to oblong or broadly fusiform with round ends, 3-celled, 2-septate, constricted at the central septum, with guttules in each cell, smooth-walled, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 10–12 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, regular, dense mycelium, white, center slightly elevated. In reverse, brown to dark brown at the center, pale brown at the edge.

Material examined – China, Yunnan Province, Kunming City, Chenggong District, Wujiaying Street, 102°51'7"E, 24°50'6"N, elevation 1,920 m, on dead twigs of *Nerium oleander* (*Apocynaceae*), 12 November 2022, H.Z. Du, S772 (HKAS 132455, holotype; HUEST 23.0580, isotype); ex-type living culture UESTCC 25.0042, ex-isotype living culture UESTCC 23.0579.

GenBank accession numbers – UESTCC 25.0042 = ITS: PQ773401, LSU: PQ773421, SSU: PQ773437, *tefl-α*: PV059193; UESTCC 23.0579 = ITS: PQ773402, LSU: PQ773422, SSU: PQ773438, *tefl-α*: PV059194.

Notes – Multi-locus phylogenetic analyses revealed that *Melomastia kevinhydei* (UESTCC 25.0042 and UESTCC 23.0579) clustered together with *M. italica* (MFLUCC 15-0160, ex-type strain) and *M. chinensis* (GMB 6242, ex-type strain) and formed a distinct lineage. This clade can be recognized as a separate species based on molecular evidence (Fig. 6). Morphologically, *M. kevinhydei* (HKAS 132455, holotype) is similar to *M. italica* (MFLU 15-0228, holotype) in having semi-immersed to erumpent, subglobose to obpyriform ascomata, 8-spored, bitunicate, cylindric asci, hyaline, uniseriate, guttulate, 2-septate ascospores with mucilaginous sheaths (Norphanphoun et al. 2017), but differs from *M. italica* by the larger ascomata (542–790 µm × 502–788 µm vs. up to 500

$\mu\text{m} \times 400\text{--}500 \mu\text{m}$), and larger ascospores ($14\text{--}17 \times 4.6\text{--}6 \mu\text{m}$ vs. $8.8\text{--}10.5 \times 2.8\text{--}4.1 \mu\text{m}$). Additionally, *M. chinensis* (GMB6242, holotype) can be distinguished from *M. kevinhydei* in having biseriate, broadly fusiform ascospores with acute ends, tapering toward the poles, 3-septate, and lacking a mucilaginous sheath. Therefore, the establishment of the new species, *M. kevinhydei*, is justified by morphological and phylogenetic evidence.



Figure 5 – *Melomastia kevinhydei* (HKAS 132455, holotype). a Host *Nerium oleander*. b–d Appearance of ascomata on host surface. e Vertical section of ascomata. f Peridium. g Hamathecium. h–k Asci. l, m Ascospores. n Ascospore stained with Indian ink showing the mucilaginous sheath. o Germinated ascospore. p, q Colonies on PDA, above (p) and below (q). Scale

bars: e = 200 μ m, f = 20 μ m, g, l–o = 10 μ m, h–k = 30 μ m.

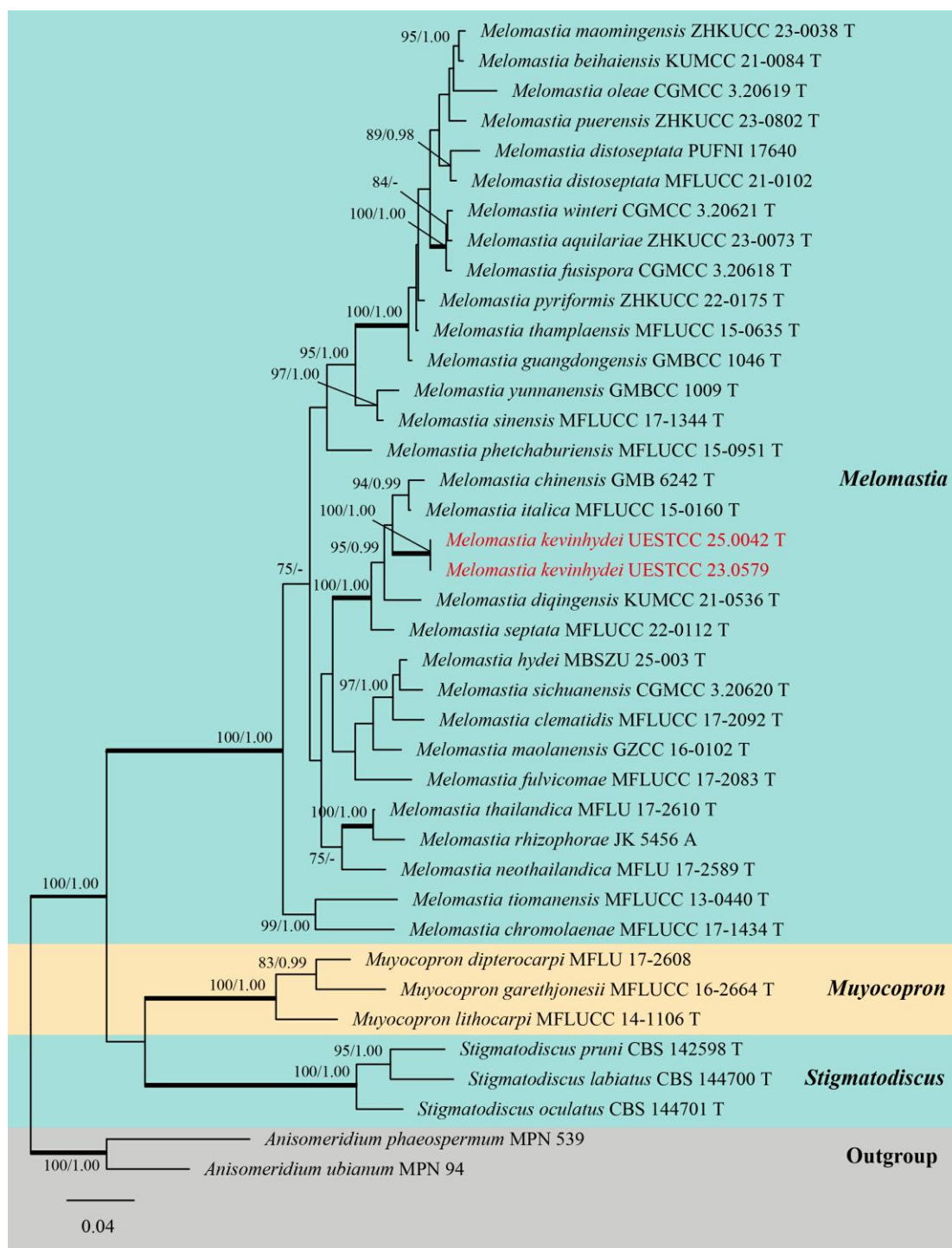


Figure 6 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined LSU, SSU, ITS, and *tefl-a* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Anisomeridium phaeospermum* (MPN539) and *A. ubianum* (MPN94). The best scoring RAxML tree with a final likelihood value of -17,393.212977 is presented. The matrix had 1,261 distinct alignment patterns, with 24.95% of undetermined characters or gaps, the tree-length is 1.501991. Estimated base frequencies were as follows: A = 0.231605, C = 0.270874, G = 0.292658, T = 0.204863, with substitution rates AC = 1.238200, AG = 2.422019, AT = 1.198883, CG = 1.109460,

CT = 8.179097, GT = 1.000000; gamma distribution shape parameter alpha = 0.240455. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009988 (the critical value for the topological convergence diagnostic is below 0.01).

Monoblastiales Lücking, M.P. Nelsen & K.D. Hyde, Fungal Diversity 63: 8 (2013)

MycoBank number: MB805299; Facesoffungi number: FoF08069

Notes – *Monoblastiales* was introduced by Hyde et al. (2013) to accommodate the single family *Monoblastiaceae*. The order includes both lichenized and non-lichenized fungi within the *Dothideomycetes*, primarily in crustose forms and typically found as epiphytes on tree bark. Compared to the other two lichenized orders, *Strigulales* and *Trypetheliales*, *Monoblastiales* is morphologically distinguished from *Strigulales* by the net-like physes and from most *Trypetheliales* in the euseptate ascospores with few septa (Hyde et al. 2013). The divergence time of *Monoblastiales* is established at approximately 148 (83–228) MYA in crown age and 254 (174–337) MYA in stem age (Liu et al. 2017).

Eriomycetaceae Huanraluek & Hyde, Fungal Diversity 100: 146 (2020)

MycoBank number: MB557099; Facesoffungi number: FoF06311

Notes – *Eriomycetaceae* was introduced by Hyde et al. (2020b) to accommodate five genera *Eriomyces* (type genus), *Funbolia*, *Heleiosa*, *Phellinocrescentia*, and *Pseudopassalora* (Crous et al. 2011a, b, 2014b, Hyde et al. 2020b). Subsequently, Zhang et al. (2023a) resurrected the family of *Eriomycetaceae* to accommodate nine non-lichenized genera, namely *Eriomyces*, *Funbolia*, *Haudseptoria*, *Heleiosa*, *Italiotungus*, *Karstiomyces*, *Neoheliosia*, *Phellinocrescentia*, and *Pseudopassalora*, and assigned *Eriomycetaceae* within *Monoblastiales* (Hongsanant et al. 2020b, Hyde et al. 2020b, Mortimer et al. 2021). The sexual morph of *Eriomycetaceae* is characterized by immersed, solitary or aggregated ascomata; 4–8-spored, or poly-spored asci, bitunicate, cylindrical to cylindric-clavate with chambers; hyaline, oblong to allantoid or ellipsoidal to fusiform ascospores. The asexual morph of coelomycetous is characterized by pycnidial conidiomata, phialidic conidiogenous cells, and hyaline, aseptate, ellipsoidal to tear-drop-shaped conidia. *Hyphomycetous* species have solitary, micronematous to macronematous conidiophores, terminal, lateral, or integrated conidiogenous cells, and fusoid-ellipsoidal to subcylindrical, aseptate to multi-septate conidia (Hyde et al. 2020b, Zhang et al. 2023a).

Neoheliosia Mortimer, Frontier in Microbiology 12 (no. 654683): 6 (2021)

MycoBank number: MB838517; Facesoffungi number: FoF11960

Notes – *Neoheliosia* was introduced by Mortimer et al. (2021) to accommodate *N. lincangensis* as the type species and was assigned to *Monoblastiaceae*. It is phylogenetically close to *Heleiosa* but differs by the ornamentation of its ascospores. *Neoheliosia* has narrowly ovoid to clavate, 1-septate, dark brown, guttulate ascospores with conically rounded ends and faint longitudinal striations, lacking any appendages, while *Heleiosa* is characterized by ellipsoidal to fusiform, two-celled, brown ascospores with numerous cilia-like subapical appendages at each end (Kohlmeyer et al. 1996, Mortimer et al. 2021).

Neoheliosia hydeispora N. Wu, H.Z. Du & Jian K. Liu, sp. nov.

Fig. 7

MycoBank number: MB855418; Facesoffungi number: FoF17969

Etymology – The epithet ‘*hydeispora*’ is a combination of Prof. Kevin D. Hyde’s last name and the ellipsoidal ascospores, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132395

Saprobic on dead twigs of *Uncaria rhynchophylla* (Miq.) Miq. (*Rubiaceae*). Visible as black dots. Sexual morph: *Ascomata* 190–260 µm diam. × 192–271 µm high ($\bar{x}$ = 225 × 231 µm, n = 20), solitary, scattered, immersed to erumpent, subglobose or obpyriform, dark brown to black, coriaceous, ostiolate, with papilla. *Ostiole* 45–60 µm wide × 49–64 µm high ($\bar{x}$ = 52 × 54 µm, n = 20), central or eccentric, brittle, filled with periphyses. *Peridium* 18–29 µm wide ($\bar{x}$ = 24.5 µm, n = 20), coriaceous,

composed of several layers of thin to thick-walled cells of *textura angularis*, with 3–5 outer layers of brown to dark brown cells and 1–2 inner layers of hyaline to pale brown cells. *Hamathecium* 1.5–2 μm wide, comprising sparse, non-septate, numerous, filamentous, hyaline, branched pseudoparaphyses, intermixed with asci. *Asci* 96.5–119 $\times$ 9–12 μm ($\bar{x}$ = 106 $\times$ 10.5 μm , n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, furcate pedicel, rounded and thick-walled at the apex, hyaline when young, brown when mature. *Ascospores* 10–19 $\times$ 5.5–9 μm ($\bar{x}$ = 15 $\times$ 7.5 μm , n = 30), slightly overlapping, uniseriate, narrowly ovoid to ellipsoidal, 1-septate and slightly constricted at the septum, initially hyaline, becoming brown to dark brown at maturity, with rounded ends, smooth-walled, tiny verrucose or two obvious guttules, without appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 12 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 35–37 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense, regular edge, surface not smooth, grayish green, center slightly elevated, and occur as a white ring at the edge. In reverse, grayish white to grayish green, with a white outer ring.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong City, Xishuangbanna South Medicinal Plant Garden, 100°47'20"E, 22°0'25"N, elevation 520 m, on dead twigs of *Uncaria rhynchophylla* (*Rubiaceae*), 8 November 2022, N. Wu & H.Z. Du, W327 (HKAS 132395, holotype; HUEST 23.0421, isotype); ex-type living culture UESTCC 24.0229, ex-isotype living culture UESTCC 23.0420.

GenBank accession numbers – UESTCC 24.0229 = ITS: PQ394058, LSU: PQ184703, *tefl- α* : PQ346504, *rpb2*: PQ379989; UESTCC 23.0420 = ITS: PQ394016, LSU: PQ184667, *tefl- α* : PQ338768, *rpb2*: PQ379931.

Notes – *Neohelleiosa hydeispora* (UESTCC 24.0229 and UESTCC 23.0420) formed a distinct lineage and was sister to *N. septata* with statistical support of 85% MLBS/1.00 BIPP (Fig. 11). However, *N. hydeispora* (UESTCC 24.0229, ex-type strain) can be distinguished from *N. septata* (CGMCC 3.27283, ex-type strain) by 9/512 bp (1.8%, 2 gaps) in ITS, 22/1146 bp (2.1%, 13 gaps) in LSU, 8/808 bp (0.99%, without gaps) in *rpb2* and 8/903 bp (0.88%, without gaps) in *tefl- α* sequence data. Morphologically, as the asexual morph of *N. hydeispora* and sexual morph of *N. verrucosisporea* are undetermined, morphological characteristics of them cannot be compared. However, comparison of the ex-type strains between *N. hydeispora* (UESTCC 24.0229) and *N. verrucosisporea* (UESTCC 24.0230) revealed the differences of 21/492 bp (4.3%, 2 gaps) in ITS, 13/825 bp (1.6%, 6 gaps) in LSU, 103/1070 bp (9.6%, 3 gaps) in *rpb2*, and 42/905 bp (4.6%, 2 gaps) in *tefl- α* sequence data. Therefore, we introduce *N. hydeispora* as a new species, isolated from *Uncaria rhynchophylla* in Yunnan Province, China.

Neohelleiosa hydeiverrucosa H.Z. Du, N. Wu & Jian K. Liu, sp. nov.

Fig. 8

MycoBank number: MB855420; Facesoffungi number: FoF17971

Etymology – The epithet '*hydeiverrucosa*' is a combination of Prof. Kevin D. Hyde's last name and the verrucose conidia, acknowledging his significant contributions to ascomycetes taxonomy.

Holotype – HKAS 132393

Saprobic on dead twigs of *Arundina graminifolia* (D. Don) Hochr. (*Orchidaceae*). Visible as black dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 140–173 μm diam. $\times$ 121–129 μm high ($\bar{x}$ = 155 $\times$ 126 μm , n = 20), solitary, scattered, immersed to slightly erumpent, globose to subglobose, dark brown to black, unilocular, glabrous. *Ostiole* indistinct. *Conidiomatal wall* 13–21.5 μm ($\bar{x}$ = 17 μm , n = 20) wide, composed of several layers of *textura angularis* with thin-walled cells, hyaline and pale brown inwardly, and becoming brown towards the apex. *Conidiophores* arising from innermost layer of basal walls, hyaline, subcylindrical, short, thick- and smooth-walled. *Conidiogenous cells* 2.5–5 μm ($\bar{x}$ = 4 μm , n = 20) long, 2–3.5 μm ($\bar{x}$ = 2.5 μm , n = 30) wide, integrated or discrete, determinate, smooth-walled, hyaline, cylindrical to subcylindrical or irregular. *Conidia* 15–32 $\times$ 3–5 μm ($\bar{x}$ = 25 $\times$ 4 μm , n = 30), hyaline, fusiform or clavate, straight or slightly curved, mostly 3–4-septate, occasionally aseptate or 1–2-septate,

verrucose, smooth-walled, with a narrow and obtuse apex, and a truncate and rounded base.



Figure 7 – *Neoheliospora hydeispora* (HKAS 132395, holotype). a Host *Uncaria rhynchophylla*. b–d Ascomata on host substrate. e, f Vertical section of ascomata. g–i Asci. j Hamathecium. k–q Ascospores. r Germinated ascospore. s, t Colonies on PDA, above (s) and below (t). Scale bars: e, f = 50 μ m, g–j = 20 μ m, k–r = 10 μ m.

Culture characteristics – Conidia germinated on PDA within 12 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense, regular edge, milky white of the whole colony, and in reverse, pale yellow in the center, white at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong City, Xishuangbanna South Medicinal Plant Garden, 100°47'20"E, 22°0'25"N, elevation 520 m, on dead twigs of *Arundina graminifolia* (Orchidaceae), 11 November 2022, H.Z. Du, S540 (HKAS 132393, holotype; HUEST 23.0419, isotype); ex-type living culture UESTCC 24.0230, ex-isotype living culture UESTCC 23.0418; *ibid.*, S543 (HUEST 23.0420, paratype), ex-paratype living culture UESTCC 23.0419.

GenBank accession numbers – UESTCC 24.0230 = ITS: PQ394060, LSU: PQ184705, *tefl-α*: PQ346506, *rpb2*: PQ379991; UESTCC 23.0418 = ITS: PQ394021, LSU: PQ184672, *tefl-α*: PQ338772, *rpb2*: PQ379935; UESTCC 23.0419 = ITS: PQ394020, LSU: PQ184671, *tefl-α*: PQ338771, *rpb2*: PQ379934.

Notes – Multi-locus phylogeny showed that *Neoheliosia hydeiverrucosa* (UESTCC 24.0230, UESTCC 23.0418, and UESTCC 23.0419) clustered together with a strong support (100% MLBS/1.00 BIPP) and formed a well-supported clade closely related to *N. hydeispora* and *N. septata* (Fig. 11). *Neoheliosia hydeiverrucosa* (HKAS 132393, holotype) shares similar asexual morphology with *N. septata* (HKAS 132391, holotype) having hyaline and shorter conidiophores, cylindrical to subcylindrical conidiogenous cells and hyaline, clavate conidia. However, the conidia of *N. septata* are larger than those of *N. hydeiverrucosa* (36–50 × 4–5 μm vs. 15–32 × 3–5 μm), and the conidial septum of *N. septata* is more than *N. hydeiverrucosa* (7–9 vs. 3–4). According to the nucleotide base pair differences of *N. hydeispora* and *N. septata*, we identify three isolates obtained in this study as a new species.

Neoheliosia septata H.Z. Du & Jian K. Liu, sp. nov.

Figs 9, 10

Mycobank number: MB855419; Facesoffungi number: FoF17970

Etymology – The epithet “*septata*” refers to the distinct septa observed in mature conidia of the asexual morph in genus *Neoheliosia*.

Holotype – HKAS 132391

Sexual morph: *Saprobia* on dead twigs of *Helwingia chinensis* Batalin (*Helwingiaceae*). Visible as black or dark brown dots. *Ascomata* 181–299 μm diam. × 154–352 μm high ($\bar{x}$ = 213 × 229 μm, *n* = 20), solitary to gregarious, scattered, immersed to erumpent, globose to subglobose or obpyriform, dark brown to black, coriaceous, ostiolate, with minute papilla. *Ostioles* 110–139 wide × 122–137 μm high ($\bar{x}$ = 125 × 129 μm, *n* = 20), papillate, blackish brown, filled with periphyses. *Peridium* 23–37 μm wide ($\bar{x}$ = 29 μm, *n* = 20), coriaceous, composed of several layers of thin to thick-walled cells of *textura angularis*, hyaline and pale brown inwardly, and becoming dark towards the apex. *Hamathecium* 1–2.5 μm wide, comprising of sparse, non-septate, numerous, filamentous, hyaline, branched pseudoparaphyses, intermixed with the asci. *Asci* 80–119 × 8.5–11.5 μm ($\bar{x}$ = 103 × 10 μm, *n* = 30), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, furcate pedicel, rounded and thick-walled at the apex, with a distinct ocular chamber. *Ascospores* 11–24 × 6–9 μm ($\bar{x}$ = 15 × 7 μm, *n* = 30), overlapping uniseriate, narrowly ovoid to ellipsoidal, 1-septate and slightly constricted at the septum, initially hyaline, becoming dark brown at maturity, with rounded ends, smooth-walled, tiny verrucose or two obvious guttules, without any appendages. Asexual morph: *Saprobia* on dead twigs of *Lonicera japonica* Thunb. (*Caprifoliaceae*). Visible as black dots. Coelomycetous. *Conidiomata* 110–207 μm diam. × 111–219 μm high ($\bar{x}$ = 136 × 134 μm, *n* = 20), solitary, scattered, immersed to slightly erumpent, globose to subglobose or obpyriform, dark brown to black, unilocular, glabrous. *Ostiole* indistinct. *Conidiomatal wall* 8.5–10.5 μm wide ($\bar{x}$ = 10 μm, *n* = 20), composed of several layers of *textura angularis* with thin-walled cells, hyaline and pale brown inwardly, and becoming brown towards the apex. *Conidiophores* arising from innermost layers of basal wall, hyaline, subcylindrical, to irregular septate, thick- and smooth-walled. *Conidiogenous cells* 5–8 μm long ($\bar{x}$ = 6 μm, *n* = 30) × 3.5–5 μm wide ($\bar{x}$ = 4 μm, *n* = 30), integrated or discrete, determinate, smooth-walled, hyaline, cylindrical to subcylindrical or irregular. *Conidia* 36–50 × 4–5 μm ($\bar{x}$ = 43 × 5 μm, *n* = 30), hyaline, fusiform or clavate, straight or slightly curved, mostly 7–9-septate, occasionally 4–5-septate, tiny verrucose, smooth-walled, with a narrow and obtuse apex, and a truncate and rounded base.

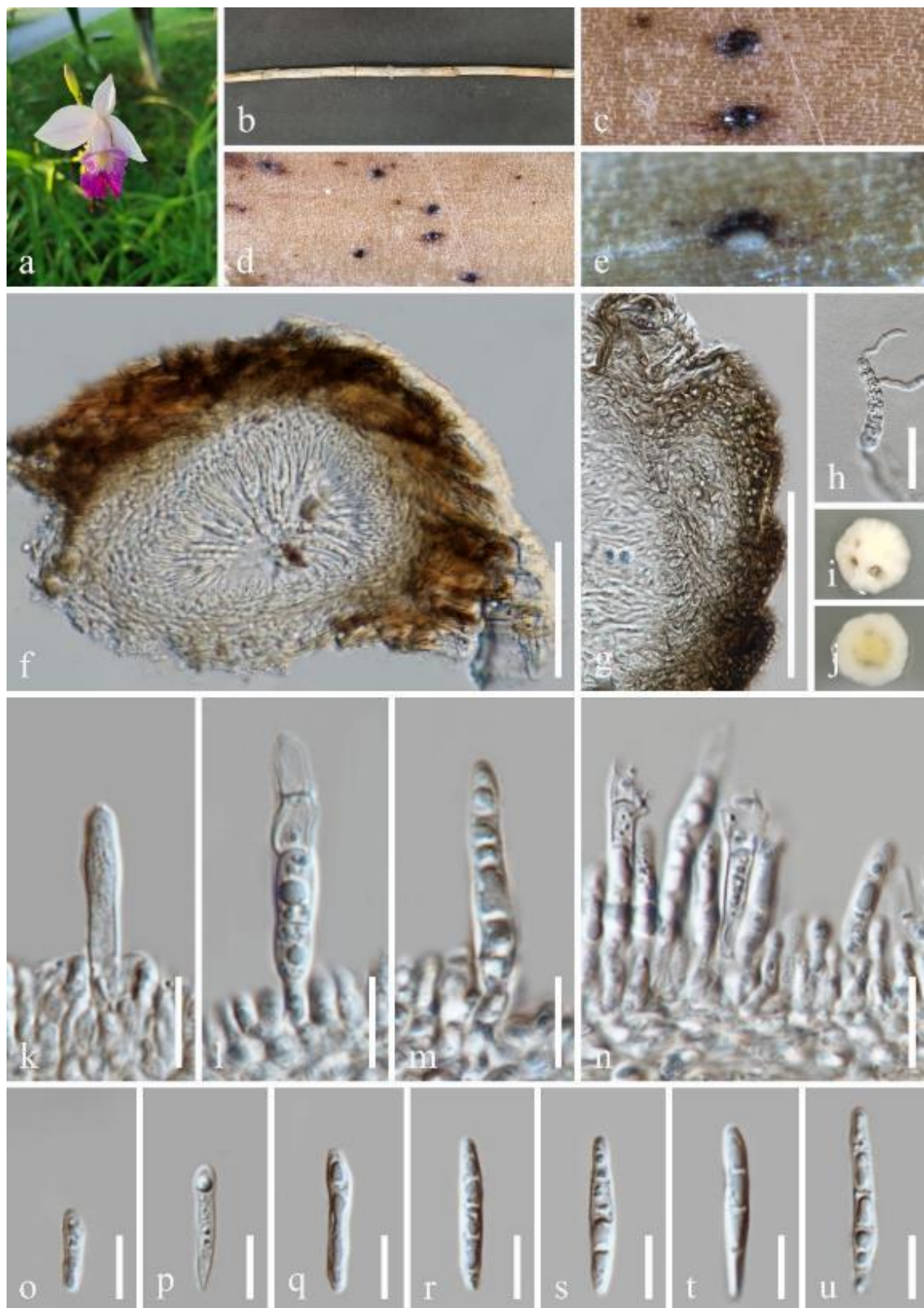


Figure 8 – *Neoheliosia hydeiverrucosa* (HKAS 132393, holotype). a Host *Arundina graminifolia*. b A twig of *A. graminifolia*. c–e Appearance of conidiomata on host surface. f Vertical section of conidiomata. g Conidiomatal wall. h Germinated conidium. i, j Colony on PDA, above (i) and below (j). k–n Conidiogenous cells and conidia. o–u conidia. Scale bars: f, g = 50 µm, h = 20 µm, k–u = 10 µm.



Figure 9 – The sexual morph of *Neoheliosia septata* (HKAS 132391, holotype). a Host *Helwingia chinensis*. b Twigs of *H. chinensis*. c–f Appearance of ascomata on host surface. g, h Vertical section of ascomata. i Structure of peridium. j Hamathecium. k–n Asci. o–v Ascospores. w Germinated ascospore. x, y Colony on PDA, above (x) and below (y). Scale bars: g, h = 100 μ m, i, j = 20 μ m, k–n = 30 μ m, o–w = 10 μ m.

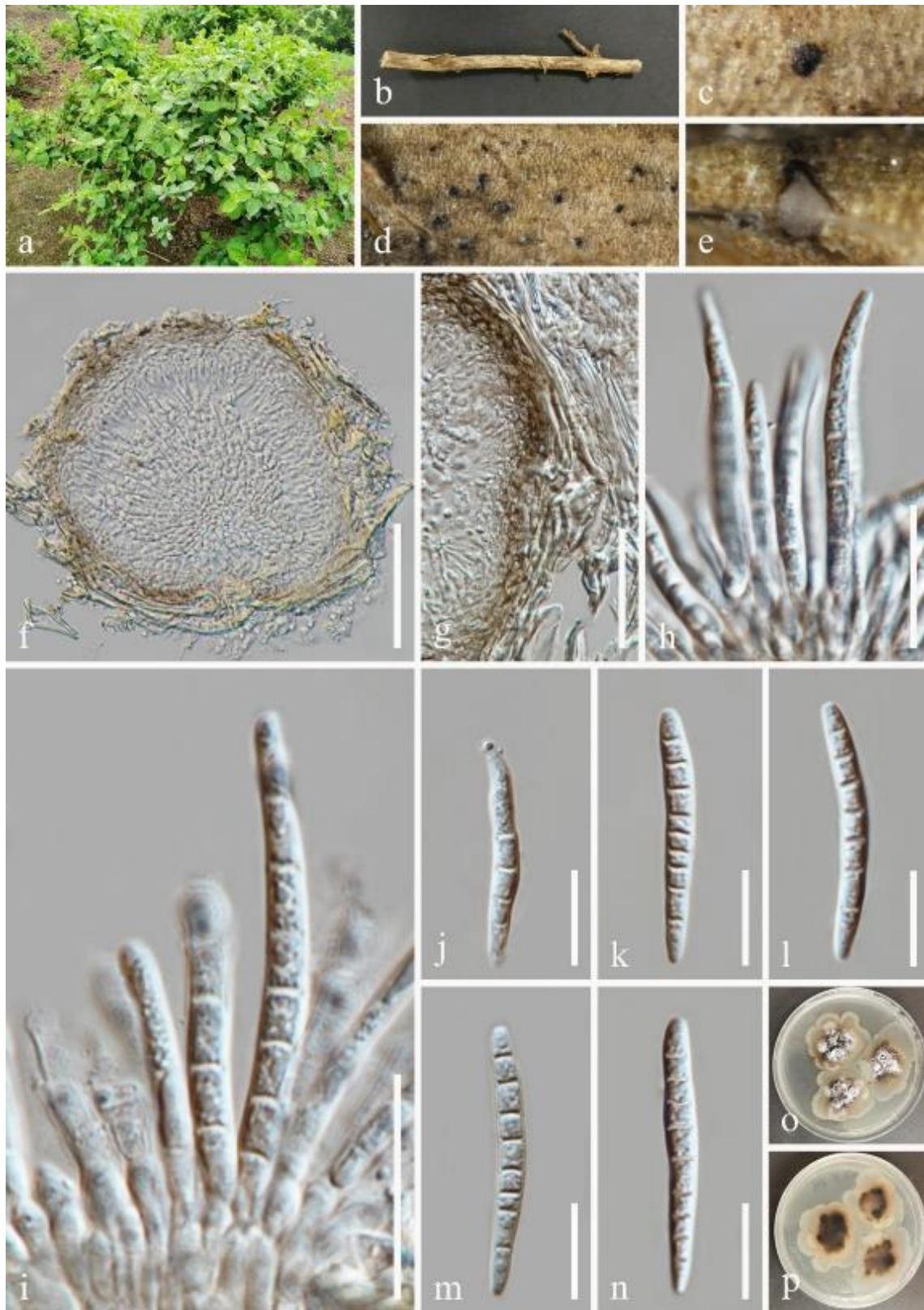


Figure 10 – The asexual morph of *Neohelleiosa septata* (HKAS 132392, paratype). a Host *Lonicera japonica*. b A twig of *L. japonica*. c–e Appearance of conidiomata on host surface. f Vertical section of conidiomata. g Conidiomatal wall. h, i Conidiogenous cells and conidia. j–n conidia. o, p Colonies on PDA, above (o) and below (p). Scale bars: f = 50 μ m, g = 30 μ m, h, i = 20 μ m, j–n = 15 μ m.

Culture characteristics – Both ascospores and conidia germinated on PDA within 12 h, and germ tubes are produced from both ends. Sexual morph: Colonies growing on PDA reached 18–22

mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense, irregular edge, milky white, with mucous substance, and the reverse is similar in color. Asexual morph: Colonies growing on PDA reached 25–27 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, irregular in shape, medium dense, slightly raised to umbonate or convex, surface rough, radially striated with lobate edge, white at the center, pale yellowish white at the edge. In reverse, brown to dark brown at the center, pale yellowish white at the edge, radiating outwards with irregular ring.

Material examined – China, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 102°44'24"E, 25°8'27"N, elevation 1,922 m, on dead twigs of *Helwingia chinensis* (*Helwingiaceae*), 11 November 2022, H.Z. Du, S718 (HKAS 132391, holotype; HUEST 23.0416, isotype); ex-type living culture CGMCC 3.27283, ex-isotype living culture UESTCC 23.0415; *ibid.*, S750 (HUEST 23.0417, paratype), ex-paratype living culture UESTCC 23.0416; *ibid.*, Dongchuan District, Tuobuka Town, 103°2'32"E, 26°19'20"N, elevation 2,348 m, on dead twigs of *Taxus wallichiana* var. *chinensis* (Pilg.) Florin (*Taxaceae*), 29 March 2022, Q. J. Shang, S515 (HUEST 23.0415, paratype), ex-paratype living culture UESTCC 23.0414; *ibid.*, Sichuan Province, Guangyuan City, Chaotian District, Qingquan Village, 105°58'35"E, 32°41'32"N, elevation 820 m, on dead twigs of *Lonicera japonica* (*Caprifoliaceae*), 19 April 2021, H.Z. Du, S224 (HKAS 132392 = HUEST 23.0418, paratype), ex-paratype living culture UESTCC 23.0417.

GenBank accession numbers – CGMCC 3.27283 = ITS: PQ394059, LSU: PQ184704, *tefl-α*: PQ346505, *rpb2*: PQ379990; UESTCC 23.0416 = ITS: PQ394017, LSU: PQ184668, *rpb2*: PQ379932; UESTCC 23.0417 = ITS: PQ394018, LSU: PQ184669, *tefl-α*: PQ338769, *rpb2*: PQ379933; UESTCC 23.0414 = ITS: PQ394019, LSU: PQ184670, *tefl-α*: PQ338770.

Notes – Multi-locus phylogeny showed that *Neoheliosia septata* (CGMCC 3.27283, UESTCC 23.0416, UESTCC 23.0417, and UESTCC 23.0414) clustered together with a strong support (95% MLBS/1.00 BIPP) and formed a distinct lineage (Fig. 11). *Neoheliosia septata* (HKAS 132391, holotype) shares similar sexual morphology with *N. ellipsoidispora* (HKAS 132395, holotype) and *N. verrucosisporea* (HKAS 132393, holotype) in having immersed to erumpent, subglobose ascomata, 8-spored, cylindrical asci and narrowly ovoid to ellipsoidal, one-septate, brown ascospores (Mortimer et al. 2021, Zhang et al. 2023a). However, *N. septata* (CGMCC 3.27283, ex-type strain) can be distinguished from *N. ellipsoidispora* (CGMCC 3.27283, ex-type strain) based on the notes under *N. ellipsoidispora* in this study, and differs from *N. verrucosisporea* (UESTCC 24.0230, ex-type strain) by 22/491 bp (4.5%, 3 gaps) in ITS, 14/843 bp (1.7%, 5 gaps) in LSU, 80/805 bp (9.9%, without gaps) in *rpb2*, and 44/904 bp (4.9%, 2 gaps) in *tefl-α* sequence data. Therefore, *N. septata* is introduced as a new species, associated with *Helwingia chinensis*, *Lonicera japonica*, and *Taxus wallichiana* var. *chinensis* in Yunnan and Sichuan Provinces, China.

Pleosporales Luttr. ex M.E. Barr, Prodrum to Class Loculoascomycetes (Amherst): 67 (1987).

MycoBank number: MB90563; Facesoffungi number: FoF08715

Notes – *Pleosporales*, the largest and most diverse order in the class *Dothideomycetes* was introduced by Nitschke (1869) and later validated by Barr (1987). Currently, about 4,700 species (Ariyawansa et al. 2018) are identified and classified into more than 400 genera and 75 families (Wijayawardene et al. 2018, Hongsanan et al. 2020b). The taxonomic circumscription of *Pleosporales* has been changed frequently in recent years due to the addition of large numbers of families, genera, and species. Pleosporalean species are characterized by pseudothecial ascomata, usually with a papilla and a peridium composed of several layers of cells (Zhang et al. 2009a, 2012b, Hyde et al. 2013, 2019, Jaklitsch & Voglmayr 2016c, Jaklitsch et al. 2018). Asexual morphs can be coelomycetous or hyphomycetous (Zhang et al. 2009a, b, Hyde et al. 2013, Ariyawansa et al. 2014, 2015b, Hernández-Restrepo et al. 2017, Valenzuela-Lopez et al. 2018). Members of *Pleosporales* are ubiquitous, occurring in various habitats, and can be recognized as epiphytes, endophytes or parasites of living leaves or twigs, hyperparasites on fungi or insects, lichenized or saprobes of dead plant twigs, leaves or bark (Zhang et al. 2012b, Hyde et al. 2013, 2020a, Ariyawansa et al. 2014).

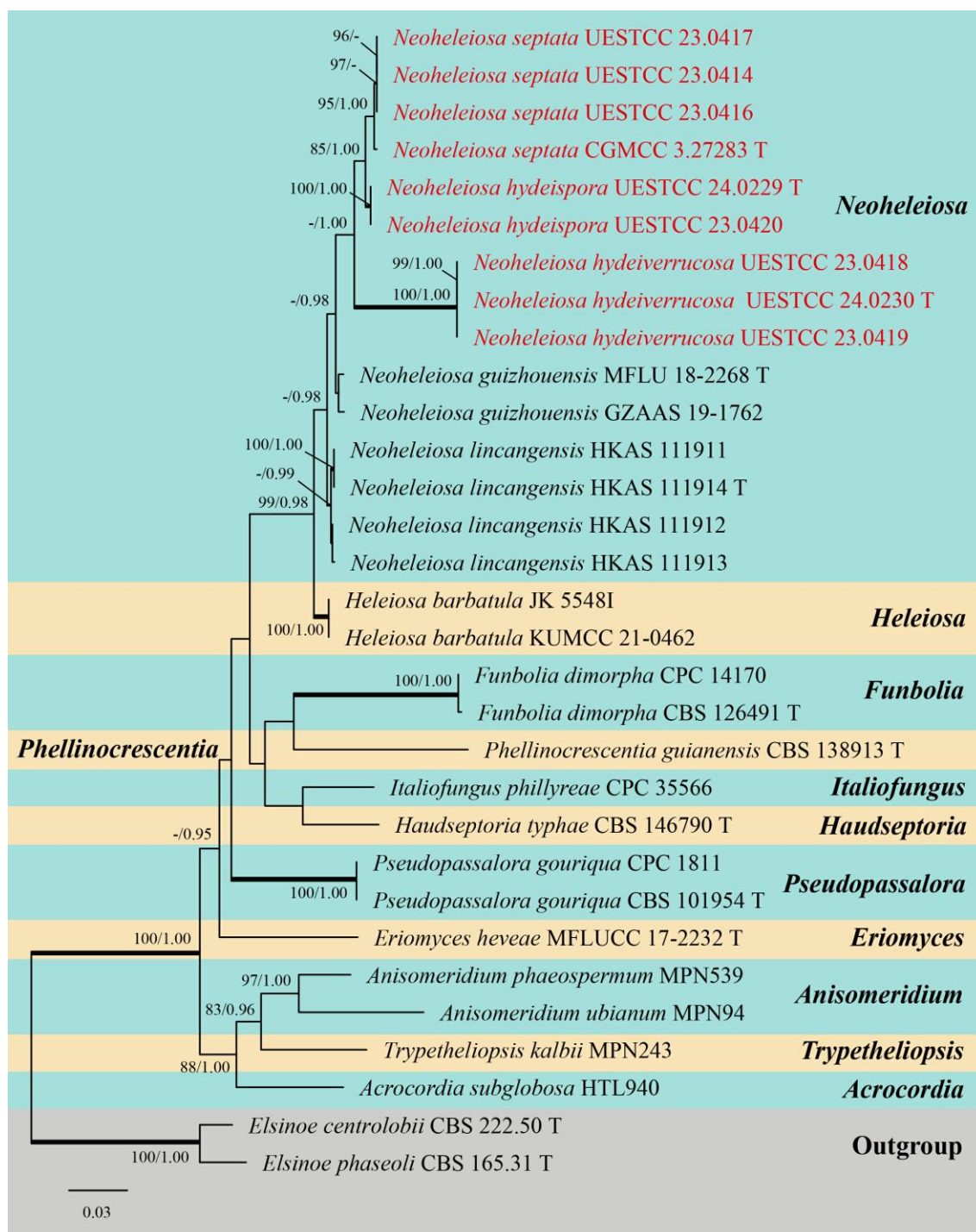


Figure 11 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined ITS, LSU, *rpb2*, and *tefl-α* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Elsinoe phaseoli* (CBS 165.31) and *E. centrolobii* (CBS 222.50). The best scoring RAXML tree with a final likelihood value of -12,724.225345 is presented. The matrix had 745 distinct alignment patterns, with 44.52% of undetermined characters or gaps, the tree-length is 1.063006. Estimated base frequencies were as follows: A = 0.232746, C = 0.264584, G = 0.287157, T = 0.215513, with substitution rates AC = 0.939319, AG = 2.111576, AT = 1.209785, CG = 1.387243, CT = 8.228254, GT = 1.000000; gamma distribution shape parameter alpha = 0.179119. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis

was 0.009934 (the critical value for the topological convergence diagnostic is below 0.01).

Acrocalymma Crous & Trakun., IMA Fungus 5 (2): 404 (2014)

MycoBank number: MB557099; Facesoffungi number: FoF08135

Notes – *Acrocalymma* was introduced by Trakuningcharoen et al. (2014) with the type genus *Acrocalymma*. The sexual morph of this family comprises globose to subglobose ascomata, cylindric to clavate asci, and hyaline, fusiform, 1–3-septate ascospores with a thick, distinct sheath. Currently, only four species with sexual morphs have been reported, viz. *A. chuxiongense*, *A. hongheense*, *A. pterocarpi*, and *A. walker* (Crous et al. 2014a, Jayasiri et al. 2019, Mortimer et al. 2021, Liu & Zeng 2022). The asexual morph is characterized by globose to subglobose conidiomata with a long pycnidial beak, hyaline, cylindrical to fusiform, aseptate, or 1–3-septate conidia, bearing mucoid appendage at one or both ends (Crous et al. 2014a, Dong et al. 2020, de Silva et al. 2022a, Li et al. 2023).

Acrocalymma Alcorn & J.A.G. Irwin, Trans. Brit. Mycol. Soc. 88 (2): 163 (1987)

MycoBank number: MB11008; Facesoffungi number: FoF05228

Notes – *Acrocalymma* was established by Alcorn & Irwin (1987) and typified by *A. medicaginis*. The sexual morph is characterized by having globose to subglobose ascomata, 8-spored, unilocular, cylindrical asci, and narrowly fusiform, hyaline to brown or pale reddish-brown, 1–3-septate ascospores with mucilaginous sheath, and the asexual morph has immersed to semi-immersed conidiomata, hyaline conidiogenous cells, with enteroblastic, cylindrical to fusiform conidia with a mucilaginous appendage at each end (Alcorn & Irwin 1987, Zhang et al. 2012a, Jayasiri et al. 2019, Calabon et al. 2023). *Acrocalymma* species were reported as pathogens and saprobes from terrestrial and freshwater habitats (Zhang et al. 2012a, Crous et al. 2014a, Trakuningcharoen et al. 2014, Jayasiri et al. 2019, Konta et al. 2023). Currently, 18 species of *Acrocalymma* are identified (<https://www.indexfungorum.org/Names/Names.asp?strGenus=Acrocalymma>; accessed on 28 February 2025).

Acrocalymma kevinii H.Z. Du, N. Wu & Jian K. Liu, sp. nov.

Fig. 12

MycoBank number: MB857556; Facesoffungi number: FoF17972

Etymology – The epithet ‘*kevinii*’ named in honor of Prof. Kevin D. Hyde for his contributions to the taxonomy of ascomycetes.

Holotype – HKAS 132427

Saprobic on dead twigs of *Kopsia arborea* Blume (*Apocynaceae*). Visible as faint black dots. Sexual morph: *Ascomata* 158–237 µm diam. × 155–270 µm high ($\bar{x}$ = 200 × 210 µm, n = 20), solitary or scattered, sometimes gregarious, immersed to slightly erumpent, globose to subglobose, or abpyriform, dark brown to black, with a minute papilla, ostiolate. *Ostioles* 65–84 µm diam. × 67–80 µm high ($\bar{x}$ = 75 × 73 µm, n = 10), central, brown to dark brown, opening by a pore, filled with periphyses. *Peridium* 16.5–21.5 µm ($\bar{x}$ = 18.5 µm, n = 20), composed of several layers of *textura angularis* cells, flattened, brown to dark brown pseudoparenchymatous cells, hyaline to pale pigmented inwardly, becoming brown to dark brown towards outside and emerging with the host tissue. *Hamathecium* composed of 2.4–3.6 µm wide, numerous, filamentous, septate, hyaline, branched pseudoparaphyses, embedded in a gelatinous matrix, longer than asci. *Asci* 75–98 × 13–17 µm ($\bar{x}$ = 86 × 15 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, with a short, narrowed, slightly furcate pedicel, and rounded at the apex with a minute ocular chamber. *Ascospores* 20–27 × 5–7 µm ($\bar{x}$ = 24.5 × 6 µm, n = 30), overlapping uni- to bi-seriate in the ascus, straight to slightly curved, hyaline, fusiform, dimidiate, widest at the center and tapering toward the ends, 1-septate, constricted at the septum, filled with 1-guttule in each cell, the upper cell is commonly slightly wider than the lower cell, smooth-walled, and surrounded by the mucilaginous sheaths. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 23–25 mm in diam. after three weeks

at 25 °C in the dark. Colonies from above, circular, medium dense, covered with white mycelium, entire, center slightly elevated, regular edge, In reverse, grayish brown in the center, yellowish white at the edge.

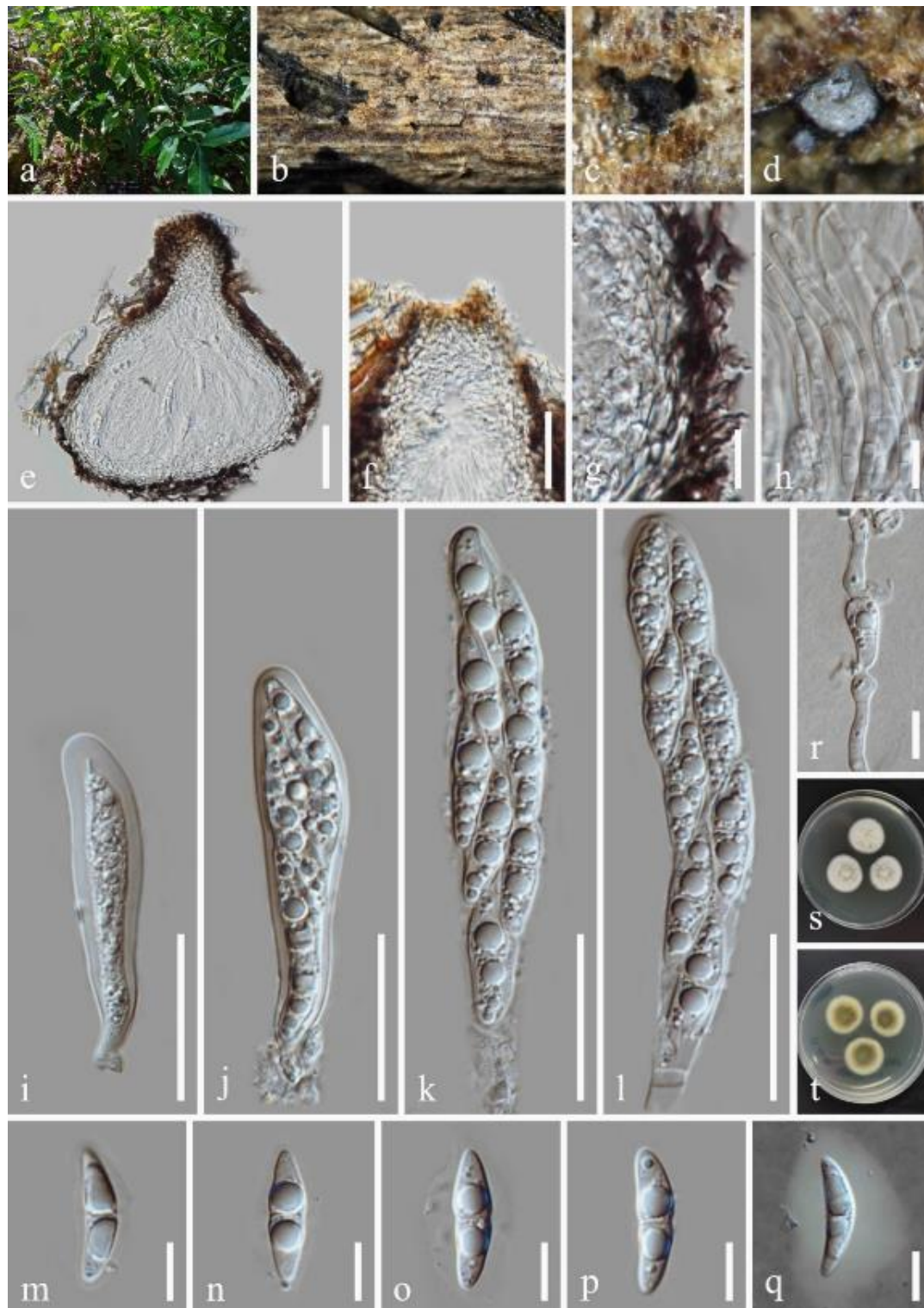


Figure 12 – *Acrocalymma kevinii* (HKAS 132427, holotype). a Host *Kopsia arborea*. b–d Appearance of ascomata on host surface. e Vertical section of ascomata. f Ostiole with periphyses. g Peridium. h Hamathecium. i–l Asci. m–p Ascospores. q Ascospore stained with Indian ink showing the mucilaginous sheath. r Germinated ascospore. s, t Colonies on PDA, above (s) and below (t). Scale bars: e = 50 μ m, f, i–l = 30 μ m, g, h, m–r = 10 μ m.

Material examined – China, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 102°44'25"E, 25°8'29"N, elevation 1,925 m, on dead twigs of *Kopsia arborea* (*Apocynaceae*), 11 November 2022, H.Z. Du, S743 (HKAS 132427, holotype; HUEST 23.0496, isotype); ex-type living culture CGMCC 3.28692; ex-isotype living culture UESTCC 23.0495.

GenBank accession numbers – HKAS 132427 = ITS: PQ773397, LSU: PQ773417, SSU: PQ773435; UESTCC 23.0495 = ITS: PQ773398, LSU: PQ773418, SSU: PQ773436.

Notes – Multi-locus phylogeny showed that *Acrocalymma kevinii* (CGMCC 3.28692 and UESTCC 23.0495) was sister to *A. walkeri* (CBS 257.93 and MFLU 23-0003) and formed a distinct lineage (Fig. 13). *Acrocalymma kevinii* (HKAS 132427, holotype) is morphologically similar to *A. walkeri* by having immersed to erumpent ascomata with minute papilla, bitunicate, 8-spored, cylindrical asci, and hyaline, fusiform, 1-septate ascospores (Shoemaker et al. 1991, de Silva et al. 2022a). However, *A. kevinii* differs from *A. walkeri* by its larger ascospores ($20\text{--}27 \times 5\text{--}7 \mu\text{m}$ vs. $16\text{--}20 \times 3\text{--}5 \mu\text{m}$) with mucilaginous sheaths, and each cell containing one distinct round guttule (de Silva et al. 2022a). Additionally, *A. kevinii* (CGMCC 3.28692, ex-type strain) can be distinguished from *A. walkeri* (CBS 257.93, ex-type strain) by 11/478 bp (2.3%, without gaps) in ITS. Therefore, based on morphological characteristics and phylogenetic evidence, *A. kevinii* associated with *Kopsia arborea*, is introduced as a new species in Yunnan Province, China.

Bambusicolaceae D.Q. Dai & K.D. Hyde, Fungal Diversity 63 (1): 49 (2013)

Mycobank number: MB804293; Facesoffungi number: FoF00586

Notes – *Bambusicolaceae* was established by Hyde et al. (2013) to accommodate *Bambusicola* as the type genus. Subsequently, three genera, *Palmiascoma* (Liu et al. 2015), *Leucaenicola* (Jayasiri et al. 2019), and *Corylicola* (Wijesinghe et al. 2020) were classified into this family based on morpho-phylogenetic evidence. At present, *Bambusicolaceae* is comprising four genera, *Bambusicola*, *Corylicola*, *Leucaenicola*, and *Palmiascoma* (Wijayawardene et al. 2022b). Morphologically, the sexual morph of *Bambusicolaceae* is characterized by having immersed to erumpent, globose to subglobose ascomata, sometimes stromatic, with anastomosing and branched pseudoparaphyses, cylindrical, bitunicate asci with well-developed ocular chambers and short furcate pedicel, and fusiform, hyaline or yellowish to brown, didymosporous ascospores, with or without gelatinous sheaths (Hongsan et al. 2020b, Wijesinghe et al. 2020). Asexual morph of *Bambusicolaceae* is characterized by having pycnothyrial conidiomata, and holoblastic, annelidic or phialidic conidiogenous cells, producing cylindrical, globose or oblong to ellipsoidal, pale to dark brown, aseptate or 1–3-septate conidia (Wijesinghe et al. 2020, Phukhamsakda et al. 2022). It is worth noting that the external appearance of ascomata, as well as the shape of ascospores and/or conidia, are the diagnostic features used to distinguish genera within this family (Hongsan et al. 2020b, Wijesinghe et al. 2020, Phukhamsakda et al. 2022).

Leucaenicola Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10 (1): 37 (2019)

Mycobank number: MB555538; Facesoffungi number: FoF05239

Notes – *Leucaenicola* was introduced by Jayasiri et al. (2019) to accommodate two coelomycetous species, *L. aseptata* (type species) and *L. phraeana*, and they were isolated from the decaying pods of *Leucaena* sp. in *Bambusicolaceae*. *Leucaenicola* is characterized by globose to subglobose, ostiolate conidiomata with thin-walled conidiomatal walls comprising *textura angularis* or *textura prismatica* cells, enteroblastic, phialidic, globose to flask-shaped conidiogenous cells and one-celled, initially hyaline, becoming brown at maturity, oblong to ellipsoidal, aseptate, smooth-walled conidia (Jayasiri et al. 2019). Currently, five species are recognized in *Leucaenicola*, namely *L. aseptata*, *L. camelliae*, *L. osmanthi*, *L. phraeana*, and *L. taiwanensis* (Index Fungorum 2025).

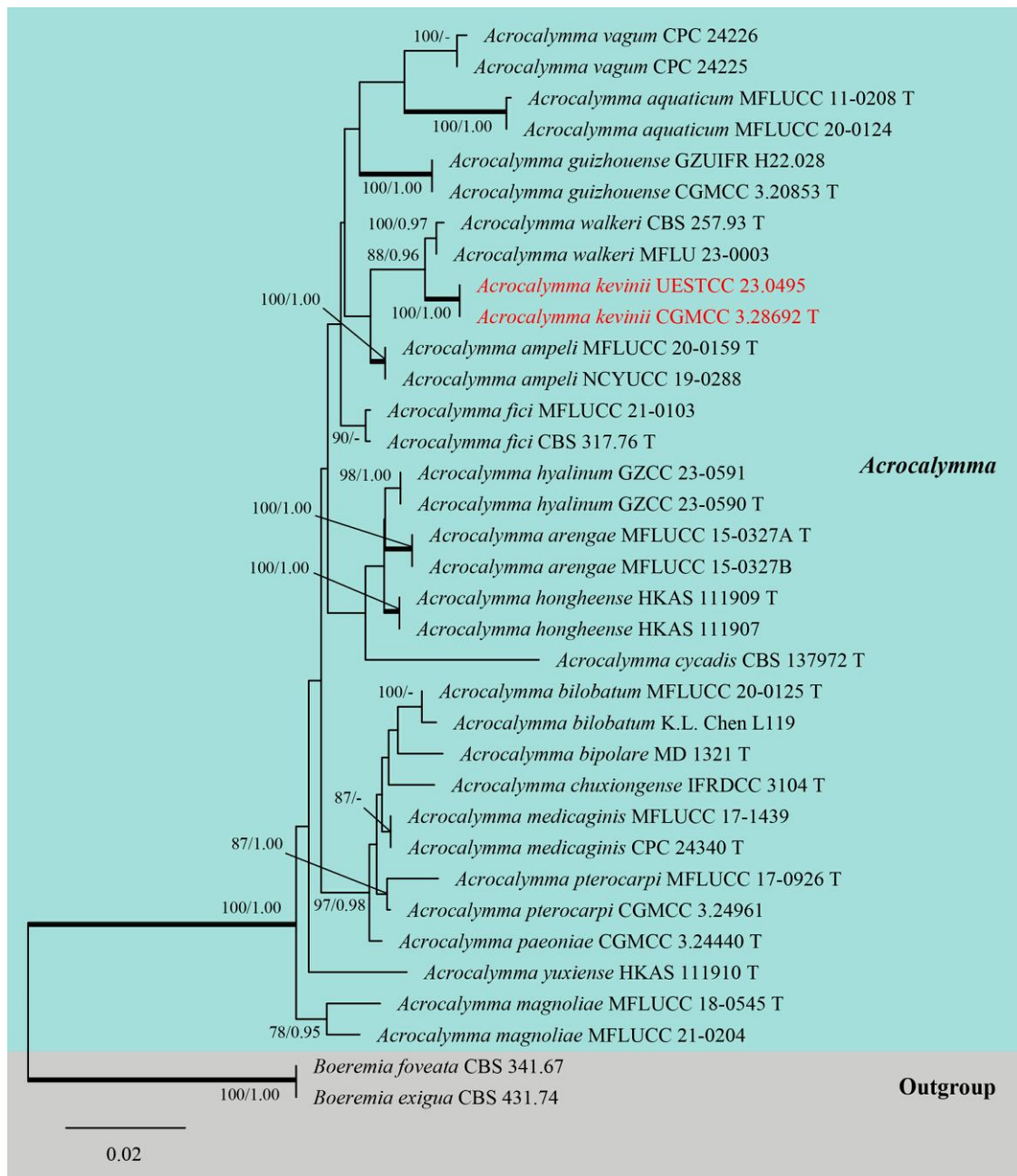


Figure 13 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined ITS, LSU, and SSU sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below the nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Boeremia foveata* (CBS 341.67) and *Boeremia exigua* (CBS 431.74). The best scoring RAxML tree with a final likelihood value of -5,960.529861 is presented. The matrix had 366 distinct alignment patterns, with 23.58% of undetermined characters or gaps, the tree-length is 0.313125. Estimated base frequencies were as follows: A = 0.249728, C = 0.215208, G = 0.271754, T = 0.263309, with substitution rates AC = 2.552816, AG = 2.269371, AT = 2.604629, CG = 0.689028, CT = 8.365842, GT = 1.000000; gamma distribution shape parameter alpha = 0.020000. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009925 (the critical value for the topological convergence diagnostic is below 0.01).

Leucaenicola hydeinandinae H.Z. Du & Jian K. Liu, sp. nov.
 MycoBank number: MB855421; Facesoffungi number: FoF17973

Fig. 14

Etymology – The epithet ‘*hydeinandinae*’ is a combination of Prof. Kevin D. Hyde’s last name and the host genus ‘*Nandina*’ from which the fungus was originally isolated, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132404

Saprobic on dead twigs of *Nandina domestica* Thunberg (*Berberidaceae*). Visible as dark brown dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 144–338 μm diam. $\times$ 116–270 μm high ($\bar{x}$ = 286 $\times$ 154 μm , n = 20), pycnidial, solitary, immersed to slightly erumpent through the host tissues, visible as black dots covered by epidermal tissues, uniloculate, globose to subglobose, glabrous. *Conidiomatal wall* 13–22 μm wide ($\bar{x}$ = 17 μm , n = 20), thin-walled, composed of several layers of hyaline to brown, pseudoparenchymatous cells of *textura angularis*. *Conidiophores* arising from basal cavity of conidiomata mostly reduced to conidiogenous cells. *Conidiogenous cells* 5–7 $\times$ 3–4 μm ($\bar{x}$ = 6 $\times$ 3.3 μm , n = 20), enteroblastic, phialidic, hyaline, smooth, ampulliform to doliiform or cylindrical, aseptate, lining the conidiomatal cavity. *Conidia* 4–7 $\times$ 3–4 μm ($\bar{x}$ = 5 $\times$ 3.5 μm , n = 30), solitary, initially hyaline, becoming brown at maturity, oblong to ellipsoidal, with rounded or obtuse ends, thin-walled, smooth, aseptate, with 1–2 guttules.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from one end. Colonies growing on PDA reached 15–17 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, circular, dense, dull with entire edge, center slightly elevated, and grayish green or olive green in reverse.

Material examined – China, Sichuan Province, Chengdu City, High-tech West District, Yaobo Park, 103°56'21"E, 30°43'57"N, elevation 505 m, on dead twigs of *Nandina domestica* (*Berberidaceae*), 11 August 2021, H.Z. Du, S331 (HKAS 132404, holotype; HUEST 23.0447, isotype); ex-type living culture CGMCC 3.27713, ex-isotype living culture UESTCC 23.0446.

GenBank accession numbers – CGMCC 3.27713 = ITS: PQ394061, LSU: PQ184706, SSU: PQ184748, *tefl- α* : PQ346507, *rpb2*: PQ379992; UESTCC 23.0446 = ITS: PQ394024, LSU: PQ184675, SSU: PQ184740, *tefl- α* : PQ346467, *rpb2*: PQ379938.

Notes – Multi-locus phylogeny (Fig. 15) showed that our two isolates (CGMCC 3.27713 and UESTCC 23.0446) formed a distinct lineage basal to other *Leucaenicola* strains. Morphologically, *L. hydeinandinae* is similar to *Leucaenicola* species in having pycnidial conidiomata, ampulliform to cylindrical conidiogenous cells, oblong to ellipsoidal conidia (Jayasiri et al. 2019, Ariyawansa et al. 2020a, b). However, *L. hydeinandinae* can be distinguished from *L. aseptata*, *L. camelliae*, *L. coffeae*, *L. osmanthi*, *L. phraeana*, and *L. taiwanensis* based on the nucleotide base pair differences of ex-type strains as shown in Table 2. Therefore, *L. hydeinandinae* is introduced as a new species based on phylogenetic evidence and associated with *Nandina domestica* in Sichuan Province, China.

Table 2 Comparison of nucleotide base pair differences of ex-type strains between *Leucaenicola hydeinandinae* (CGMCC 3.27713) and adjoining sister clade.

Species	Strain number	LSU (bp)	ITS (bp)	<i>tefl-α</i> (bp)	<i>rpb2</i> (bp)
<i>L. aseptata</i>	MFLUCC 17-2423	13/840 (1.5%, 3 gaps)	35/361 (9.7%, 6 gaps)	44/916 (4.8%, 3 gaps)	185/1055 (17.5%, 17 gaps)
<i>L. camelliae</i>	NTUCC 18-093-4	14/845 (1.7%, 2 gaps)	35/387 (9.0%, 6 gaps)	45/919 (4.9%, 3 gaps)	159/879 (18.1%, 2 gaps)
<i>L. coffeae</i>	KUNCC 24-18336	94/845 (11.1%, 1 gap)	37/387 (9.6%, 6 gaps)	46/949 (4.8%, 1 gap)	N/A
<i>L. osmanthi</i>	NTUCC 18-101-1	18/759 (2.4%, 1 gap)	30/250 (12.0%, 5 gaps)	42/813 (5.2%, 3 gaps)	129/824 (15.7%, 7 gaps)
<i>L. phraeana</i>	MFLUCC 18-0472	18/839 (2.1%, 1 gap)	23/231 (10.0%, 1 gap)	40/916 (4.4%, 3 gaps)	N/A
<i>L. taiwanensis</i>	NTUCC 18-094-1	19/845 (2.2%, 2 gaps)	35/387 (9.0%, 6 gaps)	44/918 (4.8%, 1 gap)	N/A

“N/A” denotes sequence data is unavailable in GenBank.

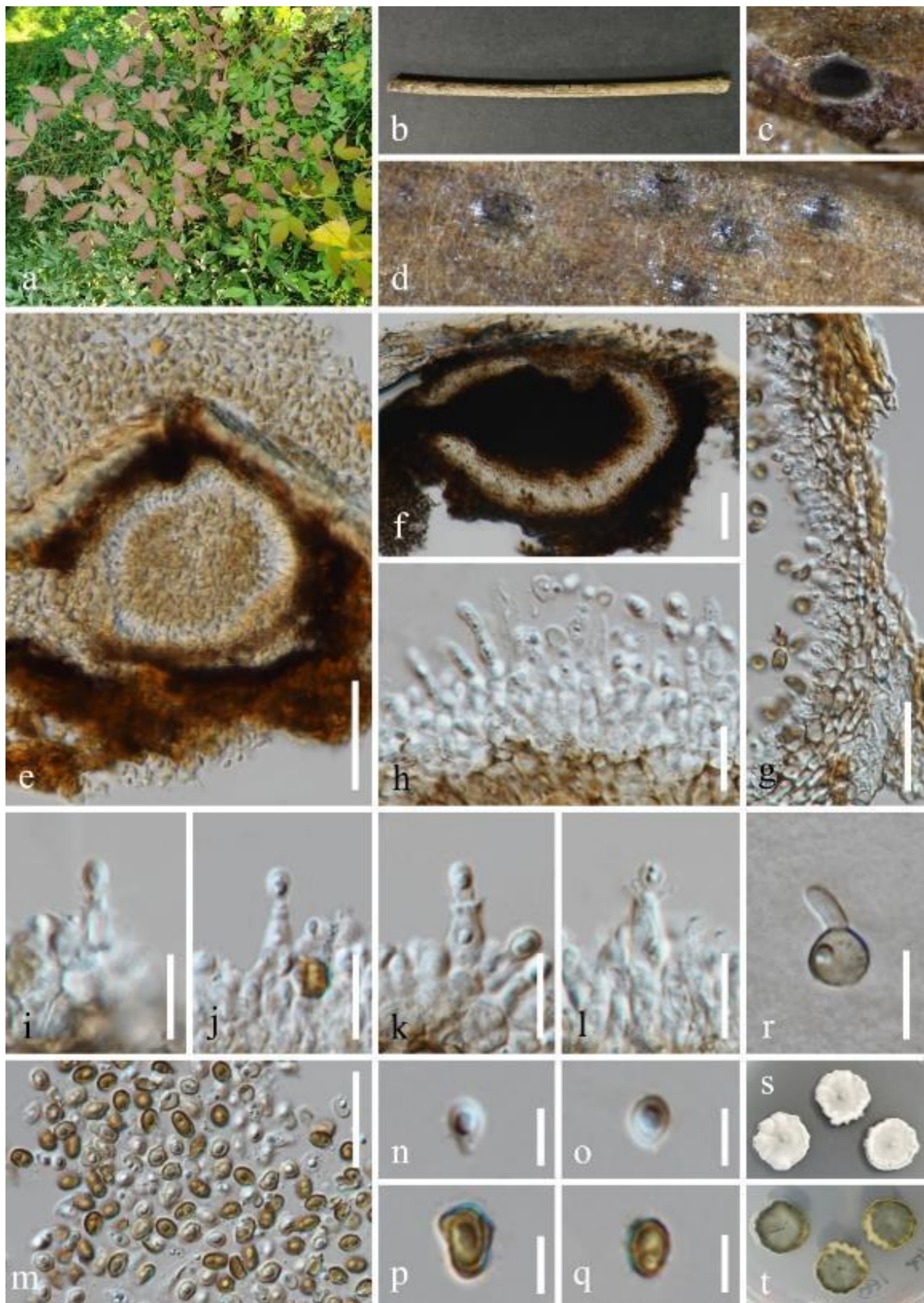


Figure 14 – *Leucaenicola hydeinandinae* (HKAS 132404, holotype). a Host *Nandina domestica*. b A twig of *N. domestica*. c, d Appearance of conidiomata on host surface. e, f Vertical section of conidiomata. g Conidiomatal wall. h–l Conidiogenous cells and conidia. m–q conidia. r Germinated conidium. s, t Colonies on PDA, above (s) and below (t). Scale bars: e, f = 50 μ m, g, m = 20 μ m, h–l, r = 10 μ m, n–q = 5 μ m.

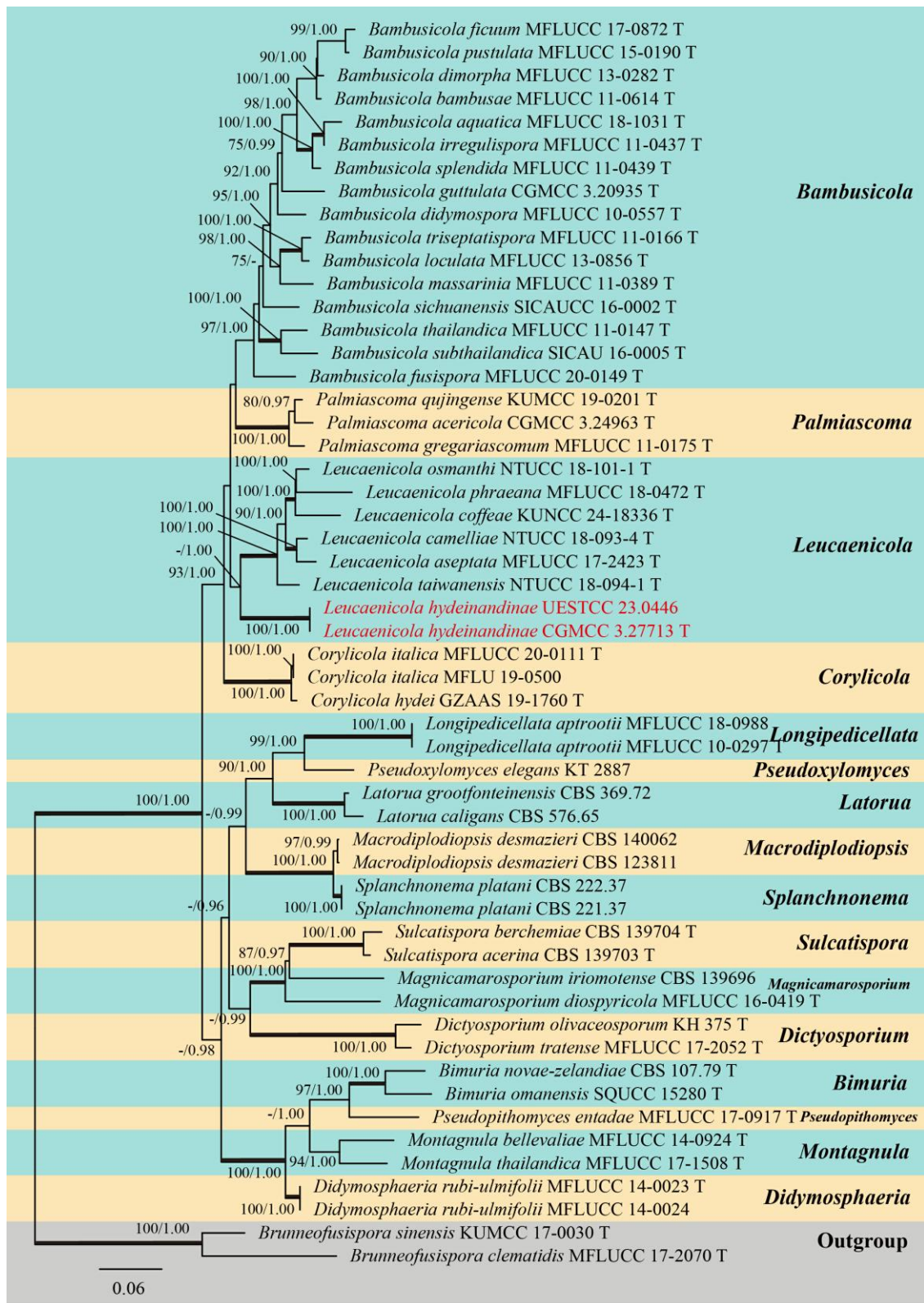


Figure 15 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined LSU, ITS, SSU, *tefl-α*, and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Brunneofusispora clematidis* (MFLUCC 17-2070) and *B. sinensis* (KUMCC 17-0030). The best scoring RAxML tree with a final likelihood value of -31,600.174200 is presented. The matrix had 1,689 distinct alignment patterns, with 24.38% of undetermined

characters or gaps, the tree-length is 2.882653. Estimated base frequencies were as follows: A = 0.243417, C = 0.254817, G = 0.269270, T = 0.232497, with substitution rates AC = 1.407466, AG = 3.216873, AT = 1.263644, CG = 1.116827, CT = 6.911925, GT = 1.000000; gamma distribution shape parameter alpha = 0.227942. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009968 (the critical value for the topological convergence diagnostic is below 0.01).

Didymosphaeriaceae Munk, Dansk botanisk Arkiv 15 (2): 128 (1953)

MycoBank number: MB80702; Facesoffungi number: FoF00200

Notes – *Didymosphaeriaceae* was introduced by Munk (1953), with *Didymosphaeria* as the type genus. In previous studies, the placement of *Didymosphaeriaceae* was not clear (Barr 1990, Lumbsch & Huhndorf 2007, Zhang et al. 2012b). Later, Ariyawansa et al. (2014) provided an updated account of the family and accepted 16 genera. Currently, the family consists of 39 genera (Hyde et al. 2024), which include isolates from different habitats, including terrestrial, aquatic, saprotrophic, parasitic, and hemibiotrophic. Among them, some genera are monotypic or contain only a few species with molecular data (Hongsanant et al. 2020a). *Didymosphaeriaceae* is characterized by immersed, gregarious or scattered ascomata and septate hamathecium. Asci bitunicate, fissitunicate, cylindrical or oblong, septate or muriform and pedicellate. Ascospores are uni-seriate or biseriate, oblong, verruculose, with or without a gelatinous sheath. The asexual morphs were known as coelomycetous and hyphomycetous taxa (Ariyawansa et al. 2014, 2015c).

Austropleospora R.G. Shivas & L. Morin, Fungal Diversity 40: 70 (2010)

MycoBank number: MB512742; Facesoffungi number: FoF00539

Notes – *Austropleospora* was introduced by Morin et al. (2010) to accommodate *A. osteospermi* as the type species. The sexual morph of *Austropleospora* has scattered and immersed, black, ostiolate ascomata, with a protruding neck, 6–8-spored, clavate to cylindrical asci and ellipsoidal, yellowish brown, smooth-walled ascospores (Morin et al. 2010). The asexual morph is coelomycetous, with pycnidial, globose conidiomata that possess central ostioles. The conidiomatal wall range from brown to reddish-brown, while the conidia are brown to yellowish-brown and vary in shape from globose to obovate (Morin et al. 2010, Ariyawansa et al. 2015a, Jayasiri et al. 2019). Currently, there are four species listed in the Index Fungorum (accessed on 25 July 2025). *Austropleospora osteospermi* (both sexual and asexual morphs) was found as a pathogen on stems of *Chrysanthemoides monilifera* (*Asteraceae*) in Australia, while *A. archidendri* (basionym: *Paraconiothyrium archidendri*) was introduced as a saprobic fungus with only an asexual morph, isolated from *Archidendron bigeminum* (*Fabaceae*) in Myanmar and *Leucaena* sp. (*Fabaceae*) in Thailand (Verkley et al. 2014, Jayasiri et al. 2019). Later, Jayasiri et al. (2019) described the coelomycetous, *A. keteleeriae*, obtained from *Keteleeria fortunei* (*Pinaceae*). The sexual morph of *A. ochracea* was newly introduced by Dissanayake et al. (2021).

Austropleospora ochracea L.S. Dissan, J.C. Kang & K.D. Hyde, Phytotaxa 491 (3): 223 (2021)

Fig. 16

MycoBank number: MB557841; Facesoffungi number: FoF07933

Saprobic on dead twigs of *Acer palmatum* Thunb. in Murray (*Sapindaceae*). Visible as raised dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 173–290 µm diam. × 199–242 µm high ($\bar{x}$ = 260 × 223 µm, n = 20), pycnidial, solitary, immersed, globose to subglobose or obpyriform, unilocular, ostiolate. *Ostioles* 61–83 µm wide × 80–93 µm high ($\bar{x}$ = 75 × 86 µm, n = 20), central, papillate, blackish brown, filled with periphyses. *Conidiomatal wall* 12–22 µm wide ($\bar{x}$ = 18 µm, n = 20), thick, 5–6-layered, outer layer composed of 4–5 layers of brown to dark brown thin-walled cells of *textura angularis*, lined with 1–2 hyaline layers bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells, arising from the base and sides of the conidiomata. *Conidiogenous cells* 4–7 × 3–5 µm ($\bar{x}$ = 5.5 × 4 µm, n = 20), phialidic, enteroblastic, determinate, ampulliform, arising from the inner layer of the pycnidium wall, hyaline, smooth, thin walled.

Conidia $5\text{--}7 \times 3\text{--}4 \mu\text{m}$ ($\bar{x} = 6 \times 3.5 \mu\text{m}$, $n = 30$), globose to obovate, solitary, aseptate, thick and smooth-walled, some cells with 1–2 guttules, with obtuse apex and base bluntly rounded, hyaline when young, becoming brown at maturity.



Figure 16 – *Austropleospora ochracea* (HUEST 23.0431, new host record). a Host *Acer palmatum*. b A twig of *A. palmatum*. c–e Appearance of conidiomata on the host surface. f Vertical section of conidiomata. g Conidiomatal wall. h–j Conidiogenous cells and conidia. k–p conidia. q Germinated conidium. r, s Colonies on PDA, above (r) and below (s). Scale bars: f = 100 μm , g = 20 μm , h = 50 μm , i–q = 5 μm .

Culture characteristics – Conidia germinated on PDA within 12 h, and germ tubes are produced from one end. Colonies growing on PDA reached 28–30 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, fluffy, circular, middle dense, irregular edge, covered with white aerial mycelium, and in reverse, yellowish brown at the center, pale brown at the edge.

Material examined – China, Sichuan Province, Chengdu City, High-tech West District, University of Electronic Science and Technology of China, 103°55'38"E, 30°45'15"N, elevation 528 m, on dead twigs of *Acer palmatum* (*Sapindaceae*), 3 April 2021, H.Z. Du, S209 (HUEST 23.0431), living culture UESTCC 23.0430; *ibid.*, Xindu District, Xinfan Street, 104°4'49"E, 30°50'51"N, elevation 550 m, on dead twigs of *Nandina domestica* Thunb. (*Berberidaceae*), 22 July 2021, H.Z. Du, S291-1 (HUEST 23.0432), living culture UESTCC 23.0431.

GenBank accession numbers – UESTCC 23.0430 = ITS: PQ394025, LSU: PQ184676, *tefl-α*: PQ346468; UESTCC 23.0431 = ITS: PQ394026, LSU: PQ184677, *tefl-α*: PQ346469.

Notes – The sexual morph of *Austropleospora ochracea* (without an asexual morph) was introduced by Dissanayake et al. (2021) and isolated from unidentified twigs in China. In the asexual morphology, our collections (HUEST 23.0431 and HUEST 23.0432) are similar to *Austropleospora* species in having solitary and pycnidial conidiomata, phialidic and enteroblastic conidiogenous cells, globose to obovate and hyaline to brown conidia. Multi-locus phylogeny showed that our two strains (UESTCC 23.0430 and UESTCC 23.0431) grouped with *A. ochracea* (KUMCC 20-0020, ex-type strain) (Fig. 20). Comparison of the nucleotide base pair between our isolates and *A. ochracea* (KUMCC 20-0020) revealed 99.4%–100% similarity in ITS, LSU, and *tefl-α*. Therefore, we identify our isolates as *A. ochracea*, and this is the first time to introduce the asexual morph of *A. ochracea* associated with *Nandina domestica* and *Acer palmatum* in Sichuan Province, China.

Chromolaenicola Mapook & K.D. Hyde, Fungal Diversity 101: 20 (2020)

MycoBank number: MB557279; Facesoffungi number: FoF07783

Notes – *Chromolaenicola* was introduced in *Didymosphaeriaceae* by Mapook et al. (2020) to accommodate *Ch. nanensis* as the type species. The sexual morph of this genus is characterized by immersed to semi-immersed and coriaceous ascomata, cylindrical asci, and uniseriate, ellipsoid, muriform ascospores (Mapook et al. 2020). And the asexual morph features pycnidial conidiomata with enteroblastic, phialidic conidiogenous cells, and oblong, oval to ellipsoid, or globose to subglobose conidia (Jayasiri et al. 2019, Mapook et al. 2020). Currently, eight species are listed in the Index Fungorum (accessed on 26 July 2025). Among them, *Ch. ananasi*, *Ch. Chiangraiensis*, *Ch. clematidis*, *Ch. lampangensis*, and *Ch. siamensis* were introduced as asexual morphs, while *Ch. nanensis*, *Ch. sapindi*, and *Ch. thailandensis* were reported as sexual morphs.

Chromolaenicola hydei H.Z. Du & Jian K. Liu, sp. nov.

Fig. 17

MycoBank number: MB855422; Facesoffungi number: FoF17974

Etymology – The epithet ‘*hydei*’ named for in honor of Prof. Kevin D. Hyde for his contribution to ascomycetes taxonomy.

Holotype – HKAS 144514

Saprobic on dead twigs of *Zanthoxylum bungeanum* Maxim. (*Rutaceae*). Visible as black dots. Sexual morph: *Ascomata* 319–485 µm diam. × 348–542 µm high ($\bar{x}$ = 392 × 422 µm, n = 20), immersed, solitary to gregarious, scattered, appearing as dark spots, coriaceous, globose to subglobose, dark brown to black. *Ostiole* 132–153 µm wide × 117–129 µm high ($\bar{x}$ = 143 × 123 µm, n = 20) central. Ostiolar neck protruding, filled with periphyses. *Peridium* 13–27 µm wide ($\bar{x}$ = 19 µm, n = 20), 3–5 layers, thin-walled, inner layers comprising hyaline to pale brown cells of *textura angularis*, outer layers comprising brown cells of *textura intricata*. *Hamathecium* comprising 2–2.5 µm wide, cylindrical to filiform, septate, hyaline, branched pseudoparaphyses. *Asci* 102–157 × 10–12 µm ($\bar{x}$ = 133 × 11 µm, n = 20), 8-spored, bitunicate, cylindrical, straight or slightly curved, apically rounded, pedicellate with an ocular chamber. *Ascospores* 18–23 × 6–9 µm ($\bar{x}$ = 20 × 7.5 µm, n = 30), slightly overlapping, uni-seriate, initially hyaline, 1-septate when immature, becoming reddish brown to brown at maturity, ellipsoid to broadly fusiform, muriform, guttulate, and 3-transversely septate,

with 1-vertical septum when mature, constricted at the central septum, straight or slightly curved, with gelatinous sheaths. Asexual morph: Undetermined.



Figure 17 – *Chromolaenicola hydei* (HKAS 144514, holotype). a Host *Zanthoxylum bungeanum*. b A twig of *Z. bungeanum*. c–e Appearance of ascomata on host surface. f Vertical section of ascomata. g Structure of peridium. h Hamathecium. i–k Asci. l–o Ascospores. p Ascospore stained with Indian ink showing the mucilaginous sheath. q Germinated ascospore. r, s Colonies on PDA, above (r) and below (s). Scale bars: f = 200 μ m, g = 30 μ m, h = 20 μ m, i–k = 40 μ m, p = 15 μ m, l–o, q = 10 μ m.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from one or both ends. Colonies growing on PDA reached 24–26 mm in diam. after three

weeks at 25 °C in the dark. Colonies from above, circular, dense, covered with white aerial mycelium, filamentous, fluffy, white to creamy white on surface. In reverse, bright yellow in the center, pale yellowish white at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'16"E, 21°55'43"N, elevation 505 m, on dead twigs of *Zanthoxylum bungeanum* (Rutaceae), 9 November 2022, H.Z. Du, S699 (HKAS 144514, holotype; HUEST 23.0438, isotype), ex-type living culture CGMCC 3.27710, ex-isotype living culture UESTCC 23.0437.

GenBank accession numbers – CGMCC 3.27710 = ITS: PQ394062, LSU: PQ184707, *tefl-α*: PQ346508; UESTCC 23.0437 = ITS: PQ394027, LSU: PQ184678, *tefl-α*: PQ346470.

Notes – Phylogenetic analyses (Fig. 20) showed that our two strains (CGMCC 3.27710 and UESTCC 23.0437) clustered together with a highly support (100% MLBS/1.00 BIPP) forming a distinct lineage. In their sexual morphs, *Chromolaenicola hydei* (HKAS 144514, holotype) is similar to *Ch. nanensis* (MFLU 20-0304, holotype), *Ch. sapinda* (HKAS 122789, holotype), and *Ch. thailandensis* (MFLU 20-0306, holotype) in having 8-spored, bitunicate asci with ocular chambers, reddish brown to brown, ellipsoid to broadly fusiform, and 3-transversely septate ascospores, with a 1-vertical septum when mature, but differs from these species in having a gelatinous sheath, which is absent in the sexual morph of other species of *Chromolaenicola* (Mapook et al. 2020, Ren et al. 2022). Therefore, based on morphological characteristics and phylogenetic evidence, *Ch. hydei* associated with *Zanthoxylum bungeanum*, is introduced as a new species in Yunnan Province, China.

Chromolaenicola hydeiwikstroemiae H.Z. Du, N. Wu & Jian K. Liu, sp. nov.

Fig. 18

MycoBank number: MB855423; Facesoffungi number: FoF17975

Etymology – The epithet ‘*hydeiwikstroemiae*’ is a combination of Prof. Kevin D. Hyde’s last name and the host genus ‘*Wikstroemia*’ from which the fungus was originally isolated, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132400

Saprobic on dead twigs of *Wikstroemia indica* (Thymelaeaceae). Visible as black dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 384–408 µm diam. × 349–367 µm high ($\bar{x}$ = 396 × 358 µm, n = 20), pycnidial, solitary, uniloculate, immersed, globose to subglobose or obpyriform, coriaceous, thick-walled, brown to dark brown, ostiolate. *Ostiole* 103–150 µm wide × 126–132 µm high ($\bar{x}$ = 127 × 129 µm, n = 20), central or eccentric, papillate, filled with periphyses. *Conidiomatal wall* 12.5–17 µm wide ($\bar{x}$ = 15 µm, n = 20), pycnidial, wider at apex, thin-walled, composed of 2–4 layers of pale brown to light brown cells of *textura angularis*, lined with a thin, hyaline layer bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells, arising from the base. *Conidiogenous cells* 2–5 × 2–4 µm ($\bar{x}$ = 3.5 × 3 µm, n = 20), enteroblastic, phialidic, determinate, discrete, truncate, hyaline, smooth, arising from the inner layer of pycnidial wall. *Conidia* 9–13 × 4.5–6 µm ($\bar{x}$ = 11 × 5 µm, n = 30), broad oblong or oval, slightly truncate at the base, rounded at the apex, hyaline to pale brown, aseptate when immature, reddish brown to dark brown at maturity, 1-septate, not constricted at the septum, rough walled, with 2 guttules in each cell.

Culture characteristics – Conidia germinated on PDA within 24 h, and the germ tubes are produced from one or both ends. Colonies growing on PDA reached 35–38 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, medium dense, filamentous, fluffy, grayish brown circle in the center, slightly raised, presented a white concentric ring in the middle, pale yellow aerial mycelium at the edge, radial. In reverse, dark brown circle in the center, pale yellow to bright yellow at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences. 101°15'16"E, 21°55'43"N, elevation 505 m, on dead twigs of *Wikstroemia indica* (Thymelaeaceae), 10 November 2022, H.Z. Du, S566 (HKAS 132400 = HUEST 23.0441, holotype; HUEST 23.0437, isotype); ex-type living culture CGMCC 3.27711 = UESTCC 23.0440; ex-isotype living culture

UESTCC 23.0436.

GenBank accession numbers – CGMCC 3.27711 = ITS: PQ394063, LSU: PQ184708, *tefl-α*: PQ346509, *rpb2*: PQ379993; UESTCC 23.0436 = ITS: PQ394030, LSU: PQ184681, *tefl-α*: PQ346473, *rpb2*: PQ379939.

Notes – Phylogenetic analyses (Fig. 20) showed that our two isolates (CGMCC 3.27711 and UESTCC 23.0436) formed a monophyletic lineage basal to other *Chromolaenicola* strains. Morphologically, *Ch. hydeiwikstroemiae* can be distinguished from other species in the size of conidiomata, conidiogenous cells, and conidia (Table 3). Therefore, based on asexual morphological characteristics and phylogenetic evidence, *Ch. hydeiwikstroemiae* is introduced as a new species, which is associated with *Wikstroemia indica* in Yunnan Province, China.

Table 3 Synopsis of asexual morph of *Chromolaenicola* species with similar morphological features discussed in this study.

Species	Holotype number	Conidiomata (μm)	Conidiogenous cells (μm)	Conidia (μm)	Distribution and Hosts	References
<i>Ch. ananasi</i>	MFLU 23-0167	–	–	7–8 × 4–5	Thailand, dead leaves of <i>Ananas comosus</i> (L.) Merr. (<i>Bromeliaceae</i>)	Tian et al. (2024a)
<i>Ch. lampangensis</i>	MFLU 20-0302	150–230 high × (155–)170–270(–345) diam.	–	12–15 × 4–6.5	Thailand, dead stems of <i>Chromolaena odorata</i> (L.) R. M. King & H. Rob. (<i>Asteraceae</i>)	Mapook et al. (2020)
<i>Ch. siamensis</i> (<i>C. Chiangraiensis</i>)	MFLU 20-0301	–	3.5–6.5 × 1–2	9–14 × 6–9	Thailand, dead stems of <i>Chromolaena odorata</i> (<i>Asteraceae</i>)	Mapook et al. (2020)
<i>Ch. siamensis</i> (<i>C. clematidis</i>)	MFLU 17-1483	76–145 high × 107–128 diam.	2.6–4.5 × 4–7	7–10 × 4–7	Thailand, dead stems of <i>Clematis subumbellata</i> Kurz. (<i>Ranunculaceae</i>)	Phukhamsakda et al. (2020)
<i>Ch. siamensis</i> (= <i>Cylindroaseptospora siamensis</i>)	MFLU 18-2147	110–165 high × 140–190 diam.	6.5–7.4 × 3.2–4.7	7.2–9.4 × 5.4–6.5	Thailand, decaying pod of <i>Leucaena</i> sp. (<i>Fabaceae</i>)	Jayasiri et al. (2019)
<i>Ch. hydeiwikstroemiae</i>	HKAS 132400	349–367 high × 384–408 diam.	2–5 × 2–4	9–13 × 4.5–6	China, dead twigs of medicinal plant <i>Wikstroemia indica</i> (<i>Thymelaeaceae</i>)	In this study

“–” refers to the unavailability of the data.

Chromolaenicola lampangensis Mapook & K.D. Hyde, Fungal Diversity 101: 23 (2020) Fig. 19
MycoBank number: MB557281; Facesoffungi number: FoF07785

= *Chromolaenicola nanensis* Mapook & K.D. Hyde, Fungal Diversity 101: 25 (2020)

Saprobic on dead twigs of *Wikstroemia indica* (Linnaeus) C. A. Meyer (*Thymelaeaceae*). No distinct spots are visible on the host surface. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 228–441 μm diam. $\times$ 154–253 μm high ($\bar{x}$ = 271 $\times$ 268 μm , n = 20), solitary, pycnidial, uniloculate, immersed, globose to subglobose, coriaceous, thick-walled, brown to light brown, ostiolate. *Conidiomatal wall* 13–22.5 μm wide ($\bar{x}$ = 18 μm , n = 20), uniform, wider at apex, thin-walled, composed of 3–5 layers of pale brown to brown cells of *textura angularis*, lined with a thin, hyaline layer bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells, arising from the base. *Conidiogenous cells* 2–4 $\times$ 2–3 μm ($\bar{x}$ = 3 $\times$ 2.5 μm , n = 20), enteroblastic, phialidic, determinate, ampulliform, discrete, truncate, hyaline, smooth, arising from the inner layer of pycnidial wall. *Conidia* 7–10 $\times$ 5–7.5 μm ($\bar{x}$ = 9 $\times$ 6.5 μm , n = 30), broad oblong or oval, rounded ends, hyaline to pale brown, aseptate when immature, reddish brown, 1-septate at maturity, not constricted at the septum, rough walled, verrucose.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from one end. Colonies growing on PDA reached 20–22 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense, covered with white aerial mycelium, filamentous, fluffy, white to creamy white on surface. In reverse, bright yellow in the center, becoming pale yellowish white at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences. 101°15'16"E, 21°55'43"N, elevation 505 m, on dead twigs of *Wikstroemia indica* (*Thymelaeaceae*), 9 November 2022, H.Z. Du, S565 (HUEST 23.0440), living culture UESTCC 23.0439; *ibid.*, 10 November 2022, H.Z. Du, S565-1 (HUEST 23.0439), living culture UESTCC 23.0438.

GenBank accession numbers – UESTCC 23.0439 = ITS: PQ394028, LSU: PQ184679, *tefl- α* : PQ346471; UESTCC 23.0438 = ITS: PQ394029, LSU: PQ184680, *tefl- α* : PQ346472.

Notes – *Chromolaenicola lampangensis* and *Ch. nanensis* were introduced by Mapook et al. (2020) and isolated from *Chromolaena odorata* in Thailand. The asexual morph of *Ch. lampangensis* (MFLU 20-0302, holotype) was discovered and failed to obtain the sexual morph, while *Ch. nanensis* (MFLU 20-0304, holotype) was only established as its sexual morph (Mapook et al. 2020). Mapook et al. (2020) introduced *Ch. lampangensis* and *Ch. nanensis* as two new species based on the nucleotide base pair comparison of 20/1068 bp (1.87%) in *rpb2* gene region. However, we could not find any significant differences in the *rpb2* gene region (530/531 bp, 99.8% similarity without gaps). In addition, the nucleotide comparison between *Ch. lampangensis* (MFLUCC 17-1462, ex-type strain) and *Ch. nanensis* (MFLUCC 17-1473, ex-type strain) showed a high similarity of 99.9% (850/851 bp, without gaps) in LSU, 100% (478/478 bp) in ITS, 100% (951/951 bp) in SSU, and 99.5% (872/876 bp, without gaps) in *tefl- α* . Thus, we synonymized *Ch. nanensis* under *Ch. lampangensis* and regard them as one species. In this study, multi-locus phylogeny showed that our two isolates (UESTCC 23.0439 and UESTCC 23.0438) were grouped with *Ch. lampangensis* (MFLUCC 17-1462, MFLUCC 17-1473, and MFLUCC 17-1477) (Fig. 20). The comparison of nucleotide base pairs between our isolates and *Ch. lampangensis* (MFLUCC 17-1462, ex-type strain) showed a high similarity (99.3%–100%) in ITS, LSU, and *tefl- α* . Therefore, we identify our new collections as *Ch. lampangensis*, which were isolated from *Wikstroemia indica* in Yunnan Province, China.

Neokalmusia Ariyaw. & K.D. Hyde, Fungal Diversity 68: 92 (2014)

MycoBank number: MB550700; Facesoffungi number: FoF00050

Notes – *Neokalmusia* was introduced in the family *Didymosphaeriaceae* to accommodate two bambusicolous taxa, *N. brevispora* (type species) and *N. scabriscora*, by transferring from the genus *Kalmusia* (Tanaka et al. 2005, Zhang et al. 2009a, Ariyawansa et al. 2014). Ten species are currently listed in the Index Fungorum (accessed on 26 July 2025). The sexual morph of *Neokalmusia* is characterized by immersed or semi-immersed ascomata under the clypeus-like structure composed of host epidermis, pedicellate asci with apical chamber, and fusiform, straight, or slightly curved, brown, septate, verrucose ascospores with or without mucilaginous sheaths, and the asexual morph

is unknown. Members of *Neokalmusia* are reported from freshwater and terrestrial habitats as saprobic fungi and known in China, Italy, Japan, and Thailand (Ariyawansa et al. 2014, Dai et al. 2016, Thambugala et al. 2017, Hu et al. 2023a, Yang et al. 2023).

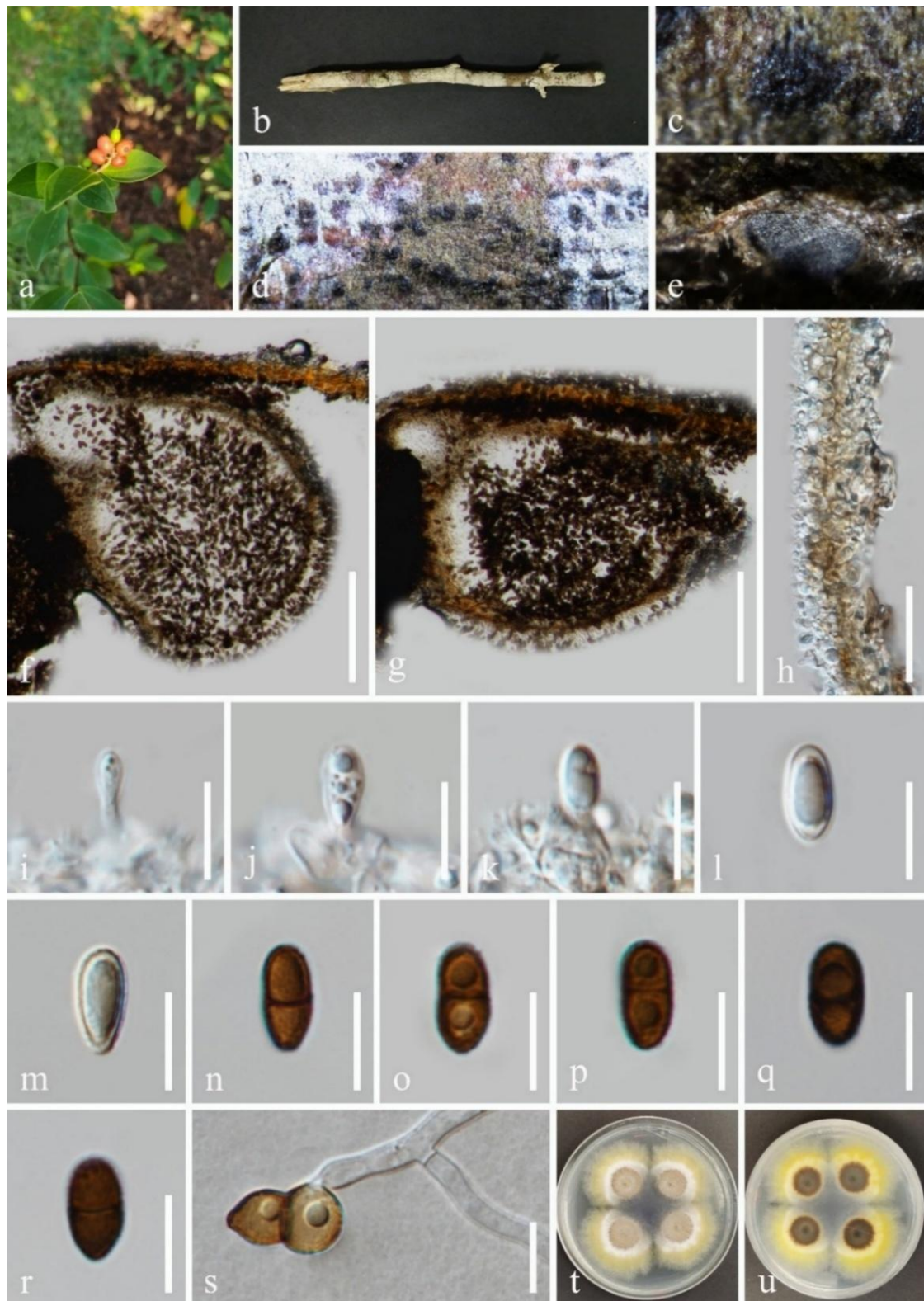


Figure 18 – *Chromolaenicola hydei wikstroemiae* (HKAS 132400, holotype). a Host *Wikstroemia indica*. b A twig of *W. indica*. c–e Appearance of conidiomata on host surface. f, g Vertical section of conidiomata. h Conidiomatal wall. i–k Conidiogenous cells and conidia. l–r Conidia. s Germinated conidium. t, u Colonies on PDA, above (t) and below (u). Scale bars: f, g = 150 μ m, h = 30 μ m,

i-s = 10 μ m.

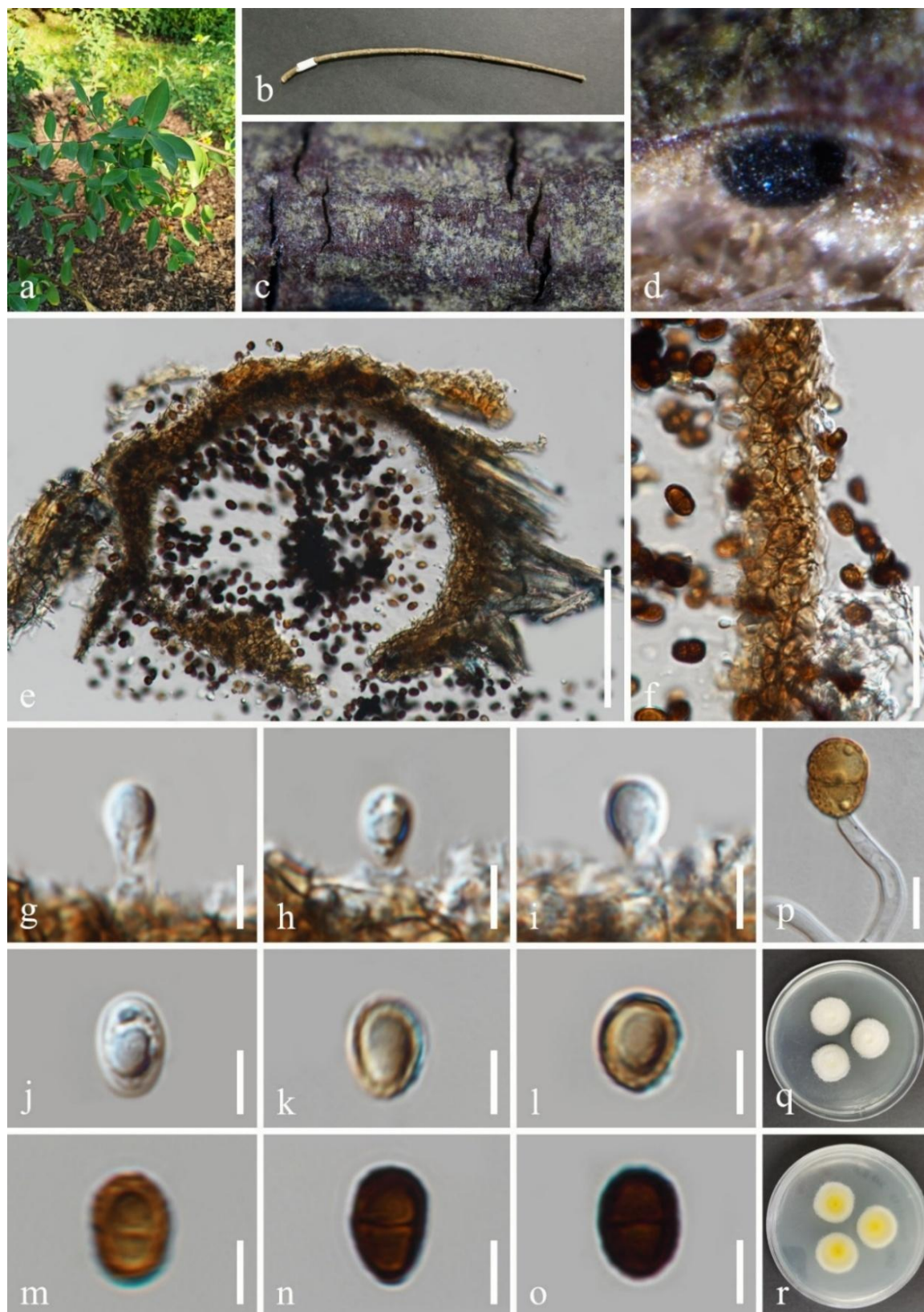


Figure 19 – *Chromolaenicola lampangensis* (HUEST 23.0440, new host and geographical records). a Host *Wikstroemia indica*. b A twig of *W. indica*. c, d Appearance of conidiomata on host surface. e Vertical section of conidiomata. f Conidiomatal wall. g–i Conidiogenous cells and conidia. j–o conidia. p Germinated conidium. q, r Colonies on PDA, above (q) and below (r). Scale bars: e = 100 μ m, f = 30 μ m, g–o = 5 μ m, p = 10 μ m.

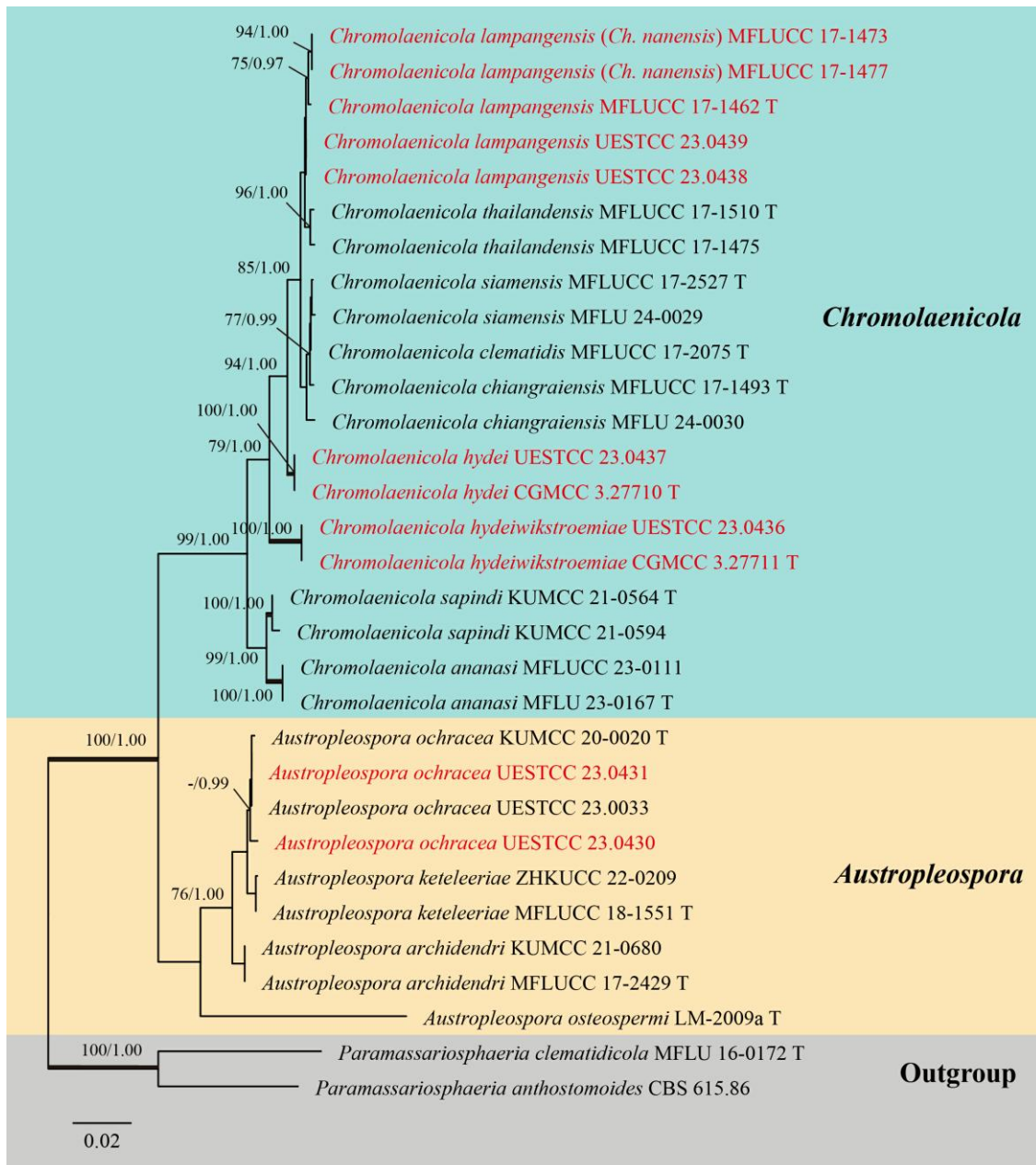


Figure 20 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined ITS, LSU, *tefl-α*, and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Paramassariosphaeria clematidicola* (MFLU 16-0172) and *P. anthostomoides* (CBS 615.86). The best scoring RAxML tree with a final likelihood value of -7,441.618293 is presented. The matrix had 396 distinct alignment patterns, with 31.66% of undetermined characters or gaps, the tree-length is 0.395472. Estimated base frequencies were as follows: A = 0.226654, C = 0.272096, G = 0.272831, T = 0.228418, with substitution rates AC = 2.011707, AG = 3.217466, AT = 1.423561, CG = 1.222563, CT = 10.173064, GT = 1.000000; gamma distribution shape parameter alpha = 0.156656. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009957 (the critical value for the topological convergence diagnostic is below 0.01).

Neokalmusia kevinitetradii H.Z. Du & Jian K. Liu, sp. nov.

Fig. 21

MycoBank number: MB855426; Facesoffungi number: FoF17976

Etymology – The epithet '*kevinitetradii*' is a combination of Prof. Kevin D. Hyde's first name and the host genus '*Tetradium*' from which the fungus was originally isolated, acknowledging his significant contributions to ascomycetes taxonomy.

Holotype – HKAS 132399

Saprobic on dead twigs of *Tetradium ruticarpum* (A. Jussieu) T. G. Hartley (*Rutaceae*). Visible as black dots. Sexual morph: *Ascomata* 167–272 μm diam. $\times$ 120–237 μm high ($\bar{x}$ = 208 $\times$ 185 μm , n = 20), immersed to erumpent in bark, solitary or scattered, globose to subglobose or obpyriform, uniloculate, coriaceous, black, ostiolate. *Ostiole* 55–63 $\times$ 41–75 μm ($\bar{x}$ = 59 $\times$ 66 μm , n = 15), central or eccentric, blackish brown, opening by a pore, filled with periphyses. *Peridium* 12–21 μm wide ($\bar{x}$ = 16 μm , n = 20), fused with host tissues, comprising 3–4 layers, thin-walled, brown to dark brown cells of *textura angularis*, uneven thickness, thickened at the side of the base. *Hamathecium* comprising 2–3 μm wide, hyaline, cylindrical to filiform, hyaline, septate, branched pseudoparaphyses. *Asci* 45–86 $\times$ 9–13 μm ($\bar{x}$ = 68 $\times$ 11 μm , n = 20), 8-spored, bitunicate, fissitunicate, clavate, slightly curved, with a small apical chamber and furcate pedicel. *Ascospores* 15–22 $\times$ 5–7.5 μm ($\bar{x}$ = 19 $\times$ 6 μm , n = 30), overlapping uni- to bi-seriate, straight to slightly curved, fusiform, smooth-walled, aseptate and hyaline when immature, becoming brown to dark brown at maturity, ellipsoid to broadly fusiform, muriform, guttulate, and 3–5-transversely septate, with 1–3-vertical septum when mature, constricted at the central septum, straight or slightly curved, without sheaths or appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA medium within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA medium reaching 17–19 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular with regular edge, dense, velvety, center elevated, covered with white aerial mycelium, and slightly brown in reverse.

Material examined – China, Sichuan Province, Yaan City, Lushan County, Siyan Town, 102°53'8"E, 30°8'37"N, elevation 708 m, on dead twigs of *Tetradium ruticarpum* (*Rutaceae*), 29 October 2021, H.Z. Du, S429 (HKAS 132399, holotype; HUEST 23.0436, isotype); ex-type living culture CGMCC 3.27709; ex-isotype living culture UESTCC 23.0435.

GenBank accession numbers – CGMCC 3.27709 = ITS: PQ252652, LSU: PQ184710, SSU: PQ184750, *rpb2*: PQ379994; UESTCC 23.0435 = ITS: PQ249234, LSU: PQ184684, SSU: PQ184742, *rpb2*: PQ379940.

Notes – Phylogenetic analyses (Fig. 22) showed that our two isolates (CGMCC 3.27709 and UESTCC 23.0435) formed a distinct lineage in *Neokalmusia*, this clade can be recognized as a separate species based on molecular evidence. Morphologically, *N. kevinitetradii* shares similar characteristics with *Neokalmusia* species, including immersed ascomata, bitunicate, clavate and 8-spored asci, and verrucose ascospores (Ariyawansa et al. 2014, Hu et al. 2023a, Yang et al. 2023). However, *N. kevinitetradii* can be distinguished from other members of *Neokalmusia* by its guttulate ascospores, which have 3–5-transverse septa and 1–3-vertical septa when mature. Therefore, we introduce *N. kevinitetradii* as a new species based on morphological differences and phylogenetic evidence, which was isolated from *Tetradium ruticarpum* in Sichuan Province, China.

Paraconiothyrium Verkley, Stud. Mycol. 50(2): 327 (2004)

MycoBank number: MB500080; Facesoffungi number: FoF00053

Notes – *Paraconiothyrium* was introduced by Verkley et al. (2004) to accommodate four species, viz., *P. brasiliense*, *P. cyclothyrioides*, *P. estuarinum* (type species), and *P. fungicola*. This genus was confirmed to be polyphyletic in the *Didymosphaeriaceae* by Ariyawansa et al. (2020b). The asexual morph of *Paraconiothyrium* is characterized by eustromatic, pycnidial conidiomata, phialidic or percurrent conidiogenous cells, and aseptate to 1-septate, hyaline to brown conidia (Verkley et al. 2004, Gonçalves et al. 2015). The sexual morph characteristics are globose or subglobose ascomata, clavate or cylindrical asci, and fusiform to ellipsoidal ascospores (Wang et al. 2021). This genus has a worldwide distribution with diverse host habitats as plant-pathogenic, saprobic, and endophytic fungi (Verkley et al. 2004, Ariyawansa et al. 2014).



Figure 21 – *Neokalmusia kevinitetradii* (HKAS 132399, holotype). a Host *Tetradium ruticarpum*. b A twig of *T. ruticarpum*. c–e Appearance of ascomata on host surface. f, g Section through ascomata. h Hamathecium. i–m Asci. n–r Ascospores. s, t Colonies on PDA, above (s) and below (t). Scale bars: f, g = 50 µm, h–m = 20 µm, n–r = 10 µm.

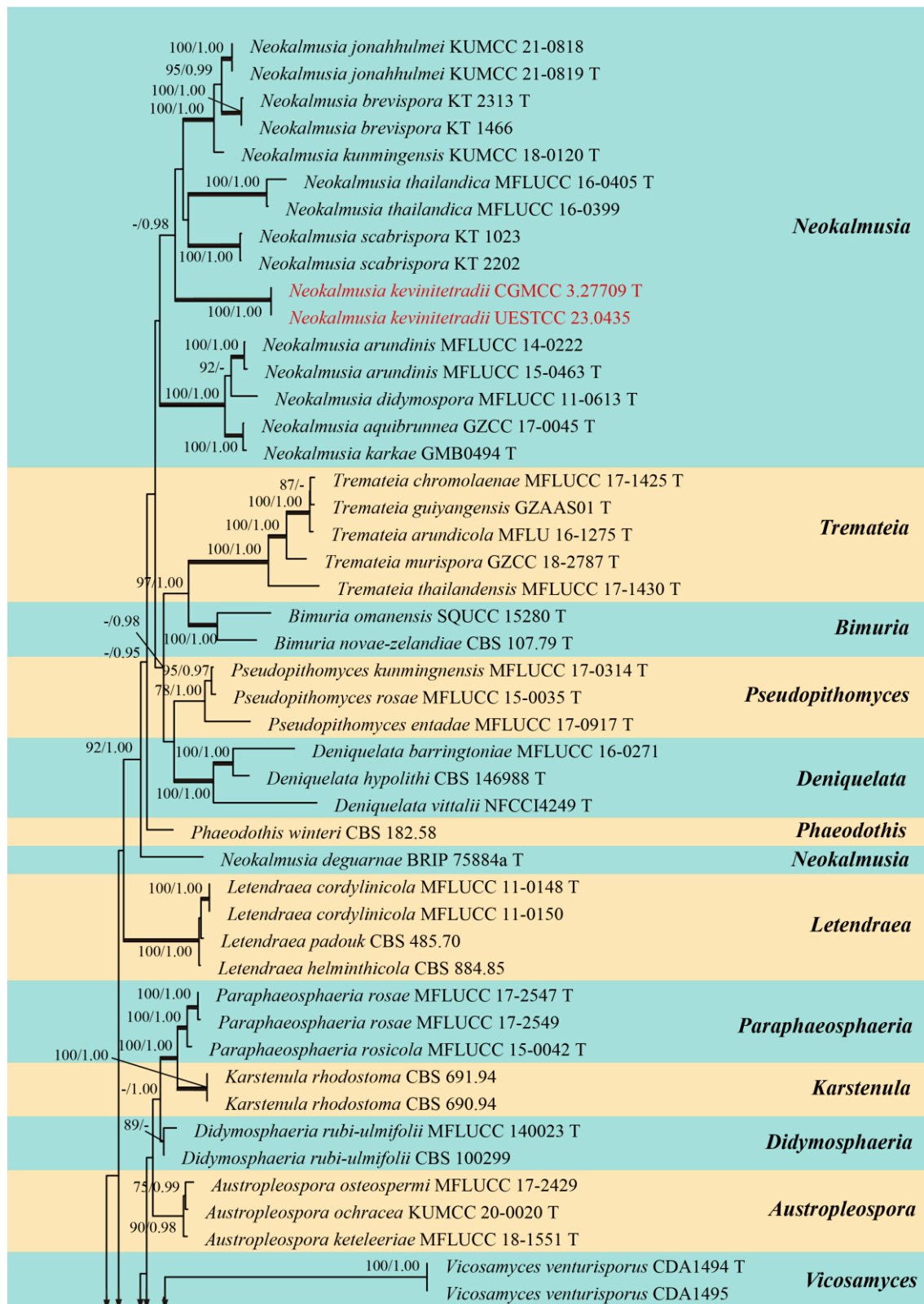


Figure 22 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined ITS, LSU, SSU, *tef1*- α , and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below the nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Bambusistroma didymosporum* (MFLU 15-0057) and *B. didymosporum* (MFLU 15-0058). The best scoring RAXML tree with a final likelihood value of -31,729.827241 is presented. The matrix had 1,710 distinct alignment patterns, with 32.39% of undetermined characters

or gaps, the tree-length is 3.207891. Estimated base frequencies were as follows: A = 0.240687, C = 0.252535, G = 0.269500, T = 0.237279, with substitution rates AC = 1.845468, AG = 3.858936, AT = 1.565072, CG = 1.313927, CT = 7.816301, GT = 1.000000; gamma distribution shape parameter alpha = 0.209323. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009973 (the critical value for the topological convergence diagnostic is below 0.01).

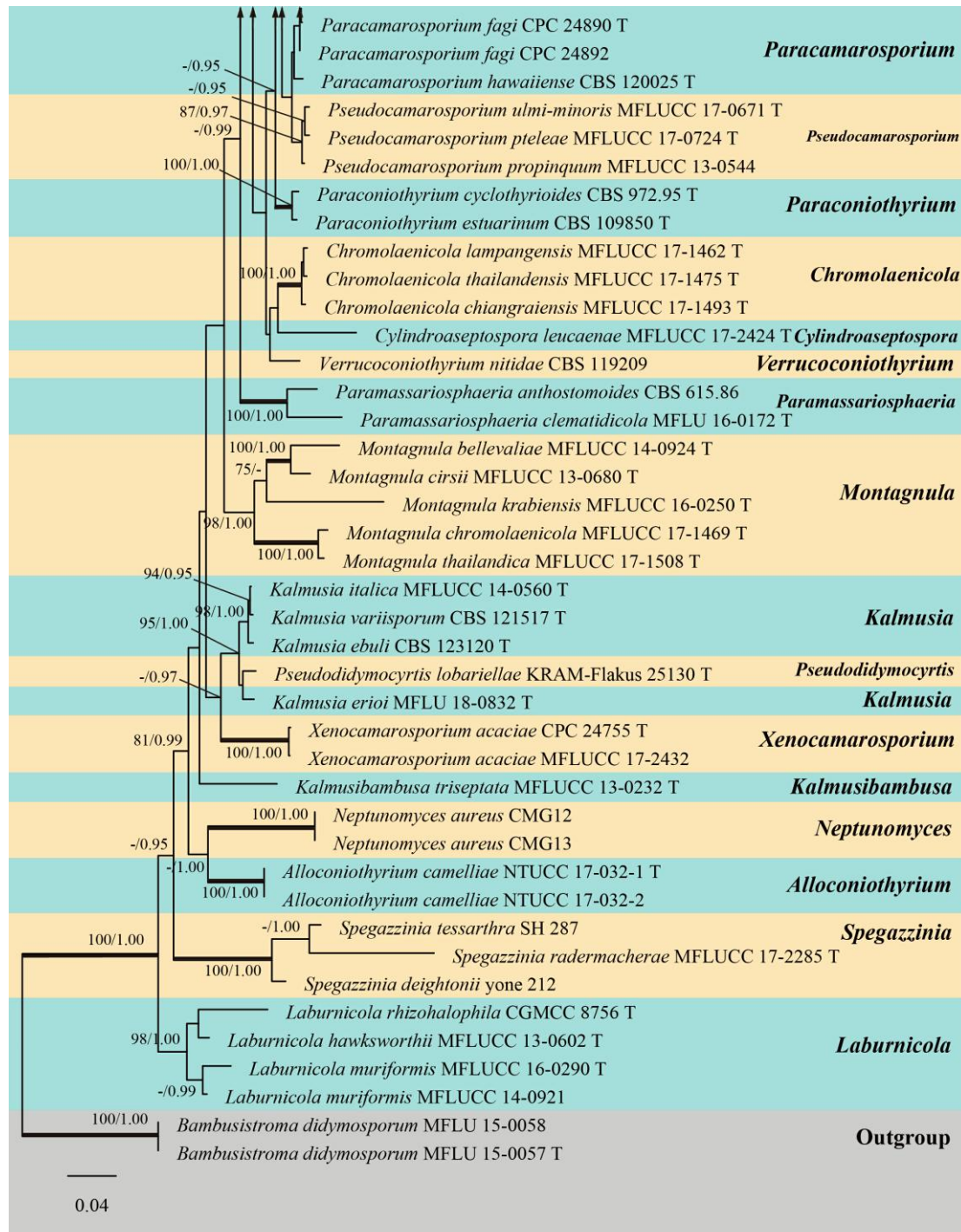


Figure 22 – Continued.

Paraconiothyrium kevinhydei H.Z. Du & Jian K. Liu, sp. nov.

Fig. 23

Mycobank number: MB855427; Facesoffungi number: FoF17977

Etymology – This morphologically remarkable species is dedicated to Prof. Kevin D. Hyde on the occasion of his seventieth birthday, in recognition of his innumerable contributions to mycology.

Holotype – HKAS 132398

Saprobic on dead twigs of *Eranthemum pulchellum* Andrews (*Acanthaceae*). Visible as black dots. Sexual morph: *Ascomata* 276–345 μm diam. $\times$ 323–374 μm high ($\bar{x}$ = 318 $\times$ 346 μm , n = 20), immersed to erumpent, conspicuous on host surface, solitary or scattered, globose to subglobose, coriaceous, black, smooth-walled, with a central ostiole. *Ostiole* short papillate, 104–126 μm wide $\times$ 116–181 μm high ($\bar{x}$ = 113 $\times$ 147 μm , n = 20), central, filled with periphyses, surrounded by pale brown stomatal tissue cells at the top of ostioles. *Peridium* 13–24 μm ($\bar{x}$ = 18 μm , n = 20), comprising 4–6 layers of thin-walled, pale brown to dark brown cells of *textura angularis*, fused with host tissues. *Hamathecium* comprising 3–5 μm wide, cylindrical to filiform, cellular, branched, hyaline, septate, guttulate, numerous pseudoparaphyses. *Asci* 68–103 $\times$ 10–15 μm ($\bar{x}$ = 85 $\times$ 12 μm , n = 20), 8-spored, bitunicate, fissitunicate, elongate clavate, slightly curved, with a long pedicel (12–17 μm long; $\bar{x}$ = 15 μm , n = 20). *Ascospores* 17–25 $\times$ 6–8 μm ($\bar{x}$ = 22 $\times$ 7 μm , n = 30), overlapping uni- to bi-seriate, hyaline or yellowish, straight to slightly curved, aseptate, hyaline to yellow brown when immature and becoming brown to reddish-brown when mature, 2-celled, fusiform to broadly fusiform, rounded ends, 1-septate, constricted at the septum, widest at the center, slightly wider upper cell and tapering towards ends, conical at both ends, smooth-walled, guttulate, without appendages and a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from one or both ends. Colonies growing on PDA reached 55–58 mm in diam. after three weeks at 25 °C in the dark, consisting of mostly immersed mycelium. Colonies from above, white aerial mycelium, medium dense, flower-like at the edge, with 2–3 layers and irregular edge, filamentous, fluffy, the color of the reverse is similar to that of the obverse, densely covered with white mycelium.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'3"E, 21°55'38"N, elevation 518 m, on dead twigs of *Eranthemum pulchellum* (*Acanthaceae*), 10 November 2022, H.Z. Du, S645 (HKAS 132398, holotype; HUEST 23.0433, isotype); ex-type living culture CGMCC 3.27707, ex-isotype living culture UESTCC 23.0432.

GenBank accession numbers – CGMCC 3.27707 = ITS: PQ249235, LSU: PQ184711, SSU: PQ184751, *tefl- α* : PQ346511, *rpb2*: PQ379995; UESTCC 23.0432 = ITS: PQ252651, LSU: PQ184685, SSU: PQ184743, *tefl- α* : PQ346476, *rpb2*: PQ379941.

Notes – Multi-locus phylogeny (Fig. 24) showed that our two isolates (CGMCC 3.27707 and UESTCC 23.0432) clustered in *Paraconiothyrium* by a strong support (100% MLBS/1.00 BIPP) and formed a monophyletic lineage basal to other *Paraconiothyrium* strains. Morphologically, the sexual morph of *P. kevinhydei* (HKAS 132398, holotype) can be distinguished from other *Paraconiothyrium* species by 1-septate ascospores with obvious guttules (Wang et al. 2021, Lu et al. 2022). Therefore, we introduce *P. kevinhydei* as a new species which associated with *Eranthemum pulchellum* in Yunnan Province, China.

Paraphaeosphaeria O.E. Erikss., Ark. Bot., Ser. 2 6: 405 (1967)

Mycobank number: MB3711; Facesoffungi number: FoF00057

Notes – *Paraphaeosphaeria* was introduced by Eriksson (1967), which was separated from *Leptosphaeria* to accommodate four species, viz. *P. castagnei*, *P. michotii*, *P. obtusispora* and *P. rusci*. Subsequently, Ariyawansa et al. (2014) confirmed the phylogenetic placement of *Paraphaeosphaeria* into *Didymosphaeriaceae*. The sexual morph characteristics of *Paraphaeosphaeria* include immersed to semi-immersed ascomata, bitunicate asci with a short pedicel, and broadly elliptical, yellowish-brown, multi-septate ascospores (Wong et al. 2000, Ariyawansa et al. 2014). The asexual morph is characterized by eustromatic or pycnidial conidiomata, phialidic, or annelidic conidiogenous cells and aseptate or 1-septate conidia (Verkley et al. 2014, Wanasinghe et al. 2018, Hongsanant et al. 2020a). Currently, there are 50 *Paraphaeosphaeria* species validly recorded in the MycoBank database (<https://www.mycobank.org/Simple%20names%20search>; accessed on 28 February 2025).



Figure 23 – *Paraconiothyrium kevinhydei* (HKAS 132398, holotype). a Host *Eranthemum pulchellum*. b A twig of *E. pulchellum*. c, d Appearance of ascomata on host surface. e Section through ascomata. f Peridium. g Ostiole. h Hamathecium. i–m Asci, n–r Ascospores. s Germinated ascospore. t, u Colonies on PDA, above (t) and below (u). Scale bars: e = 100 μ m, g = 50 μ m, f, i–m = 30 μ m, h = 20 μ m, n–s = 10 μ m.

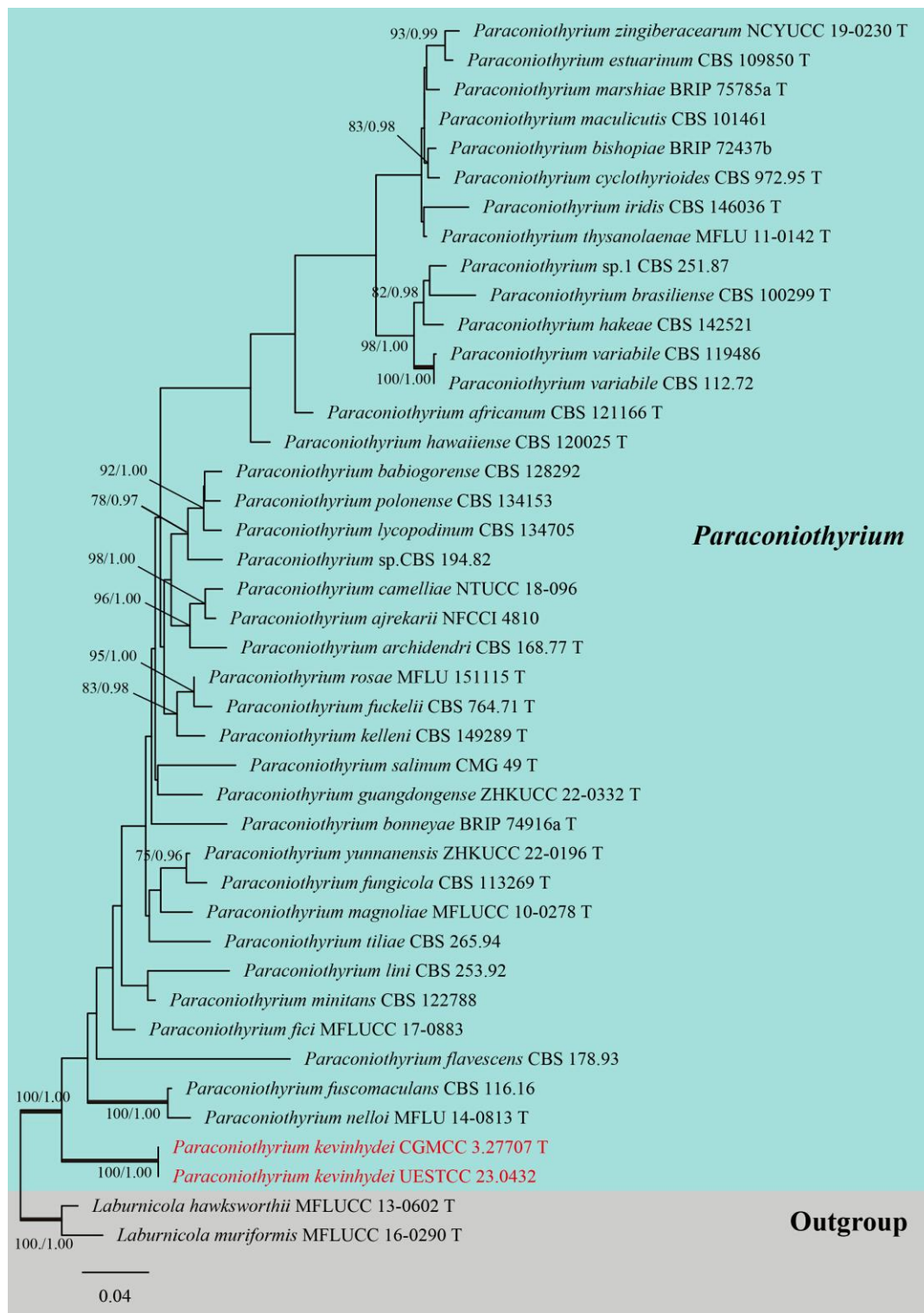


Figure 24 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined LSU, SSU, ITS, *tub2*, and *tef1-α* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Laburnicola hawksworthii* (MFLUCC 13 0602) and *L. muriformis* (MFLUCC 16 0290). The best scoring RAXML tree with a final likelihood value of -15,222.559935 is presented. The matrix had 901 distinct alignment patterns, with 42.04% of undetermined characters or gaps, the tree-length is 1.221243. Estimated base frequencies were as follows: A = 0.233889, C = 0.247878, G

= 0.276140, T = 0.242093, with substitution rates AC = 1.384716, AG = 2.382756, AT = 1.340411, CG = 0.947243, CT = 5.942569, GT = 1.000000; gamma distribution shape parameter alpha = 0.182743. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009978 (the critical value for the topological convergence diagnostic is below 0.01).

Paraphaeosphaeria hydeihelleniae H.Z. Du & Jian K. Liu, sp. nov.

Fig. 25

Mycobank number: MB855428; Facesoffungi number: FoF17978

Etymology – The epithet ‘*hydeihelleniae*’ is a combination of Prof. Kevin D. Hyde’s last name and the host genus ‘*Hellenia*’ from which the fungus was originally isolated, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 144512

Saprobic on dead twigs of *Hellenia speciosa* (J. Koenig) S. R. Dutta (*Costaceae*). Visible as dark brown dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 180–222 µm diam. × 117–158 µm high ($\bar{x}$ = 197 × 138 µm, n = 20), pycnidial, solitary, stromatic, immersed in the host, globose to subglobose, dark brown to black. Ostiole absent or not obvious. *Conidiomatal wall* 10.5–14 µm ($\bar{x}$ = 12 µm, n = 20) wide, composed of 3–4 layers, outer layer of a relatively thick-walled, orange-brown *textura angularis* and an inner layer of hyaline, thin-walled *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–2.7 × 1.6–2.3 µm ($\bar{x}$ = 2.4 × 1.9 µm, n = 20), short, discrete, globose to ampulliform, phialidic. *Conidia* 4–6 µm × 3.5–4.5 µm ($\bar{x}$ = 5 × 4 µm, n = 20), globose to subglobose or ovoid, thick-walled, initially hyaline with some small oil-droplets (< 1 µm diam.), after secession olivaceous-brown and mostly with one larger oil-droplet (> 1 µm diam.), mature conidia orange-brown to dark brown, verruculose, 0-septate.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from one end. Colonies growing on PDA reached 42–45 mm in diam. after three weeks at 25 °C in the dark, consist of mostly immersed mycelium. Colonies from above, grayish white in the center, surrounded with white aerial mycelium, circular with irregular edge, medium dense, filamentous, fluffy, the color of the reverse is similar to that of the obverse.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong City, Xishuangbanna South Medicinal Plant Garden, 100°47'19"E, 22°0'28"N, elevation 525 m, on dead twigs of *Hellenia speciosa* (*Costaceae*), 8 November 2022, H.Z. Du, S559 (HKAS 144512, holotype; HUEST 23.0430, isotype); ex-type living culture CGMCC 3.27706; ex-isotype living culture UESTCC 23.0429.

GenBank accession numbers – CGMCC 3.27706 = ITS: PQ394065, LSU: PQ184712, SSU: PQ184752, *tefl-α*: PQ346512; UESTCC 23.0429 = ITS: PQ394033, LSU: PQ184686, SSU: PQ184744, *tefl-α*: PQ346477.

Notes – *Paraphaeosphaeria hydeihelleniae* has a close phylogenetic relationship with *P. hydei* and has formed a sister lineage (Fig. 26). The nucleotide base pair comparison between *P. hydeihelleniae* (CGMCC 3.27706, ex-type strain) and *P. hydei* (CGMCC 3.19317, ex-type strain) revealed 10/846 bp (1.2%, without gaps) in LSU, 19/451 bp (4.2%, 7 gaps) in ITS, 3/56 bp (5.4%, without gaps) in *tub2*, and 28/873 bp (3.2%, without gaps) in *tefl-α* sequence data. Morphologically, *P. hydeihelleniae* (HKAS 144512, holotype) also resembles *P. hydei* (HMAS 247988, holotype) in having globose conidiomata, hyaline and ampulliform conidiogenous cells and abundant ovoid conidia (Zhang et al. 2021). However, the conidiogenous cells of *P. hydeihelleniae* are smaller than those of *P. hydei* (2–2.7 × 1.6–2.3 µm vs. 4.0–7.5 × 5.0–8.0 µm) (Zhang et al. 2021). Additionally, *P. hydeihelleniae* differs from *P. hydei* in producing conidia with oil droplets and verruculose, whereas those of *P. hydei* are smooth (Zhang et al. 2021). Therefore, the establishment of the new species, *P. hydeihelleniae*, is justified by morphological and phylogenetic evidence.

Lentitheciaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde, Studies in Mycology 64: 93 (2009)

Mycobank number: MB515470; Facesoffungi number: FoF08256



Figure 25 – *Paraphaeosphaeria hydeihelleniae* (HKAS 144512, holotype). a Host *Hellenia speciosa*. b A twig of *H. speciosa*. c–e Appearance of conidiomata on host surface. f Vertical section of conidiomata. g Ostiole. h Conidiomatal wall. i, j Conidiogenous cells and conidia. k–n conidia. o Germinated conidium. p, q Colonies on PDA, above (p) and below (q). Scale bars: f = 50 μ m, g, h = 30 μ m, i–n = 5 μ m, o = 10 μ m.

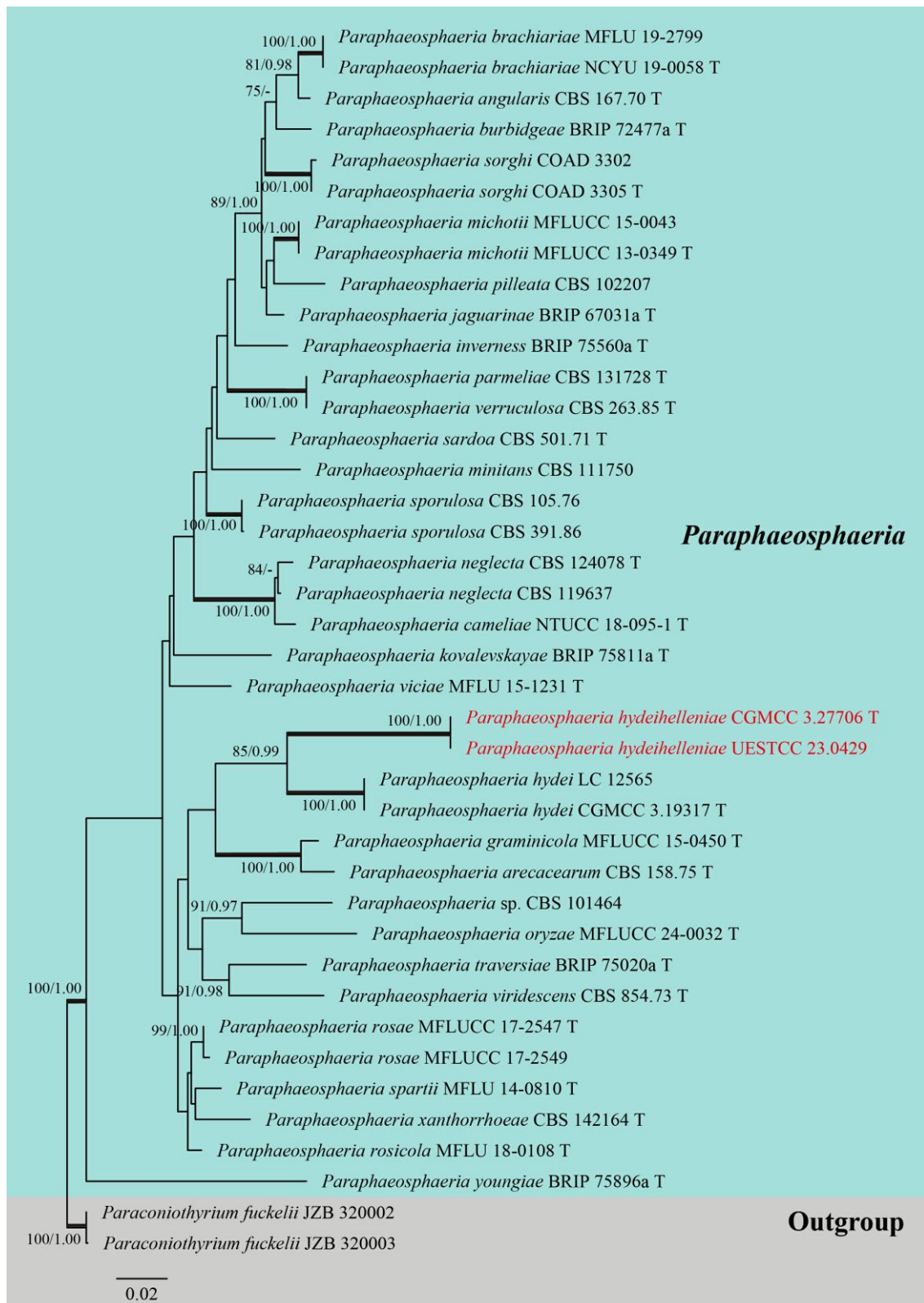


Figure 26 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined LSU, SSU, ITS, *tub2*, and *tef1-α* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below the nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Paraconiothyrium fuckelii* (JZB320002) and *P. fuckelii* (JZB320003). The best scoring RAxML tree with a final likelihood value of -12,231.008575 is presented. The matrix had 631 distinct alignment patterns, with 44.12% of undetermined characters or gaps, the tree-length

is 0.949440. Estimated base frequencies were as follows: A = 0.233972, C = 0.250858, G = 0.273731, T = 0.241438, with substitution rates AC = 1.471760, AG = 2.917236, AT = 1.588405, CG = 0.745247, CT = 6.468329, GT = 1.000000; gamma distribution shape parameter alpha = 0.107555. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009984 (the critical value for the topological convergence diagnostic is below 0.01).

Notes – Zhang et al. (2009a) introduced the family *Lentitheciaceae* with the type genus *Lentithecium*. The sexual morph of *Lentitheciaceae* is characterized by solitary to gregarious, lenticular to globose ascomata, fusiform to broadly cylindrical pseudoparaphyses, cylindrical to clavate asci, and hyaline to brown, morphologically diverse ascospores with 1–3-transverse septa, surrounded by a mucilaginous or appendage-like sheath. The asexual morphs are stagonospora-like or dendrophoma-like, having pycnidial, globose and ostiolate conidiomata, blastic or phialidic conidiogenous cells, cylindrical to oblong, hyaline to pigmented, 1-celled to muriform conidia (Zhang et al. 2009a, 2012b, Wanasinghe et al. 2018, Wijayawardene et al. 2022a, Shen et al. 2023, Tian et al. 2024b). Currently, 18 genera are accepted in *Lentitheciaceae* (Hyde et al. 2021, Liu et al. 2022, Wijayawardene et al. 2022a, Yang et al. 2022c, Rajeshkumar et al. 2023). In this study, based on the morphological characteristics and multi-locus phylogenetic analyses, we propose a new genus, *Testudiniscutum*, within the family *Lentitheciaceae*.

Testudiniscutum H.Z. Du, N. Wu & Jian K. Liu, gen. nov.

Mycobank number: MB857557; Facesoffungi number: FoF17979

Etymology – The generic epithet refers to the morphological resemblance of its conidia to a tortoise shell (from the prefix ‘Testudine-’) and a shield (from the suffix ‘-scutum’), collectively meaning ‘tortoiseshell-shield’.

Saprobic on dead twigs of *Isodon coetsa* (Buchanan-Hamilton ex D. Don) Kudô (*Lamiaceae*) in terrestrial habitats. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, solitary or gregarious, black, immersed to erumpent, unilocular, globose to subglobose, with a minute papillate ostiole. *Pycnidial wall* multi-layered, outer layer of brown to dark brown cells of *textura angularis*, thick-walled, and inner layer mostly composed of hyaline, thin-walled cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* blastic, discrete, determinate, hyaline, smooth. *Conidia* acrogenous, sub-rectangular, with rounded apex and slightly truncate base, straight, occasionally broader at the apex and narrower towards the base, hyaline to pale brown, aseptate when immature, and brown to dark brown at maturity, smooth-walled, sometimes 1-transverse septate, mostly with 4–6 transversely septa, and 5–7 longitudinal septa, constricted at the septa, which resemble a shield with intricate septations reminiscent of a tortoise shell, without appendages. Conidial secession schizolytic.

Type species – *Testudiniscutum isodonticola* H.Z. Du, N. Wu & Jian K. Liu

Notes – Phylogenetic analyses based on LSU, SSU, ITS, *tefl-α*, and *rpb2* sequence data revealed that our two isolates of *Testudiniscutum* formed a distinct clade within *Lentitheciaceae*, positioned between the genera *Murilentithecium* and *Phragmocamarosporium*. This clade was sister to *Phragmocamarosporium*, but without a significant statistical support (Fig. 28). Morphologically, *Testudiniscutum* is similar to *Murilentithecium* and *Phragmocamarosporium* in having solitary or gregarious, immersed to erumpent conidiomata, multi-layered pycnidial wall with *textura angularis* cells, and hyaline, blastic conidiogenous cells. However, *Testudiniscutum* can be distinguished from *Murilentithecium* and *Phragmocamarosporium* by its sub-rectangular conidia, which have a rounded apex, a slightly truncate base, and multiple transverse and longitudinal septa. *Murilentithecium* is characterized by oblong conidia with 3–5 transverse septa and 2–5 longitudinal septa, narrowly rounded at both ends (Wanasinghe et al. 2014, Wanasinghe et al. 2018, Phookamsak et al. 2019), while *Phragmocamarosporium* produces the clavate to ellipsoid or subcylindrical conidia, which are (2–)3(–4)-transverse septate and rarely contain a single longitudinal septum (Wijayawardene et al. 2015, Wanasinghe et al. 2018, Wijayawardene et al. 2022a, Tian et al. 2024b). Therefore, we propose a new genus, *Testudiniscutum*, to accommodate our isolates.

Testudiniscutum isodonticola H.Z. Du, N. Wu & Jian K. Liu, sp. nov.

Fig. 27

Mycobank number: MB857558; Facesoffungi number: FoF17980

Etymology – The epithet ‘*isodonticola*’ refers to the host genus ‘*Isodon*’ from which the fungus was originally isolated.

Holotype – HKAS 132437

Saprobic on dead twigs of *Isodon coetsa* (*Lamiaceae*). Visible as dark brown or black dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 135–186 µm diam. × 85–176 µm high ($\bar{x}$ = 173 × 129 µm, n = 20), pycnidial, solitary or gregarious, black, immersed, partly erumpent, sometimes scattered beneath the host tissues, unilocular, globose to subglobose, with a minute papillate ostiole. *Pycnidial wall* 13–20 µm ($\bar{x}$ = 16 µm, n = 20) wide, multi-layered, the outer layer consists of thick-walled, brown to dark brown cells of *textura angularis*, while the inner layer is mostly composed of hyaline, thin-walled cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–10 × 5–7.5 µm ($\bar{x}$ = 7.5 × 6 µm, n = 20), blastic, discrete, determinate, hyaline, smooth. *Conidia* 13–16 × 8–11 µm ($\bar{x}$ = 14 × 9.5 µm, n = 30), acrogenous, sub-rectangular, with a rounded apex and slightly truncate base, straight, occasionally broader at the apex and narrower towards the base, hyaline to pale brown, aseptate when immature, and brown to dark brown at maturity, smooth-walled, sometimes 1-transverse septate, mostly with 4–6 transversely septa, and 5–7 longitudinal septa, constricted at the septa, and composed of 5–20 subquadrate or irregularly rectangular cells, which resemble a shield with intricate septations reminiscent of a tortoise shell, without appendages. Conidial secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from each cell. Colonies growing on PDA reached 15–17 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, covered with white mycelium, circular, medium dense, entire, regular edge, center slightly elevated. In reverse, brown in the center, pale brown at the edge.

Material examined – China, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 102°44'28"E, 25°8'30"N, elevation 1,924 m, on dead twigs of *Isodon coetsa* (*Lamiaceae*), 11 November 2022, H.Z. Du, S765 (HKAS 132437, holotype; HUEST 23.0521, isotype); ex-type living culture UESTCC 25.0045, ex-isotype living culture UESTCC 23.0520.

GenBank accession numbers – UESTCC 25.0045 = ITS: PQ773403, LSU: PQ773423, SSU: PQ773439, *tefl-α*: PV059183, *rpb2*: PV075249; UESTCC 23.0520 = ITS: PQ773404, LSU: PQ773424, SSU: PQ773440, *tefl-α*: PV059184, *rpb2*: PV075250.

Notes – Multi-locus phylogeny (Fig. 35) showed that our two isolates of *Testudiniscutum isodonticola* (UESTCC 25.0045 and UESTCC 23.0520) grouped together with a strong support (100% MLBS/1.00 BIPP), and formed a sister clade to *Phragmocamarosporium*, which can be recognized as a distinct phylogenetic species (Fig. 28). Morphologically, *Testudiniscutum isodonticola* (HKAS 132437, holotype) differs from *Phragmocamarosporium* species by the sub-rectangular conidia with 4–6 transversely septate, and 5–7 longitudinal septa (Wijayawardene et al. 2015, Wanasinghe et al. 2018, Wijayawardene et al. 2022a, Tian et al. 2024b). Additionally, *T. isodonticola* can be distinguished from *Phragmocamarosporium* species based on the nucleotide base pair differences of ex-type strains (Table 4). Therefore, *T. isodonticola* is introduced as a new species based on morphological and phylogenetic evidence, which associated with *Isodon coetsa* in Yunnan Province, China.

Table 4 Comparison of nucleotide base pair differences of ex-type strains between *Testudiniscutum isodonticola* (UESTCC 25.0045) and adjoining sister clade of *Phragmocamarosporium* species.

Species	Strain number	ITS (bp)	<i>tefl-α</i> (bp)
<i>P. magnoliae</i>	GMBCC 1180	25/504 (5.0%, 3 gaps)	19/915 (2.1%, 1 gap)
<i>P. platani</i>	MFLUCC 14-1191	25/521 (4.8%, 3 gaps)	N/A
<i>P. qujingensis</i>	GMBCC 1176	27/504 (5.4%, 3 gaps)	19/917 (2.1%, without gaps)
<i>P. rosae</i>	MFLUCC 17-0797	N/A	25/902 (2.8%, without gaps)

“N/A” denotes sequence data is unavailable in GenBank.



Figure 27 – *Testudiniscutum isodonticola* (HKAS 132437, holotype). a Host *Isodon coetsa*. b–d Appearance of conidiomata on host surface. e, f Vertical section of conidiomata. g Conidiomatal wall. h, i Conidiogenous cells and conidia. j–t conidia. u Germinated conidium. v, w Colonies on PDA, above (v) and below (w). Scale bars: e, f = 50 μ m, g–u = 10 μ m.

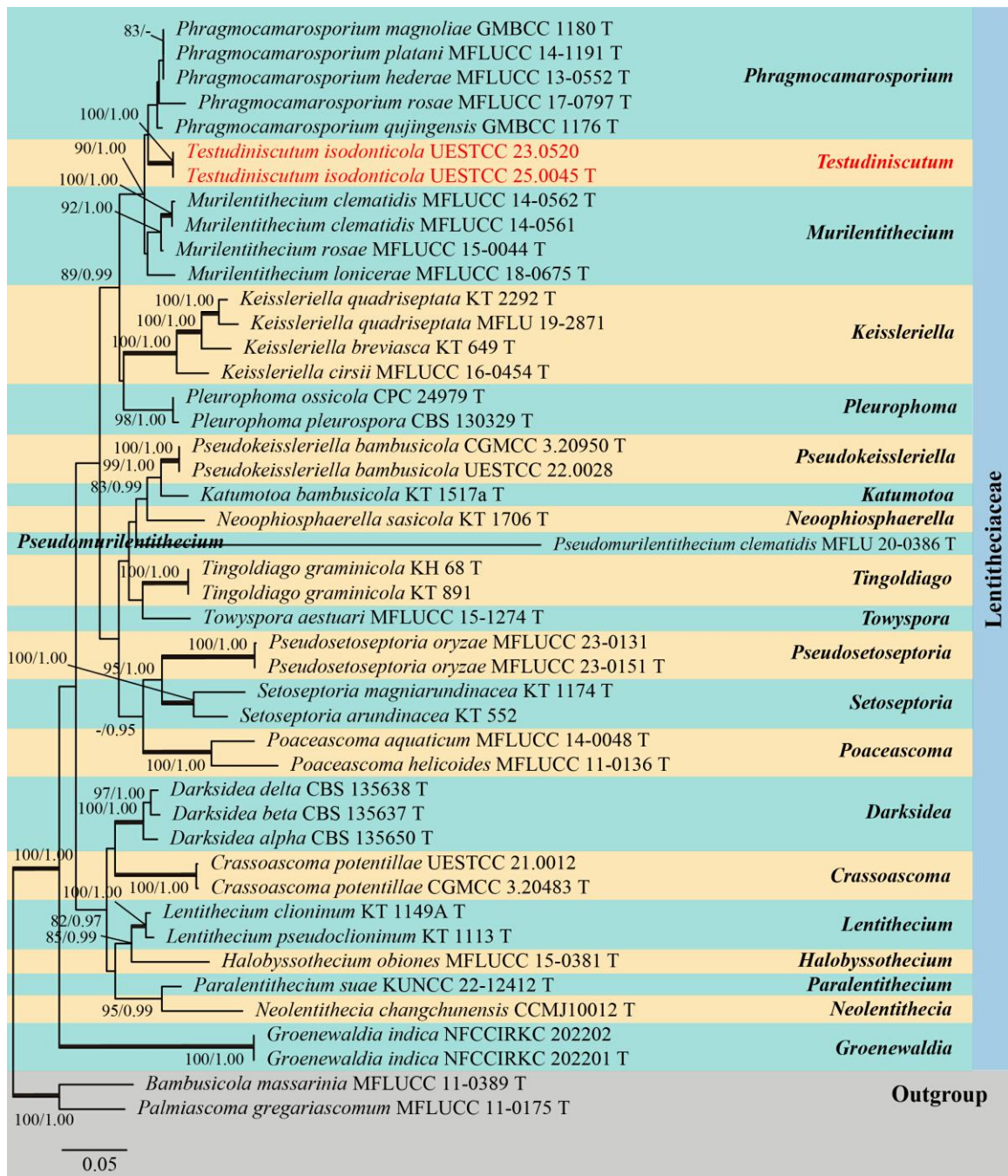


Figure 28 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined LSU, SSU, ITS, *tefl-α*, and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below the nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Bambusicola massarinia* (MFLUCC 11-0389) and *Palmiascoma gregariascomum* (MFLUCC 11-0175). The best scoring RAxML tree with a final likelihood value of -21,412.813609 is presented. The matrix had 1,294 distinct alignment patterns, with 28.62% of undetermined characters or gaps, the tree-length is 1.913579. Estimated base frequencies were as follows: A = 0.238050, C = 0.254786, G = 0.271073, T = 0.236091, with substitution rates AC = 1.446550, AG = 2.851696, AT = 1.281818, CG = 1.301276, CT = 6.658241, GT = 1.000000; gamma distribution shape parameter alpha = 0.162096. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009882 (the critical value for the topological convergence diagnostic is below 0.01).

Lophiostomataceae Sacc., Syll. fung. (Abellini) 2: 672 (1883)

MycoBank number: MB80966; Facesoffungi number: FoF00796

Notes – *Lophiostomataceae* was informally proposed by Nitschke (1869) to accommodate *Lophiostoma* as the type genus, and Saccardo (1883) formally introduced the family based on *L. macrostomum* as the type species. Previous studies had classified this family in different orders (Ainsworth et al. 1965, von Arx & Muller 1975, Barr 1987, 1992, Holm & Holm 1988, Kirk et al. 2008). *Lophiostomataceae* are mostly characterized by their coriaceous to carbonaceous ascomata with the slit-like ostiole positioned at the top of the flattened neck (Hirayama & Tanaka 2011, Hyde et al. 2013, Thambugala et al. 2015). Species of *Lophiostomataceae* are primarily found on twigs, stems or bark of herbaceous and woody plants, being saprobes or necrotrophs in terrestrial and aquatic habitats (Hirayama & Tanaka 2011, Thambugala et al. 2015). Hongsan et al. (2020a) recognized 28 genera within this family. However, Andreassen et al. (2021) synonymized 14 genera under *Lophiostoma* and accepted only 11 genera in *Lophiostomataceae*. Subsequently, Further updates by Li et al. (2023) introduced a new monotypic genus, *Oleaginea*, within this family. Currently, 32 genera were accepted by Hyde et al. (2024).

Leptoparies A. Hashim., K. Hiray. and Kaz. Tanaka, Studies in Mycology. 90: 171 (2018)

MycoBank number: MB823138; Facesoffungi number: FoF08278

Notes – A new monotypic genus, *Leptoparies* was introduced by Hashimoto et al. (2018) with the type species *L. palmarum*. The genus is characterized by a relatively thinner and non-carbonized peridium, which is composed of rectangular cells and the absence of the surrounding brown hyphae (Hashimoto et al. 2018). The sexual morph is primarily characterized by immersed, subglobose ascomata, an elongated, laterally compressed ostiolar neck, and hyaline, fusiform, one-septate ascospores with a narrow bipolar sheath (Hashimoto et al. 2018). The asexual morph remains unknown. Currently, there are two species, *Leptoparies magnoliae* and *L. palmarum*, that are accepted in the Index Fungorum (accessed on 28 July 2025).

Leptoparies hydei H.Z. Du & Jian K. Liu, sp. nov.

Fig. 29

MycoBank number: MB855429; Facesoffungi number: FoF17981

Etymology – The epithet ‘*hydei*’ named for in honor of Prof. Kevin D. Hyde for his contribution to ascomycetes taxonomy.

Holotype – HKAS 132403

Saprobic on dead twigs of *Sanchezia nobilis* Hook. f. (*Acanthaceae*). Visible as crack-like dots. Sexual morph: *Ascomata* 251–418 µm diam. × 167–326 µm high ($\bar{x}$ = 352 × 295 µm, n = 20), subglobose or triangle, dark brown to black, solitary or scattered, unilocular, immersed to slightly erumpent, with a slit-like ostiole. *Ostiolar neck* 73–118 µm wide × 100–153 µm high ($\bar{x}$ = 105 × 140 µm, n = 20), crest-like, elongated, laterally compressed, composed of brown to black cells, filled with hyaline periphyses. *Peridium* 27–34 µm ($\bar{x}$ = 30 µm, n = 20) wide, composed of several layers of small, brown to dark brown, thin-walled, cells of *textura angularis*, fusing and indistinguishable from the host tissues. *Hamathecium* comprising 1–2 µm wide, hyaline, numerous, filamentous, indistinctly septate, cellular pseudoparaphyses, anastomosing at the apex. *Asci* 64–87 × 8–13 µm ($\bar{x}$ = 76 × 11 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical clavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 15–24 × 3–5 µm ($\bar{x}$ = 19 × 4.5 µm, n = 30), overlapping, uni- to bi-seriate, hyaline, fusiform with obtuse ends, slightly constricted at the septum, smooth, guttulate, generally with four guttules, with a narrow sheath. *Sheath* drawn out 3–6 µm long ($\bar{x}$ = 4.5 µm, n = 20) at both ends, with a lateral pad, 2–3 µm wide ($\bar{x}$ = 2 µm, n = 20) at side, stained with Indian ink showing the mucilaginous sheath at the end of the ascospores. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from one end. Colonies growing on PDA reached 18–20 mm diam. after three weeks at 25 °C in the dark. Colonies from above, circular, medium dense mycelia on the surface, white, slightly elevated in the center, regular edge. In reverse, pale gray in the center, white at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture,

Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'16"E, 21°55'44"N, elevation 506 m, on dead twigs of *Sanchezia nobilis* Hook. f. (*Acanthaceae*), 10 November 2022, H.Z. Du, S616 (HKAS 132403, holotype; HUEST 23.0445, isotype), ex-type living culture CGMCC 3.27712, ex-isotype living culture UESTCC 23.0444.

GenBank accession numbers – CGMCC 3.27712 = ITS: PQ394066, LSU: PQ184713, SSU: PQ184753, *tefl-α*: PQ346513; UESTCC 23.0444 = ITS: PQ394034, LSU: PQ184687, SSU: PQ184745, *tefl-α*: PQ346478.

Notes – *Leptoparies hydei* (HKAS 132403, holotype) morphologically resembles *L. magnoliae* (MFLU 18-1291, holotype) and *L. palmarum* (HHUF 28983, holotype) by having fusiform ascospores with obtuse ends and a narrow sheath surrounding them (Hashimoto et al. 2018, de Silva et al. 2022b). However, *L. hydei* differs from *L. magnoliae* in having larger asci (64–87 × 8–13 μm vs. 40–65 × 8–11 μm), and *L. hydei* can be distinguished from *L. palmarum* in having smaller ascomata (251–418 × 167–326 μm vs. 490–650 × 210–320 μm) and asci (64–87 × 8–13 μm vs. 77–118 × 10–14 μm). Phylogenetically, the two isolates (CGMCC 3.27712 and UESTCC 23.0444) of *L. hydei* clustered together with *L. palmarum* (CBS 143653, ex-type strain) with a well support (83% MLBS/0.96 BIPP) (Fig. 30). However, comparison of the nucleotide base pair between the ex-type strains of *L. hydei* (CGMCC 3.27712) and *L. palmarum* (CBS 143653) revealed the difference of 12/494 bp (2.4%, 4 gaps) in ITS sequence data. Therefore, the establishment of the new species *L. hydei* is justified by morphological and phylogenetic evidence.

Lophiostoma Ces. & De Not., Comment. Soc. Crittog. Ital. 1 (4): 219 (1863)

Mycobank number: MB2933; Facesoffungi number: FoF00403

Notes – *Lophiostoma* was established by Cesati & de Notaris (1863) to accommodate *L. macrostomum* as the type species (Tanaka & Harada 2003a, Hyde et al. 2013). Previously, *Lophiostoma* is morphologically similar to *Lophiotrema* (Chesters & Bell 1970) but distinguished by its peridium and asci (Holm & Holm 1988). Subsequently, Hirayama & Tanaka (2011) formally regarded them as two distinct genera based on morphological characteristics and molecular analyses. The sexual morph of *Lophiostoma* is characterized by immersed to erumpent ascomata with a laterally compressed-or crest-like apex, mostly clavate asci, and septate, hyaline to dark brown ascospores with terminal appendages or mucilaginous sheaths. Members of this genus are commonly found on decaying wood and herbaceous substrates in terrestrial and aquatic habitats (Hirayama & Tanaka 2011, Hyde et al. 2013, Wijayawardene et al. 2018, 2020, Bao et al. 2019, Hongsanan et al. 2020a).

Lophiostoma japonicum (Thambug., Wanas., Kaz. Tanaka & K.D. Hyde) Andreasen, Jaklitsch & Voglmayr, Persoonia 46: 256 (2021) Fig. 31

Mycobank number: MB838983; Facesoffungi number: FoF14069

= *Biappendiculispora japonica* Thambug., Wanas., Kaz. Tanaka & K.D. Hyde, Fungal Diversity 74: 214 (2015)

Saprobic on dead twigs of *Rumex acetosa* Linnaeus (*Polygonaceae*). Visible as brown or dark brown dots. Sexual morph: *Ascomata* 271–455 μm diam. × 192–214 μm high ($\bar{x}$ = 290 × 201 μm, n = 20), solitary, immersed to papilla erumpent through host surface, subglobose, reddish brown to black, uni-loculate, glabrous, coriaceous, ostiolate. *Ostiole* 80–129 μm wide × 120–169 μm high ($\bar{x}$ = 110 × 158 μm, n = 20), rounded or slit-like, variable in shape, central, papillate, with a pore-like opening, plugged by gelatinous tissue, made up of hyaline, pseudoparenchymatous cells and occasionally in lighter color. *Peridium* 25–35 μm wide ($\bar{x}$ = 30 μm, n=20), thick-walled, wider at the apex and thinner at the base, composed of a single stratum, comprised of 5–7 layers of lightly pigmented to reddish brown, arranged in cells of *textura angularis*, inner cells hyaline, lighter, outer layer cells brown to dark brown, darker, fusing, and indistinguishable from the host tissues. *Hamathecium* comprising numerous, 2–3 μm wide, branched, septate, hyaline, cellular pseudoparaphyses, situated between and above the asci, embedded in a gelatinous matrix. *Asci* 88–111 × 11–14 μm ($\bar{x}$ = 101 × 12 μm, n = 30), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short

pedicellate, apically rounded with a minute ocular chamber. *Ascospores* $22\text{--}36 \times 4\text{--}7\text{ }\mu\text{m}$ ($\bar{x} = 32 \times 6\text{ }\mu\text{m}$, $n = 30$), overlapping uni to bi-seriate, fusiform with acute ends, straight or curved, 7–9-septate, constricted at the septa, cell above the central septum widest, hyaline when young, becoming pale yellowish to brown at maturity, with guttules, smooth-walled, with appendages at both ends, $4\text{--}6 \times 2.5\text{--}3.5\text{ }\mu\text{m}$ ($\bar{x} = 5 \times 3\text{ }\mu\text{m}$, $n = 30$). Asexual morph: Undetermined.



Figure 29 – *Leptoparies hydei* (HKAS 132403, holotype). a Host *Sanchezia nobilis*. b A twig of *S. nobilis*. c–e Appearance of ascomata on host surface. f Vertical section of ascomata. g Ostiole. h Peridium. i Hamathecium. j–l Asci. m–r Ascospores. s Ascospore stained with Indian ink showing the mucilaginous sheath. t Germinated ascospore. u, v Colony on PDA, above (u) and below (v). Scale bars: f = 100 μm , g = 50 μm , h, i, k, l = 20 μm , j = 15 μm , m–t = 10 μm .

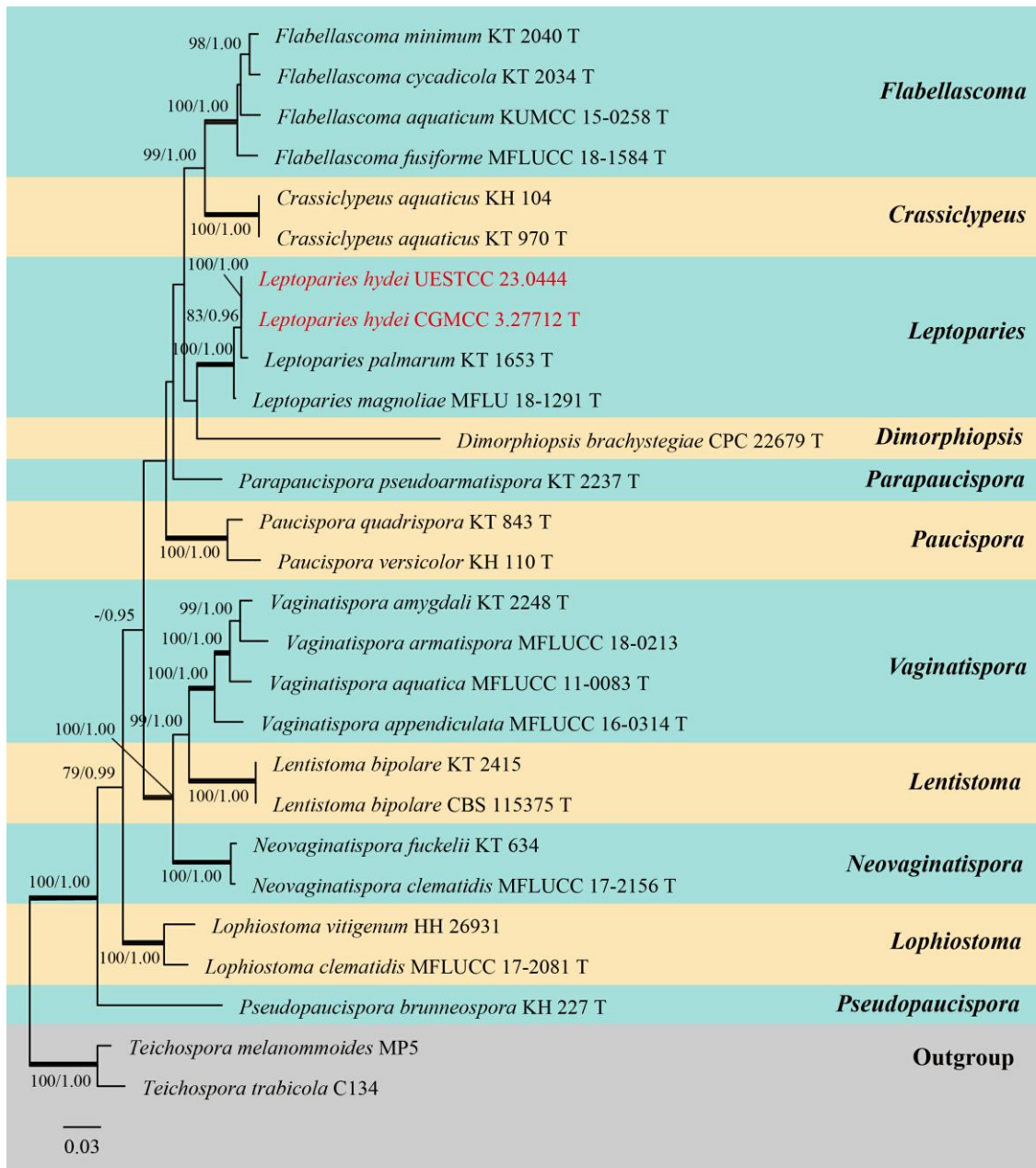


Figure 30 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined SSU, ITS, LSU, and *tefl-α* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below the nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Teichospora trabricola* (C134) and *T. melanommoides* (MP5). The best scoring RAxML tree with a final likelihood value of -14,012.441457 is presented. The matrix had 767 distinct alignment patterns, with 12.95% of undetermined characters or gaps, the tree-length is 1.186942. Estimated base frequencies were as follows: A = 0.243099, C = 0.251022, G = 0.269371, T = 0.236508, with substitution rates AC = 1.526938, AG = 3.019838, AT = 1.356099, CG = 1.600597, CT = 8.263443, GT = 1.000000; gamma distribution shape parameter alpha = 0.137728. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009953 (the critical value for the topological convergence diagnostic is below 0.01).



Figure 31 – *Lophiostoma japonicum* (HUEST 23.0446, new host record). a Host *Rumex acetosa*. b A twig of *R. acetosa*. c–e Appearance of ascomata on host surface. f Vertical section of ascomata. g Ostiole. h Peridium. i Hamathecium. j–l Asci. m–r Ascospores. s Germinated ascospore. t, u Colonies on PDA, above (t) and below (u). Scale bars: f, g = 100 μ m, h = 20 μ m, i, m–s = 15 μ m, j–l = 20 μ m.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from one or both ends. Colonies growing on PDA reached 22–35 mm diam. after three

weeks at 25 °C in the dark. Colonies from above, circular, medium dense mycelia on the surface, white, pale yellow and slightly elevated in the center, regular edge, and light yellow in the center, white at the edge from reverse.

Material examined – China, Sichuan Province, Yaan City, Lushan County, Siyan Town, 102°53'18"E, 30°8'17"N, elevation 718 m, on dead twigs of *Rumex acetosa* (*Polygonaceae*), 29 October 2021, H.Z. Du, S439 (HUEST 23.0446), living culture UESTCC 23.0445.

GenBank accession numbers – ITS: PQ394035, LSU: PQ184688, *tefl-α*: PQ346479.

Notes – Multi-locus phylogeny indicated that our isolate (UESTCC 23.0445) clustered together with *Lophiostoma japonicum* (ex-type strain MAFF 239452, MFLUCC 17-2450, GZAAS 21-2004, GZCC 19-0008) with a strong statistical support (97% MLBS/0.98 BIPP) (Fig. 37). Morphologically, our collection (HUEST 23.0446) is similar to *L. japonicum* (HHUF 27313, holotype) in having clavate asci and fusiform, 7–9-septate, guttulate ascospores with appendages at both ends, without any significant morphological or phylogenetic differences. Therefore, we identify the newly collected taxon as *L. japonicum*, and reported it as a new host record from *Rumex acetosa* in Sichuan Province, China.

Lophiotremataceae K. Hiray. & Kaz. Tanaka, Mycoscience 52: 405 (2011)

MycoBank number: MB561063; Facesoffungi number: FoF08284

Notes – *Lophiotremataceae* was introduced as a monotypic family to accommodate the type genus *Lophiotrema* by Hirayama & Tanaka (2011). The sexual morph of *Lophiotremataceae* is characterized by subglobose to globose ascomata, cylindrical, short pedicellate asci, and fusiform to cylindrical, septate, hyaline to brown ascospores (Hirayama & Tanaka 2011). The asexual morph is characterized by pycnidial, globose to subglobose, scattered, semi-immersed conidiomata, holoblastic or phialidic, cylindrical to ampliform conidiogenous cells, ellipsoidal to cylindrical conidia with rounded ends. Most species of *Lophiotremataceae* are saprobic on herbaceous and woody plants in terrestrial habitats (Hyde et al. 2013, Hashimoto et al. 2017). Currently, eight genera are classified within *Lophiotremataceae* (Hyde et al. 2024).

Lophiotrema Sacc., Michelia 1 (no. 3): 338 (1878)

MycoBank number: MB549045; Facesoffungi number: FoF08285

Notes – *Lophiotrema* was proposed by Saccardo (1878). Subsequently, Saccardo (1883) formally erected *Lophiotrema* to include fungi that have ascomata with a crest-like beak similar to those of *Lophiostoma*, and with hyaline, multi-septate ascospores. However, Chesters & Bell (1970) regarded it as a synonym of *Lophiostoma*, arguing that the color of the ascospores and the number of transverse septa are not adequate for distinguishing between genera. Holm & Holm (1988) discussed these two genera based on the different types of peridium and asci. Finally, Hirayama & Tanaka (2011) formally separated *Lophiotrema* from *Lophiostoma* based on morphological characteristics and phylogenetic analyses, while Hashimoto et al. (2017) suggested that the boundary of *Lophiotrema* should be narrowed. Therefore, the ambiguous taxa of this genus need to be studied thoroughly. *Lophiotrema* is characterized by immersed ascomata with a crest-like ostiolar neck, cylindrical asci, and hyaline, multiseptate ascospores (Hirayama & Tanaka 2011, Hyde et al. 2013). Members of *Lophiotrema* have since been reported as saprobes occurring on various plant from terrestrial, freshwater, and marine habitats, and new species are continually being discovered (Tanaka & Harada 2003b, Zhang et al. 2009b, Hyde et al. 2013, Liu et al. 2015, Hyde et al. 2016, Hashimoto et al. 2017, Mathiassen et al. 2017, 2018, Hongsanan et al. 2020a, Boonmee et al. 2021).

Lophiotrema hydei J.F. Zhang, J.K. Liu & Z.Y. Liu, Phytotaxa 379 (2): 172 (2018)

Fig. 32

MycoBank number: MB555509; Facesoffungi number: FoF05216

Saprobic on dead twigs of *Rumex acetosa* (*Polygonaceae*), visible as brown or dark brown dots. Sexual morph: *Ascomata* 188–258 µm diam. × 101–205 µm high ($\bar{x}$ = 214 × 115 µm, n = 20), immersed to semi-immersed, uni-loculate, solitary or scattered, glabrous, coriaceous, globose to subglobose, dark brown to black, ostiolate, papillate. *Ostioles* 111–141 µm wide × 95–102 µm high

($\bar{x}$ = 126 × 99 μ m, n = 20), central or lateral, carbonaceous, normally with a pore-like opening, filled with periphyses. *Peridium* up to 20–36 μ m ($\bar{x}$ = 27 μ m, n = 20) thick, composed of several layers of dark brown to black, thick-walled pseudoparenchymatous cells of *textura angularis*, fusing with host tissue at the most outside layer and pale inwardly. *Hamathecium* comprising 1.3–2.2 μ m wide, hyaline, branched, cellular pseudoparaphyses, anastomosing among and between the asci, embedded in a gelatinous matrix. *Asci* 63–94 × 6–9 μ m ($\bar{x}$ = 78 × 7.5 μ m, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, pedicellate, apically rounded with a minute ocular chamber. *Ascospores* 17.5–29 × 2.7–4 μ m ($\bar{x}$ = 25 × 3.5 μ m, n = 30), overlapping, bi-seriate, hyaline, fusiform, straight, or slightly curved, one-celled when young and become conspicuously 3-septate at maturation, slightly constricted at the septum, narrower towards both ends, smooth-walled, with guttules, surrounded by an irregular mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 28–30 mm diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense mycelia on the surface, pale grayish green in the center, slightly elevated, radial, regular edge, with a grayish white outer ring. In reverse, black in the center, grayish white ring at the edge.

Material examined – China, Sichuan Province, Yaan City, Lushan County, Siyan Town, 102°53'18"E, 30°8'17"N, elevation 718 m, on dead twigs of *Rumex acetosa* (*Polygonaceae*), 29 October 2021, H.Z. Du, S440 (HUEST 23.0451), living culture UESTCC 23.0450.

GenBank accession numbers – ITS: PQ394036, LSU: PQ184689, *tef1- α* : PQ346480, *rpb2*: PQ379942.

Notes – *Lophiotrema hydei* was introduced by Zhang et al. (2018) and isolated from an unidentified herbaceous plant in China. Morphologically, our collection (HUEST 23.0451) is identical to the holotype (MFLU 18-2075) of *Lo. hydei* (Zhang et al. 2018), and our isolate (UESTCC 23.0450) grouped with the ex-type strain of *Lo. hydei* (GZCC 18-0016) and formed a well-supported clade with 92% MLBS/1.00 BIPP (Fig. 37). Multi-locus comparison between UESTCC 23.0450 and GZCC 18-0016 showed 99.6%–100% similarity in ITS, LSU, and *tef1- α* sequence data. Therefore, we reported it as a new host record from *Rumex acetosa* in Sichuan Province, China.

Lophiotrema hydeirubicola H.Z. Du & Jian K. Liu, sp. nov.

Fig. 33

MycoBank number: MB855431; Facesoffungi number: FoF17983

Etymology – The epithet ‘*hydeirubicola*’ is a combination of Prof. Kevin D. Hyde’s last name and the host genus ‘*Rubus*’ from which the fungus was originally isolated, acknowledging his significant contributions to ascomycetes taxonomy.

Holotype – HKAS 132405

Saprobic on dead twigs of *Rubus corchorifolius* Linnaeus f. (*Rosaceae*). Visible as black dots. Sexual morph: *Ascomata* 204–336 μ m diam. × 132–229 μ m high ($\bar{x}$ = 291 × 190 μ m, n = 20), semi-immersed to erumpent through host surface, black, solitary, scattered, mammiform, with a flattened base, uni-loculate, glabrous, ostiolate, papillate. *Ostioles* 89–119 μ m wide × 60–73 μ m high ($\bar{x}$ = 100 × 67 μ m, n = 20), central or lateral, apically with crest-like papilla, filled with periphyses, carbonaceous, with a beak-like opening. *Peridium* 16–22 μ m ($\bar{x}$ = 19 μ m, n = 20) thick, composed of several layers of dark brown to black, thick-walled pseudoparenchymatous cells, fusing with host tissue at the outermost layer, and become pale pigmented inwardly. *Hamathecium* composed of branched, 1–2 μ m wide, hyaline, filamentous, indistinct septate, anastomosed pseudoparaphyses, embedded in a hyaline, gelatinous matrix. *Asci* 60–98 × 6–8 μ m ($\bar{x}$ = 72 × 7 μ m, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate with furcate to truncate pedicels, apically rounded, with well-developed ocular chambers. *Ascospores* 15–22.5 × 2.5–3 μ m ($\bar{x}$ = 18 × 3 μ m, n = 30), overlapping uniseriate or bi-seriate, hyaline, fusiform, straight, or slightly curved, one-celled when young and become 3-euseptate at maturation, slightly constricted at the septa, narrower towards both ends, smooth-walled, with guttules. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 22–24 mm diam. after three weeks at

25 °C in the dark. Colonies from above, circular, dense mycelia on the surface, grayish white, center slightly elevated, regular edge with white mycelium, visible as shining black mucoid on colony, pale grayish green in reverse, with a grayish white outer ring.



Figure 32 – *Lophiotrema hydei* (HUEST 23.0451, new host record). a Host *Rumex acetosa*. b A twig of *R. acetosa*. c–f Appearance of ascomata on host surface. g, h Vertical section of ascomata. i Peridium. j Hamathecium. k–o Asci. p–s Ascospores. t Ascospore stained with Indian ink showing the mucilaginous sheath. u Germinated ascospore. v, w Colonies on PDA, above (v) and below (w). Scale bars: g, h = 100 μ m, i = 75 μ m, j = 40 μ m, k–o, u = 20 μ m, p–t = 10 μ m.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan City, Qingcheng Mountain scenic spot, 103°28'32"E, 30°55'19"N, elevation 1,185 m, on dead twigs of *Rubus corchorifolius* (Rosaceae), 27 March 2021, H.Z. Du, S166 (HKAS 132405 = HUEST 23.0449, holotype), ex-type living culture CGMCC 3.27714 = UESTCC 23.0448; *ibid.*, S166-1 (HUEST 23.0448, isotype), ex-isotype living culture UESTCC 23.0447.

GenBank accession numbers – CGMCC 3.27714 = ITS: PQ394068, LSU: PQ184715, *tefl-α*: PQ346514, *rpb2*: PQ379946; UESTCC 23.0447 = ITS: PQ394040, LSU: PQ184693, *tefl-α*: PQ346482.

Notes – Multi-locus phylogeny (Fig. 37) showed that *Lophiotrema hydeirubicola* (CGMCC 3.27714 and UESTCC 23.0447) formed a distinct clade and was sister to *Lo. guizhouense* with the statistical support (100% MLBS, 1.00 BIPP). Morphologically, *Lo. hydeirubicola* (HKAS 132405, holotype) differs from *Lo. guizhouense* (HGUP 24-0017, holotype) by its larger ascomata (204–336 × 132–229 μm vs. 133–280 × 115–182 μm) and longer asci (60–98 μm vs. 54–62 μm) (Sun et al. 2025). Comparison of the nucleotide base pairs between *Lo. hydeirubicola* (CGMCC 3.27714) and *Lo. guizhouense* (GUCC 24-0064) revealed differences of ex-type strains, ITS = 13/541 bp (2.4%, 6 gaps) and LSU = 10/825 bp (1.2%, 1 gap). Additionally, base-pair differences between the ex-type strains of *Lo. hydeirubicola* and members of adjoining clades are shown in Table 5. Therefore, *Lo. hydeirubicola* is introduced as a new species based on morphological and phylogenetic evidence, and is associated with *Rubus corchorifolius* in Sichuan Province, China.

Table 5 Comparison of base pair differences between *Lophiotrema hydeirubicola* (CGMCC 3.27714, ex-type strain) and members of adjoining clades.

Species	Strain/Specimen number	Type materials	ITS (bp)	LSU (bp)	<i>tefl-α</i> (bp)	<i>rpb2</i> (bp)
<i>Lo. asexuale</i>	GUCC 24-0063	Ex-type strain	58/499 (11.6%, 25 gaps)	17/811 (2.1%, 1 gap)	N/A	N/A
<i>Lo. hydei</i>	GZCC 18-0016	Ex-type strain	57/500 (11.4%, 20 gaps)	17/846 (2.0%, 1 gap)	60/869 (6.9%, without gaps)	N/A
<i>Lo. karsti</i>	GZCC 19-0038	Ex-type strain	55/501 (11.0%, 25 gaps)	16/846 (1.9%, 1 gap)	59/869 (6.8%, without gaps)	N/A
<i>Lo. kevinobpyriforme</i>	CGMCC 3.27284	Ex-type strain	61/462 (13.2%, 30 gaps)	17/846 (2.0%, 1 gap)	62/827 (7.5%, 1 gap)	148/1034 (14.3%, 1 gap)
<i>Lo. lincangensis</i>	HKAS 115777	Holotype	56/494 (11.3%, 25 gaps)	15/821 (1.8%, without gaps)	52/861 (6.0%, without gaps)	158/996 (15.9%, 2 gaps)
<i>Lo. mucilaginosus</i>	LC12112	Ex-type strain	57/500 (11.4%, 20 gaps)	17/846 (2.0%, 1 gap)	61/866 (7.0%, without gaps)	153/1010 (15.1%, without gaps)
<i>Lo. myriocarpum</i>	CBS 147535	–	53/449 (11.8%, 16 gaps)	N/A	50/740 (6.8%, without gaps)	140/1039 (13.5%, 1 gap)
<i>Lo. neohysterioides</i>	KT 588		55/492 (11.2%, 23 gaps)	16/834 (1.9%, 1 gap)	64/869 (7.4%, without gaps)	150/1012 (14.8%, without gaps)

Species	Strain/Specimen number	Type materials	ITS (bp)	LSU (bp)	<i>tefl-α</i> (bp)	<i>rpb2</i> (bp)
<i>Lo. obpyriformis</i>	UESTCC 23.0448	Ex-type strain	61/462 (13.2%, 1 30 gaps)	17/846 (2.0%, 1 gap)	62/827 (7.5%, 1 gap)	148/1034 (14.3%, 1 gap)

“N/A” denotes sequence data is unavailable in GenBank.

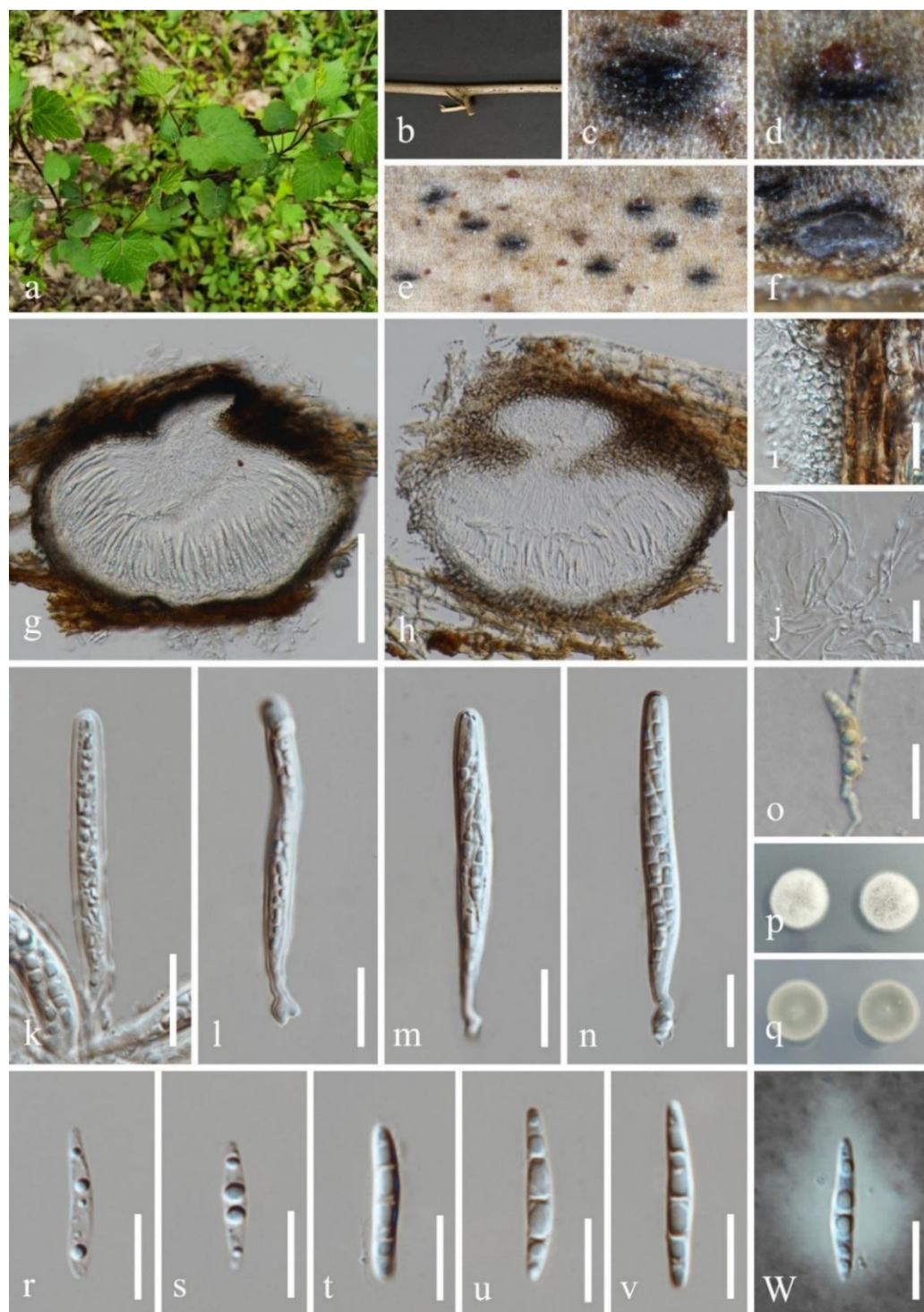


Figure 33 – *Lophiotrema hydeirubicola* (HKAS 132405, holotype). a Host *Rubus corchorifolius*. b A twig of *R. corchorifolius*. c–f Appearance of ascomata on host surface. g, h Vertical section of ascomata. i Peridium. j Hamathecium. k–n Asci. o Germinated ascospore. p, q Colonies on PDA, above (p) and below (q). r–v Ascospores. w Ascospore stained with Indian ink showing the mucilaginous sheath. Scale bars: g, h = 100 μm, i–o = 15 μm, r–w = 10 μm.

Lophiotrema kevinobpyriforme H.Z. Du & Jian K. Liu, sp. nov.

Fig. 34

MycoBank number: MB855430; Facesoffungi number: FoF17982

Etymology – The epithet ‘*kevinobpyriforme*’ is a combination of Prof. Kevin D. Hyde’s first name and the obpyriform-like ascomata, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132409

Saprobic on dead twigs of *Magnolia officinalis* Rehd. et Wils. var. *biloba* Rehd. et Wils. (*Magnoliaceae*). Visible as black dots. Sexual morph: *Ascomata* 126–140 μm diam. $\times$ 129–174 high ($\bar{x}$ = 131 $\times$ 151 μm , n = 20), immersed to semi-immersed, uni-loculate, solitary or scattered, glabrous, coriaceous, obpyriform, or globose to subglobose, dark brown to black, ostiolate, papillate. *Ostiole* 64–93 μm wide $\times$ 40–64 high ($\bar{x}$ = 82 $\times$ 53 μm , n = 20), central or lateral, carbonaceous, normally with a pore-like opening, filled with periphyses. *Peridium* 16–26 μm ($\bar{x}$ = 21 μm , n = 20) thick, composed of several layers of dark brown to black, thick-walled pseudoparenchymatous cells of *textura angularis*, fusing with host tissue at the outermost layer, and become pale pigmented inwardly. *Hamathecium* comprising 1–2 μm wide, branched, hyaline, hypha-like pseudoparaphyses, anastomosing among and between the asci, embedded in a gelatinous matrix. *Asci* 51–89 $\times$ 6–13 μm ($\bar{x}$ = 72 $\times$ 9 μm , n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, pedicellate, apically rounded with a minute ocular chamber. *Ascospores* 19–25 $\times$ 3–5 μm ($\bar{x}$ = 23 $\times$ 4 μm , n = 30), overlapping uniseriate or bi-seriate, hyaline, fusiform, straight or slightly curved, one-celled when young and become 3-euseptate at maturation, the upper cell is longer than the lower cells, slightly constricted at the septa, narrower towards both ends, smooth-walled, with guttules, with an entire mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 18–20 mm diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense mycelia on the surface, white, center slightly elevated, regular edge, and blackish green in reverse, with a white outer ring.

Material examined – China, Sichuan Province, Yaan City, Baoxing County, Lingguan Town, 102°50'57"E, 30°15'40"N, elevation 915 m, on dead twigs of *Magnolia officinalis* Rehd. et Wils. var. *biloba* Rehd. et Wils. (*Magnoliaceae*), 29 October 2021, H.Z. Du, S449 (HKAS 132409, holotype; HUEST 23.0452, isotype); ex-type living culture CGMCC 3.27284, ex-isotype living culture UESTCC 23.0451.

GenBank accession numbers – CGMCC 3.27284 = ITS: PQ394067, LSU: PQ184714, *rpb2*: PQ379945; UESTCC 23.0451 = ITS: PQ394039, LSU: PQ184692.

Notes – Multi-locus phylogeny (Fig. 37) showed that *Lophiotrema kevinobpyriforme* (CGMCC 3.27284 and UESTCC 23.0451) formed a distinct lineage and is sister to *Lo. karsti* with 77% MLBS, 0.98 BIPP statistical support. Morphologically, our new collection (HKAS 132409, holotype) resembles *Lo. karsti* (GZAAS 19-1750, holotype) in having cylindrical, short pedicellate asci as well as fusiform, hyaline, 3-euseptate ascospores at maturation (Zhang et al. 2023a). However, *Lo. kevinobpyriforme* (CGMCC 3.27284, ex-type strain) can be distinguished from *Lo. karsti* (GZCC 19-0038, ex-type strain) by 1.9% (9/470 bp, 9 gaps) in ITS and 2.0% (17/857 bp, 1 gap) in *tefl-a* differences. Therefore, *Lo. kevinobpyriforme* is identified as a new species based on phylogenetic evidence which associated with *Magnolia officinalis* in Sichuan Province, China.

Lophiotrema mucilaginosus M. Raza & L. Cai, Fungal Diversity 95: 32 (2019)

Fig. 35

MycoBank number: MB555333; Facesoffungi number: FoF04941

Saprobic on dead twigs of *Toona sinensis* (Juss.) Roem. (*Meliaceae*). Visible as black dots. Sexual morph: *Ascomata* 216–283 μm diam. $\times$ 180–223 μm high ($\bar{x}$ = 242 $\times$ 203 μm , n = 20), solitary, scattered, black, semi-immersed to erumpent through host surface, conical to mammiform, with a flattened base, uni-loculate, glabrous, ostiolate, papillate. *Ostioles* 60–95 μm wide $\times$ 74–120 μm high ($\bar{x}$ = 80 $\times$ 95 μm , n = 20), central or lateral, apically with crest-like papilla, filled with periphyses, carbonaceous, with a beak-like opening. *Peridium* 17–28 μm wide ($\bar{x}$ = 21 μm , n = 20), outer layer thick, composed of dark, coriaceous, pseudoparenchymatous cells of *textura epidermoidea*, inner

layer comprising light pigmented to hyaline cells of *textura angularis*. *Hamathecium* composed of branched, 1–2 μm wide, hyaline, filamentous, indistinct septate, anastomosed pseudoparaphyses, embedded in a hyaline, gelatinous matrix. *Asci* 68–95 $\times$ 6.5–8.5 μm ($\bar{x}$ = 83 $\times$ 7 μm , n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate with furcate to truncate pedicels, apically rounded, with a well-developed ocular chamber. *Ascospores* 24–31 $\times$ 3–4 μm ($\bar{x}$ = 26 $\times$ 3.5 μm , n = 30), overlapping 2-seriate, hyaline, sub-fusoid to fusiform, with rounded or obtuse ends, 1(–3)-septate, smooth-walled, guttulate when young, with an entire mucilaginous sheath (9–20.5 μm wide at sides). Asexual morph: Undetermined.



Figure 34 – *Lophiotrema kevinobpyriforme* (HKAS 132409, holotype). a Host *Magnolia officinalis*. b A twig of *M. officinalis*. c–f Appearance of ascomata on host surface. g Section through ascomata. h Peridium. i Hamathecium. j Germinated ascospore. k–p Asci. q–u Ascospores. v Ascospore stained in Indian ink showing the mucilaginous sheath. w, x Colony on PDA, above (w) and below (x). Scale bars: g = 50 μm , h–p = 20 μm , q–v = 10 μm .

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 18–20 mm diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense mycelia on the surface, grayish white, slightly elevated at the center, regular edge, shining black mucoid colony. In reverse, pale green in the center, brown to pale brown from center to edge.

Material examined – China, Yunnan Province, Kunming City, Dongchuan District, Tuobuka Town, 103°2'32"E, 26°19'20"N, elevation 2,348 m, on dead twigs of *Toona sinensis* (Meliaceae), 29 March 2022, H.Z. Du, S511 (HUEST 23.0450), living culture UESTCC 23.0449.

GenBank accession numbers – ITS: PQ394037, LSU: PQ184690, *tefl-α*: PQ346481, *rpb2*: PQ379943.

Notes – *Lophiotrema mucilaginosis* was introduced by Phookamsak et al. (2019) and isolated from wood litter in China. Our collection was identical to *Lo. mucilaginosis* based on morphology and phylogeny (Fig. 37) (Phookamsak et al. 2019). In addition, multi-locus comparison between our isolate (UESTCC 23.0449) and the ex-type strain of *Lo. mucilaginosis* (LC12112) showed 99.1%–100% similarity in ITS, LSU, *tefl-α*, and *rpb2*. Therefore, we report a new host record of *Lo. mucilaginosis* from *Rumex acetosa* in Yunnan Province, China.

Lophiotrema neohysterioides M.E. Barr, Mycotaxon 45: 208, 1992.

Fig. 36

Mycobank number: MB447491; Facesoffungi number: FoF05217

Saprobic on dead twigs of *Rumex acetosa* (Polygonaceae). Visible as brown or dark brown dots. Sexual morph: *Ascomata* 172–323 µm diam. × 138–227 µm high ($\bar{x}$ = 216 × 180 µm, n = 20), dark brown to black, scattered, gregarious, immersed to erumpent throughout the host tissue, globose to subglobose, uni-loculate, glabrous, coriaceous, ostiolate. *Ostioles* 88–116 µm wide × 91–121 µm high ($\bar{x}$ = 98 × 109 µm, n = 20) central, carbonaceous, with a crest-like opening, filled with periphyses. *Peridium* 17.5–27 µm wide ($\bar{x}$ = 23 µm, n = 20), thick-walled, comprised of 5–7 layers of thin to thick-walled pseudoparenchymatous cells, inner cells hyaline, outer cell layers brown to dark brown *textura angularis*. *Hamathecium* comprising dense, 1.5–2 µm wide, branched, hyaline, cellular pseudoparaphyses, anastomosing among and between the asci, embedded in a gelatinous matrix. *Asci* 58.5–76.5 × 7–10 µm ($\bar{x}$ = 70 × 8.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short pedicellate, apically rounded with a minute ocular chamber. *Ascospores* 17–33 × 3–5 µm ($\bar{x}$ = 23 × 4 µm, n = 30), overlapping bi-seriate, hyaline, fusiform, straight or slightly curved, 3-septate, with a primary median septum, normally constricted at the median septum, smooth-walled, guttulate, with a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 32–35 mm diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense mycelia on the surface, grayish white, center slightly elevated, regular edge. In reverse, dark grayish green, white at the center and the edge.

Material examined – China, Sichuan Province, Yaan City, Lushan County, Siyan Town, 102°53'18"E, 30°8'17"N, elevation 718 m, on dead twigs of *Rumex acetosa* (Polygonaceae), 29 October 2021, H.Z. Du, S436 (HUEST 23.0454), living culture UESTCC 23.0453.

GenBank accession numbers – ITS: PQ394038, LSU: PQ184691, *rpb2*: PQ379944.

Notes – The phylogenetic tree (Fig. 37) showed our isolate (UESTCC 23.0453) clustered together with *Lophiotrema neohysterioides* (GZCC 18-0015, KT 588, KT 713, KT 756, and MAFF 245619) with a strong statistical support (100% MLBS/1.00 BIPP). Morphologically, our collection (HUEST 23.0454) is similar to *Lo. neohysterioides* in having clavate asci and hyaline, fusiform, three equidistant septate ascospores (Tanaka & Harada 2003b, Zhang et al. 2018). Therefore, we identify the newly collected taxon as *Lo. neohysterioides* and reported it as a new host record from *Rumex acetosa* in Sichuan Province, China.



Figure 35 – *Lophiotrema mucilaginosus* (HUEST 23.0450, new host record). a Host *Toona sinensis*. b–d Appearance of ascomata on host surface. e, f Vertical section of ascomata. g Peridium. h Hamathecium. i–k Asci. l–p Ascospores. q Ascospore stained with Indian ink showing the mucilaginous sheath. r Germinated ascospore. s, t Colonies on PDA, above (s) and below (t). Scale bars: e, f = 100 μ m, g, h = 20 μ m, i–k = 30 μ m, l–r = 10 μ m.

Macrodiplodiopsidaceae Voglmayr, Jaklitsch & Crous, IMA Fungus 6 (1): 178 (2015)

Mycobank number: MB812794; Facesoffungi number: FoF08291

Notes – *Macrodiplodiopsidaceae* was established by Crous et al. (2015) to accommodate the

type genus of *Macrodiplodiopsis*. The sexual morph of this family is characterized by immersed, solitary or aggregated ascomata, cylindric-clavate to broadly clavate asci, dark brown, obovoid, septate ascospores. The asexual morph composed of unilocular, single or gregarious, dark brown to black conidiomata, hyaline, discrete, cylindrical conidiogenous cells, and ellipsoid to obovoid or clavate, septate conidia, occasionally with a longitudinal septum. Currently, the family consists of two genera, *Macrodiplodiopsis* and *Pseudochaetosphaeronema*, and reported as pathogens, endophytes, and saprobes from terrestrial habitats (Boonmee et al. 2021, de Silva et al. 2022a, Wijayawardene et al. 2022a, Hyde et al. 2024, Xu et al. 2024).



Figure 36 – *Lophiotrema neohysterioides* (HUEST 23.0454, new host record). a Host *Rumex acetosa*. b A twig of *R. acetosa*. c–e Appearance of ascomata on host surface. f, g Vertical section of ascomata. h Peridium. i Hamathecium. j–l Asci. m Germinated ascospore. n, o Colonies on PDA, above (n) and

below (o). p–s Ascospores. t Ascospore stained with Indian ink showing the mucilaginous sheath. Scale bars: f, g = 50 μ m, h, i, k = 20 μ m, j, l, m = 15 μ m, p–t = 10 μ m.

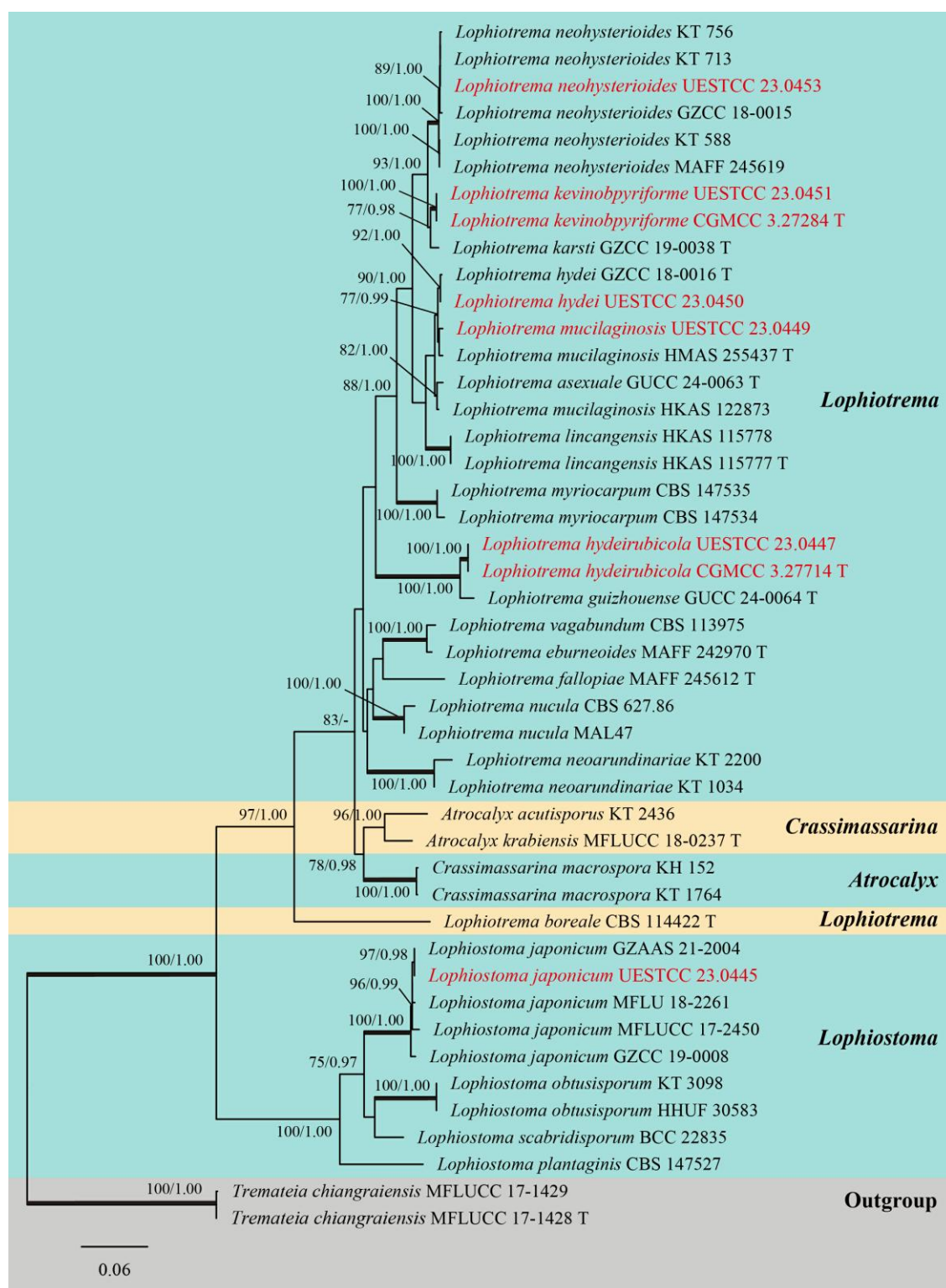


Figure 37 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined ITS, LSU, *tefl- α* , and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or below the nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Tremateia chiangraiensis* (MFLUCC 17-1428) and *T. chiangraiensis* (MFLUCC 17-1429). The best scoring RAXML tree with a final likelihood value of -19,281.673020

is presented. The matrix had 1,162 distinct alignment patterns, with 16.23% of undetermined characters or gaps, the tree-length is 1.640048. Estimated base frequencies were as follows: A = 0.242288, C = 0.274933, G = 0.268609, T = 0.214170, with substitution rates AC = 2.112399, AG = 4.893736, AT = 1.614277, CG = 1.512215, CT = 11.444314, GT = 1.000000; gamma distribution shape parameter alpha = 0.208806. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009987 (the critical value for the topological convergence diagnostic is below 0.01).

***Pseudochaetosphaeronema* Punith., Nova Hedwigia 31 (1–3): 126 (1979)**

Mycobank number: MB9562; Facesoffungi number: FoF08294

Notes – *Pseudochaetosphaeronema* was introduced by Punithalingam (1979), with *P. larense* as the type species. The sexual morph of this genus is characterized by immersed, uni-loculate ascomata, 8-spored, bitunicate, fissitunicate asci with short distinct pedicels, and hyaline, fusiform, 1-septate, guttulate ascospores (Boonmee et al. 2021, Xu et al. 2024). The asexual morph has globose to subglobose conidiomata, monoblastic or monophialidic, and cylindrical conidiogenous cells, hyaline and subglobose to oval conidia (de Silva et al. 2022a).

***Pseudochaetosphaeronema hydeiseptatum* H.Z. Du, N. Wu & Jian K. Liu, sp. nov. Fig. 38**

Mycobank number: MB857559; Facesoffungi number: FoF17984

Etymology – The epithet ‘*hydeiseptatum*’ is a combination of Prof. Kevin D. Hyde’s last name and the septum observed in mature spores of asexual morph, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132436

Saprobic on dead twigs of *Cercis chinensis* Bunge (*Fabaceae*). Visible as black or dark brown dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 172–292 µm diam. × 124–198 µm high ($\bar{x}$ = 241 × 176 µm, n = 20), pycnidial, solitary, immersed, globose to subglobose, scattered, black, glabrous, unilocular, without papilla. *Conidiomatal wall* 20–25 µm wide ($\bar{x}$ = 22 µm, n = 20), multi-layered, outer layer composed of brown to dark brown, thick-walled cells of *textura angularis*, lined with hyaline, thin-walled inner layers bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells, arising from the base and sides of the conidiomata. *Conidiogenous cells* 6.3–9.5 × 2.4–3.5 µm ($\bar{x}$ = 8.5 × 3 µm, n = 20), monoblastic, determinate, arising from the inner layer of the pycnidium wall, hyaline, cylindrical, integrated, smooth, thin-walled. *Conidia* 12.3–17 × 6–7.5 µm ($\bar{x}$ = 14 × 6.7 µm, n = 30), typically fusiform with round ends, occasionally oval, hyaline when immature, becoming brown at maturity, smooth-walled, 3-transversely septate, with 1–2-vertical septa, slightly constricted at the septum.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from each cell. Colonies growing on PDA reached 23–25 mm diam. after three weeks at 25 °C in the dark. Colonies from above, circular, regular, dense mycelium, white. In reverse, pale grayish black in the center, and grayish white at the edge.

Material examined – China, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 102°44'26"E, 25°8'42"N, elevation 1,925 m, on dead twigs of *Cercis chinensis* (*Fabaceae*), 11 November 2022, H.Z. Du, S732 (HKAS 132436, holotype; HUEST 23.0519, isotype); ex-type living culture CGMCC 3.28691, ex-isotype living culture UESTCC 23.0518.

GenBank accession numbers – HKAS 132436 = ITS: PQ773407, LSU: PQ773427, SSU: PQ773443, *tefl-α*: PV059187, *rpb2*: PV075245; UESTCC 23.0518 = ITS: PQ773408, LSU: PQ773428, SSU: PQ773444, *tefl-α*: PV059188, *rpb2*: PV075246.

Notes – *Pseudochaetosphaeronema hydeiseptatum* (CGMCC 3.28691 and UESTCC 23.0518) formed a distinct lineage and was sister to *P. kunmingense* (KUMCC 19-0215, ex-type strain) and *P. briggsiae* (BRIP 76038a, ex-type strain) with 83% MLBS, 0.99 BIPP statistical support (Fig. 39). Morphologically, our new collection (HKAS 132436, holotype) resembles *P. kunmingense* (HKAS 102564, holotype) in having immersed conidiomata without papilla, hyaline, cylindrical conidiogenous cells, and fusiform, 3-septate conidia (Hyde et al. 2020b). However, *P. hydeiseptatum*

differs from *P. kunmingense* in its conidial morphology, which has 1–2 vertical septa. Additionally, compared to *P. kunmingense*, *P. hydeiseptatum* has the larger conidiogenous cells ($6.3\text{--}9.5 \times 2.4\text{--}3.5 \mu\text{m}$ vs. $3\text{--}9 \times 1\text{--}2.5 \mu\text{m}$) and conidia ($12.3\text{--}17 \times 6\text{--}7.5 \mu\text{m}$ vs. $10\text{--}15 \times 4\text{--}6 \mu\text{m}$). Comparison of nucleotide base pairs between the ex-type strains of *P. hydeiseptatum* (CGMCC 3.28691) and *P. kunmingense* (KUMCC 19-0215) revealed 7/450 bp (1.6%, 2 gaps) in ITS, and 16/903 bp (1.8%, without gaps) in *tefl- α* differences, while *P. hydeiseptatum* (CGMCC 3.28691) can be distinguished from *P. briggsiae* (BRIP 76038a) by 11/482 bp (2.3%, 2 gaps) in ITS and 17/904 bp (1.9%, without gaps) in *tefl- α* sequence data. Therefore, according to the guidelines of Jeewon & Hyde (2016), we introduce *P. hydeiseptatum* as a new species, and associated with *Cercis chinensis* in Yunnan Province, China.

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

Mycobank number: MB557099; Facesoffungi number: FoF01973

Notes – *Occultibambusaceae* was introduced by Dai et al. (2017) to accommodate *Neooccultibambusa*, *Occultibambusa* (type genus), *Seriascoma*, and *Versicolorisporium*. Subsequently, *Brunneofusispora* was classified in this family by Phookamsak et al. (2019). *Occultibambusaceae* is represented by Bambusicola-like and Massarina-like sexual morphs, which is characterized by immersed, solitary to gregarious ascomata with ostioles, cylindrical to clavate asci, and broad-fusiform, hyaline to dark brown, usually septate ascospores (Dai et al. 2017). The asexual morphs were known as coelomycetous and hyphomycetous taxa (Hatakeyama et al. 2008, Hyde et al. 2018). The coelomycetous is characterized by annellidic conidiogenous cells and pale brown, oblong conidia (Hatakeyama et al. 2008). Most species of *Occultibambusaceae* are saprobes and have been discovered from freshwater and terrestrial habitats (Dai et al. 2017, Hyde et al. 2018, Phookamsak et al. 2019, Phukhamsakda et al. 2020).

Brunneofusispora S.K. Huang & K.D. Hyde, Fungal Diversity 95: 36 (2019)

Mycobank number: MB555599; Facesoffungi number: FoF04862

Notes – Phookamsak et al. (2019) proposed the genus *Brunneofusispora* with *Brunneofusispora sinensis* as the type species. The sexual morph of *Brunneofusispora* is characterized by immersed, uniloculate ascomata, cylindrical to clavate asci with short pedicells, and hyaline to brown, broadly fusiform ascospores (Phookamsak et al. 2019). The asexual morph has solitary, globose to subglobose conidiomata, hyaline, enteroblastic, phialidic conidiogenous cells, and hyaline, oblong to cylindrical, smooth-walled, guttulate conidia (Wanasinghe et al. 2020, Calabon et al. 2021).

Brunneofusispora kevinimucosa H.Z. Du & Jian K. Liu, sp. nov.

Fig. 40

Mycobank number: MB857560; Facesoffungi number: FoF17985

Etymology – The epithet ‘*kevinimucosa*’ is a combination of Prof. Kevin D. Hyde’s first name and the mucilaginous sheaths around the ascospores, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132429

Saprobic on dead twigs of *Smilax ferox* Wallich ex Kunth (*Smilacaceae*). Visible as black dots. Sexual morph: *Ascomata* 197–285 μm diam. $\times$ 113–152 μm high ($\bar{x} = 235 \times 137 \mu\text{m}$, $n = 20$), perithecial, immersed to erumpent, solitary or scattered, globose to subglobose, or oblate spheroid, uniloculate, coriaceous, black, ostiolate. *Ostiole* central or eccentric, blackish brown, minute papillate, opening by a pore, filled with periphyses. *Peridium* 15–26 μm wide ($\bar{x} = 19 \mu\text{m}$, $n = 20$), comprising several layers of *textura angularis* cells, some uneven thickness, the inner layer is pale brown to brown, thin-walled, and the outer wall is brown to dark brown, thick-walled. *Hamathecium* comprising 2–3 μm wide, hyaline, filamentous, un-branched, septate pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 68–86 $\times$ 15–19 μm ($\bar{x} = 80 \times 17 \mu\text{m}$, $n = 20$), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, slightly curved, short pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 18–24 $\times$ 6–9 μm ($\bar{x} = 21 \times 8 \mu\text{m}$, $n = 30$), overlapping 2-seriate,

hyaline, straight to slightly curved, 2-celled, fusiform to broadly fusiform, 1-septate, constricted at the septum, widest at the center, slightly wider upper cell and tapering towards ends, conical at both ends, smooth-walled, guttulate, surrounded by an entire mucilaginous sheath, hyaline, 2–3 μm wide. Asexual morph: Undetermined.

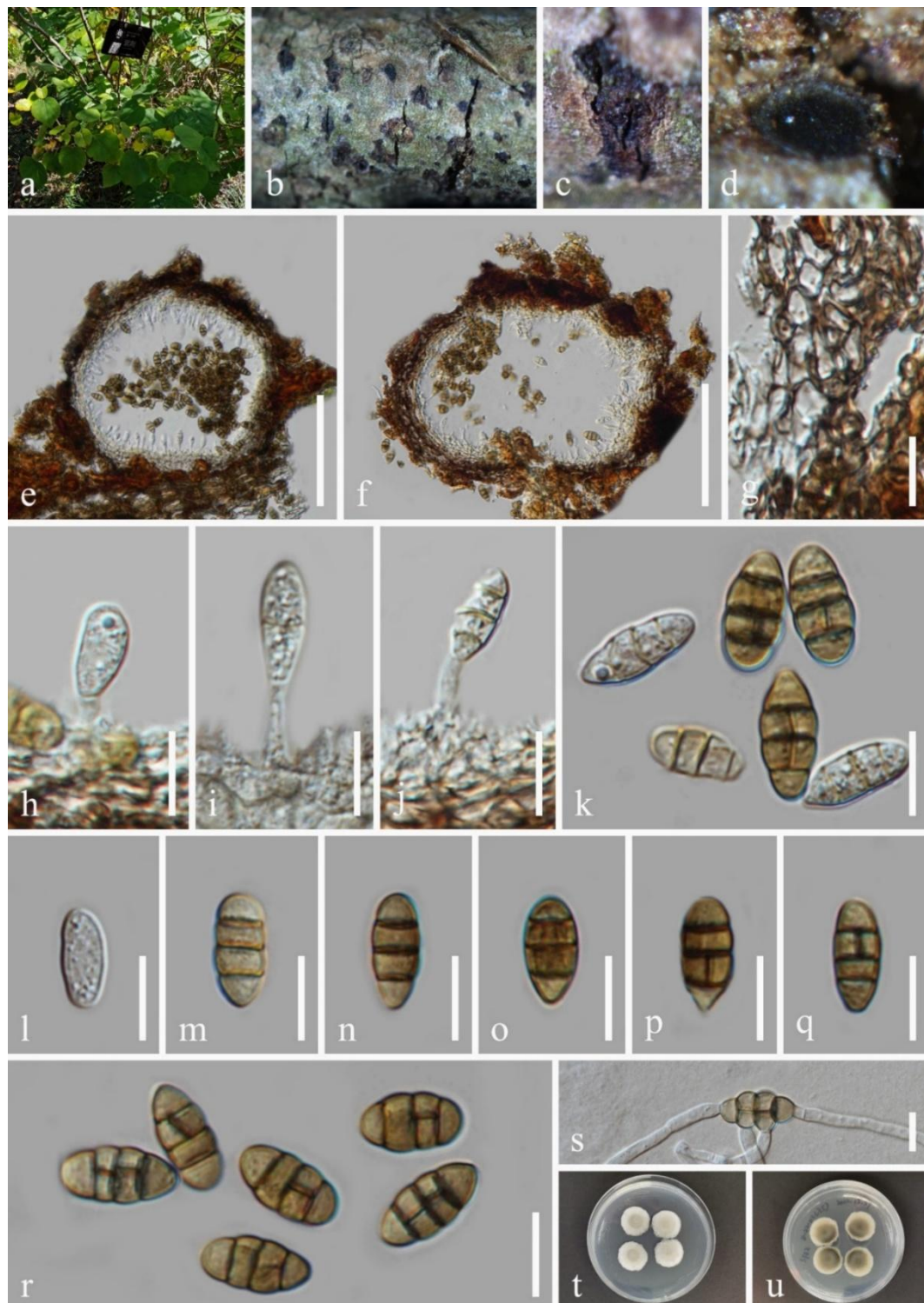


Figure 38 – *Pseudochaetosphaeronema hydeiseptatum* (HKAS 132436, holotype). a Host *Cercis chinensis*. b–d Appearance of conidiomata on host surface. e, f Vertical section of conidiomata. g Conidiomatal wall. h–j Conidiogenous cells and conidia. k–r Conidia. s Germinated conidium. t, u Colonies on PDA, above (t) and below (u). Scale bars: e, f = 100 μm , g–s = 10 μm .

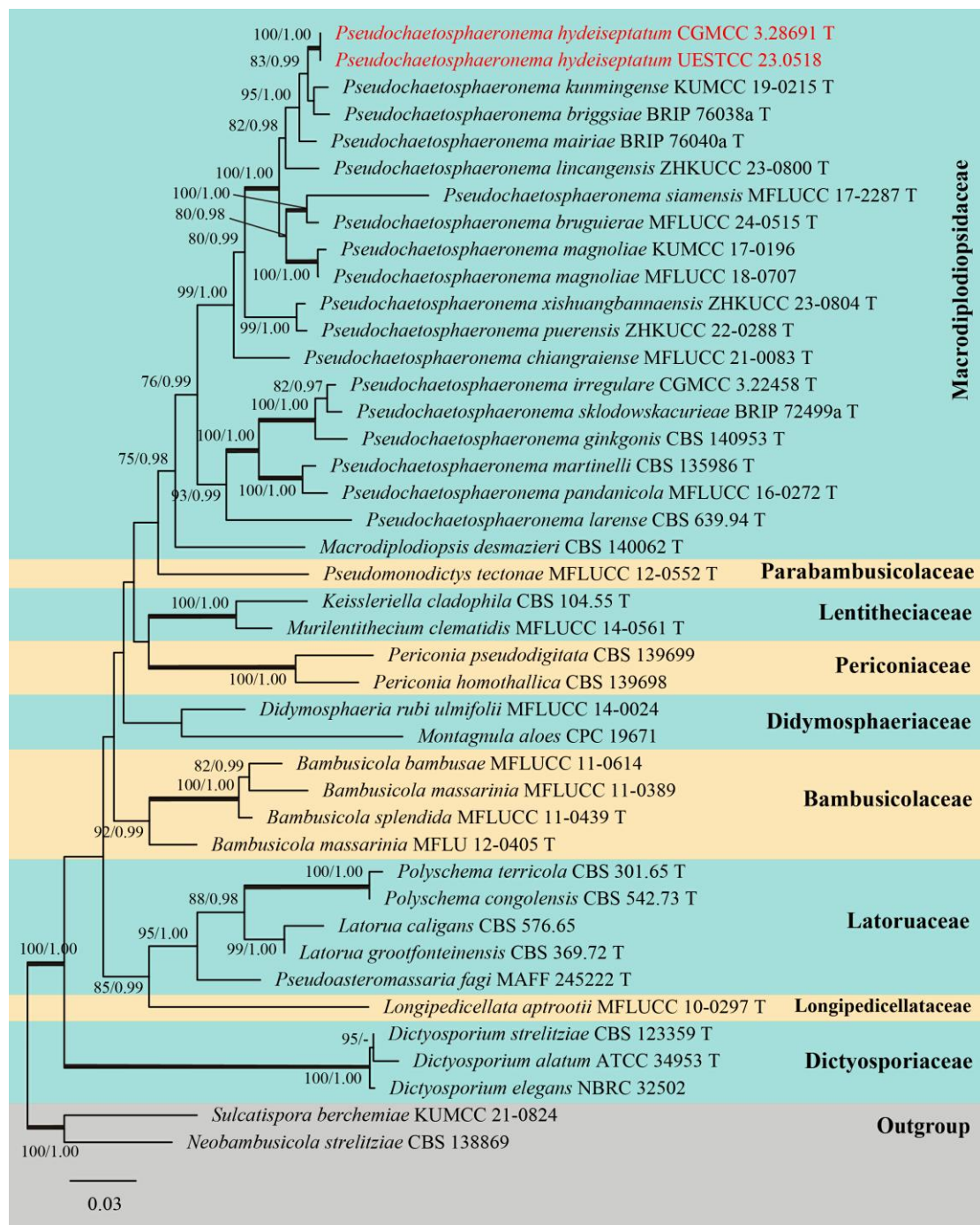


Figure 39 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined LSU, ITS, SSU, and *tefl-α* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Neobambusicola strelitziae* (CBS 138869) and *Sulcatisspora berchemiae* (KUMCC 21-0824). The best scoring RAXML tree with a final likelihood value of -17,187.629940 is presented. The matrix had 985 distinct alignment patterns, with 25.22% of undetermined characters or gaps, the tree-length is 1.719409. Estimated base frequencies were as follows: A = 0.238293, C = 0.250489, G = 0.271014, T = 0.240204, with substitution rates AC = 1.699961, AG = 3.308929, AT = 1.895027, CG = 1.520868, CT = 8.777779, GT = 1.000000; gamma distribution shape parameter alpha = 0.163160. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009588 (the critical value for the topological convergence diagnostic is below 0.01).

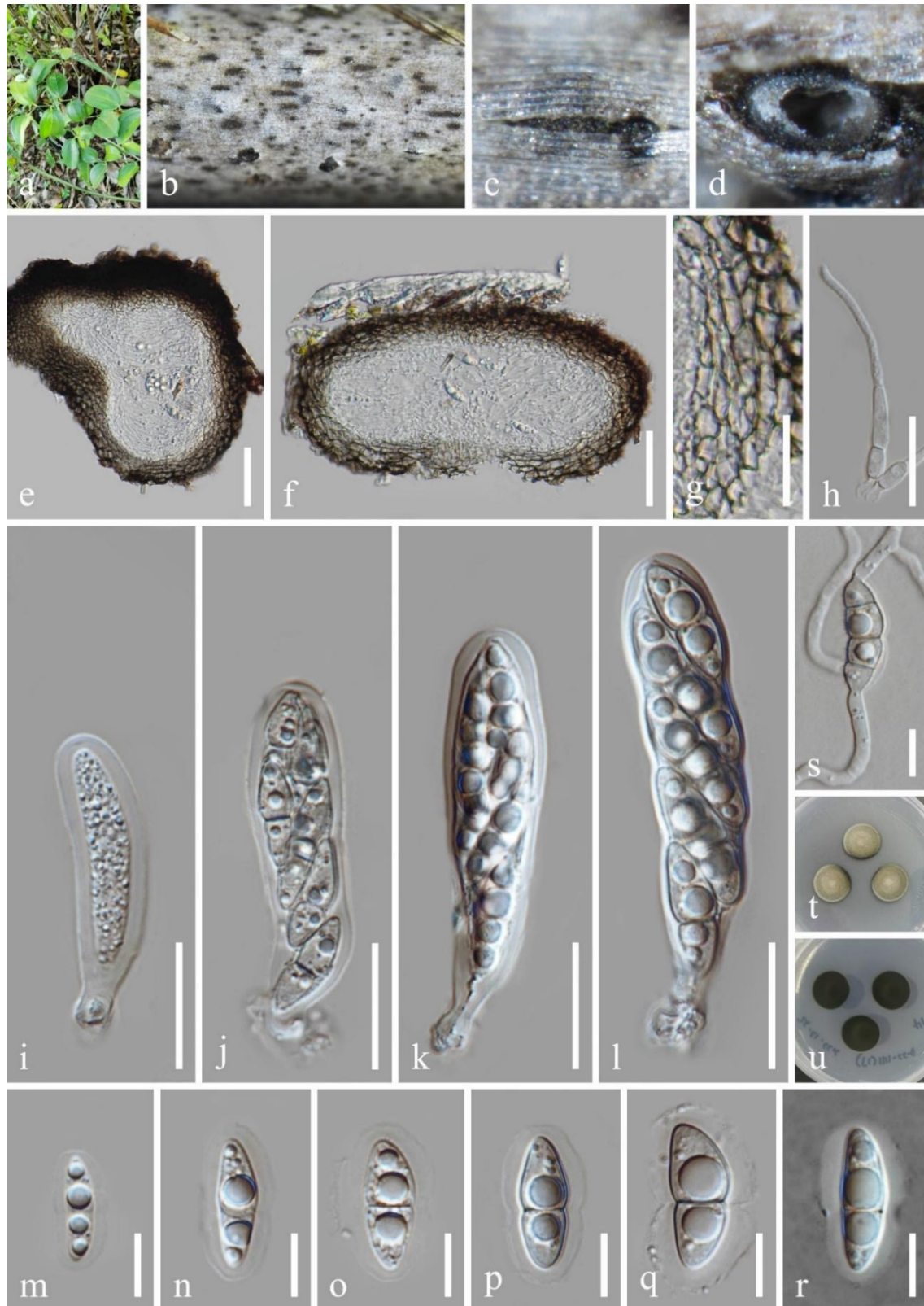


Figure 40 – *Brunneofusispora kevinimucosa* (HKAS 132429, holotype). a Host *Smilax ferox*. b–d Appearance of ascomata on host surface. e, f Section through ascomata. g Peridium. h Hamathecium. i–l Asci. m–q Ascospores. r Ascospore stained in Indian ink showing the mucilaginous sheath. s Germinated ascospore. t, u Colonies on PDA, above (t) and below (u). Scale bars: e, f = 50 μ m, g–l = 20 μ m, m–s = 10 μ m.

Culture characteristics – Ascospores germinated on PDA medium within 24 h, and germ tubes

are produced from both ends. Colonies growing on PDA reached 20–22 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense mycelium, surface smooth, velvety, grayish green, and blackish green in reverse.

Material examined – China, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 102°44'24"E, 25°8'27"N, elevation 1,922 m, on dead twigs of *Smilax ferox* (*Smilacaceae*), 11 November 2022, H.Z. Du, S714 (HKAS 132429, holotype; HUEST 23.0499, isotype); ex-type living culture CGMCC 3.28689, ex-isotype living culture UESTCC 23.0498.

GenBank accession numbers – HKAS 132429 = ITS: PQ773399, LSU: PQ773419, *tefl-α*: PV059181; UESTCC 23.0498 = ITS: PQ773400, LSU: PQ773420, *tefl-α*: PV059182.

Notes – Multi-locus phylogeny (Fig. 41) showed that *Brunneofusispora kevinimucosa* (CGMCC 3.28689 and UESTCC 23.0498) was sister to *B. mahoniae* (GUCC 24-0060) and formed a distinct lineage. Morphologically, *B. mahoniae* (HKAS 138709, holotype) can be distinguished from *B. kevinimucosa* (HKAS 132429, holotype) by the higher ascomata (165–250 µm vs. 113–152 µm diam.), papillate with a long beak when mature (Sun et al. 2025). Additionally, the nucleotide base pair comparison between ex-type strains of *B. kevinimucosa* (CGMCC 3.28689) and *B. mahoniae* (GUCC 24-0060) revealed 12/444 bp (2.7%, 5 gaps) in ITS and 25/917 bp (2.7%, without gaps) in *tefl-α* differences. Therefore, we introduce *B. kevinimucosa* as a new species based on morphological differences and phylogenetic evidence. This species was isolated from *Smilax ferox* in Yunnan Province, China.

Periconiaceae (Sacc.) Nann., Repertorio sistematico dei miceti dell' uomo e degli animali 4: 482 (1934)

MycoBank number: MB81124; Facesoffungi number: FoF06657

Notes – *Periconiaceae* was established by Nannizzi (1934) to accommodate *Periconia* as the type genus. Previously, the family was classified within *Massarinaceae* (*Pleosporales*), but Tanaka et al. (2015) revised *Massarinaceae* and placed it as a distinct family based on phylogenetic analyses. The asexual morph of *Periconiaceae* is characterized by macronematous, mononematous, pigmented, septate, and branched or unbranched conidiophores, monoblastic to polyblastic, integrated or discrete, terminal or unilaterally intercalary conidiogenous cells, with solitary, golden brown to dark brown, globose to subglobose, aseptate, verruculose, or echinulate conidia (Tanaka et al. 2015, Hongsanan et al. 2020b, Yang et al. 2022a). And the sexual morph features immersed to erumpent, scattered to grouped, subglobose to globose ascomata, 8-spored, bitunicate, fissitunicate, oblong to cylindrical asci, and hyaline, fusiform, septate, smooth-walled ascospores with an entire sheath (Adamčík et al. 2015, Tanaka et al. 2015, Hongsanan et al. 2020b). Most species of this family are well known as saprophytic fungi occurring on various hosts worldwide, and a few species were reported as endophytes and pathogens, such as *Flavomyces fueloephazae*, *Periconia circinata*, *P. digitata*, and *P. macrospinos* (Knapp et al. 2015, Sarkar et al. 2019, Hongsanan et al. 2020b, Samarakoon et al. 2021).

Periconia Tode, Fung. mecklenb. sel. (Lüneburg) 2: 2 (1791)

MycoBank number: MB9263; Facesoffungi number: FoF06658

Notes – *Periconia* was introduced by Tode (1791) and typified by *P. lichenoides*. Members of this genus are usually known as hyphomycetes, and have macronematous, mononematous and erect conidiophores, conidiophores bearing monoblastic or polyblastic, integrated or discrete, terminal or unilaterally intercalary conidiogenous cells, verruculose or echinulate, pale brown to reddish brown, unicellular conidia (Ellis 1971, Thambugala et al. 2017, Phookamsak et al. 2019, Hongsanan et al. 2020b). *Periconia* species have a worldwide distribution and are found in diverse habitats on various hosts as saprobes and endophytes (Cantrell et al. 2007, Svetlana & Kačergius 2014, Thambugala et al. 2017, Phookamsak et al. 2019, Tennakoon et al. 2021c). Additionally, some *Periconia* species, *P. atropurpurea*, *P. byssoides*, and *P. macrospinos*, also can produce valuable bioactive compounds that possess powerful pharmacological activities (Kim et al. 2004, Harnpicharnchai et al. 2009, Zhang et al. 2015, Hongsanan et al. 2020b, Azhari & Supratman 2021).

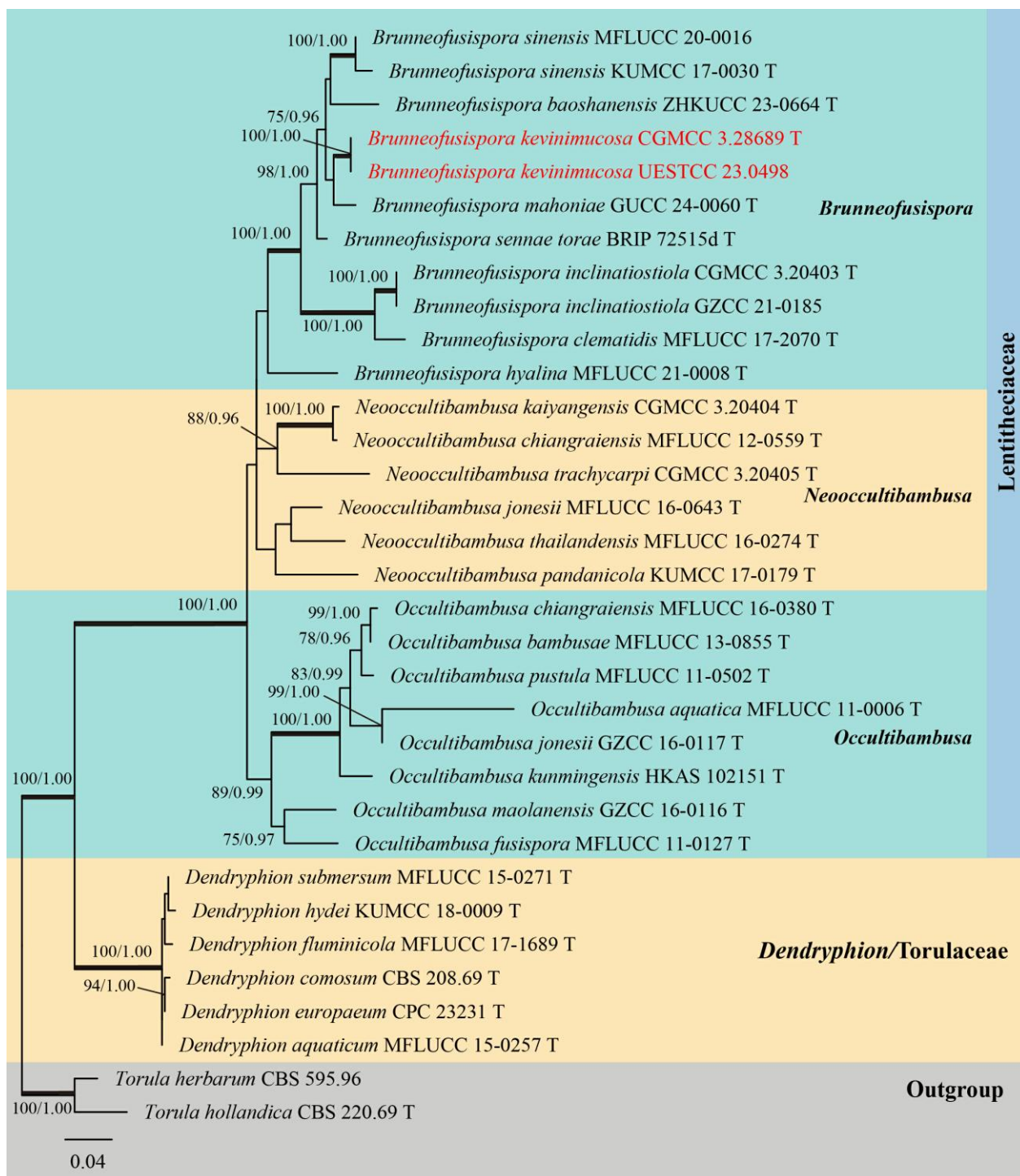


Figure 41 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined ITS, LSU, *tefl-α*, and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Torula hollandica* (CBS 220.69) and *T. herbarum* (CBS 595.96). The best scoring RAxML tree with a final likelihood value of -15,473.710060 is presented. The matrix had 1,117 distinct alignment patterns, with 26.80% of undetermined characters or gaps, the tree-length is 1.482475. Estimated base frequencies were as follows: A = 0.238958, C = 0.266290, G = 0.275221, T = 0.219531, with substitution rates AC = 1.983169, AG = 4.282419, AT = 1.833626, CG = 1.590740, CT = 10.309800, GT = 1.000000; gamma distribution shape parameter alpha = 0.20182. The final

average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009979 (the critical value for the topological convergence diagnostic is below 0.01).

Periconia alishanica Tennakoon, C.H. Kuo & K.D. Hyde, Fungal Diversity 108: 32 (2021) Fig. 42

MycoBank number: MB555315; Facesoffungi number: FoF09318

Saprobic on dead stems of *Lilium brownii* var. *viridulum* Baker (*Liliaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate superficial, hairy, effuse. *Mycelium* partly immersed, partly superficial. *Conidiophores* 275–411 μm ($\bar{x}$ = 375 μm , n = 30) long, 3–6 μm ($\bar{x}$ = 4.5 μm , n = 30) wide, macronematous, mononematous, straight or slightly flexuous, solitary, unbranched, dark brown with age, smooth, thick-walled. *Conidiogenous cells* polyblastic, brown to reddish brown, terminal, ovoid to globose. *Conidia* 10–13 μm ($\bar{x}$ = 12 μm , n = 30) diam., solitary, subglobose to globose, brown to dark brown when mature, echinulate, aseptate.

Culture characteristics – Conidia germinated on PDA within 12 h, and germ tubes are produced from one end. Colonies growing on PDA reached 43–45 mm in diam. after two weeks at 25 °C in the dark. Colonies from above, white, medium dense, circular, flat, fluffy to velvety with smooth aspects, hyaline mycelium. In reverse, brown to dark brown in the center, pale brown at the edge.

Material examined – China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, 106°41'48"E, 26°32'18"N, elevation 1,127 m, on dead stems of *Lilium brownii* var. *viridulum* (*Liliaceae*), 3 December 2020, H.Z. Du, S37 (HUEST 23.0462), living culture UESTCC 23.0461.

GenBank accession numbers – ITS: PQ394041, *tefl- α* : PQ346483.

Notes – *Periconia alishanica* was introduced by Tennakoon et al. (2021c) and isolated from dead leaves of *Ficus septica* (*Moraceae*), *Macaranga tanarius* (*Euphorbiaceae*), and *Morus australis* (*Moraceae*). In this study, our collection (HUEST 23.0462) is morphologically similar to the holotype of *Pe. alishanica* (NCYU 19-0160) in having solitary, macronematous and mononematous conidiophores, terminal, ovoid to globose conidiogenous cells, and solitary, subglobose to globose, brown to dark brown, aseptate conidia, and the size of the conidia also showed no obvious difference (10–13 μm diam. vs. 10–12 $\times$ 11–13 μm). Multi-locus phylogeny showed that our isolate (UESTCC 23.0461) clustered together with *Pe. alishanica* (MFLUCC 19-0145, ex-type strain) and formed a strongly supported clade (100% MLBS/1.00 BIPP) (Fig. 47). The comparison of nucleotide base pairs between isolate (UESTCC 23.0461) and *Pe. alishanica* (MFLUCC 19-0145) showed a high similarity in ITS (100%) and *tefl- α* (99.9%, without gaps). Therefore, we identify this taxon as *Pe. alishanica* based on morphology and phylogeny.

Periconia byssoides Pers., Synopsis methodica fungorum (Göttingen) 2: 686 (1801) Fig 43

MycoBank number: MB144538; Facesoffungi number: FoF09319

Saprobic on dead twigs of *Mentha canadensis* Linnaeus (*Lamiaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the natural substrate numerous, effuse, brown to dark brown, hairy. *Mycelium* partly immersed, partly superficial. *Conidiophores* 557–800 μm ($\bar{x}$ = 682 μm , n = 30) long, 12–23 μm ($\bar{x}$ = 19 μm , n = 30) wide, macronematous, mononematous, straight or slightly flexuous, unbranched, solitary, 2–4-septate (majority 3-septate), smooth to minutely verruculose, dark brown to black at the base, pale brown towards the apex, with spherical conidial head, rarely branched at the apex, sometimes slightly constricted near conidial head thick-walled. *Conidiogenous cells* polyblastic, discrete, terminal, pale brown to brown, subglobose, smooth or verruculose, located at nodose apices of conidiophores. *Conidia* 9–14 $\times$ 8–15 μm ($\bar{x}$ = 14 $\times$ 13 μm , n = 30), solitary or catenate, globose to subglobose, orange-brown to brown, aseptate, verruculose.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from the one end. Colonies growing on PDA reached 50–55 mm in diam. after two weeks at 25 °C in the dark. Colonies from above, white in the whole colony, medium dense, circular, cottony, flattened, hairy at the edge. In reverse, covered with cream white mycelium except for the pale yellow at the center.

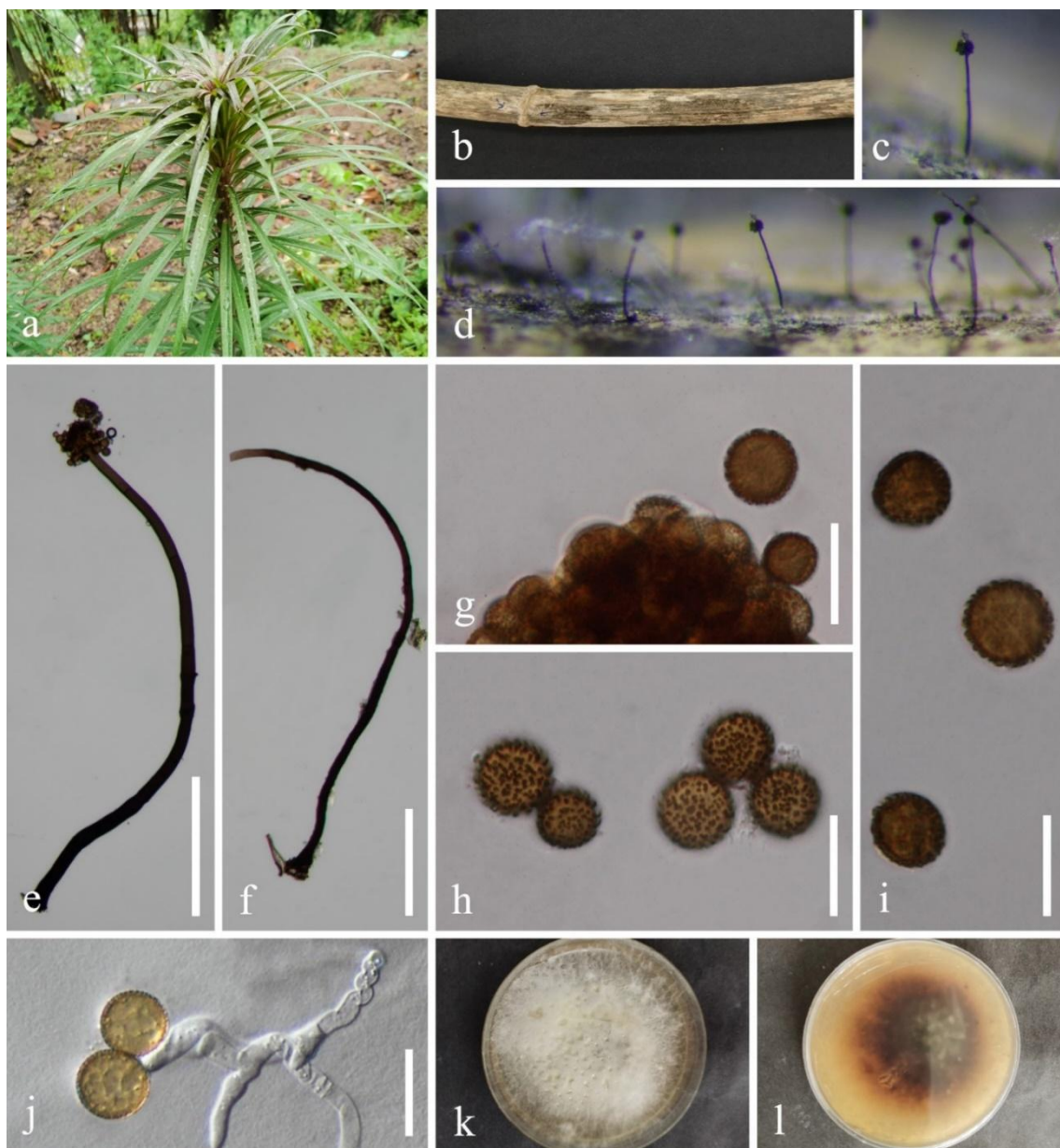


Figure 42 – *Periconia alishanica* (HUEST 23.0462, new host record). a Host *Liliun brownii* var. *viridulum*. b Stem of *L. brownii* var. *viridulum*. c, d Colonies on the host surface. e Conidiophore with conidia. f Conidiophore. g Conidiogenous cells and conidia. h, i Conidia. j Germinated conidium. k, l Colony on PDA, above (k) and below (l). Scale bars: e, f = 200 μ m, g–j = 20 μ m.

Material examined – China, Guizhou Province, Guiyang City, Huaxi District, 106°38'59"E, 26°24'23"N, elevation 1,217 m, on dead twigs of *Datura metel* L. (*Solanaceae*), 30 November 2020, H.Z. Du, S7 (HUEST 23.0459), living culture UESTCC 23.0458; *ibid.*, Nanming District, Guiyang Medicinal Botanical Garden, 106°41'48"E, 26°32'18"N, elevation 1,127 m, on dead stems of *Erythrina corallodendron* L. (*Fabaceae*), 3 December 2020, H.Z. Du, S17 (HUEST 23.0460), living culture UESTCC 23.0459; *ibid.*, Sichuan Province, Chengdu City, Xindu District, Xinfan Street. 104°4'52"E, 30°50'43"N, elevation 550 m, on dead twigs of *Mentha canadensis* (*Lamiaceae*), 22 July 2021, H.Z. Du, S272 (HUEST 23.0456), living culture UESTCC 23.0455; *ibid.*, High-tech West District, Yaobo Park, 103°55'44"E, 30°43'29"N, elevation 504 m, on dead leaves of *Bletilla striata* (Thunb. ex A. Murray) Rchb. f. (*Orchidaceae*), 8 August 2021, D24 (HUEST 24.0246), living culture UESTCC 24.0231; *ibid.*, D45 (HUEST 23.0455), living culture UESTCC 23.0454.

GenBank accession numbers – UESTCC 23.0455 = ITS: PQ394042, *tefl*- α : PQ346484; UESTCC 24.0231 = ITS: PQ394069, LSU: PQ184716, SSU: PQ184754; UESTCC 23.0454 = ITS:

PQ394043, LSU: PQ184694, SSU: PQ184746; UESTCC 23.0458 = ITS: PQ394044, *tefl-α*: PQ346485; UESTCC 23.0459 = ITS: PQ394045, *tefl-α*: PQ346486.

Notes – Multi-locus phylogenetic analyses (Fig. 47) showed that our five isolates (UESTCC 23.0455, UESTCC 23.0458, UESTCC 23.0459, UESTCC 24.0231, and UESTCC 23.0454) grouped with *Periconia byssoides* (MFLUCC 20-0172, ex-type strain), and our collections (HUEST 23.0456, HUEST 23.0459, HUEST 23.0455, HUEST D24, and HUEST 23.0460) are morphologically similar to *Pe. byssoides* by having solitary, macronematous, mononematous conidiophores with spherical conidial head, polyblastic, discrete, terminal conidiogenous cells, solitary or catenate, globose to subglobose, aseptate, verruculose conidia (Yang et al. 2022a). Additionally, comparison of the nucleotide base pairs between our isolates and *Pe. byssoides* (MFLUCC 20-0172) showed that 99.5%–100% similarity in ITS and *tefl-α* sequence data. Therefore, we identify these new isolates as *Pe. byssoides*, which associated with *Datura metel*, *Erythrina corallodendron*, and *Mentha canadensis* in Guizhou and Sichuan Provinces, China.

Periconia hydeiguttulosa H.Z. Du & Jian K. Liu, sp. nov.

Fig. 44

Mycobank number: MB855432; Facesoffungi number: FoF17986

Etymology – The epithet ‘*hydeiguttulosa*’ is a combination of Prof. Kevin D. Hyde’s last name and the guttulate conidia, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132458

Saprobic on dead stems of *Amomum kravanh* Pierre ex Gagnep. (*Zingiberaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate superficial, hairy, effuse. *Mycelium* partly immersed, partly superficial. *Conidiophores* 70–580 μm ($\bar{x}$ = 250 μm, n = 30) long, 6–15 μm ($\bar{x}$ = 10 μm, n = 30) wide, macronematous, mononematous, straight or slightly flexuous, solitary, septate, unbranched, tapering towards the apex, reddish brown to dark brown at the lower part and gradually brown to pale brown toward the apex, with spherical conidial head, smooth, thick-walled. *Conidiogenous cells* blastic, yellowish-brown to brown, terminal, integrated, ovoid to subglobose, discrete, verruculose. *Conidia* 7–10.5 × 5–8 μm ($\bar{x}$ = 8.5 × 7 μm, n = 30), solitary or catenate in short chains, ovoid to globose, reddish brown at immature stage, becoming brown to dark brown with age, aseptate, with a distinct guttula.

Culture characteristics – Conidia germinated on PDA within 12 h, and germ tubes are produced from one end. Colonies growing on PDA reached 35–38 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular with irregular edge, white, mycelium slightly raised, moderately fluffy, filiform, white aerial hyphae at the surface, pale brown ring in the middle, spreading from the center and hyaline mycelium at the edge. In reverse, brown to dark brown towards the center, yellowish white at the edge.

Material examined – China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, 106°41'46"E, 26°32'20"N, elevation 1,129 m, on dead stems of *Amomum kravanh* (*Zingiberaceae*), 5 May 2021, H.Z. Du, S266 (HKAS 132458, holotype; HUEST 23.0457, isotype), ex-type living culture UESTCC 24.0232, ex-isotype living culture UESTCC 23.0456.

GenBank accession numbers – UESTCC 24.0232 = ITS: PQ394070, LSU: PQ184717, SSU: PQ184755, *tefl-α*: PQ346515; UESTCC 23.0456 = ITS: PQ394046, LSU: PQ184695, SSU: PQ184747, *tefl-α*: PQ346487.

Notes – Phylogenetic analyses showed that our two isolates of *Periconia hydeiguttulosa* (UESTCC 24.0232 and UESTCC 23.0456) formed a distinct lineage and was sister to *Pe. yangjiangensis* (ZHKUCC 23-0997) (Fig. 47). Morphologically, *Pe. hydeiguttulosa* (HKAS 132458, holotype) is similar to *Pe. yangjiangensis* (MHZU 23-0246, holotype) in having macronematous, mononematous, solitary conidiophores, blastic conidiogenous cells, ovoid to globose, brown to dark brown conidia (Liao et al. 2024). However, *Pe. hydeiguttulosa* differs from *Pe. yangjiangensis* by the verruculose conidiogenous cells and distinctly guttulate conidia (Liao et al. 2024). In addition, Comparison of the nucleotide base pairs showed that *Pe. hydeiguttulosa* (UESTCC 24.0232, ex-type strain) can be distinguished from *Pe. yangjiangensis* (ZHKUCC 23-0997,

ex-type strain) by 21/859 bp (2.4%, 1 gap) in SSU and 14/907 bp (1.5%, 1 gap) in *tefl-α* sequence data. Therefore, according to the guidelines of Jeewon & Hyde (2016), the new species of *Pe. hydeiguttulosa* was introduced based on morphology and phylogeny.



Figure 43 – *Periconia byssoides* (HUEST 23.0456, new host record). a Host *Mentha canadensis*. b Twigs of *M. canadensis*. c, d Colonies on the host surface. e–g Conidiophores with conidia. h–j Conidiogenous cells and conidia. k, l Colonies on PDA, above (k) and below (l). m–q Conidia. Scale bars: e–g = 150 μ m, h–j = 50 μ m, m, n, p, q = 10 μ m, o = 5 μ m.



Figure 44 – *Periconia hydeiguttulosa* (HKAS 132458, holotype). a, b Host *Amomum kravanh*. c–e Colonies on the host surface. f–i Conidiophores with conidia. j, k Conidiogenous cells and conidia. l the apex of conidiophore. m, n Colonies on PDA, above (m) and below (n). o–s Conidia. Scale bars: f–i, l = 50 μ m, j, k = 20 μ m, o–r = 5 μ m, s = 10 μ m.

Periconia pseudobyssoides Markovsk. & A. Kačergius, Mycological Progress 13 (2): 293 (2014)
Fig. 45

MycoBank number: MB804763; Facesoffungi number: FoF03857

Saprobic on dead twigs of *Dahlia pinnata* Cav. (*Asteraceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate superficial, hairy, effuse. *Mycelium* partly immersed, partly superficial. *Conidiophores* 291–330 μm ($\bar{x}$ = 308 μm , n = 30) long, 16–24 μm ($\bar{x}$ = 20 μm , n = 30) wide, macronematous, mononematous, straight or slightly flexuous, solitary, septate, unbranched, tapering towards the apex, brown to dark brown at the lower part and gradually pale brown toward the apex, with spherical conidial head, smooth to minutely verruculose, thick-walled. *Conidiogenous cells* blastic, light brown to brown, ovoid to subglobose, terminal, discrete. *Conidia* 14–18 μm ($\bar{x}$ = 16 μm , n = 30) diam., catenate in short chains, globose, hyaline to reddish brown at immature stage, becoming brown to dark brown with age, aseptate, verruculose.

Culture characteristics – Conidia germinated on PDA within 12 h, and germ tubes are produced from one end. Colonies growing on PDA reached 30–33 mm in diam. after two weeks at 25 °C in the dark. Colonies from above, circular with irregular edge, white, medium dense, mycelium slightly raised, moderately fluffy, filiform, white aerial hyphae at the surface, and hyaline mycelium at the edge. In reverse, yellowish brown in the center, white mycelium at the edge, radiate outward from the center to edge.

Material examined – China, Sichuan Province, Guangyuan City, Qingchuan County, Muyu Town, 105°24'10"E, 32°38'8"N, elevation 771 m, on dead twigs of *Dahlia pinnata* (*Asteraceae*), 20 April 2021, H.Z. Du, S244 (HUEST 23.0458), living culture UESTCC 23.0457.

GenBank accession numbers – ITS: PQ394046, *tefl- α* : PQ346488.

Notes – *Periconia pseudobyssoides* was introduced by Svetlana & Kačergius (2014) and found on *Heracleum sosnowskyi* in Lithuania. Subsequently, Yang et al. (2022a) and Su et al. (2023) reported it on *Scrophularia ningpoensis* (*Scrophulariaceae*) and *Digitaria sanguinalis* (*Poaceae*) in China, respectively. Our collection (HUEST 23.0458) shares similar morphological characteristics, including the shape and color of conidiophores and conidia, with the holotype of *Pe. pseudobyssoides* (BILAS 50334). Multi-locus phylogeny showed that our strain (UESTCC 23.0457) grouped with *Pe. pseudobyssoides* (BILAS 50334, ex-type strain) (Fig. 47). Comparison of the nucleotide base pair between UESTCC 23.0457 and BILAS 50334 revealed 100% (531/531 bp) similarity in ITS. Therefore, we identify our isolate as *Pe. pseudobyssoides* which report from *Dahlia pinnata* for the first time in Sichuan Province, China.

Periconia verrucosa Phukhams., Ertz, Gerstmans & K.D. Hyde, Fungal Diversity 102: 71 (2020)
Fig. 46

Mycobank number: MB557143; Facesoffungi number: FoF07296

Saprobic on dead branches of *Bambusa tuldoidea* Munro (*Poaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the natural substrate, numerous, effuse, gregarious, hairy, dark brown. *Mycelium* partly superficial, partly immersed, composed of branched, pale brown, septate hyphae. *Conidiophores* 159–307 $\times$ 9–13 μm ($\bar{x}$ = 236 $\times$ 11 μm , n = 30), macronematous, mononematous, solitary, erect, cylindrical, straight or slightly flexuous, dark brown, unbranched, 2–4-septate, smooth to minutely verruculose, thick-walled. *Conidiogenous cells* blastic, yellow to pale brown, terminal, discrete, oblong to subglobose, smooth to verruculose. *Conidia* 7–15 μm ($\bar{x}$ = 12 μm , n = 30) diam., solitary or catenate, acrogenous, globose, aseptate, thick-walled, hyaline when immature, dark brown to reddish brown at maturity, verruculose.

Culture characteristics – Conidia germinated on PDA within 12 h, and germ tubes are produced from one end. Colonies growing on PDA reached 30–32 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, cream or white, mycelia medium dense, circular, slightly papillate, fluffy, hyaline mycelium at the edge. In reverse, pale yellow, and yellowish white mycelium at the edge.

Material examined – China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, 106°41'48"E, 26°32'18"N, elevation 1,127 m, on dead branches of *Bambusa tuldoidea* (*Poaceae*), 20 January 2021, H.Z. Du, S32 (HUEST 23.0461), living culture UESTCC 23.0460.

GenBank accession numbers – ITS: PQ394048, *tefl- α* : PQ346489.



Figure 45 – *Periconia pseudobyssoides* (HUEST 23.0458, new host record). a Host *Dahlia pinnata*. b A twig of *D. pinnata*. c, d Colonies on the host surface. e Conidiophores with conidia. f–h Conidiogenous cells and conidia. i–p Conidia. q Germinated conidium. r, s Colonies on PDA, above (r) and below (s). Scale bars: e = 100 μ m, f, g, q = 20 μ m, h–p = 10 μ m.

Notes – *Periconia verrucosa* was established by Phukhamsakda et al. (2020) which was

isolated from *Clematis viticella* in Belgium. Later, this species was reported on *Stipa tenuissima* (*Poaceae*) from terrestrial habitats in China (Su et al. 2023). Multi-locus phylogenetic tree showed our isolate (UESTCC 23.0460) clustered together with the *Periconia verrucosa* (MFLUCC 17–2158, ex-type strain) with a statistical support 88% MLBS/0.99 BIPP (Fig. 47). Morphologically, our collection (HUEST 23.0461) closely resembles the description of *Pe. verrucosa* (MFLU 17–1516, holotype) without significant differences (Phukhamsakda et al. 2020). Comparisons of nucleotide base pairs between the isolate (UESTCC 23.0460) and *Pe. verrucosa* (MFLUCC 17–2158) showed a high similarity in ITS (100%) and *tef1-α* (99.9%, without gaps). Therefore, our collection is identified as *Pe. verrucosa* which is associated with *Bambusa tuldoidea* in Guizhou Province, China.

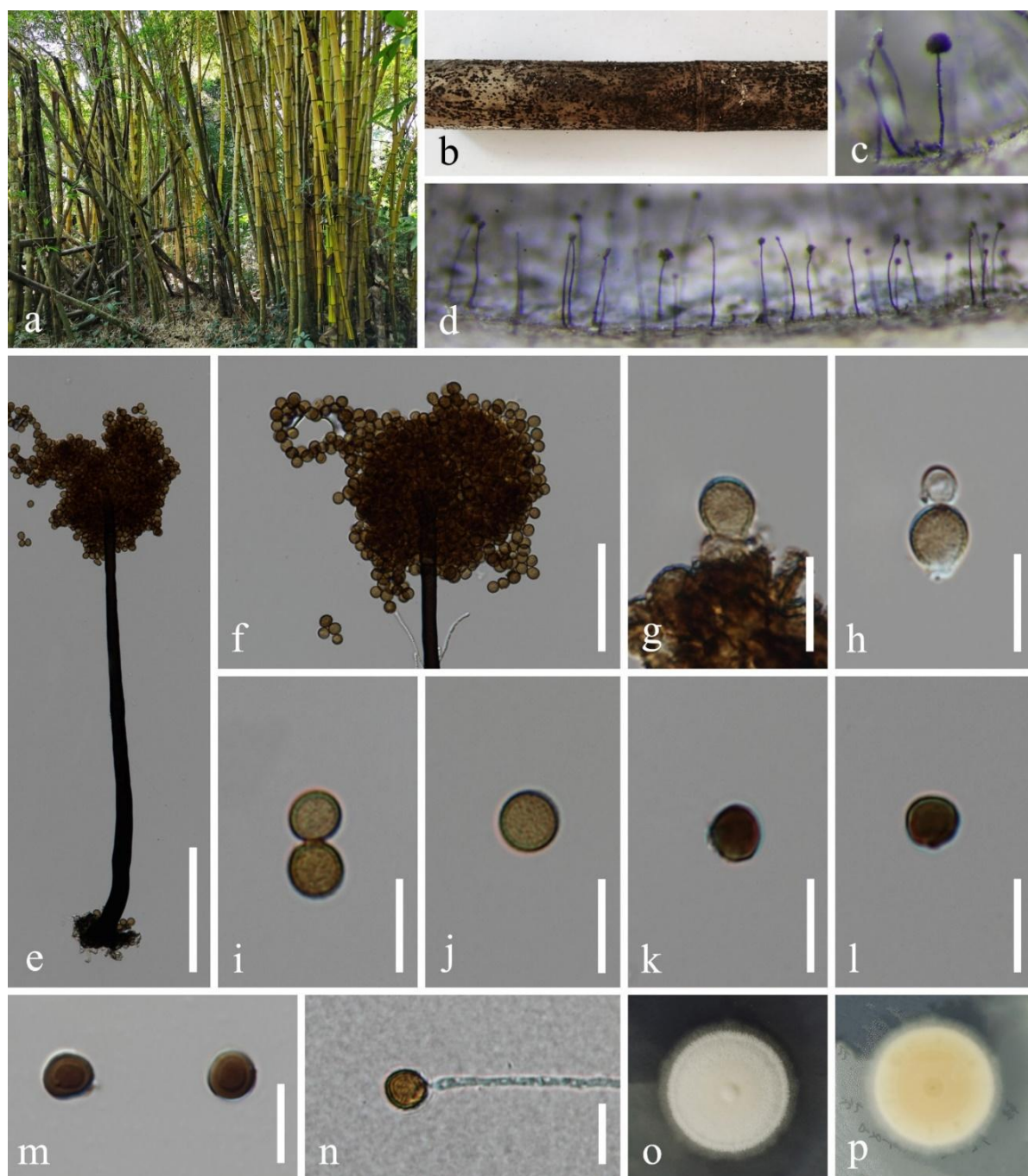


Figure 46 – *Periconia verrucosa* (HUEST 23.0461, new host record). a Host *Bambusa tuldoidea*. b Branch of *B. tuldoidea*. c, d Colonies on the host surface. e, f Conidiophores with conidia. g Conidiogenous cells and conidia. h–m Conidia. n Germinated conidium. o, p Colony on PDA, above (l) and below (m). Scale bars: e = 100 μ m, f = 50 μ m, g–n = 10 μ m.

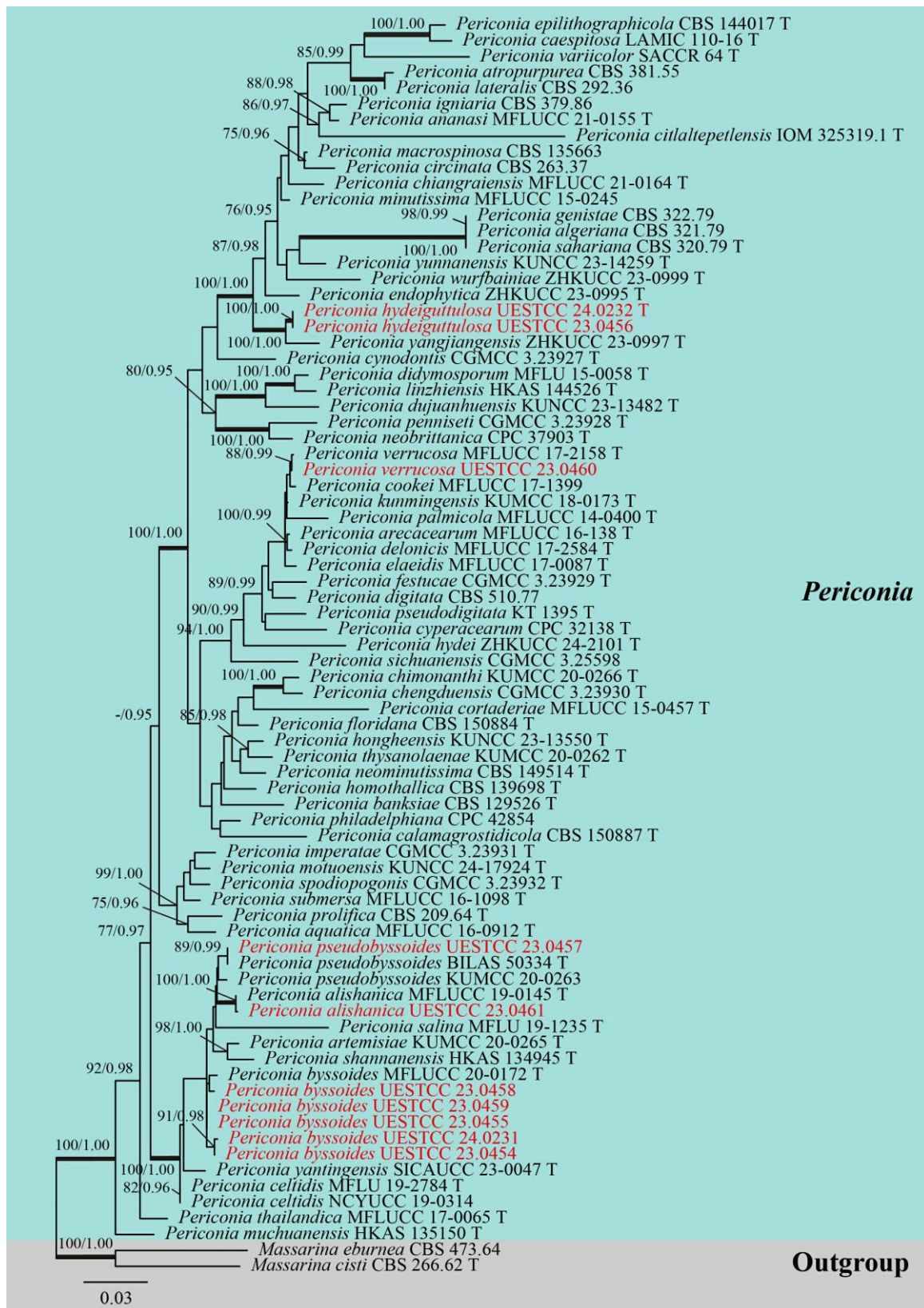


Figure 47 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined ITS, LSU, SSU, and *tef1- α* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below branches as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Massarina cisti* (CBS 266.62) and *M. eburnea* (CBS 473.64). The best scoring RAXML tree with a final likelihood value of -17,324.978215 is presented. The matrix had

983 distinct alignment patterns, with 29.83% of undetermined characters or gaps, the tree-length is 1.720617. Estimated base frequencies were as follows: A = 0.235814, C = 0.258504, G = 0.268608, T = 0.237073, with substitution rates AC = 2.135020, AG = 3.481765, AT = 2.280609, CG = 1.589738, CT = 14.544544, GT = 1.000000; gamma distribution shape parameter alpha = 0.170349. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009988 (the critical value for the topological convergence diagnostic is below 0.01).

Roussoellaceae Jian K. Liu, Phookamsak, D.Q. Dai & K.D. Hyde, Phytotaxa 181 (1): 7 (2014)

MycoBank number: MB804651; Facesoffungi number: FoF08360

Notes – *Roussoellaceae* was introduced by Liu et al. (2014) to accommodate the type genus *Roussoella*, as well as two additional genera, *Neorousoella* and *Roussoellopsis*. Later, Wijayawardene et al. (2014) proposed five genera, *Appendispora*, *Cytoplea*, *Neorousoella*, *Roussoella*, and *Roussoellopsis*, within the *Roussoellaceae*. Subsequently, the genera *Elongatopedicellata* (sexual morph) and *Immotthia* (both sexual and asexual morphs) were introduced within *Roussoellaceae* by Ariyawansa et al. (2015a) and Doilom et al. (2018), respectively. However, later, the genus *Immotthia* was transferred to Dictyosporiaceae by Jiang et al. (2021b) based on phylogenetic evidence. Phookamsak et al. (2019) transferred *Pararousoella* and *Pseudoneoconiothyrium* from *Thyridariaceae* to *Roussoellaceae*, and Mapook et al. (2020) incorporated three new genera, *Pseudorousoella*, *Setoarthopyrenia*, and *Xenorousoella* into the family *Roussoellaceae*. Previously, the family has been treated as a synonym of *Thyridariaceae* by Jaklitsch & Voglmayr (2016c). However, the latest accounts based on multigene phylogenetic analyses show that *Roussoellaceae* is well-resolved in *Pleosporales* (Dai et al. 2017, Tibpromma et al. 2017, Hyde et al. 2018, Jayasiri et al. 2019, Jiang et al. 2019, Phookamsak et al. 2019). Currently, there are 11 genera within *Roussoellaceae* as reported by Wijayawardene et al. (2022b). The sexual morph of *Roussoellaceae* is characterized by having solitary or gregarious, immersed to semi-immersed, clypeate ascostromata containing trabeculate pseudoparaphyses, bitunicate, cylindrical to cylindric-clavate asci with ocular chambers, ellipsoidal to fusiform, septate, brown to dark brown ascospores (Liew et al. 2000, Liu et al. 2014, Hongsanant et al. 2020a). The asexual morph features pycnidial, stromatic, immersed, globose to subglobose conidiomata, holoblastic, annellidic, discrete, cylindrical to ampulliform, or doliform conidiogenous cells, globose to ellipsoidal, brown to dark brown conidia with minutely warty or verrucose surface (Liu et al. 2014).

Neorousoella Jian K. Liu, Phookamsak & K.D. Hyde, Phytotaxa 181 (1): 21 (2014)

MycoBank number: MB550668; Facesoffungi number: FoF08363

Notes – *Neorousoella* was initially introduced by Liu et al. (2014) with the type species *N. bambusa*. The sexual morph of *Neorousoella* is characterized by black, semi-immersed to immersed ascomata, bitunicate, cylindrical asci, and fusiform to ellipsoidal, brown, two-celled ascospores with longitudinal striations (Liu et al. 2014). The asexual morph has black, subglobose conidiomata, phialidic, cylindrical to ampulliform conidiogenous cells, and hyaline to pale brown, ellipsoidal conidia with guttules (Liu et al. 2014, Jayasiri et al. 2019). Members of *Neorousoella* are mostly found on decaying wood as saprobes (Liu et al. 2014, Jayasiri et al. 2019, Phookamsak et al. 2019, Hyde et al. 2023), while *Neorousoella solani* was reported as pathogens and isolated from keratitis in human patients (Mochizuki et al. 2017).

Neorousoella kevinii H.Z. Du & Jian K. Liu, sp. nov.

Fig. 48

MycoBank number: MB857561; Facesoffungi number: FoF17987

Etymology – The epithet ‘*kevinii*’ named for in honor of Prof. Kevin D. Hyde for his contribution to ascomycetes taxonomy.

Holotype – HKAS 132435

Saprobic on dead twigs of *Acacia confusa* Merrill (*Fabaceae*). Visible as black or dark brown dots. Sexual morph: *Ascomata* 209–296 µm diam. × 153–286 µm high ($\bar{x}$ = 255 × 198 µm, n = 20), solitary, scattered, immersed under a clypeus or epidermis, slightly erumpent, globose to subglobose

or obpyriform, occasionally irregular in shape, dark brown to black, coriaceous, ostiolate, with minute papilla. *Ostiole* 103–125 μm wide $\times$ 69–94 μm high ($\bar{x}$ = 112 $\times$ 80 μm , n = 20), central or eccentric, brown to dark brown, minute papillate, filled with periphyses. *Peridium* 15–22 μm wide ($\bar{x}$ = 19 μm , n = 20), composed of several layers of hyaline to dark brown or black pseudoparenchymatous cells of *textura angularis*, inner layer comprising flattened, hyaline to brown cells, thin-walled, and outer layer comprising thick, dark brown to black cells. *Hamathecium* 1.0–1.6 μm wide, hyaline, comprising of sparse, non-septate, numerous, filamentous, branched pseudoparaphyses, and embedded in a gelatinous matrix. *Asci* 56–72 $\times$ 5–7 μm ($\bar{x}$ = 59 $\times$ 6 μm , n = 20), 8-spored, bitunicate, cylindrical, with a short pedicel or sessile, occasionally visible a slightly furcate pedicel, apically rounded, with an indistinct ocular chamber. *Ascospores* 7.5–11 $\times$ 2.8–3.3 μm ($\bar{x}$ = 8.3 $\times$ 3.0 μm , n = 30), uniseriate or overlapping, hyaline when young, and yellowish brown to brown when mature, ellipsoidal to fusiform, with rounded apex and slightly truncate base, 1-septate, constricted at the septum, 2-celled, mostly containing 1-guttule in each cell, with longitudinal striations, the upper cell is commonly slightly wider than the lower cell, and lack any mucilaginous sheath and appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 44–45 mm diam. after three weeks at 25 °C in the dark. Colonies from above, circular, medium dense mycelia on the surface, white, elevated in the center, regular edge. The reverse shows a color and shape similar to the obverse, except for a pale brown at the center.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong City, Xishuangbanna South Medicinal Plant Garden, 100°47'23"E, 22°0'22"N, elevation 525 m, on dead twigs of medicinal plant *Acacia confuse* (*Fabaceae*), 11 November 2022, H.Z. Du, S544 (HKAS 132435, holotype; HUEST 23.0516, isotype); ex-type living culture CGMCC 3.28685, ex-isotype living culture UESTCC 23.0515.

GenBank accession numbers – HKAS 132435 = ITS: PQ773405, LSU: PQ773425, SSU: PQ773441, *tefl- α* : PV059185, *rpb2*: PV075243; UESTCC 23.0515 = ITS: PQ773406, LSU: PQ773426, SSU: PQ773442, *tefl- α* : PV059186, *rpb2*: PV075244.

Notes – The new taxon compose of typical morphological characteristics of species in the family *Roussoellaceae*, and the multi-locus phylogenetic analyses showed that our two isolates (CGMCC 3.28685 and UESTCC 23.0515) formed a monophyletic lineage in *Neorousoella*, and was sister to *N. heveae* (MFLUCC 17-0338) (Fig. 49). Morphologically, *N. kevinii* (HKAS 132435, holotype) shares the similar sexual morph characteristics with *Neorousoella* species, including immersed ascomata, bitunicate, cylindrical asci, and fusiform to ellipsoidal, 1-septate ascospores. However, only the asexual morph of *N. heveae* has been reported since its introduction by Phookamsak et al. (2019), and its sexual morph remains undescribed, making morphological comparisons difficult. Comparison of the nucleotide base pairs between ex-type strains of *N. kevinii* (CGMCC 3.28685) and *N. heveae* (MFLUCC 17-0338) revealed 24/491 bp (4.9%, 7 gaps) in ITS and 12/824 bp (1.5%, without gaps) in LSU differences. Additionally, based on BLASTn search of NCBI GenBank, the *tefl- α* and *rpb2* sequences data of *N. kevinii* (CGMCC 3.28685) showed that 97.32% and 85.17% similarity with the closest species in *Neorousoella*, respectively (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>; accessed on 25 July 2025). Therefore, the new species of *N. kevinii* is introduced based on phylogenetic evidence, which is associated with *Acacia confusa* in Yunnan Province, China.

Teichosporaceae M.E. Barr, Mycotaxon 82: 374 (2002)

Mycobank number: MB82136; Facesoffungi number: FoF00830

Notes – Barr (2002) introduced the family *Teichosporaceae* to accommodate eight genera, *Bertiella*, *Byssothecium*, *Chaetomastia*, *Immotthia*, *Loculohypoxylon*, *Moristroma*, *Sinodidymella*, and *Teichospora* (the type genus) based on morphological characteristics. Currently, 17 genera are accepted in *Teichosporaceae* by Hyde et al. (2024). *Teichosporaceae* species were reported as saprobic fungi from terrestrial habitats (Jaklitsch et al. 2016b, Tennakoon et al. 2021b, de Silva et al.

2022a, Tian et al. 2024a). The sexual morph of this family is characterized by immersed or semi-immersed, erumpent to superficial, ostiolate ascomata, 4–8-spored, bitunicate, fissitunicate,

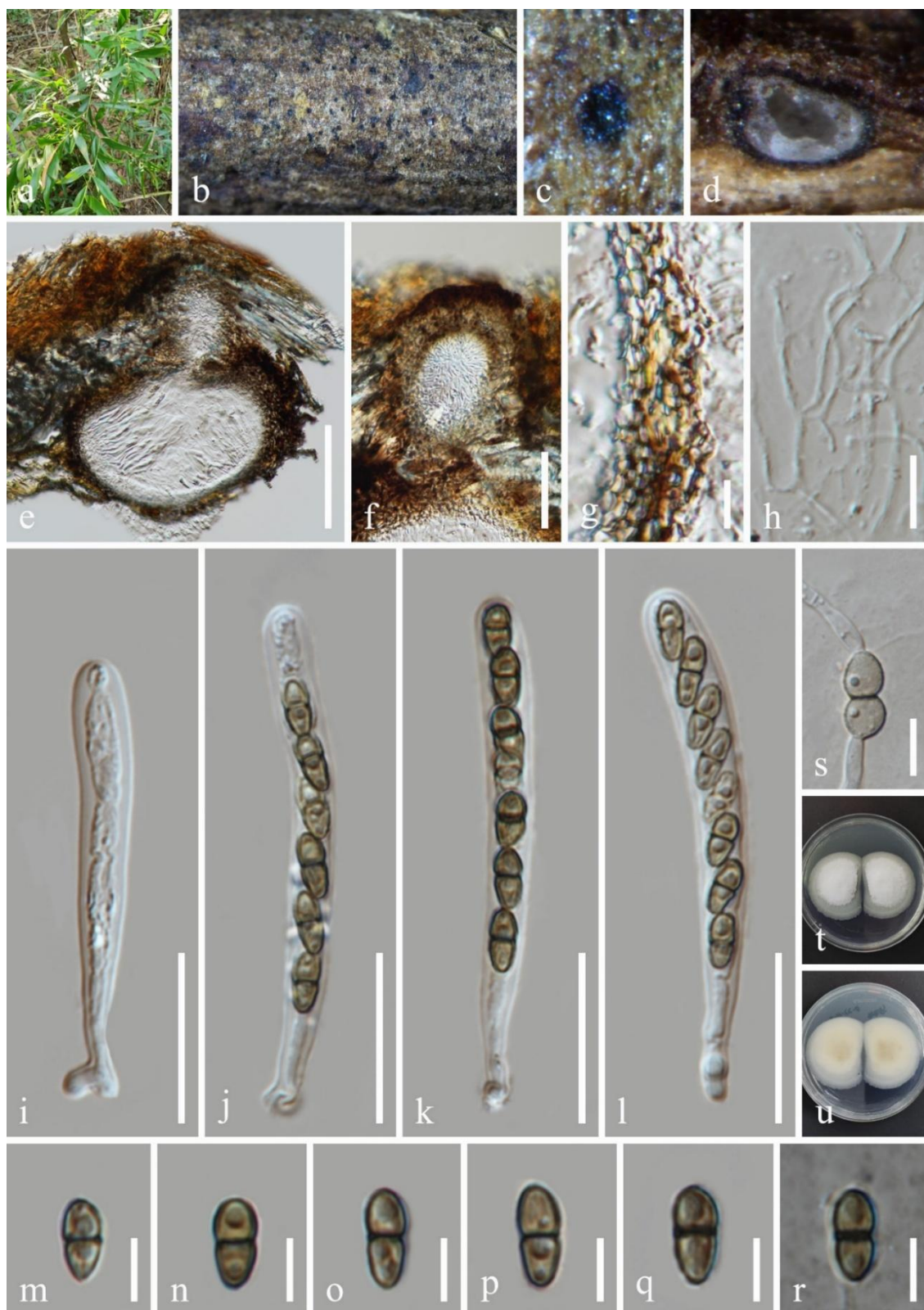


Figure 48 – *Neorousoella kevinii* (HKAS 132435, holotype). a Host *Acacia confusa*. b–d Appearance of ascomata on host surface. e Vertical section of ascomata. f Ostiole with periphyses. g Peridium. h Hamathecium. i–l Asci. m–q Ascospores. r Ascospore stained with Indian ink without a mucilaginous sheath. s Germinated ascospore. t, u Colonies on PDA, above (t) and below (u). Scale bars: e = 100 μ m, f = 50 μ m, g, h, s = 10 μ m, i–l = 20 μ m, m–r = 5 μ m.

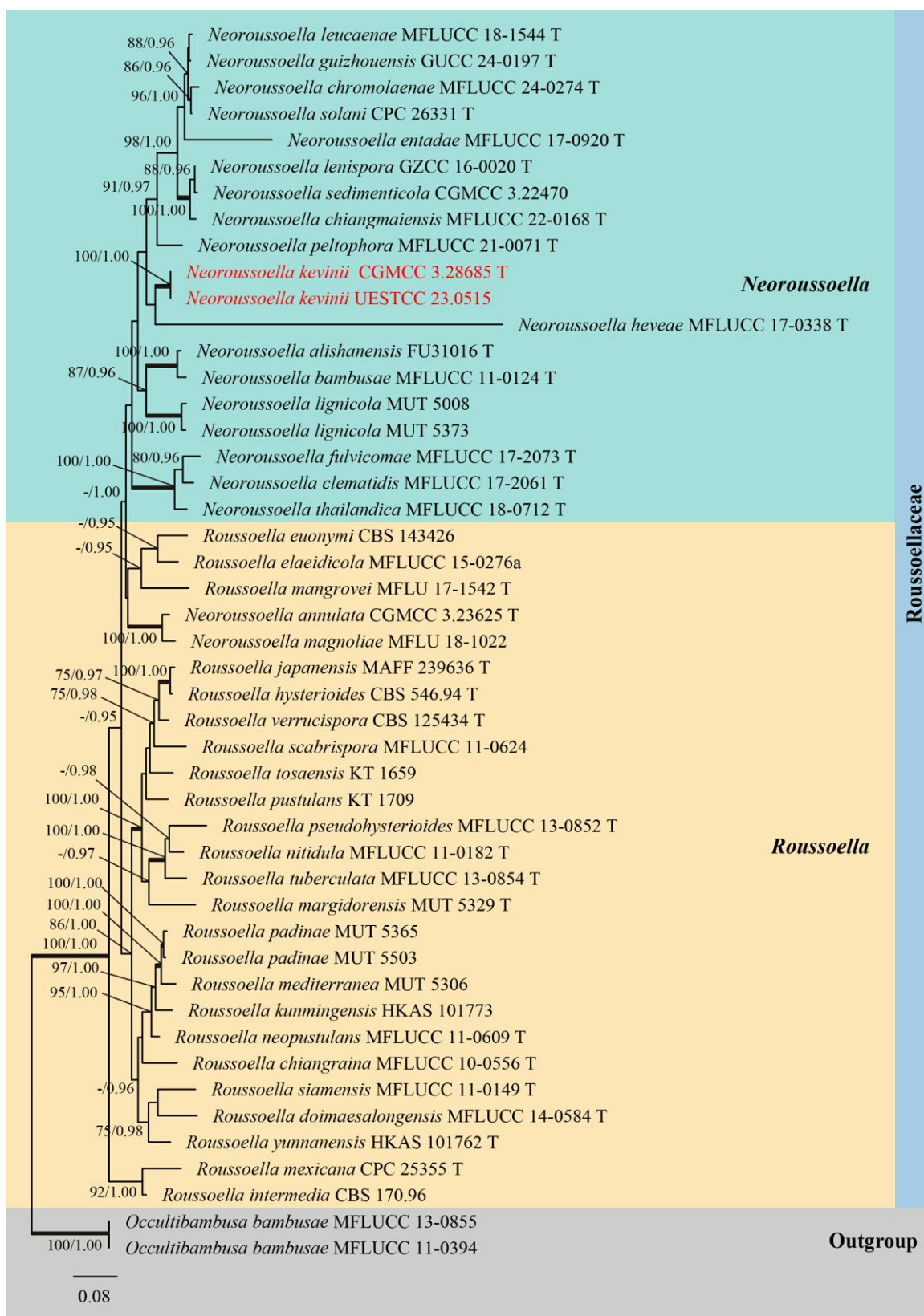


Figure 49 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined LSU, SSU, ITS, *tefl-α*, and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Occultibambusa bambusae* (MFLUCC 11-0394) and *O. bambusae* (MFLUCC 13-0855). The best scoring RAXML tree with a final likelihood value of -26,947.381133

is presented. The matrix had 1,522 distinct alignment patterns, with 27.95% of undetermined characters or gaps, the tree-length is 3.206373. Estimated base frequencies were as follows: A = 0.245146, C = 0.258061, G = 0.267988, T = 0.228805, with substitution rates AC = 1.465274, AG = 4.091412, AT = 1.656435, CG = 1.077547, CT = 7.806428, GT = 1.000000; gamma distribution shape parameter alpha = 0.188938. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009967 (the critical value for the topological convergence diagnostic is below 0.01).

cylindrical to oblong or subclavate asci, and ellipsoid to oblong or fusiform, cylindric fusiform or oblong to elliptical, ovoid to clavate, initially hyaline or pale brown to dark brown or yellowish brown, 1–3-septate or muriform ascospores. The asexual morph is coelomycetous, which mainly characterized by hyaline to brown, cylindrical to elongate, aseptate or three-distoseptate conidia (Thambugala et al. 2015, Jaklitsch et al. 2016b, Hongsanan et al. 2020a, Tennakoon et al. 2021b).

Pseudoteichospora X.G. Tian, K.D. Hyde & Tibpromma, *Mycosphere* 15 (1): 85 (2024)

MycoBank number: MB900978; Facesoffungi number: FoF14293

Notes – *Pseudoteichospora* is a monotypic genus introduced by Tian et al. (2024a) to accommodate *P. thailandensis* as the type species, which was found on dead leaves of *Ananas comosus* from a terrestrial habitat in Thailand. Currently, the asexual morph of *Pseudoteichospora* is coelomycetous, which is characterized by pycnidial, immersed to semi-immersed, dark brown to black, globose to subglobose, ostiolate conidiomata, multi-layered conidiomatal wall composed of *textura angularis* cells, hyaline, phialidic, cylindrical conidiogenous cells, and hyaline to pale brown, aseptate, ellipsoidal to oval conidia with guttules (Tian et al. 2024a), while the sexual morph of this genus has not been observed to date.

Pseudoteichospora hydei H.Z. Du & Jian K. Liu, sp. nov.

Fig. 50

MycoBank number: MB857562; Facesoffungi number: FoF17988

Etymology – The epithet ‘*hydei*’ named for in honor of Prof. Kevin D. Hyde for his contribution to ascomycetes taxonomy.

Holotype – HKAS 132432

Saprobic on dead twigs of *Arundina graminifolia* (D. Don) Hochreutiner (*Orchidaceae*). Visible as dark brown or black dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. Conidiomata 137–178 µm diam. × 95–157 µm high ($\bar{x}$ = 156 × 117 µm, n = 20), pycnidial, immersed or semi-immersed to erumpent, papillate, solitary, dark brown to black, elliptical or oblate-spheroid or conical, with a nearly flattened base, uniloculate. *Ostiole* central, papillate. *Conidiomatal wall* 14–20 µm ($\bar{x}$ = 16 µm, n = 20) wide, multi-layered, the outer layer consists of thick-walled, brown to dark brown cells of *textura angularis*, while the inner layer is mostly composed of hyaline to pale brown, thin-walled cells, bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.5–8.5 × 2.1–3.4 µm ($\bar{x}$ = 6.3 × 2.7 µm, n = 20), hyaline, phialidic, discrete, determinate, cylindrical and smooth-walled. *Conidia* 4.2–6.7 × 2.2–3.0 µm ($\bar{x}$ = 5.0 × 2.6 µm, n = 30), hyaline to pale brown, aseptate, ellipsoidal to oval with rounded apex and slightly truncate base, acrogenous, there is one granular to guttulate structure nearly at both ends of the conidial surface.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from one end. Colonies growing on PDA reached 28–30 mm diam. after three weeks at 25 °C in the dark. Colonies from above, circular, regular, dense mycelium, white. In reverse, light gray to pale grayish green in the center, with a green central spot, and white to grayish white at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong City, Xishuangbanna South Medicinal Plant Garden, 100°47'20"E, 22°0'25"N, elevation 520 m, on dead twigs of *Arundina graminifolia* (*Orchidaceae*), 11 November 2022, H.Z. Du, S539 (HKAS 132432, holotype; HUEST 23.0503, isotype); ex-type living culture CGMCC 3.28684, ex-isotype living culture UESTCC 23.0502.

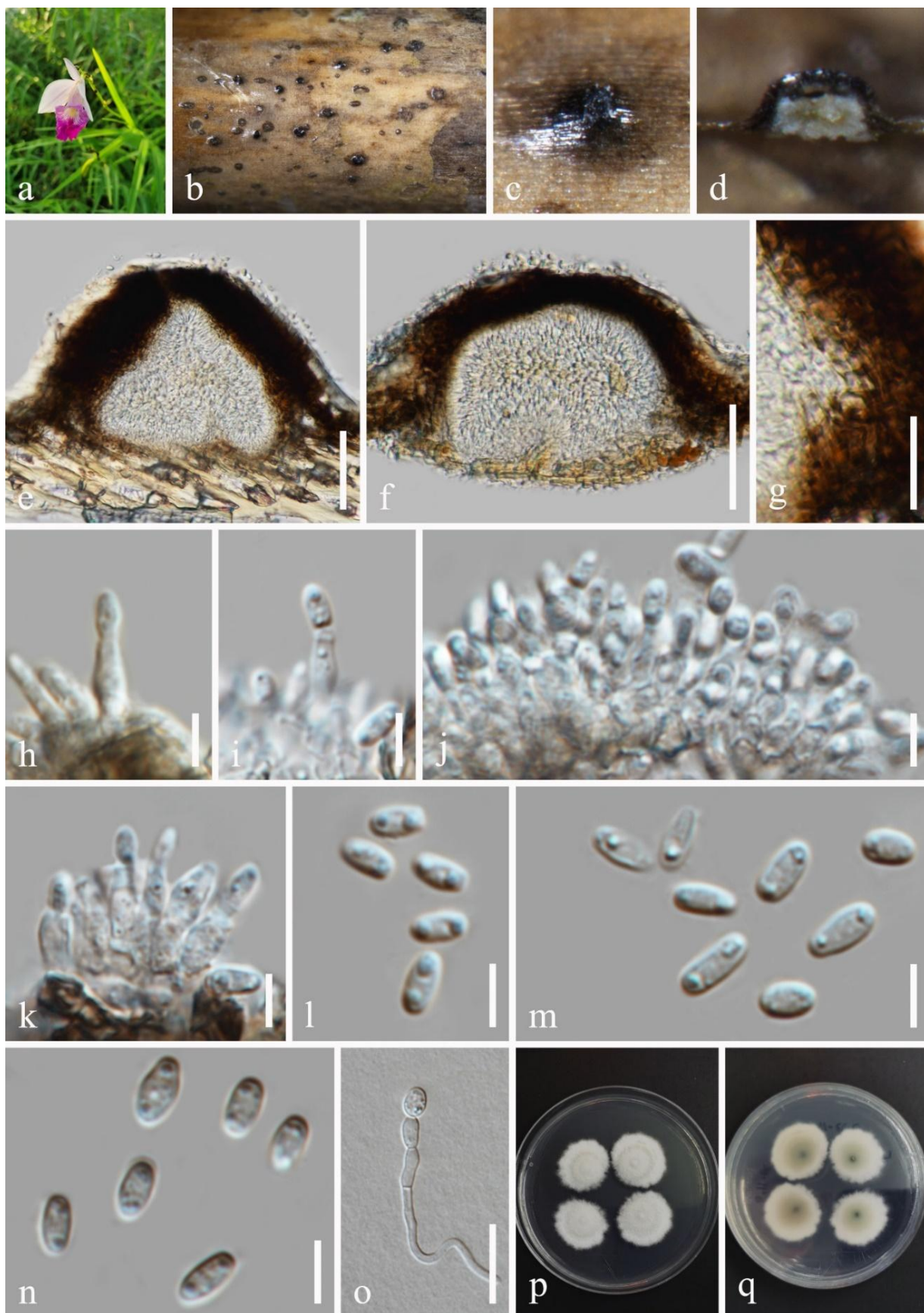


Figure 50 – *Pseudoteichospora hydei* (HKAS 132432, holotype). a Host *Arundina graminifolia*. b–d Appearance of conidiomata on host surface. e, f Vertical section of conidiomata. g Conidiomatal wall. h–k Conidiogenous cells and conidia. l–n Conidia. o Germinated conidium. p, q Colonies on PDA, above (p) and below (q). Scale bars: e, f = 50 μ m, g, o = 20 μ m, h–n = 5 μ m.

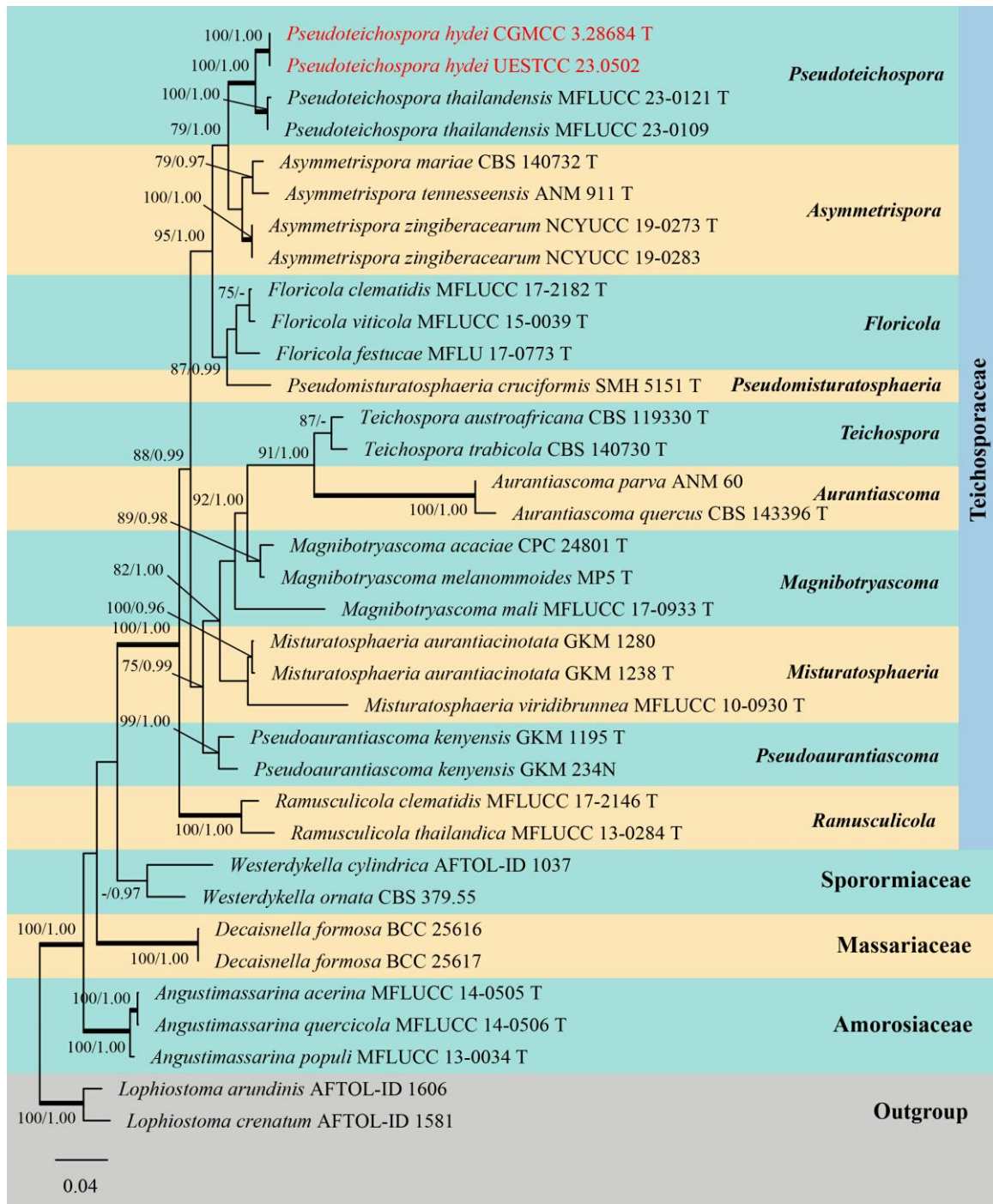


Figure 51 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined LSU, ITS, SSU, *tef1*- α , and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Lophiostoma arundinis* (AFTOL ID-1606) and *L. crenatum* (AFTOL ID-1581). The best scoring RAxML tree with a final likelihood value of -17,559.035615 is presented. The matrix had 1,188 distinct alignment patterns, with 40.90% of undetermined characters or gaps, the tree-length is 1.211785. Estimated base frequencies were as follows: A = 0.240630, C = 0.255557, G = 0.277979, T = 0.225835, with substitution rates AC = 1.134781, AG = 2.340976, AT = 1.389718, CG = 1.052202, CT = 7.212286, GT = 1.000000; gamma distribution shape parameter alpha = 0.265476. The final average standard deviation of split frequencies at the end of total MCMC

generations for BI analysis was 0.008893 (the critical value for the topological convergence diagnostic is below 0.01).

GenBank accession numbers – HKAS 132432 = ITS: PQ773409, LSU: PQ773429, SSU: PQ773445, *tefl-α*: PV059189, *rpb2*: PV075251; UESTCC 23.0502 = ITS: PQ773410, LSU: PQ773430, SSU: PQ773446, *tefl-α*: PV059190, *rpb2*: PV075252.

Notes – Multi-locus phylogeny showed that our two isolates (CGMCC 3.28684 and UESTCC 23.0502) clustered within *Pseudoteichospora*, forming a distinct lineage and was sister to *P. thailandensis* (MFLUCC 23-0121 and MFLUCC 23-0109) with a strong support (100% MLBS/1.00 BIPP) (Fig. 51). Morphologically, *P. hydei* (HKAS 132432, holotype) shares the similar asexual morphology with *P. thailandensis* (MFLU 23-0193, holotype) in having pycnidial, immersed or semi-immersed, dark brown to black conidiomata, multi-layered conidiomatal wall with *textura angularis* cells, hyaline, phialidic, cylindrical conidiogenous cells, and hyaline to pale brown, aseptate, ellipsoidal to oval conidia with guttules (Tian et al. 2024a). However, *P. hydei* differs from *P. thailandensis* by the elliptical or oblate-spheroid or conical conidiomata with a nearly flattened base, and determinate conidiogenous cells, while *P. thailandensis* has the globose to subglobose conidiomata and indeterminate conidiogenous cells (Tian et al. 2024a). Additionally, comparison of the nucleotide base pairs showed that *P. hydei* (CGMCC 3.28684, ex-type strain) can be distinguished from *P. thailandensis* (MFLUCC 23-0121, ex-type strain) by 13/479 bp (2.7%, 5 gaps) in ITS, 24/901 bp (2.7%, without gaps) in *tefl-α*, and 45/997 bp (4.5%, without gaps) in *rpb2* sequence data. Therefore, *P. hydei* is introduced as a new species based on morphological and phylogenetic evidence, and species of *Pseudoteichospora* are being reported from Yunnan Province in China for the first time.

Thyridariaceae Q. Tian & K.D. Hyde, Fungal Diversity. 63: 254 (2013)

Mycobank number: MB805172; Facesoffungi number: FoF08374

Notes – Hyde et al. (2013) established the family *Thyridariaceae* to accommodate *Thyridaria* as the type genus. Later, Jaklitsch & Voglmayr (2016c) synonymized *Roussoellaceae* under *Thyridariaceae* with the genus *Parathyridaria*, and accepted five genera, *Neoroussoella*, *Parathyridaria*, *Roussoella*, *Roussoellopsis*, and *Thyridaria*. However, Tibpromma et al. (2017) reinstated *Roussoellaceae* as a distinct family within *Pleosporales*, based on morphological characteristics and phylogenetic analyses. Subsequently, *Thyridariella* (Devadatha et al. 2018), *Liua* (Phookamsak et al. 2019), *Chromolaenomyces* (Mapook et al. 2020), and *Pseudothyridariella* (Mapook et al. 2020) were introduced within *Thyridariaceae* based on morpho-phylogenetic evidence. Currently, there are eight genera accommodated in *Thyridariaceae* (Wijayawardene et al. 2022b).

Chromolaenomyces Mapook & K.D. Hyde, Fungal Diversity 101: 96 (2020)

Mycobank number: MB557333; Facesoffungi number: FoF07824

Notes – *Chromolaenomyces* was introduced by Mapook et al. (2020) with the type species *Ch. appendiculatus* based on morphology and phylogeny. The sexual morph of the genus *Chromolaenomyces* is characterized by having cylindrical asci with a short pedicel and uni-seriate, irregularly arranged, oval to broadly fusiform, uni-septate ascospores. These ascospores have narrow sheaths that extends into polar appendages from both ends. Asexual morph is undetermined.

Chromolaenomyces davidii H.Z. Du & Jian K. Liu, sp. nov.

Fig. 52

Mycobank number: MB855434; Facesoffungi number: FoF17989

Etymology: The epithet ‘*davidii*’ refers to the Prof. Kevin D. Hyde’s second name, David, acknowledging his significant contributions to ascomycetes taxonomy.

Holotype: HKAS 132397

Saprobic on dead twigs of *Mahonia eurybracteata* Fedde (*Berberidaceae*). Visible as black dots. Sexual morph: *Ascomata* 234–445 µm diam. × 250–485 µm high ($\bar{x}$ = 377 × 337 µm, n = 20),

solitary or scattered, uniloculate, immersed, with black shiny ostioles, globose or subglobose, coriaceous, thick-walled, brown to dark brown, ostiolate. *Ostiole* 81–153 μm wide $\times$ 91–145(–244) μm high ($\bar{x}$ = 121 $\times$ 117 μm , n = 20), central or eccentric, papillate, blackish brown, opening by a pore, filled with periphyses. *Peridium* 17–33 μm ($\bar{x}$ = 25 μm , n = 20) wide, multi-layered, composed of 4–5 layers of dark brown cells of *textura angularis*, thin-walled, heavily pigmented at outer layer, reddish-brown to dark brown, cells towards the inside lighter, hyaline to pale brown. *Hamathecium* comprising 1–2 μm wide, numerous, cylindrical to filiform, septate, hyaline, smooth, branched pseudoparaphyses, and embedded in a gelatinous matrix. *Asci* 75–109 $\times$ 10–16 μm ($\bar{x}$ = 90 $\times$ 13 μm , n = 30), (4–)8-spored, bitunicate, fissitunicate, fusiform, cylindrical to clavate, straight or slightly curved, short pedicellate, apically rounded, with a small ocular chamber. *Ascospores* 20–31 $\times$ 4–9 μm ($\bar{x}$ = 27 $\times$ 7 μm , n = 30), uni-seriate, irregular arrangement, hyaline, oval to broadly fusiform, uni-septate, constricted at the septum, smooth, straight or slightly curved, stained with Indian ink showing the mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, medium dense, mycelium slightly raised, entire, white at the center and edge, with pale grayish green ring between them. In reverse, brown to dark brown in the center, pale brown at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'16"E, 21°55'43"N, elevation 505 m, on dead twigs of *Mahonia eurybracteata* (*Berberidaceae*), 9 November 2022, H.Z. Du, S569 (HKAS 132397, holotype; HUEST 23.0429, isotype); ex-type living culture UESTCC 24.0233, ex-isotype living culture UESTCC 23.0428.

GenBank accession numbers – UESTCC 24.0233 = ITS: PQ394072, LSU: PQ184719, *rpb2*: PQ379996; UESTCC 23.0428 = ITS: PQ394051, LSU: PQ184698, *rpb2*: PQ379947.

Notes – Multi-locus phylogeny showed that *Chromolaenomyces davidii* (UESTCC 24.0233 and UESTCC 23.0428) formed a distinct lineage and was sister to *Ch. appendiculatus* (Fig. 58). Morphologically, *Ch. appendiculatus* (MFLU 20-0307, holotype) can be distinguished from *Ch. davidii* (HKAS 132397, holotype) by the narrow sheath drawn out to form polar appendages from both ends of ascospores (Mapook et al. 2020), while *Ch. davidii* is characterized by obviously guttulate ascospores with mucilaginous sheaths when immersed in Indian ink. Comparison of the nucleotide base pairs showed that *Ch. davidii* (UESTCC 24.0233, ex-type strain) can be distinguished from *Ch. appendiculatus* (MFLUCC 17-1455, ex-type strain) by 26/475 bp (5.5%, 13 gaps) in ITS and 43/1044 bp (4.1%, 1 gap) in *rpb2* sequence data. Therefore, *Ch. davidii*, associated with *Mahonia eurybracteata*, is introduced as a new species based on morphology and phylogeny.

Parathyridaria Jaklitsch & H. Voglmayr, Studies in Mycology. 85: 48 (2016)

MycoBank number: MB817775; Facesoffungi number: FoF08377

Notes – *Parathyridaria* was introduced by Jaklitsch & Voglmayr (2016c) to accommodate *P. percutanea* and *P. ramulicola* (type species), which are reported as saprobes and human pathogens, respectively. The sexual morph of *Parathyridaria* is characterized by immersed and globose ascomata, pseudoparenchymatous peridium, papillate and periphysate ostioles, narrowly clavate asci, and fusoid, multi-septate, pale to grayish brown ascospores (Jaklitsch & Voglmayr 2016c). Asexual morph in this genus is characterized by solitary, immersed, globose to subglobose conidiomata, phialidic conidiogenous cells, ellipsoid, unicellular and hyaline to pale brown conidia (Jaklitsch & Voglmayr 2016c, Wanasinghe et al. 2018).

Parathyridaria ellipsoidea K. Das, S.Y. Lee & H.Y. Jung, Mycobiology 49 (1): 18 (2020)

Figs 53, 54

MycoBank number: MB835968; Facesoffungi number: FoF17990

Sexual morph: *Saprobic* on dead twigs of *Buxus sinica* (Rehder & E.H.Wilson) M. Cheng (*Buxaceae*). Visible as black dots. *Ascomata* 277–335 μm diam. $\times$ 210–289 μm high ($\bar{x}$ = 306 $\times$ 249

μm , $n = 20$), immersed in bark, solitary, scattered, globose to subglobose or obpyriform, dark brown to black, rough-walled, coriaceous, papillate, ostiolate. *Ostiole* central or eccentric, papillate,



Figure 52 – *Chromolaenomyces davidii* (HKAS 132397, holotype). a Host *Mahonia eurybracteata*. b Flowers of *M. eurybracteata*. c Twigs of *M. eurybracteata*. d–f Appearance of ascomata on host surface. g Vertical section of ascomata. h Structure of peridium. i Ostiole. j Hamathecium. k–m Asci. n–s Ascospores. t Ascospore stained with Indian ink showing the mucilaginous sheath. u Germinated ascospore. v, w Colonies on PDA, above (v) and below (w). Scale bars: g = 100 μm , h, i = 50 μm , j–m, t = 30 μm , n–s, u = 10 μm .

blackish brown, opening by a pore, filled with periphyses. *Peridium* 17–30 μm (–50 μm at apex) ($\bar{x}$ = 22 μm , n = 20), coriaceous, composed of several layers of thin to thick-walled cells of *textura angularis*, heavily pigmented at outer layer, reddish-brown to dark brown, and hyaline inner layer. *Hamathecium* composed of numerous, dense, 2–3.5 μm wide, hyaline, filamentous, branched, septate, pseudoparaphyses. *Asci* 48–76 $\times$ 5.5–9.5 μm ($\bar{x}$ = 64 $\times$ 7.5 μm , n = 30), (4–)8-spored, bitunicate, fissitunicate, fusiform, clavate, with a short pedicel, rounded and thick-walled at the apex, with a minute ocular chamber. *Ascospores* 15–21 $\times$ 3–6 μm ($\bar{x}$ = 18 $\times$ 5 μm , n = 30), overlapping uniseriate, fusoid, widest at the middle cell, tapering towards the blunt ends, or blunt at both ends, straight or slightly curved, with 1-transverse septum, constricted at the septum, hyaline, with obviously small guttules, smooth-walled, with a mucilaginous sheath present in Indian ink. Asexual morph: *Saprobia* on dead twigs of *Mahonia bealei* (Fortune) Carr. (*Berberidaceae*). Visible as dark brown or black dots. Coelomycetous. *Conidiomata* 121–182 μm high $\times$ 137–221 μm diam. ($\bar{x}$ = 146 $\times$ 174 μm , n = 20), pycnidial, solitary, aggregated, uniloculate, immersed, covered by a pseudoclypeus, globose to subglobose, coriaceous, thick-walled, dark brown to brown, papillate, ostiolate. *Ostioles* 57–62 μm high $\times$ 42.5–47 μm wide ($\bar{x}$ = 59 $\times$ 45 μm , n = 20), central, papillate, blackish brown. *Conidiomatal wall* 7.5–15 μm ($\bar{x}$ = 10 μm , n = 20) wide, outer layer composed of 4–5 layers of brown to dark brown cells of *textura angularis*, lined with a hyaline layer bearing conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–3 $\times$ 2–3 μm ($\bar{x}$ = 2.5 $\times$ 2 μm , n = 30), short, phialidic, hyaline, discrete, arising from the inner layer of pycnidium wall. *Conidia* 3.5–5 $\times$ 2–2.5 μm ($\bar{x}$ = 4 $\times$ 2.3 μm , n = 30), oval or ellipsoidal, solitary, aseptate, smooth-walled, 1(–2) guttules in each cell, with an obtuse apex and base bluntly rounded, hyaline when immature, pale brown to olivaceous brown at maturity.

Culture characteristics – Ascospores and conidia germinated on PDA within 12 h, and germ tubes are produced from both ends. Sexual morph: Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, grayish white, circular, middle dense, regular edge, umbonate, covered with white aerial mycelium, and in reverse, grayish white at the center, pale grey at the edge. Asexual morph: Colonies growing on PDA reached 27–29 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, white, medium dense, slightly raised to umbonate or convex, regular edge; and in reverse, grayish white, and pale green at the center.

Material examined – China, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 102°44'24"E, 25°8'39"N, elevation 1,922 m, on dead twigs of *Buxus sinica* (*Buxaceae*), 11 November 2022, H.Z. Du, S736 (HUEST 23.0427), living culture UESTCC 23.0426. *ibid.*, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, 106°41'49"E, 26°32'20"N, elevation 1,129 m, on dead twigs of *Mahonia bealei* (*Berberidaceae*), 12 October 2021, H.Z. Du, S375 (HUEST 23.0428), living culture UESTCC 23.0427.

GenBank accession numbers – UESTCC 23.0426 = ITS: PQ394052, LSU: PQ184699, *tefl- α* : PQ346492; UESTCC 23.0427 = ITS: PQ394053, LSU: PQ184700, *tefl- α* : PQ346493.

Notes – *Parathyridaria ellipsoidea* was introduced by Das et al. (2020) with an asexual morphology and phylogeny (ITS and LSU) and isolated from soil samples in Jeju Island, Korea. In this study, we introduced the sexual (HUEST 23.0427) and asexual (HUEST 23.0428) morphs of *P. ellipsoidea*, and the asexual morph is similar to the holotype (KNU-JJ-1829) (Das et al. 2020). Multi-locus phylogeny showed that our strains (UESTCC 23.0426 and UESTCC 23.0427) clustered together with the ex-type strain of *P. ellipsoidea* (KNU-JJ-1829) and formed a strongly supported clade (100% MLBS/1.00 BIPP) (Fig. 58). The comparison of the nucleotide base pair is not significantly different between KNU-JJ-1829 and our strains in ITS (99.6%–100%) and LSU (99.8%). Therefore, we identify these two isolates as *P. ellipsoidea* based on morphology and phylogeny. This is the first report of *P. ellipsoidea* from *Buxus sinica* and *Mahonia bealei* in Yunnan and Guizhou Provinces, China.

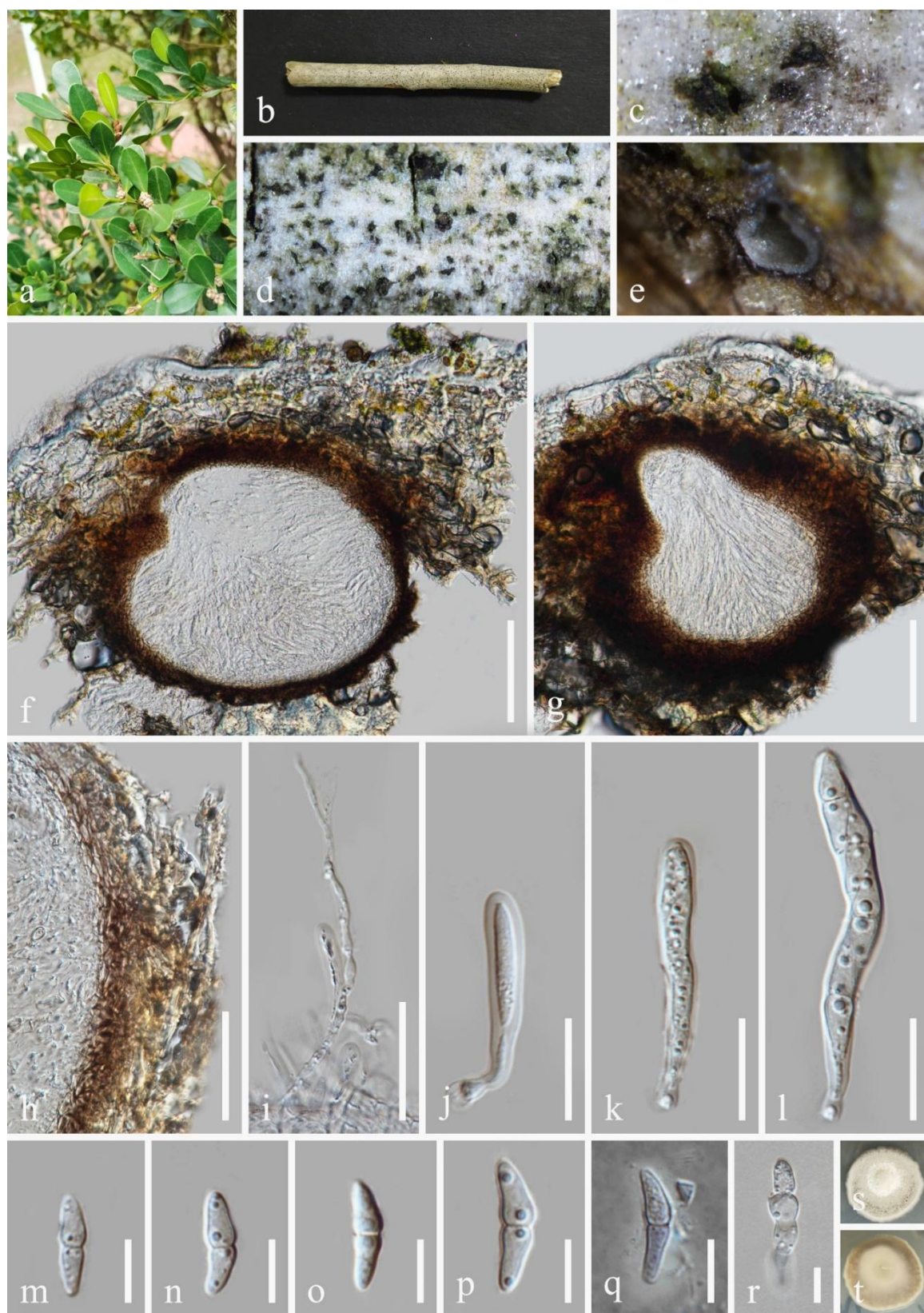


Figure 53 – The sexual morph of *Parathyridaria ellipsoidea* (HUEST 23.0427, new host and geographical records). a Host *Buxus sinica*. b A twig of *B. sinica*. c–e Appearance of ascomata on host surface. f, g Vertical section of ascomata. h Structure of peridium. i Hamathecium. j–l Asci. m–p Ascospores. q Ascospore stained in Indian ink showing the mucilaginous sheath. r Germinated ascospore. s, t Colony on PDA, above (s) and below (t). Scale bars: f, g = 100 μm , h = 40 μm , i = 30 μm , j–l = 20 μm , m–r = 10 μm .

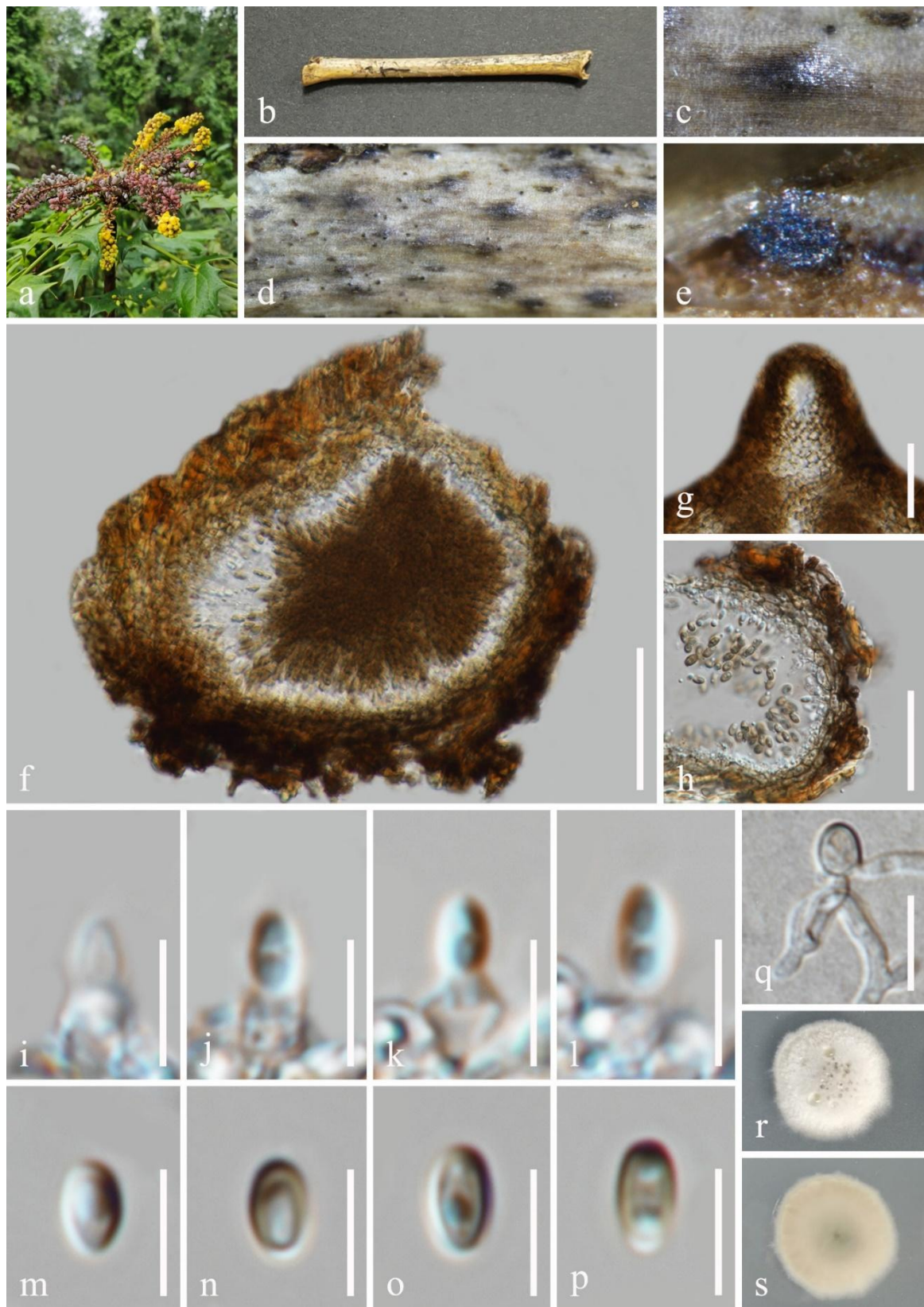


Figure 54 – The asexual morph of *Parathyridaria ellipsoidea* (HUEST 23.0428, new host and geographical records). a Host *Mahonia bealei*. b A twig of *M. bealei*. c–e Appearance of conidiomata on host surface. f Vertical section of conidiomata. g Ostiole. h Conidiomatal wall. i–l Conidiogenous cells and conidia. m–p conidia. q Germinated conidium. r, s Colony on PDA, above (r) and below (s). Scale bars: f = 50 μ m, g, h = 30 μ m, i–p = 5 μ m, q = 10 μ m.

Parathyridariella Mapook & K.D. Hyde, Fungal Diversity 101: 98 (2020)

MycoBank number: MB832836; Facesoffungi number: FoF11758

Notes – *Parathyridariella* was introduced by Poli et al. (2020) within *Thyridariaceae* to accommodate the type species *Pa. dematiacea*, which was isolated from *Pinus pinaster* and *Quercus ruber* in Italy. Currently, there are two species, *Pa. aquilariae* and *Pa. dematiacea* are listed in the Index Fungorum (accessed on 20 July 2025). The asexual morph of this species is characterized by septate, hyaline, and lightly pigmented hyphae, numerous, mostly in chains, intercalary or solitary, globose to subglobose, brown to dark brown chlamydospores, but the conidiogenesis was not observed. The sexual morph remains undetermined.

Parathyridariella davidiseptata H.Z. Du & Jian K. Liu, sp. nov.

Figs 55, 56

MycoBank number: MB855435; Facesoffungi number: FoF17991

Etymology – The epithet ‘*davidiseptata*’ is a combination of Prof. Kevin D. Hyde’s second name David, and the septum observed in the mature ascospores, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132396

Saprobic on dead twigs of *Mahonia bealei* (*Berberidaceae*). Visible as black dots. Sexual morph: *Ascomata* 177–262 μm diam. $\times$ 173–285 μm high ($\bar{x}$ = 226 $\times$ 232 μm , n = 20), immersed, solitary, scattered, appearing as black spots, coriaceous, subglobose to obpyriform, dark brown to black, with distinct papillae. *Ostiole* 86–131 μm wide $\times$ 79–114 μm high ($\bar{x}$ = 107 $\times$ 97 μm , n = 20), central, long neck, papillate, blackish brown, filled with hyaline periphyses. *Peridium* 14–32 μm wide ($\bar{x}$ = 24 μm , n = 20), coriaceous, composed of several layers of thin to thick-walled cells of *textura angularis*, heavily pigmented at outer layer, dark brown to black, and hyaline inner layer. *Hamathecium* comprising 1.5–2.5 μm wide, hyaline, cylindrical to filiform, septate, branched pseudoparaphyses. *Asci* 60–90 $\times$ 9–11 μm ($\bar{x}$ = 77 $\times$ 10 μm , n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, straight or slightly curved, with a short pedicel, apically rounded, with an ocular chamber. *Ascospores* 21–25 $\times$ 3–6 μm ($\bar{x}$ = 22 $\times$ 4 μm , n = 30), overlapping, bi-seriate, hyaline, oblong to fusiform, straight or slightly curved, smooth, with obtuse to slightly obtuse ends, 1-septate, occasionally aseptate when immature, 3-septate at maturity, surrounded by a hyaline gelatinous sheath, observed clearly when mounted in Indian ink. Asexual morph: Coelomycetous. *Conidiomata* 151–242 μm high $\times$ 177–321 μm diam. ($\bar{x}$ = 195 $\times$ 260 μm , n = 20), pycnidial, solitary, aggregated, uniloculate, immersed, globose to subglobose, coriaceous, thick-walled, brown to dark brown, slightly papillate, ostiolate. *Ostioles* eccentric, blackish brown. *Conidiomatal wall* 11–19 μm ($\bar{x}$ = 15.5 μm , n = 20) wide, composed of 3–5 layers of brown to dark brown cells of *textura angularis*, lined with a hyaline layer bearing conidiogenous cells. *Conidiophores* single, short, densely aggregated, straight or flexuous, cylindrical, hyaline, erect, septate, smooth, occasionally reduced to conidiogenous cells. *Conidiogenous cells* 4–9 $\times$ 2–3 μm ($\bar{x}$ = 6 $\times$ 2 μm , n = 30), phialidic, annellidic, hyaline, discrete, arising from the inner layer of pycnidial wall. *Conidia* 3–5 $\times$ 2–3 μm ($\bar{x}$ = 4 $\times$ 3 μm , n = 30), acrogenous, aseptate, ovoid to ellipsoidal, with 1–2-guttule in each cell, thick-walled, rounded at both ends. hyaline when immature, olivaceous to pale brown at maturity.

Culture characteristics – Ascospores and conidia germinated on PDA within 12 h, and germ tubes are produced from both ends. Sexual morph: Colonies growing on PDA reached 35–38 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, irregular, mycelium slightly raised, moderately fluffy, filiform, white aerial hyphae at the surface, spreading from the center and hyaline mycelium at the edge. In reverse, brown to olivaceous-brown in the center, with creamy white at the edge. Asexual morph: Colonies growing on PDA reached 25–28 mm in diam. after three weeks at 25 °C in the dark, and the culture characteristics (both the above and reverse) is similar to the sexual morph in the shape and color.

Material examined – China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, 106°41'49"E, 26°32'20"N, elevation 1,129 m, on dead twigs of *Mahonia bealei* (*Berberidaceae*), 12 October 2021, H.Z. Du, sexual morph, S368 (HKAS 132396, holotype; HUEST 23.0425, isotype); ex-type living culture CGMCC 3.27719; ex-isotype living culture UESTCC 23.0424. *ibid.*, asexual morph, S369 (HUEST 23.0426, paratype); ex-paratype living

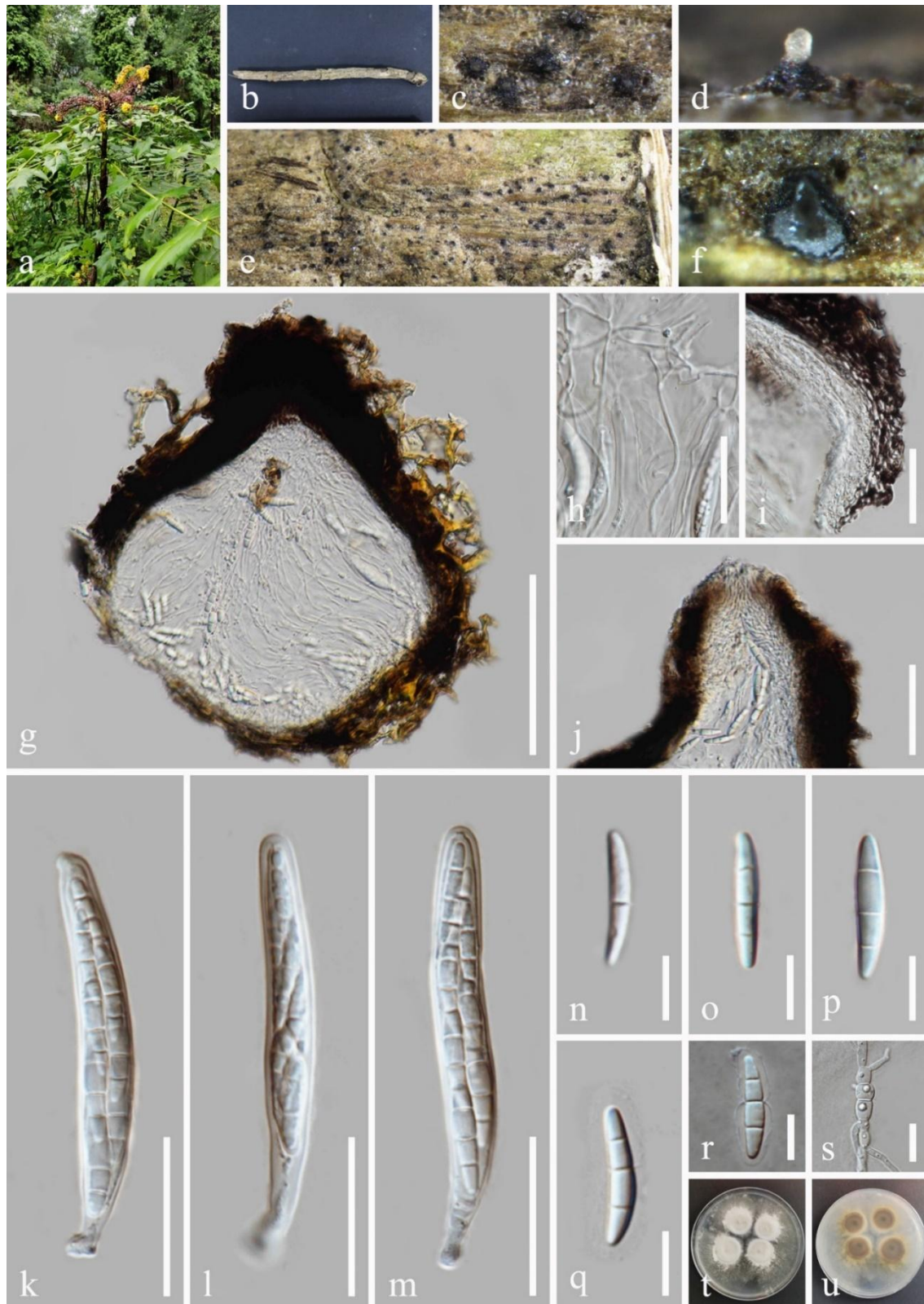


Figure 55 – The sexual morph of *Parathyridariella davidiseptata* (HKAS 132396, holotype). a Host *Mahonia bealei*. b A twig of *M. bealei*. c–f Appearance of ascomata on host surface. g Vertical section of ascomata. h Hamathecium. i Structure of peridium. j Ostiole. k–m Asci. n–q Ascospores. r Ascospore stained in Indian ink showing the mucilaginous sheath. s Germinated ascospore. t, u Colonies on PDA, above (t) and below (u). Scale bars: g = 100 μm , = 30, h, i, k–m = 30 μm , j = 50 μm , n–r = 10 μm , s = 20 μm .

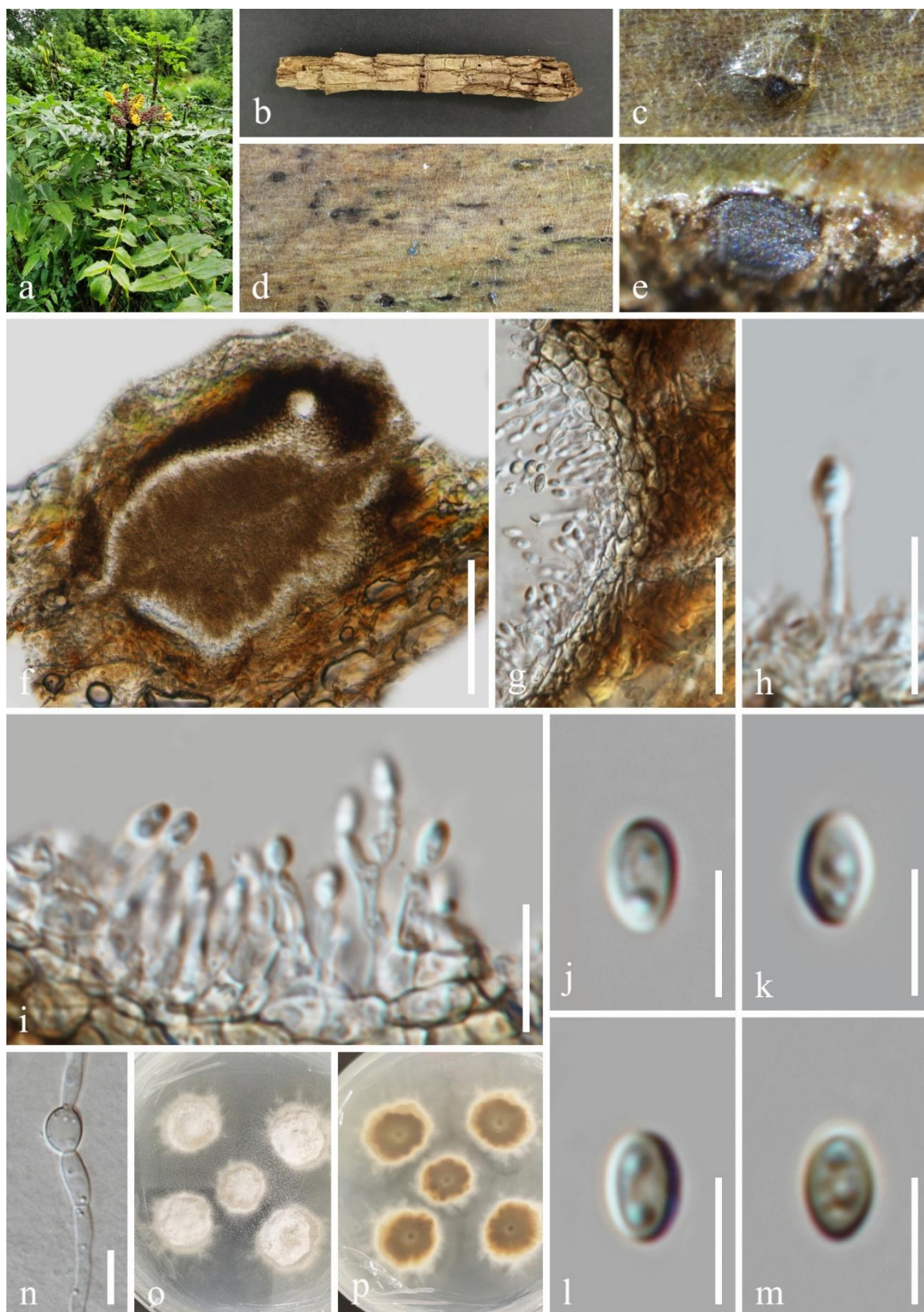


Figure 56 – The asexual morph of *Parathyridariella davidiseptata* (HUEST 23.0426, paratype). a Host *Mahonia bealei*. b A twig of *M. bealei*. c–e Appearance of conidiomata on the host surface. f Vertical section of conidiomata. g Conidiomatal wall. h, i Conidiogenous cells and conidia. j–m conidia. n Germinated conidium. o, p Colonies on PDA, above (o) and below (p). Scale bars: f = 100 μm , g = 30 μm , h, i, n = 10 μm , j–m = 5 μm .

GenBank accession numbers – CGMCC 3.27719 = ITS: PQ394073, LSU: PQ184720, *tefl-α*: PQ346517, *rpb2*: PQ379997; UESTCC 23.0425 = ITS: PQ394054, LSU: PQ184701, *tefl-α*: PQ346494, *rpb2*: PQ379948.

Notes – Multi-locus phylogeny showed that *Parathyridariella davidiseptata* (CGMCC 3.27719 and UESTCC 23.0425) formed a distinct lineage and was sister to *Par. aquilariae* (ZHKUCC 23-0074) with a well support (92% MLBS/1.00 BIPP) (Fig. 58). *Parathyridariella aquilariae* was introduced by Du et al. (2024b) based on asexual morph obtained from *Aquilaria yunnanensis* in China. Morphologically, *Par. aquilariae* (MHZU 23-0038, holotype) differs from *Par. davidiseptata* (HKAS 132396, holotype) in having larger conidiomata (200–500 × 300–550 μm vs. 151–242 μm high × 177–321 μm), and oval conidia with longitudinal striations when mature, which are absent in *Par. davidiseptata*. In addition, *Par. davidiseptata* (CGMCC 3.27719) can be distinguished from *Par. aquilariae* (ZHKUCC 23-0074) based on ITS and *rpb2* nucleotide base pair differences of ex-type strains; ITS = 18/502 bp (3.6%, without gaps) and *rpb2* = 44/462 bp (9.5%, without gaps). Therefore, considering the morpho-molecular data analysis, we establish *Par. davidiseptata* as a new species, which is associated with *Mahonia bealei* in Guizhou Province, China.

Pseudothyridariella Mapook & K.D. Hyde, Fungal Diversity 101: 98 (2020)

Mycobank number: MB557357; Facesoffungi number: FoF07826

Notes – *Pseudothyridariella* was introduced by Mapook et al. (2020) in *Thyridariaceae* with type species of *Pse. chromolaenae*. The sexual morph of *Pseudothyridariella* is similar to *Thyridariella* in having ellipsoid to broadly fusiform, muriform ascospores surrounded by a hyaline gelatinous sheath, but differs in having ascospores with a constriction at the central septum, while ascospores of *Thyridariella* are without a constriction at the central septum (Devadatha et al. 2018). The asexual morph is characterized by solitary, aggregated, immersed, globose to subglobose or obpyriform conidiomata, hyaline, discrete, holoblastic, cylindrical to lageniform conidiogenous cells, and cylindrical to ellipsoidal, septate or aseptate, guttules, olivaceous brown to dark brown conidia. Currently, there are four species, *Pse. aquilariae*, *Pse. chromolaenae*, *Pse. mahakashae*, and *Pse. idesia* are identified in this genus (<https://www.indexfungorum.org/Names/Names.asp?strGenus=Pseudothyridariella>; accessed on 20 July 2025).

Pseudothyridariella idesia L.W. Li & Jian K. Liu, Mycosphere 14 (1): 1516 (2023)

Fig. 57

Mycobank number: MB849161; Facesoffungi number: FoF14402

Saprobic on dead twigs of *Dianthus superbus* L. (*Caryophyllaceae*). Visible as dark brown or black dots. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 124–306 μm diam. × 84–199 μm high ($\bar{x}$ = 191 × 171 μm, *n* = 20), superficial, solitary, aggregated, uniloculate, immersed, globose to subglobose or obpyriform, unilocular, thick-walled, dark brown to black, papillate, ostiolate. *Ostioles* 65–69 μm wide × 70–92 μm high ($\bar{x}$ = 67 × 81 μm, *n* = 20), central, papillate, brown to dark brown. *Conidiomatal wall* 21–30 μm ($\bar{x}$ = 25 μm, *n* = 20) wide, thick, outer layer composed of several layers of thick-walled, brown cells of *textura intricata* to *textura epidermoidea*, lined with a hyaline layer bearing conidiogenous cells. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 5.5–7 × 3.5–7 μm ($\bar{x}$ = 6 × 5 μm, *n* = 30), hyaline, discrete, holoblastic, cylindrical to lageniform, indeterminate, thick- and smooth-walled, arising from the inner layer of pycnidium wall. *Conidia* 10–18 × 5.5–8 μm ($\bar{x}$ = 14 × 7 μm, *n* = 30), cylindrical to ellipsoidal, broadly rounded at ends, occasionally swollen at the basal cells, 0–4 transverse septate, straight, guttules, hyaline to pale brown when immature, olivaceous brown to dark brown at maturity.

Culture characteristics – Conidia germinated on PDA within 12 h, and the germ tubes are produced from each cell. Colonies growing on PDA reached 22–24 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, circular, middle dense, flat, regular edge, umbonate, center elevated, covered with a white aerial mycelium, and grayish white in reverse.

Material examined – China, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 102°44'24"E, 25°8'27"N, elevation 1,922 m, on dead twigs of *Dianthus superbus* (*Caryophyllaceae*), 11 November 2022, H.Z. Du, S709 (HUEST 23.0424), living culture UESTCC

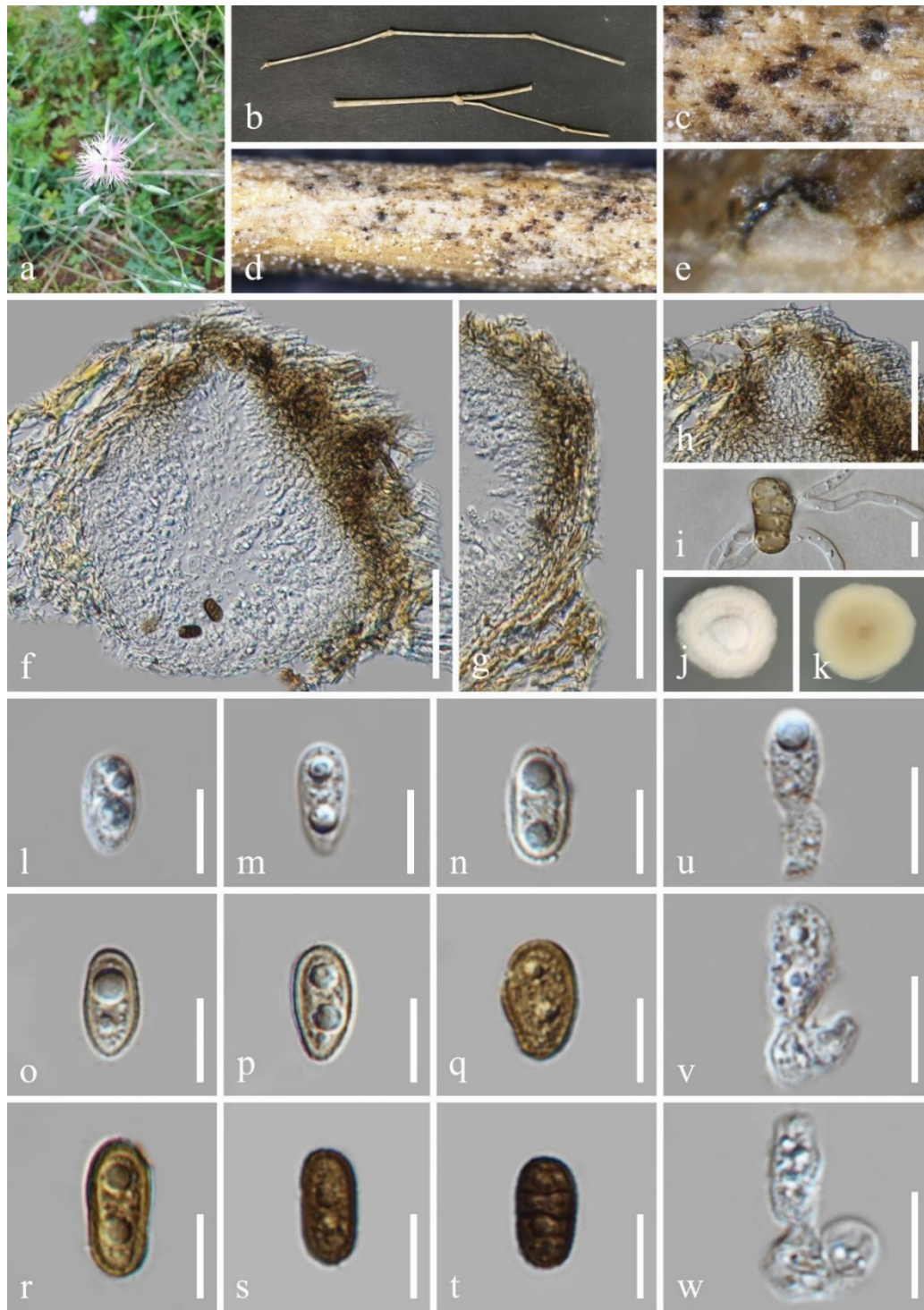


Figure 57 – *Pseudothyridariella idesiae* (HUEST 23.0424, new host record). a Host *Dianthus superbus*. b Twigs of *D. superbus*. c–e Appearance of the conidiomata on host surface. f Vertical section of conidiomata. g Conidiomatal wall. h Ostiole. i Germinated conidium. j, k Colony on PDA, above (j) and below (k). l–t conidia. u–w Conidiogenous cells and conidia. Scale bars: f–h = 50 µm, i, l–w = 10 µm.

GenBank accession numbers – ITS: PQ394055, LSU: PQ184702, *tefl-α*: PQ346495

Notes – *Pseudothyridariella idesiae* was introduced by Li et al. (2023). Multi-locus phylogeny indicated that our isolate (UESTCC 23.0423) clustered together with *Pse. idesiae* (CGMCC 3.24439,

ex-type strain) with a highly support (100% MLBS/1.00 BIPP) (Fig. 58). The morphological characteristics of our collection are similar to those of the holotype of *Pse. idesia* (HKAS 127179) (Li et al. 2023). Comparison of the nucleotide base pairs between the ex-type strain of *Pse. idesia* (CGMCC 3.24439) and our strain (UESTCC 23.0423) revealed 100% similarity in ITS, LSU, and *tefl-α*. Therefore, we identify our isolate as *Pse. idesia*, associated with *Dianthus superbis* in Yunnan Province, China.

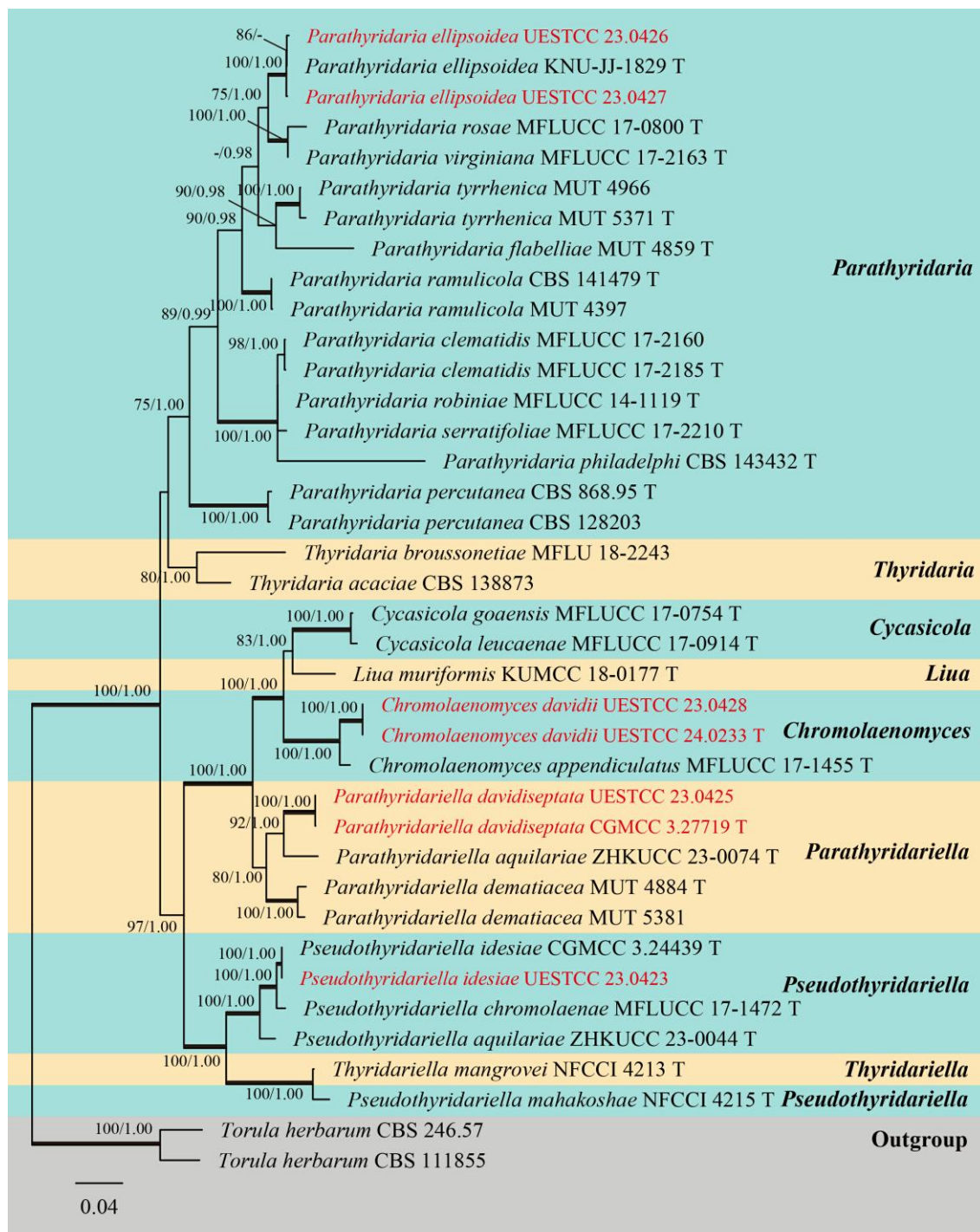


Figure 58 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined ITS, LSU, *tefl-α*, and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below the nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Torula herbarum* (CBS 246.57) and *T. herbarum* (CBS 111855). The best

scoring RAxML tree with a final likelihood value of -18,269.401092 is presented. The matrix had 1,181 distinct alignment patterns, with 18.25% of undetermined characters or gaps, the tree-length is 1.565632. Estimated base frequencies were as follows: A = 0.243027, C = 0.271397, G = 0.271148, T = 0.214428, with substitution rates AC = 1.407271, AG = 3.342724, AT = 1.631871, CG = 0.926856, CT = 8.085172, GT = 1.000000; gamma distribution shape parameter alpha = 0.209438. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009989 (the critical value for the topological convergence diagnostic is below 0.01).

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

MycoBank number: MB501481; Facesoffungi number: FoF14263

Amphisphaeriales D. Hawksw. & O.E. Erikss., Syst. Ascom. 5(1): 177 (1986)

MycoBank number: MB90458; Facesoffungi number: FoF00672

Notes – *Amphisphaeriales* was originally established by Hawksworth & Eriksson (1986) to accommodate fungal taxa in *Amphisphaeriaceae*, *Cainiaceae*, *Clypeosphaeriaceae*, and *Hyponectriaceae*. However, this order was later synonymized under *Xylariales* by Eriksson & Hawksworth (1987). Senanayake et al. (2015) reinstated the order *Amphisphaeriales*, which includes six families, *Amphisphaeriaceae*, *Bartaliniaceae*, *Clypeosphaeriaceae*, *Discosiaceae*, *Pestalotiopsidaceae*, and *Phlogicylindriaceae*. However, *Amphisphaeriales* was not accepted due to the lack of phylogenetic support (Jaklitsch et al. 2016a). Finally, Cosoveanu et al. (2018) confirmed the placement of *Amphisphaeriales*, which formed a sister clade to the *Xylariales* based on phylogenetic analysis. Following this validation, more families and genera were added within this order (Wijayawardene et al. 2020, Zhang et al. 2023b, Liu et al. 2024). The sexual morph of *Amphisphaeriales* is characterized by immersed to erumpent, mostly solitary, globose to subglobose, coriaceous ascomata, cylindrical or clavate asci with J+ or J- apical rings, and ellipsoid, apiosporous, fusiform or oval, unicellular to trans-septate, variously colored ascospores. The asexual morph features acervular or pycnidial conidiomata, with holoblastic, annellidic, ampulliform, or lageniform conidiogenous cells, and the conidia are aseptate to trans-septate, and also vary in color, often bearing appendages. Species of this order are found in various habitats and have a cosmopolitan distribution (Perera et al. 2018, Bejar et al. 2019, Zhang et al. 2023b).

Amphisphaeriaceae G. Winter, Rabenhorst's Kryptogamen-Flora, Pilze - Ascomyceten, Edn 2 1(2): 259 (1885)

MycoBank number: MB80452; Facesoffungi number: FoF00673

Notes – *Amphisphaeriaceae* was introduced by Winter (1885) to accommodate *Amphisphaeria* as the type genus. This family was initially recognized as a heterogeneous sexual morph family accommodating 36 genera (Hawksworth et al. 1995). Later, Kang et al. (1998) restricted the family to ten genera, and subsequently, Kirk et al. (2001) excluded some genera, and reduced to nine genera. Following consecutive morpho-molecular and evolutionary studies by Senanayake et al. (2015), Samarakoon et al. (2016) and Hongsanan et al. (2017), *Amphisphaeriaceae* was placed within *Amphisphaeriales*. Hyde et al. (2020c) confirmed the persistence of *Amphisphaeriaceae* within *Amphisphaeriales*. There are two genera, *Amphisphaeria* and *Griphosphaerioma*, are retained within *Amphisphaeriaceae* (Samarakoon et al. 2022). The sexual morph is characterized by immersed or erumpent perithecial ascomata, some forming in pseudostromata, with papillate ostioles, unitunicate, cylindrical asci with J- or J+ apical rings, and light to dark brown, 1-celled ascospores (Kang et al. 1998).

Amphisphaeria Ces. & De Not., Comm. Soc. crittog. Ital. 1 (4): 223 (1863)

MycoBank number: MB173; Facesoffungi number: FoF02099

Notes – *Amphisphaeria* was introduced by Cesati & de Notaris (1863) without designating a generic type (Wang et al. 2004). Petrak (1923) initially proposed *A. umbrina* (= *Sphaeria umbrina*) as the lectotype of *Amphisphaeria*, and *A. umbrina* was described by Hyde et al. (1996) but was not

as the type specimen. Hence, Hyde et al. (1996) epitypified a specimen listed by Cesati & de Notaris (1863) as *S. umbrina* and used to describe *A. umbrina* by Wang et al. (2004). Subsequently, genera *Amphisphaeria* and *Lepteutypa* was accepted within *Amphisphaeriaceae* by Wijayawardene et al. (2018). However, *Lepteutypa* was discussed and synonymized to *Amphisphaeria* by Samarakoon et al. (2020). The sexual morph of *Amphisphaeria* has perithecial, scattered, immersed, globose to subglobose ascomata, 8-spored, cylindrical asci with J+ or J- apical ring, and ellipsoidal, light brown, one-median septate ascospores. The asexual morph is characterized by solitary or aggregated, globose, dark brown conidiomata, septate, branched, hyaline conidiophores, elongate conical, septate, hyaline, annelidic conidiogenous cells, and hyaline, elongate-fusiform conidia (Senanayake et al. 2015). Members of *Amphisphaeria* are mostly discovered on dead plant materials in terrestrial and marine habitats (Dissanayake et al. 2020b, Zhang et al. 2023a, Li et al. 2024b).

***Amphisphaeria davidihuangtciae* H.Z. Du & Jian K. Liu, sp. nov.**

Fig. 59

Mycobank number: MB857563; Facesoffungi number: FoF17992

Etymology – The epithet ‘*davidihuangtciae*’ is a combination of Prof. Kevin D. Hyde’s second name David, and the host genus ‘*Huangtcia*’ from which the fungus was originally isolated, acknowledging his significant contributions to ascomycetes taxonomy.

Holotype – HKAS 132448

Saprobic on dead twigs of *Huangtcia renifolia* (L.) H. Ohashi & K. Ohashi (*Fabaceae*). Visible as dark brown or black dots. Sexual morph: *Ascomata* 315–368 µm diam. × 141–230 µm high ($\bar{x}$ = 335 × 192 µm, n = 20), immersed, solitary or scattered, conical, flattened-spherical or depressed subglobose, with a nearly flattened base, uniloculate, with a central ostiole opening, coriaceous, thick-walled, dark brown to black, micro-papillate. *Ostioles* 92–125 µm diam. × 79–105 µm high ($\bar{x}$ = 116 × 93 µm, n = 15), central, brown to dark brown, filled with periphyses. *Peridium* 9–12 µm ($\bar{x}$ = 10 µm, n = 20), comprising several layers of *textura angularis* cells, the inner layer is pale brown to brown, thin-walled, and the outer wall is brown to dark brown, thick-walled, emerging with host tissue. *Paraphyses* 4.7–6.5 µm wide ($\bar{x}$ = 5.2 µm, n = 20), hyaline, simple, cellular, constricted, septate, guttulate, embedded in a gelatinous matrix, un-branched, attenuated to pointed at the apices. *Asci* 83–96 × 5.7–7.7 µm ($\bar{x}$ = 90 × 6.5 µm, n = 20), 8-spored, unitunicate, cylindrical, thin-walled, with a short pedicel, apically rounded, with an amyloid (J+) apical ring in Melzer’s reagent. *Ascospores* 10–14 × 3.8–5.4 µm ($\bar{x}$ = 12 × 4.7 µm, n = 30), overlapping uniseriate, oblong or narrowly fusiform, guttulate, 1-distosepta, with a central scarcely constricted septum, straight to slightly curved, smooth-walled, hyaline when young, gray to grayish brown when mature. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from one or both ends. Colonies growing on PDA reached 35–38 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, circular, medium dense, slightly elevated in the center, covered with white aerial mycelium. In reverse, dark brown at the central point, and becoming yellowish brown in the middle, pale yellowish white at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'19"E, 21°55'48"N, elevation 516 m, on dead twigs of *Huangtcia renifolia* (*Fabaceae*), 10 November 2022, H.Z. Du, S627 (HKAS 132448, holotype; HUEST 23.0549, isotype), ex-type living culture UESTCC 25.0040, ex-isotype living culture UESTCC 23.0548.

GenBank accession numbers – UESTCC 25.0040 = ITS: PQ773395, LSU: PQ773415, *rpb2*: PV075241; UESTCC 23.0548 = ITS: PQ773396, LSU: PQ773416, *rpb2*: PV075242.

Notes – *Amphisphaeria davidihuangtciae* (UESTCC 25.0040 and UESTCC 23.0548) clustered together with *A. micheliae* (HKAS 107012 and MFLUCC 20-0121) and *A. sambuci* (CBS 131707 and WU 33558) with a highly support (99% MLBS/1.00 BIPP) forming a distinct lineage (Fig. 61). Morphologically, *A. sambuci* is different from *A. davidihuangtciae* (HKAS 132448, holotype) in having 3–5(–7)-distoseptate ascospores with a thick mucilaginous sheath (Jaklitsch et al. 2016a), and *A. davidihuangtciae* (HKAS 132448, holotype) can be distinguished from *A. micheliae* (HKAS

107012, holotype) by smaller asci ($83\text{--}96 \times 5.7\text{--}7.7 \mu\text{m}$ vs. $92\text{--}135 \times 7\text{--}10.5 \mu\text{m}$) and ascospores ($10\text{--}14 \times 3.8\text{--}5.4 \mu\text{m}$ vs. $15.5\text{--}21 \times 6\text{--}7.5 \mu\text{m}$) (Samarakoon et al. 2020). The nucleotide base pair comparison of ex-type strains between *A. davidihuangtciae* (UESTCC 25.0040) and *A. sambuci* (CBS 131707) revealed 39/527 bp (7.4%, 18 gaps) in ITS and 51/833 bp (6.1%, 2 gaps) in *rpb2* differences, while *A. davidihuangtciae* (UESTCC 25.0040) can be distinguished from *A. micheliae* (MFLUCC 20-0121, ex-type strain) by 28/509 bp (5.5%, 7 gaps) in ITS and 49/889 bp (5.5%, without gaps) in *rpb2* sequence data. Therefore, considering the morpho-molecular evidence, we establish *A. davidihuangtciae* as a new species, and it is associated with *Huangtcia renifolia* in Yunnan Province, China.

Amphisphaeria hydeimucosa H.Z. Du & Jian K. Liu, sp. nov.

Fig. 60

Mycobank number: MB855438; Facesoffungi number: FoF17993

Etymology – The epithet ‘*hydeimucosa*’ is a combination of Prof. Kevin D. Hyde’s last name and the mucilaginous sheath around the ascospores, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132411

Saprobic on dead twigs of *Magnolia officinalis* (*Magnoliaceae*). Visible as faint dark brown dots. Sexual morph: *Ascomata* $453\text{--}563 \mu\text{m}$ diam. $\times 205\text{--}312 \mu\text{m}$ high ($\bar{x} = 510 \times 244 \mu\text{m}$, $n = 20$), immersed, solitary or scattered, conical or subglobose with a flattened base, uniloculate, immersed under a clypeus, with a central ostiole opening, coriaceous, thick-walled, brown to dark brown, micro-papillate. *Ostioles* $82\text{--}120 \mu\text{m}$ diam. $\times 147\text{--}186 \mu\text{m}$ high ($\bar{x} = 103 \times 170 \mu\text{m}$, $n = 10$), central, brown to dark brown, filled with periphyses. *Peridium* $20\text{--}31 \mu\text{m}$ ($\bar{x} = 25 \mu\text{m}$, $n = 20$), comprising several layers of *textura angularis* cells, hyaline to pale pigmented inwardly, becoming brown towards outside and emerging with host tissue. *Paraphyses* $4.5\text{--}6.7 \mu\text{m}$ wide ($\bar{x} = 6 \mu\text{m}$, $n = 20$), hyaline, longer than asci, cellular, constricted septate, guttulate, embedded in a gelatinous matrix, unbranched. *Asci* $86\text{--}153 \times 7\text{--}15 \mu\text{m}$ ($\bar{x} = 121 \times 9.6 \mu\text{m}$, $n = 20$), 8-spored, unitunicate, cylindrical, with a short pedicel, apically rounded, with an amyloid (J+) apical ring in Melzer’s reagent. *Ascospores* $12\text{--}16 \times 5.5\text{--}7.4 \mu\text{m}$ ($\bar{x} = 14 \times 6.5 \mu\text{m}$, $n = 30$), overlapping uniseriate, ellipsoid to fusiform, guttulate, 1-septate, constricted at the septum, smooth-walled, with a clear mucilaginous sheath, hyaline when young, pale brown to yellowish brown when mature. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 48 h, and germ tubes are produced from one end. Colonies growing on PDA reached 15–17 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, circular, medium dense, slightly raised to umbonate or convex, surface rough, radially striated with lobate edge, fairly fluffy to floccose, covered with white aerial mycelium. In reverse, brown to yellowish brown at the center, pale yellowish white at the edge.

Material examined – China, Sichuan Province, Yaan City, Baoxing County, Lingguan Town, $102^{\circ}50'57''\text{E}$, $30^{\circ}15'40''\text{N}$, elevation 915 m, on dead twigs of *Magnolia officinalis* (*Magnoliaceae*), 29 October 2021, H.Z. Du, S446 (HKAS 132411, holotype; HUEST 23.0463, isotype); ex-type living culture CGMCC 3.27285; ex-isotype living culture UESTCC 23.0462.

GenBank accession numbers – CGMCC 3.27285 = ITS: PQ189779, LSU: PQ184734, *rpb2*: PQ379998, *tub2*: PQ432241; UESTCC 23.0462 = ITS: PQ191046, LSU: PQ184721, *rpb2*: PQ379951, *tub2*: PQ432242.

Notes – Multi-locus phylogenetic analyses (Fig. 61) showed that our two isolates of *Amphisphaeria hydeimucosa* (CGMCC 3.27285 and UESTCC 23.0462) grouped with *A. magna* (HKAS 130270 and HKAS 130271), *A. shangrilaensis* (HKAS 130272 and HKAS 130273), and *A. sorbi* (MFLUCC 13-0721), and formed a distinct lineage. This clade can be recognized as a separate species based on molecular evidence. Morphologically, *A. hydeimucosa* (HKAS 132411, holotype) can be distinguished from *A. magna* (HKAS 130270, holotype) in having conidia with a clear mucilaginous sheath (Dissanayake et al. 2024). Additionally, *A. sorbi* differs from *A. hydeimucosa* by the erumpent asci with a J-, apical ring (Senanayake et al. 2015), and *A. hydeimucosa* differs from *A. shangrilaensis* by the guttulate, and smaller ascospores ($12\text{--}16 \times 5.5\text{--}$

7.4 μm vs. 17–22 $\times$ 6–11 μm) (Dissanayake et al. 2024). Therefore, based on the distinct morphology and phylogenetic evidence, we establish *A. hydeimucosa* as a new species, and it is associated with *Magnolia officinalis* in Sichuan Province, China.



Figure 59 – *Amphisphaeria davidihuangticiae* (HKAS 132448, holotype). a Host *Huangticia renifolia*. b, c Appearance of ascomata on host surface. d Vertical section of ascomata. e Ostiole. f Peridium. g Paraphyses. h, i Asci. j–s Ascospores. t Ascus apex stained in Melzer's reagent with an amyloid (J +) apical ring. u Germinated ascospore. v, w Colonies on PDA, above (v) and below (w). Scale bars: d = 100 μm , e, g, h, i = 30 μm , f = 20 μm , j–u = 10 μm .

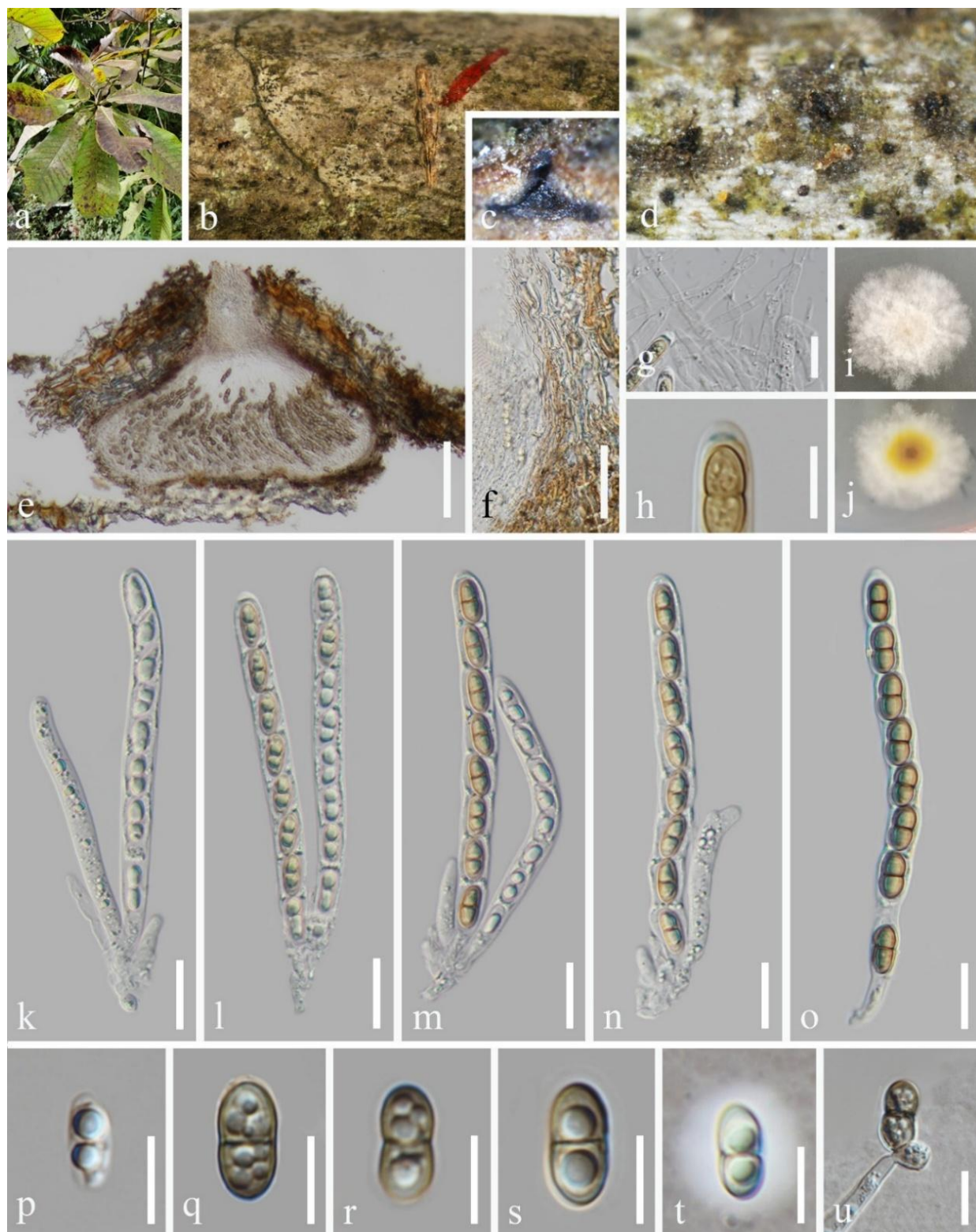


Figure 60 – *Amphisphaeria hydeimucosa* (HKAS 132411, holotype). a Host *Magnolia officinalis*. b–d Appearance of ascomata on host surface. e Vertical section of ascomata. f Peridium. g Paraphyses. h Ascus apex stained in Melzer's reagent with an amyloid (J +) apical ring. i, j Colonies on PDA, above (i) and below (j). k–o Asci. p–s Ascospores. t Ascospore stained with Indian ink showing the mucilaginous sheath. u Germinated ascospore. Scale bars: e = 100 μ m, f = 50 μ m, g, k–o = 20 μ m, h, p–u = 10 μ m.

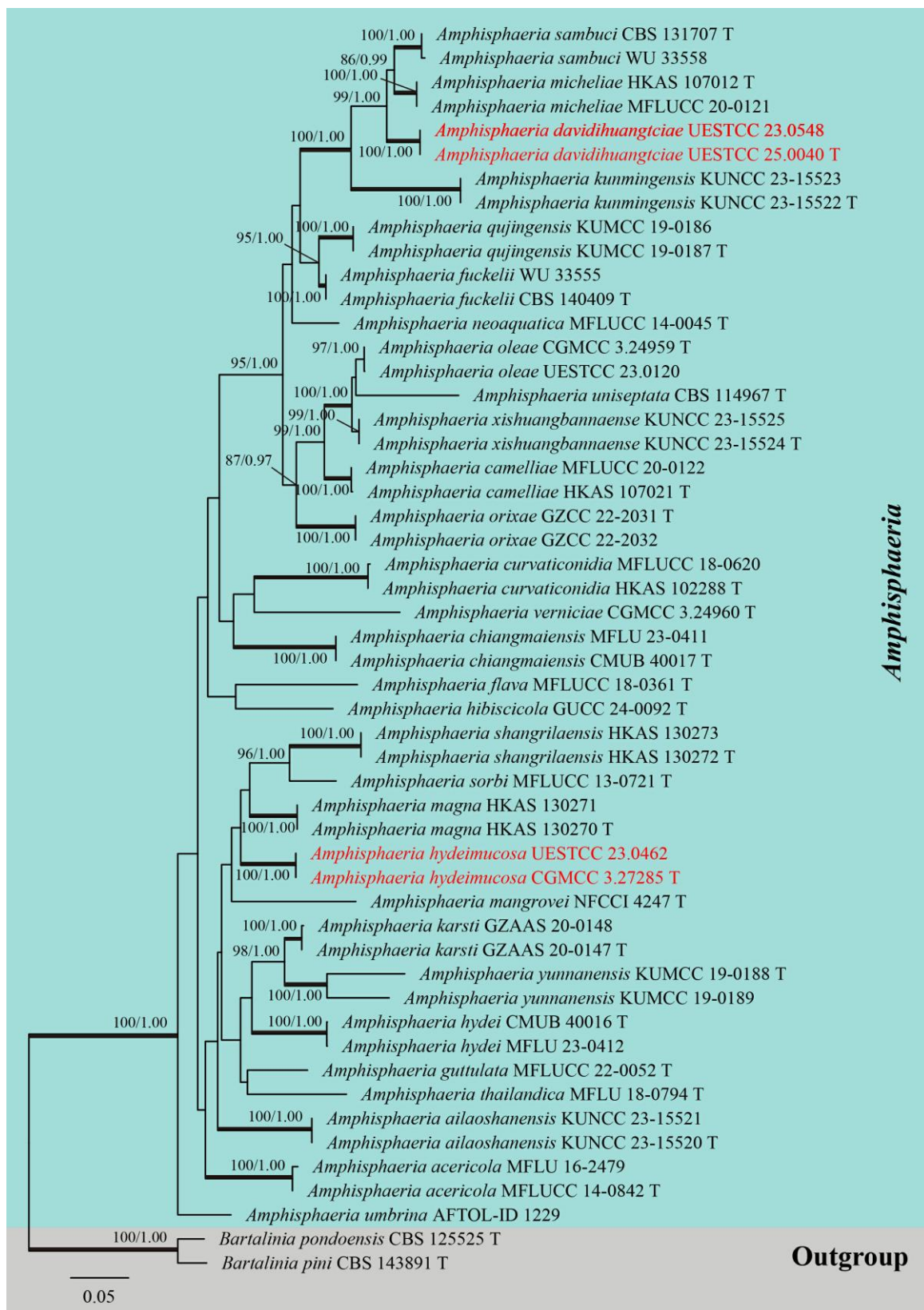


Figure 61 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined ITS, LSU, *rpb2*, and *tub2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Bartalinia pini* (CBS 143891) and *B. pondoensis* (CBS 125525). The best scoring RAXML tree with a final likelihood value of -18,754.750256 is presented. The matrix had

1,324 distinct alignment patterns, with 36.76% of undetermined characters or gaps, the tree-length is 2.582497. Estimated base frequencies were as follows: A = 0.247835, C = 0.238401, G = 0.266873, T = 0.246891, with substitution rates AC = 1.244468, AG = 3.701474, AT = 1.342985, CG = 1.338413, CT = 6.118344, GT = 1.000000; gamma distribution shape parameter alpha = 0.247073. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009987 (the critical value for the topological convergence diagnostic is below 0.01).

Sporocadaceae Corda, *Icones fungorum hucusque cognitorum* 5: 34 (1842)

MycoBank number: MB81408; Facesoffungi number: FoF06111

Notes – *Sporocadaceae* was originally established as ‘*Sporocadeae*’ by Corda (1842) with the type genus of *Sporocadus*. Following the study of Jaklitsch et al. (2016a), the families, *Bartaliniaceae*, *Discosiaceae*, *Pestalotiopsidaceae*, and *Robillardaceae*, were synonymized under the *Sporocadaceae*. And then Liu et al. (2019) confirmed the taxonomic status of *Sporocadaceae* and accepted 30 genera in the family based on morphology and phylogeny. *Sporocadaceae* was formerly in the order *Xylariales*, but later it was placed in the *Amphisphaeriales* (Hongsan et al. 2017, Wijayawardene et al. 2020). *Sporocadaceae* is a well-known fungal family containing pestalotioid fungi which are characterized by having fusiform and multi-septate conidia, with appendages at one or both ends as coelomycetous fungi (Nag Raj 1993, Maharachchikumbura et al. 2014, Liu et al. 2019). Members of *Sporocadaceae* are endophytic, plant pathogenic or saprobic, and associated with a wide range of host plants. Notably, many species within this family are important plant pathogens (Maharachchikumbura et al. 2014, Crous et al. 2015, Liu et al. 2019).

Seiridium Nees, *Syst. Pilze* (Würzburg): 22 (1816) [1816-17]

MycoBank number: MB9868; Facesoffungi number: FoF01696

Notes – *Seiridium* was introduced Nees von Esenbeck (1817) with *S. marginatum* as the type species. Later, this genus was transferred into *Sporocadaceae*, which includes acervular asexual-morphs producing distinctive appendaged conidia (Jaklitsch et al. 2016a). Bonthond et al. (2018) resolved the delimitations of *Seiridium* species, and reconfirmed the position based on morphology and phylogeny. The coelomycetous asexual morph of *Seiridium* differs from other genera in *Sporocadaceae* by having 5-septate conidia with a centric apical and single excentric basal appendage (Bonthond et al. 2018). The sexual morph is characterized by immersed to semi-immersed ascomata, cylindrical, 8-spored asci with J+, apical rings and cylindrical-oblong, euseptate, yellow to dark brown ascospores (Bonthond et al. 2018). Members of *Seiridium* are the most important pathogenic fungi from several economical plant genera, such as *Camellia*, *Cupressus*, *Eucalyptus*, *Juniperus*, and *Rosa* (Graniti 1998, Barnes et al. 2001, Tsopelas et al. 2007, Bonthond et al. 2018, Marin-Felix et al. 2019), which are the main pathogens of cypress canker and cause huge economic losses worldwide (Boesewinkel 1983, Barnes et al. 2001, Tsopelas et al. 2007).

Seiridium kevinibouchinicola H.Z. Du, N. Wu & Jian K. Liu, sp. nov.

Fig. 62

MycoBank number: MB855439; Facesoffungi number: FoF17994

Etymology – The epithet ‘*kevinibouchinicola*’ is a combination of Prof. Kevin D. Hyde’s first name and the host genus ‘*Tibouchina*’ from which the fungus was originally isolated, acknowledging his significant contributions to ascomycetes taxonomy.

Holotype – HKAS 132412

Saprobic on dead twigs of *Tibouchina urvilleana* (DC.) Cogn. (*Melastomataceae*). Visible as black dots. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 428–529 µm diam. × 224–280 µm high ($\bar{x}$ = 485 × 252 µm, n = 20), sporodochial, scattered to gregarious, immersed to erumpent from tissue, unilocular, conical or subglobose with a flattened base, dark brown to black in vertical section, later dehiscing by a split in the overlying tissue, occasionally convoluted, glabrous black. *Conidiomatal wall* 34–40 µm ($\bar{x}$ = 37 µm, n = 30) thick at the sides, not well defined, comprising brown, thin-walled cells of *textura angularis*, with lighter cells at the base fusing into the host tissue. *Conidiophores* are up to 15–22 × 1.5–2.5 µm ($\bar{x}$ = 19 × 2 µm, n = 30),

septate, cylindrical, irregularly branched, occasionally reduced to conidiogenous cells, hyaline or paler brown, thin- and smooth-walled. *Conidiogenous cells* 6–12.5 × 1.5–2.5 µm ($\bar{x}$ = 9 × 2 µm, n = 30), discrete, hyaline, cylindrical to subcylindrical with moderate periclinal thickenings in the collarette zone, smooth- and thin-walled, proliferating percurrently. *Conidia* 10.5–18.5 × 4.5–6.5 µm ($\bar{x}$ = 14 × 5 µm, n = 30) when young, acrogenous, solitary, ellipsoidal to long ellipsoidal, truncate at the base, rounded at the apex, thick-walled, uniseptate or not obvious separation, unsmooth with irregular tiny verrucae, hyaline to olive or slightly olivaceous brown. *Conidia* 20–32 × 7.5–10.5 µm ($\bar{x}$ = 26.5 × 9 µm, n = 30) when mature, lunate to falcate, straight or slightly curved, 5-septate, rarely 2 or 4-septate, basal and apical cell obconical with a truncate base, hyaline to pale brown, smooth-walled; four median cells, unsmooth with irregular tiny verrucae, short cylindrical to doliiform, thick-walled and smooth, septal pores distinctly visible, yellowish-brown to brown or dark brown, basal cell 3.1–5.8 µm wide × 3.5–4.7 µm high ($\bar{x}$ = 4.6 × 4.1 µm, n = 30), conical, hyaline to pale brown, and septa darker than the rest of the cells, second cell from base 5.9–7.6 µm wide × 7.4–7.9 µm high ($\bar{x}$ = 6.4 × 7.6 µm, n = 30), third cell 4.8–6.1 µm wide × 8.2–9.5 µm high ($\bar{x}$ = 5.3 × 9 µm, n = 30), fourth cell 4.5–5.7 µm wide × 8.1–9.7 µm high ($\bar{x}$ = 5 × 9.1 µm, n = 30), fifth cell 5–7 µm wide × 6.5–8.7 µm high ($\bar{x}$ = 5.8 × 7.5 µm, n = 30), apical cell conical, 2.2–3.9 µm wide × 3.8–4.9 µm high ($\bar{x}$ = 2.9 × 4.3 µm, n = 30), hyaline to pale brown, thin-walled, smooth.

Culture characteristics – *Conidia* germinated on PDA within 12 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 50–55 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white in the whole colony, olive grey in the center, flat, surface smooth, medium density in the middle, and sparse edges with white mycelium, filamentous. In reverse, brown or dark brown at the central point, pale yellow in the middle, white at the edge.

Material examined – China, Yunnan Province, Kunming City, Panlong District, Kunming Botanical Garden, 102°44'24"E, 25°8'27"N, elevation 1,922 m, on dead twigs *Tibouchina urvilleana* (DC.) Cogn. (*Melastomataceae*), 11 November 2022, H.Z. Du, S747 (HKAS 132412, holotype; HUEST 23.0465, isotype); ex-type living culture CGMCC 3.27720; ex-isotype living culture UESTCC 23.0464.

GenBank accession numbers – CGMCC 3.27720 = ITS: PQ189780, LSU: PQ184735, *tefl-α*: PQ346518, *rpb2*: PQ379999; UESTCC 23.0464 = ITS: PQ191047, LSU: PQ184722, *tefl-α*: PQ346498, *rpb2*: PQ379952.

Notes – Multi-locus phylogeny showed that *Seiridium kevinibouchinicola* formed a distinct subclade and was sister to *S. aquaticum* and *S. venetum* with a strong statistical support (97% MLBS/1.00 BIPP) (Fig. 63). Nucleotides comparison showed that *S. kevinibouchinicola* (CGMCC 3.27720, ex-type strain) differs from *S. venetum* (MFLU 14-0265, ex-type strain) by 19/469 bp (4.1%) in ITS. Morphologically, *S. kevinibouchinicola* can be distinguished from *S. venetum* by smaller conidiophores (15–22 × 1.5–2.5 µm vs. 60–100 × 1–2.5 µm) and conidiogenous cells (6–12.5 × 1.5–2.5 µm vs. 10–20 × 1–2.5 µm) (Maharachchikumbura et al. 2015), and the conidiophores of *S. aquaticum* are reduced to conidiogenous cells (Luo et al. 2019). Additionally, *S. kevinibouchinicola* differs from *S. aquaticum* in having smaller conidia (20–32 × 7.5–10.5 µm vs. 29–35 × 12–14 µm). Therefore, *S. kevinibouchinicola* associated with *Tibouchina urvilleana*, is introduced as a new species based on morphology and phylogeny in Yunnan Province, China.

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

Mycobank number: MB555640; Facesoffungi number: FoF01754

Notes – Multi-locus phylogenetic analyses based on LSU, SSU, *rpb2*, and *tefl-α* sequence data by Luo et al. (2019) showed that members of genera *Distoseptispora* and *Aquapteridospora* clustered together and formed a distinct clade within *Diaporthomycetidae*, and the order *Distoseptisporales* was established to accommodate *Distoseptisporaceae*. The genus *Aquapteridospora* was initially classified within the *Diaporthomycetidae* as described by Yang et al. (2015) but was considered as *genera incertae sedis*. Currently, *Aquapteridospora* and *Distoseptispora* were accepted within the order *Distoseptisporales*, and were classified under the families *Aquapteridosporaceae* and *Distoseptisporaceae*, respectively (Hyde et al. 2024).

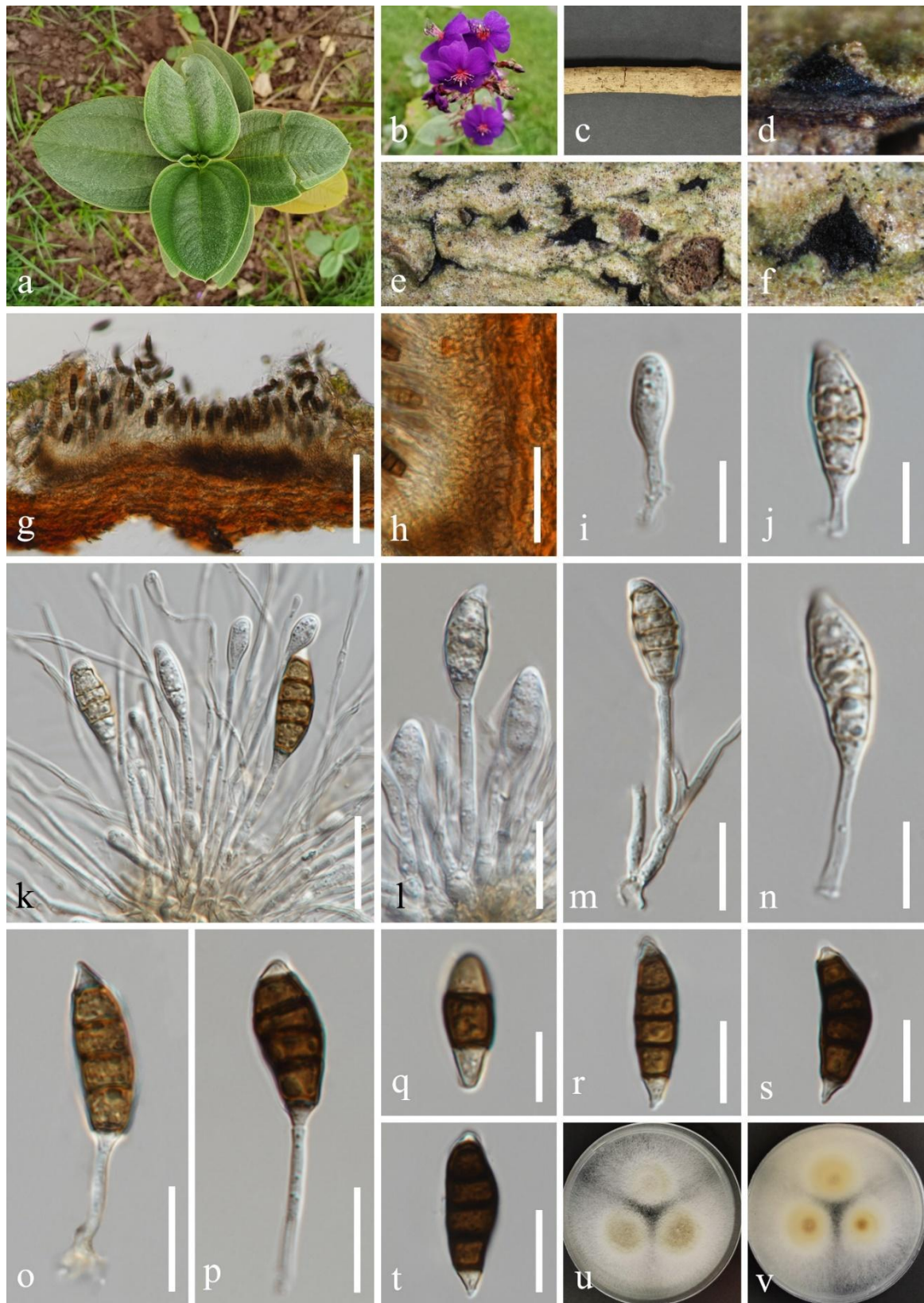


Figure 62 – *Seiridium kevinitibouchinicola* (HKAS 132412, holotype). a Host *Tibouchina urvilleana*. b Flowers of *T. urvilleana*. c A twig of *T. urvilleana*. d–f Appearance of conidiomata on host surface. g Vertical section of conidiomata. h Conidiomatal wall. i, j, l–p Conidiophores, conidiogenous cells and conidia. k Sporodochia. q–t conidia. u, v Colonies on PDA, above (u) and below (v). Scale bars: g = 100 μ m, h = 40 μ m, i, j, n, q = 10 μ m, k = 20 μ m, l, m, o, p, r–t = 15 μ m.

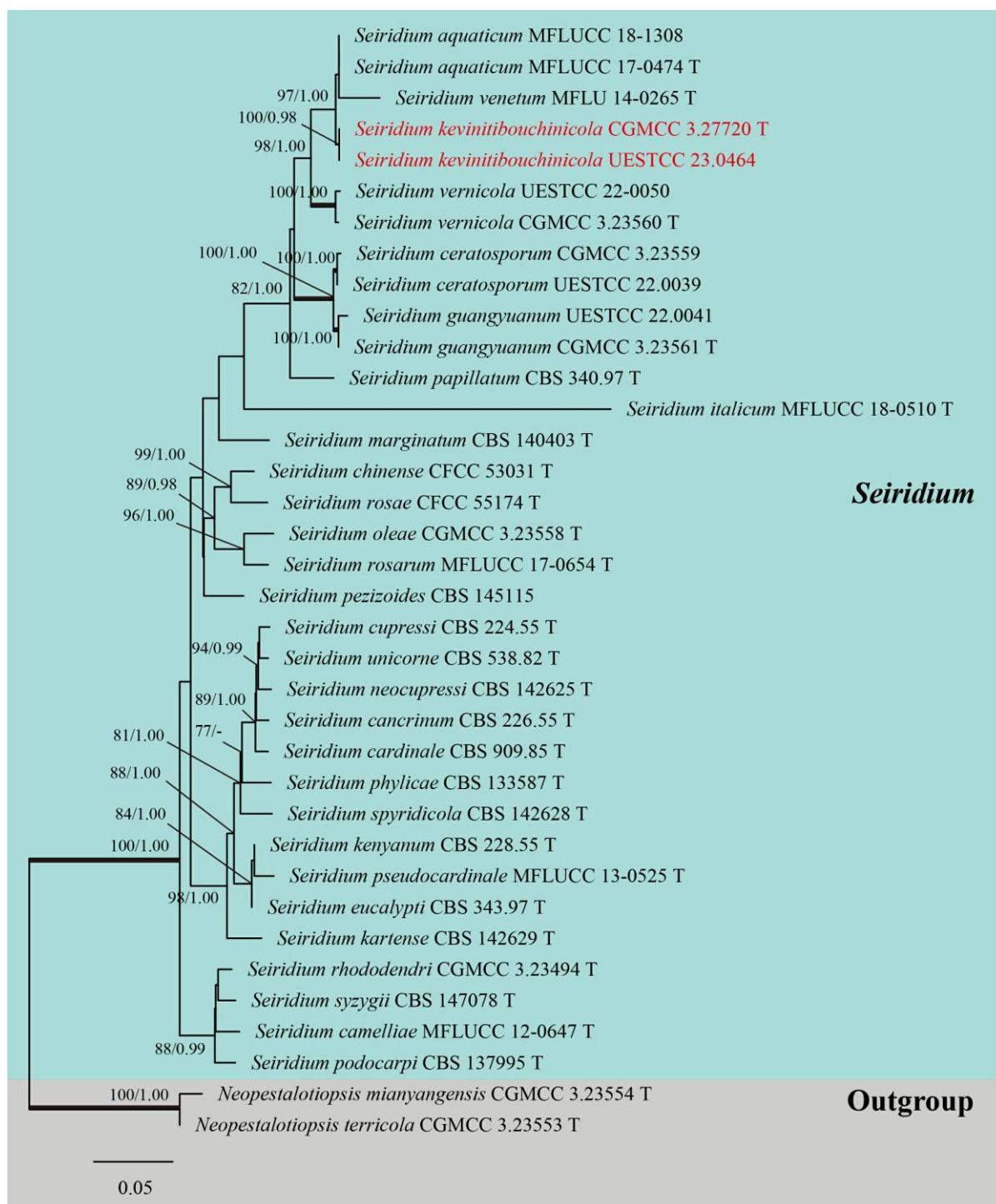


Figure 63 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined LSU, ITS, *rpb2*, and *tef1- α* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below branches as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Neopestalotiopsis mianyangensis* (CGMCC 3.23554) and *N. terricola* (CGMCC 3.23553). The best-scoring RAxML tree with a final likelihood value of -12,574.985739 is presented. The matrix had 878 distinct alignment patterns, with 22.82% of undetermined characters or gaps, the tree-length is 1.056490. Estimated base frequencies were as follows: A = 0.248368, C = 0.248751, G = 0.246338, T = 0.256543, with substitution rates AC = 0.959508, AG = 2.875872, AT = 0.871100, CG = 0.913658, CT = 5.126365, GT = 1.000000; gamma distribution shape parameter alpha = 0.219993. The final average standard deviation of split frequencies at the end of total MCMC

generations for BI analysis was 0.009988 (the critical value for the topological convergence diagnostic is below 0.01).

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

MycoBank number: MB551850; Facesoffungi number: FoF01754

Notes – *Distoseptisporaceae* was established by Su et al. (2016) to accommodate sporidesmium-like taxa based on morphology and phylogeny, and regarded *Distoseptispora* as the type genus. The family *Distoseptisporaceae* is morphologically similar to *Sporidesmiaceae* but can be distinguished by their phylogenetic placements. Additionally, the divergence time estimates revealed the stem age of *Distoseptisporaceae* and *Sporidesmiaceae* were approximately 122 MYA and 186 MYA, respectively (Hongsan et al. 2017).

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

MycoBank number: MB551833; Facesoffungi number: FoF01755

Notes – *Distoseptispora* was introduced by Su et al. (2016) with *D. fluminicola* as the type species. The asexual morph of this genus is mainly characterized by having macronematous, mononematous, septate, unbranched conidiophores, monoblastic, terminal, cylindrical conidiogenous cells, acrogenous, solitary, obclavate or long cylindrical, euseptate or distoseptate conidia (Su et al. 2016, Luo et al. 2019, Yang et al. 2021, Afshari et al. 2023). The sexual morph has solitary or gregarious, immersed to semi-immersed, erumpent ascomata, 8-spored, cylindrical asci with pedicels, overlapping, uniseriate, fusiform, septate ascospores (Yang et al. 2021). Currently, *Distoseptispora* is regarded as a saprobic lignicolous fungal genus and 98 species is listed in the Index Fungorum (accessed on 25 July 2025), each supported by comparable molecular data. Most *Distoseptispora* species have been found in freshwater and terrestrial habitats (Yang et al. 2015, Su et al. 2016, Xia et al. 2017, Crous et al. 2019a, b, Yang et al. 2021, Zhai et al. 2022, Afshari et al. 2023). Except *D. caricis* which is reported as an endophytic fungus (Crous et al. 2019a), others are saprobes.

Distoseptispora aquatica Z.L. Luo, H.Y. Su & K.D. Hyde, Fungal Diversity 80: 404 (2016)

Fig. 64

MycoBank number: MB551834; Facesoffungi number: FoF01757

Saprobic on dead twigs of *Alangium chinense* (*Alangiaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, single or clustered, brown to dark brown, hairy. *Mycelium* mostly immersed, composed of septate, branched, smooth, subhyaline to pale brown hyphae. *Conidiophores* 12–28 μm ($\bar{x}$ = 20 μm , n = 20) long, 8–9.5 μm ($\bar{x}$ = 9 μm , n = 20) wide, macronematous, mononematous, single, erect, short, unbranched, 2–3-septate, cylindrical, straight to slightly flexuous, smooth, thick-walled, tapering distally, robust at the base, dark brown. *Conidiogenous cells* 8–12 μm ($\bar{x}$ = 10 μm , n = 20) long, 7–8 μm ($\bar{x}$ = 7.5 μm , n = 30) wide, monoblastic, integrated, determinate, terminal, cylindrical, smooth, dark brown. *Conidia* (71–)100–239(–327) μm ($\bar{x}$ = 143 μm , n = 30) long, 11–18 μm ($\bar{x}$ = 15 μm , n = 30) wide at the widest part, 5–15 μm ($\bar{x}$ = 9 μm , n = 30) wide at the apex, 4.5–7 μm ($\bar{x}$ = 6 μm , n = 30) wide at the base, acrogenous, solitary, cylindrical, obclavate, elongated, straight or slightly curved, truncate at the base, smooth, 15–28-distoseptate, dark brown with bluish green, paler towards the apex. Conidial secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, circular, dense mycelium, surface smooth, velvety. In reverse, grayish white.

Material examined – China, Guizhou Province, Guiyang City, Wudang District, Xiangsihe scenic spot, 106°37'53"E, 26°26'51"N, elevation 1,125 m, on dead twigs of *Alangium chinense* (*Alangiaceae*), 22 February 2021, H.Z. Du, S116 (HUEST 23.0478), living culture UESTCC 23.0477.



Figure 64 – *Distoseptispora aquatica* (HUEST 23.0478, new host record). a Host *Alangium chinense*. b Flowers of *A. chinense*. c A twig of *A. chinense*. d Colonies on the host surface. e–h Conidiophores with conidia. i Germinated conidium. j–o Conidia. Scale bars: e–g = 100 µm, h–o = 50 µm.

GenBank accession numbers – ITS: PQ191049, LSU: PQ184724.

Notes – *Distoseptispora aquatica* was introduced by Su et al. (2016). In this study, multi-locus

phylogenetic analysis (Fig. 74) showed that our isolate (UESTCC 23.0477) grouped with *Distoseptispora aquatica* (MFLUCC 15-0374, ex-type strain) with a well support (83% MLBS/0.99 BIPP). Morphologically, our collection is identical to *D. aquatica*, and comparison of the nucleotide base pair between UESTCC 23.0477 and MFLUCC 15-0374 showed 99.44% and 100% similarity in ITS and LSU. Therefore, we identify our collection as *D. aquatica*, and reported a new host record associated with *Alangium chinense* in Guizhou Province, China.

Distoseptispora combreticola H.Z. Du & Jian K. Liu, sp. nov.

Fig. 65

Mycobank number: MB855441; Facesoffungi number: FoF17996

Etymology – The epithet ‘*combreticola*’ refers to the host genus ‘*Combretum*’ from which the fungus was originally isolated.

Holotype – HKAS 132460

Saprobic on dead twigs of *Combretum densiflorum* (Wall. ex PlanC. & Miq.) I. M. Turner (*Combretaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, single or clustered, hairy or velvety, brown to dark brown. *Mycelium* mostly immersed, composed of septate, branched, smooth, subhyaline to pale brown hyphae. Conidiophores 13–67 μm ($\bar{x}$ = 33 μm , n = 20) long, 5.5–9 μm ($\bar{x}$ = 7 μm , n = 20) wide, macronematous, mononematous, solitary, erect, unbranched, cylindrical, straight or slightly flexuous, 2–4-septate, smooth, brown to dark-brown, thick-walled, slightly tapering distally, truncate at the apex, robust at the base. Conidiogenous cells 7–13 μm ($\bar{x}$ = 9 μm , n = 20) long, 5–8 μm ($\bar{x}$ = 6 μm , n = 20) wide, holoblastic, monoblastic, integrated, terminal, determinate, cylindrical, smooth, brown to dark brown. Conidia 18–118 μm ($\bar{x}$ = 50.5 μm , n = 30) long, 9.5–17 μm ($\bar{x}$ = 14 μm , n = 30) wide at the broadest part, 4.5–13.5 μm ($\bar{x}$ = 10 μm , n = 30) wide at the apex, 4–6 μm ($\bar{x}$ = 5 μm , n = 30) wide at the truncate base, acrogenous, solitary, obclavate, rostrate 4–10-distoseptate, brown to dark brown or dark olivaceous green, slightly paler towards the apex. Conidial secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, circular, dense mycelium, surface smooth. In reverse, dark grayish green, brown at the center point.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'3"E, 21°55'34"N, elevation 520 m, on dead twigs of *Combretum densiflorum* (*Combretaceae*), 10 November 2022, H.Z. Du, S663 (HKAS 132460, holotype; HUEST 23.0471, isotype); ex-type living culture CGMCC 3.27721; ex-isotype living culture UESTCC 23.0470.

GenBank accession numbers – CGMCC 3.27721 = ITS: PQ189782, LSU: PQ184737; UESTCC 23.0470 = ITS: PQ191050, LSU: PQ184725.

Notes – Phylogenetic analyses (Fig. 74) showed that *Distoseptispora combreticola* (CGMCC 3.27721 and UESTCC 23.0470) formed a distinct lineage and was sister to *D. hainanensis* (GZCC 22-2047) by 75% MLBS/0.96 BIPP support. Morphologically, *D. combreticola* (HKAS 132460, holotype) differs from *D. hainanensis* (GZAAS 22-2047, holotype) by its shorter conidiophores (13–67 μm vs. 70–130 μm). In addition, conidia of *D. hainanensis* are up to 22-distoseptate, brown, verrucose, whereas those of *D. combreticola* are only 4–10-distoseptate, brown to dark brown or dark olivaceous green. Therefore, considering the morpho-molecular data analyses, *D. combreticola* associated with *Combretum densiflorum*, is introduced as a new species in Yunnan Province, China.

Distoseptispora davidalangii H.Z. Du & Jian K. Liu, sp. nov.

Fig. 66

Mycobank number: MB855440; Facesoffungi number: FoF17995

Etymology – The epithet ‘*davidalangii*’ is a combination of Prof. Kevin D. Hyde’s second name, David and the host genus ‘*Alangium*’ from which the fungus was originally isolated, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132478



Figure 65 – *Distoseptispora combreticola* (HKAS 132460, holotype). a Host *Combretum densiflorum*. b Twigs of *C. densiflorum*. c–e Colonies on the host surface. f–i, m, n Conidiophores with conidia. j Germinated conidium, k, l Colony on PDA, above (k) and below (l). o–t Conidia. Scale bars: f–i = 30 μ m, m–n = 50 μ m, j, o–t = 20 μ m.

Saprobic on dead twigs of *Alangium chinense* (Lour.) Harms (*Alangiaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on the substratum superficial, single or clustered, brown to black-brown, hairy. Mycelium mostly immersed, composed of septate, branched,

dark brown hyphae. *Conidiophores* 15–30 μm long ($\bar{x}$ = 22 μm , n = 20), 5–9 μm wide ($\bar{x}$ = 7 μm , n = 20), macronematous, mononematous, solitary, short, unbranched, single or in groups of two or three, 2–5-septate, cylindrical, straight or slightly flexuous, smooth, brown to dark-brown, thick-walled. *Conidiogenous cells* 4.5–7 μm ($\bar{x}$ = 6 μm , n = 20) long, 4–5.5 μm ($\bar{x}$ = 5 μm , n = 20) wide, monoblastic, integrated, terminal, determinate, cylindrical, brown to dark-brown, smooth. *Conidia* 122–367 μm ($\bar{x}$ = 255 μm , n = 30) long, 10–15 μm ($\bar{x}$ = 13 μm , n = 30) at the widest part, 6–8 μm ($\bar{x}$ = 7 μm , n = 30) wide at the apex, 4–5 μm ($\bar{x}$ = 5 μm , n = 30) wide at the base, solitary, cylindrical or obclavate, elongated, straight or curved, truncate at the base, rounded at the apex, (30–)40–55-distoseptate, smooth, brown with a green tinge. Conidial secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 35–37 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, grayish white in the middle, slightly elevated at the center point, dense mycelium, circular, surface smooth, dark black at the edge. In reverse, grayish black at the center, with a radiating black extending outward.

Material examined – China, Guizhou Province, Guiyang City, Wudang District, Xiangsihe scenic spot, 106°54'55"E, 26°46'7"N, elevation 1,125 m, on dead twigs of *Alangium chinense* (*Alangiaceae*), 25 February 2022, H.Z. Du, S137 (HKAS 132478, holotype; HUEST 23.0474, isotype), ex-type living culture UESTCC 24.0236; ex-isotype living culture UESTCC 23.0473.

GenBank accession numbers – UESTCC 24.0236 = ITS: PQ189781, LSU: PQ184736, *tefl- α* : PQ346519, *rpb2*: PQ380000; UESTCC 23.0473 = ITS: PQ191048, LSU: PQ184723, *tefl- α* : PQ346499, *rpb2*: PQ379953.

Notes – Multi-locus phylogenetic analyses showed that *Distoseptispora davidalangii* (UESTCC 24.0236 and UESTCC 23.0473) cluster together with *D. clematidis* (MFLUCC 17-2145, ex-type strain), *D. curvularia* (KUMCC 21-10725, ex-type strain), *D. dipterocarpi* (MFLUCC 22-0104, ex-type strain), *D. keviniligustrina* (UESTCC 23.0471, ex-type strain), and *D. nabanheensis* (HJAUP C2003, ex-type strain), and formed a distinct lineage (Fig. 74). Morphologically, *Distoseptispora davidalangii* differs from *D. clematidis*, *D. keviniligustrina*, and *D. nabanheensis* in having more conidial septa (Table 6). Additionally, *D. davidalangii* can be distinguished from species within its sister clade by nucleotide base pair differences in Table 6. Therefore, based on morphological and phylogenetic evidence, we establish *D. davidalangii* as a new species, which associated with *Alangium chinense* in Guizhou Province, China.

Table 6 Comparison of morphological characteristics (conidiophores and conidia) and base pair differences of ex-type strains between *Distoseptispora davidalangii* (UESTCC 24.0236) and other species within its sister clade.

Species	Conidiophores (μm)	Conidia (μm)	LSU (bp)	ITS (bp)	<i>tefl-α</i> (bp)	<i>rpb2</i> (bp)
<i>D. clematidis</i>	22–40 $\times$ 4–10 μm , 3–5-septate	120–210 $\times$ 12–20 μm , 28–35-distoseptate	5/718 (0.70%)	14/486 (2.9%)	N/A	13/663 (2.0%)
<i>D. curvularia</i>	11–28 $\times$ 5–9 μm	100–200 $\times$ 12–19 μm , 16–48-distoseptate	6/818 (0.73%)	22/536 (4.1%)	6/896 (0.67%)	9/1013 (0.89%)
<i>D. dipterocarpi</i>	14–72 $\times$ 5–7 μm , 1–7-septate	31.5–350 $\times$ 6.5–12 μm , 10–72-distoseptate	4/818 (0.49%)	7/349 (2.0%)	N/A	9/993 (0.90%)
<i>D. keviniligustrina</i>	16.5–27 $\times$ 5–9 μm , 2–5-septate	68–190 $\times$ 10.5–18.5 μm , 10–35-distoseptate	5/722 (0.69%)	22/505 (4.4%)	10/892 (1.1%)	13/1011 (1.3%)
<i>D. nabanheensis</i>	29–42 $\times$ 8–10 μm , 3–8-septate	102–214.5 $\times$ 11–14.5 μm , 18–31-distoseptate	7/556 (1.3%)	17/536 (3.2%)	8/908 (0.88%)	N/A

“N/A” denotes the sequence data is unavailable in GenBank.

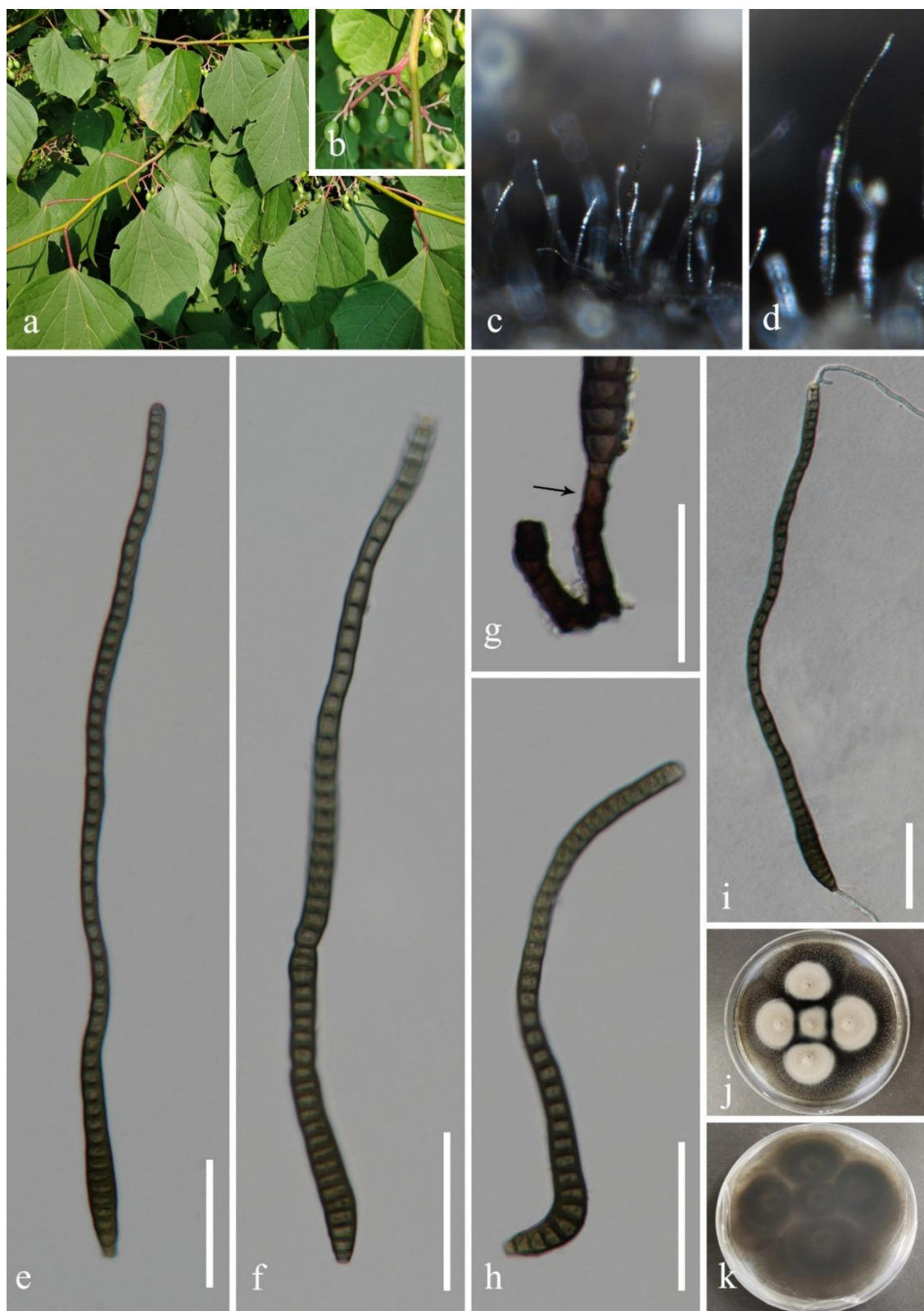


Figure 66 – *Distoseptispora davidalangii* (HKAS 132478, holotype). a Host *Alangium chinense*. b Fruits of *A. chinense*. c, d Colonies on the host surface. e, f, h Conidia. g Conidiophores with conidiogenous cell. i Germinated conidium. j, k Colonies on PDA, above (j) and below (k). Scale bars: e, f, h, i = 50 μ m, g = 40 μ m.

Distoseptispora heptapleuricola H.Z. Du & Jian K. Liu, sp. nov.
 MycoBank number: MB855442; Facesoffungi number: FoF17997

Fig. 67

Etymology – The epithet ‘*heptapleuricola*’ refers to the host genus ‘*Heptapleurum*’ from which the fungus was originally isolated.

Holotype – HKAS 132479

Saprobic on dead twigs of *Heptapleurum heptaphyllum* (L.) Y. F. Deng (*Araliaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on natural substrate effuse, single or clustered, hairy, brown to dark brown. Mycelium mostly immersed, composed of septate, branched, pale brown to brown hyphae. Conidiophores 7–29 μm ($\bar{x}$ = 17 μm , n = 20) long, 6–11 μm ($\bar{x}$ = 7.5 μm , n = 20) wide, macronematous, mononematous, single or in groups of two or three, erect, unbranched, cylindrical, straight or slightly flexuous, 2–3-septate, smooth, brown to dark brown, thick-walled, tapering distally, truncate at the apex, robust at the base. Conidiogenous cells 5.5–12 μm ($\bar{x}$ = 8 μm , n = 20) long, 5–8 μm ($\bar{x}$ = 6 μm , n = 20) wide, monoblastic, integrated, terminal, determinate, cylindrical, smooth, brown to dark brown. Conidia (67–)115–500(–590) μm ($\bar{x}$ = 250 μm , n = 30) long, 10–19 μm ($\bar{x}$ = 13 μm , n = 30) at the widest part, 4–9.5 μm wide ($\bar{x}$ = 7 μm , n = 30) at the apex, 4–6 μm wide ($\bar{x}$ = 5 μm , n = 30) at the base, acrogenous, solitary, cylindrical or obclavate, elongated, straight or flexuous, truncate at the base, tapering towards the rounded apex, 35–60-distoseptate, smooth, dark olivaceous to dark brown, slightly paler towards the apex. Conidial secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 18–20 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, dense mycelium, surface smooth, and grayish or olivaceous green in reverse.

Material examined – China, Guizhou Province, Guiyang City, Wudang District, Xiangsihe scenic spot, 106°37'53"E, 26°26'51"N, elevation 1,125 m, on dead twigs of *Heptapleurum heptaphyllum* (*Araliaceae*). 22 February 2021, H.Z. Du, S141 (HKAS 132479, holotype; HUEST 23.0475, isotype), ex-type living culture CGMCC 3.27740; ex-isotype living culture UESTCC 23.0474.

GenBank accession numbers – CGMCC 3.27740 = ITS: PQ189783, LSU: PQ184738, *tef1- α* : PQ346520, *rpb2*: PQ380001; UESTCC 23.0474 = ITS: PQ191051, LSU: PQ184726, *tef1- α* : PQ346500, *rpb2*: PQ379954.

Notes – Phylogenetic analyses (Fig. 74) showed that our two isolates (CGMCC 3.27740 and UESTCC 23.0474) cluster together with 100% MLBS/1.00 BIPP and formed a distinct lineage. This clade can be recognized as a separate species based on molecular evidence. Morphologically, *Distoseptispora heptapleuricola* (HKAS 132479, holotype) differs from other species of its sister clade in having larger conidia (Table 7). Additionally, the differences of nucleotide base pairs between *D. heptapleuricola* and ex-type strains of *D. guanshanensis*, *D. longispora*, *D. longnanensis*, *D. nanchangensis*, *D. nanpingensis*, *D. terrestris*, and *D. zhejiangensis* are presented in Table 7. Therefore, *D. heptapleuricola*, which is associated with *Heptapleurum heptaphyllum*, is described as a new species in Guizhou Province, China.

Table 7 Comparison of conidia size of holotype and base pair differences of ex-type strains between *Distoseptispora heptapleuricola* and other species within its sister clade.

Species	Conidia size (μm)	LSU (bp)	ITS (bp)	<i>tef1-α</i> (bp)	<i>rpb2</i> (bp)
<i>D. guanshanensis</i>	97–255 $\times$ 12–17	3/818 (0.37%)	5/539 (0.93%)	15/920 (1.6%)	17/886 (1.9%)
<i>D. longispora</i>	189–297 $\times$ 16–23	3/818 (0.37%)	8/538 (1.5%)	N/A	N/A
<i>D. longnanensis</i>	54– 87 $\times$ 8.2–14	4/555 (0.72%)	8/538 (1.5%)	14/918 (1.5%)	N/A
<i>D. nanchangensis</i>	149–293 $\times$ 11–18	2/572 (0.35%)	5/539 (0.93%)	20/925 (2.2%)	17/1059 (1.6%)
<i>D. nanpingensis</i>	169–282 $\times$ 12–17.5	4/575 (0.70%)	9/539 (1.7%)	N/A	19/882 (2.2%)
<i>D. terrestris</i>	54.5–91 $\times$ 11–18	4/572 (0.70%)	11/541 (2.0%)	21/925 (2.3%)	N/A
<i>D. zhejiangensis</i>	128–262 $\times$ 19–27	0/541 (0%)	25/545 (5.3%)	16/906 (1.8%)	N/A

“N/A” denotes the sequence data is unavailable in GenBank.



Figure 67 – *Distoseptispora heptapleuricola* (HKAS 132479, holotype). a Host *Heptapleurum heptaphyllum*. b, c Colonies on the host surface. d, e Colony on PDA, above (e) and below (d). f–i, k, l Conidiophores with conidia. j, m, n Conidia. Scale bars: f–n = 50 µm.

Distoseptispora keviniliguistrina H.Z. Du & Jian K. Liu, sp. nov.

Mycobank number: MB855443; Facesoffungi number: FoF17998

Etymology – The epithet '*keviniliguistrina*' is a combination of Prof. Kevin D. Hyde's first

Fig. 68

name and the host genus '*Ligustrum*' from which the fungus was originally isolated, honoring his contributions to ascomycetes taxonomy.

Holotype – HUEST 23.0472

Saprobic on dead twigs of *Ligustrum quihoui* Carrière (*Oleaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, single or clustered, hairy, brown to dark brown. *Mycelium* mostly immersed, composed of septate, branched, dark brown hyphae. *Conidiophores* 16.5–27 μm ($\bar{x}$ = 21 μm , n = 30) long, 5–9 μm ($\bar{x}$ = 7 μm , n = 30) wide, macronematous, mononematous, single or in groups of two or three, erect, unbranched, cylindrical, straight or slightly flexuous, 2–5-septate, smooth, brown to dark-brown, thick-walled, robust at the base. *Conidiogenous cells* 5–8 μm ($\bar{x}$ = 7 μm , n = 30) long, 4–6 μm ($\bar{x}$ = 5 μm , n = 30) wide, monoblastic, integrated, terminal, determinate, cylindrical, brown to dark brown, smooth. *Conidia* 68–190 μm ($\bar{x}$ = 105 μm , n = 30) long, 10.5–18.5 μm ($\bar{x}$ = 14 μm , n = 30) at the widest part, 5–11 μm ($\bar{x}$ = 8.5 μm , n = 30) wide at the apex, 4–6 μm ($\bar{x}$ = 5 μm , n = 30) wide at the base, solitary, cylindrical or obclavate, elongated, straight or slightly curved, truncate at the base, rounded at the apex, 10–35-distoseptate, smooth, brown with a green tinge. Conidial secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 38–39 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, grayish white, dense mycelium, circular, surface smooth, black at the edge, and grayish black in reverse.

Material examined – China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, 106°41'48"E, 26°32'18"N, elevation 1,127 m, on dead twigs of *Ligustrum quihoui* (*Oleaceae*). 12 October 2021, H.Z. Du, S395 (HKAS 132477 = HUEST 23.0472, holotype), ex-type living culture CGMCC 3.27722 = UESTCC 23.0471.

GenBank accession numbers – ITS: PQ191052, LSU: PQ184727, *tefl- α* : PQ346501, *rpb2*: PQ379955.

Notes – *Distoseptispora keviniligustrina* (CGMCC 3.27722, ex-type strain) has a close phylogenetic relationship with *D. curvularia* (KUMCC 21-10725, ex-type strain) with a well support (78% ML/0.98 BIPP) (Fig. 74). Morphologically, *D. keviniligustrina* is similar to *D. curvularia* in having acrogenous, obclavate, rostrate conidia and being brown with a green tinge. However, *D. keviniligustrina* (HKAS 132477, holotype) differs from *D. curvularia* (HKAS 122180, holotype) in having shorter conidia (68–190 μm vs. up to 314 μm) and fewer conidial septa (10–35 vs. up to 59) (Zhang et al. 2022). Additionally, comparison of the nucleotide base pairs between *D. keviniligustrina* (CGMCC 3.27722) and *D. curvularia* (KUMCC 21-10725) showed significant differences of 19/552 bp (3.4%, 2 gaps) in ITS locus. Therefore, we introduce *D. keviniligustrina* as a new species based on morphology and phylogeny which is isolated from *Ligustrum quihoui* in Guizhou Province, China.

Distoseptispora longispora H.Y. Song & D.M. Hu, Mycotaxon 135 (3): 516 (2020)

Fig. 69

Mycobank number: MB826916; Facesoffungi number: FoF17999

Saprobic on dead twigs of *Combretum densiflorum* (*Combretaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, single or clustered, hairy, brown to dark brown. *Mycelium* mostly immersed, composed of septate, branched, smooth, subhyaline to pale brown hyphae. *Conidiophores* 6–17 μm ($\bar{x}$ = 9 μm , n = 30) long, 6–9 μm ($\bar{x}$ = 7 μm , n = 30) wide, macronematous, mononematous, simple, erect, unbranched, 2–3-septate, cylindrical, straight to slightly flexuous, smooth, thick-walled, brown to dark brown. *Conidiogenous cells* 4–9 μm ($\bar{x}$ = 6 μm , n = 30) long, 5–7 μm ($\bar{x}$ = 6 μm , n = 30) wide, monoblastic, integrated, determinate, terminal, cylindrical, smooth, brown to dark brown. *Conidia* 81–197 μm ($\bar{x}$ = 153 μm , n = 30) long, 10.5–15 μm ($\bar{x}$ = 13 μm , n = 30) wide at the widest part, 4–7 μm ($\bar{x}$ = 5 μm , n = 30) wide at the truncate base, 5–9 μm ($\bar{x}$ = 6 μm , n = 30) wide at the apex, acrogenous, solitary, obclavate, elongated, straight or curved, truncate at the base, rounded at the apex, smooth, 30–55-distoseptate, brown to yellowish brown, slightly paler towards the apex. Conidial secession schizolytic.



Figure 68– *Distoseptispora keviniligustrina* (HKAS 132477, holotype). a Host *Ligustrum quihoui*. b A twig of *L. quihoui*. c, d Colonies on the host surface. e–h Conidiophores with conidia. i Germinated conidium. j, k Colonies on PDA, above (j) and below (k). l Conidiogenous cell. m–r Conidia. Scale bars: e–i, m–r = 50 µm, l = 10 µm.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 25–27 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense mycelium, surface smooth, velvety, grayish green in

the center, with a pale olivaceous outer ring. In reverse, blackish green, dark brown at the center point, and grayish white at the edge.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'3"E, 21°55'34"N, elevation 520 m, on dead twigs of *Combretum densiflorum* (Combretaceae), 10 November 2022, H.Z. Du, S664 (HUEST 23.0477), living culture UESTCC 23.0476.

GenBank accession numbers – ITS: PQ191053, LSU: PQ184728.

Notes – *Distoseptispora longispora* was introduced by Song et al. (2020) and isolated from a submerged wood in China. Phylogenetic analyses showed that our isolate (UESTCC 23.0476) grouped with *D. longispora* (HFJAU 0705, ex-type strain) with a strong support (96% MLBS/1.00 BIPP) (Fig. 74). Morphologically, our collection (HUEST 23.0477) is identical to the holotype of *D. longispora* (HFJAU 0705) (Song et al. 2020). Therefore, we identify our collection as *D. longispora* which is associated with *Combretum densiflorum* in Yunnan Province, China, and this was the first record to be discovered in a terrestrial habitat.

Distoseptispora pachyconidia R. Zhu & H. Zhang, Journal of Fungi 8(10): 22 (2022) Fig. 70

Mycobank number: MB559924; Facesoffungi number: FoF12581

Saprobic on dead twigs of *Sauropus androgynus* auct. non (L.) Merr. (Euphorbiaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on the substratum superficial, single or clustered, hairy or velvety, erect, dark brown or black. Mycelium mostly immersed, composed of septate, branched, smooth, hyaline to pale brown hyphae. Conidiophores 8–29 µm ($\bar{x}$ = 14 µm, n = 30) long, 5.5–8 µm ($\bar{x}$ = 6.5 µm, n = 30) wide, macronematous, mononematous, solitary, unbranched, 2–3-septate, cylindrical, straight or slightly flexuous, smooth, thick-walled, pale brown to brown, slightly tapering distally. Conidiogenous cells 5–8.5 µm ($\bar{x}$ = 7 µm, n = 30) long, 4–6 µm ($\bar{x}$ = 5 µm, n = 30) wide, monoblastic, integrated, determinate, terminal, cylindrical, smooth, pale brown to brown. Conidia 72–245 µm ($\bar{x}$ = 176 µm, n = 30) long, 11–17 µm ($\bar{x}$ = 14 µm, n = 30) at the widest part, 5–8 µm ($\bar{x}$ = 6 µm, n = 30) wide at the apex, 3.5–5 µm ($\bar{x}$ = 4 µm, n = 30) wide at the base, solitary, cylindrical or obclavate, elongated, straight or curved, truncate at the base, rounded at the apex, smooth, 8–31-distoseptate, pale brown with a green tinge. Conidial secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 15–17 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, dense mycelium on the surface, circular, smooth, fluffy. In reverse, dark blackish green, with a grayish white outer ring.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'6"E, 21°55'51"N, elevation 500 m, on dead twigs of *Sauropus androgynus* (Euphorbiaceae). 9 November 2022, H.Z. Du, S593 (HUEST 23.0470), living culture UESTCC 23.0469.

GenBank accession numbers – ITS: PQ191054, LSU: PQ184729.

Notes – *Distoseptispora pachyconidia* was introduced by Zhang et al. (2022) and found on a submerged wood in freshwater habitat from China. Multi-locus phylogeny revealed that our strain (UESTCC 23.0469) clustered together with *D. pachyconidia* (KUMCC 21-10724, ex-type strain) with a strong support (98% MLBS/1.00 BIPP) (Fig. 74). Morphologically, our collection is identical to *D. pachyconidia* (HKAS 122179, holotype) (Zhang et al. 2022). Therefore, we report it as a new host record from *Sauropus androgynus* in China, and this is the first report of *D. pachyconidia* discovered in a terrestrial habitat.

Distoseptispora tectonae Doilom & K.D. Hyde, Fungal Diversity 80: 222 (2016) Fig. 71

Mycobank number: MB552223; Facesoffungi number: FoF01877

Saprobic on dead twigs of *Asparagus cochinchinensis* (Lour.) Merr. (Asparagaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on natural substrate effuse, single or clustered, numerous, hairy, erect, brown to dark brown. Mycelium mostly immersed, composed of septate, branched, smooth, and pale brown to brown hyphae. Conidiophores 40–70 µm ($\bar{x}$ = 49 µm,

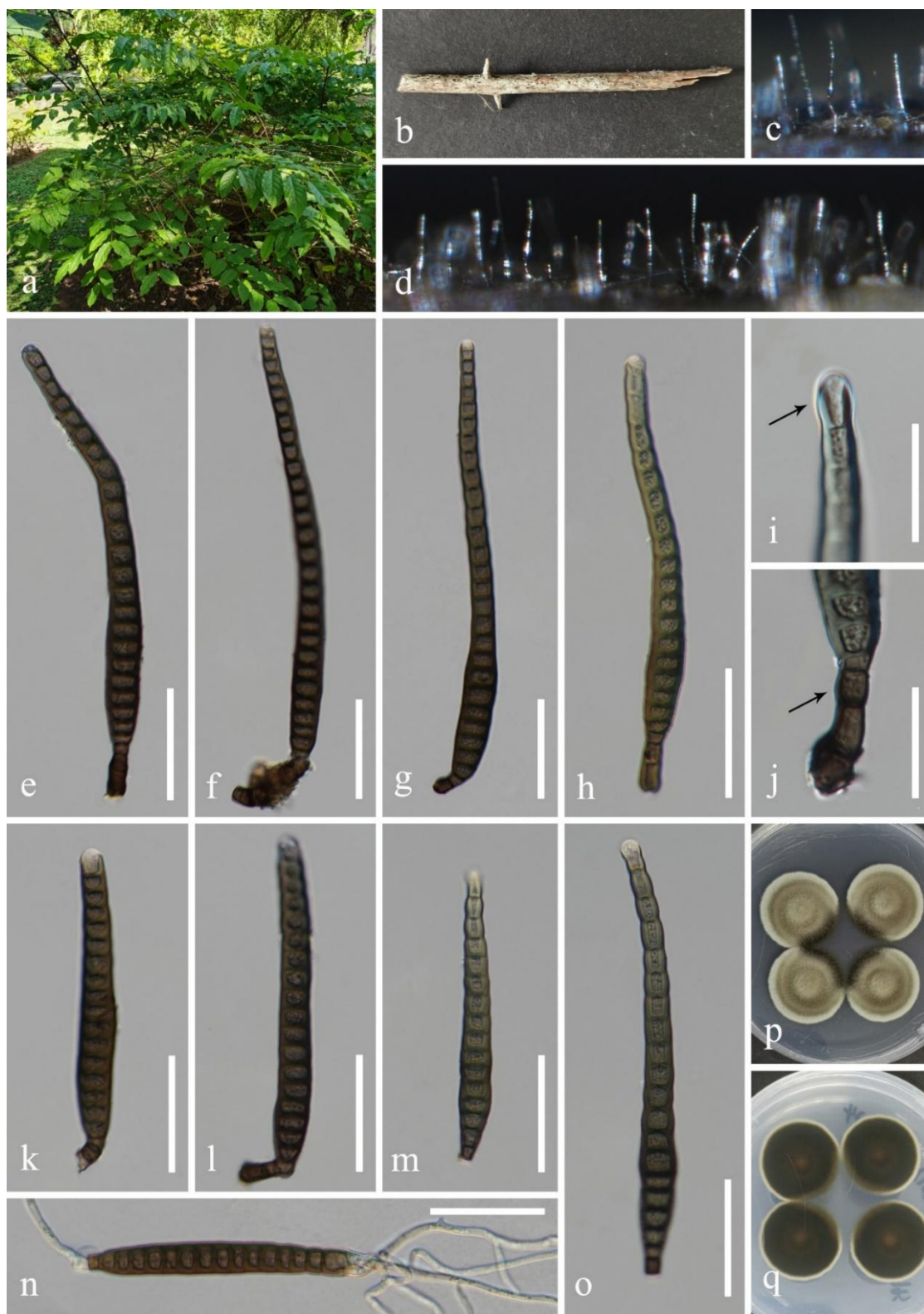


Figure 69 – *Distoseptispora longispora* (HUEST 23.0477, new host record). a Host *Combretum densiflorum*. b A twig of *C. densiflorum*. c, d Colonies on the host surface. e–h, k, l Conidiophores with conidia. i apex of conidium. j Conidiogenous cell. m, o Conidia. n Germinated conidium. p, q Colonies on PDA, above (p) and below (q). Scale bars: e–h = 40 μ m, i, j = 20 μ m, k–o = 40 μ m.



Figure 70 – *Distoseptispora pachyconidia* (HUEST 23.0470, new host record). a Host *Sauropus androgynus*. b A twig of *S. androgynus*. c–e Colonies on the host surface. f–i Conidiophores with conidia. j Germinated conidium. k–l Colony on PDA, above (k) and below (l). m–r Conidia. Scale bars: f–j, m–r = 50 µm.

n = 30) long, 5–9 µm ($\bar{x}$ = 7 µm, n = 30) wide, macronematous, mononematous, erect, unbranched, 3–6-septate, cylindrical, straight to slightly curved, smooth, thick-walled, pale brown to dark brown. *Conidiogenous cells* 7.5–12 µm ($\bar{x}$ = 10 µm, n = 30) long, 4–6 µm ($\bar{x}$ = 5 µm, n = 30) wide,

monoblastic, integrated, determinate, terminal, lageniform or cylindrical, smooth, pale brown to brown. *Conidia* (43–) 90–200 (–280) μm ($\bar{x}$ = 136 μm , n = 30) long, 10–17 μm ($\bar{x}$ = 13 μm , n = 30) at the widest part, 3–5 μm ($\bar{x}$ = 4 μm , n = 30) wide at the truncate base, 5–10 μm ($\bar{x}$ = 7 μm , n = 30) wide at the apex, acrogenous, solitary, cylindric-obclavate, elongated, straight or curved, verruculose, rounded at the apex, smooth, 5–20-distoseptate, brown to dark brown or dark reddish-brown, slightly paler towards the apex. Conidial secession schizolytic.

Culture characteristics – *Conidia* germinated on PDA within 24 h, and germ tubes are produced from one or both ends. Colonies growing on PDA reached 38–40 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense mycelium, surface smooth, velvety, aerial, radiating grayish white outwardly, olivaceous green at the edge, and dark grayish green in reverse, with a grayish point at the center.

Material examined – China, Sichuan Province, Chengdu City, High-tech West District, Yaobo Park, 103°56'22"E, 30°43'55"N, elevation 505 m, on dead twigs of *Asparagus cochinchinensis* (*Asparagaceae*), 8 August 2021, H.Z. Du, S339 (HUEST 23.0469), living culture UESTCC 23.0468.

GenBank accession numbers – ITS: PQ191055, LSU: PQ184730.

Notes – *Distoseptispora tectonae* was introduced by Hyde et al. (2016) and isolated from a dead twig of *Tectona grandis* (*Lamiaceae*) in Thailand. Our collection (HUEST 23.0469) is morphologically similar to the holotype of *D. tectonae* (MFLU 15-3417) (Hyde et al. 2016). Multi-locus phylogeny showed that our strain (UESTCC 23.0468) clustered with *D. tectonae* (MFLUCC 12-0291, ex-type strain) (Fig. 74). Therefore, we identify our collection as *D. tectonae*, and report it as a new host and geographical records from *Asparagus cochinchinensis* in China.

Distoseptispora uncariicola H.Z. Du & Jian K. Liu, sp. nov.

Fig. 72

MycoBank number: MB855444; Facesoffungi number: FoF18000

Etymology – The epithet '*uncariicola*' refers to the host genus '*Uncaria*' from which the fungus was originally isolated.

Holotype – HKAS 132480

Saprobic on dead twigs of *Uncaria rhynchophylla* (Miq.) Miq. ex Havil. (*Rubiaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, scattered, hairy, erect, dark brown to black. *Mycelium* mostly immersed, composed of septate, branched, smooth, pale brown to brown hyphae. *Conidiophores* 73–108 μm ($\bar{x}$ = 95 μm , n = 20) long, 7.5–10 μm ($\bar{x}$ = 8 μm , n = 20) wide, macronematous, mononematous, solitary, erect, unbranched, smooth, septate, cylindrical, straight or slightly flexuous, brown to dark-brown, slightly tapering distally. *Conidiogenous cells* 9–17 μm ($\bar{x}$ = 11 μm , n = 30) long, 4–6.5 μm ($\bar{x}$ = 5 μm , n = 30) wide, monoblastic, integrated, terminal, determinate, cylindrical, smooth, brown to dark brown. *Conidia* (36–)55–155(–192) μm ($\bar{x}$ = 97 μm , n = 30) long, 6–19 μm ($\bar{x}$ = 13 μm , n = 30) wide at the broadest part, 3–9 μm ($\bar{x}$ = 5 μm , n = 30) wide at the apex, 2–5.5 μm ($\bar{x}$ = 4 μm , n = 30) wide at the base, acrogenous, solitary, obclavate, 4–15-distoseptate, subhyaline to olivaceous brown when young, brown to dark brown when mature, slightly paler towards the apex. Conidial secession schizolytic.

Culture characteristics – *Conidia* germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 20–22 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, circular, dense mycelium, surface smooth, velvety, grayish white in the middle, with a pale olivaceous green outer ring, and dark grayish green in reverse.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 101°15'3"E, 21°55'34"N, elevation 520 m, on dead branches of medicinal plant *Uncaria rhynchophylla* (*Rubiaceae*), 10 November 2022, H.Z. Du, S669 (HKAS 132480, holotype; HUEST 23.0476, isotype), ex-type living culture UESTCC 24.0237; ex-isotype living culture UESTCC 23.0475.

GenBank accession numbers – UESTCC 24.0229 = ITS: PQ189784, LSU: PQ184739, *tefl- α* : PQ346521, *rpb2*: PQ380002; UESTCC 23.0420 = ITS: PQ191056, LSU: PQ184731, *tefl- α* : PQ346503, *rpb2*: PQ379957.



Figure 71 – *Distoseptispora tectonae* (HUEST 23.0469, new host and geographical records). a Host *Asparagus cochinchinensis*. b A twig of *A. cochinchinensis*. c–f Colonies on the host surface. g, h Colonies on PDA, above (g) and below (h). i–k Conidiophores with conidia. l Germinated conidium. m Conidiogenous cells. n–r Conidia. Scale bars: i–l = 50 µm, m–r = 30 µm.



Figure 72 – *Distoseptispora uncariicola* (HKAS 132480, holotype). a Host *Uncaria rhynchophylla*. b Twigs of *U. rhynchophylla*. c, d Colonies on the host surface. e–h Conidiophores with conidia. i Conidiophore. j–n Conidia. o Germinated conidium, p, q Colony on PDA, above (p) and below (q). Scale bars: e–i = 50 µm, j–m, o = 20 µm, n = 30 µm.

Notes – Phylogenetic analyses (Fig. 74) showed that our two isolates (UESTCC 24.0237 and UESTCC 23.0475) formed a distinct basal lineage and can be recognized as a distinct phylogenetic

species. Based on BLASTn search, the ITS and *tef1-α* sequence data of *D. uncaricola* (UESTCC 24.0237, ex-type strain) showed 92.27% (513/556 bp, 10 gaps) and 96.05% (875/911 bp, without gaps) similarity with the closest match species of *D. tectonae* in *Distoseptispora* (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>; accessed on 30 April 2025). Therefore, the establishment of the new species *D. uncaricola* is justified by phylogenetic evidence, which is isolated from *Uncaria rhynchophylla* in Yunnan Province, China.

Distoseptispora yichunensis Y.F. Hu & Jian Ma, Microbiology Spectrum 11(6): 13 (2023)
Fig. 73

Mycobank number: MB849135; Facesoffungi number: FoF18001

Saprobic on dead stems of *Clematis florida* Thunb. (*Ranunculaceae*). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, single or clustered, hairy, erect, brown. *Mycelium* mostly immersed, composed of septate, branched, smooth, and pale brown to brown hyphae. *Conidiophores* 16–41 μm ($\bar{x}$ = 27 μm, n = 30) long, 5–7 μm ($\bar{x}$ = 6 μm, n = 30) wide, macronematous, mononematous, solitary, unbranched, 2–3-septate, cylindrical, straight or slightly flexuous, smooth, thick-walled, brown to dark brown. *Conidiogenous cells* 5.5–9.5 μm ($\bar{x}$ = 8 μm, n = 30) long, 4–6.5 μm ($\bar{x}$ = 5.5 μm, n = 30) wide, monoblastic, integrated, determinate, terminal, cylindrical, smooth, pale brown to brown. *Conidia* (53–)90–188(–219) μm ($\bar{x}$ = 137 μm, n = 30) long, 10–14 μm ($\bar{x}$ = 12 μm, n = 30) at the widest part, 4–10 μm ($\bar{x}$ = 6 μm, n = 30) wide at the apex, 3–5 μm ($\bar{x}$ = 4 μm, n = 30) wide at the base, acrogenous, solitary, cylindrical or obclavate, straight or curved, truncate at the base, rounded at the apex, smooth, 14–35-distoseptate, pale brown to brown. Conidial secession schizolytic.

Culture characteristics – Conidia germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 32–35 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, grayish white, dense mycelium, circular, surface smooth, velvety, dark black mycelium at the edge, and grayish black in reverse.

Material examined – China, Guizhou Province, Guiyang City, Wudang District, Xiangzhigou scenic spot, 106°37'53"E, 26°26'51"N, elevation 1,125 m, on dead twigs of *Clematis florida* (*Ranunculaceae*), 22 February 2021, H.Z. Du, S103-3 (HUEST 23.0473), living culture UESTCC 23.0472.

GenBank accession numbers – ITS: PQ191057, LSU: PQ184732.

Notes – *Distoseptispora yichunensis* was introduced by Hu et al. (2023b) and was found on dead branches of an unidentified broadleaf tree. Multi-locus phylogeny revealed that our isolate (UESTCC 23.0472) formed a close relationship with *D. yichunensis* (HJAUP C1065, ex-type strain) with a well support (84% MLBS/0.98 BIPP) (Fig. 74). Our collection (HUEST 23.047) is morphologically similar to the holotype of *D. yichunensis* (HJAUP M1065) (Hu et al. 2023b). Therefore, we identify the new collection as *D. yichunensis* based on morphology and phylogeny, which is reported as a new host record (*Clematis florida*) in Guizhou Province, China.

Magnaporthales Thongk., Vijaykr. & K.D. Hyde, Fungal Diversity 34: 168 (2009)

Mycobank number: MB512852; Facesoffungi number: FoF09682

Notes – *Magnaporthales* was introduced by Thongkantha et al. (2009) to accommodate the family *Magnaporthaceae*. Klaubauf et al. (2014) added other two families *Ophioceraceae* and *Pyriculariaceae* within *Magnaporthales* based on morphological and phylogenetic evidence. Subsequently, *Pseudohalonectriaceae* and *Ceratosphaeriaceae* were included to the order by Hongsanan et al. (2017) and Luo et al. (2019). *Distoseptisporaceae* was previously considered to be classified within *Magnaporthales* (Hyde et al. 2017), but later, this family was transferred to the order *Distoseptisporales* by Luo et al. (2019). Currently, five families and 42 genera, *Ceratosphaeriaceae* (one genus), *Magnaporthaceae* (27 genera), *Ophioceraceae* (two genera), *Pseudohalonectriaceae* (one genus), and *Pyriculariaceae* (11 genera), were recognized within *Magnaporthales* (Hyde et al. 2024). The divergence time of *Magnaporthales* is established at approximately 190 MYA (Hyde et al. 2020b).



Figure 73 – *Distoseptispora yichunensis* (HUEST 23.0473, new host record). a Host *Clematis florida*. b A twig of *C. florida*. c–e Colonies on the host surface. f–i Conidiophores with conidia. j–l Conidia. m, n Colonies on PDA, above (m) and below (n). Scale bars: f–l = 40 µm.

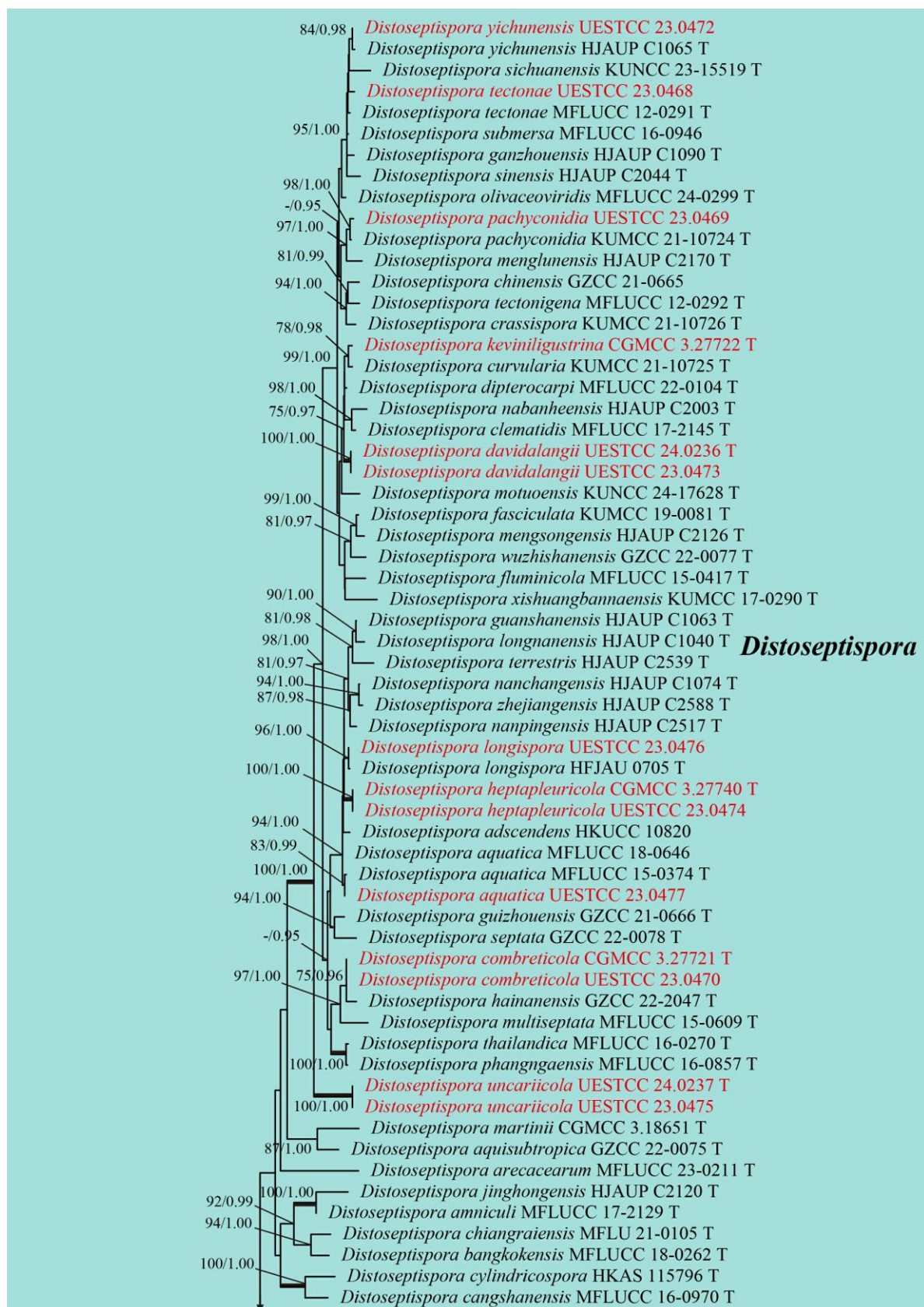


Figure 74 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined LSU, ITS, *tefl-α*, and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below branches as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa.

The tree was rooted with *Aquapteridospora fusiformis* (MFLUCC 18-1606) and *A. lignicola* (MFLUCC 15-037). The best-scoring RAXML tree with a final likelihood value of -38,008.227269 is presented. The matrix had 1,691 distinct alignment patterns, with 27.62% of undetermined characters or gaps, the tree-length is 3.821090. Estimated base frequencies were as follows: A = 0.238502, C = 0.266324, G = 0.280932, T = 0.214242, with substitution rates AC = 1.453508, AG = 3.579516, AT = 1.302158, CG = 0.893791, CT = 6.869341, GT = 1.000000; gamma distribution shape parameter alpha = 0.255355. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009989 (the critical value for the topological convergence diagnostic is below 0.01).

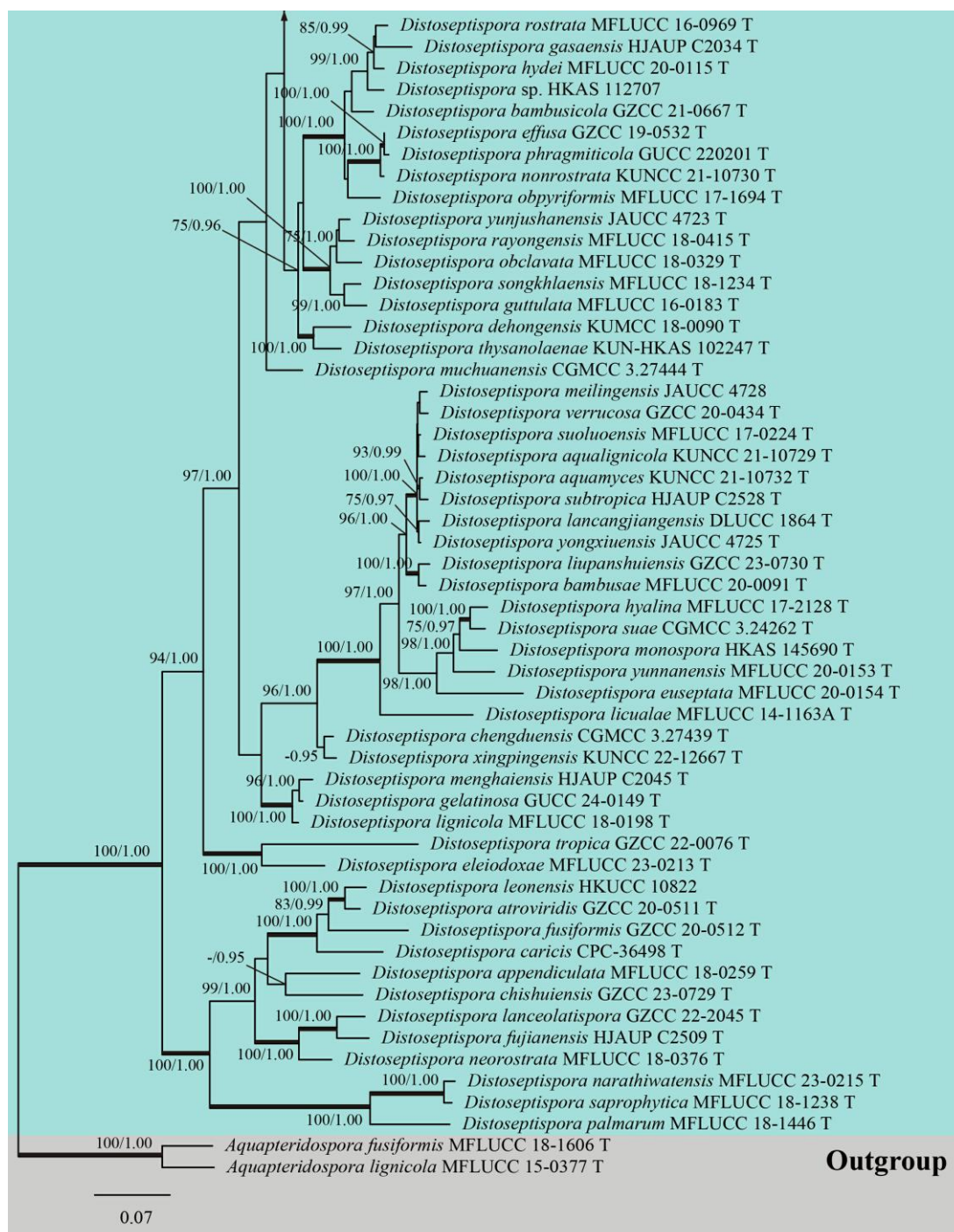


Figure 74 – Continued.

Magnaporthaceae P.F. Cannon, Systema Ascomycetum 13: 26 (1994)

MycoBank number: MB81963; Facesoffungi number: FoF01101

Notes – *Magnaporthaceae* was erected by Cannon (1994) to accommodate the type genus *Magnaporthe*, and also related genera, *Buergenerula*, *Clasterosphaeria*, *Gaeumannomyces*, *Herbampulla*, and *Omnidemtus*. Magnaporthaceous fungi has been continually reported in recent years as endophytes, saprobes, and plant pathogens (Wong 2002, Luo & Zhang 2013, Luo et al. 2015, Hernández-Restrepo et al. 2016, de Silva et al. 2019, Custódio et al. 2020, Vines et al. 2021). Currently, there are 27 genera are accepted in *Magnaporthaceae* based on the latest outline of fungi and fungus-like taxa (Hyde et al. 2024). The sexual morph of *Magnaporthaceae* is characterized by perithecial, globose to subglobose ascomata with long necks, unitunicate, cylindrical asci, filiform or spindle-shaped, morphologically variable ascospores, and the asexual morph exhibits simple conidiophores, phialidic, pigmented conidiogenous cells, and denticulate, hyaline to pale brown conidia that are septate to aseptate, variable in shape (Cannon 1994, Luo et al. 2015, Hernández-Restrepo et al. 2016, da Silva et al. 2019).

***Gaeumannomyces* Arx & D.L. Olivier, Trans. Brit. Mycol. Soc. 35 (1): 32 (1952)**

MycoBank number: MB2026; Facesoffungi number: FoF10238

Notes – von Arx & Olivier (1952) suggested the genus *Gaeumannomyces* with the type species *Gaeumannomyces graminis* (= *Ophiobolus graminis*) based on the morphological characteristics. The sexual morph of *Gaeumannomyces* is characterized by immersed to erumpent, globose to subglobose or pyriform ascomata, unitunicate, cylindrical asci, and hyaline, fusiform, multi-septate ascospores (Hernández-Restrepo et al. 2016). The asexual morph typically features phialidic conidiogenous cells with refractive collarettes and phialophora-like or lunate conidia (Hernández-Restrepo et al. 2016). As a result of these characteristics, the asexual morphs of *Gaeumannomyces* were originally referred to *Phialophora* for a long time. Later, Gams (2000) erected the genus *Harpophora* to accommodate the phialidic asexual morphs, but it was subsequently transferred to *Gaeumannomyces* (Luo et al. 2015). Species of *Gaeumannomyces* are commonly reported as saprobes, root-infecting pathogens, or endophytes (Gams 2000, Bussaban et al. 2001, Wong 2002, Vines et al. 2021).

***Gaeumannomyces hydeicoicis* H.Z. Du, N. Wu & Jian K. Liu, sp. nov.**

Fig. 75

MycoBank number: MB857564; Facesoffungi number: FoF18002

Etymology – The epithet ‘*hydeicoicis*’ is a combination of Prof. Kevin D. Hyde’s last name and the host genus ‘*Coix*’ from which the fungus was originally isolated, honoring his contributions to ascomycetes taxonomy.

Holotype – HKAS 132443

Saprobic on dead twigs of *Coix lacryma-jobi* Linnaeus (*Poaceae*). Visible as black dots. Sexual morph: *Ascomata* 225–346 µm diam. × 100–172 µm high ($\bar{x}$ = 257 × 131 µm, n = 20), perithecial, immersed to slightly erumpent, solitary or scattered, globose, subglobose to elliptical, coriaceous, brown to dark brown. *Ostiole* indistinct. *Peridium* 19.5–27 µm wide ($\bar{x}$ = 23 µm, n = 20), multi-layered, composed of 5–10 layers of *textura angularis* cells, thin-walled, outer layers brown to reddish-brown, becoming pale brown to hyaline at inner layers. *Paraphyses* 8.7–11 µm wide, numerous, hyaline, septate, often constricted at the septa, unbranched, widest at the base and gradually narrow at the apex, dissolving at maturity. *Asci* 90–142 × 15–25 µm ($\bar{x}$ = 127 × 20 µm, n = 20), 8-spored, numerous, unitunicate, cylindrical to clavate, usually curved, obtuse at the apex, shortly stalked, with apical refringent ring. *Ascospores* 92–104 × 3.9–6.2 µm ($\bar{x}$ = 99 × 4.8 µm, n = 30), overlapping, or in parallel, hyaline, filiform, straight to slightly curved, ends rounded, widest in the middle, tapering towards the base, thin-walled, guttulate, 0–5-septate, and septa often indistinct. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h, and germ tubes are produced from both ends. Colonies growing on PDA reached reaching 85 mm diam. after two weeks at 25 °C in the dark, consist of mostly immersed mycelium. Colonies from above, white aerial mycelium, fairly fluffy to floccose, margin effuse, and covered with white to yellowish white aerial

mycelium in reverse.



Figure 75 – *Gaeumannomyces hydeicoicis* (HKAS 132443, holotype). a Host *Coix lacryma-jobi*. b, c Appearance of ascomata on host surface. d Section through ascomata. e Peridium. f Hamathecium. g Apical ring. h–k Asci. l–p Ascospores. q Germinated ascospore. r, s Colonies on PDA, above (r) and below (s). Scale bars: d = 50 μ m, e–g = 10 μ m, h, q = 30 μ m.

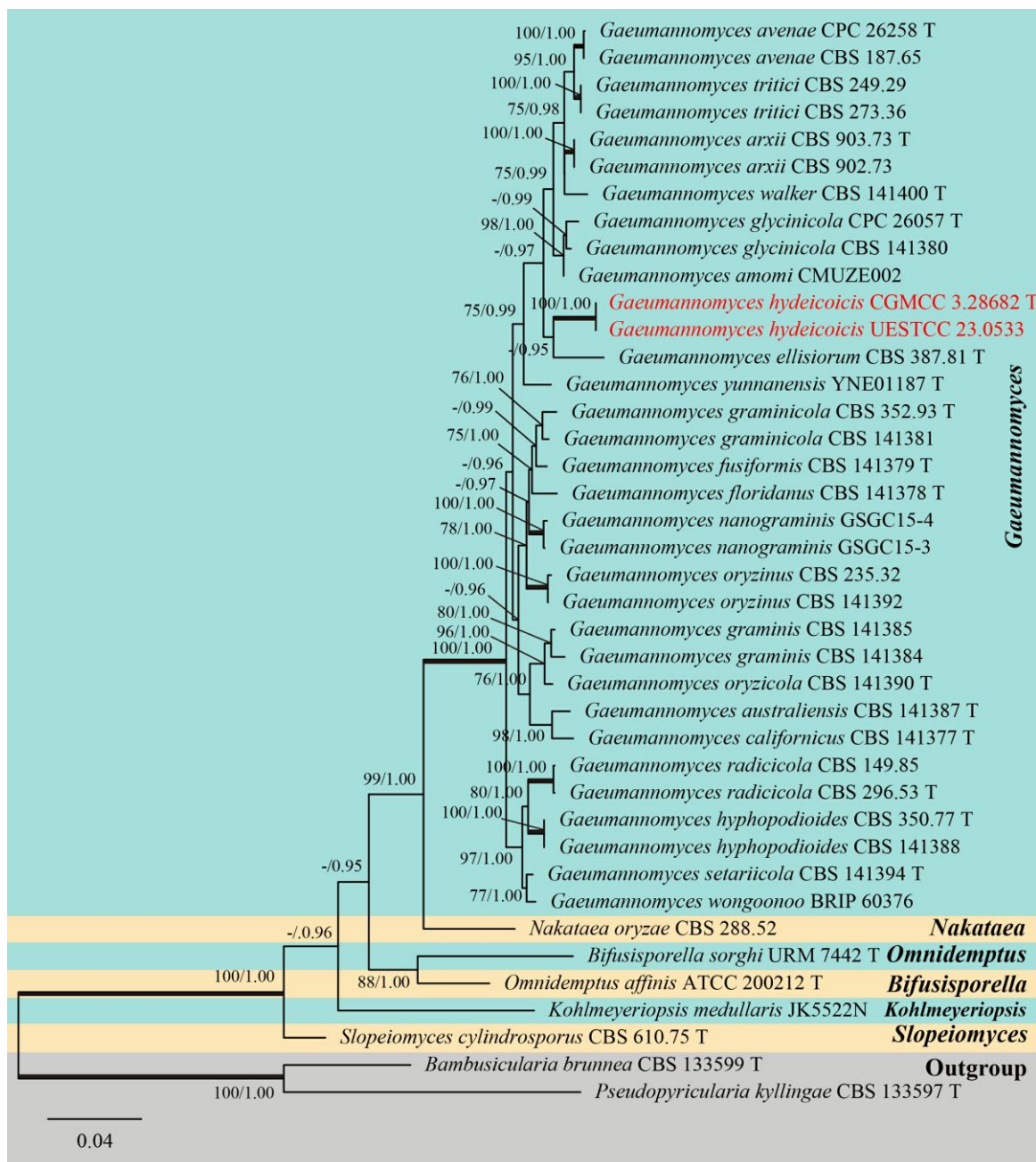


Figure 76 – Phylogenetic tree constructed from the maximum likelihood (RAXML) analyses of combined ITS, LSU, *tefl-α*, and *rpb2* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Bambusicularia brunnea* (CBS 133599) and *Pseudopyricularia kyllingae* (CBS 133597). The best scoring RAXML tree with a final likelihood value of -10,784.204825 is presented. The matrix had 670 distinct alignment patterns, with 11.64% of undetermined characters or gaps, the tree-length is 1.026763. Estimated base frequencies were as follows: A = 0.245740, C = 0.273285, G = 0.284011, T = 0.196964, with substitution rates AC = 1.297833, AG = 3.084804, AT = 2.051578, CG = 1.117451, CT = 8.944996, GT = 1.000000; gamma distribution shape parameter alpha = 0.182934. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009798 (the critical value for the topological convergence diagnostic is below 0.01).

Material examined – China, Guizhou Province, Guiyang City, Nanming District, Guiyang

Medicinal Botanical Garden, 106°41'50"E, 26°32'20"N, elevation 1,129 m, on dead twigs of *Coix lacryma-jobi* (*Poaceae*). 12 October 2021, H.Z. Du, S407 (HKAS 132443, holotype; HUEST 23.0534, isotype), ex-type living culture CGMCC 3.28682, ex-isotype living culture UESTCC 23.0533.

GenBank accession numbers – HKAS 132443 = ITS: PQ773413, LSU: PQ773433; UESTCC 23.0533 = ITS: PQ773414, LSU: PQ773434.

Notes – The multi-locus phylogeny demonstrated that *Gaeumannomyces hydeicoicis* (CGMCC 3.28682 and UESTCC 23.0533) was sister to *G. ellisiorum* (CBS 387.81, ex-type strain) based on ITS, LSU, *tefl-α*, and *rpb2* (Fig. 76). *Gaeumannomyces ellisiorum* was established by Hernández-Restrepo et al. (2016) with asexual morphology on PDA. In contrast, our collections (HKAS 132443 and HUEST 23.0534) in this study exhibit only the sexual morph. Therefore, distinguishing the morphological characteristics between the two species poses a significant challenge. However, *G. hydeicoicis* formed a monophyletic lineage in *Gaeumannomyces*, which can be recognized as a distinct phylogenetic species (Fig. 76). Additionally, comparison of the nucleotide base pairs between the ex-type strains of *G. hydeicoicis* (CGMCC 3.28682) and *G. ellisiorum* (CBS 387.81) revealed the difference of 24/481 bp (5.0%, 1 gap) in ITS sequence data. Therefore, according to the guidelines of Jeewon & Hyde (2016), the new species of *G. hydeicoicis* was introduced based on the phylogenetic evidence.

Ophioceraceae Klaubauf, M.-H. Lebrun & Crous, *Studies in Mycology* 79: 103 (2014)

MycoBank number: MB810201; Facesoffungi number: FoF01254

Notes – *Ophioceraceae* was introduced by Klaubauf et al. (2014) as a monotypic family typified by *Ophioceras*. This family is characterized by perithecial, immersed to superficial, globose to subglobose ascomata with long, periphysate necks, unitunicate, 8-spored, subcylindrical to narrowly fusoid asci with a J-, apical ring, and curved to sigmoidal, filiform, septate, hyaline to olivaceous ascospores without sheaths (Klaubauf et al. 2014, Jiang et al. 2021a, Yang et al. 2023). Species of *Ophioceraceae* are primarily known as saprobes from aquatic or terrestrial habitats (Shearer et al. 1999, Luo et al. 2019, Jiang et al. 2021a, Yang et al. 2023). Additionally, they have been reported as endophytic fungi, isolated from *Poaceae* plants (Feng et al. 2021).

Ophioceras Sacc., *Syll. fung. (Abellini)* 2: 358 (1883)

MycoBank number: MB3595; Facesoffungi number: FoF01255

Notes – *Ophioceras* was established by Saccardo (1883) with *O. dolichostomum* as the type species. Previously, *Ophioceras* was classified in *Magnaporthaceae* following Chen et al. (1999) and Inderbitzin & Berbee (2001). Subsequently, it was transferred to a separate family *Ophioceraceae* based on combined LSU and *rpb1* molecular phylogenetic analyses (Thongkantha et al. 2009, Klaubauf et al. 2014). Later, *Ceratosphaerella* was synonymized under *Ophioceras* by Jiang et al. (2021a) based on morphological and phylogenetic evidence. However, Wijayawardene et al. (2022a) and Hyde et al. (2024) reinstated *Ceratosphaerella* as a separate genus within *Ophioceraceae*. *Ophioceras* is characterized by black, immersed to semi-immersed ascomata with long necks, cylindrical to fusoid asci with small, refractive, apical rings, and hyaline, filiform ascospores (Shearer et al. 1999, Klaubauf et al. 2014, Yang et al. 2023). Species of *Ophioceras* are mostly reported as saprobes in freshwater habitats (Shearer et al. 1999, Thongkantha et al. 2009, Luo et al. 2019, Jiang et al. 2021a, Yang et al. 2023).

Ophioceras hydeanum H.Z. Du, N. Wu & Jian K. Liu, sp. nov.

Fig. 77

MycoBank number: MB857565; Facesoffungi number: FoF18003

Etymology – The epithet ‘*hydeanum*’ named for in honor of Prof. Kevin D. Hyde for his contribution to ascomycetes taxonomy.

Holotype – HKAS 145557

Saprobic on dead twigs of *Citrus medica* Linnaeus (*Rutaceae*). Visible as black dots. Sexual morph: *Ascomata* 264–512 µm diam. × 235–371 µm high ($\bar{x}$ = 340 × 304 µm, n = 20), perithecial,

immersed to slightly erumpent, solitary or scattered, globose to subglobose, or oblate spheroid, carbonaceous, black, ostiolate. *Ostiole* central or eccentric, blackish brown, opening by a pore. *Peridium* 18–23 μm wide ($\bar{x}$ = 21 μm , n = 20), comprising of multi-layered, polyhedral cells of *textura angularis*, outer layers thick-walled, brown to dark brown, becoming pale brown to hyaline

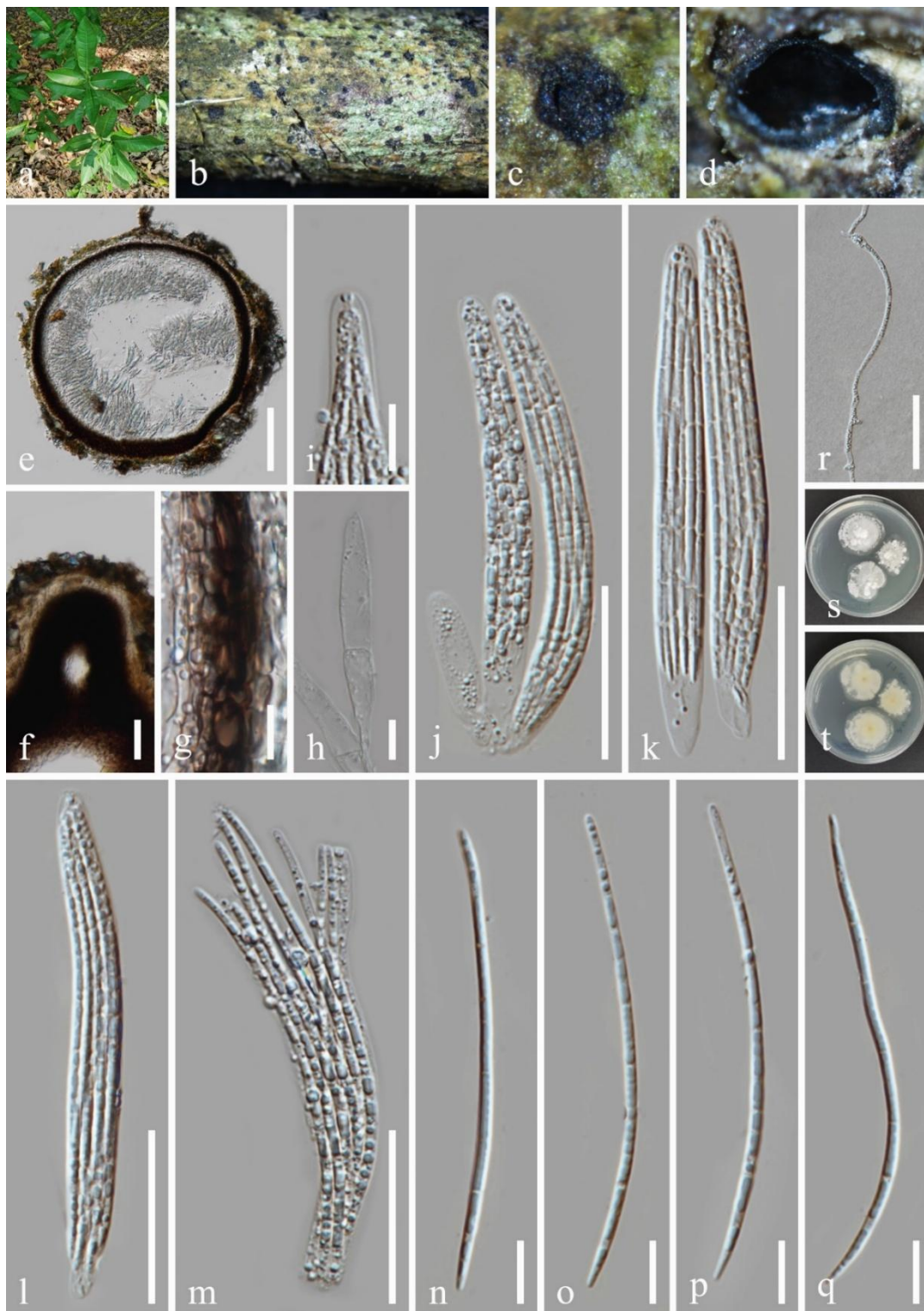


Figure 77 – *Ophioceras hydeanum* (HKAS 145557, holotype). a Host *Citrus medica*. b–d Appearance of ascomata on host surface. e Section through ascomata. f Ostiole. g Peridium. h Hamathecium. i Apical ring. j–m Asci. n–q Ascospores. r Germinated ascospore. s, t Colonies on PDA, above (s) and below (t). Scale bars: e = 100 μm , f, j–m, r = 30 μm , g–i, n–q = 10 μm .

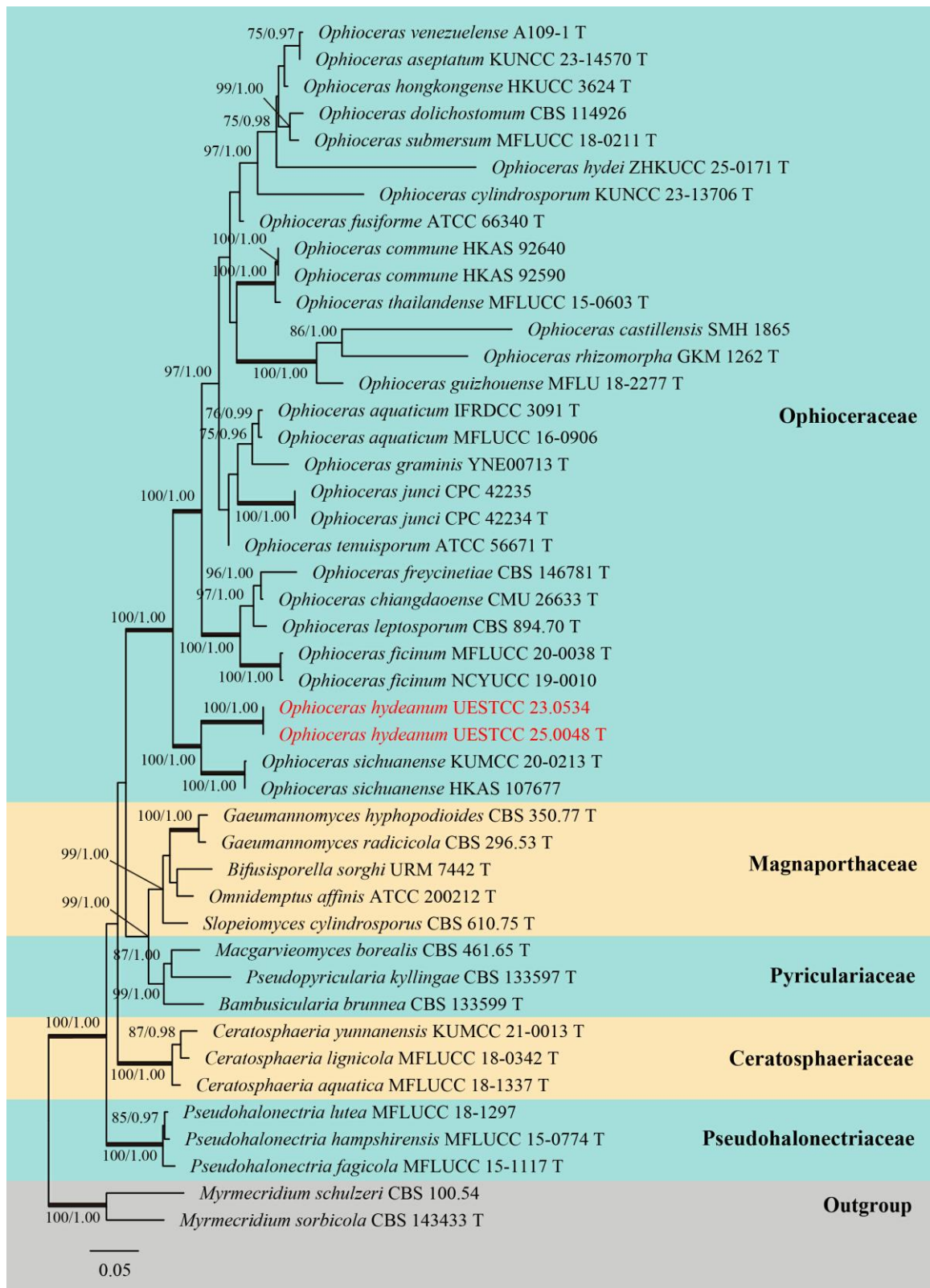


Figure 78 – Phylogenetic tree constructed from the maximum likelihood (RAxML) analyses of combined LSU, ITS, SSU, and *tefl-α* sequence data. Branches support for Maximum likelihood (MLBS) equal to or greater than 75% and Bayesian inference posterior probabilities (BIPP) equal to or greater than 0.95 are marked above or the below nodes as MLBS/BIPP. The abbreviation ‘T’ indicates the ex-type strain. Species names and culture collections in red are newly collected taxa. The tree was rooted with *Myrmecridium schulzeri* (CBS 100.54) and *M. sorbicola* (CBS 143433). The best scoring RAxML tree with a final likelihood value of -19,454.573706 is presented. The matrix had 1,103 distinct alignment patterns, with 39.49% of undetermined characters or gaps, the

tree-length is 2.290487. Estimated base frequencies were as follows: A = 0.238841, C = 0.262779, G = 0.283634, T = 0.214745, with substitution rates AC = 0.936823, AG = 1.609004, AT = 1.443333, CG = 1.157018, CT = 5.494983, GT = 1.000000; gamma distribution shape parameter alpha = 0.261027. The final average standard deviation of split frequencies at the end of total MCMC generations for BI analysis was 0.009896 (the critical value for the topological convergence diagnostic is below 0.01).

at inner layers, thin-walled. Paraphyses 7–9.5 μm wide, numerous, hyaline, septate, slightly constricted at the septa, unbranched, persistent, tapering towards the apex, swollen at the base. *Asci* 80–92 $\times$ 6.7–9.5 μm ($\bar{x}$ = 86.5 $\times$ 7.5 μm , n = 20), 8-spored, unitunicate, cylindrical to fusiform, usually curved, obtuse at the apex, sessile to subsessile, with a J-, non-amyloid apical ring. *Ascospores* 70–87 $\times$ 1.8–2.5 μm ($\bar{x}$ = 80 $\times$ 2.2 μm , n = 30), overlapping, or in parallel, hyaline, filiform, straight to slightly curved, multi-septate, smooth-walled, guttulate, thin-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 48 h, and germ tubes are produced from both ends. Colonies growing on PDA reached 35–37 mm in diam. after three weeks at 25 °C in the dark. Colonies from above, white, circular, medium dense, slightly raised, surface rough, radially striated with lobate edge, fairly fluffy to floccose, covered with white aerial mycelium, pale yellowish white in reverse.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Xishuangbanna Tropical Botanical Garden Chinese Academy of Sciences, 21°56'1"N, 101°25'33"E, elevation 505 m, on dead twigs of *Citrus medica* (Rutaceae), 10 November 2022, H.Z. Du, S654 (HKAS 145557, holotype; HUEST 23.0535, isotype); ex-type living culture UESTCC 25.0048, ex-isotype living culture UESTCC 23.0534.

GenBank accession numbers – UESTCC 25.0048 = ITS: PQ773411, LSU: PQ773431, *tefl- α* : PV059191, *rpb2*: PV075253; UESTCC 23.0534 = ITS: PQ773412, LSU: PQ773432, *tefl- α* : PV059192, *rpb2*: PV075254.

Notes – Multi-locus phylogeny (Fig. 78) showed that *Ophioceras hydeanum* (UESTCC 25.0048 and UESTCC 23.0534) formed a distinct clade and was sister to *O. sichuanense* with the statistical support (100% MLBS/1.00 BIPP). Morphologically, *O. sichuanense* (KUN-HKAS 107677, holotype) can be distinguished from *O. hydeanum* (HKAS 145557, holotype) by its ascomata with long black ostiolar necks, which are absent in *O. hydeanum* (Jiang et al. 2021a). Additionally, *O. sichuanense* differs from *O. hydeanum* by its shorter and wider asci (80–92 $\times$ 6.7–9.5 μm vs. 90–115 $\times$ 5–6.5 μm), and its narrower ascospores (1–1.5 μm vs. 1.8–2.5 μm in width) (Jiang et al. 2021a). Comparison of the nucleotide base pairs between *O. hydeanum* (UESTCC 25.0048) and *O. sichuanense* (KUMCC 20-0213) revealed differences of ex-type strains, ITS = 82/514 bp (16.0%, 31 gaps), LSU = 15/505 bp (3.0%, without gaps), and *tefl- α* = 95/954 bp (10.0%, without gaps). Therefore, *O. hydeanum*, associated with *Citrus medica*, introduced as a new species based on morphological and phylogenetic evidence.

Fungal distribution isolated from medicinal plants in Southwestern China

During our investigation of microfungi from medicinal plants in Southwestern China (Yunnan, Guizhou and Sichuan Provinces), we isolated 625 isolates following the method of Senanayake et al. (2020). Among these, 232 isolates were collected from Yunnan Province, 214 from Guizhou Province, and 179 from Sichuan Province. These included 223 ascomycetous isolates (35.68%), 211 hyphomycetous isolates (33.76%), and 191 coelomycetous isolates (30.56%) (Fig. 79).

The classification status of these isolates at the class, order, family, and genus levels was confirmed based on ITS sequence data. The results showed that our isolates distributed in 8 classes, 39 orders, 94 families and 180 genera. At the class level, the majority of isolates classified into *Dothideomycetes* (390 isolates, 62.40%), followed by *Sordariomycetes* (211 isolates, 33.76%). Other classes included *Eurotiomycetes* (10 isolates, 1.60%), *Leotiomycetes* (9 isolates, 1.44%), and smaller proportions in *Lecanoromycetes*, *Mucoromycetes*, *Orbiliomycetes*, and *Pichiomyces* (each $\leq$ 0.32%)

(Fig. 80).

In *Dothideomycetes*, the isolates distributed in 16 orders, 50 families, and 109 genera, while in *Sordariomycetes*, these isolates distributed in 16 orders, 31 families, and 58 genera. In *Eurotiomycetes*: two orders, four families, and four genera; in *Leotiomyces*: one order, five families, and five genera were obtained. Additionally, one order, one family and one genus were distributed in *Pichiomyces*, *Orbiliomyces*, *Lecanoromyces* and *Mucoromyces*, respectively (Fig. 81 to Fig. 84).

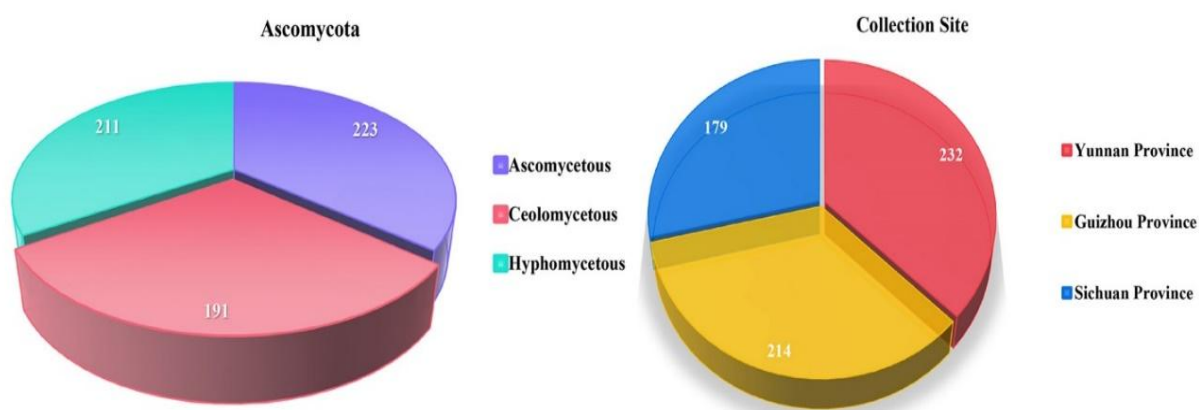


Figure 79 – The distribution of medicinal plants-associated micro-fungi in Southwestern China.

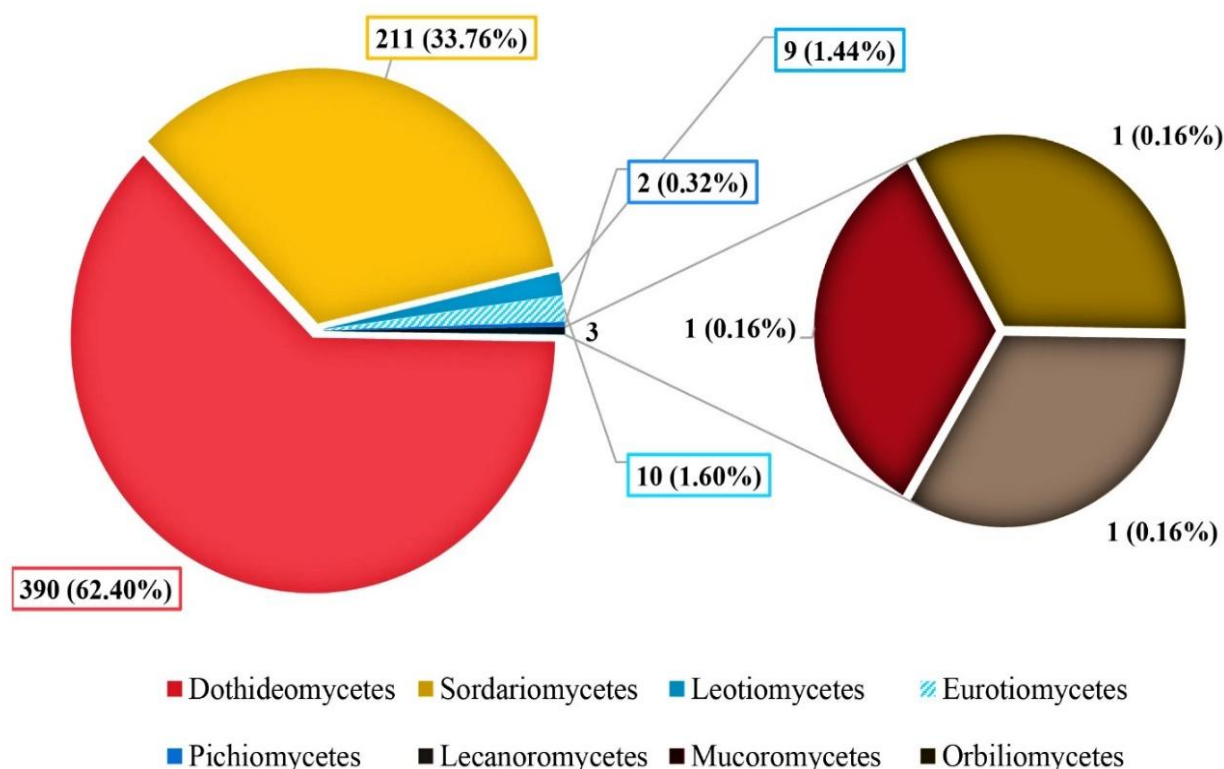


Figure 80 – The classification of microfungi on medicinal plants at class level.

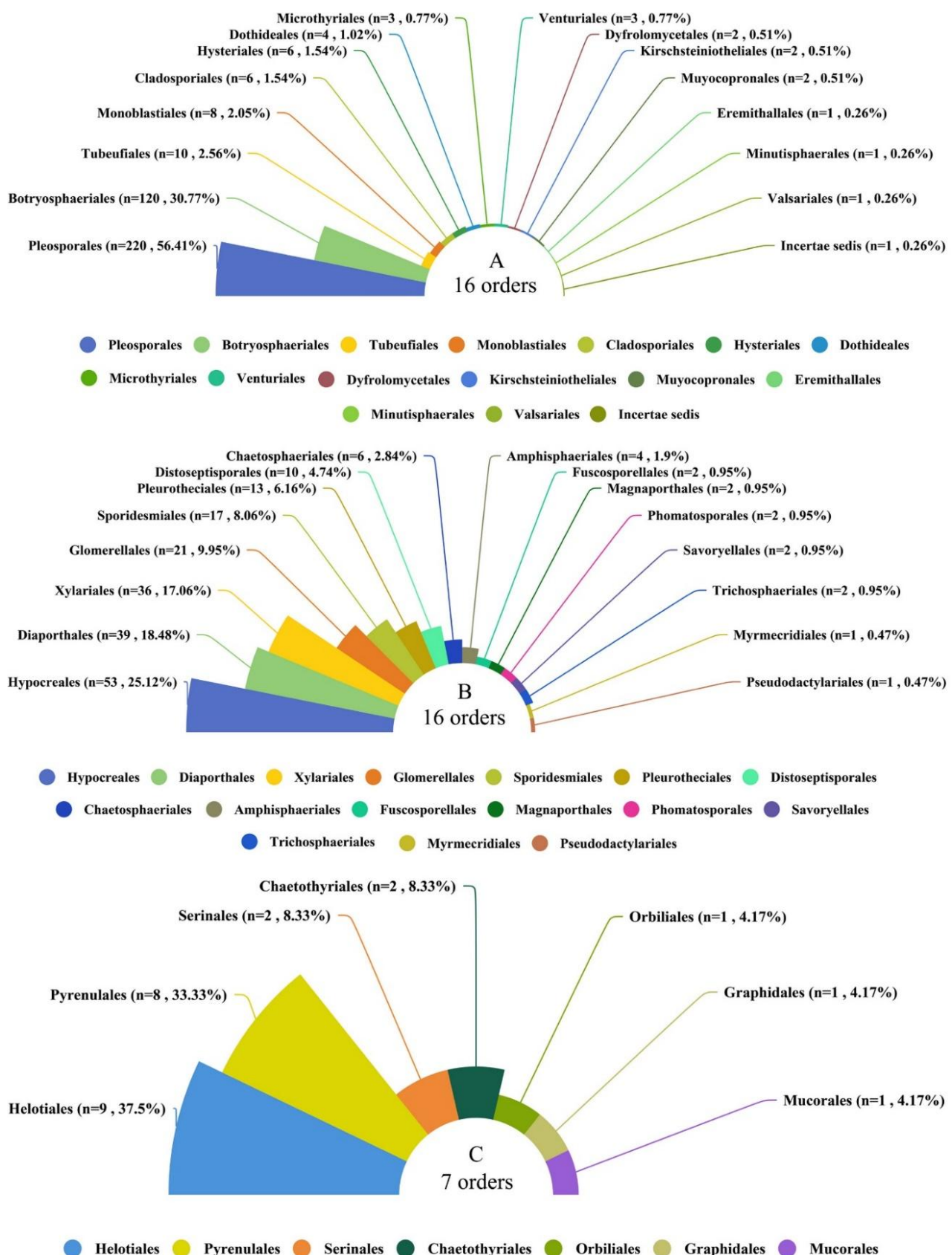


Figure 81 – The classification of microfungi on medicinal plants at order level. A *Dothideomycetes*. B *Sordariomycetes*. C *Eurotiomycetes*, *Leotiomyces*, *Pichiomyces*, *Orbiliomyces*, *Lecanoromycetes*, and *Mucoromycetes*.

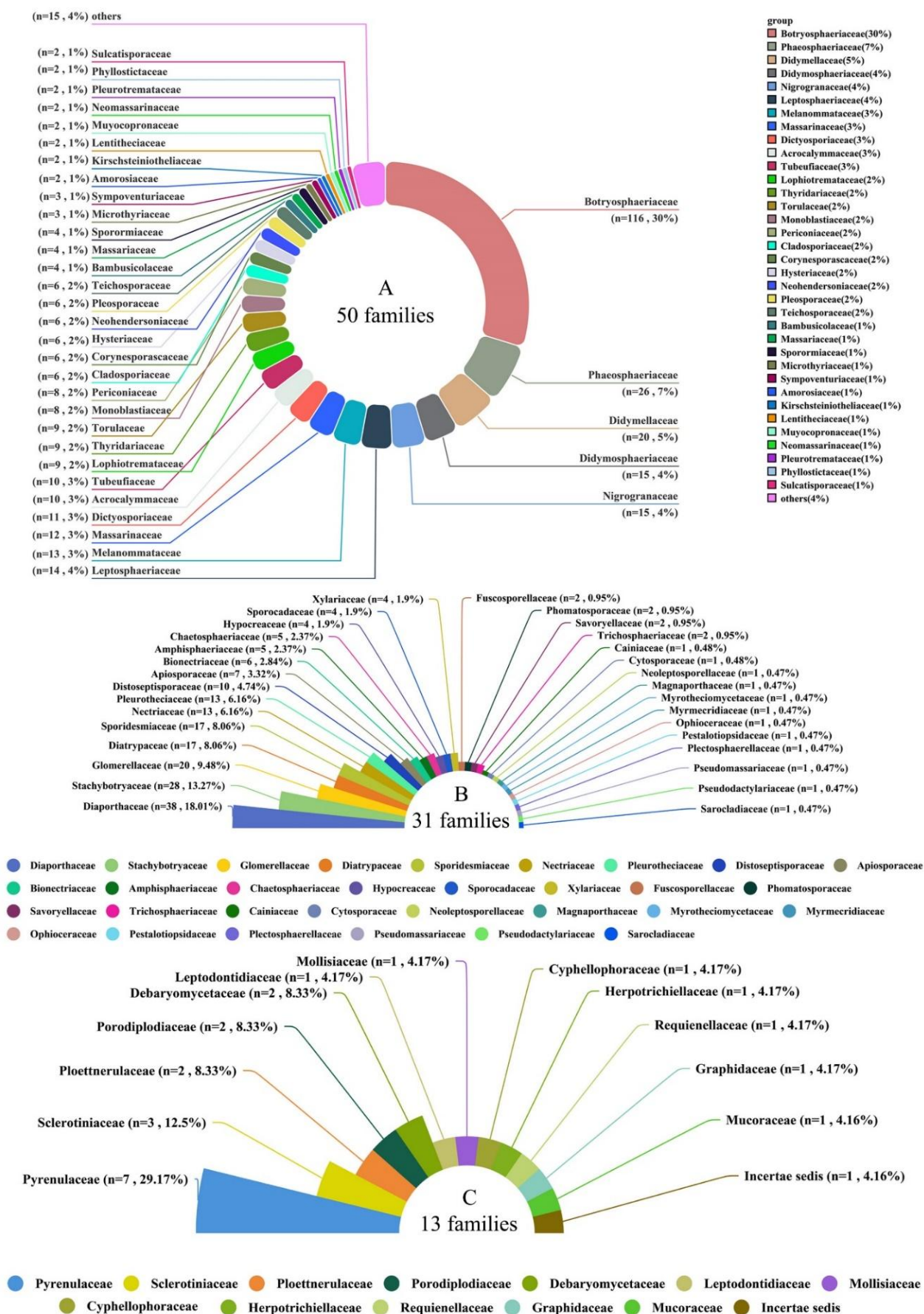


Figure 82 – The classification of microfungi on medicinal plants at the family level. A *Dothideomycetes*. B *Sordariomycetes*. C *Eurotiomycetes*, *Leotiomyces*, *Pichiomyces*, *Orbiliomyces*, *Lecanoromyces*, and *Mucoromycetes*.

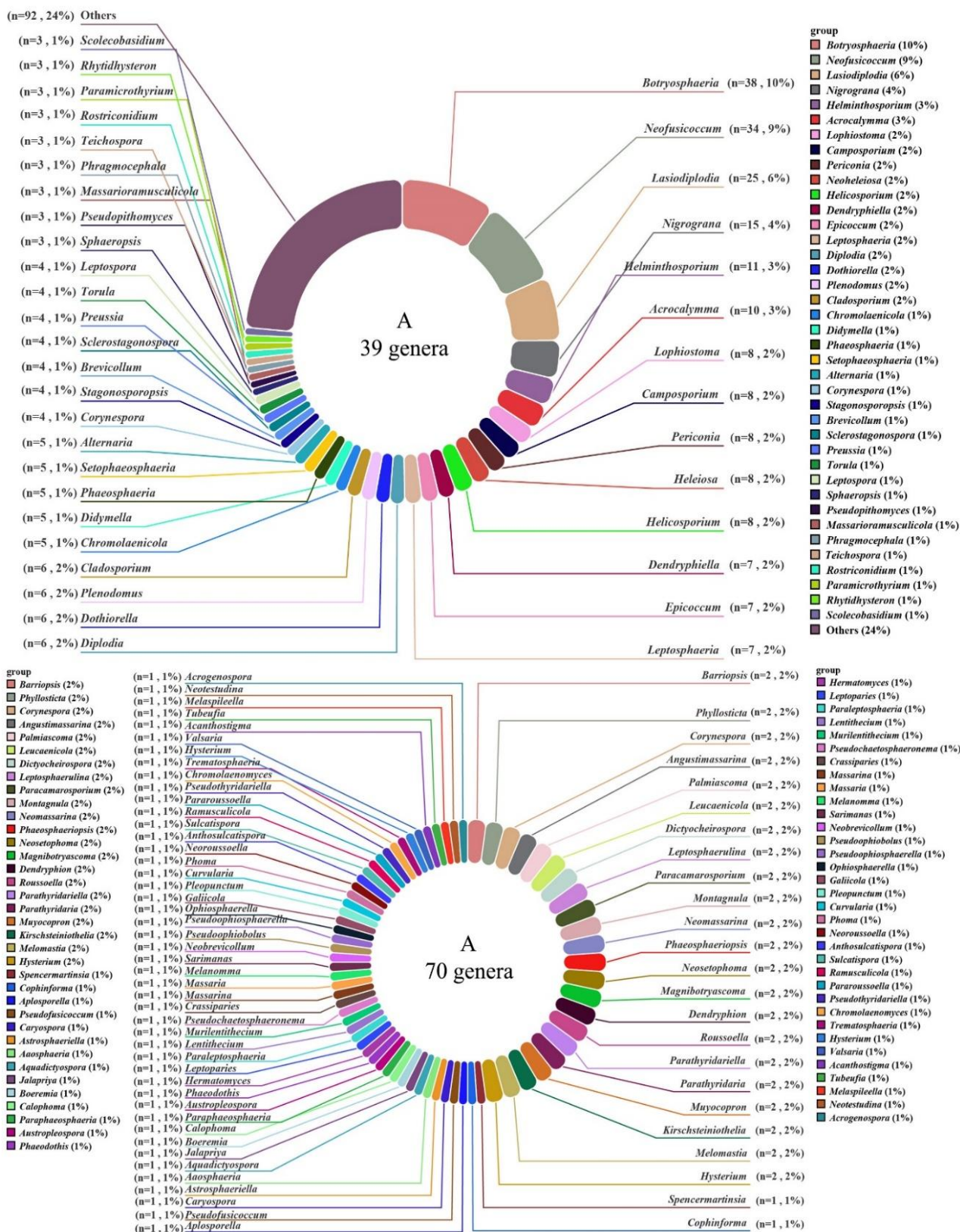


Figure 83 – The classification of microfungi on medicinal plants at genus level. A. *Dothideomycetes*.

Host distribution at the family level of medicinal plants in Southwestern China

During our investigation of fungi on medicinal plants in Southwestern China, fungi were isolated from medicinal plants which belong to 85 families, and undetermined classification status of host as *Incertae sedis*, during 2020 to 2023, viz., (1) Guizhou Province (106°39'32" – 106°41'48"E,

26°30'43" – 26°32'18"N, elevation 1000 – 1,255 m); (2) Sichuan Province (103°2'23" – 104°14'19"E, 29°29'1" – 31°8'4"N, elevation 504 – 1,200 m); (3) Yunnan Province (101°23'19" – 102°74'12"E, 21°93'15" – 25°14'27"N, elevation 505 – 1,922 m) (Fig. 85).

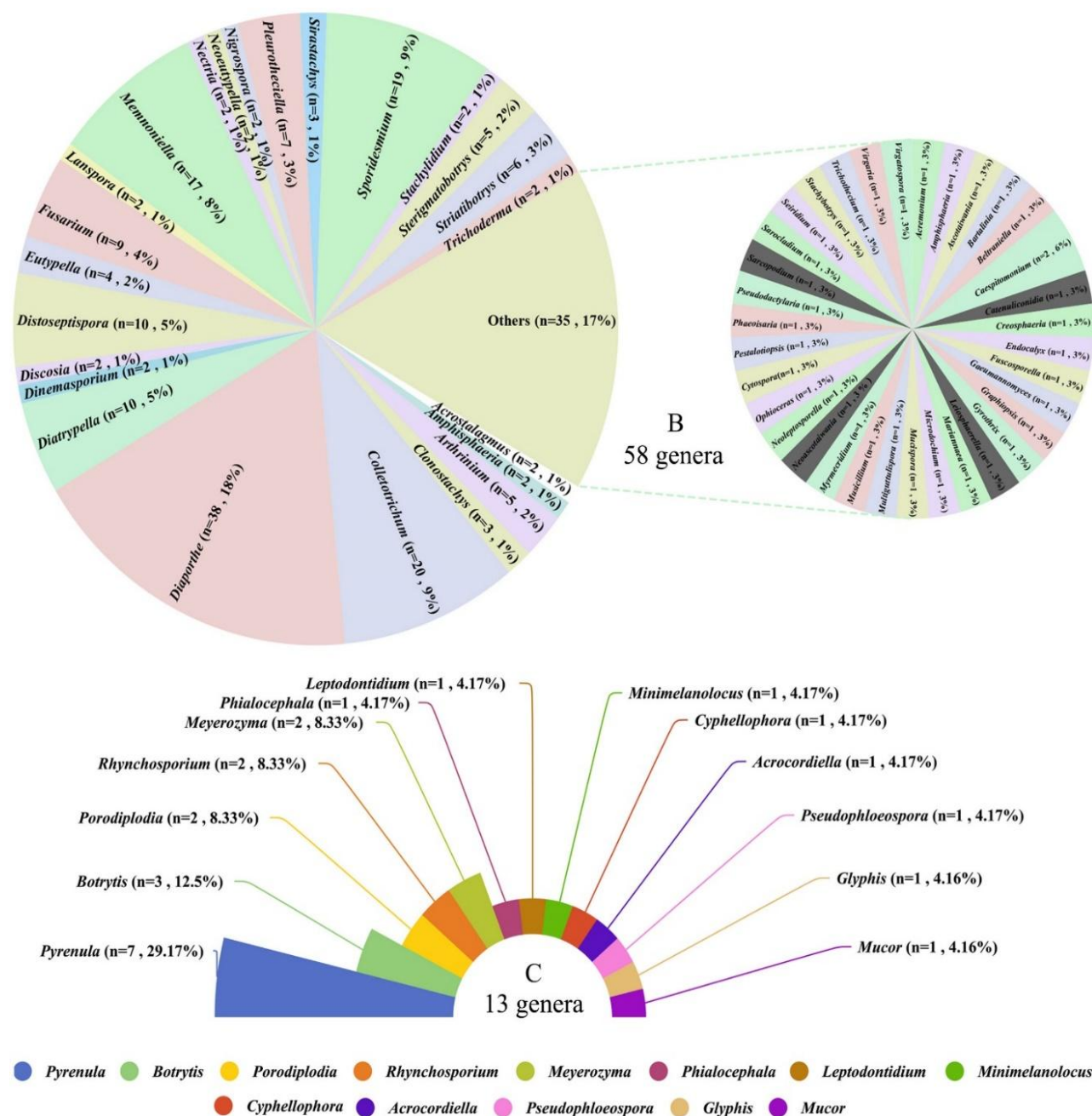


Figure 84 – The classification of microfungi on medicinal plants at genus level. B *Sordariomycetes*. C *Eurotiomycetes*, *Leotiomyces*, *Pichiomyces*, *Orbiliomyces*, *Lecanoromyces*, and *Mucoromycetes*.

DISCUSSION

In this study, we investigated saprobic fungi associated with medicinal plants in Southwestern China (Yunnan, Guizhou, and Sichuan Provinces), and revealed a remarkable assemblage of rare and distinctive taxa. A total of 90 isolates representing 49 species were recovered, including 32 novel species and 17 new records.

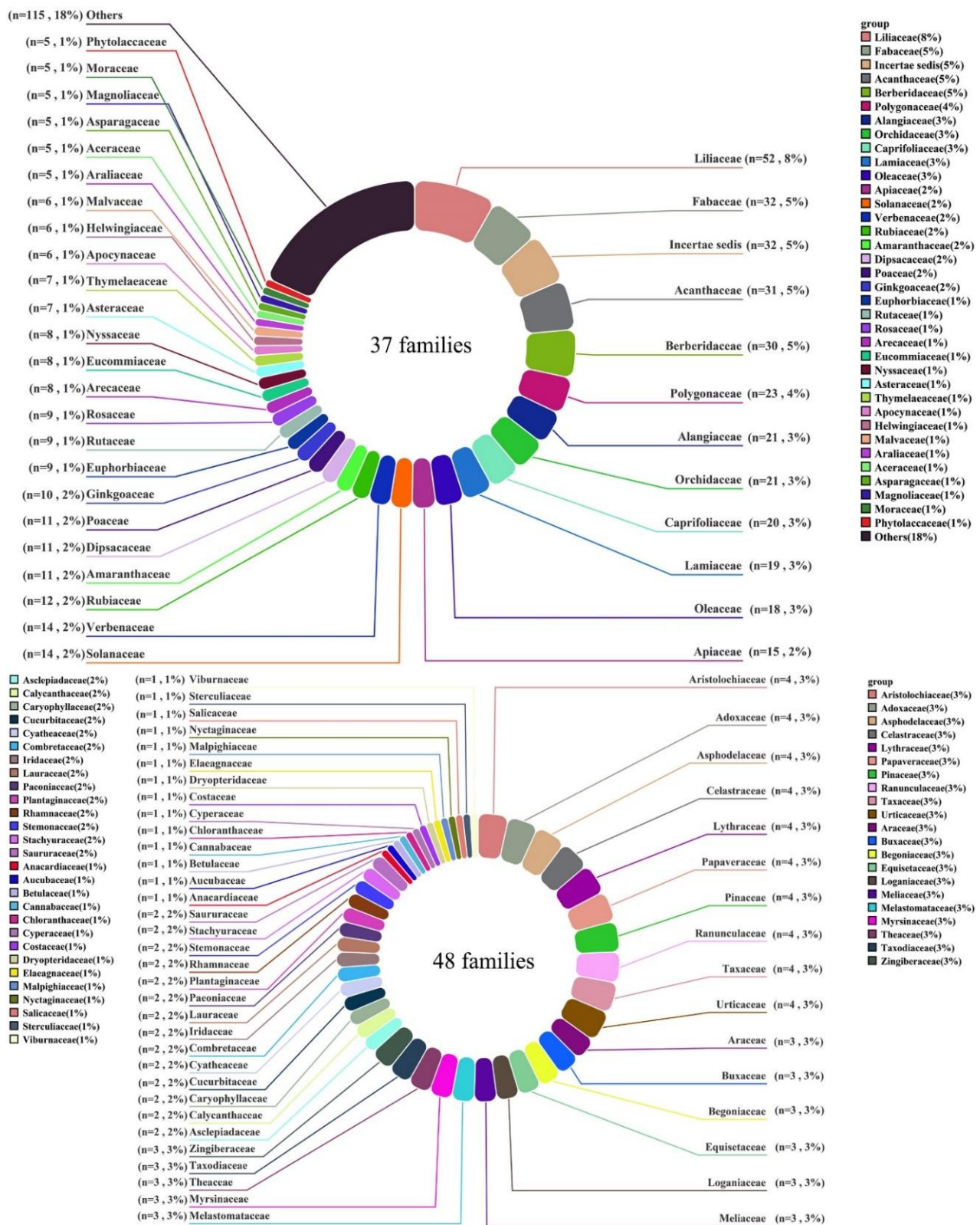


Figure 85 – The host distribution at the family level of medicinal plants in Southwestern China.

These fungi were collected 35 families of medicinal plants encompassing herbaceous, woody, and climbing hosts. While most specimens originated from wild habitats, others were obtained from cultivated plants in traditional Chinese medicine planting bases, such as *Lonicera japonica* (Caprifoliaceae), *Mentha canadensis* (Lamiaceae), and *Uncaria rhynchophylla* (Rubiaceae). Notably, several fungi were associated with endangered species, including *Taxus wallichiana* var. *chinensis* (Taxaceae) (Tang et al. 2024) and *Eucommia ulmoides* (Eucommiaceae) (Xie et al. 2023),

as well as ornamental and ethnomedicinal plants such as *Hellenia speciosa* (*Costaceae*) (Samanta et al. 2023) and *Alangium chinense* (*Alangiaceae*), a ‘Miao medicine’ resource (Xiao et al. 2024). These findings highlight the ecological importance and host diversity of fungi colonizing medicinal flora. Species delimitation in this study was based on morphological features combined with multi-locus phylogenetic analyses. Morphology alone is often inadequate for species identification, particularly within genera exhibiting only subtle differences in reproductive structures (Jeewon & Hyde 2016, Senanayake et al. 2020, Sun et al. 2023b, Wu et al. 2023, Zhang et al. 2023a, Du et al. 2024a). For instance, *Neoheliosia ellipsoidispora* closely resembles *N. guizhouensis* morphologically, but sequence divergence in ITS (2.9%), rpb2 (4.4%), and tef1- α (1.8%) clearly distinguishes them. Similarly, *Neoheliosia septata* exhibits strikingly different morphologies in its sexual and asexual states, rendering molecular data indispensable for linking the two morphs. Furthermore, some morphologically similar asexual taxa, such as *Austropleospora*, *Magnibotryascoma*, and *Paraphaeosphaeria*, were resolved as distinct lineages only through phylogenetic analyses (Jayasiri et al. 2019, Wijayawardene et al. 2020, Mortimer et al. 2021). These results reinforce the necessity of integrating morphology, molecular phylogenies, and divergence-time estimates for resolving complex taxonomic boundaries (Jeewon & Hyde 2016, Liu et al. 2017).

Saprobic fungi play a fundamental role in ecosystems by decomposing organic matter and recycling nutrients (Hyde et al. 2007). Genera such as *Aspergillus*, *Penicillium*, *Rhizopus*, and *Trichoderma* exemplify their ecological and biotechnological significance (Harman et al. 2004, Daly et al. 2020, Tyśkiewicz et al. 2022, Visagie et al. 2024, Pouris et al. 2024). Fungal lifestyles, however, are highly dynamic, with taxa shifting among saprobic, pathogenic, and endophytic modes depending on host and environmental conditions. For example, *Rhizoctonia* and *Fusarium* are typically saprobic but can become pathogenic under plant stress (Fu et al. 2022, Ekwomadu & Mwanza 2023), while *Botrytis cinerea* persists saprobically after host death (Martínez et al. 2005, Castillo et al. 2017). Likewise, *Colletotrichum* species may alternate between endophytic and pathogenic lifestyles (Tao et al. 2013, Niu et al. 2016). These shifts underscore the ecological plasticity of fungi and their capacity to adapt to diverse ecological niches (Hardoim et al. 2015, Tyśkiewicz et al. 2022). Although all collections in this study were recovered as saprobes, several genera identified here are also known to occur as endophytes or pathogens. For example, *Periconia* is usually saprobic but is also recognized as an endophyte with bioactive metabolites, including antimicrobial, antiviral, anticancer, and anti-inflammatory compounds (Li et al. 1998, Harnpicharnchai et al. 2009, Verma et al. 2011, Azhari & Supratman 2021). Conversely, some *Periconia* species are plant pathogens (Mayers 1976, Adeleke & Babalola 2021). Similarly, *Seiridium* comprises predominantly plant pathogens (Tsopelas et al. 2007, Bonthond et al. 2018), while members of *Amphisphaeria* include both endophytes and novel asexual morphs isolated from medicinal hosts (Wang et al. 2023). These examples suggest that fungi colonizing medicinal plants may harbor diverse ecological roles and bioactive potential, with possible implications for host health, growth, and the chemical quality of traditional medicines.

Fungal contamination is a critical factor influencing the quality, safety, and efficacy of traditional Chinese medicines (Zheng et al. 2017, Su et al. 2018, Altyn & Twarużek 2020, Wei et al. 2023). Many saprobes are capable of producing mycotoxins, which contaminate crops and medicinal plants during pre-harvest, post-harvest, and even processing stages (Rizzo et al. 2004, Sekar et al. 2008, Su et al. 2018, Ge et al. 2024). It is estimated that 20–25% of crops worldwide are contaminated by mycotoxins (Eskola et al. 2020). With the global rise in the consumption of herbal medicines, fungal contamination has become a major safety concern, warranting systematic evaluation of fungi colonizing medicinal hosts. Our study provides the first records of several fungal species from medicinal plants in China, laying a foundation for understanding their potential role in herbal contamination. For example, *Pseudoneoconiothyrium rosae* and *Angustimassarina kunmingensis* were isolated from *Eucommia ulmoides*, while *Lophiotrema obpyriforme* and *Amphisphaeria mucilaginis* were recovered from *Magnolia officinalis* var. *biloba*. Both *E. ulmoides* and *M. officinalis* are valued for their medicinal bark, raising the possibility that associated fungi may alter bioactive compound profiles or compromise product quality. Future work should therefore evaluate the influence of these fungi on host metabolites, efficacy, and safety. The complexity of

plant–fungus interactions, as seen in other medicinal hosts such as *Anacardium occidentale* and *Camellia japonica* (Koide et al. 2005, Tennakoon et al. 2021a), further underscores the need for integrative ecological and chemical studies. In conclusion, this study expands the known diversity of saprobic fungi associated with medicinal plants and highlights their ecological plasticity, taxonomic complexity, and applied significance. Continued exploration of these taxa is essential not only for resolving fungal systematics but also for assessing their impact on medicinal plant quality, safety, and bioactive potential. Understanding these associations will contribute to both fungal biodiversity research and the sustainable use of traditional Chinese medicines.

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DECLARATION ON CONFLICT OF INTEREST

The author list includes members of the editorial board of *Mycosphere*. They were not involved in the journal's review of, or decisions related to, this manuscript.

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