MYCOSPHERE 15(1): 1675–1793 (2024) www.mycosphere.org ISSN 2077 7019
Doi 10.5943/mycosphere/15/1/15

ARTICLE

Exploring the taxonomy and phylogeny of Sordariomycetes taxa emphasizing Xylariomycetidae in Southwestern China

Dissanayake LS[1,2], Samarakoon MC[3], Maharachchikumbura SSN[4,5], Hyde KD[1,6], Tang X[1,6], Li QR[7,8], Mortimer PE[2], Faraj T[9], Xu JC[2,10], Kang JC[1*], and Wanasinghe DN[2,9*]

[1] Engineering and Research Center for Southwest Bio-Pharmaceutical Resources of National Education Ministry of China, Guizhou University, Guiyang 550025, P.R. China
[2] Center for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Sciences, Honghe County 654400, P.R. China
[3] Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand
[4] School of Life Science and Technology, Center for Informational Biology, University of Electronic Science and Technology of China, Chengdu 611731, P.R. China
[5] Department of Biosystems Technological Studies, Faculty of Technological Studies, Uva Wellassa University, Badulla, Sri Lanka
[6] Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand
[7] State Key Laboratory of Functions and Applications of Medicinal Plants, Guizhou Medical University, Guiyang 550004, P.R. China
[8] The Key Lab of Optimal Utilization of Natural Medicine Resources, School of Pharmaceutical Sciences, Guizhou Medical University, University Town, Guian New District, Guizhou 550025, P.R. China
[9] Department of Soil Science, College of Food and Agriculture Sciences, King Saud University, P.O. Box 145111, Riyadh 11362, Saudi Arabia
[10] Department of Economic Plants and Biotechnology, Yunnan Key Laboratory for Wild Plant Resources, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, P.R. China

Citation – Dissanayake LS, Samarakoon MC, Maharachchikumbura SSN, Hyde KD, Tang X, Li QR, Mortimer PE, Faraj TK, Xu JC, Kang JC, Wanasinghe DN 2024 – Exploring the taxonomy and phylogeny of Sordariomycetes taxa emphasizing Xylariomycetidae in Southwestern China. Mycosphere 15(1), 1675–1793, Doi 10.5943/mycosphere/15/1/15

Abstract

Southwestern China has been widely acknowledged as a global biodiversity hotspot, renowned for its high levels of floral, faunal and microbial diversity. However, research on fungi, particularly microfungi, remains limited with comparison to the other kingdoms *i.e.* Plantae and Animalia. Within the fungal kingdom, the subclass Xylariomycetidae (Sordariomycetes, Ascomycota), presents a vast range of macro- and micro-morphological features, yet our knowledge of their taxonomy, diversity and geographical distribution is still lacking. To fill out this knowledge gap, our study focused on a survey of Xylariomycetidae taxa across diverse habitats in the Southwest of China, encompassing the provinces of Guizhou, Sichuan and Yunnan. The primary objective of this study was to examine fresh collections of terrestrial Xylariomycetidae and to investigate their taxonomy and phylogeny via polyphasic approaches. Employing phylogenetic analysis of targeted DNA loci within specific families and genera, encompassing all accessible ex-type and non-type strains as well as holotypes and additional herbarium material, we elucidated novel taxonomic relationships among Xylariomycetidae in Southwestern China. Our analyses revealed 30 previously unidentified species and confirmed the existence of 20 known species within the Xylariomycetidae. We also validly publish *Apiospora koreana* as a new species as it was previously invalidly published. Fourteen new species are introduced to Amphisphaeriales *viz. Amphisphaeria ailaoshanensis*, *A. kunmingensis*, *A. magna*, *A. shangrilaensis*,

Submitted: 18 April 2024; **Accepted:** 30 July 2024; **Published:** 5 September 2024
Corresponding Authors: Jichuan Kang – e-mail – jckang@gzu.edu.cn,
Dhanushka Wanasinghe – e-mail – dnadeeshan@gmail.com
Accepted by: Mingkwan Doilom

A. xishuangbannaense (Amphisphaeriaceae), *Apiospora arecacearum*, *A. koreana*, *A. menglaensis*, *A. senecionis* and *A. trachycarpi* (Apiosporaceae), *Neoamphisphaeria shangrilaensis* (Appendicosporaceae), *Iodosphaeria sichuanensis* (Iodosphaeriaceae), *Broomella meilishanguensis* and *Robillarda sichuanensis* (Sporocadaceae). In Xylariales, 14 new species were introduced *viz. Barrmaelia yunnanensis*, *B. shangrilaensis*, *Entosordaria shangrilana* (Barrmaeliaceae), *Diatrypella kunmingensis*, *Peroneutypa hongheensis* (Diatrypaceae), *Fasciatispora sichuanensis* (*Fasciatisporaceae*), *Hypoxylon guiyangense*, *H. guizhouense* (Hypoxylaceae), *Requienella shangrilana* (Requienellaceae), *Vamsapriya sichuanensis* (Vamsapriyaceae), *Collodiscula yunnanensis*, *Digitodochium ailaoshanense*, *D. yunnanensis* and *Nemania leishanensis* (Xylariaceae). We identified three new *Distoseptispora* species, *D. chishuiensis*, *D. liupanshuiensis* and *D. sichuanensis*, in Sordariomycetidae. These findings greatly enhance our understanding of fungal diversity in the region, highlighting the presence of numerous potentially novel species and providing a compelling opportunity for mycologists to explore further research avenues. Additionally, the comprehensive morphological descriptions and molecular sequences generated by this study serve as valuable resources for future taxonomic studies and contribute to a broader understanding of fungal diversity in Southwestern China.

Keywords – 31 new taxa – appendage – Ascomycota – ascospores – conidia – unitunicate

INTRODUCTION

The class Sordariomycetes exhibits a wide range of species diversity and adaptability, highlighting its ecological versatility via its widespread global distribution (Shenoy et al. 2007, Senanayake et al. 2018, Jones et al. 2020, Hyde et al. 2020a, Perera et al. 2020, Samarakoon et al. 2022, Chen et al. 2023a). Their adaptability shows in diverse ecological roles; while some species pose agricultural challenges as significant crop pathogens (Than et al 2008a, b, Crous and Groenewald 2013, Jayawardena et al. 2019a, b, Liu et al. 2019, Hyde et al. 2020a, b, Gomdola et al. 2022, Chen et al. 2023b), others establish symbiotic endophytic relationships, residing within plant tissues and potentially benefiting their hosts (Promputtha et al. 2005, 2007, U'Ren et al. 2016). Certain members of the Sordariomycetes have evolved as fungicolous taxa, while a vast number serve as saprobes and are responsible for decomposition and nutrient recycling processes in natural ecosystems (Zhang et al. 2006, Maharachchikumbura et al. 2022). Apart from their ecological importance, their influence extends to various industrial sectors. These fungi synthesize unique secondary metabolites with broad applications, from enhancing agricultural productivity to innovations in medicine and broader biotechnological aspects (Kuhnert et al. 2014, Thambugala et al. 2020). Sordariomycetes taxa are delineated into six subclasses to facilitate classification *viz.* Diaporthomycetidae, Hypocreomycetidae, Lulworthiomycetidae, Savoryellomycetidae, Sordariomycetidae and Xylariomycetidae (Wijayawardene et al. 2022) each highlighting distinct evolutionary paths and ecological strategies (Chen et al. 2023a).

Eriksson & Winka (1997) introduced the subclass Xylariomycetidae with the order Xylariales, based on both morphological and phylogenetic data. Over time, the taxonomy of this subclass has undergone extensive revision, with the most definitive and comprehensive reclassification provided recently by Samarakoon et al. (2022). This revision integrated a range of criteria, including taxonomy, phylogeny, molecular dating and ancestral state reconstruction analyses. The current subclass now encompasses 40 recognized families (Samarakoon et al. 2022). With a cosmopolitan distribution, species within Xylariomycetidae have varied life modes. These range from functioning as endophytes (U'Ren et al. 2016, Rashmi et al. 2019, Wang et al. 2023) to pathogens and even saprobes (Zhang et al. 2006, Daranagama et al. 2018, Hyde et al. 2020a). These species are typified by distinct stromata, visible or subtle stromata, often black and robust ascomata with periphyses, papillate ostioles and pigmented ascospores in their sexual phase (Samarakoon et al. 2022). Their asexual morphs are primarily hyphomycetous or coelomycetous (Samarakoon et al. 2022). This intricate morphology has been thoroughly documented in studies over the years, highlighting the rich diversity and importance of this subclass (Smith et al. 2003, Wang et al. 2004,

Zhang et al. 2006, Jaklitsch & Voglmayr 2012, Senanayake et al. 2015, Hyde et al. 2020a, Samarakoon et al. 2022).

Guizhou, Sichuan and Yunnan provinces in Southwestern China are well-known as biodiversity hotspots with high floral, faunal and microbial diversity (Xu et al. 2017). Over the past decade (2010–2020), Southwestern China has seen a surge in mycological research (Hongsanan et al. 2023). The major areas of focus include taxonomical studies of micro-fungi based on morpho-molecular analyses, investigations into fungal secondary metabolites and ethnomycological surveys (Wijayawardene et al. 2021a, b). Guizhou features a distinct topography that rises in the west and descends in the east, with slopes extending from the center towards the north, east and south. Within the core of karst regions in China, the distinctive karst climate and unique vertical altitude distribution found in Guizhou contribute to the emergence of unique biodiversity (Yang et al. 2023b, Zhang et al. 2023). This region hosts a diverse range of animals, plants and other microorganisms, distinguishing it from other areas and enriching its vegetation and fungal resources (Liu et al. 2013, Chi et al. 2017, Liu et al. 2018). A multitude of new fungal species from Xylariomycetidae have been identified in Guizhou (Su et al. 2016, Li et al. 2015, 2022, Wei et al. 2018, Xin et al. 2019, Dissanayake et al. 2021a, Wang et al. 2021, Wijayawardene et al. 2021a, Zhang et al. 2023). Adjacent to Tibet in the west, Sichuan province, boasting the third-largest forested area in China. The prominent high mountainous terrain transitions to lowland zones in the region, predominantly adorned with evergreen broad-leaved forests (Wang et al. 2008). The diminished effects of glaciation in this region contribute to the significant species diversity among both fauna and flora. Sichuan has been a focal point for fungal research, including studies on wood-inhabiting fungi (Li et al. 2023, Wanasinghe & Maharachchikumbura 2023) and soil fungi (Zhu et al. 2014, Wang et al. 2008). Recent findings have also highlighted microfungi within Xylariomycetidae (Yang et al. 2019, Li et al. 2022a, Maharachchikumbura et al. 2022). Bordering Guizhou, Sichuan, Guangxi and Tibet domestically and Vietnam, Laos and Myanmar internationally, Yunnan province presents a diverse tapestry of ecosystems. This region encompasses various vegetation types, ranging from tropical rainforests to temperate coniferous forests (Qian et al. 2020). Research on higher fungi in Yunnan traces back to the late 19th century (Feng & Yang 2018) and the province is recognized for its vast fungal biodiversity, specifically within the Ascomycota and Basidiomycota. Hawksworth (1991, 2001) proposed that the fungal count in any given region may approximate six times the local vascular plants, implying an estimated 104,000 fungal species in Yunnan. Numerous studies on Xylariomycetidae have been documented in this province (Dissanayake et al. 2020, 2021b, 2022, Wijayawardene et al. 2021a, Gao et al. 2022, Bao et al. 2023, Yang et al. 2023a, Wanasinghe & Mortimer 2022a, Wanasinghe et al. 2024).

The unique ecological landscapes of Southwestern China serve as reservoirs of rich fungal biodiversity. Given the plenteous species housed within these provinces, many of which remain undocumented or under-studied, continual research is essential. A deeper exploration into this fungal richness can provide insights into ecological interconnection and the overall health of ecosystems. Fungi, especially from groups like Xylariomycetidae, hold promise in biotechnological applications, presenting opportunities ranging from innovative industrial processes (Feng & Yang 2018). As these provinces stand as biodiversity hotspots, they are sensitive indicators of environmental changes, including those induced by climate shifts (Tedersoo et al. 2014, Casadevall et al. 2019, Nnadi & Carter 2021). Persistent monitoring and research in these areas catalyze scientific advancements and inform conservation strategies, ensuring the preservation of these ecological treasures for future generations (Wanasinghe et al. 2022b).

Given these considerations, our study embarked on an extensive collection and documentation of Sordariomycetes species from the Guizhou, Sichuan and Yunnan provinces in Southwestern China. Our research endeavors to chronicle these species and to generate detailed morphological descriptions complemented by advanced molecular sequence data analyses. Through this approach, we aimed to make a substantial contribution to the existing knowledge, paving the way for subsequent research and magnifying the potential applications of these fungi across various

sectors. Consequently, we collected many fungi from various families within Sordariomycetes. This study has documented 28 new species within the Xylariomycetidae and identified three novel species in the Sordariomycetidae. Furthermore, we present new host and geographic data for 20 previously identified species in Xylariomycetidae, along with one new record from the Sordariomycetidae.

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MATERIALS AND METHODS

Isolates and specimens

Sample collection

We collected specimens across various regions in the Southwest regions of China including Guizhou, Sichuan and Yunnan (Fig. 1). Our field trips were strategically planned during both the wet and dry seasons to capture a comprehensive understanding of the fungi in different environmental conditions. Specifically, we identified and gathered black ascomata and conidiomata, which are typical fungal structures from dead twigs. Upon collection, we ensured the specimens were safely secured and preserved by placing them in individual Ziploc bags. These bags were carefully transported to the mycology laboratory of Kunming institute of Botany for further examination. To maintain the integrity and prevent contamination or decay of the samples, they were transferred from the Ziploc bags and stored in paper envelopes once in the laboratory. We implemented single spore isolation on these samples for a more detailed analysis. This process was carried out following the standardized methods described in the comprehensive research by Senanayake et al. (2020a). Following the successful isolation, germinated spores were treated and handled carefully to ensure their viability and prevent contamination. After completing all analyses and experiments, the specimens were dried properly to ensure long-term preservation. Dried specimens were preserved at room temperature in the fungarium of the Cryptogams Kunming Institute of Botany, Academia Sinica (KUN-HKAS), and representative cultures were deposited in the Kunming Institute of Botany Culture Collection (KUMCC). Nomenclatural data for fungal novelties were deposited in the Faces of Fungi database (Jayasiri et al. 2015), MycoBank (2024) and those from the Greater Mekong Subregion in https://gmsmicrofungi.org (Chaiwan et al. 2021).

Morphological observations

In our study, we thoroughly examined the fungal structures, specifically the ascomata, conidiophores and conidia, collected from their natural substrates. The specimens were first rehydrated using regular tap water to initiate this process. For a closer and more precise observation of these rehydrated specimens, we utilized a Motic SMZ 168 Series stereomicroscope. Furthering our investigation into their morphological characteristics, we employed the technique of hand sectioning of the sporocarps. This procedure involved carefully slicing the sporocarps and placing the resultant sections onto water-mounted glass slides. Melzer's reagent and Indian ink were used where necessary. From a quantitative perspective, we measured the internal structures. Our focus was directed towards the diameter, height, color and shape of the ascomata and conidiomata. The width of the peridium, the length and diameter of the ostioles, length and width of asci, ascospores, conidiophores and conidia were accurately measured, ensuring that the width was consistently measured at the broadest point of the structures for consistency and accuracy in our findings. Microscopic photography was conducted using a Nikon ECLIPSE Ni compound microscope fitted with a Canon EOS 600D camera. We also employed an iPhone XS Max to capture macroscopic images of the fungal colonies. Measurements were made with the Tarosoft (R) Image Frame Work program. Once the raw data was collated, we used Adobe Photoshop CS6 to process and refine the images that would be incorporated into our figures, making them more illustrative and comprehensible.

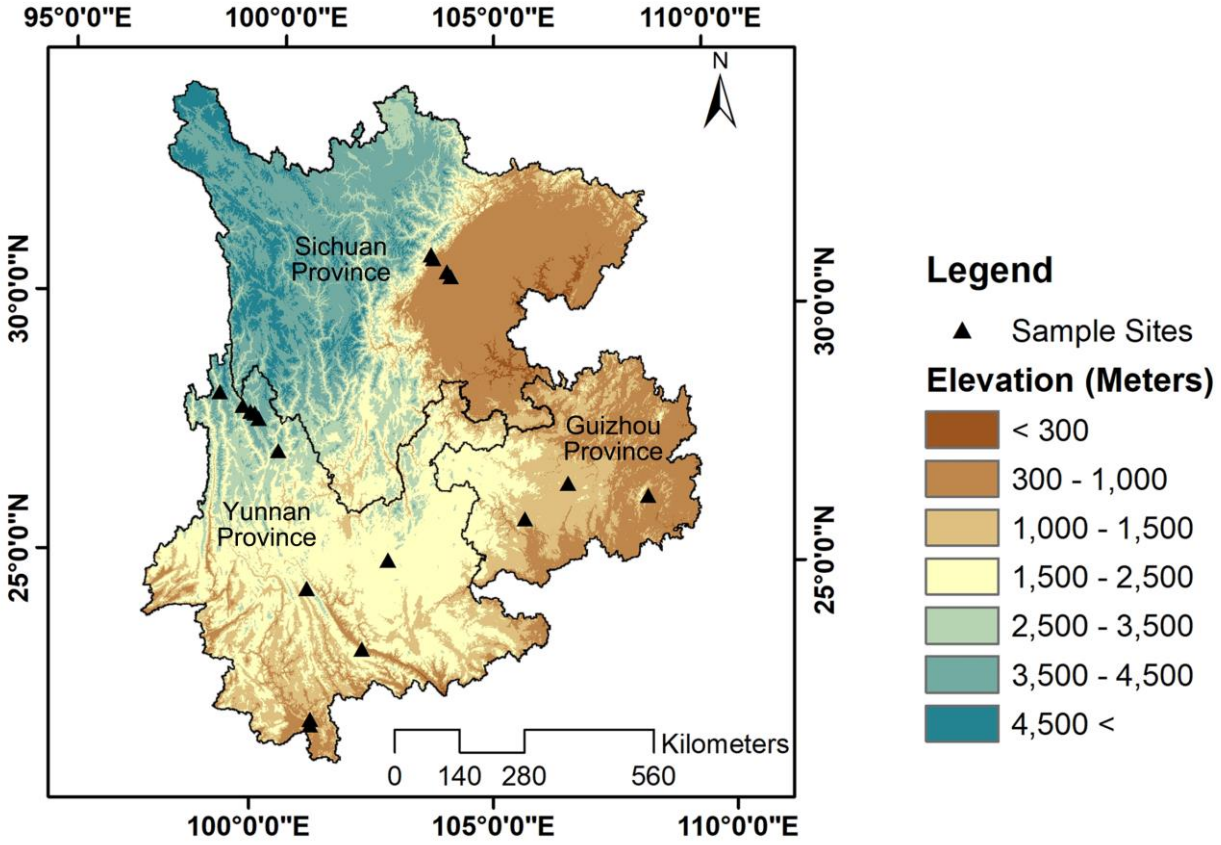

Figure 1 – Sampling locations in Southwestern China. For each site, the elevation was extracted, and the map was created with ArcGIS 15.0 (ESRI, Redlands, CA, USA).

DNA extraction, PCR amplifications and sequencing

For DNA extraction, mycelia were cultured from each fungal isolate using potato dextrose agar (PDA). This medium consisted of 39 g/L distilled water and Difco potato dextrose. The cultures were grown for 3–4 weeks under room conditions at 20 °C. Total genomic DNA was extracted from the thriving cultures, focusing on approximately 150 ± 50 mg of axenic mycelium. This mycelium was scraped from the periphery of the expanding culture to ensure its purity. The extracted mycelium was then subjected to grinding, transforming it into a fine powder. This was achieved using liquid nitrogen, which ensures the breakdown of the cell walls without causing DNA damage. The Biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (produced by BioFlux, P.R. China) was employed for the actual DNA extraction process. Throughout this extraction process, the manufacturer's guidelines were followed. However, in instances where fungi failed to grow on culture media, an alternative approach for DNA extraction was implemented. Instead of relying on cultured mycelium, the DNA was extracted directly from the fungal fruiting bodies. This procedure adhered to the protocol described by Wanasinghe et al. (2018a). DNA samples intended for use as PCR templates were preserved in two ways. For routine and immediate work, the DNA was stored at 4 °C. To ensure longevity and preserve the DNA samples, duplicates were stored at a –20 °C.

The genes, primers, references and the Polymerase Chain Reaction (PCR) protocols are summarized in Table 2. The Polymerase Chain Reaction was executed in a volume of 25 µl. This mixture incorporated 12.5 µl of 2 × Power Taq PCR MasterMix (sourced from Bioteke Co., China), 1 µl of each primer (at a concentration of 10 µM), 1 µl of the genomic DNA and 9.5 µl of deionized water. The amplified PCR fragments were sent to a commercial sequencing provider (BGI, Ltd Shenzhen, P.R. China). The nucleotide sequence data acquired were deposited in GenBank for further reference and use.

Table 1 Genes/loci used in the study with PCR primers, references and protocols.

Locus [a]	Primers	PCR: thermal cycles: (Annealing temp. in bold)	References
ITS	ITS5 ITS4	(94 °C: 30 s, **56** °C:50 s, 72 °C: 60 s) × 35 cycles	White et al. (1990)
LSU	LR0R LR5	(95 °C: 30 s, **55** °C:50 s, 72 °C: 60 s) × 35 cycles	Rehner & Samuels (1994), Vilgalys & Hester (1990)
*rpb*2	*rpb*2-5f *rpb*2-7cR	(95 ˚C: 45 s, **57** °C: 50 s, 72 °C: 90 s) × 40 cycles	Liu et al. (1999)
*tef*1-α	EF1-983F EF1-2218R	(94 °C: 30 s, **55** °C:50 s, 72 °C: 60 s) × 35 cycles	Rehner & Buckley (2005)
*tub*2	T1 T2	(95 °C: 60 s, **54** °C:110 s, 72 °C: 120 s) × 35 cycles	O'Donnell & Cigelnik (1997)
	*tub*2a *tub*2b	(95 °C: 60 s, **54** °C:110 s, 72 °C: 120 s) × 35 cycles	Glass & Donaldson (1995)

ITS: Part of rDNA 18S (3' end), the first internal transcribed spacer (ITS1), the 5.8S rRNA gene, the second ITS region (ITS2) and part of the 28S rRNA (5' end); LSU: Large subunit (28S); SSU: Small subunit rDNA (18S); *rpb*2: RNA polymerase II second largest subunit; *tef*1-α: translation elongation factor 1-alpha gene

[b] All the PCR thermal cycles include the Initiation step of 95 °C: 5 min and the final elongation step of 72 °C: 10 min and the final hold at 4 °C

Molecular Phylogenetic Analyses

Sequence alignment

Sequences obtained from different primers targeting the relevant genes were compared with other sequences sourced from GenBank. A BLAST search identified sequences with high similarity, indicating the closest matches within the Sordariomycetes taxa and referencing recently published data. The multiple alignments, which included both consensus sequences and reference sequences, were initially generated using MAFFT v. 7 (Kuraku et al. 2013, Katoh et al. 2019). Where necessary, these alignments were manually refined using BioEdit v. 7.0.5.2 (Hall 1999).

Phylogenetic Analyses

For each locus, the evolutionary models used in the Bayesian inference (BI) and maximum-likelihood (ML) analyses were independently chosen using MrModeltest v. 2.3 (Nylander 2004). The Akaike Information Criterion (AIC) served as the selection criteria and this process was executed in PAUP v. 4.0b10 (Swofford 2002). The RAxML and Bayesian analyses were carried out on the CIPRES Science Gateway platform (Miller et al. 2010). For the ML analyses, RAxML-HPC2 on XSEDE v. 8.2.10 (Stamatakis et al. 2006, Stamatakis 2014) was employed. The analysis was conducted using the GTR+I+G model and 1000 bootstrap repetitions. The MrBayes analysis was executed with settings adjusted for GTR+I+G, with 2–5 million generations and sampling at intervals of 100 generations. The run was designed to conclude automatically once the standard deviation of split frequencies fell below 0.01 and a burn-in fraction of 0.25 was set. Noteworthy phylogenetic results were represented by ML bootstrap values (MLB) equal to or greater than 60% and a posterior probability in Bayesian statistics (BYPP) equal or exceeding 0.95. These values were displayed above each node in all resulting trees. For visualization purposes, the resulting phylograms were displayed using the FigTree v1.4.0 program (Rambaut 2012). The final reorganization was accomplished using Microsoft PowerPoint (2019).

RESULTS

The taxonomic categorization and placement of *Sordariomycetes* have been followed according to the comprehensive guidelines and framework presented by Wijayawardene et al. (2022). Whenever pertinent to our discussion, we integrated and elaborated upon the phylogenetic

results we obtained. These findings are subsequently discussed in-depth, providing context, interpretation and insights in the following detailed descriptive notes.

Taxonomy
Ascomycota Caval.-Sm., Biol. Rev. Cambridge Philos. Soc. 73: 247 (1998)

Sordariomycetes O.E. Erikss. & Winka, Myconet 1: 10 (1997)
Sordariomycetidae O.E. Erikss. & Winka, Myconet 1: 10 (1997)
Distoseptisporales Z.L. Luo, H.Y. Su & K.D. Hyde, Fungal Diversity 99: 482 (2019)
Distoseptisporaceae K.D. Hyde & McKenzie, Fungal Diversity 80: 402 (2016)

Notes – The family Distoseptisporaceae was introduced by Su et al. (2016) and initially, it was established to accommodate a sole genus, *Distoseptispora*. Asexual morphs that are associated with Distoseptisporaceae are reminiscent of sporidesmium-like hyphomycetes. These fungi predominantly function as saprobes, decomposing dead wood in both terrestrial and freshwater environments (Jayawardena et al. 2022). Their global distribution has been emphasized and detailed by Yang et al. (2018).

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

Notes – *Distoseptispora* was introduced by Su et al. (2016) with the type species *Distoseptispora fluminicola*. The morphology of *Distoseptispora* is similar to other genera such as *Ellisembia* and *Sporidesmium*, which are characterized by euseptate and distoseptate conidia, respectively. Yang et al. (2021a) provided evidence that *Distoseptispora* constitutes a monophyletic lineage that is distinct from other sporidesmium-like taxa. This taxonomic distinction is further validated by Hyde et al. (2023), emphasizing that *Distoseptispora* remains the representative genus of the Distoseptisporaceae. From an ecological perspective, *Distoseptispora* species are predominant as saprobes on lignicolous substrates. These taxa are commonly associated with freshwater biotopes, though a sporadic presence in terrestrial locales has been documented (Yang et al. 2021a). The first record of a sexual morph for *Distoseptispora* was provided in a subsequent study by Yang et al. (2021a). Over recent years, there has been a notable surge in the recognition and classification of new *Distoseptispora* species. Species Fungorum (2024) lists a total of 62 epithets under this genus and recently 12 new *Distoseptispora* species have been introduced (Hu et al. 2023, Chen et al. 2024, Hyde et al. 2024, Shen et al. 2024). We expand the taxonomic account of this genus by introducing three novel species, based on morphology and LSU, ITS, *tef*1-α and *rpb*2 sequence data analyses.

Distoseptispora chishuiensis X. Tang, K.D. Hyde & J.C. Kang, sp. nov. Figs 2, 3

MycoBank number: MB852807; Facesoffungi number: FoF15544

Etymology – The specific epithet is derived from the Chishui county, where the holotype was collected.

Holotype – GZAAS 23-0805

Saprobic on the dead culms of bamboo. Sexual morph: Undetermined. Asexual morph: *Hyphomycetous*. *Colonies* on natural substrates superficial, effuse, olivaceous, or mid-brown, hairy, velvety. *Mycelium* mostly immersed, consisting of branched, septate, smooth, subhyaline to pale brown hyphae. *Conidiophores* 80–190 μm high × 4–7 μm diameter ($\overline{x}$ = 128.5 × 5.6 μm, n = 30), macronematous, mononematous, solitary, erect, straight, or flexuous, olivaceous, or brown, 5–8-septate, smooth. *Conidiogenous cells* monoblastic, holoblastic, terminal, dark brown. *Conidia* 70–130 μm high × 14.5–21 μm diameter ($\overline{x}$ = 95 × 17.2 μm, n = 30), acrogenous, solitary, obpyriform or obclavate, 13–17-distoseptate, thick-walled, olivaceous or dark brown below, hyaline towards apex, truncate at base, slender and rounded at apex.

Cultural characteristics – Conidia germinated on PDA within 24 hr and germ tube produced from the apex. Colonies on PDA reaching 15–20 mm diameter after 2 weeks at 25 °C in dark, circular, with fluffy, dense, off-white or brown, in reverse black with entire margin.

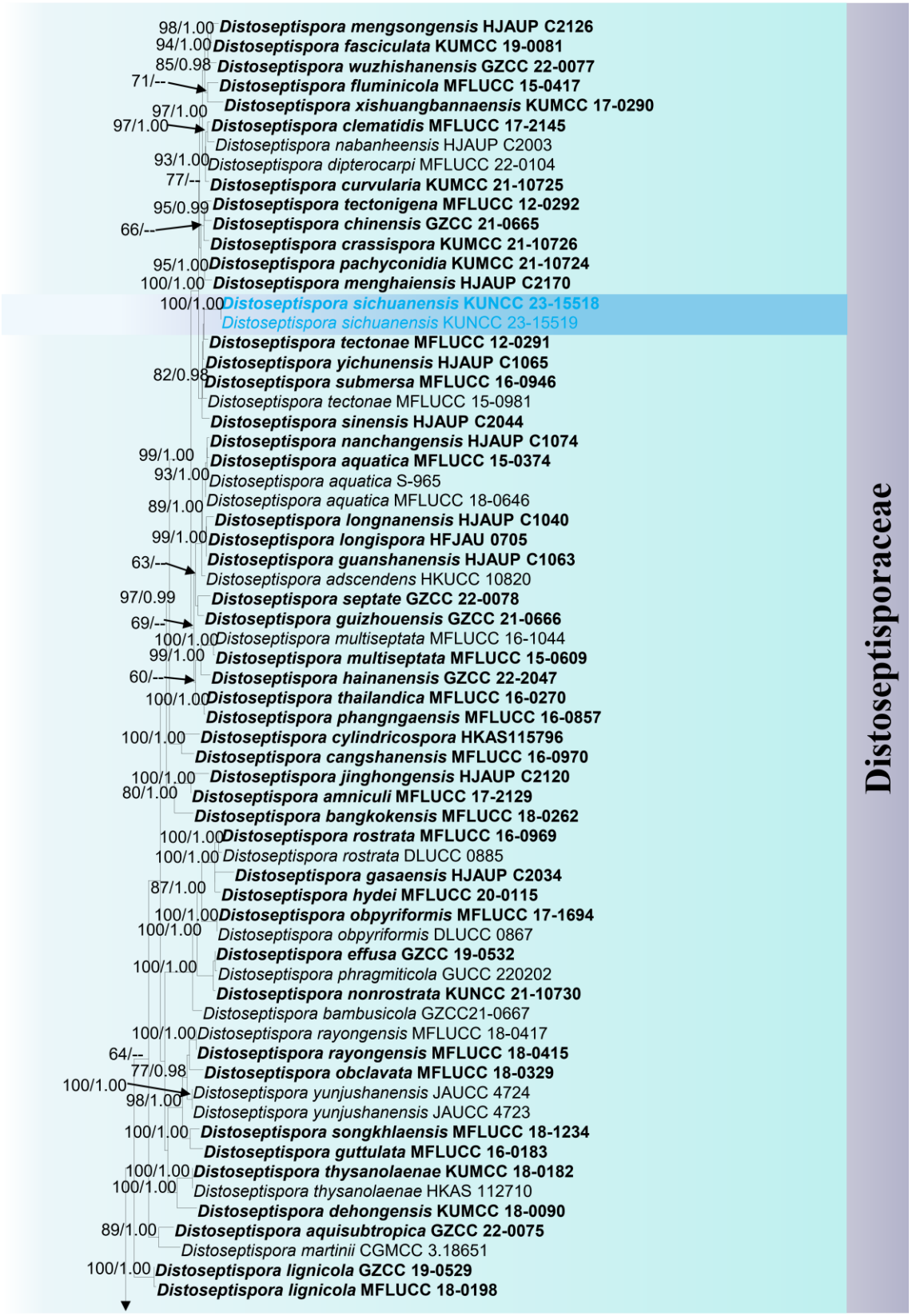

Figure 2 – RAxML phylogram generated from combined dataset of partial LSU, ITS, *tef*1-α, *rpb*2 DNA sequence analyses for Distoseptisporaceae. Final likelihood value is -30666.701188. The tree is rooted to *Aquateridospora fusiformis* (MFLUCC 18-1606) and *A. lingnicola* (MFLUCC 15-0377). The matrix had 2154 distinct alignment patterns with 27.55% undetermined characters and gaps. Estimated base frequencies were; A = 0.239293, C = 0.266824, G = 0.282677, T = 0.211206 substitution rates AC = 1.324299, AG = 2.859184, AT = 1.305312, CG = 0.791719, CT =

6.737181, GT = 1.000000; gamma distribution shape parameter α = 0.693392. Newly generated sequences are in blue. Ex-type/type strains are indicated in bold.

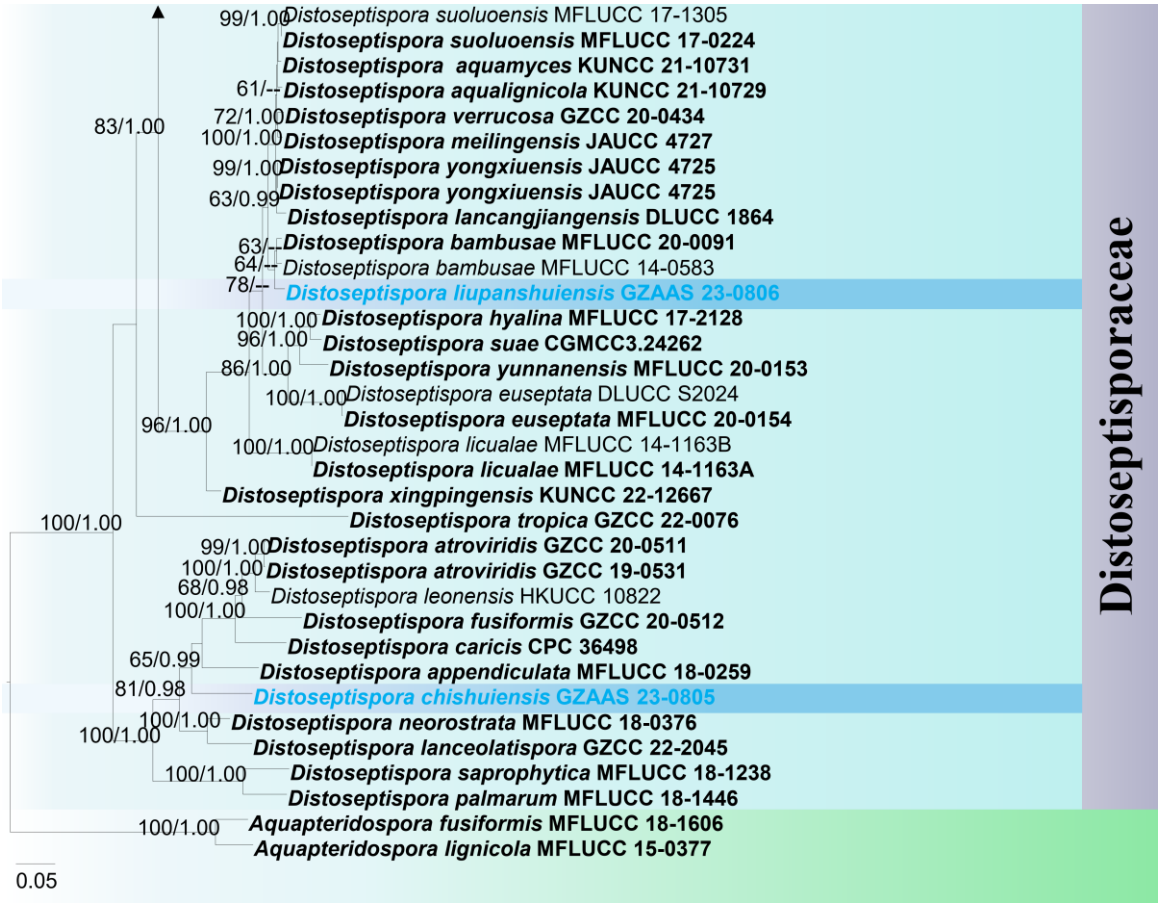

Figure 2 – Continued.

Material examined – CHINA, Guizhou Province, Zunyi City, Chishui (30.748056 N, 103.928889 E, 533m), on dead culms of bamboo, 12 April 2022, Xia Tang, CS44 (GZAAS 23-0805, holotype), ex-type, GZCC 23-0729.

GenBank accession numbers – ITS = PP584670, LSU = PP584767, *tef*1-α = PP663310.

Notes – Based on its morphological characteristics, *Distoseptispora chishuiensis* aligns well with the generic concept of *Distoseptispora*. Multi-gene analyses have demonstrated that *D. chishuiensis* is a phylogenetically distinct species, showing the closest relationship to *D. appendiculata* (MFLUCC 18-0259), a species previously collected from submerged wood in a freshwater habitat in Thailand (Luo et al. 2019). The nucleotide differences in the LSU and ITS regions between *D. appendiculata* and *D. chishuiensis* are 25/770 (3.2%) and 20/526 (3.8%), respectively. *Distoseptispora chishuiensis* is similar to *D. appendiculata* but can be differentiated by having longer conidiophores (128.5 × 5.6 µm vs. 74 × 5 µm), longer conidia (95 × 17.2 µm vs. 78 × 13 µm) and the absence of a gelatinous hyaline sheath around the tips, in comparison with *D. appendiculata*. Based on both morphological and molecular analyses (Jeewon & Hyde 2016), this study introduces *D. chishuiensis* as a new species from Guizhou province, China.

Distoseptispora liupanshuiensis X. Tang, K.D. Hyde & J.C. Kang, sp. nov. Figs 2, 4

MycoBank number: MB853452; Facesoffungi number: FoF15748

Etymology – The specific epithet is derived from the Liupanshui City, where the holotype was collected.

Holotype – GZAAS 23-0806

Saprobic on the dead culms of bamboo. Sexual morph: Undetermined. Asexual morph: *Hyphomycetous*. *Colonies* effuse, brown to dark-brown, hairy. *Mycelium* mostly immersed, composed of pale to dark brown, septate, branched, smooth, hyaline to subhyaline hyphae. *Conidiophores* 70–340 μm high × 3.5–7 μm diameter ($\overline{x}$ = 179 × 7.8 μm, n = 30), macronematous, mononematous, solitary, erect, straight or flexuous, brown, 5–8-septate, smooth. *Conidiogenous cells* monoblastic, holoblastic, terminal, dark brown. *Conidia* 55–90 μm high × 6–11 μm diameter ($\overline{x}$ = 74 × 8.8 μm, n = 30), acrogenous, solitary, straight, obpyriform, 8–10-distoseptate, thick-walled, light brown below, hyaline towards apex, rounded at the apex, truncate at base, tapering towards the apex.

Cultural characteristics – Conidia germinated on PDA within 24 hr and germ tube produced from the apex. Colonies on PDA reaching 15–20 mm diameter after 2 weeks at 25 °C in dark, circular, with fluffy, dense, off-white or brown, in reverse black with entire margin.

Material examined – CHINA, Guizhou Province, Liupanshui City, Yushe National Forest Park (30.748056 N, 103.928889 E, 533m), on dead culms of bamboo, 25 February 2023, Xia Tang, TY91 (GZAAS 23-0806, holotype), ex-type, GZCC 23-0730.

GenBank accession numbers – ITS = PP584669, LSU = PP584766, *tef*1-α = PP663309.

Notes – Multi-gene analysis revealed that our new species, GZCC 23-0730, shares a close relationship with *Distoseptispora bambusae*, with 64% MLB statistical support and this was not supported by the BYPP (Fig. 2). *Distoseptispora bambusae*, which was introduced by Sun et al. (2020), was collected from dead bamboo culms in China and Thailand. We also found our new isolate from dead culms of bamboo in China. The morphological characteristics of our new collection, GZCC 23-0730, closely resemble those of the holotype of *Distoseptispora bambusae* (MFLUCC 20-0091), with the exception that our isolate has larger conidia, measuring 74 × 8.8 μm, compared to the 60 × 7.5 μm conidia of *D. bambusae*. The nucleotide differences in the ITS and TEF regions between *Distoseptispora bambusae* and the new isolate are 15/495 (3%) and 16/845 (1.9%), respectively. Based on both morphological and molecular analyses, this study introduces *Distoseptispora liupanshuiensis* as a new species from Guizhou Province, China.

Distoseptispora sichuanensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 2, 5

MycoBank number: MB850205; Facesoffungi number: FoF14895

Etymology – The specific epithet is derived from the Sichuan Province, where the holotype was collected.

Holotype – HKAS 130264

Saprobic on a dead twig of an unidentified host. Sexual morph: Undetermined. Asexual morph: *Hyphomycetous*. *Colonies* on natural substrates superficial, effuse, dark brown to black, hairy. *Mycelium* mostly immersed, consisting of branched, dark brown, smooth, septate hyphae. *Conidiophores* 15–25 μm high × 4–6 μm diameter ($\overline{x}$ = 20 × 5 μm, n = 5), macronematous, mononematous, erect, solitary or in small group, cylindrical, yellowish brown to dark brown, 1–4-septate, unbranched. *Conidiogenous cells* 6–12 μm high × 6–8 μm high ($\overline{x}$ = 9 × 7.2 μm, n = 10), monoblastic, terminal, determinate, cylindrical, brown. *Conidia* 80–145 μm high × 6–17 μm diameter ($\overline{x}$ = 114 × 12.8 μm, n = 20), solitary, obclavate, elongated, straight or slightly curved, truncate at the base, rounded at the apex and hyaline, straight or slightly curved, 12–20-distoseptate, yellowish brown to brown, truncate and darkened at the base.

Cultural characteristics – Conidia germinated on PDA within 24 hr and germ tube produced from the apex. Colonies on PDA reaching 15–20 mm diameter after 2 weeks at 25 °C in dark, circular, with fluffy, dense, dark purple to black, in reverse black with entire margin.

Material examined – CHINA, Sichuan Province, Chengdu, Chenghua District (30.748056 N, 103.928889 E, 533m), on dead twigs of unidentified host, 3 January 2023, L.S. Dissanayake, SCCETU23–16 (HKAS 130264, holotype), ex-type, KUNCC 23-15518. *ibid*. SCCETU23–16A (HKAS 130265, isotype), ex-isotype, KUNCC 23-15519.

GenBank accession numbers – ITS = PP584671, PP584672, LSU = PP584768, PP584769, *tef*1-α = PP663311, PP663312.

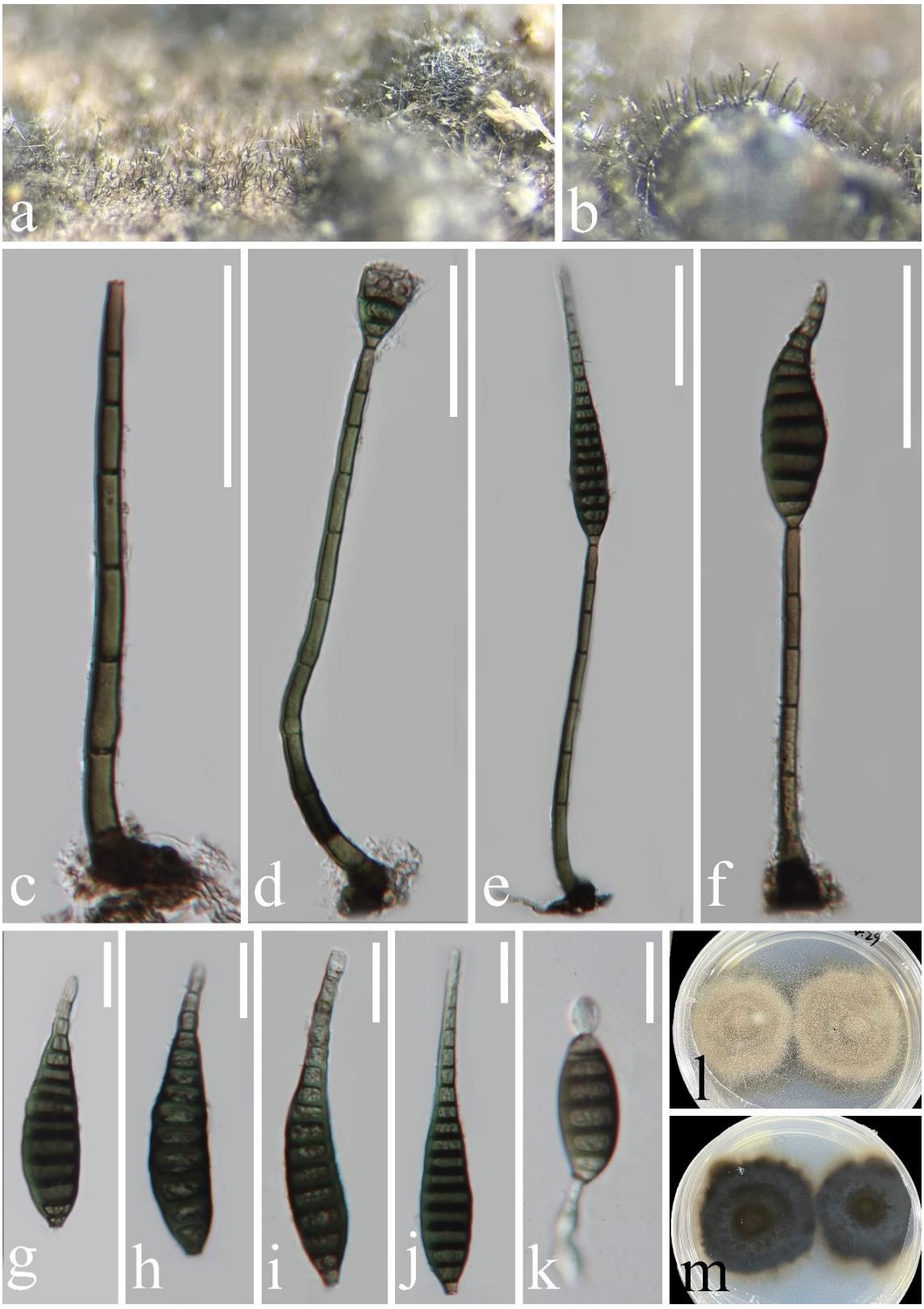

Figure 3 – *Distoseptispora chishuiensis* (GZAAS 23-0805, holotype). a, b Colonies on natural substrate. c–f Conidiophores, conidiogenous cells baring conidia. g–k Conidia. (k = Germinated conidium). l upper view. m Reverse view of the one-week-old colony on PDA. Scale bars: c–f = 50 μm, g–k = 20 μm.

Notes – We introduce *Distoseptispora sichuanensis* as a distinct species, differentiated from other known *Distoseptispora* species based on both morphological and phylogenetic distinctions.

Phylogenetic analysis shows that the two strains of *Distoseptispora sichuanensis* form a monophyletic group, with 100% MLB and 1.00 BYPP support values. These strains exhibit a close phylogenetic relationship to three strains of *Distoseptispora tectonae*, supported by 95% MLB and 1.00 BYPP values. The nucleotide differences of LSU and ITS between *Distoseptispora sichuanensis* and *D. tectonae* are 20/770 (2.6%) and 18/526 (3.4%) respectively. It is noteworthy that the sexual morphs of both species remain elusive, with current reports focusing solely on their hyphomycetous asexual morphs. While the conidia of both species exhibit similar morphology, there is a marked difference in their septation. Specifically, *Distoseptispora tectonae* has conidia with 20–28 distosepta (Hyde et al. 2016), whereas *D. sichuanensis* is characterized by 12–20 distosepta.

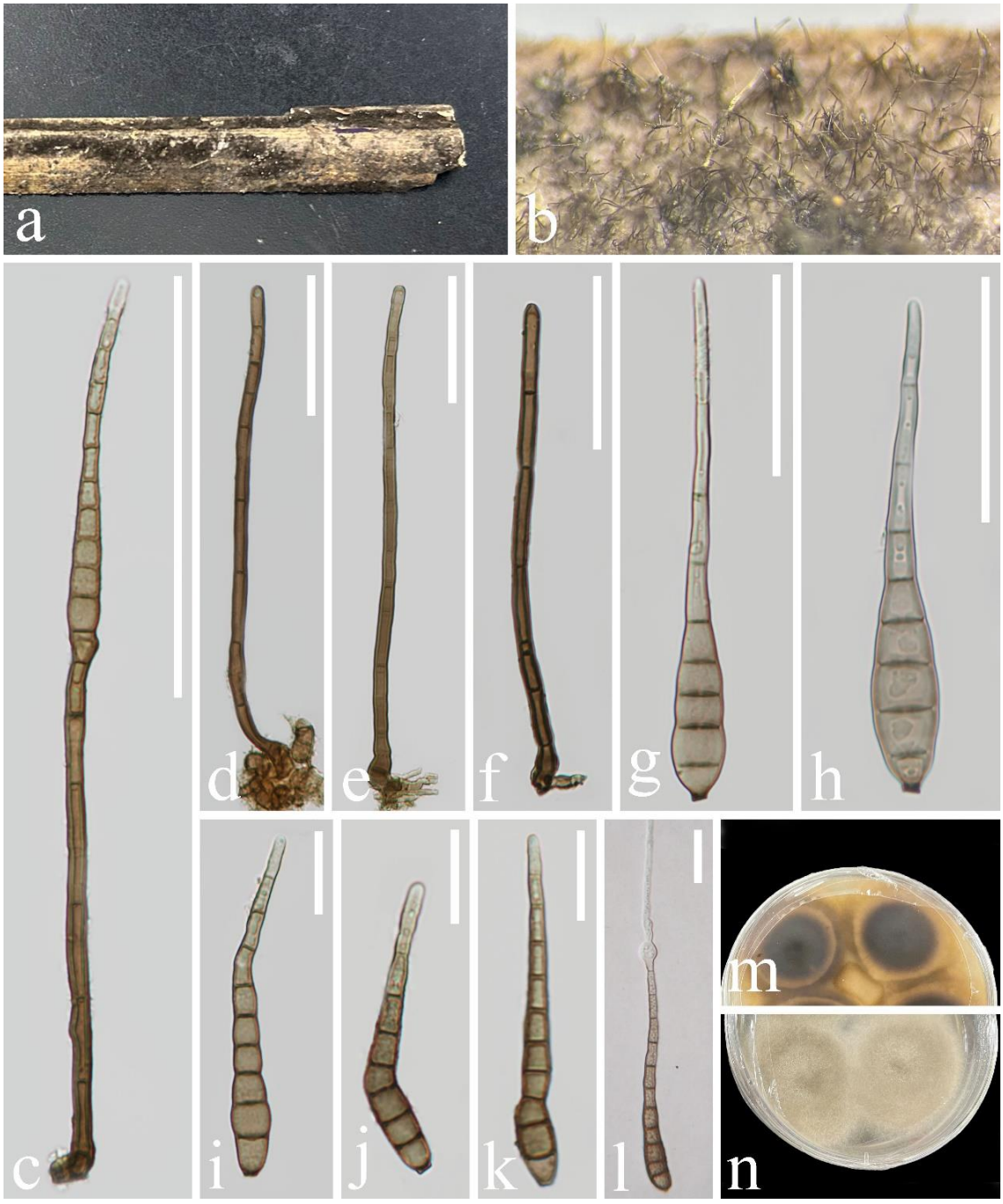

Figure 4 – *Distoseptispora liupanshuiensis* (GZAAS 23-0806, holotype). a Dead twig of bamboo. b Colonies on natural substrate. c–f Conidiophores, conidiogenous cells baring conidia. g–l Conidia

(l = Germinated conidium). m Upper view. n Reverse view of the one-week-old colony on PDA. Scale bars: c = 100 μm, d–h = 50 μm, i–l = 20 μm.

Xylariomycetidae O.E. Erikss. & Winka, Myconet 1: 12 (1997)

Amphisphaeriales D. Hawksw. & O.E. Erikss., Systema Ascomycetum 5: 177 (1986)
Amphisphaeriaceae G. Winter, Rabenhorst's Kryptogamen-Flora, Pilze – Ascomyceten, Edn 2 1(2): 259 (1885)

Notes – Amphisphaeriaceae was introduced by Winter (1885), highlighting its type genus, *Amphisphaeria*. Samarakoon et al. (2020) recognized Amphisphaeriaceae within the order Amphisphaeriales and identified two constituent genera *viz*. *Amphisphaeria* and *Griphosphaerioma*. Primarily, members of this family are saprobic, thriving in terrestrial, aquatic and marine environments, with occasional reports of endophytic occurrences (Wang et al. 2004, 2023, Senanayake et al. 2015, Jaklitsch et al. 2016, Liu et al. 2024).

Figure 5 – *Distoseptispora sichuanensis* (HKAS 130264, holotype). a Substrate. b, c Colonies on natural substrate. d–f Young to mature conidia attached to conidiophores. g–k Matured conidia. l Upper view. m Reverse view of the one-week-old colony on PDA. Scale bars: d–f = 20 μm, g–k 100 μm.

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

Notes – *Amphisphaeria* was introduced by Cesati & De Notaris (1863) with type species *A. umbrina*. This genus is recognized for producing both coelomycetous and hyphomycetous asexual morphs and is characterized by saprobic and endophytic lifestyles (Samarakoon et al. (2020, Wang et al. 2023, Hyde et al. 2024). *Amphisphaeria* comprises 33 species which are in terrestrial habitats (Li et al. 2024). We update the phylogenetic classification for the genus *Amphisphaeria*, incorporating DNA analyses from LSU, ITS, *rpb*2 and *tub*2 markers. Based on morphological and phylogenetic assessments, we identified five new species within this genus: *Amphisphaeria ailaoshanensis*, *A. kunmingnensis*, *A. magna*, *A. shangrilaensis* and *A. xishuangbannanensis*. Out of 33 species, only 22 have had molecular data and we provide five species with molecular data, further improving the phylogenetic classification of this genus.

Amphisphaeria ailaoshanensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 6, 5

MycoBank number: MB850206; Facesoffungi number: FoF14896

Etymology – The specific epithet is derived from the Ailaoshan, where the holotype was collected

Holotype – HKAS 130266

Saprobic on dead twigs of an unidentified host. Sexual morph: *Ascomata* 100–140 μm high × 250–350 μm diameter ($\overline{x}$ = 124.6 × 319 μm, n = 5), immersed, visible as black spots solitary or aggregated, scattered, globose to subglobose, clypeus absent, papillate, conical with mostly flattened base. *Ostioles* 120–170 μm high × 80–130 μm wide ($\overline{x}$ = 152 × 111 μm, n = 5), long neck, ostiolar canal long periphysate, hyaline periphyses. *Peridium* 30–50 μm wide ($\overline{x}$ = 42 μm), multi-layered; outer layer comprising bright-brown, thick-walled cells of *textura angularis*, inner layer comprising hyaline, thin-walled cells of *textura angularis. Paraphyses* 3–6 μm ($\overline{x}$ = 4.5 μm) wide, hyaline, highly delicate, cellular, constricted septate, with a blunt end, guttulate, embedded in a gelatinous matrix. *Asci* 70–100 μm × 7–10 μm (86.9 × 8 μm, n = 10), 8-spored, unitunicate, cylindrical, thin-walled, short-pedicellate, apically rounded, with a J- apical ring. *Ascospores* 14–20 μm × 5–8 μm ($\overline{x}$ = 16.6 × 6.6 μm, n = 30), uniseriate, fusiform, hyaline, guttulate, turning brown, 1–3 septate, smooth-walled, without mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – colonies on PDA, reaching 20 mm diameter after one week at 25 °C; colonies are raised, white and dense, uneven margin, media becoming pale brown; reverse blackish at center and light brown to yellow edges.

Material examined – CHINA, Yunnan Province, Ailaoshan (24.536944 N, 101.019444 E, 2500m), on dead twigs of an unidentified host, 20 August 2022, L. Qinxing, DWALS10 (HKAS 130266, holotype), ex-type, KUNCC 23-15520. *ibid*. DWALS10A (HKAS 130267, isotype), ex-isotype, KUNCC 23-15521.

GenBank accession numbers – ITS = PP584673, PP584674, LSU = PP584770, PP584771.

Notes – *Amphisphaeria ailaoshanensis* exhibits solitary or aggregated, scattered, globose to subglobose and papillate ascomata, with 8-spored, unitunicate asci and brown, guttulate ascospores, similar to other species within the *Amphisphaeria*. In phylogenetic analyses, *Amphisphaeria ailaoshanensis* (HKAS 130266) forms a cluster with *A. umbrina*; however, their relationship is not statistically supported by either ≥60% MLB or 0.95 BYPP. The LSU and ITS sequence of *A. ailaoshanensis* differs from that of *A. umbrina* 35/697 (5%) and 48/574 (8.4%) respectively. *Amphisphaeria ailaoshanensis* has immersed ascomata measuring 100–140 μm in height by 250–350 μm in diameter, has comparatively longer ostioles at 120–170 μm with hyaline periphyses and smaller asci measuring 70–100 × 7–10 μm with J- apical ring. Additionally, its 1–3 septate ascospores are 14–20 × 5–8 μm and lacks a mucilaginous sheath. In contrast, *Amphisphaeria umbrina* ascomata are immersed beneath a clypeus, larger (560–640 × 400–480 μm) and have shorter ostioles. The asci are larger, measuring 150–170 × 11–13 μm, with J+ apical ring and the 1-septate ascospores are 18–22 × 6–8 μm (Wang 2000).

Amphisphaeria kunmingensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 6, 8

MycoBank number: MB850207; Facesoffungi number: FoF14897

Etymology – The specific epithet is derived from the Kunming city, where the holotype was collected.

Holotype – HKAS 130268

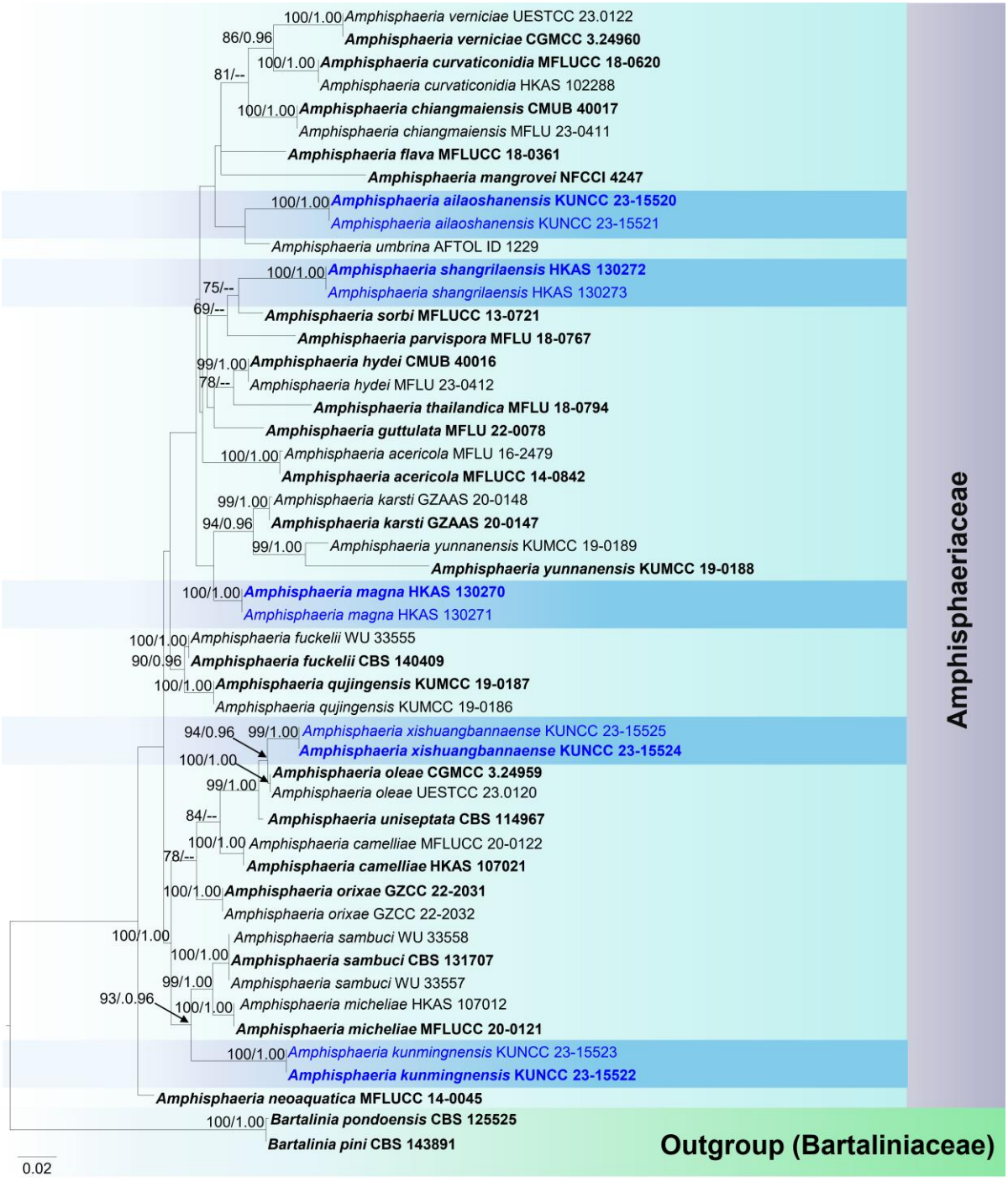

Figure 6 – RAxML phylogram generated from combined dataset of partial LSU, ITS, *rpb*2 and *tub*2 DNA sequence analyses for Amphisphaeriaceae. The final likelihood value is -4433.852252. The tree is rooted to *Bartalinia pini* (CBS 143891) and *B. pondoensis* (CBS 125525). The matrix had 1220 distinct alignment patterns with 4.05% undetermined characters and gaps. Estimated base frequencies were; A = 0.255304, C = 0.207359, G = 0.286377, T = 0.250960 substitution rates AC = 0.958930, AG = 3.001692, AT = 1.628390, CG = 0.938530, CT = 9.041500, GT = 1.000000; gamma distribution shape parameter α = 0.632688. Newly generated sequences are in blue. Ex-type/type strains are indicated in black bold.

Saprobic on dead twigs of an unidentified deciduous host. Sexual morph: *Ascomata* 170–240 µm high × 300–400 µm diameter ($\bar{x}$ = 200 × 356 µm, n = 5), immersed, visible as black spots, solitary or aggregated, scattered, globose to subglobose, papillate, conical with mostly flattened base. *Ostioles* 70–100 µm high × 60–90 µm wide ($\bar{x}$ = 89 × 80 µm, n = 10), ostiolar canal periphysate, orange periphyses. *Peridium* 20–40 µm wide ($\bar{x}$ = 29 µm, n = 10), wider at the apex and near to ostioles, multi-layered, outer layer comprising blackish-brown, thick-walled cells of *textura angularis*, inner layer composed of pale brown, thin-walled cells of *textura angularis*. *araphyses* 4–6 µm ($\bar{x}$ = 5 µm, n = 10) wide, longer than asci, hyaline, cellular, constricted septate, blunt ends, guttulate, embedded in a gelatinous matrix. *Asci* 80–120 µm × 6–12 µm ($\bar{x}$ = 97.8 × 8.3 µm, n = 15), 8-spored, unitunicate, cylindrical, thin-walled, apically rounded, with a J-, apical ring, short-pedicellate. *Ascospores* 12–20 µm × 6–8 µm ($\bar{x}$ = 15.7 × 7.6 µm, n = 20), uniseriate, oblong or narrowly fusiform, first hyaline, guttulate, turning yellow to yellowish-brown, with a median septum, slightly constricted at the septum, straight to slightly curved, smooth-walled, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – colonies on PDA, reaching 20 mm diameter after one week at 25 °C; colonies are flat, circular and dense, with a smooth surface, entire margin, concentrically zonate, black, grey to white, media becoming pale brown, reverse blackish at center and light brown edges.

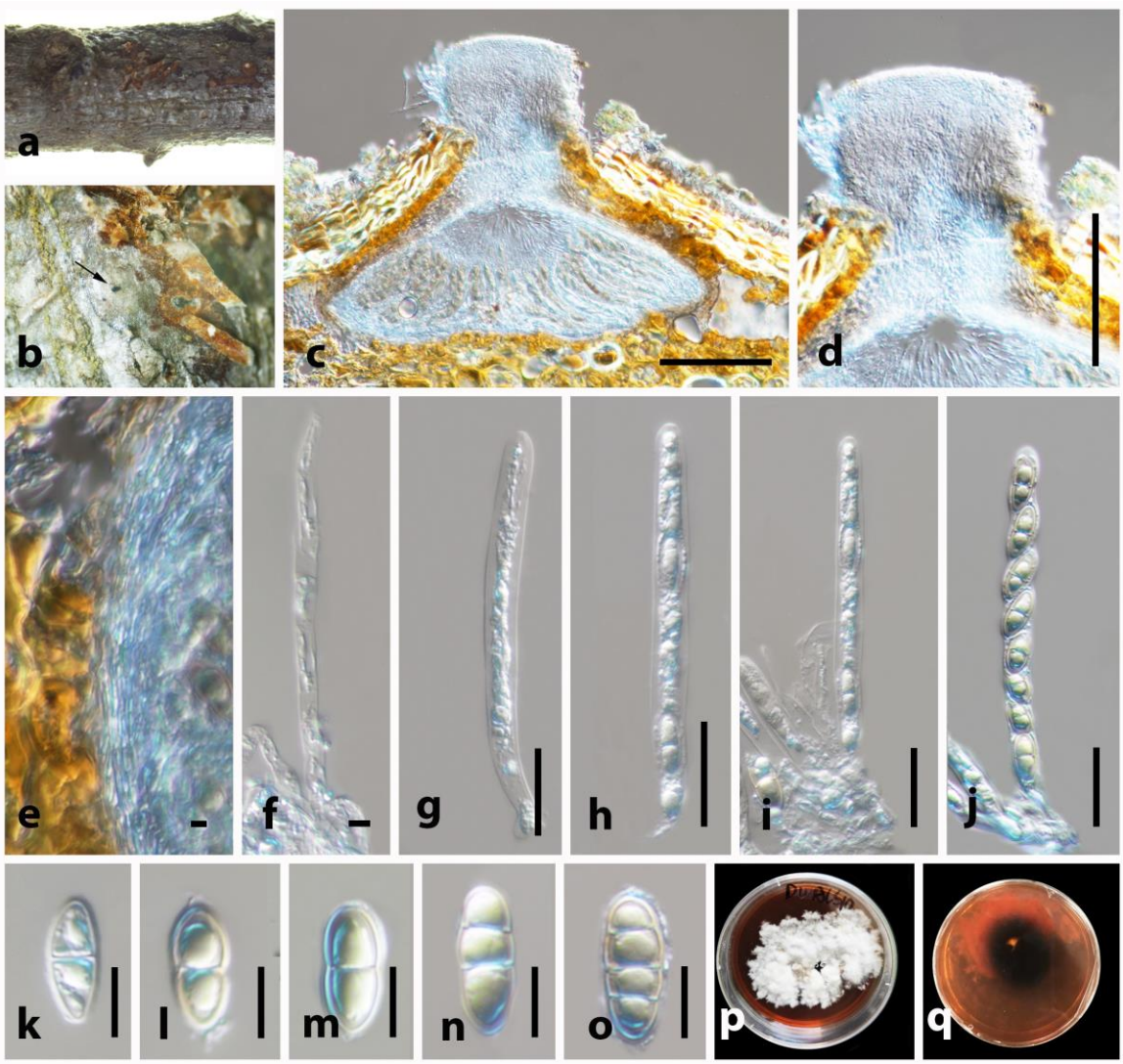

Figure 7 – *Amphisphaeria ailaoshanensis* (HKAS 130266, holotype). a Substrate. b Ascomata on the host surface (arrowed). c Section of an ascoma. d Close up of an ostiole. e Peridium. f Paraphyses. f–j Asci. k–o Ascospores. p, q Colonies on PDA after 6 weeks. Scale bars: c = 100 µm, d = 50 µm, f = 5 µm, g–j = 20 µm e, k–o = 10 µm.

Material examined – CHINA, Yunnan Province, Botanical Garden, Kunming Institute of Botany (25.140833 N, 102.739444 E, 1892 m), on dead twigs of an unidentified deciduous host, 4 April 2022, L. Qinxian, KIB22-24 (HKAS 130268, holotype), ex-type, KUNCC 23-15522. *ibid*. KIB22-24A (HKAS 130269, isotype), ex-isotype, KUNCC 23-15523.

GenBank accession numbers – ITS = PP584675, PP584676, LSU = PP584772, PP584773.

Notes – *Amphisphaeria kunmingensis* form a distinct lineage from other *Amphisphaeria* species in the phylogenetic results, supported by 93% MLB and 0.96 BYPP statistical values (Fig. 4). Multi-gene phylogenetic analysis reveals that our novel species is closely related to *A. micheliae* (MFLUCC 20-0121, HKAS 107012) and *A. sambuci* (CBS 131707, WU 33557, and WU 33558), with statistical support values of 99% ML and 1.00 BYPP. The LSU sequence of *Amphisphaeria kunmingensis* differs from that of *A. micheliae* and *A. sambuci* in 36/697 (5.2%) and 24/697 (3.5%), respectively, while the ITS is in 41/574 (7.1%) and 42/574 (7.3%), respectively. *Amphisphaeria kunmingensis* resembles *A. micheliae*, in having ascomata with prominent ostioles, short pedicellate and apically rounded asci with 1-septate, light brown, guttulate ascospores. However, *Amphisphaeria kunmingensis* differs from both *A. micheliae* and *A. sambuci* in having conical ascomata with a predominant flat base, larger ostioles with orange periphyses (89 × 80 μm *vs* 68 × 42 μm), and a J- apical ring in Melzer's reagent (Samarakoon et al. 2020). Based on morphology and molecular data we introduce *Amphisphaeria kunmingensis* as new species.

Amphisphaeria magna L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 6, 9

MycoBank number: MB850208; Facesoffungi number: FoF14898

Etymology – The specific epithet is derived from the Latin word meaning 'large', in reference to the large ascomata.

Holotype – HKAS 130270

Saprobic on dead twigs of an unidentified host. Sexual morph: *Ascomata* 300–350 μm high × 450–520 μm diameter ($\overline{x}$ = 322.7 × 503.6 μm, n = 5), immersed, visible as black spots solitary or aggregated, scattered, globose to subglobose, beneath a poorly developed clypeus, papillate, in cross section conical with mostly flattened base. *Ostioles* 90–120 μm high × 50–100 μm diameter ($\overline{x}$ = 77.7 × 107.1 μm), ostiolar canal periphysate light brown to yellowish short periphyses. *Peridium* 20–40 μm wide ($\overline{x}$ = 28 μm, n = 5) multi-layered, outer layer comprising blackish-brown, thick-walled cells of *textura angularis*, inner layer composed of pale brown to hyaline, thin-walled cells of *textura angularis*, thin-walled, loosely arranged. *Paraphyses* 4–5 μm ($\overline{x}$ = 4.9 μm, n = 10) wide, hyaline, highly delicate, cellular, constricted septate, guttulate, longer than asci, with a blunt end, embedded in a gelatinous matrix. *Asci* 100–150 μm × 12–20 μm diameter ($\overline{x}$ = 133 × 14 μm, n = 20), 8-spored, unitunicate, cylindrical, straight to slightly curved, thin-walled, short-pedicellate, apically rounded, with a J- apical ring, *Ascospores* 15–25 μm × 9–13 μm ($\overline{x}$ = 20.4 × 11 μm, n = 20), uniseriate, fusiform, hyaline when immature, turning brown when mature, bi-guttulate, with a median septum, straight to slightly curved, smooth-walled, without mucilaginous sheath. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Shangri-La, Deqen, Skied filed (27.935833 N, 99.608056 E, 2250m), on dead twigs of unidentified host, 18 August 2021, L. Qinxian, SF17-1 (HKAS 130270, holotype). *ibid*. SF17-1A (HKAS 130271, isotype).

GenBank accession numbers – ITS = PP584677, PP584678, LSU = PP584774, PP584775.

Notes – *Amphisphaeria magna* shows characteristics typical of the genus *Amphisphaeria*, including solitary, immersed, ostiolate ascomata, 8-spored, unitunicate asci and brown, septate ascospores. While *Amphisphaeria magna* has a close phylogenetic relationship with *A. yunnanensis*, their affiliation does not receive strong statistical support (Fig. 4). The nucleotide differences in the LSU and ITS between *Amphisphaeria magna* and *A. yunnanensis* are 41/697 (5.8%) and 84/574 (14.6%), respectively. However, *Amphisphaeria magna* can be distinguished from *A. yunnanensis* by its immersed ascomata, which are situated beneath a poorly developed clypeus and appear conical in cross-section with a mostly flattened base. Furthermore, *Amphisphaeria magna* is characterized by larger ascomata, with measurements of 322.7 × 503.6

μm, in contrast to the globose to sub-globose, dark reddish-brown and smaller ascomata of *A. yunnanensis*, which are 352.5 × 415 μm (Dissanayake et al. 2020). Other distinguishing features of *Amphisphaeria magna* include a shorter ostiole (77.7 × 107.1 μm vs. 132.5 × 30 μm), longer asci (133 × 14 μm vs. 85.5 × 7.5 μm) and large (20.4 × 11 μm), bi-guttulate, straight to slightly curved ascospores, compared to the smaller (13.5 × 5 μm), multi-guttulate, straight to slightly pointed ascospores of *A. yunnanensis* (Dissanayake et al. 2020). Based on phylogenetic evidence and morphological differences, we have introduced our new collection as a distinct species, *Amphisphaeria magna*.

Amphisphaeria shangrilaensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 6, 10

MycoBank number: MB850209; Facesoffungi number: FoF14899

Etymology – The specific epithet is derived from the Shangri-La, the location where the holotype was collected.

Holotype – HKAS 130272

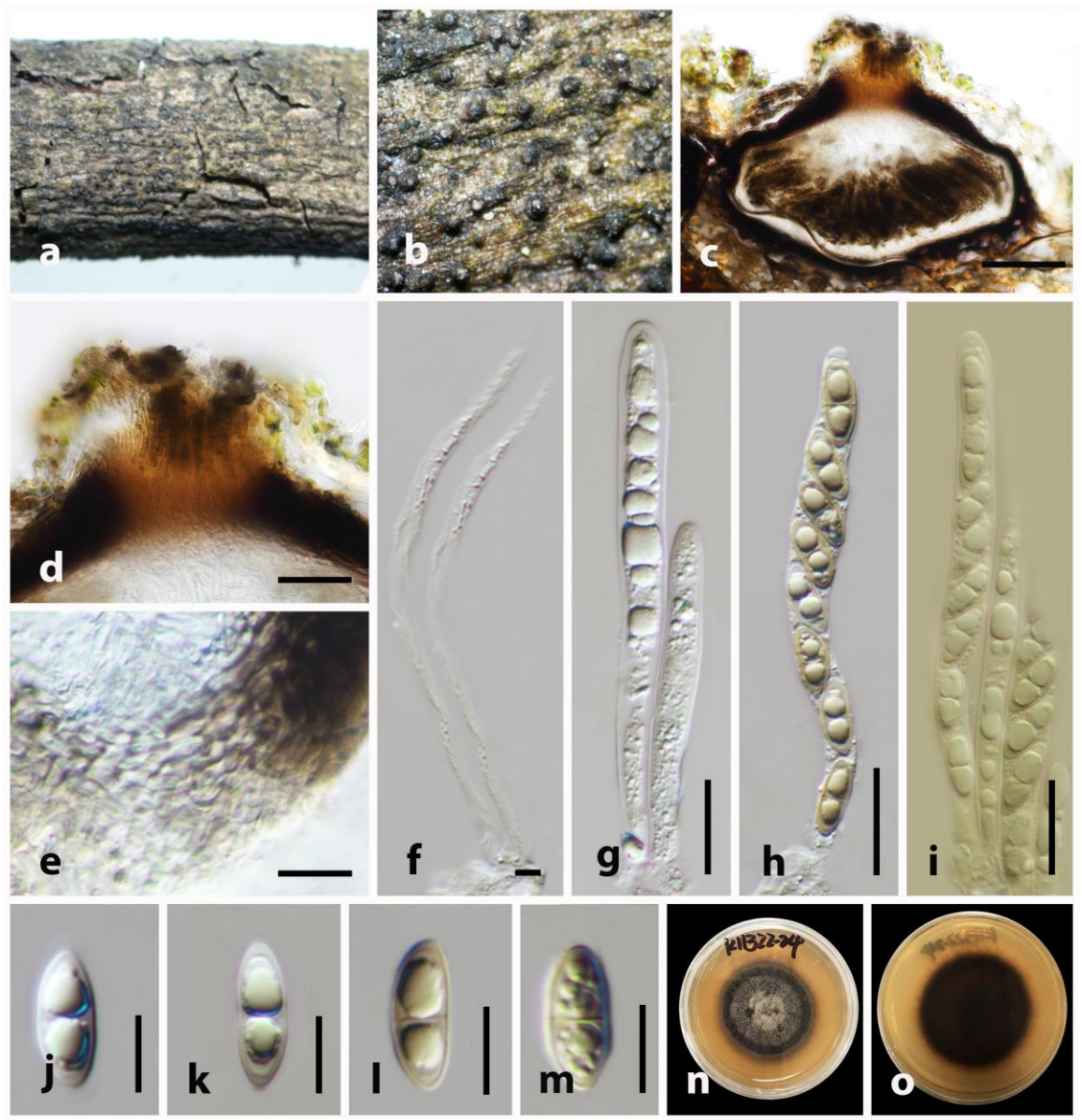

Figure 8 – *Amphisphaeria kunmingensis* (HKAS 130268, holotype). a Substrate. b Ascomata on the host surface. c Section of an ascoma. d Section through an ostiole. e Peridium. f Paraphyses. g–i Asci (i = Asci in Melzer's reagent). j–m Ascospores. n, o Colonies on PDA after 6 weeks. Scale bars: c = 100 μm, d = 50 μm, e, g–i = 20 μm, f, j–m = 5 μm.

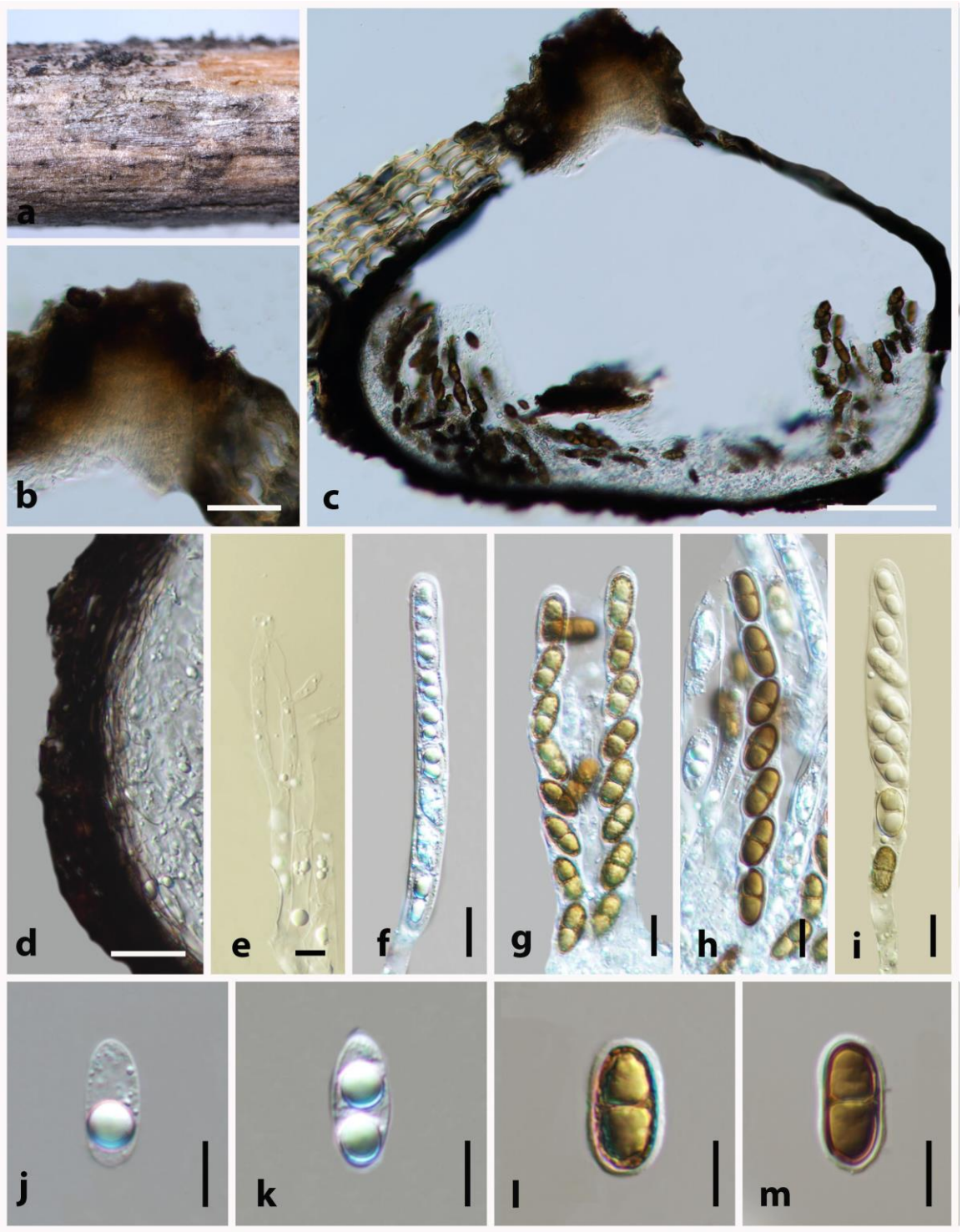

Figure 9 – *Amphisphaeria magna* (HKAS 130270, holotype). a Substrate. b Section through ostioles. c Section of an ascoma. d Peridium. e Paraphyses (in Melzer's reagent). f–i Asci (i Asci in Melzer's reagent). j–m Ascospores. Scale bars: b = 50 μm, c = 100 μm, d = 20 μm, e = 5 μm, f–i = 20 μm, j–m = 10 μm.

Saprobic on dead twigs of an unidentified host. Sexual morph: *Ascomata* 200–300 μm high × 400–500 μm diameter ($\overline{x}$ = 271.9 × 454.7 μm, n = 5), immersed, visible as black spots solitary or aggregated, scattered, globose to subglobose, beneath a poorly developed clypeus, papillate. *Ostioles* 60–90 μm diameter ($\overline{x}$ = 70.6 μm, n = 5), ostiolar canal periphysate, with hyaline periphyses. *Peridium* 50–80 μm wide ($\overline{x}$ = 58.9 μm, n = 10) multi-layered, outer layer comprising brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of

textura angularis. *Paraphyses* 4–6 μm (5.3 μm, n = 10) wide, hyaline, highly delicate, cellular, constricted septate, with a blunt end, guttulate, embedded in a gelatinous matrix. *Asci* 90–120 μm × 9–13 μm ($\overline{x}$ = 105.2 × 10.5 μm) 8-spored, unitunicate, cylindrical, thin-walled, short-pedicellate, apically rounded, with a J+, apical ring. *Ascospores* 17–22 μm × 6–11 μm ($\overline{x}$ = 19.8 × 8.9 μm) uniseriate, fusiform, bi-guttulate, at first hyaline, turning brown, with a median septum, slightly constricted at the septum, smooth-walled, with thin mucilaginous sheath. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Beng Chinandang, Shangri-La (28.040556 N, 99.443333 E, 3390m), on dead twigs of an unidentified host, 18 August 2021, L. Qinxian, BNCD17 (HKAS 130272, holotype). *ibid*. BNCD17A (HKAS 130273, isotype).

GenBank accession numbers – ITS = PP584679, PP584680, LSU = PP584776, PP584777.

Notes – In our phylogenetic analysis, *Amphisphaeria shangrilaensis* has a close phylogenetic affinity to *A. sorbi*, supported by 75% MLB. The nucleotide differences in the LSU and ITS between *A. shangrilaensis* and *A. sorbi* are 35/698 (5%) and 32/574 (5.6%), respectively. *Amphisphaeria shangrilaensis* has asci that are immersed beneath a poorly developed clypeus, with a J+, discoid, apical ring and bi-guttulate ascospores. In contrast, *Amphisphaeria sorbi* has erumpent asci, opening through the cracks of the host surface a J-, apical ring and multi-guttulate ascospores (Senanayake et al. 2015).

Amphisphaeria xishuangbannaense L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 6, 11

MycoBank number: MB850210; Facesoffungi number: FoF14900

Etymology – The specific epithet is derived from Xishuangbanna, where the holotype was collected.

Holotype – HKAS 130451

Saprobic on dead woody branches of an unidentified host. Sexual morph: *Ascomata* 250–300 μm high × 350–400 μm diameter ($\overline{x}$ = 274 × 380 μm, n = 5), immersed, visible as black spots, solitary or aggregated, scattered, globose to subglobose, papillate. *Ostioles* 50–90 μm wide ($\overline{x}$ = 70 μm, n = 10) wide, centric, prominent, conical, periphysate, hyaline with short periphyses. *Peridium* 15–20 μm wide ($\overline{x}$ = 17 μm, n = 5) multi-layered, outer layer comprising reddish-brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of *textura angularis*. *Paraphyses* 5.5–8.5 μm ($\overline{x}$ = 6.8 μm, n = 10) wide, hyaline, highly delicate, cellular, constricted septate, guttulate, longer than asci, embedded in a gelatinous matrix. *Asci* 130–160 × 8–12 μm ($\overline{x}$ = 141 × 10.8 μm, n = 20) 8-spored, unitunicate, cylindrical, thin-walled, long-pedicellate (18–28 μm long), apically rounded, with a J-, apical ring. *Ascospores* 12–16 μm × 5–6 μm ($\overline{x}$ = 14 × 5.7 μm, n = 20) uniseriate, oblong or narrowly fusiform, hyaline when immature, guttulate, turning pale yellow when mature, with a median septum, slightly constricted at the septum, straight to slightly curved, smooth-walled, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – colonies on PDA, reaching 20–22 mm diameter after one week at 25 °C; colonies are flat, circular and dense, with a smooth surface, entire margin, concentrically zonate, White to pale yellow, media becoming pale brown; reverse blackish at center and light brown to yellow edges.

Material examined – CHINA, Yunnan Province, Pineapple Garden, Xishuangbanna (21.868381 N, 101.199819 E), on dead woody branches of unidentified host, 16 February 2023, L.S. Dissanayake, XBPG23-19 (HKAS 130451, holotype), ex-type, KUNCC 23-15524. *ibid*. XBPG23-19A (HKAS 130452, isotype), ex-isotype, KUNCC 23-15525.

GenBank accession numbers – ITS = PP584681, PP584682, LSU = PP584778, PP584779.

Notes – Based on the phylogenetic analysis of multiple genes, *Amphisphaeria xishuangbannaense* has a close relationship with *A. oleae* (UESTCC: 23.0120, CGMCC: 3.24959), supported by 96% MLB and 0.96 BYPP, and *A. uniseptata* (CBS 114967), supported by 96% MLB and 0.98 BYPP (Fig. 4). The LSU sequence of *Amphisphaeria xishuangbannaense* differs from *A. oleae* and *A. uniseptata* by 38/697 (5.5%) and 35/697 (5%), respectively, while the ITS sequence differences are 40/574 (7.5%) and 42/574 (7.3%), respectively. *Amphisphaeria xishuangbannaense*

shares similarities with both *A. oleae* and *A. uniseptata*, exhibiting immersed, solitary or aggregated, scattered ascomata that are globose to subglobose and papillate. It also has hyaline, septate, and guttulate paraphyses that are constricted at the septum. The asci are 8-spored, unitunicate, and cylindrical and apically rounded, while the ascospores are uniseriate, oblong or narrowly fusiform, guttulate, and feature a median septum slightly constricted at the septum.

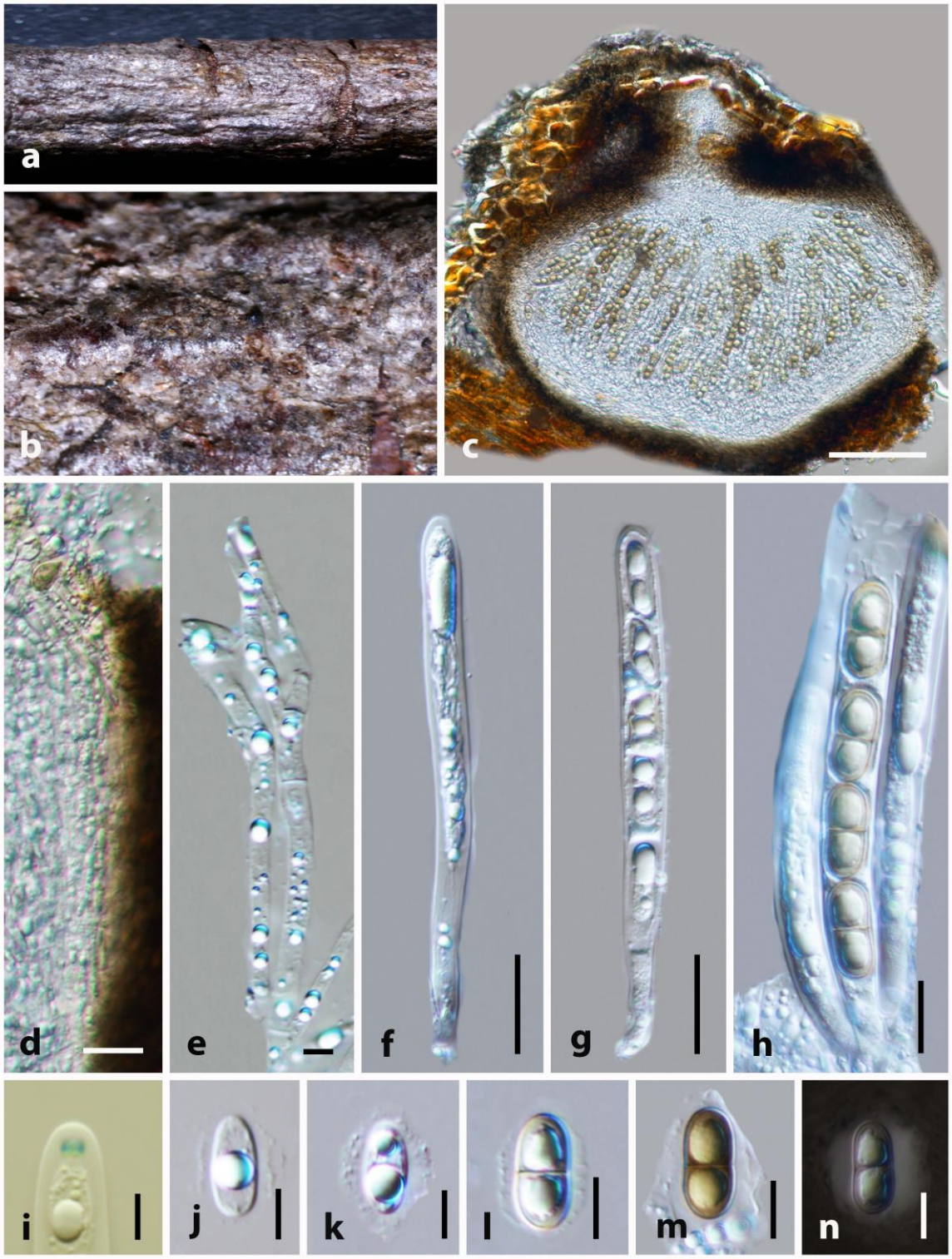

Figure 10 – *Amphisphaeria shangrilaensis* (HKAS 130272, holotype). a Substrate. b Ascomata on the host surface. c Section of an ascoma. d Peridium. e Paraphyses. f–h Asci. i Apical ring bluing in Melzer's reagent. j–n Ascospores (n stain with Indian ink). Scale bars: c = 100 μm, d = 50 μm, e = 5 μm, f–h = 20 μm, i–n = 10 μm.

However, *Amphisphaeria xishuangbannaense* can be differentiated from *A. uniseptata* by its J- asci, which have a comparatively longer pedicel, in contrast to the J+ asci with a shorter pedicel found in the others (Tsui et al. 2001). *Amphisphaeria xishuangbannaense* differs from *A. oleae* in having larger ascomata (274 × 380 μm vs. 230 × 320 μm) and longer asci (141 × 10.8 μm vs. 101 × 7.5 μm). *Amphisphaeria oleae* was collected from decaying branches of *Olea europaea* in Sichuan Province, China (Li et al. 2024). In this study, we introduce *Amphisphaeria xishuangbannaense* as a new species from dead woody twigs in Yunnan province, China.

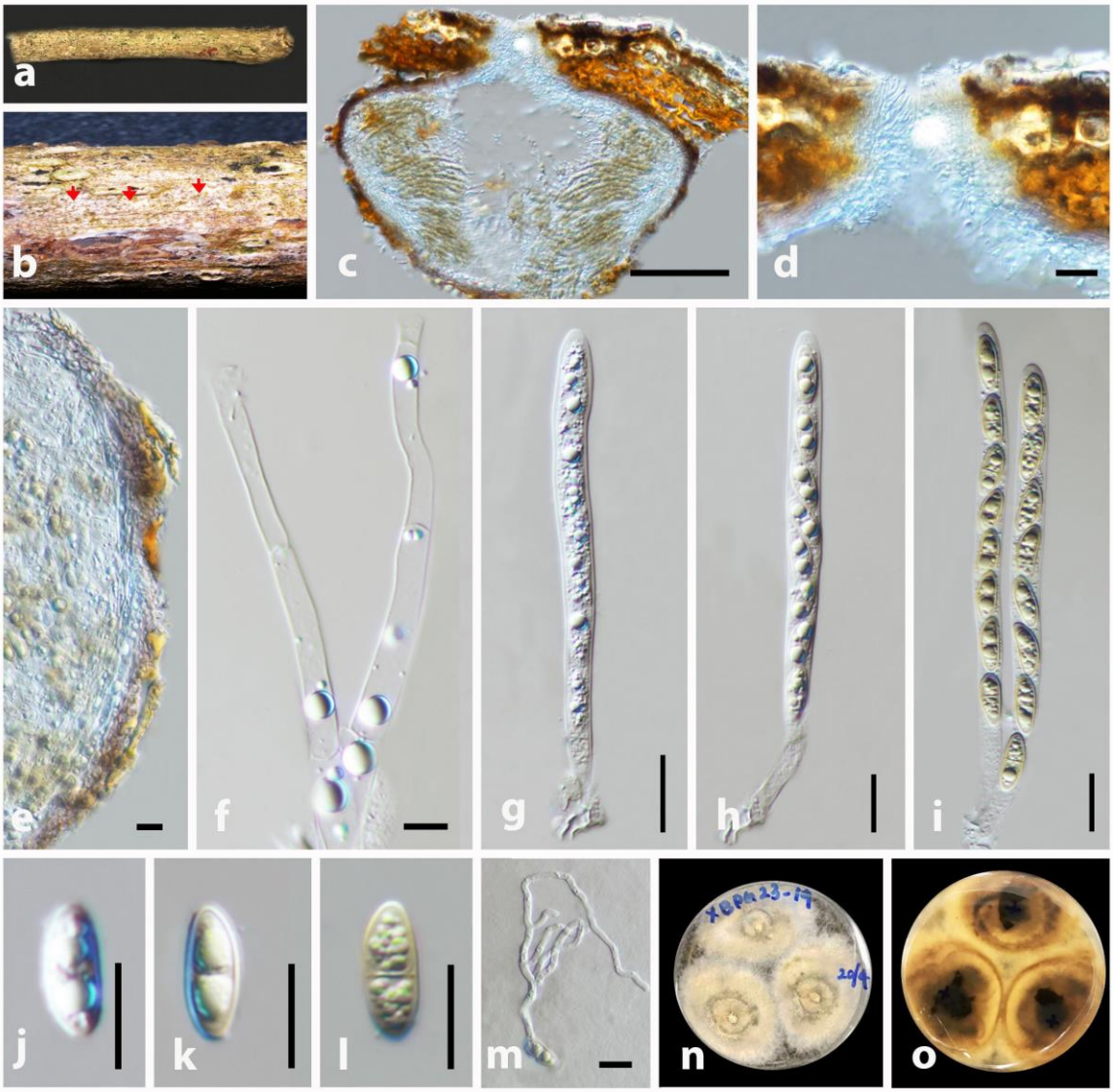

Figure 11 – *Amphisphaeria xishuangbannaense* (HKAS 130451, holotype). a Substrate. b Ascomata on the surface. c Section of an ascoma. d Section through ostiole. e Peridium. f Paraphyses. g–i Asci. j–n Ascospores. m Germinated ascospore. n, o One-week-old colony on PDA (o from the bottom). Scale bars: c = 100 μm, d, g–i = 20 μm, e, f = 5 μm, j–m = 10 μm.

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr, Sydowia 50(1): 23 (1998)

Notes – The family Apiosporaceae was introduced by Hyde et al. (1998), with *Apiospora* designated as its type genus (Yuan et al. 2020). The family was established to encompass taxa characterized by the apiospores and a basauxic, arthrinium-like conidiogenesis (Samuels et al. 1981, Senanayake et al. 2015, Dai et al. 2017, Wang et al. 2018, Pintos et al. 2019). Currently, the family includes three genera: *Apiospora*, *Arthrinium* and *Nigrospora* (Pintos & Alvarado 2021, Senanayake et al. 2023). Members of the Apiosporaceae are saprobes and pathogens affecting plants, lichens and soil, and on rare occasions, they can infect humans (Seifert et al. 2011, Crous &

Groenewald 2013, Pintos et al. 2019, Senanayake et al. 2020b, Feng et al. 2021). Consequently, species within the Apiosporaceae hold significant economic, environmental and medicinal importance (de Hoog et al. 2000, Jiang et al. 2018b).

Apiospora Sacc., Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 4 4: 85 (1875)

Notes – *Apiospora* was initially introduced by Saccardo (1875) without specifying a type species. Later, Saccardo et al. (1931) designated *Apiospora montagnei* as the lectotype of the genus. The sexual morph of *Apiospora* is characterized by multi-locular, perithecial stromata with hyaline ascospores that are surrounded by a thick gelatinous sheath (Senanayake et al. 2015, Pintos & Alvarado 2021). The asexual morph of this genus is known for its basauxic conidiogenesis, with pale brown to brown, globose to sub-globose, obovoid to fusiform conidia (Hyde et al. 1998, 2024, Dai et al. 2016). Due to the morphological similarities among *Apiospora* species, molecular data are required to distinguish between them. *Apiospora* was synonymized under *Arthrinium* by Crous & Groenewald (2013). Pintos & Alvarado (2021) demonstrated that some *Arthrinium* species form a monophyletic basal clade to *Apiospora*, suggesting this clade as distinct within *Arthrinium*. *Apiospora* species are cosmopolitan, with a wide range of hosts and substrates. They can be endophytes, phytopathogens, or saprobes and some are associated with lichens, air, or soil-borne (Dai et al. 2017, Wang et al. 2017, 2018, Hyde et al. 2020a, Senanayake et al. 2020b, 2023, Pintos & Alvarado 2021). A few species have been identified as pathogens in animals and humans, capable of causing Onychomycosis (Goodenough et al. 2017, Dyląg et al. 2017). Some species of *Apiospora* produce antifungal metabolites, such as Apiosporamide, which was discovered by Alfatafta et al. (1994). Currently, there are 121 species listed in this genus (Species Fungorum 2024).

Apiospora arecacearum L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 12, 13

MycoBank number: MB852801; Facesoffungi number: FoF15545

Etymology – Referring to the host family Arecaceae, from which the holotype was collected.

Holotype – HKAS 133084

Saprobic on dry branches of *Trachycarpus fortunei*. Sexual morph: Undetermined Asexual morph: Colonies on natural substrate are dry, dark brown to black, velvety, dull, consisting of a sterile mycelial outer zone and round, sporulating centre, with conidia readily liberated when disturbed. *Hyphae* 2–4 μm diameter micronematous, hyaline, branched, thick-walled, septate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* arising from hyphae, holoblastic, monoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* 8–11 μm diameter ($\overline{x}$ = 10 μm, n = 20), globose to subglobose, aseptate, golden yellow to dark brown, with an equatorial germ-slit.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colony surfaces are white to off white, flat, spreading, filiform, with abundant aerial mycelia and reverse yellow.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.075 N, 103.564167 E, 1065.01m), on dead stem of *Trachycarpus fortunei* (Arecaceae), 5 January 2023, L. S. Dissanayake, SCCFP23-01 (HKAS 133084, holotype). ex-type KUNCC23-15554. *ibid*. SCCFP23-01A (HKAS 133083, isotype), ex-isotype KUNCC23-15555. SCCFP23-05. *ibid*. SCCFP23-05 (HKAS 133085).

GenBank accession numbers – ITS = PP584683, PP584684, PP584685, LSU = PP584780, PP584781, PP584782, *tef*1-α = PP933191, PP933192, *tub*2 = PP982282, PP982283, PP982284.

Notes – Three strains (KUNCC23-15554, KUNCC23-15555 and SCCFP23-05), representing *Apiospora arecacearum*, formed a clade and appeared closely related to *A. lageniformis* and *A. jiangxiensis*, with 97% MLB and 1.00 BYPP support (Fig. 12). Base-pair comparisons of the ITS, *tef*1-α and tub2 gene regions showed differences of 2% (8/392 bp), 2.4% (10/414 bp) and 2.6% (12/460 bp) between *Apiospora arecacearum* and *A. lageniformis*, and differences of 2.8% (11/392 bp), 3.8% (16/414 bp), and 4.5% (21/460 bp) between *A. arecacearum* and *A. jiangxiensis*.

Apiospora arecacearum is distinguishable from *A. lageniformis* and *A. jiangxiensis* by having holoblastic, monoblastic, hyaline, cylindrical, straight conidiogenous cells and globose to subglobose, golden yellow to dark brown conidia. In contrast, *Apiospora lageniformis* has polyblastic, lageniform conidiogenous cells and globose to ellipsoid, green to dark brown conidia (Known et al. 2022), while *A. jiangxiensis* has aggregated hyphae, ampulliform conidiogenous cells, and globose to ellipsoid, brown conidia (Wang et al. 2018). Based on these molecular and morphological differences, we introduce *Apiospora arecacearum* as a novel species, with three strains acquired from the *Trachycarpus fortunei* (Arecaceae) in Sichuan Province, China.

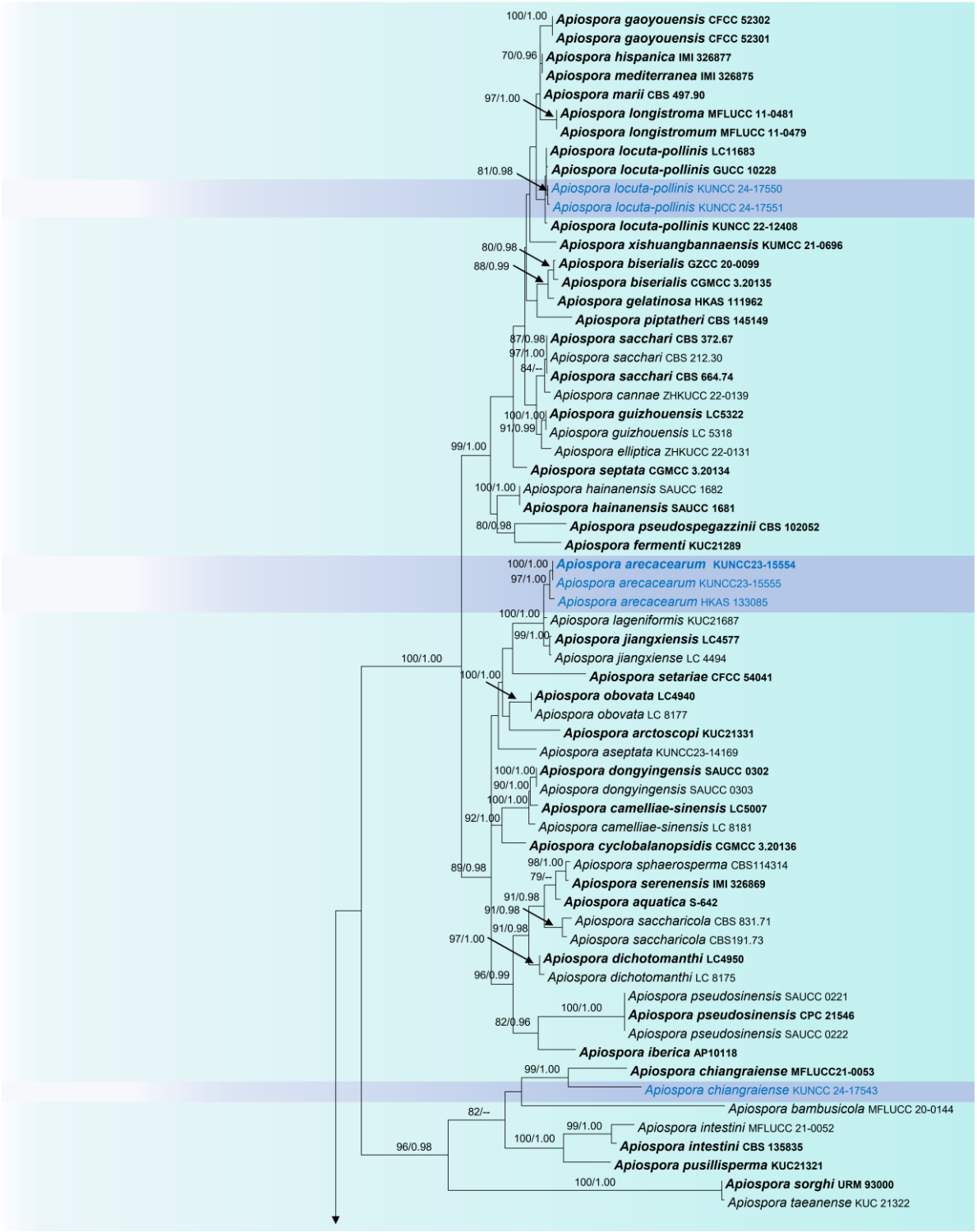

Figure 12 – RAxML phylogram generated from combined dataset of partial LSU, ITS, *tef*1-α and

*tub*2 DNA sequence analyses for Apiosporaceae. The final likelihood value is -25665.118197. The tree is rooted to *Nigrospora camelliae-sinensis* (CGMCC 3.18125) and *N. chinensis* (CGMCC 3.18127). The matrix had 2300 distinct alignment patterns with 20.73% undetermined characters and gaps. Estimated base frequencies were; A = 0.235281, C = 0.247771, G = 0.263297, T = 0.253651 substitution rates AC = 1.214508, AG = 2.842115, AT = 1.106454, CG = 0.974982, CT = 4.448903, GT = 1.000000; gamma distribution shape parameter α = 0.271762. Newly generated sequences are in blue. Ex-type/type strains are indicated in black bold.

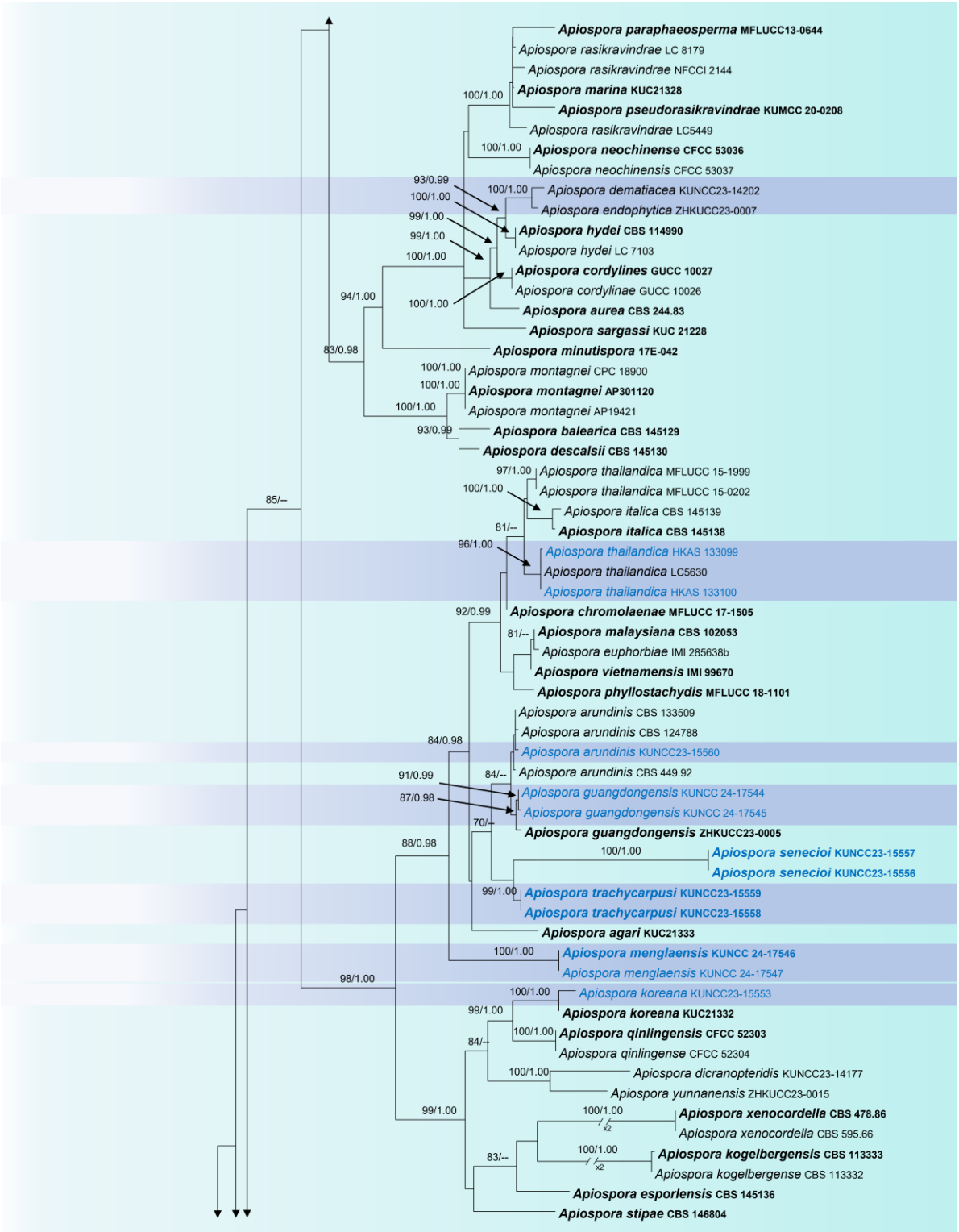

Figure 12 – Continued.

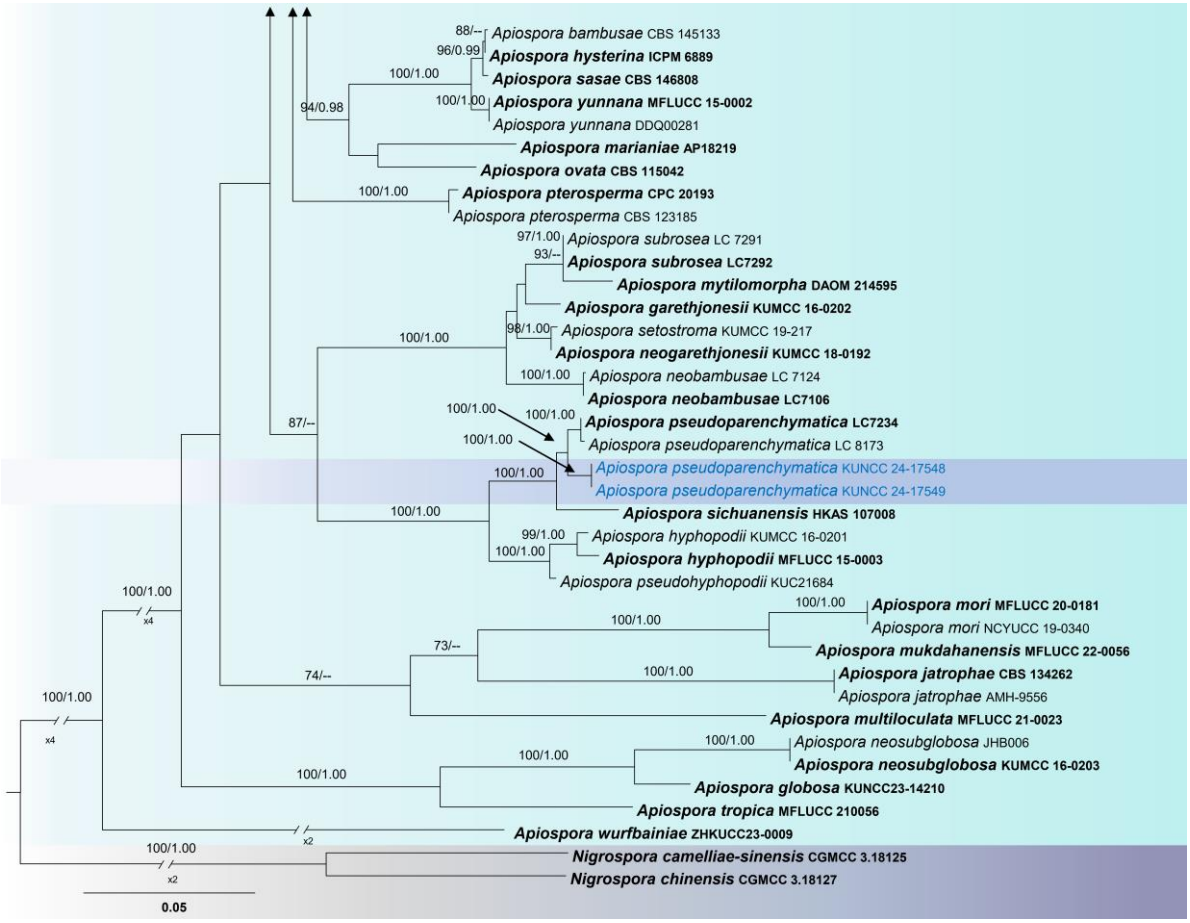

Figure 12 – Continued.

Apiospora arundinis (Corda) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 205 (2021) Figs 12, 14

MycoBank number: MB837742; Facesoffungi number: FoF13417

Saprobic on dry stems of unidentified host. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after one month, spore mass visible as black, scattered to aggregated on white colonies. *Hyphae* 3–5 µm diameter, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–6 µm diameter holoblastic, monoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* 4–10 µm diameter (x = 7 µm, n = 20) globose to subglobose in surface view, lenticular in side view, golden brown to dark brown, rough walled with a pale equatorial slit.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colonies' surfaces are white, woolly, flat, spreading, filiform, with abundant aerial mycelia and reverse off-white.

Material examined – CHINA, Sichuan Province, Chengdu, Qingyang District, Huanhuaxi park (23.389921 N, 102.225556 E, 1186m), on dead twigs of an unidentified host, 5 January 2023, L.S. Dissanayake, UF23-26 (HKAS 127246), living culture KUNCC23-15560.

GenBank accession numbers – ITS = PP584686, LSU = PP584783, *tef*1-α = PP933193, *tub*2 = PP982285.

Notes – In this study, new isolates designated as HKAS 127246 clustered with *Apiospora arundinis*, as illustrated in Fig. 12. This new collection resembles the *A. arundinis* species as described by Li et al. (2023), in having conidia of a similar size to those reported in previous studies (Chen et al. 2014, Jiang et al. 2021a, Liao et al. 2022). *Apiospora arundinis* has been collected from terrestrial habitats associated with a variety of hosts in China, including *Phyllostachys praecox*, *Castanea mollissima*, *Saccharum officinarum*, *Polygonatum cyrtonema* and

Brunfelsia brasiliensis (Chen et al. 2014, Jiang et al. 2021a, Liao et al. 2022, Li et al. 2023). It has mostly been reported as a pathogen on plants (Chen et al. 2014, Gong et al. 2023, Li et al. 2023).

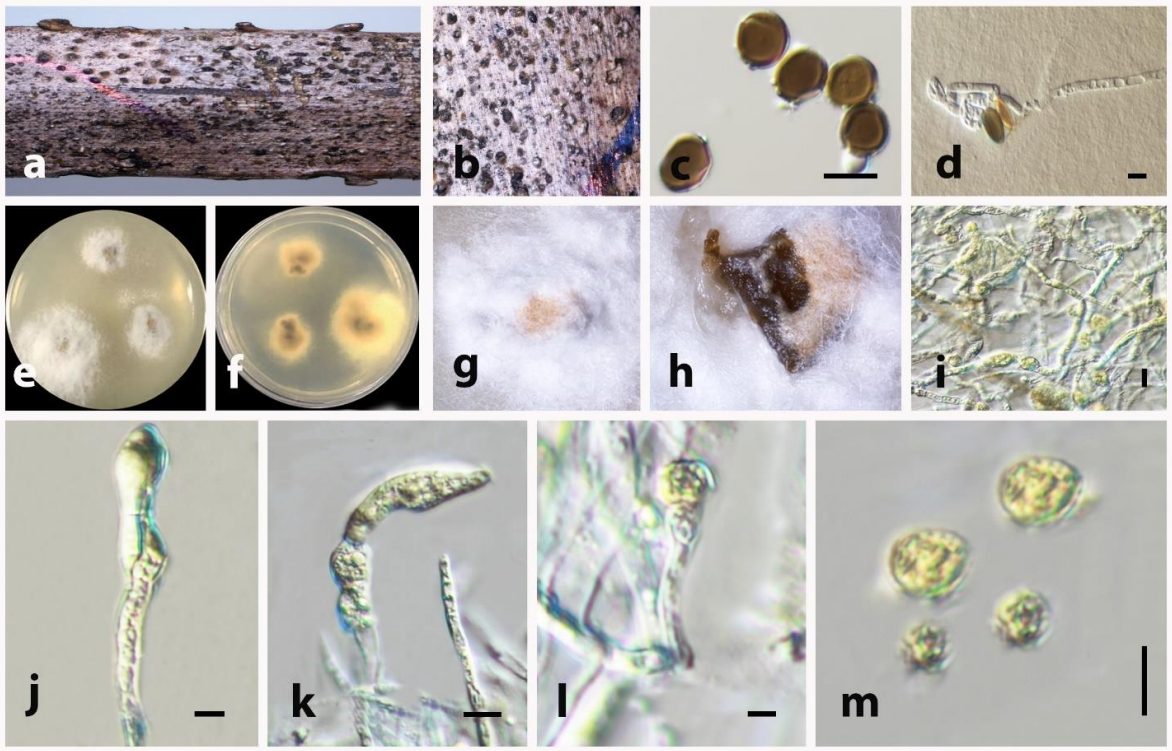

Figure 13 – *Apiospora arecacearum* (HKAS 133084, holotype). a Host. b Conidia on host surface. c, m Conidia. d Germinated conidium. e Upper view. f Reverse view of the two-week-old colony on PDA. g, h Colony on PDA producing conidial masses. i Hyphae. j–l Conidiogenous cells giving rise to conidia. Scale bars: c, d, m = 10 μm, i–l = 2 μm.

Apiospora chiangraiense X.G. Tian & Tibpromma, Life 11(no. 1071): 11 (2021) Fig. 12

MycoBank number: MB558492; Facesoffungi number: FoF09905

See the description in Tian et al. (2021).

Material examined – CHINA, Yunnan Province, Mengla, Xishuangbanna (21.580788 N, 101.434776 E, 776 m), on dead stalk of Poaceae sp. 29 January 2023, L. Qinxian, ML23-01 (HKAS 133090), living culture, KUNCC 24-17543.

GenBank accession numbers – ITS = PP584687, LSU = PP584784, *tef*1-α = PP933194, *tub*2 = PP982286.

Notes – According to the phylogenetic analysis, the new species forms a closely related clade with *Apiospora chiangraiense* (MFLUCC21-0053), supported by 99% MLB and 1.00 BYPP statistical values (Fig. 12). ML23-01 is also similar to *Apiospora chiangraiense*, exhibiting similar shape and size of conidia. *Apiospora chiangraiense* (MFLUCC21-0053) was introduced by Tian et al. (2021), having been collected from dead culms of bamboo in Thailand. In this study, we report an additional collection of *Apiospora chiangraiense*, collected from a dead stalk of grass in Yunnan Province, China.

Apiospora guangdongensis C.F. Liao & Doilom, Journal of Fungi 9(no. 1087): 12 (2023)

Figs 12, 15

MycoBank number: MB900357; Facesoffungi number: FoF14659

Saprobic on dead culms of Poaceae sp. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after one month, spore mass visible as black, scattered to aggregated on white colonies. *Hyphae* 2–4 μm diameter, micronematous, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 μm diameter

arising from hyphae, holoblastic, monoblastic, hyaline, cylindrical, straight, discrete, aseptate, smooth-walled. *Conidia* 5–7 μm diameter ($\bar{x}$ = 6 μm, n = 20), globose to ellipsoidal, aseptate, initially hyaline to dark brown, smooth-walled with a broad equatorial germ-slit.

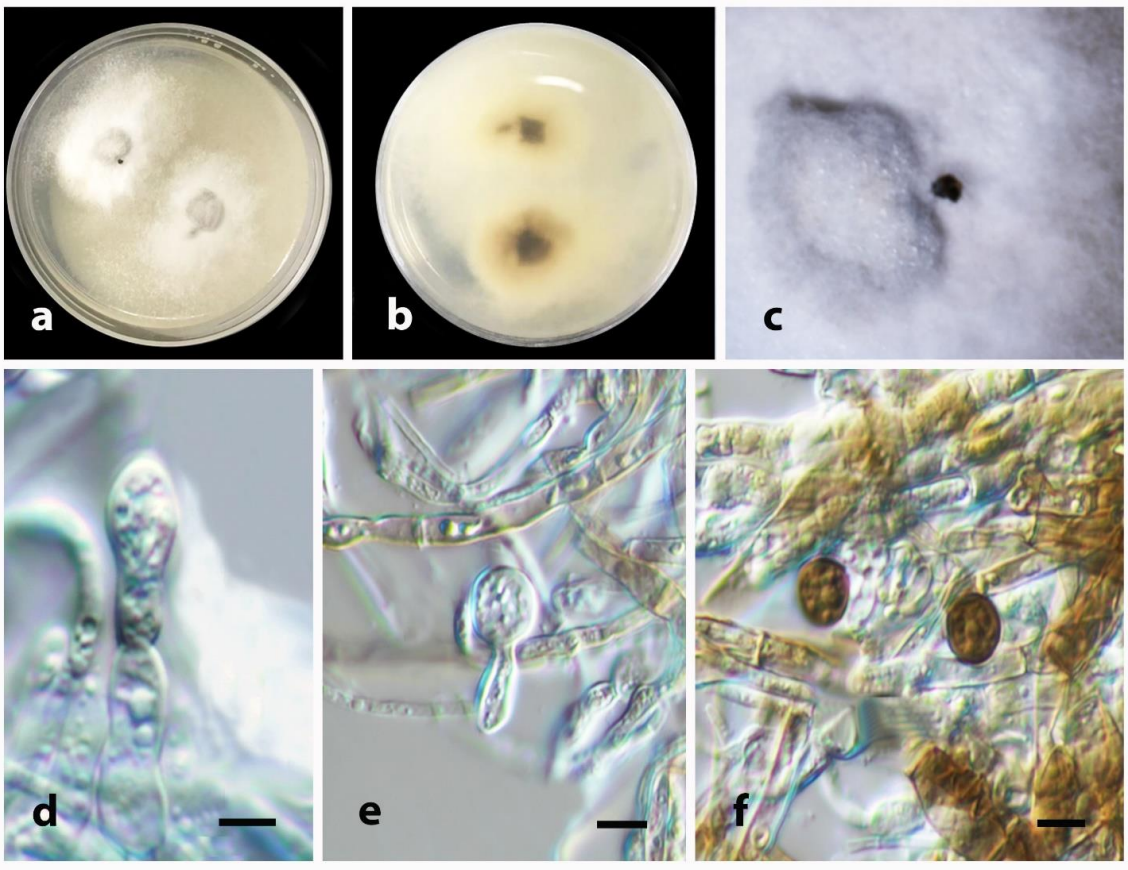

Figure 14 – *Apiospora arundinis* (HKAS 127246). a Upper view. b Reverse view of the two-week-old colony on PDA. c Colony on PDA producing conidial masses. d, e Conidiogenous cells giving rise to conidia. f Conidia. Scale bars: d, e = 5 μm, f = 10 μm.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colony surface is white, yellowish flat, spreading, filiform, with abundant aerial mycelia and reverse yellow.

Material examined – CHINA, Yunnan Province, Mengla, Xishuangbanna (21.580788 N, 101.434776 E, 776 m), on dead culms of Poaceae sp., 29 January 2023, L. Qinxian, ML23-23 (HKAS 133092), living culture, KUNCC 24-17544. *ibid*. ML23-23A (HKAS 133091), living culture KUNCC 24-17545.

GenBank accession numbers – ITS = PP584688, PP584689, LSU = PP584785, PP584786, *tub*2 = PP982287, PP982288, *tef*1-α = PQ001003, PQ001004.

Notes – *Apiospora guangdongensis* (ZHKUCC23-0005), collected from asymptomatic leaves of *Wurfbainia villosa* in Guangdong Province, China, was reported as an endophyte in asymptomatic leaves by Liao et al. (2023). Phylogenetically, *A. guangdongensis* forms a sister branch to *A. arundinis*, receiving high statistical support. *Apiospora guangdongensis* differs from *A. arundinis* in having shorter conidiogenous cells and larger conidia. The conidiogenous cells of *Apiospora guangdongensis* are described as cylindrical or ampulliform and sometimes ovate or obpyriform, in contrast to the ampulliform conidiogenous cells of *A. arundinis* (Liao et al. 2023). In our multigene phylogenetic analysis, two new strains (ML23-23 and ML23-23A) were found to share a close relationship with *A. guangdongensis* based on ML and BI analyses, supported by 87% MLB and 0.98 BYPP (Fig. 12). These new strains are similar to *Apiospora guangdongensis*, by its

globose to ellipsoidal, aseptate, initially hyaline to dark brown, smooth-walled conidia with a broad equatorial germ-slit. Therefore, we consider these strains to be new collections of *Apiospora guangdongensis*, from Poaceae in Yunnan Province, China.

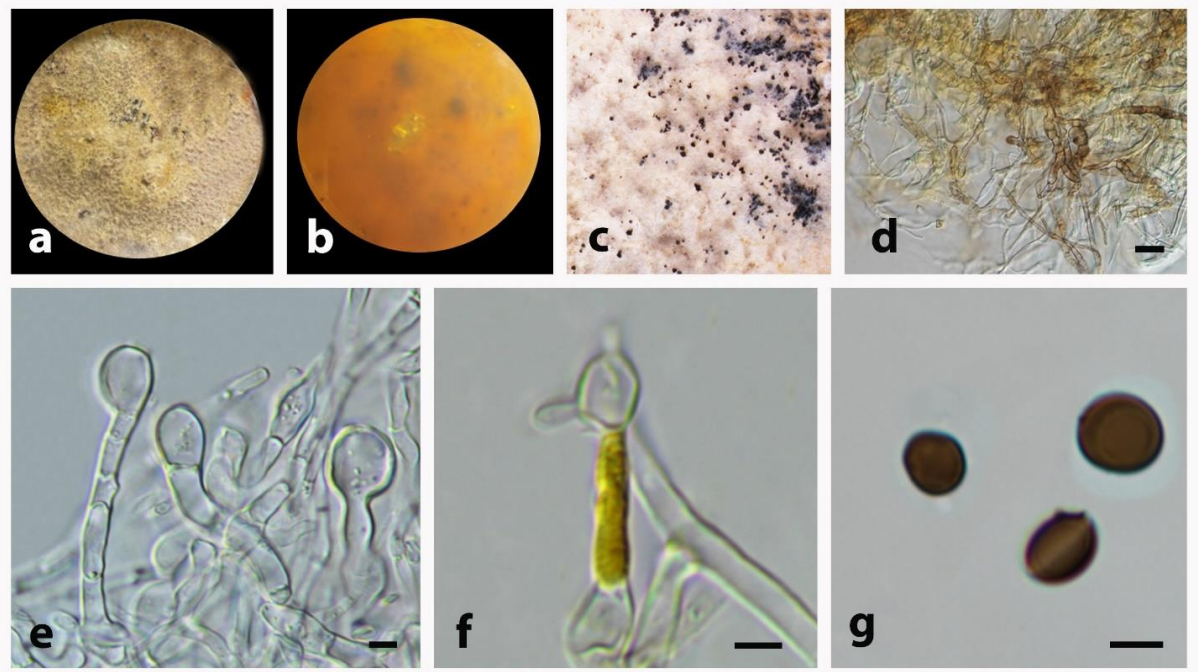

Figure 15 – *Apiospora guangdongensis* (HKAS 133092). a Upper view. b Reverse view of the two-week-old colony on PDA. c Colony on PDA producing conidial masses. d Hyphae. e-f Conidiogenous cells giving rise to conidia. g Conidia. Scale bars: d, e = 2 μm, f, g = 5 μm.

Apiospora koreana L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 12, 16

MycoBank number: MB853454; Facesoffungi number: FoF15546

= *Apiospora koreana* (S.L. Kwon, S. Jang & J.J. Kim) S.L. Kwon & J.J. Kim, in Kwon et al., Mycobiology 50 (1): 52 (2022); Nom. inval., Art. F.5.1 (Shenzhen)

≡ *Arthrinium koreanum* S.L. Kwon, S. Jang & J.J. Kim, in Kwon et al., IMA Fungus 12 (no. 13): 16 (2021)

Typification details – Korea, Gangwon-do, Goseong-gun, 38°28'44.0"N, 128°26'18.9"E, isolated from egg masses of *Arctoscopus japonicus*, 10 November 2016, M.S. Park (Herb. KCTC 46908, holotype), ex-types (KUC21332 = NIBRFGC000501587, SFC20200506-M06).

Saprobic on dead culms of bamboo sp. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after one month. *Hyphae* 3–4 μm diameter, micronematous, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–4 μm diameter aggregated in clusters on hyphae, holoblastic, monoblastic, hyaline, cylindrical, straight, discrete, aseptate, smooth-walled. *Conidia* 6–9 μm diameter ($\overline{x}$ = 7 μm, n = 20) globose to subglobose, aseptate, initially hyaline to golden brown, dark brown when mature, rough walled with an equatorial germ-slit.

Culture characteristics – Conidia germinating on PDA within 24 h at cold temperature (4 °C). On the PDA, the surface of the colony is white, flat, spreading, filiform, with abundant aerial mycelia and reverse white.

Material examined – CHINA, Sichuan Province, Chengdu City, Dayi County, Xiling Snow Mountain (30.684421 N, 103.164434 E, 3163 m), on dead culms of bamboo sp., 3 January 2023, L.S. Dissanayake, SCCSM23-12 (HKAS 127253), living culture, KUNCC23-15553.

GenBank accession numbers – ITS = PP584690, LSU = PP584787, *tef*1-α = PP933195, *tub*2 = PP982289.

Notes – *Arthrinium koreanum*, originally collected from marine habitats (the egg masses of *Arctoscopus japonicus*) in Korea, was described with an asexual morph (Kwon et al. 2021). Later, Kwon et al. (2022) synonymized *Arthrinium koreanum* with *Apiospora koreana* based on molecular analyses. However, *Apiospora koreana* was shown as invalid in Index Fungorum (2024, Nom. inval., Art. F.5.1 Shenzhen). The identifier cited in the protologue (MycoBank number: MB834596), was not assigned to the name that was published since the names had not been registered prior to publication. In this study, we hereby validly establish the same name to accommodate *Apiospora koreana*. Morphologically and phylogenetically, *Apiospora koreana* is similar to *A. qinlingensis*; however, it can be differentiated from *A. qinlingensis* by its larger conidia (7.5–11 × 5.5–10 μm vs. 5–8 μm). In this study, our new strain, KUNCC 23-15553, showed a close phylogenetic relationship to *Apiospora koreana* (KUC21332), with 100% MLB and 1.00 BYPP statistical support (Fig. 12). The new strain KUNCC23-15553 closely resembles the type species of *Apiospora koreana* (KUC21332), in having micronematous, hyaline, branched, thick-walled, septate, guttulate hyphae, and conidia that are globose to subglobose, aseptate, initially hyaline to golden brown, turning dark brown upon maturation, with a rough wall and an equatorial germ-slit (Kwon et al. 2021). It is noteworthy that our new collection, originating from an extreme environment on a Snow Mountain in China, where temperatures approximate –2 °C, demonstrates the wide adaptation of this species. *Apiospora koreana* efficiently obtains nutrients from diverse substrates, including animal-based sources (e.g. egg masses of sailfin sandfish) and woody-based sources (e.g. bamboo), showing its ability to survive in both aquatic and terrestrial habitats (Kwon et al. 2021).

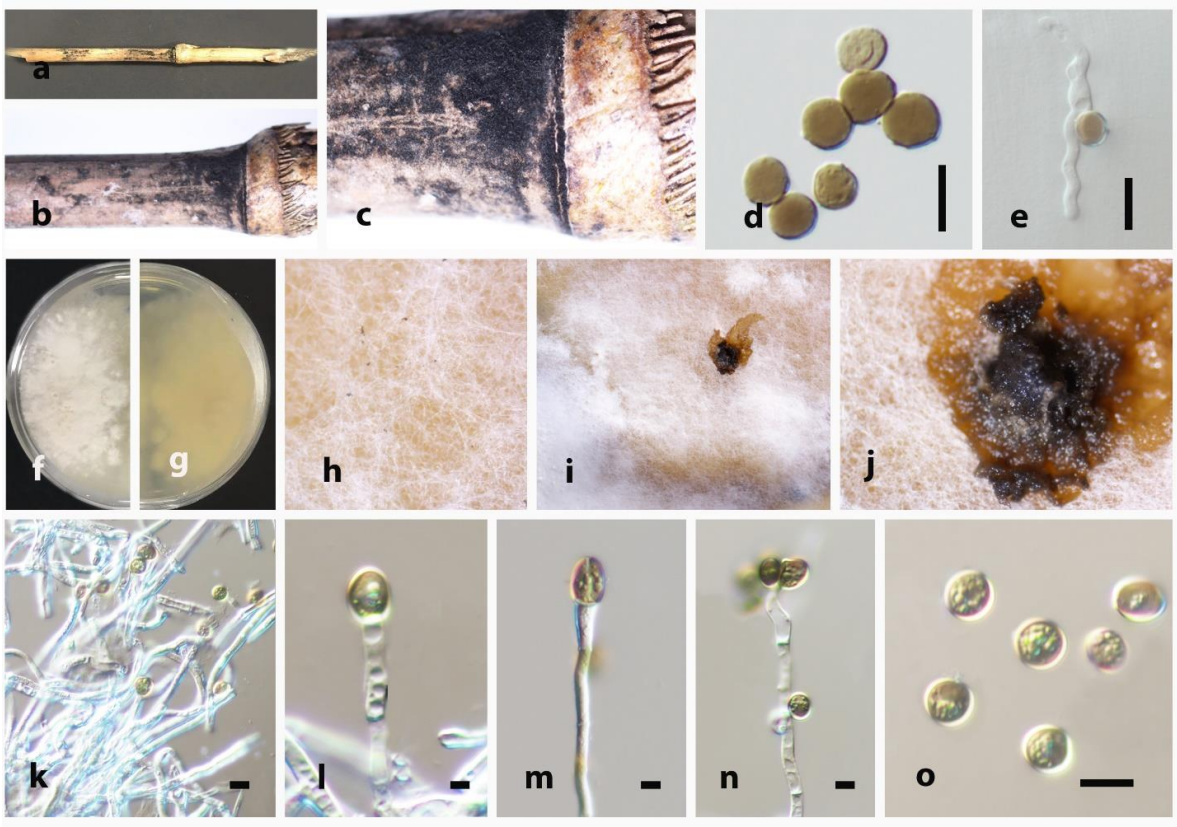

Figure 16 – *Apiospora koreana* (HKAS 127253). a, b Host. c Conidia on the host surface. d Conidia. e Germinated conidium. f Upper view. g Reverse view of the two-week-old colony on PDA. h-j Colony on PDA producing conidial masses. k Hyphae. l–n Conidiogenous cells giving rise to conidia. o Conidia. Scale bars: k–n = 5 μm, d–f, o = 10 μm.

Apiospora locuta-pollinis (F. Liu & L. Cai) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 206 (2021) Figs 12, 17

MycoBank number: MB558496; Facesoffungi number: FoF15204

Saprobic on dry culms of Bamboo sp. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after one month, spore mass visible as black, scattered to aggregated on white colonies. Hyphae 3–4 µm diameter, hyaline, branched, thick-walled, septate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 µm diameter holoblastic, monoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* 6–8 µm diameter ($\bar{x}$ = 7 µm, n = 20) globose in surface view, lenticular in side view, dark brown, smooth walled with a pale equatorial slit.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colony surfaces are white, woolly, flat, spreading, filiform, with abundant aerial mycelia and reverse off-white to yellow.

Material examined – CHINA, Yunnan Province, Botanical Garden, Kunming Institute of Botany (25.140833 N, 102.739444 E, 1892 m), on dead culms of Bamboo sp., 12 December 2022, L.S. Dissanayake, KIB22-64 (HKAS 133093), KIB22-67 (HKAS 133094), living cultures, KUNCC 24-17550, KUNCC 24-17551.

GenBank accession numbers – ITS = PP584691, PP584692, LSU = PP584788, PP584789, *tef*1-α = PP933196, PP933197, *tub*2 = PP982290, PP982291.

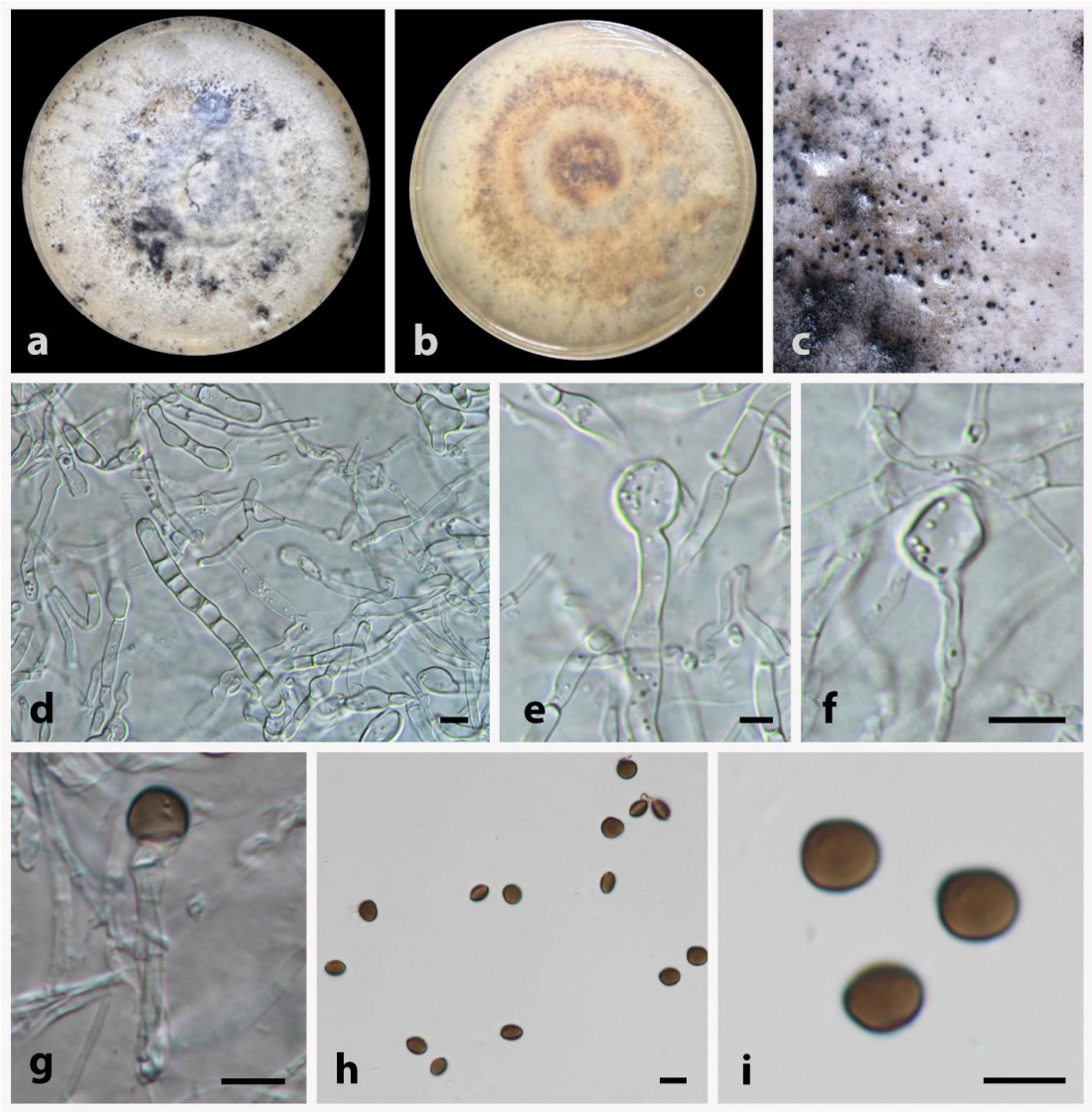

Figure 17 – *Apiospora locuta-pollinis* (HKAS 133093). a Upper view. b Reverse view of the two-week-old colony on PDA. c Colony on PDA producing conidial masses. d Hyphae. e–g Conidiogenous cells giving rise to conidia. h, i Conidia. Scale bars: d = 5 µm, h–i = 10 µm.

Notes – Chen et al. (2021a) originally described *Arthrinium pseudomarii* from the leaves of *Aristolochia debilis* in Yunnan Province, China. Subsequently, Tian et al. (2021) found that *Arthrinium pseudomarii* was phylogenetically and morphologically similar to *Apiospora locuta-pollinis* (= *Ar. locuta-pollinis*), leading them to synonymize *Arthrinium pseudomarii* under *Apiospora locuta-pollinis*. *Apiospora locuta-pollinis* (= *Ar. locuta-pollinis*), introduced by Zhao et al. (2018), was collected from hive-stored pollen on *Brassica campestris* in Hubei Province, China. Monkai et al. (2022) later reported two new records of *Apiospora locuta-pollinis* from dry culms of bamboo in Yunnan Province, China. In our study, two *Apiospora* strains (KIB22-64 and KIB22-67) were found to be phylogenetically closely associated with *A. locuta-pollinis* (GUCC 10228, KUNCC 22-12408 and LC11683) as shown in Fig. 12. These strains are similar to *Apiospora locuta-pollinis*, characterized by the brown and pale equatorial slit, globose to subglobose conidia of similar size, and hyaline, smooth, septate hyphae (Chen et al. 2021a, Tian et al. 2021, Monkai et al. 2022). Therefore, in this study, we recognise our new specimens belonging to *Apiospora locuta-pollinis* from bamboo in Yunnan Province, China.

Apiospora menglaensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 12, 18

MycoBank number: MB852803; Facesoffungi number: FoF15547

Etymology – The specific epithet is derived from Mengla county, where the holotype was collected

Holotype – HKAS 133096

Saprobic on dead culms of bamboo. Sexual morph: Undetermined Asexual morph: Colonies on natural substrate are dry, dark brown to black, velvety, dull, consisting of a sterile mycelial outer zone and round, sporulating centre, with conidia readily liberated when disturbed. *Hyphae* 2–5 µm diameter, micronematous, hyaline, branched, thick-walled, septate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* arising from hyphae, holoblastic, monoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* 7–10 µm diameter ($\bar{x}$ = 8 µm, n = 20), globose to subglobose, aseptate, pale brown to dark brown, with a central scar, globose in the surface view, a lenticular inside view.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colonies' surfaces are white to off white, flat, spreading, filiform, with abundant aerial mycelia and reverse yellow.

Material examined – CHINA, Yunnan Province, Mengla County, Xishuangbanna (21.580788 N, 101.434776 E, 776 m), on dead culms of bamboo sp., 29 January 2023, L. Qinxing, ML24 (HKAS 133096, holotype), ex-type KUNCC 24-17546, ML24A (HKAS 133095, isotype), ex-isotype, KUNCC 24-17547.

GenBank accession numbers – ITS = PP584693, PP584694, LSU = PP584790, PP584791, *tef*1-α = PP933198, PP933199, *tub*2 = PP982292, PP982293.

Notes – *Apiospora menglaensis* (strains KUNCC 24-17546 and KUNCC 24-17547) was found to be phylogenetically related to *A. agari* (KUC21333), with 88% MLB and 0.98 BYPP support (Fig. 12). Nucleotide base pair comparisons across three gene regions (ITS, *tef*1-α and tub2) between these two species revealed differences of 3.8% (15/392 bp), 3.3% (14/414 pb) and 4% (19/460 bp), respectively. *Apiospora menglaensis* closely resembles *A. agari*, sharing similar characteristics such as smooth, hyaline, branched, septate mycelium and brown conidia, globose in surface view, and lenticular in side view (Kwon et al. 2021). However, *Apiospora menglaensis* can be differentiated from *A. agari* by the shape of its conidiogenous cells. *Apiospora menglaensis* has cylindrical conidiogenous cells, whereas *A. agari* has ampulliform conidiogenous cells (Kwon et al. 2021).

Apiospora pseudoparenchymatica (M. Wang & L. Cai) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021) Figs 12, 19

MycoBank number: MB837707; Facesoffungi number: FoF15548

Saprobic on dead stalk of grass (Poaceae sp.). Sexual morph: Undetermined Asexual morph: Colonies on natural substrate are dry, dark brown to black, velvety, dull, consisting of a sterile mycelial outer zone and round, sporulating centre, with conidia readily liberated when disturbed. *Hyphae* 3–4 μm diameter, micronematous, hyaline, branched, thick-walled, septate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* arising from hyphae, holoblastic, monoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* 4–7 μm diameter ($\bar{x}$ = 6 μm, n = 20) globose to subglobose, aseptate, pale brown to dark brown, with an equatorial germ-slit.

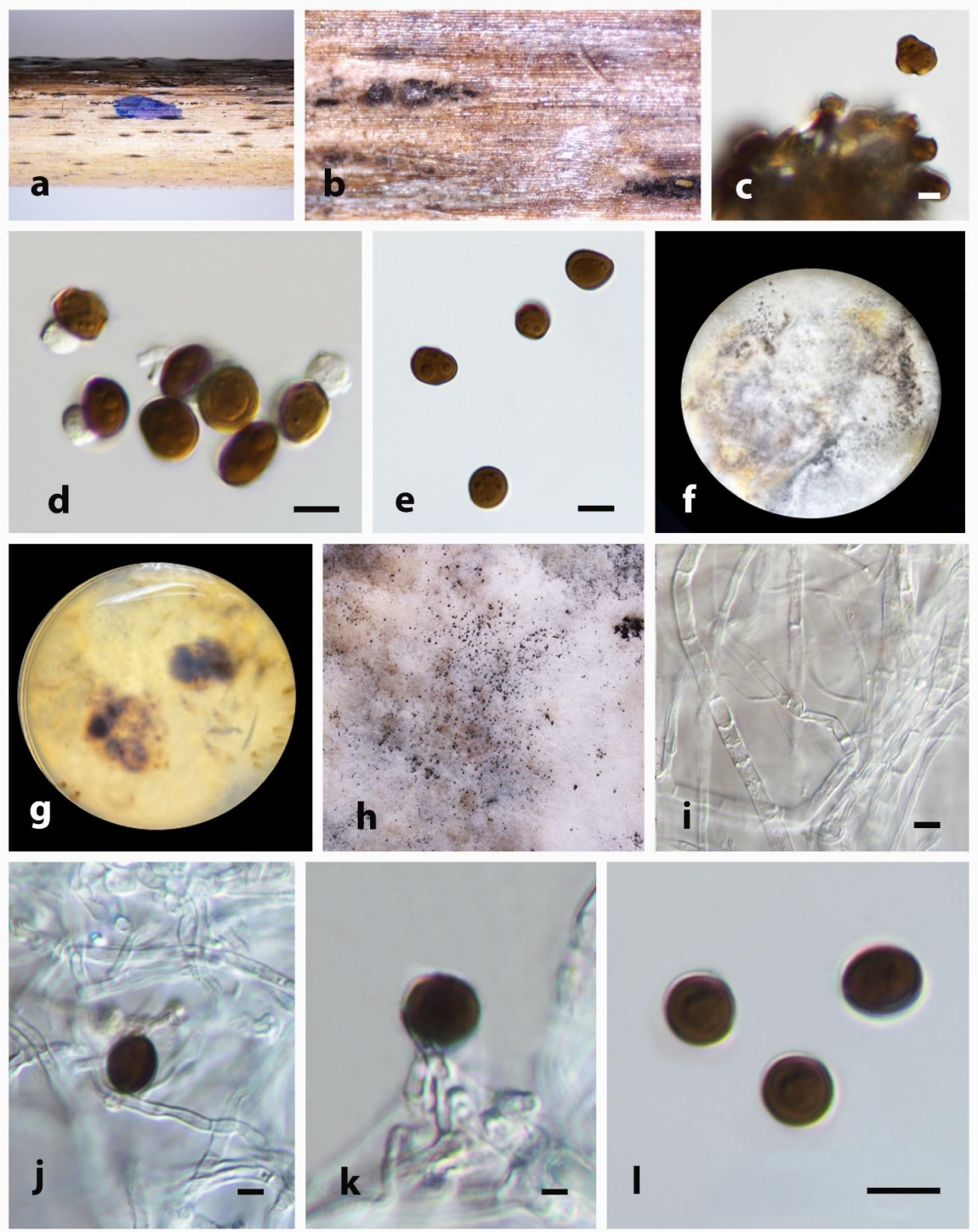

Figure 18 – *Apiospora menglaensis* (HKAS 133096, holotype). a Host. b Conidia on host surface. c Conidiophore mother cell. d, e Conidia. f Upper view. g Reverse view of the two-week-old colony on PDA. h Colony on PDA producing conidial masses. i Hyphae. j, k Conidiogenous cells giving rise to conidia. l Conidia. Scale bars: c, i–k = 2 μm, d, e, l = 10 μm.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colony surfaces are white to off white, flat, spreading, filiform, with abundant aerial mycelia and reverse yellow.

Material examined – CHINA, Yunnan Province, Mengla, Xishuangbanna (21.580788 N, 101.434776 E, 776 m), on dead stalk of a Poaceae sp., 2 February 2023, L. Qinxing, ML03 (HKAS 133097), ML03A (HKAS 133098), living cultures KUNCC 24-17548, KUNCC 24-17549.

GenBank accession numbers – ITS = PP584695, PP584696, LSU = PP584792, PP584793, *tef*1-α = PP933200, PP933201, *tub*2 = PP982294, PP982295.

Notes – Our new strains, KUNCC 24-17548 and KUNCC 24-17549, demonstrate a close phylogenetic relationship to *Apiospora pseudoparenchymatica*, supported by 100% MLB and 1.00 BYPP (Fig. 12). These strains resemble *A. pseudoparenchymatica*, but they exhibit distinct differences, notably having much smaller conidia (4–7 μm vs. 13.5–27 μm × 12–23.5 μm) and the absence of dentate conidia (Wang et al. 2018). The nucleotide differences in the ITS and *tef*1-α gene regions between our strains and *A. pseudoparenchymatica* are 10/392 (2.5%) and 6/414 (1.4%), respectively. *Arthrinium pseudoparenchymatica* was originally identified by Wang et al. (2018) from bamboo in Guangdong Province, China. Subsequently, Pintos & Alvarado (2021) synonymized it under *Apiospora pseudoparenchymatica* following a phylogenetic analysis. In this current study, we report two additional specimens of *Apiospora pseudoparenchymatica* collected from dead stalks of grass (Poaceae) in Yunnan Province, China, serving as a new host record.

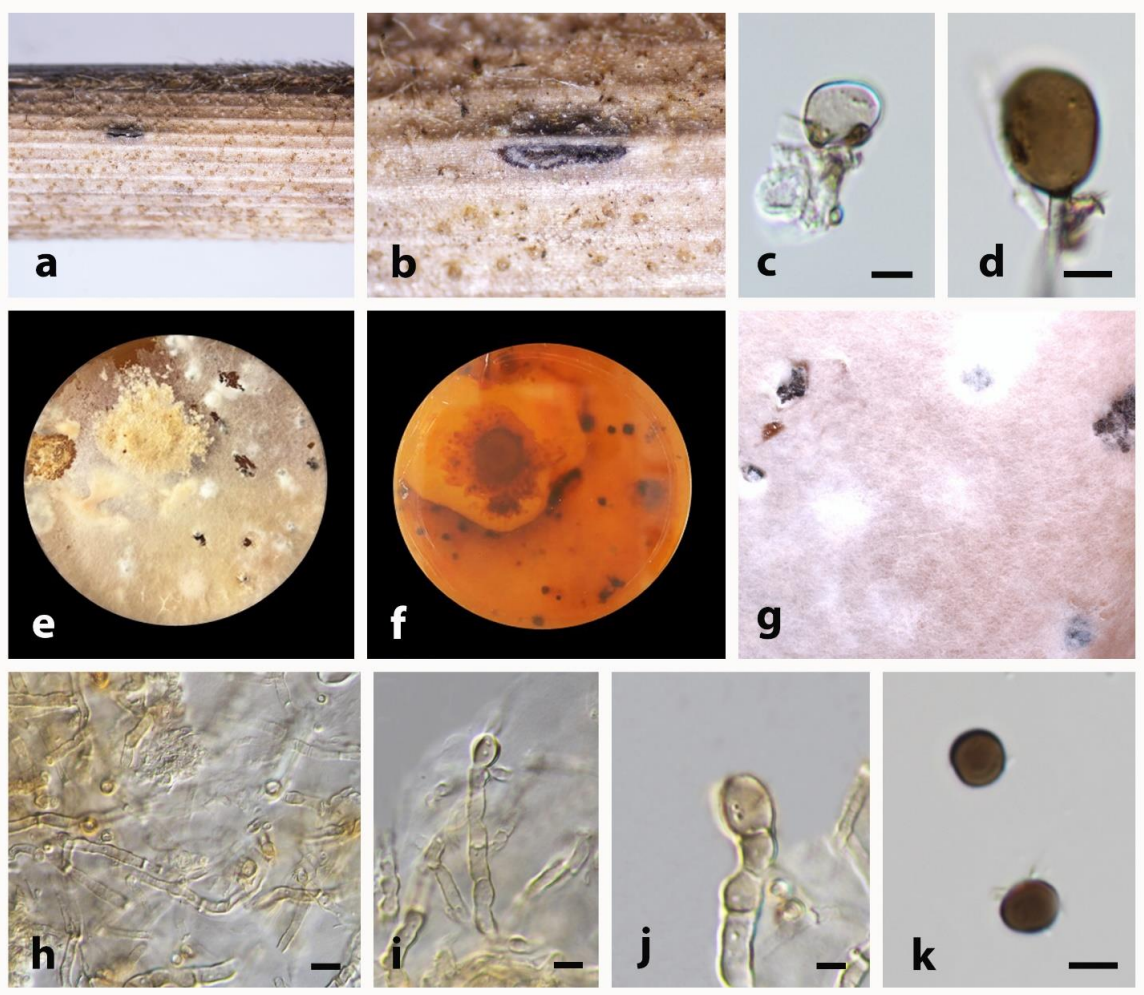

Figure 19 – *Apiospora pseudoparenchymatica* (HKAS 133097). a Host. b Conidia on host surface. c Conidiophore mother cell. d, k Conidia. e Upper view. f Reverse view of the two-week-old colony on PDA. g Colony on PDA producing conidial masses. h Hyphae. i, j Conidiogenous cells giving rise to conidia. Scale bars: c, d, h–j = 2 μm, k = 5 μm.

Apiospora senecionis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 12, 20

MycoBank number: MB852804; Facesoffungi number: FoF15549

Etymology – The specific epithet is derived from genus of *Senecio scandens*, which the holotype was collected.

Holotype – HKAS 127245

Saprobic on dead twigs of *Senecio scandens* Buch.-Ham. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after one month. *Hyphae* 3–6 µm diameter, micronematous, hyaline to golden brown, branched, thick-walled, septate, guttulate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–7 µm diameter arising from hyphae, holoblastic, monoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. *Conidia* 8–17 µm diameter ($\bar{x}$ = 13 µm, n = 20), globose to subglobose, aseptate, golden yellow to light brown when mature, rough walled with an equatorial germ-slit.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colony surfaces are black, flat, spreading, filiform, with abundant aerial mycelia and reverse black.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.075 N, 103.564167 E, 1065.01 m), on dead twigs of *Senecio scandens* (Asteraceae), 5 January 2023, L. S. Dissanayake, SCCFP23-14 (HKAS 127245, holotype), ex-type, KUNCC23-15556, *ibid*. SCCFP23-14A (HKAS 133102, isotype), ex-isotype, KUNCC23-15557.

GenBank accession numbers – ITS = PP584697, PP584698, LSU = PP584794, PP584795, *tef*1-α = PP993513, PP993514.

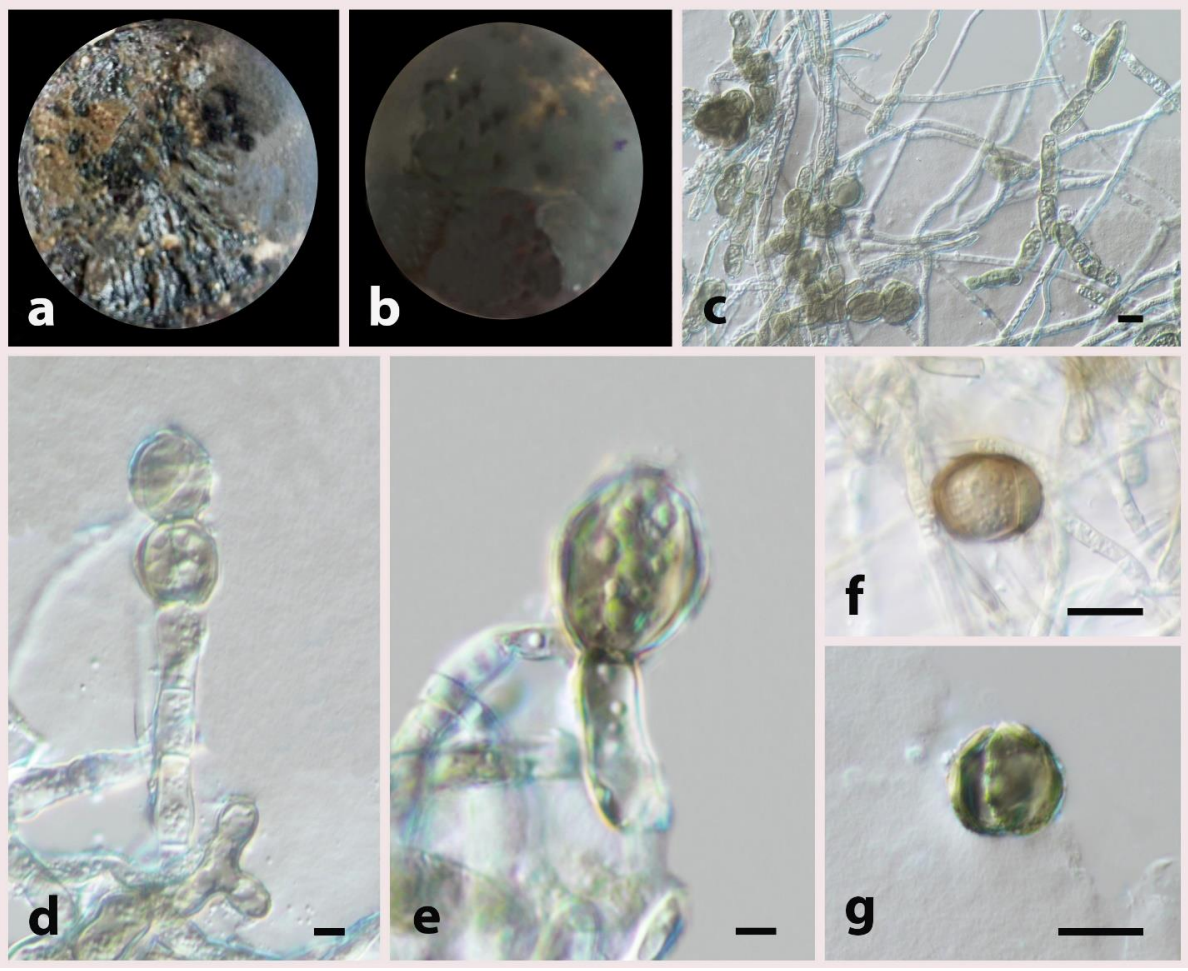

Figure 20 – *Apiospora senecionis* (HKAS 127245, holotype). a Upper view. b Reverse view of the two-week-old colony on PDA. c Hyphae. d, e Conidiogenous cells giving rise to conidia. f, g Conidia. Scale bars: c–e = 5 µm, f, g = 10 µm.

Notes – Based on phylogenetic analysis, our new strains, KUNCC23-15556 and KUNCC23-15557 (*Apiospora senecionis*), form a sister branch with *A. arundinis* and *A. guangdongensis*, with 84% MLB support (Fig. 12). Our new strains exhibit distinct differences from *A. guangdongensis* (ZHKUCC23-0005) and *A. arundinis*, particularly in terms of conidia size, with our strains having larger conidia (8–17 μm in diameter vs. 6–9 × 5–9 μm and 6–7 μm in diameter, respectively). The conidiogenous cells of our new strains are holoblastic, monoblastic, hyaline, cylindrical and straight, whereas *A. guangdongensis* has cylindrical or ampulliform, sometimes ovate or obpyriform conidiogenous cells, and *A. arundinis* has ampulliform conidiogenous cells, as reported by (Li et al. 2023, Liao et al. 2023). Comparative analysis of the ITS, *tef*1-α and *tub2* sequence data between our isolate KUNCC23-15556 (ex-type) and *A. guangdongensis* (ZHKUCC23-0001; ex-type) revealed nucleotide differences of 3% (12/392 bp), 3.6% (15/414 bp), and 3.4% (16/460 bp), respectively. Comparisons with *A. arundinis* (CBS 449.92) indicated differences of 3.8% (15/392 bp), 3.3% (12/414 pb) and 3.6% (17/460 bp), respectively. Considering both the morphological and molecular data, we have introduced *Apiospora senecionis* as a new species.

Apiospora thailandica (D.Q. Dai & K.D. Hyde) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 207 (2021) Figs 12, 21

MycoBank number: MB837735; Facesoffungi number: FoF06794

Saprobic on dead stem of unidentified host. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after one month. *Hyphae* 2–3 μm diameter, hyaline, branched, thick-walled, septate, guttulate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 μm diameter holoblastic, monoblastic, hyaline, cylindrical, straight, aseptate, smooth-walled. Conidia 5–7 μm diameter ($\bar{x}$ = 6 μm, n = 20) globose to subglobose, dark brown, smooth walled with a pale equatorial germ-slit.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colony surfaces are white to brownish, woolly, flat, spreading, filiform, with abundant aerial mycelia and reverse off-white to yellow.

Material examined – CHINA, Yunnan Province, Honghe Autonomous Prefecture, Honghe County, (23.389394 N, 102.226167 E, 1186 m), on dead stem of unidentified host, 12 March 2023, L. Qinxian, HH23-22 (HKAS 133099), HH23-30 (HKAS 133100).

GenBank accession numbers – ITS = PP584699, PP584700, LSU = PP584796, PP584797, *tef*1-α = PP933202, PP933203, *tub*2 = PP982296, PP982297.

Notes – Dai et al. (2016) described and illustrated both the sexual and asexual morphs of *Arthrinium thailandicum*, collected from dead culms of bamboo in Thailand. Wang et al. (2018) provided another strain of *Ar. thailandicum* from rotten wood in China. Subsequently, Pintos and Alvarado et al. (2021) synonymized *Ar. thailandicum* with *Apiospora thailandica* based on molecular analysis. Our phylogenetic analysis revealed that two new isolates, HH23-22 and HH23-30, clustered with the strain of *Apiospora thailandica* (LC5630), with 96% ML and 1.00 BYPP support values (Fig. 12). These new isolates closely resembled the holotype of *Apiospora thailandica* (MFLUCC 15-0202), in having globose to subglobose, dark brown, smooth-walled conidia with a pale equatorial germ-slit, and similar size (Dai et al. 2016, Wang et al. 2018). Therefore, we identify the two new isolates as *Apiospora thailandica*, representing a new record in China.

Apiospora trachycarpi L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 12, 22

MycoBank number: MB852805; Facesoffungi number: FoF06794

Etymology – The specific epithet is derived from *Trachycarpus fortunei*, from which the holotype was collected.

Holotype – HKAS 127244

Saprobic on dead twigs of *Trachycarpus fortune* (Hook.) H. Wendl. Sexual morph: Undetermined. Asexual morph: Sporulating on PDA after one month. *Hyphae* 2–4 μm diameter, micronematous, hyaline to brown, branched, thick-walled, septate, guttulate. *Conidiophores*

reduced to conidiogenous cells. *Conidiogenous cells* 3–5 µm diameter arising from hyphae, holoblastic, monoblastic, hyaline, cylindrical, straight, discrete, aseptate, smooth-walled. *Conidia* 5–7 µm diameter ($\bar{x}$ = 6 µm, n = 20), globose to subglobose or ellipsoidal, aseptate, hyaline to dark brown when mature, globose in the surface view, a lenticular inside view, with an equatorial germ-slit.

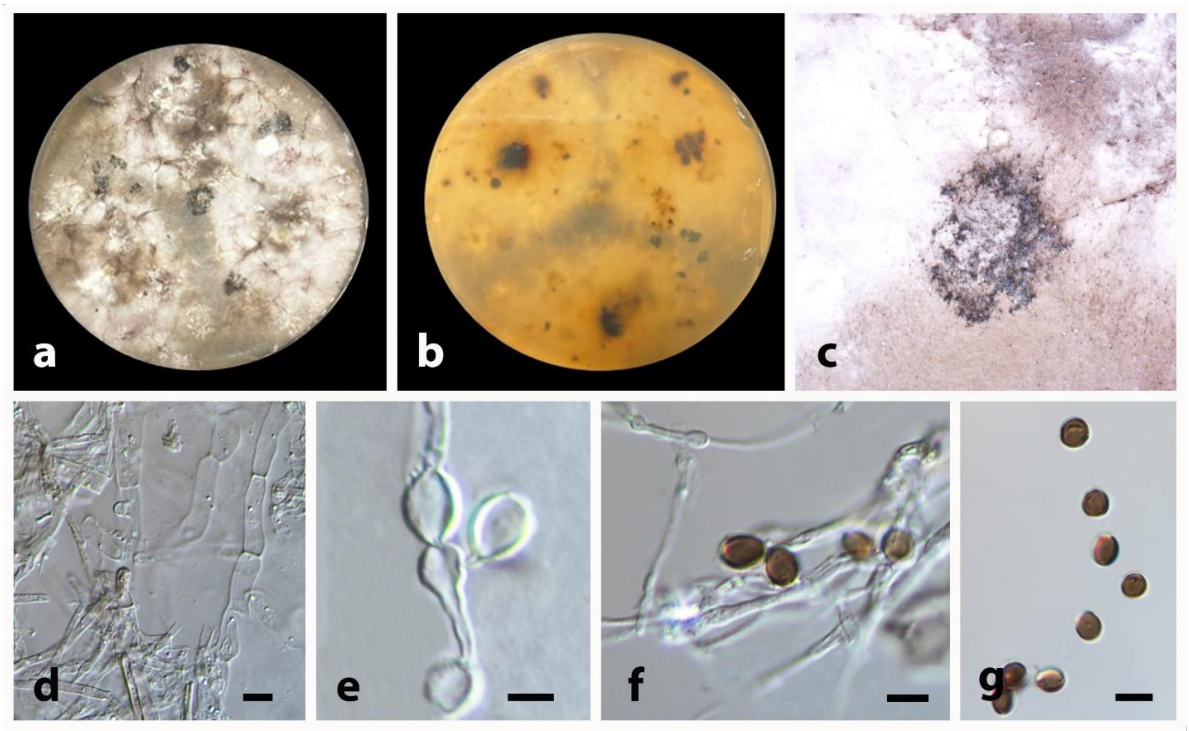

Figure 21 – *Apiospora thailandica* (HKAS 133099). a Upper view. b Reverse view of the two-week-old colony on PDA. c Colony on PDA producing conidial masses. d Hyphae. e–g Conidiogenous cells giving rise to conidia. h, i Conidia. Scale bars: d = 2 µm, h–i = 5 µm.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). On the PDA, the colony surfaces are white to off white, flat, spreading, filiform, with abundant aerial mycelia and reverse yellow.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.075 N, 103.564167 E, 1065 m), on dead twigs of *Trachycarpus fortune* (Arecaceae), 5 January 2023, L. S. Dissanayake, SCCFP23-03 (HKAS 127244, holotype), ex-type, KUNCC23-15558. *ibid*. SCCFP23-03A (HKAS 133101, isotype), ex-isotype, KUNCC23-15559.

GenBank accession numbers – ITS = PP584701, PP584702, LSU = PP584798, PP584799, *tef*1-α = PP933204, PP933205, *tub*2 = PP982298, PP982299.

Notes – In our phylogenetic analysis, *Apiospora trachycarpi* (strains KUNCC23-15558 and KUNCC23-15559) formed a distinct branch with *A. senecionis*, with a 99% MLB and 1.00 BYPP support (Fig. 12). The comparison of ITS, *tef*1-α and *tub2* sequence data between our isolate, *Apiospora trachycarpi* and *A. senecionis* (KUNCC23-15558, the ex-type) revealed nucleotide differences of 2% (8/392 bp), 2.8% (12/414 bp), and 2% (10/460 bp), respectively. *Apiospora trachycarpi* is distinguished from *A. senecioi* by its smaller conidia size (5–7 µm vs. 8–17 µm in diameter) and its globose appearance in surface view, transitioning to lenticular in side view, whereas *A. senecionis* did not have its conidia side view observed in this study. Based on these phylogenetic and morphological distinctions, we have introduced *Apiospora trachycarpi* as a novel species collected from the *Trachycarpus fortunei* in Sichuan Province, China.

Appendicosporaceae Samarak. & K.D. Hyde, Fungal Diversity 112: 22 (2022)

Notes – Samarakoon et al. (2022) introduced Appendicosporaceae, designating *Appendicospora* as the type genus. Previously, *Appendicospora* had been grouped with *Apiospora* and *Pseudomassaria*, both of which had uncertain taxonomic placements (Hyde et al. 1995). Wang & Hyde (1999) and Smith et al. (2003) demonstrated that *Appendicospora* consistently grouped with *Hyponectria* and was thus placed under Hyponectriaceae. Samarakoon et al. (2022) indicated that *Appendicospora* forms a distinct clade separate from Apiosporaceae within the Amphisphaeriales. Based on morphological evidence, phylogeny, and divergence time estimates, Samarakoon et al. (2022) introduced Appendicosporaceae, which includes two genera *viz*. *Appendicospora* and *Neoamphisphaeria*. Members of this family are saprobic on terrestrial habitats.

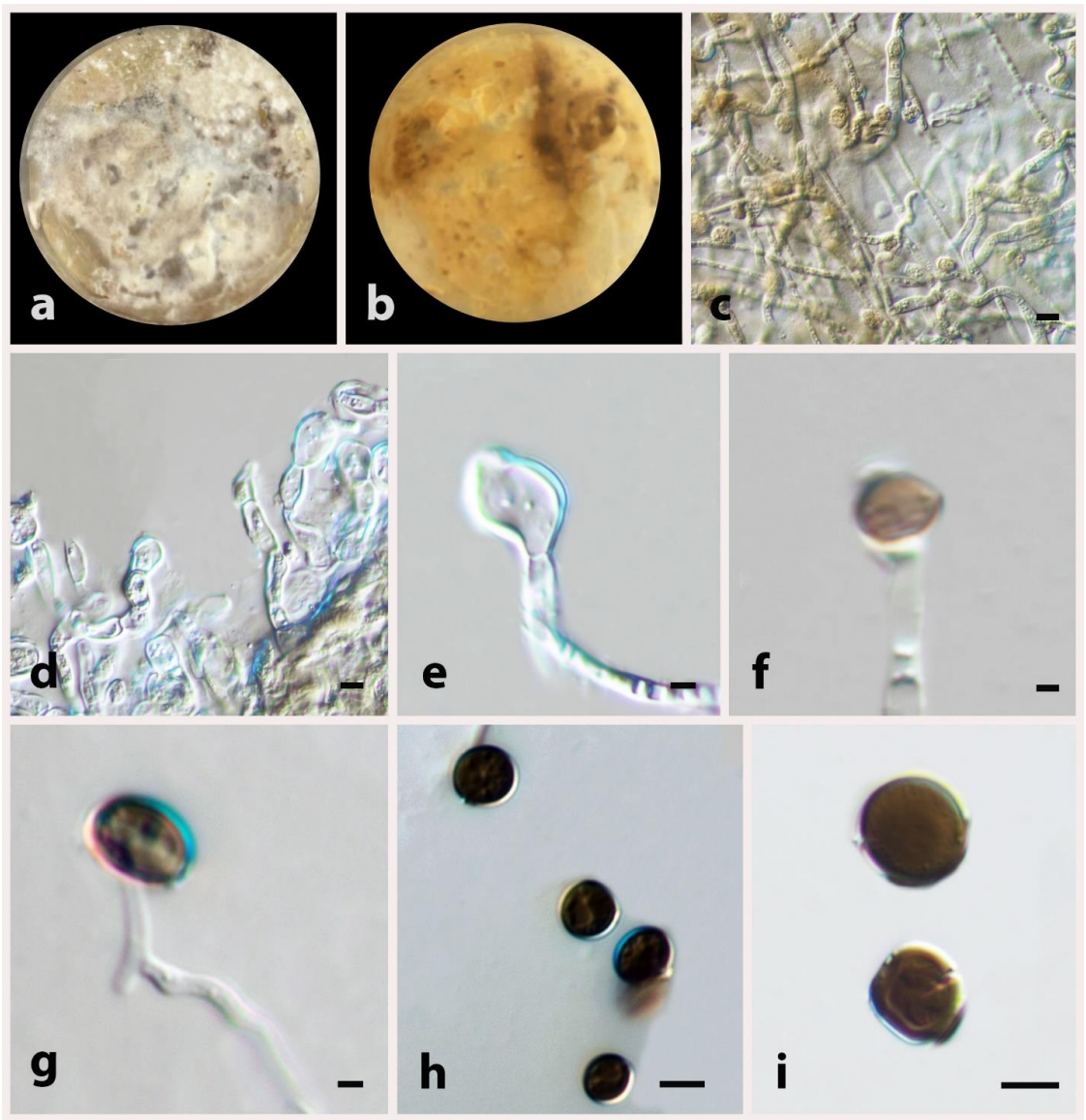

Figure 22 – *Apiospora trachycarpi* (HKAS 127244, holotype). a Upper view. b Reverse view of the two-week-old colony on PDA. c Hyphae. d–g Conidiogenous cells giving rise to conidia. h, i Conidia. Scale bars: c–i = 5 µm.

Neoamphisphaeria Samarak. & K.D. Hyde, Fungal Diversity 112: 23 (2022)

Notes – *Neoamphisphaeria*, a novel genus introduced by Samarakoon et al. (2022) with *N. hyalinospora* as the type species. *Neoamphisphaeria hyalinospora* was introduced with sexual morph as saprobic in terrestrial habitats. During their study, they made the tentative decision to classify *Neoamphisphaeria* under *Appendicosporaceae*. In our in-depth research, we have found

compelling evidence that supports this decision. Specifically, our data demonstrates that *Neoamphisphaeria* exhibits a close clustering relationship with *Appendicospora*. This affiliation was supported by a 93% MBL and a 1.00 MYPP. To ensure the placement of the genus, we used multi-genes, LSU, ITS, *tef*1-α, *rpb*2, and *tub*2 analysis, as shown in Fig. 9. When we combined the genetic results with morphological observations, we were able to identify a new species within *Neoamphisphaeria*, which we have named *N. shangrilaensis*. We suggest that to ascertain the precise taxonomic placement of *Neoamphisphaeria* and to validate our findings further, it will be important to conduct additional research, ideally with new and diverse collections from different localities.

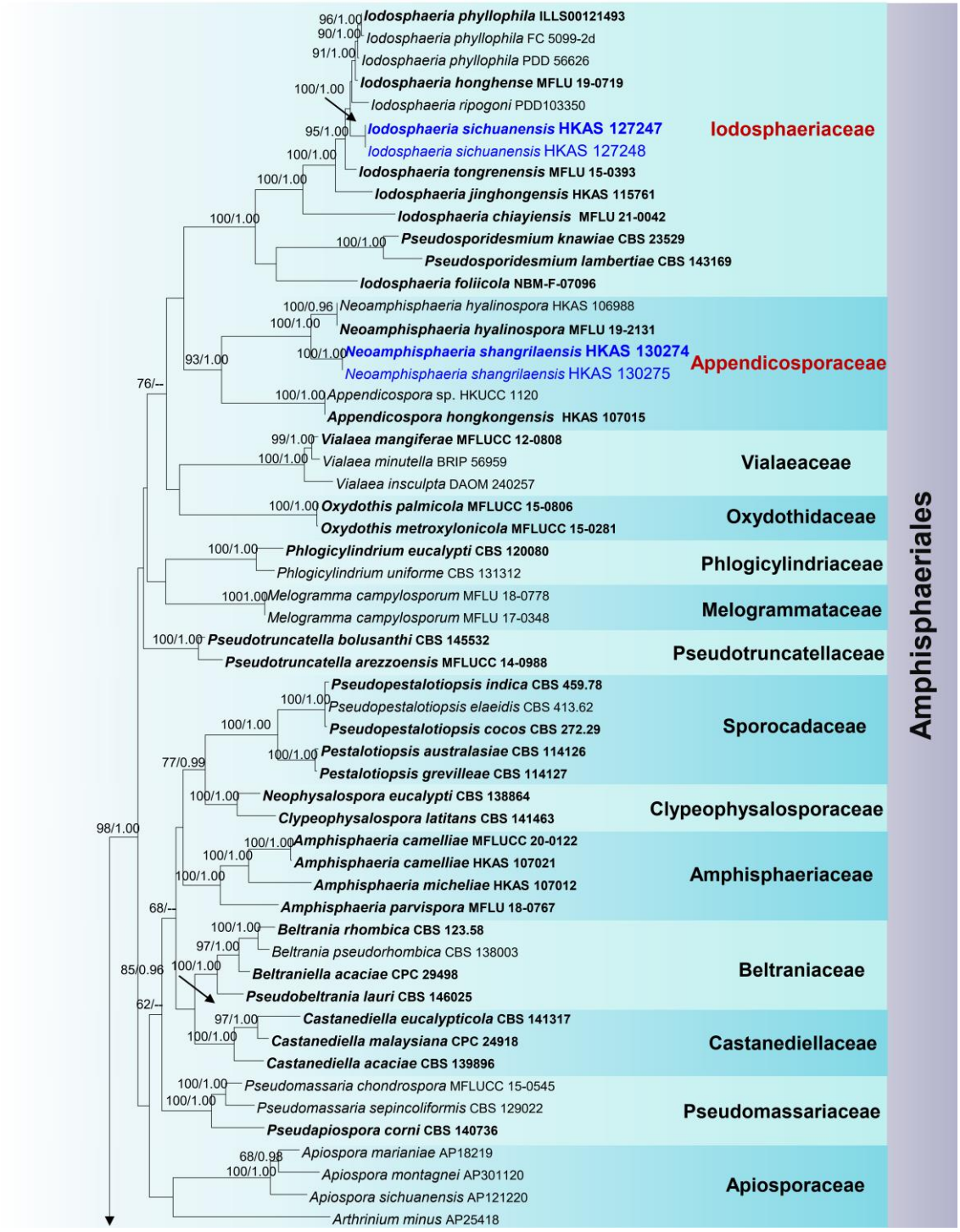

Figure 23 – RAxML phylogram generated from the combined dataset of partial LSU, ITS, *tef*1-α, *rpb*2 and *tub*2 DNA sequence analyses for Amphisphaeriales and Xylariales. The final likelihood

value is -55447.430720. The tree is rooted to *Chaetomium globosum* (CBS 371.66), (CGMCC 3.12915), (CBS 164.62) and *Sordaria fimicola* (CBS 723.96). The matrix had 4675 distinct alignment patterns with 51.75% undetermined characters and gaps. Estimated base frequencies were; A = 0.242209, C = 0.257679, G = 0.268892, T = 0.231221 substitution rates AC = 1.201800, AG = 2.837039, AT = 1.552940, CG = 1.115755, CT = 5.822438, GT = 1.000000; gamma distribution shape parameter α = 0.707392. Newly generated sequences are in blue. Ex-type/type strains are indicated in black bold.

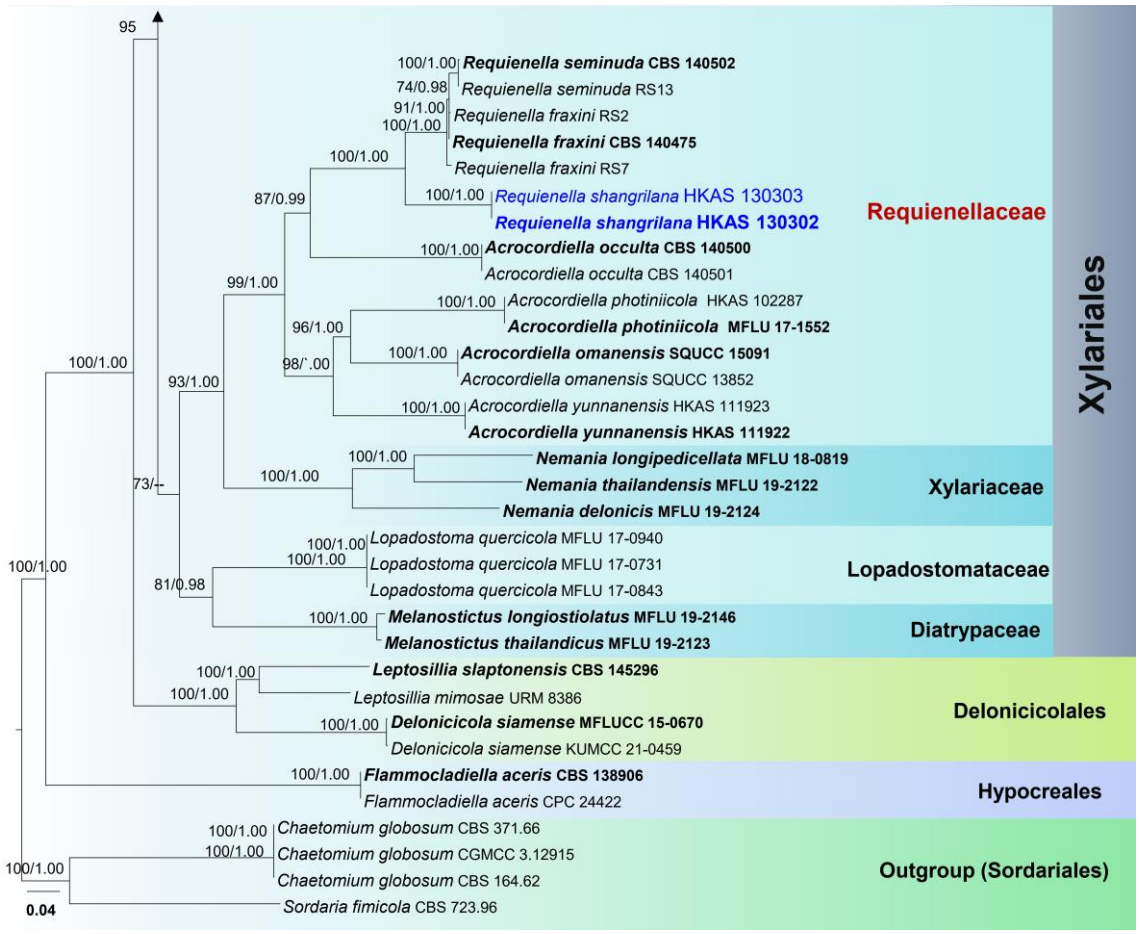

Figure 23 – Continued.

Neoamphisphaeria shangrilaensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 23, 24

MycoBank number: MB850211; Facesoffungi number: FoF14901

Etymology – The specific epithet is derived from the Shangri-La, where the holotype was collected.

Holotype – HKAS 130274

Saprobic on dead twigs of an unidentified host. Sexual morph: *Ascomata* 200–350 µm high × 180–320 µm diameter ($\bar{x}$ = 248 × 263.8 µm, n = 5), immersed, visible as black dots, solitary or aggregated, pear-shaped, in cross-section conical with mostly flattened base or less globose. *Ostioles* 90–120 µm high × 100–150 µm wide ($\bar{x}$ = 113 × 121 µm, n = 5), filled with white amorphous tissue. *Peridium* 20–40 µm wide ($\bar{x}$ = 28 µm, n = 5), multi-layered, outer layer comprising reddish brown, thick-walled cells of *textura prismatica*, inner layer composed of hyaline, thin-walled cells of *textura prismatica*. *Paraphyses* 5–6 µm wide, hyaline, long, septate, guttulate, easily delicate, embedded in a gelatinous matrix. *Asci* 140–200 µm × 10–15 µm ($\bar{x}$ = 159 × 13 µm, n = 10), 8-spored, unitunicate, cylindrical, slightly curved or straight, long pedicellate (24–34 µm), with a bilobed or dome-shaped, J- apical ring in Melzer's reagent, apically rounded. *Ascospores* 15–30 µm × 10–13 µm ($\bar{x}$ = 24 ×11.4 µm, n = 30), uniseriate, broadly ellipsoidal,

aseptate when immature, 1-septate when mature, hyaline, guttulate, lacking a mucilaginous sheath. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Meilishangu, Shangri-la (28.276389 N, 98.915833 E, 2910m), on dead twigs of unidentified host, 15 August 2021, L. Qinxian, MLSG3-2 (HKAS 130274, holotype). *ibid*. MLSG3-2A (HKAS 130275, isotype).

GenBank accession numbers – ITS = PP584703, PP584704, LSU = PP584800, PP584801.

Notes – *Neoamphisphaeria shangrilaensis* has a close phylogenetic relationship with *N. hyalinospora*; supported by 100% MLB and 1.00 BYPP (Fig. 23). The comparison of nucleotide differences in LSU and ITS are 33/867 (4%) and 44/710 (6%) respectively. *Neoamphisphaeria shangrilaensis* is characterized by immersed ascomata, a peridium with *textura prismatica* cells, asci that can reach up to 200 μm in length, a long pedicel (24–34 μm) and larger ascospores measuring 24 × 11.4 μm. In contrast, *Neoamphisphaeria hyalinospora* features ascomata that are immersed but have slightly raised areas, a peridium with *textura angularis* cells, asci that can reach up to 120 μm in length, a short pedicel and smaller ascospores measuring 16 × 6.5 μm (Samarakoon et al. 2022). While *Neoamphisphaeria shangrilaensis* was collected from China and *N. hyalinospora* was collected from Thailand (Samarakoon et al. 2022). In this study, we introduce *N. shangrilaensis* as the second species of this genus, marking the first report of a *Neoamphisphaeria* species from China.

Iodosphaeriaceae O. Hilber, The genus *Lasiosphaeria* and allied taxa: 7 (2002)

Notes – Iodosphaeriaceae was introduced by Hilber & Hilber (2002) to accommodate *Iodosphaeria*, but its placement was obscure with a paraphyletic relationship (Jeewon et al. 2003a). Initially, it was placed within Amphisphaeriales. However, the family was transferred to the Xylariales by Maharachchikumbura et al. (2016a) and Samarakoon et al. (2016). Subsequent placements categorized Iodosphaeriaceae within Xylariomycetidae as families *incertae sedis* (Hyde et al. 2017, Hongsanan et al. 2017, Wijayawardene et al. 2018). Currently, Iodosphaeriaceae is recognized within the Amphisphaeriales with a single genus, *Iodosphaeria* (Wijayawardene et al. 2022). Members of this family are saprobic in terrestrial and aquatic habitats (Hyde et al. 2020a, Dissanayake et al. 2022).

Iodosphaeria Samuels, E. Müll. & Petrini, Mycotaxon 28 (2): 486 (1987)

Notes – *Iodosphaeria* was introduced by Samuels et al. (1987) with the type species *I. phyllophila*. The genus is known for its selenosporella-like or ceratosporium-like asexual morphs and a saprobic lifestyle (Hyde et al. 2020a, Dissanayake et al. 2022). While there are 13 *Iodosphaeria* species according to MycoBank (2023), only eight are supported with molecular data (Li et al. 2015a, Marasinghe et al. 2019, Miller & Réblová 2021, Dissanayake et al. 2022). We introduce *Iodosphaeria sichuanensis*, further expanding our understanding of the ecological and morphological characteristics within the genus.

Iodosphaeria sichuanensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 23, 25

MycoBank number: MB850213; Facesoffungi number: FoF14902

Etymology – The specific epithet is derived from Sichuan Province, where the holotype was collected.

Holotype – HKAS 127247

Saprobic on dead twigs of an unidentified host. Sexual morph: *Ascomata* 280–350 μm high × 170–370 μm diameter ($\overline{x}$ = 313 × 262 μm, n = 5), globose to subglobose, superficial, black, solitary to gregarious, consisting of numerous long, flexuous setae. *Setae* 4–6 μm wide, arising from cells at the peridium surface, brown, unbranched, septate, apex flattened. *Ostiole* ostiolar canal periphysate, hyaline periphyses. *Peridium* 40–60 μm wide, multi-layered, outer layer comprising brown to black, thick-walled cells of *textura angularis*, inner layer composed of light brown to hyaline, thin-walled cells of *textura angularis*. *Paraphyses* 4–9 μm wide, shorter or longer than asci, hyaline, thin-walled, highly delicate, cellular, tiny-guttulate, embedded in a gelatinous matrix. *Asci* 110–140

μm × 10–14 μm ($\bar{x}$ = 123 × 12 μm, n = 10), 8-spored, unitunicate, cylindrical, short- pedicellate, apex rounded, straight or slightly curved, with a J-, wedge-shaped apical ring. *Ascospores* 16–21 μm × 5–9 μm ($\bar{x}$ = 19 × 7 μm, n = 10), overlapping uniseriate, ellipsoidal, aseptate, hyaline, guttulate, lacking a mucilaginous sheath. Asexual morph: Undetermined.

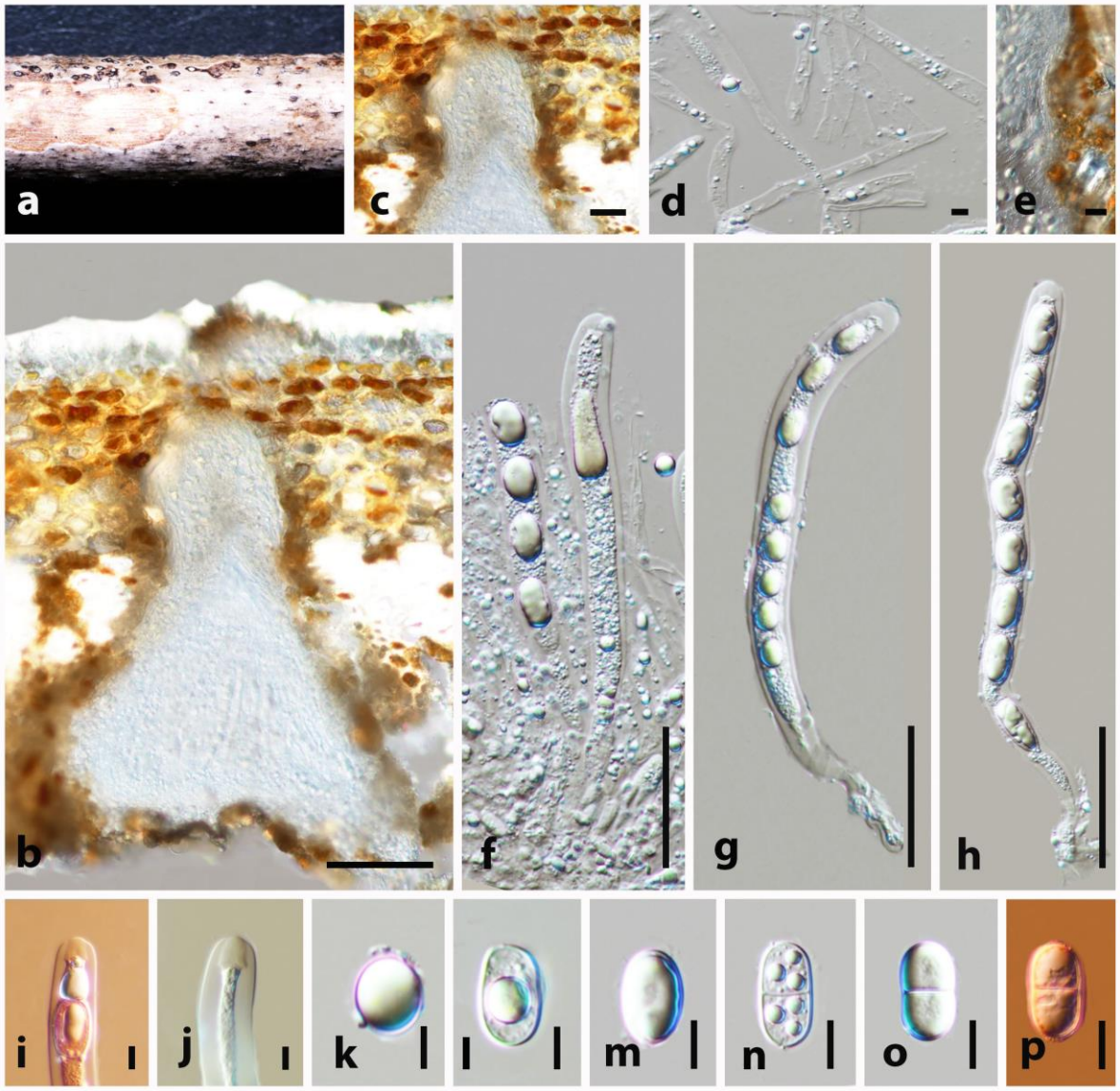

Figure 24 – *Neoamphisphaeria shangrilaensis* (HKAS 130274, holotype). a Ascomata on the host surface. b Section of an ascoma. c Section through an ostiole. d Paraphyses. e. Peridium. f–h Asci. i Apical ring in Melzer's reagent. j Apical ring in Congo red. k–p Ascospores (p with Congo red). Scale bars: b = 100 μm, c, f–h = 50 μm, d, i, j = 5 μm, e = 20 μm, k–p = 10 μm.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.075 N, 103.564167 E, 1065.01m), on dead twigs of unidentified host, 5 January 2023, L. S. Dissanayake, SCCFP23-30 (HKAS 127247, holotype). *ibid*. SCCFP23-30A (HKAS 127248, isotype).

GenBank accession numbers – ITS = PP584705, PP584706, LSU = PP584802, PP584803.

Notes – The combined gene phylogeny (Fig. 23) indicates that *Iodosphaeria sichuanensis* is closely related to *I. tongrenensis*, with 100% MLB, 1.00 BYPP statistical support (Fig. 23). Comparisons of the LSU and ITS base pairs revealed 25/867 (3%) and 42/710 (6%) differences, respectively. *Iodosphaeria tongrenensis* possesses longer and wider asci with J+, apical ring, measuring 150–210 × 12–16 μm *vs*. 110–140 × 9–13 μm and its ascospores have a mucilaginous

sheath (Li et al. 2015a). This contrasts with *Iodosphaeria sichuanensis*, which has asci with a J-, wedge-shaped apical ring and ascospores that lack a mucilaginous sheath.

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

Notes – Corda (1842) introduced the family Sporocadaceae with *Sporocadus* as the type genus. Typically, appendage bearing coelomycetous genera are included in this family. Taxonomic reclassifications have been made periodically (Crous et al. 2015, Senanayake et al. 2015, Jaklitsch et al. 2016, Maharachchikumbura et al. 2016a, Liu et al. 2019). Currently, this family comprises 35 genera (Wijayawardene et al. 2022). Members of this family have been reported as saprobes, endophytes, and pathogens on various hosts. They are also known to be parasitic on humans and animals (NagRaj 1993, Jaklitsch et al. 2016, Maharachchikumbura et al. 2016a, b, Liu et al. 2019, Hyde et al. 2019, 2020b, Ma et al. 2021, Zhang et al. 2022). We provide an updated multigene tree for Sporocadaceae.

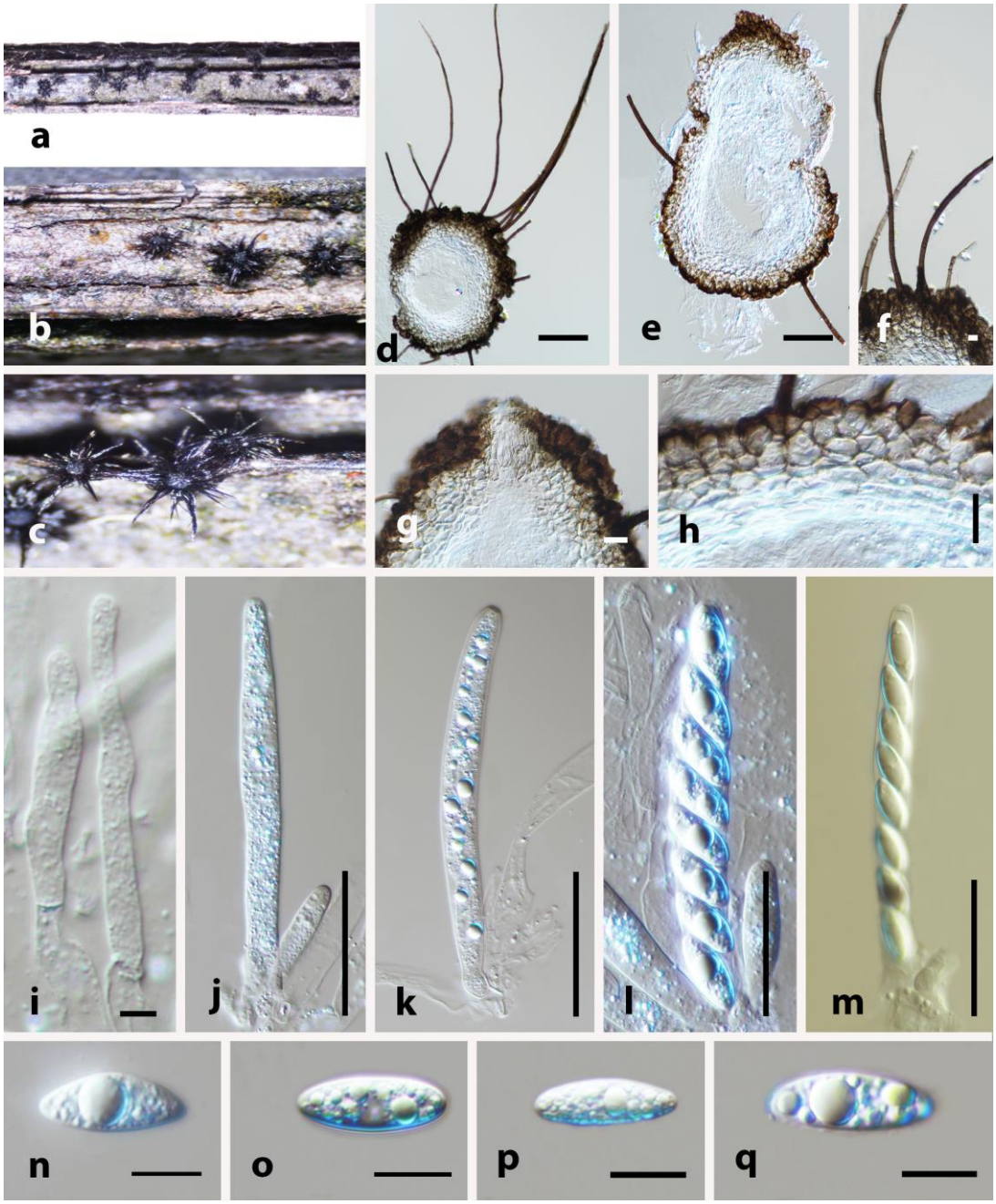

Figure 25 – *Iodosphaeria sichuanensis* (HKAS 127247, holotype). a Substrate. b, c Ascomata on the host surface. d, e Section of ascoma. f Appearance of setae on peridium. g Ostiole. h Peridium.

i paraphyses. j–m Asci (m = Asci with Melzer's reagent). n–q Ascospores. Scale bars: d, e = 100 µm, f, i = 5 µm, g, h = 20 µm, j–m = 50 µm, n–q = 10 µm.

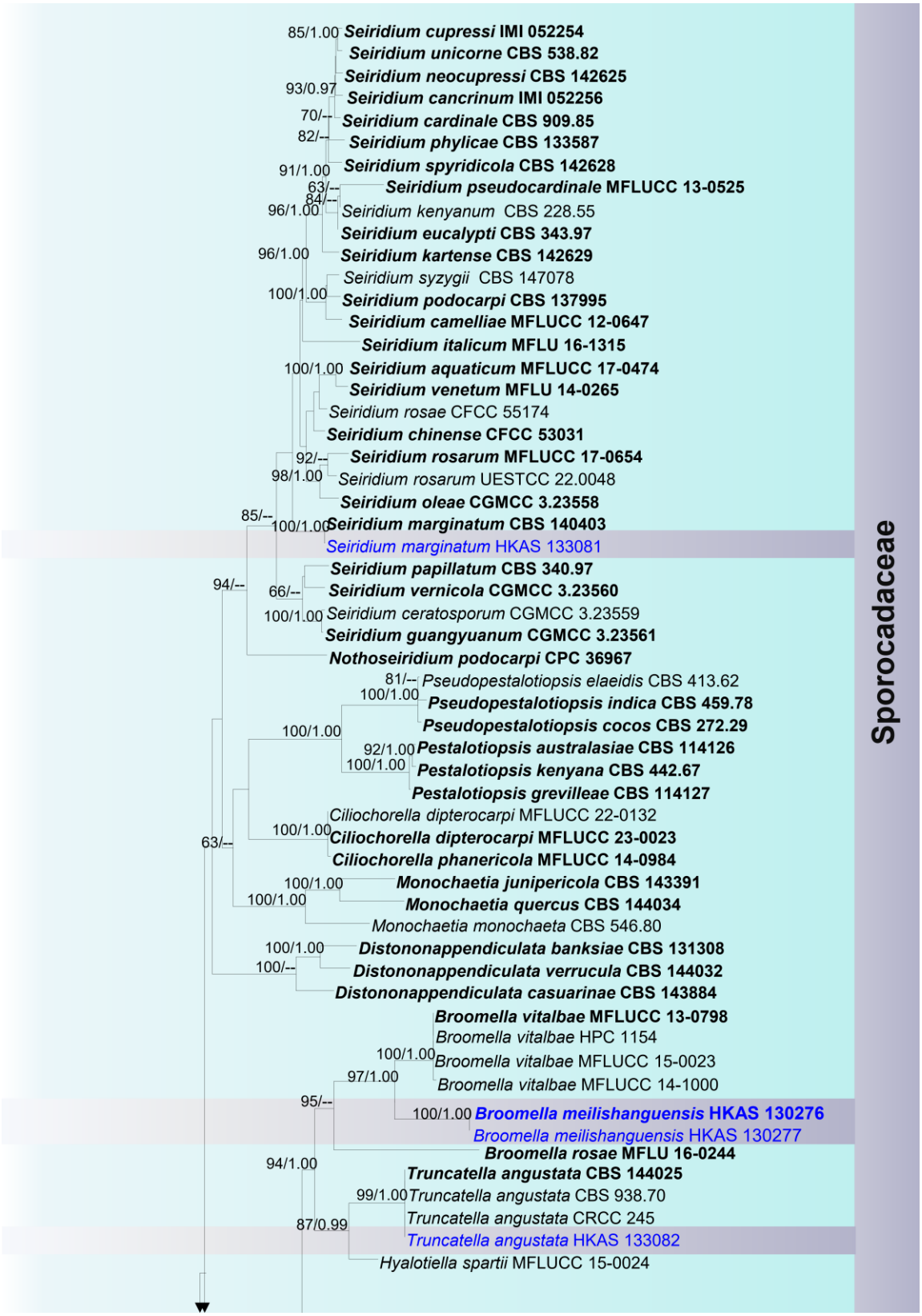

Figure 26 – 16 RAxML phylogram generated from combined dataset of partial LSU, ITS, *rpb*2, *tef*1-α, *tub*2 DNA sequence analyses for Sporocadaceae. Final likelihood value is -10991.575373. The tree is rooted to *Phlogicylindrium uniforme* (CBS 131312) and *P. eucalypti* (CBS 120080). The matrix had 3850 distinct alignment patterns with 30.45% undetermined characters and gaps.

Estimated base frequencies were; A = 0.249135, C = 0.254814, G = 0.243814, T = 0.252236 substitution rates AC = 1.574051, AG = 4.079871, AT = 1.473741, CG = 1.125690, CT = 6.182017, GT = 1.000000; gamma distribution shape parameter α = 0.895100. Newly generated sequences are in blue. Ex-type/type strains are indicated in bold.

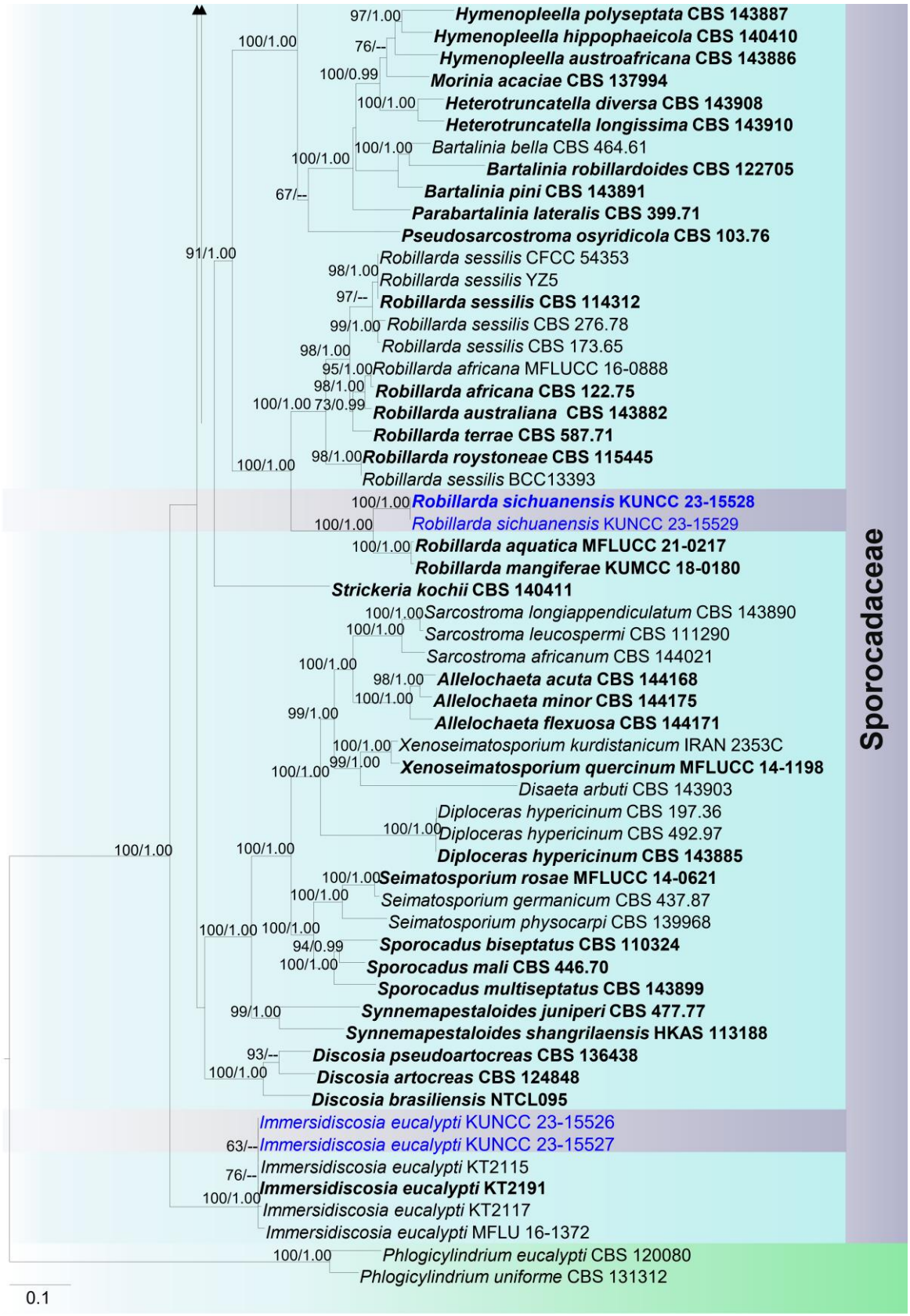

Figure 26 – Continued.

Broomella Sacc., Sylloge Fungorum 2: 557 (1883)

Notes – Saccardo (1883) introduced *Broomella*, typified by *B. vitalbae*. It was later placed in Amphisphaeriaceae (Kang et al. 1999). Li et al. (2015a) provided DNA and morphological data for *B. vitalbae*, detailing both its sexual and asexual morphs. Senanayake et al. (2015) described the coelomycetous asexual morph of *Broomella vitalbae* and positioned it in the family Bartaliniaceae with phylogenetic support. Later, Jaklitsch et al. (2016) provided DNA data for *Broomella vitalbae* and as a result, *Broomella* was placed under the family Sporocadaceae (= Bartaliniaceae) based on phylogenetic analysis. Wanasinghe et al. (2018a) introduced a new species, *Broomella rosae* (MFLU 16-0244), with a sexual morph. *Broomella* currently comprises 15 accepted species (Species Fungorum 2024). We introduce *Broomella meilishanguensis* with asexual morphology and phylogeny.

Broomella meilishanguensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 26, 27

MycoBank number: MB850213; Facesoffungi number: FoF14903

Etymology – The specific epithet is derived from Meilishangu county, where the holotype was collected.

Holotype – HKAS 130276

Saprobic on a decaying wood of an unidentified host. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 100–150 high μm × 120–220 diameter ($\overline{x}$ = 133 × 181 μm, n = 5), pycnidial, black, immersed, visible as black appendages, uni-loculate, solitary, scattered, globose, ostiolate. *Ostiole* 110–140 μm long × 40–100 μm diameter (125 × 74 μm), centric, prominent, cylindrical, wide, long neck, ostiolar canal brown, long periphysate. *Conidiomatal wall* 15–30 μm wide, thick-walled, slightly thick at the pycnidial upper wall, composed of two layers, light brown, thick-walled cells in outer layer, arranged in *textura angularis*, becoming hyaline towards the inner layer. *Conidiophores* reduced to conidiogenous cells lining the cavity of the conidiomata. *Conidiogenous cells* 8–12 μm length, holoblastic, proliferating sympodial at apex, ampulliform to subcylindrical, hyaline, aseptate, smooth and thin-walled. *Conidia* 30–60 μm high × 10–20 diameter ($\overline{x}$ = 42 × 13 μm, n = 30), cylindrical to ellipsoidal, 3-septate, smooth and thin-walled, apical cell modified into an appendage, basal cell obconic with an obtuse base, hyaline, with 2 subcylindrical to ellipsoidal, thick-walled, yellowish to brown, median cells constricted at septa, two prominent guttulate, hyaline apical cell, apical appendages 40–50 μm long, tubular, acellular, often irregularly or dichotomously branched at the base, filiform, flexuous, hyaline.

Material examined – CHINA, Yunnan Province, Meilishangu, Shangri-La (28.276389 N, 98.915833 E, 2910m), on decaying wood of an unidentified host, 15 August 2021, L. Qinxian, MLSG13 (HKAS 130276, holotype). *ibid*. MLSG13A (HKAS 130277, isotype).

GenBank accession numbers – ITS = PP584707, PP584708, LSU = PP584804, PP584805, *tef*1-α = PP933206, PP933207.

Notes – The combined genes phylogeny indicates that *Broomella meilishanguensis* is a sister species to *B. vitalbae*, with 97% MLB and 1.00 BYPP statistical support (Fig. 26). The nucleotide difference of LSU and ITS between *Broomella meilishanguensis* and *B. vitalbae* 10/827 (1.2%) and 25/538 (5%) respectively. *Broomella meilishanguensis* differs from *B. vitalbae* whereas the former has conidia that are cylindrical to ellipsoidal, an apical cell that is modified into an appendage, a basal cell that is obconic with an obtuse base and is hyaline with two prominent guttules on the median cells. Its apical appendages are 40–50 μm long, tubular, acellular, often irregularly or dichotomously branched at the base, filiform, flexuous, and hyaline. In contrast, *B. vitalbae* has conidia that are fusiform to aciculate with unequal ends; its basal cell is obconic and pale brown with two doliiform median cells that are thin-walled and pale brown. It also has a 6–15 μm long tubular, unbranched, filiform, flexuous, and hyaline appendage (Li et al. 2015d, Senanayake et al. 2015). The asexual morph of *Broomella meilishanguensis* is mostly similar to that of *Truncatella*. Both possess conidia with brown median cells and hyaline apical and basal cells, a branched cellular appendage, and are conical at the apical cell, with one or more appendages. However, *Broomella meilishanguensis* differs from *Truncatella* species in having conidiomata with a clear

ostiole and conidia with a cylindrical to ellipsoidal shape (Senanayake et al. 2015). From this study, the introduction of *Broomella meilishanguensis* with its asexual morph as a new species, providing asexual morphological characters for *Broomella* with molecular data.

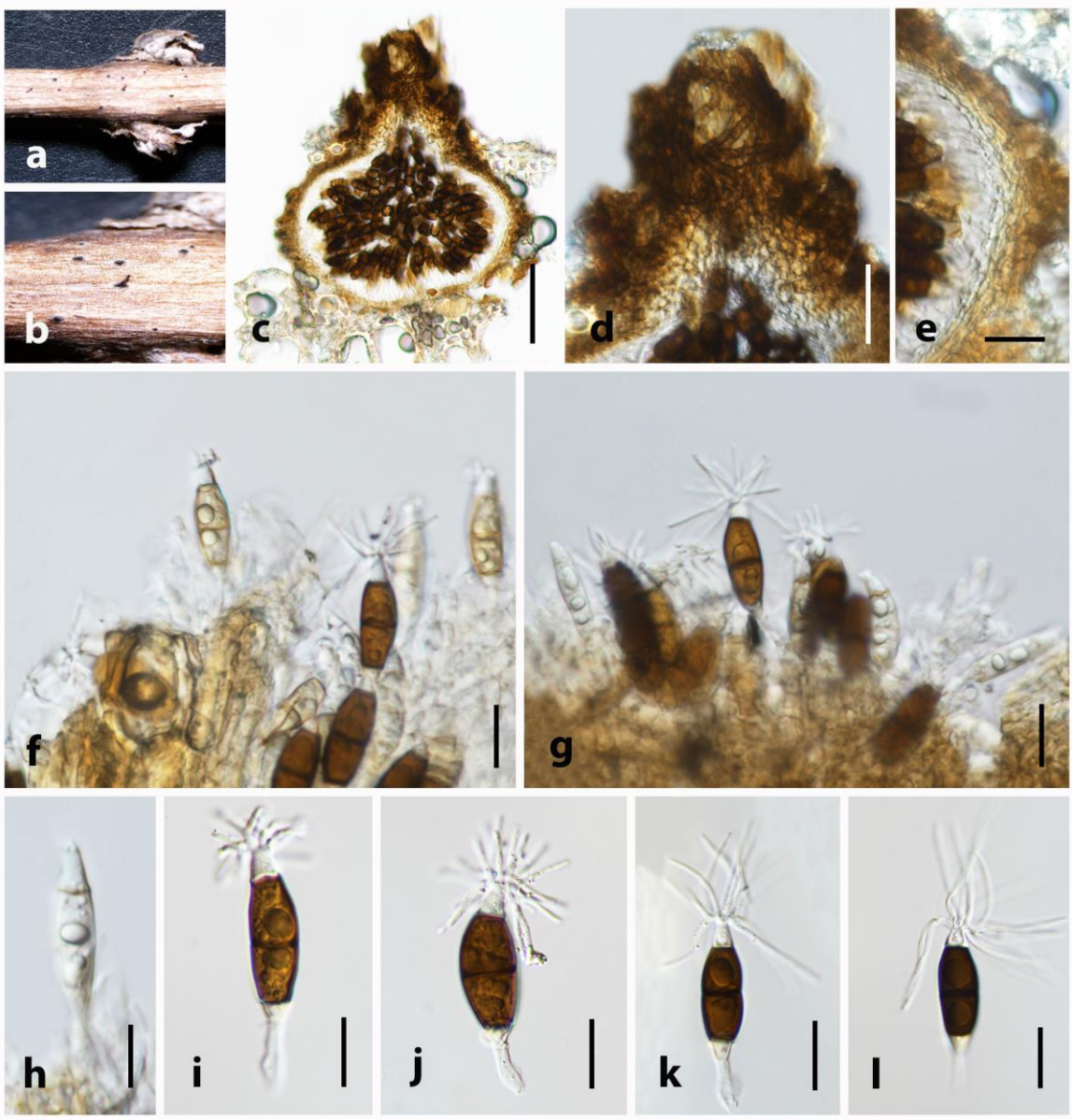

Figure 27 – *Broomella meilishanguensis* (HKAS 130276, holotype). a Host. b. Black conidiomata on the host surface. c Vertical section of a conidioma. d Section of ostiole. e Peridium. f, g. Conidiophores, conidiogenous cells and developing conidia. h–l Conidia. Scale bars: c, d = 50 μm, e–l = 20 μm.

Immersidiscosia Kaz. Tanaka, Okane & Hosoya, Persoonia 26: 94 (2011)

Notes – *Immersidiscosia* was introduced by Tanaka et al. (2011) with the *I. eucalypti* as the type species. Since its introduction, the observations of this species have been limited. Up until now, it has been documented exclusively in France, Italy, Japan and Tunisia. The sexual morph of *Immersidiscosia* remains unidentified and unknown to researchers. From our study, we identified and documented *Immersidiscosia eucalypti*, marking its presence in China on *Dichotomanthes tristaniicarpa*.

Immersidiscosia eucalypti (Pat.) Kaz. Tanaka, Okane & Hosoya, Persoonia 26: 94 (2011) Figs 26, 28

MycoBank number: MB519747; Facesoffungi number: FoF03385

Saprobic on dead leaves of *Dichotomanthes tristaniicarpa* Kurz. Sexual morph Undetermined. Asexual morph *Coelomycetous*. *Conidiomata* 40–70 μm high × 100–220 μm diameter ($\bar{x}$ = 141 × 59.3 μm, n = 5), conspicuous, pycnidial, subglobose to sometimes lenticular in section view, semi-immersed, scattered or aggregated and confluent, with relatively thin stromatic base, black, glabrous, epidermal, unilocular or multilocular and rounded. *Peridium* 10–25 μm wide, composed of multi-layers with outer light brown and inner layer hyaline. *Conidiogenous cells* 5–10 μm, subcylindrical, developing directly on the inner-most layer of peridium-wall, phialidic, each producing a single conidium, integrated, hyaline, smooth-walled. *Conidia* 30–40 μm long × 5–8 μm wide ($\bar{x}$ = 33.2 × 10.6 μm), cylindrical to subcylindrical, slightly curved, 3-septate, slightly constricted at the septa, hyaline, with cells of unequal width, basal cell obconic, two median cells subcylindrical, apical cell conical with a rounded apex; apical and basal cells with an unbranched, filiform, flexuous or straight appendage; apical appendage 10–20 μm ($\bar{x}$ = 14.6 μm), basal appendage 12–20 μm ($\bar{x}$ = 15.1 μm).

Culture characteristics – Colonies on PDA, reaching 20 mm diameter after one week at 25 °C; colonies are not flat, circular and dense, with a smooth surface, entire margin, concentrically zonate, white and brown at the centre, yellowish to light brown at the margin, media becoming pale brown; reverse brown at centre and light-yellow edges.

Material examined – CHINA, Yunnan Province, Botanical Garden, Kunming Institute of Botany (25.140833 N, 102.739444 E, 1892 m), on dead leaves of *Dichotomanthes tristaniicarpa* (Rosaceae), 12 December 2022, L.S. Dissanayake, KIB22-07 (HKAS 127242), living culture, KUNCC 23-15526. *ibid*. KIB22-07A (HKAS 127243), living culture, KUNCC 23-15527.

GenBank accession numbers – ITS = PP584709, PP584710, LSU = PP584806, PP584807, *tef*1-α = PP943006, PP943007.

Notes – *Immersidiscosia eucalypti* has been described on several host plants, including *Ardisia japonica* (Japan), *Eucalyptus* sp. (Tunisia), *Laurus nobilis* (France), *Quercus myrsinifolia* (Japan) and *Q. pubescens* (Italy) (Tanaka et al. 2011, Hyde et al. 2017, Lawrence et al. 2018). The LSU and ITS sequences from our two collections are similar to those of KT2117 and KT2091. Microscopically, the characteristics of our two collections align closely with the descriptions of *Immersidiscosia eucalypti* provided by Tanaka et al. (2011) and Hyde et al. (2017). This study represents a new record of *Immersidiscosia eucalypti* on *Dichotomanthes tristaniicarpa* in China. Additionally, we provide protein sequence data for this genus.

Neopestalotiopsis Maharachch., K.D. Hyde & Crous 2014

Notes – *Neopestalotiopsis* was established by Maharachchikumbura et al. (2014) with *N. protearum* as the type species. This genus is morphologically similar to *Pestalotiopsis*, characterized by 4-septate conidia, which are distinguished by one or several filiform or attenuated tubular apical appendages and a single basal tubular appendage (Jeewon et al. 2002, 2003b). The differentiation between *Neopestalotiopsis* and *Pestalotiopsis* also relies on conidial pigmentation and molecular phylogenetic analyses (Maharachchikumbura et al. 2014, Jayawardena et al. 2016, Liu et al. 2021, Chaiwan et al. 2022). Species within the *Neopestalotiopsis* are known to be pathogenic, causing a range of plant diseases including post-harvest diseases, leaf spots, fruit rots, fruit cankers, diseases of flowers and root rot across various hosts. The significance of these pathogens has been highlighted in various studies, such as those by Darapanit et al. (2021), Gualberto et al. (2021), Prasannath et al. (2021), Sun et al. (2021a), Ul Haq et al. (2021) and Konta et al. (2023) indicating the wide impact of *Neopestalotiopsis* species on agriculture and plant health globally.

Neopestalotiopsis rhododendri Qi Yang & Yong Wang bis, Biodiversity Data Journal 9(no. e70446): 9 (2021) Figs 29, 30

MycoBank number: MB840066; Facesoffungi number: FoF12918

Saprobic on dead twigs of unidentified host. Sexual morph: Undetermined. Asexual morph: *Conidiomata* conspicuous, scattered or aggregated, rounded, black. *Conidiophores* reduced to conidiogenous cells, smooth, hyaline. *Conidiogenous cells* discrete, thin walled, lageniform, subcylindrical or irregular. *Conidia* 18–28 μm × 6–8 μm ($\overline{x}$ = 22.6 × 6.9 μm, n = 20) fusoid, ellipsoid to subcylindrical, straight to slightly curved, 4-septate, basal cell 3–6 μm ($\overline{x}$ = 4.3 μm) conic to obconic with a truncate base, hyaline, minutely verruculose and thin walled, three median cells 12.5–17.5 μm ($\overline{x}$ = 15.2 μm) doliiform, versicolourous, second cells from base pale brown to olivaceous, third cell honey brown, forth cell brown, apical cell 3.5–5 μm ($\overline{x}$ = 4.2 μm) hyaline, subcylindrical, rugose and thin walled, with 2–3 tubular apical appendages, arising from the apical appendages, arising from the apical crest, unbranched, filiform 9–18 μm long, basal appendage present, 3–7.5 μm long.

Culture characteristics – Colonies on PDA reaching up to 60 mm in 14 days, dense aerial mycelium on the surface with undulate edge, white, fruiting bodies were observed after 21 days. reverse light-yellow.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.075 N, 103.564167 E, 1065.01m), on dead twigs of an unidentified host, 5 January 2023, L.S. Dissanayake, SCCFP23-16 (HKAS 133075), living culture KUNCC 24-17635, *ibid*. SCCFP23-16A (HKAS 133076), living culture, KUNCC 24-17636.

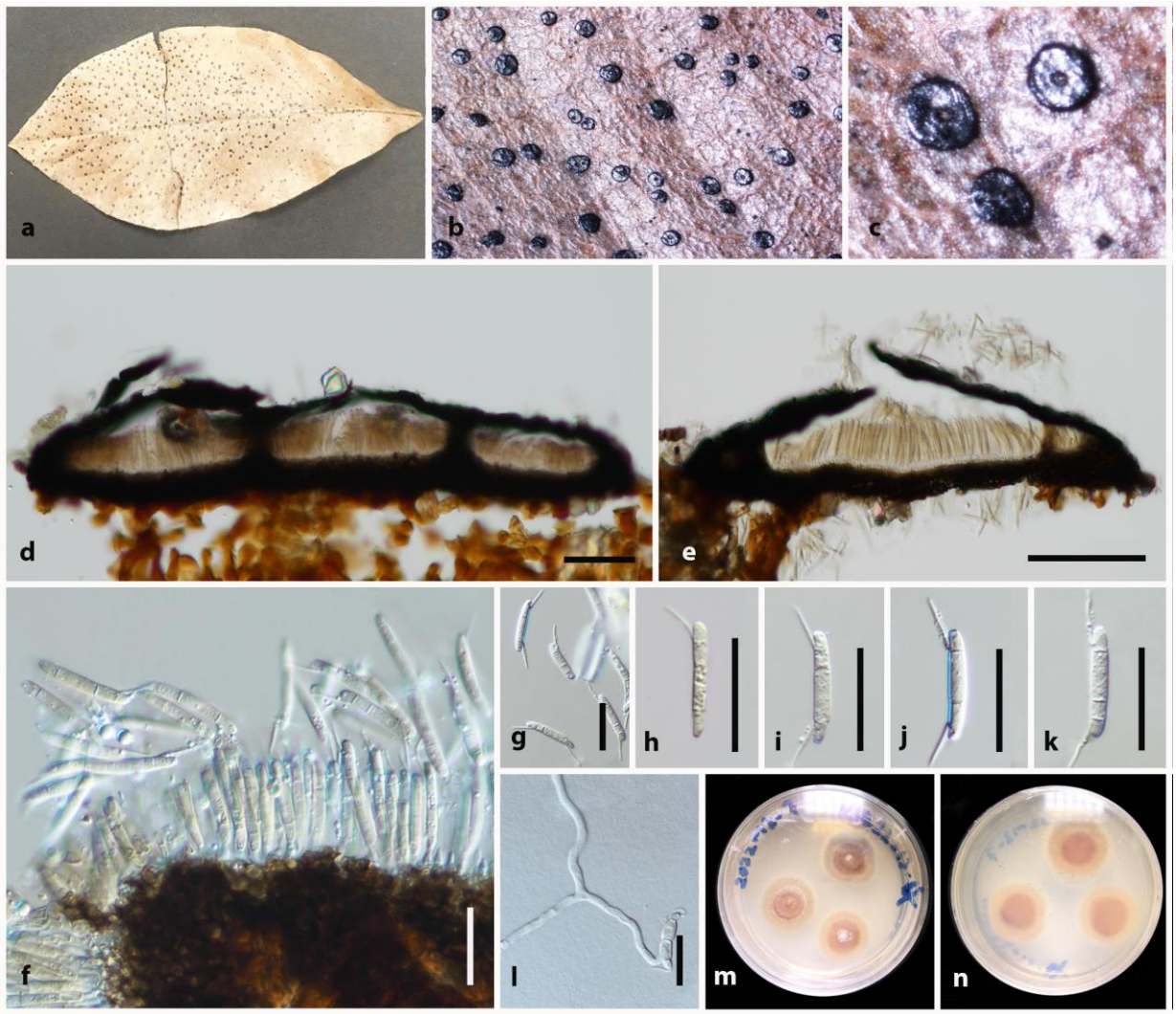

Figure 28 – *Immersidiscosia eucalypti* (HKAS 127242). a. Host. b, c Conidiomata on host surface. d, e Vertical sections of conidiomata. f Conidiogenous cells. g–l Conidia (l Germinating conidium). Colonies on PDA from above (m) and below (n). Scale bars: d, e = 50 μm, f–l = 30 μm.

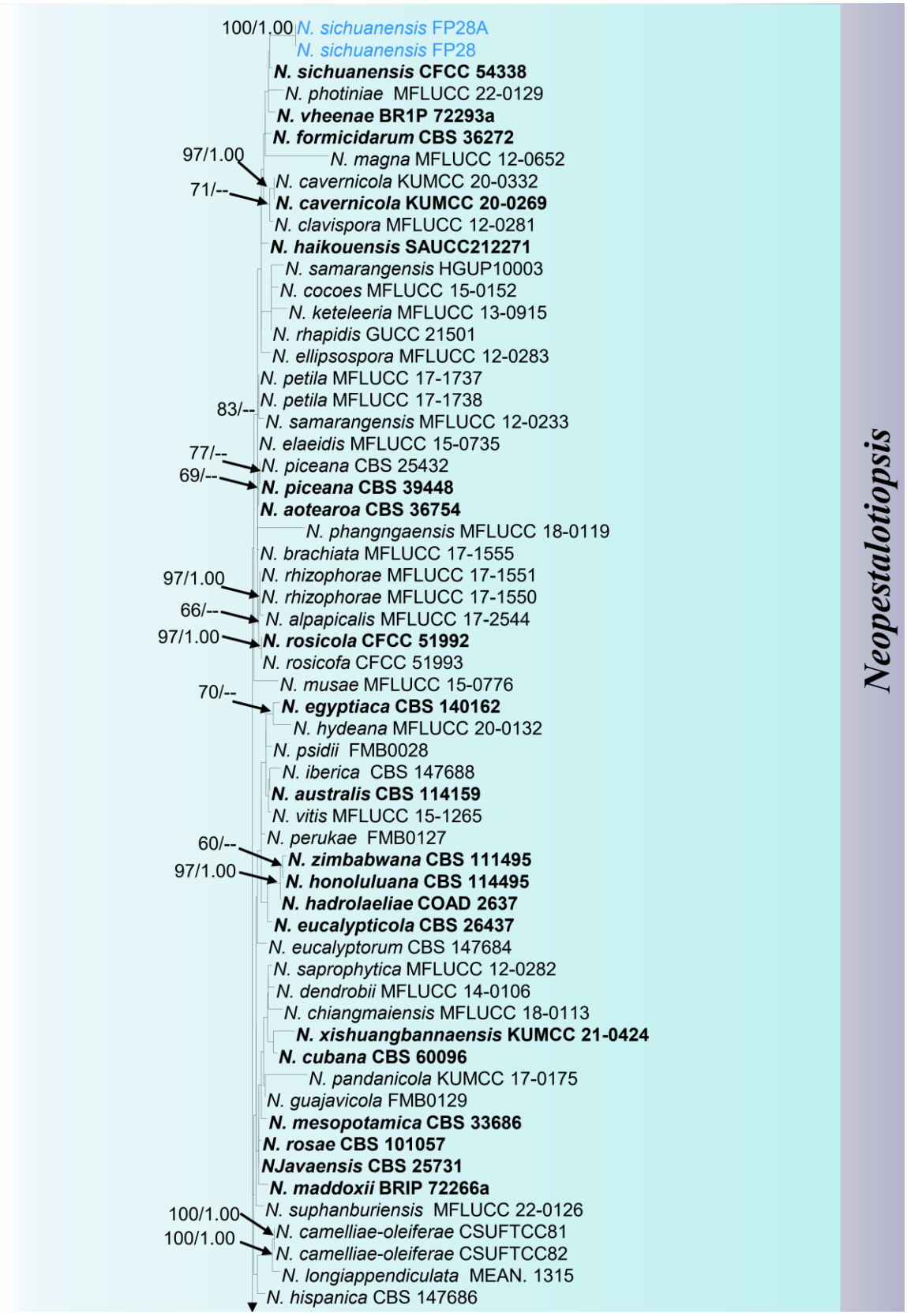

Figure 29 – RAxML phylogram generated from combined dataset of partial LSU, ITS, *rpb*2, *tef*1-α, *tub*2 DNA sequence analyses for *Neopestalotiopsis*. Final likelihood value is -7770.177449. The tree is rooted to *Pestalotiopsis diversiseta* (MFLUCC 12-0287) and *P. spathulata* (CBS 35686). The matrix had 1562 distinct alignment patterns with 11.95% undetermined characters and gaps. Estimated base frequencies were; A = 0.233280, C = 0.268485, G = 0.214908, T = 0.283327 substitution rates AC = 1.091046, AG = 4.314693, AT = 1.671304, CG = 0.875432, CT =

5.931999, GT = 1.000000; gamma distribution shape parameter α = 0.715430. Newly generated sequences are in blue. Ex-type/type strains are indicated in bold.

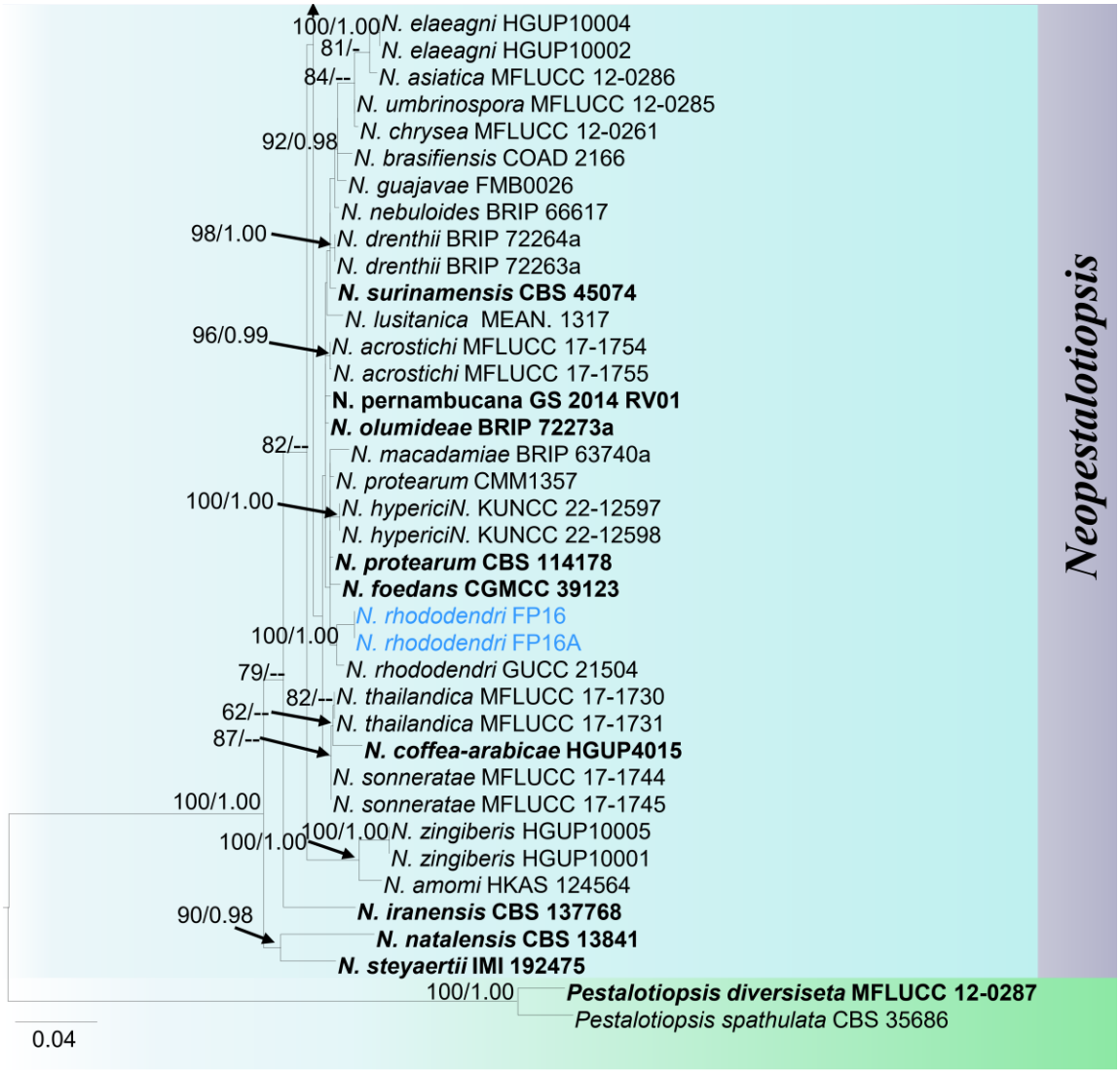

Figure 29 – Continued.

GenBank accession numbers – ITS = PP584711, PP584712, LSU = PP584808, PP584809, *tef*1-α = PP943008, PP943009, *tub*2 = PP977148, PP977149.

Notes – In our phylogenetic analysis, our strains (SCCFP23-16 and SCCFP23-16A) closely resembled *Neopestalotiopsis rhododendri*, a species originally collected from *Rhododendron simsii* leaves showing pathogenic spots in Yunnan and Guizhou provinces, China (Yang et al. 2021b). Our strains (FP16 and FP16A) are similar to *Neopestalotiopsis rhododendri*, sharing comparable size, shape and colour of conidia with those described in Yang et al. (2021b). Based on these findings, we report a new record for *Neopestalotiopsis rhododendri* from Sichuan Province, China.

Neopestalotiopsis sichuanensis (FP28) C. M. Tian & N. Jiang, Journal of Fungi 7 (1, no. 64): 22 (2021) Figs 29, 31

MycoBank number: MB837792; Facesoffungi number: FoF15550

Saprobic on dead twigs of an unidentified host. Sexual morph: Undetermined. Asexual morph: *Conidiomata* conspicuous, scattered or aggregated, rounded, black. *Conidiophores* reduced to conidiogenous cells, smooth, hyaline. *Conidiogenous cells* discrete, thin-walled, lageniform, subcylindrical or irregular. *Conidia* 20–25 × 6–9 µm ($\overline{x}$ = 22.3 ×7.2 µm, n = 20) fusoid, ellipsoid to

subcylindrical, straight to slightly curved, 4-septate, basal cell 4–5 µm ($\bar{x}$ = 4.7 µm) conic to obconic with a truncate base, hyaline, minutely verruculose and thin walled, three median cells 14–18.5 µm ($\bar{x}$ = 16.3 µm) doliiform, versicolourous, second cells from base pale brown to olivaceous, third cell honey brown, forth cell brown, apical cell 4.5–6.5 µm ($\bar{x}$ = 5.2 µm) hyaline, subcylindrical, rugose and thin walled, with 2–3 tubular apical appendages, arising from the apical appendages, arising from the apical crest, unbranched, filiform 11–20 µm long, basal appendage present, 4.2–6.6 µm long.

Culture characteristics – Colonies on PDA reaching up to 60 mm in 14 days, dense aerial mycelium on the surface with undulate edge, white, fruiting bodies were observed after 21 days. reverse light-yellow.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.075 N, 103.564167 E, 1065.01m), on dead twigs of an unidentified host, 5 January 2023, L.S. Dissanayake, SCCFP23-28 (HKAS 133078), living culture, KUNCC 24- 17633. *ibid*. SCCFP23-28A (HKAS 133077), living culture, KUNCC 24- 17634.

GenBank accession numbers – ITS = PP584713, PP584714, LSU = PP584810, PP584811, *tef*1-α = PP943010, PP943011, *tub*2 = PP977150, PP977151.

Notes – In our phylogenetic analysis, new strains (FP28 and FP28A) showed a close phylogenetic affinity to *Neopestalotiopsis sichuanensis* (Fig. 29). *Neopestalotiopsis sichuanensis* and our new collections are similar, with comparable conidia shapes and sizes (Jiang et al. 2021b). Initially *Neopestalotiopsis sichuanensis* was described from leaf spots on *Castanea mollissima* in Sichuan Province, China. In this study, we report two new strains of *Neopestalotiopsis sichuanensis* from the same province in China.

Pestalotiopsis Steyaert, Bull. Jard. bot. État Brux. 19: 300 (1949)

Notes – Steyaert (1949) initially categorized *Pestalotia* into three separate genera based on conidial forms: *Pestalotia* for species with 6-celled conidia, *Pestalotiopsis* for those with 5-celled conidia, and *Truncatella* for species with 4-celled conidia. Advancements in DNA-based phylogenetic analysis led Maharachchikumbura et al. (2014) to further refine the classification of

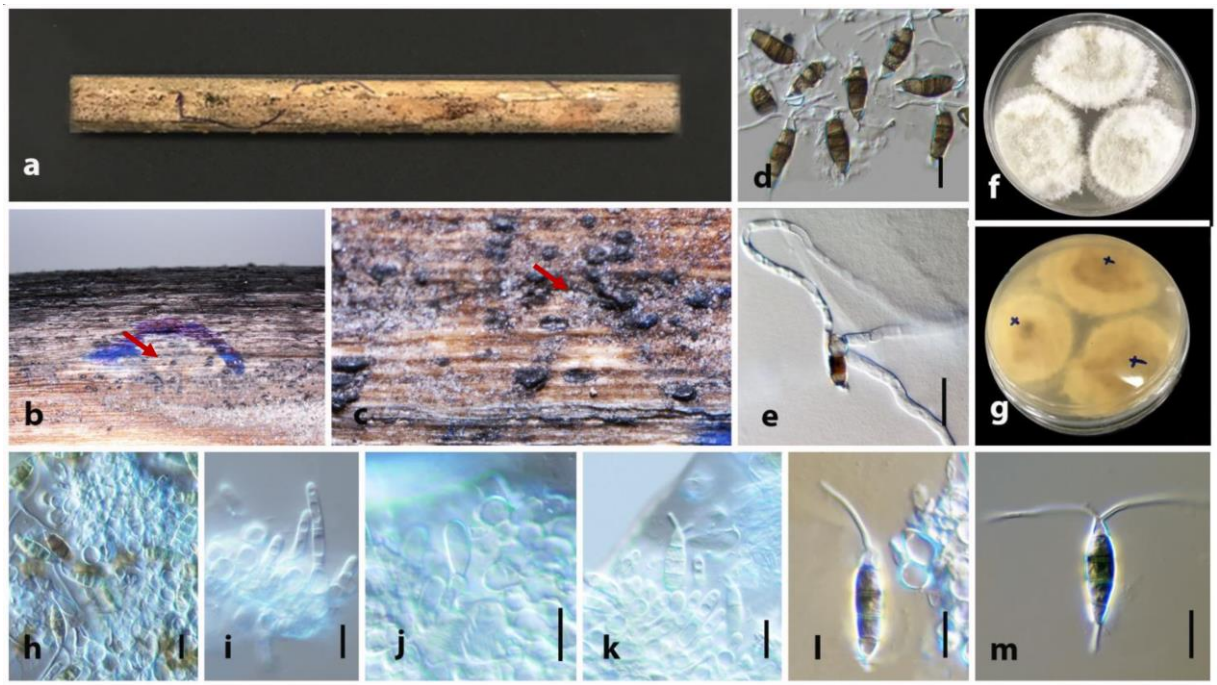

Figure 30 – *Neopestalotiopsis rhododendri* (HKAS 133075). a Host. b, c Conidiomata on host surface. d, e, l, m Conidia (e Germinated conidium). f Colonies on PDA from above. g Colonies on PDA from below. h–k Conidia attached to the conidiogenous cells. Scale bars: d, e = 5 µm, h–m = 10 µm.

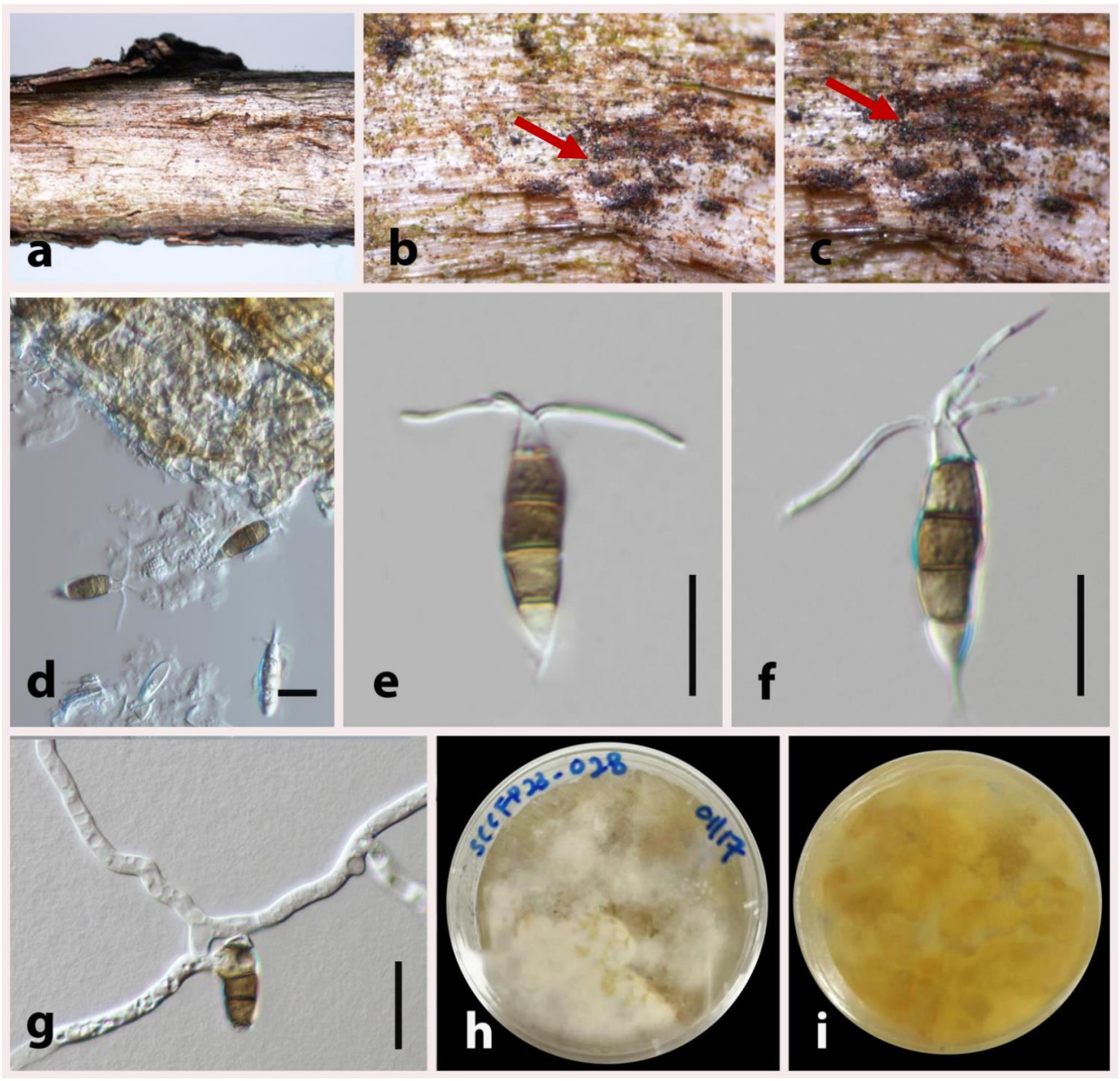

Figure 31 – *Neopestalotiopsis sichuanensis* (HKAS 133078). a Host. b, c Conidiomata on host surface. d Conidia attached to the conidioma. e–g Conidia (g Germinated conidium). Colonies on PDA from above (h) and below (i). Scale bars: e, f = 10 μm, d, g = 20 μm.

pestalotioid fungi. According to their research, the pestalotioid complex was divided into three genera *viz*. *Neopestalotiopsis*, *Pestalotiopsis* and *Pseudopestalotiopsis*, with all species across these genera exhibiting 4-conidial forms. *Pestalotiopsis maculans*, recognized as the type species of *Pestalotiopsis*, differentiates from *Pseudopestalotiopsis* through sequence data and typically features dark coloured, concolourous median cells with indistinct conidiophores. In contrast, *Neopestalotiopsis* is characterized by versicolourous median cells with indistinct conidiophores. The contemporary classification places *Pestalotiopsis* species within the Xylariales, under the family Sporocadaceae. *Pestalotiopsis* taxa are prevalent in both tropical and temperate regions, engaging with various plants as pathogens, endophytes or saprobes (Hu et al. 2007, Liu et al. 2010, Xu et al. 2010, Gu et al. 2022, Xiong et al. 2022, Sun et al. 2023, Pandey et al. 2024). This genus has garnered increasing attention due to its role as a phytopathogen and its potential in producing novel chemical metabolites. Currently, there are 410 species epithets are listed in Index Fungorum (2024), reflecting the diversity and significance of this fungal group in various ecological and research contexts.

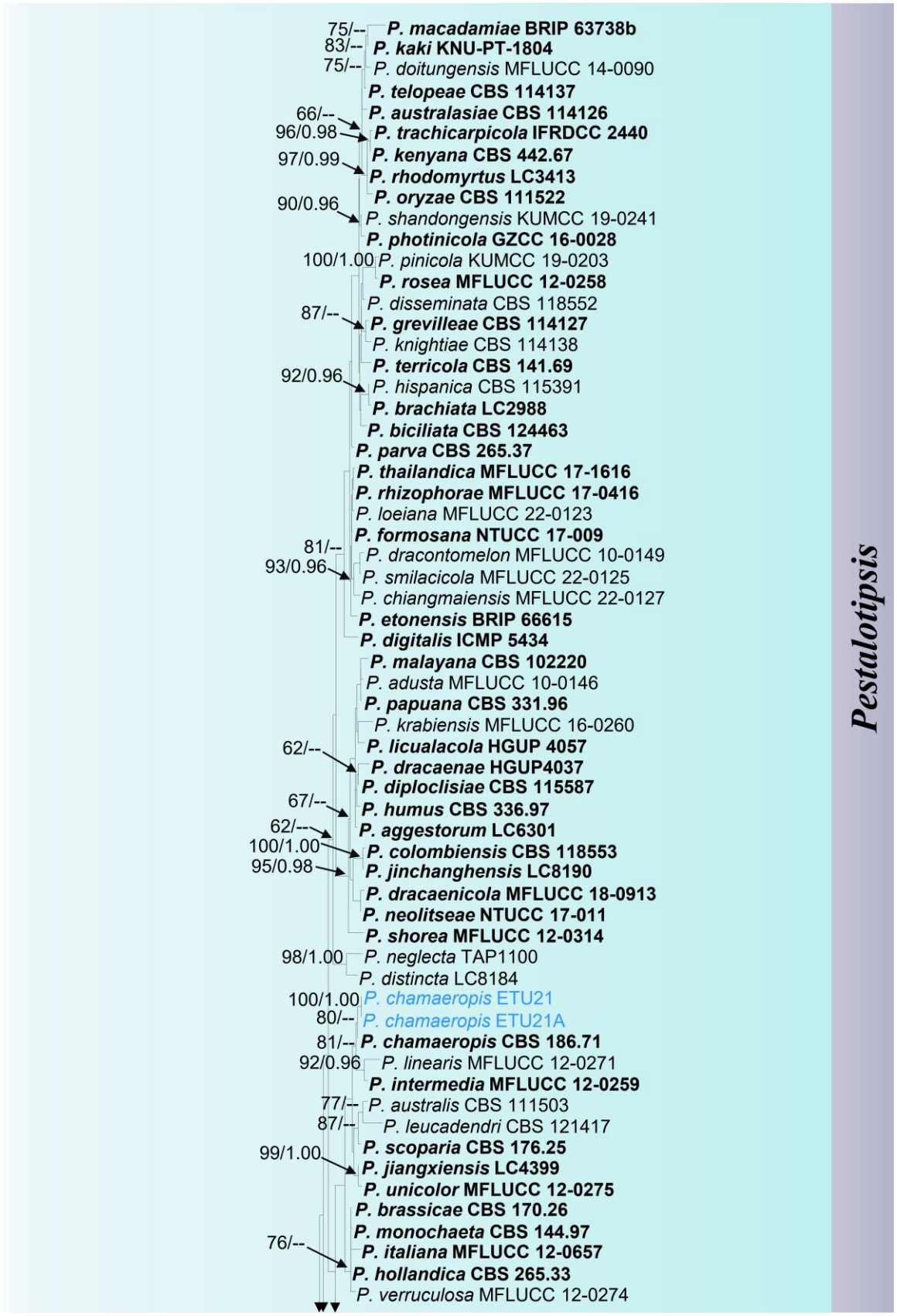

Figure 32 – 16 RAxML phylogram generated from combined dataset of partial LSU, ITS, *rpb*2, *tef*1-α, *tub*2 DNA sequence analyses for *Pestalotiopsis*. Final likelihood value is -8980.105245. The tree is rooted to *Neopestalotiopsis hypericin* (KUNCC 22-12597) and *N. protearum* (CBS 114178). The matrix had 1562 distinct alignment patterns with 10.03% undetermined characters and gaps. Estimated base frequencies were; A = 0.233719, C = 0.289733, G = 0.217421, T = 0.259127

substitution rates AC = 0.894635, AG = 3.100211, AT = 1.092177, CG = 0.941697, CT = 4.277126, GT = 1.000000; gamma distribution shape parameter α = 0.633467. Newly generated sequences are in blue. Ex-type/type strains are indicated in bold.

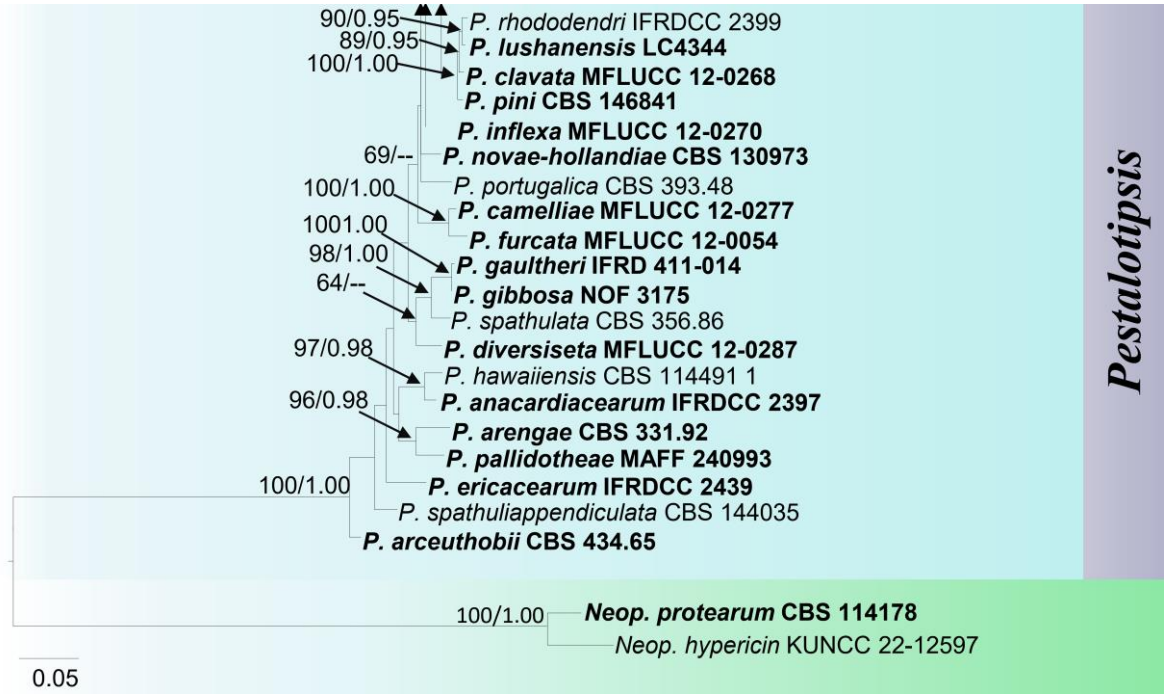

Figure 32 – Continued.

Pestalotiopsis chamaeropis Maharachch., K.D. Hyde & Crous, Studies in Mycology 79: 158 (2014) Figs 32, 33

MycoBank number: MB809735; Facesoffungi number: FoF11691

Saprobic on dry culms of Poaceae sp. Sexual morph: Undetermined. Asexual morph: *Conidiomata* conspicuous, scattered or aggregated, rounded, black. *Conidiophores* reduced to conidiogenous cells, smooth, hyaline. *Conidiogenous cells* discrete, thin-walled, lageniform, subcylindrical or irregular. *Conidia* 17–26 × 5–7.5 μm ($\overline{x}$ = 21 × 6.3 μm) fusoid, ellipsoid to subcylindrical, straight to slightly curved, 4-septate, basal cell 4–6 μm ($\overline{x}$ = 4.7 μm) conic to obconic with a truncate base, hyaline, minutely verruculose and thin walled, three median cells 12–16.5 μm ($\overline{x}$ = 14.7 μm) doliiform, versicolourous, second cells from base pale brown to olivaceous, third cell honey brown, forth cell brown, apical cell 3.7–5.1 μm ($\overline{x}$ = 4 μm) hyaline, subcylindrical, rugose and thin walled, with 2–3 tubular apical appendages, arising from the apical appendages, arising from the apical crest, unbranched, filiform 9.5–14.6 μm long, basal appendage single, tubular, unbranched 3.2–5.2 μm long.

Culture characteristics – Colonies on PDA reaching up to 60 mm in 14 days, dense aerial mycelium on the surface with undulate edge, white to off-white, fruiting bodies were observed after 21 days. reverse light-yellow.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.075 N, 103.564167 E, 1065.01 m), on dry culms of Poaceae sp., 5 January 2023, L.S. Dissanayake, SCCETU23-21 (HKAS 133080), living culture, KUNCC 24- 17631. *ibid*. SCCETU23-21A (HKAS 133079), living culture, KUNCC 24- 17632.

GenBank accession numbers – ITS = PP584715, PP584716, LSU = PP584812, PP584813, *tef*1-α = PP943012, PP943013, *tub*2 = PP977152, PP977153.

Notes – Based on ITS, *tef*1-α and *tub*2 combined phylogenetic analysis, our new strains (HKAS 133079 and HKAS 133080) clustered with *Pestalotiopsis chamaeropis* and both showing considerable morphological similarities, including the size of conidia. *Pestalotiopsis chamaeropis*

was initially introduced by Maharachchikumbura et al. (2014) from leaves of *Chamaerops humilis* in Italy. Subsequently, *Pestalotiopsis chamaeropis* has been collected from various hosts and in different life modes: by Chen et al. (2021b) on tea leaves in China and by Hsu et al. (2024) on the stroma of *Ophiocordyceps* sp., parasitic on a cocoon (Lepidoptera) in Taiwan. In this study, we report another record for *Pestalotiopsis chamaeropis*, collected from Poaceae sp. in China.

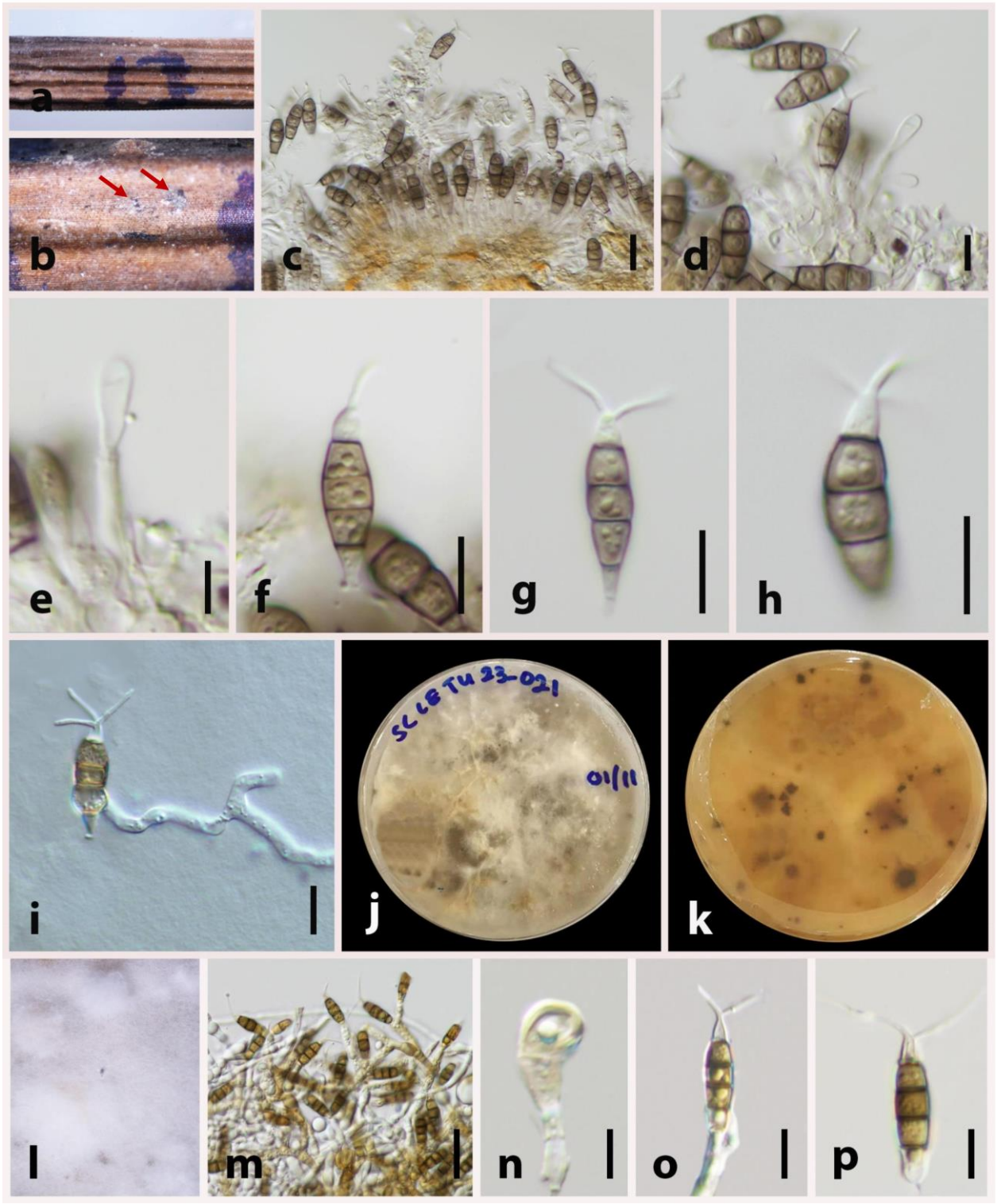

Figure 33 – *Pestalotiopsis chamaeropis* (HKAS 133080). a Host. b Conidiomata on host surface. c–e Conidia attached to the conidiomata. f–i, p Conidia (i Germinating conidium). j Colonies on PDA from above. k Colonies on PDA from below. l Colony on PDA. m–o Conidia attached to the conidiogenous cells. Scale bars: c–i = 20 μm, n–p = 10 μm.

Robillarda Sacc., Michelia 2 (6): 8 (1880)

Notes – Saccardo (1880) introduced *Robillarda* to accommodate the type species *R. sessile*. Various ecosystems, including terrestrial and freshwater environments, have reported the presence of *Robillarda* species (Phookamsak et al. 2019, Manawasinghe et al. 2022). *Robillarda* species are characterized by solitary or gregarious, scattered, subglobose, unicellular, immersed, ostiolate, glabrous pycnidia, holoblastic, ampulliform, hyaline, conidiogenous cells, 1-septate, smooth-walled, hyaline conidia with a single branched, apical appendage (Crous et al. 2015, Borse et al. 2016, Wijayawardene et al. 2016). Index Fungorum (2024) listed 34 species epithets under *Robillarda*. We report multigene phylogenetic description for *Robillarda* and introduced a new species, *R. sichuanensis*.

Robillarda sichuanensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 26, 34

MycoBank number: MB850214; Facesoffungi number: FoF14904

Etymology – The specific epithet originates from the Sichuan Province, where the holotype was collected.

Holotype – HKAS 127250

Saprobic on decaying wood of an unidentified host. Sexual morph: Undetermined. Asexual morph: *Coelomycetous*. *Conidiomata* 90–160 μm high × 150–250 μm diameter ($\overline{x}$ = 123 × 217 μm, n = 10), pycnidial, black, immersed, visible as black dots, uni-loculate, solitary, scattered, globose, minutely ostiolate. *Conidiomatal wall* 15–40 μm wide, thick-walled, slightly thick at the pycnidial upper wall, composed of two layers, dark brown to black, thick-walled cells in outer layer, arranged in *textura angularis*, becoming hyaline towards the inner layer. *Conidiophores* reduced to conidiogenous cells lining the cavity of the conidiomata. *Conidiogenous cells* 4–10 × 3–5 μm ($\overline{x}$ = 7 × 4 μm, n = 20), holoblastic, proliferating sympodial at apex, ampulliform to subcylindrical, hyaline, aseptate, smooth and thin-walled. *Conidia* 10–15 μm long × 3–5 μm wide ($\overline{x}$ = 12.4 × 4.2 μm, n = 40), hyaline, oblong to ellipsoidal, narrow towards the basal cell, straight, 1-septate, smooth and thin-walled, slightly constricted at the septum, apical cell modified into an appendage; appendages 15–30 × 1–2 μm ($\overline{x}$ = 22 × 1.8 μm, n = 40), dividing into 3–4 divergent branches, devoid of cell contents, flexuous, attenuated toward the apex, slightly swollen at the apex.

Culture characteristics – Conidia germinating on PDA within 24 h. Colonies on PDA reaching 25–30 mm diameter after 2 weeks at 25 °C. *Mycelia* superficial, circular, flat, surface slightly rough, with entire margin, forming small, from above, white to light brown; reverse, dark brown at the center and becoming light brown towards margin, not producing pigmentation in agar.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.075 N, 103.564167 E, 1065.01m), on dead twigs of an unidentified host, 5 January 2023, L.S. Dissanayake, SCCFP23-32 (HKAS 127250, holotype), ex-type, KUNCC 23-15528. *ibid*. SCCFP23-32A (HKAS 127251, isotype), ex-isotype, KUNCC 23-15529.

GenBank accession numbers – ITS = PP584719, PP584720, LSU = PP584816, PP584817, *tef*1-α = PP961245, PP961246, *tub*2 = PP971773, PP971774.

Notes – The combined LSU, ITS, *rpb*2, *tef*1-α and *tub*2 phylogeny indicates that *Robillarda sichuanensis* clusters with *R. aquatica* (MFLU 21-0253) and *R. mangiferae* (KUMCC 18-0180), with 100% MLB and 1.00 BYPP support (Fig. 26). The LSU and ITS nucleotide of *Robillarda sichuanensis* differs from that of *R. mangiferae* and *R. aquatica* by 13/827 (1.5%), 28/538 (5.2%) and 15/827 (1.8%), 30/538 (5.6%) respectively. *Robillarda sichuanensis* differs from *R. aquatica* in having immersed ascomata vs. semi-immersed to erumpent ascomata, comparatively smaller conidia (10–15 μm vs. 15–20 μm) and shorter appendages (15–30 μm vs. 30–45 μm) (Manawasinghe et al. 2022). *Robillarda mangiferae* has large conidiomata (250–310 μm high, 300–340 μm diameter vs. 90–160 high μm × 150–250 diameter) compared to *R. sichuanensis*. *Robillarda mangiferae* is characterized by having 2–3 divergent branches on the conidia appendages while *R. sichuanensis* characterized with 3–4 divergent branched conidia (Phookamsak et al. 2019).

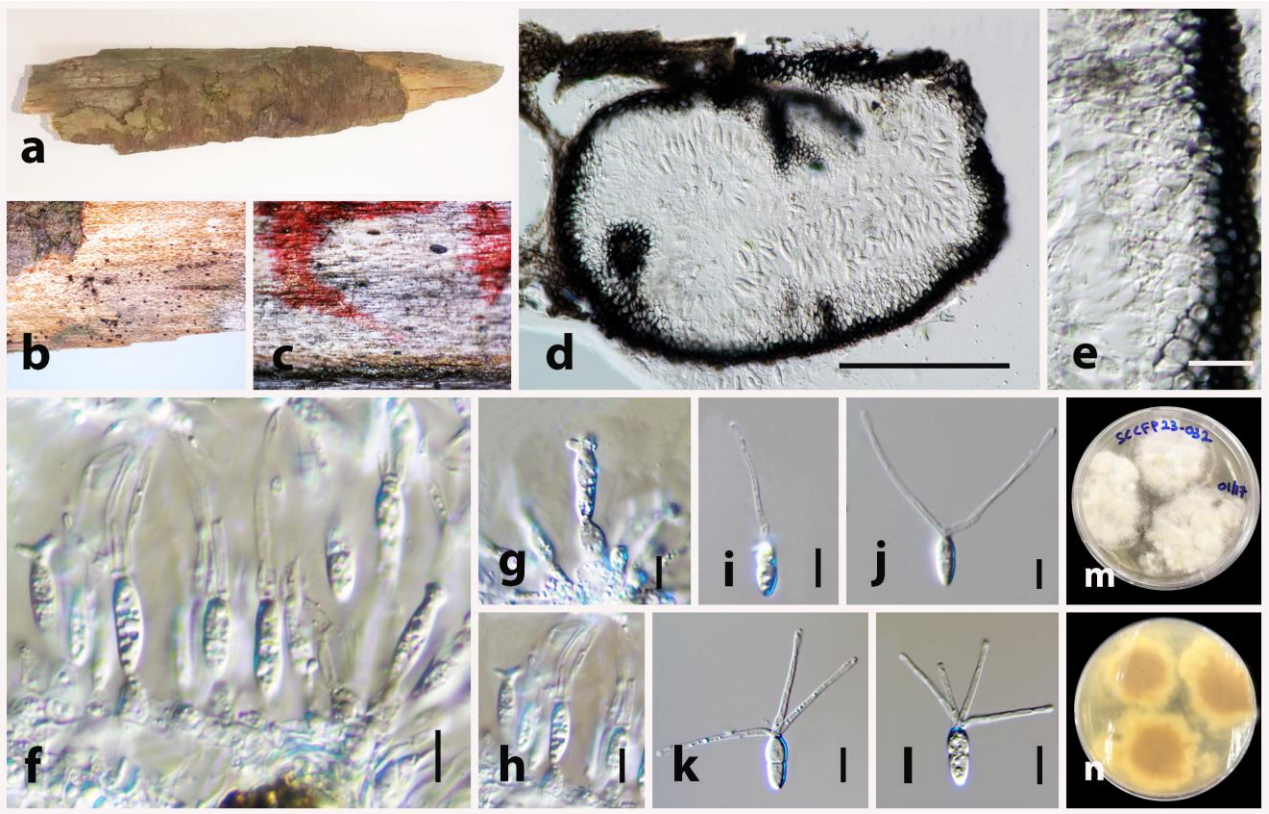

Figure 34 – *Robillarda sichuanensis* (HKAS 127250, holotype). a Host. b, c Appearance of conidiomata. d Vertical section of conidioma. e Conidioma wall. f–h Conidiogenous cells. i–l Conidia. m, n Colonies on PDA (n from the bottom). Scale bars: d = 100 μm, e = 20 μm, f–l = 10 μm.

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

Notes – *Seiridium*, established by Nees (1816) with *S. marginatum* as the type species, has been subject to extensive phylogenetic analysis to clarify its relationships within the Sporocadaceae. Bonthond et al. (2018) employed a multi-loci phylogenetic analysis, incorporating ITS, *tef*1-α, *tub*2 and *rpb*2, to resolve the phylogenetic placement of *Seiridium*. This genus is distinguished from others within the Sporocadaceae by its 5-septate conidia and is known to occur as both saprobes and plant pathogens (Jeewon (2003b, Maharachchikumbura et al. 2014, Li et al. 2021, 2022). *Seiridium* species are distributed in both tropical and temperate regions (Jiang et al. (2019). Senanayake et al. (2015) identified *Blogiascospora* and *Lepteutypa* as the sexual morphs of this genus. Subsequently, Jaklitsch et al. (2016) epitypified *Seiridium marginatum* and confirmed its sexual morph as *Blogiascospora marginata*, based on molecular data.

Seiridium marginatum Nees, Syst. Pilze (Würzburg): 5 (1817) Figs 23, 35

MycoBank number: MB165487; Facesoffungi number: FoF06881

Associated with dead twigs of unidentified host. Sexual morph: Undetermined. Asexual morph: *Conidiomata* pycnidial, globose to clavate, solitary or aggregated, semi-immersed, dark brown, exuding globose, dark brown, glistening conidial masses. *Conidiophores* long, lining the cavity of conidioma, septate, irregularly branched, colorless, smooth-walled, invested in mucus. *Conidiogenous cells* discrete, cylindrical, with minute apical periclinal thickenings, colorless, smooth, proliferating 2–5 times percurrently. *Conidia* 20–30 × 6.5–8.5 ($\overline{x}$ = 24.5 × 7.6 μm), fusiform to ellipsoid, straight or somewhat curved, basal cell obconic with a truncate base, hyaline, smooth-walled, 4 median cells doliiform, unequal, brown, thick-walled, together 13–22 μm long; apical cell, conical, hyaline, smooth-walled, 2–4 μm long; apical appendages tubular, attenuated,

flexuous single, unbranched 10–35 μm long; basal appendage single, unbranched, centric, 20–25 μm long.

Material examined – CHINA, Yunnan Province, Meilishangu, Shangri-La (28.276389 N, 98.915833 E, 2910m), on decaying wood of an unidentified host, 15 August 2021, L. Qinxian, MLSG12 (HKAS 133081).

GenBank accession numbers – ITS = PP584717, LSU = PP584814, *tef*1-α = PP961243, *tub*2 = PP977154.

Notes – In this study, a new strain (HKAS 133081) was phylogenetically closely related to *Seiridium marginatum* (CBS 140403), with 100% MLB and 1.00 BYPP support values (Fig. 26). It is similar to *Seiridium marginatum*, having conidia and conidiomata of similar size, color and shape. Jaklitsch et al. (2016) revisited *Seiridium* and epitypified *S. marginatum*, collected from *Rosa canina* in Europe (France, Germany, Switzerland). From our research, we report a new record for *Seiridium marginatum* collected from an unidentified host in Yunnan Province, China, expanding the known distribution and potential host range of this species.

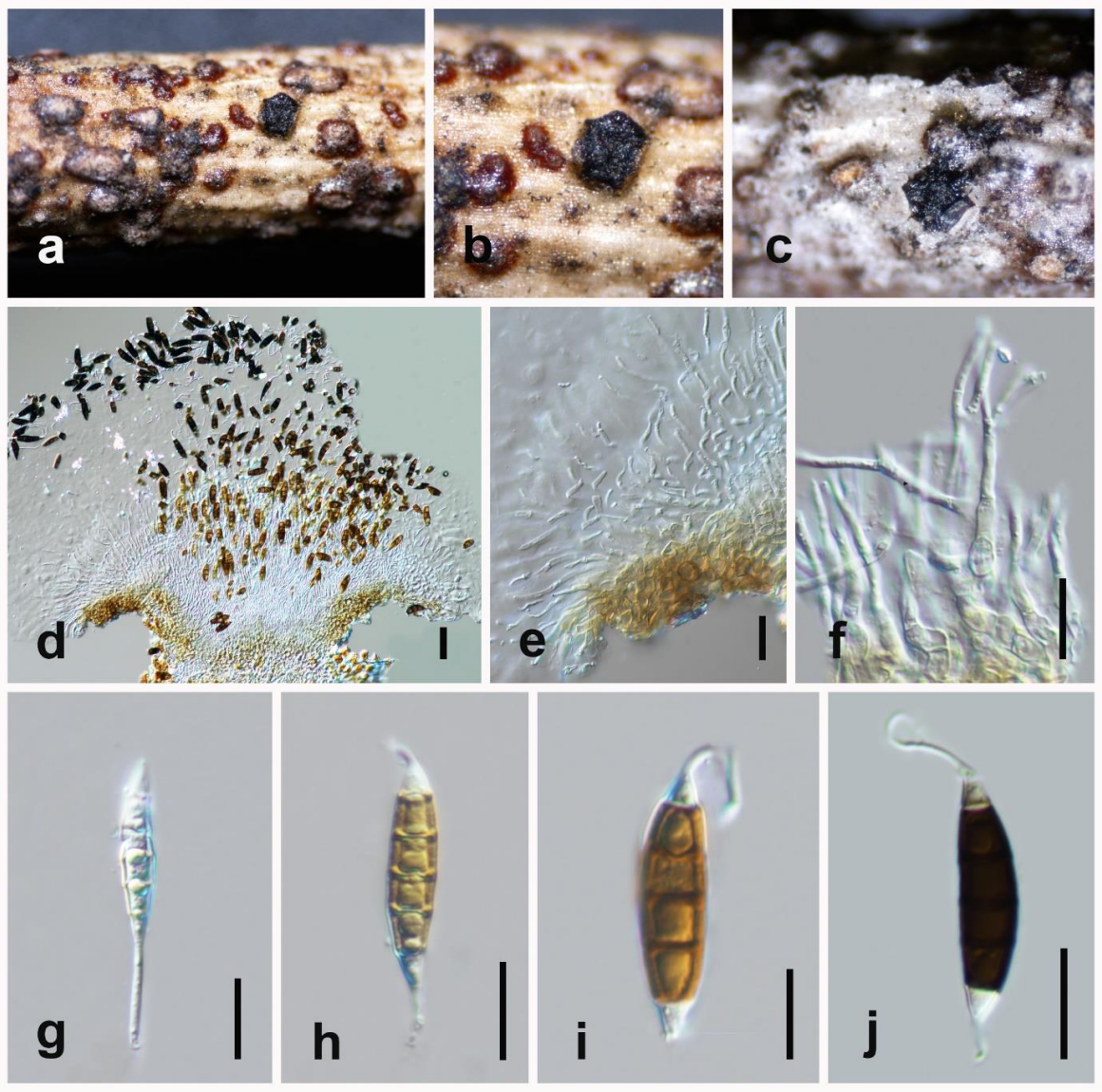

Figure 35 – *Seiridium marginatum* (HKAS 133081). a. Host. b, c Conidiomata on host surface. d, e Conidiomata. f Conidia attached to the conidiomata wall. g–j Conidia. Scale bars: d–f = 20 μm, g–j = 10 μm.

Truncatella Steyaert, Bull. Jard. bot. État Brux. 19: 293 (1949)

Notes – *Truncatella*, established by Steyaert (1949) with *T. truncata* as its type species, has undergone various taxonomic placements over the years. Initially classified in the Amphisphaeriaceae and later with the Xylariales and Bartaliniaceae (Jeewon et al. 2003b, Lumbsch and Huhndorf 2010, Senanayake et al. 2015), it is now accepted within the Sporocadaceae (Hyde et al. 2020a). *Truncatella* species are characterized by their 3-septate, verruculose, and pigmented conidia (Steyaert 1949, Jeewon et al. 2002, Maharachchikumbura et al. 2012, 2015). *Truncatella* species primarily function as saprobes, and endophytes, with some species being notable as destructive pathogens causing diseases in several economically important crops (Maharachchikumbura et al. (2016a).

Truncatella angustata (Pers.) S. Hughes, Can. J. Bot. 36: 822 (1958) Figs 26, 36

MycoBank number: MB307155; Facesoffungi number: FoF04092

Pathogenic on diseased branches of unidentified host. Sexual morph: Undetermined. Asexual morph: *Conidiomata* are 110–190 × 160–190 µm ($\overline{x}$ = 141.6 × 179.8 µm), pycnidial to sporodochial, mostly solitary, immersed to semi-erumpent, unilocular, conical, or subglobose with a flattened base, and dark brown to black. The Conidiomata wall is 12–18 µm 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 septate, cylindrical, irregularly branched, with branch lengths variable (up to 40 µm long), hyaline or paler brown, thin-and smooth-walled. *Conidiogenous cells* are discrete, hyaline, cylindrical, and proliferating percurrently. *Conidia* 16–22 × 6.5–8 µm ($\overline{x}$ = 19 × 7 µm, n = 20), fusoid, ellipsoid to subcylindrical, 4-septate, not striate, bearing a hyaline appendage at both ends, euseptate, basal cell obconic with a truncate base, hyaline to light brown, 1.5–2.5 µm long; two median cells, 7–15 µm long, verruculose, cylindrical to doliiform, and brown to dark brown, guttulate, with septa darker than the rest of the cells, the apical cell is conical, with hyaline to pale brown, and a smooth, 3.5–5.2 µm long, apical appendage mostly single, centric, and 1.7–5.5 µm long, occasionally branched; the basal appendage is single, cylindrical, excentric, unbranched, and 16–35 µm long.

Material examined – CHINA, Yunnan Province, Shangri-La (28.276389 N, 98.915833 E, 2910m), on decaying wood of an unidentified host, 15 August 2021, L. Qinxian, GLD02 (HKAS 133082).

GenBank accession numbers – ITS = PP584718, LSU = PP584815, *tef*1-α = PP961244, *tub*2 = PP977155.

Notes – A new collection (HKAS 133082), was found from dead twigs of an unidentified host in Yunnan Province, China. This new strain shows a close phylogenetic affinity to *Truncatella angustata* based on combined LSU, ITS, *rpb*2, *tef*1-α and *tub*2 sequence data analyses (Fig. 26). *Truncatella angustata* is known to cause grapevine trunk disease in northern Iran and is responsible for yield losses in grapes (Arzanlou et al. 2012). It has been recorded on many plant species in various countries, including *Olea europaea* fruits in Kazakhstan, *Rosa canina*, *Malus domestica* in the Netherlands, *Origanum vulgare* in Latvia, *Vaccinium* spp. (Blueberry) in Chile, *Quercus brantii* (Persian Oak) in Iran and *Picea schrenkiana* in China (Zhang et al. 1999, Espinoza et al. 2008, Eken et al. 2009, Wenneker et al. 2016, Alidadi et al. 2018, Sokolova et al. 2022). This study reports another record of *Truncatella angustata* from an unidentified host in China.

Xylariales Nannf., Nova Acta Regiae Societatis Scientiarum Upsaliensis Ser. IV. 8 (2): 66 (1932)

Barrmaeliaceae Voglmayr & Jaklitsch, Mycol. Progr. 17 (1-2): 162 (2017)

Notes – Barrmaeliaceae was introduced by Voglmayr et al. (2018) to accommodate the *Barrmaelia* and *Entosordaria*. In their study, Voglmayr et al. (2018) epitypified three species of *Barrmaelia viz. B. macrospora*, *B. moravica* and *B. rhamnicola*. They also epitypified one species of *Entosordaria, E. perfidiosa*. Members are saprobic specially on wood and bark inhabiting species.

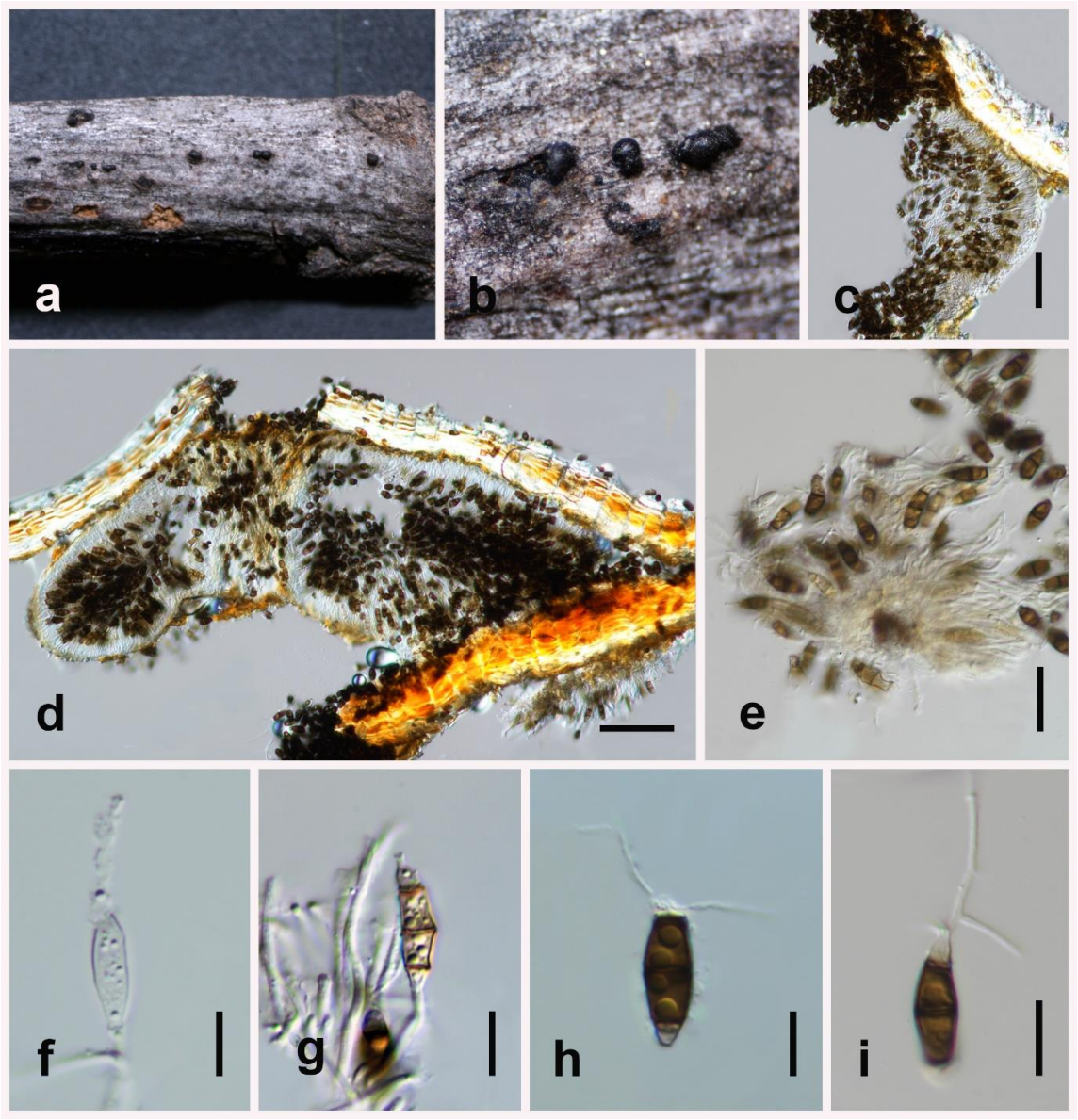

Figure 36 – *Truncatella angustata* (HKAS 133082). a. Host. b Conidiomata on host surface. d Conidiomata. c, e Conidia attached to the conidiomata. f–i Conidia. Scale bars: d = 50 μm, e = 20 μm, f–i= 10 μm.

Barrmaelia Rappaz, Mycologia Helvetica 7: 130 (1995)

Notes – *Barrmaelia* was introduced by Rappaz (1995) to accommodate *B. rhamnicola* as the type species. This genus is characterized by its often slightly curved, relatively large ascospores filled with conspicuous oil drops and it lacks a germ slit in its sexual morph while having a libertella-like asexual morph. More recently, *B. rappazii* and *B. serenoae* were introduced (Voglmayr et al. 2018, Crous et al. 2020). Nine species epithets are listed in the Index Fungorum (2024). In this study, we introduce two new *Barrmaelia* species with sexual morphs and a multi-gene (ITS, LSU, *rpb*2, *tub*2) phylogenetic analysis. This study represents the first report of *Barrmaelia* from China.

Barrmaelia shangrilaensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 37, 38

MycoBank number: MB850215; Facesoffungi number: FoF14905

Etymology – The specific epithet is derived from the Shangri-La, where the holotype was collected.

Holotype – HKAS 130280

Saprobic on dead twigs of an unidentified host. Sexual morph: *Ascomata* 220–380 µm high × 300–400 µm diameter ($\bar{x}$ = 297 × 339 µm, n = 5), scattered or gregarious, solitary, immersed, black, appear as small black dots, with a papillate ostioles. *Peridium* 30–40 µm wide, multi-layered, outer layer comprising brown, thick-walled cells of *textura prismatica*; inner layer composed of light brown to hyaline, thin-walled cells of *textura prismatica*. *Paraphyses* 2–5 µm wide, hyaline,

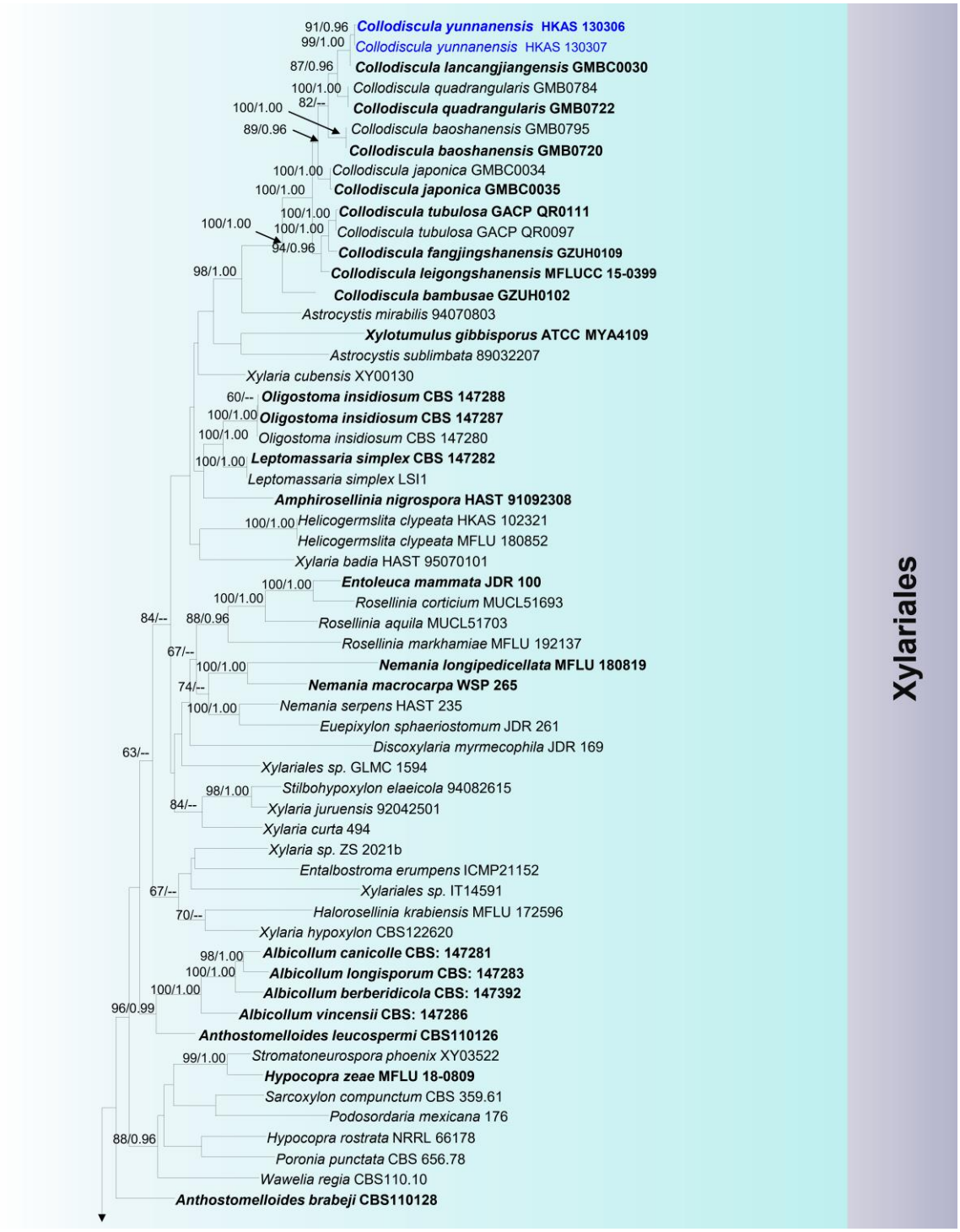

Figure 37 – RAxML phylogram generated from combined dataset of partial ITS, LSU, *rpb*2 and *tub*2 DNA sequence analyses for Xylariaceae. Final likelihood value is -74641.196756. The tree is rooted to *Cainia desmazieri* (WU 33597) *Cainia graminis* (IT 1462) *Endocalyx cinctus* (JCM 7946) *Endocalyx metroxyli* (MFLUCC 15-0723) *Requienella fraxini* (CBS 140475) and *Requienella seminuda* (CBS 140502). The matrix had 3261 distinct alignment patterns with 34.99% undetermined characters and gaps. Estimated base frequencies were; A = 0.240297, C = 0.261724,

G = 0.263816, T = 0.234163 substitution rates AC = 1.341240, AG = 3.679357, AT = 1.122932, CG = 1.040753, CT = 6.899725, GT = 1.000000; gamma distribution shape parameter α = 0.724091. Newly generated sequences are in blue. Ex-type/type strains are indicated in bold.

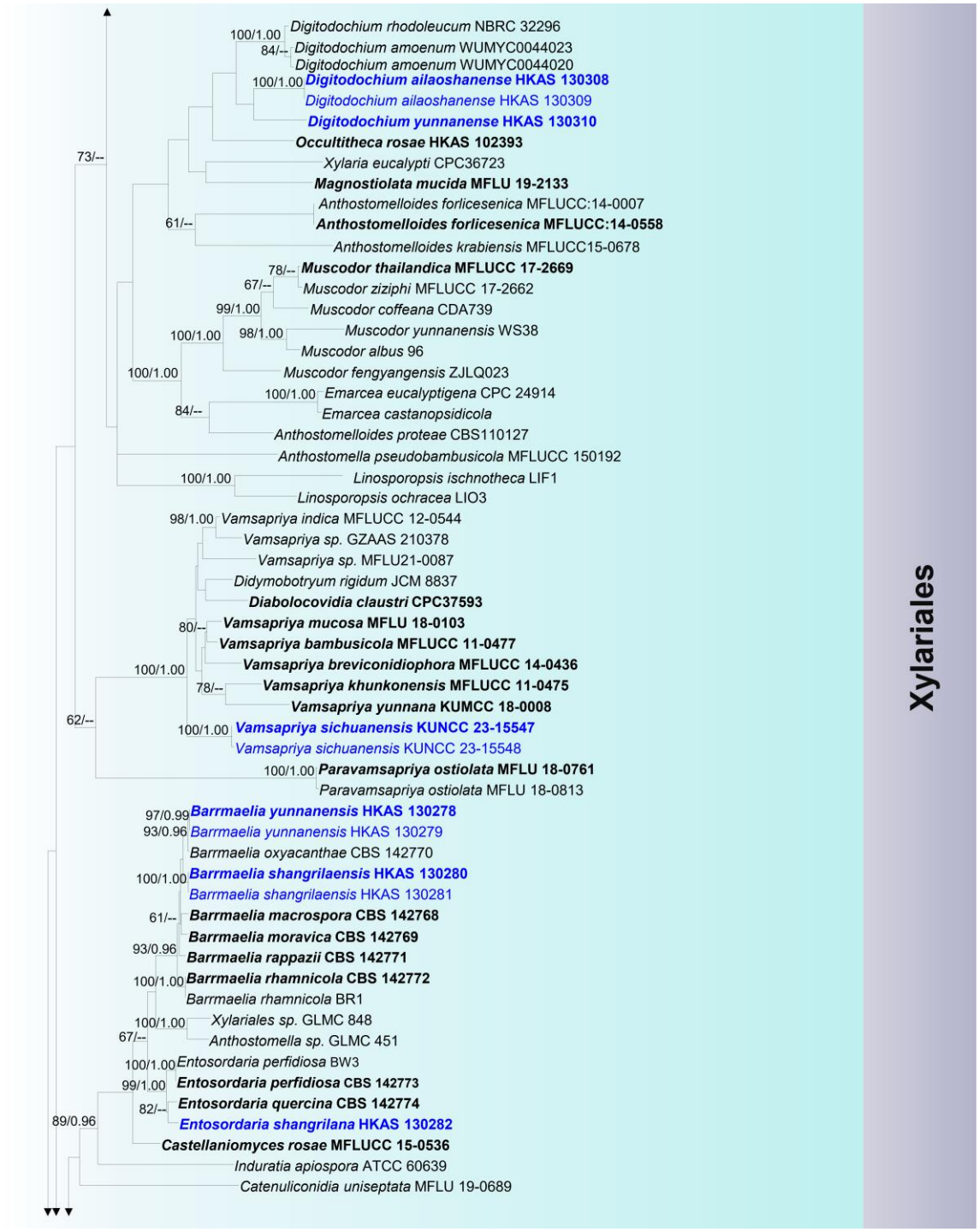

Figure 37 – Continued.

aseptate, unbranched, cellular, minutely guttulate, embedded in a gelatinous matrix. *Asci* 80–120 × 6–9 µm ($\overline{x}$ = 102 × 8 µm, n = 10), 8-spored, unitunicate, long-pedicellate, apically rounded, J- apical ring in Melzer's reagent. *Ascospores* 13–16 × 4–6 µm ($\overline{x}$ = 14 × 5 µm, n = 30), overlapping uniseriate, ellipsoid, one-celled, slightly inequilaterally, with a straight germ slit of spore-length, light brow to brown, filled with two and several small guttules in the poles, smooth-walled, lacking a mucilaginous sheath or appendages. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Shangri-La (27.801111 N, 99.808056 E, 3390m), on dead twigs of an unidentified host, 15 August 2021, L. Qinxian, TSB2 (HKAS 130280, holotype). *ibid*. TSB2A (HKAS 130281, isotype).

GenBank accession numbers – ITS = PP584721, PP584722, LSU = PP584818, PP584819.

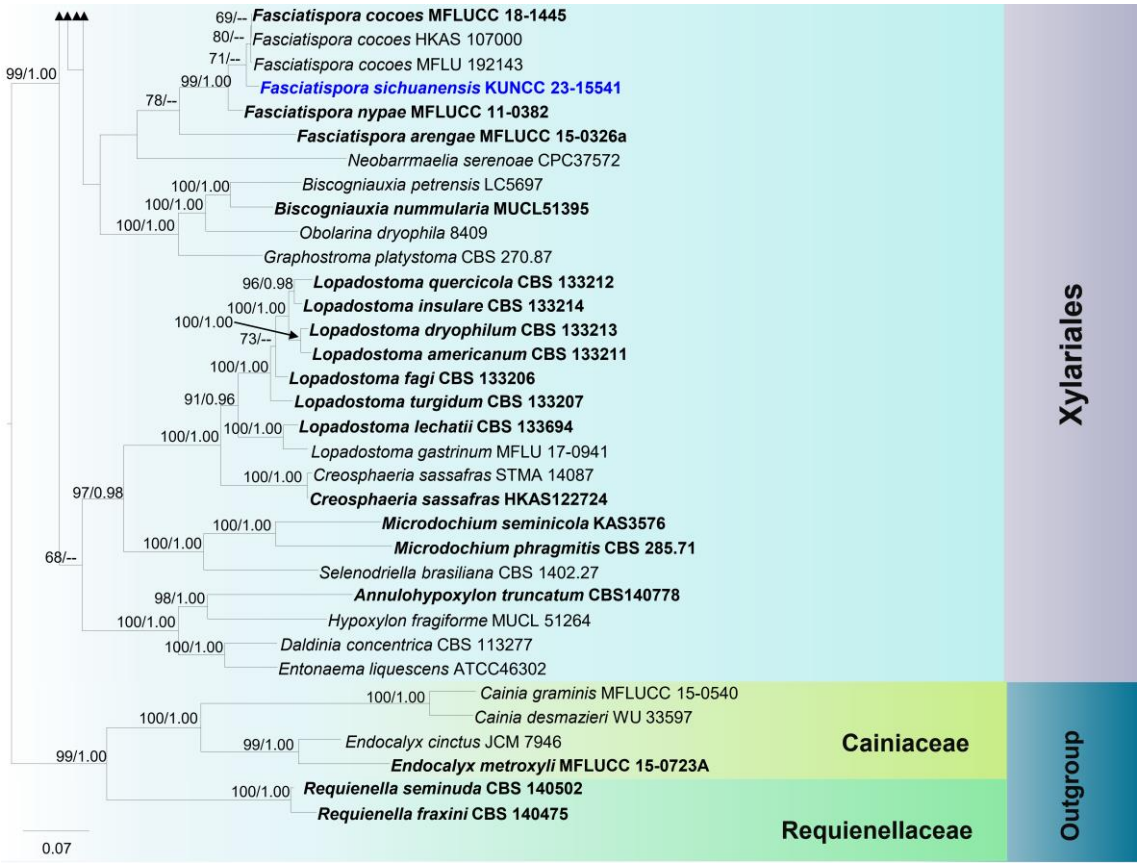

Figure 37 – Continued.

Notes – In the multi-gene phylogenetic analyses (Fig. 37), *Barrmaelia shangrilaensis* (HKAS 130280) has a close affinity to *B. oxyacanthae* (CBS 142770) and *B. yunnanensis* (HKAS 130280) with support of 100% MLB and 1.00 BYPP. *Barrmaelia shangrilaensis* is similar to both *B. oxyacanthae* and *B. yunnanensis* by the shapes of its asci and ascospores. However, *Barrmaelia shangrilaensis* can be differentiated from *B. oxyacanthae* and *B. yunnanensis* by its comparatively small ascomata, (220–380 × 300–400 µm vs. 335–473 × 604–630 µm vs. 300–500 × 300–700 µm, respectively) (Voglmayr et al. 2018). Further, *Barrmaelia shangrilaensis* differs from *B. oxyacanthae* by having immersed ascomata with a thicker peridium (20–30 µm), compared to the semi-immersed ascomata and thinner peridium (15–20 µm) of *B. oxyacanthae* (Voglmayr et al. 2018). Materials of *Barrmaelia oxyacanthae* have been examined from various parts of the world: the holotype from France and other type materials from Austria, Germany, Italy and the USA (South Dakota) (Voglmayr et al. 2018). The LSU and ITS nucleotide of *B. shangrilaensis* and *B. oxyacanthae* reveal 28/835 (3.3%), 36/690 (5.2%) and *B. shangrilaensis* and *B. yunnanensis* reveal 18/835 (2.1%), 26/690 (3.8.2%) respectively. In our study, we have introduced *Barrmaelia shangrilaensis* and *B. yunnanensis* to the family Barrmaeliaceae, both from the Yunnan Province of China.

Barrmaelia yunnanensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 37, 39

MycoBank number: MB850216; Facesoffungi number: FoF14906

Etymology – The specific epithet is derived from the Yunnan Province, where the holotype was collected.

Holotype – HKAS 130278

Saprobic on dead stalks of an unidentified host. Sexual morph *Ascomata* 300–500 μm high × 550–650 μm diameter ($\overline{x}$ = 418 × 615 μm, n = 5), scattered or gregarious, solitary, semi-immersed, showing slight discoloration around the ascomata, with a papillate ostiole. *Peridium* 40–60 μm wide, multi-layered, outer layer comprising brown, thick-walled cells of *textura prismatica*, inner layer composed of light brown to hyaline, thin-walled cells of *textura prismatica*. *Paraphyses* 2–5 μm wide, hyaline, aseptate, unbranched, cellular, minutely guttulate, embedded in a gelatinous matrix. *Asci* 90–130 × 7–10 μm ($\overline{x}$ = 115 × 7.4 μm, n = 10), 8-spored, unitunicate, pedicellate, apically rounded, crown-shaped J- apical ring in Melzer's reagent. *Ascospores* 15–20 × 5–7 μm ($\overline{x}$ = 17.6 × 6.1 μm, n = 30), overlapping uniseriate, one-celled, ellipsoid, slightly inequilaterally, with a straight germ slit of spore-length, golden brow to brown, guttulate in the poles, smooth-walled, lacking a mucilaginous sheath or appendages. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Shangri-La (27.203333 N, 100.276111 E, 3130m), on a dead stalk of an unidentified host, 15 August 2021, L. Qinxian, DDX18 (HKAS 130278, holotype). *ibid*. DDX18A (HKAS 130279, isotype).

GenBank accession numbers – ITS = PP584723, PP584724, LSU = PP584820, PP58482.

Notes – In the multi-gene phylogenetic analyses (Fig. 37), *Barrmaelia yunnanensis* (HKAS 130278, HKAS 130279 isolate) shows a close affinity to *B. oxyacanthae* (CBS 142770) with 93% MLB and 0.96 BYPP support. *Barrmaelia yunnanensis* shares certain morphological similarities with *B. oxyacanthae* and other *Barrmaelia* species. However, *B. yunnanensis* can be distinguished from *B. oxyacanthae* by its comparatively thicker peridium (40–60 μm) and golden brown ascospores (15–20 μm). In contrast, *B. oxyacanthae* has a thinner ascomata peridium (15–20 μm), and dark brown ascospores measuring 12–14 μm (Voglmayr et al. 2018). The LSU and ITS sequence of *B. yunnanensis* and *B. oxyacanthae* reveal 18/835 (2.1%) and 42/690 (6.1%) nucleotide differences respectively.

Entosordaria (Sacc.) Höhn., Sitzungsber. Kaiserl. Akad. Wiss., Wien. Math.-Naturwiss. Cl., Abt. 1 129: 167 (1920)

Notes – *Entosordaria* was initially described as a subgenus of *Anthostomella* by Saccardo (1882). Voglmayr et al. (2018) later re-described and validated *Entosordaria*, placing it in Barrmaeliaceae. In their work, Voglmayr et al. (2018) introduced *Entosordaria quercina*, providing details of its sexual morph and molecular data. *Entosordaria* comprises 18 species epithets listed in Index Fungorum (2024), but molecular data has been provided for only two species.

Entosordaria shangrilana L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 37, 40

MycoBank number: MB850217; Facesoffungi number: FoF14907

Etymology – The specific epithet is derived from the Shangri-La, where the holotype was collected.

Holotype – HKAS 130282

Saprobic on dead twigs of an unidentified host. Sexual morph *Ascomata* 300–400 μm high × 400–500 μm diameter ($\overline{x}$ = 367 × 471.6 μm, n = 5), scattered or gregarious, solitary, immersed below bark and raising it, globose to ellipsoid, with a papillate ostiole. *Ostioles* 100–140 μm long × 60–100 μm wide ($\overline{x}$ = 127 × 83 μm, n = 5), prominent, centric. *Peridium* 30–40 μm wide, multi-layered, outer layer comprising brown, thick-walled cells of *textura prismatica*, inner layer composed of light brown to hyaline, thin-walled cells of *textura prismatica*. *Paraphyses* 3–4 μm wide, hyaline, aseptate, unbranched, cellular, minutely guttulate, embedded in a gelatinous matrix. *Asci* 100–200 × 10–15 μm ($\overline{x}$ = 145 × 12 μm, n = 10), 8-spored, unitunicate, short-pedicellate, apically rounded, discoid amyloid apical ring. *Ascospores* 20–25 × 8–12 μm ($\overline{x}$ = 22.9 × 9 μm, n = 30), uniseriate, ellipsoid, with subacute to rounded ends, two-celled with septum near one end, the small cell hyaline, the large cell dark brown at maturity, hyaline when immature and becoming golden brown to brown at maturity, often with a large and several small guttules, smooth-walled,

surrounded by a thick mucilaginous sheath (10–20 μm thick), thinner at the ends and thicker at the middle. Asexual morph: Undetermined.

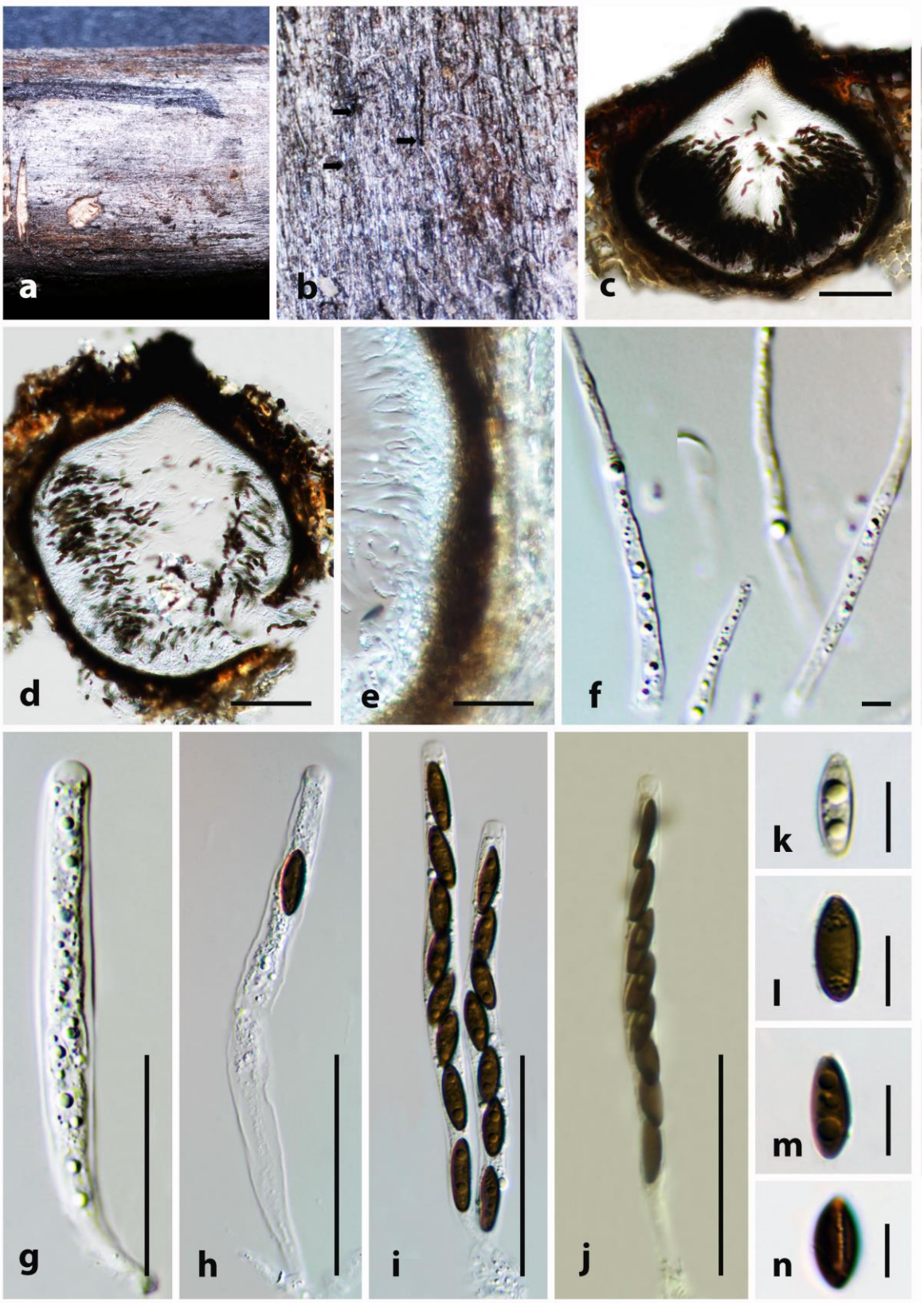

Figure 38 – *Barrmaelia shangrilaensis* (HKAS 130280, holotype). a Host. b Ascomata on the host surface (arrow showing ascomata on host). c, d Vertical section of an ascoma. e Peridium. f Paraphyses. g–j Asci (j in Melzer's reagent). k–n Ascospores (n with germ slit). Scale bars: c, d = 100 μm, e = 20 μm, f = 5 μm, g–j = 50 μm, k–n = 10 μm.

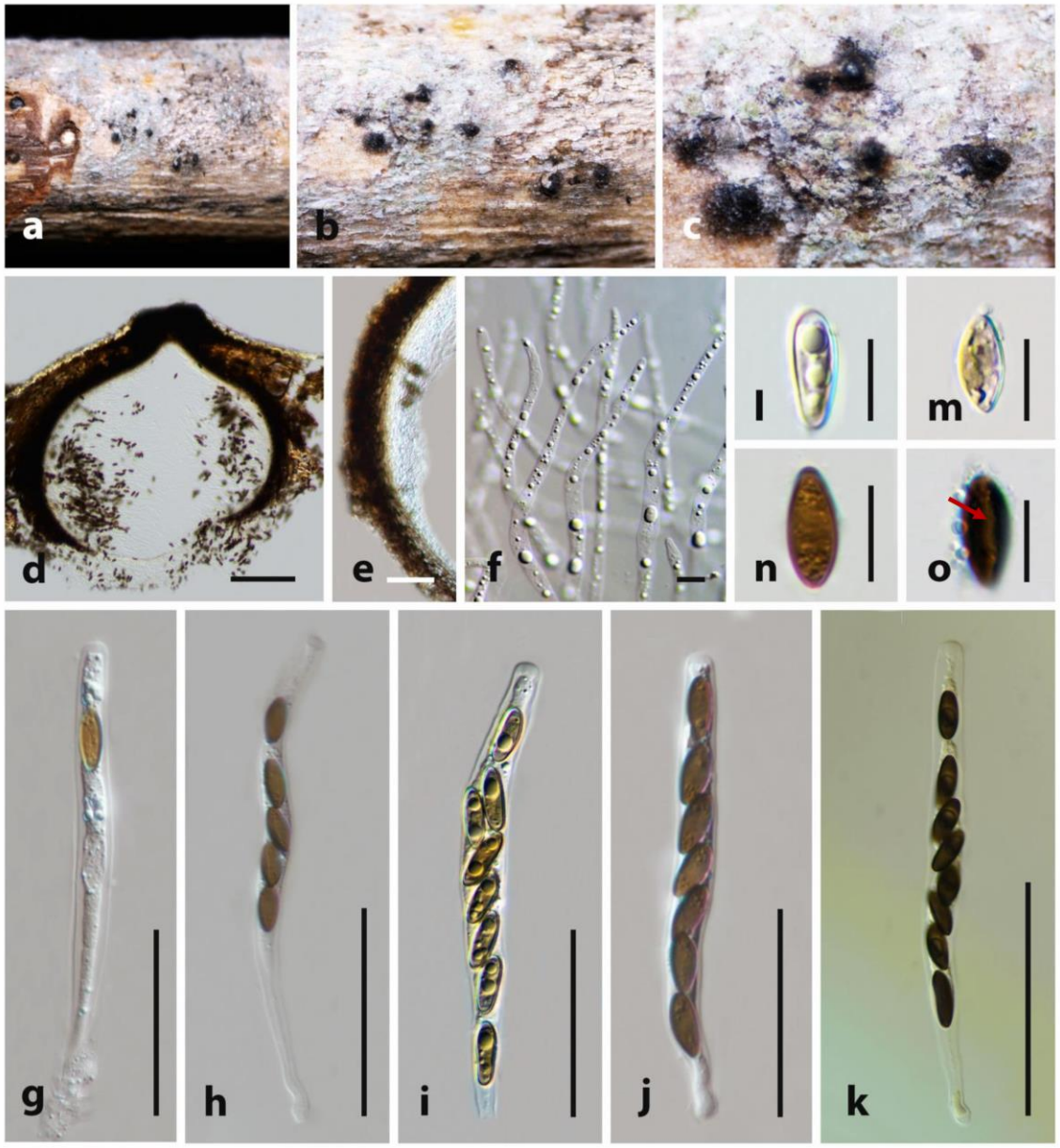

Figure 39 – *Barrmaelia yunnanensis* (HKAS 130278, holotype). a Host. b, c Ascomata on the host surface. d Vertical section of ascoma. e Peridium. f Paraphyses. g–k Asci (k in Melzer's reagent). l–o Ascospores (o. arrow showing Ascospores with germ slit). Scale bars: d = 200 μm, f = 5 μm, e, g–k = 50 μm, l–o = 10 μm.

Material examined – CHINA, Yunnan Province, Shangri-La (30.169722 N, 98.245278 E, 3020m), on dead twigs of an unidentified host, 15 August 2021, L. Qinxian, NYR13, (HKAS 130282, holotype).

GenBank accession numbers – ITS = PP584725, LSU = PP584822, *tef*1-α = PP993515.

Notes – In the multi-gene phylogenetic analyses (Fig. 37), *Entosordaria shangrilana* (HKAS 130282) was nested with *E. quercina* (CBS 142774), indicating an 82% MLB support value. However, this affiliation was not supported by Bayesian analysis. *Entosordaria shangrilana* is characterized by its comparatively smaller asci, measuring 100–200 × 10–15 μm, with a J- apical ring and ellipsoidal ascospores (20–25 × 8–12 μm) with subacute to rounded ends. In contrast, *Entosordaria quercina* features larger asci (270–293 × 18.5–21.5 μm) with a J+ discoid amyloid apical ring and ellipsoid to allantoid, brown ascospores that measure 34–38 × 12–13.5 μm. *Entosordaria shangrilana* resembles *E. perfidiosa*, as both possess a J- discoid amyloid apical ring in their asci and ellipsoidal ascospores with subacute to rounded ends. *Entosordaria quercina* was

identified on dead twigs of *Quercus coccifera* in Greece, while *E. perfidiosa* was found on old trunks of living *Acer pseudoplatanus* in Italy (Voglmayr et al. 2018). The nucleotide comparison of LSU and ITS of *Entosordaria shangrilana* and *E. quercina* reveal 25/835 (3.1%) and 38/690 (5.5%) respectively. Our collection originates from dead twigs of an unidentified host in Yunnan Province, China.

Diatrypaceae Nitschke, Pyrenomycetes Germanici 1: 62 (1867)

Notes – Diatrypaceae was introduced by Nitschke (1869) and typified by *Diatrype*. Recent studies, including those by Dissanayake et al. (2021a), Zhu et al. (2021) and Li et al. (2023), have provided phylogenetic analyses that demonstrate strong support for the family placement within Xylariomycetidae, specifically in Xylariales (Fig. 21). Twenty-six genera are currently accepted in Diatrypaceae (Li et al. 2023). Species of the Diatrypaceae are found in both terrestrial and aquatic habitats and exhibit various life modes, including saprobic, endophytic and pathogenic behaviours (Trouillas et al. 2010, Urbez-Torres et al. 2012, Senanayake et al. 2015, Dayarathne et al. 2020 a, b).

Allodiatrype Konta & K.D. Hyde, Mycosphere 11 (1): 247 (2020)

Notes – *Allodiatrype* was introduced by Konta et al. (2020) and is typified by *A. arengae*. In their study, Konta et al. (2020) introduced three new species one novel combination under *Allodiatrype*, including *A. arengae*, *A. elaeidicola*, *A. elaeidis* and *A. thailandica* (= *Diatrype thailandica*). Species of *Allodiatrype* possess a close resemblance to those of *Diatrype*. However, *Allodiatrype* can be distinguished by its characteristic multi-ascomata immersed within a single stroma and may or may not have a black stromatic zone. In contrast, the stromata of *Diatrype* species typically spread across a broader area, sometimes even covering the surface of the host. Currently, seven *Allodiatrype* species epithets are listed in the Index Fungorum (2024).

Allodiatrype albelloscutata H.X. Wu & X.H. Li, Chiang Mai Journal of Science 49 (3): 573 (2022) Fig. 41

MycoBank number: MB841214; Facesoffungi number: FoF15749

See the description in Li et al. (2022b).

Material examined – CHINA, Yunnan Province, Xishuangbanna, Yinchang Mountain (21.968333 N, 101.1975 E, 1188 m), on dead twigs of an unidentified host, 16 February 2023, L.S. Dissanayake, Y24 (HKAS 130284), living culture, KUNCC 23-15530. *ibid*. Y24A (HKAS 130285), living culture, KUNCC 23-15531.

GenBank accession numbers – ITS = PP584726, PP584727.

Notes – Li et al. (2022) introduced *Allodiatrype albelloscutata* (IFRD9100) from Pu'er in Yunnan Province, China. In this study, we identified two additional specimens from the same province, specifically from Xishuangbanna, collected from unidentified hosts.

Diatrype Fr., Summa veg. Scand., Sectio Post. (Stockholm): 384 (1849)

Notes – Fries (1849) established *Diatrype*, designating *D. disciformis* as the type species. The genus is characterized by widely effuse or verrucose stromata that are flat or slightly convex, with discoid or sulcate ostioles at the surface, as well as by eight-spored and long-stalked asci and hyaline or brownish, allantoid ascospores (Rappaz 1987, Vasilyeva & Stephenson 2009, Senwanna et al. 2017, Hyde et al. 2020a, Zhu et al. 2021, Yang et al. 2023c). Recently, Zhu et al. (2021) and Yang et al. (2022) introduced new *Diatrype* species with polysporous asci into the genus based on a phylogenetic approach. Currently, 182 species are listed in Species Fungorum (2024).

Diatrypella (Ces. & De Not.) De Not., Comment. Soc. Crittog. Ital. 1 (4): 205 (1863)

Notes – *Diatrypella* was introduced by Cesati & De Notaris (1863) and is typified by *D. verruciformis*. *Diatrypella* is characterized by pustule-like stromata that emerge through the host surface, polysporous asci, allantoid ascospores and libertella-like asexual morphs (Hyde et al.

2020a, Dissanayake et al. 2021a). Distinguishing between *Diatrypella* and *Cryptovalsa* based solely on morphological characters is challenging. As a result, a multi-locus phylogeny that includes more representative taxa is essential to clarify the relationships among species within *Diatrypella* (Mehrabi et al. 2015, Zhu et al. 2021). In this study, we introduce a new species and provide additional sequence data for a new geographical record of *Diatrypella vulgaris*.

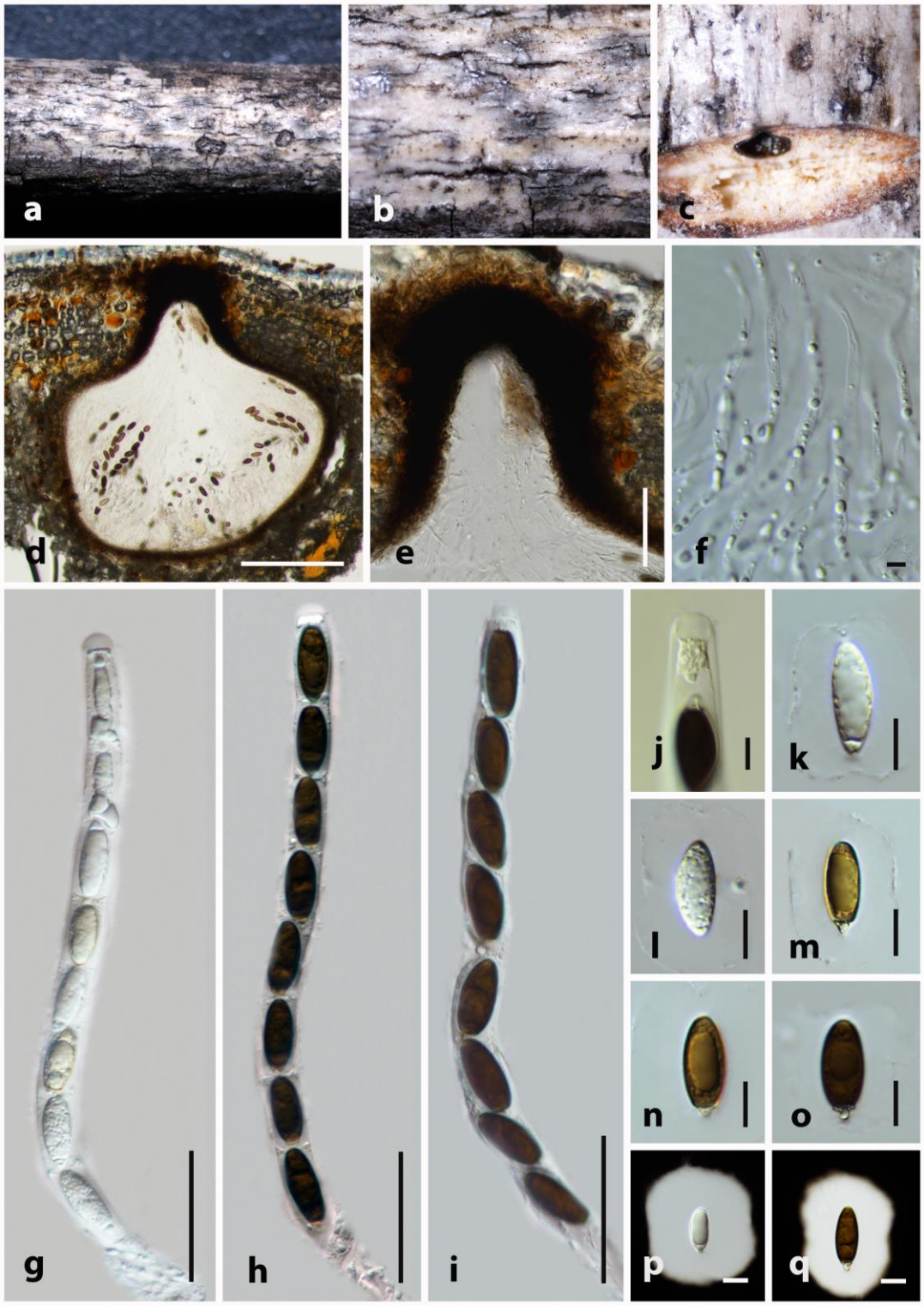

Figure 40 – *Entosordaria shangrilana* (HKAS 130282, holotype). a, b Ascomata appear on the host surface. c, d Vertical sections of ascomata. e Ostiole. f Paraphyses. g–j Asci (j Asci in Melzer's reagent). k–q Ascospores (p immature, q mature ascospores in Indian ink). Scale bars: d = 200 μm, e = 50 μm f, j = 5 μm, g–i = 20 μm, k–q = 10 μm.

Diatrypella elaeidis Konta & K.D. Hyde, Mycosphere 11(1): 256 (2020) Fig. 41

MycoBank number: MB556572; Facesoffungi number: FoF05122

Material examined – CHINA, Yunnan Province, Yuxi, Eshan Yi Autonomous County, (24.095650, N, 102.171782 E, 1407 m), on dead twigs of Fagaceae sp., 14 March 2019, D.N. Wanasinghe, DW0822-02 (HKAS 133105), *ibid*. DW0822-05 (HKAS 133106).

GenBank accession numbers – ITS = PP584730, PP584731, *tub*2 = PP82302, PP82303.

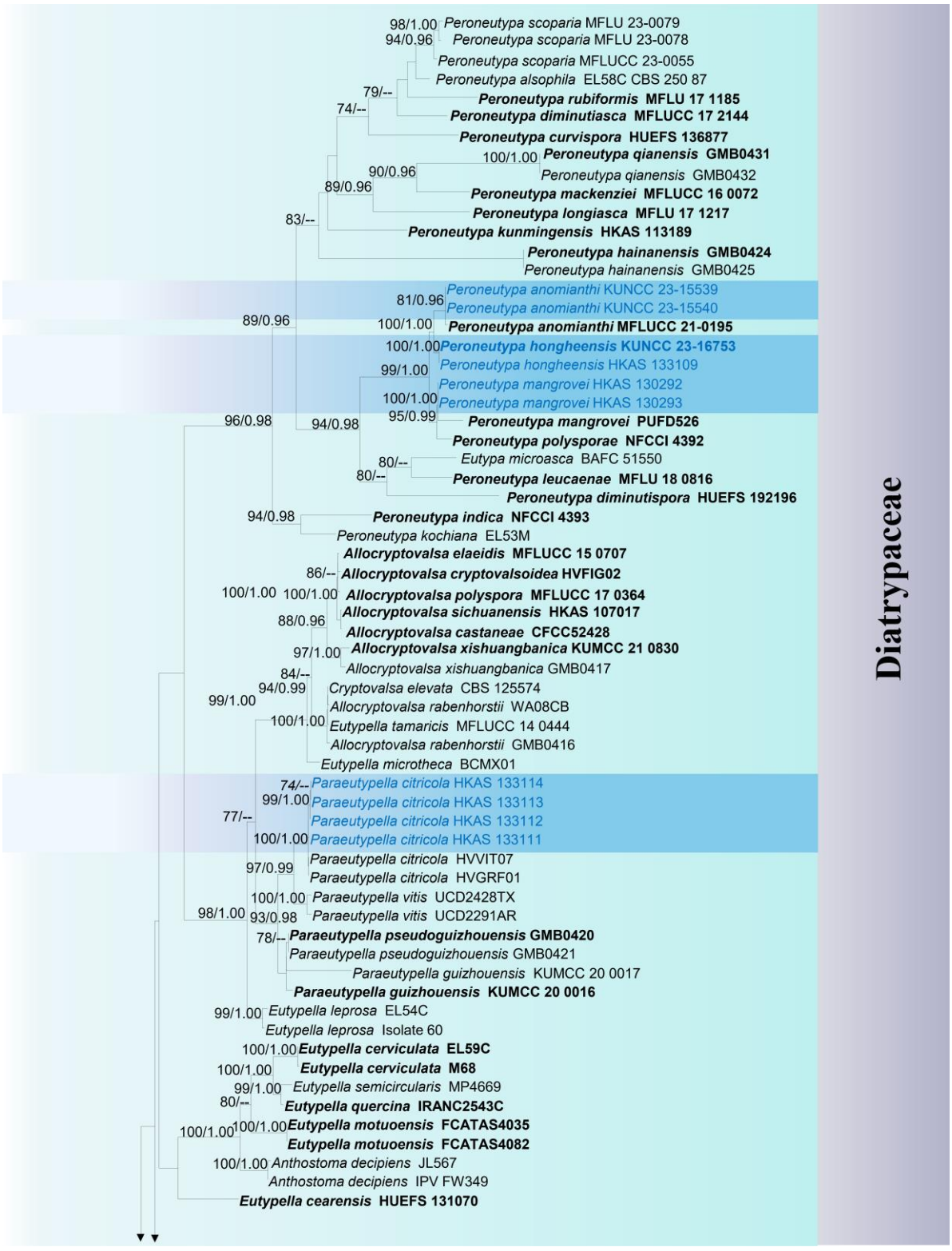

Figure 41 – RAxML phylogram generated from combined dataset of partial ITS and *tub*2 DNA sequence analyses for Diatrypaceae. Final likelihood value is -29649.533802. The tree is rooted to

Kretzschmaria deusta (CBS 82672) and *Xylaria hypoxylon* (CBS 122620). The matrix had 1903 distinct alignment patterns with 53.28% undetermined characters and gaps. Estimated base frequencies were; A = 0.220516, C = 0.275247, G = 0.234359, T = 0.971147, AG = 3.165289, AT = 1.242456, CG = 0.878246, CT = 3.928602, GT = 1.000000; gamma distribution shape parameter α = 0.865004. Newly generated sequences are in blue. Ex-type/type strains are indicated in bold.

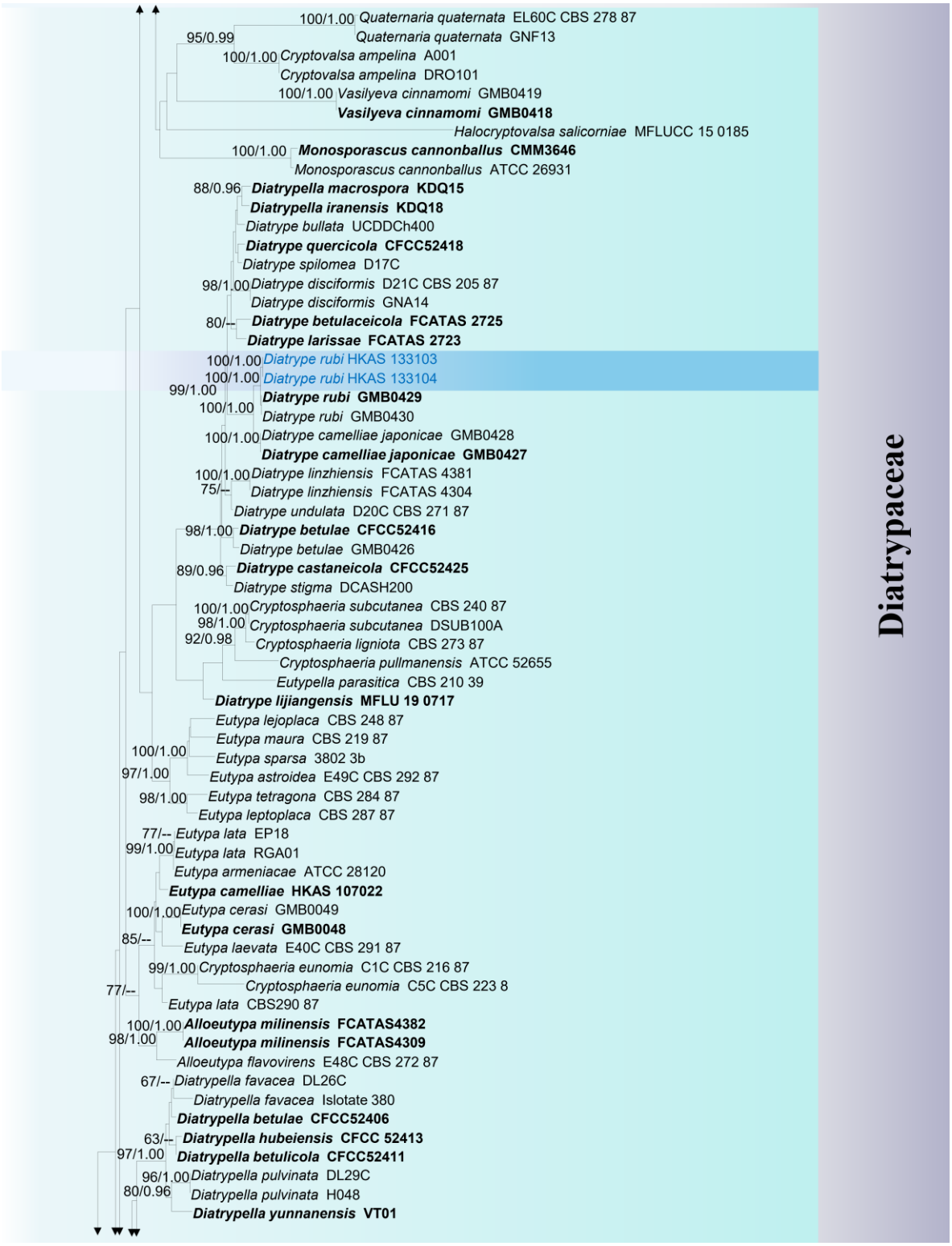

Figure 41 – Continued.

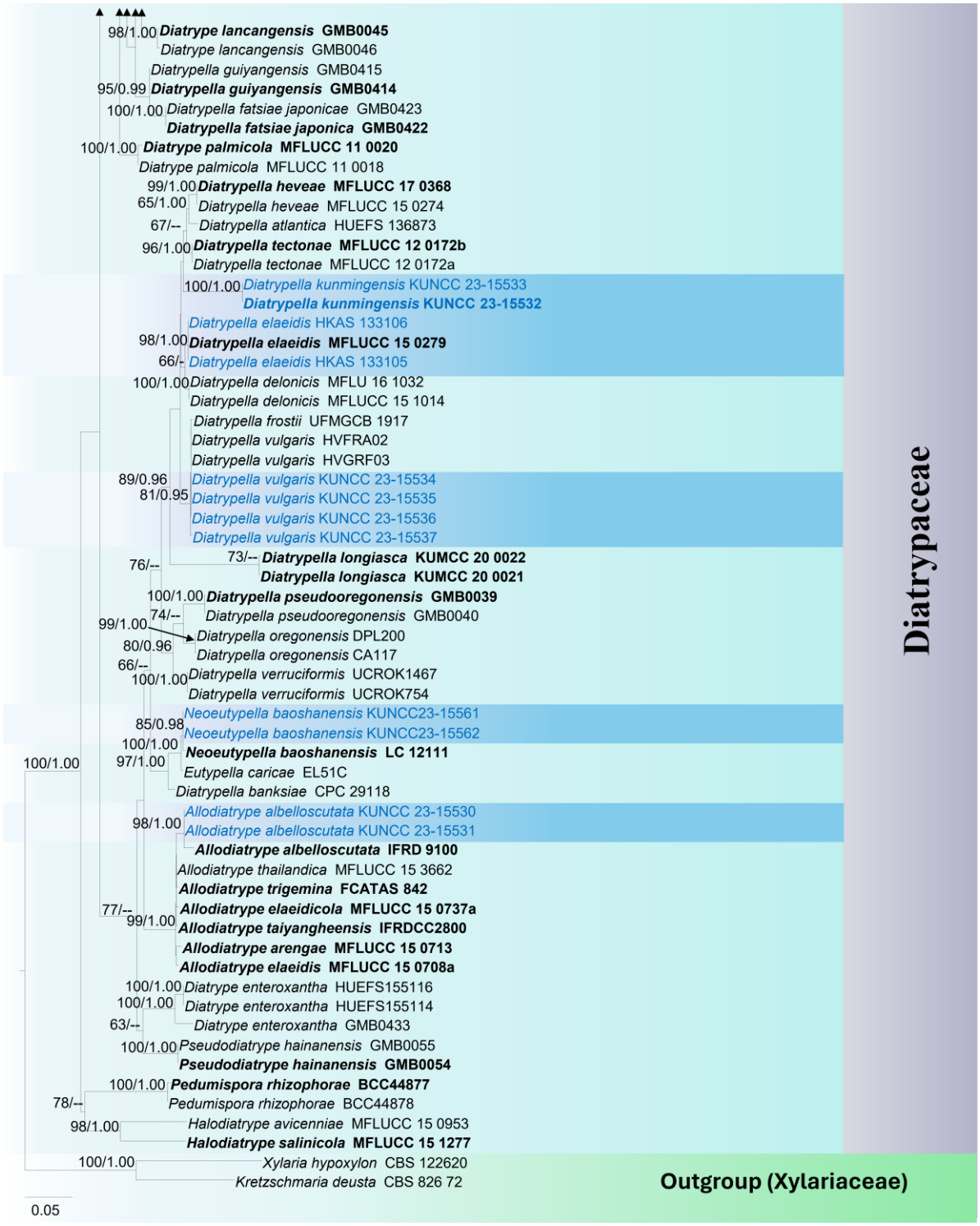

Figure 41 – Continued.

Notes – The phylogenetic results indicate that our strains belong to the same species as *Diatrypella elaeidis*. Their morphological characteristics closely match those of *Diatrypella elaeidis*, with similarities in the size and color of the ascomata, ostiolar canals, peridia, asci and ascospores (Konta et al. 2020). The ITS and *tub*2 sequence data are identical to those of the ex-type strain. *Diatrypella elaeidis* was originally collected from a dead petiole of *Elaeis guineensis* (Arecaceae) in Chiang Rai Province, Thailand (Konta et al. 2020). In this study, we introduce two *Diatrypella elaeidis* strains collected from dead twigs of woody litter from a Fagaceae species in Yunnan Province, China, marking a new country record.

Diatrypella kunmingensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 41, 42

MycoBank number: MB850218; Facesoffungi number: FoF14912

Etymology – The specific epithet is derived from Kunming, where the holotype was collected.

Holotype – HKAS 130286

Saprobic on dead twigs on an unidentified host. Sexual morph *Stromata* well developed, solitary to gregarious, erumpent, black, immersed, globose to sub-globose. *Ascomata* 300–400 μm high × 250–450 μm diameter ($\overline{x}$ = 344 × 382 μm, n = 10), perithecial, surrounded by white entostroma, immersed in stromata, 4–5 perithecia arranged in a valsoid configuration, sub-globose, individual ostiole with a long neck. *Ostioles* 90–120 μm high × 80–120 μm diameter ($\overline{x}$ = 112 × 104 μm, n = 10), cylindrical, ostiolar canal periphysate, yellowish periphyses. *Peridium* 20–40 μm wide, composed of two layers with outer layer of brown, thick-walled cells, inner layer hyaline, thick-walled cells forming *textura angularis*. *Paraphyses* 2–4 μm arising from base of perithecia, hyaline, long, narrow, unbranched, septate, guttulate, narrowing and tapering towards apex. *Asci* 70–170 × 10–20 μm ($\overline{x}$ = 146 × 15 μm, n = 10), polysporous, unitunicate, clavate, apically round, long pedicellate (50–55 μm). *Ascospores* 6–9 × 2–4 μm ($\overline{x}$ = 7 × 3 μm, n = 30), overlapping, allantoid, hyaline, yellowish in mass, aseptate, guttulate, smooth-walled. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Botanical Garden, Kunming Institute of Botany (25.140833 N, 102.739444 E, 1892 m), on dead leaves of unidentified host, 12 December 2022, L.S. Dissanayake, KIB22-08 (HKAS 130286, holotype), ex-type, KUNCC 23-15532. *ibid*. KIB22-08A (HKAS 130287, isotype), ex-isotype KUNCC 23-15533.

GenBank accession numbers – ITS = PP584732, PP584733, *tub*2 = PP82304, PP82305.

Notes – Phylogenetic analyses based on ITS and *tub*2 sequence data (Fig. 41) indicate that *Diatrypella kunmingensis* forms a distinct lineage sister to *D. hevea*, *D. atlantica* and *D. tectonae*. However, their affiliation is not statistically supported. The new species, *Diatrypella kunmingensis*, is similar to *D. hevea*, *D. atlantica* and *D. tectonae* (de Almeida et al. 2016, Senwanna et al. 2017, Shang et al. 2017). Nevertheless, the presence of yellow cells in the ostiole distinguishes *Diatrypella kunmingensis*. When comparing the ITS and *tub*2 sequences of *Diatrypella kunmingensis* with *D. tectonae*, there are 5.6% (35/621) and 11.6% (32/275) base pair differences in the gene loci respectively. Based on both morpho and molecular data we introduce *Diatrypella kunmingensis* as new species.

Diatrypella vulgaris Trouillas, W.M. Pitt & Gubler, Fungal Diversity 49: 212 (2011) Fig. 41

MycoBank number: MB519404; Facesoffungi number: FoF03591

See the description in Trouillas et al. (2010).

Material examined – CHINA, Sichuan Province, Chengdu, Qingyang District, Huanhuaxi park (23.39 N, 102.225556 E, 1186m), on dead twigs of an unidentified host, 5 January 2023, L.S. Dissanayake, SCCHHX23-28 (HKAS 130288), living culture, KUNCC 23-15534. *ibid*. SCCHHX23-09 (HKAS 130291), living culture, KUNCC 23-15535. *ibid*. SCCHHX23-10 (HKAS 130290), living culture, KUNCC 23-15536. *ibid.* Kunming institute of botany, Kunming, Yunnan Province (25.140833 N, 102.739444 E, 1892 m) on dead twigs of an unidentified host, 12 April 2023, L.S. Dissanayake, HH11 (HKAS 130289), living culture, KUNCC 23-15537.

GenBank accession numbers – ITS = PP584734, PP584735, PP584736, PP584737, *tub*2 = PP82306, PP82307, PP82308, PP82309.

Notes – Trouillas et al. (2011) designated a reference specimen for *Diatrypella vulgaris* (HVGRF03) from a dead branch of *Citrus paradisi* in Hunter Valley, NSW, Australia. Isotypes were collected from dead branches of *Fraxinus angustifolia* and *Schinus molle* in the same location. Zhang et al. (2023) added six new collections for *Diatrypella vulgaris* collected on dead culm of herbaceous plant and dead branch of woody plant from Guizhou Province, China. Our study presents data from specimens collected in Sichuan and Yunnan provinces, China. These specimens are morphologically and phylogenetically similar to *Diatrypella vulgaris* type strain. Therefore,

these new specimens are identified as *Diatrypella vulgaris*, which has been reported from Australia, China and Thailand (Trouillas et al. 2011, Hyde et al. 2017, Long et al. 2021, Zhang et al. 2023).

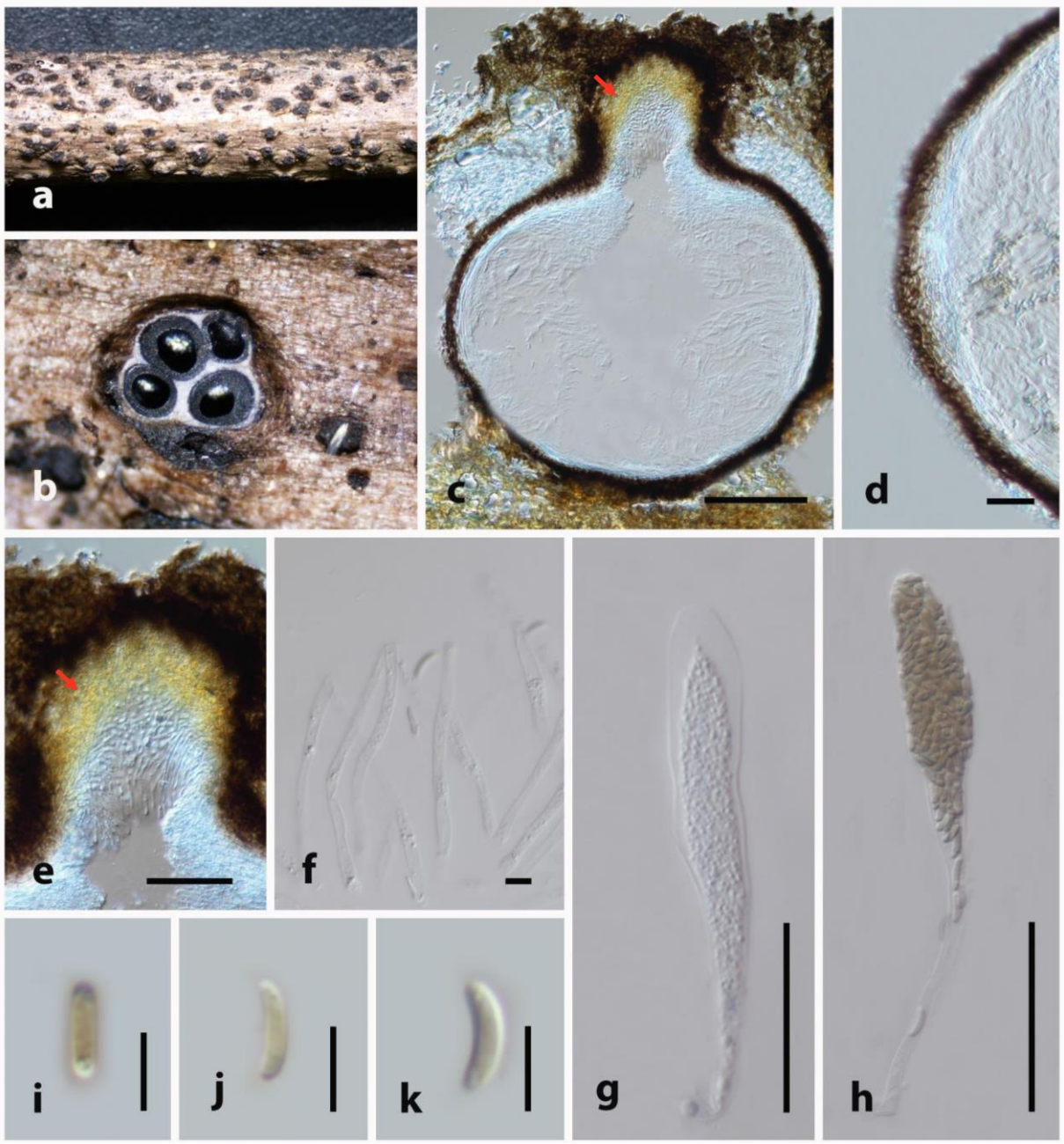

Figure 42 – *Diatrypella kunmingensis* (HKAS 130286, holotype). a Ascomata on host. b Horizontal section through an ascostroma. c Vertical section of ascoma. d Peridium. e Ostiole (red arrow shows yellow cells on ostiole neck). f Paraphyses. g, h Asci. i–k Ascospores. Scale bars: c = 100 μm, d = 20 μm, e, g, h = 50 μm, f, i–k = 5 μm.

Neoeutypella M. Raza, Q.J. Shang, Phookamsak & L. Cai, Fungal Divers. 95 (1): 1–273 (2019)

Notes – *Neoeutypella* was introduced by Phookamsak et al. (2019) to accommodate *N. baoshanensis* as its type species. This genus is characterized by carbonaceous stromata that are erumpent through the host epidermis, producing yellow pigments surrounding the stroma. The asci are 8-spored, spindle-shaped, with long pedicellate, apically rounded and contain refractive cytoplasmic strands. The ascospores are pale yellowish to pale brown. Currently, *Neoeutypella* is recognized as a monotypic genus, hosting only the type species, *N. baoshanensis* (Species Fungorum 2024).

Neoeutypella baoshanensis M. Raza, Q.J. Shang, Phookamsak & L. Cai, Fungal Divers. 95: 169 (2019) Figs 41, 43

MycoBank number: MB555372; Facesoffungi number: FoF04928

Saprobic on dead twigs on an unidentified host. Sexual morph *Stromata* well developed, solitary to gregarious, erumpent, black, immersed, globose to sub-globose. *Ascomata* 240–280 μm high × 180–210 μm diameter ($\overline{x}$ = 266 × 200 μm, n = 10), perithecial, surrounded by white entostroma, immersed in stromata, 5–6 perithecia arranged in a valsoid configuration, sub-globose, individual ostiole with a long neck. *Ostioles* 140–150 μm high × 60–80 μm diameter ($\overline{x}$ = 148 × 75 μm, n = 10), cylindrical, ostiolar canal periphysate, hyalin periphyses. *Peridium* 25–30 μm wide, composed of two layers with outer layer of brown, thick-walled cells, inner layer hyaline, thick-walled cells forming *textura angularis*. *Paraphyses* 3–5 μm arising from base of perithecia, hyaline, long, narrow, unbranched, septate, guttulate, narrowing and tapering towards apex. *Asci* 80–110 × 7–10 μm ($\overline{x}$ = 94 × 8 μm, n = 10), polysporous, unitunicate, spindle-shaped, apically round, long pedicellate. *Ascospores* 12–15 × 2–4 μm ($\overline{x}$ = 13 × 3 μm, n = 30), overlapping, allantoid, hyaline, light brown, aseptate, guttulate, smooth-walled. Asexual morph: Undetermined.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Yeleishan park (31.075 N, 103.564167 E, 1065.01m), on dead twigs of an unidentified host, 5 January 2023, L.S. Dissanayake, SCCYL23-05 (HKAS 133108), living culture KUNCC23-15562. *ibid*. SCCHHX23-14 (HKAS 133107), living culture KUNCC23-15561.

GenBank accession numbers – ITS = PP584738, PP584739, *tub*2 = PP82310, PP82311.

Notes – Based on phylogenetic results, our new strains (SCCYL23-05, SCCHHX23-14) are closely affiliated with *Neoeutypella baoshanensis*, with 85% MLB and 0.98 BYPP statistical support (Fig. 41). Phookamsak et al. (2019) originally introduced *Neoeutypella baoshanensis* from Baoshan City, Yunnan Province, China, collected from dead wood of *Pinus armandii* (Pinaceae). The morphological characteristics of our strains closely resemble those of *Neoeutypella baoshanensis*, including similar sizes of asci, ascomata and spindle-shaped asci with hyaline to light brown ascospores. However, our new strains exhibit differences from the type species of *N. baoshanensis* (LC 12111), such as having smaller ascomata (266 × 200 μm vs. 500–770 × 450–530 μm) with a thinner peridium (25–30 μm vs. 145–240 μm) (Phookamsak et al. 2019). The sequence data of ITS and *tub*2 are identical to those of the ex-type. Therefore, we report additional specimens for *Neoeutypella baoshanensis* from another province in China.

Peroneutypa Berl., Icon. fung. (Abellini) 3(3–4): 80 (1902)

Notes – *Peroneutypa* was introduced by Berlese (1902) to accommodate *P. bellula*, *P. corniculata* and *P. heteracantha* without designating a type species. Rappaz (1987) proposed *Peroneutypa bellula* as the type species and synonymized *Peroneutypa* under *Eutypella*. However, based on characteristics and phylogenetic data as presented by Acero et al. (2004), *Peroneutypa* was reinstated by Carmarán et al. (2006). The genus is characterized by valsoid stromata, featuring packed, long prominent necks, sessile to long pedicels, small asci with truncate apices and allantoid ascospores (Carmarán et al. 2006, 2014, Senwanna et al. 2017, Shang et al. 2017). This study introduces a new species, *Peroneutypa honghensis* and provides additional sequence data for *P. anomianthi* and *P. mangrovei*.

Peroneutypa anomianthi N.I. de Silva, Lumyong & K.D. Hyde, Mycosphere 13(1): 1048 (2022) Figs 41, 44

MycoBank number: MB559525; Facesoffungi number: FoF010722

Saprobic on dead twigs of an unidentified host. Sexual morph: *Stromata* poorly developed interior, solitary to gregarious, 1–10 locules, immersed, becoming raised to erumpent by a small ostiolar canal, dark brown to black, glabrous, circular. *Ascomata* 250–320 μm high × 300–400 μm diameter ($\overline{x}$ = 279 × 354 μm, n = 5), perithecial, immersed in a stroma, dark brown to black, globose to subglobose, glabrous, individual ostioles. *Peridium* 20–30 μm wide, multi-layered, outer layer comprising brown, thick-walled cells of *textura angularis*, inner layer composed of light

brown to hyaline, thin-walled cells of *textura angularis* to *textura prismatica*. *Paraphyses* 4–6 µm wide, dense, cylindrical, septate, constricted at the basal septa, hyaline. *Asci* 20–30 × 3–5 µm ($\overline{x}$ = 28 × 4 µm, n = 10), 8-spored, unitunicate, urn-shaped, long stalked (15–20 µm), apically rounded to truncate. *Ascospores* 4–6 × 1–2 µm ($\overline{x}$ = 4.5 × 1.5 µm, n = 20), overlapping 1–2-seriate, oblong to allantoid, sometimes slightly curved, aseptate, hyaline to pale yellowish, smooth-walled, with two small guttules. Asexual morph: Undetermined.

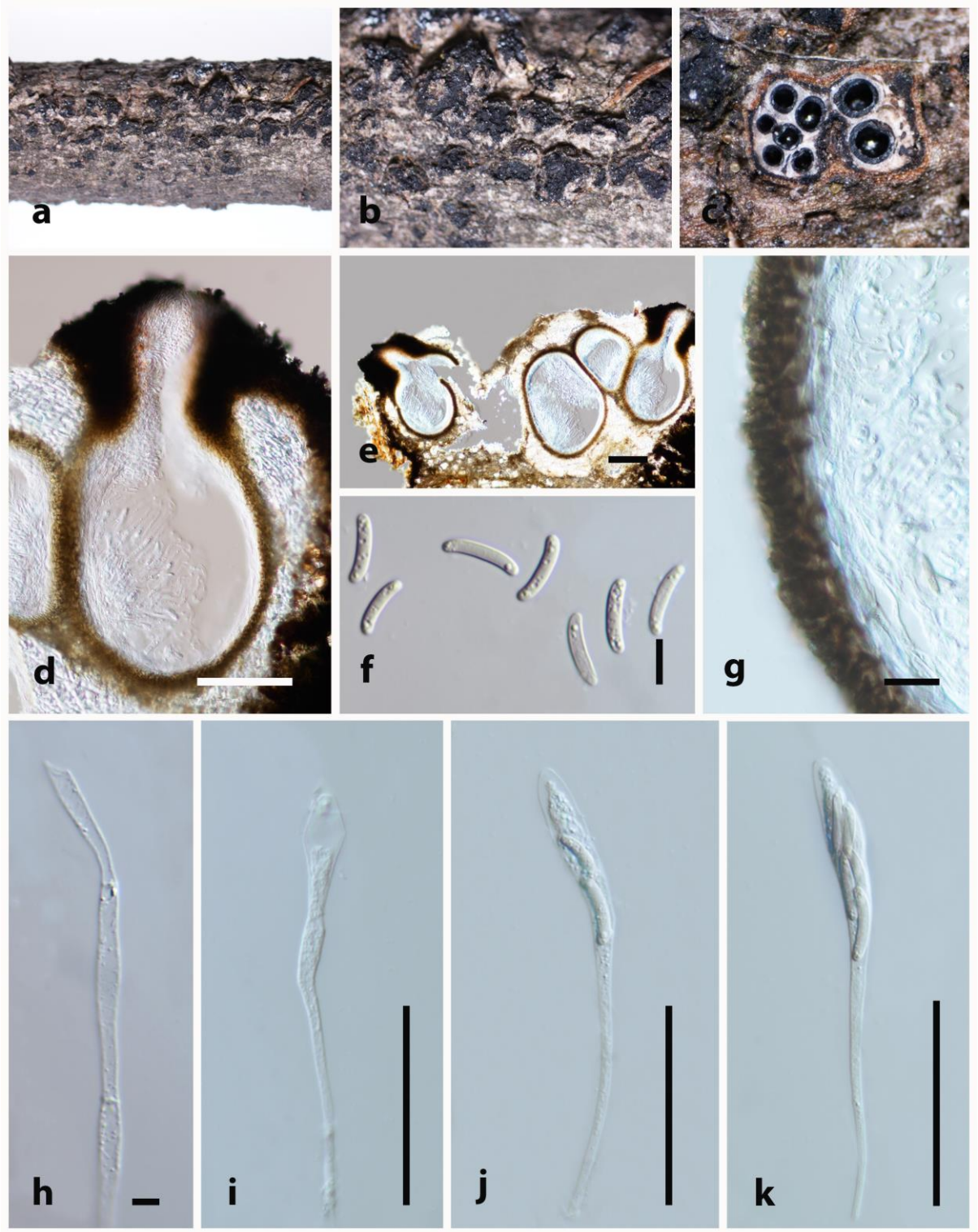

Figure 43 – *Neoeutypella baoshanensis* (HKAS 133108). a, b Ascomata on host. c Horizontal section through an ascostroma. d, e Vertical section of a Locule. g Peridium. f. Ascospores. h Paraphyses. i–k Asci. Scale bars: d, e = 100 µm, f = 10 µm, g = 20 µm, h = 5 µm, i–k = 50 µm.

Material examined – CHINA, Yunnan Province, Xishuangbanna, Yinchang Mountain (21.968333 N, 101.1975 E, 1188 m), on dead twigs of an unidentified host, 6 February 2023, L.S. Dissanayake, Y21 (HKAS 130294), living culture, KUNCC 23-15539. *ibid*. Y21A (HKAS 130295), living culture, KUNCC 23-15540.

GenBank accession numbers – ITS = PP584740, PP584741.

Notes – In our ITS and *tub*2 phylogenetic analysis (Fig. 41), our strains align closely with *Peroneutypa anomianthi*, supported by 81% MLB and 0.96 BYPP. De Silva et al. (2022) introduced *Peroneutypa anomianthi* from Thailand, collected from dead twigs attached to *Anomianthus dulcis* (Annonaceae). Our specimen is morphologically similar to *Peroneutypa anomianthi*, with immersed stromata that are raised to erumpent by a small ostiolar canal, and similarities in size concerning ascomata, asci, and ascospores (de Silva et al. 2022). In this study, we report two strains of *Peroneutypa anomianthi* as a new country record.

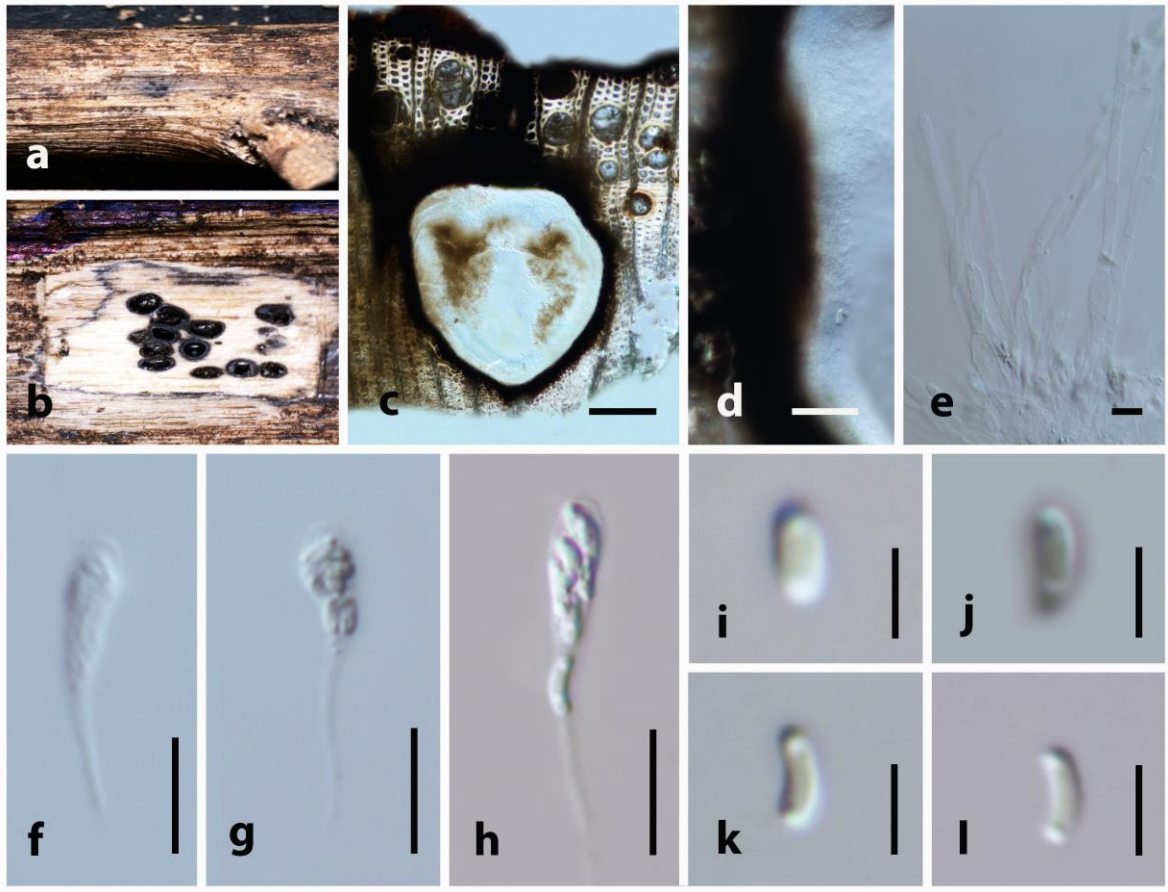

Figure 44 – *Peroneutypa anomianthi* (HKAS 130294). a Appearance of stromata on substrate. b Cross section through stroma. c Vertical section of stroma. d Peridium. e Paraphyses. f–h Asci. i–l Ascospores. Scale bars: c = 100 μm, d = 20 μm, f–h = 10 μm, e, i–l = 5 μm.

Peroneutypa hongheensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 41, 45

MycoBank number: MB852806; Facesoffungi number: FoF04928

Etymology – The specific epithet is derived from the Honghe County, where the holotype was collected.

Holotype – HKAS 133110

Saprobic on dead twigs of Rosaceae. Sexual morph: *Stromata* with poorly developed interior, solitary to gregarious, with 3–5 locules, immersed, becoming raised to erumpent by a small ostiolar canal, dark brown to black, glabrous, circular. *Ascomata* 250–280 μm high × 190–220 μm diameter ($\bar{x}$ = 274 × 207 μm, n = 5), perithecial, immersed in a stroma, dark brown to black, globose to subglobose, glabrous, with individual ostioles. *Ostiole* 60–70 μm high × 20–30 μm diameter ($\bar{x}$ =

69 × 24 μm, n = 5), cylindrical, sulcate, periphysate. *Peridium* 8–12 μm wide, multi-layered, outer layer comprising brown, thick-walled cells of *textura angularis*, inner layer composed of light brown to hyaline, thin-walled cells of *textura angularis* to *textura prismatica*. *Paraphyses* 4–6 μm wide, dense, cylindrical, septate, hyaline. *Asci* 30–40 × 3–6 μm ($\overline{x}$ = 34 × 4.8 μm, n = 10), 8-spored, unitunicate, urn-shaped, apically rounded to truncate. *Ascospores* 4–6 × 1–2 μm ($\overline{x}$ = 4.7 × 1.7 μm, n = 20), overlapping 1–2-seriate, oblong to allantoid, sometimes slightly curved, aseptate, hyaline to pale yellowish, smooth-walled, with two small guttules. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Honghe Autonomous Prefecture, Honghe County, (23.391098 N, 102.224279 E, 1198 m), on dead twigs of Rosaceae sp., 12 March 2023, D.N. Wanasinghe, DWHH01 (HKAS 133110, holotype), ex-type KUNCC 23-16753. *ibid*. DWHH03 (HKAS 133109, isotype), ex-isotype KUNCC 24-17630.

GenBank accession numbers – ITS = PP584742, PP584743, *tub*2 = PP951427, PP951428.

Notes – Two new strains (KUNCC 23-16753 and KUNCC 24-17630) form an independent lineage that is closely related to *Peroneutypa anomianthi* (MFLUCC 21-0195), supported by 100% MLB and 1.00 BYPP in our phylogenetic analysis of combined ITS and *tub*2 sequence data (Fig. 41). These new strains differ from *Peroneutypa anomianthi* by having comparatively smaller ascomata (250 × 280 μm vs. 320 × 400 μm) with shorter ostioles (69 × 24 μm vs. 340 × 100 μm). *Peroneutypa anomianthi* was introduced by de Silva et al. (2022) from dead twigs attached to *Anomianthus dulcis* (Annonaceae) in Thailand. The base pair differences in ITS and *tub*2 between *Peroneutypa anomianthi* and the new species are 4.5% (28/621) and 13.8% (38/275) respectively. The new strains were collected from dead twigs of Rosaceae in Honghe County, Yunnan Province, China. Therefore, we introduce *Peroneutypa hongheensis* as a novel species based on morphology and phylogenetic analysis.

Peroneutypa mangrovei Devadatha & V.V. Sarma, Fungal Diversity 95: 169 (2019) Fig. 41

MycoBank number: MB554285; Facesoffungi number: FoF04271

See the description in Phookamsak et al. (2019).

Material examined – CHINA, Sichuan Province, Chengdu, Qingyang District, Huanhuaxi Park (30.662222 N, 104.026111 E, 501m), on dead twigs of *Senecio scandens* (Asteraceae), 3 January 2023, L.S. Dissanayake, HHX04 (HKAS 130292), living culture, KUNCC 23-15538. *ibid*. HHX04A (HKAS 130293).

GenBank accession numbers – ITS = PP584744, PP584745, *tub*2 = PP951429, PP951430.

Notes – Phookamsak et al. (2019) introduced *Peroneutypa mangrovei*, found on decaying wood of *Avicennia marina* (Acanthaceae) in the Thengaithittu mangroves of Puducherry, India. In our study, we detail two additional specimens (HKAS 130292, HKAS 130293) from dead twigs of *Senecio scandens* (Asteraceae) in Huanhuaxi Park, Qingyang District, Chengdu, Sichuan Province, China. These new findings expand the known habitats and distribution range of *Peroneutypa mangrovei*.

Paraeutypella L.S. Dissan., J.C. Kang, Wijayaw. & K.D. Hyde, Biodiversity Data Journal 9: e63864, 11 (2021)

Notes – *Paraeutypella* was introduced by Dissanayake et al. (2021a) to accommodate *P. citricola* and *P. vitis*, two species previously placed in *Eutypella* sensu lato, with *Paraeutypella guizhouensis* as the type species. *Paraeutypella* is distinguished from *Eutypella* species by having stromata with groups of 4–25 perithecia arranged in a valsoid configuration and ostiolar necks that are 3–6 sulcate and long, whereas *Eutypella* species have stromata comprising groups of 20–70 perithecia with comparatively shorter ostiolar necks, which can be sulcate or smooth. *Paraeutypella* species function as saprobes on twigs and deadwood materials.

Paraeutypella citricola (Speg.) L.S. Dissan., Wijayaw., J.C. Kang & K.D. Hyde, Biodiversity Data Journal 9: e63864, 14 (2021) Figs 41, 46

MycoBank number: MB558003; Facesoffungi number: FoF15551

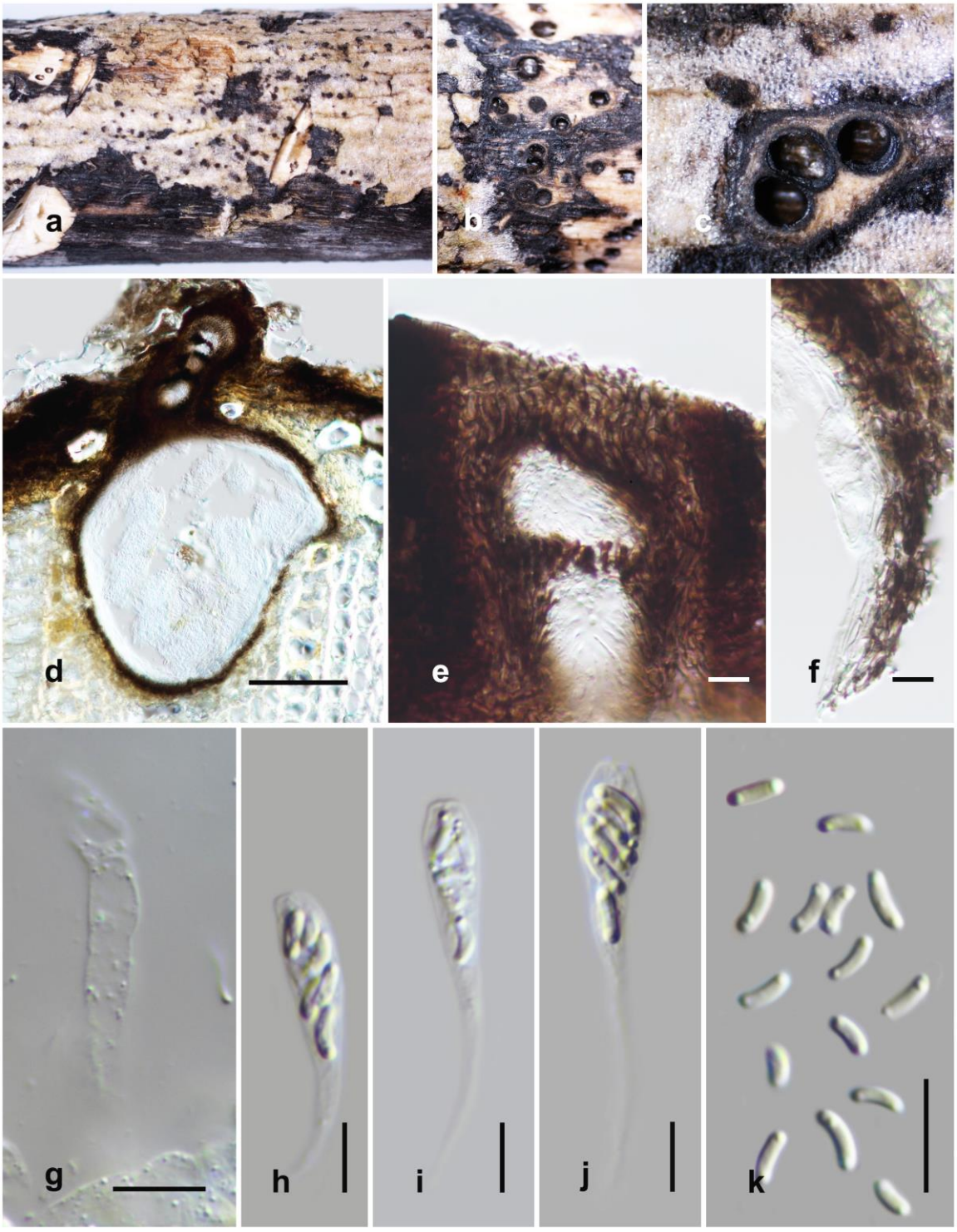

Figure 45 – *Peroneutypa hongheensis* (HKAS 133110, holotype). a Appearance of stromata on substrate. b, c Cross section through stroma. d Vertical section of stroma. e Ostiole. f Peridium. g Paraphyses. h–j Asci. k Ascospores. Scale bars: c = 100 µm, d = 20 µm, f–h = 10 µm, e, i–l = 5 µm.

Saprobic on dead twigs of unidentified host. Sexual morph: *Stromata* immersed in the substrate, erumpent, aggregated, circular to irregular, blackening the periderm, surface black, rugose due to the necks of perithecia, surrounded by a black line in the host tissue, with groups of 6–10 perithecia. *Ascomata* 300–400 µm high × 300–360 µm diameter ($\overline{x}$ = 395 × 340.5 µm, n = 10), dark brown, black, globose to subglobose, compressed, necks of the perithecia arranged in a valsoid configuration. *Ostiolar canals* 250–300 µm high × 60–80 µm diameter ($\overline{x}$ = 279.5 × 69 µm,

n = 10), dark brown, opening separately, sulcate or smooth, periphysate. *Peridium* 30–40 μm thick, comprising several layers of cells of *textura angularis*; inner layer cells hyaline, outer layer cells brown to dark brown. *Paraphysis* 3–4 μm wide, dense, cylindrical, septate, constricted at the basal septa, hyaline. *Asci* 60–100 × 6–10 μm ($\overline{x}$ = 70 × 7 μm, n = 20), 8-spored, unitunicate, cylindrical, with rounded apex, apical rings inamyloid, long-stalked. *Ascospores* 8–10 × 2–3 μm ($\overline{x}$ = 9 × 2.5 μm, n = 30), uniseriate to irregularly arranged, sometimes agglomerated at the base of the ascus, hyaline, becoming pale brown, allantoid, aseptate, smooth-walled. Asexual morph: Undetermined.

Material examined – CHINA, Sichuan Province, Chengdu, Qingyang District, Huanhuaxi park (23.39 N, 102.225556 E, 1186m), on dead twigs of an unidentified host, 5 January 2023, L.S. Dissanayake, SCCHHX23-15 (HKAS 133113), SCCHHX23-17 (HKAS 133114). Dujiangyan City, Yeleishan park (31.075 N, 103.564167 E, 1065.01m) on dead twigs of an unidentified host, 5 January 2023, L.S. Dissanayake, SCCYL23-12 (HKAS 133112), SCCUF23-10 (HKAS 133111).

GenBank accession numbers – ITS = PP584746, PP584747, PP584748, PP584749, *tub*2 = PP951426, PP951425, PP951424, PP951423.

Notes – *Eutypella citricola* was originally introduced by Spegazzini (1898) from *Citrus* in Argentina. Based on a phylogeny that combined ITS and *tub*2 sequence data, Dissanayake et al. (2021a) reclassified *Eutypella citricola* as *Paraeutypella citricola*. In our phylogenetic analysis, the new strains (HKAS 133111, HKAS 133112, HKAS 133113 and HKAS 133114) clustered with *Paraeutypella citricola* (HVVIT07, HVGRF01). Previously, *Paraeutypella citricola* was found on various hosts in warm temperate and tropical countries, including *Acer*, *Citrus limon*, *C. sinensis*, *C. paradisi*, *Magnolia lilifera*, *Salix* spp., *Schinus molle*, *Ulmus procera*, and *Vitis vinifera* (Trouillas et al. 2011 Mehrabi et al. 2016, Farr and Rossman 2020, Dissanayake et al. 2021a, de Silva et al. 2022). In this study, we report four *Paraeutypella citricola* strains from different unidentified hosts in Sichuan Province, China.

Fasciatisporaceae S.N. Zhang, K.D. Hyde & J.K. Liu, Fungal Diversity 100: 227 (2020)

Notes – Hyde et al. (2020b) introduced the family Fasciatisporaceae to accommodate *Fasciatispora*, which has distinct morphology and phylogeny within the Xylariales. Species of Fasciatisporaceae can be distinguished from other members of Xylariales by their unicellular ascospores with a central pallid band (Hyde et al. 2020a). *Fasciatispora* is currently the sole genus in the family (Wijayawardene et al. 2022). Members of this family are saprobes in both marine and terrestrial habitats (Hyde et al. 2020b).

Fasciatispora K.D. Hyde, Transactions of the Mycological Society of Japan 32: 265 (1991)

Notes – Hyde et al. (1991) introduced *Fasciatispora* with type species of *F. nypae*. *Fasciatispora* species are saprobes found on palms and other monocotyledons and are distributed in terrestrial and coastal habitats. Eleven *Fasciatispora* species have been introduced, but only five have been described using both molecular and morphological data (Hyde et al. 2020a). This study introduces *Fasciatispora sichuanensis* and provides an updated and comprehensive phylogenetic classification, incorporating LSU, ITS, *rpb*2 and *tub*2 sequence analyses.

Fasciatispora sichuanensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 37, 47

MycoBank number: MB850220; Facesoffungi number: FoF14914

Etymology – The specific epithet is derived from the Sichuan Province, where the holotype was collected.

Holotype – HKAS 130296

Saprobic on dead twigs of Poaceae sp. Sexual morph: *Ascomata* 170–250 μm high × 220–300 μm diameter ($\overline{x}$ = 210 × 260 μm, n = 5), immersed, visible as black, circular dots, indistinct, mostly solitary, sometimes aggregated into small groups, globose, beneath a clypeus, with prominent ostioles. *Ostioles* 80–120 μm high × 40–80 μm wide ($\overline{x}$ = 106 × 57 μm), ostiolar canal periphysate, light brown to yellowish periphyses. *Peridium* 20–35 μm wide, multi-layered, outer layer comprising brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline, thin-

walled cells of *textura angularis*. *Paraphyses* 2–3 μm wide, aseptate, unbranched, hyaline, numerous, filamentous, flexuous, tapering. *Asci* 70–120 × 7–14 μm ($\overline{x}$ = 102 × 11 μm), 8-spored, unitunicate, cylindrical, short pedicellate, apical ring wedge-shaped, J+ in Melzer's reagent, apex rounded. *Ascospores* 14–17 × 6–9 μm ($\overline{x}$ = 16 × 7.7 μm), uniseriate, ellipsoidal to obovoid, aseptate, hyaline when immature, yellowish brown with wide equatorial pallid band when mature, guttulate (1–2 large guttules at the center), without a mucilaginous sheath and lacking a germ slit. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinating on PDA within 24 h. Colonies on PDA reaching 20 mm diameter after 2 weeks at 25 °C. Mycelia superficial, umbonate shape, surface slightly rough, with undulate margin, forming small, from above, white; reverse, blackish brown, not producing pigmentation in agar.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Yuleishan park (31.075 N, 103.564167 E, 1065.01m), on a dead twig of Poaceae sp., 5 January 2023, L. S. Dissanayake, SCCYL23-06 (HKAS 130296, holotype), ex-type, KUNCC 23-15541.

GenBank accession numbers – ITS = PP584750, LSU = PP584823.

Notes – *Fasciatispora sichuanensis* aligns well within *Fasciatispora* and clusters with *F. cocoes* in our phylogenetic analysis (Fig. 37), with 99% MLB and 1.00 BYPP statistical support. *Fasciatispora cocoes* was identified on decaying rachides of *Cocos nucifera* from Thailand, while *F. sichuanensis* was examined on Poaceae from the Sichuan Province in China (Hyde et al. 2020a). *Fasciatispora sichuanensis* is different from *F. cocoes* in having a thick peridium (24–35 μm) and ascospores without a mucilaginous sheath vs. a thinner peridium (9–18) and ascospores with a mucilaginous sheath (Hyde et al. 2020a). The nucleotide difference of LSU and ITS of *Fasciatispora sichuanensis* and *F. cocoes* reveal 15/835 (1.7%) and 32/690 (4.6%) respectively.

Hypoxylaceae DC., Flore française 2: 280 (1805)

Notes – Wendt et al. (2018) validated the family Hypoxylaceae within the Xylariales based on multi-locus phylogeny, morphology and chemotaxonomy studies. Molecular data provided evidence confirming the position of Hypoxylaceae within Xylariales further (Hongsanan et al. 2017, Chen et al. 2023a). Daranagama et al. (2018) recognized 18 genera, including *Alloanthostomella*, *Neoanthostomella* and *Pseudoanthostomella* within the Hypoxylaceae. However, based on phylogenetic studies by Voglmayr et al. (2018) and Wendt et al. (2018), these three genera cluster as distinct clades in Xylariaceae *sensu stricto*. As a result, they were placed within the Xylariales as *genera incertae sedis*. Hyde et al. (2020a) accepted 19 genera within the Hypoxylaceae. Recently, Cedeño-Sanchez et al. (2023) introduced *Parahypoxylon* segregated from Hypoxylon based on polyphasic taxonomic approach.

Hypoxylon Bull., Histoire des champignons de la France 1: 168 (1791)

Notes – Bulliard (1791) introduced *Hypoxylon* with *H. fragiforme* as the type species. *Hypoxylon* is an extensively studied genus, rich in species with over 200 accepted taxa (Hyde et al. 2020a, Song et al. 2022). Index Fungorum (2024) lists 1,188 species epithets for the genus. *Hypoxylon* species are mainly found on dead wood, acting as saprobes and are distributed worldwide (Ju & Rogers 1996, Wendt et al. 2018). Some species of *Hypoxylon* also function as endophytes and facultative parasites on diseased hosts (Ju & Rogers 1996, Kuhnert et al. 2014). Numerous secondary metabolites have been isolated in *Hypoxylon* species (Helaly et al. 2018). Recently, *Hypoxylon aurantium* and *H. teeravasati* were discovered in decaying wood on submerged mangrove habitats (Phookamsak et al. 2019, Dayarathne et al. 2020a). In this study, we introduce two *Hypoxylon* species from Guizhou Province, China with both morphological and molecular data.

Hypoxylon guiyangense L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 48, 49

MycoBank number: MB850221; Facesoffungi number: FoF14915

Etymology – The specific epithet is derived from Guiyang City, where the holotype was collected.

Holotype – HKAS 130300

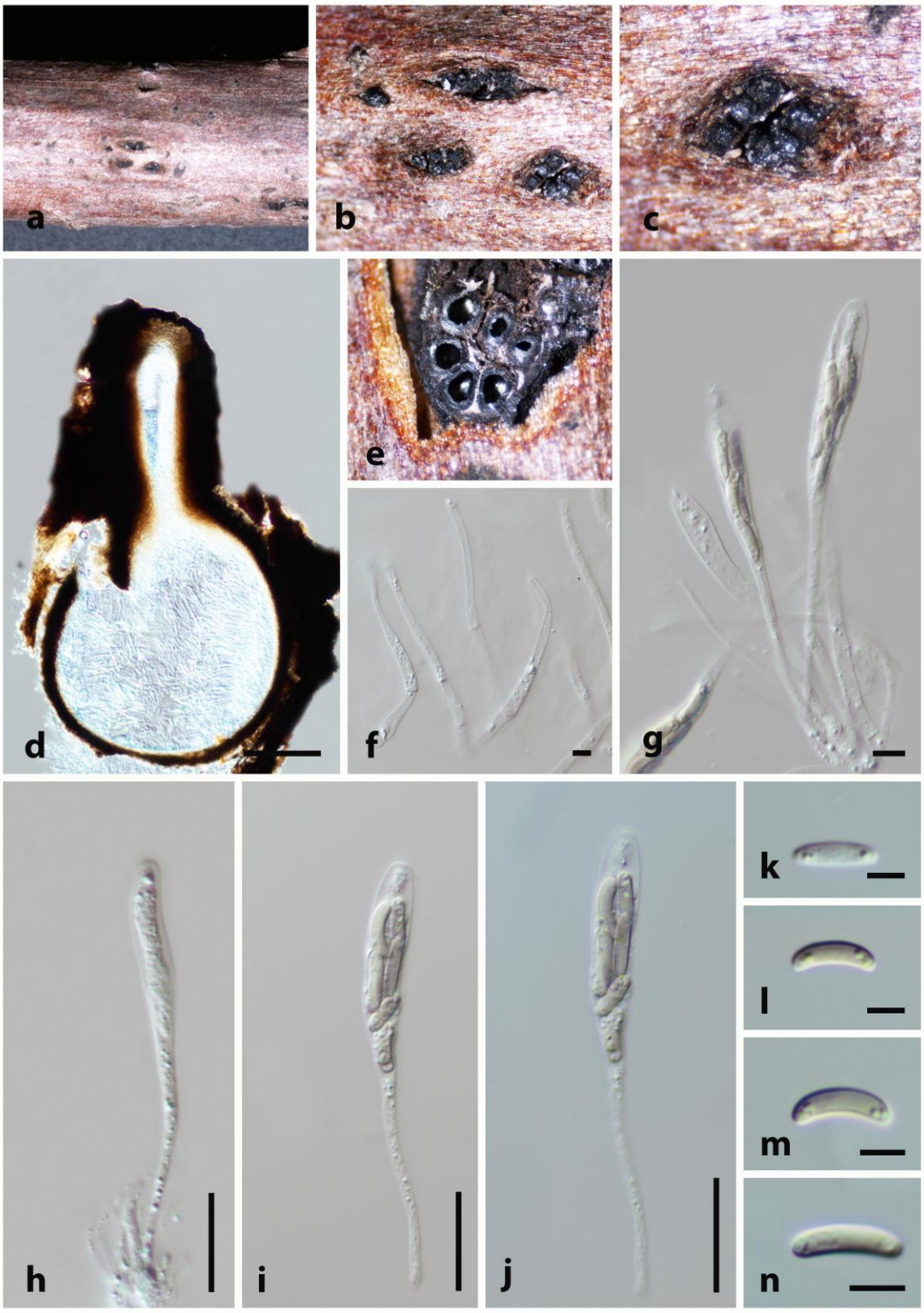

Figure 46 – *Paraeutypella citricola* (HHX15 HKAS). a–c Appearance of stromata on substrate. d Vertical section of stroma. e Cross section through stroma. f Paraphyses. g–j Asci. k–n Ascospores. Scale bars: c = 100 μm, d = 20 μm, f–h = 10 μm, e, i–l = 5 μm.

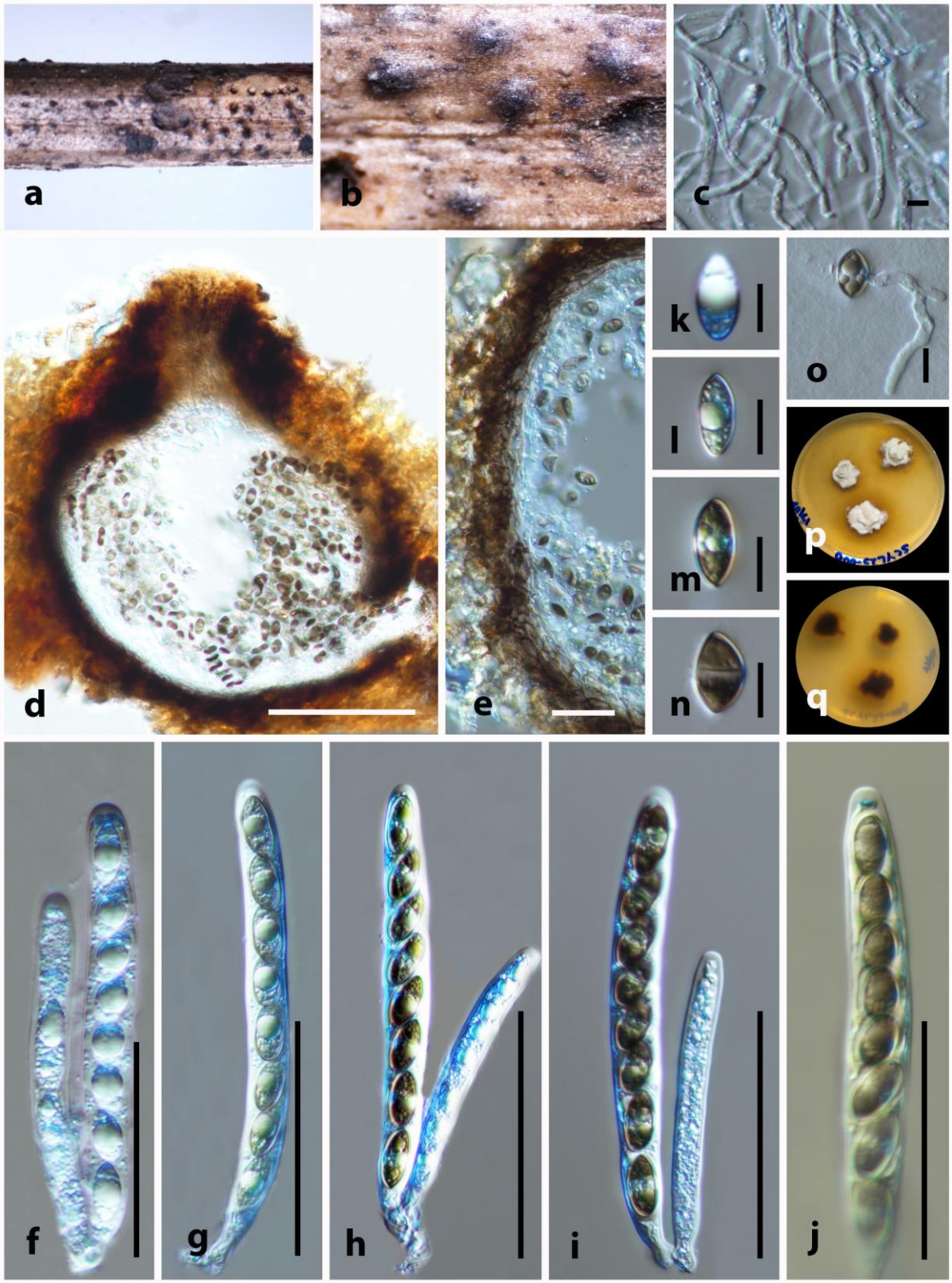

Figure 47 – *Fasciatispora sichuanensis* (HKAS 130296, holotype). a Substrate. b Ascomata on the host surface. c Paraphyses. d Section of an ascoma. e Peridium. f–j Asci (j = Asci in Melzer's reagent). k–n Ascospores. o Germinated ascospore. p, q One-week-old colony on PDA (q from the bottom). Scale bars: c = 5 μm, d = 100 μm, e = 20 μm, f–j = 50 μm, k–o = 10 μm.

Saprobic on dead twigs of an unidentified host. Sexual morph: *Stromata* superficial, pulvinate to effused-pulvinate, gregarious, with inconspicuous perithecial mounds, surface yellowish brown, blackish granules immediately beneath surface, multi-layered perithecial mound,

grayish-yellow pigments in 10% KOH. *Ascostromata* 120–150 μm high × 120–160 μm diameter ($\overline{x}$ = 135 × 143 μm, n = 5), globose to sub-globose, dark brown, with an ostiole. *Ostioles* 60–90 μm high × 40–60 μm wide, ostiolar canal periphysate, hyaline periphyses. *Peridium* 25–40 μm wide, multi-layered, outer layer comprising brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of *textura prismatica*. *Paraphyses* 3–5 μm wide, rarely septate, unbranched, hyaline, cellular, minutely guttulate, embedded in a gelatinous matrix. *Asci* 80–100 × 7–10 μm ($\overline{x}$ = 93 × 8.4 μm, n = 10), 8-spored, unitunicate, cylindrical or clavate, long pedicellate (25–35 μm long), J+ apical ring in Melzer's reagent. *Ascospores* 9–12 × 5–7 μm ($\overline{x}$ = 9.4 × 4.8 μm, n = 30), uniseriate to overlapped, ellipsoidal-inequilateral, with narrowly rounded ends, smooth at surface, aseptate, hyaline to yellowish brown when immature, dark brown at maturity, 1–5 guttulate (mostly 3 guttules), with straight germ slit spore length, aseptate, perispore dehiscent in 10% KOH. Asexual morph: Undetermined.

Material examined – CHINA, Guizhou Province, Guiyang City (26.646999 N, 106.629997 E, 1075.55 m), on dead twigs of unidentified host, 11 November 2022, G.C. Ren, GYR22-23 (HKAS 130300, holotype), ex-type, KUNCC 23-15543. *ibid*. GYR22-23A (HKAS 130301, isotype), ex-isotype, KUNCC 23-15546.

GenBank accession numbers – ITS = PP584751, PP584752, LSU = PP584824, PP584825, *tub*2 = PP951417, PP951418.

Notes – Strains of *Hypoxylon guiyangense* form a distinct clade (100% MLB, 1.00 BYPP) adjacent to *H. guizhouense* (Fig. 48). *Hypoxylon guiyangense* differs from *H. guizhouense* in that it has yellowish-brown stromata that spread over a smaller area of the host substrate with 1–5 guttulate (mostly 3 guttules) ascospore. In contrast, *Hypoxylon guizhouense* features stromata with a violet-brown surface that covers a broader area on the host surface with 1–3 guttulate (mostly 2 guttules) ascospore. The nucleotide differences between *Hypoxylon guiyangense* and *H. guizhouense* are 2% (12/560) for ITS, 2% (27/1217) for LSU, 5% (33/669) for *rpb*2 and 3% (38/1175) for *tub*2.

Hypoxylon guizhouense L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 48, 50

MycoBank number: MB850222; Facesoffungi number: FoF14916

Etymology – The specific epithet is derived from the Guizhou Province, where the holotype was collected.

Holotype – HKAS 130298

Saprobic on dead twigs of an unidentified host. Sexual morph: *Stromata* superficial, pulvinate to effused-pulvinate, gregarious, with inconspicuous perithecial mounds, surface violet-brown, white granules immediately beneath surface, with a multi-layered perithecial mound, spreading over a large area of the host surface, yellow pigments in 10% KOH. *Ascostromata* 150–250 μm high × 150–270 μm diameter ($\overline{x}$ = 195 × 203 μm, n = 5), globose to sub-globose, dark brown, with an ostiole. *Ostioles* 40–60 μm high × 70–80 μm wide, ostiolar canal periphysate, with hyaline periphyses. *Peridium* multi-layered, outer layer comprising brown, thick-walled cells of *textura angularis*, inner layer composed of light brown to hyaline, thin-walled cells of *textura angularis*. *Paraphyses* 3–5 μm wide, rarely septate, unbranched, hyaline, cellular, minutely guttulate, embedded in a gelatinous matrix. *Asci* 80–100 × 6–10 μm ($\overline{x}$ = 89 × 8 μm, n = 10) 8-spored, unitunicate, cylindrical or clavate, long pedicellate (30–35 μm long), with a J+, apical ring in Melzer's reagent. *Ascospores* 9–11 × 4–5 μm ($\overline{x}$ = 10 × 4.8 μm), uniseriate to overlapping, ellipsoidal, narrow at both ends, smooth at surface, aseptate, initially hyaline to yellowish brown, dark brown at maturity, 1–3 guttulate (mostly 2 guttules), with conspicuously straight germ slit same as spore-length on the convex side, perispore dehiscent in 10% KOH. Asexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA within 24 h. Colonies on PDA reaching 12–18 mm diameter after 3 weeks at 25 °C. Mycelia superficial, umbonate shape, surface slightly rough, with undulate margin, forming small, from above, white; reverse, blackish brown, not producing pigmentation in agar.

Material examined – CHINA, Guizhou Province, Guiyang City (26.646999 N, 106.629997 E, 1075.55 m), on dead twigs of an unidentified host, 11 November 2022, G.C. Ren, GYR22-20 (HKAS 130298, holotype), ex-type, KUNCC 23-15544. *ibid*. GYR22-19 (HKAS 130299), ex-isotype, KUNCC 23-15545.

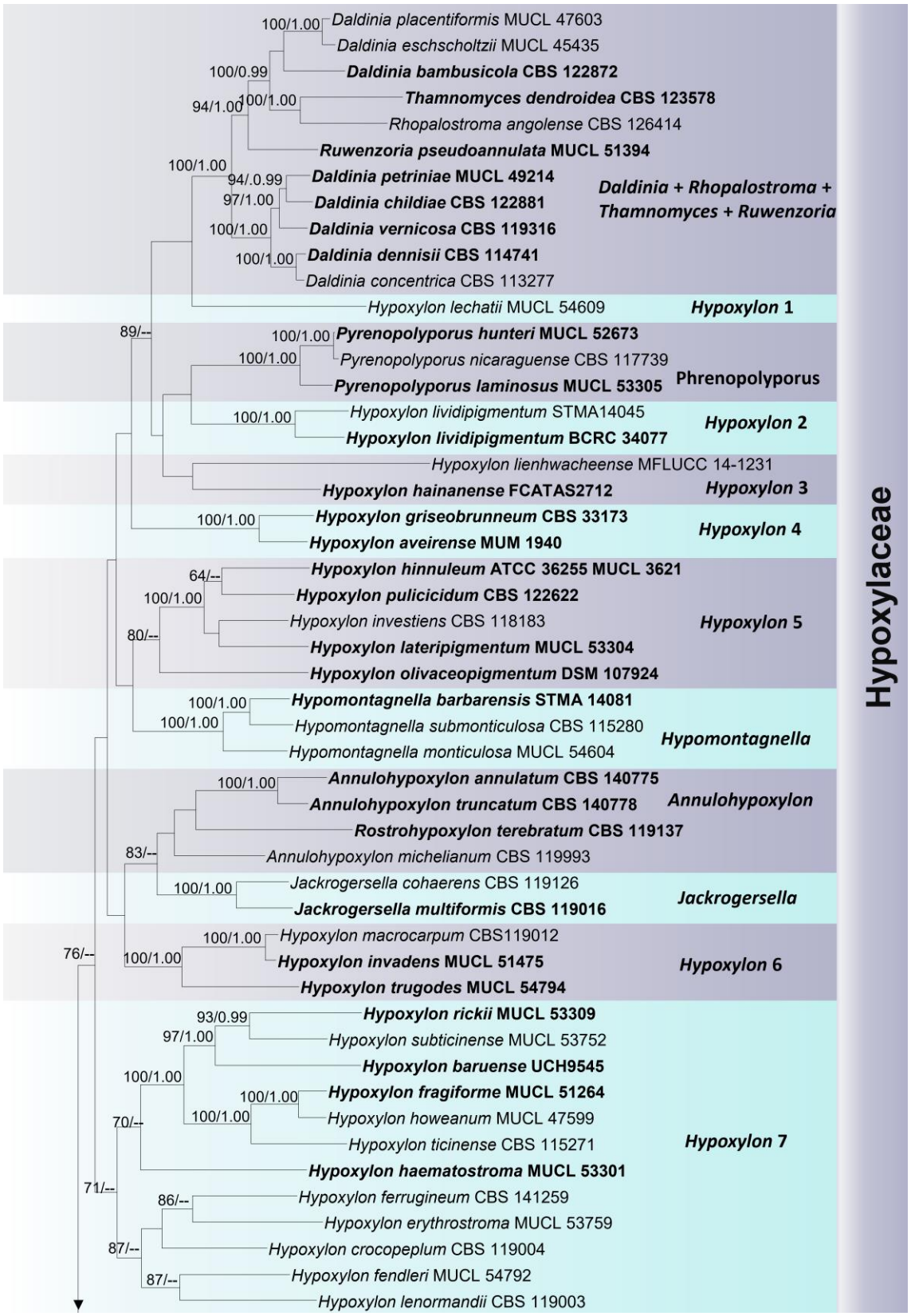

Figure 48 – RAxML phylogram generated from combined dataset of partial ITS and *tub*2 DNA sequence analyses for Hypoxylaceae. Final likelihood value is -123263.528767. The tree is rooted

to *Graphostroma platystomum* (CBS 27087), *Natonodosa speciosa* (CLM-RV86), *Xylaria arbuscula* (CBS 126415) and *X. hypoxylon* (CBS 122620). The matrix had 3972 distinct alignment patterns with 29.55% undetermined characters and gaps. Estimated base frequencies were; A = 0.087127, C = 0.033474, G = 0.088612, T = 0.058542 substitution rates AC = 0.312229, AG = 2.081526, AT = 3.217693, CG = 0.095403, CT = 0.138768, GT = 0.260191; gamma distribution shape parameter α = 0.443095. Newly generated sequences are in blue. Ex-type/type strains are indicated in bold.

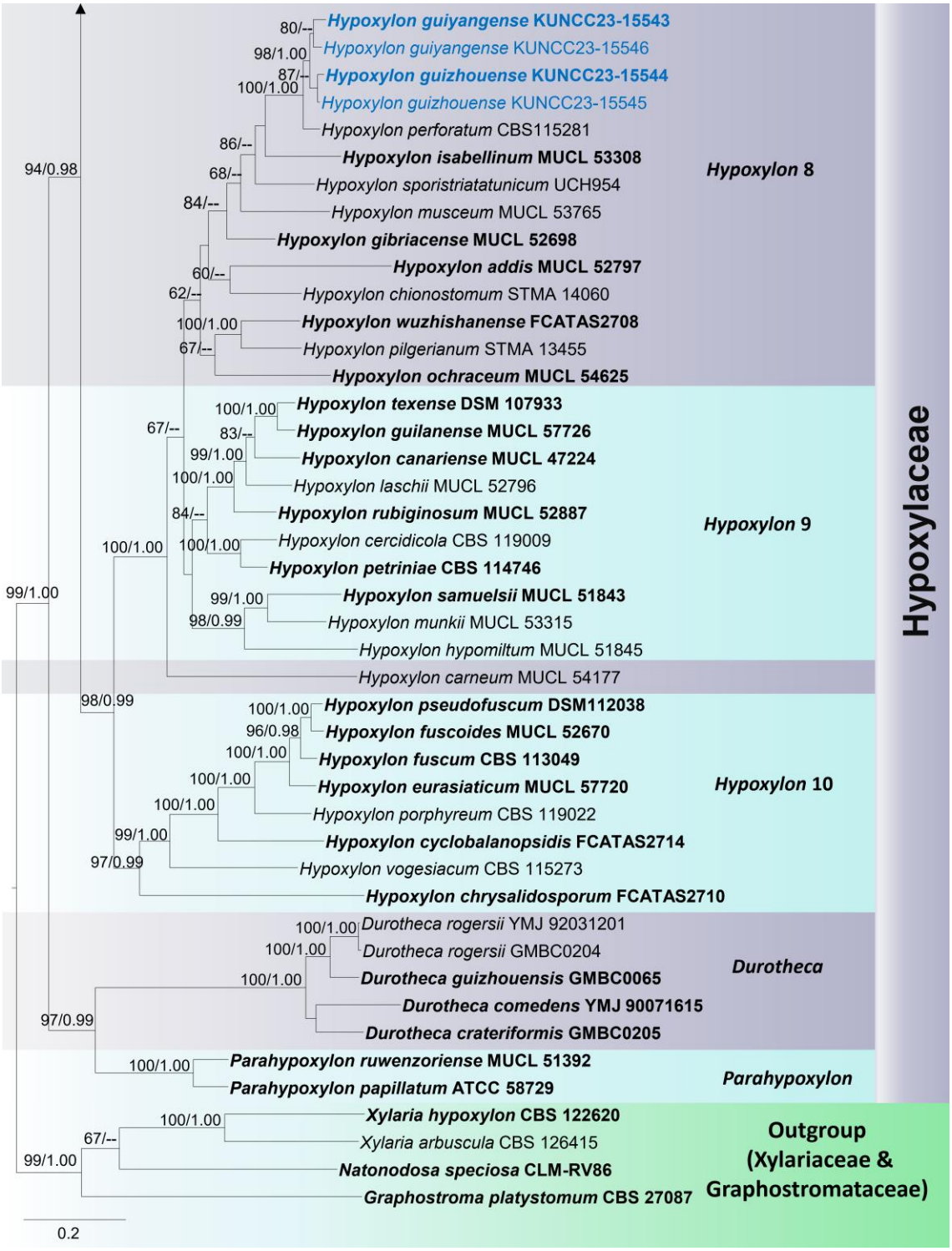

Figure 48 – Continued.

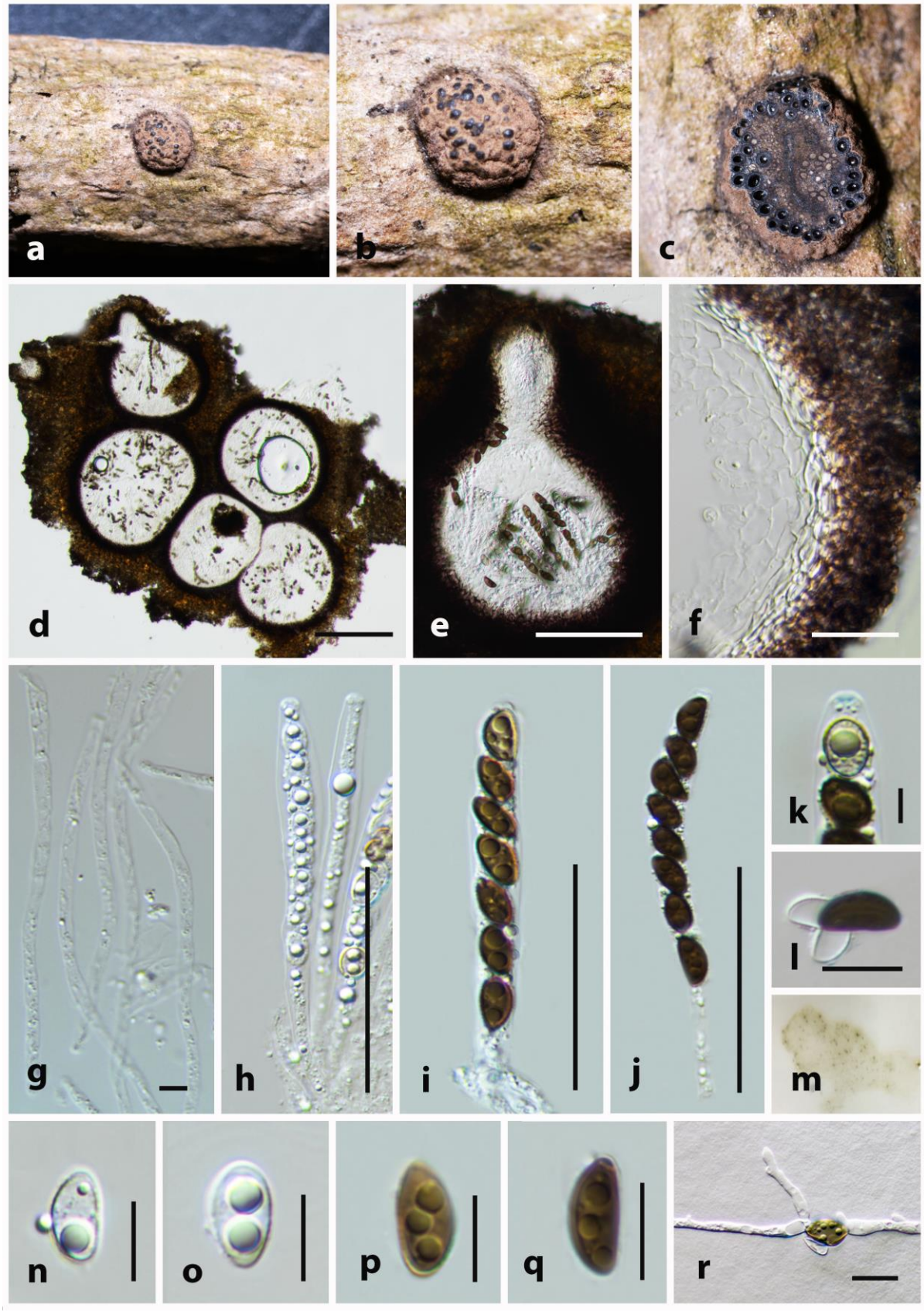

Figure 49 – *Hypoxylon guiyangense* (HKAS 130300, holotype). a Stromata on substrate. b Stromata surface. c–e Horizontal sections through stroma. f Peridium. g Paraphyses. h–k Asci (k = Asci in Melzer's reagent). l–q Ascospores (l = ascospore in 10% KOH, m = KOH-extractable pigments, r = germinated ascospore). Scale bars: d, e = 100 μm, f = 20 μm, g = 5 μm, h–j = 50 μm, k–r = 10 μm.

GenBank accession numbers – ITS = PP584753, PP584754, LSU = PP584826, PP584827, *tub*2 = PP951419, PP951420, *rpb*2 = PP993509, PP993509.

Notes – In the multi-gene phylogenetic analyses (Fig. 48), our collections of *Hypoxylon guizhouense* and *H. guiyangense* show a close affinity to *H. perforatum* (CBS 115281) with 100% MLB and 1.00 BYPP support. *Hypoxylon guizhouense* and *H. guiyangense* differ as detailed in the notes under *H. guiyangense*. *Hypoxylon guizhouense* differs from *H. perforatum*, which has stromata with violet-brown surface, and white granules immediately beneath the surface. While in *Hypoxylon perforatum* the stromata surface is dark brick, grayish to brown, dark brown or blackish granules immediately beneath the surface or umber. *Hypoxylon guiyangense* differs from *H. perforatum* that it has yellowish-brown stromata that is spread over a smaller area of the host substrate, whereas *H. perforatum* features stromata with a grayish-brown surface that covers a broader area on the host surface. The nucleotide differences between *Hypoxylon guizhouense* and *H. perforatum* are 3% (15/560) for ITS, 4% (48/1217) for LSU, 7% (45/669) for *rpb*2 and 4% (47/1175) for *tub*2. Between *Hypoxylon guiyangense* and *H. perforatum*, the differences are 3% (17/560) for ITS, 3% (40/1217) for LSU, 7% (38/669) for *rpb*2 and 3% (35/1175) for *tub*2.

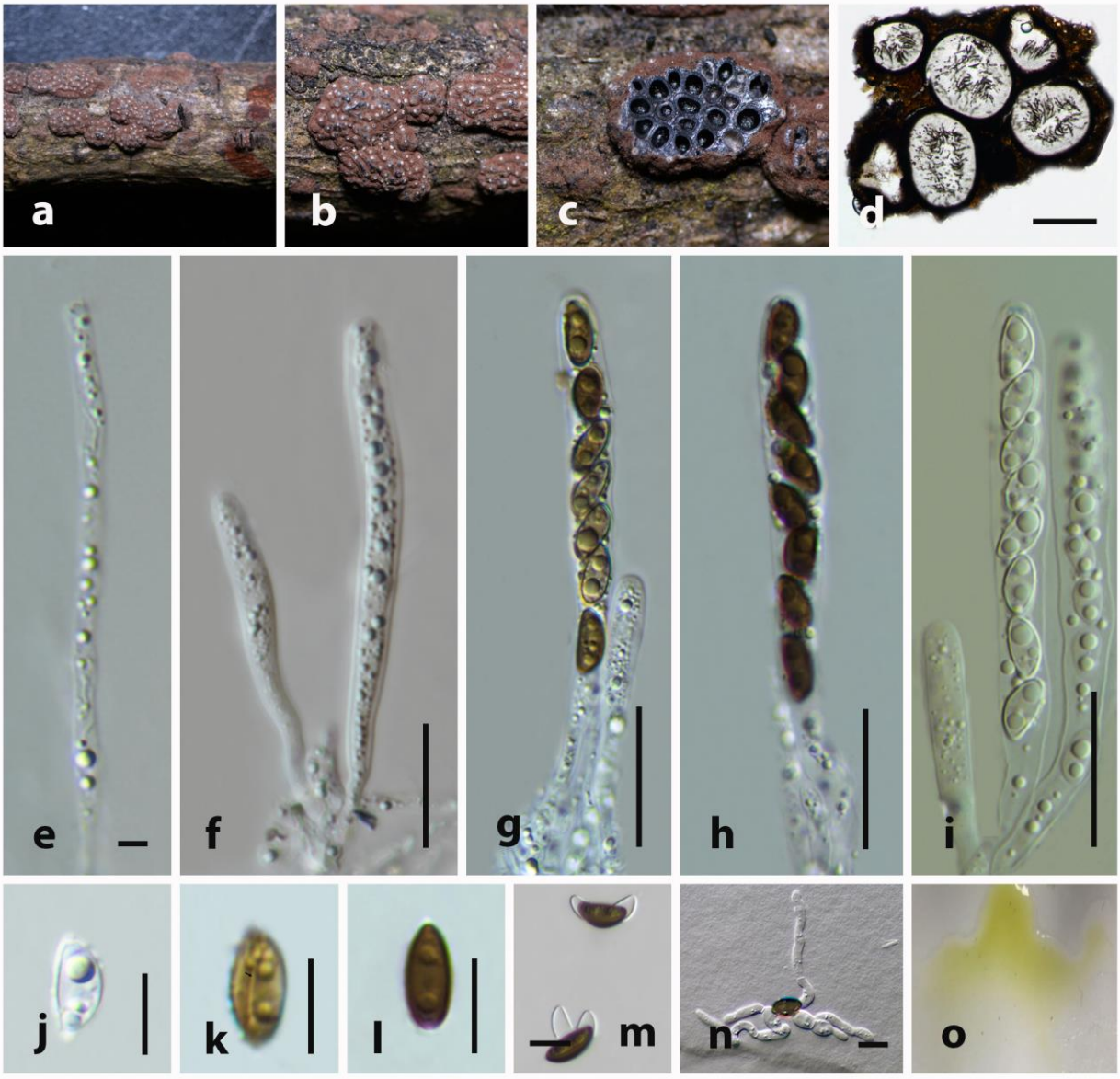

Figure 50 – *Hypoxylon guizhouense* (HKAS 130298, holotype). a, b Stromata on substrate. c, d Horizontal sections through stroma. e Paraphyses. f–i Asci (I = Apical ring blueing in Melzer's reagent). j–m Ascospores (k = ascospore with germ slit, m = Ascospore in 10% KOH,

n = Germinated ascospore). o KOH-extractable pigments. Scale bars: d = 200 μm, e = 5 μm, f–i = 20 μm, j–n = 10 μm.

Requienellaceae Boise, Mycologia 78: 37 (1986)

Notes – Boise (1986) introduced Requienellaceae in the class Dothideomycetes, with *Requienella* as the type genus. The taxonomic placement of Requienellaceae was initially uncertain. However, based on phylogenetic analysis and morphological comparisons, Jaklitsch et al. (2016) transferred Requienellaceae to Xylariales as a distinct family. Requienellaceae comprises four genera *viz*. *Acrocordiella*, *Lacrymospora*, *Parapyrenis* and *Requienella* (Wijayawardene et al. 2022). Species within Requienellaceae are widely distributed, acting as saprobes on dead wood or as pathogens on plants and can be found inhabiting bark (Hyde et al. 2020a, Dissanayake et al. 2021b).

Requienella Fabre, Ann. Sci. Nat., Bot. ser. 6, 15: 55 (1883)

Notes – *Requienella* was introduced by Fabre (1883) with three species; however, these were later transferred to other genera. Boise (1986) reinstated *Requienella* by typifying the genus with *R. seminuda* (= *Sphaeria seminuda*). Jaklitsch et al. (2016) revisited this genus, studying *R. seminuda*, introducing a new species (*R. fraxini*) and confirming that *Requienella* belongs to Xylariales. Only three *Requienella* species are listed in Species Fungorum (2024), with two having molecular data. We introduce one new species, providing both morphological evidence and molecular data to stabilize the genus further.

Requienella shangrilana L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 23, 51

MycoBank number: MB850223; Facesoffungi number: FoF14918

Etymology – The specific epithet is derived from the Shangri-La, where the holotype was collected.

Holotype – HKAS 130302

Saprobic on dead twigs of an unidentified host. Sexual morph: *Ascomata* 400–520 μm high × 480–620 μm diameter ($\overline{x}$ = 473 × 547 μm, n = 5), immersed, solitary, scattered, globose to sub-globose, black clypeus present, appearing as black spots on the substrate, ostiolate bell-shaped to cap-like. *Ostioles* periphysate, with hyaline periphyses. *Peridium* 25–40 μm wide, multi-layered, outer layer comprising light brown, thick-walled cells of *textura angularis*, inner layer composed hyaline, thin-walled cells of *textura prismatica*. *Paraphyses* 3–6 μm wide, longer than asci, aseptate, hyaline, filiform, unbranched, highly delicate, minutely guttulate, embedded in a gelatinous matrix. *Asci* 100–160 × 10–18 μm ($\overline{x}$ = 127 × 14 μm, n = 20), 8-spored, arising from basal and lateral cavity-surface of the ascoma, cylindrical, unitunicate, with a short pedicel, knob-like at the base, ascal apex thickned, inversely funnel-shaped dome, with J- apical ring in Melzer's reagent. *Ascospores* 20–30 × 9–12 μm ($\overline{x}$ = 23.7 × 10.4 μm, n = 30), obliquely uniseriate, ellipsoid, inequilaternal, narrowly rounded to nearly acute at the ends, 3-septate, becoming 4-distoseptate, inner cells are similar in size and rhomboid shape, multi-guttulate, at first hyaline, greyish when young, olivaceous to medium brown mature, smooth and thick-walled, without a mucilaginous sheath. Asexual morph: Undetermind.

Material examined – CHINA, Yunnan Province, Shangri-la (27.801111 N, 99.808056 E, 3390m), on dead twigs of an unidentified host, 15 August 2021, L. Qinxing, BNCD18 (HKAS 130302, holotype). *ibid*. BNCD18A (HKAS 130303, isotype).

GenBank accession numbers – ITS = PP584755, PP584756, LSU = PP584828, PP584829.

Notes – *Requienella shangrilana* is similar to both *R. fraxini* and *R. seminuda*, sharing characteristics such as globose to sub-globose ostiolate ascomata, cylindrical, thick-walled, short pedicellate asci with a J- apical ring and ellipsoid, single-celled, distoseptate ascospores. However, *Requienella shangrilana* can be differentiated from *R. fraxini* and *R. seminuda* by its immersed ascomata measuring 400–520 μm × 480–620 μm, cylindrical asci measuring 100–160 × 10–20 μm and 4-distoseptate, olivaceous to medium brown ascospores that are 20–30 μm long. In contrast,

both *Requienella fraxini* and *R. seminuda* possess perithecioid, erumpent ascomata measuring 500–1100 × 450–1000 µm and 600–1200 × 450–900 µm, respectively, with oblong to narrowly clavate asci (153–206 × 20–30 µm for *R. fraxini* and 158–178 × 23.5–29 µm for *R. seminuda*) and 5-distoseptate ascospores measuring 26.7–31.5 µm for *R. fraxini* and 28.3–32.7 µm for *R. seminuda* (Jaklitsch et al. 2016).

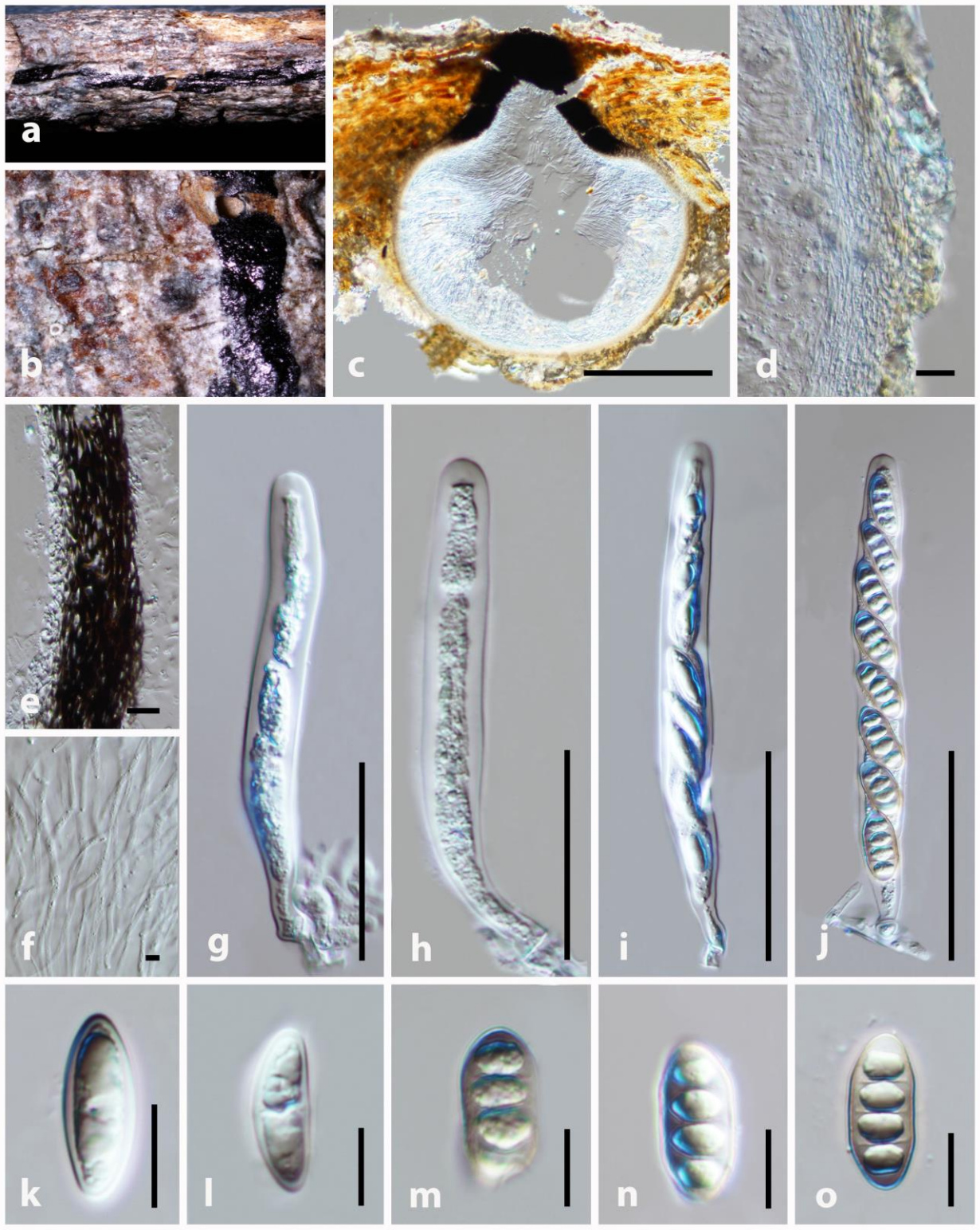

Figure 51 – *Requienella shangrilana* (HKAS 130302, holotype). a Host. b Ascomata on the host surface. b Horizontal section of an ascoma. d Peridium. e Peridium of clypeus. f Paraphyses. g–i Asci. k–o Ascospores. Scale bars: c = 200 µm, f = 5 µm, g–j = 50 µm, d, e, k–o = 10 µm.

Vamsapriyaceae Y.R. Sun, Yong Wang bis & K.D. Hyde, Journal of Fungi 7 (11, no. 891): 7 (2021)

Notes – The family Vamsapriyaceae was introduced by Sun et al. (2021b) to accommodate *Vamsapriya*, which had previously been assigned to Xylariaceae (Dai et al. 2014). However, phylogenetic analyses by Sun et al. (2021b) indicated that *Vamsapriya* forms a distinct clade within Xylariales. Morphological comparisons further highlight its distinctiveness from other families in Xylariales. Currently two genera *viz*. *Paravamsapriya* and *Vamsapriya* belong to Vamsapriyaceae. Most members of Vamsapriyaceae are saprobes in terrestrial and aquatic habitats (Bao et al. 2021, Sun et al. 2021b).

Vamsapriya Gawas & Bhat, Mycotaxon 94: 150 (2005)

Notes – Gawas & Bhat (2005) introduced *Vamsapriya* based on its asexual morphs. It is characterized by erect, cylindrical, dark brown, synnematous conidiophores; monotretic, clavate to cylindrical conidiogenous cells and cylindrical, broadly fusiform, or obclavate, and brown to dark-brown conidia (Gawas et al. 2005, Ling et al. 2018). Dai et al. (2017) described the first sexual morph of *Vamsapriya*, which features solitary, immersed ascomata visible as black dots, 8-spored, unitunicate asci and hyaline, and fusiform ascospores. The genus comprises 12 species epithets in Index Fungorum (2024). In this study, we introduce *Vamsapriya sichuanensis* as a new species, showcasing its sexual morph.

Vamsapriya sichuanensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 37, 52

MycoBank number: MB850224; Facesoffungi number: FoF14919

Etymology – The specific epithet is derived from the Sichuan Province, where the holotype was collected.

Holotype – HKAS 130304

Saprobic on dead bamboo culms. Sexual morph: *Ascomata* 250–400 high × 350–500 diameter μm ($\overline{x}$ = 327.1 × 466.4 μm, n = 10), immersed, visible as black dots, with clypeus-like tissue around the ostiolar opening, surrounded by a light brown, depressed margin, solitary, scattered, in cross-section subglobose. *Ostioles* centric, raised, ostiolar canal periphysate. *Peridium* 50–60 μm wide, multi-layered, outer layer comprising yellowish brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of *textura angularis*. *Paraphyses* 4–6 μm wide, long, septate, constricted at septa, guttulate, curve ends, in a gelatinous matrix. *Asci* 100–160 × 7–10 μm ($\overline{x}$ = 130.7 × 8.5 μm, n = 20), 8-spored, unitunicate, cylindrical, short pedicellate, with a rhomboid apical ring, J+ in Melzer's reagent, apex rounded. *Ascospores* 18–23 × 5–7 μm ($\overline{x}$ = 20 × 6.4 μm, n = 10), uniseriate or overlapping uniseriate, ellipsoidal to fusiform, 1-septate, smooth-walled, guttulate, pointed, hyaline, constricted apiosporous with a large cell (13–17 μm long) and basal cell (4–6 μm long), surround a thin gelatinous mucilaginous sheath present. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 24 h. Colonies on PDA reaching 25–30 mm diameter after 2 weeks at 25 °C. Mycelia superficial, circular, flat, surface slightly rough, with entire margin, forming small, white from above; reverse, dark brown at the center and becoming light brown towards the margin, not producing pigmentation in agar.

Material examined – CHINA, Sichuan Province, Dujiangyan City, Sichuan Longchi National Forest Park (31.003611 N, 103.611944 E, 837m), on dead bamboo culms, 5 January 2023, L.S. Dissanayake, SCCFP23-23 (HKAS 130304, holotype), ex-type, KUNCC 23-15547. *ibid*. SCCFP23-23A (HKAS 130305, isotype), ex-isotype, KUNCC 23-15548.

GenBank accession numbers – ITS = PP584757, PP584758, LSU = PP584830, PP584831, *rpb2* = PP993507, PP993508.

Notes – *Vamsapriya sichuanensis* is the first sexual morph reported in China representing *Vamsapriya*. Another sexual morph of this genus (*V. bambusicola, V. chiangmaiensis* and *V. mucosa*) were reported from Thailand. *Vamsapriya sichuanensis* is similar to *V. bambusicola*, characterized by solitary, subglobose ascomata, 8-spored, unitunicate, cylindrical asci with a J+

apical ring and fusiform, hyaline, 1-septate, apiosporous ascospores. It can be distinguished by its thicker peridium (50–60 μm compared to 10–15 μm in *V. bambusicola*). Furthermore, the nucleotide differences in the LSU and ITS regions between *Vamsapriya sichuanensis* and *V. bambusicola* are 42/835 (5%) and 35/690 (5%) respectively. *Vamsapriya sichuanensis* differs from *V. chiangmaiensis*, having smaller ascomata (466.4 × 327.1 μm compared to 845 × 750 μm) and smaller asci (130.7 × 8.5 μm vs. 160 × 9 μm) with a J+ apical ring. In the multi-gene phylogenetic analysis (Fig. 37), our strain of *Vamsapriya sichuanensis* closely aligns with *V. khunkonensis* and *V. yunnana*, supported by an 81% MLB and 0.98 BYPP bootstrap. However, direct comparisons with *Vamsapriya khunkonensis* and *V. yunnana* are not feasible since they are only known from their asexual morphs (Jiang et al. 2018a).

Xylariaceae Tul. & C. Tul., Selecta Fungorum Carpologia, Tomus Secundus. Xylariei – Valsei – Sphaeriei 2: 3 (1863)

Notes – Species of the Xylariaceae are distributed worldwide and can be found as saprobes, pathogens and endophytes in wood, leaves and fruits or in association with insects. Maharachchikumbura et al. (2016a) recognized 87 genera within the family. Upon re-examining herbarium specimens, Daranagama et al. (2018) accepted only 37 genera. Following several subsequent studies, Wijayawardene et al. (2022) recognized 38 genera within the Xylariaceae.

Collodiscula I. Hino & Katum., Bulletin of the Faculty of Agriculture Yamaguchi University 6: 55 (1955)

Notes – *Collodiscula* was introduced by Hino & Katumoto (1955), typified by *C. japonica*, which was found on bamboo culms in Japan. Based on morphological features, including stromatal ontogeny, heavily carbonized stromata, J+ apical rings in Melzer's reagent, short-stipitate asci, *Collodiscula* was placed within Xylariaceae (Samuels & Rossman 1992, Læssøe & Spooner 1994, Kang et al. 1999). A phylogenetic study by Jaklitsch & Voglmayr (2012), based on LSU and ITS sequences, confirmed the inclusion of *Collodiscula* in Xylariaceae. To date, seven species of *Collodiscula* have been reported (Hino & Katumoto 1955, Li et al. 2015b, c, Hyde et al. 2017, Xie et al. 2020, Wu et al. 2021). To date, six *Collodiscula* species are reported from China. Except *Collodiscula chiangraiensis*, all other *Collodiscula* species were observed on bamboo. Our study documents a new *Collodiscula* species on bamboo twigs in Yunnan Province, China.

Collodiscula yunnanensis L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 37, 53

MycoBank number: MB850225; Facesoffungi number: FoF14920

Etymology – The specific epithet is derived from the Yunnan Province, where the holotype was collected.

Holotype – HKAS 130306

Saprobic on the dead stalks of bamboo, forming on the host surface. Sexual morph: Stromata scattered or gregarious, solitary, superficial, black, a hexagonal prism, coronated with the top of stroma sulcate, containing 1 ascomata, with a circle of black tissue at the base, with a papillate ostiole. *External stromata* layer black, carbonaceous, easily chipped away to reveal the thin, black ascomata. *Ostioles* papillate in the centre, black. *Paraphyses* 4–6 μm hyaline, septate, unbranched, cellular, minutely guttulate, embedded in a gelatinous matrix. *Asci* 100–180 × 8–15 μm ($\overline{x}$ = 147.9 × 11 μm, n = 30), 8-spored, unitunicate, long-pedicellate, apically rounded, with a J+ wedge-shaped apical ring in Melzer's reagent. *Ascospores* 27–36 × 5–8 μm ($\overline{x}$ = 31.1 × 6.4 μm, n = 30), overlapping uniseriate, fusiform to narrowly fusiform, not constricted at septa, with narrow ends, smooth-walled, hyaline to golden brown, 3-septate, guttulate at each septum, lacking a germ slit, or appendages. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Ailaoshan Forest Mountain (24.536944 N, 101.019444 E, 2500m), on dead stalk of bamboo, 7 April 2023, L.S. Dissanayake, ALF23-09 (HKAS 130306, holotype). *ibid*. ALF23-09A (HKAS 130307, isotype).

GenBank accession numbers – ITS = PP584759, PP584760, LSU = PP584832, PP584833, *rpb*2 = PP993511, PP993512.

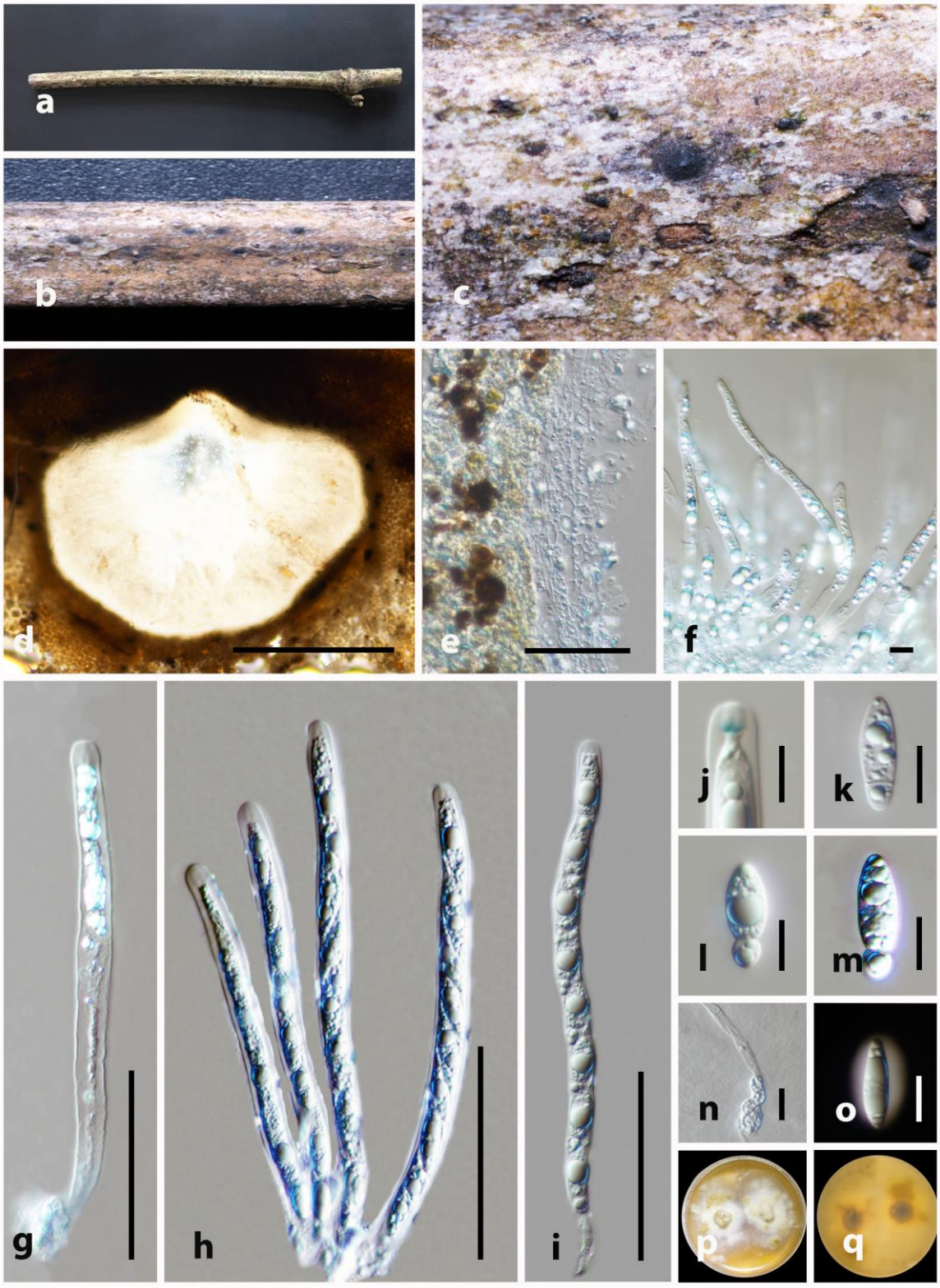

Figure 52 – *Vamsapriya sichuanensis*. (HKAS 130304, holotype). a Substrate. b, c Ascomata on the host surface. d Section of ascoma. e Peridium. f Paraphyses. g–i Asci. j Apical ring blueing in Melzer's reagent. k–o Ascospores (n germinated ascospore, o in Indian ink). p, q One-week-old colony on PDA (q from the bottom). Scale bars: d = 200 µm, e, g–i = 50 µm, f = 5 µm, j–o = 10 µm.

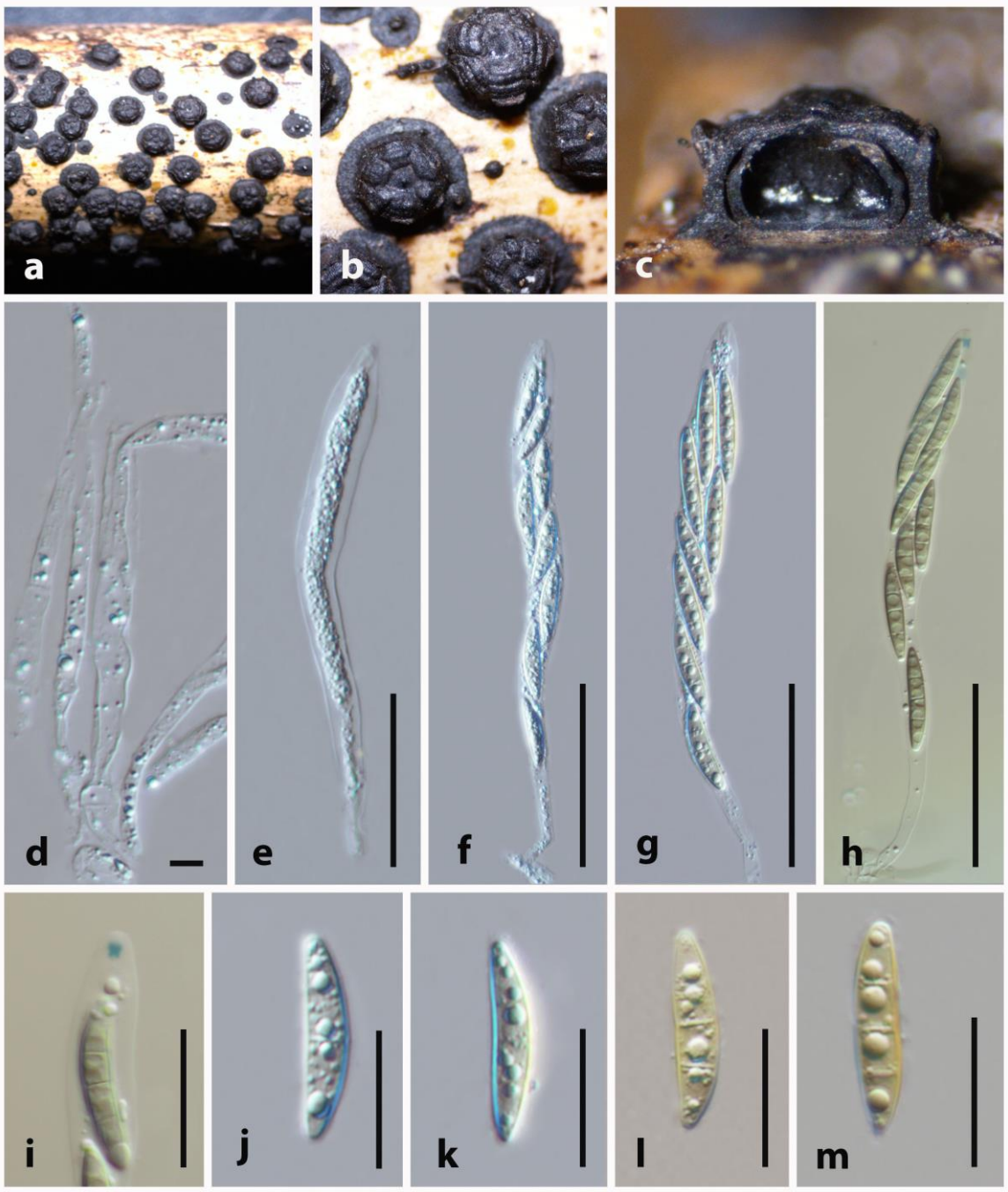

Figure 53 – *Collodiscula yunnanensis* (HKAS 130306, holotype). a, b Ascomata on the host surface. c Vertical section of an ascoma. d Paraphyses. e–h Asci (h. Asci in Melzer's reagent). i Apical ring bluing in Melzer's reagent. j–m Ascospores. Scale bars: d = 5 μm, e–h = 50 μm, i–m = 20 μm.

Notes – Phylogenetic analyses indicate that *Collodiscula yunnanensis* is closely related to *C. lancangjiangensis* (GMBC0030) with 99% MLB and 1.00 BYPP statistical support (Fig. 37), forming a distinct lineage. Our new specimen *Collodiscula yunnanensis* resembles *C. lancangjiangensis* with overlapping scattered or gregarious stromata, solitary, superficial, hexagonal prism and long-pedicellate, J+, wedge-shaped, apical ring in Melzer's reagent. However, *Collodiscula yunnanensis* can be differentiated from *C. lancangjiangensis* by its stromata containing a single ascoma, its hexagonal prism shape, its flower-like coronation at the top of the stroma and the presence of guttules on each septum of its ascospores. In contrast, *Collodiscula lancangjiangensis* has stromata with 1–2 ascomata, a hexagonal prism shape and ascospores that

lack guttules (Wu et al. 2021). Furthermore, the nucleotide differences in the LSU and ITS regions between *Collodiscula yunnanensis* and *C. lancangjiangensis* were 18/835 (2.2%) and 25/690 (4%) respectively. Based on morphological and phylogenetic evidence, we introduce *C. yunnanensis* as a new species.

Digitodochium Tubaki & Kubono, Sydowia 41: 344 (1989)

Notes – *Digitodochium* was introduced by Tubaki & Kubono (1989), typified by *D. rhodoleucum* which was described from the corticated twigs of *Fagus crenata* in Japan. *Digitodochium* was placed under Ascomycota genera *incertae sedis* (Wijayawardene et al. 2022) However, Voglmayr et al. (2022) re-examined *Digitodochium amoenum* and their collection of the asexual morph matched that of *D. amoenum* and the illustrations of *D. rhodoleucum*. As a result, Voglmayr et al. (2022) provided the first report on the sexual morphology of *Digitodochium*. Their phylogenetic analysis showed a close relationship with *Digitodochium rhodoleucum*, positioning it as the most basal clade of Xylariaceae. Thus, Voglmayr et al. (2022) placed *Digitodochium* within Xylariaceae. *Digitodochium* is phylogenetically closely related to *Occultitheca* (Voglmayr et al. 2022, Fig. 17). When comparing morphological characters, *Occultitheca* has similar characters (immersed ascomata and brown ascospores with hyaline dwarf cells) to *Digitodochium*. Therefore, further study of the asexual morph and molecular data of *Occultitheca* is needed to determine whether it is a distinct genus.

We conducted a multi-gene analysis using ITS, LSU, *rpb*2, *tub*2 and our two species closely aligned with *Digitodochium*, forming a distinct lineage with 93% MLB and 0.93 BYPP statistical support (Fig. 17). This research provides an updated and comprehensive phylogenetic classification for *Digitodochium*. By integrating morphological and phylogenetic data, we identified two new species, *Digitodochium ailaoshanense* and *D. yunnanensis*.

Digitodochium ailaoshanense L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 37, 54

MycoBank number: MB850226; Facesoffungi number: FoF14921

Etymology – The specific epithet is derived from the Ailaoshan mountain, where the holotype was collected.

Holotype – HKAS 130308

Saprobic on the dead stalk of bamboo, forming on the host surface. Sexual morph: *Ascomata* 150–250 μm high × 300–400 μm diameter ($\bar{x}$ = 188.4 × 347.2 μm, n = 5), scattered or gregarious, solitary, immersed, black, with a small black clypeus, and papillate ostioles. *Ostioles* 40–60 μm high × 12–20 μm wide ($\bar{x}$ = 46.9 × 15.8 μm, n = 5), ostiolar canal periphysate, with hyaline periphyses. *Paraphyses* 3–7 μm hyaline, septate, unbranched, cellular, minutely guttulate, embedded in a gelatinous matrix. *Asci* 70–110 × 6–9 μm ($\bar{x}$ = 85.9 × 8.1 μm, n = 30), 8-spored, unitunicate, cylindrical to slightly fusiform, short-pedicellate, apically rounded, J- blue in Melzer's reagent. *Ascospores* 12–16 × 3–5 μm ($\bar{x}$ = 14 × 4.6 μm, n = 30), overlapping uniseriate, apiosporous, hyaline to dark brown, aseptate, ellipsoid to narrowly ellipsoid, with slightly pinched ends, with a small cell at the base, smooth-walled, mostly with 2 large guttules, and thick mucilaginous sheath. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Ailaoshan Forest Mountain (24.536944 N, 101.019444 E, 2500m), on dead stalk of bamboo, 7 April 2023, L.S. Dissanayake, ALF23-14 (HKAS 130308, holotype). *ibid*. ALF23-14A (HKAS 130309, isotype).

GenBank accession numbers – ITS = PP584761, PP584762, LSU = PP584834, PP584835.

Notes – *Digitodochium ailaoshanense* is phylogenetically closely related to *D. yunnanense*, in the multigene phylogenetic analysis, with 94% MLB and 0.99 MYPP statistical support (Fig. 37). Both *Digitodochium ailaoshanense* and *D. yunnanense* are similar to *D. amoenum*. They all have 8-spored, unitunicate, cylindrical to slightly fusiform, short-pedicellate asci and hyaline to dark brown, aseptate, ellipsoid to narrowly ellipsoid apiospores with a small, inconspicuous, basal cell. However, they can be distinguished from *Digitodochium amoenum* by its comparatively shorter asci (70–110 × 6–9 μm, 90–140 × 8–12 μm vs. (170–197 × 12–14.5 μm), smaller

ascospores (12–16 × 3–5 µm, 13–18 × 4–6 µm vs. 12–13 × 21–29.6 µm) and ascospores with a thick mucilaginous sheath vs. apiospores and conspicuous, pad-like, mucilaginous, secondary appendages. Moreover, there is a morphological difference between *D. ailaoshanense* and *D. yunnanense*. The former has a J- apical ring in Melzer's reagent, while the latter has a J+ apical ring in Melzer's reagent (Voglmayr et al. 2022). The nucleotide differences between *Digitodochium ailaoshanense* and *D. yunnanense* for LSU and ITS reveal 41/835 (5%), and 52/690 (7.5%) differences respectively.

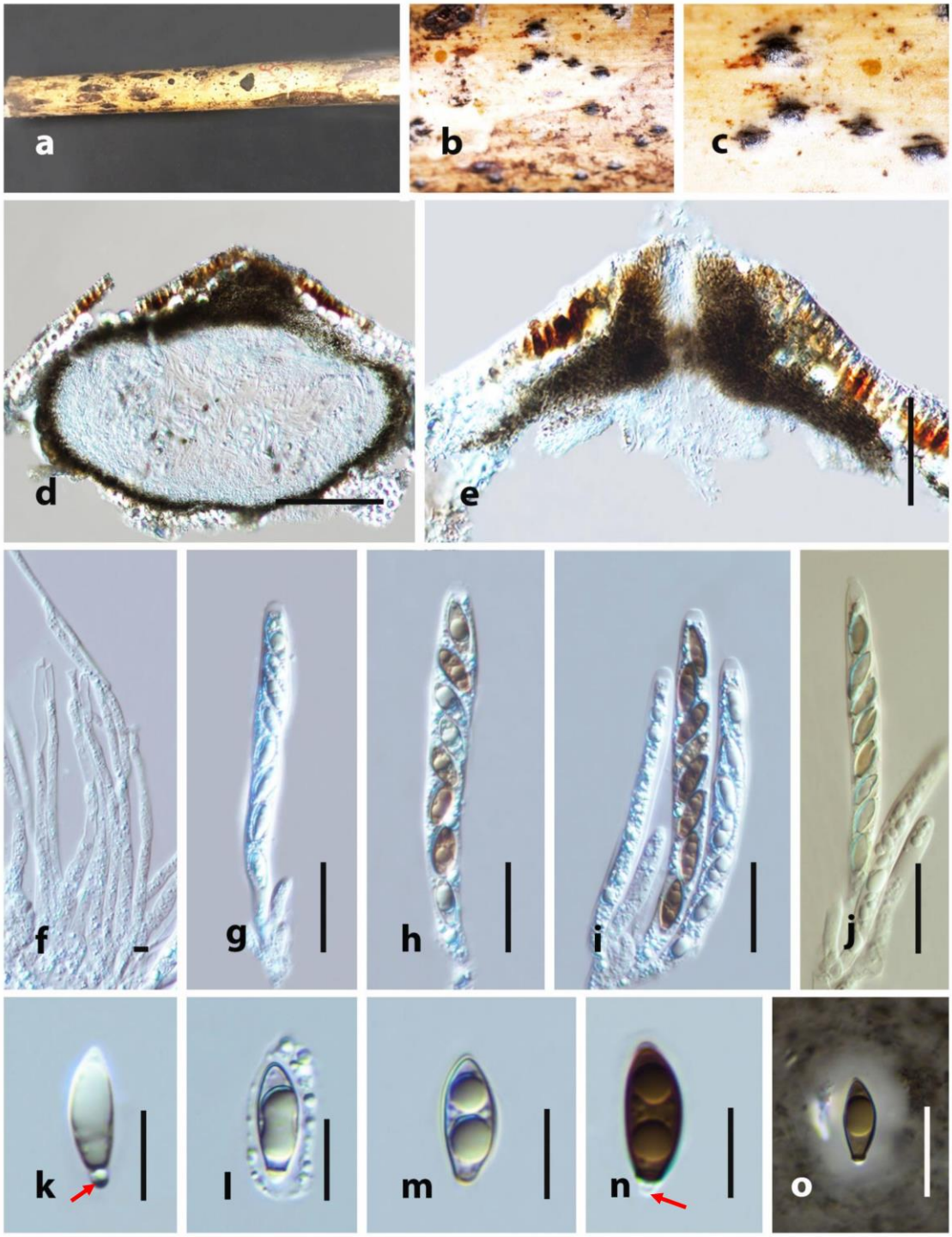

Figure 54 – *Digitodochium ailaoshanense* (HKAS 130308, holotype). a–c Ascomata on the host surface. d Vertical section of an ascoma. e Ostiole. f Paraphyses. g–j Asci (j with Melzer's reagent). k–n Ascospores (Arrows showing the basal cell). o Ascospores stain with Indian ink. Scale bars: d = 100 µm, e = 50 µm, f = 5 µm, g–j = 20 µm, k–o = 10 µm.

Digitodochium yunnanense L.S. Dissan., K.D. Hyde & J.C. Kang, sp. nov. Figs 37, 55

MycoBank number: MB850227; Facesoffungi number: FoF14922

Etymology – The specific epithet is derived from the Yunnan Province, where the holotype was collected.

Holotype – HKAS 130310

Saprobic on the dead stalk of bamboo, forming on the host surface. Sexual morph: *Ascomata* in rows, solitary, immersed, black, globose to subglobose. *Paraphyses* 2–5 μm hyaline, septate, unbranched, cellular, minutely guttulate, embedded in a gelatinous matrix. *Asci* 90–130 × 8–12 μm ($\overline{x}$ = 109 × 10 μm, n = 30), 8-spored, unitunicate, cylindrical to slightly fusiform, short-pedicellate, apically rounded, bipartite apical ring, crown-like basal part with sharp lateral rims, with a J+ apical ring in Melzer's reagent. *Ascospores* 13–18 × 4–6 μm ($\overline{x}$ = 15.3 × 5 μm, n = 30), overlapping uniseriate, apiosporous, hyaline to brown, aseptate, ellipsoid to narrowly ellipsoid, with a small basal cell, smooth-walled, mostly 2 large guttules, and thick mucilaginous sheath. Asexual morph: Undetermined.

Material examined – CHINA, Yunnan Province, Ailaoshan Forest Mountain (24.536944 N, 101.019444 E, 2500m), on dead stalk of bamboo, 14 June 2023, L.S. Dissanayake, ALLS23-11 (HKAS 130310, holotype).

GenBank accession numbers – ITS = PP584763, LSU = PP584836.

Notes – Refer the note section in *Digitodochium ailaoshanense.*

Nemania Gray, A natural arrangement of British plants 1: 516 (1821)

Notes – Gray (1821) introduced *Nemania*, which is typified by *N. serpens*. *Nemania* is a species-rich genus within Xylariaceae that encompasses endophytes, saprobes and pathogens (U'Ren et al. 2016, Daranagama et al. 2018, Wendt et al. 2018). *Nemania* are characterized by stromata that are not associated with bark rupturing structures, an absence of KOH extractable pigments, finely papillate ostioles, unitunicate cylindrical asci and ascospores with a germ slit in their sexual morph. They also have a geniculosporium-like asexual morph (Daranagama et al. 2018). We introduce *Nemania leishanensis* based on morphological and molecular data.

Nemania leishanensis S.H. Long, K.D. Hyde & Q.R. Li. sp. nov. Figs 56, 57

MycoBank number: MB850271; Facesoffungi number: FoF15711

Etymology – The specific epithet is derived from the Leishan town, where the holotype was collected.

Holotype – GMB0768

Saprobic on the surface of decaying wood of an unidentified plant. Sexual morph: *Stromata* pulvinate, attached to substrate along entire area of the base, frequently confluent, 0.3–1 mm long × 0.4–0.55 mm diameter × 0.5–0.6 mm thick, with inconspicuous perithecial mounds, carbonaceous between the perithecia, surface dull black and slightly shiny at maturity, carbonaceous, interior white, loosely fibrous to cottony; not releasing a coloured pigment in 10% KOH. *Perithecia* 300–540 μm high × 300–450 μm diameter, subglobose. *Ostioles* slightly higher than the stromatal surface, with openings slightly papillate. *Asci* 107.5–129 × 5–7.5 μm ($\overline{x}$ = 117.3 × 6.6 μm, n = 30), 8-spored, unitunicate, cylindrical, long-stipitate, spore-bearing parts 65–75 μm long, apically rounded with a J+ apical ring in Melzer's reagent, 1–2 × 1–2 μm ($\overline{x}$ = 1.8 × 1.5 μm, n = 30), tubular with a faint upper rim. *Ascospores* 9–11.5 × 4–6.5 μm ($\overline{x}$ = 10.5 × 5.2 μm, n = 30), uniseriate unicellular, slightly inequilateral, with narrowly rounded ends, light brown, smooth wall, inconspicuous or lack germ slits. Asexual morph: Undetermined.

Culture characteristics – The colony grows slowly on the PDA with a diameter of 4.5 cm after 2 weeks at 25 °C. The colony on the surface is white, thick and flat in the middle, edges are shallow, irregular bands and rosettes. Colony reverse is orange and intermediate colour darker.

Material examined – CHINA, Guizhou Province, Leishan Town, Leigongshan Nature Reserve (26.381412 N, 108.363821 E, 867 m), on branches of an unidentified plant, 7 August 2021, S. H. Long & Q. R. Li., LGS58 (GMB0768, holotype), ex-type, GMBC0768.

GenBank accession numbers – ITS = PP584764, PP584764, LSU = PP584837, PP584838, *tub*2 = PP951421, PP951422.

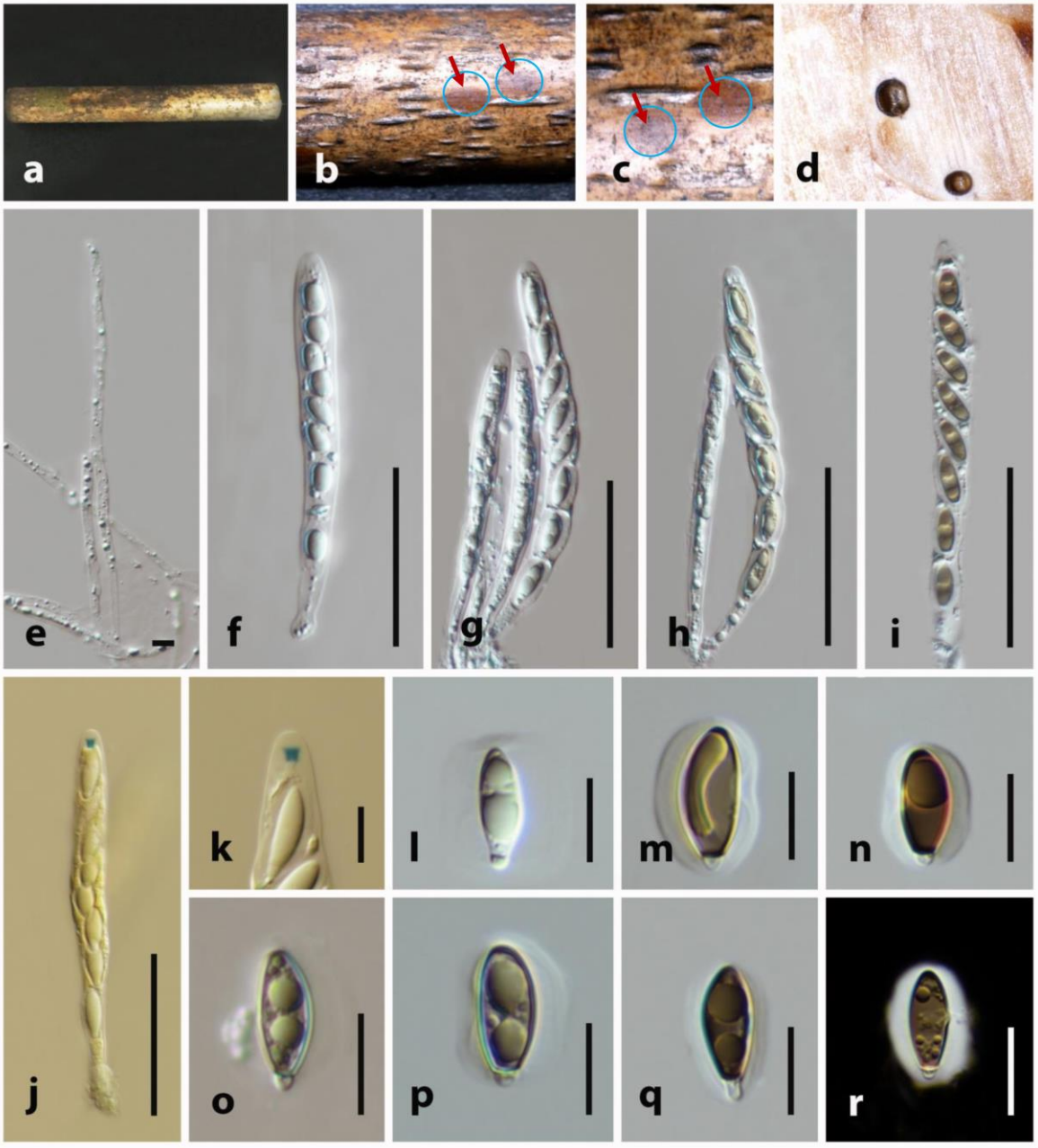

Figure 55 – *Digitodochium yunnanense* (HKAS 130310, holotype). a Host. b–d Ascomata on the host surface. (arrow showing the ascomata). e Paraphyses. f–j Asci (j. Asci in Melzer's reagent). l–q Ascospores (Apical appendages showing arrow). r Ascospore with Indian ink. Scale bars: d = 100 µm, e = 50 µm, e = 5 µm, f–j = 20 µm, k–r = 10 µm.

Notes – In the phylogenetic analysis, *Nemania leishanensis* (GMB0768) clusters proximate to *N. caries* with 100% MLB and 1.00 BYPP statistical support (Fig. 56). Yet, distinctions arise in their morphological features. Ascospores of *N. leishanensis* are devoid of germ slits, contrasting the *N. caries* ascospores which exhibit broadly rounded ends and an indistinct germ slit occupying approximately 1/4 to 1/3 of spore length. Further, the apical ring dimensions in *N. leishanensis* (1–2 × 1–2 µm) are marginally reduced relative to those in *N. caries* (2.5 × 2.5 µm) (Ju and Rogers 2002). Comparatively, *N. leishanensis* and *N. colubrina* share ascospore dimensions and exhibit narrowly tapered ends. However, the latter is discernible by its subtle, off-center germ slit (Fournier

et al. 2018). The nucleotide differences between *N. leishanensis* and *N. caries* for LSU and ITS reveal 32/825 (8.1%), 25/587 (4.3%) differences, respectively.

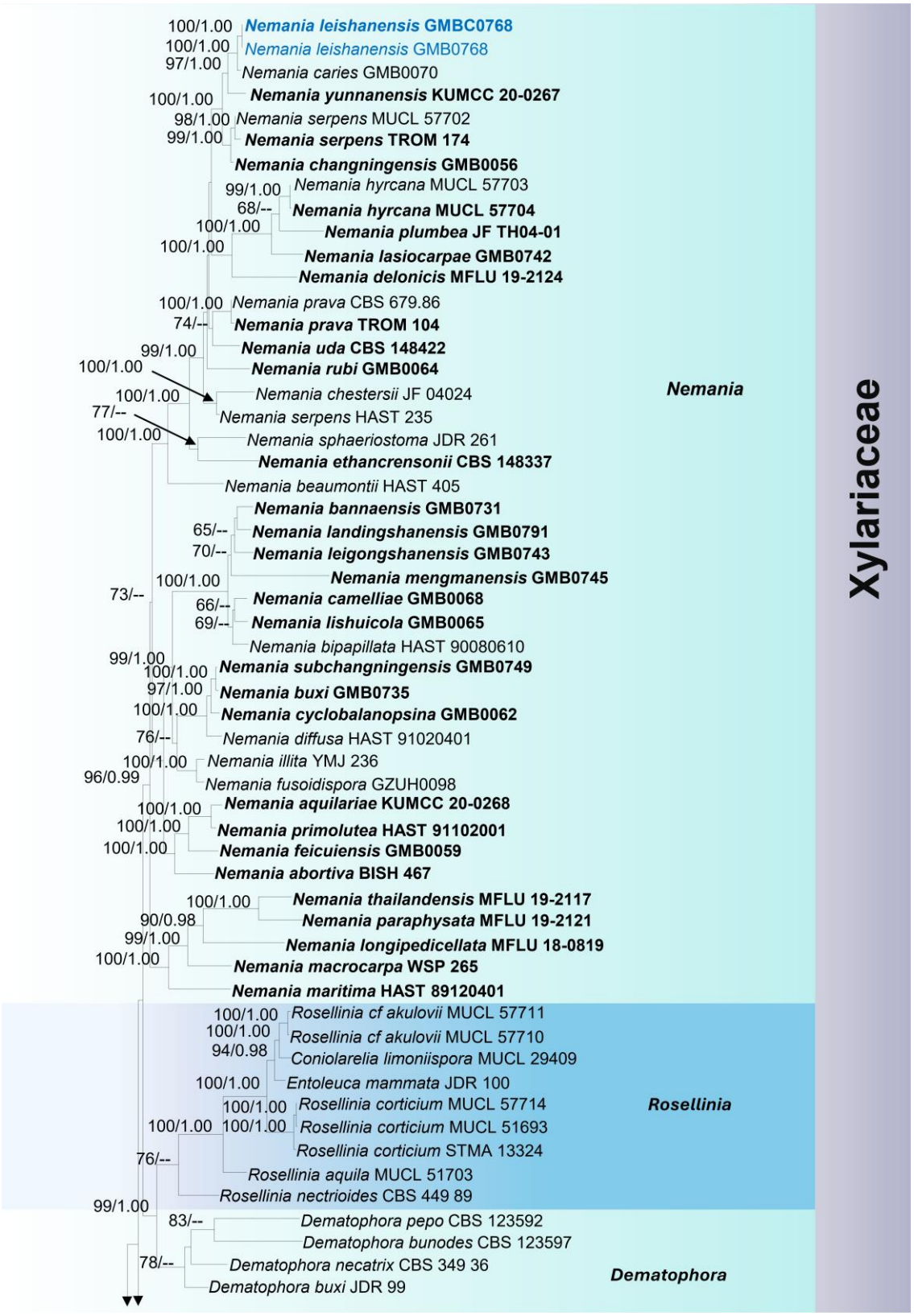

Figure 56 – RAxML phylogram generated from combined dataset of partial ITS, LSU, *rpb*2 and *tub*2 DNA sequence analyses for Xylariaceae. Final likelihood value is -58219.730356. The tree is rooted to *Biscogniauxia nummularia* (MUCL 51395), *Graphostroma platystomum* (CBS 270.87), *Hypoxylon fragiforme* (MUCL 51264) and *H. howeanum* (MUCL 47599). The matrix had 3611

distinct alignment patterns with 25.20% undetermined characters and gaps. Estimated base frequencies were; A = 0.234647, C = 0.270338, G = 0.261230, T = 0.233784 substitution rates AC = 1.632496, AG = 5.273767, AT = 1.357473, CG = 1.265651, CT = 8.468220, GT = 1.000000; gamma distribution shape parameter α = 0.803484. Newly generated sequences are in blue. Ex-type/type strains are indicated in bold.

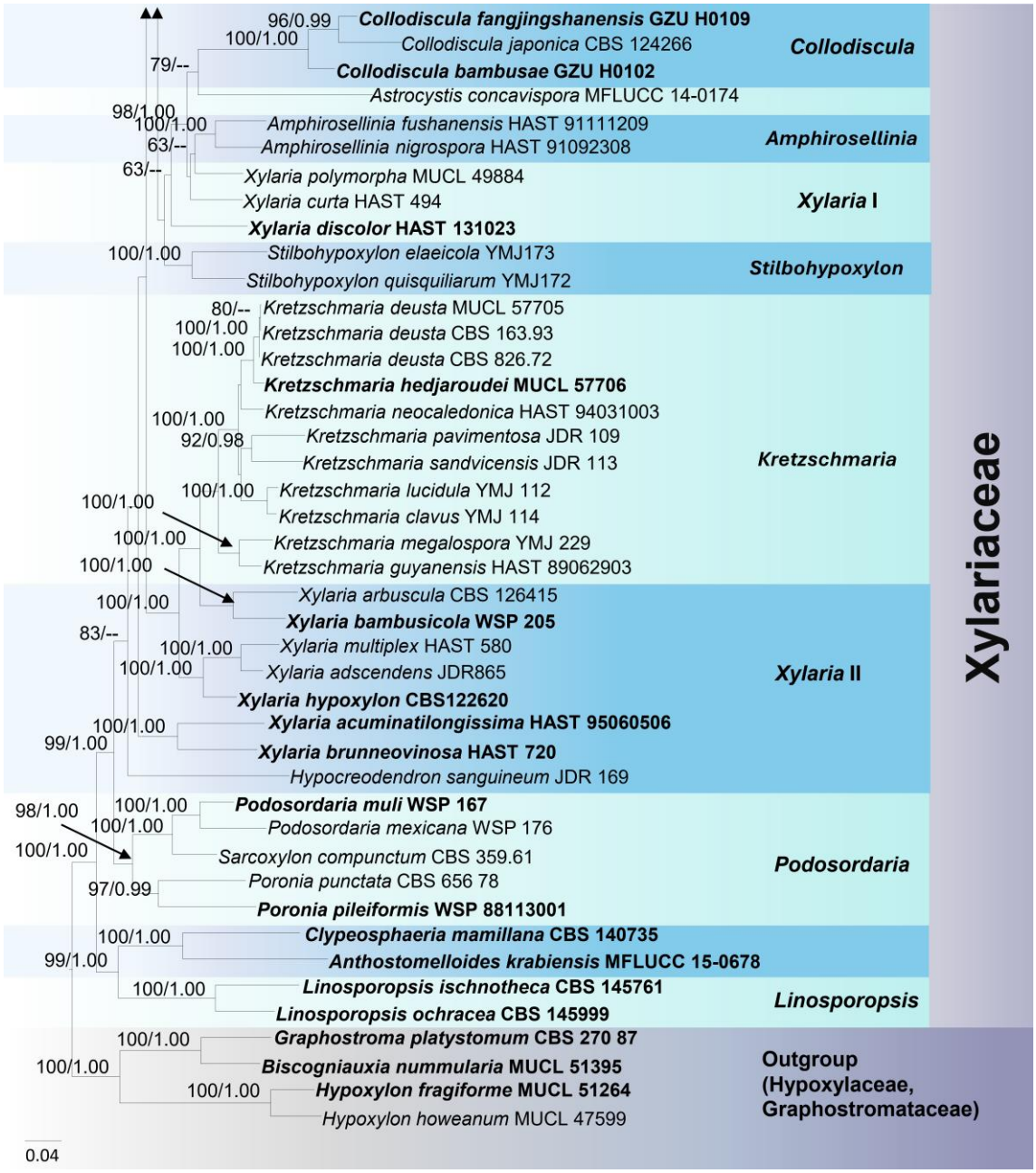

Figure 56 – Continued.

DISCUSSION

The present study deals with the taxonomy of a heterogeneous group of fungi. We refined their classification and discussed the morphological aspects and applied DNA sequence data to identify and characterize the taxa accurately. Throughout this investigation, the taxonomic details of novel species in Amphisphaeriaceae, Apiosporaceae, Appendicosporaceae, Barrmaeliaceae, Diatrypaceae, Distoseptisporaceae, Fasciatisporaceae, Hypoxylaceae, Iodosphaeriaceae, Requienellaceae, Sporocadaceae, Vamsapriyaceae and Xylariaceae were explained. A noteworthy

observation was the morphological resemblance (such as ascomata, asci and ascospore features) observed amongst members of families including Apiosporaceae, Diatrypaceae and Hypoxylaceae.

Figure 57 – *Nemania leishansis* (GMB0768, holotype). a Type material. b Stromata on the surface of host. c Transverse section of stroma. d Longitudinal section of stroma. e Pigments in 10% KOH. f Ascus apical ring (stained in Melzer's Reagent). g–j Asci with ascospores. l–n Ascospores. Scale bars: b, c = 500 μm, d = 200 μm, f–n = 10 μm.

Similar results have been reported before and even with the incorporation of DNA sequence data analysis, relationships among these groups of fungi are still obscure (Tang et al. 2009, Pinnoi et al. 2010, Daranagama et al. 2016). These similarities make it difficult to tell them apart just by appearance, both at their generic and individual species levels. Families with morphological heterogeneity among their genera (*i.e*. Sporocadaceae and Xylariaceae) can be differentiated at the genus level through characteristics of ascomata, asci, and spores. These morphological features thus hold some phylogenetic relevance. However, their reliability decreases at the species level. A more effective approach for species identification across various taxonomic levels combines multiple morphological characteristics such as the shape of ascomata, ostioles, peridium, and asci, along with variations in ascospores. To enhance accuracy, it is essential to supplement the morphological data with additional relevant information *i.e*. DNA sequence data and ecological data (Karunarathna et al. 2017, Wanasinghe et al. 2017, 2018b, Jayasiri et al. 2019).

From a phylogenetic standpoint, our study employed a broader taxonomic sampling to determine the relationships of specific genera or families relative to their neighbouring taxa. This approach resulted in a more refined topology with robust bootstrap support within our phylogenetic analyses. Of particular mention is our strategic decision to employ diverse dataset combinations to derive reliable phylogenetic interpretations. The concatenated datasets resulted in a phylogenetic topology largely consistent with the outcomes from our primary single-gene data analyses (data not shown). Even though the LSU marker is sometimes too consistent to give clear evolutionary patterns, we had to include it because of the large amount of sequence data available for this region and it has also been shown to be an appropriate phylogenetic marker at the generic level (Jeewon et al. 2003a, b, Pem et al. 2019, Xu et al. 2021, Ren et al. 2022). On the other hand, ITS1, ITS2 and certain protein markers such as *rpb*2, *tef*1-α and *tub*2 have been proven to be reliable indicators, confirming the accuracy of our species classifications (*i.e*. Apiosporaceae, Diatrypaceae, Hypoxylaceae, Sporocadaceae). However, in this study, we encountered occasional difficulties when trying to sequence these protein markers for phylogenetic analysis (for ex: *Amphisphaeria* and *Iodosphaeria*). These situations reinforce the need for a comprehensive strategy in fungal systematics research (Chethana et al. 2021).

Our study focused on exploring and documenting Xylariomycetidae species in the provinces of Guizhou, Sichuan and Yunnan in Southwestern China. The aim was to introduce these species and to provide detailed morphological descriptions supported by rigorous molecular sequence data analyses. We have integrated morphological, ecological and molecular approaches allowing for a comprehensive understanding of the studied species (Maharachchikumbura et al. 2021). The documentation of 28 new species within Xylariomycetidae and three within Sordariomycetidae emphasises the richness of fungi in these provinces, which may have been previously overlooked. The significance of our research extends beyond the acquisition of knowledge. It highlights the importance of continued exploration and research efforts in recognizing the hidden fungal diversity within different ecological niches, such as various types of dead twigs. By expanding our understanding of the fungal kingdom, we can gain insights into the intricate relationships between fungi and their ecosystems, contributing to broader ecological studies and potentially yielding practical applications in various fields.

ACKNOWLEDGEMENTS

Kang JC thanks the National Natural Science Foundation of China (NSFC grants Nos. 32170019 & 31670027) and the Open Fund Program of Engineering Research Center of Southwest Bio-Pharmaceutical resources, Ministry of Education, Guizhou University (No. gZukey 20160705). We thank CAS President's International Fellowship Initiative (number 2021FYB0005), the National Science Foundation of China (NSFC) under project code 32150410362, Smart Yunnan Project (Young Scientists) under project code E13K281261 and the Postdoctoral Fund from Human Resources and Social Security Bureau of Yunnan Province and Yunnan Department of Sciences and Technology of China (Grant No: 202101AS070045, 202205AM070007, 202302AE090023, 202303AP140001). Samarakoon MC thanks the Office of the Permanent Secretary, Ministry of

Higher Education, Science, Research and Innovation (OPS MHESI), Thailand Science Research and Innovation (TSRI). (grant no. RGNS 65-078). Dhanushka Wanasinghe and Turki Kh. Faraj gratefully acknowledge the financial support provided by the Distinguished Scientist Fellowship Program (DSFP) at King Saud University in Riyadh, Saudi Arabia. We thank the Chinese Academy of Sciences for providing molecular laboratory facilities. We would also like to thank Shaun Pennycook for checking the nomenclature. Dissanayake thanks Li Qinxian and Yuan Lingling for their help with sample collection, DNA extraction, PCR amplification and specimen and culture preservation. Yang Jianbo is thanked for his contribution to mapping the geographical elevation data.

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