

Research Article



New and notable taxa of Ascomycota on the Qinghai-Xizang Plateau and its surrounding areas: Filamentous and entomopathogenic fungi

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Received: 06 August 2025 / Accepted: 18 August 2026 / Published: 21 September 2026

Abstract

This paper represents the third installment in our series dedicated to the documentation of novel and noteworthy fungal taxa inhabiting the Qinghai-Xizang Plateau and its surrounding areas. In this study, we concentrate on filamentous and entomopathogenic fungi endemic to the Q-X Plateau, an area that has historically received limited taxonomic attention. We describe a total of 67 newly identified species classified within four classes, 19 orders, 35 families, and 52 genera of the Ascomycota. Comprehensive morphological assessments, coupled with robust phylogenetic analyses, substantiate the taxonomic identities of these newly described species, affirming their placements within the established fungal classification framework. One new genus *Zangmuomyces*, and 44 new species, viz. *Beauveria lanceolata*, *Chalara aquatica*, *Chalara guttulata*, *Cladophialophora biguttulata*, *Clonostachys habaensis*, *Cordana pohuashanensis*, *Cordana tumida*, *Cordyceps biclavata*, *Corynespora xinjiangensis*, *Dictyocheiropora luojiensis*, *Digitodochium lacustre*, *Falholtia linzhienensis*, *Fusarium highlandense*, *Helminthosporium xinjiangense*, *Hermatomyces motuoensis*, *Juncigena hyalina*, *Kernia xizangensis*, *Metarhizium luteum*, *Moelleriella yusheensis*, *Neodictyosporium lacustre*, *Ophiocordyceps fusispora*, *Ophiocordyceps hutiaoxiaensis*, *Ophiocordyceps multiseptata*, *Ophiocordyceps polyphialidica*, *Ophiocordyceps yuhongii*, *Papiliomyces aurantiacus*, *Perenicordyceps woodihabitata*, *Periconia xizangensis*, *Phaeoisaria linzhienensis*, *Phialocephala guizhouensis*, *Phialosporostilbe gaoligongensis*, *Ramophialophora ramosa*, *Samsoniella daiae*, *Savoryella submersa*, *Setophoma manglietiae*, *Simplicillium tengchongense*, *Sporidesmiella gezaensis*, *Sporidesmium fluviale*, *Stanjehughesia motuoensis*, *Thysanorea linzhienensis*, *Torula motuoensis*, *Trichoderma habaense*, *Trichoderma xinpingense* and *Zangmuomyces xizangensis* are introduced. In addition, 23 new hosts, geographical, habitat, recollected records and new combinations comprise *Acrogenospora carmichaeliana*, *Akanthomyces phariformis*, *Aquaphila albicans*, *Chloridium fuscum*, *Conioscypha aquatica*, *Corynespora yunnanensis*, *Cylindrotrichum clavatum*, *Dichotomopilus ramosissimus*, *Fusarium rubellum*, *Ilyonectria liriodendri*, *Kylindria cryptomeriae*, *Mariannaea elegans*, *Ophiocordyceps sporangifera*, *Petchia siamensis*, *Pleurocordyceps sinensis*, *Pleurocordyceps yunnanensis*, *Polycephalomyces formosus*, *Polycephalomyces tengchongensis*, *Samsoniella hepiali*, *Sporoschisma longicatenatum*, *Sterigmatobotrys uniseptatus*, and *Tetraploa hainanensis*. By providing a comprehensive checklist of fungal taxa, this paper lays the groundwork for future studies aimed at exploring the fungal diversity of the Q-X Plateau. Such research is essential for understanding the evolutionary processes that have shaped the region's biodiversity and for informing conservation strategies.

Key words: Dothideomycetes, Multi-gene, New taxa, Phylogeny, Sordariomycetes, Taxonomy

Citation: Xu, R.-J., Wang, Y.-B., Chen, B.-Z., Li, J.-N., He, S.-C., Shen, H.-W., Luo, Z.-L., Lu, Y.-Z., Ma, J., Xiao, Y.-P., Li, Y., Yang, H.-D., Zhao, Y.-W., Fan, Q., Liao, H.-F., Wei, C.-Y., Tang, M., Wang, X.-M., Yang, Z.-L., Al-Otibi, F., Hyde, K.-D., Zhao, Q. (2026) New and notable taxa of Ascomycota on the Qinghai-Xizang Plateau and its surrounding areas: Filamentous and entomopathogenic fungi. Fungal Diversity 136: 136012. <https://doi.org/10.65390/fdiv.2026.136012>

Introduction

Ascomycota is the largest and most species-rich group of fungi (Thiyagaraja et al. 2025), with approximately 111,903 known species worldwide (Catalogue of Life, August 16, 2026). Of these, around 16,474 species have been reported from China, accounting for about one-sixth of the global Ascomycota diversity (Bánki et al. 2025). Ascomycota play a pivotal role in global ecosystems, encompassing both microfungi and macrofungi, and contribute an estimated USD 54.57 trillion to the global economy (Niego et al. 2023a, b). These fungi are extensively distributed across terrestrial and aquatic environments and exhibit a diverse array of lifestyles, including saprotrophic, symbiotic, parasitic, and endophytic modes of existence (Liu et al. 2024a; Liao et al. 2025; Thiyagaraja et al. 2025). Notably, certain micro-ascomycetes are significant plant pathogens, as well as pathogens affecting animals and humans (Jayawardena et al. 2019). Notable examples include *Aspergillus fumigatus*, *Botrytis cinerea*, *Candida albicans*, *Colletotrichum gloeosporioides*, *Fusarium oxysporum*, *Magnaporthe oryzae* and *Sclerotinia sclerotiorum* (Gordon et al. 2017; Latgé & Chamilos 2019; Jayawardena et al. 2021).

The Qinghai-Xizang Plateau (abbreviated as Q-X Plateau) is bounded to the west by the Pamirs and to the north by the West Kunlun-Qilian-Altun Mountains, and gradually merges with the adjacent Qinling Mountains, Yunnan-Guizhou Plateau and lower mountains in southern Yunnan along the line of Minshan-Daxushan-Yulongshan (Wang et al. 2025b). In the Q-X Plateau, characterized by its challenging environmental conditions that restrict plant growth, fungi emerge as essential players in maintaining ecosystem balance. They contribute significantly by decomposing organic matter and recycling nutrients into the soil, thereby supporting overall ecological health (Bucher et al. 2004). Despite previous studies on fungi on the Q-X Plateau, including a number of published research papers (Wang & Zang 1983; Mao et al. 1993; Zang et al. 1996; He et al. 2024a, b, c, 2025; Xu et al. 2022, 2023, 2024a, b, c, d, e, 2025; Shen et al. 2025) and regional monographs, such as “Notes on the fungi from western Kunlun Mountains” (Zang & Xia 1989), “Economic Macrofungi of Tibet” (Mao et al. 1993), “Economic Macrofungi from Southwestern China” (Ying & Zang 1994), and different volumes of “Flora Fungorum Sinicorum” (Zang 1979, 1980, Yang 1997), the area is home to a vast variety of fungi, many of which require exploration. Therefore, we initiated the series of fungal diversity in the Q-X Plateau to publish fungal species systematically and promptly, and focused on the fungi in a special habitat, viz. macroscopic basidiomycetes in the first paper (Wang et al. 2025b), lignicolous freshwater fungi in the second paper (Xu et al. 2025). In the third paper of this series, we focus on entomopathogenic and filamentous fungi occurring in the pan Q-X Plateau.

Our investigation encompassed comprehensive fieldwork across the pan Q-X Plateau, resulting in the collection of over 14,000 specimens and samples representing diverse ascomycete taxa. By employing an integrative approach that synthesizes morphological assessments, phylogenetic analyses.

Materials and methods

Fungal specimens were collected from woody substrates, insect hosts, leaves and plant litter in terrestrial and freshwater habitats across Gansu, Guizhou, Qinghai, Sichuan, Xizang, Xinjiang and Yunnan, from 2019 to 2025. Morphological observations, macro- and microscopic photography, and isolation were conducted using the methods described by Wang et al. (2020a) and Xu et al. (2025), with necessary adaptations. Voucher specimens, ex-type cultures and living cultures were deposited in the following herbaria and culture collections. HKAS: Herbarium of Cryptogams, Kunming Institute of Botany, Chinese Academy of Sciences, China; KUMCC: Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China; KUNCC: Kunming Institute of Botany Culture Collection, China. DNA extraction was performed using both pure fungal cultures and fruiting bodies when cultures were not available. Procedures for DNA extraction, polymerase chain reaction (PCR), gel electrophoresis, and sequencing were conducted as outlined by Su et al. (2025). The sequence results generated in the study have been submitted to GenBank.

To delineate species boundaries, phylogenetic analyses were conducted using multiple methodologies. Maximum likelihood (ML) analyses were performed using RAxML-HP2 v.8.2.12 (Silvestro & Michalak 2012; Stamatakis 2014) and the CIPRES Science Gateway portal (Miller et al. 2012), while Bayesian inference (BI) analyses were conducted using MrBayes v3.1.2 (Ronquist et al. 2012), and via the same web portal as in ML. Maximum parsimony (MP) analysis was executed using PAUP* version 4.0b10 (Swofford & Sullivan 2003). Pairwise homoplasy index (PHI) tests were conducted using Split Tree software, as described by Quaedvlieg et al. (2014), to assess the level of recombination among closely related species when necessary. Species delimitation was based on an integrative taxonomic approach combining morphology and multi-gene phylogenetic analyses following the recommendations of Jeewon & Hyde (2016), Chethana et al. (2021a) and Xu et al. (2025). Newly introduced fungal species were registered with Index Fungorum (Index Fungorum, June 30, 2025) and the Faces of Fungi database (Jayasiri et al. 2015).

Results

Checklist of species

This study presents a checklist of filamentous and entomopathogenic fungi from the pan Q-X Plateau, comprising 6 classes, 42 orders, 99 families, 228 genera, and 644 species, and encompassing representative taxa from various ecological niches (Table 1). These fungi are commonly found on substrates such as decaying wood, insect carcasses, leaf litter, soil, freshwater, plant tissues and other fungi, highlighting their broad ecological adaptability in the high-altitude environment. As previous records are somewhat scattered, the taxonomy and phylogenetic placement of certain species remain to be clarified. With the increasing application of high-throughput sequencing technologies, more undocumented fungal taxa are expected to be discovered, providing fundamental data for understanding fungal diversity on the Q-X Plateau.

Table 1 Checklist of accepted freshwater fungi and entomopathogenic fungi on the Q-X Plateau.

Species	Regions	References
Dothideomycetes (9 orders) (43 families) (88 genera) (241 species)		
Botryosphaeriales (2 families)		
Botryosphaeriaceae (4 genera, 4 species)		
<i>Botryosphaeria dothidea</i> (Moug.) Ces. & De Not	Yunnan Province	Jayawardena et al. (2022)
<i>Diplodia salicicola</i> N. Jiang	Xinjiang Autonomous Region	Zhou et al. (2025)
<i>Phaeobotryon xizangense</i> N. Jiang	Xinjiang Autonomous Region	Zhou et al. (2025)
<i>Tiarosporella paludosa</i> (Sacc. & Fiori) Höhn	Yunnan Province	Luo et al. (2004)
Phyllostictaceae (1 genus) (1 species)		
<i>Phyllosticta cangshanensis</i> Z.Y. Huang, H.W. Shen & Z.L. Luo	Yunnan Province	Huang et al. (2024)
Jahnulales (1 family)		
Aliquandostipitaceae (3 genera) (7 species)		
<i>Brachiosphaera radiaticonidiosa</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Brachiosphaera tropicalis</i> Nawawi	Yunnan Province	Cai et al. (2002)
<i>Jahnula granulosa</i> K.D. Hyde & S.W. Wong	Yunnan Province	Cai et al. (2002)
<i>Jahnula poonythii</i> K.D. Hyde & S.W. Wong	Yunnan Province	Cai et al. (2002)
<i>Jahnula rostrata</i> Raja & Shearer	Yunnan Province	Dong et al. (2020)
<i>Xylomyces chlamydosporus</i> Goos, R.D. Brooks & Lamore	Yunnan Province	Luo et al. (2004)
<i>Xylomyces pusillus</i> Goh, W.H. Ho, K.D. Hyde & C.K.M. Tsui	Yunnan Province	Cai et al. (2002)
Kirschsteinioteliales (1 family)		
Kirschsteinioteliaceae (1 genus) (13 species)		
<i>Kirschsteiniotelia aethiops</i> (Sacc.) D. Hawks	Yunnan Province	Su et al. (2016b)
<i>Kirschsteiniotelia aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2018)
<i>Kirschsteiniotelia cangshanensis</i> Z.L. Luo, D.F. Bao, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2018)
<i>Kirschsteiniotelia distoseptata</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Kirschsteiniotelia dujuanhuensis</i> H.W. Shen & Z.L. Luo	Yunnan Province	Manawasinghe et al. (2024)
<i>Kirschsteiniotelia fluminicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2018)
<i>Kirschsteiniotelia linzhienensis</i> S.C. He, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	He et al. (2025)
<i>Kirschsteiniotelia longiconidiophora</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Kirschsteiniotelia mucosa</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Kirschsteiniotelia pini</i> Y. Jin, W.H. Tian & Maharachch	Yunnan Province	Wang et al. (2024b)
<i>Kirschsteiniotelia rostrata</i> J. Yang & K.D. Hyde	Yunnan Province	Bao et al. (2018)
<i>Kirschsteiniotelia submersa</i> H.Y. Su & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Kirschsteiniotelia yadongensis</i> S.C. He, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	He et al. (2025)
Microthyriales (1 family)		
Microthyriaceae (4 genera) (5 species)		
<i>Hyalobisporella drungiorum</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Hyalobisporella reniformis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Keqinzhangia aquatica</i> Z.F. Yu, M. Qiao & R.F. Castañeda	Sichuan Province	Zheng et al. (2022)
<i>Paramirandina guttulata</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024c)
<i>Triscelophorus monosporus</i> Ingold	Sichuan Province	Hu et al. (2013)
Minutisphaerales (1 family)		

Species	Regions	References
Acrogenosporaceae (1 genus) (12 species)		
<i>Acrogenospora alticampestricola</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Acrogenospora aquatica</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2020)
<i>Acrogenospora basalicellularispora</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2020)
<i>Acrogenospora carmichaeliana</i> (Berk.) Rossman & Crous	Xinjiang Autonomous Region	Xu et al. (2025)
<i>Acrogenospora ellipsoidea</i> D.M. Hu, L. Cai & K.D. Hyde	Yunnan Province	Hu et al. (2010)
<i>Acrogenospora guttulatispora</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2020)
<i>Acrogenospora obovoidispora</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2020)
<i>Acrogenospora olivaceospora</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2020)
<i>Acrogenospora submersa</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2020)
<i>Acrogenospora subprolata</i> Goh, K.D. Hyde & C.K.M. Tsui	Yunnan Province and Xizang Autonomous Region	(Bao et al. 2020; Xu et al. 2025)
<i>Acrogenospora verrucispora</i> H. Zhu, L. Cai & K.Q. Zhang	Yunnan Province	Bao et al. (2020)
<i>Acrogenospora yunnanensis</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province and Xizang Autonomous Region	(Bao et al. 2020; Xu et al. 2025)
Mycosphaerellales (1 family)		
Neodevriesiaceae (1 genus) (1 species)		
<i>Tripospermum camelopardus</i> Ingold, Dann & P.J. McDougall	Sichuan Province	Hu et al. (2013)
Natipusillales (1 family)		
Acronigrasporaceae (1 genus) (2 species)		
<i>Acronigraspora subsphaerica</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Acronigraspora zhuomulariensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
Pleosporales (35 families)		
Acrocalymmacae (1 genus) (1 species)		
<i>Acrocalymma medicaginis</i> Ingold, Dann & P.J. McDougall	Yunnan Province	Wang et al. (2024b)
Amniculicolaceae (4 genera) (8 species)		
<i>Amniculicola aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Hyde et al. (2019)
<i>Amniculicola guttulata</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Hyde et al. (2019)
<i>Amniculicola longissima</i> (Sacc. & P. Syd.) Nadeeshan & K.D. Hyde	Sichuan Province	Hu et al. (2013)
<i>Murispora aquatica</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2019b)
<i>Murispora cicognanii</i> Wanas., Camporesi, E.B.G. Jones & K.D. Hyde	Yunnan Province	Hyde et al. (2019)
<i>Murispora fagicola</i> Wanas., Camporesi, E.B.G. Jones & K.D. Hyde	Yunnan Province	Bao et al. (2019b)
<i>Pithomyces flavus</i> Berk. & Broome	Yunnan Province	Cai et al. (2002)
<i>Vargamyces aquaticus</i> (Dudka) Tóth	Xinjiang Autonomous Region	Xu et al. (2025)
Astrosphaeriellaceae (3 genera) (4 species)		
<i>Astrosphaeriella stellata</i> (Pat.) Sacc	Yunnan Province	Luo et al. (2004)
<i>Astrosphaeriella yunnanensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Triseptatospora yadongensis</i> S.C. He, Jayaward. & Q. Zhao	Xizang Autonomous Region	He et al. (2025)
<i>Xenoastrosphaeriella tornata</i> (Cooke) Jayasiri & K.D. Hyde	Yunnan Province	Cai et al. (2002)
Bambusicolaceae (1 genus) (1 species)		
<i>Bambusicola aquatica</i> W. Dong, H. Zhang & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
Caryosporaceae (1 genus) (2 species)		
<i>Caryospora aquatica</i> H. Zhang, K.D. Hyde & Ariyaw	Yunnan Province	Dong et al. (2020b)

Species	Regions	References
<i>Caryospora minima</i> Jeffers	Yunnan Province	Luo et al. (2004)
<i>Corynesporascaceae</i> (1 genus) (4 species)		
<i>Corynespora lignicola</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Hyde et al. (2020a)
<i>Corynespora submersa</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Hyde et al. (2020a)
<i>Corynespora yunnanensis</i> J.W. Liu & J. Ma	Xizang Autonomous Region	Xu et al. (2025)
<i>Corynespora xinjiangensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	This study
<i>Cryptocoryneaceae</i> (1 genus) (1 species)		
<i>Cryptocoryneum sinense</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Dictyosporiaceae</i> (9 genera) (33 species)		
<i>Aquadictyospora aquatica</i> L. Zhang & Z.L. Luo	Yunnan Province	Zhang et al. (2024b)
<i>Aquadictyospora lignicola</i> Z.L. Luo, W.L. Li, K.D. Hyde & H.Y. Su	Yunnan Province and Xizang Autonomous Region	(Li et al. 2017b; Xu et al. 2025)
<i>Aquadictyospora nujiangensis</i> S. Luan, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024c)
<i>Cheirosporium triseriale</i> L. Cai & K.D. Hyde	Yunnan Province	Cai et al. (2008)
<i>Dictyocheiropora appendiculata</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Dictyocheiropora aquadulcis</i> Sorvongxay, Boonmee & K.D. Hyde	Yunnan Province	Zhang et al. (2024b)
<i>Dictyocheiropora aquatica</i> Z.L. Luo, Bhat & K.D. Hyde	Yunnan Province	Wang et al. (2016a)
<i>Dictyocheiropora garethjonesii</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	Cai et al. (2002)
<i>Dictyocheiropora heptaspora</i> (Garov.) M.J. D'souza, Boonmee & K.D. Hyde	Yunnan Province	Wang et al. (2016a)
<i>Dictyocheiropora luojiensis</i> R.J. Xu, Q. Zhao & Boonmee	Yunnan Province	This study
<i>Dictyocheiropora multiappendiculata</i> H.W. Shen & Z.L. Luo	Yunnan Province	Shen et al. (2022)
<i>Dictyocheiropora rotunda</i> M.J. D'souza, Bhat & K.D. Hyde	Yunnan Province	(Wang et al. 2016a, 2024a; Zhang et al. 2024b)
<i>Dictyocheiropora splendida</i> Y. Wang & Z.L. Luo	Yunnan Province	Wang et al. (2025)
<i>Dictyocheiropora suae</i> H.W. Shen & Z.L. Luo	Yunnan Province	Shen et al. (2022)
<i>Dictyocheiropora taiwanense</i> Tennakoon, C.H. Kuo & K.D. Hyde	Yunnan Province	Wang et al. (2024b)
<i>Dictyocheiropora tetraploides</i> (L. Cai & K.D. Hyde) J. Yang & K.D. Hyde	Yunnan Province	Cai (2003)
<i>Dictyosporium biseriale</i> D.M. Hu, L. Cai & K.D. Hyde	Yunnan Province	Hu et al. (2010)
<i>Dictyosporium canisporum</i> L. Cai & K.D. Hyde	Yunnan Province	Cai (2003)
<i>Dictyosporium fluminicola</i> L. Zhang & Z.L. Luo	Yunnan Province	Zhang et al. (2024b)
<i>Dictyosporium lakefuxianense</i> L. Cai, K.D. Hyde & McKenzie	Yunnan Province	Cai et al. (2003)
<i>Dictyosporium polystichum</i> (Höhn.) Damon	Yunnan Province	Luo et al. (2004)
<i>Dictyosporium tetrasporum</i> L. Cai & K.D. Hyde	Yunnan Province	Cai & Hyde (2007a)
<i>Dictyosporium tubulatum</i> J. Yang, K.D. Hyde & Z.Y. Liu	Yunnan Province	Shen et al. (2022)
<i>Dictyosporium yunnanense</i> L. Cai, K.D. Hyde & McKenzie	Yunnan Province	Cai et al. (2003)
<i>Digitodesmium heptasporum</i> L. Cai & K.D. Hyde	Yunnan Province	Cai (2003)
<i>Jalapriya guttulata</i> Y. Wang & Z.L. Luo	Yunnan Province	Wang et al. (2025)
<i>Jalapriya pulchra</i> M.J. D'souza, Hong Y. Su, Z.L. Luo & K.D. Hyde	Yunnan Province	Boonmee et al. (2016)
<i>Neodigitodesmium cheirosporium</i> W. H. Tian & Maharachch	Sichuan Province	Tian et al. (2022)
<i>Pseudodictyosporium wauense</i> Matsush	Yunnan Province	Li et al. (2017b)
<i>Vikalpa dujuanhensis</i> H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Vikalpa grandispora</i> H.W. Shen, S. Boonmee & Z.L. Luo	Yunnan Province	Shen et al. (2022)

Species	Regions	References
<i>Vikalpa lignicola</i> M.J. D'souza, Bhat, Hong Y. Su & K.D. Hyde	Yunnan Province	Boonmee et al. (2016)
<i>Vikalpa sphaerica</i> H.W. Shen & Z.L. Luo	Yunnan Province	Shen et al. (2022)
<i>Hermatomyces</i> (1 genus) (2 species)		
<i>Hermatomyces hongheensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Hermatomyces motuoensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	This study
<i>Lentitheciaceae</i> (4 genera) (15 species)		
<i>Halobyssothecium aquifusiforme</i> J. Yang, J.K. Liu & K.D. Hyde	Yunnan Province	(Shen et al. 2023, Zhang et al. 2024b)
<i>Halobyssothecium cangshanense</i> (Z.L. Luo, X.J. Su & K.D. Hyde) M.S. Calabon, K.D. Hyde & E.B.G. Jones	Sichuan Province	Liu et al. (2024b)
<i>Halobyssothecium phragmitis</i> M.S. Calabon, E.B.G. Jones, S. Tibell & K.D. Hyde	Yunnan Province	Shen et al. (2023)
<i>Halobyssothecium sichuanense</i> Y. Qing & H. Zhang	Sichuan Province	Liu et al. (2024b)
<i>Halobyssothecium unicellulare</i> (Abdel-Aziz) M.S. Calabon, K.D. Hyde & E.B.G. Jones	Yunnan Province	Shen et al. (2023)
<i>Lentithecium cangshanense</i> Z.L. Luo, X.J. Su & K.D. Hyde	Yunnan Province	Su et al. (2016a)
<i>Lentithecium kunmingense</i> W. Dong, H. Zhang & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Lentithecium pseudocloninum</i> Kaz. Tanaka & K. Hiray	Yunnan Province	Shen et al. (2023)
<i>Lentithecium yunnanensis</i> W.H. Lu, Karun. & Tibpromma	Yunnan Province	Shen et al. (2023)
<i>Paralentithecium aquaticum</i> (Ying Zhang, J. Fourn. & K.D. Hyde) H.W. Shen & Z.L. Luo	Yunnan Province	Shen et al. (2023)
<i>Paralentithecium suae</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2023, 2024d)
<i>Setoseptoria arundinacea</i> (Sowerby) Kaz. Tanaka & K. Hiray	Yunnan Province	Luo et al. (2004)
<i>Setoseptoria bambusae</i> J. Yang, Jian K. Liu & K.D. Hyde	Yunnan Province	Shen et al. (2023)
<i>Setoseptoria phragmitis</i> Quaeadl., Verkley & Crous	Yunnan Province	Shen et al. (2024d)
<i>Setoseptoria suae</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2023)
<i>Lindgomycetaceae</i> (5 genera) (12 species)		
<i>Aquimassariosphaeria aquatica</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Aquimassariosphaeria kunmingensis</i> W. Dong, Doilom & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Clohesyomyces aquaticus</i> K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Hongkongmyces brunneisporus</i> D.F. Bao, Z.L. Luo & H.Y. Su	Yunnan Province	Dao et al. (2021)
<i>Hongkongmyces cylindricisporus</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Hongkongmyces fusiformis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Hongkongmyces guttulatus</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Hongkongmyces hongheensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Hongkongmyces sichuanensis</i> X.D. Yu, K.D. Hyde & Jian K. Liu	Sichuan Province	Yu et al. (2023b)
<i>Hongkongmyces yunnanensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Lindgomyces yunnanensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Liu et al. (2024b)
<i>Lolia fusiformispora</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Longirostraceae</i> (1 genus) (1 species)		
<i>Longirostrum aquaticum</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Lophiostomataceae</i> (6 genera) (8 species)		
<i>Biappendiculispora japonica</i> Thambug., Wanas., Kaz. Tanaka & K.D. Hyde	Yunnan Province	Bao et al. (2019a)
<i>Flabellascoma aquaticum</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2019a)
<i>Flabellascoma fusiforme</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2019a)

Species	Regions	References
<i>Lentistoma bipolare</i> (K.D. Hyde) A. Hashim., K. Hiray. & Kaz. Tanaka	Yunnan Province	Luo et al. (2004)
<i>Lentistoma motuoense</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Neovaginatisspora fuckelii</i> (Sacc.) A. Hashim., K. Hiray. & Kaz. Tanaka	Yunnan Province	Bao et al. (2019a)
<i>Pseudocapulatispora longiappendiculata</i> Mapook & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Sigarispora clavata</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Bao et al. (2019a)
Massarinaceae (1 genus) (3 species)		
<i>Helminthosporium aquaticum</i> H.Y. Su, Z.L. Luo & K.D. Hyde	Yunnan Province	Zhu et al. (2016)
<i>Helminthosporium velutinum</i> Link	Yunnan Province	(Zhu et al. 2016; Wang et al. 2024b)
<i>Helminthosporium xinjiangense</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xinjiang Autonomous Region	This study
Melanommataceae (1 genus) (3 species)		
<i>Camposporium appendiculatum</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Hyde et al. (2020b)
<i>Camposporium multiseptatum</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Hyde et al. (2020b)
<i>Camposporium pellucidum</i> (Grove) S. Hughes	Yunnan Province	Hyde et al. (2020b)
Morosphaeriaceae (2 genera) (7 species)		
<i>Aquihelicascus thalassioideus</i> (K.D. Hyde & Aptroot) W. Dong & H. Zhang	Yunnan Province	Luo et al. (2004)
<i>Aquihelicascus yunnanensis</i> W. Dong, H. Zhang & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Neohelicascus aquaticus</i> (H. Zhang & K.D. Hyde) W. Dong, K.D. Hyde & H. Zhang	Yunnan Province	Dong et al. (2020b)
<i>Neohelicascus elaterascus</i> (Shearer) W. Dong, K.D. Hyde & H. Zhang	Yunnan Province	(Luo et al. 2004, Wang et al. 2024b)
<i>Neohelicascus gallicus</i> (Y. Zhang & J. Fourn) W. Dong, K.D. Hyde & H. Zhang	Yunnan Province	Wang et al. (2024b)
<i>Neohelicascus submersus</i> H. Yang, W. Dong, K.D. Hyde & H. Zhang	Yunnan Province	(Dong et al. 2020b, Wang et al. 2024b)
<i>Neohelicascus uniseptatus</i> (J. Yang, J.K. Liu & K.D. Hyde) W. Dong, K.D. Hyde & H. Zhang	Yunnan Province	Wang et al. (2024b)
Nigrogranaceae (1 genus) (1 species)		
<i>Nigrograna cangshanensis</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	Tibpromma et al. (2017)
Occultibambusaceae (2 genera) (5 species)		
<i>Occultibambusa clavata</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Occultibambusa jonesii</i> J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu	Yunnan Province	Shen et al. (2024d)
<i>Occultibambusa kunmingensis</i> C.X. Liu, H. Zhang & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Occultibambusa pustula</i> D.Q. Dai & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Seriascoma didymosporum</i> Phook., D.Q. Dai, Karun. & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
Parabambusicolaceae (4 genera) (4 species)		
<i>Lonicericola qujingensis</i> D.Q. Dai, Wanas. & Wijayaw	Yunnan Province	Shen et al. (2024d)
<i>Paramonodictys dispersa</i> R.J. Xu, Q. Zhao & Boonmee	Yunnan Province	Xu et al. (2023b)
<i>Paratrimmatostroma helicosporum</i> J. Ma, H.W. Shen, K.D. Hyde & Y.Z. Lu	Yunnan Province	Ma et al. (2024)
<i>Scolecohyalosporium submersum</i> Phookamsak, Hongsanan & N. Xie	Yunnan Province	Xie et al. (2022)
Paradictyoarthrinaceae (1 genus) (1 species)		
<i>Paradictyoarthrinium hydei</i> N.G. Liu & J.K. Liu	Yunnan Province	Xu et al. (2023b)
Pararamichloridiaceae (1 genus) (1 species)		
<i>Pararamichloridium caricicola</i> Crous	Yunnan Province	Wang et al. (2024b)
Periconiaceae (1 genus) (13 species)		
<i>Periconia aquatica</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	Hyde et al. (2017)
<i>Periconia byssoides</i> Pers	Yunnan Province	Luo et al. (2004)

Species	Regions	References
<i>Periconia digitata</i> (Cooke) Sacc	Yunnan Province	Luo et al. (2004)
<i>Periconia dujuanhuensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Periconia hongheensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Periconia linzhiensis</i> S.C. He, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	He et al. (2025)
<i>Periconia minutissima</i> Corda	Yunnan Province	Luo et al. (2004)
<i>Periconia motuoensis</i> B.B. Sun, S.C. He & Q. Zhao	Xizang Autonomous Region	Sun et al. (2025)
<i>Periconia shannanensis</i> T. Cai, S. C. He, & Q. Zhao	Xizang Autonomous Region	Cai et al. (2024)
<i>Periconia submersa</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	Hyde et al. (2017)
<i>Periconia thysanolaenae</i> E.F. Yang, H.B. Jiang & Phookamsak	Yunnan Province	Wang et al. (2024b)
<i>Periconia xizangensis</i> R.J. Xu, Q. Zhao & Boonmee	Xizang Autonomous Region	This study
<i>Periconia yunnanensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
Phaeoseptaceae (2 genera) (7 species)		
<i>Catenatimuriformis sporodochialis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Pleopunctum ellipsoideum</i> N.G. Liu, K.D. Hyde & J.K. Liu	Yunnan Province	Xu et al. (2023b)
<i>Pleopunctum baoshanense</i> G.C. Ren & Tibpromma	Yunnan Province	Ren et al. (2024)
<i>Pleopunctum megalosporum</i> R.J. Xu, Q. Zhao & Boonmee	Yunnan Province	Xu et al. (2023b)
<i>Pleopunctum multicellularum</i> R.J. Xu, Q. Zhao & Boonmee	Yunnan Province	Xu et al. (2023b)
<i>Pleopunctum pseudoellipsoideum</i> N.G. Liu, K.D. Hyde & J.K. Liu	Yunnan Province	(Dong et al. 2020b; Xu et al. 2023b)
<i>Pleopunctum rotundatum</i> R.J. Xu, Q. Zhao & Boonmee	Yunnan Province	Xu et al. (2023b)
Pleomassariaceae (1 genus) (2 species)		
<i>Beverwykella grandispora</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Beverwykella pulmonaria</i> (Beverw.) Tubaki	Yunnan Province	Cai et al. (2002)
Pleomonodictydaceae (1 genus) (1 species)		
<i>Pleomonodictys capensis</i> (R.C. Sinclair, Boshoff & Eicker) Hern.-Restr., J. Mena & Gené	Xizang Autonomous Region	Bao et al. (2021)
Pleosporaceae (2 genera) (3 species)		
<i>Alternaria xizangensis</i> F. Liu, S. Song & L. Cai	Xizang Autonomous Region	Phurbu et al. (2024)
<i>Curvularia eragrostidis</i> (Henn.) J.A. Mey	Yunnan Province	Su et al. (2015)
<i>Curvularia verruculosa</i> Tandon & Bilgrami ex M.B. Ellis	Yunnan Province	Su et al. (2015)
Pseudoastrospheariellaceae (1 genus) (1 species)		
<i>Pseudoastrospheariella papillata</i> (K.D. Hyde & J. Fröhl.) Phook. & K.D. Hyde	Yunnan Province	Luo et al. (2004)
Pseudoberkleasmiaceae (1 genus) (1 species)		
<i>Pseudoberkleasmium chiangmaiense</i> Y.Z. Lu & K.D. Hyde	Yunnan Province	Bao et al. (2021)
Roussoellaceae (2 genera) (5 species)		
<i>Neorousoella bambusae</i> Phook, Jian K. Liu & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Neorousoella leucaenae</i> Jayasiri, E.B.G. Jones & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Roussoella aquatica</i> W. Dong, H. Zhang & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Roussoella dujuanhuensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Roussoella saprophytica</i> X.D. Yu & Jian K. Liu	Sichuan Province	Yu et al. (2023b)
Sporormiaceae (1 genus) (2 species)		
<i>Preussia cylindricalis</i> F. Liu, S. Song & L. Cai	Xizang Autonomous Region	Phurbu et al. (2024)
<i>Preussia sedimenticola</i> F. Liu, S. Song & L. Cai	Xizang Autonomous Region	Phurbu et al. (2024)
Teichosporaceae (1 genus) (1 species)		

Species	Regions	References
<i>Aurantiascoma xinjiangensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xinjiang Autonomous Region	Xu et al. (2025)
Tetraplophaeriaceae (6 genera) (11 species)		
<i>Neotriplosphaeria yadongensis</i> S.C. He, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	He et al. (2025)
<i>Pseudopolypliosphaeria guizhouensis</i> J.F. Zhang, Y.Y. Chen & Jian K. Liu	Sichuan Province	Yu et al. (2023b)
<i>Pseudotetraploa aquatica</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
<i>Shrungabeeja vadirajensis</i> V.G. Rao & K.A. Reddy	Yunnan Province	Zhang et al. (2019)
<i>Tetraploa aquatica</i> W.L. Li & H.Y. Su	Yunnan Province	Li et al. (2020)
<i>Tetraploa lignicola</i> J.N. Li, R.J. Xu & Y.A. Zhu	Yunnan Province	Li et al. (2023)
<i>Tetraploa linzhiensis</i> S.C. He, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	He et al. (2025)
<i>Tetraploa longiappendiculata</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Tetraploa puzheheiensis</i> W. Dong, H. Yang & H. Zhang	Yunnan Province	Dong et al. (2020b)
<i>Tetraploa yunnanensis</i> W. Dong, H. Yang & H. Zhang	Yunnan Province	Dong et al. (2020b)
<i>Triplosphaeria yunnanensis</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024d)
Torulaceae (4 genera) (25 species)		
<i>Dendryphion aquaticum</i> H.Y. Su & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Dendryphion fluminicola</i> Z.L. Luo, D.J. Bhat & K.D. Hyde	Yunnan Province	Su et al. (2018)
<i>Dendryphion hydei</i> J.F. Li, Phookamsak & Jeewon	Yunnan Province	(Boonmee et al. 2021; Wang et al. 2024b)
<i>Dendryphion nanum</i> (Nees) S. Hughes	Yunnan Province	Su et al. (2016b)
<i>Dendryphion verrucosum</i> S. Luan, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024c)
<i>Dendryphion submersum</i> Hong Y. Su & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Neotorula aquatica</i> Z.L. Luo & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Neotorula submersa</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Rostriconidium aquaticum</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Su et al. (2018)
<i>Rostriconidium cangshanensis</i> H.W. Shen, Z.L. Luo & H.Y. Su	Yunnan Province	Shen et al. (2021)
<i>Rostriconidium pandanicola</i> Tibpromma & K.D. Hyde	Yunnan Province	Shen et al. (2021)
<i>Torula aquatica</i> Z.L. Luo, K.D. Hyde, X.J. Su & H.Y. Su	Yunnan Province	Su et al. (2018)
<i>Torula dingjieensis</i> S.C. He, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	He et al. (2025)
<i>Torula yadongensis</i> S.C. He, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	He et al. (2025)
<i>Torula canangae</i> N.I. de Silva, S. Lumyong & K.D. Hyde	Yunnan Province	Wang et al. (2023)
<i>Torula chinensis</i> W.H. Tian, Y.P. Chen & Maharachch	Yunnan and Sichuan Provinces	(Tian et al. 2023; Wang et al. 2024b)
<i>Torula fici</i> P.W. Crous	Yunnan Province	(Su et al. 2018; Wang et al. 2024b)
<i>Torula gaodangensis</i> J. Yang & K.D. Hyde	Yunnan Province	Wang et al. (2024b)
<i>Torula lancangjiangensis</i> H.W. Shen, Boonmee, Z.L. Luo & K.D. Hyde	Yunnan Province	Boonmee et al. (2021)
<i>Torula luguhuensis</i> S. Luan, H.W. Shen & Z.L. Luo	Yunnan Province	Luan et al. (2023)
<i>Torula mackenziei</i> J.F. Li, Phookamsak & K.D. Hyde	Yunnan Province	(Boonmee et al. 2021; Wang et al. 2024b)
<i>Torula masonii</i> Crous	Yunnan Province	Su et al. (2018)
<i>Torula suae</i> W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2023)
<i>Torula submersa</i> W.H. Tian, Y.P. Chen & Maharachch	Yunnan and Sichuan Provinces	Wang et al. (2023, 2024a)
<i>Torula sundara</i> (Subram.) Y.R. Sun, Yong Wang bis & K.D. Hyde	Yunnan Province	(He et al. 2024; Wang et al. 2023)

Species	Regions	References
Trematosphaeriaceae (1 genus) (1 species)		
<i>Hadrospora fallax</i> (Mouton) Boise	Yunnan Province	Luo et al. (2004)
Pleosporales genera incertae sedis (2 genera) (2 species)		
<i>Ascorhombispora aquatica</i> L. Cai & K.D. Hyde	Yunnan Province	Cai & Hyde (2007b)
<i>Mangifericomes aquilariae</i> T.Y. Du, K.D. Hyde, Tibpromma & Karun.	Yunnan Province	Du et al. (2025)
Tubeufiales (2 families)		
Tubeufiaceae (10 genera) (26 species)		
<i>Aquaphila albicans</i> Goh, K.D. Hyde & W.H. Ho	Xizang Autonomous Region	This study
<i>Camporesiomyces bhatii</i> M.Y. Han & Tibpromma	Yunnan Province	Han et al. (2025)
<i>Camporesiomyces coffeae</i> M.Y. Han & Tibpromma,	Yunnan Province	Han et al. (2025)
<i>Camporesiomyces puerensis</i> M.Y. Han & Tibpromma	Yunnan Province	Han et al. (2025)
<i>Helicoma rufum</i> Y.Z. Lu, J.C. Kang & K.D. Hyde	Yunnan Province	Li et al. (2022b)
<i>Helicoma rugosum</i> (C. Booth) Boonmee & K.D. Hyde	Yunnan Province	Li et al. (2022b)
<i>Helicoma yunnanense</i> J. Ma, H.W. Shen, K.D. Hyde & Y.Z. Lu	Yunnan Province	Ma et al. (2024)
<i>Muripulchra aquatica</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2017)
<i>Neohelicomyces aquaticus</i> Z.L. Luo, Bhat & K.D. Hyde	Yunnan Province	Luo et al. (2017)
<i>Neohelicomyces dehongensis</i> H. Zhang, W. Dong & K.D. Hyde	Yunnan Province	Dong et al. (2020b)
<i>Neohelicomyces grandisporus</i> Z.L. Luo, Boonmee & K.D. Hyde	Yunnan Province	Luo et al. (2017)
<i>Neohelicomyces melaleucae</i> Crous	Yunnan Province	Ma et al. (2024)
<i>Neohelicomyces submersus</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	(Luo et al. 2017)
<i>Neohelicomyces yunnanensis</i> J. Ma, H.W. Shen, K.D. Hyde & Y.Z. Lu	Yunnan Province	Ma et al. (2024)
<i>Neohelicosporium suae</i> L.L. Li, H.W. Shen & Z.L. Luo	Yunnan Province	Li et al. (2022b)
<i>Neohelicosporium xinjiangense</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xinjiang Autonomous Region	Xu et al. (2025)
<i>Neomanoharachariella aquatica</i> L.L. Li, H.W. Shen & Z.L. Luo	Yunnan Province	Li et al. (2022b)
<i>Neomanoharachariella xizangensis</i> Y. Y. Yang & Q. Zhao	Xizang Autonomous Region	Yang et al. (2024)
<i>Parahelicomyces hyalosporus</i> (Y.Z. Lu, J.K. Liu & K.D. Hyde) S. Y. Hsieh, Goh & C. H. Kuo	Yunnan Province	Li et al. (2022b)
<i>Parahelicomyces suae</i> L.L. Li, H.W. Shen & Z.L. Luo	Yunnan Province	Li et al. (2022b)
<i>Parahelicomyces yunnanensis</i> H.W. Shen, L.L. Li, H.Y. Su & Z.L. Luo	Yunnan Province	Li et al. (2022a)
<i>Pseudohelicomyces hyalosporus</i> Y.Z. Lu, J.K. Liu & K.D. Hyde	Yunnan Province	Luo et al. (2017)
<i>Tubeufia aquatica</i> Z.L. Luo, Bhat & K.D. Hyde	Yunnan Province	Luo et al. (2017)
<i>Tubeufia cylindrothecia</i> (Seaver) Höhn	Yunnan Province	(Luo et al. 2017; Li et al. (2022b)
<i>Tubeufia nigroseptum</i> H.W. Shen, L.L. Li, H.Y. Su & Z.L. Luo	Yunnan Province	Li et al. (2022a)
Wiesneriomycetaceae (1 genus) (1 species)		
<i>Wiesneriomyces aquaticus</i> R.J. Xu, K.D. Hyde & Q. Zhao	Xizang Autonomous Region	Xu et al. (2025)
Eurotiomycetes (2 orders) (2 families) (6 genera) (22 species)		
Chaetothyriales (1 family)		
Herpotrichiellaceae (3 genera) (17 species)		
<i>Cladophialophora biguttulata</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xinjiang Autonomous Region	This study
<i>Cladophialophora kaiduensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xinjiang Autonomous Region	Xu et al. (2025)
<i>Minimelanolocus clavatus</i> Y.L. Wan, D.F. Bao & H.Y. Su	Yunnan Province	Wan et al. (2021)
<i>Minimelanolocus nujiangensis</i> Y.L. Wan, Z.L. Luo & H.Y. Su	Yunnan Province	Wan et al. (2021)

Species	Regions	References
<i>Minimelanolocus submersus</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	Hyde et al. (2016)
<i>Minimelanolocus yunnanensis</i> Q. Tian & K.D. Hyde	Yunnan Province	Tian et al. (2016)
<i>Thysanorea amniculi</i> J. Yang, Jian K. Liu & K.D. Hyde,	Xizang Autonomous Region	Xu et al. (2025)
<i>Thysanorea asiatica</i> (Hong Y. Su, Udayanga & K.D. Hyde) Hern.-Restr. & Crous	Yunnan Province	Liu et al. (2015)
<i>Thysanorea curvata</i> (Hong Y. Su, Udayanga & K.D. Hyde) Hern.-Restr. & Crous	Xizang Autonomous Region	Xu et al. (2025)
<i>Thysanorea fusiformis</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Thysanorea hyaloconidia</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Thysanorea linzhienensis</i> R.J. Xu, Q. Zhao & Boonmee	Xizang Autonomous Region	This study
<i>Thysanorea lotorum</i> (Morgan-Jones) Hern.-Restr. & Crous	Yunnan Province	Wang et al. (2024b)
<i>Thysanorea melanica</i> (H.Y. Su, Udayanga & K.D. Hyde) Hern.-Restr. & Crous	Yunnan Province	Liu et al. (2015)
<i>Thysanorea nonramosa</i> (X.D. Yu, G.N. Wang & H. Zhang) Hern.-Restr. & Crous	Yunnan Province	Wang et al. (2024b)
<i>Thysanorea obscura</i> (Matsush.) Hern.-Restr. & Crous	Yunnan Province	Liu et al. (2015)
<i>Thysanorea yunnanensis</i> Hern.-Restr. & Crous	Yunnan Province	(Liu et al. 2015; Wang et al. 2024b)
Chaetothyriales genera incertae sedis (1 genus) (2 species)		
<i>Uncispora sinensis</i> G.Z. Yang & Z.F. Yu	Yunnan Province	Yang et al. (2011)
<i>Uncispora wuzhishanensis</i> L.P. Chen & Z.F. Yu	Yunnan Province	Liu et al. (2018)
Sclerococcales (1 family)		
Dactylosporaceae (2 genera) (3 species)		
<i>Gamsomyces aquaticus</i> (W. Dong, H. Zhang & K.D. Hyde) J. Yang & K.D. Hyde	Yunnan Province	Yang et al. (2023)
<i>Gamsomyces namco</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Pseudobactrodesmium aquaticum</i> W. Dong, H. Zhang & K.D. Hyde	Yunnan Province	Dong et al. (2020a)
Leotiomycetes (3 orders) (3 families) (7 genera) (16 species)		
Helotiales (2 families)		
Discinellaceae (3 genera) (5 species)		
<i>Lemonniera aquatica</i> De Wild	Sichuan Province	Hu et al. (2013)
<i>Lemonniera terrestris</i> Tubaki	Sichuan Province	Hu et al. (2013)
<i>Tetrachaetum elegans</i> Ingold	Yunnan and Sichuan Provinces	(Yang & Ding 1986; Hu et al. 2013)
<i>Tetrachladium setigerum</i> (Grove) Ingold	Sichuan Province	Hu et al. (2013)
<i>Tetrachladium marchalianum</i> De Wild	Sichuan Province	Hu et al. (2013)
Tricladiaceae (1 genus) (1 species)		
<i>Tricladium angulatum</i> Ingold	Sichuan Province	Hu et al. (2013)
Helotiales genera incertae sedis (1 genus) (5 species)		
<i>Dactylaria hoogi</i> R.F. Castañeda & W.B. Kendr	Yunnan Province	Cai et al. (2002)
<i>Dactylaria longidentata</i> Cazau, Aramb. & Cabello	Yunnan Province	Luo et al. (2004)
<i>Dactylaria splendida</i> R.F. Castañeda & W.B. Kendr	Yunnan Province	Luo et al. (2004)
<i>Dactylaria triseptata</i> (Matsush.) R.F. Castañeda & W.B. Kendr	Yunnan Province	Luo et al. (2004)
<i>Dactylaria uniseptata</i> Matsush	Yunnan Province	Cai et al. (2002)
Leotiales genera incertae sedis (2 genera) (2 species)		
<i>Alatospora acuminata</i> Ingold	Sichuan Province	Hu et al. (2013)
<i>Flagellospora curvula</i> Ingold	Sichuan Province	Hu et al. (2013)
Thelebolales (1 family)		
Pseudeurotiaceae (1 genus) (2 species)		

Species	Regions	References
<i>Pseudeurotium desertorum</i> Mouch	Xizang Autonomous Region	Phurbu et al. (2024)
<i>Pseudeurotium sedimenticola</i> F. Liu, S. Song & L. Cai	Xizang Autonomous Region	Phurbu et al. (2024)
Orbiliomycetes (1 order) (1 family) (1 genus) (12 species)		
Orbiliales (1 family)		
Orbiliaceae (1 genus) (12 species)		
<i>Arthrobotrys cibiensis</i> F. Zhang, S. Boonmee & X.Y. Yang	Yunnan Province	Zhang et al. (2024a)
<i>Arthrobotrys dianchiensis</i> (Y. Hao & K.Q. Zhang) Z.F. Yu	Yunnan Province	Hao et al. (2004)
<i>Arthrobotrys eryuanensis</i> F. Zhang & X.Y. Yang	Yunnan Province	Zhang et al. (2022a)
<i>Arthrobotrys heihuiensis</i> F. Zhang, S. Boonmee & X.Y. Yang	Yunnan Province	Zhang et al. (2024a)
<i>Arthrobotrys jinpingensis</i> F. Zhang & X.Y. Yang	Yunnan Province	Zhang et al. (2022a)
<i>Arthrobotrys jinshaensis</i> F. Zhang, S. Boonmee & X.Y. Yang	Yunnan Province	Zhang et al. (2024a)
<i>Arthrobotrys lanpingensis</i> F. Zhang & X.Y. Yang	Yunnan Province	Zhang et al. (2022a)
<i>Arthrobotrys luquanensis</i> F. Zhang & X.Y. Yang	Yunnan Province	Zhang et al. (2022a)
<i>Arthrobotrys tachengensis</i> F. Zhang & X.Y. Yang	Yunnan Province	Manawasinghe et al. (2024)
<i>Arthrobotrys yangbiensis</i> F. Zhang, S. Boonmee & X.Y. Yang	Yunnan Province	Zhang et al. (2024a)
<i>Arthrobotrys yangjiangensis</i> F. Zhang, S. Boonmee & X.Y. Yang	Yunnan Province	Zhang et al. (2024a)
<i>Arthrobotrys zhaoyangensis</i> F. Zhang & X.Y. Yang	Yunnan Province	Zhang et al. (2022a)
Pezizomycetes (1 order) (1 family) (1 genus) (1 species)		
Pezizales (1 family)		
Pezizaceae (1 genus) (1 species)		
<i>Aquapeziza globispora</i> D.M. Hu, L. Cai & K.D. Hyde	Yunnan Province	Hu et al. (2012c)
Sordariomycetes (26 orders) (48 families) (122 genera) (352 species)		
Amphisphaeriales (2 families)		
Amphisphaeriaceae (2 genera) (2 species)		
<i>Amphisphaeria hongheensis</i> R.M. Liu & Karun.	Yunnan Province	Liu et al. (2024b)
<i>Arthrimum aquaticum</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
Sporocadaceae (2 genera) (2 species)		
<i>Hymenoplella lakefuxianensis</i> (L. Cai, Jeewon & K.D. Hyde) F. Liu, L. Cai & Crous	Yunnan Province	Jeewon et al. (2003)
<i>Seiridium aquaticum</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
Annulatascales (1 family)		
Annulatascaceae (3 genera) (4 species)		
<i>Annulatascus fusiformis</i> K.D. Hyde & S.W. Wong	Yunnan Province	Cai et al. (2006)
<i>Annulatascus menglensis</i> D.M. Hu, L. Cai & K.D. Hyde	Yunnan Province	Hu et al. (2012a)
<i>Aqualignicola vaginata</i> D.M. Hu, L. Cai & K.D. Hyde	Yunnan Province	Hu et al. (2012a)
<i>Clohiesia curvispora</i> L. Cai & K.D. Hyde	Yunnan Province	Cai & Hyde (2007c)
Atractosporales (1 family)		
Atractosporaceae (1 genus) (2 species)		
<i>Atractospora aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Atractospora ellipsoidea</i> (W.H. Ho, C.K.M. Tsui, Hodgkiss & K.D. Hyde) Réblová & J. Fourn.	Yunnan Province	Dong et al. (2021)
Barbatosphaeriales (1 family)		
Barbatosphaeriaceae (2 genera) (2 species)		
<i>Appendopyricularia guttulata</i> Y. Wang, H.W. Sheng & Z.L. Luo	Yunnan Province	Wang et al. (2024b)

Species	Regions	References
<i>Barbatosphaeria lignicola</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2019)
Chaetosphaeriales (2 families)		
Chaetosphaeriaceae (12 genera) (34 species)		
<i>Anacraspedodidymum submersum</i> Z.F. Yu & R.F. Castañeda	Yunnan Province	Zheng et al. (2021)
<i>Chaetosphaeria aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Chaetosphaeria aseptata</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Chaetosphaeria catenulata</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Chaetosphaeria cubensis</i> Hol.-Jech	Yunnan Province	Luo et al. (2019)
<i>Chaetosphaeria guttulata</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Chaetosphaeria myriocarpa</i> (Fr.) C. Booth	Yunnan Province	Luo et al. (2019)
<i>Chaetosphaeria submersa</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Chloridium fuscum</i> (Corda) Réblová & Hern.-Restr	Xizang Autonomous Region	This study
<i>Chloridium gonytrichii</i> (F.A. Fernández & Huhndorf) Réblová & Seifert	Yunnan Province	Luo et al. (2019)
<i>Codinaea yunnanensis</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Cylindrotrichum clavatum</i> W. Gams	Yunnan Province and Xizang Autonomous Region	(Maharachchikumbura et al. 2018; This study)
<i>Cylindrotrichum gorii</i> Lunghini	Yunnan Province	Maharachchikumbura et al. (2018)
<i>Cylindrotrichum submersum</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2019)
<i>Dematiosporium aquaticum</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Dictyochaeta cangshanensis</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Dictyochaeta ellipsoidea</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Dictyochaeta lignicola</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2019)
<i>Dictyochaeta submersa</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Exserticlava yunnanensis</i> L. Cai & K.D. Hyde	Yunnan Province	Cai & Hyde (2007b)
<i>Falholtia linzhiensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	This study
<i>Sporoschisma chiangraiense</i> N.G. Liu & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Sporoschisma hemipsilum</i> (Berk. & Broome) Zelski, A.N. Mill. & Shearer	Yunnan Province and Xizang Autonomous Region	(Luo et al. 2016; Xu et al. 2025)
<i>Sporoschisma hyalomucilaginosum</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Sporoschisma juvenile</i> Boud	Yunnan Province	Luo et al. (2019)
<i>Sporoschisma lignicola</i> R.J. Xu & Q. Zhao	Yunnan Province	Xu et al. (2024f)
<i>Sporoschisma longicatenatum</i> J. Yang, Jian K. Liu & K.D. Hyde	Xizang Autonomous Region	This study
<i>Sporoschisma mirabile</i> Berk. & Broome	Yunnan Province and Xizang Autonomous Region	(Luo et al. 2016; Xu et al. 2025)
<i>Sporoschisma nigroseptatum</i> D. Rao & P.Rag. Rao	Yunnan Province	Luo et al. (2016)
<i>Sporoschisma phaeocentron</i> W.H. Ho, K.D. Hyde & Goh	Yunnan Province	Luo et al. (2016)
<i>Sporoschisma taitense</i> (Mugambi & Huhndorf) A.N. Mill	Yunnan Province	Luo et al. (2016)
<i>Sporoschisma verruculosa</i> R.J. Xu & Q. Zhao	Xizang Autonomous Region	Xu et al. (2024f)
<i>Stanjehughesia motuoensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	This study
<i>Tainosphaeria lunata</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
Helminthosphaeriaceae (1 genus) (1 species)		
<i>Hilberina breviseta</i> (P. Karst.) Huhndorf & A.N. Mill	Yunnan Province	Luo et al. (2004)
Reticulascaceae (1 genus) (2 species)		

Species	Regions	References
<i>Kylindria aquatica</i> Z.L. Luo, Maharachch. & Cheew	Yunnan Province	Maharachchikumbura et al. (2018)
<i>Kylindria chinensis</i> Maharachch., H.Y. Su & Cheewangkoon	Yunnan Province	Maharachchikumbura et al. (2018)
Coniochaetales (1 family)		
Cordanaceae (1 genus) (8 species)		
<i>Cordana aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Cordana crassa</i> Tóth	Xizang Autonomous Region	Xu et al. (2025)
<i>Cordana lignicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Cordana linzhienensis</i> R.J. Xu, Boonmee & Q. Zhao	Xizang Autonomous Region	Xu et al. (2024f)
<i>Cordana reniformis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Cordana terrestris</i> (Timonin) Hern.-Restr., Gené & Guarro	Yunnan Province	Luo et al. (2019)
<i>Cordana tumida</i> R.J. Xu, Q. Zhao, K.D. Hyde & S. Boonmee	Xizang Autonomous Region	This study
<i>Cordana uniseptata</i> L. Cai, McKenzie & K.D. Hyde	Yunnan Province	Cai (2004)
Conioscyphales (1 family)		
Conioscyphaceae (1 genus) (9 species)		
<i>Conioscypha aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province and Xizang Autonomous Region	(Luo et al. 2019; This study)
<i>Conioscypha breviconiophora</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Conioscypha motuoensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Conioscypha punctiformis</i> H.W. Shen, Y.R. Sun & K.D. Hyde	Yunnan Province	Liu et al. (2024a)
<i>Conioscypha reniformis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Conioscypha subglobosa</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Conioscypha submersa</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Conioscypha xizangensis</i> R.J. Xu, Boonmee & Q. Zhao	Xizang Autonomous Region	Xu et al. (2024e)
<i>Conioscypha yunnanensis</i> L. Li, Bhat & Phookamsak	Yunnan Province	Xu et al. (2024e)
Conlariales (1 family)		
Conlariaceae (1 genus) (4 species)		
<i>Conlarium aquaticum</i> W. Dong, H. Zhang & K.D. Hyde	Yunnan Province	Dong et al. (2021)
<i>Conlarium multiseptatum</i> H.W. Shen, Z.L. Luo & K.D. Hyde	Yunnan Province	Hyde et al. (2024b)
<i>Conlarium sichuanense</i> T. Zhang & J. K. Liu	Yunnan Province	Hyde et al. (2024b)
<i>Conlarium yunnanense</i> H.W. Shen, Z.L. Luo & K.D. Hyde	Yunnan Province	Hyde et al. (2024b)
Coronophorales genera incertae sedis (1 genus) (1 species)		
<i>Papulaspora sepedonioides</i> Preuss	Yunnan Province	Cai et al. (2006)
Diaporthales (2 families)		
Diaporthaceae (1 genus) (2 species)		
<i>Diaporthe alnicola</i> Ning Jiang	Xizang Autonomous Region	Li et al. (2025)
<i>Diaporthe linzhienensis</i> Ning Jiang	Xizang Autonomous Region	Li et al. (2025)
Lamproconiaceae (1 genus) (1 species)		
<i>Zangia xizangensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	This study
Distoseptisporales (2 families)		
Aquapteridosporaceae (1 genus) (4 species)		
<i>Aquapteridospora fusiformis</i> Z.L. Luo, D.F. Bao, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2019)
<i>Aquapteridospora linzhienensis</i> R.J. Xu, Q. Zhao & Boonmee	Xizang Autonomous Region	Xu et al. (2025)

Species	Regions	References
<i>Aquapteridospora submersa</i> R.J. Xu, Q. Zhao & Boonmee	Xizang Autonomous Region	Xu et al. (2024d)
<i>Aquapteridospora yadongensis</i> R.J. Xu, Q. Zhao & Boonmee	Xizang Autonomous Region	Xu et al. (2024d)
<i>Distoseptisporaceae</i> (1 genus) (27 species)		
<i>Distoseptispora aqualignicola</i> C.X. Li & H. Zhang	Sichuan Province	Zhang et al. (2022b)
<i>Distoseptispora aquamyces</i> R. Zhu & H. Zhang	Sichuan Province	Zhang et al. (2022b)
<i>Distoseptispora aquatica</i> Z.L. Luo, Hong Y. Su & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Distoseptispora aquisubtropica</i> J. Ma & Y.Z. Lu	Xizang Autonomous Region	Xu et al. (2025)
<i>Distoseptispora bambusae</i> Y.R. Sun, I.D. Goonasekara, Yong Wang bis & K.D. Hyde	Sichuan Province	Zhang et al. (2022b)
<i>Distoseptispora bambusicola</i> X. Tang, Jayaward., J.C. Kang & K.D. Hyde	Sichuan Province	Xu et al. (2025)
<i>Distoseptispora cangshanensis</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2018b)
<i>Distoseptispora clematidis</i> Phukhams., M.V. de Bult & K.D. Hyde	Yunnan Province	Zhang et al. (2022b)
<i>Distoseptispora crassisporea</i> R. Zhu & H. Zhang	Yunnan Province	Zhang et al. (2022b)
<i>Distoseptispora curvularia</i> R. Zhu & H. Zhang	Yunnan Province	Zhang et al. (2022b)
<i>Distoseptispora cylindricospora</i> D.F. Bao, Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Phukhamsakda et al. (2022)
<i>Distoseptispora euseptata</i> W.L. Li, H.Y. Su & Jian K. Liu	Yunnan Province	Li et al. (2021)
<i>Distoseptispora fluminicola</i> McKenzie, Hong Y. Su, Z.L. Luo & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Distoseptispora gasaensis</i> Y.F. Hu & J. Ma	Yunnan Province	Hu et al. (2023)
<i>Distoseptispora longisporea</i> H.Y. Song & D.M. Hu	Yunnan Province	Song et al. (2020)
<i>Distoseptispora menghaiensis</i> Y.F. Hu & Jian Ma	Yunnan Province	Hu et al. (2023)
<i>Distoseptispora motuoensis</i> J.N. Li, R.J. Xu, Q. Zhao & Y.A. Zhu	Xizang Autonomous Region	Li et al. (2024a)
<i>Distoseptispora nonrostrata</i> Y. Qing & H. Zhang	Sichuan Province	Zhang et al. (2022b)
<i>Distoseptispora obpyriformis</i> Z.L. Luo & H.Y. Su	Yunnan Province	Dong et al. (2021)
<i>Distoseptispora pachyconidia</i> R. Zhu & H. Zhang	Yunnan Province	Zhang et al. (2022b)
<i>Distoseptispora rostrata</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	(Luo et al. 2018b; Wang et al. 2024b)
<i>Distoseptispora suae</i> H.W. Shen & Z.L. Luo	Yunnan Province	Shen et al. (2024a)
<i>Distoseptispora submersa</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2018b)
<i>Distoseptispora suoluensis</i> J. Yang, Maharachch. & K.D. Hyde	Yunnan Province	Luo et al. (2018b)
<i>Distoseptispora tectonae</i> Doilom & K.D. Hyde	Yunnan and Sichuan Provinces	(Zhang et al. 2022b; Wang et al. 2024b)
<i>Distoseptispora xipingensis</i> H.W. Shen & Z.L. Luo	Yunnan Province	Shen et al. (2024a)
<i>Distoseptispora yunnanensis</i> W.L. Li, H.Y. Su & Jian K. Liu	Yunnan Province	Li et al. (2021)
<i>Fuscosporellales</i> (1 family)		
<i>Fuscosporellaceae</i> (6 genera) (7 species)		
<i>Bactrodesmiastrum pyriforme</i> Hern. -Restr., J. Mena, Gené & Guarro	Xizang Autonomous Region	Xu et al. (2025)
<i>Fuscosporella xingyiensis</i> X. Xu, Q.R. Li, Y.Q. Kang & Wijayaw	Xizang Autonomous Region	Xu et al. (2025)
<i>Mucispora hydei</i> Wijayaw., Q.R. Li, Y.C. Deng, L.S. Dissan. & D.Q. Dai	Xizang Autonomous Region	Xu et al. (2025)
<i>Parafuscosporella menglensis</i> D.M. Hu, L. Cai & K.D. Hyde	Yunnan Province	Hu et al. (2010)
<i>Pseudoascotaiwania aquatica</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Vanakripa chiangmaiensis</i> X.G. Tian & Karun	Xizang Autonomous Region	Xu et al. (2025)
<i>Vanakripa mucosa</i> (Jing Yang, Bhat & K.D. Hyde) Goh, S.Y. Hsieh, C.H. Kuo	Xizang Autonomous Region	Xu et al. (2025)
<i>Hypocreales</i> (9 families)		
<i>Bionectriaceae</i> (4 genera) (9 species)		
<i>Clonostachys aquatica</i> D.F. Bao, Z.L. Luo & K.D. Hyde	Yunnan Province	Bao et al. (2023a)

Species	Regions	References
<i>Clonostachys habaensis</i> Y.B. Wang, B.Z. Chen, F. Xiong, & Zhu L. Yang	Yunnan Province	This study
<i>Clonostachys linzhiensis</i> S.C. He, K.D. Hyde & Q. Zhao	Xizang Autonomous Region	He et al. (2025)
<i>Clonostachys motuoensis</i> S.C. He, K.D. Hyde & Q. Zhao	Xizang Autonomous Region	He et al. (2025)
<i>Clonostachys rosea</i> (Link) Schroers, Samuels, Seifert & W. Gams	Yunnan Province	Bao et al. (2023a)
<i>Clonostachys yadongensis</i> S.C. He, K.D. Hyde & Q. Zhao	Xizang Autonomous Region	He et al. (2025)
<i>Emericellopsis ovoidea</i> F. Liu, S. Song & L. Cai	Xizang Autonomous Region	Phurbu et al. (2024)
<i>Fusariella sarniensis</i> M.B. Ellis	Gansu Province	Hu et al. (2013)
<i>Glomastix masseei</i> (Sacc.) Matsush	Yunnan Province	Bao et al. (2023a)
Clavicipitaceae (3 genera) (3 species)		
<i>Metarhizium luteum</i> Y.B. Wang, C.Y. Wei, B.Z. Chen, & Zhu L. Yang	Yunnan Province	This study
<i>Papiliomyces aurantiacus</i> Y.B. Wang, C.Y. Wei, B.Z. Chen & Zhu L. Yang	Yunnan Province	This study
<i>Petchia siamensis</i> Thanakitp., Mongkols. & Luangsa-ard	Yunnan Province	This study
Cordycipitaceae (5 genera) (11 species)		
<i>Akanthomyces phariformis</i> Khons., Thanakitp. & Luangsa-ard	Yunnan Province	This study
<i>Akanthomyces zaquensis</i> Y.Hui Wang, W.J. Wang, Ke Wang, C.H. Dong, J.R. Hao, P.M. Kirk & Y.J. Yao	Qinghai Province	Wang et al. (2023)
<i>Beauveria lanceolata</i> Y.B. Wang, B.Z. Chen & Zhu L. Yang	Yunnan Province	This study
<i>Beauveria medogensis</i> Imoulan & Y.J. Yao	Xizang Autonomous Region	Imoulan et al. (2016)
<i>Cordyceps biclavata</i> Y.B. Wang, B.Z. Chen, M. Tang & Zhu L. Yang	Yunnan Province	This study
<i>Cordyceps subtenuipes</i> H. Yu, Y.B. Wang, Y. Wang, D.E. Duan & Zhu L. Yang	Yunnan Province	Wang et al. (2020a)
<i>Samsoniella alpina</i> H. Yu, Y.B. Wang, Y. Wang & Zhu L. Yang	Yunnan Province	Wang et al. (2020a)
<i>Samsoniella daiae</i> Y.B. Wang, B.Z. Chen, M. Tang & Zhu L. Yang sp. nov.	Yunnan Province	This study
<i>Samsoniella hepiali</i> (Q.T. Chen & R.Q. Dai ex R.Q. Dai, X.M. Li, A.J. Shao, Shu F. Lin, J.L. Lan, Wei H. Chen & C.Y. Shen) H. Yu, R.Q. Dai, Y.B. Wang, Y. Wang & Zhu L. Yang	Yunnan Province	Wang et al. (2020a); This study
<i>Samsoniella yunnanensis</i> H. Yu, Y.B. Wang, Y. Wang, D.E. Duan & Zhu L. Yang	Yunnan Province	Wang et al. (2020a)
<i>Simplicillium tengchongense</i> Y.B. Wang, B.Z. Chen, M. Tang & Zhu L. Yang	Yunnan Province	This study
Hypocreaceae (1 genus) (2 species)		
<i>Trichoderma habaense</i> Y.B. Wang, B.Z. Chen & Zhu L. Yang	Yunnan Province	This study
<i>Trichoderma xinpingense</i> Y.B. Wang, B.Z. Chen & Zhu L. Yang	Yunnan Province	This study
Nectriaceae (15 genera) (71 species)		
<i>Aquanectria jacinthicolor</i> S.K. Huang, R. Jeewon & K.D. Hyde	Yunnan Province	Huang et al. (2018)
<i>Aquanectria penicillioides</i> (Ingold) L. Lombard & Crous	Yunnan Province	(Luo et al. 2019, Bao et al. 2023a)
<i>Atractium fusiformis</i> D.F. Bao, K.D. Hyde & Z.L. Luo	Yunnan Province	Bao et al. (2023a)
<i>Chaetopsina beijingensis</i> Crous & Y. Zhang ter	Yunnan Province	Luo et al. (2019)
<i>Chaetopsina motuoensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Chaetopsina penicillata</i> Samuels	Yunnan Province	Bao et al. (2023a)
<i>Cosmospora aquatica</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province, Xizang Autonomous Region	Luo et al. (2019), Zhao et al. (2025)
<i>Cosmospora butyri</i> (J.F.H. Beyma) Gräfenhan, Seifert & Schroers	Xizang Autonomous Region	Zhao et al. (2025)
<i>Cosmospora cylindricospora</i> D.F. Bao, K.D. Hyde & Z.L. Luo	Yunnan Province	Bao et al. (2023a)
<i>Cosmospora fomiticola</i> C.S. Herrera & P. Chaverri	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium altiplanum</i> Y.B. Wang, B.Z. Chen, Q. Fan & Zhu L. Yang	Yunnan Province	This study
<i>Fusarium acuminatum</i> Ellis & Everh.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium amerosporum</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)

Species	Regions	References
<i>Fusarium annulatum</i> Bugnic.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium asiaticum</i> O'Donnell, T. Aoki, Kistler & Geiser	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium avenaceum</i> (Fr.) Sacc.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium cerealis</i> (Cooke) Sacc.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium citri</i> M.M. Wang, Qian Chen & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium clavus</i> J.W. Xia, L. Lombard, Sand.-Den., X.G. Zhang & Crous	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium commune</i> K. Skovg., O'Donnell & Nirenberg	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium equiseti</i> (Corda) Sacc.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium fecundum</i> S.L. Han, M.M. Wang & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium flocciferum</i> Corda	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium fujikuroi</i> Nirenberg	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium gamsii</i> Torbati, Arzanlou & Sand.-Den.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium hydei</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium iranicum</i> Torbati, Arzanlou & Sand.-Den.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium kangmaense</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium kyushuense</i> O'Donnell & T. Aoki	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium medogense</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium meridionale</i> T. Aoki, Kistler, Geiser & O'Donnell	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium microsporellum</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium nedongense</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium neoequiseti</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium nyingchiense</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium odoratissimum</i> Maryani, L. Lombard, Kema & Crous	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium paeoniae</i> M.M. Wang & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium paraclavum</i> S.L. Han & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium purangense</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium redolens</i> Wollenw.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium rubellum</i> P. Zhao & L. Cai	Qinghai Province, Xizang Autonomous Region	Zhao et al. (2025); This study
<i>Fusarium scabridum</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium shigatseense</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium sympodiale</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium taii</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium toxicum</i> L. Lombard & J.W. Xia	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusarium wereldwysianum</i> Crous & Sand.-Den.	Xizang Autonomous Region	Zhao et al. (2025)
<i>Fusicolla acetilerea</i> (Tubaki, C. Booth & T. Harada) Gräfenhan & Seifert	Xizang Autonomous Region	Zhao et al. (2025)
<i>Gliocladiopsis tenuis</i> (Bugnic.) Crous & M.J. Wingf	Yunnan Province	Bao et al. (2023a)
<i>Ilyonectria liriodendri</i> (Halleen, Rego & Crous) P. Chaverri & Salgado	Xizang Autonomous Region	This study
<i>Mariannaea cinerea</i> D.M. Hu & L. Cai	Yunnan Province	Hu et al. (2017)
<i>Mariannaea dimorpha</i> Z.Q. Zeng & W.Y. Zhuang	Yunnan Province	Bao et al. (2023a)
<i>Mariannaea elegans</i> (Corda) Samson	Yunnan Province	This study
<i>Mariannaea samuelsii</i> Seifert & Bissett	Yunnan Province	Luo et al. (2019)
<i>Mariannaea suae</i> D.F. Bao, K.D. Hyde & Z.L. Luo	Yunnan Province	Bao et al. (2023a)
<i>Mariannaea superimposita</i> (Matsush.) Samuels	Yunnan Province	(Luo et al. 2019; Bao et al. 2023a)

Species	Regions	References
<i>Mariannaea yunnanensis</i> D.F. Bao, K.D. Hyde & Z.L. Luo	Yunnan Province	Bao et al. (2023a)
<i>Neocosmospora aquatica</i> D.F. Bao, K.D. Hyde & Z.L. Luo	Yunnan Province	Bao et al. (2023a)
<i>Neocosmospora brevis</i> Sand.-Den. & Crous	Yunnan Province	Bao et al. (2023a)
<i>Neocosmospora solani</i> (Mart.) L. Lombard & Crous	Xizang Autonomous Region	Zhao et al. (2025)
<i>Neocosmospora stercicola</i> Šišić, Al-Hatmi, Baćanović-Šišić, S.A. Ahmed & Finckh) Sand.-Den. & Crous	Xizang Autonomous Region	Zhao et al. (2025)
<i>Neocosmospora tonkinensis</i> (Bugnic.) Sand.-Den. & Crous	Xizang Autonomous Region	Zhao et al. (2025)
<i>Neocosmospora xizangensis</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Neonectria aquatica</i> D.F. Bao, K.D. Hyde & Z.L. Luo	Yunnan Province	Bao et al. (2023a)
<i>Neonectria borealis</i> Spetik, Eichmeier & Gramaje		
<i>Paracremonium binnewijzendii</i> Houbraken, van der Kleij & L. Lombard	Yunnan Province	(Luo et al. 2019; Bao et al. 2023a)
<i>Paraniesslia aquatica</i> L. Cai & K.D. Hyde	Yunnan Province	Cai & Hyde (2007c)
<i>Payosphaeria minuta</i> H.Y.M. Leung	Yunnan Province	Cai et al. (2006)
<i>Thelonectria cylindricospora</i> D.F. Bao, K.D. Hyde & Z.L. Luo	Yunnan Province	Bao et al. (2023a)
<i>Thelonectria hydei</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
<i>Thelonectria xizangensis</i> P. Zhao & L. Cai	Xizang Autonomous Region	Zhao et al. (2025)
Ophiocordycipitaceae (1 genus) (10 species)		
<i>Ophiocordyceps albastroma</i> Hong Yu bis, Y.D. Dai, T. Sun & Y. Chen	Yunnan Province	Sun et al. (2024)
<i>Ophiocordyceps fusispora</i> Y.B. Wang, H.F. Liao & Zhu L. Yang	Yunnan Province	This study
<i>Ophiocordyceps hutiaoxiaensis</i> Y.B. Wang, H.F. Liao & Zhu L. Yang	Yunnan Province	This study
<i>Ophiocordyceps liangshanensis</i> (M. Zang, D.Q. Liu & R.Y. Hu) H. Yu, Y. Wang, Y.D. Dai, Zhu L. Yang & Y.B. Wang	Sichuan Province	Wang et al. (2021)
<i>Ophiocordyceps polystromata</i> Y.B. Wang, H.F. Liao & Zhu L. Yang	Yunnan Province	Liao et al. (2025)
<i>Ophiocordyceps multiseptata</i> Y.B. Wang, H.F. Liao & Zhu L. Yang	Yunnan Province	This study
<i>Ophiocordyceps nigrstroma</i> Hong Yu bis, T. Sun, W.Q. Zou & Y.D. Dai	Yunnan Province	Sun et al. (2024)
<i>Ophiocordyceps nujiangensis</i> Hong Yu bis, T. Sun & W.Q. Zou	Yunnan Province	Sun et al. (2022)
<i>Ophiocordyceps sporangifera</i> Y.P. Xiao, T.C. Wen & K.D. Hyde	Yunnan Province	This study
<i>Ophiocordyceps yuhongii</i> Y.B. Wang, H.F. Liao & Zhu L. Yang	Yunnan Province	This study
Polycephalomycetaceae (4 genera) (7 species)		
<i>Perennicordyceps lutea</i> Y.B. Wang, Hong Yu bis & Y.P. Xiao	Sichuan Province	Xiao et al. (2023)
<i>Perennicordyceps woodihabitata</i> Y.B. Wang, B.Z. Chen, X.M. Wang & Zhu L. Yang	Yunnan Province	This study
<i>Pleurocordyceps sinensis</i> (Q.T. Chen, S.R. Xiao & Z.Y. Sh) Y.J. Yao, Y.H. Wang, S. Ban, W.J. Wang, Yi Li, Ke Wang & P.M. Kirk	Yunnan Province and Sichuan Province	Wang et al. (2012); This study
<i>Pleurocordyceps yunnanensis</i> (Hong Yu bis, Y.B. Wang & Y.D. Dai) Y.H. Wang, S. Ban, W.J. Wang, Yi Li, Ke Wang, P.M. Kirk & Y.J. Yao	Guizhou Province and Yunnan Province	Wang et al. (2015); This study
<i>Polycephalomyces formosus</i> Kobayasi	Yunnan Province	This study
<i>Polycephalomyces tengchongensis</i> Y. Wang tris & T.C. Wen	Yunnan Province	This study
<i>Volutella ciliata</i> (Alb. & Schwein.) Fr	Yunnan Province	Bao et al. (2023a)
Sarocladiaceae (1 genus) (1 species)		
<i>Sarocladium kiliense</i> (Grütz) Summerb	Yunnan Province	Bao et al. (2023a)
Stachybotryaceae (3 genera) (5 species)		
<i>Memnoniella echinata</i> (Rivolta) Galloway	Yunnan Province	Bao et al. (2023a)
<i>Memnoniella oenanthes</i> (M.B. Ellis) L. Lombard & Crous	Yunnan Province	Bao et al. (2023a)
<i>Myxospora motuoensis</i> S.C. He, K.D. Hyde & Jayaward	Xizang Autonomous Region	He et al. (2024)

Species	Regions	References
<i>Stachybotrys chartarum</i> (Ehrenb.) S. Hughes	Yunnan Province and Xinjiang Autonomous Region	(Luo et al. 2019; Bao et al. 2023a; Xu et al. 2025)
<i>Stachybotrys chlorohalonata</i> B. Andersen & Thrane	Yunnan Province	(Luo et al. 2019; Bao et al. 2023a)
Hypocreomycetidae incertae sedis (1 genus) (1 species)		
<i>Campylospora chaetocladia</i> Ranzoni	Sichuan Province	Hu et al. (2013)
Magnaporthales (4 genera)		
Ceratosphaeriaceae (1 genus) (1 species)		
<i>Ceratosphaeria aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
Magnaporthaceae (2 genera) (2 species)		
<i>Aquafiliformis lignicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Falciphoriella hyalina</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
Ophioceraeae (1 genus) (4 species)		
<i>Ophioceras aquaticum</i> D.M. Hu, L. Cai & K.D. Hyde	Yunnan Province	Hu et al. (2012b)
<i>Ophioceras aseptatum</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Ophioceras cylindrosporum</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Ophioceras guttulatum</i> C.K.M. Tsui, H.Y.M. Leung, K.D. Hyde & Hodgkiss	Yunnan Province	Cai et al. (2006)
Pseudohalonectriaceae (1 genus) (3 species)		
<i>Pseudohalonectria fuxianii</i> L. Cai, C.K.M. Tsui, K.Q. Zhang & K.D. Hyde	Yunnan Province	Cai et al. (2002)
<i>Pseudohalonectria lignicola</i> Minoura & T. Muroi	Yunnan Province	Cai et al. (2002)
<i>Pseudohalonectria lutea</i> Shearer	Yunnan Province	(Cai et al. 2002; Zhang et al. 2024b)
Microascales (2 families)		
Halosphaeriaceae (5 genera) (5 species)		
<i>Clavatospora tentacula</i> Sv. Nilsson	Sichuan Province	Hu et al. (2013)
<i>Halosphaeriopsis mediosetigera</i> (Cribb & J.W. Cribb) T.W. Johnson, J. Elisha	Xinjiang Autonomous Region	Xu et al. (2025)
<i>Natantispora retorquens</i> (Shearer & J.L. Crane) J. Campb., J.L. Anderson & Shearer	Yunnan Province	Cai et al. (2002)
<i>Phaeonectriella lignicola</i> R.A. Eaton & E.B.G. Jones	Yunnan Province	Luo et al. (2004)
<i>Pseudocirrenalia aquialpina</i> J. Ma, R.J. Xu, K.D. Hyde & Y.Z. Lu	Xinjiang Autonomous Region	Ma et al. (2024)
Microascaceae (3 genera) (3 species)		
<i>Kernia xizangensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	This study
<i>Parascodosporium putredinis</i> (Corda) Lackner & de Hoog	Yunnan Province	Bao et al. (2023a)
<i>Scedosporium minutisporum</i> (Gilgado, Gené, Cano & Guarro) Lackner & de Hoog	Xizang Autonomous Region	Xu et al. (2025)
Myrmecridiales (1 family)		
Myrmecridiaceae (2 genus) (10 species)		
<i>Myrmecridium aquaticum</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Myrmecridium hydei</i> Asghari, Phukhams & E.B.G. Jones	Yunnan Province	Zhang et al. (2024b)
<i>Myrmecridium iridis</i> Crous	Xinjiang Autonomous Region	Xu et al. (2023a)
<i>Myrmecridium schulzeri</i> (Sacc.) Arzanlou, W. Gams & Crous	Yunnan Province	Xu et al. (2023a)
<i>Myrmecridium submersum</i> L. Zhang & Z.L. Luo	Yunnan Province	Zhang et al. (2024b)
<i>Myrmecridium thailandicum</i> Crous & Cheew	Yunnan Province	Wang et al. (2024b)
<i>Neomyrmecridium fusiforme</i> L. Zhang & Z.L. Luo	Yunnan Province	Zhang et al. (2024b)
<i>Neomyrmecridium gaoligongense</i> R.J. Xu, Q. Zhao & Boonmee	Yunnan Province	Xu et al. (2023a)

Species	Regions	References
<i>Neomyrmecridium luguense</i> R.J. Xu, Q. Zhao & Boonmee	Yunnan Province	Xu et al. (2023a)
<i>Neomyrmecridium sichuanense</i> Y.P. Chen & Maharachch.	Sichuan Province	Chen et al. (2025)
Parasymphodiellales (1 family)		
Parasymphodiellaceae (1 genus) (1 species)		
<i>Parasymphodiella lauri</i> Hern.-Restr., Gené & Guarro	Yunnan Province	Wang et al. (2024b)
Phomatosporales (1 family)		
Phomatosporaceae (2 genera) (2 species)		
<i>Conicotenuis fusiformis</i> W. Dong & K.D. Hyde	Yunnan Province	Dong et al. (2023)
<i>Minimispora superficialis</i> W. Dong & K.D. Hyde	Yunnan Province	Dong et al. (2023)
Pisoriisporiales (1 family)		
Xizangmycetaceae (1 genus) (1 species)		
<i>Xizangmyces aquaticus</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
Pleurotheciales (1 family)		
Pleurotheciaceae (6 genera) (34 species)		
<i>Phaeoisaria aquatica</i> Z.L. Luo, X.J. Su & K.D. Hyde	Yunnan Province	Luo et al. (2018a)
<i>Phaeoisaria clematidis</i> (Fuckel) S. Hughes	Yunnan Province and Xizang Autonomous Region	(Luo et al. 2018a; Xu et al. 2024a)
<i>Phaeoisaria ellipsoidea</i> R. Zhu & H. Zhang	Yunnan Province	Yang et al. (2023)
<i>Phaeoisaria mononematosa</i> W.P. Wang & Z.L. Luo	Xizang Autonomous Region	Wang et al. (2025)
<i>Phaeoisaria motuoensis</i> K. Xu, R.J. Xu & Y.A. Zhu	Xizang Autonomous Region	Xu et al. (2024a)
<i>Phaeoisaria obovata</i> W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Phaeoisaria pseudoclematidis</i> D.Q. Dai & K.D. Hyde	Yunnan Province	Wang et al. (2024b)
<i>Phaeoisaria sedimenticola</i> X.L. Cheng & Wei Li	Xizang Autonomous Region	Xu et al. (2024a)
<i>Phaeoisaria synnemata</i> P.N. Singh & S.K. Singh	Yunnan Province	Wang et al. (2024b)
<i>Phaeoisaria yadongensis</i> Y. Li, S.C. He, & Q. Zhao	Xizang Autonomous Region	Li et al. (2025)
<i>Phragmocephala atra</i> (Berk. & Broome) E.W. Mason & S. Hughes	Yunnan Province	Su et al. (2015)
<i>Phragmocephala garethjonesii</i> H.Y. Su, Udayanga & K.D. Hyde	Yunnan Province	Su et al. (2015)
<i>Pleurotheciella aquatica</i> Z.L. Luo, D.J. Bhat, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2018a)
<i>Pleurotheciella atroseptata</i> W.P. Wang & Z.L. Luo	Xizang Autonomous Region	Wang et al. (2025)
<i>Pleurotheciella bambusisiliquosa</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Pleurotheciella brachyspora</i> W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Pleurotheciella fusiformis</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2018a)
<i>Pleurotheciella guttulata</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2018a)
<i>Pleurotheciella hyalospora</i> J. Ma & Y.Z. Lu	Yunnan Province	Wang et al. (2024b)
<i>Pleurotheciella longidenticulata</i> W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Pleurotheciella lunata</i> Z.L. Luo, D.J. Bhat & K.D. Hyde	Yunnan Province	Luo et al. (2018a)
<i>Pleurotheciella obliqua</i> W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Pleurotheciella saprophytica</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2018a)
<i>Pleurotheciella submersa</i> Z.L. Luo & K.D. Hyde	Yunnan Province	Luo et al. (2018a)
<i>Pleurotheciella uniseptata</i> (Matsush.) Seifert	Yunnan Province	(Luo et al. 2018a; Wang et al. 2024b)
<i>Pleurotheciella xizangensis</i> W.P. Wang & Z.L. Luo	Xizang Autonomous Region	Wang et al. (2025)
<i>Pleurothecium aquaticum</i> Z.L. Luo, H.Y. Su & K.D. Hyde	Yunnan Province	Luo et al. (2018a)
<i>Pleurothecium pisiformis</i> W.P. Wang & Z.L. Luo	Xizang Autonomous Region	Wang et al. (2025)

Species	Regions	References
<i>Pleurothecium pulneyense</i> Subram. & Bhat	Yunnan Province	Luo et al. (2018a)
<i>Pleurothecium recurvatum</i> (Morgan) Höhn.	Yunnan Province and Xizang Autonomous Region	(Luo et al. 2019; Xu et al. 2025)
<i>Saprodesmium dematiosporum</i> W. Dong, Doilom & K.D. Hyde	Yunnan Province	(Dong et al. 2020a; Xu et al. 2025)
<i>Sterigmatobotrys macrocarpus</i> (Corda) S. Hughes	Xizang Autonomous Region	Xu et al. (2025)
<i>Sterigmatobotrys rudis</i> (Sacc.) Heuchert, U. Braun & Ertz	Yunnan Province and Xizang Autonomous Region	(Yang et al. 2023; Xu et al. 2025)
<i>Sterigmatobotrys uniseptatus</i> H.S. Chang	Yunnan Province	(Luo et al. 2019; This study)
Rhamphoriales (1 family)		
Rhamphoriaceae (2 genera) (2 species)		
<i>Rhodoveronea aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Xylolentia subhyalina</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
Savoryellales (1 family)		
Savoryellaceae (6 genera) (14 species)		
<i>Bactrodesmium brunneosporum</i> W.P. Wang & Z.L. Luo	Yunnan Province	Wang et al. (2025)
<i>Bactrodesmium diversum</i> Hern.-Restr., J. Mena, Gené & Guarro	Yunnan Province	Xu et al. (2025)
<i>Bactrodesmium obovatum</i> (Oudem.) M.B. Ellis	Xizang Autonomous Region	Xu et al. (2025)
<i>Canalisporium jinghongense</i> L. Cai, K.D. Hyde & McKenzie	Yunnan Province	(Cai et al. 2003; Wang et al. 2024b)
<i>Dematiosporium aquaticum</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Sichuan Province	Yu et al. (2023a)
<i>Dematiosporium bambusicola</i> X.D. Yu, S.N. Zhang & Jian K. Liu	Sichuan Province	Yu et al. (2023a)
<i>Dematiosporium dictyosporum</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Dematiosporium phaeohyphum</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Neoscotaiwania aquatica</i> D.F. Bao, H.Y. Su, K.D. Hyde & Z.L. Luo	Yunnan Province	Yang et al. (2022)
<i>Rhexoacrodictys melanospora</i> S.X. Bao, R.J. Xu & Q. Zhao	Yunnan Province	Bao et al. (2023b)
<i>Savoryella bambusicola</i> X.D. Yu, S.N. Zhang & Jian K. Liu	Sichuan Province	Yu et al. (2023a)
<i>Savoryella claviformis</i> R.J. Xu, S. Boonmee, K.D. Hyde & Q. Zhao	Xinjiang Autonomous Region	Xu et al. (2024c)
<i>Savoryella daemonocula</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Savoryella submersa</i> R.J. Xu, Q. Zhao & Boonmee	Xizang Autonomous Region	This study
Sordariales (3 families)		
Chaetomiaceae (3 genera) (3 species)		
<i>Chaetomium globosum</i> Kunze	Yunnan Province	Luo et al. (2019)
<i>Myceliophthora xizangica</i> F. Liu, S. Song & L. Cai	Xizang Autonomous Region	Phurbu et al. (2024)
<i>Trichocladium lignicola</i> I. Schmidt	Yunnan Province	Cai et al. (2002)
Lasiosphaeriaceae (2 genera) (2 species)		
<i>Xizangia sedimenticola</i> F. Liu, S. Song & L. Cai	Xizang Autonomous Region	Phurbu et al. (2024)
<i>Zopfiella latipes</i> (N. Lundq.) Malloch & Cain	Yunnan Province	Cai et al. (2002)
Schizotheciaceae (1 genus) (1 species)		
<i>Cercophora caudata</i> (Sacc.) N. Lundq	Yunnan Province	Luo et al. (2019)
Sordariales genera incertae sedis (4 genera) (7 species)		
<i>Ascolacicola coffeae</i> (L. Lu & Karun.) W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Ascolacicola minispora</i> W.P. Wang, H.W. Shen, K. D. Hyde & Z.L.	Yunnan Province	Wang et al. (2024b)
<i>Ascolacicola uniseptata</i> (H. S. Chang & S.-Y. Hsieh) W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024b)

Species	Regions	References
<i>Cuspidatispora xiphiago</i> Shearer & Bartolata	Yunnan Province	Luo et al. (2019)
<i>Lunulospora curvula</i> Ingold	Sichuan Province	Hu et al. (2013)
<i>Ramophialophora ramosa</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xinjiang Autonomous Region	This study
<i>Ramophialophora vesiculosa</i> M. Calduch, Stchigel, Gené & Guarro	Xizang Autonomous Region	Xu et al. (2025)
Sporidesmiales (1 family)		
Sporidesmiaceae (1 genus) (17 species)		
<i>Sporidesmium aquaticivaginatium</i> J. Yang & K.D. Hyde	Yunnan Province	Wang et al. (2024b)
<i>Sporidesmium aturbinatum</i> (S. Hughes) M.B. Ellis	Yunnan Province	Bao et al. (2021)
<i>Sporidesmium bostenicum</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xingjiang Autonomous Region	Xu et al. (2025)
<i>Sporidesmium brachypus</i> (Ellis & Everh.) S. Hughes	Yunnan Province	Luo et al. (2019)
<i>Sporidesmium cangshanense</i> Z.L. Luo & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Sporidesmium dulongense</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Hyde et al. (2020c)
<i>Sporidesmium filiforme</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Sporidesmium fluminicola</i> H.Y. Su & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Sporidesmium fluviale</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan province	This study
<i>Sporidesmium guttulatum</i> W.P. Wang, H.W. Shen, K. D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Sporidesmium lageniforme</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province and Xizang Autonomous Region	(Luo et al. 2019; Xu et al. 2025)
<i>Sporidesmium lignicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Sporidesmium mucilaginosum</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
<i>Sporidesmium napaense</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan province	Xu et al. (2025)
<i>Sporidesmium nujiangense</i> D.F. Bao, H.Y. Su, K.D. Hyde & Z.L. Luo	Yunnan Province and Xizang Autonomous Region	(Bao et al. 2021; Xu et al. 2025)
<i>Sporidesmium submersum</i> H.Y. Su & K.D. Hyde	Yunnan Province	Su et al. (2016b)
<i>Sporidesmium tropicale</i> M.B. Ellis	Yunnan Province	Bao et al. (2021)
Togniniales (1 family)		
Togniniaceae (1 genus) (2 species)		
<i>Phaeoacremonium aquaticum</i> (D.M. Hu, L. Cai & K.D. Hyde) Gramaje, L. Mostert & Crous	Yunnan Province	Hu et al. (2012b)
<i>Phaeoacremonium ovale</i> S.K. Huang, R. Jeewon & K.D. Hyde	Yunnan Province	Huang et al. (2018)
Vermiculariopsiellales (1 family)		
Vermiculariopsiellaceae (1 genus) (1 species)		
<i>Chloridiopsiella septata</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
Xenospadicoidales (1 family)		
Xenospadicoidaceae (2 genera) (6 species)		
<i>Neospadicoides aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Neospadicoides lignicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province and Xizang Autonomous Region	(Luo et al. 2019; Xu et al. 2025)
<i>Neospadicoides yunnanensis</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Spadicoides bambusicola</i> D.Q. Zhou, Goh & K.D. Hyde	Yunnan Province	Cai et al. (2006)
<i>Spadicoides hydei</i> R.J. Xu & Q. Zhao	Xizang Autonomous Region	Xu et al. (2025)
<i>Spadicoides minuta</i> L. Cai, McKenzie & K.D. Hyde	Yunnan Province	Cai (2004)
Xylariales (4 families)		
Cainiaceae (1 genus) (1 species)		

Species	Regions	References
<i>Amphibambusa aquatica</i> Doilom	Yunnan Province	Manawasinghe et al. (2024)
Diatrypaceae (1 genus) (1 species)		
<i>Quaternaria dissepata</i> (Fr.) Tul. & C. Tul	Yunnan Province	Hu et al. (2013)
Hypoxylaceae (1 genus) (2 species)		
<i>Hypoxylon lignicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Gansu Province	Luo et al. (2019)
<i>Hypoxylon malongense</i> G.Q. Zhang, Wijayaw., & Q.R. Li	Yunnan Province	Zhang et al. (2025)
Vamsapriaceae (1 genus) (3 species)		
<i>Vamsapriya aquatica</i> D.F. Bao, H.Y. Su, K.D. Hyde & Z.L. Luo	Yunnan Province	Bao et al. (2021)
<i>Vamsapriya indica</i> Gawas & Bhat	Yunnan Province	Bao et al. (2021)
<i>Vamsapriya yadongensis</i> Z.Y. Wang, S.C. He & Q. Zhao	Xizang Autonomous Region	Wang (2024)
Xylariales genera incertae sedis (2 genera) (2 species)		
<i>Xenostanjehughesia polypora</i> (W.P. Wu) N.G. Liu, H.W. Shen & Jian K. Liu	Yunnan Province	Liu et al. (2024a)
<i>Brachysporium sinense</i> H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Shen et al. (2024b)
Sordariomycetes incertae sedis		
Diaporthomycetidae families incertae sedis (7 families)		
Acrodictyceae (1 genus) (2 species)		
<i>Acrodictys altitudinalis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Sichuan Province	Xu et al. (2025)
<i>Acrodictys fluminicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
Junewangiaceae (4 genera) (15 species)		
<i>Dictyospora ellipsoidea</i> W. Dong, H. Zhang & K.D. Hyde	Yunnan Province	Bao et al. (2021)
<i>Dictyospora hydei</i> H.Y. Song & D.M. Hu	Yunnan Province	Song et al. (2018a)
<i>Dictyospora yunnanensis</i> X.G. Tian & Tibpromma	Yunnan Province	Hyde et al. (2023)
<i>Jennwenomyces navicularis</i> (R.F. Castañeda & Heredia) Goh & C.H. Kuo	Xinjiang Autonomous Region	Xu et al. (2025)
<i>Junewangia aquatica</i> H.Y. Song & D.M. Hu	Yunnan Province	Song et al. (2018b)
<i>Junewangia chen Yue</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	This study
<i>Sporidesmiella aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Sporidesmiella gezaensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	This study
<i>Sporidesmiella hyalosperma</i> (Corda) P.M. Kirk	Yunnan Province and Xizang Autonomous Region	(Dong et al. 2021; Xu et al. 2025)
<i>Sporidesmiella indistincta</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Sporidesmiella junci</i> Crous & Osieck	Xizang Autonomous Region	Xu et al. (2025)
<i>Sporidesmiella motuoensis</i> Y.C. Xiong, R.J. Xu, & Q. Zhao	Xizang Autonomous Region	Xiong et al. (2024)
<i>Sporidesmiella novae-zelandiae</i> (S. Hughes) Madrid, Hern.-Restr. & Crous	Yunnan Province	Luo et al. (2019)
<i>Sporidesmiella obovoidia</i> (X.H. Li, H.Y. Song & D.M. Hu) X.D. Yu, W. Dong & H. Zhang	Xizang Autonomous Region	Xu et al. (2025)
<i>Sporidesmiella yadongensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
Papulosaceae (1 genus) (4 species)		
<i>Wongia aquatica</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Wongia flava</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Wongia fusiformis</i> D.F. Bao, H.Y. Su, K.D. Hyde & Z.L. Luo	Yunnan Province	(Bao et al. 2021; Wang et al. 2024b)
<i>Wongia suae</i> L. Zhang, H.W. Shen & Z.L. Luo	Yunnan Province	Zhang et al. (2023)
Trichosphaeriaceae (2 genera) (2 species)		
<i>Brachysporium nielamuense</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)

Species	Regions	References
<i>Stachylidium chayuense</i> C. Ma, S.C. He & Q. Zhao	Xizang Autonomous Region	Ma et al. (2025)
Woswasiaceae (1 genus) (1 species)		
<i>Xylochrysis aquatica</i> J.Y. Song & X.D. Yu	Sichuan Province	Song et al. (2023)
Savoryellomycetidae genus incertae sedis (3 genera) (4 species)		
<i>Gohteikhimycetes dulongjiangensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Yunnan Province	Xu et al. (2025)
<i>Obliquifusoideum triseptatum</i> W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
<i>Pseudostanjehughesia lignicola</i> Z.L. Luo, K.D. Hyde & H.Y. Su	Yunnan Province	Luo et al. (2019)
<i>Pseudostanjehughesia nielamuensis</i> R.J. Xu, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	Xu et al. (2025)
Sordariomycetes genera incertae sedis (1 genus) (1 species)		
<i>Ascoyunnania aquatica</i> L. Cai & K.D. Hyde	Yunnan Province	Cai et al. (2005)
Dothideomycetes incertae sedis (2 genera) (2 species)		
<i>Clavariopsis aquatica</i> De Wild	Sichuan Province	Hu et al. (2013)
<i>Pseudorobillarda multiguttulata</i> W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo	Yunnan Province	Wang et al. (2024b)
Ascomycota incertae sedis (5 genera) (5 species)		
<i>Candelabrum brocchiatum</i> Tubaki	Yunnan Province	Luo et al. (2004)
<i>Culicidospora gravida</i> R.H. Petersen	Sichuan Province	Hu et al. (2013)
<i>Neopodoconis yunnanensis</i> W.P. Wang, H.W. Shen & Z.L. Luo	Yunnan Province	Wang et al. (2023)
<i>Pseudofuscophialis lignicola</i> Sivan. & H.S. Chang	Yunnan Province	Cai & Hyde (2007b)
<i>Trichobotrys motuoensis</i> S.C. He, Q. Zhao & K.D. Hyde	Xizang Autonomous Region	He et al. (2025)
Dyfolomycetales (1 family)		
Pleurotremataceae (1 genus)(1 species)		
<i>Melomastia puerensis</i> R.F. Xu & Tibpromma	Yunnan Province	Xu et al. (2024b)
Neopyrenochaetaceae (1 genus)(1 species)		
<i>Nigrograna lincangensis</i> R.F. Xu & Tibpromma	Yunnan Province	Xu et al. (2024b)
Macrodiplodopsidaceae (1 genus) (2 species)		
<i>Pseudochaetosphaeronema lincangensis</i> R.F. Xu & Tibpromma	Yunnan Province	Xu et al. (2024b)
<i>Pseudochaetosphaeronema xishuangbannaensis</i> R.F. Xu & Tibpromma	Yunnan Province	Xu et al. (2024b)
Cytosporaceae (1 genus) (1 species)		
<i>Cytospora qujingensis</i> G.Q. Zhang, Wijayaw. & Q.R. Li	Yunnan Province	Zhang et al. (2025)
Thyridiales (2 families)		
Thyridiaceae (1 genus) (1 species)		
<i>Thyridium livistonae</i> Song Jing & Senan.	Yunnan Province	Song et al. (2025)
Peniophoraceae (1 genus) (1 species)		
<i>Asterostroma roseoalbum</i> J.H. Dong & C.L. Zhao	Yunnan Province	Dong et al. (2024)

Taxonomy

The classification followed here is from Hyde et al. (2024). The guidelines of Chethana et al. (2021a), and Maharachchikumbura et al. (2021) are followed when determining if species are novel or new collections.

Ascomycota Caval.-Sm

Dothideomycetes O.E. Erikss & Winka

The class *Dothideomycetes*, a significant group within the phylum *Ascomycota*, with approximately 32,621 species

worldwide (Pem et al. 2024; Bánki et al. 2025; [Catalogue of Life](#)), encompasses a diverse array of fungi characterized by their unique morphological traits and ecological roles. This class is primarily defined by the presence of perithecial ascomata, which are typically dark and globose, facilitating the production of asci that contain ascospores (Hongsanan et al. 2020). In this study, a phylogenetic framework of *Dothideomycetes* is constructed using four loci (LSU, SSU, *rpb2* and *tef1-α*) from approximately 600 strains. Further details are provided in Supplementary (Fig. 1).

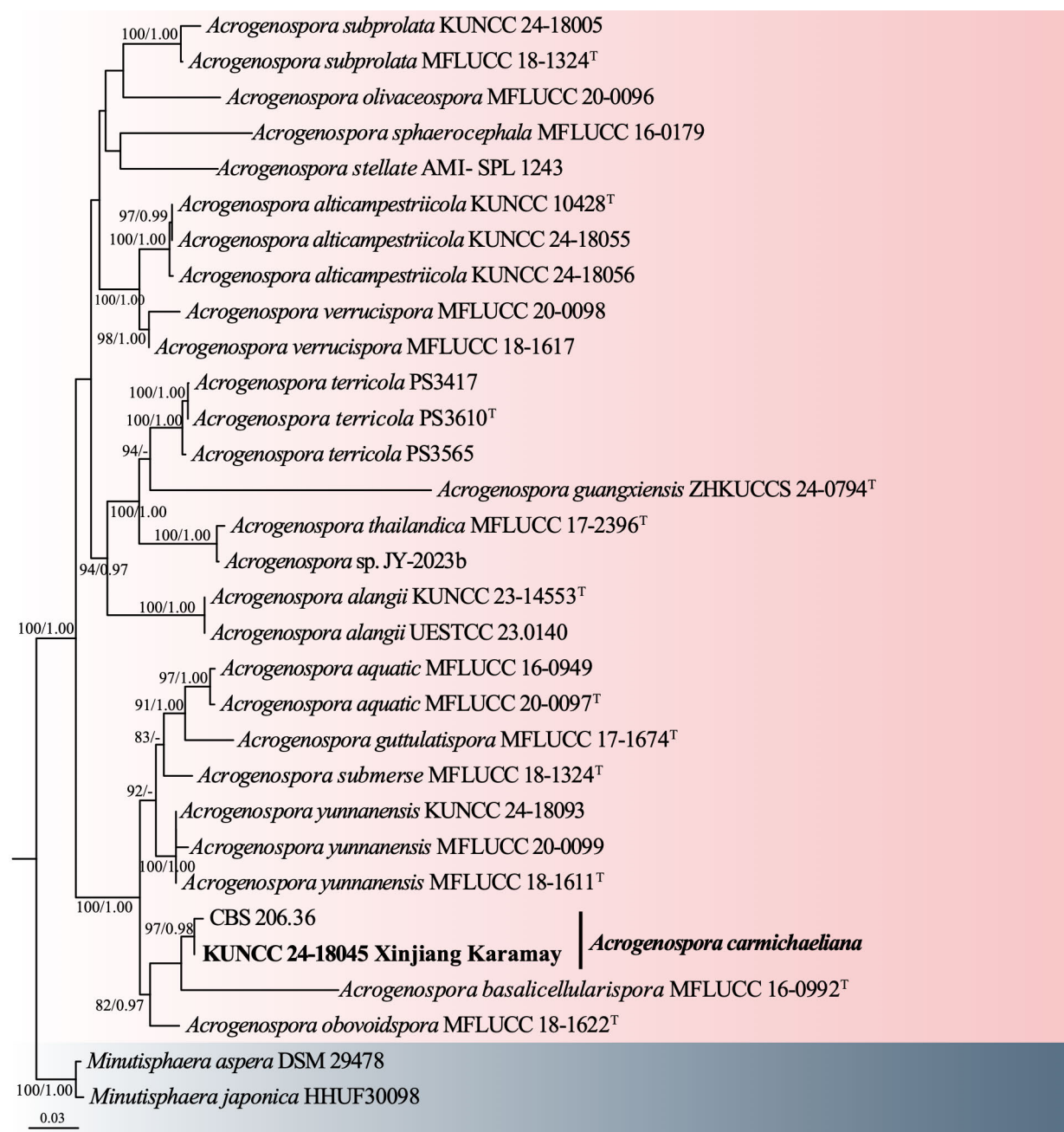


Fig. 1 Maximum likelihood majority rule consensus tree for *Acrogenospora* using ITS, LSU, SSU, *rpb2* and *tef1-α* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Minutisphaera aspera* (DSM 29478) and *M. japonica* (HHUF 30098). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Minutisphaerales Raja, Oberlies, Shearer & A.N. Mill.

Acrogenosporaceae Jayasiri & K.D. Hyde

Acrogenospora M.B. Ellis

Acrogenospora was established by Ellis (1971). It is characterized by macronematous, mononematous, and brown conidiophores that frequently proliferate percurrently. The conidiogenous cells are monoblastic, either terminal or intercalary, and its conidia are globose, ellipsoid, or obovoid, ranging from olivaceous to brown (Hughes 1978; Goh et al. 1998c; Bao et al. 2020; Harrington et al. 2022; Li et al. 2024b). Initially, *Acrogenospora* comprised two species, *A. carmi-*

chaeliana and *A. sphaerocephala*, both described solely by their asexual morphs. Goh et al. (1998c) expanded the genus by adding *A. ovalia* and *A. subprolata*, while Bao et al. (2020) further refined its taxonomy by accommodating nine species, including seven new taxa and two previously described ones, based on phylogenetic and morphological analyses. Currently, *Acrogenospora* encompasses 27 species, primarily from freshwater habitats (21 species), and terrestrial habitats (six species) (Bao et al. 2020; Li et al. 2024b; Cao et al. 2025; Xu et al. 2025).

1. *Acrogenospora carmichaeliana* (Berk.) Rossman & Crous, in Rossman, Crous & Hyde, IMA Fungus 6(2): 509 (2015) Fig. 2

Chinese name: – 卡迈克尔顶生孢 (ka mai ke er ding sheng bao)

Index Fungorum number: IF 814513; **Facesoffungi number:** FoF 08065

Saprobic on decaying wood submerged in freshwater stream. **Sexual morph:** Undetermined. **Asexual morph:** Colonies effuse on natural substrate, hairy, dark brown, with masses of conidia on conidiophores. **Mycelium** mostly immersed, composed of grayish-brown, septate, branched, smooth hyphae. **Conidiophores** 267–354 × 8–10 µm ($\bar{x}$ = 308 × 8 µm, n = 10), mononematous, macronematous, solitary, erect, straight or slightly flexuous, cylindrical, unbranched, brown to dark brown, paler toward apex, septate, smooth-walled. **Conidiogenous cells** holoblastic, monoblastic, integrated, initially terminal, later becoming intercalary, cylindrical, smooth-walled, pale brown, proliferating percurrently. **Conidia** 31–38 × 25–31 µm ($\bar{x}$ = 35 × 28 µm, n = 25), acrogenous or acropleurogenous, solitary, spherical or subspherical, truncate at base, aseptate, hyaline when young, dark brown to black when mature, smooth-walled.

Material examined: CHINA, Xinjiang Autonomous Region, Karamay City, Lengshuigou, 43°58'11.99" N, 85°6'47.30" E, 1785 m a.s.l., on decaying wood submerged in a freshwater stream, 16 July 2021, R.J. Xu, MD-369 (HKAS 136217), living culture KUNCC 24-18045.

Notes: The taxonomic status of *Acrogenospora carmichaeliana* and its relationship with *Farlowiella carmichaeliana* have long been complex issues in mycological research. Historically, based on culture studies, *Acrogenospora megalospora* was considered as the asexual morph of *Farlowiella carmichaeliana*. Ellis (1971a) reported the asexual morph of *F. carmichaeliana* as *Acrogenospora carmichaeliana*, and Goh et al. (1998c) confirmed this relationship and synonymized *A. carmichaeliana* under *Farlowiella carmichaeliana*. The asexual-sexual connection between these two genera (*Farlowiella* and *Acrogenospora*) was also confirmed by Jayasiri et al. (2018) and Hyde et al. (2019) based on phylogenetic analysis. Therefore, *Acrogenospora* was given priority over *Farlowiella*. However, Jayasiri et al. (2018) found that *Acrogenospora sphaerocephala* clustered with *Farlowiella carmichaeliana* (the sexual morph of *Acrogenospora carmichaeliana*), supporting their connection. However, recent studies, Hyde et al. (2019) and Bao et al. (2020), showed that *Acrogenospora sphaerocephala* forms different clades from *Acrogenospora carmichaeliana*. Thus, whether *A. sphaerocephala* was the asexual morph of *Farlowiella carmichaeliana* and whether *Acrogenospora megalospora* was wrongly introduced as the asexual morph of *Farlowiella carmichaeliana* needs further study. In this study, our collection KUNCC 24-18045 is identified as *Acrogenospora carmichaeliana* based on morphological traits and molecular evidence (Fig. 1).

Pleosporales Luttrell ex M.E. Barr

Corynesporascaceae Sivan.

Corynespora Güssow, J

Corynesporasca, established by Sivanesan (1996) and typified by *C. carotae*, represents the sexual morph of a *Corynespora* species found on tropical plants. *Corynespora* typified by *C. mazei* and now synonymised with *C. cassicola*,

comprises about 200 species. The leaf spot fungus *Corynespora cassicola* is particularly widespread, infecting numerous plant hosts predominantly in tropical regions (Smith et al. 2007). Due to the extensive usage and historical priority of the name *Corynespora*, especially in the context of plant pathogenic fungi, it is recommended to continue using this name. *Corynespora* species are mainly tropical and subtropical, found on a wide range of plant hosts, and known for causing leaf spot diseases. They exhibit notable morphological features such as distinct, determinate or percurrently extending conidiophores and monotretic, integrated, terminal conidiogenous cells producing solitary or sometimes catenate, distoseptate conidia. Liu et al. (2023a) and Zhang et al. (2025) provided a detailed description and explanation of the genus.

2. *Corynespora yunnanensis* Jing W. Liu & Jian Ma, in Liu, Hu, Luo, Castañeda-Ruiz, Xia, Xu, Cui, Shi, Zhang & Ma, Journal of Fungi 9 (no. 107): 11 (2023) Fig. 4

Chinese name: – 云南棒孢霉 (yun nan bang bao mei)

Index Fungorum number: IF 900078; **Facesoffungi number:** FoF 17390

Saprobic on decaying stems of wood submerged in a freshwater stream habitat. **Sexual morph:** Undetermined. **Asexual morph:** Colonies superficial, effuse, velvety, gregarious, pale brown, **Mycelium** immersed, subhyaline to pale brown, composed of branched, septate hyphae. **Conidiophores** 406–603 × 12–19 µm ($\bar{x}$ = 490 × 16 µm, n = 20), macronematous, mononematous, erect, straight or slightly flexuous, solitary or group, tapering towards the apex, septate, unbranched, cylindrical, dark brown or brown, becoming paler towards the apex, with several successive cylindrical extensions. **Conidiogenous cells** 21–38 × 10–16 µm ($\bar{x}$ = 29 × 12 µm, n = 20), integrated, terminal, monotretic, cylindrical, pale brown to brown, smooth. **Conidia** 122–154 × 20–28 µm ($\bar{x}$ = 134 × 23 µm, n = 25), acrogenous, solitary, obclavate, rostrate, rounded at the apex, straight or slightly curved, multi-distoseptate, olivaceous to brown, smooth-walled, truncate at the base.

Culture characteristics: Conidia germinating on PDA medium within 24 h, and germ tubes produced from both ends. Colonies grown on PDA reached 60 mm diameter at room temperature in two weeks, circular, with velvety, flat, brown mycelium on the surface, from below dark brown with entire margin.

Material examined: CHINA, Xizang Autonomous Region, Shannan Prefecture, Cuona City, Lebugou, 27°52'38.19" N, 91°47'54.64" E, 3560 m a.s.l., on decaying wood submerged in a freshwater stream, 3 August 2023, R.J. Xu, LJN-45 (HKAS 135995), living culture KUNCC 24-17961.

Notes: *Corynespora yunnanensis* was isolated from dead branches of an unidentified tree in Yunnan Province, China (Liu et al. 2023a). Morphologically, our collection (KUNCC 24-17961) shares identical morphological characters to the holotype of *C. yunnanensis* but has larger conidia (122–154 × 20–28 vs. 80–128 × 16–19 µm). The phylogenetic position of our strain is unclear (Fig. 3). However, comparisons of ITS sequences demonstrate 100% similarity between the ex-type strain HJAUP M2132 and KUNCC 24-17961. Therefore, based on the current evidence, we tentatively retain our strain as *C. yunnanensis*. Further collections and additional evidence are needed to clarify their relationship.

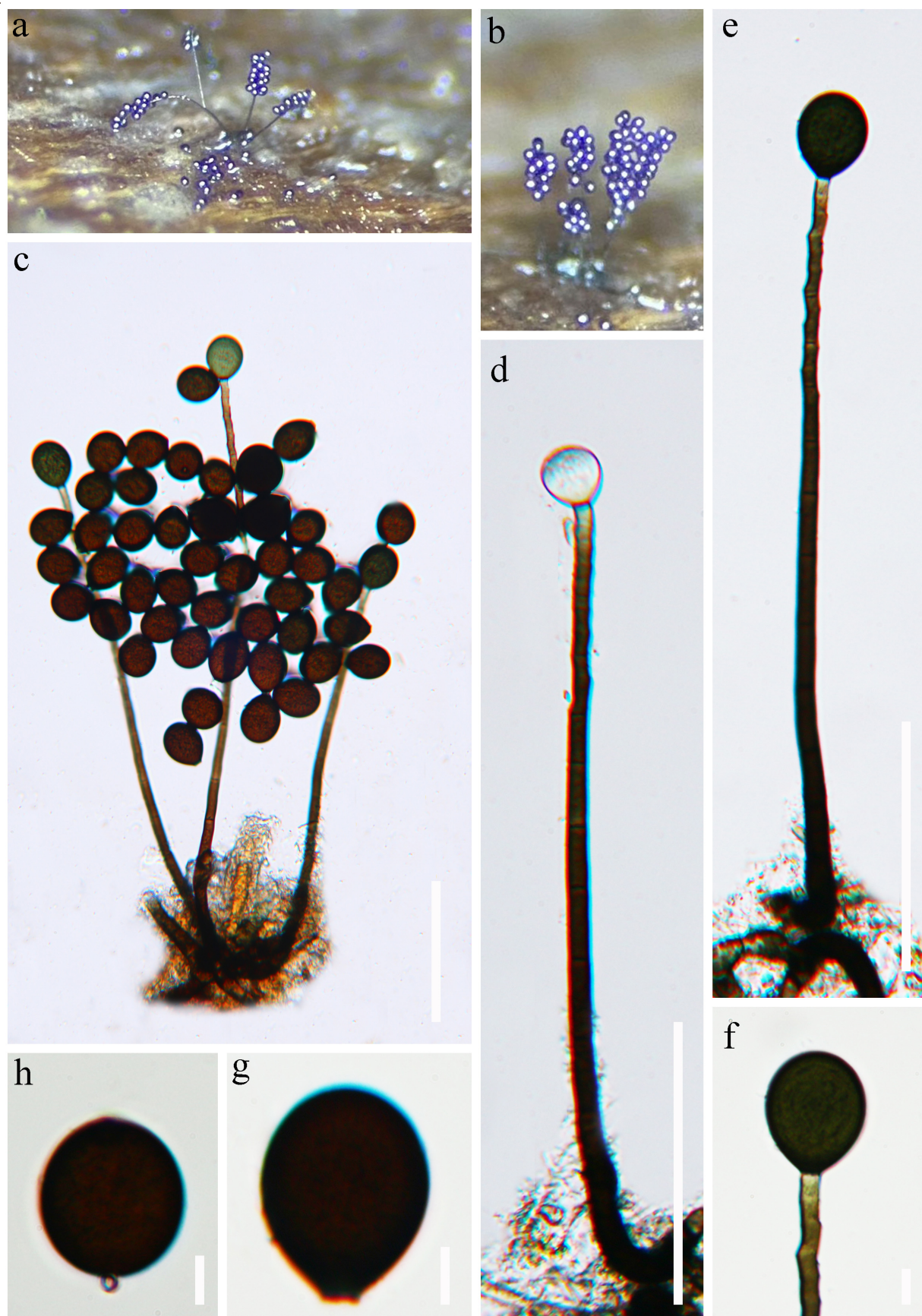


Fig. 2 *Acrogenospora carmichaeliana* (HKAS 136217) a, b Colony on natural substrates. c–f Conidiophores with conidia. g, h Conidia. Scale bars: c–e = 100 μ m, f–h = 10 μ m.

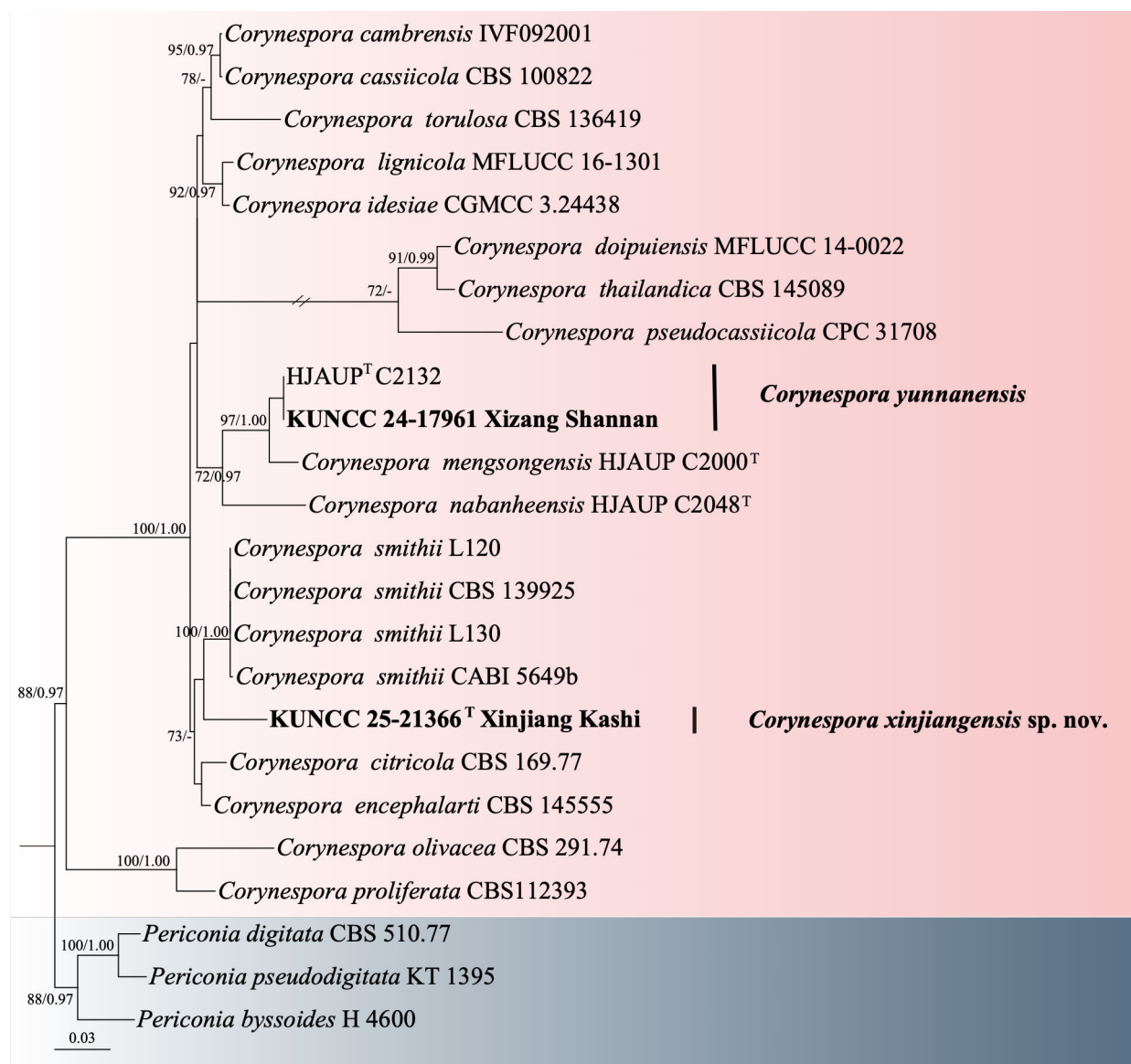


Fig. 3 Maximum likelihood majority rule consensus tree for *Corynespora* using ITS and LSU sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML BS/PP. The scale bar represents the expected number of changes per site. The tree is rooted with *Periconia byssoides* (H 4600), *P. digitata* (CBS 510.77) and *P. pseudodigitata* (KT 1395). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

3. *Corynespora xinjiangensis* R.J. Xu, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 5

Chinese name: – 新疆棒孢霉 (xin jiang bang bao mei)

Index Fungorum number: IF 905026; **Facesoffungi number:** FoF 19296

Etymology: Refers to Xinjiang Autonomous Region in China, where the type specimen of this species was collected.

Holotype: HKAS 151641

Saprobic on decaying wood in a freshwater habitat.

Sexual morph: Undetermined. **Asexual morph:** Colonies on natural substratum, superficial, effuse, filiform, pale brown. Mycelium mostly immersed, composed of branched, septate, pale brown to brown, smooth-walled hyphae. *Conidiophores* macronematous, mononematous, fasciculate, filamentous, cylindrical, septate, unbranched, pale brown to brown, sometimes with multiple consecutive proliferations. *Conidiogenous cells* monotretic, integrated, terminal,

cylindrical, pale brown to brown, smooth-walled, often percurrently proliferating. *Conidia* 63–114 × 6–35 μm ($\bar{x}$ = 84 × 12 μm, n = 30), acrogenous, solitary, obclavato-cylindrical, straight to slightly flexuous, light olivaceous-brown, truncate at the base, obtuse to rounded at the apex, distoseptate, sometimes proliferates 1 to 3 times at the tip of the conidia.

Culture characteristics: Conidia germinating on PDA medium within 24 hours, with germ tubes arising from both ends of the conidium. Colonies grown on PDA reaching 60 mm diam at room temperature under natural light after two weeks, circular, flat, with velvety, with filiform edge, brown to dark brown from above and below.

Material examined: CHINA, Xinjiang Autonomous Region, Kashi Prefecture, Yecheng City, 37° 45' 8.87" N, 77° 25' 7.71" E, 1490 m a.s.l., on decaying wood submerged in a freshwater habitat, 18 July 2021, R.J. Xu, MD-172A (HKAS 151641, holotype), ex-type culture KUNCC 25-21366.

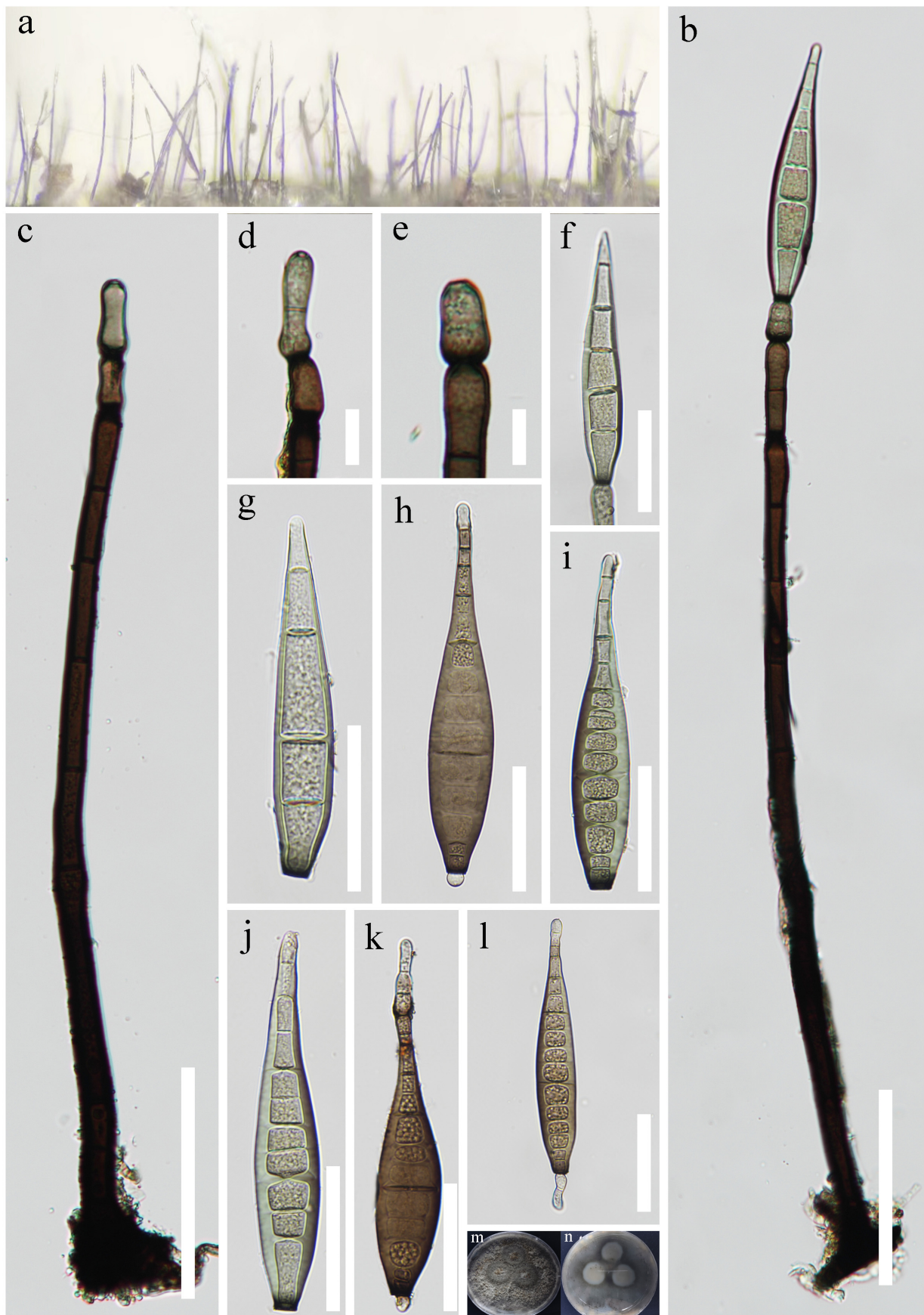


Fig. 4 *Corynespora yunnanensis* (HKAS 135995) a Colony on natural substrates. b, c Conidiophores and conidiogenous cells. d–f Conidiogenous cells with young conidia. g–k Conidia. l Germinated conidium. m, n Culture on PDA medium, m from above, n from below. Scale bars: b–c = 100 μ m, d–l = 50 μ m.

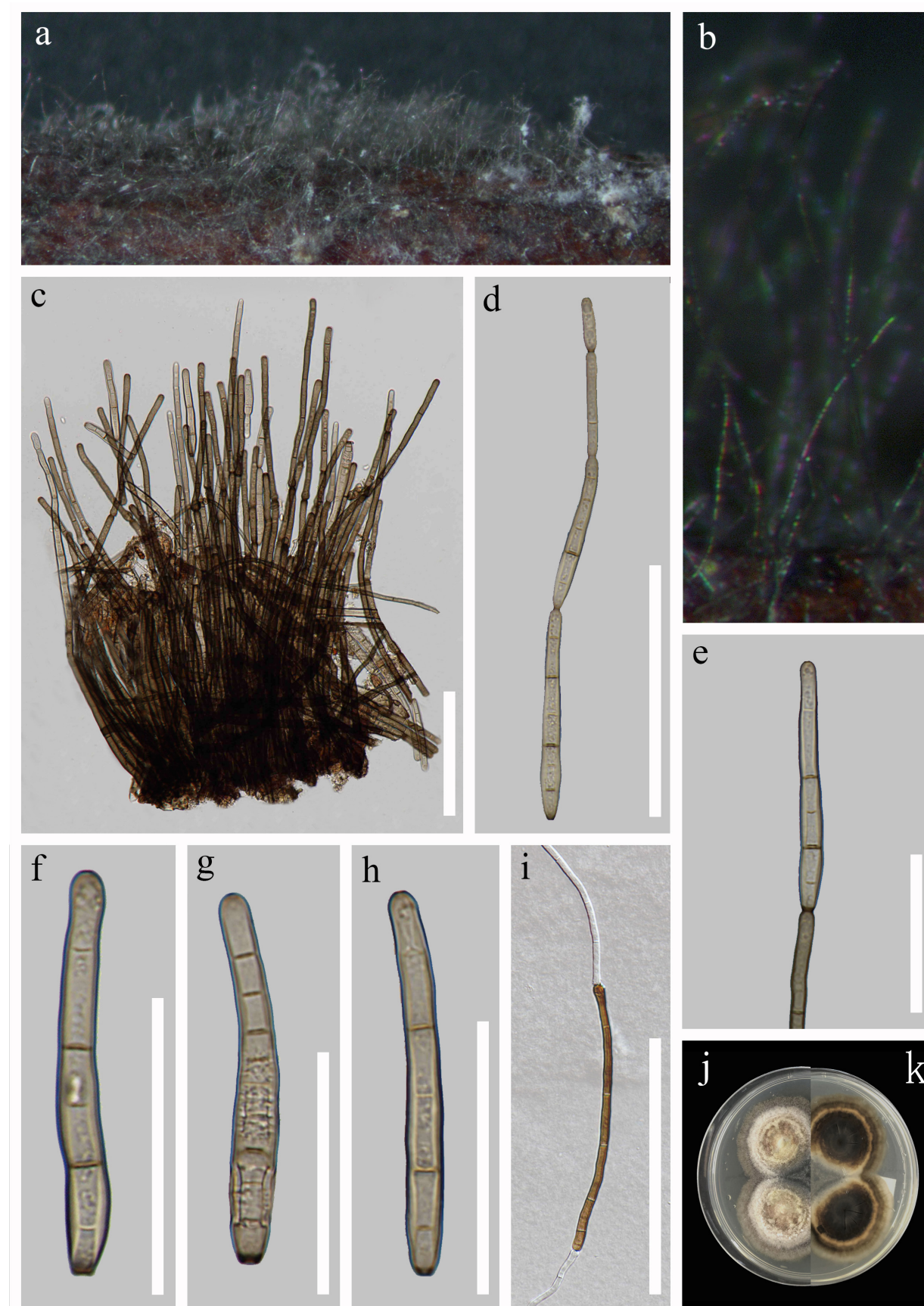


Fig. 5 *Corynespora xinjiangensis* (HKAS 151641, **holotype**) a, b Colony on natural substrates. c, d Short conidiophores and conidia. e Conidiogenous cells with young conidia. f–h Conidia. i Germinated conidium. j, k Culture on PDA medium, j from above, k from below. Scale bars: c, d = 100 μ m, e–i = 50 μ m.

Notes: *Corynespora xinjiangensis* is morphologically typical of *Corynespora*, characterized by macronematous, mononematous conidiophores, monotretic conidiogenous cells, and obclavato-cylindrical, distoseptate conidia (Smith et al. 2007). The conidia of *C. xinjiangensis* are relatively large, measuring 63–114 × 6–35 µm, with an average size of 84 × 12 µm, with 1–3 proliferations at the apex. *Corynespora xinjiangensis* differs from *C. mengsongensis* and *C. nabanheensis*, by having short, multiple consecutive proliferations conidiophores and obclavato-cylindrical conidia (Liu et al. 2023a). Furthermore, a comparison of the ITS nucleotide bases in *C. xinjiangensis* (KUNCC 25-21366) and *C. smithii* (MFLU 19-0688) revealed that they differ in 83/869 bp (9.55%) of ITS, and the phylogenetic analyses (Fig. 3) place *C. xinjiangensis* in a distinct lineage, supporting its separation from the known species.

Dictyosporiaceae Boonmee & K.D. Hyde

Dictyocheiropora M.J. D'souza, S. Boonmee & K.D. Hyde

Dictyocheiropora was established by Boonmee et al. (2016) with *D. rotunda* as the type species. *Dictyocheiropora* is distinguished from its close relative genus *Dictyosporium*, by its unique conidial morphology. The conidia in *Dictyocheiropora* are cheiroid, non-complanate, or cylindrical, often tightly grouped at the apex, contrasting with the conidial arrangement in *Dictyosporium* (Boonmee et al. 2016; Wang et al. 2016a; Shen et al. 2022). The asexual morphs of *Dictyocheiropora* are characterized by dark sporodochial colonies producing aeroaquatic conidia, while its sexual morphs are noted for subglobose ascomata, cylindrical asci, and hyaline, fusiform, uniseptate ascospores, with or without a sheath (Boonmee et al. 2016; Tibpromma et al. 2018; Liu et al. 2023b; Tennakoon et al. 2023).

The phylogenetic placement of *Dictyocheiropora* within the *Dictyosporiaceae* family has been validated through analyses employing multiple-gene phylogenies in various studies (Liu et al. 2015a; Tanaka et al. 2015; Boonmee et al. 2016). *Dictyocheiropora* currently comprises 33 accepted species, identified through both morphological characteristics and phylogenetic analysis (Boonmee et al. 2016; Wang et al. 2016a; Hyde et al. 2017; Hyde et al. 2019; Yang et al. 2018a; Tibpromma et al. 2018; Jayasiri et al. 2019; Phookamsak et al. 2019; Dong et al. 2020; Phukhamsakda et al. 2020; Shen et al. 2022; Tennakoon et al. 2023; Wang et al. 2025c; Sun et al. 2025).

4. Dictyocheiropora luojiensis R.J. Xu, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 7

Chinese name: – 洛吉砖隔掌状孢 (luo ji zhuan ge zhang zhuang bao)

Index Fungorum number: IF 903471; **Facesoffungi number:** FoF 17391

Etymology: Referring to the location “Luoji River” where the holotype of this fungus was collected.

Holotype: HKAS 136148

Saprobic on decaying stems of wood submerged in a freshwater river. **Sexual morph:** Undetermined. **Asexual morph:** Colonies sporodochial, punctiform, scattered or in small groups, compactly, water-stained, dark brown to black. **Mycelium** immersed, subhyaline to pale brown, composed of branched, septate hyphae. **Conidiophores** macronematous, mononematous, septate, cylindrical, pale brown to subhyaline, smooth-walled, sometimes reduced to conidiogenous

cells. **Conidiogenous cells** holoblastic, cylindrical to subglobose, hyaline to pale brown, smooth-walled. **Conidia** 56–71 × 22–40 µm ($\bar{x}$ = 64 × 28 µm, n = 25), acrogenous, solitary, cheiroid, brown or dark brown, closely appressed, composed of seven rows of cells, non-complanate, cylindrical, each row with 8–12 cells. Conidial secession was schizolytic.

Culture characteristics: Conidia germinating on PDA medium within 72 h and germ tubes arising from terminal end of conidium. Colonies grown on PDA reached 30 mm diam at room temperature in one month, circular, with velvety, raised, white mycelium on the surface, from below cream to light brown with entire margin.

Material examined: CHINA, Yunnan Province, Shangri-La City, Luoji River, 27°42'23.30" N, 99°59'31.51" E, 3539 m a.s.l., on decaying wood submerged in a freshwater river, 18 June 2022, R.J. Xu, LTS-25 (HKAS 136148, holotype), ex-type culture KUNCC 24-17999.

Notes: Phylogenetic analysis combining SSU, ITS, LSU and *tef1-α* sequence data showed that *Dictyocheiropora luojiensis* clustered within the *Dictyocheiropora* clade and formed an independent lineage (Fig. 6). *Dictyocheiropora luojiensis* is closely related to *D. lithocarpus*, *D. multiappendiculata*, and *D. suae* (Fig. 6). *Dictyocheiropora luojiensis* is morphologically similar to these species in having cheiroid, ellipsoid to cylindrical, not complanate, septate, closely appressed conidia, and with or without appendages (Jayasiri et al. 2019; Shen et al. 2022). However, *D. luojiensis* can be distinguished from *D. lithocarpus* by its larger conidia (56–71 × 22–40 µm vs. 35–40 × 12–18 µm) with appendages, and with more rows of cells (7 rows vs. 6 rows) (Jayasiri et al. 2019). *Dictyocheiropora luojiensis* differs from *D. multiappendiculata* by having larger conidia (56–71 × 22–40 µm vs. 55–62 × 19–22 µm) and rare appendages, whereas appendages are common in *D. multiappendiculata* (Shen et al. 2022). *Dictyocheiropora luojiensis* differs from *D. suae* by its smaller conidia (56–71 × 22–40 µm vs. 72–79 × 20–25 µm), and fewer cells in each row of cells (8–12 cells vs. 12–15 cells) (Shen et al. 2022). Conidial size is one of the important criteria for distinguishing dictyosporium-like taxa (Goh et al. 1999). Based on the unique morphological characters and phylogenetic distance, we therefore introduce *D. luojiensis* as a new species here.

Massarinaceae Munk

Helminthosporium Link

Helminthosporium was introduced by Link (1809) with *H. velutinum* as the type species. Species of *Helminthosporium* are widely distributed and mainly saprobic on a broad range of natural substrates such as decaying wood, plant stems, bark, dung, and occasionally insects, and some species have been reported as opportunistic human pathogens (Luttrell 1964; Alcorn 1988; Konta et al. 2023; Hyde et al. 2023, 2024). The genus is classified in *Massarinaceae* (*Pleosporales*), and is characterized by macronematous, cylindrical, septate, erect conidiophores with polytretic conidiogenous cells and acropleurogenous, clavate or obclavate, distoseptate conidia with a flat, ringed pore at the base (Luttrell 1964; Liu et al. 2022; Hyde et al. 2023). Although over 780 names have been listed under *Helminthosporium* (Index Fungorum 2026), many were reclassified based on morphological inconsistencies with the characteristics of the genus. In addition, recent phylogenetic analyses based on molecular data indicate that

Helminthosporium is polyphyletic (Konta et al. 2021; Chen et al. 2022). In this study, we introduce a new species of *Helminthosporium* based on morphological characteristics and phylogenetic analysis.

5. *Helminthosporium xinjiangense* R.J. Xu, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 9

Chinese name: – 新疆长蠕孢 (xin jiang chang ru bao)

Index Fungorum number: IF 905028; **Facesoffungi number:** FoF 19297

Etymology: Refers to Xinjiang Autonomous Region in China, where the type specimen of this species was collected.

Holotype: HKAS 151642

Saprobic on decaying wood in a freshwater habitat.

Sexual morph: Undetermined. **Asexual morph:** Colonies on natural substratum, superficial, effuse, scattered, hairy, dark brown. *Mycelium* mostly immersed, composed of branched, septate, brown to dark brown, smooth-walled hyphae.

Conidiophores 214–433 × 9–12 µm ($\bar{x}$ = 329 × 11 µm, n = 20), macronematous, mononematous, solitary or in groups, erect, cylindrical, straight or flexuous, unbranched, dark brown to black, smooth-walled. *Conidiogenous cells* 47–112 × 5–9 µm ($\bar{x}$ = 75 × 8 µm, n = 20), polytretic, integrated, terminal and intercalary, cylindrical, brown, smooth-walled. *Conidia* 55–89 × 8–11 µm ($\bar{x}$ = 66 × 10 µm, n = 20), acropleurogenous, solitary, obclavate-rostrate, straight or curved, usually curved, tapering towards the rounded apex, brown, subhyaline at the apex, 6–9-distoseptate, smooth-walled, with a conspicuous black scar at the base.

Culture characters: Conidium germinating on PDA within 24 h and germ tubes produced from both ends or middle. Colonies on PDA reaching 10 mm diam., in a week at room temperature, effuse, hairy, mycelium radiating outwards, fimbriate edge, dense, pale. Mycelium superficial and partly immersed, light brown.

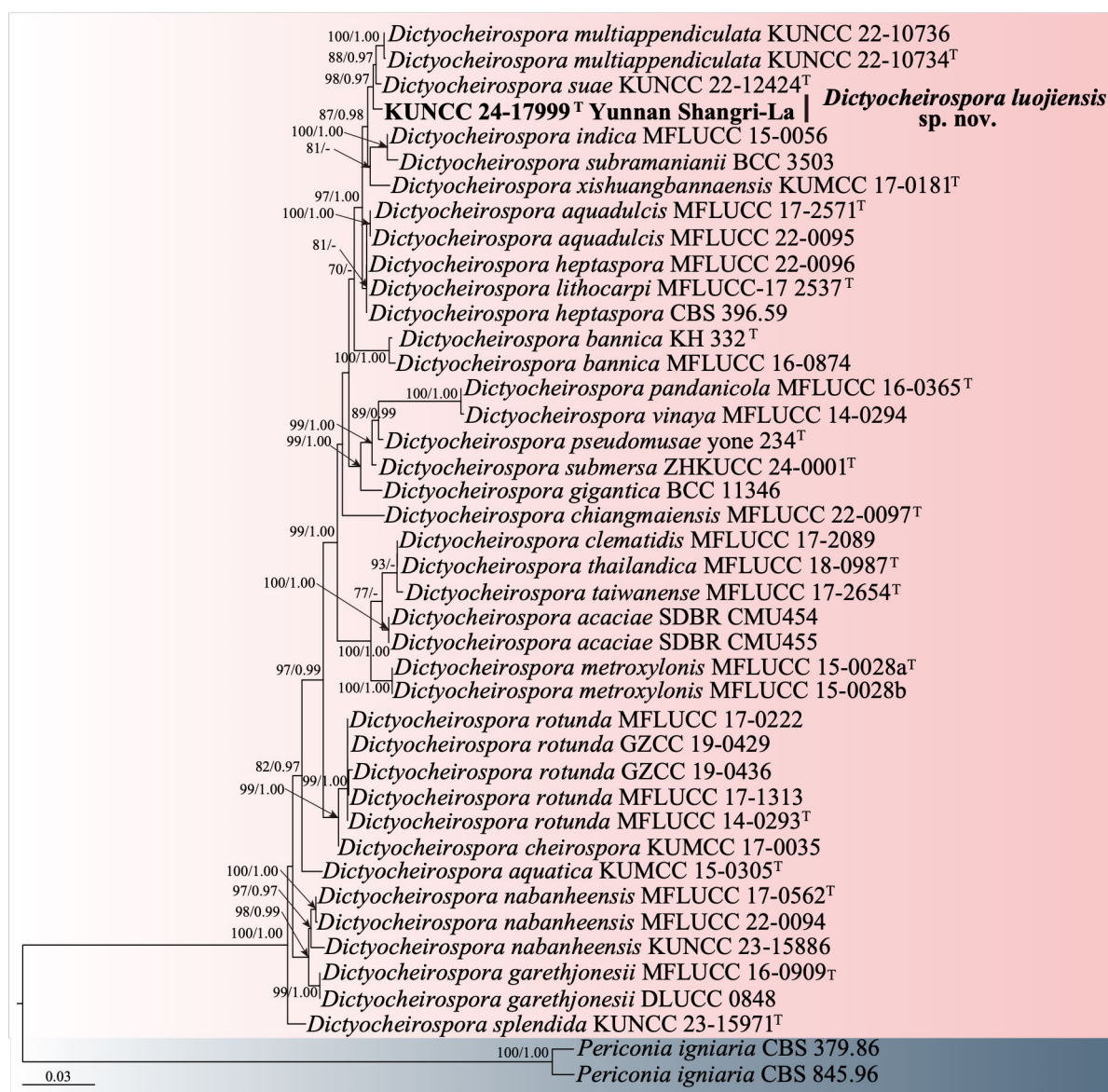


Fig. 6 Maximum likelihood majority rule consensus tree for *Dictyocheirospora* using SSU, ITS, LSU and *tef1-α* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Periconia igniaria* (CBS: 379.86 and CBS: 845.96). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

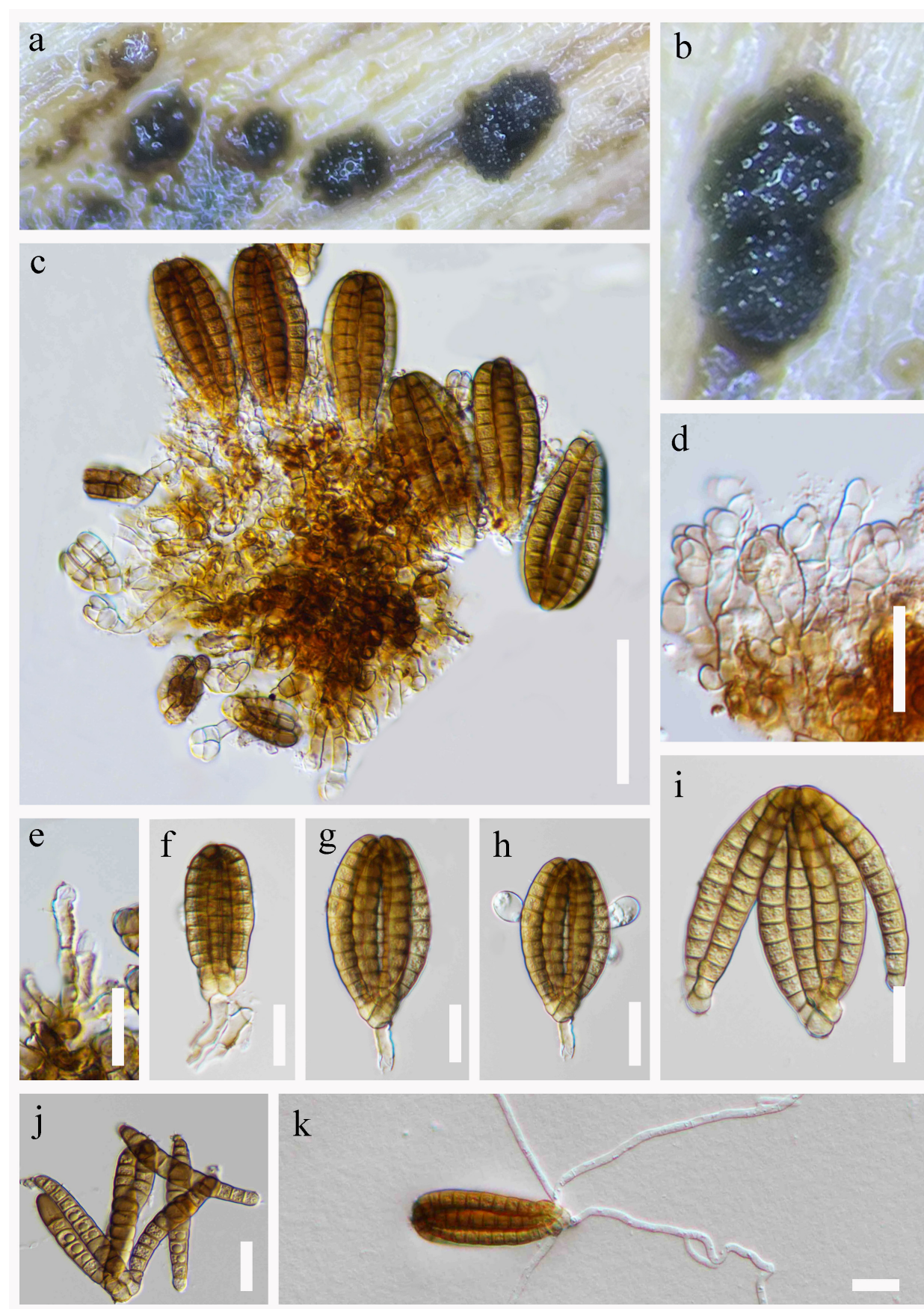
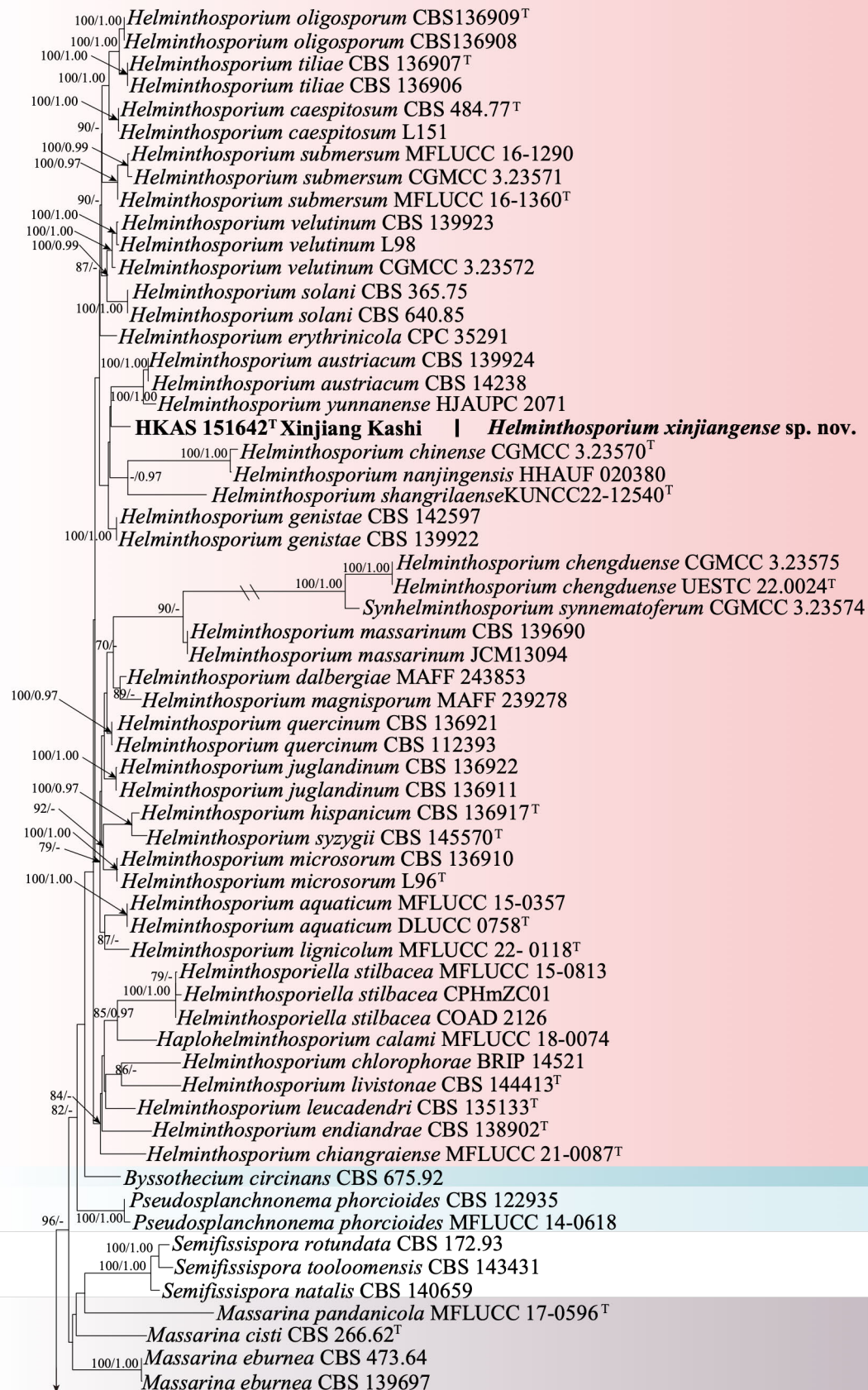


Fig. 7 *Dictyocheirospora luojiensis* (HKAS 136148, **holotype**) a, b Colony on natural substrates. c Conidiophores and conidia. d, e Conidiophores and conidiogenous cells. f–j Conidia. k Germinated conidium. Scale bars: c = 50 μ m, d–k = 20 μ m.

Material examined: CHINA, Xinjiang Autonomous Region, Kashi, Yecheng City, 37° 45' 8.87" N, 77° 25' 7.71" E, 1490 m a.s.l., on decaying wood submerged in a freshwater habitat, 18 July 2021, R.-J. Xu, MD-176A (HKAS 151642, holotype), ex-type culture KUNCC 25-21367.

Notes: In phylogenetic analyses, our isolate formed a sister clade with *Helminthosporium austriacum* and *H. yunnanense* (Fig. 8). Sequence comparison of the ITS region



◀ **Fig. 8** Maximum likelihood majority rule consensus tree for *Helminthosporium* using SSU, LSU, ITS, *rpb2* and *tef1*-α sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML BS/PP. The scale bar represents the expected number of changes per site. The tree is rooted with *Periconia pseudodigitata* (CBS 139699). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

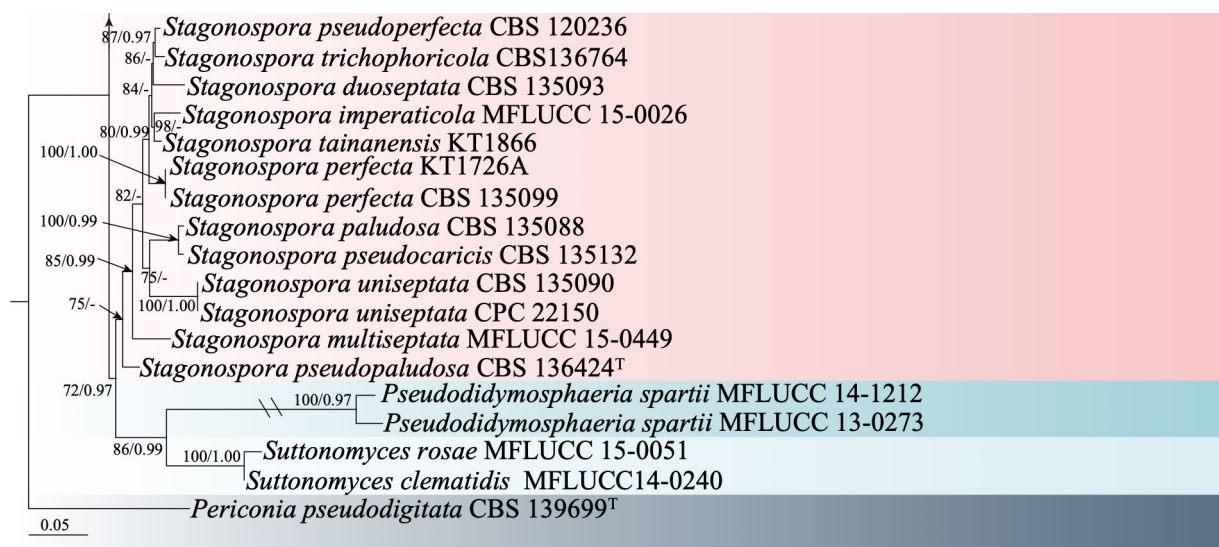


Fig. 8 (continued)

showed nucleotide differences of 13.64% (70/513 bp, excluding gaps) and 15.20% (78/513 bp, excluding gaps) between *H. xinjiangense* and *H. austriacum*, *H. xinjiangense* and *H. yunnanense*, respectively. Morphologically, *H. xinjiangense* differs from *H. austriacum* by having shorter conidiophores (214–433 × 9–12 μm vs. 275–700 × 11.5–19 μm), and more slender, usually curved conidia (55–89 × 8–11 μm vs. 35–48 × 13.7–16.5 μm) (Voglmayr et al. 2017), and differs from *H. yunnanense* in shorter conidiophores (214–433 × 9–12 μm vs. 560–680 × 12.5–15.5 μm) without one cylindrical, enteroblastic percurrent extension, and larger, obclavate-rostrate conidia (55–89 × 8–11 μm vs. 30.5–55.5 × 9–11 μm) with a higher number of distosepta (6–9 vs. 4–7) (Liu et al. 2022). Therefore, we introduce *H. xinjiangense* as a new species.

***Hermatomyces* Locq. ex A. Hashim. & Kaz. Tanaka**

Hermatomyces was informally introduced by Locquin (1984) and later validated by Hashimoto et al. (2017) to accommodate the monotypic genus *Hermatomyces*. Members of *Hermatomyces* are saprobic on various plant substrates. The sexual morph has not yet been observed. Asexual structures include sporodochial, pulvinate conidiomata that are dark brown to black. Conidiophores are pale brown and mononematous, bearing monoblastic, integrated, terminal conidiogenous cells that are cylindrical (Castañeda & Heredia 2000; Ren et al. 2021).

***Hermatomyces* Speg**

Hermatomyces has a wide geographic range, occurring in both tropical and temperate regions, including Brazil, China, Cuba, Japan, Panama, the Philippines, Thailand, and Venezuela (Doilom et al. 2017; Hashimoto et al. 2017b; Koukol et al. 2018; Tibpromma et al. 2018). To date, host specificity within *Hermatomyces* remains unclear, as species have been identified on hosts from multiple plant families, including

Acanthaceae, *Arecaceae*, *Asteraceae*, *Fabaceae*, and *Pandanaceae* (Doilom et al. 2017; Hashimoto et al. 2017; Koukol et al. 2018; Tibpromma et al. 2018). The sexual-asexual connection in *Hermatomyces* has not yet been established, since no sexual morph has been documented for any species in the genus (Hashimoto et al. 2017b; Tibpromma et al. 2018). Up to now, 34 species have been accepted within *Hermatomyces* (Hyde et al. 2024a; Shen et al. 2024; Koukol et al. 2025).

6. *Hermatomyces motuoensis* R.J. Xu & Q. Zhao, sp. nov. Fig. 11

Chinese name: – 墨脱柱格孢 (mo tuo zhu ge bao)

Index Fungorum number: IF 905256; **Facesoffungi number:** FoF 19298

Etymology: The epithet refers to Motuo County, located in Xizang of China, where the type specimen was collected.

Holotype: HKAS 151643

Saprobic on decaying wood in a freshwater habitat.

Sexual morph: Undetermined. **Asexual morph:** Colonies on natural substrate effuse, superficial, scattered, conspicuous, flattened, consisting of a sterile mycelial outer zone and a round, glistening, brown to black. **Mycelium** mostly immersed, composed of branched, septate, brown to dark brown, smooth-walled hyphae. **Conidiophores** micronematous, mononematous, unbranched, straight or flexuous, hyaline, septate, smooth. **Conidiogenous cells** 11–20 × 2–7 μm ($\bar{x}$ = 16 × 4 μm, n = 20), holoblastic, monoblastic, integrated, terminal, cylindrical, hyaline to subhyaline. **Conidia** 19–33 × 17–27 μm ($\bar{x}$ = 28 × 22 μm, n = 30), dimorphic, thick-walled, smooth. lenticular conidia, subglobose to ellipsoidal, muriform, smooth, central cells dark brown to black, peripheral cells narrow, flattened, subhyaline to pale brown, obovoid or oblong in side view, cylindrical conidia, 2–3-celled, symmetrical or asymmetrical, distinctly constricted at the septum, guttulate, straight or flexuous, hyaline, the upper

cells usually subcylindrical and the apex rounded or slightly flattened, often slightly attenuated and dark brown or black, the lower cells are ellipsoidal.

Cultural characteristics: Conidia germinating on PDA and germ tubes produced from peripheral cells of conidium

within 24 h. Colonies on PDA, reaching 30 mm after one month at room temperature, colony circular, edge smooth, surface hyphae grey-brown, fluffy, flocculent, reverse side grey-brown to brown, dense, cracked in the middle.

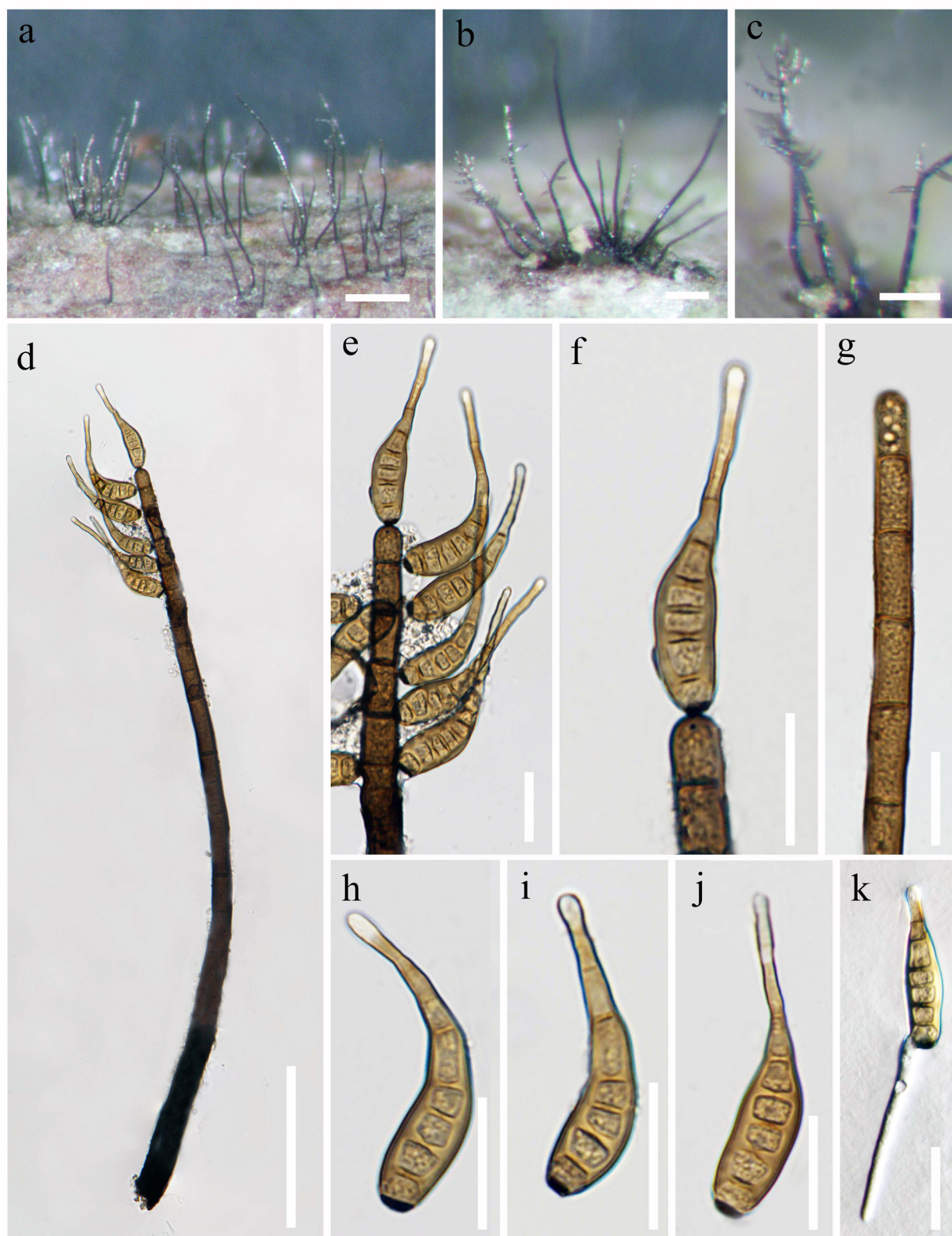


Fig. 9 *Helminthosporium xinjiangense* (HKAS 151642, holotype) a–c Colony on natural substrates. d, e Conidiophores and conidiogenous cells. f, g Conidiogenous cells with conidia. h–j Conidia. k Germinated conidium. Scale bars: d = 50 μm, e–k = 20 μm.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, Beibong Township, 29° 14' 35.76" N, 95° 10' 6.94" E, 1278 m a.s.l., on decaying wood submerged in a freshwater stream, 12 July 2022, R.J. Xu, MD-200A (HKAS 151643, holotype), ex-type culture KUNCC 25-21368.

Notes: Phylogenetic analysis revealed that *Hermatomyces motuoensis* clustered with *H. hongheensis*, *H. constrictus*, *H. iriomotensis*, *H. krabiensis* and *H. griseomarginatus* with 84% ML/0.68 BYPP support (Fig. 10). Morphologically, *H. motuoensis* displays dimorphic conidia, characterized by both lenticular and cylindrical forms. This morphological trait aligns with the conidial characteristics observed in *H. constrictus*, *H. iriomotensis*, and *H. krabiensis*, thereby indicating a potential phylogenetic relationship among these

taxa (Spegazzini 1910; Tibpromma et al. 2016; Hashimoto et al. 2017; Koukol et al. 2018; Ren et al. 2021). However, *H. motuoensis* can be distinguished from *H. constrictus* in having larger conidiogenous cells (11–20 µm vs. 4–7 µm), and the cylindrical conidia with more cells (2–3-cells vs. 2-cells) (Koukol et al. 2018). Compared to *H. iriomotensis*, *H. motuoensis* has smaller lenticular conidia (28 × 22 µm avg. vs. 33.6 × 23.5 µm, avg.) and fewer septa (1–2-septate vs. 3–7-septate) in cylindrical conidia (Tibpromma et al. 2016). Furthermore, a megablast search of NCBI's GenBank nucleotide database, the best matching result of the ITS sequence is *H. bifurcatus* (voucher: PMA:116075, sequence ID: LS398263, similarities: 616/656 (94%), 10 gaps. Therefore, based on morphological and molecular sequence evidence, *H. motuoensis* is herein introduced as a novel species.

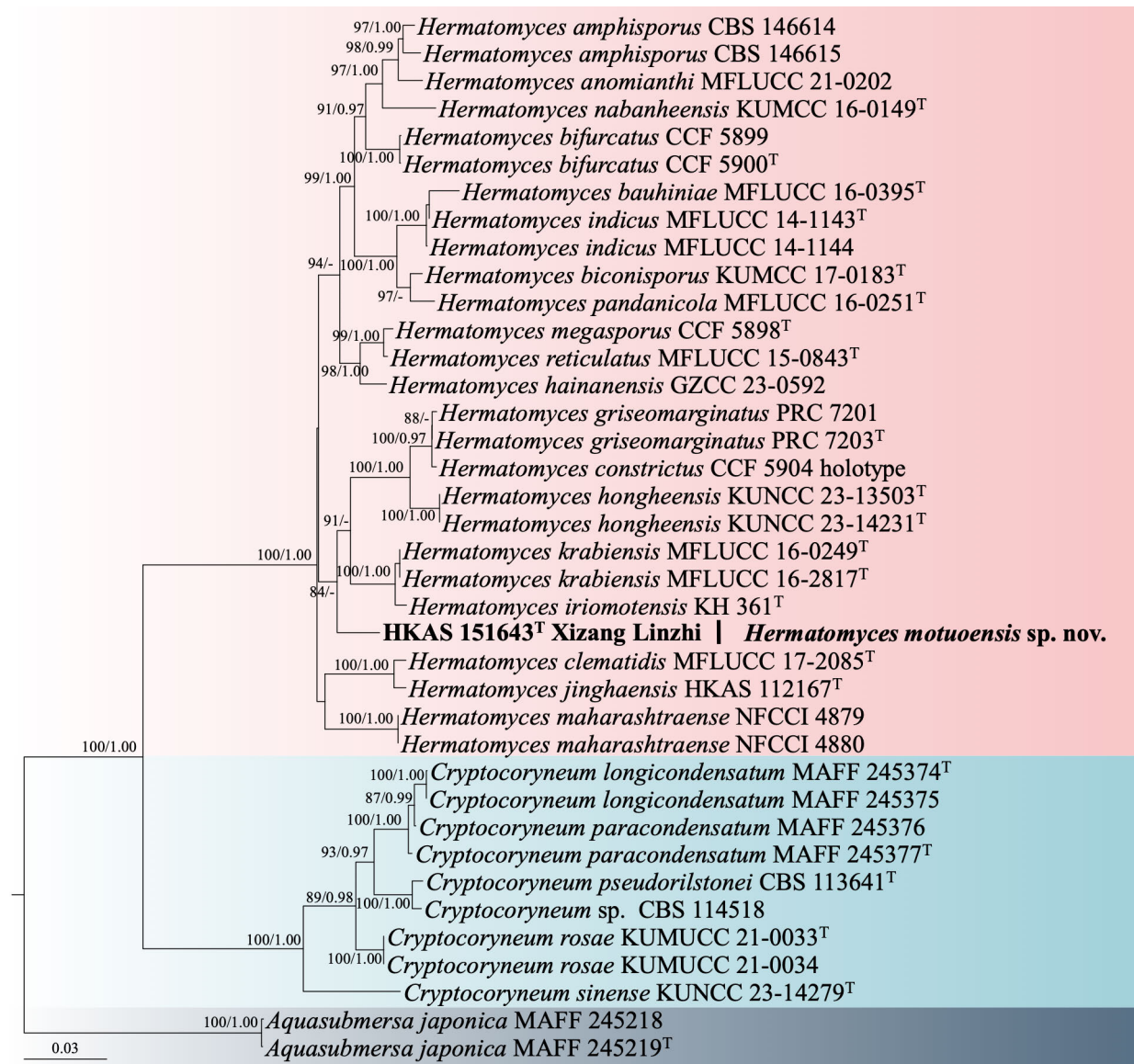


Fig. 10 Maximum likelihood majority rule consensus tree for *Hermatomyces* using ITS, LSU, SSU, *tef1*-α and *rpb2* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Aquasubmersa japonica* (MAFF 245218 and MAFF 245219). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

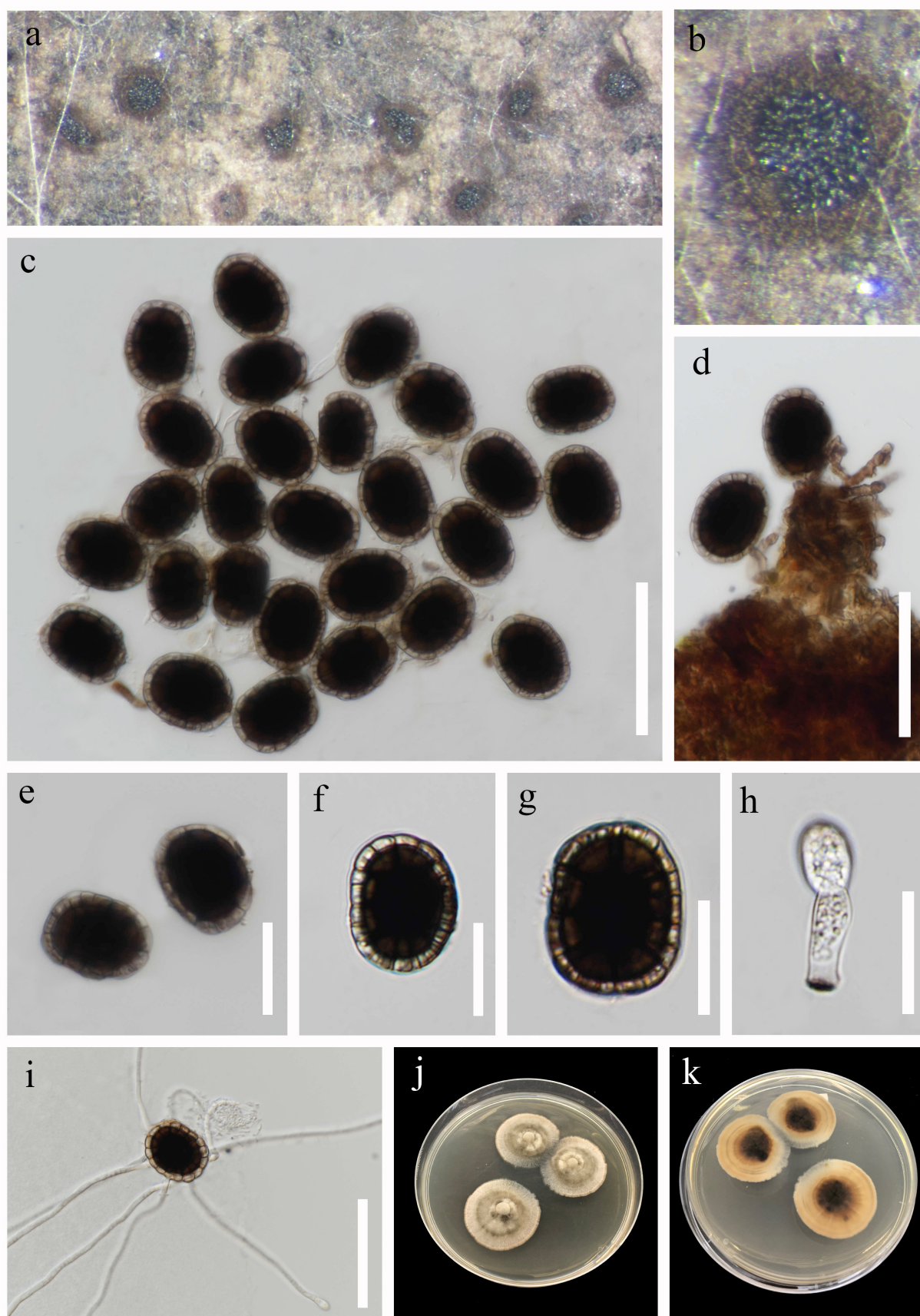


Fig. 11 *Helminthosporium motuoensis* (HKAS 151643, holotype) a, b Colonies on natural substrate. c, d Conidiophores, conidiogenous cells and conidia. e–h Conidia. i Germinated conidium. j, k Culture on PDA medium, j from above, k from below. Scale bars: c, d, i = 50 μ m, e–h = 20 μ m.

Periconiaceae Nann**Periconia** Tode

Periconiaceae was delineated by Nannizzi (1934) and represented by the genus *Periconia*. The family was resurrected by Tanaka et al. (2015) and placed in *Pleosporales* based on morphological and phylogenetic evidence. Currently, the family comprises a single genus *Periconia*. Subsequent taxonomic reassessments by Yang et al. (2022a) led to the synonymization of *Bambusistroma* and *Noosia* under *Periconia*, based on morphological traits observed in sexual reproductive structures and multilocus phylogenetic studies. Additionally, Liao et al. (2024a) suggest that *Flavomyces fulophazii* should be synonymized with *Periconia*. However, further corroborative data is essential to affirm the taxonomic placement of *F. fulophazii*.

Periconia was introduced by Tode (1790) with *P. lichenoides* as the type species. *Periconia* was re-classified by Tanaka et al. (2015) based on the multi-locus phylogenetic analysis and placed in *Periconiaceae*. Species of *Periconia* are mostly reported as saprobes as their asexual morph, and also have some species as endophytes and pathogens, such as *P. endophytica* was isolated as an endophytic fungus from asymptomatic leaves of *Wurfbainia villosa* in China (Liao et al. 2024a). *Periconia circinata* was isolated as a pathogen causing blackening and rotting of wheat roots and stem bases (Goga 2000). To date, *Periconia* has 201 epithets listed in Species Fungorum.

7. *Periconia xizangensis* R.J. Xu, Q. Zhao & K.D. Hyde, sp. nov. Fig. 13

Chinese name: – 西藏黑团孢 (xi zang hei tuan bao)

Index Fungorum number: IF 905030; **Facesoffungi number:** FoF 17397

Etymology: The epithet refers to Xizang, China, where the type specimen was collected.

Holotype: HKAS 136110

Saprobic on decaying wood submerged in a freshwater stream. **Sexual morph:** Undetermined. **Asexual morph:** Colonies effuse, hairy, velvety, scattered or in small groups, with glistening, pale brown to brown conidial masses at the apex. **Mycelium** is mostly superficial, partially immersed, consisting of branched, septate, smooth, subhyaline hyphae. **Conidiophores** 366–601 × 13–19 µm ($\bar{x}$ = 467 × 16 µm, n = 20), macronematous, mononematous, solitary, erect, unbranched or occasionally 2–3-branched, septate, straight or flexuous, cylindrical, tapering towards at the apex, with cylindrical to elliptical heads at the apex, often swollen at the base, dark brown at the base, light brown towards the apex. **Conidiogenous cells** polyblastic, pale brown to brown, terminal, subglobose or elliptical, smooth-walled. **Conidia** 6–8.5 × 5.6–8 µm ($\bar{x}$ = 7.3 × 7.3 µm, n = 40), solitary or aggregated in masses, globose, brown, aseptate, verruculose.

Culture characteristics: Conidia germinating on PDA medium within 24 h and germ tubes produced from both ends. Colonies grown on PDA reached 60 mm diam at room temperature in two weeks, filamentous, with velvety, flat, dark brown mycelium, aerial mycelium on the surface, from below dark brown with undulate margin.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, 29°19'43.69" N, 95°21'19.27" E, 798 m a.s.l., on decaying wood submerged in a freshwater

stream, 12 July 2022, R.J. Xu, XK-14 (HKAS 136110, holotype), ex-type culture KUNCC 10433.

Notes: Phylogenetic analyses showed that our collection (KUNCC 10433) formed a distinct clade within *Periconia*, and formed a sister relationship with the ex-type strain of *P. thailandica* (MFLUCC 17-0065) (Fig. 12). *Periconia xizangensis* differs from *P. thailandica* in having conidiophores sometimes with 2–3-branched and cylindrical to elliptical heads (Liu et al. 2017).

Phaeosphaeriaceae M.E. Barr

Phaeosphaeriaceae, typified by *Phaeosphaeria*, currently comprises 84 genera and remains one of the largest families within *Pleosporales* (Wanasinghe & Maharachchikumbura 2023). Species in this family exhibit high diversity and are widely distributed in terrestrial environments worldwide, functioning as plant pathogens, saprobes, endophytes, and lichenicolous fungi (Phookamsak et al. 2014). Many species are significant plant pathogens that affect economically important crops, such as *Phaeosphaeria* and *Paraconiothyrium* which cause leaf spots on wheat and rice (Phookamsak et al. 2014). Although ongoing research integrating morphological and phylogenetic methods has led to considerable progress in identifying these taxa, the classification is still not fully resolved.

Setophoma Gruyter, Aveskamp & Verkley

Setophoma was originally published to accommodate *Phoma terrestris* and *Pyrenochaeta sacchari* (Liu et al. 2019a). Currently, 19 species are listed in Index Fungorum. They were thought to be well-resolved, since many of them are available of molecular data and colour illustrate (Phookamsak et al. 2014). Species in this genus are commonly found in asexual morph, living as plant pathogens (Crous et al. 2014, 2016). Morphologically, they are characterised by phialidic conidiogenous cells, and hyaline, ellipsoidal to subcylindrical, aseptate conidia (Liu et al. 2019a).

8. *Setophoma manglietiae* H.D. Yang, K.D. Hyde & Q. Zhao, sp. nov. Fig. 15

Chinese name: – 木莲壳霉 (mu lian ke mei)

Index Fungorum number: IF905257; **Facesoffungi number:** FoF 19299

Etymology: Referring to the host plant *Manglietia fordiana* (*Magnoliaceae*).

Holotype: HKAS 154724

Leaf spots amphigenous, angular, brown to grey. **Sexual morph:** Undetermined. **Asexual morph:** Colony on PDA grows slowly, reaching 66 mm after 65 days. Upper surface, flat, cottony, white at the beginning, forming pink patches near the centre at the later, undulate to entire edge, lower surface brown with pink plaque, white at the edge. Colony on SNA, upper white, flat, with abundant aerial mycelium, undulate to entire edge, lower surface white. Colony on WA, mycelium sparse, growth zone appears grey. The hyphae measure 1.8–3.3 µm in diameter, are septate, hyaline to lightly pigmented brown, and contain abundant guttules commonly aggregate to form inflated, globose, or bead-like structures.

Material examined: CHINA, Yunnan Province, Kunming City, on leaf of *Manglietia fordiana*, 14 March 2022, Hong-De Yang14 (HKAS 154724, holotype), ex-type culture KUNCC 23-14872.

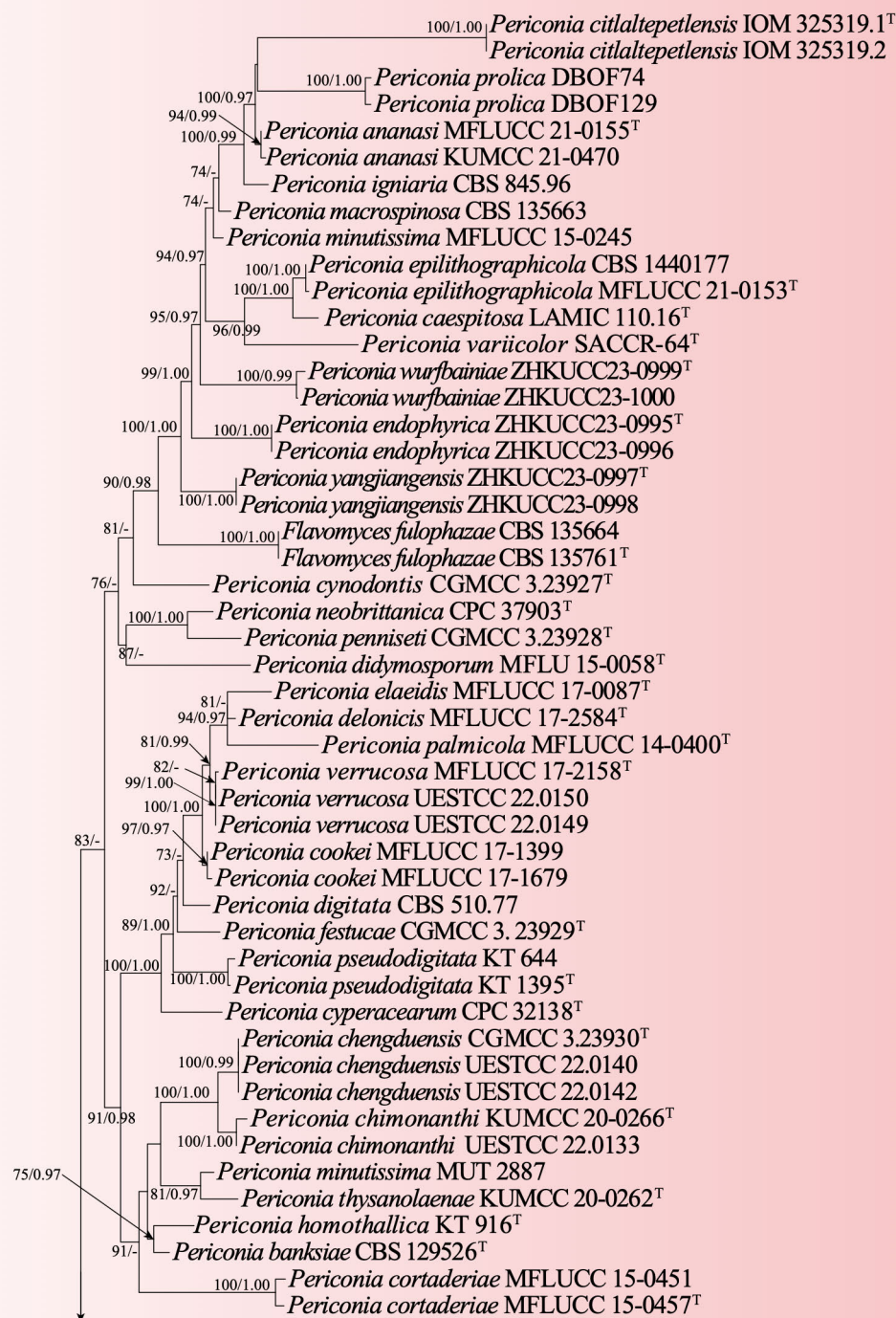


Fig. 12 Maximum likelihood majority rule consensus tree for *Periconia* using ITS, LSU, SSU and *tef1-α* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Morosphaeria ramunculicola* (KH 220) and *M. velatispora* (KH 221). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Notes: *Setophoma manglietiae* exhibits a phylogenetic affinity with *S. chromolaenae*, *S. vernoniae*, and *S. syzygii* (Fig. 14), all of which have been isolated from foliar tissues and associated with leaf pathologies. Our isolate presents shared phenotypic traits, such as the formation of colony patches and an undulate to entire margin; however, it is distinguished by its pigmentation, which varies from white to grey and pink (Quaedvlieg et al. 2013; Crous et al. 2014, 2021). Due to an inability to induce sporulation on various media, including

PDA, SNA, and WA, micromorphological characteristics could not be assessed. Consequently, identification was primarily based on colony morphology and molecular data. It is noteworthy that *S. chromolaenae*, *S. vernoniae* and *S. syzygii* are characterized by the production of hyaline, aseptate, subcylindrical conidia (Quaedvlieg et al. 2013; Crous et al. 2014, 2021). Thus, further investigations are warranted to confirm the morphological attributes of our species.

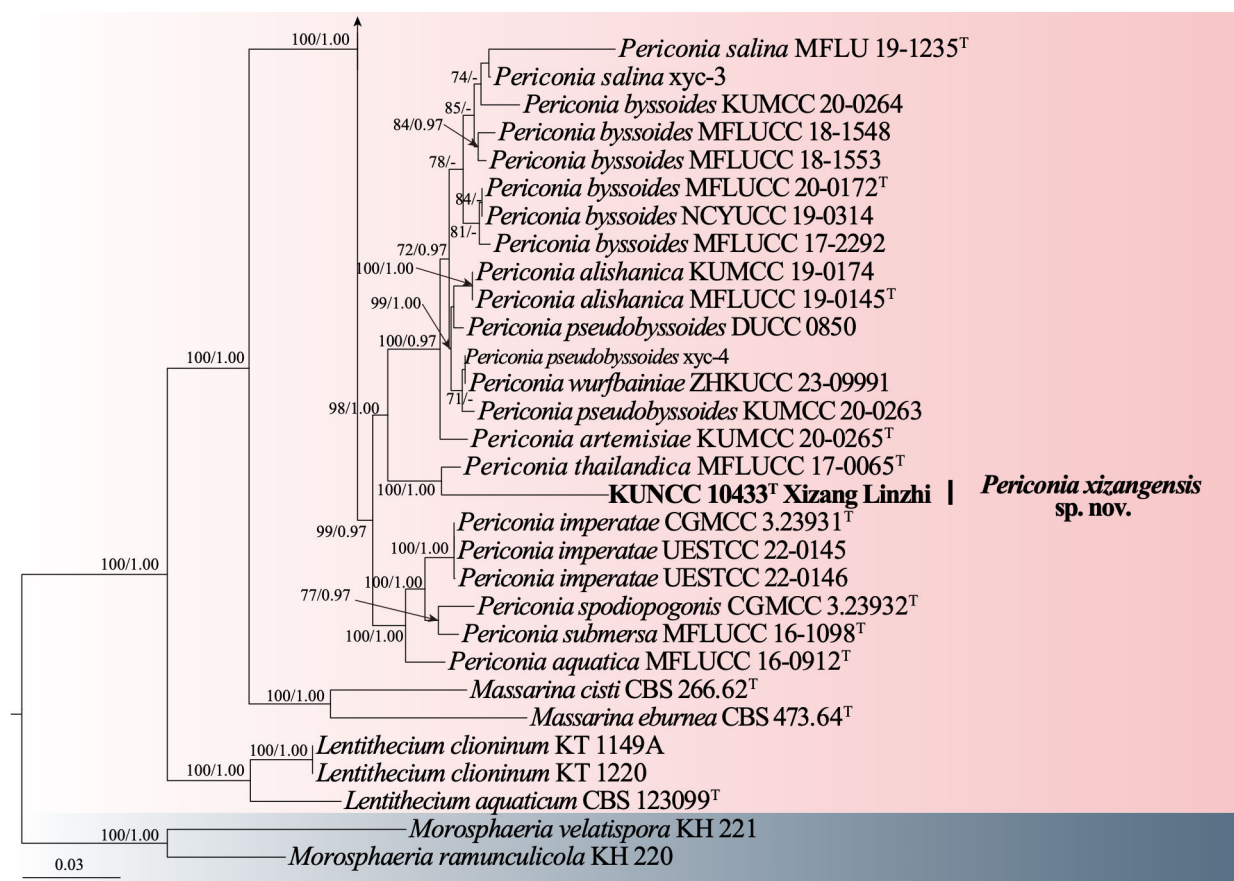


Fig. 12 (continued)

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray.**Tetraploa** Berk. & Broome

Tetraploa (synonym *Tetraplosphaeria*) was described by Berkeley & Broome in 1850 to accommodate the type species *T. aristata*. Species of the genus *Tetraploa* are predominantly isolated from bamboos, various herbaceous plants, and decaying wood across both terrestrial and aquatic ecosystems (Ando 1992; Dong et al. 2020; Hyde et al. 2020b; Phookamsak et al. 2022; Li et al. 2023; Liao et al. 2024b). This genus exhibits both sexual and asexual reproductive strategies. The asexual morph is distinguished by the absence of conidiophores, featuring monoblastic conidiogenous cells, and producing verrucose, short cylindrical to obpyriform conidia arranged in several columns, each adorned with setose appendages at the apex (Tanaka et al. 2009; Hyde et al. 2013). In contrast, the sexual morph is characterized by the presence of immersed to superficial, globose to subglobose ascomata, short-pedicellate asci, and septate, hyaline ascospores that are narrowly fusiform to broadly cylindrical, often enveloped by a mucilaginous sheath-like appendage (Tanaka et al. 2009; Hyde et al. 2013; He et al. 2025). There are about 30 species epithets linked to the genus *Tetraploa* (Hyde et al. 2024a).

9. *Tetraploa hainanensis* X. Tang, Jayaward., R. Jeewon & J.C. Kang, in Tang, Jeewon, Lu, Alrefaei, Jayawardena, Xu, Ma, Chen & Kang, MycoKeys 100: 189 (2023) Fig. 17

Chinese name: – 海南四绺孢 (hai nan si liu bao)

Index Fungorum number: IF 900952; **Facesoffungi number:** FoF 14667

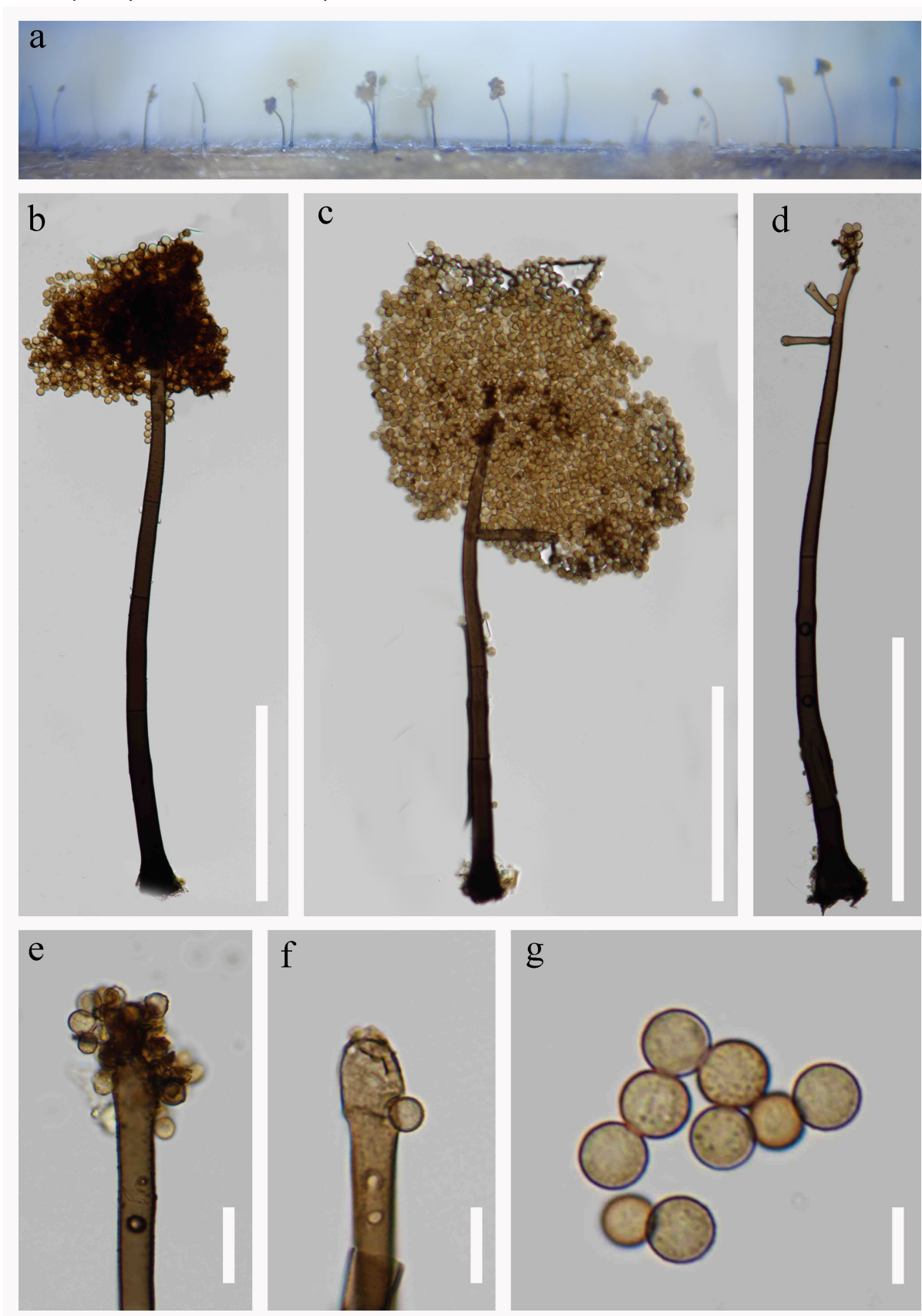
Saprobic on the dead stem of *Zea mays*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. **Colonies** effuse, brown to dark brown, hairy, gregarious on the host substrate. **Mycelium** partly superficial, partly immersed, septate, branched and pale brown. **Conidiophores** absent. **Conidiogenous cells** integrated, monoblastic, determinate. **Conidia** 29–44 × 17–31 µm ($\bar{x}$ = 36 × 25 µm, n = 20), cylindrical with obtuse ends, dark brown, solitary, verrucose, smooth, composed of four columns of cells, sometimes five columns of cells, 2–6-septate in each column, with four apical appendages. **Appendages** 59–193 × 4–6 µm ($\bar{x}$ = 131 × 5 µm, n = 30), cylindrical, solitary, straight or slightly flexuous, smooth-walled, unbranched, pale brown to brown, guttulate, 4–8-septate in each column, wide at the base, tapering toward the apex with hyaline.

Material examined: CHINA, Yunnan Province, on a dead stem of *Zea mays*, 9 September 2022, Yanyan Yang, YYY333 (HKAS 144363), culture KUNCC 25-20221. Yunnan Province, Xishuangbanna, Mengyang Town, on a dead stem of *Zea mays*, 6 September 2022, Yanyan Yang, YYY333-1 (HKAS 144364), culture KUNCC 25-20222.

Notes: In the integrated phylogenetic analyses encompassing LSU, ITS, and SSU, our isolates exhibited a robust clustering with *Tetraploa hainanensis* (GZCC 23-0601), attaining statistical support values of 100% ML/1.00 BYPP (Fig. 16). Sequence comparison at the nucleotide level between our new isolate and *T. hainanensis* (GZCC 23-0601) highlighted divergences of 0.25% (807/809 bp) for LSU, 1.2% (492/498 bp) for ITS, and 0% (780/780 bp) for SSU. Furthermore, both taxa exhibit analogous morphological traits, characterized by cylindrical, verrucose conidia

arranged in four columns of cells, accompanied by cylindrical and septate appendages. However, our isolate differs from the *T. hainanensis* (GZCC 23-0601) in having lower number of septate of appendages (4–8-septate vs. 5–16-septate) (Tang et al. 2023). *Tetraploa hainanensis* was reported from the

unidentified decaying wood in Hainan Province, China. This study provides the first host record of *T. hainanensis* on a dead stem of *Zea mays* with evidence of morpho-molecular characterizations.



◀ **Fig. 13** *Periconia xizangensis* (HKAS 136110, **holotype**) a Colonies on natural substrate. b, c Conidiophores and conidiogenous cells. d–f Conidiogenous cells with developing conidia. g Conidia. Scale bars: b–d = 200 μ m, e, f = 20 μ m. g = 10 μ m.

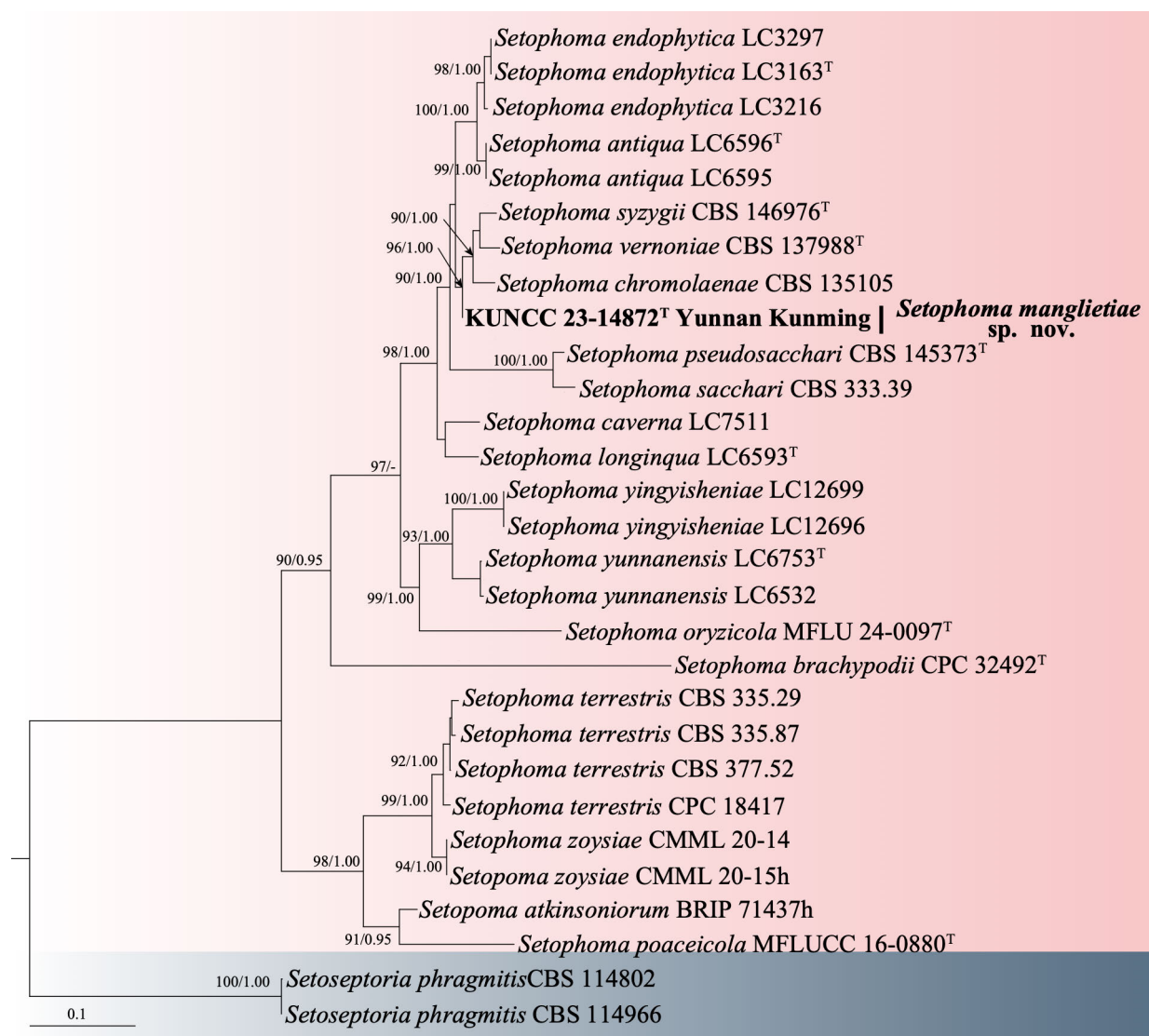


Fig. 14 IQ-tree based on ITS, LSU, *tef1-α*, *rpb2* and *tub2* sequences, SH-aLRT support (greater than 90, left) and Bayesian Posterior Probability (greater than 0.9, right) are shown in nodes. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Torulaceae Corda

Torula Pers

Torula was introduced by Persoon in 1795, and is characterized by its type species *T. herbarum*. This genus is primarily recognized through its asexual reproductive structures, which include macronematous, mononematous conidiophores, holoblastic conidiogenous cells that exhibit a clavate to ellipsoidal morphology, and acrogenous, verrucose structures bearing septate conidia (Jayawardena et al. 2022; Hyde et al. 2023; He et al. 2024a, 2025). Most species within the *Torula* are found inhabiting freshwater and terrestrial environments (Crous et al. 2015a; Li et al. 2017a; He et al. 2024b). *Torula* is a widely distributed genus, having been documented across various regions including Asia (China,

India, Thailand), Europe (France, Germany, Italy), North America (Crous et al. 2015a; Li et al. 2017a; Su et al. 2018; Boonmee et al. 2021; He et al. 2025; Zhang et al. 2025). It holds the distinction of being the largest genus within *Torulaceae* (He et al. 2024b), with 571 epithets in Index Fungorum (accessed on April 20, 2026). However, it is noteworthy that the majority of these species lack molecular data (Crous et al. 2015a), with only 34 species being corroborated by molecular data (He et al. 2025; Zhang et al. 2025). In this study, based on phylogenetic and morphological analysis and following the guidance of Maharachchikumbura et al. (2021), we introduced a new species, *T. motuoensis*, from Xizang, China.

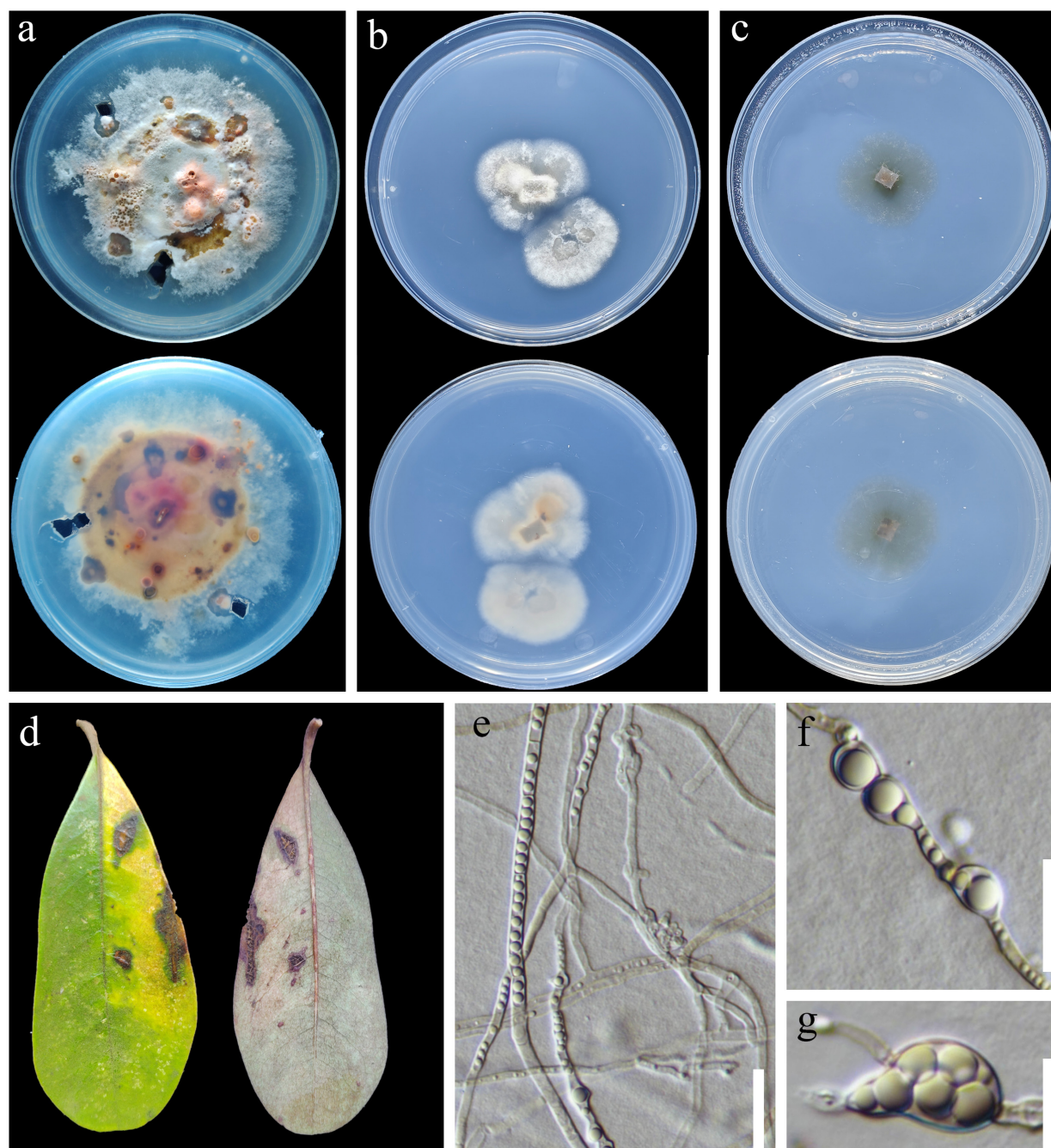


Fig. 15 *Setophoma manglietiae* (HKAS 154724, holotype). a Colony on PDA. b Colony on SNA, HMAS 287387. c Colony on WA. d appearance of leaf spots. e hypha. f, g Chlamydospores. Scale bars: e = 30 μ m, f = 20 μ m, g = 10 μ m.

10. *Torula motuoensis* S.C. He, Q. Zhao & K.D. Hyde, sp. nov. Fig. 19

Chinese name: – 墨脱色串孢 (mo tuo se chuan bao)

Index Fungorum number: IF 905258, **Facesoffungi number:** FoF 19300

Etymology: Referring to the location “Motuo County” where the holotype of this fungus was collected.

Holotype: HKAS 150299

Saprobic on dead stems of *Ageratina adenophora*. **Sexual morph:** Undetermined. **Asexual morph:** Colonies effuse, medium dense, hairy, black brown on the host. **Mycelium** immersed on the substrate, composed of septate, chained, branched, black brown hyphae. **Conidiophores** macronema-

tous, mononematous, erect, flexuous, branched, verruculose, septate, cylindrical, brown to dark brown, $18.6\text{--}54.4 \times 6\text{--}8.8 \mu\text{m}$ ($\bar{x} = 32.5 \times 7.2 \mu\text{m}$, $n = 20$). **Conidiogenous cells** holoblastic, terminal, erect, ellipsoid, with melanized basal regions, bowl, pale brown to brown. **Conidia** phragmospores, catenate, acropleurogenous, moniloid, simple, dry, verruculose, guttulate, thick-walled, rough-walled, 0–multi-septate, pale brown to brown, $10\text{--}62 \times 6\text{--}9 \mu\text{m}$ ($\bar{x} = 38 \times 8 \mu\text{m}$, $n = 30$).

Culture characteristics: germinating within 24 h on PDA at 25 °C, reaching 6.4–6.6 cm after 30 days incubation, above colony black, reverse dark brown, edge entire, undulate, umbonate, surface rough, mycelia dense, no pigment.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, 29°35'N, 95°14'E, 1730 m a.s.l., on dead stems of *Ageratina adenophora* (Asteraceae), 12 July 2022, Shu-Cheng He, HSC821 (HKAS 150299, holotype), ex-type culture: KUNCC 23-17479. *ibid.* HSC805, (HKAS 150300), culture: KUNCC 23-17350.

Notes: The phylogenetic analysis indicated that our isolates of *T. motuoensis* (KUNCC 23-17479 and KUNCC 23-17350) clustered with *T. calceiformis* (HKAS 125551 and HKAS 125552) (Fig. 18). *Torula calceiformis* is known to exhibit saprobic associations with unidentified wood samples

sourced from Guizhou, China (Hyde et al. 2023). Our isolates were collected from *Ageratina adenophora* in Linzhi City, Xizang, China. Morphologically, *T. motuoensis* resembles *T. calceiformis* in having phragmospores, and moniloid, verruculose, multi-septate conidia. Compared to *T. calceiformis*, *T. motuoensis* has longer conidiophores (32.5×7.2 vs. 5.5×6.5 μm) and conidia (38×8 vs. 27.6×9.2 μm). Therefore, based on phylogenetic and morphological analyses, we introduce a new species, *T. motuoensis*, from Linzhi City, Xizang, China.

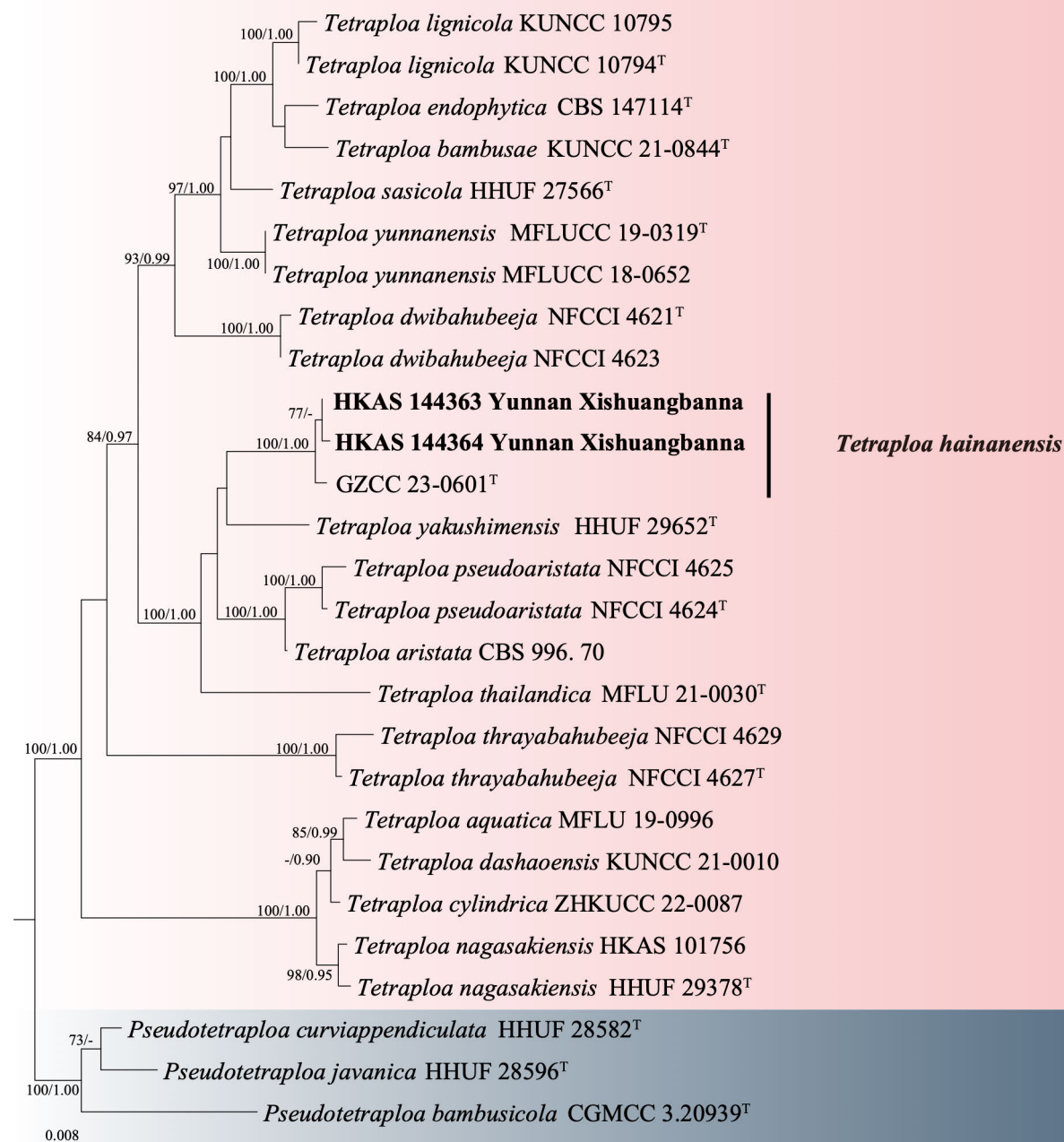


Fig. 16 Maximum likelihood majority rule consensus tree for *Tetraploa* using ITS, LSU and SSU sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML / BYPP. The tree is rooted with *Pseudotetraploa bambusicola* (CGMCC 3.20939), *P. curviappendiculata* (HHUF 28582) and *P. javanica* (HHUF 28596). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

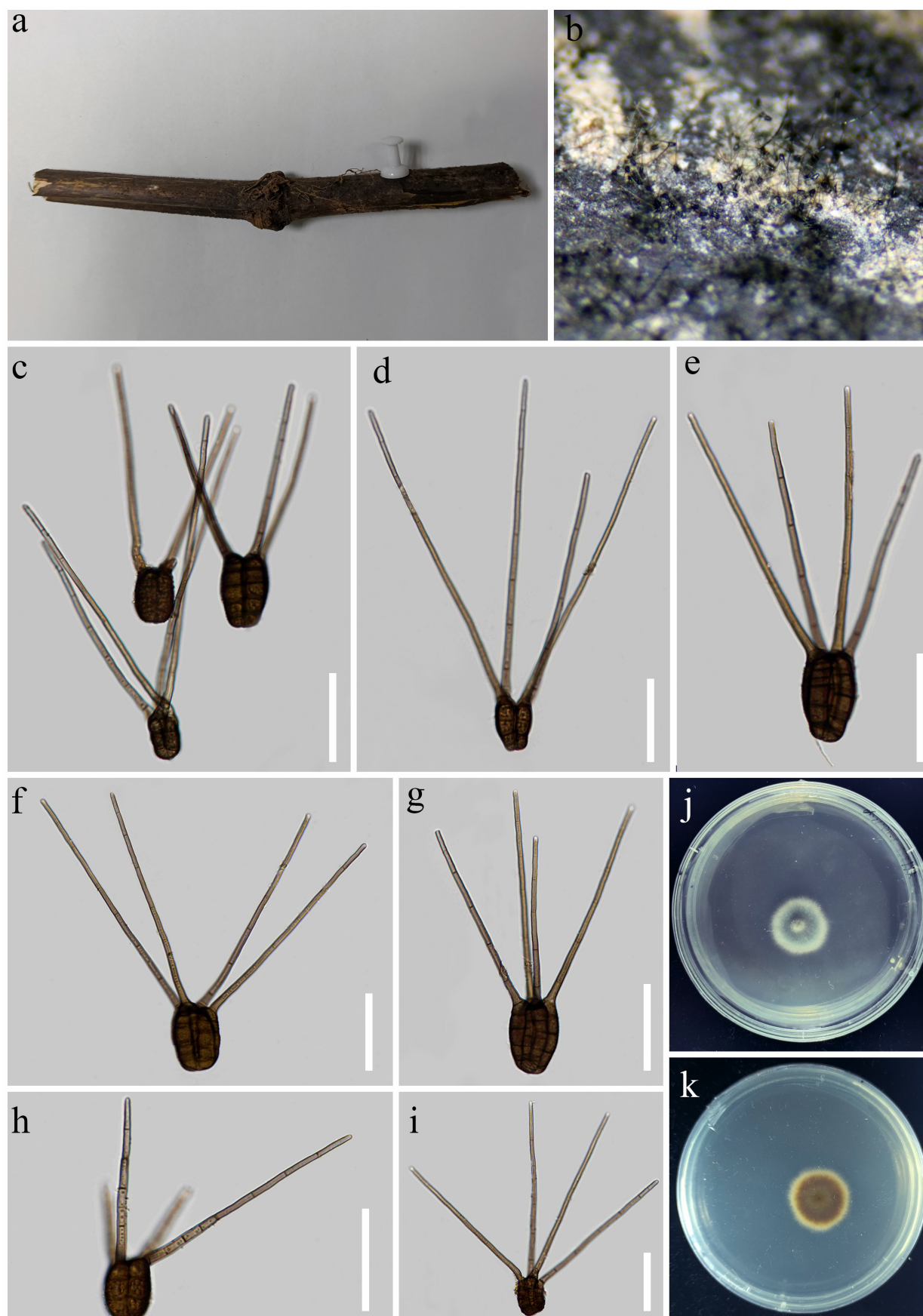
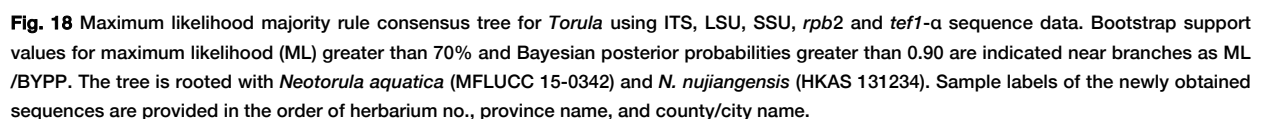


Fig. 17 *Tetraploa hainanensis* (HKAS 144363) a, b Colony on natural substrates. c–e Conidiophores with conidia. f Conidiogenous cells with conidia. g, h Conidia. Scale bars: c–e = 100 μ m, f–h = 10 μ m.



Saprobic on decaying wood submerged in freshwater habitats. **Sexual morph:** Undetermined. **Asexual morph:** *Colonies* superficial, hairy, velvety, white, conidia arising from

aerial hyphae. *Mycelium* partly immersed in the woody substratum and partly superficial, consisting of septate, branched, hyaline, smooth, repent hyphae. *Conidiophores* 15–52 × 4–8 µm ($\bar{x}$ = 30 × 5 µm, n = 10), semi-macronematous, arising singly as lateral branches from the procumbent hyphae, cylindrical, simple or branched, septate, thin-walled, smooth, indistinctly septate, hyaline, flexuous or geniculate. *Conidiogenous cells* monoblastic or polyblastic, denticulate, sympodial proliferations, cylindrical. *Conidia* 58–78 × 8–10 µm

($\bar{x}$ = 65 × 9 µm, n = 30), holoblastic, solitary, borne acrogenously on conidiogenous denticles, becoming lateral after proliferation of the conidiophore, hyaline or very pale yellowish, predominantly fusoid to sickle-shaped, sometimes sigmoid, very rarely straight and obclavate, thin-walled, smooth, 9–12-euseptate, not constricted at the septa, heavily guttulate, conically rounded at both ends slightly broad at the base, basal cell obconical but not pedicellate.

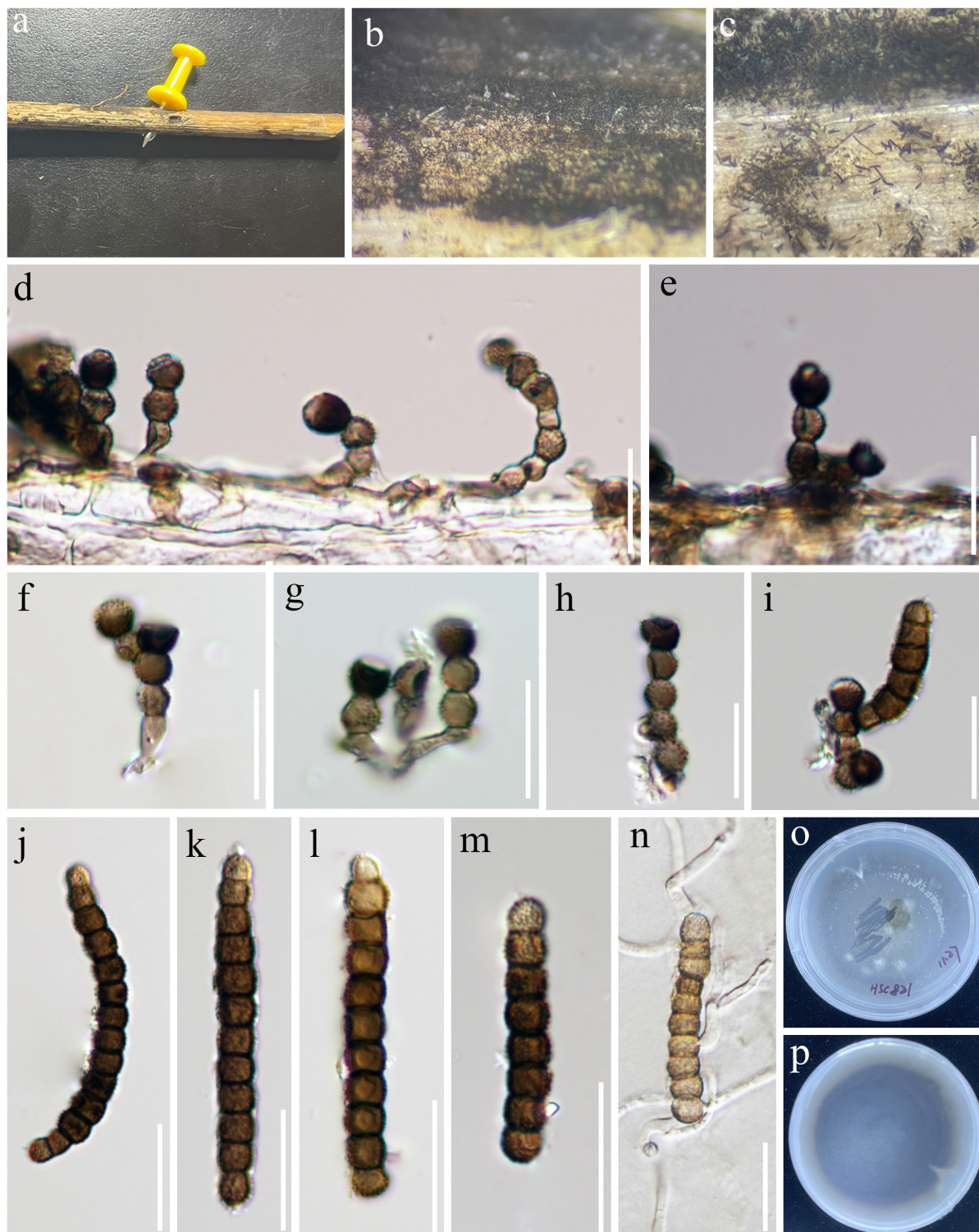


Fig. 19 *Torula motuoensis* (HKAS 150299, holotype) a–c Colony on natural substrates. d, e Conidiophores. f–i Conidiogenous cells. j–m Conidia. n Germinated conidia on PDA. o, p Culture on the PDA. Scale bars: d–i = 20 µm, j–n = 25 µm.

Culture characteristics: Conidia germinating on PDA medium within 48 h and germ tubes produced from both ends. Colonies grown on PDA reached 30 mm diam at room temperature in two weeks, circular, with velutinous appearance, flat, light brown aerial mycelium on the surface, from below dark brown with entire margin.

Material examined: CHINA, Xizang Autonomous Region, Shigatse City, Yadong County, Xiayadong Township, 27°23'38.03" N, 88°50'15.01" E, 4070 m a.s.l., on decaying wood submerged in a freshwater stream, 26 July 2023, R.J. Xu, LJN-56 (HKAS 135977), culture KUNCC 24-17963.

Notes: Goh et al. (1998b) introduced *Aquaphila albicans* from submerged wood in a tropical habitat. Our newly isolated strain (KUNCC 24-17963) clusters with *A. albicans* (MFLUCC 16-0010 and KUMCC 19-0078) with 100% ML/1.00 BYPP support (Fig. 20). Morphologically, our new isolate shares the same morphological characteristics with the holotype (HKU(M) 2856) of *A. albicans*, thus we identified our new isolate as *A. albicans*.

Eurotiomycetes O.E. Erikss & Winka

Chaetothyriales M.E. Barr

Herpotrichiellaceae Munk

***Cladophialophora* Borelli**

Cladophialophora was established by Borelli (1980), with *C. ajelaloi* designated as the type species, now synonymized with *C. carrionii* (Badali et al. 2008). It is characterized by the production of branched or unbranched chains of conidia through blastic conidiogenesis, a process distinguished by hyaline conidial scars (Sutton et al. 2009). Members of this genus exhibit remarkable ecological adaptability, with approximately 85 accepted species inhabiting a range of environments, from soil and plants in terrestrial ecosystems to unusual substrates such as sports drinks and lichens (Obase et al. 2015; Tang et al. 2017; Wijayawardene et al. 2022; Chang et al. 2023; Thitla et al. 2023; Hyde et al. 2024a). *Cladophialophora* exhibits a widespread geographical distribution, being found across the continents of Africa, Asia, Europe, North America, Oceania, and South America (De Hoog et al. 1995; Thitla et al. 2023). Species such as *C. nyingchiensis* and *C. tumulicola* have been isolated from rocks, demonstrating the genus's ability to colonize various substrates, including aquatic and semi-aquatic environments (Isola et al. 2016; Kiyuna et al. 2017; Sun et al. 2020; Chang et al. 2023; Thitla et al. 2023).

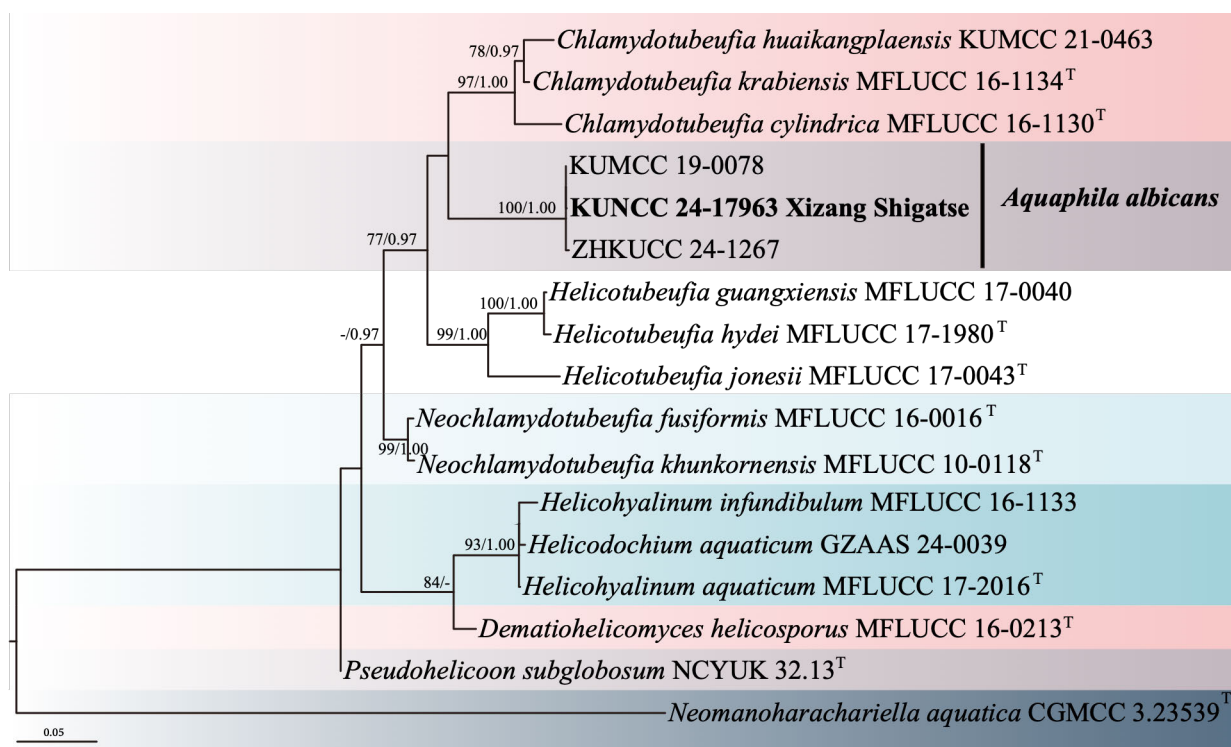


Fig. 20 Maximum likelihood majority rule consensus tree for Tubeufiaceae using ITS, LSU, SSU, *rpb2* and *tef1-α* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.90 are indicated near branches as ML /BYPP. The tree is rooted with *Honghemycetes pterolobii* (KUMCC 20-0218 and KUMCC 21-0030). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

12. *Cladophialophora biguttulata* R.J. Xu & Q. Zhao, sp. nov. Fig. 23

Chinese name: – 大油滴枝孢瓶霉 (da you di zhi bao ping mei)

Index Fungorum number: IF 903480; **Facesoffungi number:** FoF 17403

Etymology: the species epithet "*biguttulata*" refers to the presence of two large guttules within the conidia, which is a characteristic feature of this species.

Holotype: HKAS 136223

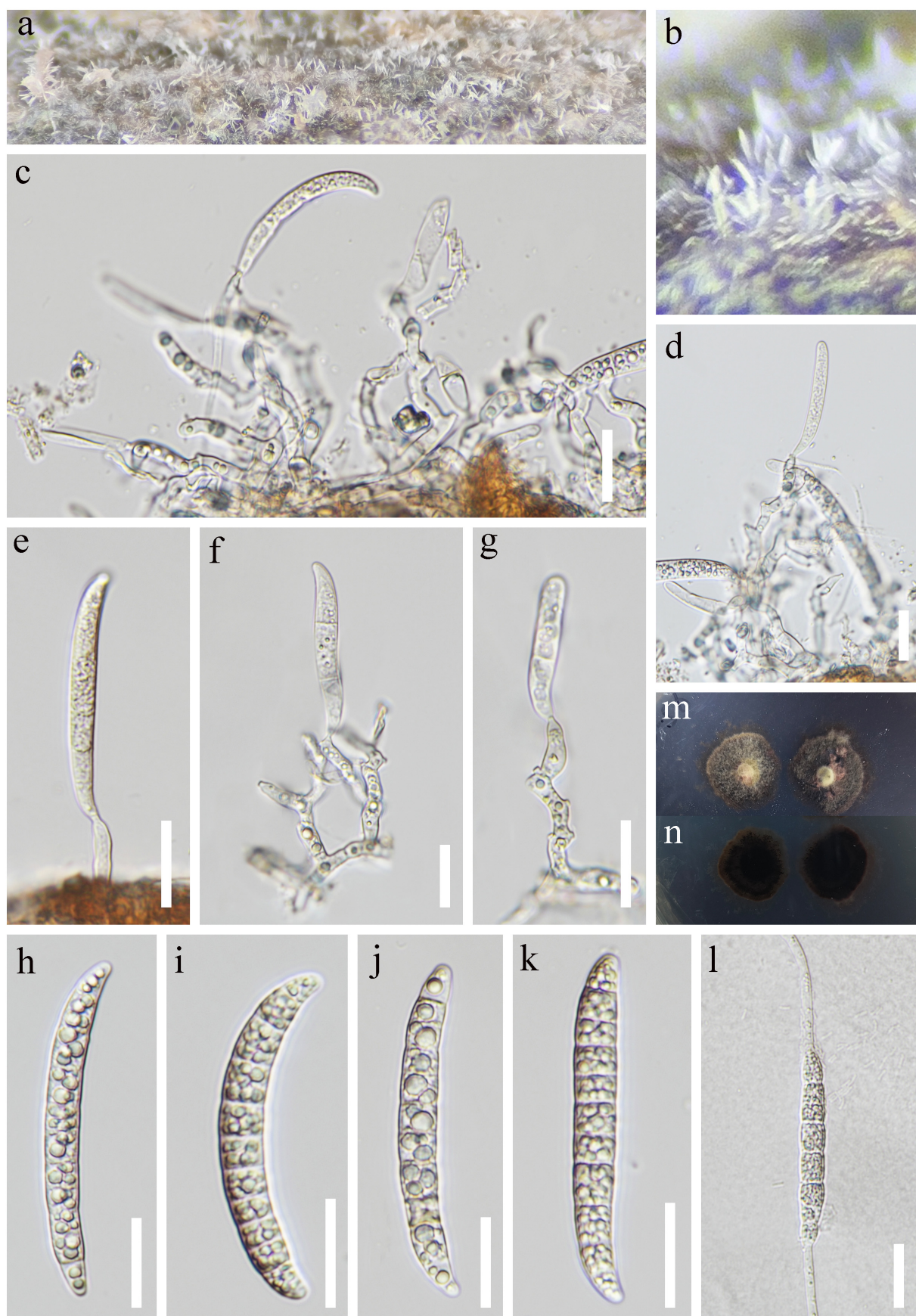


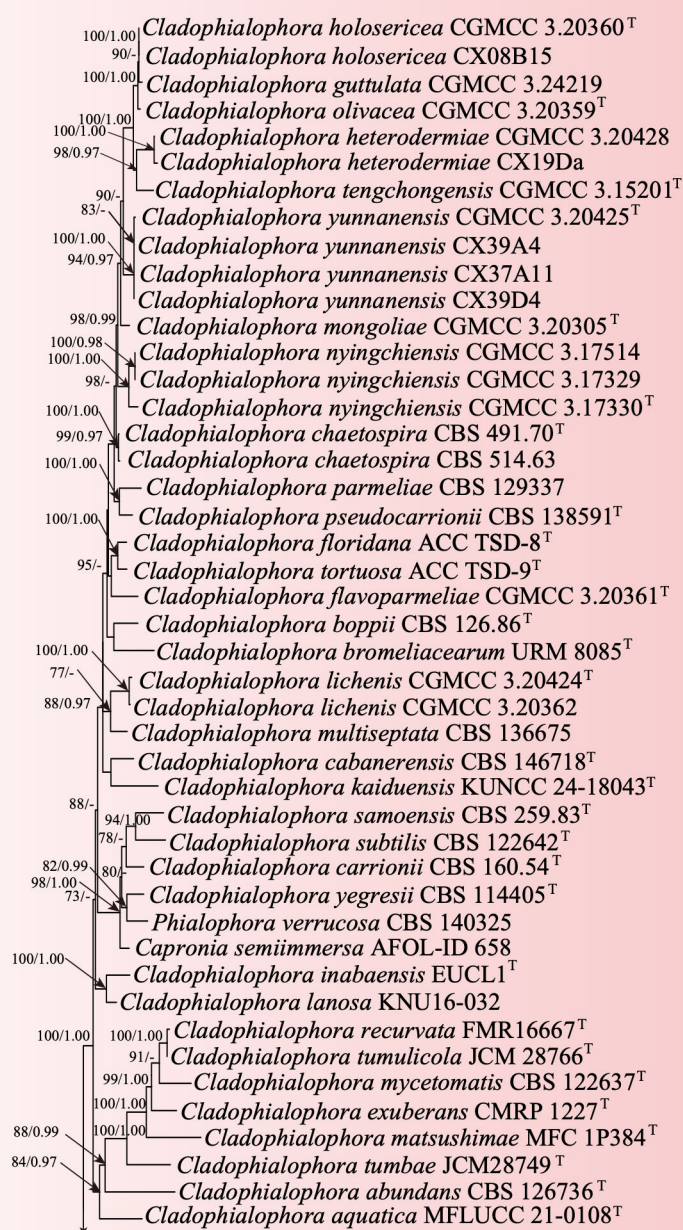
Fig. 21 *Aquaphila albicans* (HKAS 135977) a, b Colony on natural substrates. c, d Conidiophores with conidiogenous denticles. e–g Conidiophores with holoblastic conidia during development. h–k Conidia. l Conidia germination. m, n Culture on PDA medium, m from above, n from below. Scale bars: c–l = 20 μ m.

Saprobic on decaying wood submerged in freshwater habitats. **Sexual morph:** Undetermined. **Asexual morph:** Colonies superficial, effuse, velvety, gregarious, with masses white of conidia on the natural substrate. **Mycelium** immersed, consisting of hyaline, smooth-walled, branched, septate. **Conidiophores** semi-macronematous or macronematous, mononematous, cylindrical, straight or slightly flexuous, branched, dark brown or brown, capitate. **Conidiogenous cells** polyphialidic, with several sympodial proliferations, sometimes with conspicuous denticles, pale brown to subhyaline. **Conidia** 12–17 × 4–6 µm ($\bar{x}$ = 16 × 5 µm, n = 25), polyphialidic, reniform or cymbiform, curving, subhyaline, 1-septate, smooth, with two distinct guttules, short subhyaline pedicels.

Culture characteristics: Colonies grown on PDA reached 50 mm diam at room temperature in one month, circular, with dense, viscous, raised, dark brown mycelium on the surface, viscous, immersed mycelium on the surrounding, from below dark brown with entire margin.

Material examined: CHINA, Xinjiang Autonomous Region, Yili, Tacheng City, Dongdatang Scenic Spot, 43°52'42" N, 85°39'7.2" E, 1779 m a.s.l., on decaying wood submerged in a freshwater habitat, 17 July 2021, R.J. Xu, MD-345 (HKAS 136223, holotype), ex-type culture KUNCC 10438.

Notes: Recent morphological studies of *Cladophialophora* have primarily focused on the asexual forms produced on culture media (Obase et al. 2015; Sun et al. 2020; Boonmee et al. 2021; Cometto et al. 2023). Our collection was isolated from a natural substrate of submerged decaying wood. Morphologically, our collection differs from other species within *Cladophialophora* in having polyphialidic, with several sympodial proliferations conidiogenous cells and polyphialidic, reniform or cymbiform, with two distinct guttules, short subhyaline pedicels conidia (Sutton et al. 2009; Chang et al. 2023; Thitla et al. 2023). In addition, phylogenetic analyses also reveal that our collection *C. biguttulata* (KUNCC 10438) forms a separate, basal clade in *Cladophialophora* (Fig. 22), indicating it represents a new species.



◀ **Fig. 22** Maximum likelihood majority rule consensus tree for *Cladophialophora* using SSU, ITS, LSU and *tef1-α* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Arachnomyces bostrychodes* (CBS H-24452) and *A. jinanicus* (CGMCC 3.14173). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

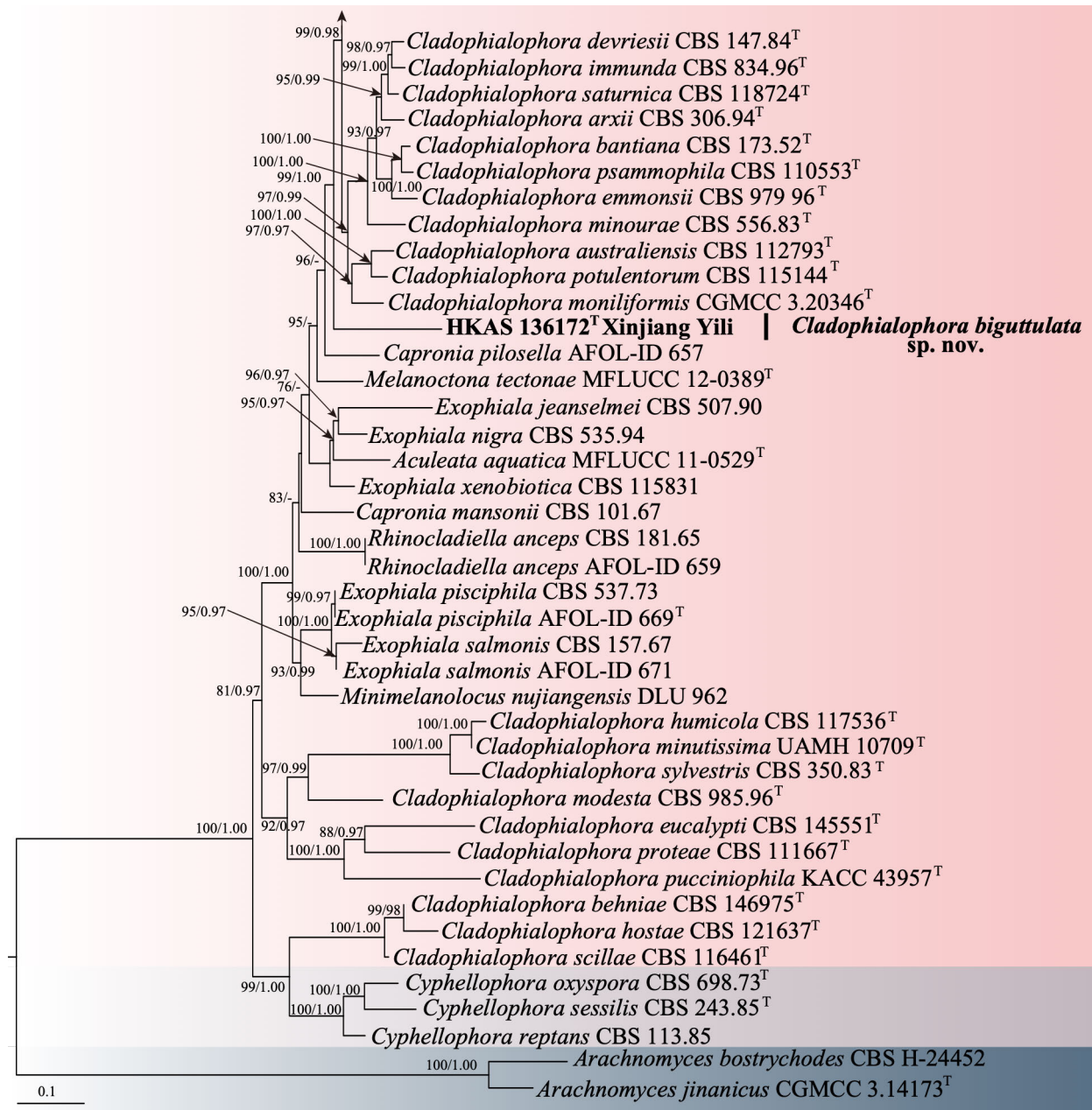


Fig. 22 (continued)

***Thysanorea* Arzanlou, W. Gams & Crous**

Thysanorea was established by Arzanlou et al. (2007), with *T. papuana*, formerly known as *Periconiella papuana*, as the type species. *Thysanorea* is characterized by micro- or macronematous, erect conidiophores that are either simple or apically branched, occasionally proliferating percurrently at the apex. The conidiogenous cells are terminal or intercalary, polyblastic, and exhibit a color gradient, transitioning from brown at the base to a paler shade towards

the apex. The conidia are generally pale brown and vary in shape, including oblong, obovoid, and cylindrical forms (Hernández-Restrepo et al. 2020; Yang et al. 2023). Hernández-Restrepo et al. (2020) later transferred species from *Minimelanolocus* to *Thysanorea*, citing their congeneric nature based on phylogenetic analyses. However, this reclassification has been debated, with Wan et al. (2021) challenging the move due to differences in the branching pattern of the conidiophores.

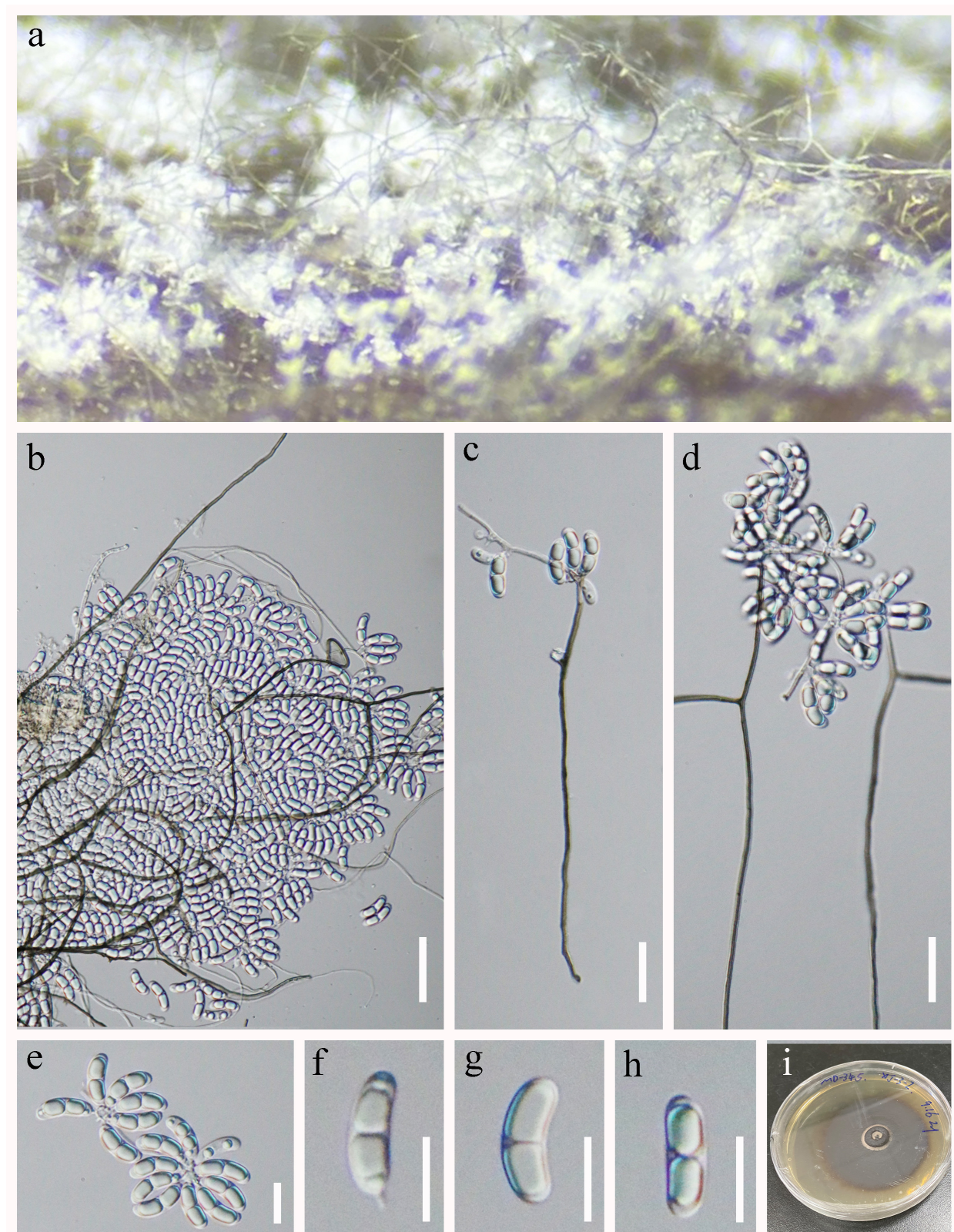


Fig. 23 *Cladophialophora biguttulata* (HKAS 136223, holotype) a Colony on natural substrates. b–d Conidiophores with conidia. e Conidiogenous cells with conidia. f–h Conidia. i Culture on PDA medium. Scale bars: b–d = 20 μ m, e–h = 10 μ m.

13. *Thysanorea linzhiensis* R.J. Xu, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 25

Chinese name: – 林芝金花茶菌 (lin zhi jin cha hua jun)

Index Fungorum number: IF 905033; **Facesoffungi number:** FoF 19301

Etymology: The epithet refers to Linzhi City, located in the Xizang Autonomous Region of China, where the type specimen was collected.

Holotype: HKAS 136140

Saprobic on decaying submerged wood in a freshwater stream. **Sexual morph:** Undetermined. **Asexual morph:** Colonies on natural substrates effuse, hairy, scattered or in small groups, brown, with glistening conidial masses at apex. **Mycelium** is partly superficial, partly immersed, composed of septate, smooth, pale brown hyphae. **Conidiophores** 201–320 × 3–9 µm ($\bar{x}$ = 263 × 6 µm, n = 20), macronematous, mononematous, erect, solitary, straight or flexuous, cylindrical, smooth-walled, septate, unbranched, dark brown, becoming pale brown or subhyaline towards the apex, thick-walled. **Conidiogenous cells** polyblastic, integrated, terminal, denticulate, sympodial proliferations, cylindrical, slightly constricted at septa, pale brown or subhyaline. **Conidia** 14–18 × 3–4 µm ($\bar{x}$ = 16 × 3 µm, n = 20), acrogenous or acropleurogenous, clavate, with a narrow truncate base, truncate at the base, aseptate when young, 1–4-septate when mature, smooth-walled, subhyaline.

Culture characteristics: Conidia germinating on PDA medium within 24 h and germ tubes produced from both ends. Colonies grown on PDA reached 30 mm diam at room temperature in two weeks, circular, with velvety, raised, grayish-green aerial mycelium on the surface, from below grayish-green with entire margin.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Chayu County, 28°39′55.76″ N, 97°28′15.71″ E, 4118 m a.s.l., on decaying wood submerged in a freshwater stream, 14 July 2022, R.J. Xu, LTS-36 (HKAS 136140, holotype), ex-type culture KUNCC 24-18006.

Notes: *Thysanorea linzhiensis* resembles *T. obscurus* in possessing mononematous, macronematous, septate conidiophores, as well as polyblastic, integrated, sympodially proliferating conidiogenous cells, and clavate conidia with a narrow truncate base. However, *T. linzhiensis* can be distinguished from *T. obscurus* by its denticulate conidiogenous cells and longer conidiophores (201–320 × 3–9 µm vs. 123–219 × 5–6 µm) (Liu et al. 2015b). In the phylogenetic analysis using combined ITS, LSU, and SSU sequence data, *T. linzhiensis* formed a distinct clade within *Thysanorea* (Fig. 24), closely related to but clearly separate from *T. obscurus*, with a genetic divergence of 2.8% in ITS sequences (16/564 bp difference). The introduction of *T. linzhiensis* as a new species is supported by both morphological and phylogenetic evidence.

Leotiomyces O.E. Erikss. & Winka

Helotiales Nannf. ex Korf & Lizoñ

Mollisiaceae Rehm

Phialocephala W.B. Kendrick

Phialocephala was introduced by Kendrick (1961) to accommodate *P. dimorphospora* (type species) and *P. bactrospora*, the latter was recently transferred to

Parasporendocladia (Wu & Diao 2022). *Phialocephala* is a polyphyletic genus throughout *Mollisiaceae* (Tanney & Seifert 2020; Visagie et al. 2024). Tanney & Seifert (2020) defined the *Phialocephala sensu stricto* which contains 14 species. *Phialocephala* is characterized by macronematous, mononematous, brown conidiophores, monophialidic, discrete conidiogenous cells arranged penicillately, and often catenate, subglobose to ellipsoidal, hyaline or pigmented, aseptate conidia (Ellis 1971b; Onofri et al. 1994; Tanney et al. 2016; Tanney & Seifert 2020; Senanayake et al. 2023). *Phialocephala* also has diplococcium-like synasexual morph, e.g., *P. catenospora*, and synnematus synasexual morph, e.g., *P. oblonga* (Tanney et al. 2016).

14. *Phialocephala guizhouensis* J. Ma & Y.Z. Lu, *sp. nov.* Fig. 27

Chinese name: – 贵州瓶头霉 (gui zhou ping tou mei)

Index Fungorum number: IF 573589; **Facesoffungi number:** FoF 19302

Etymology: the species epithet "guizhouensis" refers to the location where this species was collected

Holotype: GZAAS 23-0033

Saprobic on decaying wood in a terrestrial habitat. **Sexual morph:** Undetermined. **Asexual morph:** Colonies on natural substrate effuse, black, hairy. **Mycelium** mostly partly immersed, partly superficial, composed of brown, branched, septate, smooth hyphae. **Conidiophores** up to 220 µm long, macronematous, mononematous, erect, cylindrical, brown to reddish-brown, septate, thick-walled. **Conidiogenous cells** polytretic, integrated, terminal and intercalary, brown to reddish-brown. **Conidia** 6–13 × 3–5 µm ($\bar{x}$ = 8.5 × 4 µm, n = 30), catenate, formed in acropetal, branched chains, oblong with obtuse ends, brown to slight dark brown, 1–2-septate, darkened and slightly constricted at the septa, smooth.

Culture characteristics: Conidia germinate on water agar within 24 hrs. Germ tubes are produced from the apex or base. Colonies superficial, irregularly circular, flat, with entire edge, from above grey to whitish-grey in the center, brownish-grey at the edge, and from below, pale grey in the middle, brownish-grey at the edge.

Material examined: CHINA, Guizhou Province, Qiannan Buyi Autonomous Prefecture, Longli County, on decaying wood in a terrestrial habitat, 2 September 2020, Jian Ma, LLZB3 (GZAAS 23-0033, holotype), ex-type cultures GZCC 24-0159.

Notes: Our collection morphologically resembles the synasexual morph of *Phialocephala catenospora*, which has oblong and brown conidia (Tanney et al. 2016). However, the conidia of *P. catenospora* are larger than those of ours, (6–13 × 3–5 vs. 12–22.5 × 5–6 µm). Besides, *P. catenospora* (DAOMC 250108) is phylogenetically distant from our strain LLZB3 in the analyses (Fig. 26). In the phylogenetic tree, our strain LLZB3 formed an internal subclade with *P. amethystea* (DAOMC 251552) and *P. compacta* (CBS 507.94) with 99% ML/1.00 BYPP support (Fig. 26). ITS comparison shows there are 7.11% (53 out of 746 bp, including 7 gaps) and 4.97% (37 out of 745 bp, including 1 gap) differences with the strains DAOMC 251552 and CBS 507.94, respectively. Therefore, we introduce our collection as a new species.

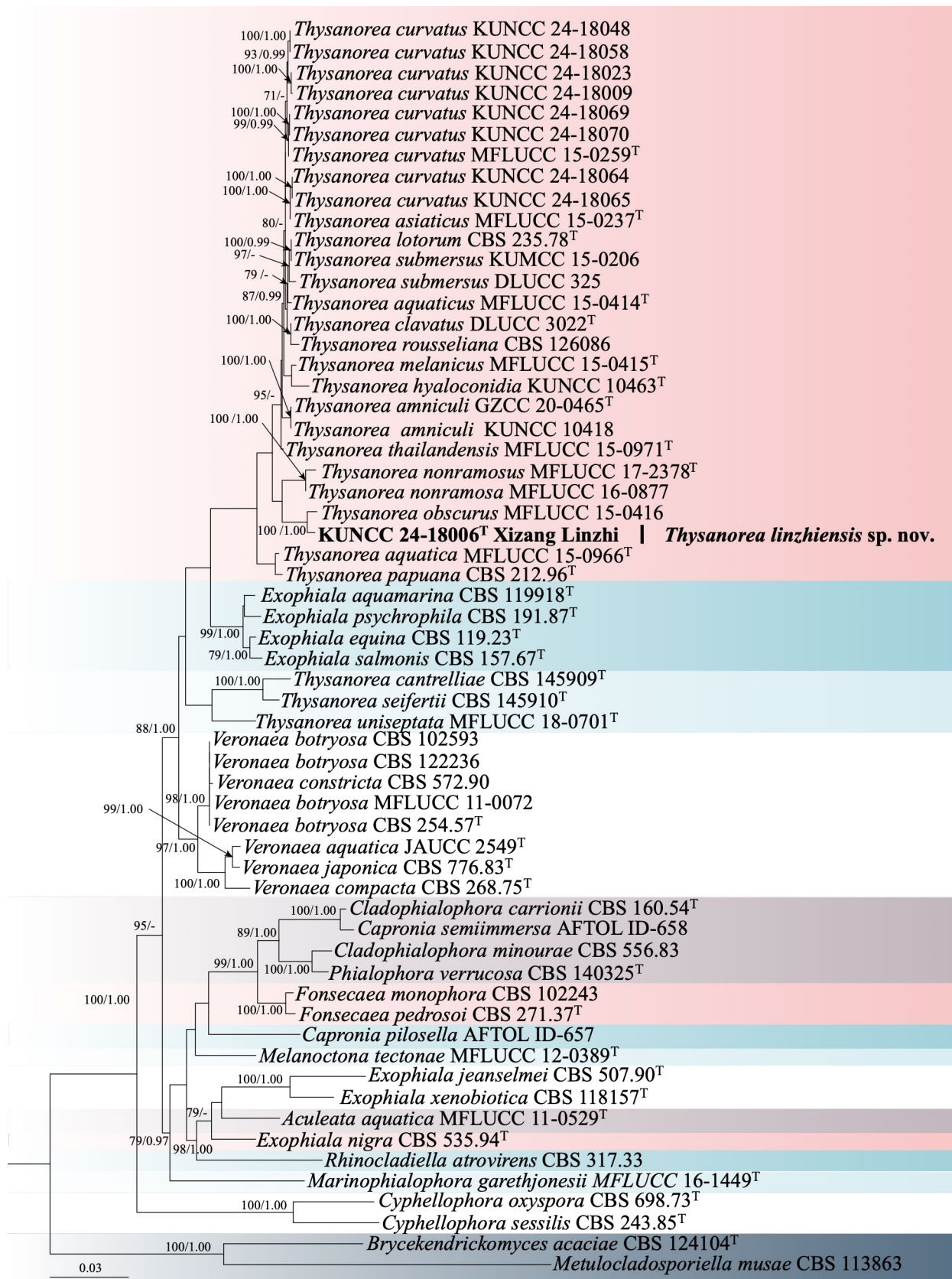


Fig. 24 Maximum likelihood majority rule consensus tree for *Thysanorea* using ITS, LSU and SSU sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Brycekendrickomyces acaciae* (CBS 124104) and *Metulocladosporiella musae* (CBS 113863). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.



Fig. 25 *Thysanorea linzhensis* (HKAS 136140, holotype) a Colony on natural substrates. b, c Conidiophores with conidia. d–g Conidiogenous cells with developmental conidia. h–r Conidia. s Germinated conidium. t, u Culture on PDA medium, t from above, u from below. Scale bars: b–e = 50 μm, f, g = 20 μm, h–k = 10 μm.

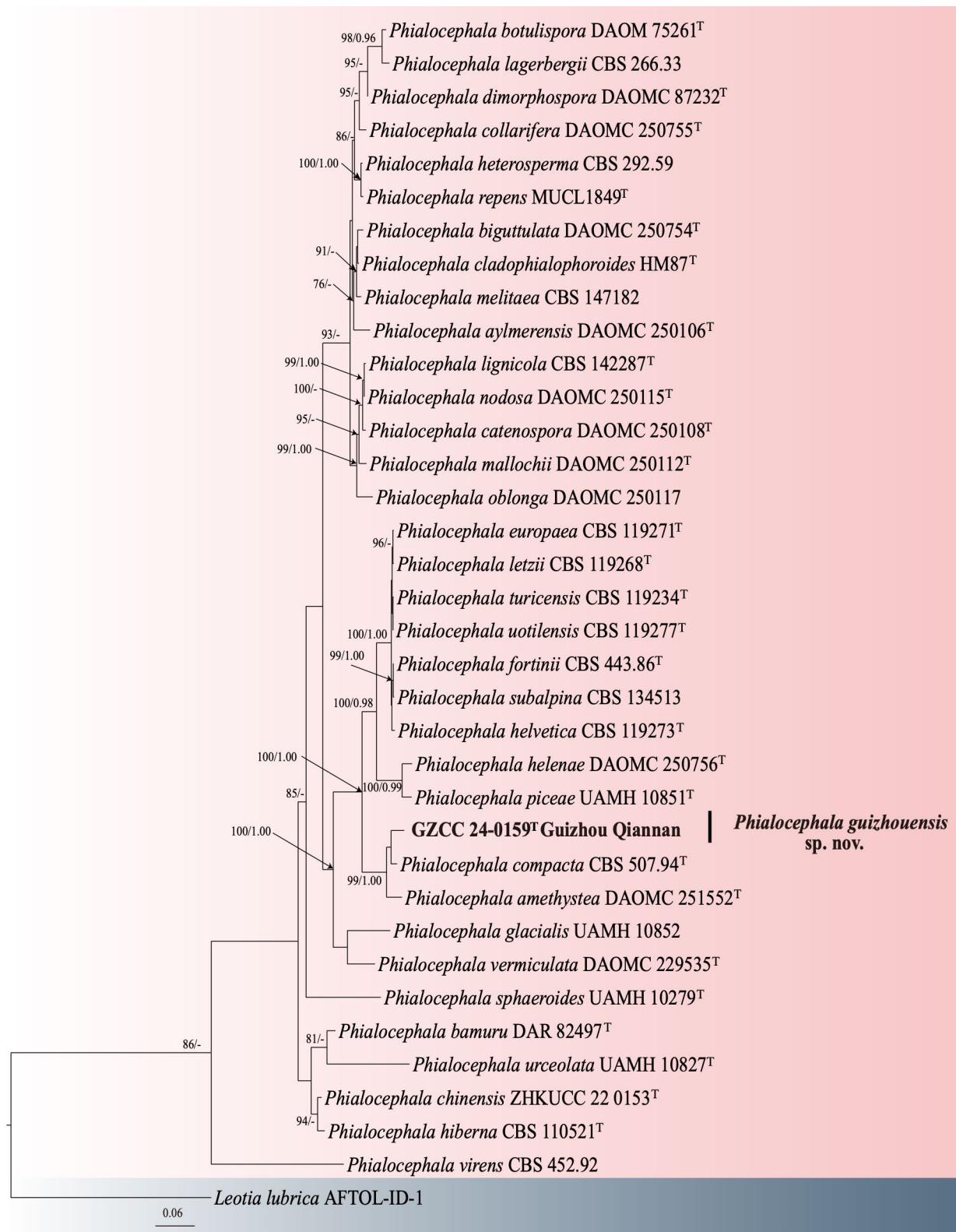


Fig. 26 ML tree ($-\ln L = 16244.186$) based on the combined ITS-LSU-LNS2-7 *rpb1*-TOP1 sequences. The combined dataset comprises 36 strains, including the new collection. The alignment comprises 3,919 characters (ITS: 1–659, LSU: 660–1870, LNS2: 1871–2151, *rpb1*: 2152–2965, TOP1: 2966–3919) including gaps. Among them, number of constant sites is 2,853, and number of parsimony informative sites are 676. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Leotia lubrica* (AFTOL-ID 1). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

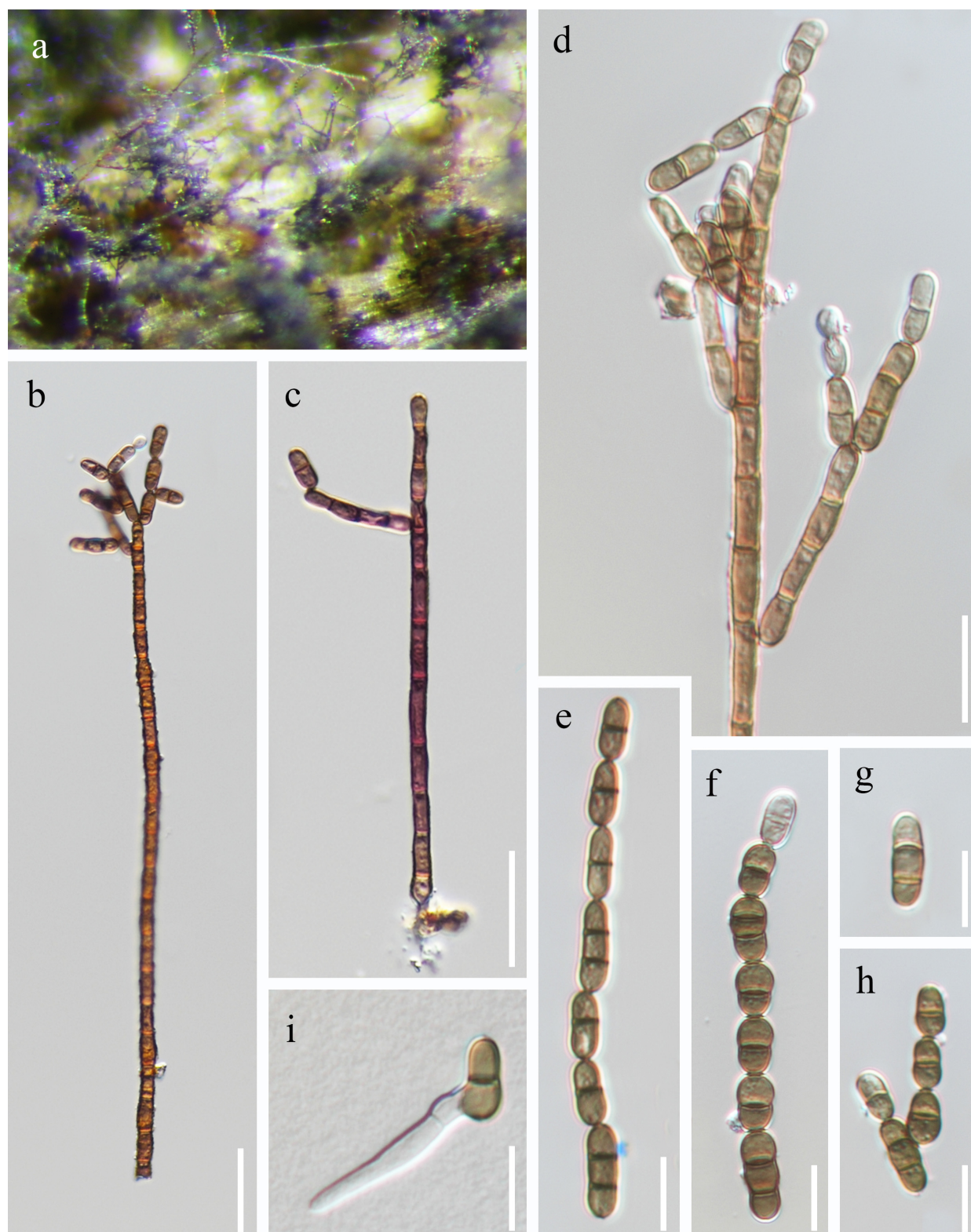


Fig. 27 *Phialocephala guizhouensis* (GZAAS 23-0033, **holotype**) a Colonies on natural substrate. b, c Conidiophores and conidia. d Conidiogenous cells and conidia. e–h Conidia. Scale bars: b–c = 50 μ m, d = 30 μ m, e–i = 10 μ m.

Pezizellaceae Velen

Chalara (Corda) Rabenh

Chalara was originally introduced by Corda (1837) as a subgenus of *Torula* to accommodate the hyphomycete *Chalara fusidioides*, characterized by a granular, effuse stroma, simple conidiophores, lageniform, cylindrical

conidiogenous cells, and cylindrical, hyaline conidia. Rabenhorst (1844) elevated *Chalara* to the generic level. The genus *Chalara* comprises a group of hyphomycetes characterized by the presence or absence of stroma and setae; conidiophores are scattered or aggregated, erect, simple, subcylindrical to cylindrical, smooth or verrucose,

septate or aseptate; conidiogenous cells ampulliform, lageniform, obclavate, ellipsoidal, or subcylindrical, with a venter and a collarette; conidia cylindrical to obclavate, hyaline, aseptate, and extruded in short chains (Nag Raj & Kendrick 1975; Wu & Diao 2023). Based on morphological and phylogenetic analyses, Wu & Diao (2023) revised the genus *Chalara*, typified by *C. fusidioides*, into a narrowly concept monophyletic genus to accommodate seven species that formed a distinct clade separate from other *Chalara*-like fungi in their phylogenetic reconstruction. These species include *Chalara africana*, *C. bambusicola*, *C. clidemiae*, *C. cylindrosperma*, *C. longiphora*, *C. platanicola*, and *C. qinlingensis* (Wu & Diao 2023). In addition to these phylogenetically supported species, *Chalara sensu stricto* also includes nine other species for which molecular data are currently lacking (Wu & Diao 2023). Species of *Chalara* s. str. are saprobic and occur on various plant substrates and in soil (Nag Raj & Kendrick 1975; Kirk 1986; Christiansen 1993; McKenzie et al. 2002; Wu 2004; Pratibha et al. 2005; Wu & Diao 2023).

15. *Chalara aquatica* H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 28

Chinese name: – 水生鞘孢霉 (shui sheng qiao bao mei)

Index Fungorum number: IF 905259; **Facesoffungi number:** FoF 19303

Etymology: The specific epithet “*aquatica*” refers to the *aquatica* habitat, which is where this species was collected.

Holotype: HKAS 151651

Saprobic on submerged decaying wood in a freshwater habitat. **Sexual morph:** Undetermined. **Asexual morph:** Colonies on natural substrate, superficial, effuse, scattered, hairy, dark brown, solitary or in small groups. *Mycelium* partly immersed and partly superficial, composed of branched, septate, pale brown hyphae. *Stroma* absent. *Setae* absent. *Conidiophores* (85–)115–171(–183) × 5.3–8.5 µm ($\bar{x}$ = 143 × 7.2 µm, *n* = 20), macronematous, mononematous, cylindrical, straight or slightly flexuous, unbranched, septate, basal cells slightly swollen, brown to dark brown, smooth-walled. *Conidiogenous cells* (30–)36–42(–44) × 7.4–9.3 µm ($\bar{x}$ = 39 × 8.3 µm, *n* = 25), integrated, terminal, lageniform, pale to medium brown, consisting of the wider venter and the narrower collarette, transition from venter to collarette abrupt. *Venter* 10–21 × 7–9 µm, ellipsoid to subcylindrical, medium brown. *Collarette* 18–26 × 4–6 µm, cylindrical, pale to medium brown. *Conidia* (3.5–)5.2–7.8(–8.6) × 3.5–5 µm ($\bar{x}$ = 6.5 × 4.2 µm, *n* = 30), endogenous, subglobose to barrel-shaped to rectangular, truncate or obtuse at both ends, hyaline, aseptate, guttulate, smooth-walled.

Culture characteristics: Conidia germinated on PDA within 12 h and germ tubes produced from around the conidium. Colonies on PDA reaching 2–3 cm diameter after one month at room temperature (around 22 °C) in the dark, dense, velvety, gray to brown, with smooth margins and bulge center from above, dense, gray to brown, with smooth margins from below.

Material examined: CHINA, Yunnan Province, Lijiang City, on the unidentified decaying wood, October 2021, L.L. Li, L944 (HKAS 151651, holotype), ex-type culture KUNCC 23-14304.

Notes: Phylogenetic analysis revealed that *Chalara aquatica* is closely related to *C. cylindrosperma*, *C. longiphora*, and *C. platanicola*, forming a robustly supported

clade within the phylogenetic framework (Fig. 29). Morphologically, *C. aquatica* is similar to all three species, but can be distinguished from *C. cylindrosperma* by its larger venter (10–21 × 7–9 µm vs. 10–12.5 × 5–7 µm) and collarette (18–26 × 4–6 µm vs. 17.5–20 × 2.5–3.5 µm), as well as by its smaller conidia (5.2–7.8 × 3.5–5 µm vs. 10–17 × 1.5–2.5 µm) (Wu & Diao 2023). *Chalara aquatica* differs from *C. longiphora* in having a larger collarette (18–26 × 4–6 µm vs. 14–17 × 2.5–2.7 µm), wider conidia (3.5–5 µm vs. 2–2.5 µm), and subglobose to barrel-shaped or rectangular conidia, whereas the conidia of *C. longiphora* are cylindrical (Wu & Diao 2023). Compared to *C. platanicola*, *C. aquatica* has longer conidiogenous cells (36–42 µm vs. 26–27 µm), venter (10–21 × 7–9 µm vs. 10–12.5 × 5.7–6.5 µm), and collarette (18–26 × 4–6 µm vs. 17–18 × 2.8–3.3 µm), but produces shorter and wider conidia (5.2–7.8 × 3.5–5 µm vs. 9–10.5 × 2.2–2.5 µm) (Wu & Diao 2023). Based on both phylogenetic distinction and morphological differences, we introduce *C. aquatica* as a new species.

16. *Chalara guttulata* H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 30

Chinese name: – 油滴鞘孢霉 (you di qiao bao mei)

Index Fungorum number: IF 905260; **Facesoffungi number:** FoF 19304

Etymology: The specific epithet “*guttulata*” refers to the guttulate conidia of this species.

Holotype: DLU 3129

Saprobic on submerged decaying wood in a freshwater habitat. **Sexual morph:** Undetermined. **Asexual morph:** Colonies on natural substrate, superficial, effuse, scattered, hairy, dark brown, solitary or in small groups. *Mycelium* partly immersed and partly superficial, composed of branched, septate, pale brown hyphae. *Stroma* absent. *Setae* absent. *Conidiophores* 82–88 × 4.3–6 µm ($\bar{x}$ = 85 × 5 µm, *n* = 15), macronematous, mononematous, cylindrical, straight or slightly flexuous, unbranched, 3–septate, basal cells slightly swollen, brown to dark brown, smooth-walled. *Conidiogenous cells* 50–60 × 5–6.4 µm ($\bar{x}$ = 56 × 5.5 µm, *n* = 15), integrated, terminal, long-lageniform, pale to medium brown, consisting of the wider venter and the narrower collarette, transition from venter to collarette abrupt. *Venter* 21–31 × 4.5–6 µm, subcylindrical to long-clavate, medium brown. *Collarette* 25.5–32 × 2.8–3.1 µm, cylindrical, pale to medium brown. *Conidia* 7.8–12 × 1.8–2.5 µm ($\bar{x}$ = 10 × 2.2 µm, *n* = 40), endogenous, cylindrical, truncate or obtuse at both ends, hyaline, aseptate, guttulate, smooth-walled.

Material examined: CHINA, Yunnan Province, Dali City, on undetermined decaying wood, May 2021, S. Luan, S3129 (DLU3129, holotype), ex-type culture DLUCC 3129.

Notes: Phylogenetic analysis placed *Chalara guttulata* within the *Chalara* clade, where it formed a distinct and with 100% ML/1.00 BYPP support (Fig. 29). Morphologically, *C. guttulata* resembles *C. versicolor* in having cylindrical, unbranched, septate conidiophores, integrated, terminal, lageniform conidiogenous cells, consisting of the wider venter and the narrower collarette, and cylindrical, hyaline, aseptate conidia, truncate or obtuse at both ends (Wu & Diao 2023). However, it differs by its longer conidiophores (82–88 µm vs. 15–50 µm), longer conidiogenous cells (50–60 µm vs. 47–50 µm), and smaller conidia (7.8–12 × 1.8–2.5 µm vs. 6.5–15 × 2.5–3 µm) (Wu & Diao 2023). A BLASTn search of the ITS sequence against NCBI GenBank revealed the closest match to be *Chalara* sp. (Specimen voucher: HAY-F-011218,

Sequence ID: PV742674.1), with 98% identity (485/496 bp, including 2 gaps). The closest match for the LSU sequence was *Endoradiciella communis* (Strain: P2333, Sequence ID: NG_149040.1), showing 99% identity (857/864 bp, including 1 gap). Based on both morphological characteristics and molecular phylogenetic evidence, we introduce *C. guttulata* as a novel species.

Sordariomycetes O.E. Erikss. & Winka

Sordariomycetes is one of the largest classes within *Ascomycota*, widely distributed worldwide and predominantly comprising terrestrial taxa, although several members also occur in aquatic habitats (Luo et al. 2019; Hyde et al. 2020c). In the present study, a phylogenetic framework of *Sordariomycetes* is reconstructed based on sequence data from three loci (LSU, *rpb2* and *tef1-α*) using approximately 1,000 strains. Further details are provided in Supplementary (Fig. 2).

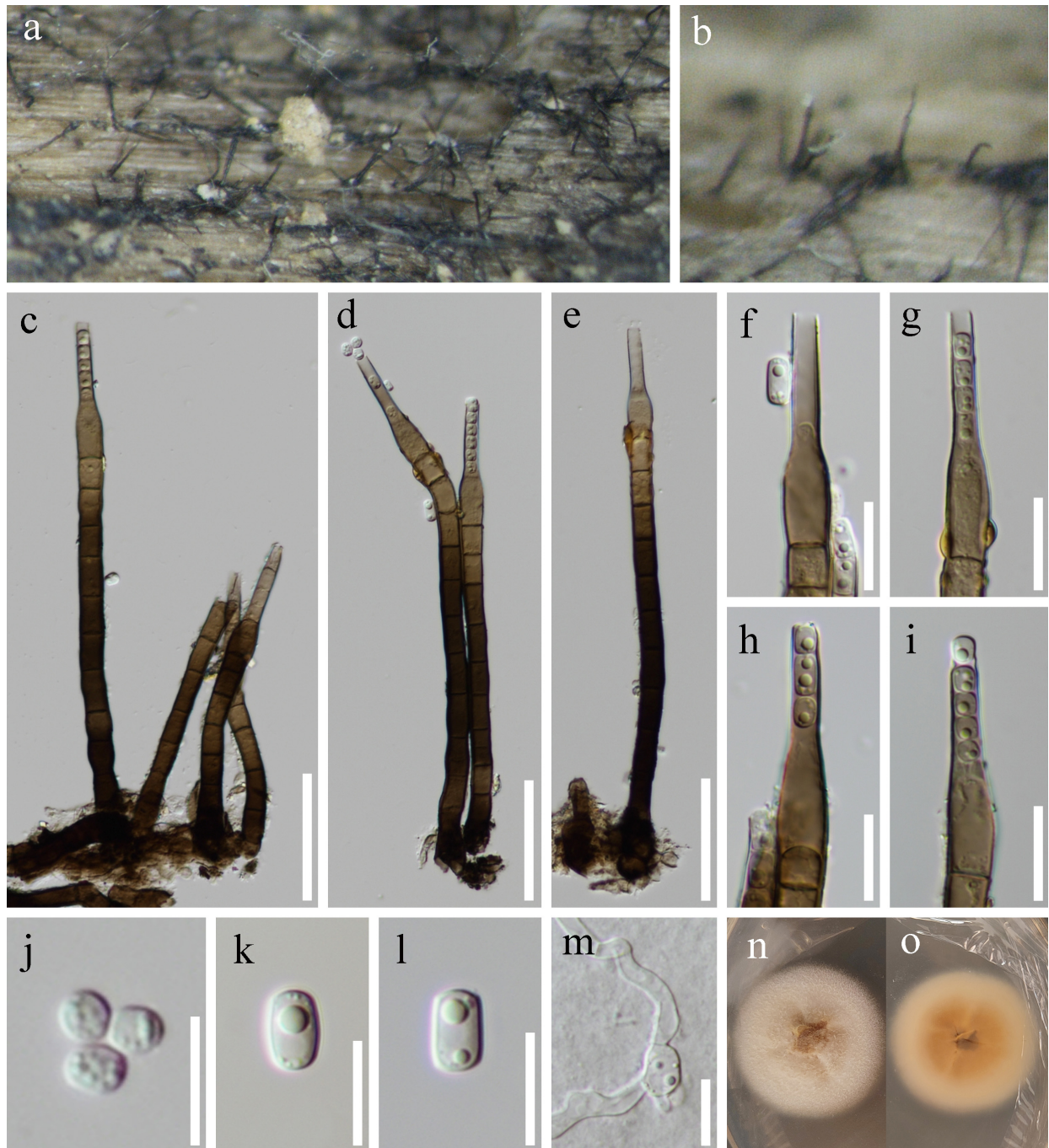


Fig. 28 *Chalara aquatica* (HKAS 151651, holotype) a, b Colonies on woody substrates. c–e Conidiophores. f Conidiogenous cell and conidium. g–i Conidiogenous cells with developing conidia. j–l Conidia. h, i Conidia. m Germinated conidium. n Culture on PDA, left from surface, right from back. Scale bars: c–e = 40 μ m, f–i = 15 μ m, j–m = 10 μ m.

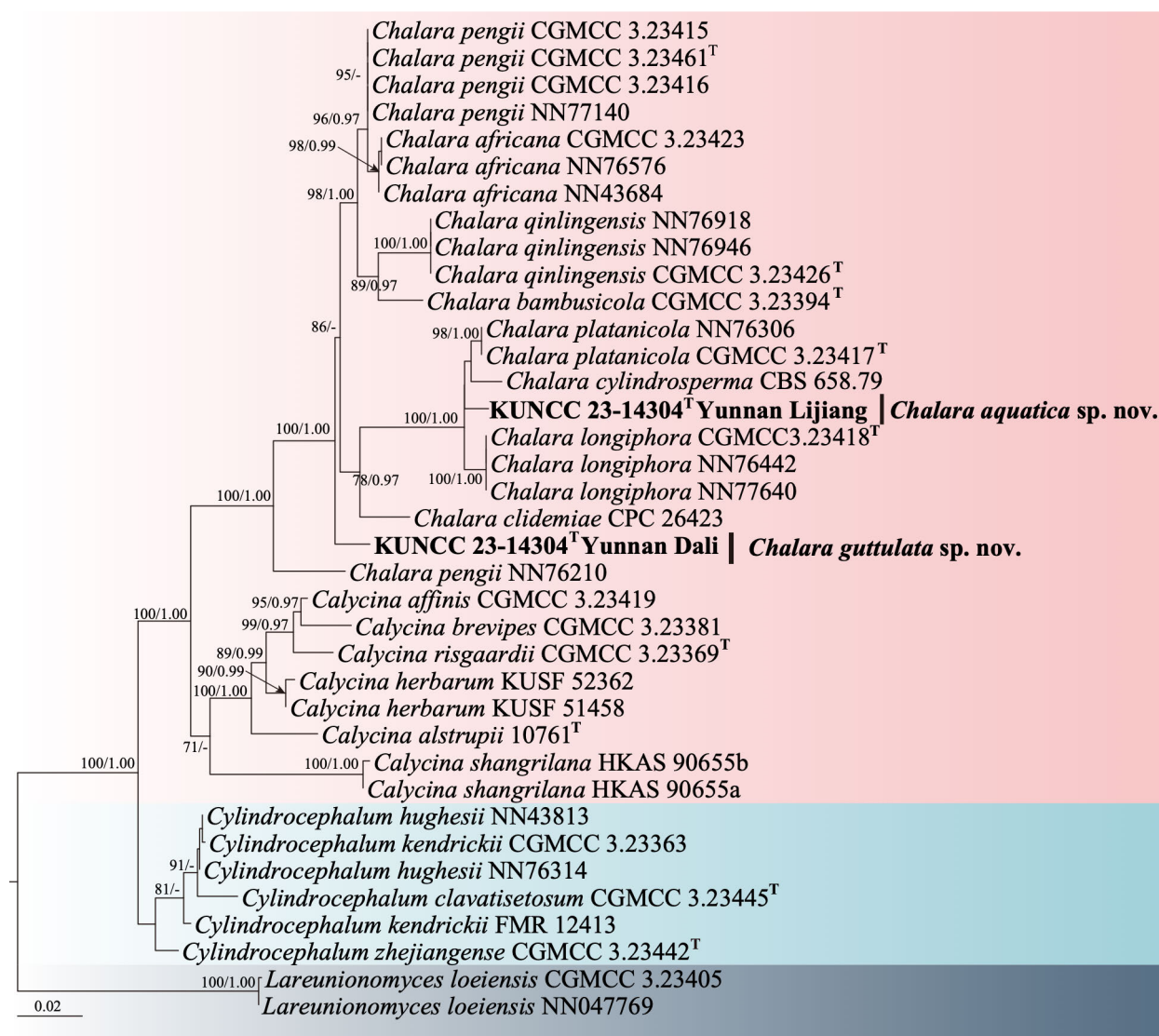


Fig. 29 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU. Thirty-seven strains were included in the combined sequence analyses, which comprised 3817 characters with gaps (ITS = 464 and LSU = 825). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. *Lareunionomyces loeiensis* (CGMCC3.23405 and NN047769) strains were used as the outgroup taxa. The final ML optimization likelihood is -27926.145972. The matrix included 1676 distinct alignment patterns, with 21.83% undetermined characters or gaps. Estimated base frequencies were obtained as follows: A = 0.234861, C = 0.271796, G = 0.258425, T = 0.234918; substitution rates AC = 1.379110, AG = 3.330310, AT = 1.229619, CG = 1.122043, CT = 5.312755, GT = 1.000000; gamma distribution. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.95 are given above or below the nodes. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Chaetosphaeriaceae was established by Réblová et al. (1999a) to accommodate *Chaetosphaeria* with the closely related genera including: *Ascocodinaea*, *Melanochaeta*, and *Sporoschisma*. *Chaetosphaeriaceae* is a major family within *Sordariomycetes*, known for its complex pleomorphism and diverse asexual morphologies. Previous, the phylogenetic analyses have revealed that both *Stanjehughesia* and *Linkosia* are polyphyletic (Shenoy et al. 2006; Su et al. 2016a; Hyde et al. 2020c; Hsieh et al. 2021), and the type species *S. hormiscioides* lacks molecular data, leaving the phylogenetic position of the genus unresolved. However, Réblová et al. (2024) re-evaluated species previously classified in the genera *Exserticlava*, *Phaeostalagmus*, *Phialocephala*, and several *Chalara* and *Stanjehughesia*-like fungi, and

reassigned them to *Chaetosphaeriaceae* based on living cultures and DNA sequence data obtained from numerous type species. Currently, 101 genera are accepted in *Chaetosphaeriaceae* and phylogenetic analysis based on combined ITS, LSU, and *tef1-α* sequence data (Hyde et al. 2024a; Réblová et al. 2024).

Chloridium Link

Chloridium is known for its cosmopolitan distribution, thriving on decaying plant tissues in terrestrial and freshwater habitats, notably on wood buried in moist soil or leaf litter. *Chloridium* was introduced with *C. virescens* as the type species, characterized by pigmented, unbranched, erect conidiophores with globose conidia forming green masses (Link 1809; Réblová et al. 2022). The taxonomy of *Chloridium* has been complex, with early classifications based on

morphological features and later, molecular data. Recent molecular analyses have further refined the understanding of phylogeny of *Chloridium*, revealing its paraphyletic nature

and close relationships with other genera such as *Adautomilanezia* and *Sporoschisma* (Réblová et al. 2022).

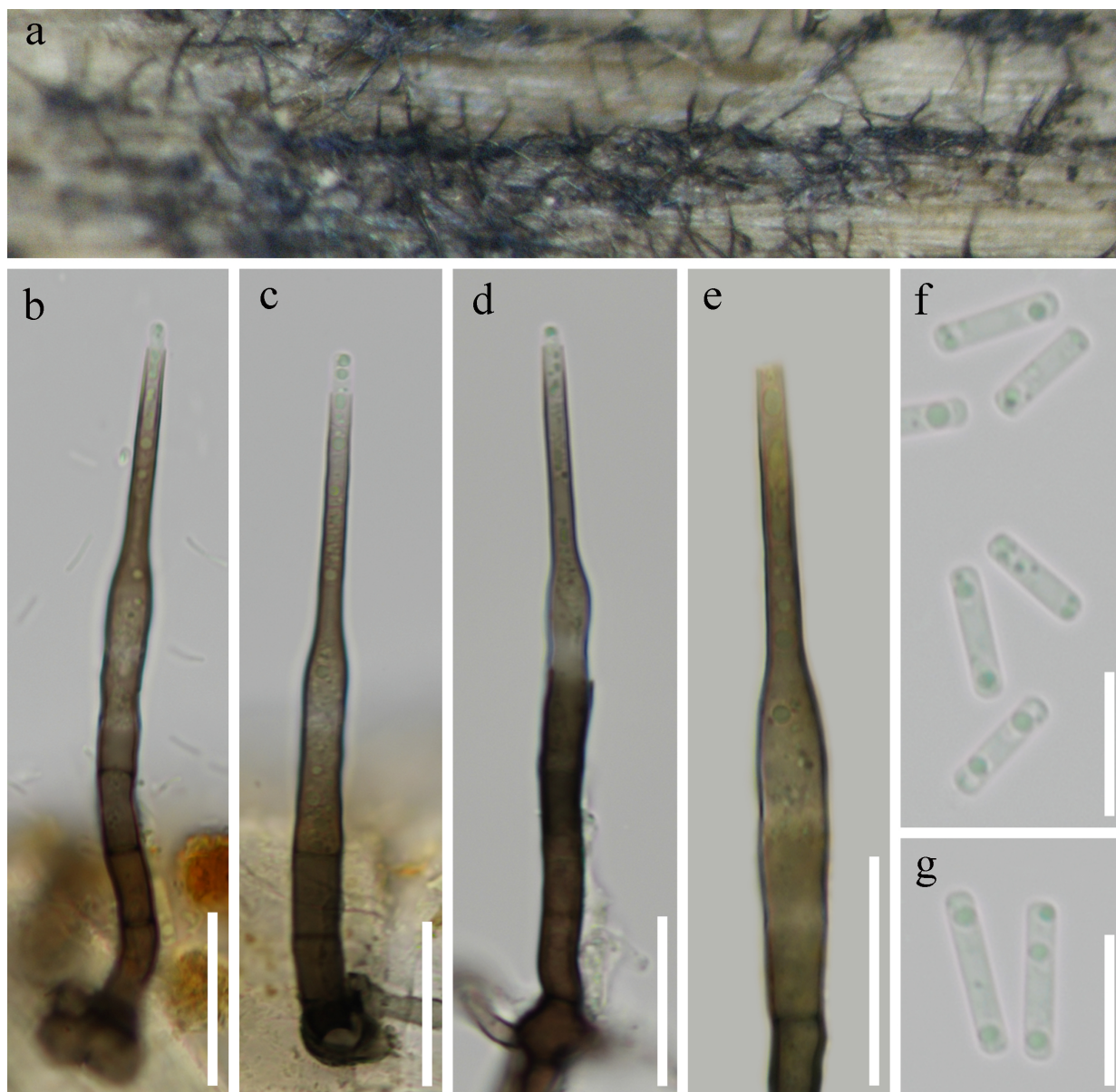


Fig. 30 *Chalará guttulata* (DLU3129, holotype) a Colonies on woody substrates. b–d Conidiophores. e Conidiogenous cell f, g Conidia. Scale bars: b–e = 20 µm, f, g = 10 µm.

17. *Chloridium fuscum* (Corda) Réblová & Hern. - Restr., Stud. Mycol. 103: 176 (2022) Fig. 32

Chinese name: – 暗褐暗梗单孢霉 (an he an geng dan bao mei)

Index Fungorum number: IF 555386; **Facesoffungi number:** FoF 04950

Saprobic on decaying wood submerged in a freshwater habitat. **Sexual morph:** Undetermined. **Asexual morph:** Colonies effuse, dark brown, olivaceous brown to olivaceous grey, with long hairy mycelium. **Mycelium** partly immersed, partly superficial, consisting of branched, septate, brown hyphae. **Conidiophores** 158–241 × 3–6 µm ($\bar{x}$ = 195 × 5 µm, n = 15), macronematous, solitary or crowded, erect, straight, septate, unbranched, cylindrical, 4–6-septate, dark brown, pale brown to subhyaline towards the apex, slightly tapering

towards the apex. **Conidiogenous cells** 11–31 × 3–5 µm ($\bar{x}$ = 21 × 4 µm, n = 20), monophialidic, discrete, phialide, sometimes extending percurrently, subulate to cylindrical, pale brown to subhyaline, hyaline towards the apex, in 5–10 cylindrical located in the two lower thirds of the conidiophore in the nodes at intervals. **Conidia** 4–5 × 3–4 µm ($\bar{x}$ = 5 × 3 µm, n = 20), acrogenous, ellipsoidal, subhyaline to pale brown, aseptate, smooth,

Culture characteristics: Conidia germinating on PDA medium within 24 h and germ tubes produced from both ends, Colonies grown on PDA reached 50 mm diam at room temperature in two weeks, circular, with velvety, flat, dark brown mycelium on the surface, from below dark brown to grayish-brown with entire margin.

Material examined: CHINA, Xizang Autonomous Region, Rikaze City, Yadong County, 27° 21' 11" N, 88° 58' 10" E, 3061 m a.s.l., on decaying wood submerged in a freshwater habitat, 01 July 2022, R.J. Xu, LTS-8 (HKAS 136133), culture KUNCC 24-17992. Linzhi City, Motuo County, Dexing Township, 29°21'14.97" N, 95°8'53.19" E, 2172 m a.s.l., on decaying wood submerged in a freshwater stream, 10 August 2023, R.J. Xu, LJN-42 (HKAS 135976), culture KUNCC 24-17960. Shannan City, Luozha County, 28°11'3.15" N, 90°59'57.88" E, 3491 m a.s.l., on decaying wood submerged in a freshwater habitat, 08 July 2022, R.J. Xu, XK-68 (HKAS 136102), culture KUNCC 24-18124. Linzhi City, Chayu County, Guyu Township, 29°19'31.89" N, 97°8'52.91" E, 3858 m a.s.l., on decaying wood submerged in a freshwater habitat, 12 August 2023, R.J. Xu, LJN-72 (HKAS 135984), culture KUNCC 24-17972.

Notes: *Chloridium fuscum* was initially described by Corda (1837) as *Chaetopsis fusca*. It was later synonymized with *Gonytrichum* and subsequently reclassified under *Chloridium* based on comprehensive phylogenetic analyses (Saccardo 1880; Hughes 1951; Réblová et al. 2022). Synonyms of this species include *Mesobotrys simplex* and *Chl. aseptatum*. *Chl. fuscum* is closely related to *Chl. volubile*, sharing similar conidiophore characters, but can be distinguished based on specific morphological differences (Réblová et al. 2022).

Chloridium fuscum is a widely distributed saprobic species that can be found in both terrestrial and freshwater environments, including soil, decaying wood and bark, thriving on a variety of plant remnants. This species exhibits a broad geographic presence, recorded in regions such as Australia, Canada, China, the Czech Republic, Germany, Italy, Korea, Puerto Rico, South Africa, Thailand, the United Kingdom, and the USA (Réblová et al. 2022). Morphologically, our collection fits well with the species concept of *Chl. fuscum*, and phylogenetic analyses showed that our collections of *Chlo. fuscum* clustered closely with *Chl. fuscum* (CBS 195.60) (Fig. 31). Consequently, we identified the four strains as *Chl. fuscum* and reported as a new collection from Xizang, China.

Reticulascus was established by Réblová et al. (2011a), based on a combined of ITS, LSU and SSU phylogeny and to accommodate two holomorph *Chaetosphaeria* species. Whereafter, Réblová et al. (2016a) given its widespread use, priority, and greater number of names, therefore recommend the use of *Cylindrotrichum* rather than *Reticulascus*. The genus is characterized by brown to black, hairy, effuse colonies *in vivo*. Setae are absent. Conidiophores are macronematous, mononematous, cylindrical, and straight. Conidiogenous cells are usually monophialidic, rarely polyphialidic with up to two lateral enteroblastic openings, with collarette hyaline to subhyaline. Conidia are cylindrical, slightly tapering, rounded at the apex, obtuse at the base, 1-septate, not constricted at the septum, hyaline, guttulate, and smooth-walled.

18. *Cylindrotrichum clavatum* W. Gams & Hol. -Jech., Stud. Mycol. 43: 54. 1976 Fig. 34

= *Reticulascus clavatus* Réblová & J. Fourn., in Réblová, Gams & Seifert, Stud. Mycol. 68: 181 (2011)

Chinese name: – 棒状柱孢霉 (bang zhuang zhu bao mei)

Index Fungorum number: IF 555386; **Facesoffungi number:** FoF 04950

Saprobic on decaying wood submerged in a freshwater river. **Sexual morph:** *Reticulascus clavatus*. **Asexual morph:** Colonies superficial, effuse, glistening, hairy or velvety, pale brown to brown. *Mycelium* immersed, consisting of hyaline, smooth-walled, branched, septate. *Conidiophores* 105–182 × 3–5 µm ($\bar{x}$ = 153 × 4 µm, n = 15), macronematous, mononematous, solitary or 2-group, erect, unbranched, 4–8-septate, straight or flexuous, cylindrical, dark brown at the base, light brown towards the apex. *Conidiogenous cells* 22–27 × 4–5 µm ($\bar{x}$ = 24 × 4 µm, n = 20), monophialidic, polyphialidic, collarette hyaline to subhyaline. *Conidia* 7–11 × 3–4 µm ($\bar{x}$ = 9 × 3 µm, n = 25), acrogenous, cylindrical or clavate, rounded at apex, slightly tapering, obtuse at base, 0–1-septate, hyaline, smooth-walled.

Culture characteristics: Conidia germinating on PDA medium within 24 h and germ tubes produced from both ends. Colonies grown on PDA reached 30 mm diam at room temperature in two weeks, irregular, with velvety, flat, aerial mycelium on the surface, from below dark brown with entire margin.

Material examined: CHINA, Xinjiang Autonomous Region, Aksu City, Aksu River, 41° 8' 13.8" N, 80° 8' 42.8" E, 1112 m a.s.l., on decaying wood submerged in a freshwater river, 02 August 2021, R.J. Xu, MD-306 (HKAS 136202), culture KUNCC 24-18038.

Notes: Réblová et al. (2011a) introduced the new holomorph genus *Reticulascus* for two species, based on multi-gene phylogenetic analyses. This included the new species *R. clavatus*, with *Cylindrotrichum clavatum* identified as its anamorph. However, Réblová et al. (2016a) later advised using the name *Cylindrotrichum* instead of *Reticulascus*. This recommendation was based on the discovery that the type species of *Cylindrotrichum*, *Cy. oligospermum*, is the asexual morph of *Chaetosphaeria tulasneorum*, which is the type species of *Reticulascus* (Réblová 1999; Réblová et al. 2011a). Consequently, *Cylindrotrichum* and *Reticulascus* are synonymous.

Cylindrotrichum clavatum, originally found on submerged wood in freshwater habitats in France, was later reported by Maharachchikumbura et al. (2018) in the Lancang River, Yunnan Province. Our phylogenetic analyses showed that the isolate (KUNCC 24-18038) clusters with *Cy. clavatum* (DLUCC 0575, DLUCC 0572, CBS 125296, CBS 125297, CBS 125239 and CBS 428.76) (Fig. 33). The morphology of our strain's conidiophores, conidiogenous cells, and conidia aligns with those of *Cy. clavatum*, leading to its identification as a new collection from Xinjiang, China.

Falholtia W.P. Wu & Y.Z. Diao

Falholtia is a monotypic genus established by Wu & Diao (2022) to accommodate a synnematus *Stanjehughesia*-like taxon previously described as *Stanjehughesia kaohsiungensis* (Hsieh et al. 2021). This genus is morphologically distinct within *Chaetosphaeriaceae* by producing cylindrical, septate conidiophores aggregated into conspicuous synnemata, and determinate, monoblastic conidiogenous cells. The conidia are holoblastic, obclavate-rostrate, multi-euseptate (up to 27 septa), and brown to dark olivaceous, with the base truncate and the apex paler and often slightly curved. These features, particularly the well-developed synnemata and the unique conidial morphology, clearly distinguish *Falholtia* from *Stanjehughesia*, in which conidiophores are usually solitary or in clusters, and conidia are less complex.

Phylogenetically, *Falholtia* forms a distinct, well-supported clade within *Chaetosphaeriaceae* (Hsieh et al. 2021; Wu & Diao 2022), separated from *Stanjehughesia* and other *Sporidesmium*-like genera such as *Ellisembia*, *Morisiella*, and *Paliphora* (Réblová et al. 2021; Luo et al. 2019). *Falholtia* represents one of the few genera in *Chaetosphaeriaceae* with non-phialidic, holoblastic

conidiogenous cells. It adds to the diversity of non-phialidic anamorphs in the family, which are otherwise represented mainly by *Sporidesmium*-like fungi. Other related genera with similar conidiogenesis include *Paliphora* and *Chaetosphaeria*, though their conidial and conidiophore structures are notably different (Sivanesan & Sutton 1985; Luo et al. 2019).

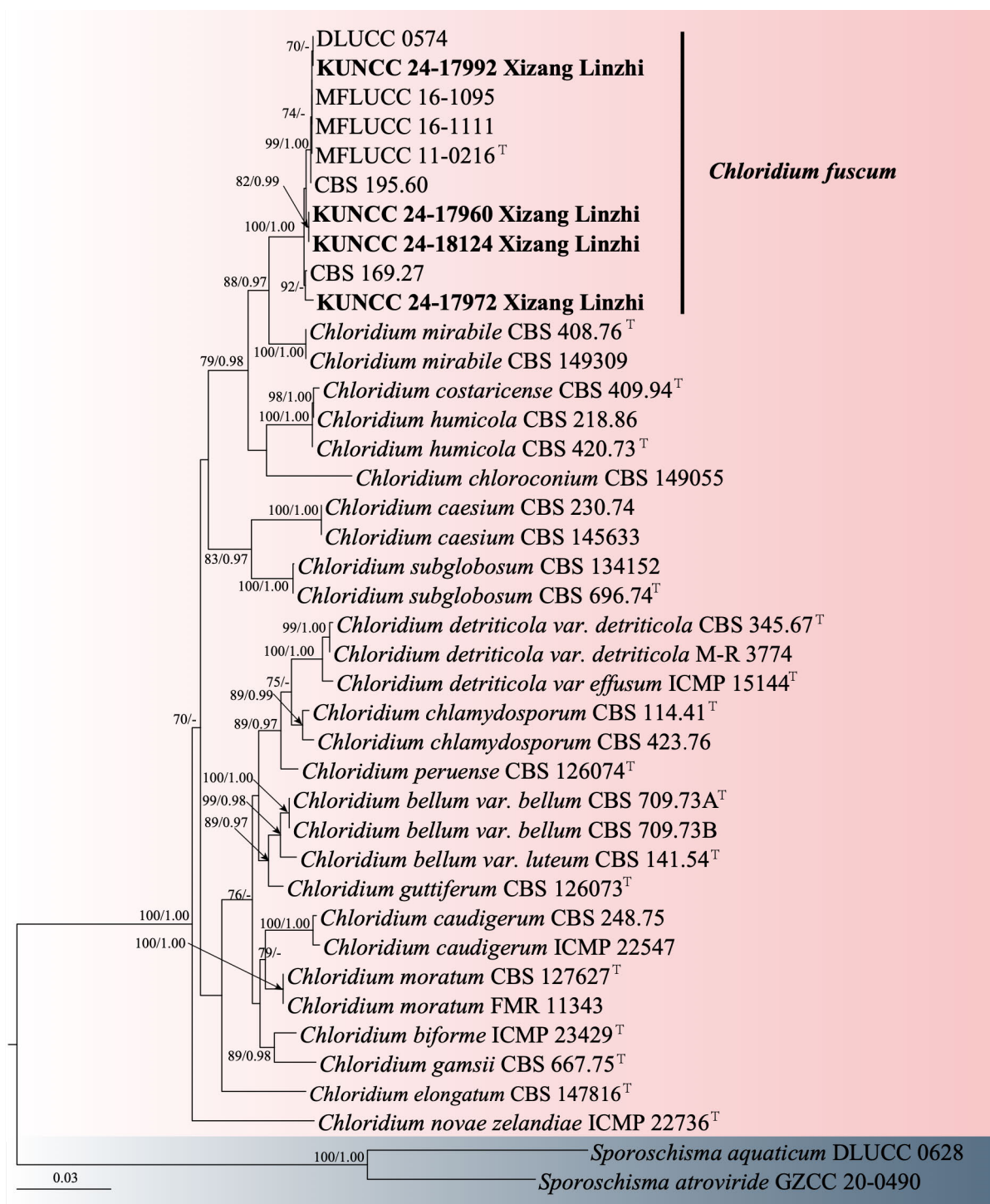


Fig. 31 Maximum likelihood majority rule consensus tree for *Chloridium* using ITS, LSU and SSU sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Sporoschisma aquaticum* (DLUCC 0628) and *S. atroviride* (GZCC 20-0490). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

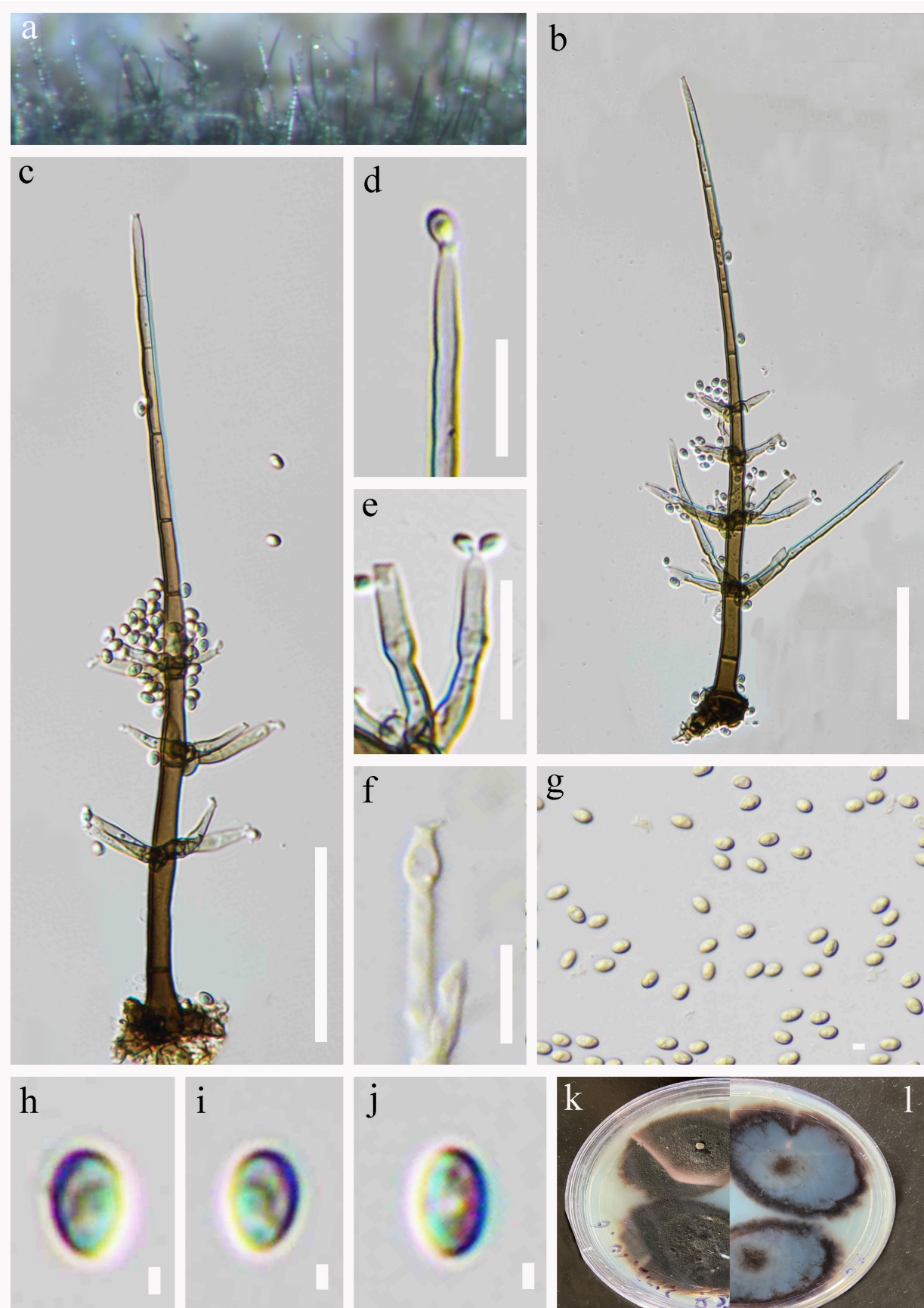


Fig. 32 *Chloridium fuscum* (HKAS 136133) a Colonies on natural substrate. b, c Conidiophores with conidiogenous cell. d–f Conidiogenous cell with developing conidia. g–j Conidia. k, l Culture on PDA medium, k from above, l from below. Scale bars: b, c = 50 μ m, d–f = 10 μ m, g–j = 1 μ m.

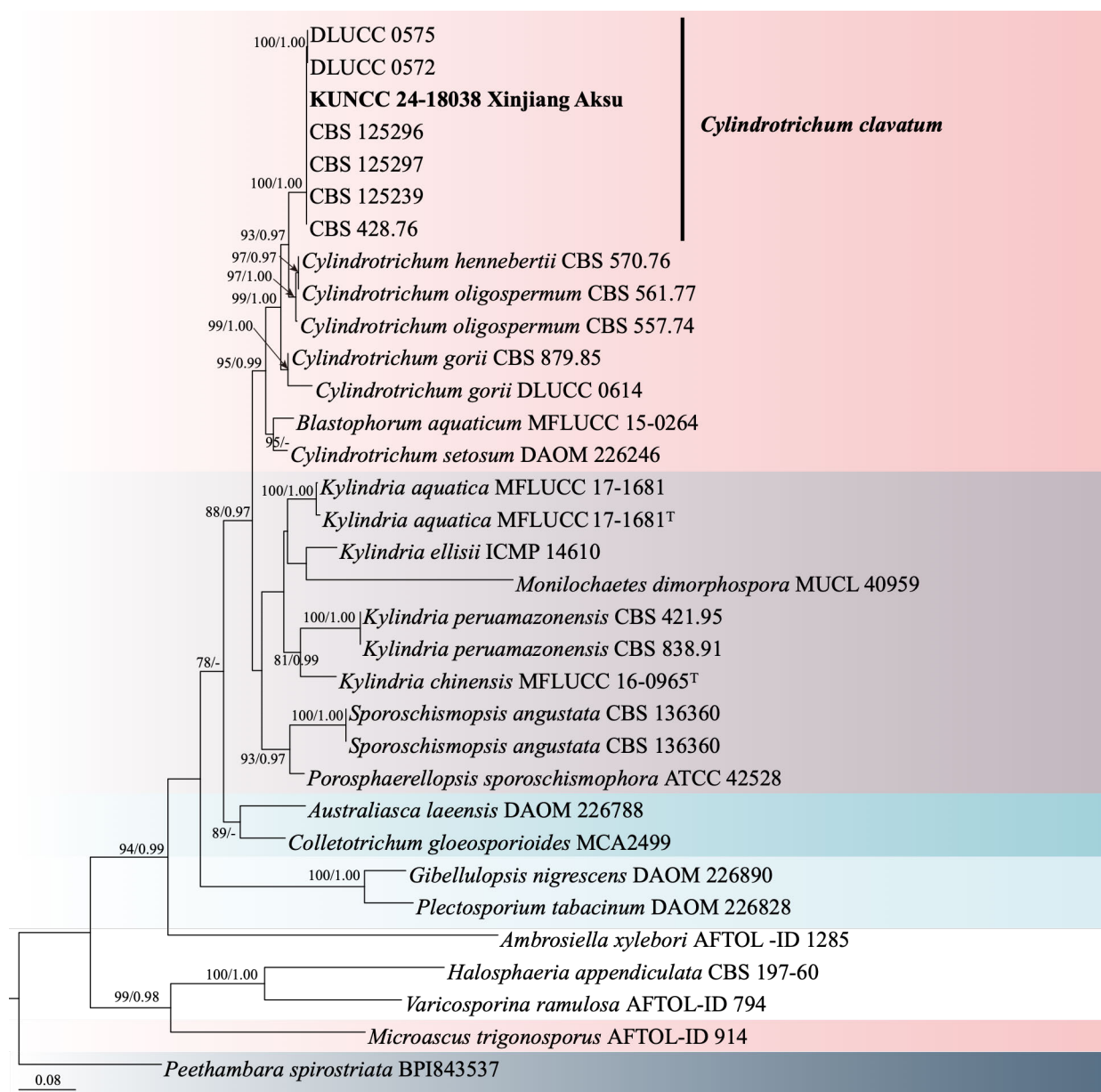


Fig. 33 Maximum likelihood majority rule consensus tree for *Cylindrotrichum* using ITS, LSU and SSU sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML /BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Peethambara spirostriata* (BPI843537). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

19. *Falholtia linzhiensis* R.J. Xu, Q. Zhao & K.D. Hyde, sp. nov. Fig. 36

Chinese name: – 林芝法霍尔提亚菌 (lin zhi fa huo er ti ya jun)

Index Fungorum number: IF 905035; **Facesoffungi number:** FoF 19305

Etymology: the term “linzhiensis” refers to the locality where the type specimen was found.

Holotype: HKAS 141644

Saprobic on decaying wood in a freshwater habitat.

Sexual morph: Undetermined. **Asexual morph:** Colonies on natural substratum, superficial, effuse, scattered, hairy, dark brown. **Mycelium** partly immersed and partly superficial, composed of branched, septate, brown to dark brown, smooth-walled hyphae. **Conidiomata** 480–1128 × 34–50 μm ($\bar{x}$

= 640 × 40 μm, n = 20), synnematos, solitary or in group, erect, cylindrical, dark brown to black, tapering towards the apex, composed of closely compacted conidiophores and hyphae. **Conidiophores** 16–23 × 4–6 μm ($\bar{x}$ = 19 × 5 μm, n = 20), short, 1(2)-septate, cylindrical, unbranched, dark brown to black, smooth-walled. **Conidiogenous cells** monoblastic, integrated, terminal, determinate, cylindrical, brown to dark brown, smooth-walled. **Conidia** 73–152 × 11–15 μm ($\bar{x}$ = 98 × 13 μm, n = 20), acrogenous, solitary, straight to slightly flexuous, obclavate-rostrate, tapering towards the rounded apex, truncate at the base, brown to dark olivaceous brown, hyaline at the apex, base cells cuneiform, 8–15-euseptate, slightly constricted at the septa, sometimes with a sheath at the apex.

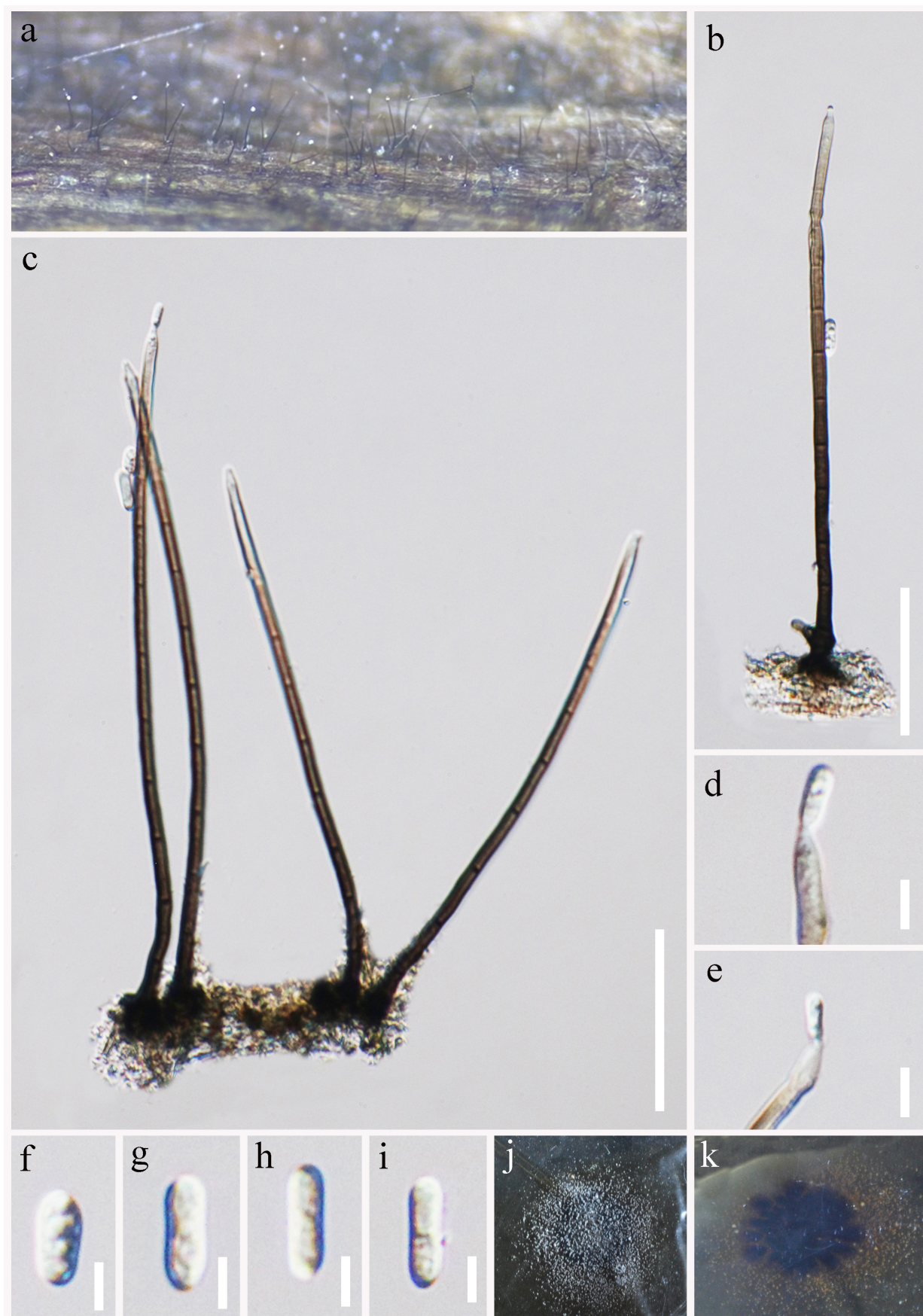


Fig. 34 *Cylindrotrichum clavatum* (HKAS 136202) a Colony on natural substrates. b, c Conidiophores with conidia. d, e Conidiogenous cells with developmental conidia. f–i Conidia. j, k Culture on PDA medium, j from above, k from below. Scale bars: b–c = 50 μ m, d–e = 10 μ m, f–i = 5 μ m.

Culture characteristics: Conidia germinate on PDA within 48 h, with germ tubes emerging from a subtruncate base. Colonies on PDA reach a diameter of 3 cm within one month at room temperature. These colonies are circular with irregular margin, raised in the middle, cream-colored mycelium that covers the entire colony.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Chayu County, 28° 29' 39.27" N, 96° 59' 35.25" E, 1537 m a.s.l., on decaying wood submerged in a freshwater stream, 14 July 2022, R.J. Xu, MD-152A (HKAS 141644, holotype), ex-type culture KUNCC 25-21369.

Notes: *Falholtia linzhiensis* shares the generic features of *Falholtia* by having compact synnemata composed of cylindrical, septate conidiophores, terminal, determinate, monoblastic conidiogenous cells, and holoblastic, obclavate-

rostrate, euseptate conidia with a truncate base and paler apex (Hsieh et al. 2021; Wu & Diao 2022). However, *F. linzhiensis* is morphologically distinct from the type species *F. kaohsiungensis* in having shorter (16–23 µm vs. 13–34 µm), and conidia with fewer septa (8–15 vs. up to 27), often bearing an apical sheath, this feature not reported in the type. Additionally, *F. linzhiensis* forms conidiomata that are often scattered and hairy on the substrate surface, differing from the more compact and erect synnemata of *F. kaohsiungensis*.

Phylogenetic analysis based on ITS and LSU sequences places *F. linzhiensis* within *Chaetosphaeriaceae*, forming a well-supported and independent clade sister to *F. kaohsiungensis* (Fig. 35), thus supporting its recognition as a distinct taxon within the genus.

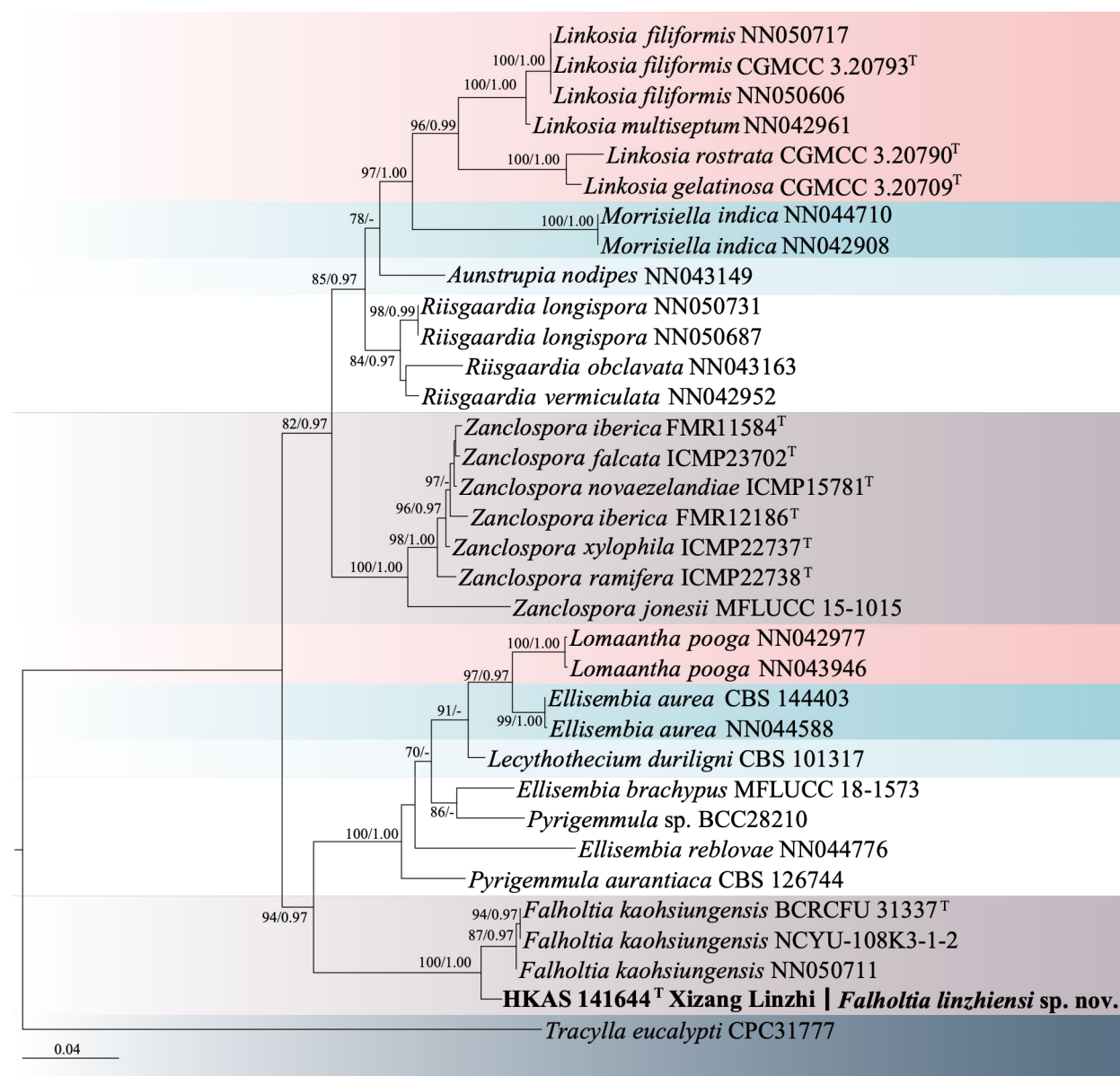


Fig. 35 Maximum likelihood consensus tree inferred from the combined ITS, LSU, and *rpb2* multiple sequence alignments. ML support equal to or greater than 75% and BYPP value equal to or greater than 0.95 are given near the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Tracylella eucalypti* (CPC 31777). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

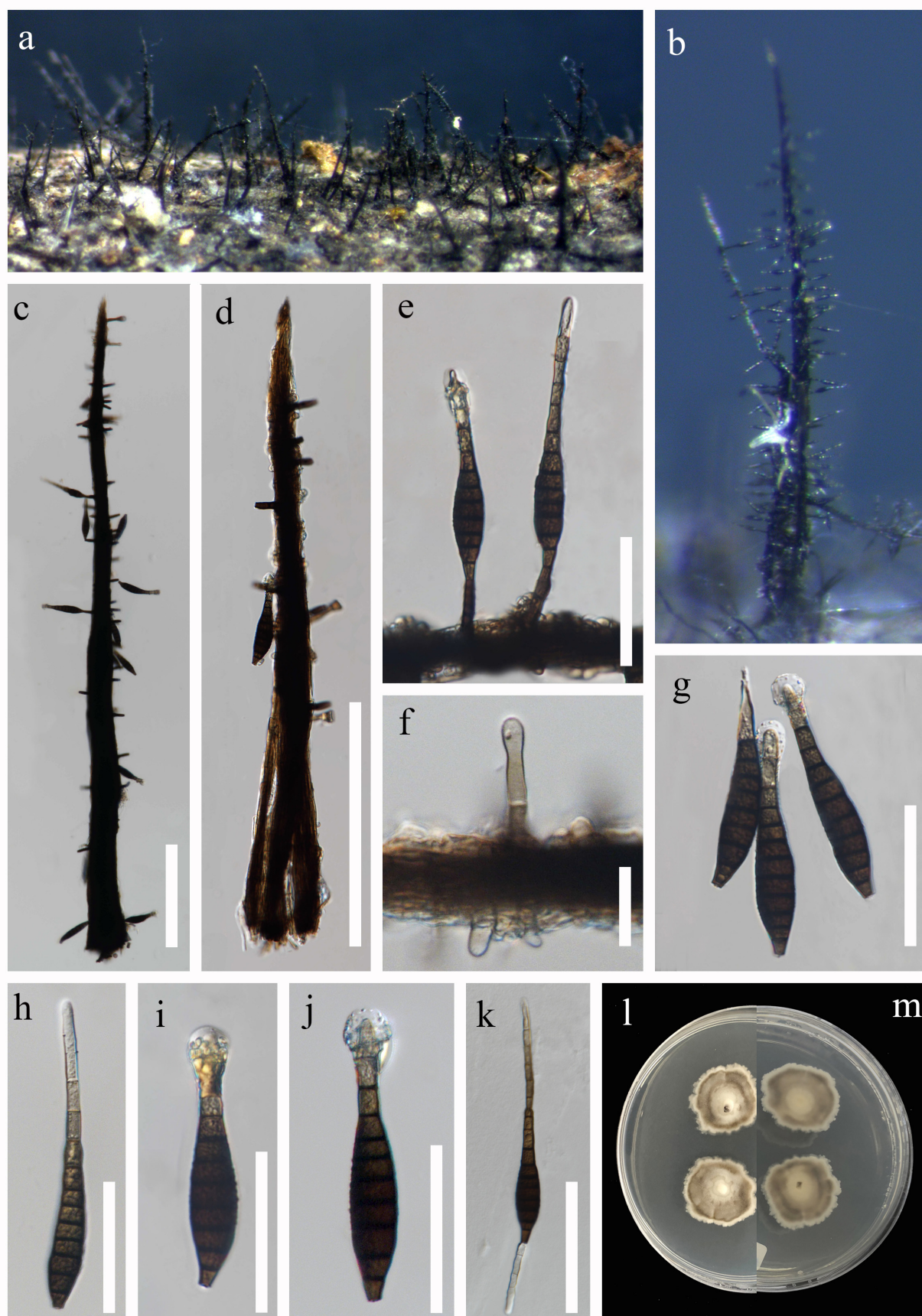


Fig. 36 *Falholtia linzhiensis* (HKAS 141644, **holotype**) a, b Synnemata on natural substrates. c, d Synnemata, conidiophores and conidia. e Conidiophores with conidia. f conidiophores. g–j Conidia. k Germinated conidium. l, m Culture on PDA, l from above, m from below. Scale bars: b–f = 50 µm, g–l = 20 µm.

***Phialosporostilbe* Mercado & J. Mena**

Phialosporostilbe was established by Sierra & Portales (1985) to accommodate *P. turbinata*. Members of *Phialosporostilbe* are characterized by the production of synnematus conidiophores bearing integrated, monophialidic or annellidic conidiogenous cells at the apices. The conidia are typically acrogenous, phialidic, catenate, and range from turbinate to cuneiform or cordiform in shape, colourless to pale brown, smooth-walled, and amerosporous, often with short subapical or apical appendages, such as setulae.

To date, seven species have been recognized worldwide: *Phialosporostilbe catenata*, *P. dendroidea*, *P. gregariclava*, *P. scutiformis*, *P. setosa*, *P. turbinata* and *P. yadongensis*, described from various habitats and geographic regions including Asia and the Americas (Sierra & Portales 1985; Bhat & Kendrick 1993; Shirouzu & Harada 2004; Sureshkumar et al. 2005; Wu & Zhang 2009; Yang et al. 2018b). Although similar in conidial shape and conidiogenesis to species of *Nawawia*, *Phialosporostilbe* is distinguishable by its synnematus rather than mononematous conidiophores, which has been the key feature supporting its separation at the generic level. Nonetheless, due to the similarities in conidial morphology and development, some authors previously considered *Phialosporostilbe* and *Nawawia* to be congeneric (Yang et al. 2018b), warranting further phylogenetic investigation to clarify their relationships.

20. *Phialosporostilbe gaoligongensis* R.J. Xu, Y. Li & Q. Zhao, sp. nov. Fig. 38

Chinese name: – 高黎贡瓶梗孢柱菌 (gao li gong ping geng zhu bao jun)

Index Fungorum number: IF905261; **Facesoffungi number:** FoF 19307

Etymology: The term “gaoligongensis” refers to the locality where the type specimen was found.

Holotype: HKAS 149332

Saprobic on decaying wood submerged in a freshwater stream. **Sexual morph:** Undetermined. **Asexual morph:** Colonies effuse, scattered or in small groups, dark brown, with masses of conidia on the apex of conidiophores. Mycelium immersed, consisting of pale brown, smooth-walled, branched, septate, smooth, subhyaline hyphae. Conidiophores 131–253 × 4–7 µm ($\bar{x}$ = 175 × 5 µm, n = 20), macronematous, mononematous, straight or slightly flexuous, solitary or 2–3-group, cylindrical, smooth-walled, 4–6-septate, unbranched, dark brown or brown, becoming paler towards the apex, rounded at the apex. Conidiogenous cells 26–44 × 4–7 µm ($\bar{x}$ = 35 × 6 µm, n = 20), monophialidic, terminal, integrated, pale brown, subhyaline towards the apex, cylindrical to cylindric-clavate, with an inconspicuous apical collarette. Conidia 8–12 × 6–10 µm ($\bar{x}$ = 10 × 8 µm, n = 30), acrogenous, solitary, round-tetrahedral, pyramidal, smooth, aseptate, thin-walled, guttulate, with 3–4 radiating from each corner appendages 1.6–3.3 µm ($\bar{x}$ = 2.4 µm, n = 30) long.

Culture characteristics: Conidia germinating on PDA medium within 48 h and germ tubes arising from terminal end of conidium. Colonies grown on PDA reached 30 mm diam at room temperature in three weeks, irregular, with velvety, dry, raised, grayish-white mycelium on the surface, from below cream to light brown, producing cream pigments, with entire margin.

Material examined: CHINA, Yunnan Province, Tengchong City, Gaoligong Mountain, 25° 12' 36.00" N, 98° 19' 48.00" E, 1852 m a.s.l., on decaying wood submerged in a freshwater stream, 12 November 2024, Y. Li, ly42 (HKAS 149332, holotype), ex-type culture KUNCC 25-19643.

Notes: *Phialosporostilbe gaoligongensis* possess its conidial characteristics that fit with *Phialosporostilbe* (Sierra & Portales 1985; Wu & Zhang 2009; Yang et al. 2018b), but differs from *P. catenate*, *P. dendroidea*, *P. scutiformis*, *P. setosa*, *P. turbinata* and *P. yadongensis* in having macronematous, mononematous, unbranched conidiophores. *Phialosporostilbe gaoligongensis* resembles *P. gregariclava* in having macronematous, mononematous, conidiophores, acrogenous, solitary, pyramidal conidia, with 3–4 radiating subapical appendages. However, *P. gregariclava* differs from *P. gaoligongensis* in having conidiophores of *P. gregariclava* sometimes with percurrently proliferate, and more septa (5–15 septa vs. 4–6 septa).

Phylogenetic analysis showed that *Phialosporostilbe gaoligongensis* (KUNCC 25-19643) isolates formed a distinct lineage within the genus, and sister clade with *P. scutiformis* (MFLU 18-1502 and MFLUCC 18-1288) (Fig. 37). but it differs from *P. scutiformis* in having unbranched conidiophores and shorter appendages (1.6–3.3 µm vs. 3.5–7.5 µm) (Yang et al. 2018b).

***Sporoschisma* Berk. & Broome**

Sporoschisma was introduced by Berkeley (1847), with *S. mirabile* as the type species. Significant revisions of the genus were made by Hughes (1966) and Goh et al. (1997), who provided historical collection details and comprehensive illustrations. *Sporoschisma* is characterized by scattered, capitate setae and straight, smooth, unbranched brown conidiophores, typically consisting of a cylindrical stipe, a swollen venter, and a long cylindrical neck. The conidiogenous cells are phialidic, while the conidia are cylindrical, often truncate at both ends, and form in chains endogenously in basipetal succession (Seifert & Gams 2011; Wu & Diao 2022; Yang et al. 2023; Xu et al. 2024f).

21. *Sporoschisma longicatenatum* Jing Yang, Jian K. Liu & K.D. Hyde, in Yang, Liu, Hyde, Bhat, Gareth Jones & Liu, Phytotaxa 289(2): 152 (2016) Fig. 40

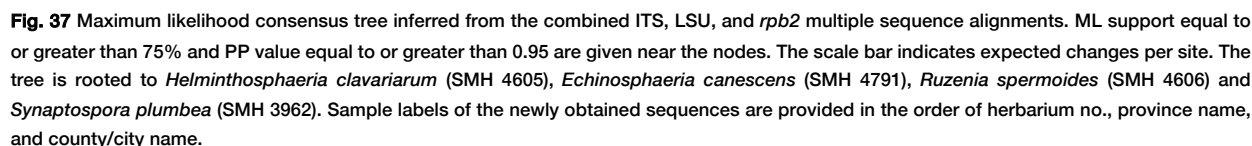
Chinese name: – 长链裂孢菌 (chang lian lie bao jun)

Index Fungorum number: IF 552182; **Facesoffungi number:** FoF 02243

Saprobic on decaying wood submerged in a freshwater habitat. **Sexual morph:** Undetermined. **Asexual morph:** Colonies effuse, black, hairy, chain-like conidia at the apex. Mycelium immersed, composed of pale to dark brown hyphae. Setae 105–156 × 5–7 µm ($\bar{x}$ = 127 × 6 µm, n = 10), scattered or in groups mixed with conidiophores, capitate, usually at the swollen apex, straight or flexuous, septate. Conidiophores 293–359 × 12–15 µm ($\bar{x}$ = 318 × 14 µm, n = 15), macronematous, mononematous, smooth, dark brown to black, paler at the torn apex, straight or slightly flexuous, solitary or in groups, setae, arising from dark brown to black bulbous base, composed of a cylindrical stipe and a swollen venter with a long cylindrical neck, erect. Conidiogenous cells monophialidic, percurrent, integrated, terminal, determinate, brown, lageniform, frayed at the apex. Conidia 66–87 × 19–25 µm ($\bar{x}$ = 74 × 21 µm, n = 20), cylindrical, 5-septate, hyaline when young, olivaceous to brown at maturity, with hyaline to

brown mycelium on the surface, from below dark brown with undulate margin.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, 29°19'43" N, 95°21'19" E, 677 m a.s.l., on decaying wood submerged in a freshwater habitat, 13 July 2022, R.J. Xu, MD-109 (HKAS 136183), living culture KUNCC 24-18020.



longicatenatum (KUNCC 24-18020) clustered together with *S. longicatenatum* (MFLUCC16-0180 and GZCC15-0072) with strong statistical support (100% ML/1.00 BYPP) (Fig. 39). Therefore, we reported a new record for *S. longicatenatum* on the Q-X Plateau, China.



Fig. 38 *Phialosporostilbe gaoligongensis* (HKAS 149332, **holotype**) a Specimen. b Colonies on woody substrate. c–e Conidiophores. f, g Conidiogenous cell with conidia. h Conidia. i Germinated conidium. j, k Culture on PDA medium, j from above, k from below. Scale bars: c–e = 50 μ m, f–i = 10 μ m.

***Stanjehughesia* Subram**

Stanjehughesia was established by Subramanian (1992) during his taxonomic revision of the heterogeneous *Sporidesmium*, in which he segregated several genera based on morphological features such as the presence or absence of conidiophores, the nature of conidial septation (euseptate vs. distoseptate), and percurrent proliferation. Species within *Stanjehughesia* are characterized by lacking well-developed conidiophores and producing obclavate to obclavate-rostrate, euseptate conidia, which may be smooth or verrucose, directly on simple, monoblastic conidiogenous cells (Subramanian 1992; Wu & Zhuang 2005; Seifert et al.

2011). To date, approximately 21 species have been reported in this genus (Hsieh et al. 2021). Cultural studies have linked the sexual morphs *Umbrinosphaeria caesariata* syn. *Chaetosphaeria caesariata* and *Miyoshiella larvata* linked to *Stanjehughesia* (Réblová 1999b). Morphologically similar genera such as *Linkosia* also possess reduced conidiophores and comparable conidial features. However, *Linkosia* can be distinguished by its distoseptate conidia (Hernández-Gutiérrez & Sutton 1997). Phylogenetic analyses have revealed that both *Stanjehughesia* and *Linkosia* as distinct lineages in *Chaetosphaeriaceae*, *Chaetosphaeriales* (Hyde et al. 2024a; Réblová et al. 2024).

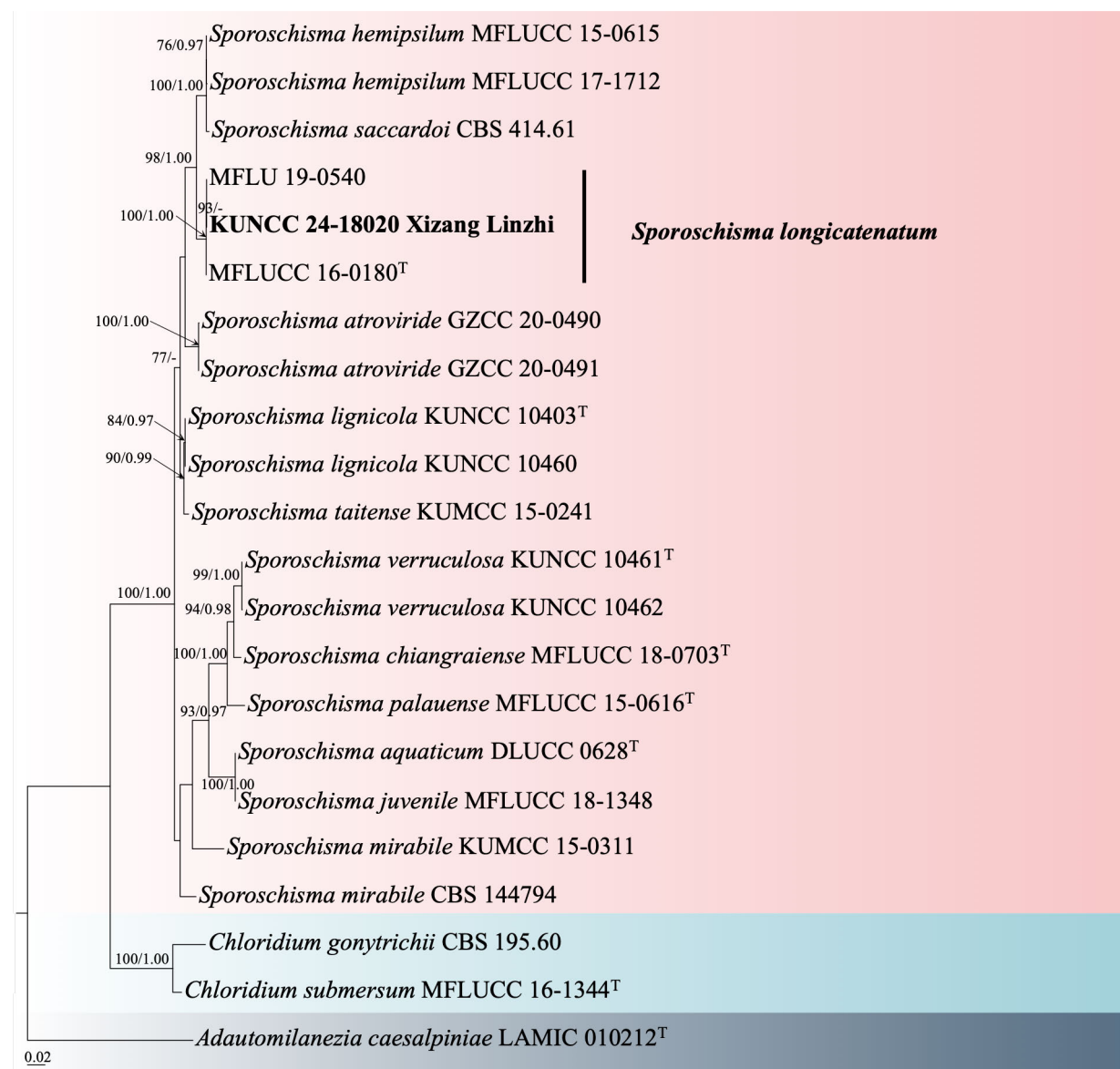


Fig. 39 Maximum likelihood consensus tree inferred from the combined ITS, LSU, and *rpb2* multiple sequence alignments. ML support equal to or greater than 75% and PP value equal to or greater than 0.95 are given near the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Adautomilanezia caesalpiniae* (LAMIC 010212). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

22. *Stanjehughesia motuoensis* R.J. Xu, Q. Zhao & K.D. Hyde, sp. nov. Fig. 42

Chinese name: – 墨脱休氏霉 (mo tuo xiu shi mei)

Index Fungorum number: IF 905037; **Facesoffungi number:** FoF 19308

Etymology: the term “motuoensis” refers to the locality where the type specimen was found.

Holotype: HKAS 151645

Saprobic on decaying wood in a freshwater habitat.

Sexual morph: Undetermined. **Asexual morph:** Colonies on

wood effuse, scattered or in small groups, hairy, dark brown, glistening. Mycelium mostly immersed, composed of septate, branched, hyaline to brown, smooth-walled hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–6 × 3–4 µm ($\bar{x}$ = 5 × 3 µm, n = 20), monoblastic, integrated, terminal, determinate, erect, solitary or fasciculate, straight, cylindrical or lageniform, aseptate, slight olivaceous green, brown to dark brown, smooth-walled. *Conidia* 30–110 × 9–12 µm ($\bar{x}$ = 90 × 11 µm, n = 20), acrogenous, solitary, lanceolate, rostrate, straight or slightly curved, 14–19-euseptate, brown to dark brown with olive green tint, pale

brown to subhyaline at the apex, guttulate, tip swollen and gradually tapers towards the base part when young, the lower middle part swollen and gradually tapers towards both ends when mature, rounded at the apex and truncate at the base, smooth-walled.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, 29°19'43.6" N, 95°21'19.2" E, 798 m a.s.l., saprobic on submerged decaying wood in a freshwater habitat, 12 July 2022, R.J. Xu, MD-381A (HKAS 151645, holotype), ex-type culture KUNCC 10488.

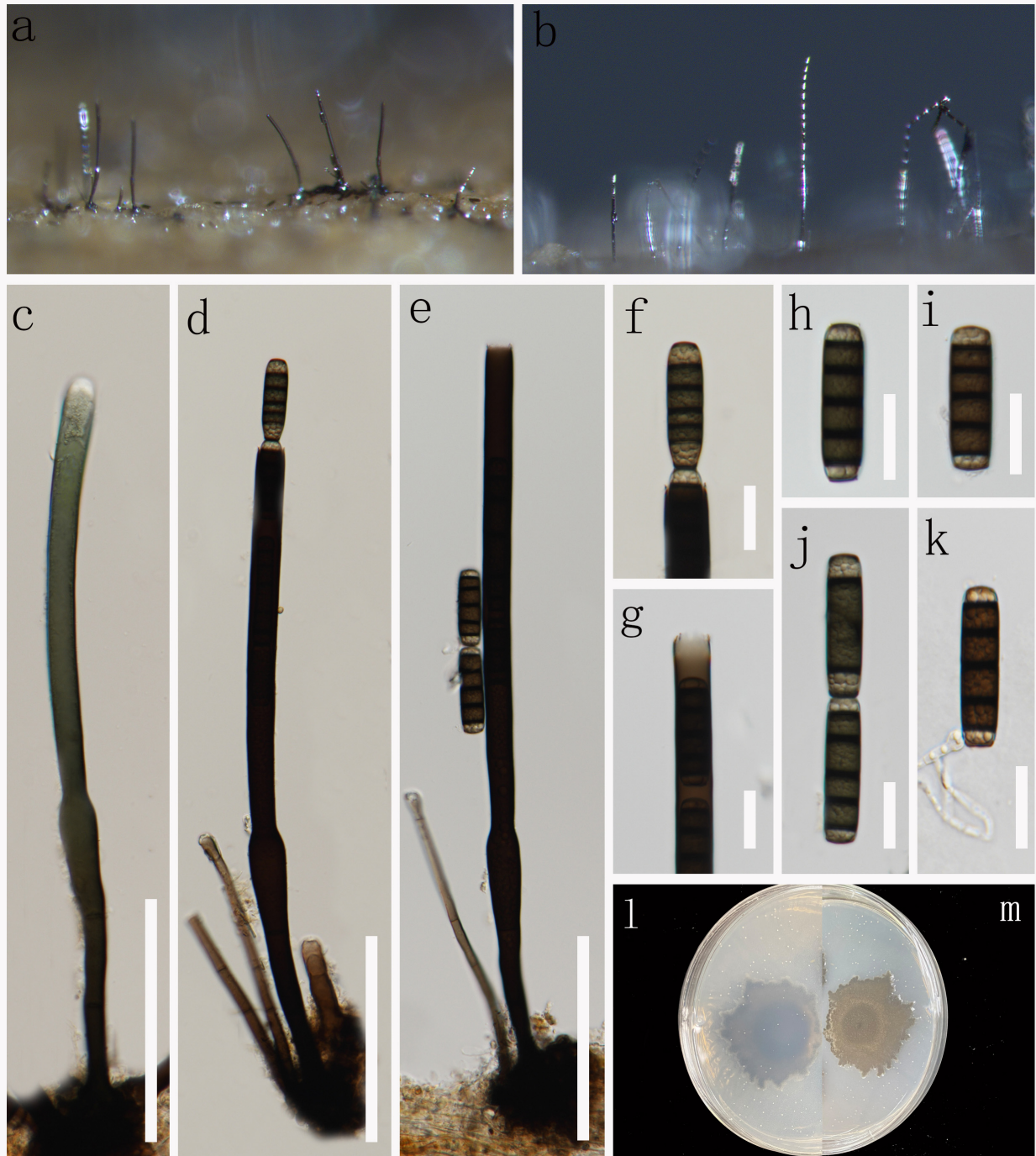


Fig. 40 *Sporoschisma longicatenatum* (HKAS 136183) a, b Colony on wood with long conidia chains. c–e Conidiophores with setae. f, g Conidiogenous cell with conidia. h–k Conidia. l, m Culture on PDA medium, l from above, m from below. Scale bars: c–e = 100 µm, f–k = 20 µm.

Notes: *Stanjehughesia motuoensis* was collected from decaying wood in a freshwater habitat in Q-X Plateau, China. In the multi-gene phylogenetic analysis based on combined LSU, SSU, ITS, and *tef1*- α sequence data, *S. motuoensis* forms a distinct, well-supported clade within *Chaetosphaeriaceae* (Fig. 41), clearly separated from other known species of the genus (Wu & Diao 2022). Although *S. motuoensis* shares the typical lanceolate, multi-septate conidia characteristic of *Stanjehughesia*, it is readily distinguished from *S. hormiscioides* by its longer conidia (30–110 μ m vs. 30–60 μ m), higher septation (14–19 vs. 7–14), and more pronounced tapering at both ends. Compared to *S. kaohsiungensis*, which has shorter (35–70 μ m), less septate (7–13) conidia and a broader apex, *S. motuoensis* also exhibits a distinctive rostrate shape and a darker pigmentation with an olive tint. *Stanjehughesia motuoensis* is introduced herein as a new species based on its unique morphological characteristics and distinct phylogenetic placement within *Stanjehughesia*.

Glomerellales Chadeff. ex Réblová, W. Gams & Seifert

Reticulascaceae Réblová & W. Gams

Kylindria DiCosmo, S.M. Berch & W.B. Kendr.

DiCosmo et al. (1983) established *Kylindria* to accommodate *Cylindrotrichum triseptatum* ($\equiv$ *K. triseptata*, type species), along with four other *Cylindrotrichum* species. The asexual morphs are characterized by solitary, unbranched, multi-septate, dark brown conidiophores, monophialidic, integrated, terminal, ampulliform conidiogenous cells with narrow apertures at the apex and with or without a conspicuous collarette, and unicellular or euseptate, hyaline conidia with or without an excentric lateral or basal hilum (DiCosmo et al. 1983; Zhang et al. 2010). *Kylindria* species are predominantly saprobic fungi that flourish on decomposing organic matter, including dead branches, decaying leaves, rotting rachides, and desiccated twigs, found in both aquatic and terrestrial ecosystems (Maharachchikumbura et al. 2018; Tian et al. 2024a). Currently, 18 species epithets are listed in Index Fungorum (accessed on 16 July 2025), however, sequence data are available for only 6 species.

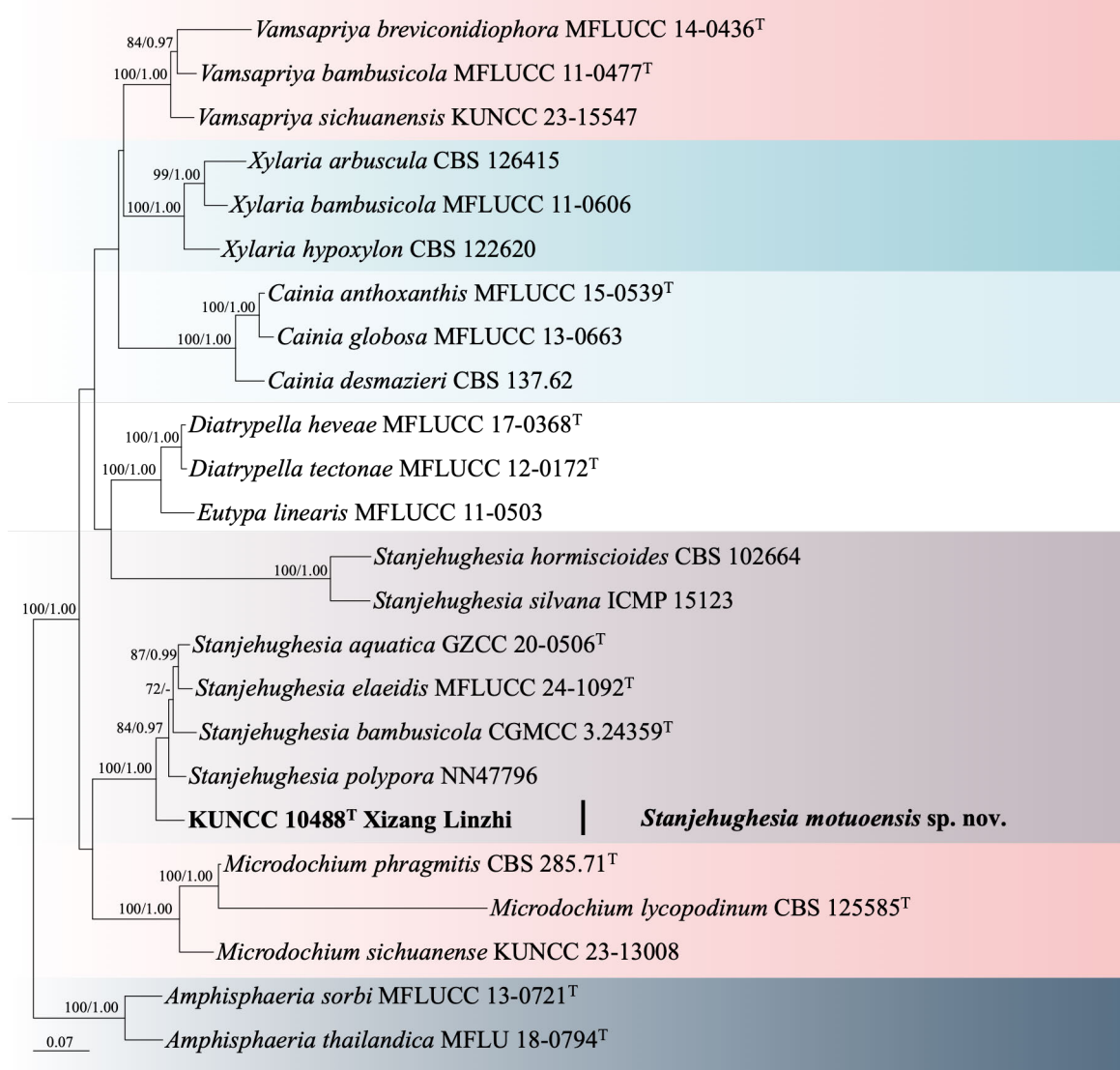


Fig. 41 Maximum likelihood consensus tree inferred from the combined ITS, LSU, and *rpb2* multiple sequence alignments. ML support equal to or greater than 75% and PP value equal to or greater than 0.95 are given near the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Amphisphaeria sorbi* (MFLUCC 13-0721) and *A. thailandica* (MFLU 18-0794). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

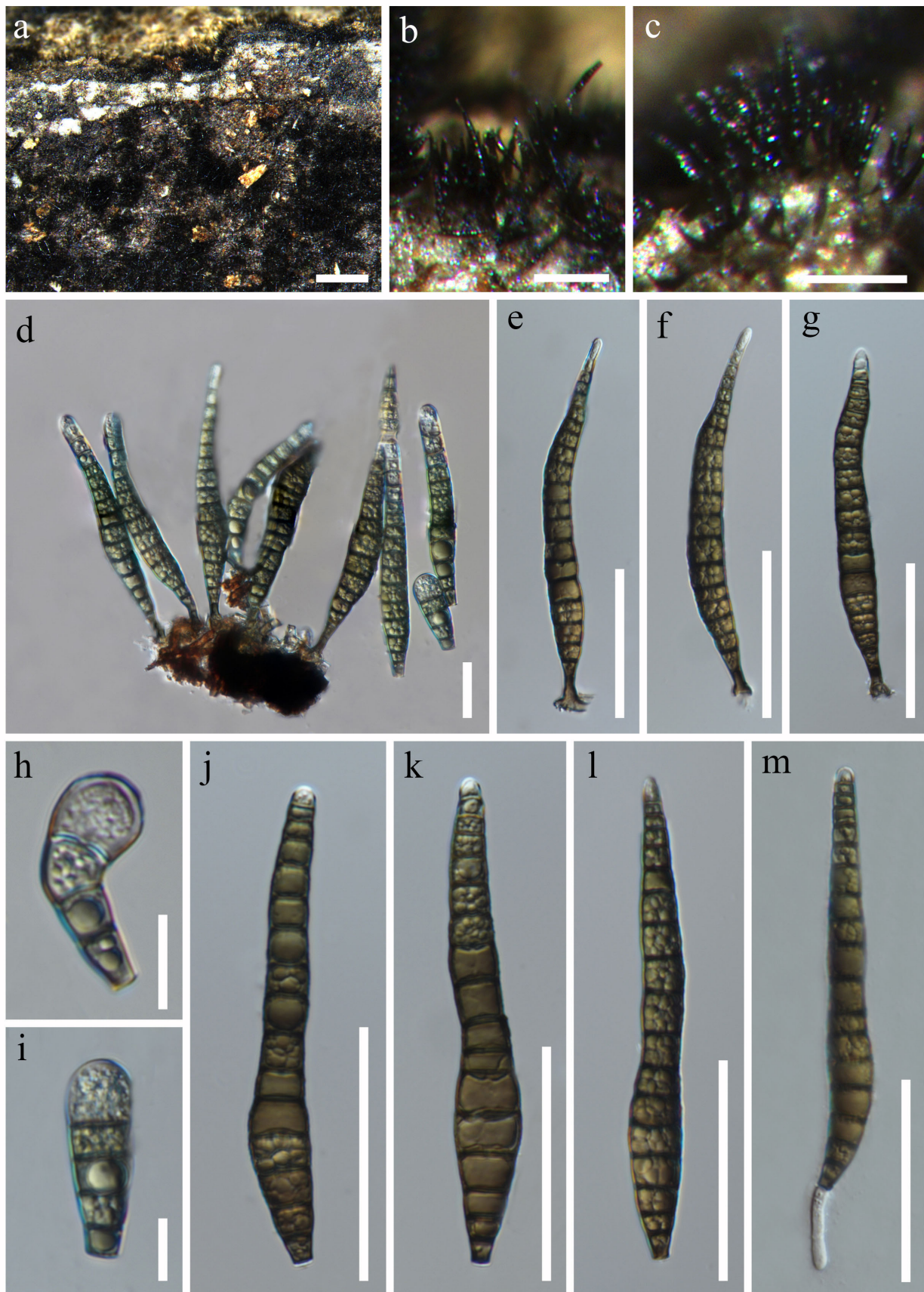


Fig. 42 *Stanjehughesia motuoensis* (HKAS 151645, holotype) a–c Colony on natural substrates. d Conidiogenous cells with conidia. e–g Conidia. h, i Conidiogenous cells with developmental conidia. j–l Conidia. m Germinated conidium. Scale bars: b–c = 50 µm, d–e = 10 µm, f–i = 5 µm.

23. *Kylindria cryptomeriae* W.H. Tian, K.D. Hyde & Maharachch., *Mycosphere* 15 (1): 1861 (2024) **Fig. 44**

Chinese name: – 柳杉隐管菌 (liu shan yin guan jun)

Mycobank number: MB 851891; **Facesoffungi number:** FoF 16281

Saprobic on decaying submerged wood in a freshwater habitat. **Sexual morph:** Undetermined. **Asexual morph:** Colonies on natural substrate, superficial, effuse, gregarious, brown to dark brown, hairy, with white glistening conidial masses at the apex. *Mycelium* partly immersed, composed of branched, septate, brown to dark brown, smooth hyphae. *Conidiophores* 204–305 × 9–16 µm ($\bar{x}$ = 268 × 12 µm, *n* = 20), mononematous, macronematous, straight to slightly curved, erect, unbranched, multi-septate, dark brown at base, paler toward the apex, thick-walled. *Conidiogenous cells* 41–53 × 9–15 µm ($\bar{x}$ = 46 × 13 µm, *n* = 20), phialidic, terminal, integrated, ampuliform, broadest above the middle, tapering near the apex, with an inconspicuous apical collarette. *Conidia* 24–34 × 9–14 µm ($\bar{x}$ = 30 × 11 µm, *n* = 30), arranged in a slimy head, solitary, oblong with obtuse ends, hyaline, 0–3-septate, with a slimy mucilaginous coating around.

Culture characteristics: Conidia germinating on PDA medium within 24 hours, with germ tubes arising from polar cells of the conidium. Colonies grown on PDA reached a diameter of 12 mm at room temperature under natural light in one month, edges regular, flat, white to pale yellow on the surface, pale yellow on the reverse.

Material examined: CHINA, Guizhou Province, Liupanshui City, Shuicheng County, Yushe National Forest Park, N 26°27'17" N, 104°48'26" E, 2232 m a.s.l., on decaying submerged wood in a freshwater habitat, 27 February 2023, Xingjuan Xiao, YSS89 (HKAS 145867), culture GZCC 24-0088.

Note: Phylogenetically, our new collection is closely allied with *Kylindria cryptomeriae* (UESTCC 23.0231) with 96% ML/1.00 BYPP support (Fig. 43). Comparison of the ITS, LSU, and *rpb2* sequences between the new collection and *K. cryptomeriae* (UESTCC 23.0231) showed 99% identity (481/483 bp, 1 gap), 100% identity (801/801 bp), and 99% identity (1019/1023 bp, 1 gap), respectively. Morphologically, the new collection displays nearly identical characteristics, including conidiophore dimensions (204–305 × 9–16 µm vs. 180–310 × 6–11 µm) and conidia (24–34 × 9–14 µm vs. 22–32 × 9–12 µm) with the holotype (HKAS 131279) of *K. cryptomeriae* (Tian et al. 2024a). Consequently, we classify our collection as *K. cryptomeriae*, marking the first report of this species from a freshwater habitat.

Conioscyphales Réblová & Seifert

Conioscyphaceae Réblová & Seifert

Conioscypha Höhn

Conioscypha was established by von Höhnelt (1904), with *C. lignicola* as the type species. Species within this genus are widely distributed across terrestrial and freshwater habitats globally. The sexual morphs of *Conioscypha* are characterized by inconspicuous ascomata, which are either superficial or immersed, ostiolate, and subhyaline to pale orange. These ascomata contain hyaline, 8-spored, unitunicate asci with a refractive J-apical annulus, and fusiform, 3–7-septate ascospores that lack mucilaginous sheaths or appendages (Réblová & Seifert 2004; Zelski et al. 2014; Réblová et al. 2016b; Hyde et al. 2020b). The asexual morphs are defined by micronematous, mononematous, erect, hyaline, and smooth-walled conidiophores. The conidiogenous cells are enteroblastic, terminal, or intercalary,

and exhibit cyathiform to doliiform shapes with multilayered, cup-like collarettes. The conidia are dark brown to black, ranging from globose to subglobose or elliptical, with smooth surfaces (Shearer & Motta 1973; Goh & Hyde 1998a; Chuaseeharonnachai et al. 2017; Luo et al. 2019). Currently, *Conioscypha* comprises 29 accepted species (Index Fungorum 2026; Liu et al. 2019b; Xu et al. 2024e, 2025; Li et al. 2024b; Sun et al. 2025).

24. *Conioscypha aquatica* (Z.L. Luo, K.D. Hyde & H.Y. Su) R.J. Xu, Q. Zhao & K.D. Hyde, **comb. nov.** **Fig. 46**

Chinese name: – 水生锥壳孢 (shui sheng zhui ke bao)

Index Fungorum number: IF 905262; **Facesoffungi number:** FoF 05450

Synonym: *Conioscypha submersa* Z.L. Luo, K.D. Hyde & Hong Y. Su, *Fungal Diversity* 99: 560 (2019)

Saprobic on decaying wood submerged in a freshwater habitats. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies on natural substrate effuse, scattered, gregarious, punctiform, dark brown or black. *Mycelium* immersed, composed of hyaline, septate, branched, smooth hyphae. *Conidiophores* micronematous, mononematous, hyaline, often reduced to conidiogenous cells. *Conidiogenous cells* sessile or on short conidiophores, and arising directly from the hyphae. *Conidia* 17–23 × 14–22 µm ($\bar{x}$ = 20 × 18 µm, *n* = 40), acrogenous, globose, subglobose, or obovoid, aseptate, pale brown when young, dark brown to black when mature, smooth-walled, subtruncate at base.

Culture characteristics: Conidia germinating on PDA within 48 h and germ tubes produced from base cell. Colonies on PDA reaching 5–10 mm diam, at one month at room temperature, circular, with sparse dark brown mycelium in the middle, sparse pale brown mycelium on the outer ring with irregular margin. Sporulated conidia in cultures. *Conidiophores* micronematous, branched, sometimes reduced to a moniliform conidiogenous cell, hyaline to pale brown. *Conidiogenous cells* monoblastic, integrated, cylindrical, hyaline. *Conidia* 9–17 × 8–14 µm ($\bar{x}$ = 12 × 11 µm, *n* = 40), acrogenous, subglobose or elliptical, olivaceous or pale brown.

Material examined: CHINA, Xizang Autonomous Region, Rikaze City, Nyalam County, 27° 59' 13.09" N, 85° 59' 0.93" E, 2236 m a.s.l., on decaying wood submerged in a freshwater stream, 06 July 2022, R.J. Xu, MD-680 (HKAS 136019), culture KUNCC 10475. Xizang Autonomous Region, Rikaze City, Dingjie County 27° 53' 8.72" N, 87° 27' 36.21" E, 3042 m a.s.l., on decaying wood submerged in a freshwater stream, 05 July 2022, R.J. Xu, MD-681 (HKAS 136027), culture KUNCC 10473.

Notes: *Conioscypha aquatica* and *C. submersa* were initially described by Luo et al. (2019), based on comprehensive phylogenetic analyses and morphological assessments. Our multigene phylogenetic analyses, coupled with meticulous morphological comparisons, indicate that our collected specimens (KUNCC 10475 and KUNCC 10473) group together with ex-type of *C. aquatica* (MFLUCC 18-1333) and ex-type of *C. submersa* (DLUCC 0904) (Fig. 45). Despite the observed differences in their ITS sequences, which amount to 7/528 bp (1.3%, excluding gaps), these intraspecific variabilities do not satisfy the standard thresholds commonly employed for species delineation (Jeewon & Hyde 2016; Chethana et al. 2021a). Furthermore, morphological analysis reveals a notable congruence among

these specimens regarding conidiophore architecture and the morphology, dimensions, and shape of the spores, thereby reinforcing the hypothesis that they constitute a singular species.

Given these findings, we consolidate *Conioscypha aquatica* and *C. submersa* into a single species. In accordance with the International Code of Nomenclature for

algae, fungi, and plants (ICN), we recommend the retention of the name *C. aquatica*, as it is supported by the earlier collection date of its type specimen (2015) in contrast to that of *C. submersa* (2016). Additionally, we have updated the molecular phylogenetic data for this species and provided a comprehensive description of its colonies cultivated on potato dextrose agar (PDA) medium.

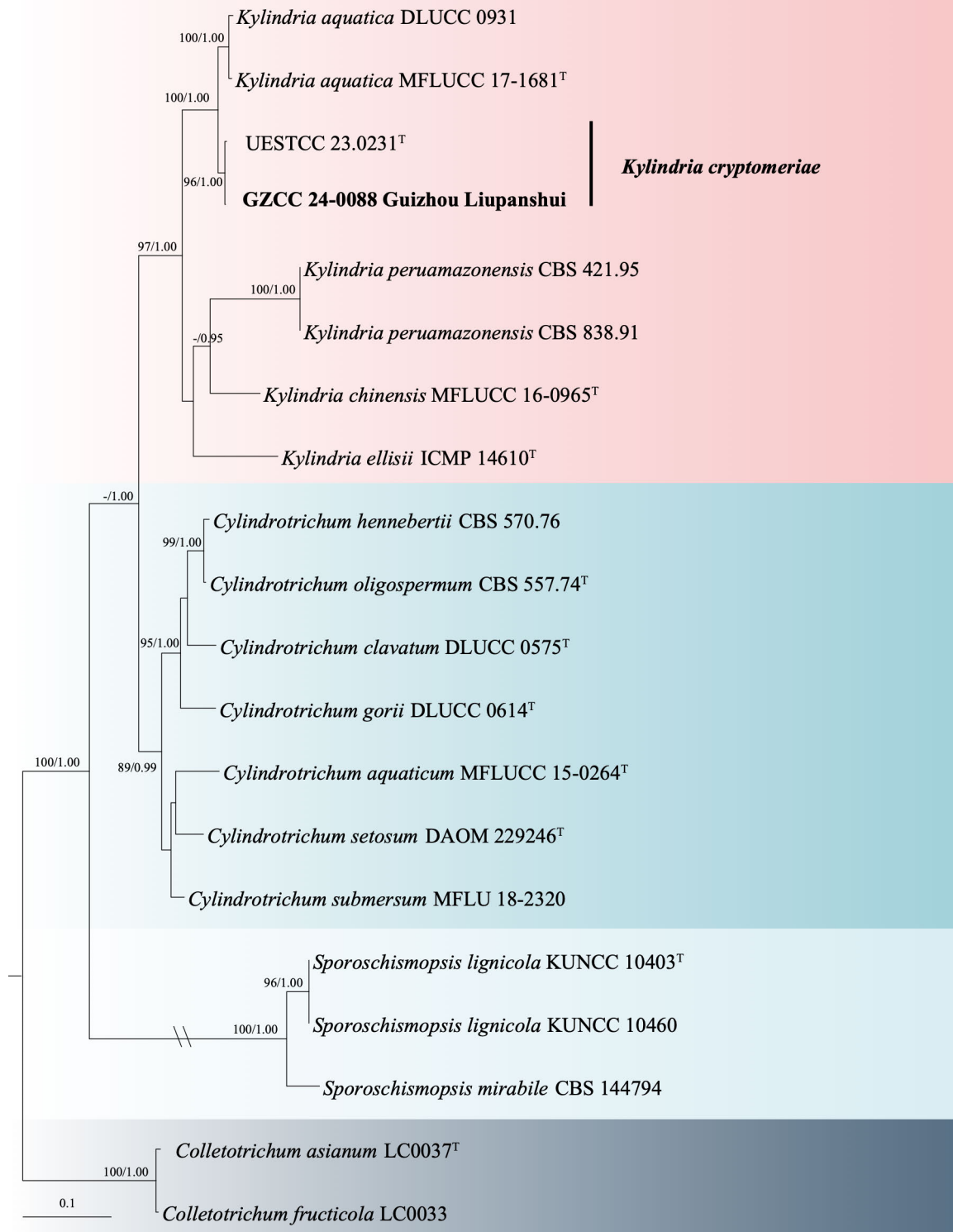


Fig. 43 Maximum likelihood consensus tree inferred from the combined ITS, LSU, and *rpb2* multiple sequence alignments. ML support equal to or greater than 75% and PP value equal to or greater than 0.95 are given near the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Colletotrichum asianum* (LC0037) and *C. fruticola* (LC0033). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

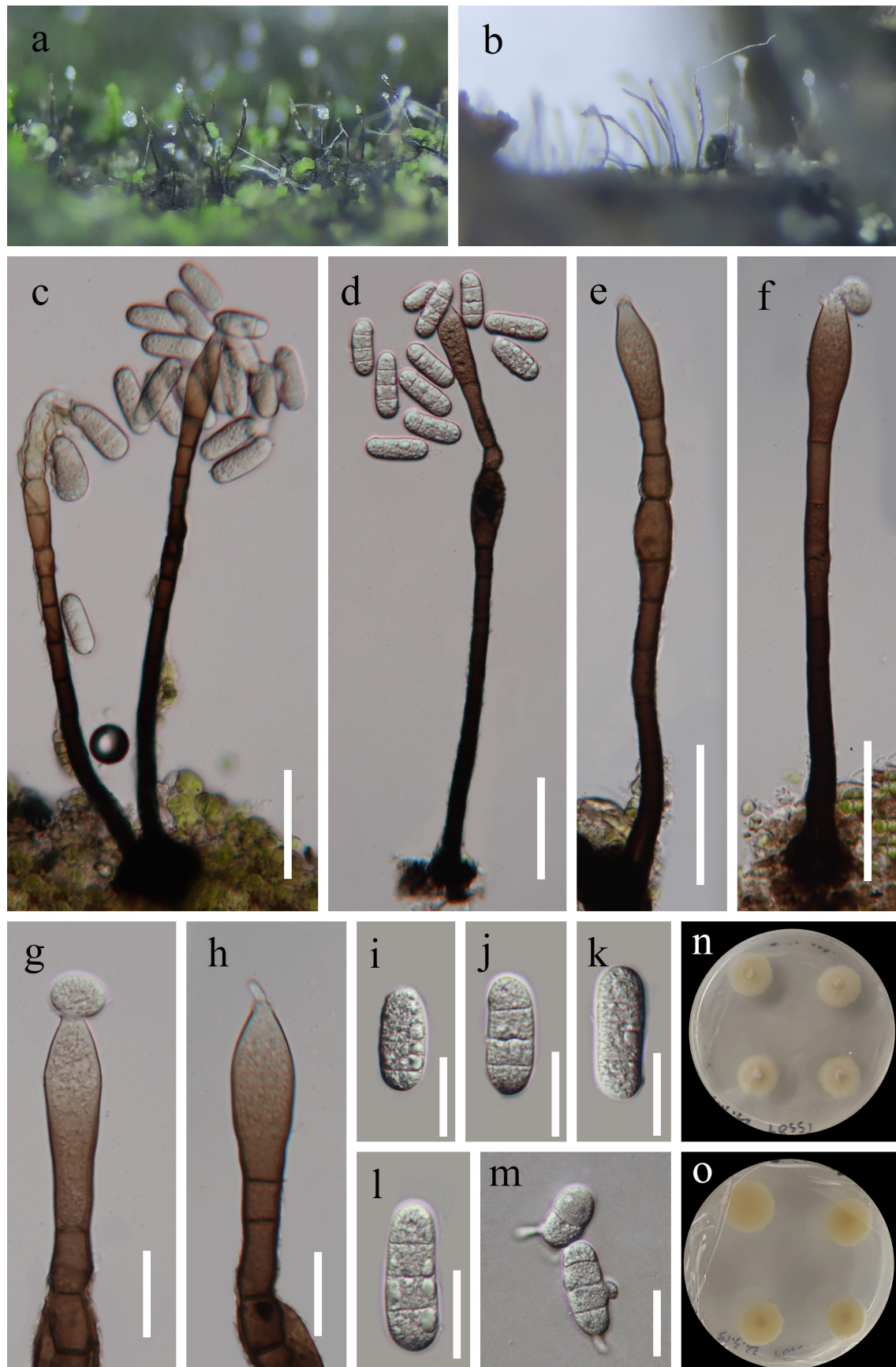


Fig. 44 *Kylandria cryptomeriae* (HKAS 145867, new habitat records) a, b Colonies on dead wood. c–f Conidiophores and conidia. g, h Conidiogenous cells and young conidium. i–l Conidia, m Germinating conidia. n, o Colonies on PDA medium, n from above, o from below. Scale bars: c–f = 50 µm, g–m = 20 µm.

Coniochaetales Huhndorf, A.N. Mill. & F.A. Fernández
Cordanaceae Nann.

Cordana Preuss, Linnaea 24: 129 (1851)

Cordana was established by Preuss (1851) to include three species *C. polyseptata*, *C. pauciseptata*, and *C. pedunculata*, though no type species was initially designated (Hernández-Restrepo et al. 2014; Hyde et al. 2020c). *Cordana* is defined by macronematous, mononematous conidiophores with polyblastic, inflated, integrate or discrete conidiogenous cells that are terminal or intercalary, nodose, and swollen or umbellate at the apices. Its conidia are acropleurogenous,

ovoid to ellipsoid, and typically bear a protuberant hilum (Castañeda Ruiz et al. 1999; Ai et al. 2019; Yang et al. 2022b).

Members of *Cordana* are globally distributed and commonly found on various substrates, including soil, plant debris, and other fungal organisms (De Hoog et al. 1983; Cai 2004; Soares et al. 2005). Currently, 21 species are recognized in the genus, with some species, such as *C. abramovii*, *C. aquatica*, *C. reniformis*, *C. uniseptata* and *C. xizangensis* also identified in freshwater environments (Cai 2004; Hernández-Restrepo et al. 2014; Zelski et al. 2014; Luo et al. 2019; Xu et al. 2024e, 2025).

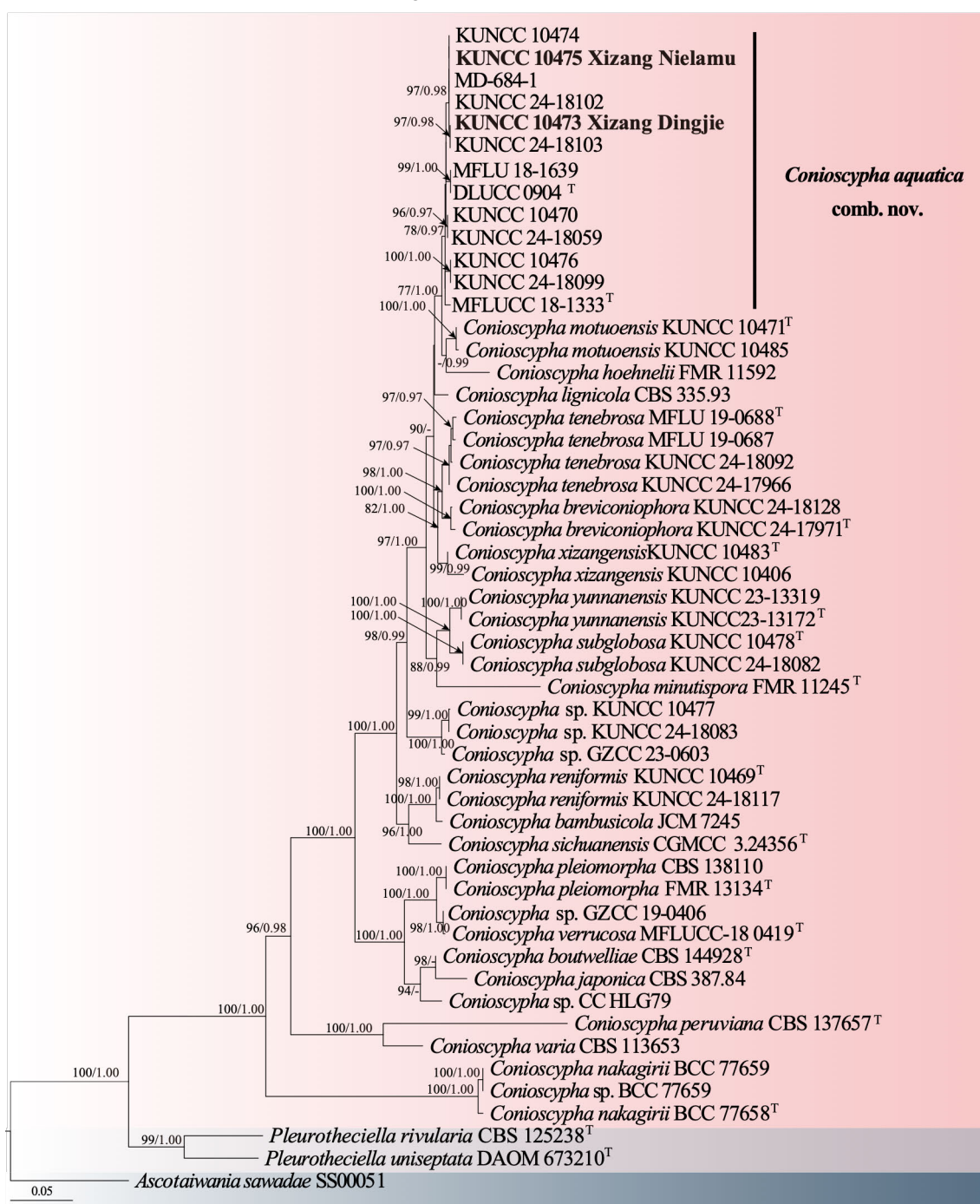


Fig. 45 Maximum likelihood majority rule consensus tree for *Conioscyphaceae* using ITS, LSU, SSU and *rpb2* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML BS/PP. The scale bar represents the expected number of changes per site. The tree is rooted with *Ascotaiwania sawadae* (SS00051). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

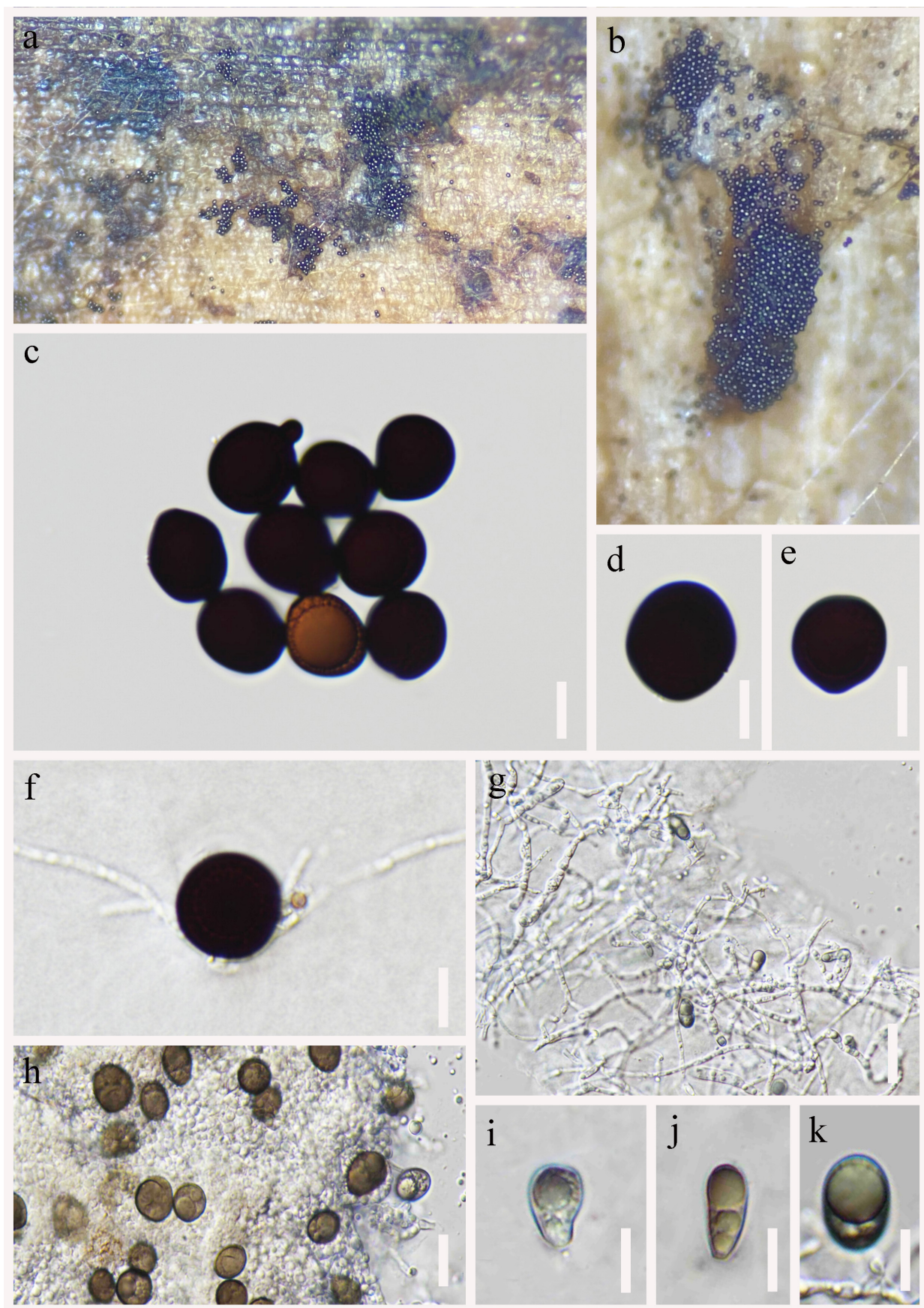


Fig. 46 *Conioscypha aquatica* (HKAS 136019) a, b Colony on natural substrates. c–e Conidia. f Germinated conidium. g, h Colony on PDA. i–k Conidia on PDA. Scale bars: c–k = 10 μm.

25. *Cordana pohuashanensis* S.C. He, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 48

Index Fungorum number: IF905263; **Facesoffungi number:** FoF 19309

Chinese name: 花楸暗双孢 (hua qiu an shuang bao)

Etymology: Name reflects the host, *Sorbus pohuashanensis*, from which the fungus was collected.

Holotype: HKAS 144626

Saprobic on decaying of *Sorbus pohuashanensis* (Rosaceae). **Sexual morph:** Not observed. **Asexual morph:** Hyphomycetous. **Colonies** on the host surface, effuse, medium sparse, dark brown. **Mycelium** immersed, septate, branched, smooth. **Conidiophores** macronematous, mononematous, erect, straight or slightly flexuous, branched, rough-walled, thick-walled, septate, cylindrical, 0–10-inflated, brown to hyaline, conidiophores have multiple conidiogenous loci, 51–260 × 4–7.7 µm ($\bar{x}$ = 160 × 6 µm, n = 20). **Conidiogenous cell** polyblastic, integrated, terminal. **Conidia** didymospores, solitary, acropleurogenous, simple, dry, oblong with obtuse ends, smooth, thin-walled, 1-septate, guttulate when immature, constricted at septate, darker at septum hyaline, hyaline to brown, 8.7–12 × 3.8–5.7 µm ($\bar{x}$ = 10.5 × 5 µm, n = 30).

Culture characteristics: Conidia germinating within 12 h on PDA media at 25 °C, reaching 2.2–2.4 cm after 15 days incubation, colony surface pale olivaceous-grey, reverse pale

black, dense, circular, slightly raised, smooth, entire, hairy, pigmentation not produced.

Material examined: CHINA, Xizang, Linzhi City, Motuo County, 29°15'N, 95°15'E, 1663 m a.s.l., on the *Sorbus pohuashanensis* (Rosaceae), June 27, 2022, collected by Yun-Wei Zhao, ZYW221 (HKAS 144626, holotype), ex-type culture, KUNCC24-19008.

Notes: *Cordana aquatica* was introduced by Luo et al. (2019), based on phylogenetic and morphological analyses, and was collected from aquatic environments in Yunnan, China. Our specimen (HKAS 144626) was collected in Xizang, China, from a terrestrial environment of *Sorbus pohuashanensis*. Morphologically, our specimen (HKAS 144626) are similar to *C. aquatica*, with conidiophores that are macronematous, mononematous, and cylindrical, and conidia that are didymospores, acropleurogenous, and 1-septate (Luo et al. 2019). However, the conidiophores of our samples are shorter (160 × 6 µm vs. 209 × 6 µm), and the conidia are larger (10.5 × 5 µm vs. 9 × 4 µm). Through base pair comparison, the ITS and LSU sequence of *C. aquatica* differs from that of our specimen (HKAS 144626) in 17/482 (3.5 %) and 7/759 (1 %) respectively, and phylogenetic analysis showed that *C. pohuashanensis* sister group with *C. reniformis* (Fig. 47). Therefore, we introduce a new species, *C. pohuashanensis*, from Xizang, China, based on phylogenetic analysis, morphology, and habitat.

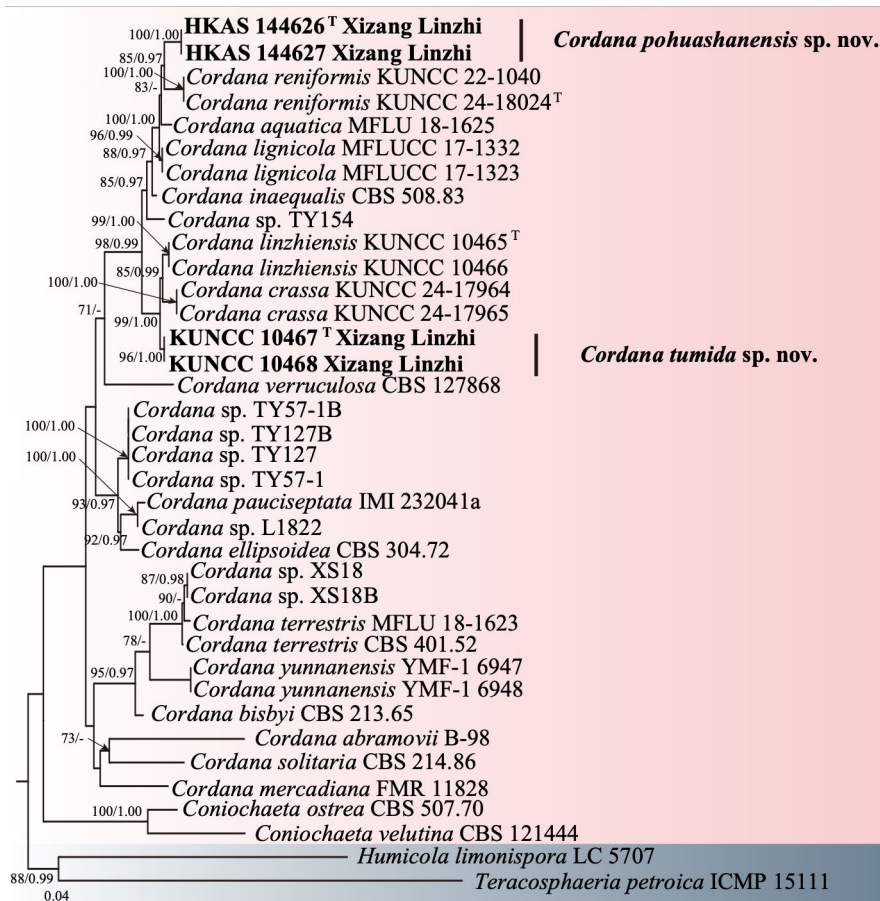


Fig. 47 Maximum likelihood majority rule consensus tree for *Cordanaceae* using LSU and ITS sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Humicola limonispora* (LC 5707) and *Teracosphaeria petroica* (ICMP 15111). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.



Fig. 48 *Cordana pohuashanensis* (HKAS 144626, **holotype**) a Host. b Colonies on the substrate surface. c-g Conidiophores. h, i Conidiogenous cell. j Conidium. k Germinated conidia. l-m Culture on PDA. Scale bars: c-g = 50 μ m, h-k = 10 μ m.

26. *Cordana tumida* R.J. Xu, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 49**Chinese name:** – 膨突暗双孢 (peng tu an shuang bao)**Index Fungorum number:** IF 903488; **Facesoffungi number:** FoF 17412**Etymology:** The epithet "tumida" refers to the swollen conidiophores.**Holotype:** HKAS 136033

Saprobic on decaying wood submerged in a freshwater stream. **Sexual morph:** Undetermined. **Asexual morph:** Colonies superficial, effuse, scattered, hairy, dark brown. **Mycelium** immersed, consisting of pale brown, smooth-walled, branched, septate. **Conidiophores** 197–357 × 4–6 µm ($\bar{x}$ = 273 × 5 µm, n = 10), macronematous, mononematous, solitary, erect, straight or flexuous, unbranched, multi-septate, with swollen, fertile, intercalary nodes in the upper middle, cylindrical, slightly constricted at septa, dark brown at the base, lighter towards the apex. **Conidiogenous cells** 30–66 × 5–7 µm ($\bar{x}$ = 36 × 6 µm, n = 20), polyblastic, integrated, terminal, becoming intercalary, percurrent, sympodial, denticulate, usually swollen at the conidiogenous loci. **Conidia** 13–17 × 7–10 µm ($\bar{x}$ = 14 × 9 µm, n = 30), acropleurogenous, calabash-shaped, or cylindrical, smooth, 1-septate, pale brown, apparent constricted at the septa, elliptical at the apex, rounded at the base, guttulate.

Culture characteristics: Conidia germinating on PDA medium within 48 h and germ tubes arising from terminal end of conidium. Colonies grown on PDA reached 30 mm diam at room temperature in three weeks, circular, with velvety, flat, grayish-white mycelium on the surface, from below cream with entire margin.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, 29°19'36.31" N, 95°21'22.18" E, 1481 m a.s.l., on decaying wood submerged in a freshwater stream, 13 July 2022, R.J. Xu, MD-676 (HKAS 136033, holotype), ex-type culture KUNCC 10467. Linzhi City, Chayu County, 28°29'39.27" N, 96°59'35.25" E, 1537 m a.s.l., on decaying wood submerged in a freshwater stream, 14 July 2022, R.J. Xu, MD-676-2 (HKAS 136032, paratype), culture KUNCC 10468.

Notes: Among the known species of *Cordana*, only *C. aquatica*, *C. lignicola*, *C. lushanensis* and *C. verruculose* resemble *C. tumida* in having intercalary nodes (Hernández-Restrepo et al. 2014; Ai et al. 2019; Luo et al. 2019). However, *C. aquatica* differs from *C. tumida* by its smaller conidia (8–10 × 3–5 µm vs. 13–17 × 7–10 µm), and mostly oblong, sometimes ellipsoid conidia (Luo et al. 2019). *Cordana lignicola* differs from *C. tumida* by its narrower conidia (3.5–4.5 µm vs. 7–10 µm). *Cordana lushanensis* differs from *C. tumida* by its branched conidiophores and aseptate conidia (Ai et al. 2019). *Cordana verruculose* differs from *C. tumida* by its aseptate and verruculose conidia (Hernández-Restrepo et al. 2014).

In the phylogenetic analysis, *Cordana tumida* was grouped with *C. linzhiensis* and *C. crassa* forming a distinct clade separate from other species within *Cordana* (Fig. 47). However, *C. tumida* differs from *C. linzhiensis* in having smaller conidia (13–17 × 7–10 vs. 20–28 × 11–15 µm) and in the presence or absence of intercalary nodes in the conidiophores. Additionally, the conidia of *C. linzhiensis* are characterized by a hyaline mucoid sheath (Xu et al. 2024e). By contrast, *C. crassa* differs from *C. tumida* in that the conidiophores of the former absence intercalary nodes. In

addition, a comparison of the ITS nucleotide bases in *C. tumida* (KUNCC 10467) and *C. crassa* (KUNCC 24-17964) revealed that they differ in 10/491 bp (2%) of ITS. Therefore, the new species *C. tumida* is introduced based on the recommendation of Jeewon & Hyde (2016) and the polyphasic approach recommended by (Chethana et al. 2021a).

Diaporthales* Nannf**Lamproconiaceae* Norph., T.C. Wen & K.D. Hyde**

Lamproconiaceae was established to accommodate *Lamproconium* and *Hercospora* by Norphanphoun et al. (2016) based on both morphological and phylogenetic evidence. This family includes both pathogenic and saprobic fungi, typically found on dead herbaceous twigs (Norphanphoun et al. 2016; Crous et al. 2020). The sexual morph is characterized by prosenchymatous stromata surrounding the perithecia, externally demarcated by a greenish-black, dense pseudoparenchymatous layer, while the interior is whitish, composed of interwoven hyphae intermixed with host tissue, each stroma generally contains 3–5 perithecia. The asexual morph produces pycnidial conidiomata that are solitary, partially embedded in host tissues, and either uniloculate, multiloculate, or convoluted, conidiogenous cells are holoblastic, cylindrical to subcylindrical, forming single conidia at the apex, or annellidic, and may appear colorless to olivaceous with smooth walls, conidia are aseptate, fusiform to ellipsoid, thick-walled, containing granular contents (Norphanphoun et al. 2016). Currently this family contains 27 epithets in three genera, viz., *Hercospora*, *Lamproconium*, and *Neolamproconium* (Index Fungorum 2025; Hyde et al. 2024a).

27. *Zangmuomyces* R.J. Xu, K.D. Hyde & Q. Zhao, *gen. nov.***Chinese name:** – 臧穆菌属 (Zang mu jun shu)**Index Fungorum number:** IF 905264; **Facesoffungi number:** FoF 19310

Etymology: The genus name *Zangmuomyces* is established to honor Professor Zang Mu for his outstanding contributions to the field of mycology in China.

Saprobic on decaying unidentified wood in terrestrial habitat. **Sexual morph:** Undetermined. **Asexual morph:** **Conidiomata** 378–481 µm high, 660–858 µm diam ($\bar{x}$ = 428 × 740 µm, n = 15), pycnidial, solitary, scattered, semi-immersed or superficial, black, uni-loculate, ellipsoid or irregular when viewed from above, like a raised cylindrical barrel when viewed from the front, a large opening in the middle, glabrous. **Peridium** 69–120 µm wide, composed of brown to dark brown, irregular, thick-walled cells arranged in a textura angularis, the side walls are significantly thicker than the bottom, fused with the host tissue. **Paraphyses** interspersed within conidiophores. **Conidiophores** 15–78 × 2–4 µm ($\bar{x}$ = 47 × 3 µm, n = 20), arising from the outermost wall layer at the basal of pycnidium, filiform or cylindrical, hyaline, aseptate, unbranched, smooth-walled. **Conidiogenous cells** cylindrical to subcylindrical, filiform, hyaline, thin-walled, becoming swollen towards the apex. **Conidia** 26–35 × 10–13 µm ($\bar{x}$ = 31 × 12 µm, n = 25), hyaline, ellipsoidal to long ellipsoidal, rounded at both ends, straight or slightly curved, 3-septate, slightly constricted at septum, hyaline sheath around conidia, smooth-walled, guttulate.

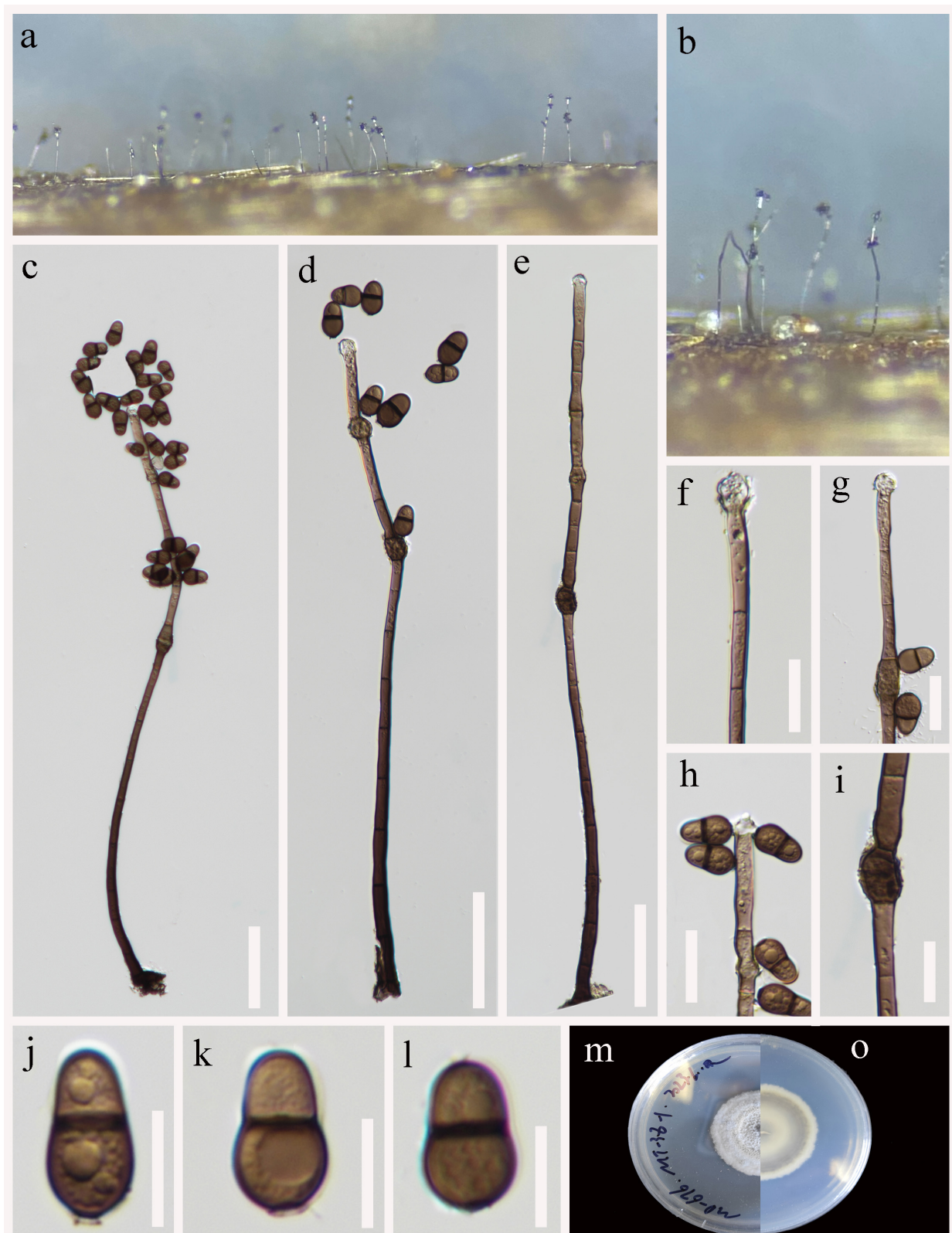


Fig. 49 *Cordana tumida* (HKAS 136033, holotype) a, b Colony on natural substrates. c–e Conidiophores with conidia. f–h Conidiogenous cells with conidia. i Swollen, intercalary conidiogenous cells. j–l Conidia. m, o Culture on PDA medium. m from above, o from below. Scale bars: c–e = 50 μ m, f–i = 20 μ m, j–l = 10 μ m.

Type species: *Zangmuomyces xizangensis* R.J. Xu, K.D. Hyde & Q. Zhao (HKAS 151647)

Notes: In the phylogenetic analyses, strains of *Zangmuomyces* were clustered with *Hercospora*, *Lamproconium*, and *Neolamproconium* in the *Lamproconiaceae*. In morphology, *Z. xizangensis* shows unique features: conidiomata like a raised cylindrical barrel when viewed from the front, conidiogenous cells becoming swollen towards apex, and conidia ellipsoidal to long ellipsoidal, rounded at both ends, 3-septate. It can be distinguished from other three genera in *Lamproconiaceae*. Therefore, this study introduces *Zangmuomyces* as a new genus to accommodate *Z. xizangensis*.

28. *Zangmuomyces xizangensis* R.J. Xu, K.D. Hyde & Q. Zhao, *sp. nov.* Fig. 51

Chinese name: – 西藏臧穆菌 (xi zang zang mu jun)

Index Fungorum number: IF 905043; **Facesoffungi number:** FoF 19311

Etymology: refers to Xizang Autonomous Region in China, where the type specimen was collected.

Holotype: HKAS 151647

Saprobic on decaying unidentified wood in a freshwater habitat. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* 378–481 µm high, 660–858 µm diam ($\bar{x}$ = 428 × 740 µm, *n* = 15), pycnidial, solitary, scattered, semi-immersed or superficial, black, uni-loculate, ellipsoid or irregular when viewed from above, like a raised cylindrical barrel when viewed from the front, a large opening in the middle, glabrous. *Peridium* 69–120 µm wide, composed of brown to dark brown, irregular, thick-walled cells arranged in a textura angularis, the side walls are significantly thicker than the bottom, fused with the host tissue. *Paraphyses* filamentous, aseptate, interspersed within conidiophores. *Conidiophores* 15–78 × 2–4 µm ($\bar{x}$ = 47 × 3 µm, *n* = 20), arising from the outermost wall layer at the basal of pycnidium, filiform or cylindrical, hyaline, aseptate, unbranched, smooth-walled. *Conidiogenous cells* cylindrical to subcylindrical, filiform, hyaline, guttulate, thin-walled, becoming swollen towards apex. *Conidia* 26–35 × 10–13 µm ($\bar{x}$ = 31 × 12 µm, *n* = 25), hyaline, ellipsoidal to long ellipsoidal, rounded at both ends, straight or slightly curved, 3-septate, slightly constricted at septum, hyaline sheath around conidia, smooth-walled, guttulate.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, 29°19'43.69" N, 95°21'19.27" E, 677 m a.s.l., on decaying wood submerged in a freshwater stream, 13 July 2022, R.J. Xu, MD-308A (HKAS 151647, holotype), ex-type culture KUNCC 25-21370.

Notes: In the phylogenetic tree, *Zangmuomyces xizangensis* clustered with strains of *Hercospora*, *Lamproconium*, and *Neolamproconium* with 99% ML/1.00 BYPP statistical support (Fig. 50). Morphologically, *Zangmuomyces* and other three genera of *Lamproconiaceae* show differences on conidiomata, conidiogenous cells, and conidia. The conidiomata of *Z. xizangensis* are like a raised cylindrical barrel when viewed from the front, conidiogenous cells become swollen towards the apex, and conidia are 3-septate, ellipsoidal to long ellipsoidal, often with a hyaline sheath, and rounded at both ends, while *Hercospora* has conidiomata with a superficial cap of sterile tissues, elongate conidiophores (conidiogenous cells not mentioned), and

ovoid to ellipsoid, one-celled conidia (Norphanphoun et al. 2016). *Lamproconium* has dark blue conidiomata, with a raised centre, conidiogenous cells with flared periclinal thickenings in the collarette zone, and conidia are fusiform, ellipsoid, with narrowly rounded ends, aseptate, bluish to glistening dark blue (Norphanphoun et al. 2016). The stromata of *Neolamproconium* are characterized by aggregated rosettes of up to 15 pycnidia, phialidic conidiogenous cells, with prominent periclinal thickenings, and conidia are dimorphic, with macroconidia 1(–3)-septate, and microconidia aseptate (Crous et al. 2020).

Therefore, based on its obvious branching in the phylogenetic tree and unique morphological structure, this study introduces *Zangmuomyces xizangensis* as a new species of a new genus *Zangmuomyces*.

Hypocreales Lindau

Bionectriaceae Samuels & Rossman

Clonostachys

The asexual morph-typified genus *Clonostachys*, described by Corda (1839), is anchored by its type species, *Clo. araucaria*, distinguished by its penicillate conidiophores and imbricate conidia organized in columns (Schroers et al. 1999). *Clonostachys* is typified by its penicillate, sporodochial, or dimorphic conidiophores and phialidic conidiogenous cells, which generate hyaline conidia (Schroers 2001). The teleomorph, originally described as *Bionectria* (Spegazzini 1919), is characterized by ascomata typically situated on a pseudoparenchymatous stroma or directly arising from the substrate, ascomata exhibit a color range from white, pale yellow, to orange and dark brownish-orange, remaining unchanged in appearance when exposed to 3% KOH or lactic acid (Schroers 2001; Lechat & Fournier 2018; Perera et al. 2023). Currently, 136 records have been listed in the Index Fungorum ([Index Fungorum Name Search](#), April 18, 2026).

29. *Clonostachys habaensis* Y.B. Wang, B.Z. Chen & Zhu L. Yang, *sp. nov.* Fig. 53

Chinese name: – 哈巴螺旋聚孢霉 (ha ba luo xuan ju bao mei)

Index Fungorum number: IF 905265; **Facesoffungi number:** FoF 19312

Etymology: The epithet *habaensis* refers to Haba Snow Mountain (Haba Xueshan) in Shangri-La City, Yunnan Province, China, where the type specimen was collected.

Diagnosis: *Clonostachys habaensis* produces slightly smaller ellipsoidal conidia compared to its close relatives.

Holotype: HKAS 135029

Endophytic from the root of *Rhododendron decorum*.

Sexual morph: Undetermined. **Asexual morph:** *Conidiophores* broadly penicillate, arising from the agar surface or aerial mycelium ter- to quinquiesverticillate, aggregated in pustules or sporodochia, *phialides* slightly divergent or adpressed, in whorls of 1–3, flask-shaped, widest in the lower third or almost cylindrical, slightly tapering in the upper part towards the tip, without a visible collarette, (11.3–) 11.4–18.9 (–19.2) × (1.9–) 2–3.2 (3.2) µm ($\bar{x}$ = 15.5 × 2.7 µm, *n* = 20). *Conidia* aseptate, hyaline, smooth-walled, ellipsoid, some slightly curved or asymmetric with one more flattened side, with a laterally displaced hilum, 5.1–7.6 (–9) × (2.9–) 3–5.2 (–5.8) µm ($\bar{x}$ = 6.3 × 4 µm, *n* = 30).

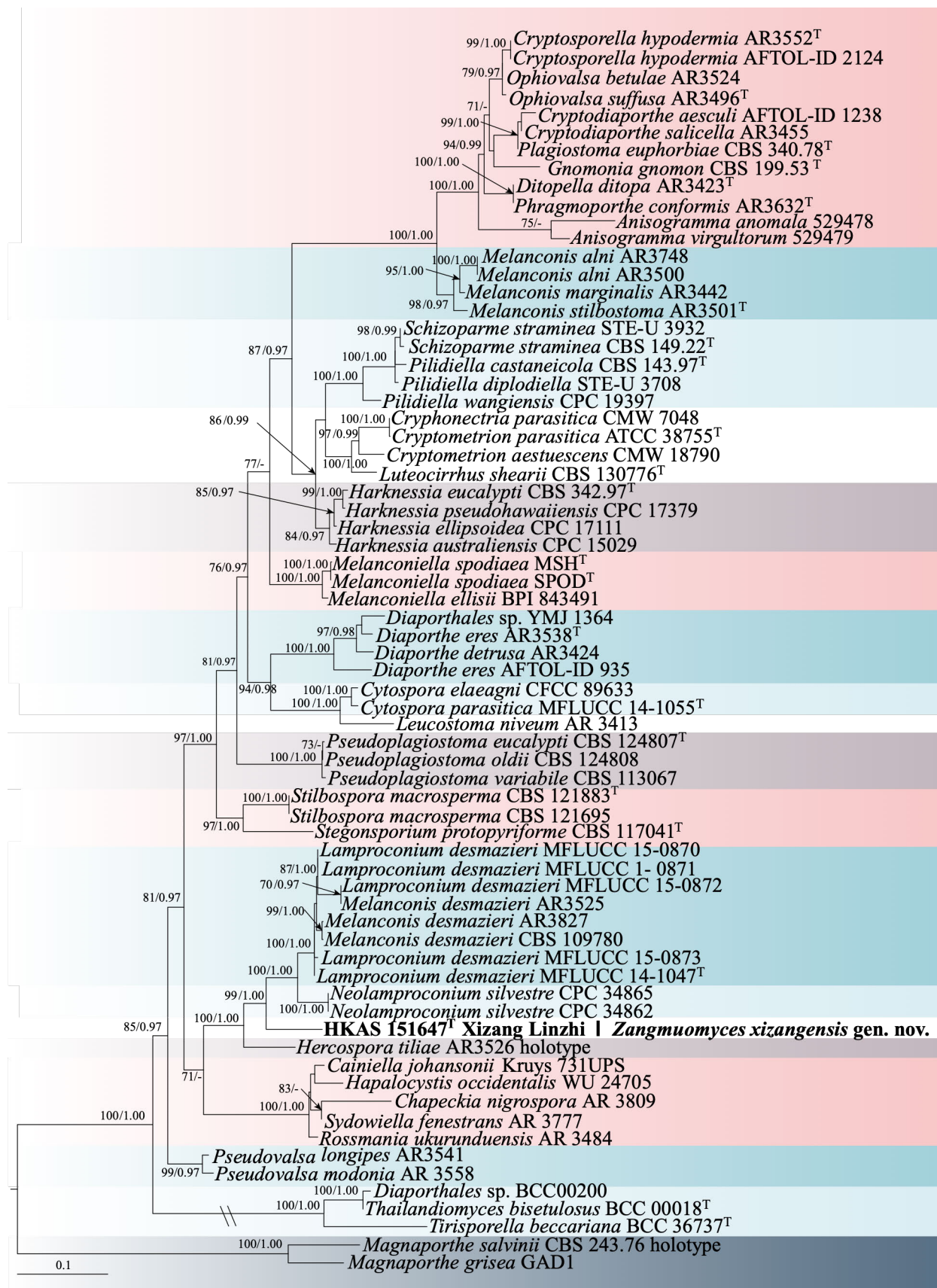


Fig. 50 Maximum likelihood majority rule consensus tree for *Diaporthales* using ITS and LSU sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Magnaporthe salvinii* (CBS 243.76) and *M. grisea* (GAD1). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

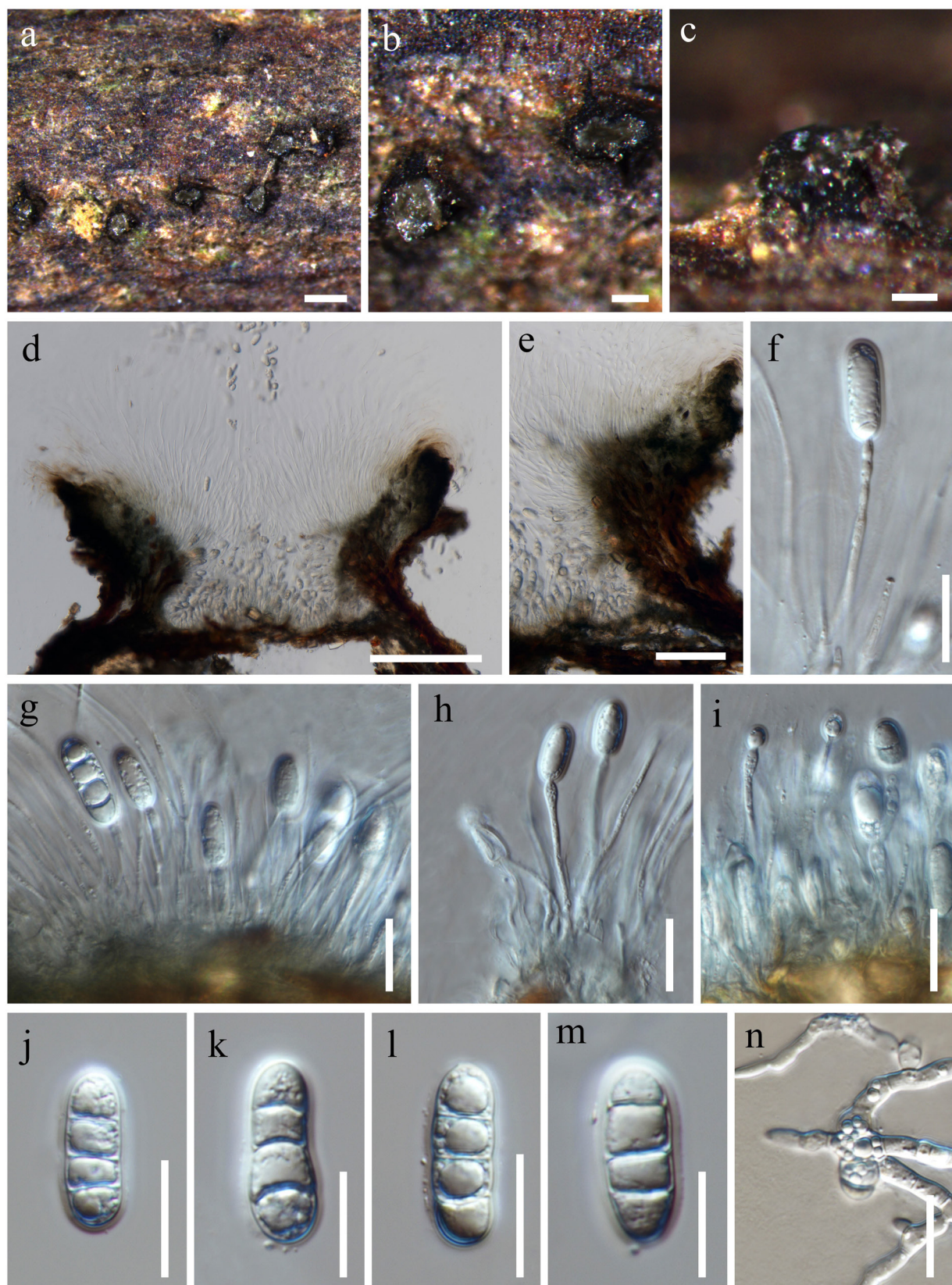


Fig. 51 *Zangmuomyces xizangensis* (HKAS 151647, holotype) a–c Conidiomata on host. c–e Conidiophores with conidia. d, e Cross section of a conidioma. f–i Conidiogenous cells with attached conidia. j–m Conidia. n Germinated conidium. Scale bars: f–i = 20 μ m, j–n = 10 μ m.

Culture characteristics: Colonies on PDA reaching 54–61 mm diameter after 8 days at 25 °C, flat, with entire margin, aerial mycelium abundant, cottony, pale yellow, reverse yellowish.

Material examined: CHINA, Yunnan Province, Diqing, Shangri-La City, Haba Snow Mountain, isolated as an endophyte from *Rhododendron decorum* root, 15 March 2023, collected by Q. Fan (HKAS 135029, holotype, dried culture on PDA, ex-type culture KUNCC 11234), other collection: *Ibid.*, Q. Fan (culture KUNCC 11233).

Notes: *Clonostachys habaensis* is closely related to *Clo. pseudostrata* and *Clo. palmae*, as strongly supported by multi-gene phylogenetic inference. However, it shows clear sequence divergence from its sister species *Clo. pseudostrata* (CBS 120.87^T) (Fig. 52), with 99.4% identity in ITS (2 bp differences), 99.8% in LSU (1 bp), 98.7% in *rpb2* (9 bp), 98.4% in *tef1-α* (12 bp), and 95.6% in *tub* (39 bp). Morphologically, *Clo. habaensis* produces ellipsoidal conidia that are slightly smaller than those of *Clo. palmae* (Schroers 2002; Zhao et al. 2023).

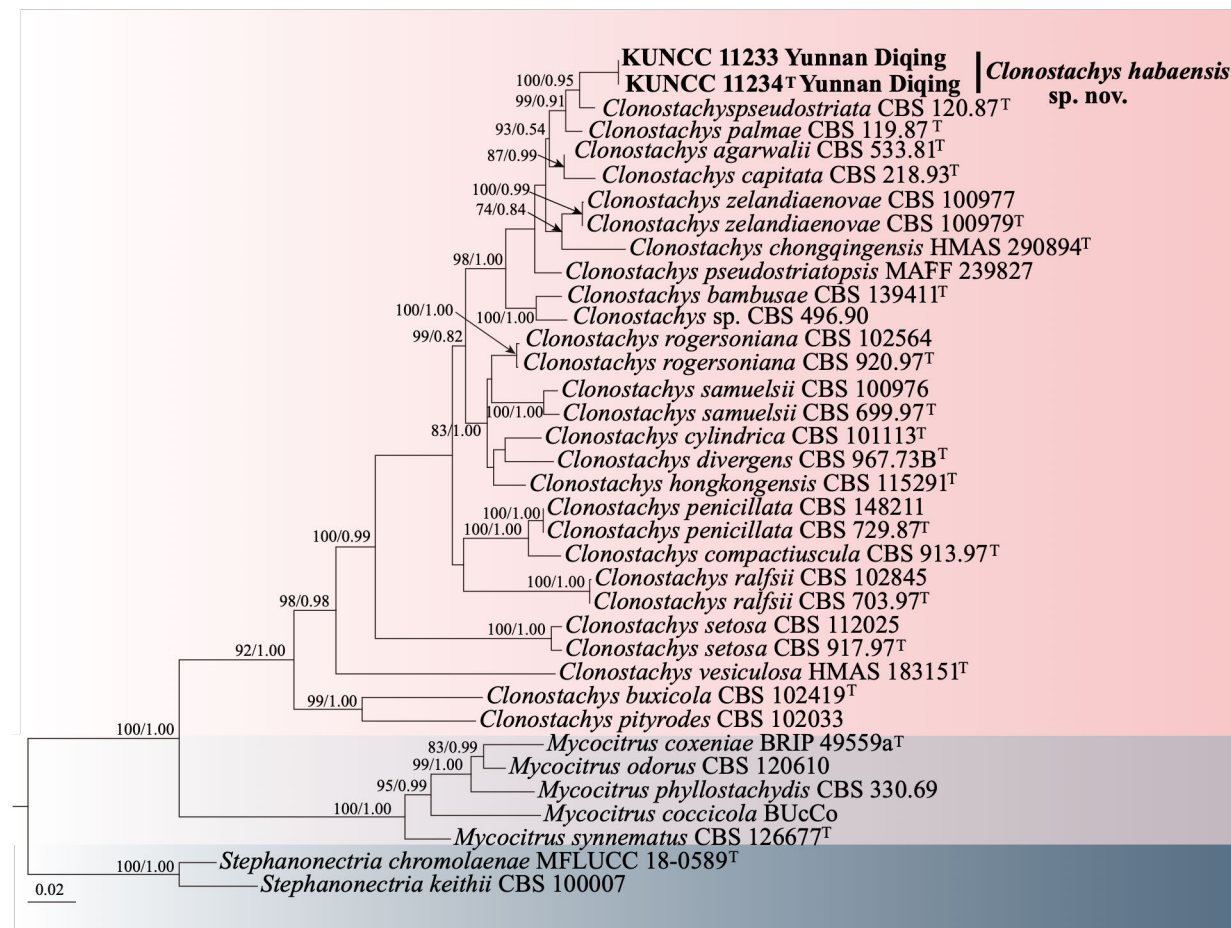


Fig. 52 The maximum likelihood tree using IQ-Tree (Web-IQ-TREE) inferred from combined LSU, *tef1-α*, ITS, *tub* and *rpb2* sequences. *Stephanonectria chromolaenae* R.H. Perera & K.D. Hyde and *Ste. keithii* (Berk. & Broome) Schroers & Samuels were designated as the outgroup taxa. Values at the nodes before and after the backslash are ML bootstrap proportions (ML-BP > 70%) and BI posterior probabilities (BI-PP > 0.70), respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Clavicipitaceae Rogerson

Clavicipitaceae was initially treated as a subfamily of *Hypocreaceae* (Earle 1901). It was later placed within *Hypocreales* by Spatafora & Blackwell (1993). Sung et al. (2007) further divided it into three monophyletic families: *Clavicipitaceae*, *Cordycipitaceae*, and *Ophiocordycipitaceae*. Xiao et al. (2023) introduced a fourth family, *Polycephalomycetaceae*. Currently, *Clavicipitaceae* includes over 40 genera, such as *Aciculosporium*, *Claviceps*, *Epichloë*, and *Metarhizium* (Kepler et al. 2014). Many species are entomopathogenic, often parasitizing insects or forming symbiotic relationships with plants (Kepler et al. 2012;

Khonsanit et al. 2021). The sexual morph features dark or brightly colored, fleshy to tough stromata or subiculum, with perithecial ascomata that can be superficial or immersed and are arranged in ordinal or oblique patterns, containing cylindrical asci with thickened apices and typically cylindrical, multiseptate ascospores that may disarticulate into part-spores (Sung et al. 2007; Kepler et al. 2014). The asexual morphs include genera like *Aschersonia*, *Ephelis*, *Metarhiziopsis*, *Metarhizium*, *Neotyphodium*, *Nomuraea*, *Pochonia*, and *Rotiferophthora* (Sung et al. 2007; Kepler et al. 2012; Mongkolsamrit et al. 2020).

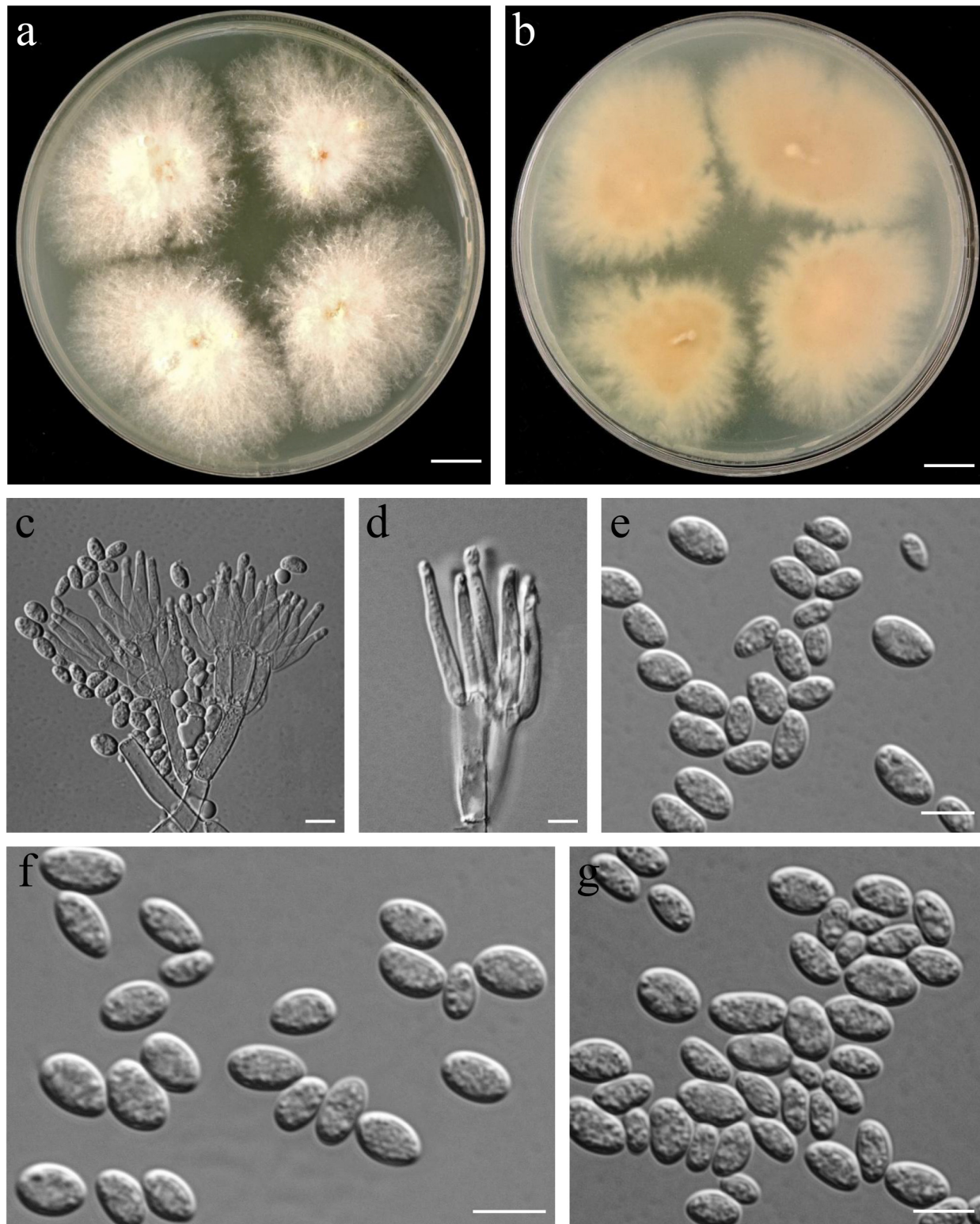


Fig. 53 *Clonostachys habaensis* (HKAS 135029, **holotype**) a, b Colonies on PDA, front and back. c, d Conidiophores and Phialides. e–g conidia. Scale bar: a = 1 cm, c–g = 5 µm.

***Metarhizium* Sorokin**

Metarhizium is of paramount significance in the study of entomopathogenic fungi, catalyzing two molecular phylogenetic revisions that have robustly validated and refined the morphological classification delineated by Rombach et al. (1987). The species classified within

Metarhizium are acknowledged as entomopathogens, effectively targeting insect hosts and resulting in their mortality or incapacitation. Furthermore, these fungi have been documented to promote plant growth and enhance biomass accumulation (Elena et al, 2011; Khan et al, 2012; Mongkolsamrit et al. 2020).

30. *Metarhizium luteum* Y.B. Wang, C.Y. Wei, B.Z. Chen & Zhu L. Yang, *sp. nov.* Fig. 54

Chinese name: – 土黄绿僵菌 (tu huang lv jiang jun)

Index Fungorum number: IF 905266; **Facesoffungi number:** FoF 19313

Etymology: The stromata are earthy yellow.

Diagnosis: Different from all other *Metarhizium* members by color of its stromata.

Holotype: HKAS 126260

Parasitic on larvae of *Scarabaeidae*. **Sexual morph:** *Stromata* from the head of the *Scarabaeidae* (Coleoptera) buried in soil, solitary, occasionally branched, fleshy, glabrous, 7–10 cm long. *Stipes* cylindrical, easily bent, white to orange, 2–4 mm wide. *Fertile parts* terminal, cylindrical, orange, tapering upwards, contains infertile tip, 70–100 × 2–4 mm. *Perithecia* obliquely immersed, dense, ovate, 600–800 × 100–400 µm. *Asci* linear, (100–) 150–300 (–350) × 3.5–5 (–5.5) µm ($\bar{x}$ = 207.6 × 4.3 µm), apical caps prominent, hemispherical, (3–) 3.5–6 (–6.5) × 1.5–2 (–2.5) µm ($\bar{x}$ = 4.9 × 1.9 µm). *Ascospores* hyaline, filiform multiseptate, breaking into secondary ascospores, 15–25 (–30) × (0.5–) 1–1.5 µm ($\bar{x}$ = 22.5 × 1.2 µm). Secondary ascospores cylindrical, rounded at both ends, (8.5–) 8.6–10.4 (–10.5) × 1–1.5 µm ($\bar{x}$ = 9.5 × 1.1 µm). **Asexual morph:** *Conidiophores* smooth-walled, cylindrical, apically branched. *Phialides* smooth-walled, cylindrical with semi-papillate apices, arranged in whorls of 3–5 at the apex of conidiophores, (6–) 6.5–10.5 (–11) × (1–) 1.5–3 (–3.5) µm ($\bar{x}$ = 8.3 × 2.3 µm). *Conidia* hyaline, cylindrical, (6.5–) 7–10 (–10.5) × (2–) 2.5–3.5 (–4.0) µm ($\bar{x}$ = 8.3 × 2.9 µm).

Culture characteristics: Colonies on PDA attaining a diam of 23 mm in 14 d, white, flocculent, high mycelial density, intact edges, reverse white cream. Center of the colony is dark green due to the production of conidia. Hyphae smooth-walled, colorless, septate.

Material examined: CHINA, Yunnan Province, Baoshan City, parasite on larvae of *Scarabaeidae* buried in soil, 2 August 2022, C.Y. Wei, (HKAS 126260 holotype, ex-type culture KUNCC 10831), other collection: *Ibid.*, C.Y. Wei (HKAS 126261, culture KUNCC 10832; HKAS 126262, culture KUNCC 10833).

Notes: As shown in the phylogenetic tree, *Met. luteum* forms a distinct terminal lineage (Fig. 57), strongly supported by multi-locus phylogenetic analyses. *Metarhizium luteum* shares similarity with *Met. candelabrum* and *Met. cercopidarum* in the production of cylindrical phialides with rounded ends (Mongkolsamrit et al. 2020). However, *Met. luteum* parasitize *scarabaeidae* larvae while *Met. candelabrum* and *Met. cercopidarum* infect adult leafhopper. In *Met. luteum* the conidia on PDA are wider than in *Met. candelabrum* and *Met. cercopidarum*. Further, *Met. luteum* is distinguished from *Met. candelabrum* and *Met. cercopidarum* by growth rate on PDA, and *Met. luteum* is significantly faster than *Met. candelabrum* and *Met. cercopidarum*.

Moelleriella Bres

Moelleriella, an entomopathogenic genus within the *Clavicipitaceae* (*Hypocreales*, *Ascomycota*), is distinguished from related genera like *Conoideocrella*, *Hypocrella* and *Samuelsia* by unique features such as disarticulating ascospores and fusiform conidia produced by its anamorph (Bresadola 1897; Chaverri et al. 2008). *Moelleriella* species engage in a dual parasitic role, acting as necrotrophic

parasites of scale insects and whiteflies, and biotrophic parasites of plants, often presenting as vibrant stromata on insect hosts (Chaverri et al. 2008; Mongkolsamrit et al. 2015). Molecular analyses, especially of LSU, *tef1-α* and *rpb1* genes, have clarified their taxonomy, ecological roles, and evolutionary relationships, enhancing our understanding of fungal biodiversity and ecosystem dynamics (Khonsanit et al. 2021).

31. *Moelleriella yusheensis* Y. Yang, K.D. Hyde & Y.P. Xiao, *sp. nov.* Fig. 56

Chinese name: – 玉舍莫勒菌 (yu she mo le jun)

Index Fungorum number: IF 903156; **Facesoffungi number:** FoF 17061

Etymology: in reference to the place where the fungus was collected, China, Guizhou Province, Liupanshui City, Shuicheng County, Yushe forest Park.

Holotype: HKAS 132266

Sexual morph: *Teleomorphic stromata* flat to umbonate, globose to subglobose, 2.5–4.5 mm in diam, orange to dark orange. *Perithecia* scattered or fused together, embedded, numerous perithecia per stroma (≥30), obpyriform, 180–360 × 80–150 µm ($\bar{x}$ = 296 × 110 µm, n = 30). Ostioles pale yellow to light orange. *Asci* hyaline, cylindrical, 130–180 × 5–11 µm ($\bar{x}$ = 162 × 7 µm, n = 50). *Asci caps* inconspicuous. *Ascospores* hyaline, disarticulating into part-spores. *Secondary spores* oblong to cylindrical with round or blunt ends, 7.2–9.7 × 2.3–3.5 µm ($\bar{x}$ = 8.6 × 2.9 µm, n = 50), smooth, hyaline, thin-walled, guttulate. **Asexual morph:** undetermined.

Material examined: CHINA, Guizhou Province, Liupanshui City, Shuicheng County, Yushe forest Park. *Parasitism* on scale insects (*Coccidae*), found on the upper surfaces of dicotyledonous leaves, 1 August 2022, Yu Yang SC186 (HKAS 132266, holotype).

Notes: *Moelleriella yusheensis* clusters with *Moe. gracilispora* and *Moe. kanchanaburiensis* in the phylogenetic tree, with 100% MLBP, 0.99 BYPP support (Fig. 55). The sequences of six loci of *Moe. gracilispora* and *Moe. kanchanaburiensis* share 97–98% identity with *Moe. yusheensis* in LSU, 94–95% in *tef1-α*, and 91–92% in *rpb1*. *Moe. gracilispora* infects whitefly nymphs (Hemiptera), while *Moe. yusheensis* and *Moe. kanchanaburiensis* both infect scale insects (*Coccidae*) (Yuan et al. 2020; Khonsanit et al. 2021). Morphologically, *Moe. yusheensis* can be easily distinguished from other *Moelleriella* species by its flat to umbonate, orange to dark orange teleomorphic stromata, numerous embedded perithecia, hyaline asci, and cylindrical thin-walled, and guttulate secondary spores. In this study, we introduce a novel species, *Moe. yusheensis*, from China.

Papiliomyces Luangsa-ard, Samson & Thanakitp. 2020

Papiliomyces was introduced by Mongkolsamrit et al. (2020) within the *Clavicipiteae*, to accommodate *Pap. liangshanensis* and *Pap. shibinensis*. The teleomorph of *Papiliomyces* encompass solitary to multiple (branched and robust to wiry) stromata, superficial to entirely immersed perithecia within the stroma, and ampulliform, ellipsoid to ovoid asci, with ascospores that are whole, exhibiting septation or fragmentation into cylindrical part-spores (Kepler et al. 2012a; Kepler et al. 2012b; Mongkolsamrit et al. 2020; Wang et al. 2021).

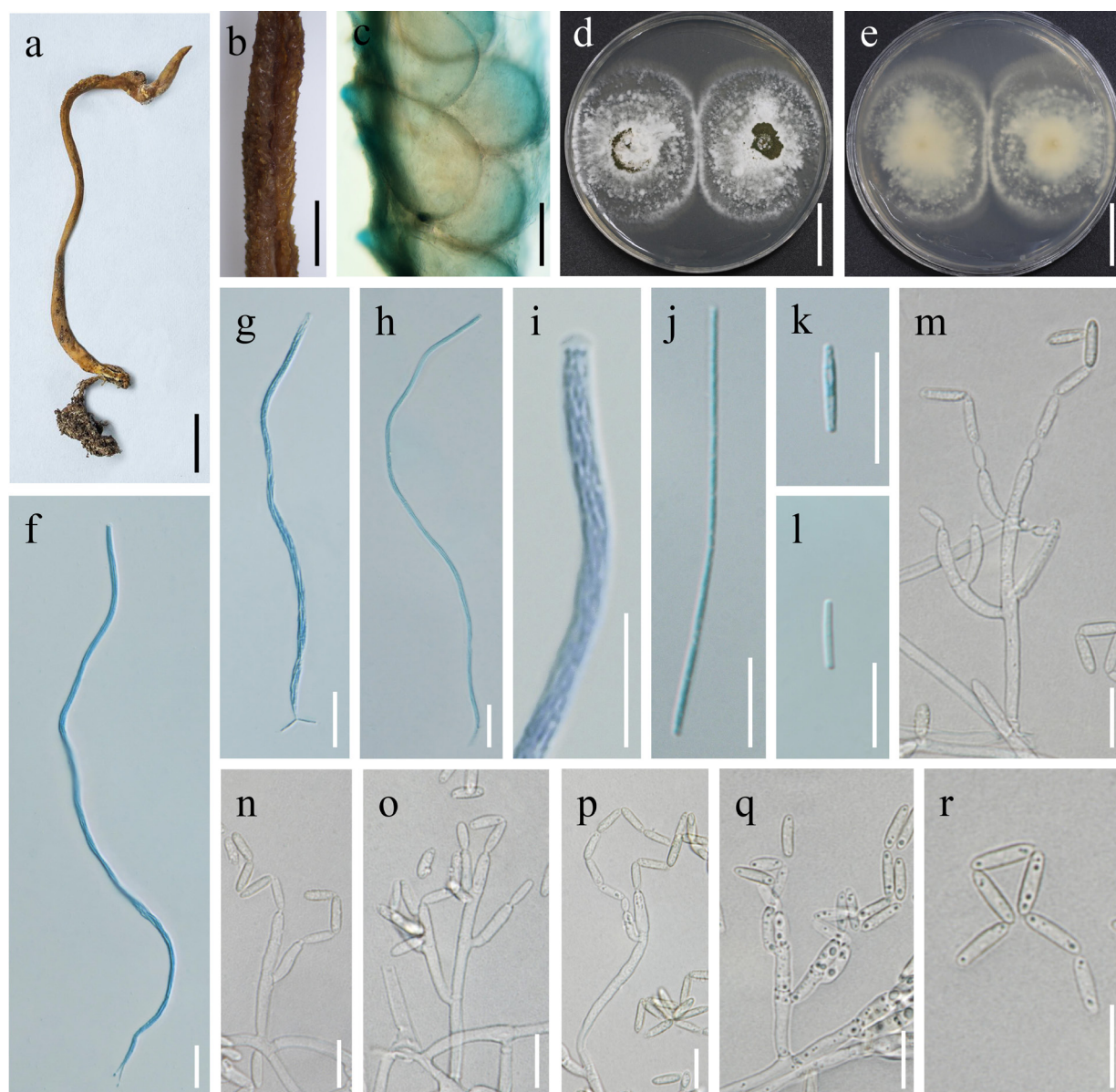


Fig. 54 *Metarhizium luteum* (HKAS 126260, holotype) a Stroma arising from a larva of *Coleoptera*. b Fertile part. c Perithecia. d, e Colonies on PDA. f–i Asci. j Ascospore. k, l Secondary ascospores. m–q Conidiophores, phialides and conidia on PDA. r Conidia on PDA. Scale bars: a = 1 cm, b = 1 mm, c = 200 μ m, d, e = 2 cm, f–h = 20 μ m, i–r = 10 μ m.

32. *Papiliomyces aurantiacus* Y.B. Wang, C.Y. Wei, B.Z. Chen & Zhu L. Yang, *sp. nov.* Fig. 58

Chinese name: – 橙黄蝶蛾菌 (cheng huang die e jun)

Index Fungorum number: IF 905267; **Facesoffungi number:** FoF 19314

Etymology: Fertile parts are orange

Diagnosis: Different from all other *Papiliomyces* members by color of its fertile parts.

Holotype: HKAS 126283

Parasitic on larvae of *Scarabaeidae*. **Sexual morph:** **Stromata** from the head of lepidopteran larvae buried in the soil, solitary, occasionally branched, 30–45 mm long. Stipe cylindrical, white to orange-yellow, 1.5–3 mm wide. **Fertile parts** cylindrical, orange, 5–10 $\times$ 2.5–3 mm. **Perithecia** embedded, dense, ovate or long oval, 445–503 $\times$ 176–239 μ m ($\bar{x}$ = 465.5 $\times$ 214.7 μ m). **Asci** transparent, linear, 114–202 $\times$ 4.8–6.7 μ m ($\bar{x}$ = 152.7 $\times$ 5.5 μ m), apical caps prominent, hemispherical, (4–) 4.5–5.5 (–6) $\times$ 2.5–3.5 (–4) μ m ($\bar{x}$ = 4.9 $\times$ 3

μ m). **Ascospores** columnar, multiseptate, composed of numerous cells, 162–175 $\times$ 2.4–3.2 μ m ($\bar{x}$ = 168.8 $\times$ 2.8 μ m), not breaking into secondary ascospores. **Asexual morph:** **Conidiophores** smooth-walled, cylindrical, top branch. **Phialides** smooth-walled, colorless, flask-shaped, base thinning upward, arising singly from the hyphae or in whorls of 3–4 at the top of the conidiophores, (11–) 11.5–15 (–15.5) $\times$ (0.5–) 1–2 (–2.5) μ m ($\bar{x}$ = 13.4 $\times$ 1.6 μ m). **Conidia** smooth-walled, unicellular, globose to subglobose, surface tooth teeth, often arranged into chains, and 3.5–4.5 (–5) $\times$ 3.5–4 (–4.5) μ m ($\bar{x}$ = 4.2 $\times$ 4.1 μ m).

Culture characteristics: Colonies on PDA attaining a diam of 30 mm in 14 d, dense, pulvinate, white, intact edges. Hyphae smooth-walled, colorless.

Material examined: CHINA, Yunnan Province, Nujiang, parasite on larvae of *Hepialidae* buried in soil. 12 August 2023, C.Y. Wei (HKAS 126283 holotype, ex-type culture KUNCC 10852), other collection: *Ibid.*, C.Y. Wei (HKAS 126282).



Fig. 55 Maximum likelihood consensus tree inferred from the combined LSU, *tef1*-α, and *rpb1* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 75% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.90 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Ophiocordyceps aphrophoridarum* YTS19061912 and *O. aphrophoridarum* YTS19061907. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

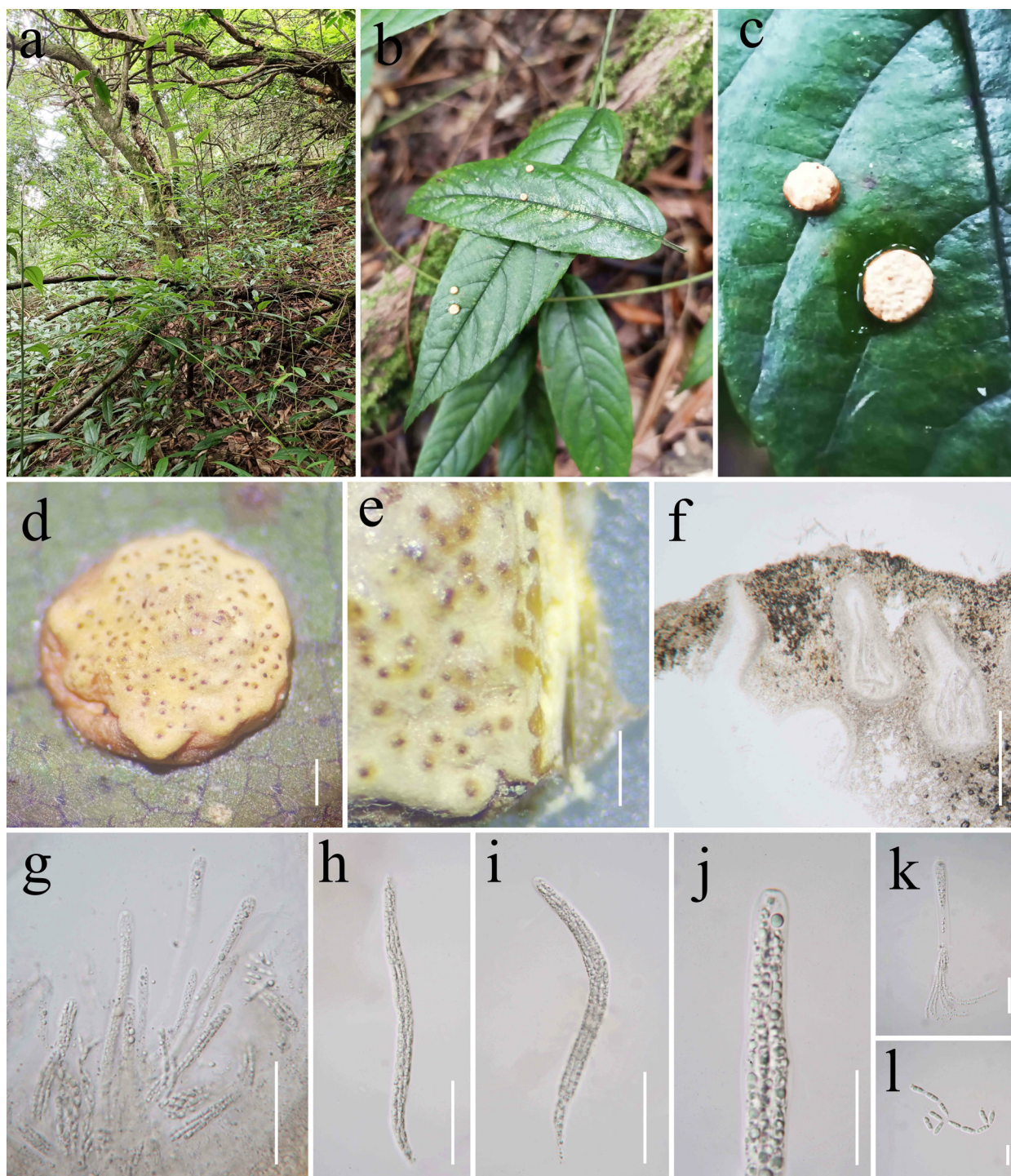


Fig. 56 *Moelleriella yusheensis* (HKAS 132266, holotype) a Habitat. b-e Teleomorphic stroma. f Perithecia. g-i Asci. j Apical cap of asci. k part of Ascospores. l Secondary spores. Scale bars: d = 0.1 cm, e = 0.5 mm, f = 200 μ m, g-i = 50 μ m, j-k = 20 μ m, l = 10 μ m.

Notes: As shown in the phylogenetic tree, *Pap. aurantiacus* represents a distinct terminal lineage (Fig. 57), strongly supported by multi-locus phylogenetic analyses. *Papiliomyces aurantiacus* exhibits similarities to *Pap. shibinensis*, as both species share the same host, namely the larvae of *Lepidoptera*. However, they differ in the size and

color of fertile parts and ascospores. *Papiliomyces aurantiacus* has orange fertile parts, whereas *Pap. shibinensis* is faint yellow (Mongkolsamrit et al. 2020). In *Pap. aurantiacus* (162–175 $\times$ 2.4–3.2 μ m), the fertile parts are wider than in *Pap. shibinensis* (120–170 $\times$ 1.4–2.1 μ m).

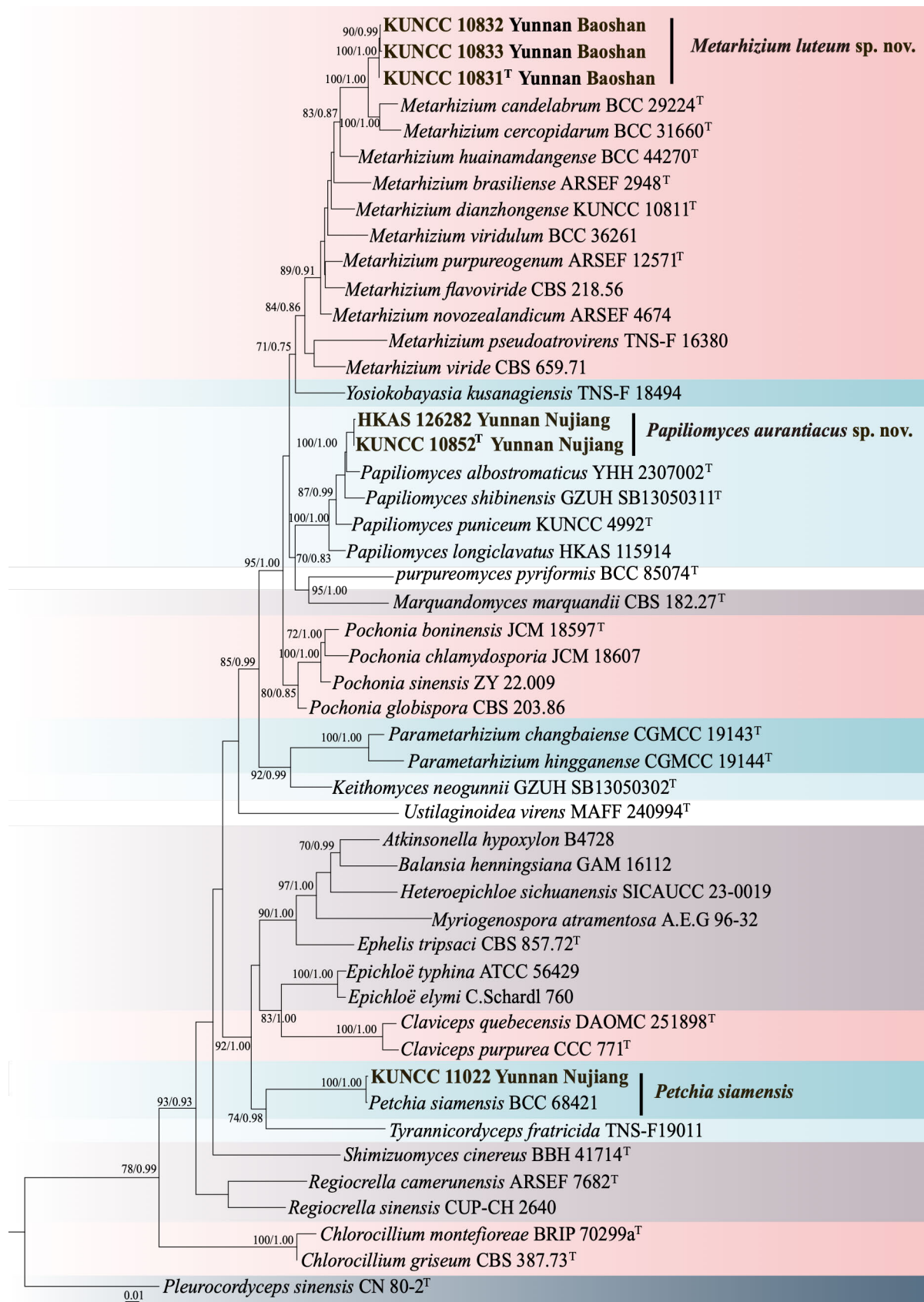


Fig. 57 The maximum likelihood tree using IQ-Tree ([Web-IQ-TREE](https://iqtree.bioinformatics.org/)) inferred from combined LSU, SSU, *tef1-α*, *rpb1* and *rpb2* sequences. *Pleurocordyceps sinensis* (Q.T. Chen, S.R. Xiao & Z.Y. Shi) Y.J. Yao, Y.H. Wang, S. Ban, W.J. Wang, Yi Li, Ke Wang & P.M. Kirk was designated as outgroup taxon. Values at the nodes before and after the backslash are ML bootstrap proportions (ML-BP > 70%) and BI posterior probabilities (BI-PP > 0.70), respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

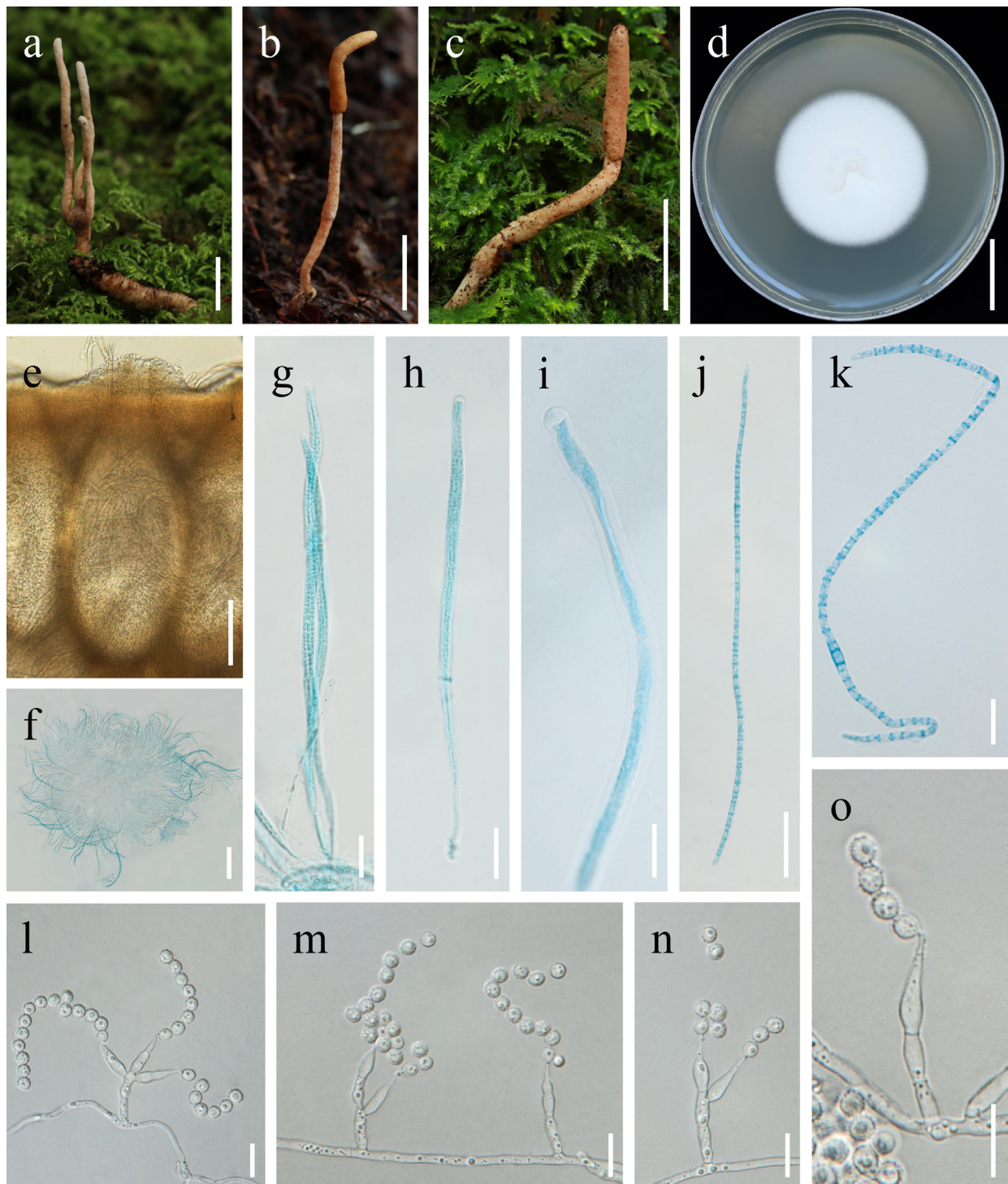


Fig. 58 *Papillomyces aurantiacus* (HKAS 126283, **holotype**) a, b Stromata arising from lepidopteran larvae. c Fertile parts, d Colonies on PDA. e Perithecia. f–i Asci. j, k Ascospores. l–o Conidiophores, phialides and conidia on PDA. Scale bars: a–c = 1 cm, d = 2 cm, e, f = 100 μ m, g, h = 20 μ m, i = 10 μ m, j = 20 μ m, k–o = 10 μ m.

Petchia Thanakitp., Mongkols. & Luangsa-ard 2020

Petchia was proposed by Mongkolsamrit et al. (2020) within the *Clavicipiteae*. *Petchia* is distinguished from related genera by stromata arising from the egg cases of praying mantis (Mantidae), multiple, mostly erect up to 2 cm high, fertile region is located at the apical end of the stroma, exhibiting a pale cream coloration, with a globose

morphology measuring 1.5–1.8 cm in diameter, perithecia are narrowly ovoid, exhibiting a brown hue, and are immersed with dense mycelial encasement around each perithecium (Mongkolsamrit et al. 2020). Currently, only two species in the genus, all are saprotrophic, on the egg cases of praying mantis (Mongkolsamrit et al. 2020).

33. *Petchia siamensis* Thanakitp., Mongkols. & Luangsa-ard, in Thanakitpipattana, Tسانathai, Mongkolsamrit, Khonsanit, Lamlerthon & Luangsa-ard, Persoonia 44: 154 (2020) **Fig. 59**

Chinese name: – 暹罗佩奇菌 (xian luo pei qi jun)

Index Fungorum number: IF 830168; **Facesoffungi number:** FoF 14494

Diagnosis: The specimen examined in this study shares the same phylogenetic position as *Petchia siamensis*.

Parasitic on the ootheca of praying mantis (*Mantidae*).

Sexual morph: *Stromata* grow from the ootheca of praying mantis (*Mantidae*), several produced on a single host, each stroma unbranched, easily bent, length 5–7 mm. *Stipe* cylindrical, curved, smooth, glabrous, light yellow, with a diameter of 0.8–1 mm. The fertile part is globose apical, light yellow, measuring 2 × 1.5 mm. *Perithecia* are immersed, oval, brown, (550–)578–624(–650) × (400–)413–434(–450) µm, ($\bar{x}$ = 596 × 434 µm). *Asci* are cylindrical, slender, (170–)179–250 × 3–4.8(–5) µm ($\bar{x}$ = 203 × 4 µm). The apical cap is prominent, hemispherical, thickened, measuring 3–3.5 × 1.5–2 µm, ($\bar{x}$ = 3.1 × 1.8 µm). *Ascospores* are transparent, thread-like, multi-septate, (200–)215–275(–300) × 1–1.5 µm, ($\bar{x}$ = 246 × 1.3 µm), and break into secondary ascospores when mature. *Secondary ascospores* are short-cylindrical, (5.5–)5.7–9.8(–10) × (0.5–)0.7–1.2(–1.5) µm, ($\bar{x}$ = 8.1 × 0.9 µm). **Asexual morph:** *Hyphae* smooth-walled, colorless, branched. *Conidiophores* smooth-walled, cylindrical, branched at the apex. *Phialides* smooth-walled, base cylindrical and gradually tapering upwards, bottle-shaped, whorled at the top of the conidiophores, 12.5–18.8(–20) × (1–)1.3–3.3(–3.5) µm, ($\bar{x}$ = 14.9 × 1.9 µm). *Conidia* unicellular, colorless, ellipsoidal, 3–5 × (1.5–)1.7–2.8(–3) µm, ($\bar{x}$ = 4.4 × 2.3 µm).

Culture characteristics: Colonies on PDA reach 25 mm in diameter within 14 days, tightly attached, flat, cushion-like, fuzzy, gray-purple, clear edges.

Material examined: CHINA, Yunnan Province, Nujiang, Gongshan County, on the ootheca of praying mantis (*Mantidae*), August 3, 2024, J.L. Jia (HKAS 135119, culture KUNCC 11022).

Notes: Thanakitpipattana et al. (2020) discovered a fungus parasitizing the oothecae of praying mantises in Khao Yai National Park, Thailand. Morphologically, this fungus showed similarities to *Cor. mantidicola*, but exhibited significant differences in the size of its perithecia and the shape of its ascospores. Based on a combination of multigene phylogenetic analysis and morphological data, researchers confirmed that it belongs to the family *Clavicipitaceae* and is distinct from other known genera. Consequently, Thanakitpipattana et al. (2020) established the new genus *Petchia*, with *Pet. siamensis* as the type species. In this study, phylogenetic analyses (Fig. 57), clearly demonstrated that the newly collected specimen belongs to the same species as *Pet. siamensis* were observed emerging from various parts of the host's body, and their microscopic characteristics were highly consistent with those previously reported. This specimen represents a new distribution record for the genus *Petchia*, specifically for the species *Pet. siamensis*.

Cordycipitaceae Kreisel ex G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora

Akanthomyces Lebert 1858

Akanthomyces, described by Lebert in 1858, is typified by *Aka. aculeatus*, a species originally identified on a moth in Europe (Mains, 1950). Specific insect targeted by *Akanthomyces* include *Hemiptera* (*Aka. lecanii*), *Coleoptera* (*Aka. neocoleopterorum*), *Lepidoptera* (*Aka. pistillariiformis*), and *Orthoptera* (*Aka. fragilis*) (Hodge et al, 2003; Mongkolsamrit et al, 2018; Chen et al, 2020). Overall, the host range of *Akanthomyces* remains consistent for both its teleomorph and anamorph forms. Additionally, the genus encompasses *Cordyceps tuberculata*, which parasitizes adult moths and is taxonomically linked to the anamorphic stage *Aka. pistillariiformis*. Furthermore, *Akanthomyces* holds taxonomic precedence over *Lecanicillium*, a member of the family *Cordycipitaceae* characterized by its verticillium-like morphology.

34. *Akanthomyces phariformis* Khons., Thanakitp. & Luangsa-ard, in Khonsanit, Thanakitpipattana, Mongkolsamrit, Kobmoo, Phosrithong, Samson, Crous & Luangsa-ard, Fungal Syst. Evol. 14: 285 (2024) **Fig. 60**

Chinese name: – 灯塔刺束梗孢 (deng ta ci shu geng bao)

Index Fungorum number: IF 842455; **Facesoffungi number:** FoF 19315

Diagnosis: The molecular data showed a high level of identity with *Akanthomyces phariformis*.

Parasitic on the adult of moth clinging to the stone. **Sexual morph:** *Stromata* numerous, arising from the head, thorax and abdomen of the insect host, 3.6 mm long, 0.6 mm wide. *Stipes* cylindrical to clavate, white. *Fertile parts* terminal, slightly curved, yellow, 2 mm long, 1.2 mm wide. *Perithecia* superficial, ovoid, 424–678 × 217–401 µm. *Asci* cylindrical, 8-spored, 176–433 × 4–9 µm. *Ascal cap* hemispherical, 3.6–4.9 × 2.2–3.5 µm. *Ascospores* hyaline, entire, cylindrical, 39–187 × 0.6–1.8 µm, with 10–16 septa. *Secondary ascospores* cylindrical, 5–10 µm long, smooth, hyaline. **Asexual morph:** *Hyphae* smooth-walled, hyaline, measuring 1.4–4.5 µm in width. *Phialides* 11.2–21.2 µm long, arising singly from vegetative hyphae; base cylindrical, middle portion swollen, tapering gradually or abruptly towards the apex; base 1.9–4.8 µm wide, neck 0.2–1.5 µm wide. *Conidia* 4.3–6.5 × 2.4–3.8 µm, smooth-walled, hyaline, globose to ellipsoidal.

Culture characteristics: Colonies on PDA attaining 15–30 mm in diameter after 14 days at 25 °C, with dense, centrally elevated mycelia, margins radiating and creeping. Colony center pale yellow, margins white, reverse white to pale yellow.

Material examined: CHINA, Yunnan Province, Nujiang, Fugong County, on the adult of moth clinging to the stone, 5 September 2023, M. Tang, (HKAS 135021, culture KUNCC 11410).

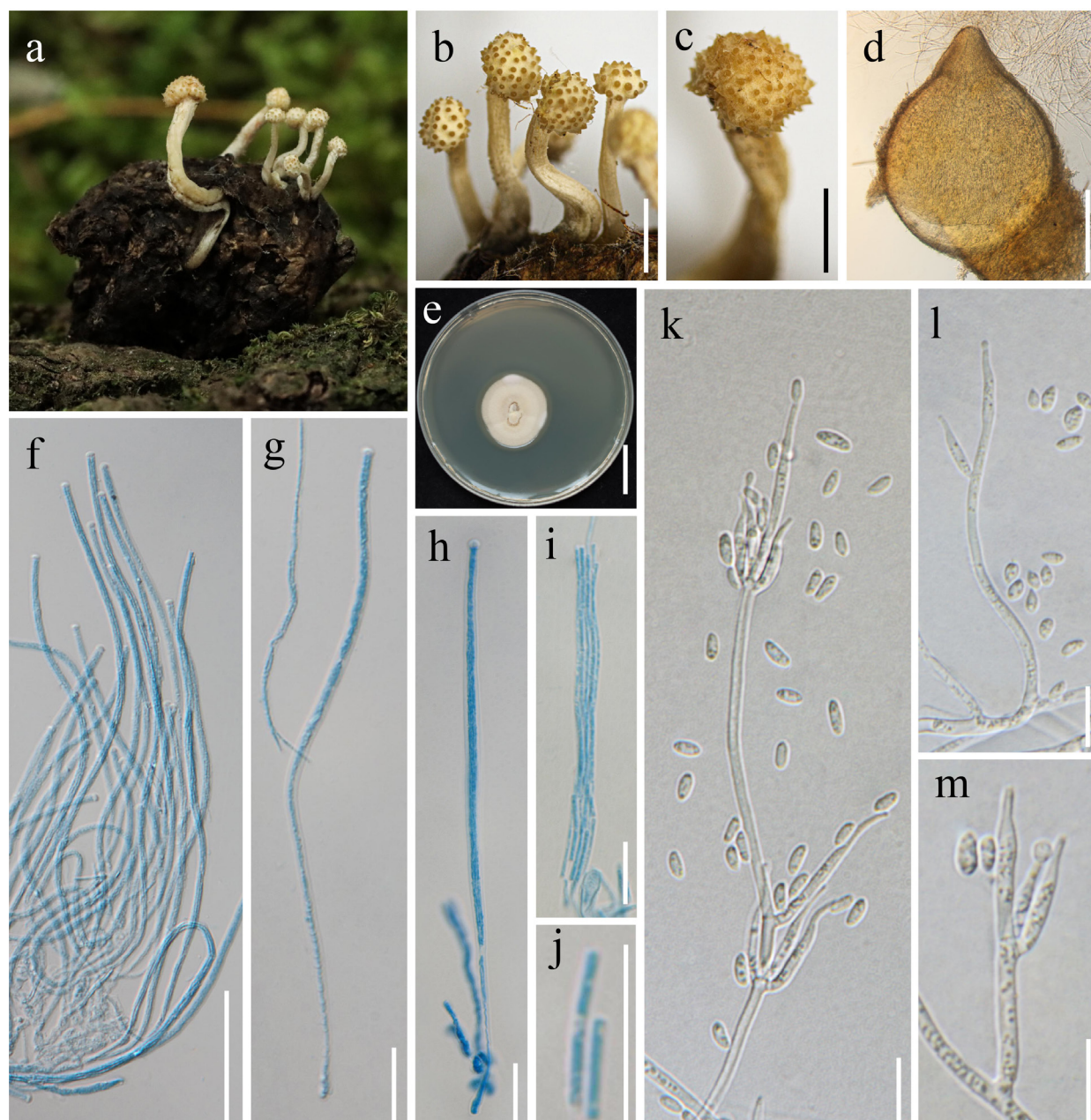


Fig. 59 *Petchia siamensis* (HKAS 135119) a Stromata arising from ootheca of praying mantis. b, c Fertile parts. d Perithecia. e Colonies on PDA. f–h. Asci, i Ascospore. j Secondary ascospores. k–m Conidiophores, phialides and conidia on PDA. Bars: b, c = 2 mm, d = 200 μ m, e = 2 cm, f = 50 μ m, g = 20 μ m, h–m = 10 μ m.

Notes: *Akanthomyces phariformis* is characterized by numerous stromata, with a terminal, slightly curved, yellow fertile part, superficial ovoid perithecia, and cylindrical asci bearing filiform ascospores. Phylogenetic analyses placed the specimen within *Akanthomyces* and showed that it is closely related to *Aka. taiwanicus*. Morphologically, *Aka. phariformis* can be distinguished from *Aka. taiwanicus* by its phialides. In *Aka. phariformis*, phialides arise singly from vegetative hyphae, with a cylindrical base, a swollen middle

portion, and a tapering apex that narrows gradually or abruptly, whereas these features are absent in *Aka. taiwanicus*. In addition, *Aka. phariformis* has a wider phialide base (1.9–4.8 μ m) compared to that of *Aka. taiwanicus* (2.5–3 μ m) (Chuang et al. 2024). Phylogenetic analysis of the present specimen showed that its clusters with *Aka. phariformis*, and morphological observations are consistent with the original description. Therefore, *Aka. phariformis* is reported here as a new record from China (Fig. 63).

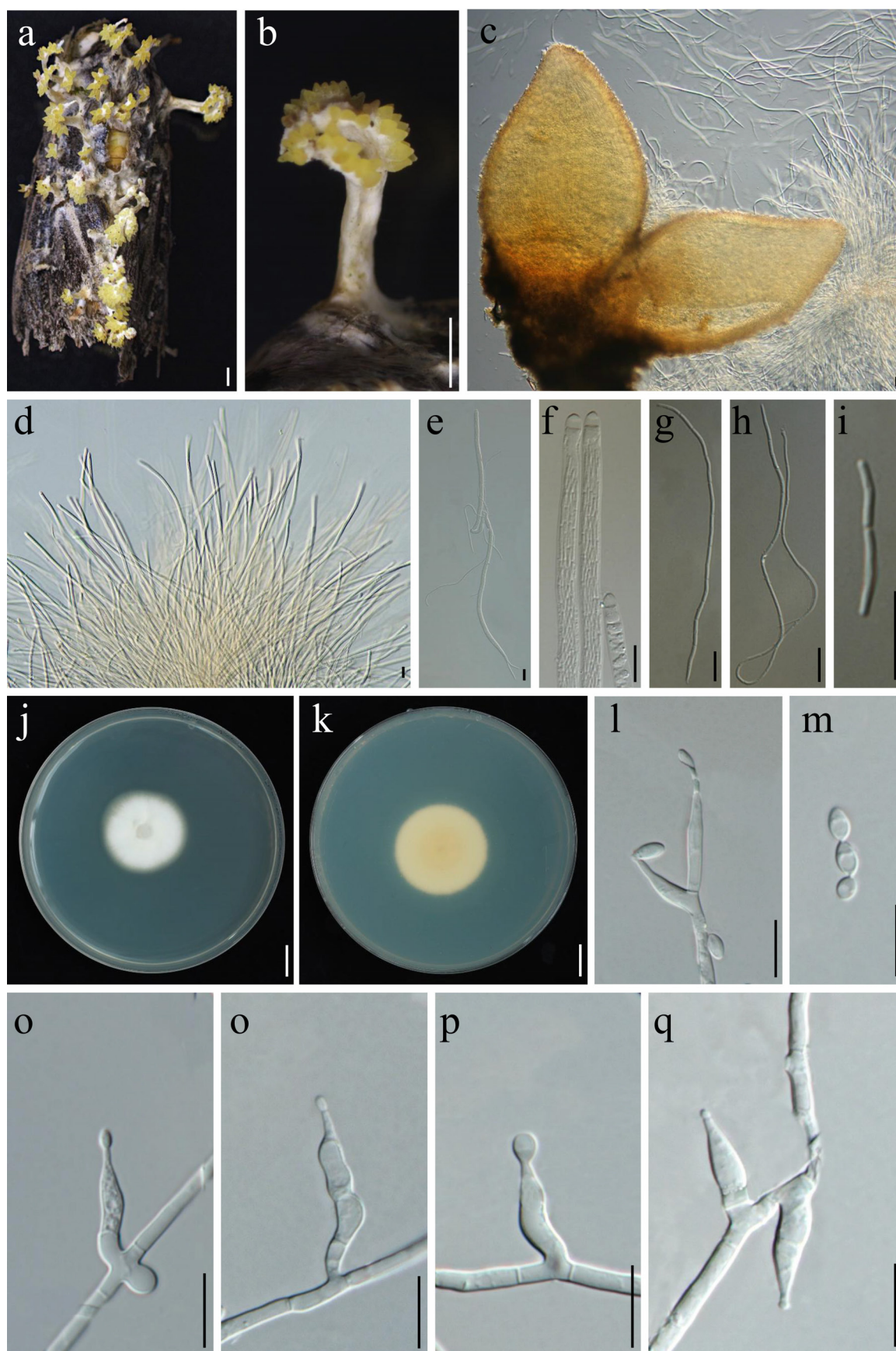


Fig. 60 *Akanthomyces phariformis* (HKAS 135021) a Fungus on the adult of *Lepidoptera*. b Fertile part. c Section of perithecia. d–e Asci. f Ascocarp caps. g–h Ascospores. i Secondary ascospores. j–k Colony on PDA, front and back. l–q Phialides and conidia. Scale bars: a–b = 1000 μ m, c–i = 10 μ m, j–k = 1 cm, l–q = 10 μ m.

Beauveria Vuill. 1912

Beauveria was proposed by Vuillemin in 1912, with *B. bassiana* (Bals.-Criv.) Vuill. as the type species. Since its inception, numerous investigations have been conducted to elucidate and delineate the distinct taxa within *Beauveria* (Petch 1926; MacLeod 1954; De Hoog 1972; Rehner & Buckley 2005). The identification of species within *Beauveria* utilizing solely ITS as a DNA barcode has reached a resolution threshold. Recently, there has been a discernible shift towards employing an integrative multi-locus delimitation framework for closely related species. To date, 81 records in the Index Fungorum ([Index Fungorum](#) July 18, 2025), and 17 species have been accepted in *Beauveria* (Imoulan et al. 2017).

35. Beauveria lanceolata Y.B. Wang, B.Z. Chen & Zhu L. Yang, *sp. nov.* Fig. 62

Chinese name: – 矛尖白僵菌 (mao jian bai jiang jun)

Index Fungorum number: IF 905268; **Facesoffungi number:** FoF 19316

Etymology: The specific epithet “lanceolata” refers to the narrowly elongated and tapering stroma, resembling a spearhead.

Diagnosis: *Beauveria lanceolata* is distinguished by narrowly elongated, spearhead-shaped stroma arising from coleopteran larva, pale yellow to orange, with superficial, densely arranged ovoid to ellipsoidal perithecia.

Holotype: HKAS 135020

Parasitic on the larva of *Coleoptera* buried in soil and adult of *Dermaptera* clinging to the fallen leaves. **Sexual morph:** *Stroma* 2–5 cm long, solitary, unbranched, arising from larvae of *Coleoptera*, pale yellow to orange. *Fertile part* 1–4 cm long, orange, cylindrical or flattened, 2–10 mm wide. *Perithecia* 200–540 × 160–320 µm, superficial, densely aggregated, and ovoid to ellipsoidal. *Asci* 120–250 × 2–3 µm, cylindrical, slender. *Ascospore caps* 2–3.5 × 1.5–2.5 µm, hemispherical. **Asexual morph:** *Hyphae* 0.5–4 µm wide, hyaline, septate, smooth-walled. *Conidiophores* 8–12.5 × 1–2 µm, smooth, hyaline, cylindrical, branched at the apex. *Phialides* 4–18 × 1–2 µm, smooth-walled, cylindrical or flask-shaped, produced in clusters at the tips of conidiophores or directly from hyphae, with zigzag-shaped apices. *Conidia* 3–6 × 2–4 µm, single-celled, hyaline, smooth, ovoid to ellipsoidal, produced at the tips of phialides.

Culture characteristics: Mycelia emerge from the entire host body, forming white to pale yellow powdery conidia. Colonies on PDA reach 30–40 mm in diameter after 14 days at 25 °C, surface white to pale yellow, darkening outward, with smooth margins and a dense or slightly floccose texture, reverse side darker, centrally pale yellow and fading toward the edge.

Material examined: CHINA, Yunnan Province, Kunming City, 12 September 2023, on the adult of *Dermaptera* clinging to the fallen leaves, W.B. Zeng (HKAS 135020 holotype, ex-type culture KUNCC 11286). CHINA, Yunnan Province, Kunming City, on the larva of *Coleoptera* buried in soil, 12 September 2023, Y.B. Wang (culture KUNCC 8665).

Notes: In the multigene phylogenetic analyses based on *tef1-α*, *rpb1*, *rpb2*, and *Bloc* sequences, *B. lanceolata* clusters closely with *B. pseudobassiana* within the same clade but is clearly separated with strong support (Fig. 61). Morphologically, *B. lanceolata* is distinct from *B. pseudobassiana* and *B. varroae* in producing ovoid to

ellipsoidal conidia, whereas the latter species bear globose to broadly ellipsoidal conidia (Rehner et al. 2011).

Cordyceps Fr.

Cordyceps, a fascinating group of fungi, has garnered significant attention within scientific and medical communities due to its unique parasitic lifestyle and potential therapeutic properties. The diversity within *Cordyceps* is vast, encompassing over 300 identified species, with ongoing research continually broadening our understanding of this intriguing fungal group (Wang et al. 2020a). To date, 607 records have been listed in the Index Fungorum ([Index Fungorum](#) July 18, 2025).

36. Cordyceps biclavata Y.B. Wang, B.Z. Chen, M. Tang & Zhu L. Yang, *sp. nov.* Fig. 64

Chinese name: – 双棒虫草 (Shuang bang chong cao)

Index Fungorum number: IF905269; **Facesoffungi number:** FoF 19317

Etymology: The epithet “*biclavata*” refers to the two clavate stromata emerging from the head of lepidopteran pupa.

Diagnosis: *Cordyceps biclavata* differs from related species by producing two clavate stromata from the head of lepidopteran pupa, and the verticillium-like asexual morph.

Holotype: HKAS 135022

Parasitic on the pupae of *Lepidoptera*. **Sexual morph:** *Stromata* arising from the head of lepidopteran pupa buried in soil, two in number, unbranched, 30–35 mm long and 3–8 mm wide, orange to orange-yellow, cylindrical or flattened at the base and cylindrical toward the apex. *Fertile parts* cylindrical to clavate, 15–20 mm long and 2–6 mm wide, orange-yellow. *Perithecia* semi-immersed, ovoid, 280–499 × 134–379 µm. *Asci* eight-spored, hyaline, cylindrical. *Ascal cap* hemispherical, 2.8–4 × 1.3–3.3 µm. **Asexual morph:** *Hyphae* 1.5–3.3 µm wide, smooth, hyaline. *Phialides* 15.7–47.2 µm long, typically solitary or arising laterally from vegetative hyphae or terminally from conidiogenous cells; base cylindrical, tapering gradually toward the apex; basal width 1.3–3 µm, neck 0.3–1.2 µm wide. *Conidia* 3.4–5.2 × 1.8–3.3 µm, hyaline, ellipsoidal. Two types of conidia are observed, all are one-celled, occurring singly or more commonly aggregated into subglobose to ellipsoidal heads at the apex of phialides.

Culture characteristics: Colonies on PDA at 25 °C for 14 days grow rapidly, reaching 30–35 mm in diameter, with a floccose texture, white to pale yellow.

Material examined: CHINA, Yunnan Province, Baoshan City, the host is a pupa of *Lepidoptera* found underground. 5 September 2023, M. Tang, (HKAS 135022 holotype, ex-type culture KUNCC 11366), other collection: *Ibid.*, M. Tang (culture KUNCC 11367).

Notes: *Cordyceps biclavata* is phylogenetically closely related to *Cor. militaris*, *Cor. shuifuensis*, and *Cor. changbaiensis* (Fig. 63), but forms a distinct and well-supported clade within this lineage, indicating that it represents a separate species. Morphologically, the stromata of *Cor. biclavata* are cylindrical or flattened at the base and cylindrical toward the apex, differing from the solitary, cylindrical to slightly clavate stromata observed in *Cor. militaris* and *Cor. shuifuensis* (Wang et al. 2020a). Among these related species, *Cor. biclavata* is most similar to *Cor. militaris*, sharing characteristics such as cylindrical to slightly clavate stromata with yellowish to reddish-orange coloration,

superficial perithecia, and a verticillium-like asexual morph. However, it can be distinguished by its overall smaller size and the absence of an isaria-like asexual morph, which is present in *Cor. militaris* (Wang et al. 2020a). In contrast, *Cor. changbaiensis* differs significantly from *Cor. biclavata* in

having longer stromata covered with white mycelia and in parasitizing coleopteran larvae rather than lepidopteran hosts (Hu et al. 2021). These phylogenetic and morphological distinctions support the recognition of *Cor. biclavata* as a novel species within the genus *Cordyceps*.

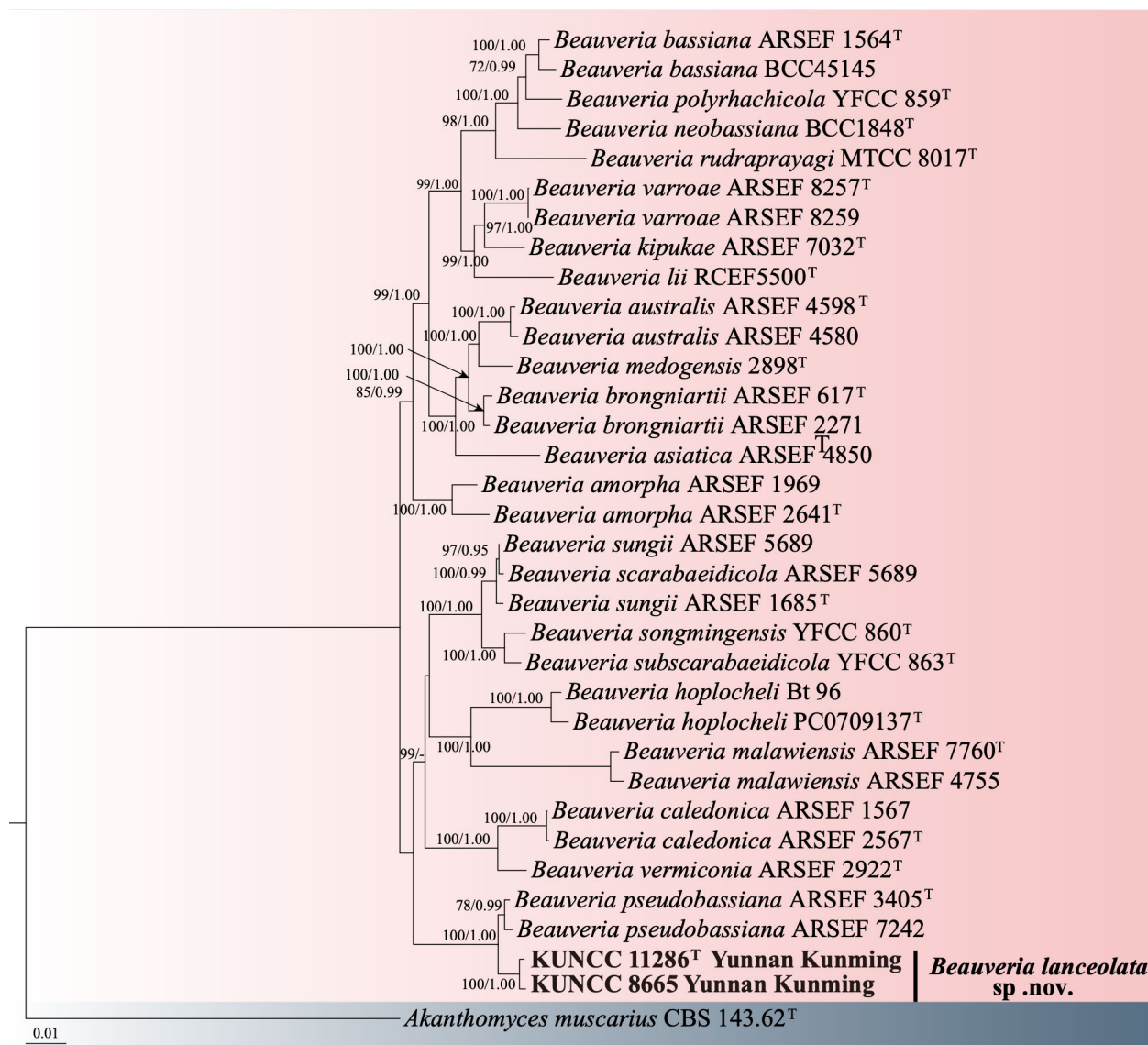


Fig. 61 The maximum likelihood tree using IQ-Tree (Web-IQ-TREE) inferred from combined *tef1*- α , *rpb1*, *rpb2* and *Bloc* sequences. *Akanthomyces muscarius* (Petch) Spatafora, Kepler & B. Shrestha was designated as the outgroup taxon. Values at the nodes before and after the backslash are ML bootstrap proportions (ML-BP > 70%) and BI posterior probabilities (BI-PP > 0.70), respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Samsoniella Mongkols., Thanakitp., Spatafora & Luangsa-ard

Samsoniella, as described by Mongkolsamrit et al. (2018), was established through molecular phylogeny of isaria-like morphotypes within the *Cordycipitaceae*. This genus is characterized by the presence of oval to fusiform conidia, along with striking bright red-orange teleomorphic stromata and anamorphic synnemata (Mongkolsamrit et al. 2018). Additionally, the species *Penicillium alboaurantium* G. Sm. was reclassified under the genus *Samsoniella*, and two novel species, *Sam. aurantia* and *Sam. inthanonensis*, have been formally described (Wang et al. 2020a). Currently, 45 species, viz. *Sam. alboaurantia*, *Sam. alpina*, *Sam. anhuiensis*, *Sam.*

antleroides, *Sam. aranea*, *Sam. asiatica*, *Sam. aurantia*, *Sam. cardinalis*, *Sam. coccinellidicola*, *Sam. coleopterorum*, *Sam. cristata*, *Sam. doupengshanensis*, *Sam. duyunensis*, *Sam. eruceae*, *Sam. farinospora*, *Sam. formicae*, *Sam. fusiformispora*, *Sam. guizhouensis*, *Sam. haniiana*, *Sam. hepiali*, *Sam. hymenopterorum*, *Sam. inthanonensis*, *Sam. kunmingensis*, *Sam. lanmaoa*, *Sam. lasiocampidarum*, *Sam. lepidopterorum*, *Sam. lurida*, *Sam. neopupicola*, *Sam. pseudogunnii*, *Sam. pseudotorricidae*, *Sam. pupicola*, *Sam. ramosa*, *Sam. sanmingensis*, *Sam. sapaensis*, *Sam. scoliopterygis*, *Sam. sinensis*, *Sam. subasiatica*, *Sam. tiankengensis*, *Sam. torquatistipitata*, *Sam. tortricidae*, *Sam. vallis*, *Sam. winandae*, *Sam. yuanzuiensis* and *Sam.*

yunnanensis, species have been accepted in *Samsoniella* (Index Fungorum July 18, 2025). This study introduces two new *Samsoniella* species that was reported during the survey

of microfungi in Southwestern China. The new species is established based on the evidence from morphological characterization and multigene phylogenetic analyses.

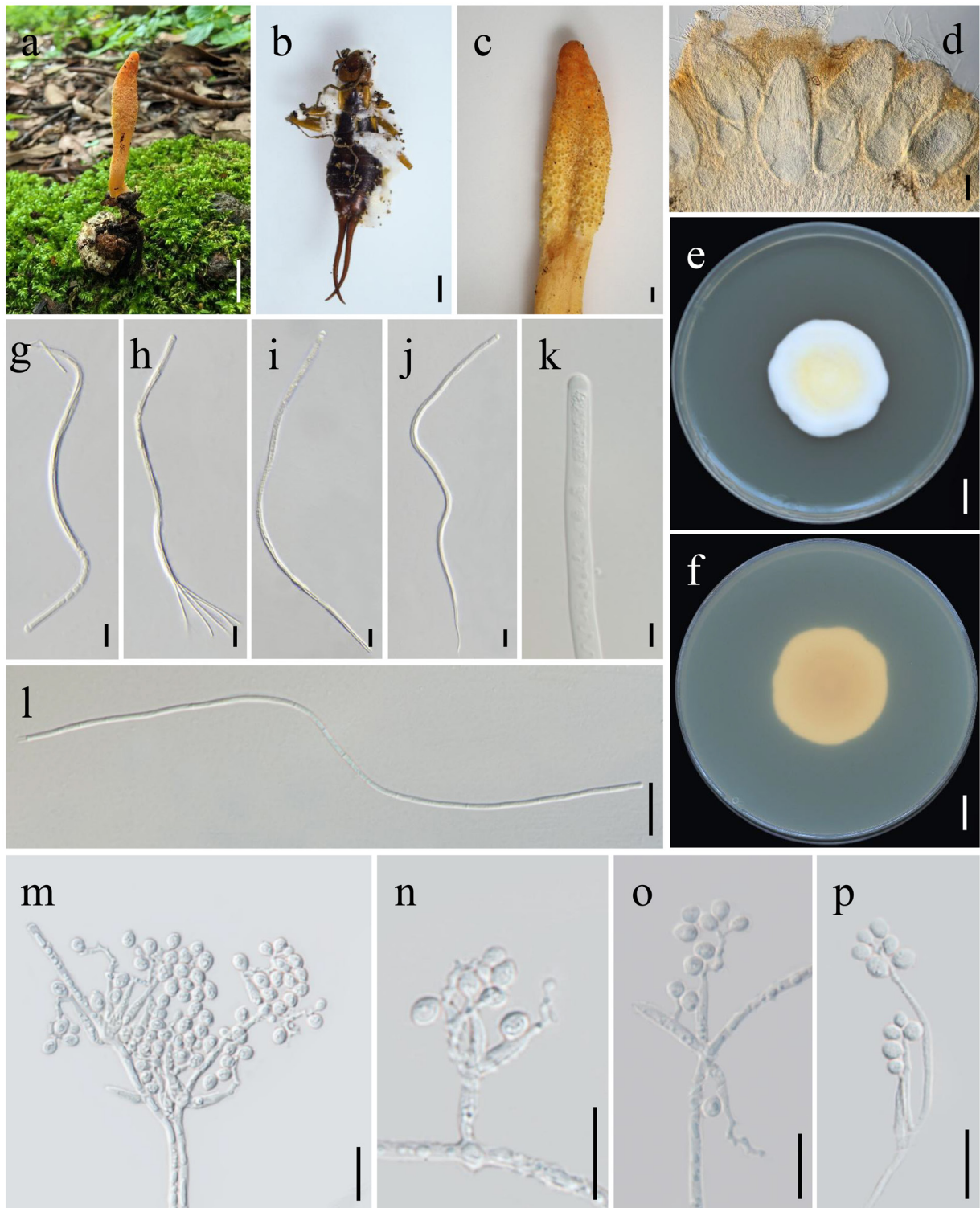


Fig. 62 *Beauveria lanceolata* (HKAS 135020, holotype) a Fruiting body of *B. lanceolata* parasitic on the larva of *Coleoptera*. b Mycelia of *B. lanceolata* growing on the adult of *Dermaptera*. c Fertile structure. d Perithecia. e, f Colonies on PDA. g–l Ascospores, ascus caps, and secondary ascospores. m–p Conidiophores, conidiogenous cells, and conidia. Scale bar: a = 5 cm, b = 1 mm, c = 1 cm, d = 1 mm, e, f = 1 cm, g–p = 10 μm.

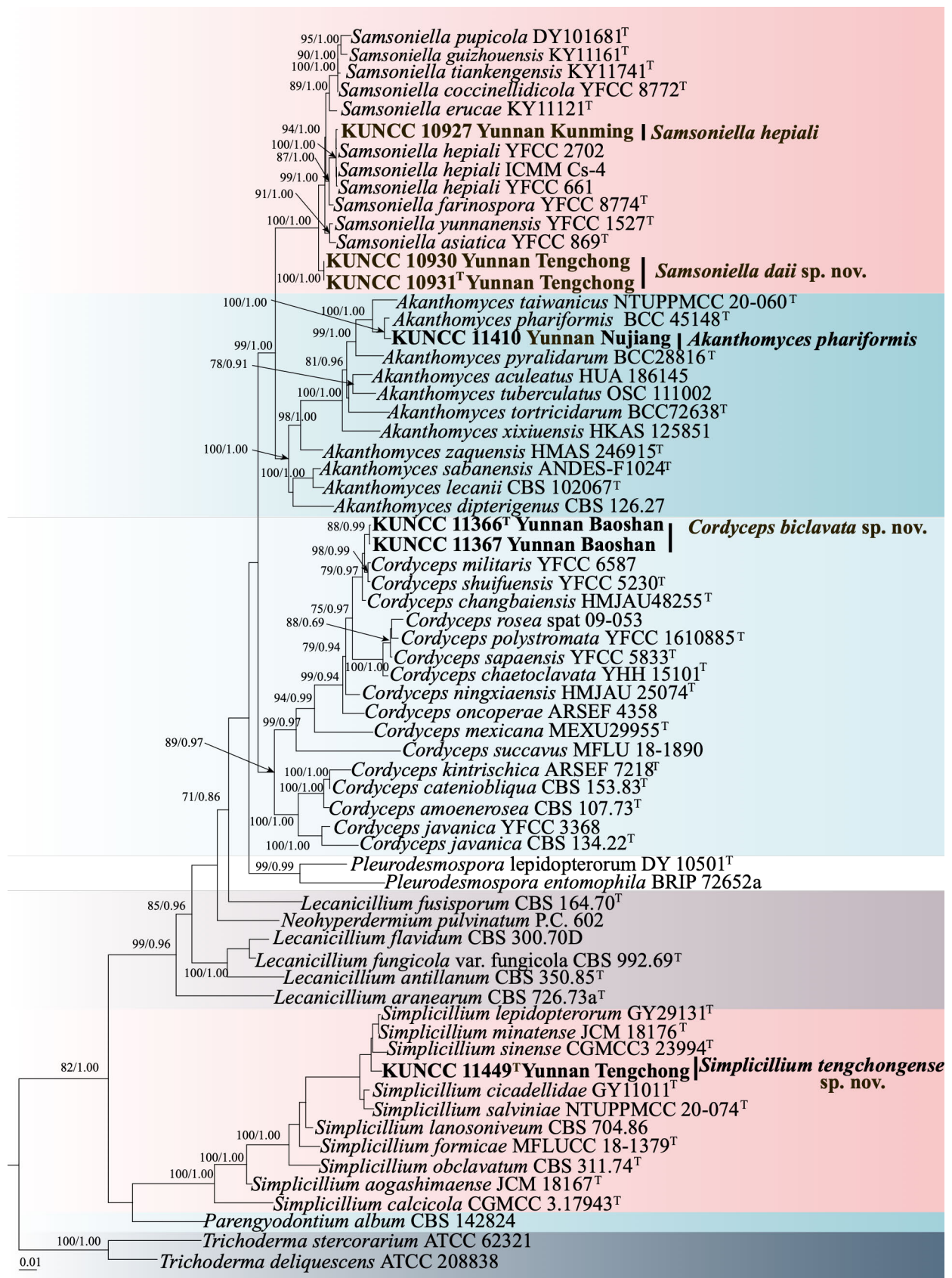


Fig. 63 The maximum likelihood tree using IQ-Tree (Web-IQ-TREE) inferred from combined *tef1*-α, LSU, and *rpb1* sequences of representative species of *Tri. stercorarium* (Barrasa, A.T. Martínez & G. Moreno) Jaklitsch & Voglmayr and *Tri. deliquescens* (Sopp) Jaklitsch were designated as outgroup taxa. Values at the nodes before and after the backslash are ML bootstrap proportions (ML-BP > 70%) and BI posterior probabilities (BI-PP > 0.70), respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

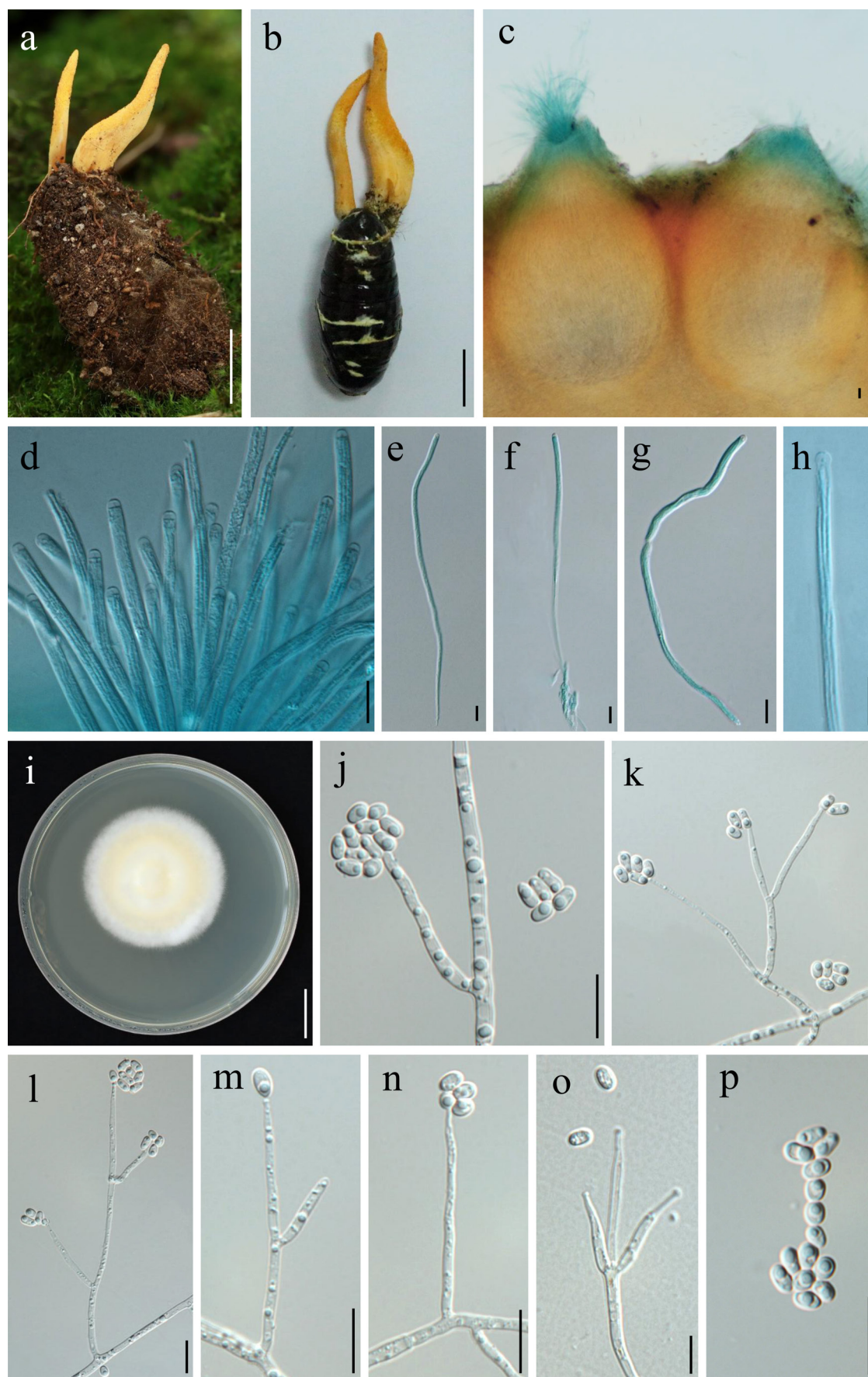


Fig. 64 *Cordyceps biclavata* (HKAS 135022, holotype) a–b Fungus on the larva of *Lepidoptera*. c Perithecia. d–g Asci. h Ascus cap. i Colony on PDA. j–p Conidiophores, phialides and conidia. Scale bars: a–b = 1 cm, c–h = 10 μ m, i = 1 cm, j–o = 10 μ m.

37. *Samsoniella hepiali* (Q.T. Chen & R.Q. Dai ex R.Q. Dai, X.M. Li, A.J. Shao, Shu F. Lin, J.L. Lan, Wei H. Chen & C.Y. Shen) H. Yu, R.Q. Dai, Y.B. Wang, Y. Wang & Zhu L. Yang. **Fig. 65**

Chinese name: – 蝙蝠蛾虫草 (bian fu e chong cao)

Index Fungorum number: IF 833114; **Facesoffungi number:** FoF 13965

Diagnosis: The molecular data were consistent with *Samsoniella hepiali*

Parasitic on the pupa of *Lepidoptera*. **Sexual morph:** Undetermined. **Asexual morph:** The strain was isolated from the stroma of *Cordyceps militaris*. **Hyphae** smooth-walled, hyaline, 1.4–2.5 µm wide. **Conidiophores** smooth-walled, cylindrical, 5.1–20.8 × 1.7–3.5 µm. **Phialides** on conidiophores verticillate, in whorls of two to six, basal portion cylindrical to narrowly lageniform, tapering gradually or abruptly toward the apex; 6.9–19.6 µm long, 1–1.8 µm wide at the base, 0.5–0.8 µm wide at the apex. **Conidia** smooth, hyaline, one-celled, fusiform or oval, 2.3–3.4 × 1.5–2.2 µm, often in chains.

Culture characteristics: Colonies on PDA fast-growing, 35–40 mm diameter in 14 days at 25 °C, white to yellowish, cottony with high mycelial density, Reverse white to yellowish.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany, isolated from *Cor. militaris* on the pupa of *Lepidoptera* buried in soil, 10 September 2023, M. Tang, (HKAS 126362, dried culture on PDA, living culture KUNCC 10927).

Notes: *Samsoniella hepiali* has isaria-like asexual morph and is characterized by branched or unbranched synnemata arising from the whole body of lepidopteran insects, cylindrical or clavate stipes with powdery conidia clusters at the apex (Wang et al. 2020a). However, a notable difference is that *Sam. hepiali* was isolated from a stroma of *Cor. militaris* in this study. Similarities include conidiophores cylindrical, phialides on conidiophores verticillate, basal portion cylindrical to narrowly lageniform, conidia fusiform or oval, often in chains. Phylogenetic analysis showed that the specimen clustered with *Sam. hepiali* (Fig. 63), and morphological studies confirmed that the isolated strain was *Sam. hepiali*. Therefore, *Cor. militaris* is reported as the new host of *Sam. hepiali*.

38. *Samsoniella daiae* Y.B. Wang, B.Z. Chen, M. Tang & Zhu L. Yang, **sp. nov.** **Fig. 66**

Chinese name: – 戴氏鳞翅虫草 (dai shi lin chi chong cao)

Index Fungorum number: IF 905270; **Facesoffungi number:** FoF 17504

Etymology: Named after Prof. Ruqin Dai for her contributions to cordycipitoid fungi.

Diagnosis: The species is characterized by reddish-orange and occasionally branched stromata, narrowly ovoid perithecia.

Holotype: HKAS 126364

On the larvae of *Lepidoptera*. **Sexual morph:** Stromata arising from the head of insects buried in soil, solitary, occasionally branched, 25 mm long, 2 mm wide. **Stipes** orange, cylindrical. Fertile parts reddish-orange, cylindrical to clavate, 5 mm long, 2.5 mm wide. **Perithecia** semi-immersed, narrowly ovoid, 301–481 × 99–240 µm. **Asci** cylindrical, eight-

spored, 84–230 × 2.5–4.5 µm. **Ascal caps** hemispherical, 1.8–3.9 × 1.8–2.9 µm. **Ascospores** hyaline, filiform, 45–110 × 0.7–0.9 µm. **Asexual morph:** Hyphae smooth-walled, hyaline, 1.1–2.7 µm wide. **Conidiophores** smooth-walled, cylindrical, solitary, 6.5–14.9 × 1.2–2.6 µm. **Phialides** on conidiophores verticillate, in whorls of three to six, basal portion cylindrical, tapering gradually or abruptly toward the apex; 6.2–22.6 µm long, 1.3–2.4 µm wide at the base, 0.2–1.4 µm wide at the apex. **Conidia** hyaline, smooth, one-celled, fusiform or oblong, 2–3.9 × 1–2.6 µm, often in chains.

Culture characteristics: Colonies on PDA fast-growing, 40–45 mm diameter in 14 days at 25 °C, cottony with high mycelium density, white. Reverse white to yellowish.

Material examined: CHINA, Yunnan Province, Tengchong City, Wuhe Township, on the larva of *Lepidoptera* buried in soil, 5 September 2023, M. Tang (HKAS 126364, holotype, ex-type culture KUNCC 10931), other collection: *Ibid.*, M. Tang (HKAS 126363, culture KUNCC 10930).

Notes: *Samsoniella daiae* is characterized by solitary stromata, occasionally branched, clavate, fertile parts reddish-orange, cylindrical to clavate, perithecia semi-immersed, narrowly ovoid, and cylindrical asci with filiform ascospores. *Samsoniella daiae* was phylogenetically closely related to *Sam. farinospora* (Fig. 63). However, the difference is that stromata of *Sam. daiae* arise from the head of insects, whereas *Sam. farinospora* on the hepialid hosts occurs asexual synnemata bearing powdery conidia at the apex, along with isaria-like conidiogenous structures (Wang et al. 2020a). Morphological observations reveal a significant difference in conidia sizes between *Sam. daiae* (2–3.9 × 1–2.6 µm) and *Sam. farinospora* (1.6–2.8 × 0.6–1.2 µm).

***Simplicillium* W. Gams & Zare**

Simplicillium was initially established with *Sim. lanosoniveum* as the type species, aiming to define a putatively monophyletic group comprising *Sim. lanosoniveum*, *Sim. lamellicola*, *Sim. obclavatum*, and *Sim. wallacei* within the family *Clavicipitaceae* (Wang et al. 2020a). *Simplicillium* exhibits a broad host range and is distributed globally. Several species within this genus are associated with plant pathogenic rust fungi and are recognized for their considerable potential in biological control (Gomes et al. 2018). To date, 37 species and 2 varietal taxa, viz. *Sim. album*, *Sim. aogashimaense*, *Sim. araneae*, *Sim. calcicola*, *Sim. chinense*, *Sim. cicadellidae*, *Sim. coccinellidae*, *Sim. coffeanum*, *Sim. coleopterorum*, *Sim. cylindrosporium*, *Sim. filiforme*, *Sim. formicae*, *Sim. formicidarum*, *Sim. guizhouense*, *Sim. humicola*, *Sim. hymenopterorum*, *Sim. lamellicola*, *Sim. lanosoniveum*, *Sim. lanosoniveum* var. *lanosoniveum*, *Sim. lanosoniveum* var. *tianjinense*, *Sim. larvatum*, *Sim. lepidopterorum*, *Sim. minatense*, *Sim. neolepidopterorum*, *Sim. niveum*, *Sim. obclavatum*, *Sim. pechmerlense*, *Sim. pseudocercosporicola*, *Sim. puwenense*, *Sim. salviniae*, *Sim. scarabaeoidea*, *Sim. sinense*, *Sim. spumae*, *Sim. subtropicum*, *Sim. sympodiophorum*, *Sim. wallacei* and *Sim. yunnanense* were restricted to *Simplicillium*, based on the phylogenetic analyses of ITS sequence data and strong morphological evidence (Index Fungorum, July 18, 2025).

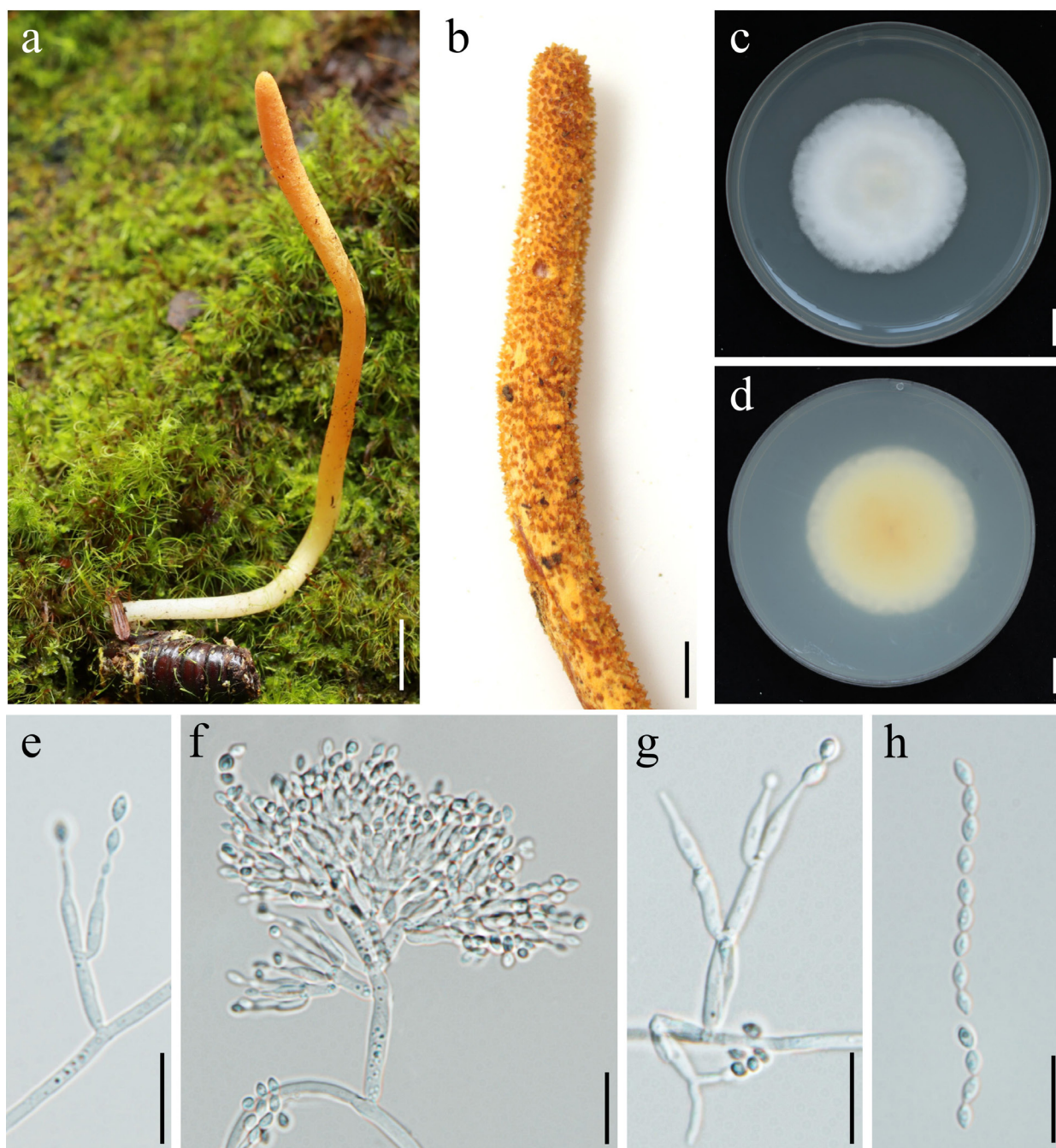


Fig. 65 *Samsoniella hepiali* (HKAS 126362) a The host *Cordyceps militaris* on a pupa of *Lepidoptera*. b Fertile part of *Cor. militaris*. c, d Colony on PDA. e–g Conidiophores and phialides. h Conidia. Scale bars: a–d = 1 cm, e–h = 10 μm.

39. *Simplicillium tengchongense* Y.B. Wang, B.Z. Chen, M. Tang & Zhu L. Yang, *sp. nov.* **Fig. 67**

Chinese name: – 腾冲单梗霉 (teng chong dan geng mei)

Index Fungorum number: IF 905271; **Facesoffungi number:** FoF 19318

Etymology: The epithet *tengchongense* refers to Tengchong City, Yunnan Province, China, where the holotype specimen was collected.

Diagnosis: *Simplicillium tengchongense* is distinguished by its solitary phialides on hyphae or paired on conidiophores, and ellipsoidal to subglobose conidia in chains.

Holotype: HKAS 135023

Endophytic from *Nigella martialis* which parasite on the larva of *Lepidoptera*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphae are 1.5–3.1 μm wide, smooth-walled, and hyaline. Phialides 9.4–32.4 μm long, typically solitary on vegetative hyphae or in pairs at the apex of conidiophores; base cylindrical, tapering gradually toward the apex; basal width 1.3–3.3 μm, neck 0.5–1.4 μm wide. Conidia 1.9–5.6 × 2.2–4.5 μm, smooth, hyaline, ellipsoidal to subglobose, commonly arranged in chains.

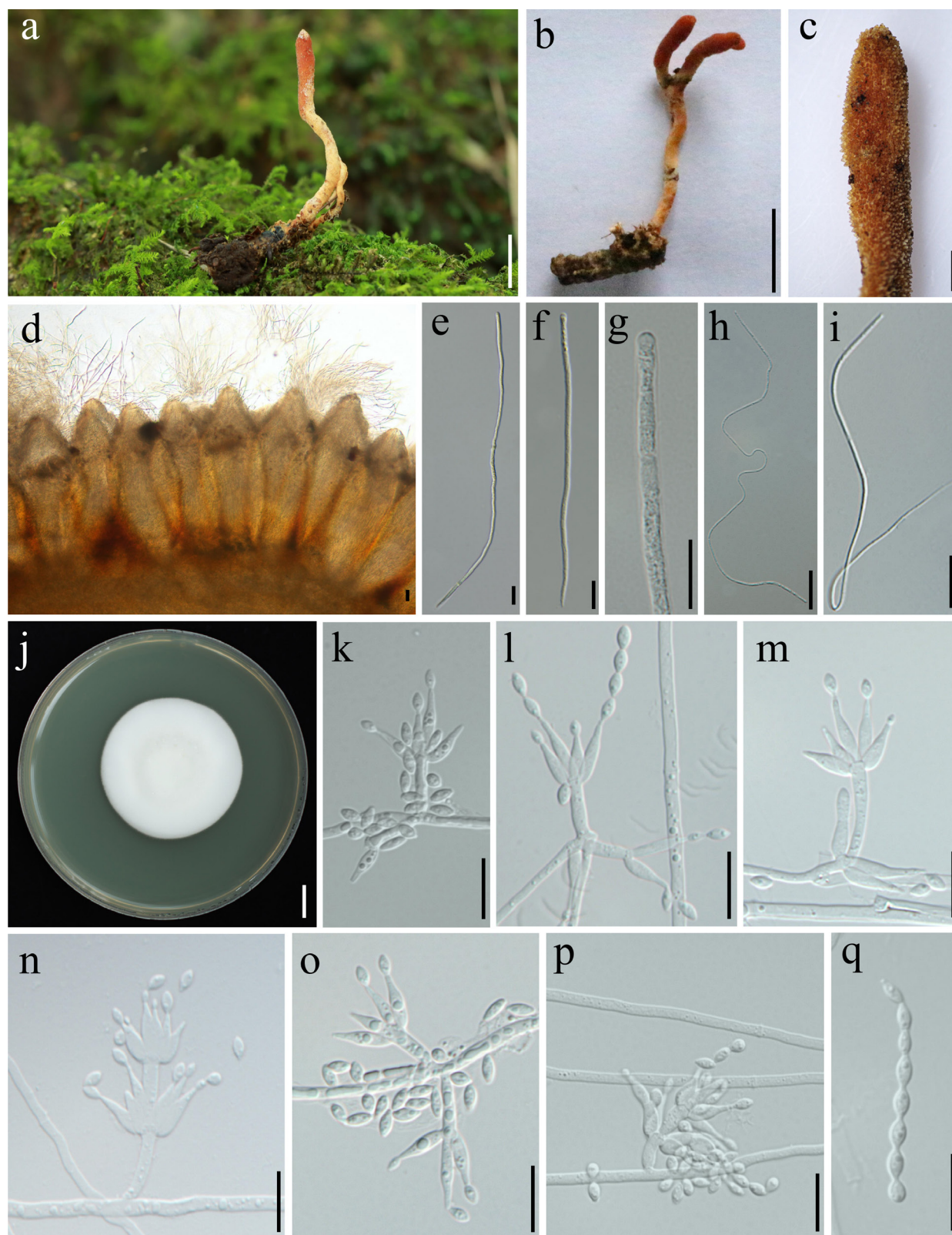


Fig. 66 *Samsoniella daiae* (HKAS 126364, **holotype**) a–b Fungus on the larvae of *Lepidoptera*. c Fertile part. d Perithecia. e, f Asci. g Ascospores. h, i Ascospores. j Colony on PDA. k–p Conidiophores and phialides. q Conidia. Scale bars: a–b = 1 cm, c = 1000 μ m, d–i = 10 μ m, j = 1 cm, k–q = 10 μ m

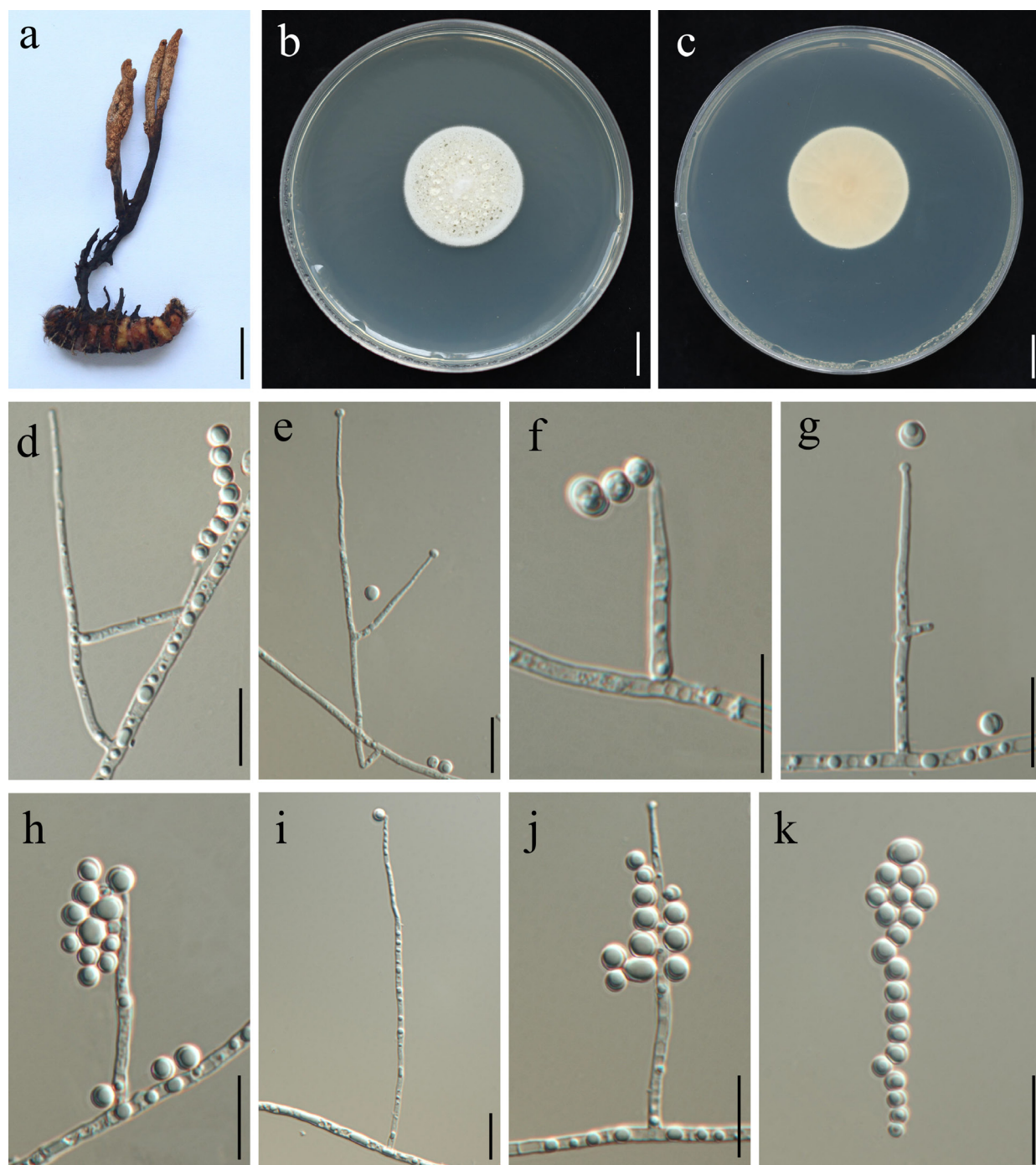


Fig. 67 *Simplicillium tengchongense* (HKAS 135023, holotype) a *Nigella martialis* on a larva of *Lepidoptera*. b, c Colony on PDA. d–j Phialides and conidia. k Conidia on PDA. Scale bars: a–c = 1 cm, d–k = 10 μ m.

Culture characteristics: Colonies on PDA at 25°C for 14 days reach 30–35 mm in diameter, with dense mycelia and abundant production of hyaline exudate droplets. Colonies are white to pale yellow on the surface, and white to cream on the reverse, with conspicuous longitudinal furrows.

Material examined: CHINA, Yunnan Province, Tengchong City, Houqiao Township, isolated from the sclerotium of *Nig. martialis* parasitic on the larva of *Lepidoptera* buried in soil, 5 September 2023, M. Tang, (HKAS 135023 holotype, ex-type culture KUNCC 11449).

Notes: *Simplicillium tengchongense* was described as a member of the genus *Simplicillium* due to its solitary phialides

and conidia adhering in globose slimy heads. In our five-gene phylogenetic analyses (Fig. 63), *Sim. tengchongense* forms a distinct clade within *Simplicillium* and is closely related to *Sim. lepidopterorum* and *Sim. sinense* (Chen et al. 2019; Yan et al. 2023). However, *Sim. tengchongense* can be distinguished from *Sim. lepidopterorum* by its production of ellipsoidal to subglobose conidia, whereas *Sim. lepidopterorum* produces ellipsoidal to fusiform conidia (Chen et al. 2019). It also differs from *Sim. sinense* in its ecological origin, having been isolated from the sclerotium of *Nig. martialis* rather than from human skin (Yan et al. 2023).

Hypocreaceae De Not**Trichoderma** Pers

Trichoderma is a genus of widely distributed filamentous fungi that exhibit considerable biotechnological promise, primarily due to their remarkable ability to colonize a variety of substrates across diverse environmental contexts (Jaklitsch 2011). This genus is also known for its proficiency in secreting an array of hydrolytic enzymes, including cellulases, chitinases, glucanases, and proteases, alongside a variety of secondary metabolites such as pyrones, peptaibols, and terpenes (Jaklitsch & Voglmayr 2015). Certain species like *Tri. reesei* serve as vital sources of enzymes for various biotechnological applications. Currently, 563 described within *Trichoderma* (Index Fungorum July 18, 2025).

40. *Trichoderma habaense* Y.B. Wang, B.Z. Chen & Zhu L. Yang, sp. nov. Fig. 69

Chinese name: – 哈巴木霉 (ha ba mu mei)

Index Fungorum number: IF 905272; **Facesoffungi number:** FoF 19319

Etymology: The epithet “*habaense*” refers to Haba Snow Mountain (Haba Xueshan) in Shangri-La City, Yunnan Province, China, where the type specimen was collected.

Diagnosis: *Trichoderma habaense* produces smaller, globose to ellipsoid conidia without oblong forms.

Holotype: HKAS 135027

Endophytic from the root of *Rho. decorum*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiophores* typically straight, verticillium-like or regularly branched in a treelike pattern, mostly slender, rarely forming long, distinct main axes. They emerged radially from the reticulum and occasionally extended as short, fertile outgrowths bearing 1–3 terminal phialides. Branches (2–)2.5–4.5(–5) μm wide, sometimes widening to 8 μm ; lateral branches arranged at right angles or slightly inclined upward, loose and short, typically single-celled and terminated by a solitary phialide; higher-order branches often formed 2–3 rebranching levels. Phialides solitary or in divergent whorls of 2–4, lageniform, with or without distal wall thickening, measuring (6.9–)7.6–14.8(–19) $\times$ (2.6–)3.1–4.1(4.4) μm ($\bar{x}$ = 10.7 $\times$ 3.6 μm , n = 29). **Terminal phialides** in each whorl often distinctly longer; most phialides straight, rarely curved. **Conidia** (3.5–)3.8–5.2(–5.5) $\times$ (3.2–)3.4–4.8(–5.5) μm ($\bar{x}$ = 4.4 $\times$ 4.1 μm , n = 34), green, globose to ellipsoid, smooth-walled, containing a few small guttules. *Chlamydospores* not observed.

Culture characteristics: Colonies on PDA reaching 29–30 mm in radius at 25 °C and 6–9 mm at 30 °C after 72 h, covering the entire plate after 7 days at 25 °C. Colonies circular, dense, with abundant aerial hyphae forming a thick white cottony mat that ascended in concentric zones and reached the lid of the Petri dish. Autolytic exudates inconspicuous, hyphal coilings absent, no diffusing pigments or distinct odour observed.

Material examined: CHINA, Yunnan Province, Diqing, Shangri-La City, Haba Snow Mountain, isolated as an endophyte from *Rho. decorum* root, 15 March 2023, F. Xiong (HKAS 135027 holotype, ex-type culture, KUNCC 11229), other collection: *Ibid.*, Q. Fan (culture KUNCC 11230).

Notes: As shown in the phylogenetic tree, *Tri. habaense* forms a distinct terminal lineage (Fig. 68), strongly supported by multi-locus phylogenetic analyses (Cai & Druzhinina 2021). BLAST comparisons against the NCBI database revealed 98.8% identity to *Tri. cremeoides* S112 in *tef1*- α (14 bp differences) and 99.3% identity in *rpb2* (5 bp differences). Morphologically, the conidia of *Tri. cremeoides* are larger than those of *Tri. habaense*. In addition, the conidia of *Tri. habaense* are predominantly globose to ellipsoid, with oblong forms rarely observed (Jaklitsch & Voglmayr 2015).

41. *Trichoderma xinpingense* Y.B. Wang, B.Z. Chen & Zhu L. Yang, sp. nov. Fig. 70

Chinese name: – 新平木霉 (xin ping mu mei)

Index Fungorum number: IF 905273; **Facesoffungi number:** FoF 19320

Etymology: The epithet *xinpingense* refers to Xinping Yi & Dai Autonomous County, Gasa Town in Yuxi City, Yunnan Province, China, where the type specimen was collected.

Diagnosis: Differs from *T. phellinicola* by shorter, wider phialides and smaller conidia.

Holotype: HKAS 135028

Endophytic from *Ophiocordyceps* sp. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiophores* simple or rebranching 1 (–2) times, i.e. 1 main axis of variable length, tapering from 2 to 3 μm at the base to 1–2 μm wide terminally, with 1–2 celled, often asymmetric terminal branches, replaced by phialides in apical regions. Phialides solitary or divergent in whorls of 1–2, often distinctly inclined upwards, arising from cells 2–4 μm thick. **Phialides** (10.1–)10.5–20.8(–21.2) $\times$ (1.9–)2–3.3(3.4) μm ($\bar{x}$ = 15.3 $\times$ 2.5 μm , n = 30), subulate or cylindrical, widest at or slightly above the base, straight or curved. Conidia formed in minute wet heads, rarely exceeding 50 μm diam, distributed across the whole plate, denser around the margin. **Conidia** (3.2–)3.9–7(–7.4) $\times$ (2–)2–3(–3.3) μm ($\bar{x}$ = 4.9 $\times$ 2.5 μm , n = 30), oblong, cylindrical, less commonly sub-ellipsoidal, hyaline, smooth, with few minute guttules; scar indistinct.

Culture characteristics: Colonies on PDA 53–57 mm in radius after 72 h at 25 °C, covering the plate after 4–5 d. Colonies circular, aerial hyphae abundant. No pigment and distinct odor produced on this medium.

Material examined: CHINA, Yunnan Province, Yuxi City, Xinping, Gasa Town, isolated as an endophyte from *Ophiocordyceps* sp., 19 July 2024, F.W. Lou (HKAS 135028, holotype, ex-type culture KUNCC 11231), other collection: *Ibid.*, Q. Fan (culture KUNCC 11232).

Notes: As shown in the phylogenetic tree, *Tri. xinpingense* forms a distinct terminal lineage (Fig. 68), strongly supported by multi-locus phylogenetic analyses. BLAST comparisons against the NCBI database revealed 88% identity to *Tri. phellinicola* in *tef1*- α (88 bp differences) and 95.6% identity in *rpb2* (33 bp differences). Morphologically, the conidia of *Tri. xinpingense*, measuring (3.2–)3.9–7(–7.4) $\times$ (2–)2–3(–3.3) μm , are smaller than those of *Tri. phellinicola*, which measure (5–)6–11(–15) $\times$ (2–)2.2–2.7(–3) μm . Furthermore, the phialides of *Tri. xinpingense* (10.1–)10.5–20.8(–21.2) $\times$ (1.9–)2–3.3(3.4) μm are notably shorter and slightly wider than those of *Tri. phellinicola* (11–)19–33(–41) $\times$ (1.8–)2–3(–3.2) μm (Jaklitsch 2011).

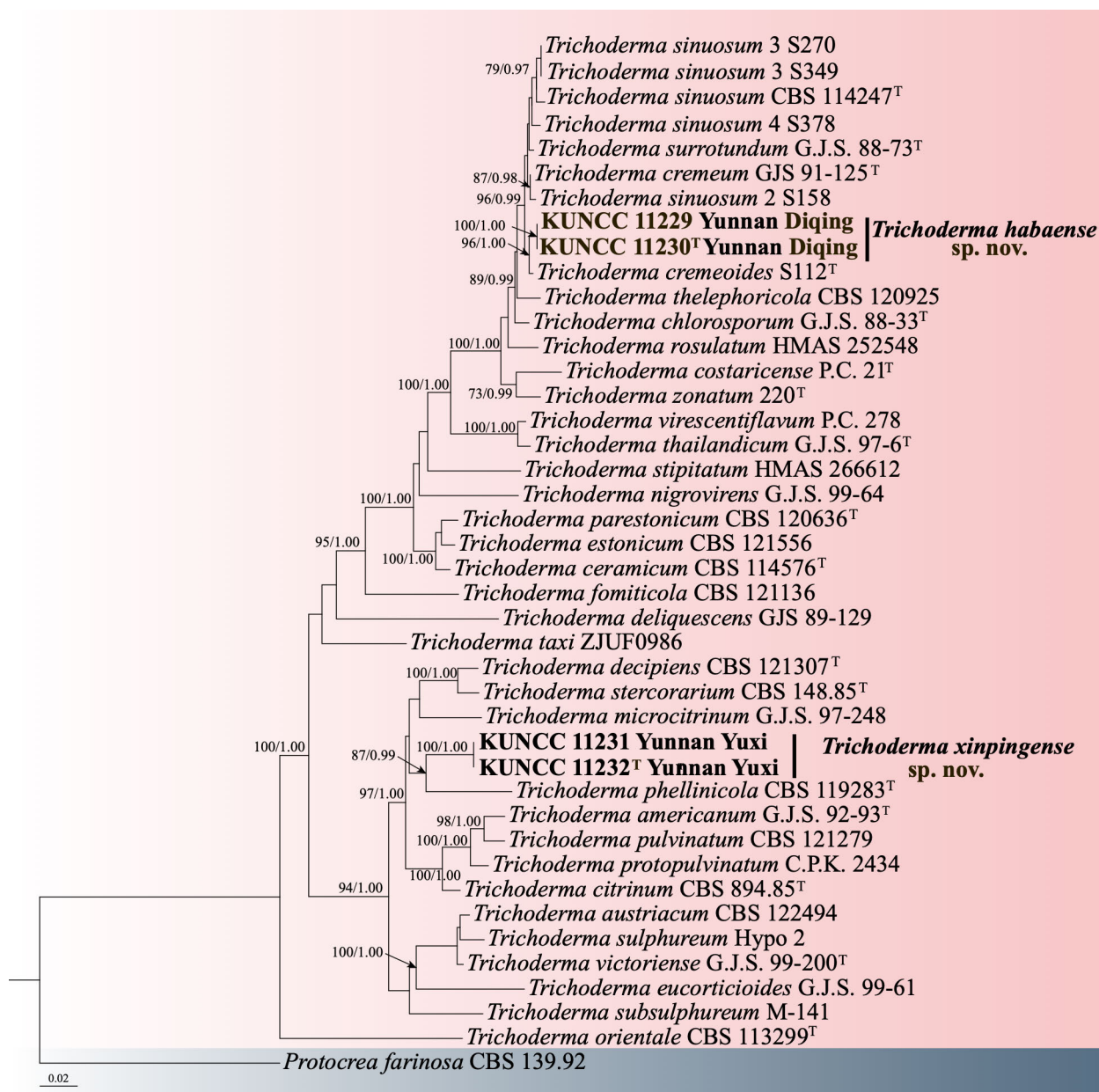


Fig. 68 The maximum likelihood tree using IQ-Tree ([Web-IQ-TREE](#)) inferred from combined *tef1*-α and *rpb2* sequences. *Protocrea farinosa* (Berk. & Broome) Petch was designated as outgroup taxon. Values at the nodes before and after the backslash are ML bootstrap proportions (ML-BP > 70%) and BI posterior probabilities (BI-PP > 0.70), respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Hypocreales Lindau

Nectriaceae Tul. & C. Tul.

Fusarium Pers

Fusarium is recognized as one of the most widespread filamentous fungal pathogens globally. Multi-locus sequence analysis encompassing *tef1*-α, *tub2*, calmodulin, and *rpb2* genes has elucidated the existence of multiple cryptic species within each morphospecies of clinically significant *Fusarium* taxa (John F. Leslie & Summerell 2006; Balajee et al. 2009). *Fusarium*, currently encompasses more than 712 names (Crous et al. 2021; [Fusarium Database](#)), and 1863 lists within the indexfungorum ([Index Fungorum](#) July 18, 2025).

42. *Fusarium highlandense* Y.B. Wang, B.Z. Chen, Q. Fan & Zhu L. Yang, **sp. nov.** **Fig. 72**

Chinese name: – 高原镰刀菌 (gao yuan lian dao jun)

Index Fungorum number: IF 905274; **Facesoffungi number:** FoF 19321

Etymology: "highlandense" refers to samples collected from high-altitude plateau regions.

Diagnosis: *Fusarium highlandense* is distinguished by producing cream to orange, translucent sporodochia and 2–7-septate falcate macroconidia with blunt to slightly curved apical cells and foot-shaped basal cells.

Holotype: HKAS 135030

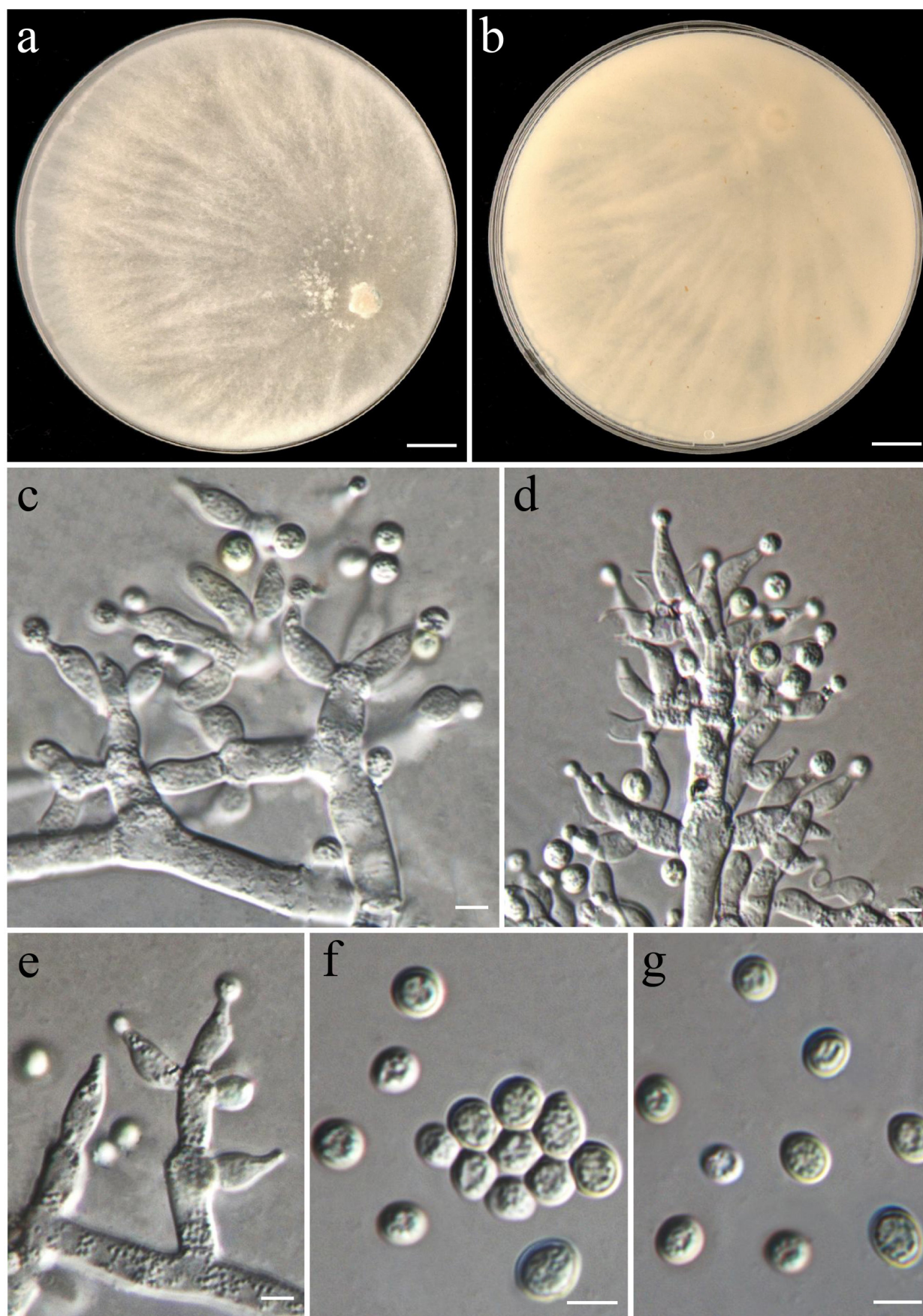


Fig. 69 *Trichoderma habaense* (HKAS 135027, holotype) a, b Colony on PDA, front and back. c–e Conidiophores and Phialides. f, g conidia. Scale bar: a, b = 1 cm, c–g = 5 µm.

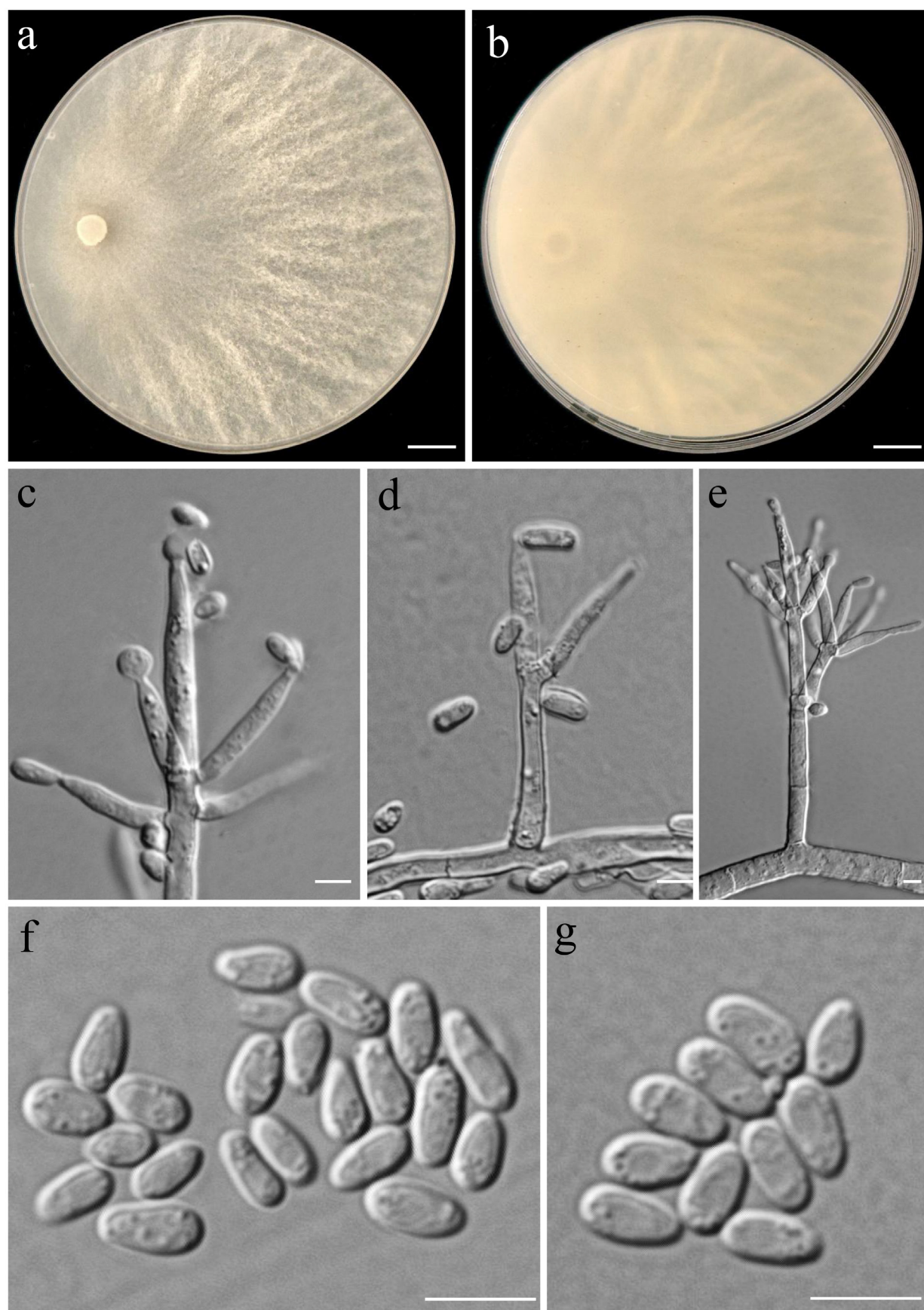


Fig. 70 *Trichoderma xinpingense* (HKAS 135028, **holotype**) a, b Colonies on PDA, front and back. c-e Conidiophores and phialides. f, g Conidia. Scale bar: a, b = 1 cm, c-e = 3 μm, f, g = 5 μm.

Parasitic from the symptomatic leaves of *Erianthus rufipilus*. **Sexual morph:** Undetermined. **Asexual morph:** *Sporodochial conidiophores* densely, irregularly branched, 12–21.5 × 3–4.5 µm, bearing apical whorls of 2–3 phialides, sporodochial phialides monophialidic, subulate to subcylindrical, 14.5–22.5 × 3–3.5 µm, ($\bar{x}$ = 17 × 3.5 µm), smooth and thin-walled, apical collarettes absent and periclinal thickening inconspicuous. *Sporodochial microconidia* absent. *Sporodochial macroconidia* falcate, straight to slightly dorsiventrally curved, broadest at the middle portion, tapering towards both ends, apical cell blunt to slightly curved, basal cell stunted to well-developed, foot-shaped, 2–6(–7)-septate, predominantly 5-septate, hyaline, smooth- and thick-walled; 2-septate conidia: 21–24 × 3.5–4.5 µm, ($\bar{x}$ = 23 × 4 µm); 3-septate conidia: 29–38.5 × 3–4.5 µm ($\bar{x}$ = 34 × 3.5 µm); 4-septate conidia: 40–47.5 × 3.5–4 µm, ($\bar{x}$ = 44 × 3 µm); 5-septate conidia: 45–60(–64.5) × 3.5–5 µm ($\bar{x}$ = 52.5 × 4 µm); 6-septate conidia: 58–68 × 4–4.5 µm ($\bar{x}$ = 62 × 4 µm); 7-septate conidia: 69.5–78.5 × 3.5–4.5 µm, ($\bar{x}$ = 73.5 × 4 µm). *Chlamydospores* not observed.

Culture characteristics: Colonies on PDA exhibiting 6.5–7 cm diam in 7 d at 25°C, aerial mycelia abundant, flat, colony margin regular, surface white to magenta, reverse cream to magenta. On SNA reaching 3.5–4 cm diam in 7 d, aerial

mycelia scant, flat, colony margin regular, surface white to cream, reverse white to cream. On OA reaching 5.5–6 cm diam in 7 d, felty, with abundant aerial mycelia, colony margin lightly regular, surface white, reverse pale brown. Aerial conidiophores and conidia were not observed. Sporodochia cream to orange, translucent, formed richly on the carnation leaves and on the agar, often covered with aerial mycelia.

Material examined: CHINA, Yunnan Province, Shangri-La City, from the symptomatic leaves of *Erianthus rufipilus*, August 2023, Q. Fan (HKAS 135030 holotype, dried culture on PDA; ex-type culture KUNCC 11103), other collection: *Ibid.*, Q. Fan, (culture KUNCC 3449).

Notes: Phylogenetic analysis based on the concatenated dataset of *CaM*, *rpb1*, *rpb2*, *tef1-α*, ITS and *tub2* loci resolved the *Fus. highlandense* isolates as a monophyletic clade within the *Fusarium*, with strong statistical support (Fig. 71). *Fusarium highlandense* is closely related to *Fus. avenaceum*, but differs by 63 bp from *Fus. avenaceum* in the 3-locus (*rpb1-rpb2-tef1-α*) dataset (ITS, *CaM* and *tub2* sequences are not available for *Fus. avenaceum*). Morphologically, *Fus. highlandense* can be distinguished from related species through the septation (3–5-septate in *F. avenaceum* vs. 2–7-septate in *Fus. highlandense*) (John F. Leslie & Summerell 2006).

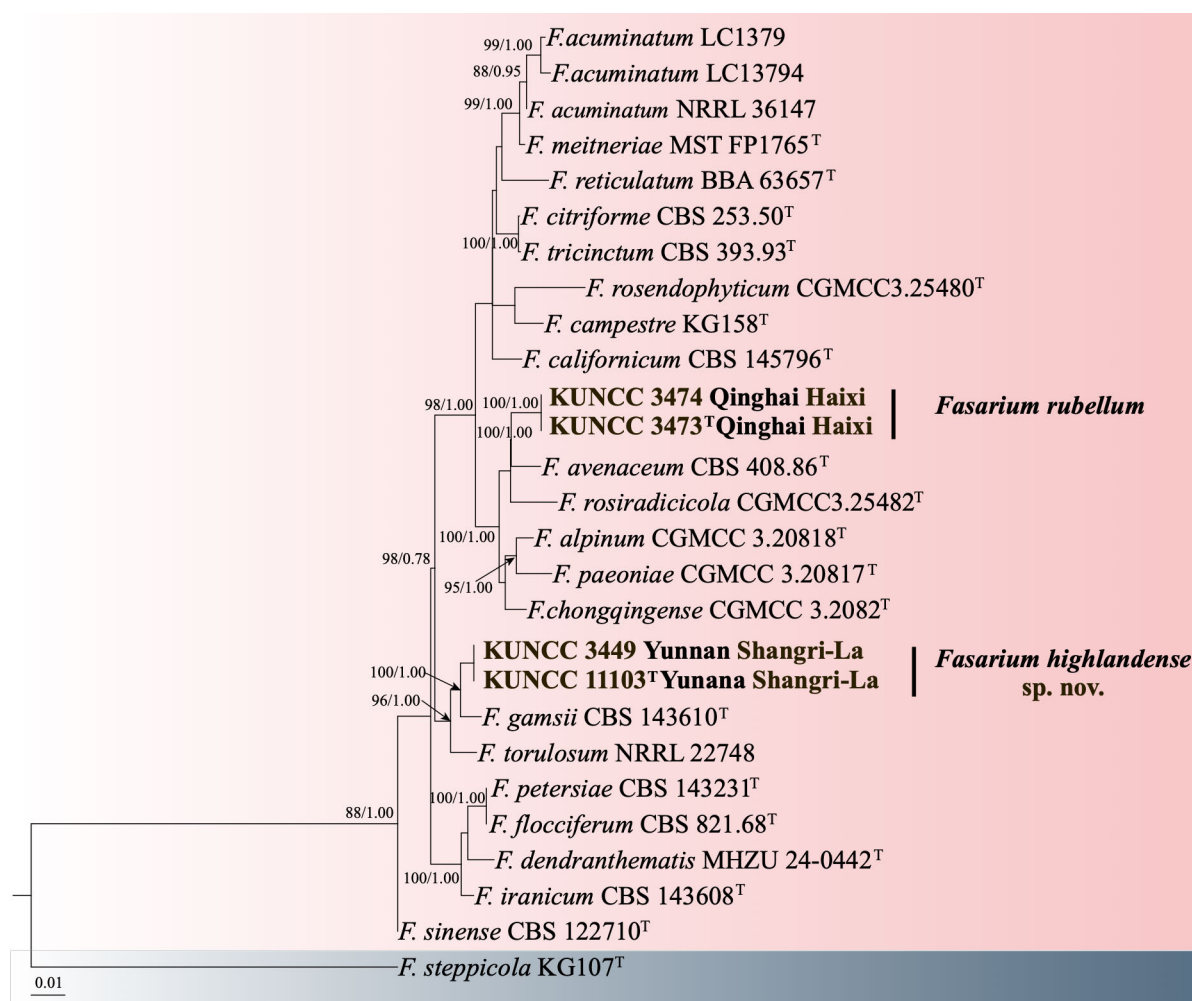


Fig. 71 The maximum likelihood tree using IQ-Tree (Web-IQ-TREE) inferred from combined ITS, *tub2*, *CaM*, *tef1-α*, *rpb1* and *rpb2* sequences. *Fusarium steppicola* Akhmetova, D.G. Knapp, Kovács & O. Molnár was used as outgroup taxa. Values at the nodes before and after the backslash are ML bootstrap proportions (ML-BP > 70%) and BI posterior probabilities (BI-PP > 0.70), respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

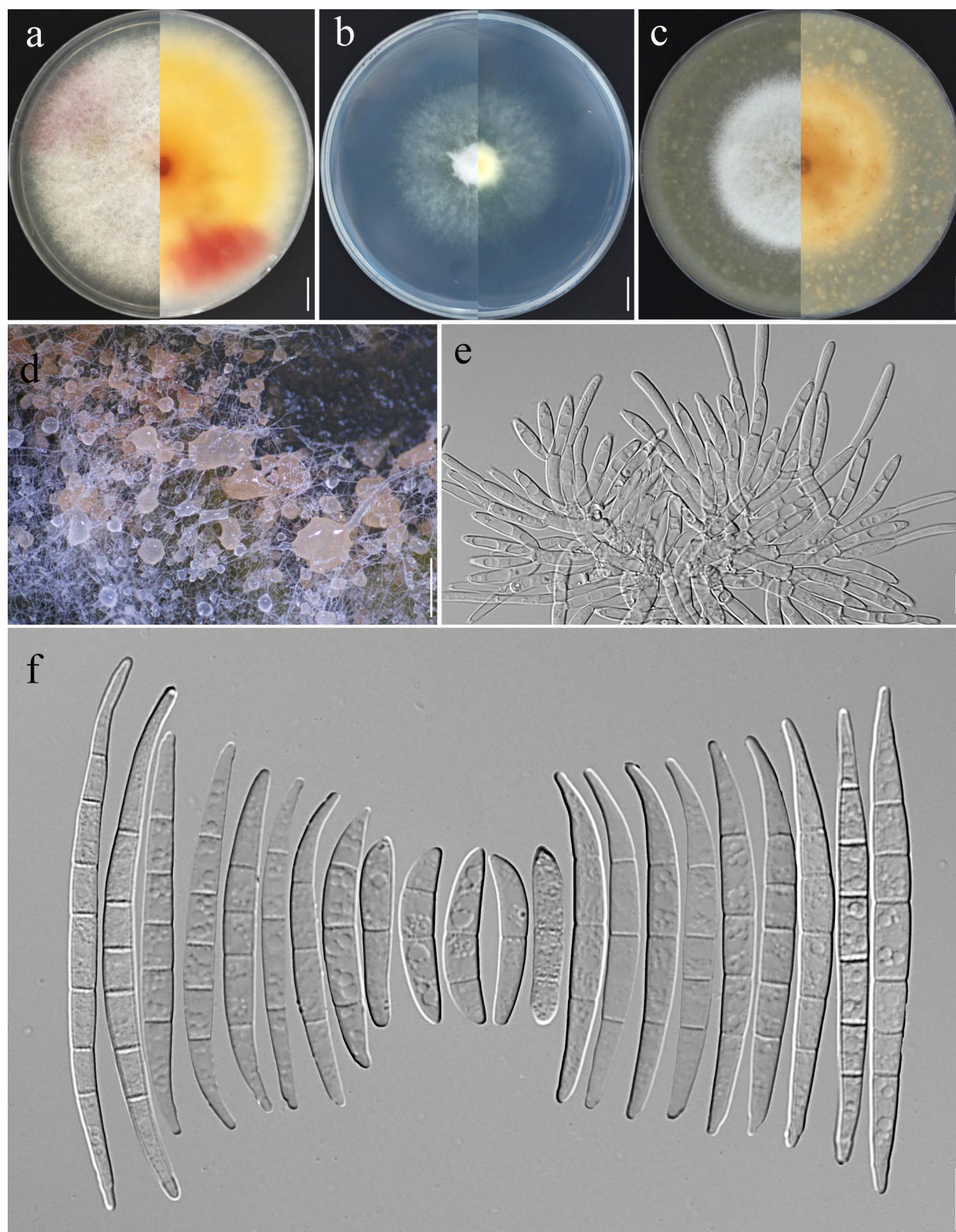


Fig. 72 *Fusarium highlandense* (HKAS 135030, holotype) a–c Colonies on PDA, SNA, and OA (left: surface, right: reverse). d Sporodochia. e Sporodochial conidiophores and conidiogenous cells. f Sporodochial macroconidia. Scale bars: a–c 1 cm, d–f = 10 μ m.

43. *Fusarium rubellum* P. Zhao & L. Cai. Fig. 73

Chinese name: – 粉红镰刀菌 (fen hong lian dao jun)

Index Fungorum number: IF 572668; **Facesoffungi number:** FoF 19322

Endophytic from *Ophicordyceps sinensis*. Sexual morph: Undetermined. **Asexual morph:** Conidiophores on aerial mycelia 12–28 μ m tall, simple or rarely irregularly branched, bearing terminal single phialides or whorls of 1–2 phialides, sometimes reduced to solitary conidiogenous cells borne

laterally on hyphae; aerial conidiogenous cells monophialidic, subulate to subcylindrical or lageniform, smooth- and thin-walled, $11\text{--}24 \times 3\text{--}4.5 \text{ }\mu\text{m}$ ($\bar{x} = 18 \times 4 \text{ }\mu\text{m}$), apical collarettes absent and periclinal thickening inconspicuous. *Aerial macroconidia* falcate to navicular, hyaline, smooth- and thin-walled, almost straight to slightly dorsiventrally curved, tapering towards both ends, apical cell blunt or papillate, basal cell stunted to well-developed, foot-shaped, 1–6-septate, predominantly 5-septate, 1-septate conidia: $22\text{--}30 \times 4\text{--}5 \text{ }\mu\text{m}$ ($\bar{x} = 26 \times 4.5 \text{ }\mu\text{m}$); 2-septate conidia: $29.5\text{--}41 \times$

$4\text{--}6 \text{ }\mu\text{m}$ ($\bar{x} = 34 \times 5 \text{ }\mu\text{m}$); 3-septate conidia: $31.5\text{--}43.5 \times 4.5\text{--}6 \text{ }\mu\text{m}$ ($\bar{x} = 37.5 \times 5 \text{ }\mu\text{m}$); 4-septate conidia: $(35\text{--}) 37\text{--}52 \text{ }\mu\text{m}$ ($\bar{x} = 43.5 \times 5 \text{ }\mu\text{m}$); 5-septate conidia: $38.5\text{--}56.5 \times 5\text{--}6.5 \text{ }\mu\text{m}$, ($\bar{x} = 46.5 \times 5.5 \text{ }\mu\text{m}$); 6-septate conidia: $43.5\text{--}52.5 \times 5\text{--}6.5 \text{ }\mu\text{m}$, ($\bar{x} = 48 \times 6 \text{ }\mu\text{m}$); overall: $22\text{--}56.5 \times 4\text{--}6.5 \text{ }\mu\text{m}$ ($\bar{x} = 39.5 \times 5 \text{ }\mu\text{m}$). *Sporodochia and Sporodochial conidia* not observed. *Chlamydospores* obovoidal, subglobose to globose, hyaline, smooth-walled to slightly roughened, thick-walled, $6\text{--}8.5 \text{ }\mu\text{m}$, terminal or intercalary.

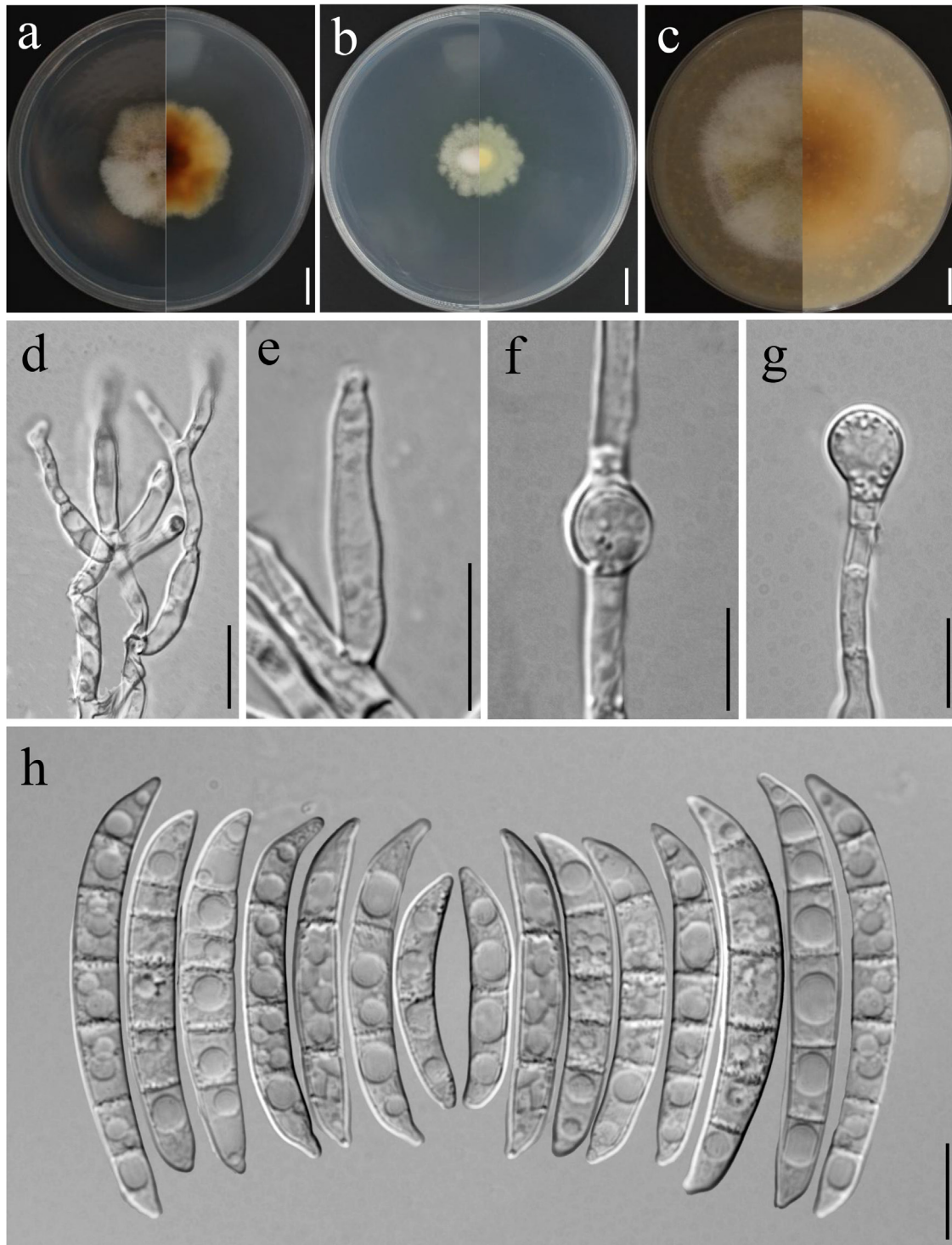


Fig. 73 *Fusarium rubellum* (HKAS 126169) a–c Colony on PDA, SNA, and OA (left: surface, right: reverse). d, e Sporodochial conidiophores and conidiogenous cells. f, g Chlamydospores. h Sporodochial macroconidia. Scale bars: a–c 1 cm, d–h = 10 μm .

Culture characteristics: Colonies on PDA exhibiting 4–4.5 cm diam in seven days at 25°C, cottony, with abundant aerial mycelium, colony margin undulate, surface white to pale brown, reverse pale brown to brown. On SNA reaching 2.5–3 cm diam in seven days, flat, colony margin undulate, surface white to cream, reverse cream. On OA reaching 5.5–6 cm diam in seven days, cottony, with abundant aerial mycelium, colony margin regular, surface cream to pale brown, reverse cream to pale brown.

Material examined: CHINA, Qinghai Province, Haixi, isolated from *O. sinensis*, May 2022, Q. Fan (HKAS 126169 holotype, ex-type culture KUNCC 3473), other collection: *Ibid.*, Q. Fan (culture KUNCC 3474).

Note: Phylogenetic analysis based on the concatenated dataset of *CaM*, *rpb1*, *rpb2*, *tef1*-α, ITS, and *tub2* loci revealed that the isolates form a monophyletic clade with *Fus. rubellum*, with strong statistical support (Fig. 71). *Fusarium rubellum* is phylogenetically closely related to *Fus. gamsii* but differs by 14 bp in the combined *tef1* and *rpb2* dataset. It should be noted that sequences of *rpb1*, *tub2*, and *CaM* are unavailable for *Fus. gamsii*, which limits further comparative analyses. Morphologically, *Fus. rubellum* can be distinguished from related species by the size of macroconidia (22–56.5 × 4–6.5 μm vs. 17–46 × 4–6 μm in *Fus. gamsii*) and septation (1–6-septate vs. 1–4-septate in *Fus. gamsii*) (Torbat et al. 2019). Based on both phylogenetic and morphological evidence, the isolates are identified as *Fus. rubellum*. In this study, this species was isolated from *O. sinensis*, representing a new host record for *Fus. rubellum* (Torbat et al. 2019; Zhao et al. 2025).

Ilyonectria P. Chaverri & C. Salgado

Ilyonectria was introduced with type species *I. radicola*, having asexual morphs and belonging to *Neonectria radicola*-group (Booth 1959, 1996; Chaverri et al. 2011; Lombard et al. 2014). Sexual morphs are mostly found on herbaceous material, rarely on woody parts while asexual morphs are in soil, with diseased roots (Chaverri et al. 2011). *Ilyonectria* sexual morph are characterized with perithecia loosely attaching to substratum, red, globose to subglobose, and having smooth, ellipsoidal, 1-septate ascospores (Chaverri et al. 2011; Lombard et al. 2014). Asexual morphs are produced cylindrocarpon-like conidia, characterized by ellipsoidal to ovoid, 0–1-septate, chlamydospores present, microconidia and straight, 1–3-septate macroconidia (Chaverri et al. 2011; Lombard et al. 2014). Recent studies have evaluated the paraphyletic nature of *Ilyonectria* (Cabral et al. 2012a; Cabral et al. 2012b; Lombard et al. 2014).

44. *Ilyonectria liriodendri* (Halleen, Rego & Crous) P. Chaverri & Salgado, in Chaverri, Salgado, Hirooka, Rossman & Samuels, Stud. Mycol. 68: 71 (2011) Fig. 74

Chinese name: – 鵝掌楸土赤壳菌 (e zhang qiu tu chi qiao jun)

Index Fungorum number: IF 518561; **Facesoffungi number:** FoF 14355

Saprobic on decaying wood submerged in freshwater habitats. **Sexual morph:** See Halleen et al. (2006). **Asexual**

morph: *Mycelium* immersed, consisting of hyaline, smooth-walled, branched, septate, smooth, subhyaline hyphae. *Conidiophores* 68–149 × 3–5 μm ($\bar{x}$ = 95 × 4 μm, n = 15), macronematous, semi-macronematous, irregularly branched, solitary or group, phialides cylindrical, smooth, 2–3-septate, subhyaline. *Conidiogenous cells* monophialidic, integrated, cylindrical, subhyaline, truncate at the apex. *Conidia* 22–43 × 5–9 μm ($\bar{x}$ = 31 × 7 μm, n = 25), acrogenous, solitary, fusiform or obclavate, 1–2-septate, smooth, subhyaline, rounded at the apex.

Culture characteristics: Conidia germinating on PDA medium within 24 h and germ tubes arising from terminal end of conidium. Colonies grown on PDA reached 50 mm diam at room temperature in one month, circular, with velvety, glistening, dry, flat, cream to light brown mycelium on the surface, from below dark brown with entire margin.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, 29°19'36.31" N, 95°21'22.17" E, 1481 m a.s.l., on decaying wood submerged in a freshwater stream, 13 July 2022, R.J. Xu, XK-2 (HKAS 136098), culture (KUNCC 24-18108).

Notes: *Ilyonectria liriodendri* was described as *Neonectria liriodendri* and was isolated from *Vitis vinifera* in France, Portugal and South Africa, as well as from *Liriodendron tulipifera* in the USA. It is the ex-type strain of *Cylindrocarpon liriodendri* by (Halleen et al. 2006). Later, Chaverri et al. (2011) synonymized *N. liriodendri* as *I. liriodendri* due to molecular phylogenetic analysis revealing five distinct genera, with *Ilyonectria* including some species from the *N. radicola* group. Morphologically, our collection perfectly matches the ex-type strain of *I. liriodendri*. Therefore, we identify our collection as *I. liriodendri* and report it as a new record for China.

Mariannaea G. Arnaud ex Samson

Mariannaea was established by Samson (1974) and includes species *M. camptospora* and *M. elegans* var. *punicea*, with *M. elegans* designated as the type species. *Mariannaea* is characterized by branched, septate conidiophores and flask-shaped phialides that produce 1–2-celled, hyaline conidia, typically arranged in overlapping chains or slimy clusters (Samson 1974, Samson and Bigg 1988, Hu et al. 2017). The taxonomy of *Mariannaea* was later reassessed by Hu et al. (2017) using both morphological and molecular data, and an epitype was designated for *M. elegans*. More recently, Bao et al. (2023) introduced two new species, *M. yunnanense* and *M. suae*, and reported two additional *Mariannaea* species from freshwater habitats based on phylogenetic and morphological analyses. To date, 23 species have been recognized within the genus (Hyde et al. 2024a).

45. *Mariannaea elegans* (Corda) Samson, Stud. Mycol. 6: 75 (1974) Fig. 76

Chinese name: – 优雅马利亚霉 (you ya ma li ya mei)

Index Fungorum number: IF 300242; **Facesoffungi number:** FoF 17424

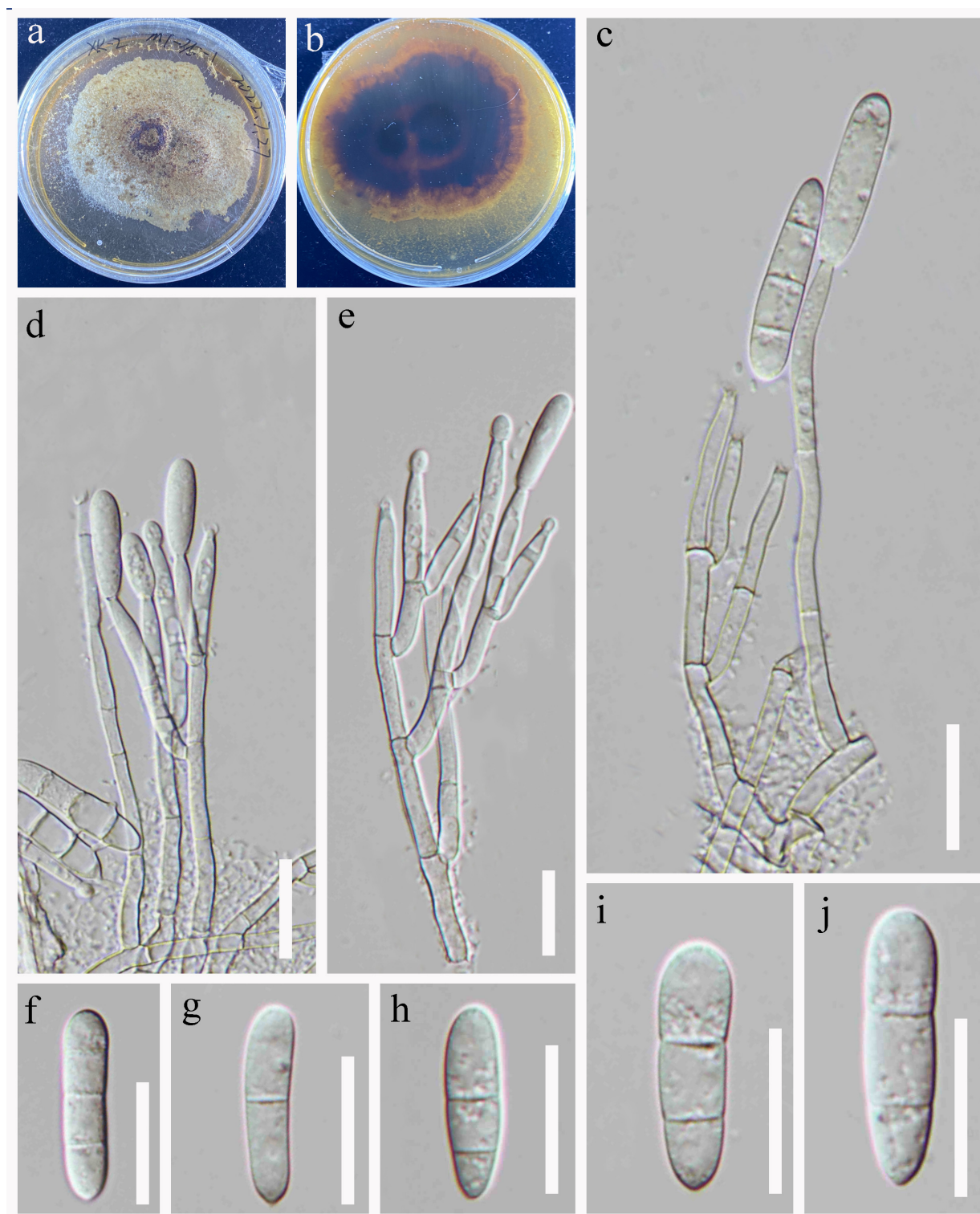


Fig. 74 *Ilyonectria llirodendri* (HKAS 136098) a, b Culture on PDA medium, a from above, b from below. c–e Conidiophores and conidiogenous cells with developmental conidia. f–j Conidia. Scale bars: c–j = 20 μm.

Saprobic on submerged decaying wood. **Sexual morph:** Undetermined. **Asexual morph:** Colonies on the substratum superficial, effuse, white, hairy. **Mycelium** immersed, subhyaline to pale brown, composed of branched, septate hyphae. **Conidiophores** 202–636 × 6–10 μm ($\bar{x}$ = 481 × 8 μm, n = 15), macronematous, mononematous, cylindrical, erect, straight or slightly flexuous, septate, smooth-walled, hyaline when young, becoming orange brown at base and gradually

paler towards apex, hyaline at the apex. **Conidiogenous cells** phialides, flask-like, hyaline, slightly swollen at base, tapering at apex, smooth-walled. **Conidia** 5–6 × 2–3 μm ($\bar{x}$ = 5 × 3 μm, n = 10), ellipsoidal to fusiform, acuminate at apex, pointed at base, aseptate, hyaline.

Culture characteristics: Conidia germinating on PDA medium within 24 h and germ tubes produced from both ends. Colonies grown on PDA reached 30 mm diam at room

temperature in two weeks, circular, with velvety, flat, light brown mycelium in the middle and sparse, dark brown at the edge, producing reddish-brown pigment, from below dark brown with entire margin.

Material examined: CHINA, Yunnan Province, Shangri-La City, Gonda Village, 27°58'24.94" N, 99°46'39.32" E, 3222 m a.s.l., on decaying wood submerged in a freshwater stream, 19 June 2022, R.J. Xu, LTS-10 (HKAS 136147), culture (KUNCC 24-17993).

Notes: *Mariannaea elegans* was originally described by (Samson 1974), based on samples collected from the bark of rotten trunks of fir trees (*Pinaceae*) in Brezina. Based on strain (CBS 217.73A). Hu et al. (2017) confirmed that the resulting

colony generally matches the description of *M. elegans*, thereby designating it as the epitype. *Mariannaea elegans* is saprobic and lignicolous, occurring on submerged decaying woody debris in terrestrial environments. It has been reported from the Brezina, Czechoslovakia, Europe and, Netherlands (Hu et al. 2017).

In the phylogenetic analyses (Fig. 75), our collection (KUNCC 24-17993) clustered with *Mariannaea elegans* (Ducc 400). Morphologically, these new isolates closely resemble *M. elegans* Hu et al. (2017), therefore, we have identified our new isolates as *M. elegans*. This represents the first report of *M. elegans* from a freshwater habitat on the Yunnan Province, China.

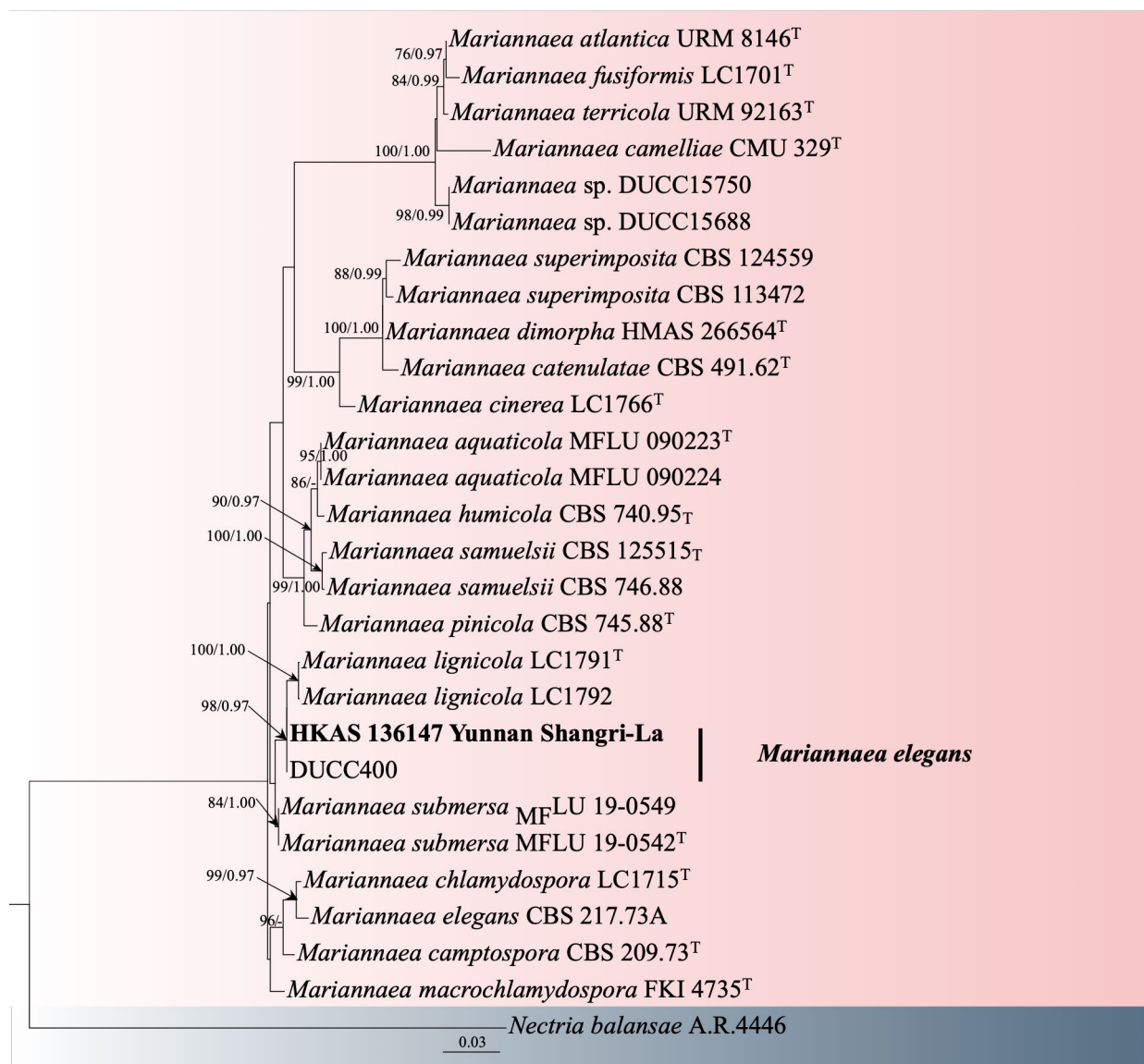


Fig. 75 Maximum likelihood majority rule consensus tree for *Mariannaea* using ITS and LSU sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Nectria balansae* (A.R. 4446). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

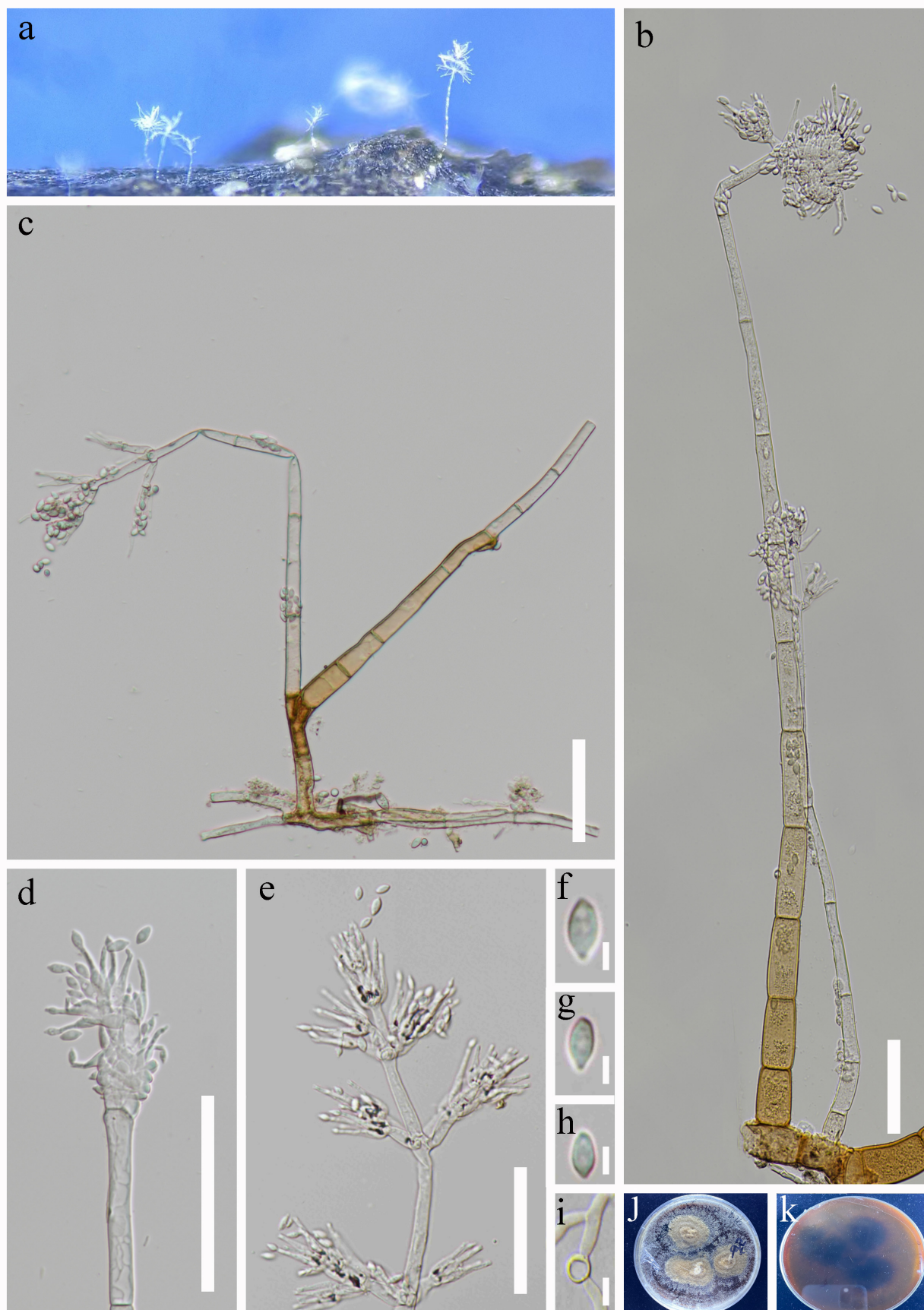


Fig. 76 *Mariannaea elegans* (HKAS 136147) a Colony on natural substrates. b, c Conidiophores with conidia. d, e Conidiogenous cell with conidia. f–h Conidia. i Germinated conidium. j, k Culture on PDA medium j from above, k from below. Scale bars: b–e = 50 µm, f–i = 2 µm.

Ophiocordycipitaceae G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora

Ophiocordycipitaceae separated from *Clavicipitaceae* to include nine genera based on morphological and phylogenetic analyses (Sung et al. 2007; Quandt et al. 2014; Simmons et al. 2015). Asexual morphs display varied synnemata, conidiophores, and conidia, while sexual morphs feature dark or bright, tough stromata or subicula with cylindrical, unitunicate asci and multi-septate, often disarticulating ascospores (Mains 1950; Samson & Evans 1975; Sung et al. 2007; Simmons et al. 2015; Maharachchikumbura et al. 2016, 2021). Currently, this family contains over 500 distinct species. However, more than 30 species were introduced within two years, indicating that the taxonomic diversity of this family has not been sufficiently investigated (Tang et al. 2023; Mongkolsamrit et al. 2024; Yang et al. 2024)

Ophiocordyceps Petch, Trans. Br

Ophiocordyceps, established by Petch to classify *Cordyceps* species with non-disarticulating ascospores (Petch 1931). Later, it was designated as a subgenus based on spore morphology (Kobayasi 1941) and subsequently included in *Cordyceps sensu lato* (Mains 1958). The genus, known for infecting insects, sexual morphs is characterized by darkly pigmented, tough, fibrous stromata that may be stipitate or sessile, with perithecia that range from superficial to fully immersed and ascospores that either remain intact or disarticulate into secondary spores (Sung et al. 2007; Simmons et al. 2015). Asexual morphs associated with *Ophiocordyceps* include *Hirsutella*, *Syngliocladium*, *Stilbella*, *Paraisaria*, *Hymenostilbe* and *Sorosporella* (Evans & Samson 1982; Araújo & Hughes 2016; Xiao et al. 2019; Yang et al. 2021).

46. Ophiocordyceps fusispora Y.B. Wang, H.F. Liao & Zhu L. Yang, *sp. nov.* Fig. 78

Chinese name: – 梭孢线虫草 (suo bao xian chong cao)

Index Fungorum number: IF 905275; **Facesoffungi number:** FoF 19323

Etymology: The species is named for its fusiform secondary ascospores.

Diagnosis: Different from other *Ophiocordyceps* species by its fusiform secondary ascospores.

Holotype: HKAS 126122

Parasitic on ants buried in soil. **Sexual morph:** *Stromata* arising from the heads of hymenopteran ants, 25–58 × 1.2–1.9 mm ($\bar{x}$ = 41 × 1.5 mm, n = 10), solitary, pale yellow to yellow. *Fertile parts* 1.6–2.5 × 1.8–2.8 mm ($\bar{x}$ = 2.1 × 2.3 mm, n = 10), nearly spherical, terminal, spinous surface due to protruding ostioles, distinctly demarcated from the stipe, colored yellow to orange-yellow. *Perithecia* 566.8–825.6 × 85.3–118.6 μ m ($\bar{x}$ = 692 × 102 μ m, n = 20), longitudinal, immersed, lageniform, and parallel to the stipe. *Asci* 189.6–394.7 × 5.8–9.6 μ m ($\bar{x}$ = 292.2 × 7.8 μ m, n = 20), hyaline, cylindrical, 8-spores. *Ascospores* disintegrated into secondary ascospores, 8.6–11.4 × 1.8–3.2 μ m ($\bar{x}$ = 10.0 × 2.5 μ m, n = 20), hyaline, fusiform.

Asexual morph: Undetermined.

Culture characteristics: Undetermined

Material examined: CHINA, Yunnan, Nujiang Prefecture, Lanping County, Fuhe Village, on ants buried in soil, 8 August 2022, H.F. Liao (HKAS 126122, holotype), *ibid.* (HKAS 126123).

Notes: Phylogenetic analysis based on five genes indicates that *Ophiocordyceps fusispora* is most closely

related to *O. formicarum* (Fig. 77). These two species share similar morphological characteristics and are both parasitic on hymenopteran ants, with their perithecia being immersed (Yahagi et al. 2004). The differences are reflected in the arrangement of the perithecia, *O. fusispora* has longitudinal perithecia, whereas *O. formicarum* has obliquely immersed perithecia. Furthermore, the perithecia (566.8–825.6 × 85.3–118.6 μ m), asci (189.6–394.7 × 5.8–9.6 μ m), and secondary ascospores (8.6–11.4 × 1.8–3.2 μ m) of *O. fusispora* are comparatively larger than those of *O. formicarum*, which measures perithecia (300–500 × 100–150 μ m), asci (100–160 × 3–5 μ m), and secondary ascospores (6–9 × 1–2 μ m) (Yahagi et al. 2004).

47. Ophiocordyceps hutiaoxiaensis Y.B. Wang, H.F. Liao & Zhu L. Yang, *sp. nov.* Fig. 79

Chinese name: – 虎跳峡线虫草 (hu tiao xia xian chong cao)

Index Fungorum number: IF905276; **Facesoffungi number:** FoF 19324

Etymology: The species is named after the Hutiaoxia Town in Shangri-La City, where the type specimen was collected.

Diagnosis: Different from related *Ophiocordyceps* species by its smaller perithecia, more narrower and slender asci

Holotype: HKAS 126128

Parasitic on adult stink bugs buried in fallen leaves.

Asexual morph: Undetermined. **Sexual morph:** *Stromata* arising from the thoracic sides of the adults of Pentatomidae, 80–138 × 0.8–1.6 mm ($\bar{x}$ = 105 × 1.2 mm, n = 5), woody, solitary, straight, black or dark brown, a red-orange stipe below the fertile part. *Fertile parts* 12–16 × 2.1–2.8 mm ($\bar{x}$ = 14 × 2.5 mm, n = 5), cylindrical, unbranched, longer than the stroma's end, yellow to orange. *Perithecia* obliquely immersed, narrowly obpyriform or lageniform, 360–480 × 160–220 μ m ($\bar{x}$ = 420 × 195 μ m, n = 20). *Asci* 420–780 × 1.8–3.8 μ m ($\bar{x}$ = 600 × 2.8 μ m, n = 20), hyaline, filiform. *Apical caps* hemispherical 3.5–5.1 × 4.9–6.6 μ m ($\bar{x}$ = 4.3 × 5.8 μ m, n = 10). *Ascospores* broke into secondary ascospores, hyaline, cylindrical, 10.2–12.8 × 0.7–1.2 μ m ($\bar{x}$ = 11.4 × 1.1 μ m, n = 20).

Culture characteristics: Undetermined.

Material examined: CHINA, Yunnan, Shangri-La City, Hutiaoxia Town, on adult stink bugs buried in fallen leaves, 16 July 2021, Y.B. Wang (holotype, HKAS 126128); *ibid.* (HKAS 126060).

Notes: Phylogenetic analysis based on five genes indicates that *Ophiocordyceps hutiaoxiaensis* is closely related to *O. tessaratomidarum* and *O. asiana* (Fig. 77), yet it forms a distinct new evolutionary clade (Khao-ngam et al. 2021). These species exhibit morphological similarities, parasitize on insects of *stink bugs* (Hemiptera) produce orange-colored stromata, possess obliquely immersed perithecia, and their ascospores undergo fragmentation into secondary ascospores (Khao-ngam et al. 2021). However, the perithecia of *O. hutiaoxiaensis* (360–480 × 160–220 μ m) are smaller compared to those of *O. asiana* ((750–)896–1124(–1200) × (200 –)214–298(–300) μ m), and its asci are slender than *O. asiana* (420–780 × 1.8–3.8 μ m). The asci of *O. tessaratomidarum* (240–790 × 5–6 μ m) are wider than those of *O. hutiaoxiaensis* (420–780 × 1.8–3.8 μ m) (Khao-ngam et al. 2021).

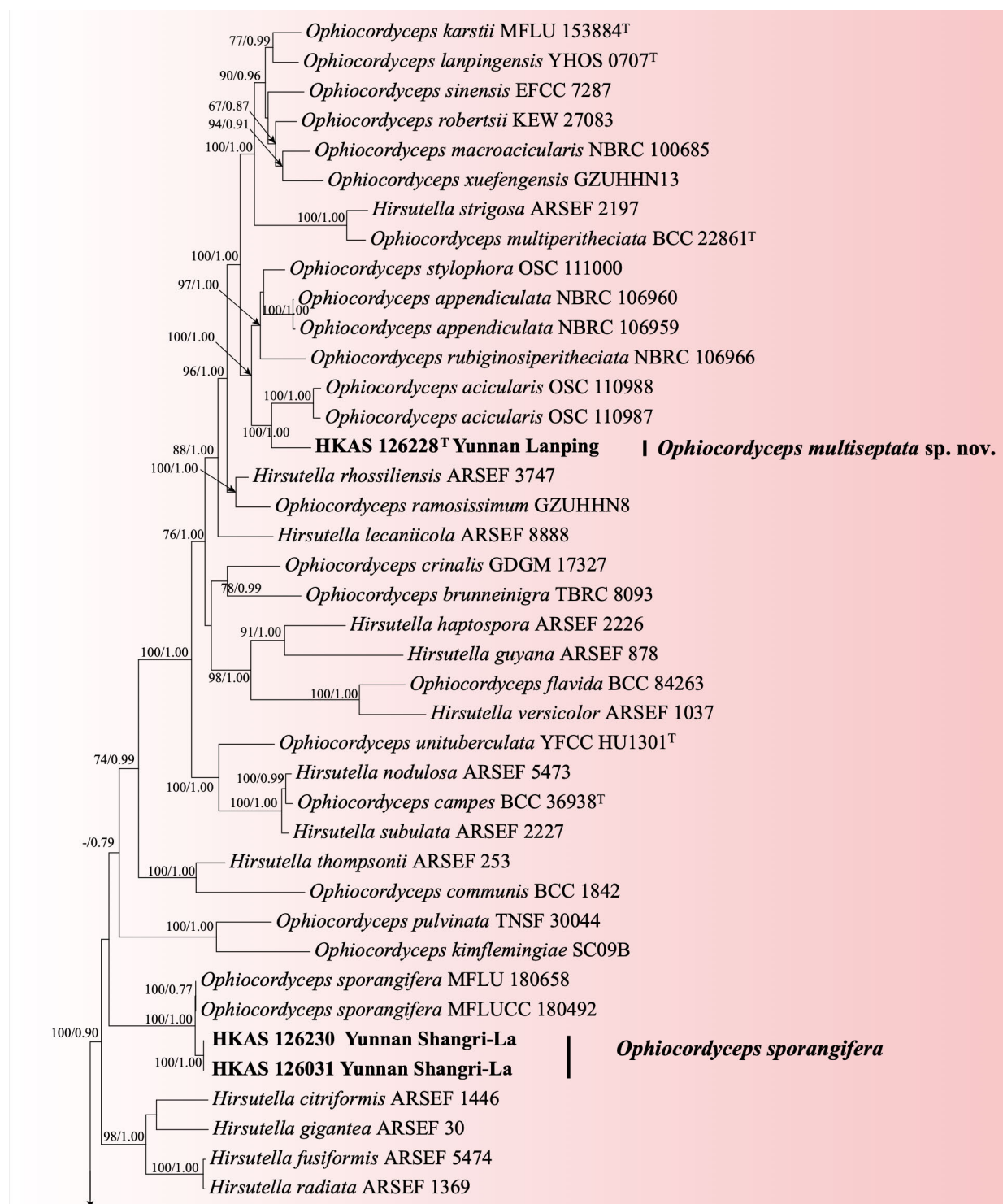


Fig. 77 Phylogenetic tree based on the combined dataset of SSU, LSU, *tef1-α*, *rpb1* and *rpb2*, showing the phylogenetic relationships of the species identified in this study from Q-X Plateau and other *Ophiocordyceps* species. Values at the nodes before and after the backslash are BI posterior probabilities (BI-PP greater than 0.70) and ML bootstrap proportions (ML-BP greater than 70%), respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

48. *Ophiocordyceps multiseptata* Y.B. Wang, H.F. Liao & Zhu L. Yang, sp. nov. Fig. 80

Chinese name: – 多隔线虫草 (duo ge xian chong cao)

Index Fungorum number: IF905277; **Facesoffungi number:** FoF 19325

Etymology: The species is named after the ascospore with multiple septa.

Diagnosis: Different from related *Ophiocordyceps* species by its slender stromata and ascospores with multiple septa.

Holotype: HKAS 126228

Parasitic on larvae of *Buprestidae* buried in soil. **Sexual morph:** Stromata arising bilaterally from the head of larva of *Buprestidae*, 63 mm in length and 0.7 mm in width, woody

and rigid, solitary, with the lower half black and the upper half brown. *Fertile heads* 12 mm in length and 0.6 mm in width. *Perithecia* 490–560 × 380–440 µm ($\bar{x}$ = 525 × 412 µm, n = 20), are vertical, initially yellowish-brown and mature to dark brown. *Asci* 210–280 × 12–16 µm ($\bar{x}$ = 253 × 15 µm, n = 20), hyaline, cylindrical, 8-spores, with an incomplete apical cap. *Ascospores* 168–220 × 3.1–3.7 µm ($\bar{x}$ = 188 × 3.2 µm, n = 20), hyaline, multiseptate, non-disarticulating, septate cells 4.2–7.6 µm ($\bar{x}$ = 5.1 µm, n = 20). **Asexual morph:** Undetermined.

Culture characteristics: Undetermined.

Material examined: CHINA, Yunnan, Nujiang Prefecture, Lanping County, Jinding Town, on a larva of *Buprestidae* buried in soil, 9 August 2022, H.F. Liao (holotype, HKAS 126228).

Notes: Phylogenetic analysis based on five-gene data reveals *Ophiocordyceps multiseptata* is closely related to *O.*

acicularis (Fig. 77), as both species exhibit identical morphological characteristics, and are parasitic on larvae of *Buprestidae* (Coleoptera) (Petch 1933). *Ophiocordyceps acicularis* was introduced by Petch in 1933 and was later redescribed in the "Field Guide to the Natural World of *Cordyceps*" by the Japanese *Cordyceps* Society (Petch 1933, Japanese *Cordyceps* Society 2018). The difference between *O. multiseptata* and *O. acicularis* is that the stromata of *O. multiseptata* (63 mm long, 0.7 mm wide) are slenderer than those of *O. acicularis* (3–10 cm long, 1–1.5 mm wide). Additionally, the perithecia of *O. multiseptata* are immersed and predominantly clustered at the upper portion of the stroma, exhibiting a clear demarcation from the stipe, and are significantly wider (490–560 × 380–440 µm) (Japanese *Cordyceps* Society 2018).

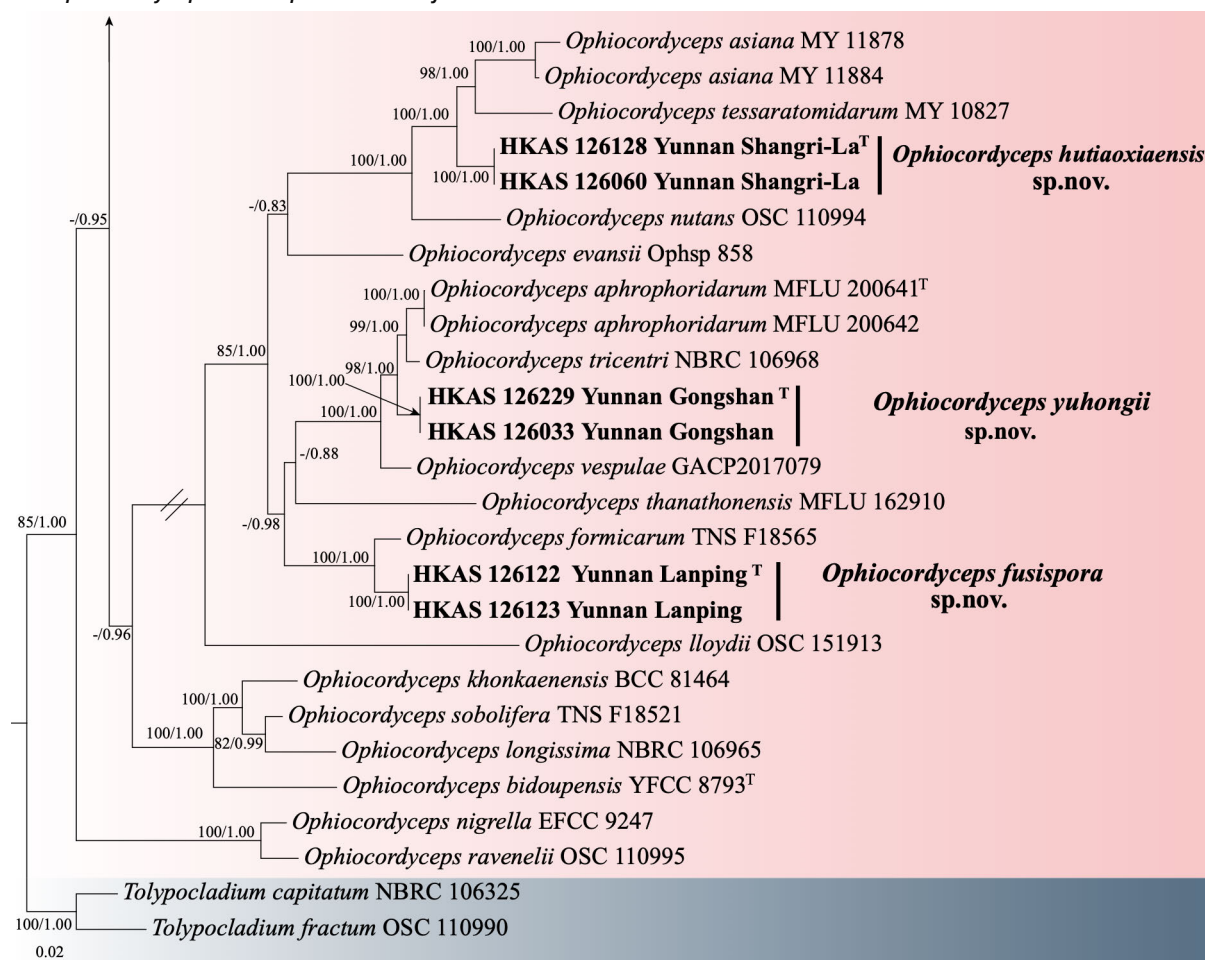


Fig. 77 (continued)

49. *Ophiocordyceps polyphialidica* Y.P. Xiao, K.D. Hyde & Y. Yang, *sp. nov.* Fig. 81

Chinese name: – 多瓶梗线虫草 (duo ping geng xian chong cao)

Index Fungorum number: IF 903157; **Facesoffungi number:** FoF 17062

Etymology: in reference to polyphialidic of conidiogenous cells.

Holotype: HKAS 144591

Parasitism on Larvae of *Lepidoptera*, buried in the leaf litter. **Sexual morph:** Undetermined. **Asexual morph:**

Hirsutella-like. *Synnemata* 1.5–3.5 cm long, 0.3–0.8 mm wide, white to pale gray, solitary or multiple, on the insect body, without fertile head. *Phialide* solitary along synnemata, monophialidic or polyphialidic, 8.3–14.5 × 1.3–4.5 µm ($\bar{x}$ = 11.4 × 2.9 µm, n = 50), mostly with pyriform inflated basal portion 4.5–8.8 × 2.3–4.5 µm ($\bar{x}$ = 6.6 × 3.4 µm, n = 50), tapering gradually or abruptly into a thin neck 3.5–6.8 µm long. *Conidia* 4.4–6.2 × 1.4–2.3 µm ($\bar{x}$ = 5.3 × 1.8 µm, n = 60), fusiform, 1-celled, hyaline, smooth-walled.

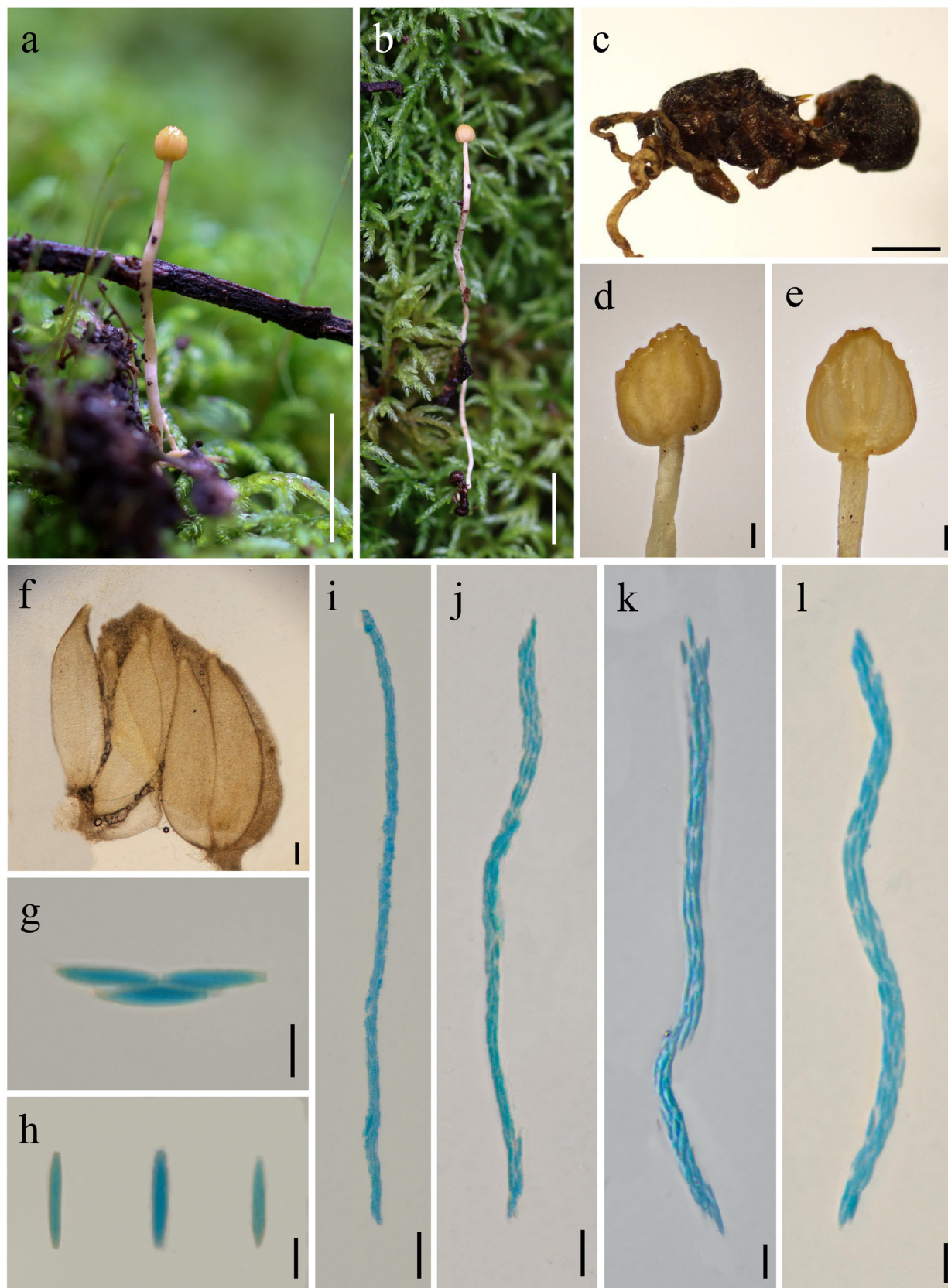


Fig. 78 *Ophlocordyceps fusispora* (HKAS 126122, **holotype**) a, b Stromata arising from host. c Host. d Fertile head. e Vertical section of fertile head. f Section of perithecia. g, h Secondary ascospores. i-l Asci. Scale bars: a, b = 1 cm, c = 1 mm, d, e = 200 μm, f = 100 μm, g, h = 5 μm, i-l = 10 μm.

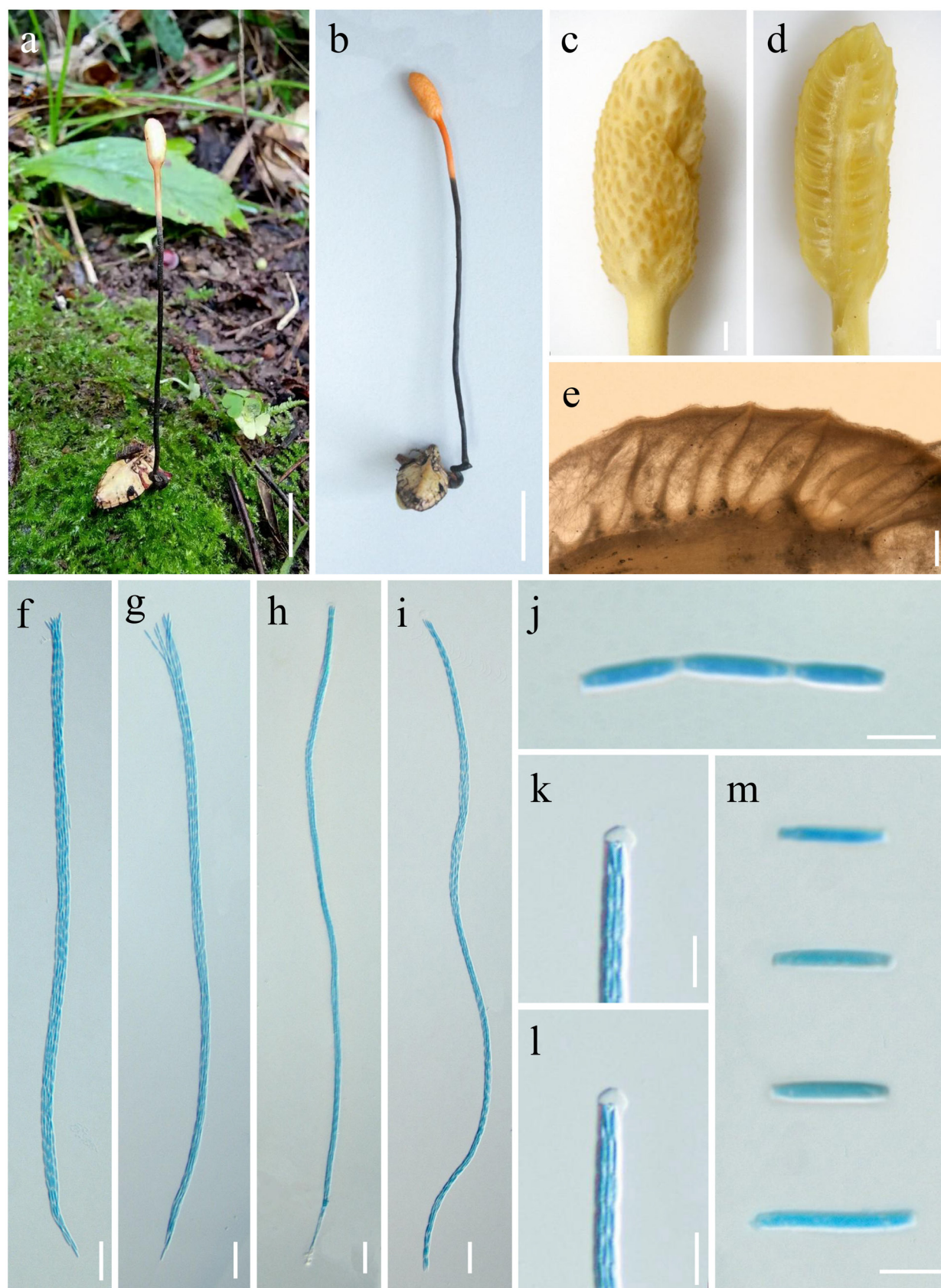


Fig. 79 *Ophiocordyceps hutiaoxiaensis* (HKAS 126128, **holotype**) a, b Stromata arising from host. c Fertile head. d Vertical section of fertile head. e Section of perithecia. f–i Asci. j Ascospores. k, l Apical caps. m Secondary ascospores. Scale bars: a, b = 1 cm, c, d = 300 μ m, e = 200 μ m, f–i = 20 μ m, j = 5 μ m, k, l = 10 μ m, m = 5 μ m.

Material examined: CHINA, Xizang Autonomous Region, Linzhi, Bomi County, parasitism on Larvae of Lepidoptera, 31 August 2024, Xingjuan Xiao 242605 (HKAS 144591, holotype), 242607 (HKAS 144589, paratype).

Notes: *Ophiocordyceps polyphialidica* was phylogenetically retrieved as a sister species of *O. unituberculata* with strong statistical support (100% ML/1.00 BYPP) (Fig. 82). Base pair differences of ITS, *tef1-α*, *rpb1* and *rpb2* genes loci of *O. unituberculata* are 3.09% (15/485), 6.12% (42/686), 3.05%

(20/655) and 3.16% (29/916) respectively. Morphologically, *O. unituberculata* produces monophialidic, longer phialide (31.9–128.3 × 1.2–5 μm vs. 8.3–14.5 × 1.3–4.5 μm), bigger conidia (6.3–10.6 × 1.9–3.7 vs. 4.4–6.2 × 1.4–2.3 μm), compared to *O. polyphialidica* (Wang et al. 2018). Both morphological observation and phylogenetic analyses of combined ITS, SSU, *tef1-α*, *rpb1* and *rpb2* sequence data support that this fungus is a distinctive species in *Ophiocordyceps*.

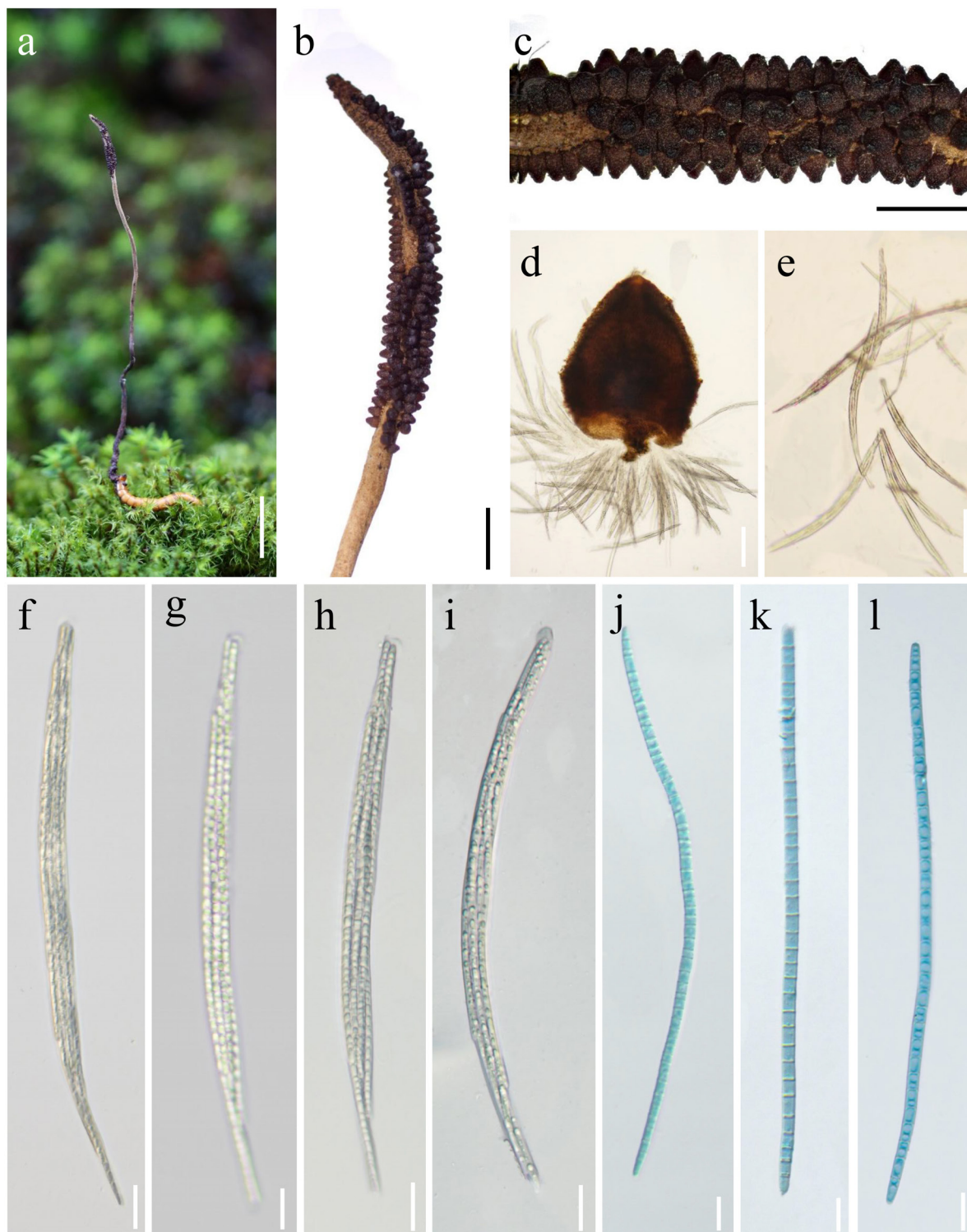


Fig. 80 *Ophiocordyceps multiseptata* (HKAS 126228, holotype) a Stroma arising from host. b, c Fertile head. d Perithecia. e–i Asci. j–l Ascospores. Scale bars: a = 1 cm, b = 0.2 cm, c = 1000 μm, d = 100 μm, e = 100 μm, f–i = 20 μm, j–l = 10 μm.

50. *Ophiocordyceps sporangifera* Y.P. Xiao, T.C. Wen & K.D. Hyde, in Xiao, Hongsanan, Hyde, Brooks, Xie, Long & Wen, MycoKeys 47: 63 (2019) **Fig. 83**

Chinese name: – 孢囊线虫草 (bao nan xian chong cao)

Index Fungorum number: IF 555324; **Facesoffungi number:** FoF 04865

Sexual morph: Unknown. **Asexual morph:** *Primary synnemata* arise from the head region of bugs (*Cydnidae*, *Hemiptera*), paired to multiple, simple, cylindrical, Flexuous, not smooth, brown to deep brown, with a white fertile head at the apex, 80–120 × 0.9–1.2 mm ($\bar{x}$ = 100 × 1.1 mm, n = 10). *Fertile heads* cylindrical, 0.5–1.8 × 0.3–0.9 mm ($\bar{x}$ = 1.1 × 0.7 mm, n = 10), white to brown, with sporangia on their surfaces. No other morphological features were observed.

Culture characteristics. Colony growth on PDA medium is slow; after 5 weeks of incubation at a constant temperature

of 25°C, the diameter reaches 2 cm, with a raised white center and felty margins. The surface features circular, dense mycelia. After 7 weeks, the colony color deepens gradually from the periphery towards the center, shifting from white to brown, with circular rings. By the 9th week, vesicular structures are produced. The mycelium is septate and smooth. *Phialides* 52–96 × 2–6.3 µm ($\bar{x}$ = 74 × 4.2 µm, n = 20), enlarged base, ampulla, gradually tapering towards an attenuated apex, displaying slight verrucose protrusions. Most are solitary, with a few dichotomous branching. *Conidia* 6.1–9.4 × 2.3–4.8 µm ($\bar{x}$ = 7.8 × 3.6 µm, n = 20) 1 cell, hyaline, ovoid, bound in mucilaginous spheres. *Mucilaginous spheres* 7.6–11.2 × 4.2–7.3 µm ($\bar{x}$ = 9.5 × 6.1 µm, n = 20), hyaline to brown, 1–3 conidia, lemon-shaped or semispherical.

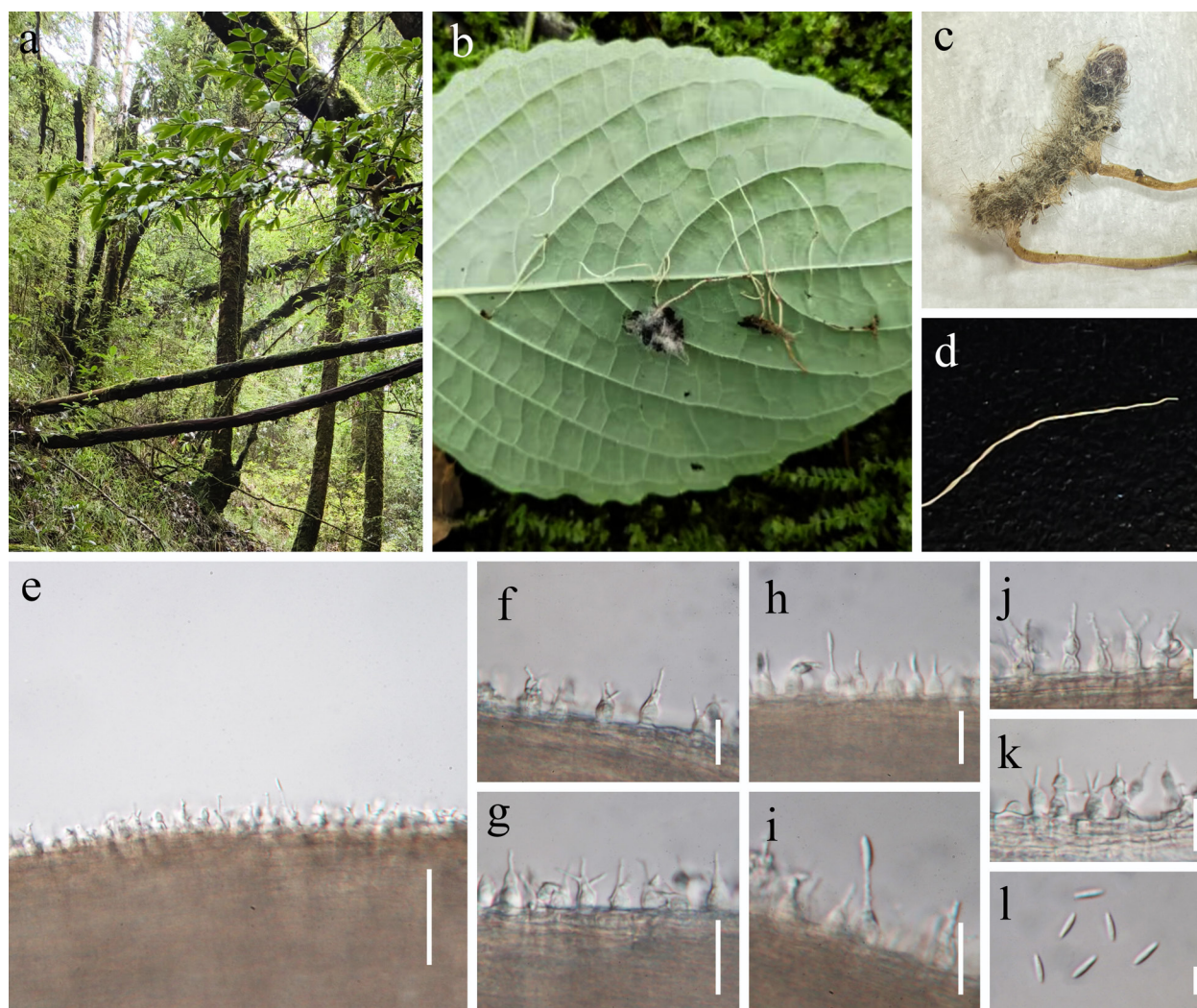


Fig. 81 *Ophiocordyceps polyphialidica* (HKAS 144591, holotype) a Habitat. b Overview of the host and synnemata. c Host. d Synnemata. e–k Phialides and conidia. l Conidia. Scale bars: e = 30 µm, f–k = 10 µm, l = 5 µm.

Material examined: CHINA, Yunnan, Shangri-La City, Hutiaoxia Town; collected from the surface layer of leaf litter in a broad-leaved forest, 8 August 2023, Y.B. Wang & H.F. Liao, (HKAS 126230, KUNCC 10936); *ibid.* (HKAS 126031).

Notes: *Ophiocordyceps sporangifera* was discovered as a new species by Xiao et al. (2019) in Thailand. Multigene phylogenetic analysis demonstrates that this species, along

with *O. sporangifera* Y.P. Xiao, T.C. Wen & K.D. Hyde (Fig. 77), is closely related within the same clade on the *Hirsutella* subclade (Xiao et al. 2019). They exhibit a very close phylogenetic relationship. Morphologically, both species are remarkably similar in the size and shape of their primary synnemata and fertile heads. In culture characteristics, the growth characteristics on PDA medium are nearly identical,

with phialides and mucilaginous spheres that are similar in size, shape, and color. Therefore, they should be considered the same species. However, they differ in their host species; the hosts for the specimens collected in this study are adults of *Cydnidae*, *Hemiptera*, whereas the hosts for *O.*

sporangifera are larvae of *Elateridae* (Coleoptera). Furthermore, this species was discovered in China for the first time, indicating an expansion in both its host range and geographical distribution (Xiao et al. 2019).

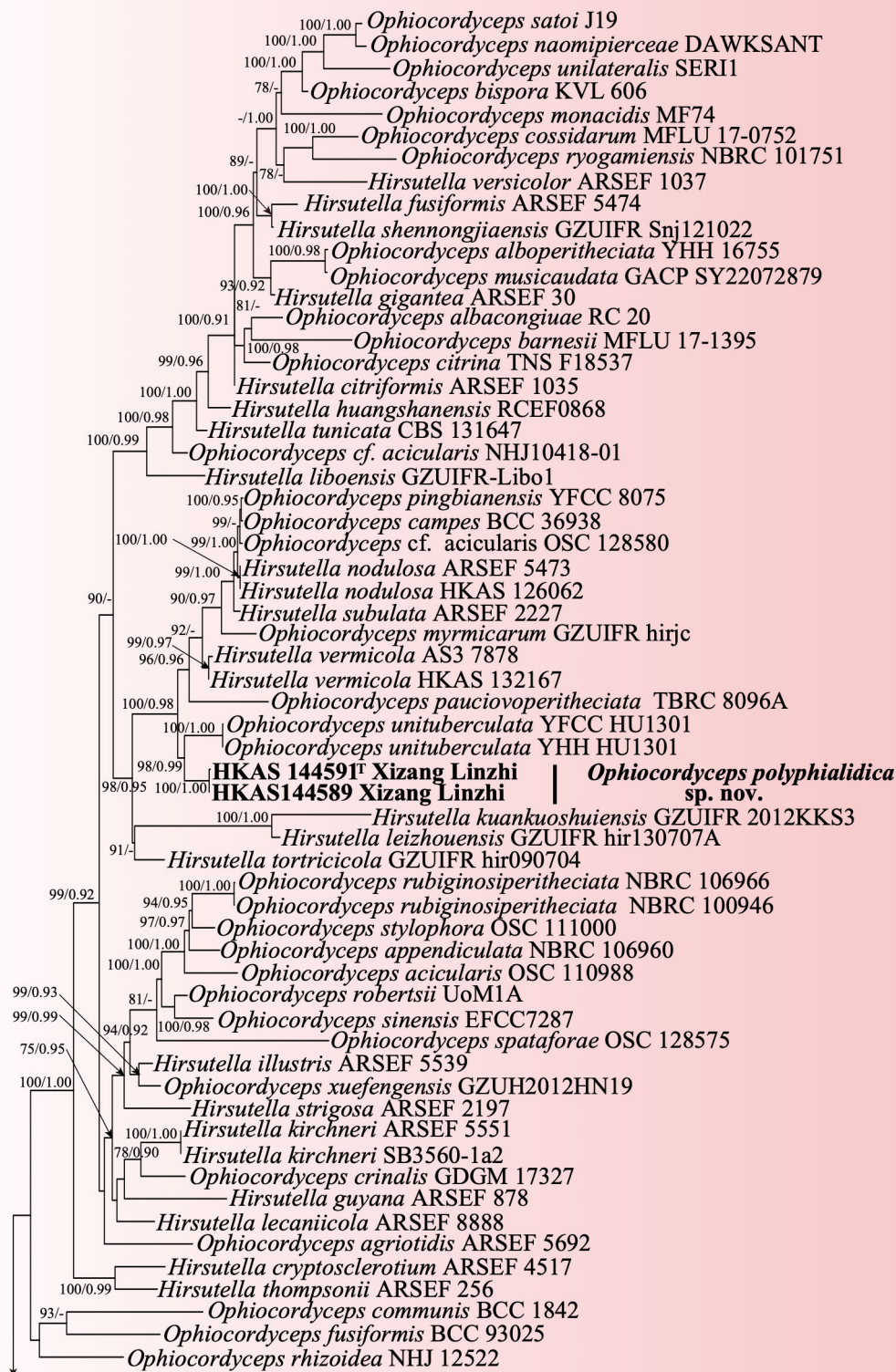


Fig. 82 Maximum likelihood consensus tree inferred from the combined ITS, SSU, *tef1* - α , *rpb1* and *rpb2* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 75% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.90 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Paraisaria coenomyia* NBRC 108993 and *Par. pseudoheteropoda* OSC-M-052009. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

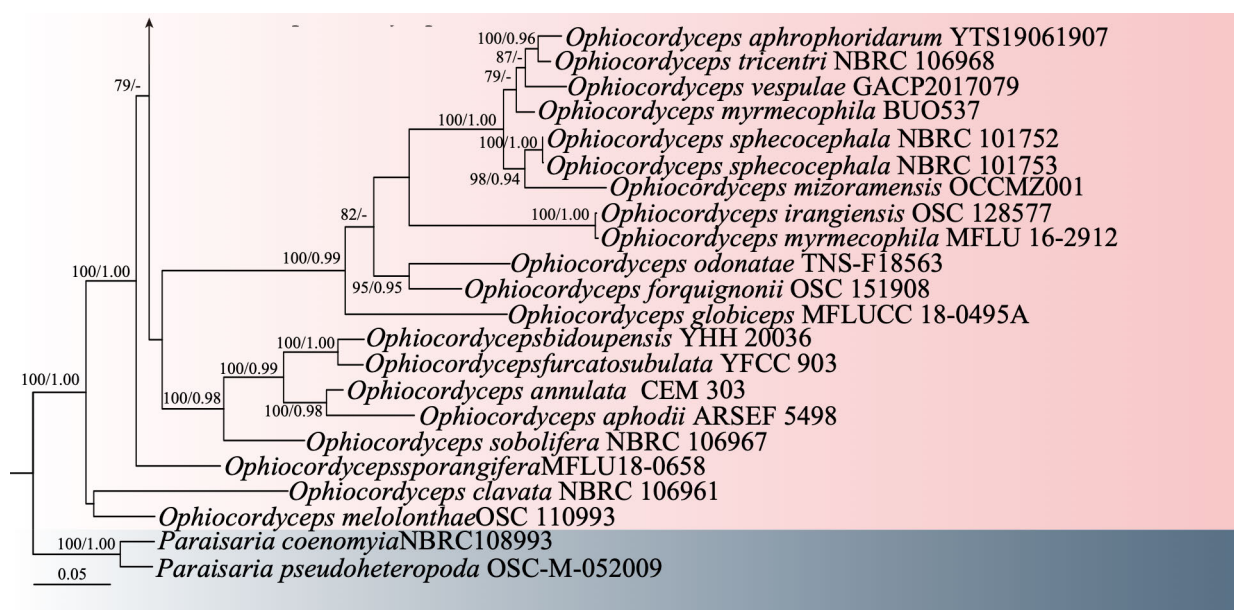


Fig. 82 (continued)

51. *Ophiocordyceps yuhongii* Y.B. Wang & H.F. Liao, sp. nov. Fig. 84

Chinese name: – 虞泓线虫草 (yu hong xian chong cao)

Index Fungorum number: IF 905278; **Facesoffungi number:** FoF 19326

Etymology: The species is named after Professor Yu Hong, acknowledging his contributions to the research on cordycipitoid fungi.

Diagnosis: Different from related *Ophiocordyceps* species by its shorter stromata and larger perithecia, occurring from the head of insect hosts.

Holotype: HKAS 126229

Parasitic on adult of *Aphrophoridae* cling to the surface of leaf litter. **Sexual morph:** Stromata 25–50 × 0.4–0.6 mm ($\bar{x}$ = 32 × 0.5 mm, n = 5), arising from the heads of adult frog hopper insects (Hemiptera), solitary, simple, yellow to orange-yellow. **Fertile heads** 3.4–4.2 × 1.8–2.2 mm ($\bar{x}$ = 3.8 × 2.0 mm, n = 5), ovoid, surface spinous due to the protruding ostioles, orange-yellow. **Perithecia** 765–910 × 210–290 μm ($\bar{x}$ = 837 × 250 μm, n = 20), immersed, inclined aggregated, ostioles opening on the upper surface of the head, flask-shaped to elongated obpyriform. Asci 450–698 × 6.1–7.7 μm ($\bar{x}$ = 574 × 6.9 μm, n = 20), hyaline, filiform, thickened apices, with the apical cap disappearing upon maturation. **Apical caps** 6.1–6.8 × 5.2–5.5 μm ($\bar{x}$ = 6.5 × 5.3 μm, n = 20), hyaline, conspicuous, hemispherical. **Ascospores** 280–610 × 0.9–1.8 μm ($\bar{x}$ = 498 × 1.4 μm, n = 20), filiform, multiseptate, which upon maturation, breaking into secondary ascospores. **Secondary ascospores** 11.1–13.1 × 1.9–2.4 μm, ($\bar{x}$ = 12.5 × 2.1 μm, n = 20) hyaline, lanceolate. **Asexual morph:** Undetermined.

Culture characteristics: Undetermined

Material examined: CHINA, Yunnan Province, Nuijiang, Gongshan County, Dulongjiang Township, on adult of *Aphrophoridae* cling to the surface of leaf litter, 24 July 2023, H.F. Liao (HKAS 126229, holotype); *ibid.* (HKAS 126033).

Notes: Phylogenetic analysis based on the five-gene data indicates that *O. yuhongii* is closely related to *O. aphrophoridarum* and *O. tricornis* (Fig. 77), sharing similar

morphological characteristics (Shrestha & Sung 2005; Yang et al. 2021). The hosts for all three species are the adult frog hopper insects of Hemiptera. *Ophiocordyceps tricornis* was initially described in Japan as *Cor. tricornis* Yasuda (1922) and was subsequently redescribed by Shrestha and Sung (Shrestha & Sung 2005). *Ophiocordyceps yuhongii* differs from *O. aphrophoridarum* and *O. tricornis* by its thinner and shorter stromata (25–50 × 0.4–0.6 mm), as well as larger perithecia (765–910 × 210–290 μm), asci (450–698 × 6.1–7.7 μm), ascospores (280–610 × 0.9–1.8 μm), and secondary ascospores (11.1–13.1 × 1.9–2.4 μm). Additionally, while *O. aphrophoridarum* emerges from the thorax of its insect host, *O. yuhongii* occurs from the head of its insect host. This distinction highlights notable differences in morphological characteristics as well as host interactions across the genus (Yang 2021; Shrestha & Sung 2005). Therefore, both morphological and molecular phylogenetic analyses provide strong evidence to support *O. yuhongii* as a new species within the genus *Ophiocordyceps*.

Polycephalomycetaceae Y.P. Xiao, Y.B. Wang, T.C. Wen, H. Yu & K.D. Hyde

Polycephalomycetaceae was separated from *Ophiocordycipitaceae* by Xiao, based on morphological and phylogenetic analyses, to accommodate three genera: *Polycephalomyces*, *Perennicordyceps*, and *Pleurocordyceps*, comprising 30 species (Xiao et al. 2023, 2024; Liu et al. 2024c). Unlike *Ophiocordycipitaceae*, *Polycephalomycetaceae* parasitizes insects or fungi and has a thick peridium (Xiao et al. 2023). Species within this family have a cosmopolitan distribution, with most species found in tropical and subtropical regions (Xiao et al. 2023). The insect orders most commonly associated with this family include *Coleoptera*, *Formicidae*, *Hemiptera*, *Hymenoptera*, *Lepidoptera*, *Orthoptera*, *Pentatomidae*, and *Psocoptera* (Kobayasi 1939; Kobayasi & Shimizu 1982; Ban et al. 2009; Xiao et al. 2018).



Fig. 83 *Ophiocordyceps sporangifera* (HKAS 126230) a, b Synnemata on host. c Synnemata. d Host. e Colonies on PDA. f Reverse of colonies. g–j Phialides. k Conidia. Scale bars: a, b = 1 cm, c, d = 0.2 cm, e, f = 1 cm, g–k = 10 µm.

52. *Perennicordyceps woodihabitata* Y.B. Wang, B.Z. Chen, X.M. Wang & Zhu L. Yang, *sp. nov.*

Chinese name: – 木栖多年生虫草 (mu qi duo nian sheng chong cao)

Index Fungorum number: IF 905279; **Facesoffungi number:** FoF 19327

Etymology: Collected from rotten wood.

Diagnosis: *Perennicordyceps woodihabitata* differs from related species by having smaller perithecia, larger ascus caps and secondary ascospores, and larger ellipsoidal to subellipsoidal conidia.

Holotype: HKAS 135026

Parasitic on coleopteran larva inhabiting decayed wood.

Sexual morph: *Stromata* arising from the dorsal surface or both ends of coleopteran larvae, leathery, clavate. *Fertile parts* located at the apical region of the stroma, solitary, orange, 0.2–0.5 mm long, with irregular protuberances, pale

yellow to orange. White ostioles of perithecia present on the protruding areas. *Perithecia* superficial, ovoid, 180.54–241.45 µm long, 69.16–113.13 µm wide at the base, 75.88–169.59 µm at the middle, and 26.85–33.56 µm at the neck. *Asci* narrowly clavate, 35.68–47.12 × 8.5–16 µm. *Apical caps* hemispherical, 33–4.89 × 0.48–2.66 µm. *Secondary ascospores* hyaline, short-clavate, 140–310 × 1.7–2.41 µm. **Asexual morph:** *Hyphae* branched, hyaline, smooth-walled, 2.3–4.8 µm wide. *Conidiophores* cylindrical, 7.88–17.71 µm long, 1.43–23 µm wide at the base, 1.8–2.25 µm at the middle, and 1.79–2.86 µm at the neck. *Phialides* solitary or in whorls of 2–4 on hyphae, mostly lanceolate, occasionally narrowly flask-shaped, 18.26–21.5 µm long, 1.47–2.19 µm wide at the base, 1.81–2.41 µm at the middle, and 1.1–1.23 µm at the neck. *Conidia* hyaline, smooth-walled, aseptate, ellipsoidal to subellipsoidal, 2.44–3.88 × 0.72–1.69 µm.

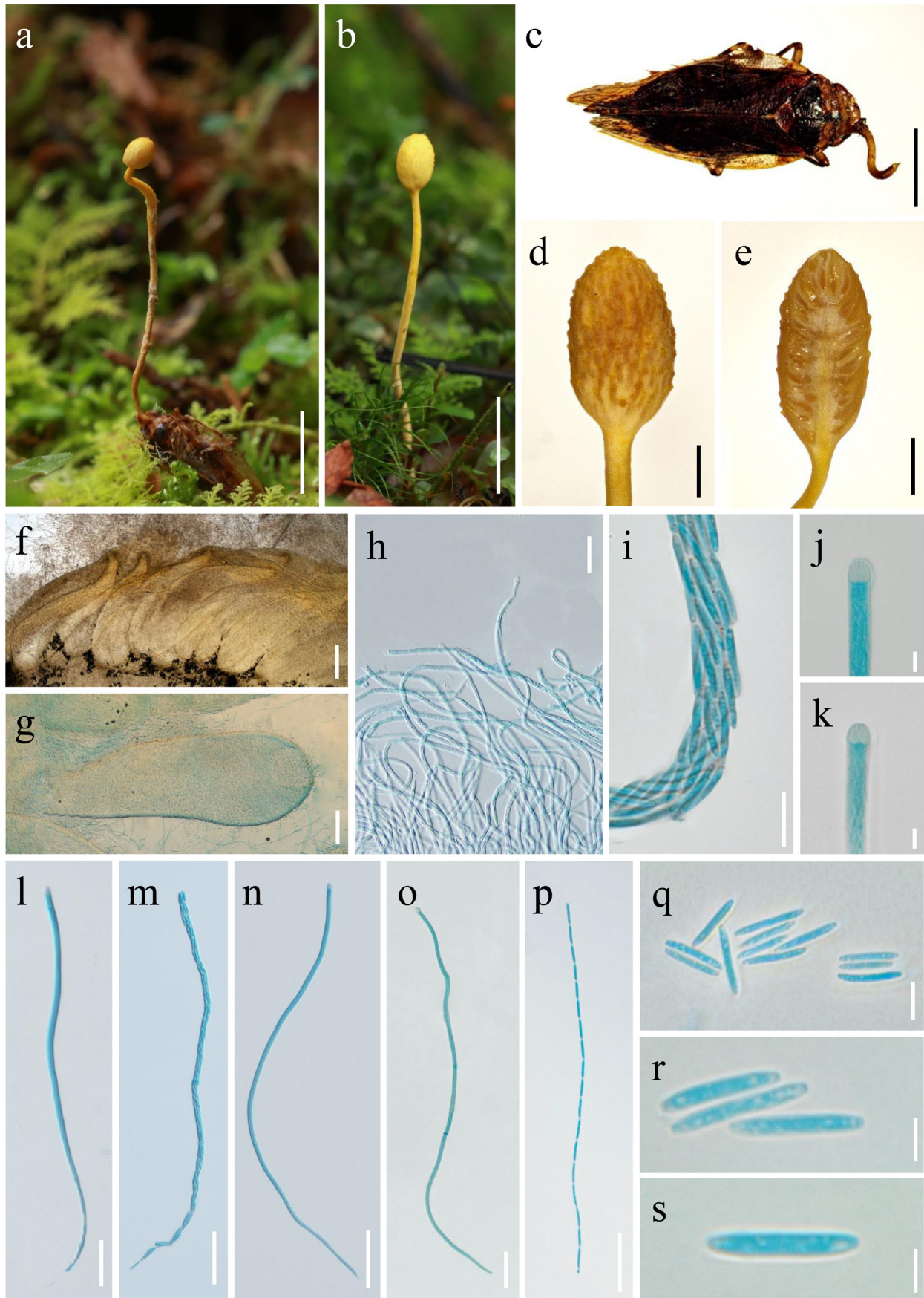


Fig. 84 *Ophlocordyceps yuhonglii* (HKAS 126229, **holotype**) a–c Stromata arising from Host, c Host. d Fertile head. e Vertical section of fertile head. f, g Perithecia. h Aggregated asci. i Asci. j, k Apical caps. l–o Asci. p Ascospore. q–s Secondary ascospores. Scale bars: a, b = 1 cm, c = 3 mm, d, e = 1 mm, f, g = 100 μ m, h = 40 μ m, i = 10 μ m, j, k = 10 μ m, l–o = 30 μ m, p = 10 μ m, q = 10 μ m, r–s = 5 μ m.

Culture characteristics: Colonies on PDA grew slowly, reaching only 2.8 cm in diameter after 21 days at 25°C. Reverse surface yellow-brown, surface floccose, spreading from the center to the margin, changing from pale yellow to white. No synnemata observed. After 40 days, dark yellowish-brown aggregated structures formed on the colony surface.

Material examined: CHINA, Yunnan Province, Tengchong City, on larva of *Coleoptera* inhabiting decayed wood, 26 May 2024, X.M. Wang (HKAS 135026, holotype, ex-type culture, KUNCC 11459), *ibid.*, X.M. Wang (culture KUNCC 11458).

Notes: *Perennicordyceps woodihabitata* is phylogenetically closely related to *P. paracuboidea* (Matočec et al. 2014), as strongly supported by multi-gene phylogenetic inference

(Fig. 85). However, it shows clear sequence divergence from *P. paracuboidea* (CBS 120.87), with 96.1% identity in ITS (26 bp differences), 99.9% in LSU (21 bp differences), 97.8% in *rpb2* (21 bp differences), 98.7% in *rpb1* (8 bp differences), and 98% in *tef1-α* (20 bp differences). Morphologically, *P. woodihabitata* differs from *P. paracuboidea* by having significantly smaller perithecia, but larger ascus caps and ascospores. Its secondary ascospores exhibit a more pronounced length-to-width ratio, and its conidia are larger. In the asexual morph, the phialides are borne in whorls of 2–4 in *P. woodihabitata*, and the conidia are slightly smaller than those of the other two related species.

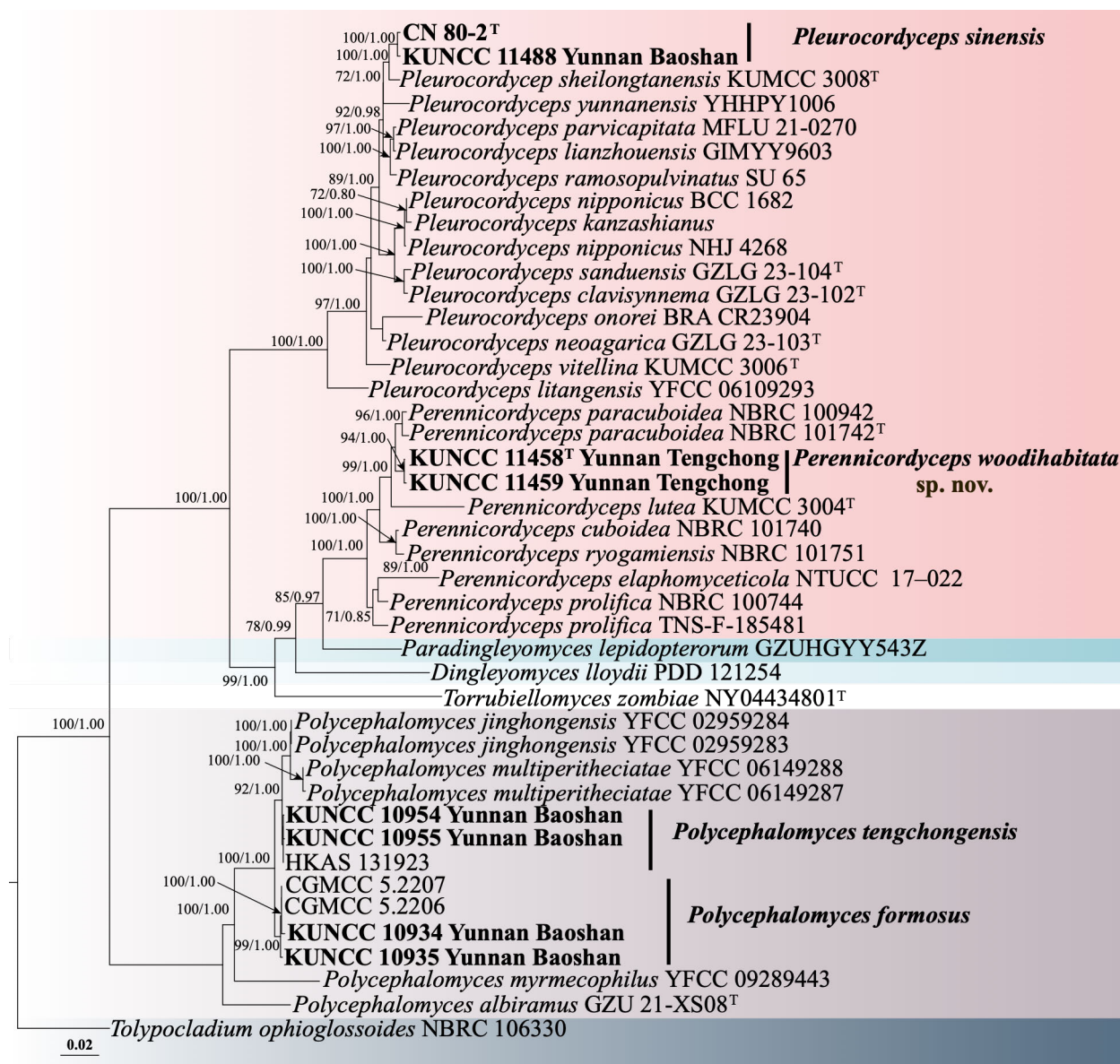


Fig. 85 Maximum likelihood consensus tree inferred from the combined ITS, LSU, SSU, *tef1-α* and *rpb2* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 75% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.90 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Tolypocladium ophioglossoides* NBRC 106330. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

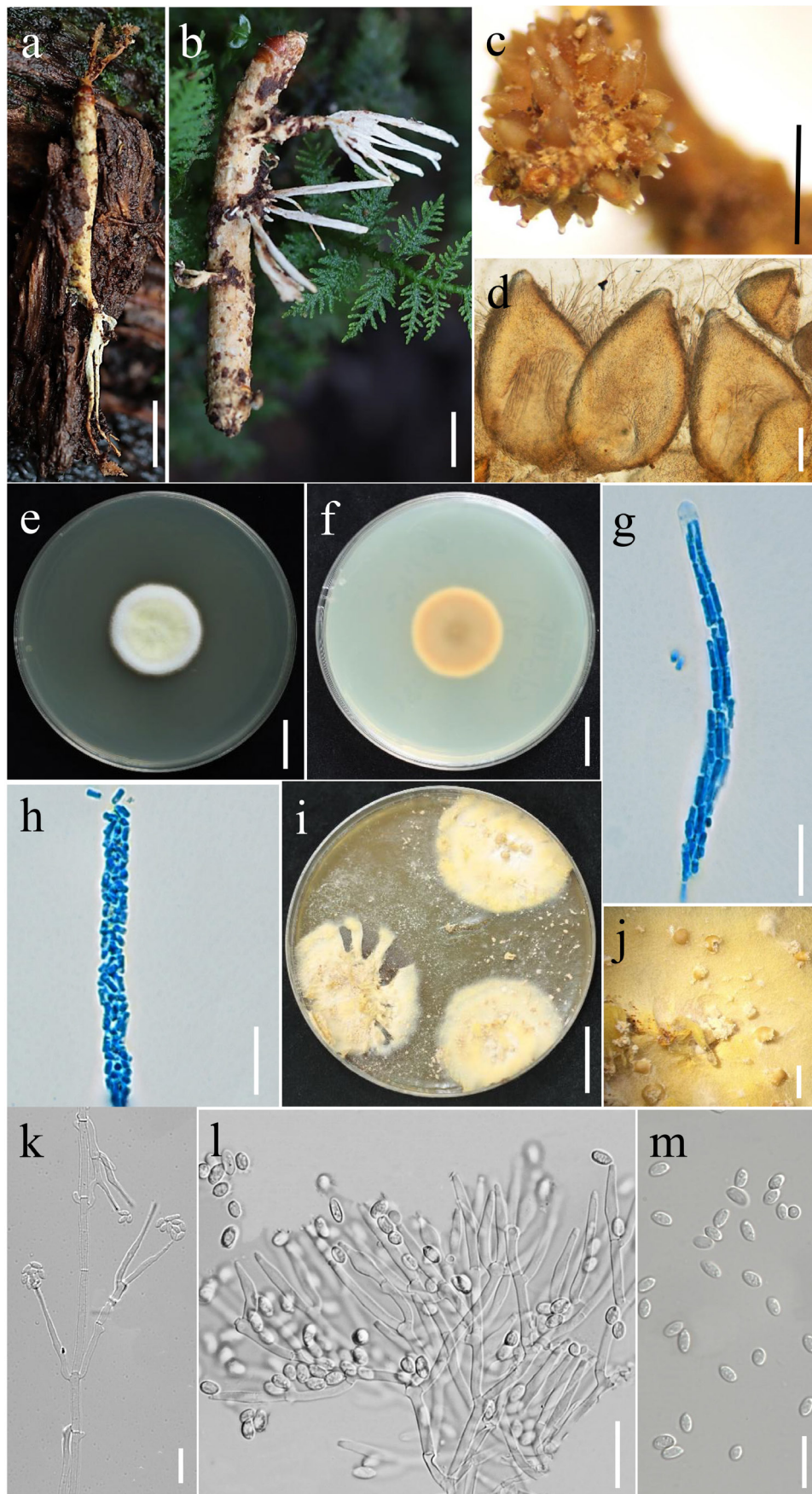


Fig. 86 *Perennicordyceps woodihabitata* (HKAS 135026, **holotype**) a, b Fungus on larvae of *Coleoptera*. c Intact fertile head. d Perithecia. e, f Colonies on PDA front and back. g, h Ascus and secondary ascospores. i, j Mucous mass growing on the colonies. k–m = Phialides and conidia. Scale bars: a, b = 1 mm, c = 100 μ m, d = 45 μ m, e, f = 2 cm, g, h = 10 μ m, i, j = 2000 μ m, k–m = 10 μ m.

Pleurocordyceps Y.J. Yao, Y.H. Wang, S. Ban, W.J. Wang, Yi Li, Ke Wang & P.M. Kirk

Pleurocordyceps, established by Wang et al. (2021) with the type species *Ple. sinensis*, is characterized by its lateral fertile pulvinate stromata near the tip of the sexual morph and two distinct types of phialides and conidia in the asexual morph (Wang et al. 2021; Xiao et al. 2023). This genus, associated with various insect hosts and fungi, holds promise for producing secondary metabolites with potential medicinal applications, such as antibacterial and anti-inflammatory compounds (Sangdee et al. 2017; Xiao et al. 2024).

53. *Pleurocordyceps sinensis* (Q.T. Chen, S.R. Xiao & Z.Y. Shi) Y.J. Yao, Y.Hui Wang, S. Ban, W.J. Wang, Yi Li, Ke Wang & P.M. Kirk, in Wang, Ban, Wang, Li, Wang, Kirk, Bushley, Dong, Hawksworth & Yao, *Journal of Systematics and Evolution* 59(5): 1075 (2021) **Fig. 87**

Chinese name: – 中国侧生虫草 (zhong guo ce sheng chong cao)

Index Fungorum number: IF 550007; **Facesoffungi number:** FoF 10739

Parasitic on adult of *Aphrophoridae* sp. buried in soil. **Sexual morph:** Undetermined. **Asexual morph:** *Hyphae* were smooth-walled, hyaline, septate, and measured 1.19–4.89 μm in width. *Conidiophores* measured 5.66–10.99 μm in length, with a basal width of 1.11–1.67 μm , a middle width of 1.35–2.62 μm , and a neck width of 1.17–1.79 μm . Two types of phialides and conidia were observed. β -type phialides ranged from 3.57 to 11.19 μm in length, with basal, middle, and neck widths of 1.55–2.31 μm , 1.96–4.2 μm , and 0.93–1.69 μm , respectively. α -type phialides were observed by mounting the pale-yellow mucilaginous mass from the apex of synnemata collected from wild material. These phialides were smooth-walled, hyaline, and either short-flask-shaped or lanceolate, usually arising from hyphae or conidiophores in a terminal or lateral position. Their length ranged from 5.38 to 15.76 μm , with basal, middle, and neck widths of 1.12–1.55 μm , 0.93–1.92 μm , and 0.74–1.36 μm , respectively. *Conidia* were all unicellular and hyaline. β -type conidia were fusiform and often formed in chains, measuring 2.18–4.39 μm in length and 1.28–2.09 μm in width. α -type conidia were nearly ellipsoidal, also hyaline, and measured 2.18–3.39 μm in length and 1.7–3.22 μm in width.

Culture characteristics: On PDA medium, Colonies exhibited a relatively regular growth pattern. After 28 days of incubation, it reached a diameter of 4.5 cm. The colony formed a distinctly circular outline in the Petri dish, expanding radially and uniformly from the initial inoculation point, with a neatly defined margin. The colony surface was fluffy, displaying a typical cottony texture. The reverse side of the colony showed a gradient of coloration, with the center appearing light brown—indicating pigment deposition or dense hyphal aggregation—and gradually transitioning to a pale yellow toward the edge, where the color remained even and soft.

Material examined: CHINA, Yunnan Province, Baoshan City, on adult of *Aphrophoridae* sp. buried in soil, 10 September 2023, X. M. Wang (HKAS 135024, culture KUNCC 11488).

Notes: In the present study, six-gene phylogenetic analyses clearly demonstrated that the newly collected specimens belong to the same species as *Ple. sinensis* (Wang

et al. 2020b) (Fig. 85). Synnemata were observed emerging from various parts of the host's body, and their microscopic characteristics were highly consistent with those previously described for *Ple. sinensis*. This specimen represents a new host record for *Ple. sinensis*, with the host identified as *Aphrophoridae* sp.

54. *Pleurocordyceps yunnanensis* (Hong Yu, Y.B. Wang & Y.D. Dai) Y.H. Wang, S. Ban, W.J. Wang, Yi Li, Ke Wang, P.M. Kirk & Y.J. Yao 2021 **Fig. 88**

Chinese name: – 云南侧生虫草 (yun nan ce sheng chong cao)

Index Fungorum number: IF 570681; **Facesoffungi number:** FoF 17063

Parasitism on fertile head of *Ophiocordyceps aphrophoridarum*, buried in the leaf litter. **Sexual morph:** undetermined. **Asexual morph:** Hyphomycetous. *Synnemata* 0.3–0.5 cm long, 0.2–0.6 mm wide, pale yellow to yellow, solitary or multiple, with fertile head. *Phialides* of two types: α -phialides arising from the fertile head of the synnema; β -phialides developing from the stipe of the synnema. α -phialides 8.6–22.5 $\times$ 0.9–2.1 μm ($\bar{x}$ = 15.5 $\times$ 1.5 μm , n = 50), β -phialides 9.5–13.5 $\times$ 1.3–2.3 μm ($\bar{x}$ = 11.5 $\times$ 1.8 μm , n = 40), smooth, hyaline, solitary. α -conidia 2.2–3.5 $\times$ 0.9–1.5 μm ($\bar{x}$ = 2.8 $\times$ 1.2 μm , n = 50) diam, smooth-walled, globose to ellipsoid, one-celled; β -conidia 4.1–5.5 $\times$ 1.1–2.3 μm ($\bar{x}$ = 4.8 $\times$ 1.7 μm , n = 50), hyaline, fusiform or droplets shape, one-celled, smooth-walled.

Material examined: CHINA, Guizhou Province, Hezhang County, parasitism on fertile head of *Ophiocordyceps aphrophoridarum*, 31 July 2022, Yuanpin Xiao HZ158 (HKAS 132195); HZ158J (GZCC 24-0148, culture).

Notes: The new collections clustered with *Ple. yunnanensis* with strong support (100% ML/1.00 BYPP, Fig. 85). The morphology of the new collections is similar to that of *Ple. yunnanensis*, showing no significant differences (Wang et al. 2015). Previously, *Ple. yunnanensis* was reported to parasitize *Ophiocordyceps nutans* and stink bugs as its hosts, with the holotype obtained from forest litter in Guizhou Province, China (Wang et al. 2015). However, in this study, *Oph. aphrophoridarum* were identified as the new hosts of *Ple. yunnanensis*.

Polycephalomyces Kobayasi

Polycephalomyces was introduced by Kobayasi to accommodate a monotypic anamorph genus for the species *Pol. formosus* Kobayasi and the diagnostic characteristic of highly branched synnemata (Kobayasi 1941). The asexual morph is hyphomycetous, with stipitate synnemata on the host surface or in culture, light-colored divergent conidiophores, phialidic hyaline conidiogenous cells, and monomorphic, hyaline, smooth-walled, one-celled conidia (Xiao et al. 2023). Now, this genus has been reported over 13 species from tropic and subtropic regions (Xiao et al. 2023; Liu et al. 2024c).

55. *Polycephalomyces formosus* Kobayasi, *Sci. Rep. Tokyo Bunrika Daig., Sect. B* 5: 245 (1941) **Fig. 89**

Chinese name: – 美丽多头菌 (mei li duo tou jun)

Index Fungorum number: IF 289806; **Facesoffungi number:** FoF 10731

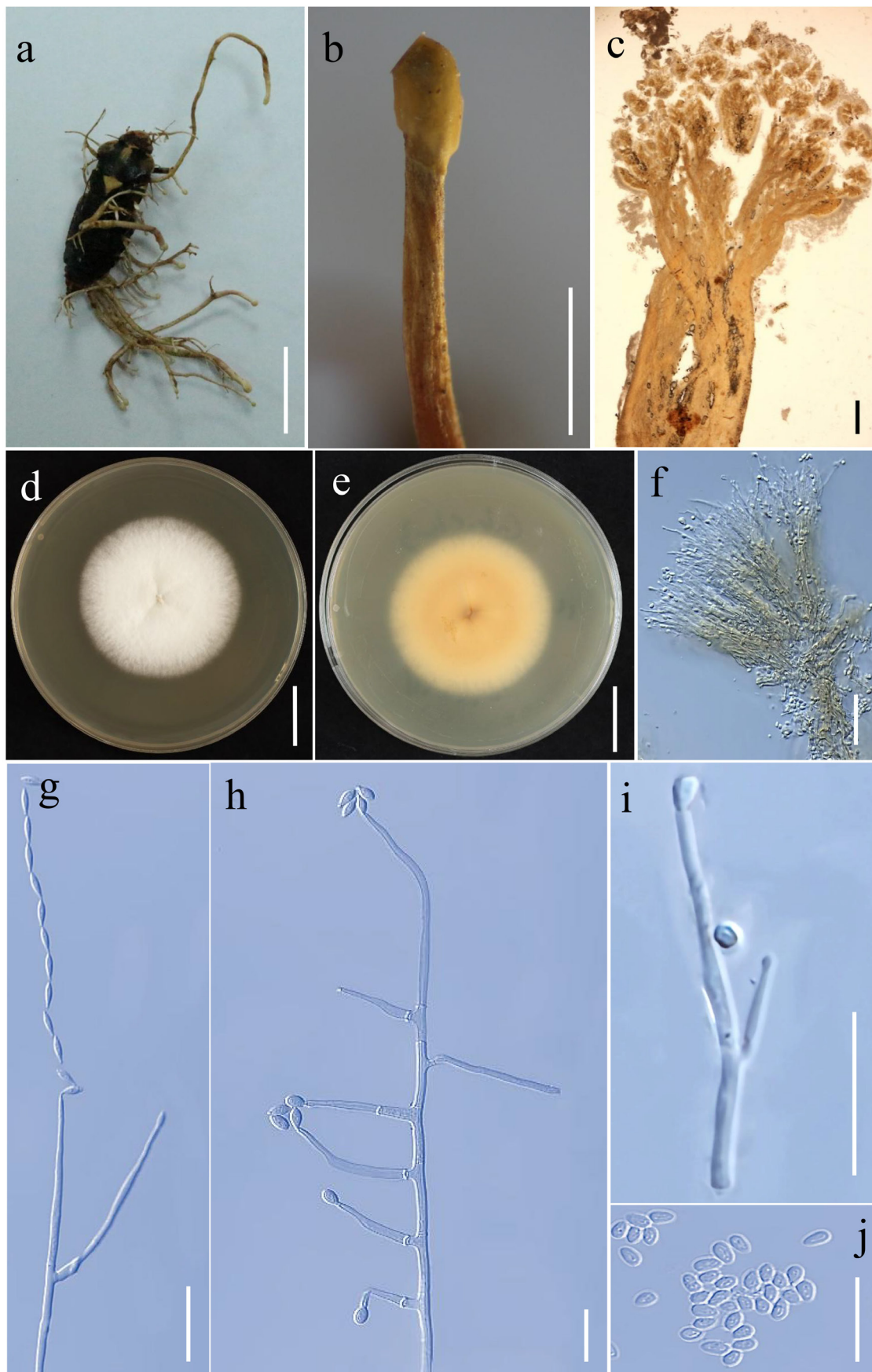


Fig. 87 *Pleurocordyceps sinensis* (HKAS 135024) a Fungus on adult of *Aphrophoridae* sp. b, c Synnemata on the wild specimen. d, e Colony on PDA culture, front and back. g, h β-phialides and β-conidia. f–j α-phialides and α-conidia. Scale bars: a = 1 cm, b = 500 μm, c = 200 μm, d, e = 2 cm, f–j = 10 μm.

Parasitic on adult of *Cicada* buried in soil. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Synnemata* 1–25 mm long, 0.1–1 mm wide, scattered or gathered on the *Cicada*, stipitate, solitary or forming 2–4 branches, white to pale yellow, cylindrical or rhizoid with or without an enlarged globose fertile head at the apex. *Fertile heads* 0.1–0.3 mm wide, globose to subglobose, white to pale yellow, covered with masses conidia. *Stipes* 0.5–5 mm long, 0.1–0.3 mm wide, cylindrical or rhizoid, white. *Phialides* 6–19 × 0.9–2.3 µm ($\bar{x}$ = 16 × 1.8 µm, n = 30), tapering gradually from middle to the apex, narrowly cylindrical to subulate, 1.3–2 µm wide at the base and 1–1.6 µm wide at the apex, one-type, hyaline, smooth-walled. *Conidia* 1.7–3 × 1.2–2.1 µm ($\bar{x}$ = 2.5 × 1.6 µm, n = 30), one-celled, one-type, hyaline. The conidia on wild material were oval-shaped obovoid, and the conidia on cultured mycelium were oblong ellipsoid. Colonies derived from single spore isolation.

Culture characteristics: Colonies on PDA reaching 4 cm diam in 28 days at 25 °C, white mixed with some pale yellow, radial with dense mycelium, reverse yellow. *Synnemata* 1.5–4 cm long, 0.2–2 mm wide, stipitate, gathered, white, cylindrical or flaky, growing and spreading from one branch to multiple branches, conidia masses on the surface, without fertile head.

Material examined: CHINA, Yunnan Province, Baoshan City, on adult of *Cicada* buried in soil, 10 September 2023, X.M. Wang (HKAS 135019, culture KUNCC 10935), other collection: *Ibid.*, X.M. Wang (HKAS 135018, culture KUNCC 10934).

Notes: The new collections clustered with other *Pol. formosus* sequences in the same clade with strong statistical support (Fig. 85). The morphology of the new collections is similar to *Pol. formosus* (Xiao et al. 2023). These specimens represent a new host record for *Pol. formosus*, with the host identified as adult of *Cicada* (*Cicadidae*, *Hemiptera*).

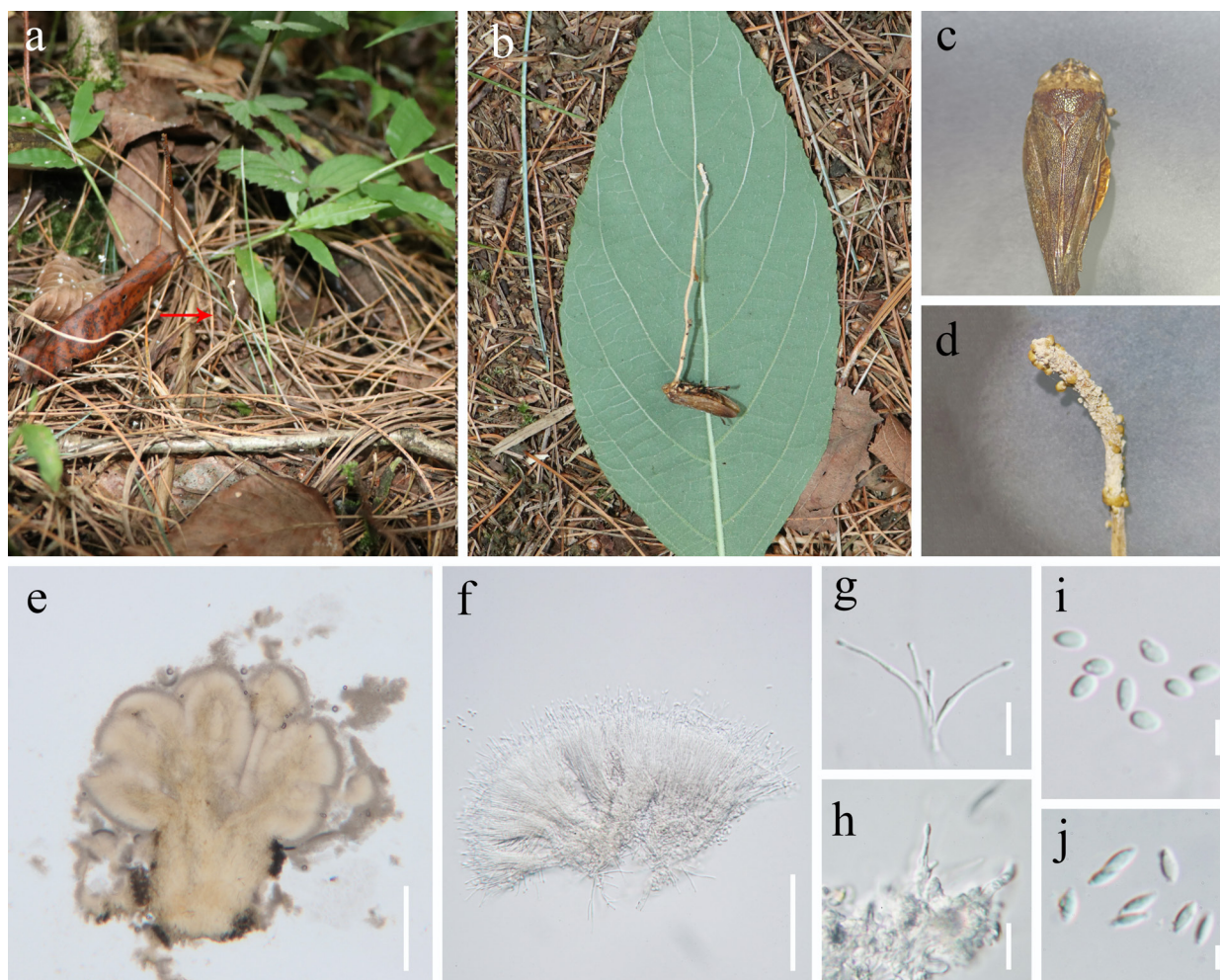


Fig. 88 *Pleurocordyceps yunnanensis* (HKAS 132195) a Habitat. b Overview of *Pleurocordyceps yunnanensis*. c Host of *Ophiocordyceps aphrophoridarum*. d Synnemata on the host. e Synnemata. f Conidiophores. g α -phialides. h β -phialides. i α -conidia. j β -conidia. Scale bars: e = 300 µm, f = 50 µm, g–h = 10 µm, i–j = 5 µm.

56. *Polyccephalomyces tengchongensis* Y. Wang & T.C. Wen, in Wang, Wei, Peng, Kang, Li, Li, Zhang, Wang, Zhou, He, Chomnunti & Wen, MycoKeys 110: 195 (2024) **Fig. 90**

Chinese name: – 腾冲多头菌 (teng chong duo tou jun)

Index Fungorum number: IF 901449; **Facesoffungi number:** FoF 19328

Parasitic on larva of *Coleoptera* buried in soil. **Sexual morph:** Undetermined. **Asexual morph:** *Hyphae* hyaline, smooth-walled, septate, 1.72–3.3 µm wide. *Conidiophores* cylindrical, 3–7 µm long, 1–2 µm wide at the base, and 1.69–2.46 µm at the neck. *Phialides* borne in whorls of 2–4 on the necks of conidiophores or terminal hyphae, flask-shaped, hyaline, smooth-walled, 8.95–14.38 µm long, 1.48–2.15 µm

wide at the base, 1.51–2.46 μm at the middle, and 0.52–1.16 μm at the neck. *Conidia* hyaline, smooth-walled, aseptate, subellipsoidal to fusiform, 2.19–3.51 $\times$ 1.01–1.97 μm .

Culture characteristics: Colonies on PDA grew slowly, reaching 3.9 cm in diameter after 21 d at 25 °C. Colony center grey, expanding outward to pale yellow; surface pale yellow to milky white, producing highly branched, coral-like, flattened synnemata.

Material examined: CHINA, Yunnan Province, Baoshan City, on larva of *Coleoptera* buried in soil, 11 September 2023, X.M. Wang (HKAS 135025, culture KUNCC 10954), other collections: *Ibid.*, X. M. Wang (culture KUNCC 10955).

Notes: The new collections cluster together with previously published sequences of *Pol. tengchongensis* with strong statistical support. Morphologically, it is also consistent with *Pol. tengchongensis* (Wang et al. 2024e) (Fig. 85). However, it differs in host species, which in this case is a larva of *Coleoptera*, whereas the original described specimens of *Pol. tengchongensis* were found on *Lepidopteran* hosts (Wang et al. 2024e). These specimens represent a new host record for *Pol. tengchongensis*, with the host identified as larvae of *Coleoptera*.

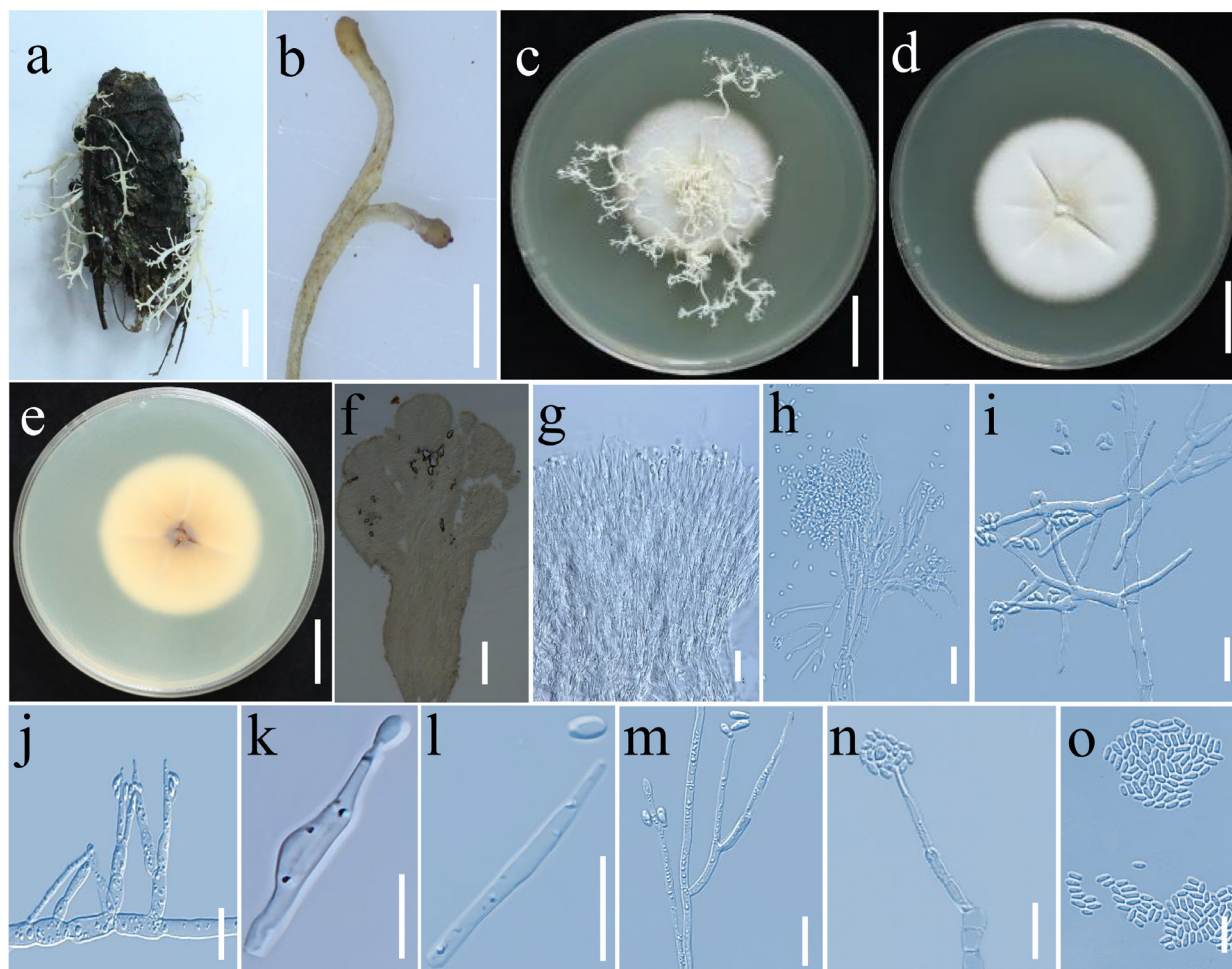


Fig. 89 *Polycephalomycetes formosus* (HKAS 135019) a Fungus on adult of *Cicada*. b–d Synnemata. e, f Colonies on PDA. g Conidiophores. h, i Phialides and conidia on hyphae cultured on PDA. j, k Phialides and conidia on wild material. l, m Phialides and conidiophores cultured on PDA. n Conidia cultured on PDA. Scale Bars: a = 1 cm, b = 1 mm, c = 1000 μm , d = 200 μm , e, f = 2 cm, g = 20 μm , h, i = 10 μm , j, k = 5 μm , l–n = 10 μm .

Microascales Luttr. ex Benny & Kimbr

Microascaceae Luttr. ex Malloch

Kernia Nieuwl

Kernia was established by Nieuwland (1916), with *K. nitida* as the type species. Malloch & Cain (1970) positioned *Kernia* within the *Microascaceae*, citing its absence of croziers, the presence of dextrinoid ascospores with germ pores, and the intricate annellophore-type conidial stages as key taxonomic features. Currently, the genus comprises 20 taxa recorded in Index Fungorum (Index Fungorum). Su et al. (2020) distinguished *Kernia* from *Acaulium* based on multigene (ITS, LSU, *tub*, *tef1*- α) phylogenetic analyses and morphological characteristics. *Kernia* is typically collected from animal dung,

although *K. retardata* and *K. peruviana* have been isolated from soil (Su et al. 2020). The sexual morph of *Kernia* is distinguished by its superficial, dark cleistothecia, which can exhibit triangular, rectangular, or globose shapes, often adorned with appendages—either elongated or abbreviated—at the angles, resulting in a depressed morphology. These appendages display an olive, green to brown coloration, and can be straight or arcuate, occasionally undulating, terminating in one or two circinate or recurved tips. They are septate, with thick walls and a smooth surface. The asci are unitunicate, irregularly arranged within the fruiting body, pyriform or clavate in shape, possessing short stalks, and are characteristically 8-spored. The ascospores are hyaline to

light olive-green, ellipsoidal, and exhibit either acute or rounded apices (Malloch & Cain 1970; Malloch 1971; Su et al. 2020). Some species of *Kernia* produce both sexual and asexual morphs in culture (Su et al. 2020). The genus has

been reported in Canada, China (Beijing, Taiwan), France, Germany, South America, and Uganda (Nieuwland 1916; Malloch et al. 1971; Su et al. 2020).

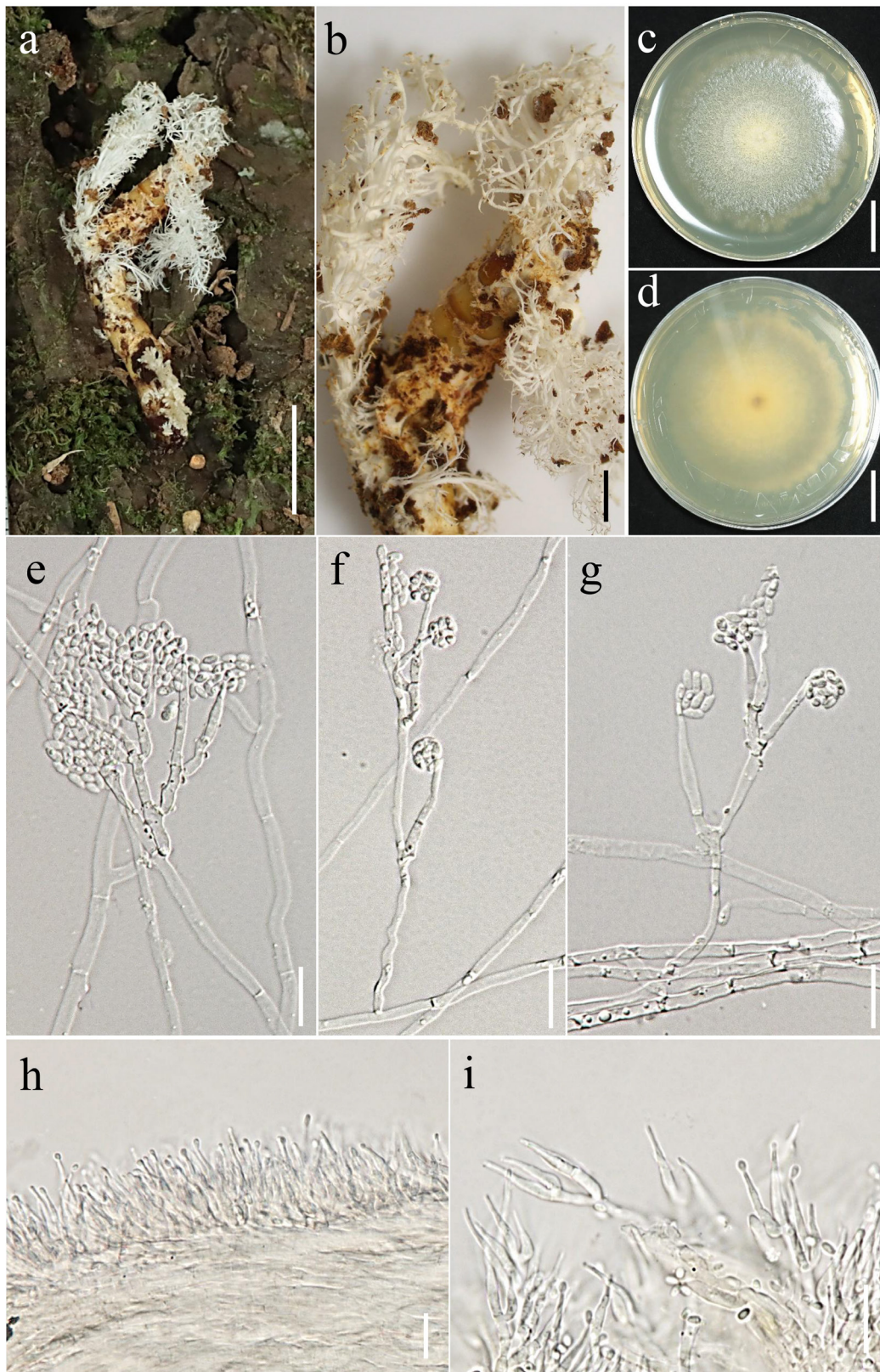


Fig. 90 *Polycephalomyces tengchongensis* (HKAS 135025) a, b Fungus on larvae of *Coleoptera*. c, d PDA culture colonies front and back. e–i Phialides and conidia. Scale bars: a = 1 cm, b = 2000 μ m, c, d = 2 cm, e–i = 10 μ m.

57. *Kernia xizangensis* R.J. Xu & Q. Zhao, *sp. nov.* Fig. 92**Chinese name:** – 西藏闭小囊菌 (xi zang bi xiao nang jun)**Index Fungorum number:** IF 905280; **Facesoffungi number:** FoF 19329**Etymology:** The species is named after the Xizang, where the type specimen was collected.**Holotype:** HKAS 136196

Saprobic on decaying wood submerged in freshwater stream. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* on the natural substrate scattered or caespitose, with glistening conidial masses at apex. *Synnemata* 244–406 × 11–23 µm ($\bar{x}$ = 322 × 15 µm, n = 20), septate, pale brown to subhyaline, smooth, penicillately branched at the apex. *Conidiogenous cells* polyblastic, hyaline to pale brown, percurrent, ampulliform, terminal. *Conidia* 5–7 × 3–5 µm ($\bar{x}$ = 6 × 4 µm, n = 30), obovoid, ellipsoidal to irregularly fusiform with a truncate base and rounded or bluntly pointed apex, hyaline, smooth, aseptate, collecting in wet masses at the apices of the conidiophores.

Culture characteristics: Conidia germinated on PDA media within 24 hours and germ tube were produced from base. Colonies grown on PDA reached 50 mm diam at room temperature in two weeks, circular, flat, sparse, dark brown mycelium, with radialized margin.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, on decaying wood submerged in a freshwater stream, 19 July 2021, R.J. Xu, MD-303 (HKAS 136196, holotype), ex-type culture (KUNCC 24-18037).

Notes: Phylogenetic analysis shows that our collection clusters within *Kernia* and is a sister group to *K. anthracina* and *K. hipporrepida*, with 96 ML/ 0.98 BYPP statistical support (Fig. 91). Morphologically, our collection resembles *K. anthracina* with a scopulariopsis-like branching pattern and the production of acrospores, and obovoid to ellipsoidal conidia (Su et al. 2020). However, our collection differs from *K. anthracina* by having pale brown to subhyaline synnemata, with penicillately branched at the apex and percurrent, ampulliform conidiogenous cells. In addition, our collection differs from *K. hipporrepida* in having longer synnemata (244–406 × 11–23 µm vs. 16–90 × 2.5–3.5 µm), and aseptate conidia (Malloch & Cain 1970).

Pleurotheciales Réblová & Seifert**Pleurotheciaceae** Réblová & Seifert***Phaeoisaria*** Höhn. 1909

Phaeoisaria was introduced by Höhnelt (1909) with *P. clematidis* as the type species and was distinguished in *Pleurotheciaceae* by Réblová et al. (2016b). *Phaeoisaria* is a widespread genus with 27 species currently reported (Li et al. 2025). Morphologically, *Phaeoisaria* asexual morph is characterized by macronematous, synnematus, brown to dark brown synnemata, polyblastic, hyaline to brown, sympodial, terminal conidiogenous cells, ellipsoidal to obovoid, hyaline, smooth-walled, aseptate conidia (Hyde et al. 2018; Luo et al. 2018, 2019; Xu et al. 2024a; Li et al. 2025), the sexual morph is characterized by black ascomata, paraphyses, branched, septate, smooth and asci with 8 spores. Ascospores are tapering at both ends, multi-septate, hyaline (Luo et al. 2019). Species of *Phaeoisaria* are commonly collected from freshwater habitats and decaying wood (Crous et al. 2015b; Luo et al. 2019; Xu et al. 2024a).

Following reports of *Phaeoisaria* species in Xizang by Xu et al. (2024a) and Li et al. (2025). In this study, based on morphological and phylogenetic analyses, we describe a new species *Phaeoisaria xizangensis* from Xizang.

58. *Phaeoisaria linzhiensis* S.C. He, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 94**Chinese name:** – 林芝暗棒束孢 (lin zhi an bang shu bao)**Index Fungorum number:** IF 905281; **Facesoffungi number:** FoF 19330**Etymology:** Referring to the location “Linzhi City” where the holotype of this fungus was collected.**Holotype:** HKAS 145479

Saprobic on decaying stems of *Lilium* spp. **Sexual morph:** Undetermined. **Asexual morph:** *Colonies* effuse, solitary, brown, hairy. *Mycelium* immersed, superficial, branched, pale brown hyphae. *Synnemata* 328–462 × 8–15 µm ($\bar{x}$ = 390 × 12 µm, n = 10) µm, scattered, erect, brown to dark black, straight or flexuous, pale at the apex, composed of conidiophores, branched at the apex. *Conidiophores* 270–350 × 2.1–3.8 µm ($\bar{x}$ = 330 × 2.8 µm, n = 30), macronematous, synnematus, septate, cylindrical, branched, straight or flexuous, pale brown to brown, thick-walled, smooth-walled. *Conidiogenous cells* polyblastic, integrated, terminal and intercalary, rough, cylindrical, subhyaline to pale brown, with several small denticulate conidiogenous loci. *Conidia* 7–10 × 3–4 µm ($\bar{x}$ = 8 × 3.5 µm, n = 30) µm, amero-spores solitary, acropleurogenous, simple, subglobose to obovoidal, smooth and guttulate, aseptate, hyaline to subhyaline.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, on *Lilium* spp, 22 August 2023, Shucheng He, ZYW74 (HKAS 145479, holotype).

Notes: *Phaeoisaria linzhiensis* formed a distinct clade within *Phaeoisaria* (Fig. 93). Its morphology fits well with the generic concept of *Phaeoisaria* with amero-spores, acropleurogenous, subglobose to obovoidal, smooth, aseptate, hyaline (Xu et al. 2024a). Morphologically, *P. linzhiensis* resembles *P. obovata* in having macronematous, synnematus, septate, cylindrical conidiophores, terminal and intercalary, polyblastic, curved to recurved conidiogenous cells, and solitary, subglobose, hyaline, aseptate conidia (Wang et al. 2024a). However, *P. obovata* have bigger synnemata (727.4 × 14.6 µm vs. 390 × 12 µm). Based on morphological and phylogenetic analyses, we introduce a new species *P. linzhiensis* from Linzhi City, Xizang, China.

Sterigmatobotrys Oudem

Sterigmatobotrys comprises dematiaceous hyphomycetes commonly found on decaying wood in terrestrial and freshwater habitats. Initially described by Oudemans (1886), the genus included *S. elata* and *S. papyrogena*. Rabenhorst (1844) later classified *Sterigmatobotrys* as a subgenus of *Stachybotrys*, basing this placement on an illustration of *Stachybotrys elata*. However, subsequent studies re-established *Sterigmatobotrys* as a distinct genus, with *S. elata* lectotyped and *S. macrocarpa* designated as the type species. This reclassification was based on reassessments of historical type material by Hughes (1958) and Jong & Davis (1971). The teleomorph of *S. macrocarpa*, identified in the Czech Republic, is characterized by conical to subglobose, dark brown perithecia containing asci with eight hyaline, elongate-fusiform ascospores (Réblová & Seifert 2011b).



Fig. 91 Maximum likelihood majority rule consensus tree for Microascaceae using LSU, ITS, *tef1*-α and SSU sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Stilbohypoxylon elaeidis* (MFLUCC 15-0295a), *Xylaria acuta* (AFTOL ID 63) and *X. hypoxylon* (AFTOL ID 51). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

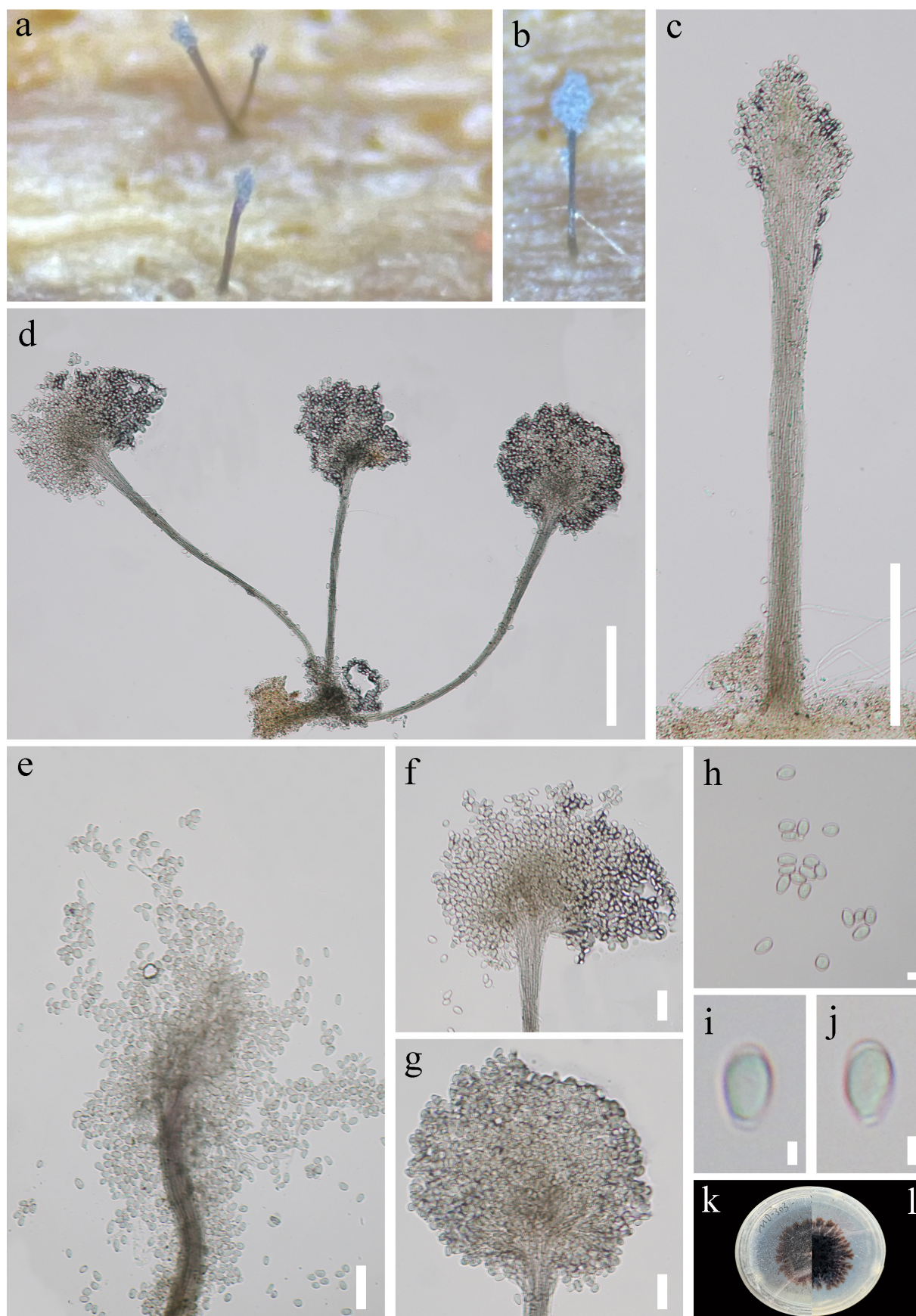


Fig. 92 *Kernia xizangensis* (HKAS 136196, holotype) a, b Colony on natural substrates. c, d Synnema and conidiogenous cells. e–g Conidiogenous cells and conidia. h–i Conidia. k, l Culture on PDA medium, k from above, l from below. Scale bars: c, d = 100 μ m, e–g = 20 μ m, h–j = 2 μ m.

The asexual morph of *Sterigmatobotrys* is distinguished by macronematous, irregularly biverticillate to terverticillate conidiophores with stout, septate, and darkly pigmented stipes. These terminate in polyblastic conidiogenous cells bearing minute, sympodially arranged denticles. The hyaline, septate conidia mature to a brown color and are embedded in slime (Chang 1991; Réblová & Seifert 2011; Ertz et al. 2016; Luo et al. 2019). Currently, the genus includes three accepted

species: *S. macrocarpa*, *S. rudis*, and *S. uniseptate*. *S. macrocarpa* is characterized by 2-septate, cylindrical to fusiform, hyaline conidia with a truncate base. In contrast, *S. rudis* features catenate, obclavate to fusiform, 3–12-septate conidia, while *S. uniseptate* is distinguished by its 1-septate, hyaline conidia (Réblová & Seifert 2011; Ertz et al. 2016; Luo et al. 2019; Yang et al. 2023).

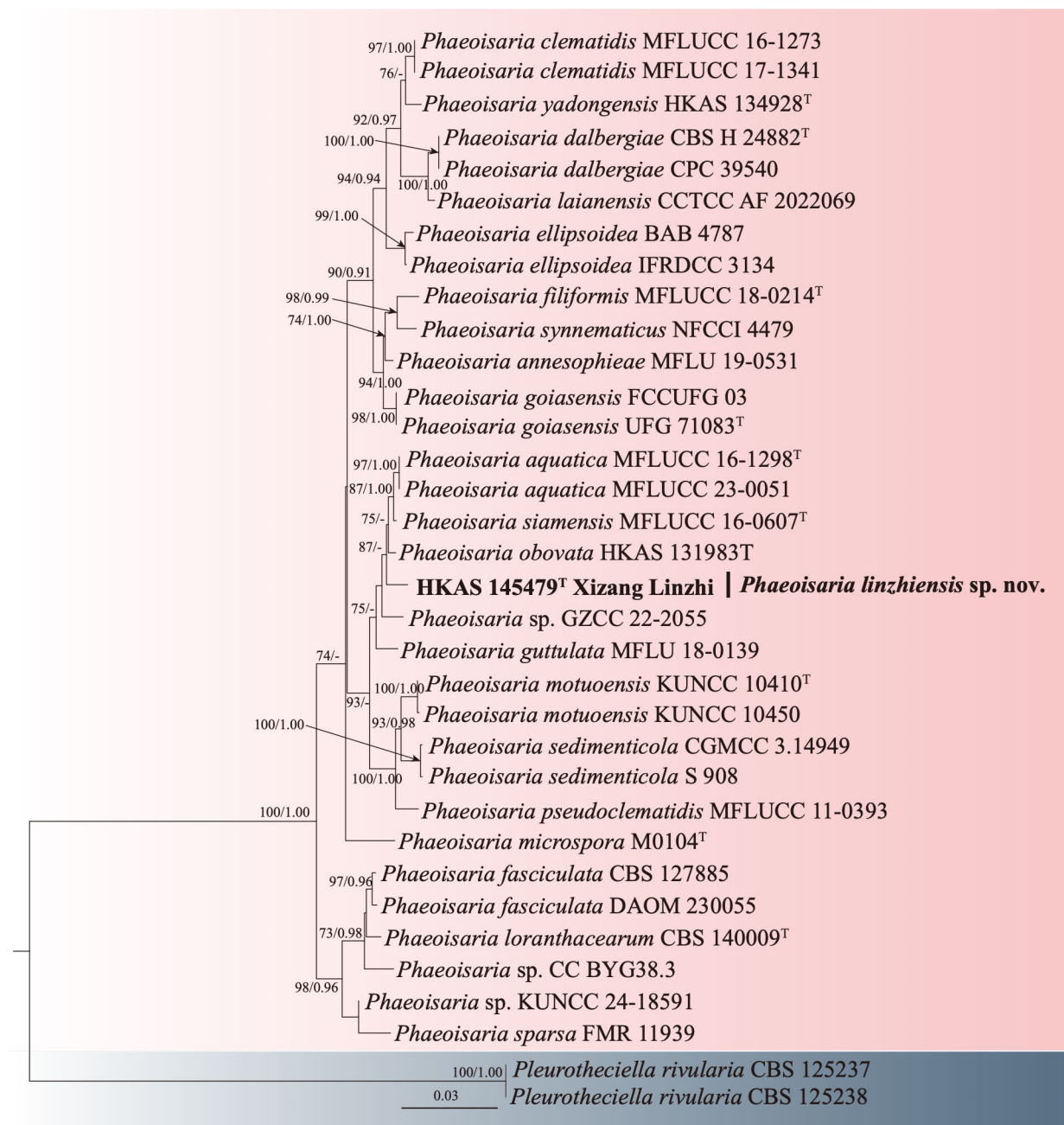


Fig. 93 Maximum likelihood consensus tree of *Phaeoisaria* inferred from the combined LSU, ITS and SSU multiple sequence alignments. Bootstrap support values for maximum likelihood (ML) equal to or greater than 70% and Bayesian posterior probabilities from MCMC analyses (BYPP) equal to or greater than 0.90 are given above the nodes. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.



Fig. 94 *Phaeoisaria linzhensis* (HKAS 145479, holotype) a, b Colony on natural substrates. c–e Conidiophores with conidia. f Conidiogenous cells with conidia. g, h Conidia. Scale bars: c–e = 100 µm, f–h = 10 µm.

59. *Sterigmatobotrys uniseptatus* H.S. Chang [as 'uniseptata'], Mycol. Res. 95(9): 1142 (1991) Fig. 96

Chinese name: – 单隔头梗孢 (dan ge tou geng bao)

Index Fungorum number: IF 626943; **Facesoffungi number:** FoF 17432

Saprobic on submerged decaying wood. **Sexual morph:** Undetermined. **Asexual morph:** *Colonies* on the substratum superficial, effuse, with white, glistening conidial masses at apex. *Mycelium* immersed, subhyaline to pale brown, composed of branched, septate hyphae. *Conidiophores* 132–181 × 7–11 µm ($\bar{x}$ = 151 × 9 µm, n = 15), macronematous, mononematous, cylindrical, terminating in an irregularly biverticillate to terverticillate head, erect, straight or slightly flexuose, solitary, septate, smooth, unbranched, dark brown or brown. *Conidiogenous cells* terminal, parallel, polyblastic, smooth, cylindrical, hyaline, bearing multiple sympodially produced denticles from which conidia develop holoblastically. *Conidia* 14–19 × 4–6 µm ($\bar{x}$ = 16 × 5 µm, n = 20), aggregated in slimy masses, ellipsoidal to fusoid, 1-septate, smooth-walled, hyaline, sometimes constricted at the septa.

Culture characteristics: Conidia germinating on PDA medium within 48 h and germ tubes produced from both ends. Colonies grown on PDA reached 20 mm diam at room temperature in three weeks, circular, with velvety, dry, umbonate, light brown mycelium on the surface, from below dark brown with entire margin.

Material examined: CHINA, Yunnan Province, Nujiang, Gongshan County, Dizhengdang Village, 28°4'47.37" N, 98°19'32.06" E, 2030 m a.s.l., on decaying wood submerged in a freshwater stream, 20 October 2019, R.J. Xu, MD-214 (HKAS 136182), culture KUNCC 24-18026. Yunnan Province, Nujiang, Gongshan County, Dizhengdang Village, 28°4'47.37" N, 98°19'32.06" E, 2030 m a.s.l., on decaying wood submerged in a freshwater stream, 20 October 2019, R.J. Xu, MD-243 (HKAS 136208), culture KUNCC 10411. Xizang Autonomous Region, Shannan City, Longzi County, Zhari Township, 28°39'50.06" N, 93°22'25.27" E, 3023 m a.s.l., on decaying wood submerged in a freshwater stream, 05 August 2023, R.J. Xu, LJN-60 (HKAS 135979), culture KUNCC 24-17967. Yunnan Province, Shangri-La City, Bitu Lake, 27°45'21.04" N, 99°56'46.56" E, 2306 m a.s.l., on decaying wood submerged in a freshwater river, 23 July 2020, R.J. Xu, MD-239 (HKAS 136161), culture KUNCC 24-18030.

Notes: *Sterigmatobotrys uniseptata* was described by Chang (1991), collected from unidentified twigs in Taiwan, and was later found on decaying wood submerged in freshwater in Yunnan Province, China (Luo et al. 2019). This species is characterized by its macronematous, mononematous conidiophores, which arise from stromatic cells. Each conidiophore features a well-defined stipe and a complex penicillate head composed of a series of penicillate branches, terminating in conidiogenous cells. These cells produce a head of slimy conidia. The conidiogenous cells are polyblastic and hyaline, while the conidia are solitary, slimy, thin-walled, hyaline, straight, cylindrical to subclavate, and 1-septate.

Phylogenetic analysis revealed that our collections (KUNCC 24-18026, KUNCC 10411, KUNCC 24-17967 and KUNCC 24-18030) clustered with *Sterigmatobotrys uniseptata* (MFLUCC 15-0358) (Fig. 95). The shape and size

of conidiophores, conidiogenous cells, and conidia in our strains are identical to those described in strains of *S. uniseptata* by Chang (1991) and Luo et al. (2019). Therefore, we identify our collections as *S. uniseptata*.

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

Savoryellaceae Jaklitsch & Réblová

Savoryella E.B.G. Jones & R.A. Eaton

Savoryella was established by Jones & Eaton (1969), with *S. lignicola* as the type species. The sexual morphs of *Savoryella* are defined by ascostromata that are immersed, partially immersed, or superficial, and globose, subglobose, or ellipsoidal in shape. These structures typically contain 8-spored, occasionally 2-spored, cylindrical or clavate, unitunicate asci, and ellipsoidal, three-septate ascospores. In contrast, the asexual morphs are distinguished by glistening, punctiform colonies; micronematous, mononematous conidiophores; holoblastic, determinate, integrated, terminal, or intercalary conidiogenous cells; and solitary or aggregated, pyriform to obovoid, septate conidia. Zhang et al. (2019) synonymized *Trichocladium nypae* with *Savoryella nypae* and introduced the asexual species *S. sarushimana* into the genus based on morphological and phylogenetic data. Subsequently, Tian et al. (2024) reported two more asexual species, *S. cocois* and *S. chiangraiensis*, from decaying leaves of *Arecaceae*, supported by phylogenetic analysis and morphological evidence. *Savoryella*, a holomorphic genus, predominantly inhabits submerged decaying woody debris in both aquatic and terrestrial ecosystems. The genus has been extensively studied and systematically illustrated by mycologists worldwide (Cai et al. 2002, 2003; Luo et al. 2004), and is widely distributed across diverse freshwater habitats globally, with particularly abundant occurrences in plateau lakes of Yunnan Province, China. Furthermore, all known genera in *Savoryellales* have been found to be distributed in the Q-X Plateau region (Wang et al. 2025a; Xu et al. 2025).

60. *Savoryella submersa* R.J. Xu, K.D. Hyde & Q. Zhao, sp. nov. Fig. 98

Chinese name: – 沉木小萨沃里菌 (chen mu xiao sa wo li jun)

Index Fungorum number: IF 905046; **Facesoffungi number:** FoF 17439

Etymology: the species epithet "*submersa*" refers to the submerged wood where this species was collected.

Holotype: HKAS 136193

Saprobic on decaying stems of wood submerged in a freshwater stream habitat. **Sexual morph:** Undetermined. **Asexual morph:** *Colonies* effuse, scattered, black, glistening, punctiform. *Mycelium* immersed, subhyaline to pale brown, composed of branched, septate hyphae. *Conidiophores* inconspicuous or micronematous, mononematous, hyaline to pale brown, smooth. *Conidiogenous cells* holoblastic, determinate, integrated, pale brown to brown, cylindrical. *Conidia* 18–28 × 13–23 µm ($\bar{x}$ = 21 × 19 µm, n = 30), acrogenous, solitary, obovoid to subspherical, 1-septate, distinct constricted at septa, dividing the conidium into two unequal cells, smooth, brown when mature, the basal cell pale brown.

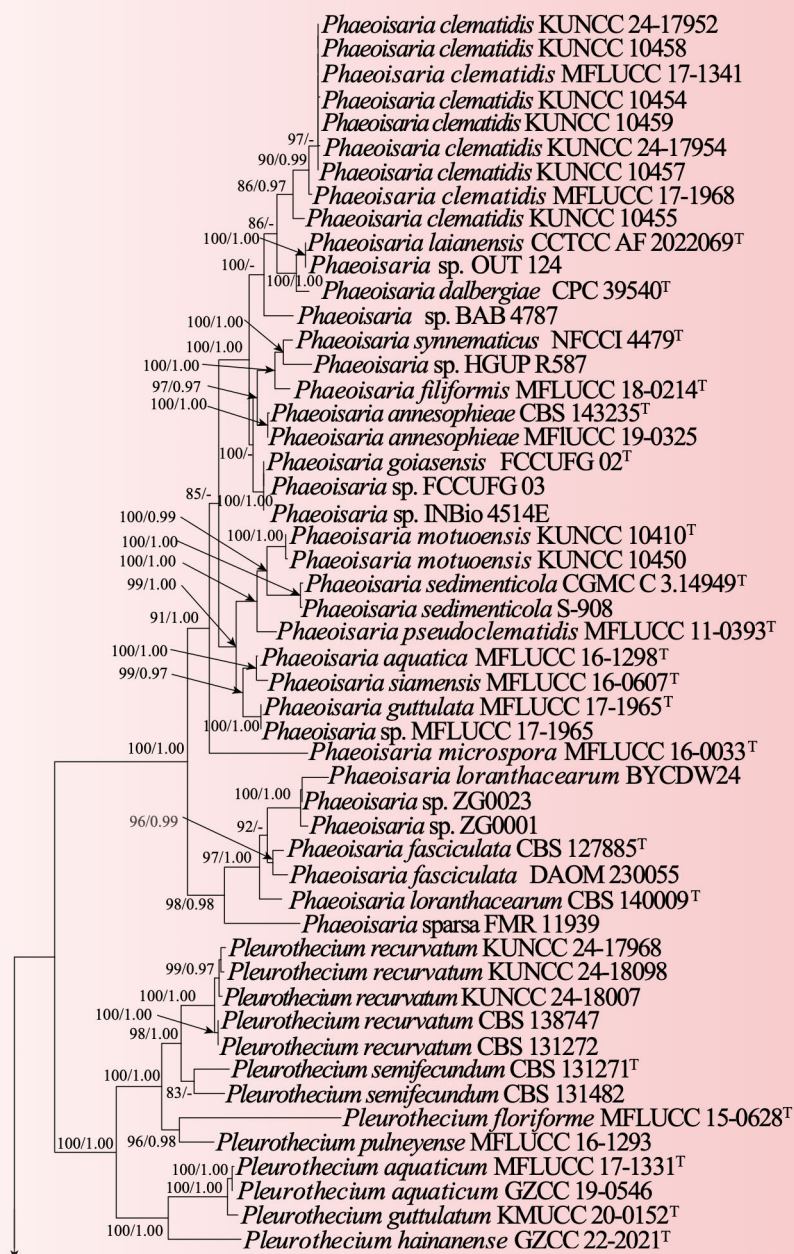


Fig. 95 Maximum likelihood majority rule consensus tree for *Pleurotheciaceae* using ITS, LSU, SSU and *rpb2* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Conioscypha tenebrosa* (GZCC 19-0217) and *C. minutispora* (CBS 137253). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Culture characteristics: Conidia germinating on PDA medium within 24 h and germ tubes arising from terminal end of conidium. Colonies grown on PDA reached 30 mm diam at room temperature in two weeks, circular, with velvety, flat, dark brown mycelium on the surface, from below dark brown to black with entire margin.

Material examined: CHINA, Xizang Autonomous Region, Linzhi City, Motuo County, 29° 23' 36.31" N, 95° 35' 22.18" E, 667 m a.s.l., on decaying wood submerged in a freshwater stream, 13 July 2022, R.J. Xu, MD-99 (HKAS 136193, holotype), ex-type culture (KUNCC 24-18017).

Notes: Zhang et al. (2019) synonymized *Trichocladium nypae* with *Savoryella nypae* and introduced an asexual

species, *S. sarushimana*, into the genus *Savoryella*, based on morphological and phylogenetic analyses. Subsequently, Tian et al. (2024) reported two additional asexual species, *S. cocois*, and *S. chiangraiensis*, collected from decaying leaves of the *Arecaceae*. Later, Xu et al. (2024f) introduced a unique asexual species, *S. claviformis*, which can be distinguished from all asexual species in *Savoryella* by its fusiform, claviform conidia. So far, five asexual species have been reported in *Savoryella* (Zhang et al. 2019; Tian et al. 2024b; Xu et al. 2024c).

Among the asexual species of *Savoryella*, *S. submersa* is distinguished by its obovoid to subspherical, 1-septate conidia, which are distinctly constricted at the septa (Zhang

et al. 2019; Tian et al. 2024b; Xu et al. 2024c). *Savoryella submersa* differs from *S. nypae* in having 1-septate, obovoid to subspherical conidia, while the conidia of *S. nypae* are pyriform to obovoid with 2(–3)-septa. In addition, in the phylogenetic analysis (Fig. 97), *S. submersa* (KUNCC 24-

18017) formed a distinct branch within *Savoryella*, clearly separating it from other asexual species, and clustered as a sister group to *S. aquatica*, *S. verrucosa*, and *S. yunnanensis* with (100% ML/1.00 BYPP) statistical support.

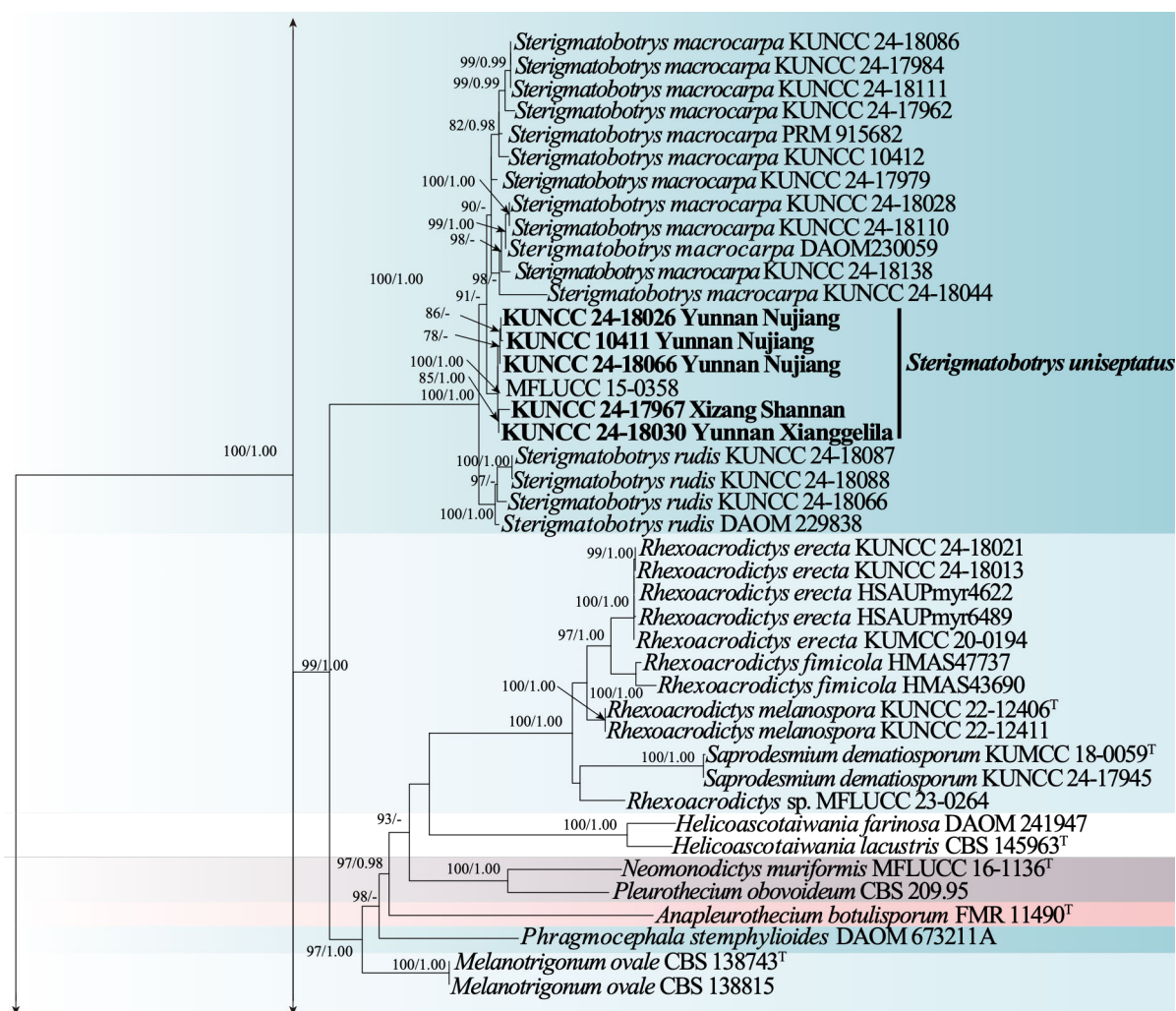


Fig. 95 (continued)

Sordariales Chad. Ex D. Hawksw. & O.E. Erikss.

Bombardiaceae S.K. Huang & K.D. Hyde

Ramophialophora M. Calduch, Stchigel, Gené & Guarro

Ramophialophora was introduced by Calduch et al. (2004), with *R. vesiculosa* designated as the type species. The conidiophores of *Ramophialophora* resemble those of *Gonytrichum*, *Dicyma*, and *Surculiseries*, but the genus differs significantly in its conidiogenesis and the arrangement of conidiogenous cells on the conidiophore (Calduch et al. 2004). *Ramophialophora* is characterized by macronematous, mononematous, erect, cylindrical, septate, and branched conidiophores with subhyaline, subspherical to clavate vesicles. The conidiogenous cells are monophialidic or polyphialidic, discrete, terminal or lateral, lageniform, pale olivaceous, and smooth-walled, with conspicuous, slightly darker collarettes. The conidia are one-celled, spherical, and possess a protuberant basal hilum (Calduch et al. 2004).

61. *Ramophialophora ramosa* R.J. Xu, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 100

Chinese name: – 分枝瓶孢霉 (fen zhi ping bao mei)

Index Fungorum number: IF 905047; **Facesoffungi number:** FoF 17440

Etymology: the species epithet "*ramosa*" refers to the branched conidiophores characteristic of this species.

Holotype: HKAS 136227

Saprobic on decaying wood submerged in freshwater habitats. **Sexual morph:** Undetermined. **Asexual morph:** Colonies on natural substrate effuse, hairy, velvety, pale brown. *Mycelium* superficial and immersed in the substrate, pale brown, septate, branched. *Conidiophores* macronematous, mononematous, erect, cylindrical, septate, branched, brown to dark brown, becoming paler towards the apex. *Conidiogenous cells* polyphialidic, discrete, terminal and lateral, lageniform or cylindrical, pale brown to subhyaline, cup-like collarette. *Conidia* 2–3 × 2–3 μm ($\bar{x}$ = 3 × 3 μm, n = 35), solitary, spherical, subglobose, one-celled at the base, brown to subhyaline, smooth.

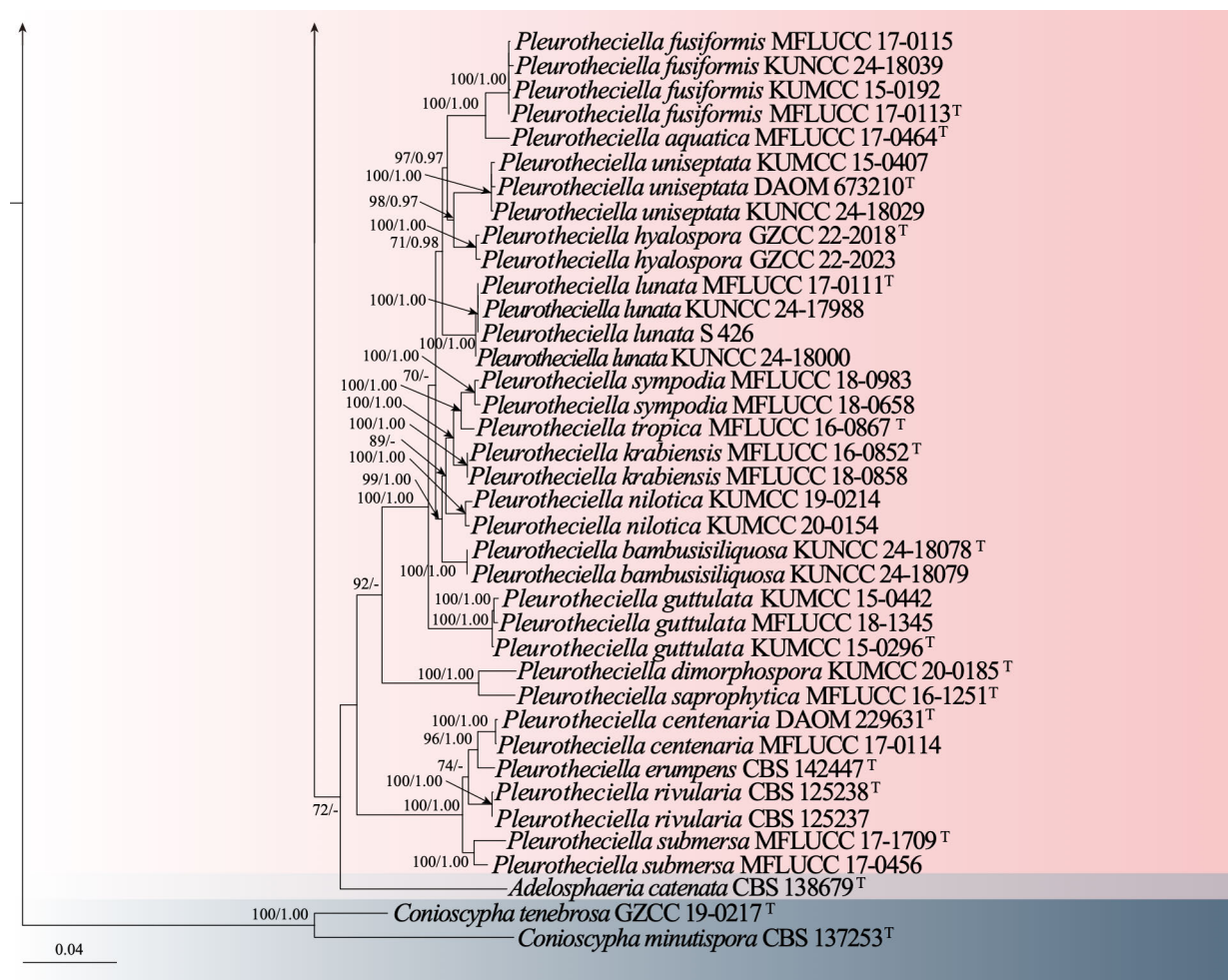


Fig. 95 (continued)

Culture characteristics: Conidia germinating on PDA medium within 24h. Colonies grown on PDA reached 60 mm diam at room temperature in one week, circular, with velvety, flat, dark brown mycelium on the surface, from below dark brown with entire margin.

Material examined: CHINA, Xinjiang Autonomous Region, Yili Kazak Autonomous Prefecture, Gongliu County, Yuhu lake, 42°41'55.19" N, 81°4'51.31" E, 1955 m a.s.l., on decaying wood submerged in a freshwater lake, 05 August 2021, R.J. Xu, MD-318 (HKAS 136227, holotype), ex-type culture KUNCC 10414. Xinjiang Autonomous Region, Yili Kazak Autonomous Prefecture, Gongliu County, Kiziltar Village, 43°20'12.61" N, 82°30'56.54" E, 921 m a.s.l., on decaying wood submerged in a freshwater stream, 04 August 2021, R.J. Xu, MD-318-1 (HKAS 136226, paratype), ex-paratype culture KUNCC 24-18041.

Notes: Phylogenetic analysis showed that our collections (KUNCC 10414 and KUNCC 24-18041) clustered together and formed a sister group with *Ramophialophora vesiculosa* with (98% ML/1.00 BYPP) statistical support (Fig. 99). *Ramophialophora ramosa* resembles *R. vesiculosa* in having macronematous, mononematous, branched, brown conidiophores; monophialidic or polyphialidic, lageniform conidiogenous cells; and subhyaline conidia (Calduch et al. 2004). However, *R. ramosa* can be easily distinguished from

R. vesiculosa by its lageniform or cylindrical conidiogenous cells with a cup-like collarette (Calduch et al. 2004). *Ramophialophora globispora* can be distinguished from *R. ramosa* by its unbranched conidiophores and chained conidia (Zhang et al. 2017b). In addition, they are located on different clade of the phylogenetic tree.

Chaetomiaceae G. Winter

Dichotomopilus X. Wei Wang, Samson & Crous

Wang et al. (2014) introduced *Chaetomium indicum*. Subsequently, based on the produces dichotomously-branched terminal hairs, Wang et al. (2016b) transferred *Chaetomium indicum* to *Dichotomopilus* and introduced *Dichotomopilus indicus* as the type species. There are currently 13 species reported in *Dichotomopilus* (Kedves et al. 2021; Wang et al. 2016b; Hyde et al. 2024a), mainly distributed in the China, Germany, Iran and USA, found in corn straw, soil, discarded sheep dung, straw of *Triticum aestivum*, and stored cotton (Wang et al. 2014). Morphologically, terminal hairs seta-like and the beginning, then developing into dichotomously or irregularly branched, lateral hairs unbranched, seta-like, tapering towards tips. Asci fasciculate, clavate, with 8 biseriate or irregularly arranged ascospores (Wang et al. 2016b).

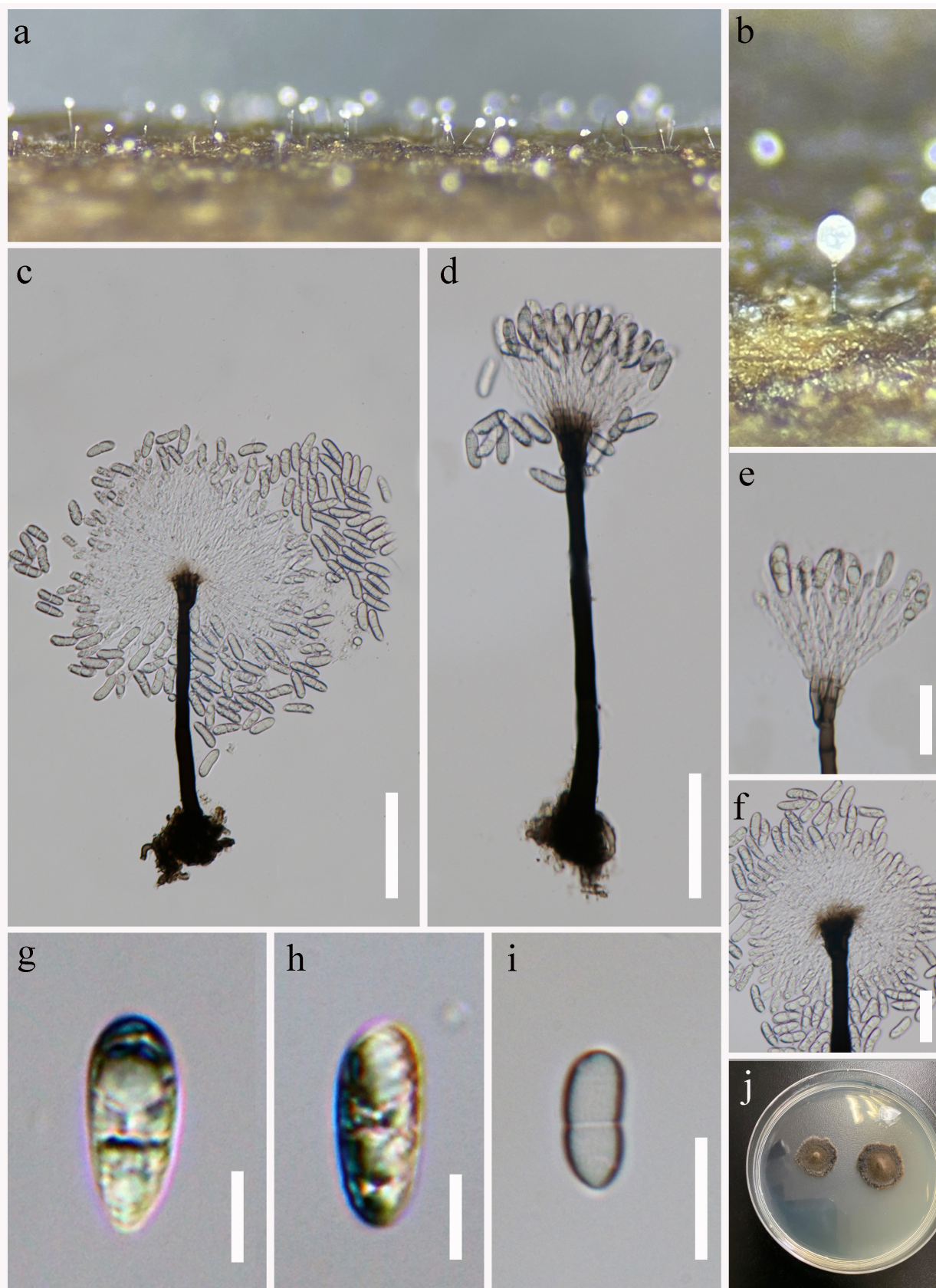


Fig. 96 *Sterigmatobotrys uniseptatus* (HKAS 136208) a, b Colony on natural substrates. c, d Conidiophores and conidia. e, f Conidiogenous cells with conidia. g-i Conidia. j Culture on PDA medium. Scale bars: c, d = 50 μm ; e, f = 20 μm . g-i = 10 μm .

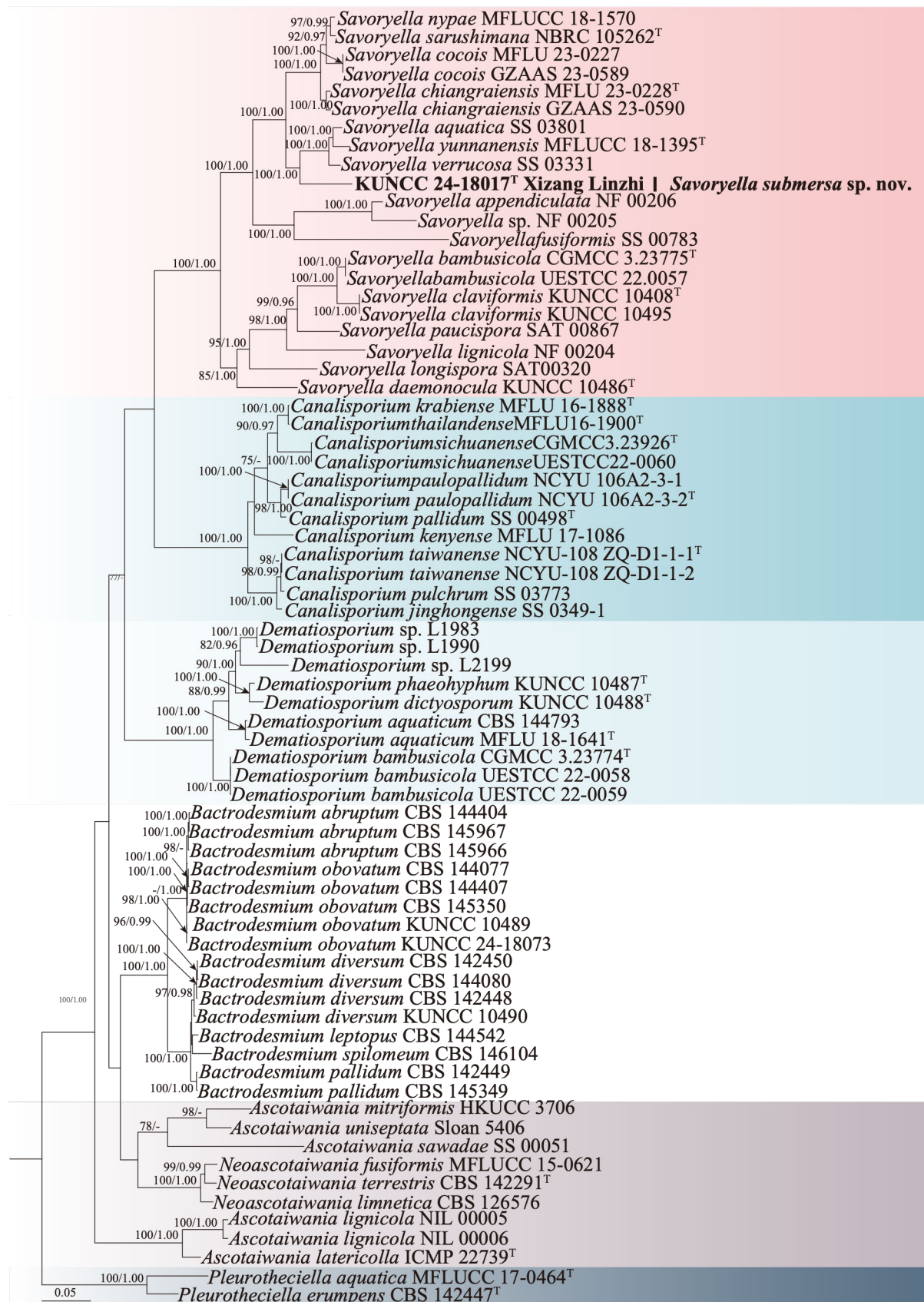


Fig. 97 Maximum likelihood majority rule consensus tree for *Savoryellales* using SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML BS/PP. The scale bar represents the expected number of changes per site. The tree is rooted with *Pleurotheciella aquatica* (MFLUCC 17-0464) and *P. erumpens* (CBS 142447). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

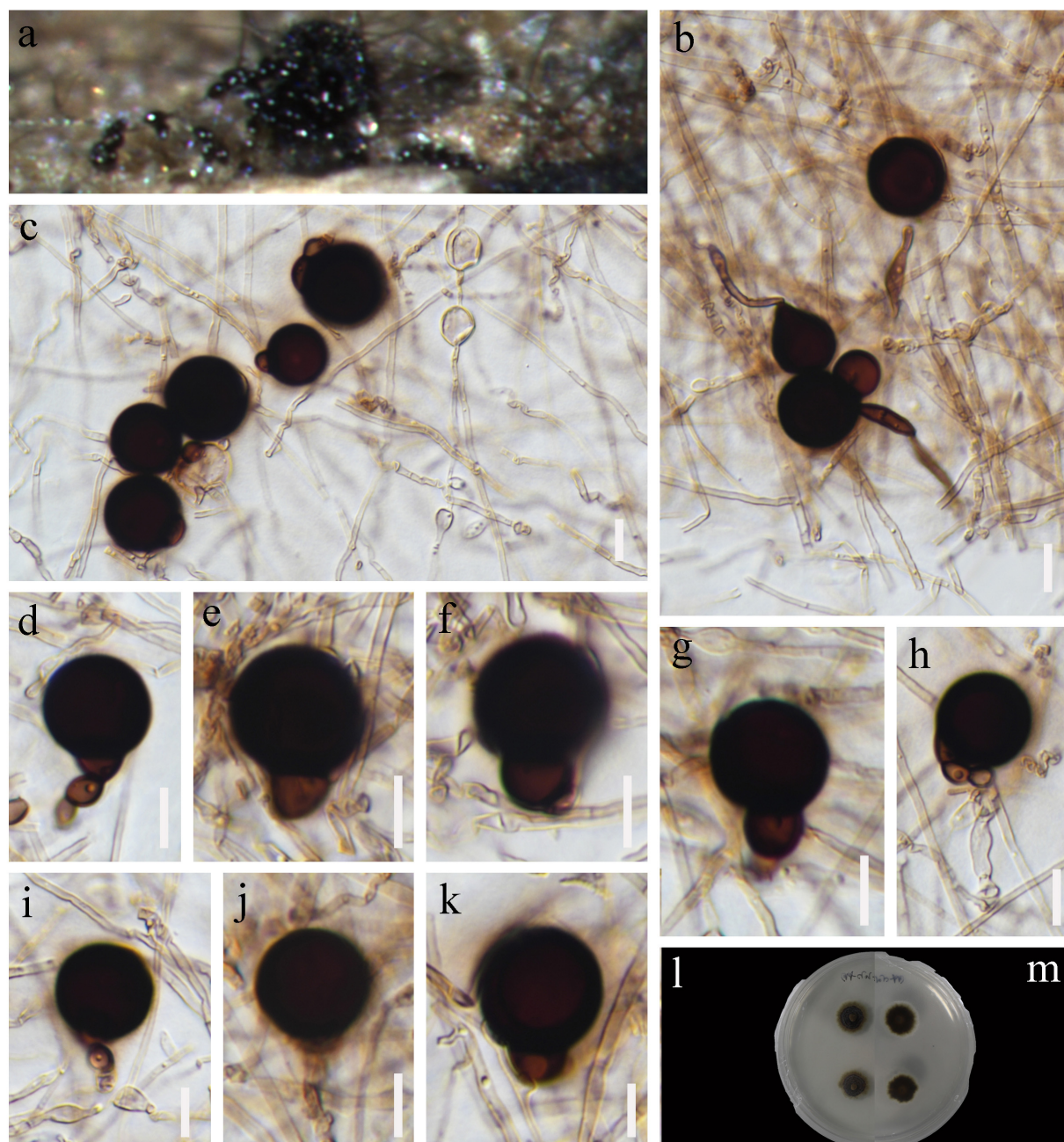


Fig. 98 *Savoryella submersa* (HKAS 136193, **holotype**) a Colony on natural substrates. b, c Conidiophores and conidia. d–k Conidia. l, m Culture on PDA medium, l from above, m from below. Scale bars: b–k = 10 µm.

62. *Dichotomopilus ramosissimus* X. Wei Wang & Samson, Studies in Mycology 84, 217 (2016)

= *Chaetomium ramosissimum* X. Wei Wang & L. Cai, Mycological Progress 13, 725 (2014)

Chinese name: – 多分枝二叉孢 (duo fen zhi er cha bao)

Index Fungorum number: IF 818869; **Facesoffungi number:** FoF 07245

Saprobic on decaying stems of *Chromolaena odorata*.

Sexual morph: Ascomata (on PDA) 700 × 500 µm diam, superficial, subglobose or ellipsoidal, brown to black, ostiolate. *Peridium* comprising brown, angular, or elongated cell structures that resemble hyphae. Terminal hairs erect, irregular in length, dark brown, dichotomously branched at wide to acute angles starting, verrucose. Thinner hairs resembling terminal setae, aseptate. Lateral hairs reduced to

short spines. *Asci* already deliquescent. *Ascospores* 5–8 × 3–5 µm ($\bar{x}$ = 6.5 × 4, n = 30), pale brown when young, rather brown when mature, ovate to limoniform, thin-walled, smooth-walled, aseptate. **Asexual morph:** Undetermined.

Culture characteristics: Colonies on PDA, entire edge, about 50 mm diam. after 20 days of incubation at 25°C, white to pale yellow, sparse, floccose aerial hyphae, without pigment, reverse yellow, Ascomata is produced after 80 days.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Jinghong City, on dead twigs of *Chromolaena odorata*, 7 September 2022, Shu-Cheng He, HSC1042 (HKAS 150298).

Known distribution: India, China, UK (Wang et al. 2016b; Chethana et al. 2021b).

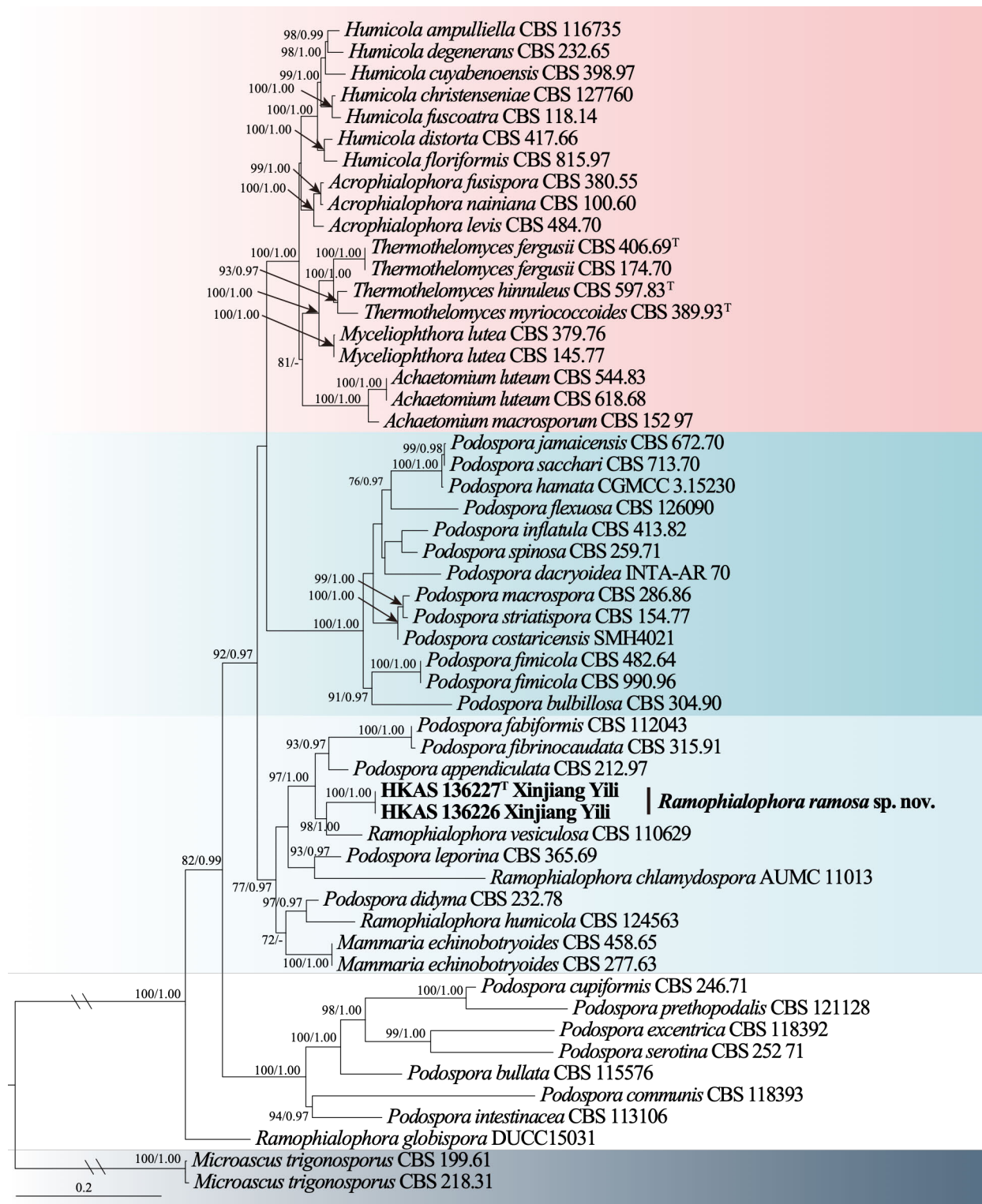


Fig. 99 Maximum likelihood majority rule consensus tree for *Bombardiaceae* using SSU, ITS, LSU, *rpb2* and *tef1-α* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML/BYPP. The scale bar represents the expected number of changes per site. The tree is rooted with *Microascus trigonosporus* (CBS 199.61 and CBS 218.31). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Known hosts: *Clematis vitalba*, *Dolichandrone spathacea*, *Panax notoginseng* (Wang et al. 2016b; Chethana et al. 2021b), *Chromolaena odorata* (this study).

Notes: Wang et al. (2014) introduced *Chaetomium ramosissimum* (Wang et al. 2014), which was subsequently reclassified as *Dichotomopilus ramosissimus* within the genus *Dichotomopilus* by Wang et al. (2016b). Based on multigene phylogenetic (ITS-LSU-*rpb2-tub2*) analysis, our isolate clusters with *D. ramosissimus* (Fig. 101).

Morphologically, our isolate is similar to *D. ramosissimus*, both having dichotomously or irregularly branched. *D. ramosissimus* is by Wang et al. (2016b) first report (Wang et al. 2014, 2016). In addition, the sexual morph has been reported from China (Zhang et al. 2017a) and India (Chethana et al. 2021b). Thus, we report this collection as a new host record of *D. ramosissimus* from Yunnan Province, China, and provide additional molecular and morphological photoplates for this species.

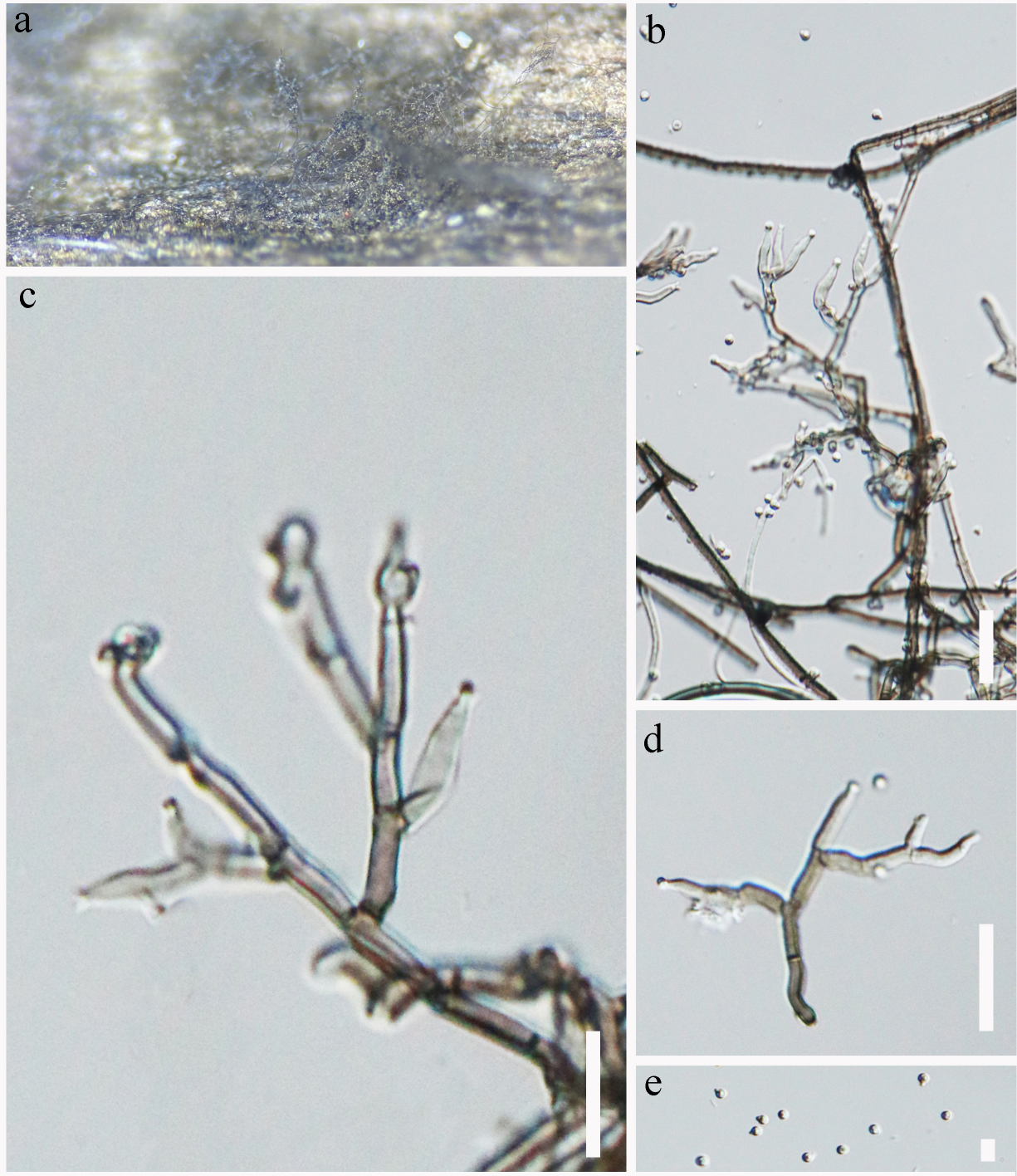


Fig. 100 *Ramophialophora ramosa* (HKAS 136227, holotype) a Colony on natural substrates. b, c Conidiophores and conidia. d Conidiogenous cells. e Conidia. Scale bars: b–d = 20 µm, e = 5 µm.

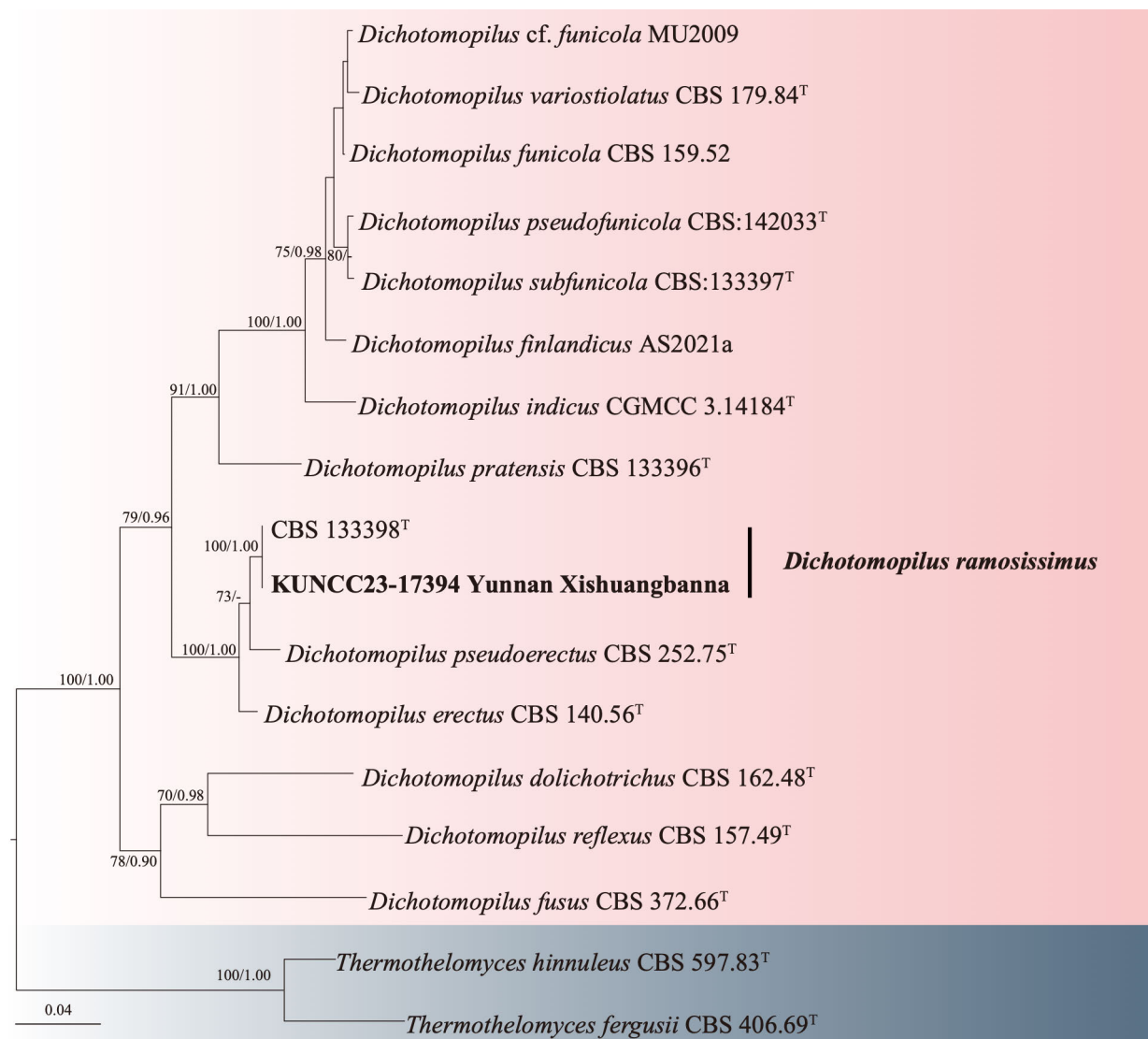


Fig. 101. Phylogram generated from the maximum likelihood analysis based on the combined LSU, ITS, *tub2* and *rpb2* sequence data of the genus *Dichotomopilus*. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Sordariaceae G. Winter

Neodictyosporium Tennakoon, C.H. Kuo & K.D. Hyde

Neodictyosporium was established by Tennakoon et al. (2021) to accommodate a dictyosporium-like coelomycetous fungus that produces cheirosporous conidia. The asexual morph is characterized by pycnidial, superficial, subglobose conidiomata, holoblastic, determinate, terminal, cylindrical to subcylindrical, subhyaline to pale brown conidiogenous cells, and dimorphic conidia; the cheirosporous conidia are hyaline to pale brown, consisting of arms, euseptate, with a basal connecting cell; the clavate to obovoid conidia are hyaline, septate, guttulate, smooth-walled (Tennakoon et al. 2021; Crous et al. 2024; Yu et al. 2024). Phylogenetic analyses based on a multi-locus dataset (LSU, SSU, and *rpb2*) placed this genus within *Sordariales* genera *incertae sedis* (Tennakoon et al. 2021). Subsequent studies by Yu et al. (2024) on fungi associated with bamboo substrates revealed the sexual morph of *Neodictyosporium*, which is characterized by immersed to semi-immersed, subglobose ascomata, hyaline,

septate paraphyses, 8-spored, unitunicate, cylindrical asci with long pedicellate, and an apical ring, and fusiform, hyaline, septate ascospores, with or without a mucilaginous sheath (Yu et al. 2024). Based on comprehensive phylogenetic analyses, Yu et al. (2024) elevated *Neodictyosporium* to familial rank, resulting in the establishment of *Neodictyosporiaceae*, a monotypic family that currently comprises only this genus. Species of *Neodictyosporium* are saprobic and inhabit terrestrial environments, typically occurring on decaying plant material such as *Macaranga tanarius*, *Juncus maritimus*, and various bamboo species (Tennakoon et al. 2021; Crous et al. 2024; Yu et al. 2024). To date, six species have been described within the genus, among which *N. bambusae* and *N. sexuale* represent the sexual morphs. These species have been recorded only from China and the Netherlands, suggesting a geographically restricted and potentially underexplored distribution (Tennakoon et al. 2021; Crous et al. 2024; Yu et al. 2024).

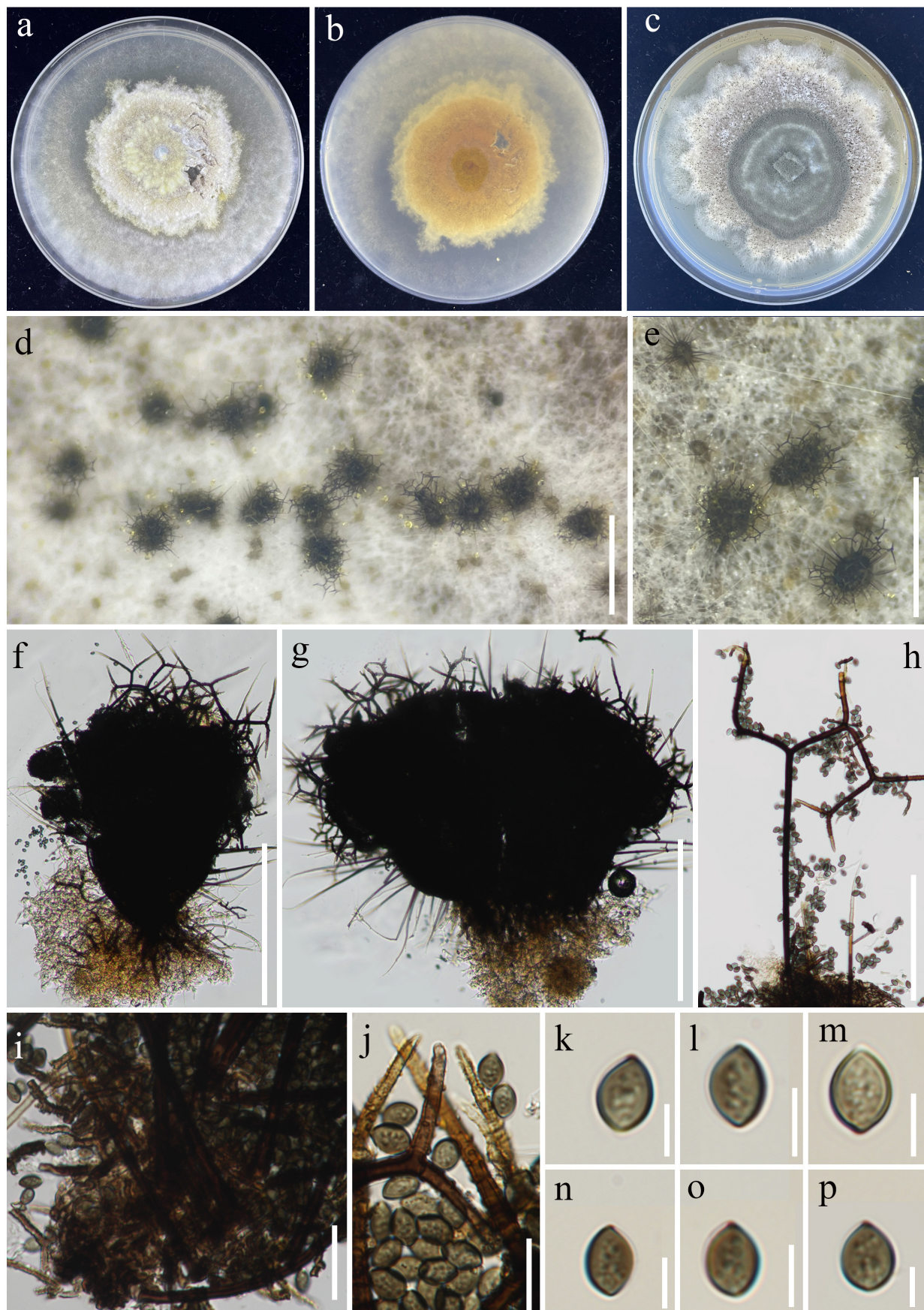


Fig. 102 *Dichotomopilus ramosissimus* (HKAS 150298, new host record). a–c Strain on PDA. d, e Ascomata on PDA. f, g Ascomata. h Mature ascomata on lacatophenol mount. i, j Terminal and Lateral ascomatal hairs. k–p Ascospores. Scale bars: d, e = 1000 μ m, f, g = 250 μ m, h = 100 μ m, i, j = 10 μ m, k–p = 5 μ m.

63. *Neodictyosporium lacustre* H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 104

Chinese name: – 杜鹃湖新砖格孢 (du juan hu xin zhuan ge bao)

Index Fungorum number: IF 905282; **Facesoffungi number:** FoF 19331

Etymology: “lacustre” refers to the Dujuanhu Lake in Yunnan Province, China, where the species was collected.

Holotype: HKAS 132049

Saprobic on submerged decaying wood in freshwater habitat. **Sexual morph:** Ascomata 354–382 µm high, 328–366 µm diam, semi-immersed to immersed, scattered, solitary, subglobose or ellipsoidal, dark brown to black, carbonaceous, uniloculate, biloculate, ostiolate. Ostiolar neck central or oblique, short, 86–114 µm long, 138–168 µm wide, papillate, rounded, dark brown. Peridium 22–35 µm thick, composed of several layers of pale brown to dark brown, thick-walled cells of *textura angularis*. Paraphyses 2 µm wide, branched, septate, hyaline, numerous, hyphae-like, anastomosing above the asci. Asci 97–129 × 13–16 µm ($\bar{x}$ = 113 × 14 µm, n = 20) µm, 8-spored, unitunicate, inoperculate, cylindrical, straight or slightly curved, apex rounded, long pedicellate, with an apical annulus. Ascospores (20–)24–27 × 7–8 µm ($\bar{x}$ = 25 × 8 µm, n = 40), overlapping, uniseriate, fusiform, straight or slightly curved, hyaline, 3-septate, slightly constricted at the septa, guttulate, smooth or verrucous, without mucilaginous sheath. **Asexual morph:** Undetermined.

Culture characteristics: Conidia germinating on PDA within 12 h and germ tubes produced from both ends and around conidia. Colonies on PDA reaching 2–3 cm diameter after two months at room temperature (around 22 °C) in the dark, dense, velvety, pale brown to dark brown, smooth margins from above; dense, brown to dark brown, smooth margins from below.

Material examined: CHINA, Yunnan Province, Dujuanhu Lake, 24°32'15.6" N, 100°1'30.00" E, 2500 m a.s.l., on the unidentified submerged decaying wood, 23 February 2023, H.W. Shen, L2085 (HKAS 132049, holotype), ex-type culture KUNCC 23-13778 = DLUC 2090.

Notes: Phylogenetic analyses showed that *Neodictyosporium lacustre* (KUNCC 23-13778 = DLUC 2090) formed a distinct clade at the base of the *N. bambusae* (CGMCC 3.27440 and ESTCC 24.0111), *N. cheirosporum* (CGMCC 3.27450 and UESTCC 24.0121), and *N. sichuanense* (CGMCC 3.27593) lineages, with 100% ML and 1.00 PP statistical support (Fig. 103). Among these, only *N. bambusae* is known to possess a sexual morph. *Neodictyosporium lacustre* is morphologically similar to *N. bambusae* in having semi-immersed, subglobose, uni- or multi-loculate ascomata, numerous, hyphae-like, unbranched, hyaline, septate paraphyses, 8-spored, unitunicate, cylindrical asci with long pedicellate and an apical ring, and fusiform, hyaline, septate ascospores (Yu et al. 2024). However, *N. lacustre* differs from *N. bambusae* in having larger ascospores and lacking a gelatinous sheath (Yu et al. 2024). Nucleotide comparisons revealed that *N. lacustre* differs from *N. bambusae* by 13 bp (including 5 gaps) in the ITS region, 2 bp in the LSU region, and 15 bp in the *tef1*-α region. In comparison to *N. cheirosporum*, *N. lacustre* shows 15 bp (including 6 gaps) differences in ITS, 3 bp in LSU, and 14 bp in the *tef1*-α, while differences between *N. lacustre* and *N. sichuanense* are 16 bp (including 7 gaps) bp in ITS, 3 bp in LSU, and 15 bp in the *tef1*-α. Based on both morphological characteristics and

molecular evidence, we introduce *N. lacustre* as a novel species. Notably, it represents the first species of *Neodictyosporium* documented from freshwater habitats.

Sporidesmiales* Crous**Sporidesmiaceae* Fr.*****Sporidesmium* Link**

Sporidesmiaceae was established by Fries (1849) and later redefined by Su et al. (2016) to delineate a monophyletic clade of *Sporidesmium* species, designated as *Sporidesmiaceae* sensu stricto. Members of this family are saprobic, predominantly found on woody plant material in both aquatic and terrestrial environments. They exhibit diverse morphologies but are primarily hyphomycetous fungi. Asexual morphs are characterized by brown, cylindrical conidiophores and conidia with distinctive septation. *Sporidesmium* was introduced by Link (1809) without the designation of a type species. Initially, the genus encompassed a vast array of species, reflected in nearly 500 epithets listed in Index Fungorum (2025). However, Shenoy et al. (2006) revealed that *Sporidesmium* sensu lato was polyphyletic within Ascomycota. Su et al. (2016) redefined the genus as a concise, monophyletic clade (*Sporidesmium* sensu stricto). Morphologically, *Sporidesmium* is distinguished by macronematous, mononematous, erect conidiophores, and monoblastic, holoblastic, percurrently proliferating conidiogenous cells. The conidia vary in shape, including ovoid, obpyriform, and rostrate forms, and are either euseptate or distoseptate, sometimes with an appendage or mucilaginous sheath (Su et al. 2016; Luo et al. 2019; Bao et al. 2021; Yang et al. 2018c, 2023a).

64. *Sporidesmium fluviatile* R.J. Xu, Q. Zhao & K.D. Hyde, sp. nov. Fig. 106

Chinese name: – 河流基孢菌 (he liu shen bao jun)

Index Fungorum number: IF 905049; **Facesoffungi number:** FoF 17442

Etymology: referring to the riverine habitat where the species is typically found

Holotype: HKAS 136180

Saprobic on submerged decayed wood in freshwater habitats. **Sexual morph:** Undetermined. **Asexual morph:** Colonies effuse, velvety, scattered or in small groups, pale brown, glistening. **Mycelium** partly immersed, mostly immersed, composed of septate, smooth. **Conidiophores** 38–54 × 3–5 µm ($\bar{x}$ = 48 × 4 µm, n = 15), macronematous, mononematous, erect, straight or slightly flexuous, solitary or 2-groups, cylindrical, smooth-walled, 2–4-septate, unbranched, pale brown to brown, truncate at the apex, often with hyphopodium at the base. **Conidiogenous cells** 17–19 × 3–4 µm ($\bar{x}$ = 18 × 4 µm, n = 15), holoblastic, monoblastic, terminal, integrated, determinate, cylindrical, pale brown. **Conidia** 40–51 × 9–14 µm ($\bar{x}$ = 45 × 10 µm, n = 20), acrogenous, solitary, lageniform, obclavate, rostrate, straight or slightly curved, 2–8-distoseptate, pale brown to brown, tapering at apex, truncate at the base, with a darkened scar at the base, smooth-walled, with a mucilaginous sheath over the apex.

Culture characteristics: Conidia germinating on PDA medium within 48 h and germ tubes arising from terminal end of conidium. Colonies grown on PDA reached 30 mm diam at room temperature in one month, irregular, with dense, wrinkled, viscous, pulvinate, grayish-white mycelium in the middle, sparse, mostly immersed mycelium which producing

dark brown to black pigment at the edge, from below dark brown to black with entire margin.

Material examined: CHINA, Yunnan Province, Gongshan County, Dizhengdang Village, Dulong River, 28° 4' 47" N, 98° 19' 32" E, 1680 m a.s.l., on decaying wood submerged in a freshwater river, 10 July 2020, R.J. Xu, MD-271 (HKAS 136180, holotype), ex-type culture KUNCC 24-18035.

Notes: Morphologically, *Sporidesmium fluviatile* shares common characteristics with *S. aquaticivaginatum* and *S. olivaceoconidium* in having macronematous, mononematous, erect, straight or slightly, cylindrical conidiophores and conidia possess a mucilaginous sheath (Hyde et al. 2016; Luo et al. 2019; Bao et al. 2021). However, *S. fluviatile* differs from *S. aquaticivaginatum* in having smaller conidiophores (38–54 × 3–5 vs. 60–125 × 4–6 µm) and fewer conidia septate (2–8 vs. 6–10 distoseptate). It differs from *S. olivaceoconidium* in pale brown to brown, rostrate conidia. In addition, the phylogenetic analyses showed that *S. fluviatile* formed a distinct branch in *Sporidesmium* (Fig. 105).

Torpedosporales E.B.G. Jones, Abdel-Wahab & K.L. Pang

Juncigenaceae E.B.G. Jones, Abdel-Wahab & K.L. Pang

Juncigena Kohlm., Volk. -Kohlm. & O.E. Erikss.

Juncigena was introduced by Kohlmeyer et al. (1997) based on the type species *J. adarca*, which was collected from senescent leaves of *Juncus roemerianus* from Atlantic coast in the USA. It is characterized by immersed, subglobose to pyriform, ostiolate, coriaceous, fuscous ascomata with cylindrical, periphysate neck, 8-spored, fusiform to cylindrical, short pedunculate, unitunicate asci with a non-amyloid apical ring, and uni- to biseriate, fusiform to ellipsoidal, 3-septate, hyaline ascospores (Kohlmeyer et al. 1997). Its asexual morph was described as *Cirrenalia adarca* with helicoid and brown conidia (Kohlmeyer et al. 1997). Abdel-Wahab et al. (2010) transferred *Cirrenalia adarca* to *Moheitospora* based on phylogenetic and morphological evidence. Subsequently, Réblová et al. (2016a) synonymized *Moheitospora* under *Juncigena*.

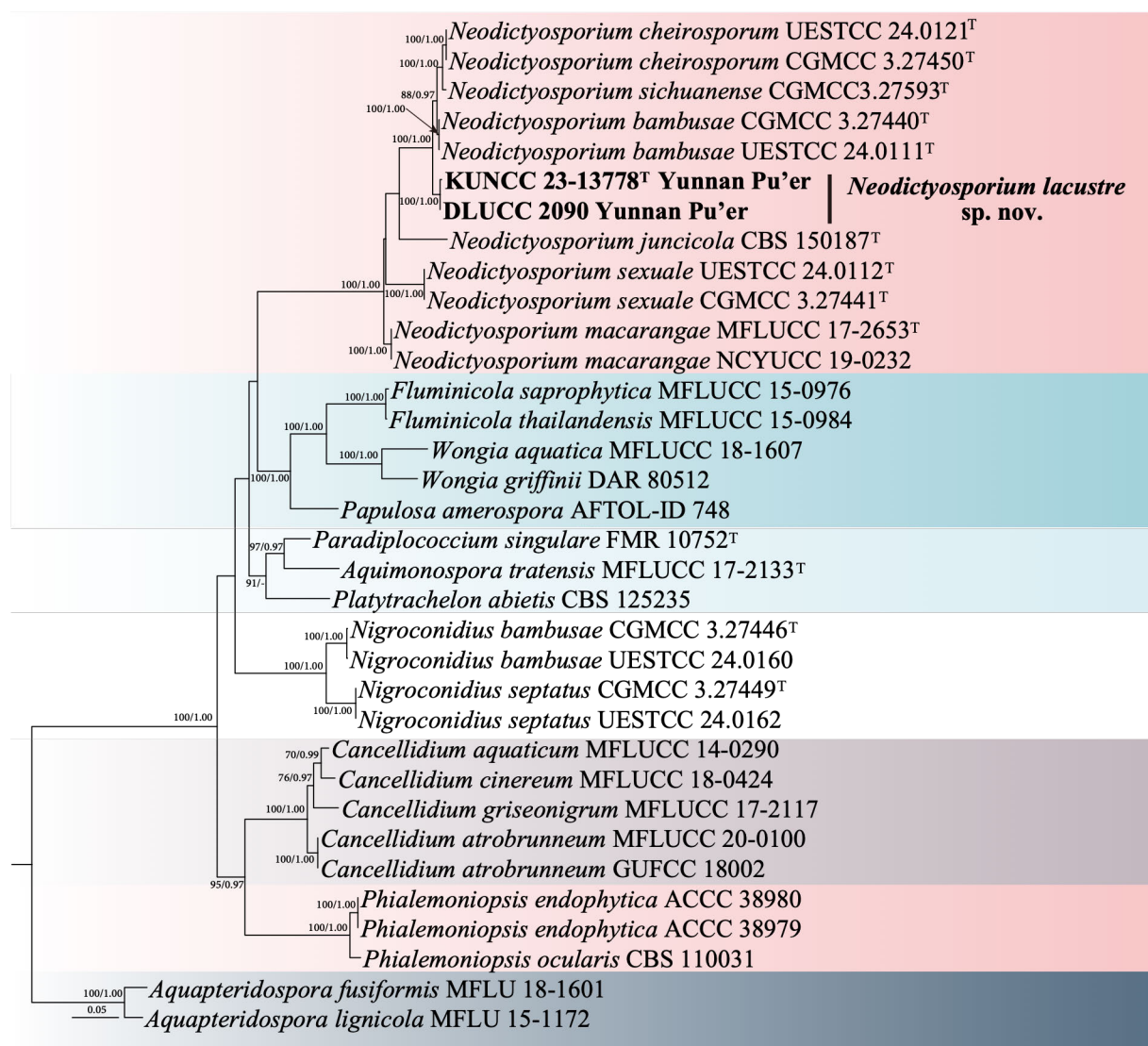


Fig. 103 Phylogram generated from the maximum likelihood analysis based on the combined LSU, ITS, *tub2* and *rpb2* sequence data of the genus *Sordariaceae*. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

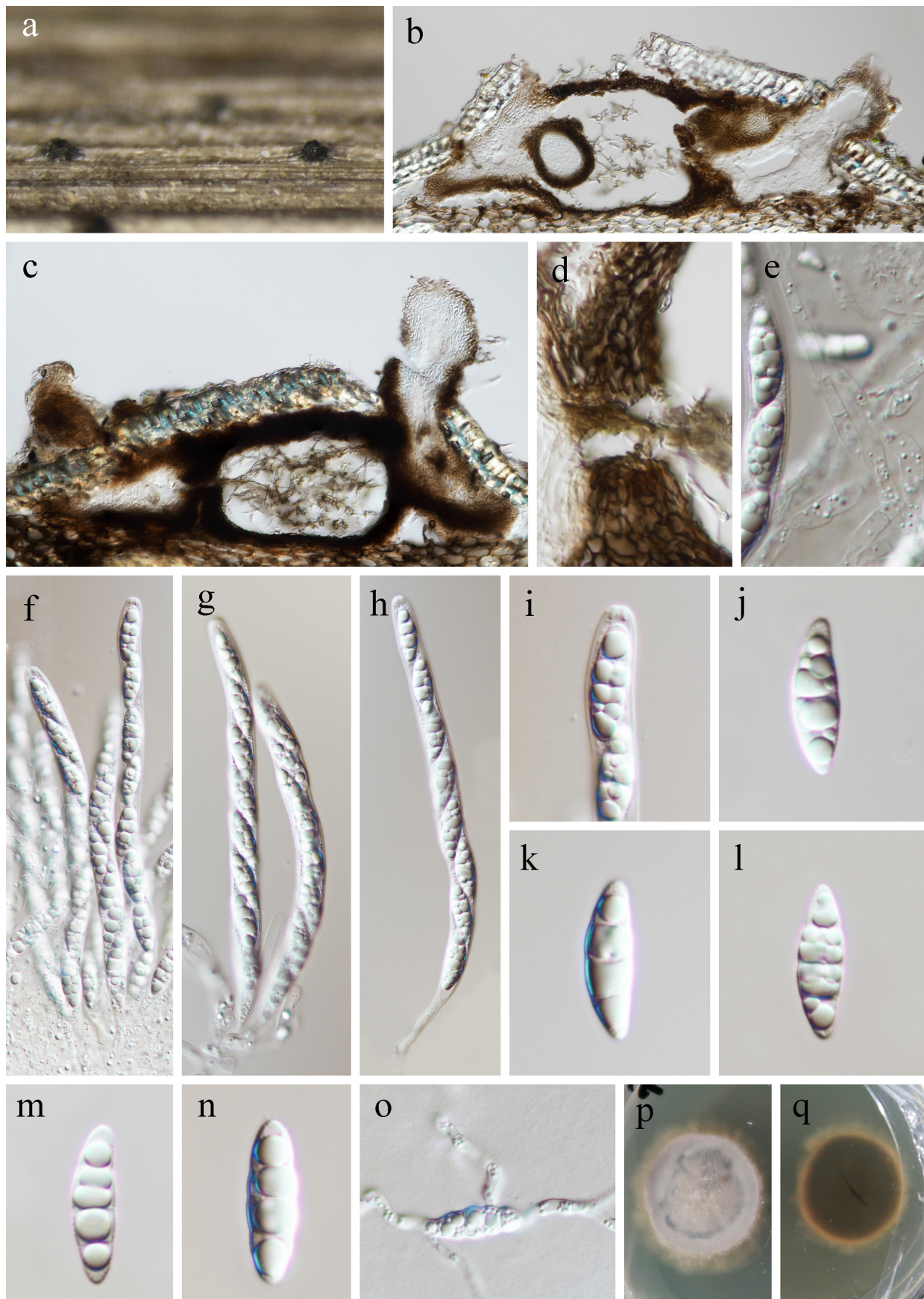


Fig. 104 *Neodictyosporium lacustre* (HKAS 132049, **holotype**). a Appearance of ascomata on the host. b, c Sections of ascomata. d Section of peridium. e Paraphyses. f–h Asci. i Apex of ascus with apical annulus. j–n Ascospores. o Germinated ascospore. p, q Culture on PDA, surface (p) and back (q). Scale bar: c–e 50 μ m, f, g 10 μ m, h–n 20 μ m.

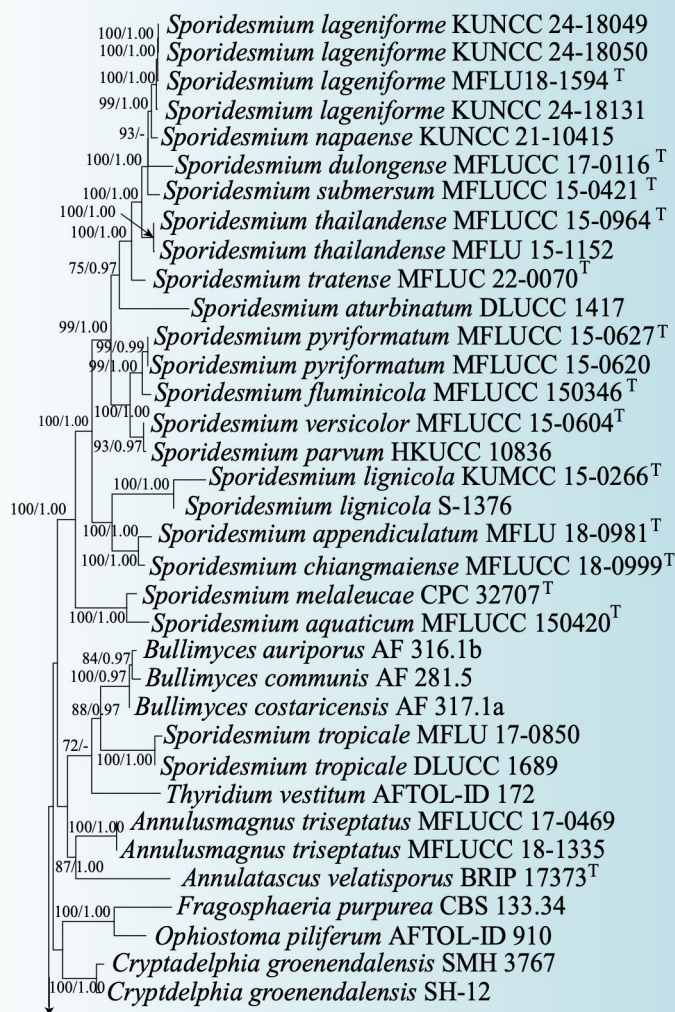


Fig. 105 Phylogram generated from the maximum likelihood analysis based on the combined LSU, ITS, *tub2* and *rpb2* sequence data of the genus *Sporidesmiales*. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes, respectively. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

65. *Juncigena hyalina* J. Ma & Y.Z. Lu, sp. nov. Fig. 108

Chinese name: – 透明灯草菌 (tou ming deng cao jun)

Fungal Names number: FN 573590; **Facesoffungi number:** FoF 19332

Etymology: the species epithet "hyalina" refers to its hyaline ascospores

Holotype: GZAAS 23-0032

Saprobic on submerged decaying twigs in freshwater habitats. **Sexual morph:** Ascomata 100–150 µm high, 110–210 µm wide, subglobose to pyriform, completely submersed under the cortex, ostiolate, papillate, coriaceous, fuscous, single. **Neck** cylindrical, curved, dark brown, ostiolar canal periphysate. **Peridium** 8–25 µm thick, comprising several layers of pale brown to brown cells of textura angularis. **Hamathecium** composed of numerous unbranched, septate pseudoparaphyses, attached at the top and bottom. **Asci** not observed. **Ascospores** 29–47 × 4.5–6.5 µm ($\bar{x}$ = 40.5 × 5.5 µm, n = 25), fusiform to elongate ellipsoidal, hyaline, 3-septate, slightly curved, guttulate, thin-walled, smooth. **Asexual morph:** Undetermined.

Culture characteristics: Ascospores germinated on PDA within 12 h, at room temperature and germ tubes produced

from both ends of the ascospores. Colonies on PDA reaching 4 cm diam after four weeks. Colonies superficial, dense, circular, with slightly raised center and entire edge, white from above, pale yellow from below.

Material examined: CHINA, Xinjiang Autonomous Region, Bayingolin, Bohu County, 41°51'54" N, 86°43'46" E, 991 m a.s.l., on decaying wood submerged in a freshwater river, 22 July 2021, Y.Z. Lu, Lu 1 (GZAAS 23-0032, holotype), ex-type culture (GZCC 23-0483).

Notes: In the phylogenetic analyses (Fig. 107), our strain GZCC 23-0483 grouped with *Juncigena adarca* (JK5548A) and *J. fruticosae* (EF14) with 94% ML/1.00 BYPP support. Our collection resembles the type species *J. adarca* in having subglobose to pyriform, ostiolate ascomata, and fusiform to ellipsoidal, hyaline, 3-septate ascospores (Kohlmeyer et al. 1997). However, our collection has smaller ascomata (100–150 × 110–210 µm vs. 225–400 × 135–200 µm) and longer and thinner ascospores (29–47 × 4.5–6.5 µm vs. 26.5–34.5 × 6–7 µm) (Kohlmeyer et al. 1997). *Juncigena fruticosae* is characterized by its hyphomycetous asexual morph, thus, their morphology is incomparable. However, phylogenetic analyses show our collection is a distinct species.

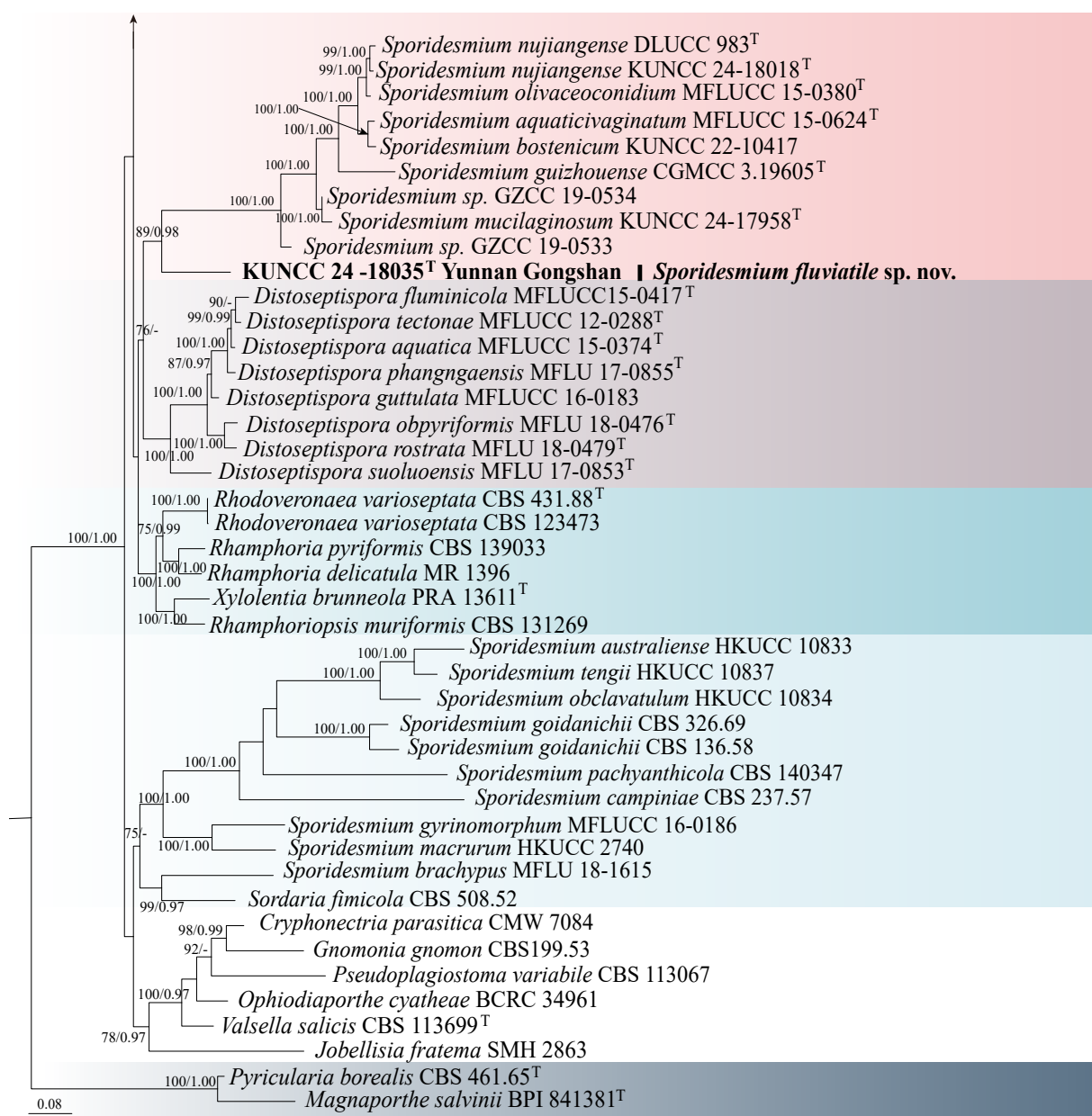


Fig. 105 (continued)

Xylariaceae Tul. & C. Tul.***Digitodochium*** Tubaki & Kubono

Digitodochium was established by Tubaki & Kubono (1989) to accommodate an asexual species, *D. rhodoleucum* (the type species), originally described from corticated twigs of *Fagus crenata* in Japan. For over three decades, no additional reports of this genus were published until recently, when Voglmayr et al. (2020) linked the sexual and asexual morphs of *Digitodochium*. Subsequently, six additional species were introduced within *Digitodochium*, five from China and one from Australia (Dissanayake et al. 2024; Liu et al. 2025; Tian et al. 2025). Currently, eight species are accepted in the genus, they occurring as saprobes on decaying branches or leaves of *Grevillea sessilis*, *Fagus sylvatica* and various bamboo species (Voglmayr et al. 2020; Dissanayake et al. 2024; Liu et al. 2025; Tian et al. 2025). Both sexual and asexual morphs are known in the genus; the sexual morph is characterized by scattered or gregarious, solitary, immersed,

subglobose, black ascomata, with a small black clypeus; papillate, central, black ostioles, with a conical neck; hyaline, septate, unbranched, cellular paraphyses; unitunicate, cylindrical to slightly fusiform asci, apically rounded, with a wedge-shaped, apical ring; uniseriate, aseptate, ellipsoid to fusiform ascospores, with or without sheath. And the asexual morph is characterized by sporodochial, immersed, cushion-shaped, subglobose to irregular conidiomata; aggregated, hyaline, branched conidiophores; integrated, holoblastic conidiogenous cells; subhyaline, staurosporous conidia, consisting of a cylindrical main axis with whorls of lateral branches arising at wide angles from the basal 1–3 cells of the main axis, septate, gradually tapering towards the top, narrowly rounded tips (Voglmayr et al. 2020; Dissanayake et al. 2024; Liu et al. 2025; Tian et al. 2025). In this study, we discuss a novel saprobic taxon collected on submerged decaying bamboo wood from freshwater habitat in Yunnan Province, China.

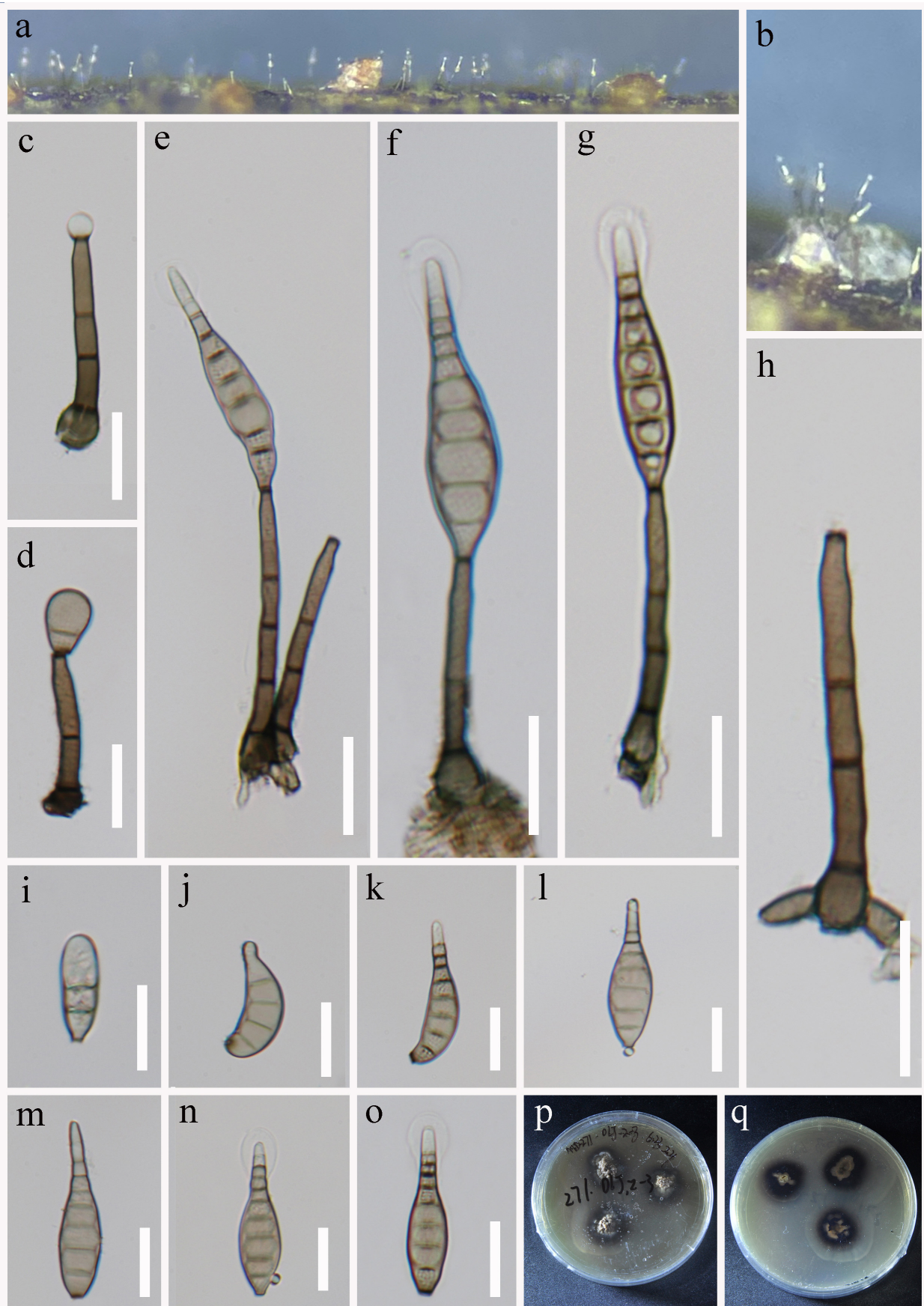


Fig. 106 *Sporidesmium fluviatile* (HKAS 136180, holotype) a, b Colony on natural substrates. c–g Conidiophores with conidia. h Conidiophores with conidiogenous cells. i–o Conidia. p, q Culture on PDA medium, p from above, q from below. Scale bars: c–o = 20 µm.

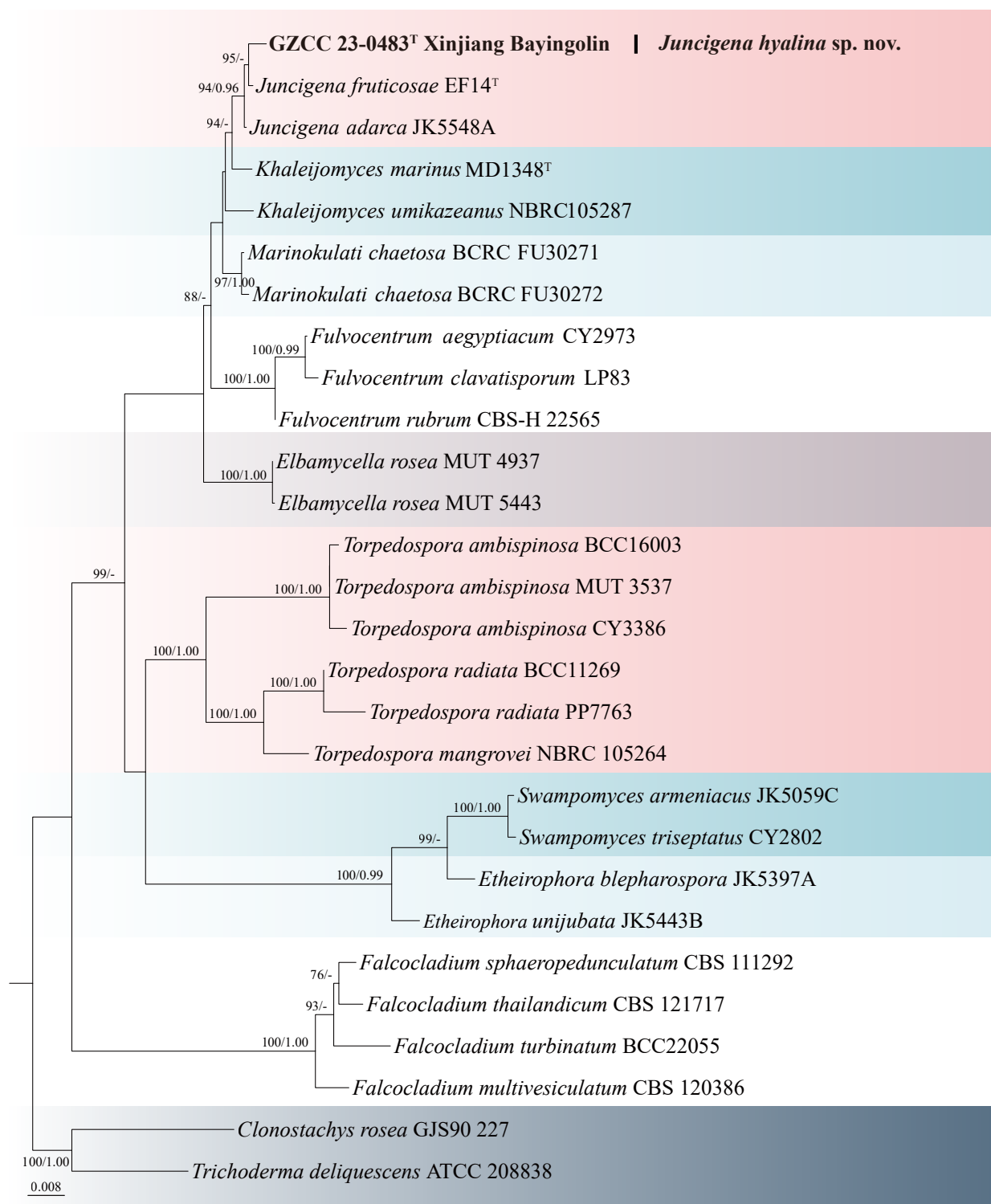


Fig. 107 *Clonostachys rosea* (GJS90 227) and *Trichoderma deliquescens* (ATCC 208838). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

66. *Digitodochium lacustre* H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 110

Chinese name: – 湖生指孢霉 (hu sheng zhi bao mei)

Index Fungorum number: IF 905283; **Facesoffungi number:** FoF 19887

Etymology: “lacustre” refers to the freshwater lake where the species was collected.

Holotype: HKAS 132103.

Saprobic on decaying submerged bamboo wood in a lake.

Sexual morph: *Ascomata* 430–490 µm high, 580–670 µm diam, scattered or gregarious, solitary, immersed, black, subglobose, papillate ostioles. *Ostioles* papillate, central, black, with a conical neck. *Peridium* uneven in thickness, 30–60 µm wide, composed of several layers of thick, dark brown to black, irregular cells of *textura angularis*. *Paraphyses* 2–3 µm wide, composed of numerous, filamentous, cellular, septate, guttulate, embedded in a gelatinous matrix. *Asci*

130–187(–208) × 10–13 µm ($\bar{x}$ = 162 × 11 µm, n = 20), 8-spored, unitunicate, cylindrical to slightly fusiform, straight or slightly curved, short-pedicellate, rounded at the apex. Ascospores 13–17 × 4.5–6 µm ($\bar{x}$ = 15 × 5.3 µm, n = 40), overlapping uniseriate, aseptate, ellipsoid to narrowly ellipsoid, hyaline to dark brown, smooth-walled, usually malachite green, slightly rounded ends, with a small cell at the base, 2–4 guttules, mostly with 2 large guttules, surrounded by a mucilaginous sheath, 15–21 µm wide. **Asexual morph:** Undetermined.

Culture characteristics: Ascospore germinated on PDA within 12 h and germ tubes produced from the ends of the ascospore. Colonies on PDA reaching 2.8–3 cm diam. after six weeks at room temperature, colony circular, smooth edge, surface hyphae cream to pale brown, flocculent, dense; reverse side cream, smooth, dense, smooth.

Material examined: CHINA, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'15.6" N, 100°1'30.00" E, 2500 m a.s.l., on a rotten bamboo branch submerged in water, 19 February 2023, H.W. Shen, L2087 (HKAS 132103, holotype); ex-type culture (KUNCC 23-13817).

Notes: Multigene phylogenetic analysis revealed that *Digitodochium lacustre* clustered with *D. zhangjiajieense* with 99% ML/1.00 BYPP bootstrap support (Fig. 109). Morphologically, *D. lacustre* resembles *D. ailaoshanense* in having scattered or gregarious, subglobose, immersed, black ascomata; unitunicate, cylindrical to slightly fusiform asci and aseptate, hyaline to dark brown, guttulate ascospores, with a small cell at the base, and surrounded by a mucilaginous sheath. However, *D. lacustre* is distinguished from *D. ailaoshanense* by having larger asci (130–187 × 10–13 µm vs. 70–110 × 6–9 µm). Comparison of ITS and LSU sequences between *D. lacustre* (KUNCC 23-13817) and *D. ailaoshanense* (HKAS 130308) showed nucleotide differences of 25 bp (excluding gaps) and 16 bp, respectively. Similarly, comparisons of ITS, LSU and *tub2* sequences between *D. lacustre* (KUNCC 23-13817) and *D. zhangjiajieense* (GMB5607) revealed nucleotide differences of 9 bp (including 2 gaps), 7 bp and 24 bp, respectively. Based on both morphological characteristics and molecular evidence, we introduce *D. lacustre* as a new species, marking the first record of a *Digitodochium* species from a freshwater habitat.

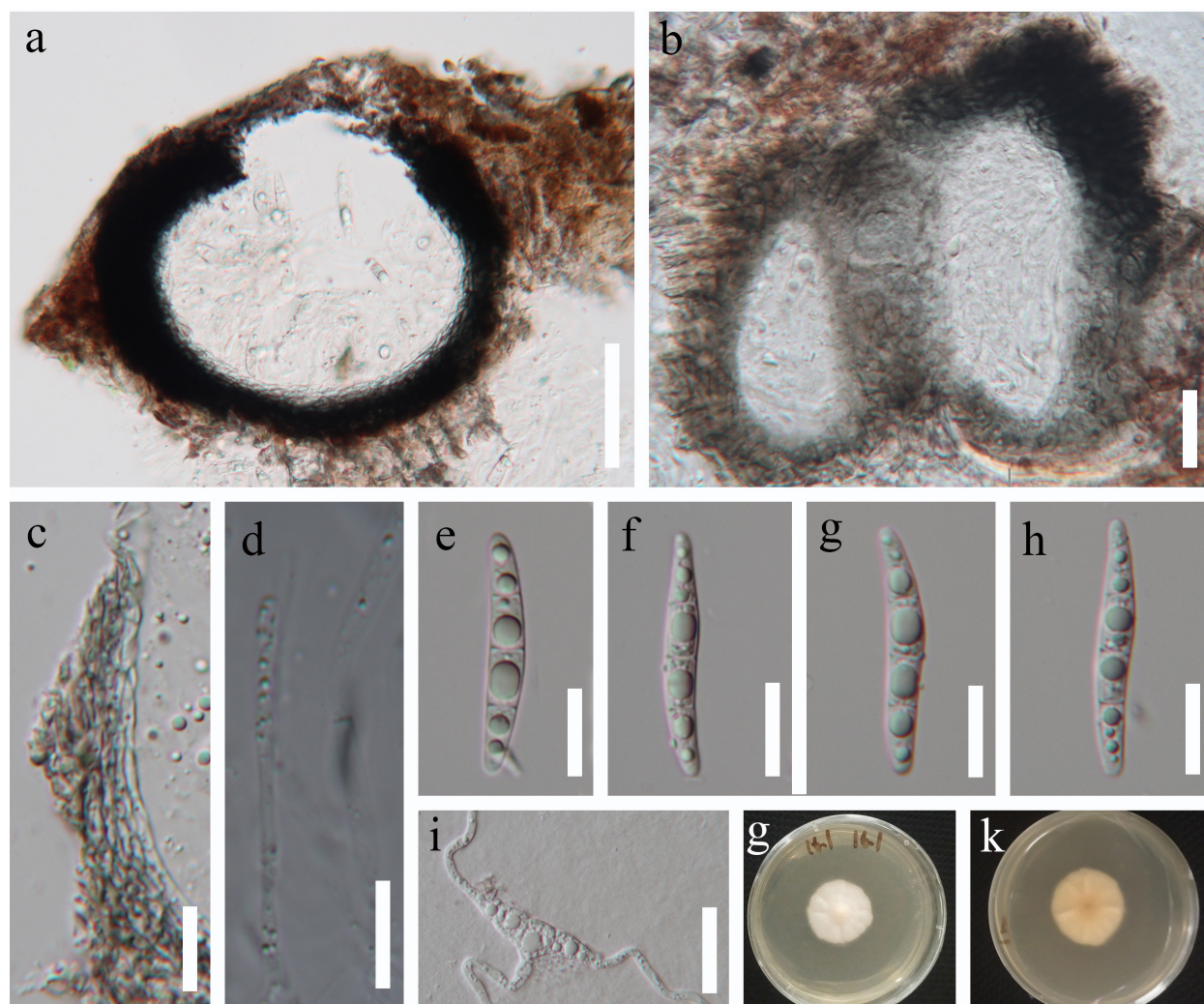


Fig. 108 *Juncigena hyalina* (GZAAS 23-0032, holotype) a, b Section through ascomata. c Peridium. d Pseudoparaphyses. e–h Ascospores. i Germinating ascospore. g, k Colonies on PDA. Scale bars: a, b, i = 10 µm, c, e–h = 20 µm, d = 5 µm.

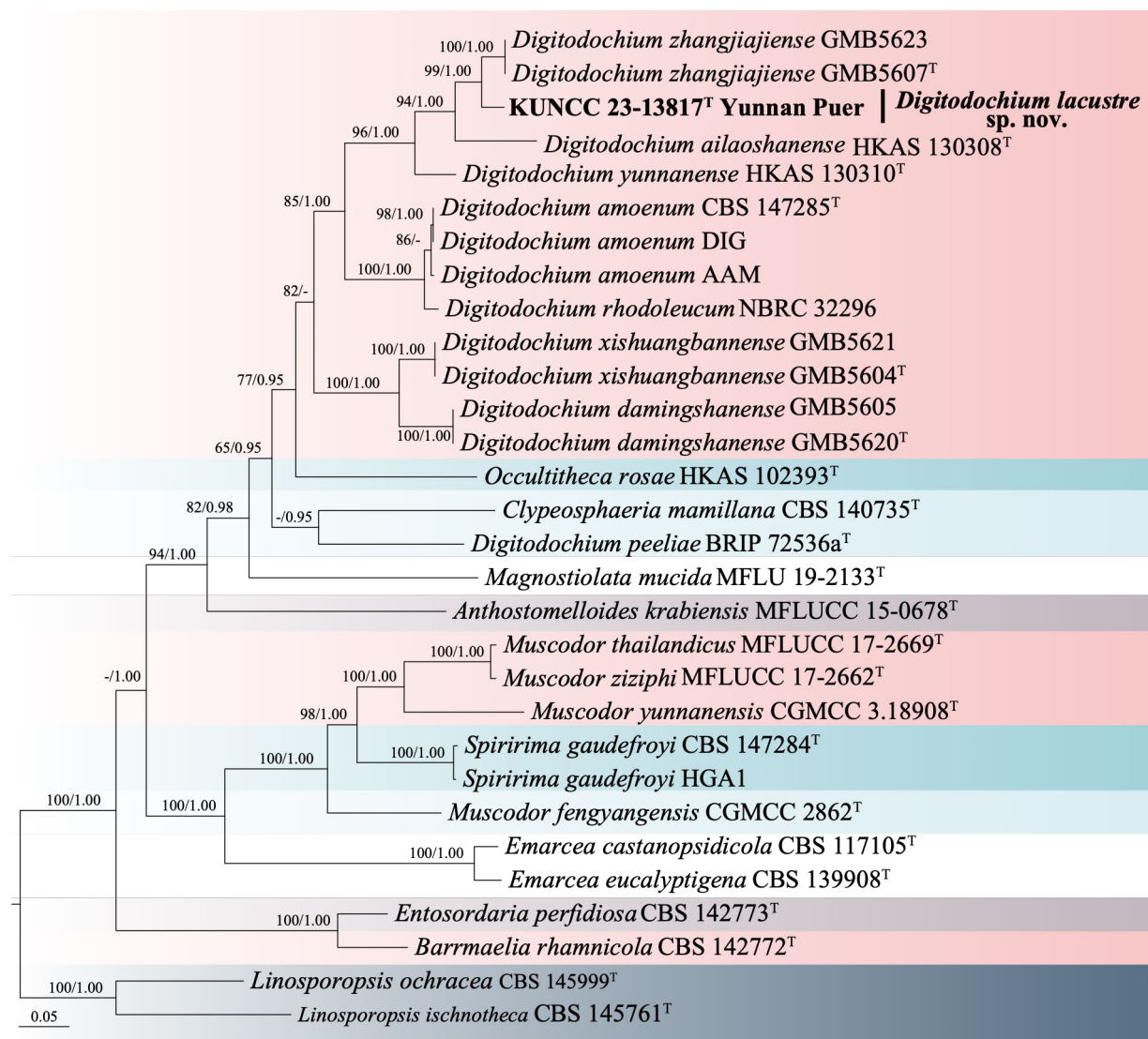


Fig. 109 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *rpb2* and *tub2* sequenced data. Thirty strains were included in the combined sequence analyses, which comprised 3817 characters with gaps (LSU = 787, ITS = 588, *rpb2* = 1022, *tub2* = 1420). Single gene analyses were also performed, and topology and clade stability were compared from the combined gene analyses. *Linosporopsis ischnotheca* (CBS 145761) and *L. ochracea* (CBS 145999) strains were used as the outgroup taxa. The final ML optimization likelihood is -27926.145972. The matrix included 1676 distinct alignment patterns, with 21.83% undetermined characters or gaps. Estimated base frequencies were obtained as follows: A = 0.234861, C = 0.271796, G = 0.258425, T = 0.234918; substitution rates AC = 1.379110, AG = 3.330310, AT = 1.229619, CG = 1.122043, CT = 5.312755, GT = 1.000000; gamma distribution. Bootstrap support values for ML (first set) equal to or greater than 70%, BYPP equal to or greater than 0.95 are given above or below the nodes. Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Sordariomycetes families incertae sedis

Junewangiaceae J.W. Xia & X.G. Zhang

Sporidesmiella P.M. Kirk

Sporidesmiella was established by Kirk (1982), with *S. claviformis* designated as the type species. It is characterized by clavate to obovoid or cuneate conidia with a few distosepta, rounded or coronate at the apex, which secede schizolytically from monoblastic, integrated, terminal, annellidic, or occasionally sympodially extending conidiogenous cells (Kirk 1982; Ma et al. 2012; Luo et al. 2019; Xiong et al. 2024). *Sporidesmiella* has been reported in various countries, including China, Mexico, Brazil, the Netherlands, and Thailand, and spans tropical and

subtropical regions (Wang 2005; Monteiro et al. 2014; Heredia et al. 2015; Luo et al. 2019; Crous et al. 2021; Dong et al. 2021).

Based on multigene phylogenetic analysis, Luo et al. (2019) placed *Sporidesmiella* within *Junewangiaceae*. Hyde et al. (2020b) classified the genus as *Diaporthomycetidae* genera *incertae sedis*, observing that *Sporidesmiella* clustered in a separate clade with *Junewangiaceae*. However, further phylogenetic evidence from Dong et al. (2021a) strongly supported its placement within *Junewangiaceae*. Currently, *Sporidesmiella* has 54 records listed in Index Fungorum (2025), but only 13 species have corresponding DNA sequences in GenBank. While taxonomic revisions have been made for some species, the classification of many others remains uncertain due to insufficient sequence data.

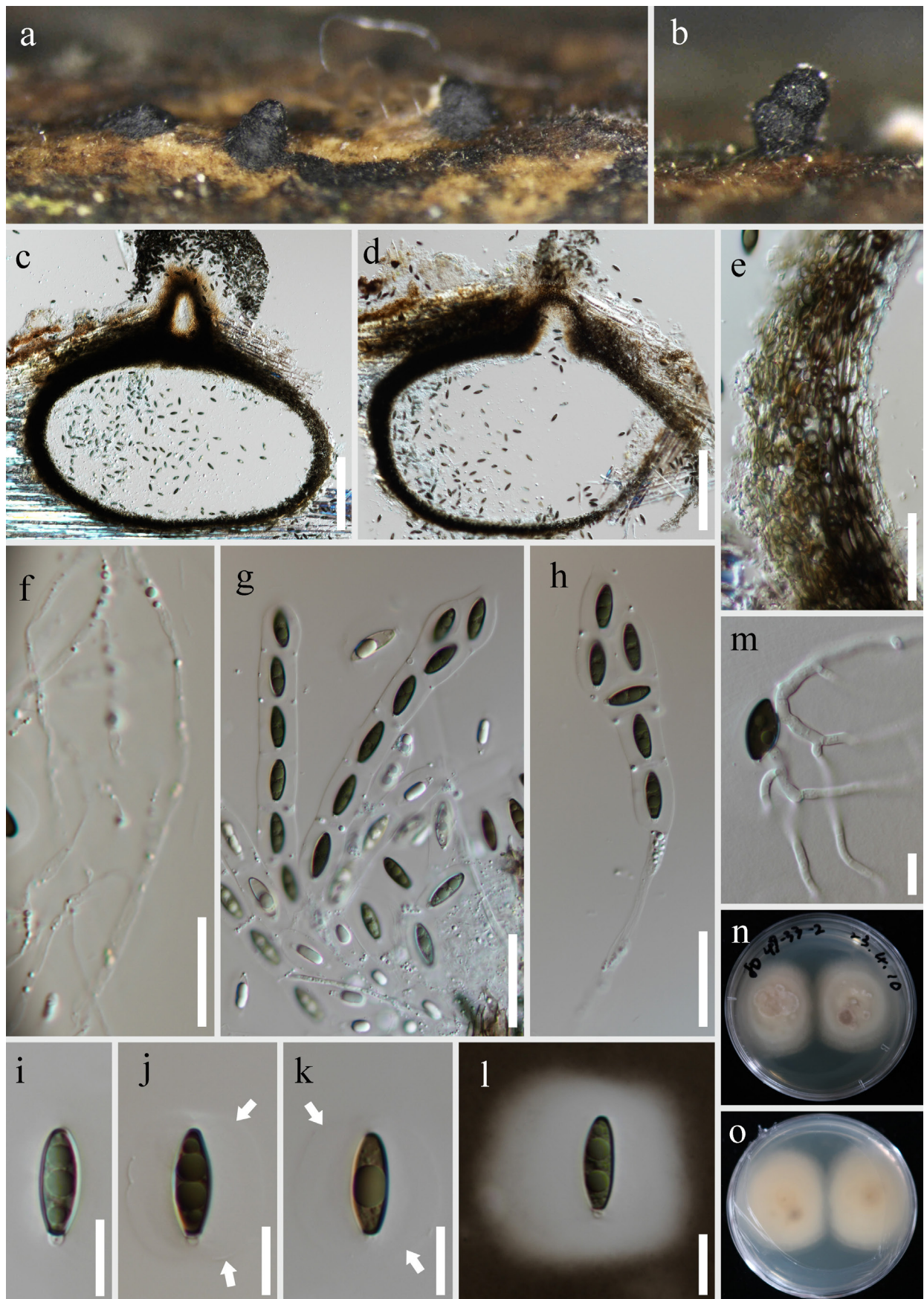


Fig. 110 *Digitodochium lacustre* (HKAS 132103, **holotype**). a, b Appearance of ascomata on host substrate. c, d Sections of ascomata. e Peridium. f Paraphyses. g, h Asci. i–k Ascospores (arrows show the sheath of ascospores). l Ascospore stained with Indian ink. m Germinated ascospore. n, o Colony on PDA, upper (n) and lower (o). Scale bars: c, d = 150 μ m, e, g, h = 30 μ m, f = 20 μ m, i–m = 10 μ m.

67. *Sporidesmiella gezaensis* R.J. Xu, Q. Zhao & K.D. Hyde, *sp. nov.* Fig. 112

Chinese name: – 格咱小基孢 (ge za xiao shen bao)

Index Fungorum number: IF 905284; **Facesoffungi number:** FoF 19888

Etymology: It is named after Geza Township, where the type specimen was collected.

Holotype: HKAS 136093

Saprobic on submerged decaying wood in freshwater stream. **Asexual morph:** Colonies superficial, effuse, glitter, pale brown to brown. *Mycelium* superficial, partly immersed, consisting of branched, septate, smooth, hyaline to pale brown hyphae. *Conidiophores* 161–202 × 4–5 µm ($\bar{x}$ = 185 × 5 µm, *n* = 20), macronematous, mononematous, unbranched, single or 2–3-groups, erect, cylindrical, straight or slightly flexuous, slightly constricted at septa, brown, pale toward the apex, 4–8-septate, smooth. *Conidiogenous cells* 17–63 × 4–5 µm ($\bar{x}$ = 34 × 4 µm, *n* = 15), holoblastic, polyblastic, integrated, with sympodial proliferations, terminal and intercalary, with several sympodial proliferations, conspicuous denticles, cylindrical, hyaline, smooth. *Conidia* 18–25 × 9–15 µm ($\bar{x}$ = 21 × 11 µm, *n* = 25), acrogenous or intercalary, solitary, obovoid, rounded at the apex, narrow towards truncate at the base, hyaline to pale brown, becoming brown at maturity, 0–1-distoseptate when young, 3–4-euseptate when mature, guttulate, smooth-walled. **Sexual morph:** Undetermined.

Culture characteristics: Conidia germinating on PDA medium within 24 h and germ tubes arising from terminal end of conidium. Colonies grown on PDA reached 20 mm diam at room temperature in two weeks, irregular, dense, glistening, dry, flat, grayish-white mycelium on the surface, cream, butyrous, immersed mycelium on the surrounding, from below cream with entire margin.

Material examined: CHINA, Yunnan Province, Shangri-La City, Geza Township, 27°58′24.94″ N, 99°46′39.32″ E, 3307 m a.s.l., on decaying wood submerged in a freshwater stream, 19 June 2022, R.J. Xu, XK-33-1 (HKAS 136093, holotype); ex-type culture KUNCC 10426. CHINA, Yunnan Province, Shangri-La City, Geza Township, 27°58′24.94″ N, 99°46′39.32″ E, 3307 m a.s.l., on decaying wood submerged in a freshwater stream, 19 June 2022, R.J. Xu, XK-33-1-1 (HKAS 136092, paratype), ex-paratype culture KUNCC 24-18116.

Notes: Morphologically, the macronematous, mononematous, unbranched, cylindrical conidiophores, holoblastic, integrated, sympodial, cylindrical conidiogenous cells that with proliferating percurrently, and solitary, obovoid, distoseptate conidia are the typical characteristics in *Sporidesmiella*.

Sporidesmiella gezaensis was previously confused with *S. aquatica*, but the new species differs from the latter in having smaller conidia (18–25 × 9–15 µm vs. 51–59 × 18–22 µm) (Luo et al. 2019). Phylogenetic analyses showed that our collections form a distinct clade within *Sporidesmiella*, closely related to *S. yadongensis* (KUNCC 24-17996) (Fig. 111). However, a comparison of ITS nucleotide sequences reveals that *S. gezaensis* differs from *S. yadongensis* (KUNCC 24-17996) by 12/525 bp (2.3%, excluding gaps). Therefore, *Sporidesmiella gezaensis* is introduced as a new species based on morphological distinctiveness, phylogenetic evidence, and species delimitation criteria proposed by Jeewon and Hyde (2016) and Chethana et al. (2021a).

Discussion

The Q-X Plateau, renowned for its unique ecological and geographical characteristics, has long been an area of interest for researchers across various disciplines. However, the mycological diversity of this region has not been extensively documented until recent years. This paper, the third in a series dedicated to documenting novel fungal taxa in this region, focuses on filamentous-fungi and entomopathogenic fungi that are endemic to the Q-X Plateau. Based on molecular evidence and morphological characteristics, 4 classes, 19 orders, 35 families, and 52 genera, viz. *Acrogenospora*, *Akanthomyces*, *Aquaphila*, *Beauveria*, *Chalara*, *Chloridium*, *Cladophialophora*, *Clonostachys*, *Conioscypha*, *Cordana*, *Cordyceps*, *Corynespora*, *Cylindrotrichum*, *Dichotomopilus*, *Dictyocheirospora*, *Digitodochium*, *Falholtia*, *Fusarium*, *Helminthosporium*, *Hermatomyces*, *Ilyonectria*, *Juncigena*, *Kernia*, *Kylindria*, *Mariannaea*, *Metarhizium*, *Moelleriella*, *Neodictyosporium*, *Ophiocordyceps*, *Papiliomyces*, *Perennicordyceps*, *Periconia*, *Petchia*, *Phaeoisaria*, *Phialocephala*, *Phialosporostilbe*, *Polycephalomyces*, *Ramophialophora*, *Samsoniella*, *Savoryella*, *Setophoma*, *Simplicillium*, *Sporidesmiella*, *Sporidesmium*, *Sporoschisma*, *Stanjehughesia*, *Sterigmatobotrys*, *Tetraploa*, *Thysanorea*, *Torula*, *Trichoderma* and *Zangmuomyces*, are identified. Among these genera, some have garnered attention due to their cosmopolitan distribution, while others are notable for their unique presence in specific regions such as the Q-X Plateau.

Acrogenospora, *Akanthomyces*, *Beauveria*, *Cladophialophora*, *Clonostachys*, *Cordyceps*, *Fusarium*, *Helminthosporium*, *Metarhizium*, and *Trichoderma*, exhibit a remarkable ability to thrive in diverse environments, are characterized by their widespread occurrence, often facilitated by their adaptability to various ecological niches and their interactions with a wide range of hosts. For instance, *Beauveria*, *Cladophialophora*, *Fusarium*, and *Trichoderma* are renowned for their entomopathogenic properties, making them pivotal in biological control strategies against agricultural pests (Agrawal et al. 2014; Robène-Soustrade et al. 2015). Their taxonomic classification has been refined through molecular phylogenetic studies, which have elucidated their evolutionary relationships and underscored the importance of genetic diversity within these genera. In contrast, the Q-X Plateau, characterized by its distinctive climatic and geographical conditions, is home to several endemic fungal genera, such as *Zangmuomyces*, that have evolved specific adaptations to thrive in this extreme environment. Notably, *Cordyceps*, along with its allied genera such as *Ophiocordyceps* and *Metarhizium*, are well-known for their entomopathogenic species, some of which are highly valued in traditional medicine, including the renowned caterpillar fungus, exhibit specialized traits that enable their survival in the high-altitude, low-oxygen milieu of the plateau (Xiao et al. 2023). The taxonomic investigation of these endemic genera is essential for elucidating their evolutionary trajectories and ecological functions. Advanced molecular techniques, including DNA sequencing and phylogenetic analysis, have proven pivotal in deciphering the intricate taxonomy of these fungi, thereby uncovering their unique genetic lineages and adaptive mechanisms.

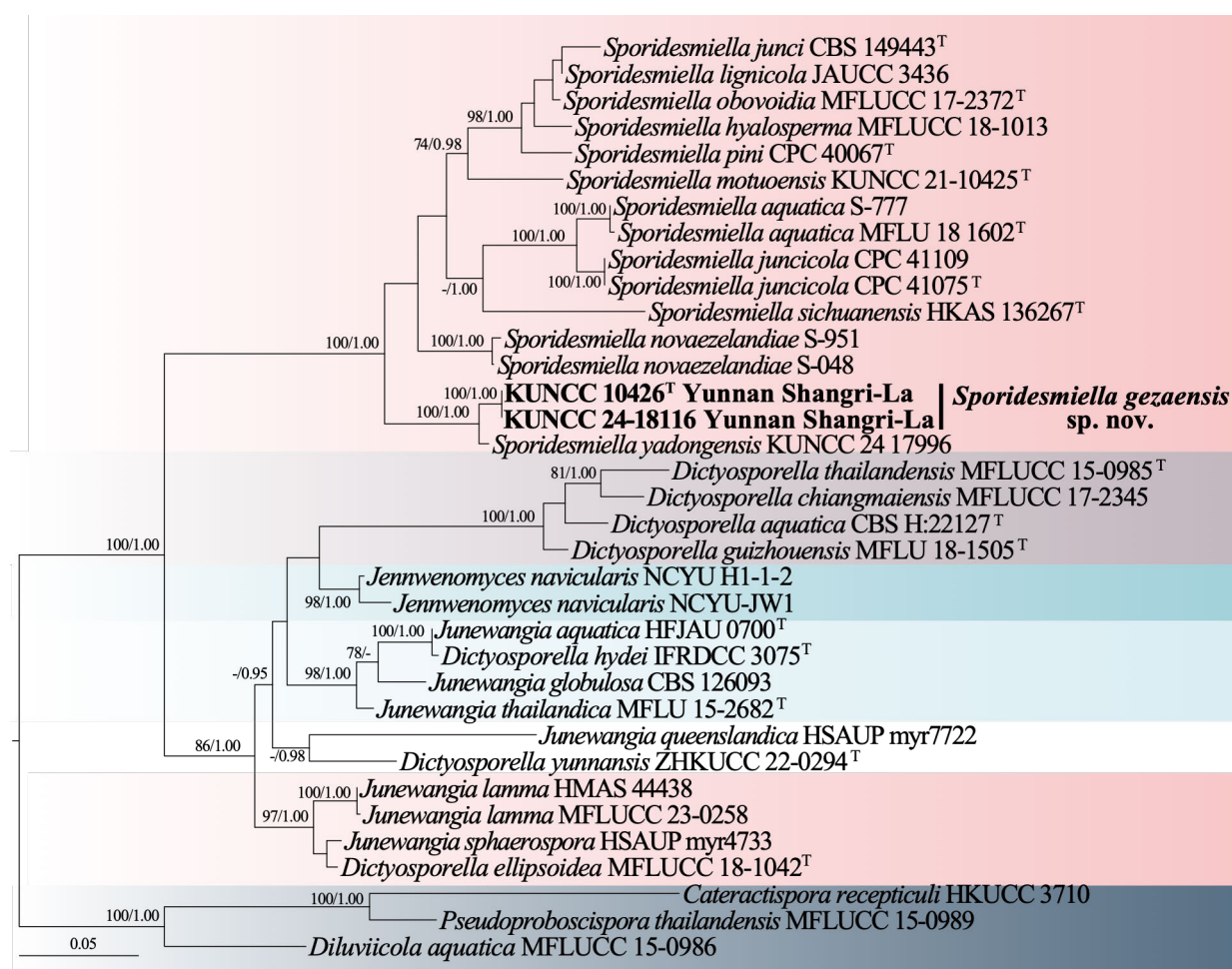


Fig. 111 Maximum likelihood majority rule consensus tree for *Sporidesmiella* using ITS, LSU, *tef1*-α and *rpb2* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 70% and Bayesian posterior probabilities greater than 0.95 are indicated near branches as ML BS/PP. The scale bar represents the expected number of changes per site. The tree is rooted with *Cateractispora recepticuli* (HKUCC 3710), *Pseudoproboscisporea thailandensis* (MFLUCC 15-0989) and *Diluviicola aquatica* (MFLUCC 15-0986). Sample labels of the newly obtained sequences are provided in the order of herbarium no., province name, and county/city name.

Entomopathogenic fungi, also known as insect-pathogenic fungi, play a crucial role in the natural regulation of insect populations. Among the 47 genera documented in this study, *Akanthomyces*, *Beauveria*, *Cordyceps*, *Metarhizium*, *Ophiocordyceps*, *Papiliomyces*, *Perenicordyceps*, *Pleurocordyceps*, *Polycephalomyces* and *Samsoniella* are recognized as typical entomopathogenic fungi, known for their ability to infect and kill insects (Wang et al. 2022; Xiao et al. 2023). *Beauveria* is one of the most well-known entomopathogenic fungi, particularly *Beauveria bassiana*. The discovery of new species, such as *Cordyceps biclavata*, *Ophiocordyceps fusispora*, *O. hutiaoxiaensis*, *O. multiseptata*, *O. polyphialidica*, *O. yuhongii* and *O. sporangifera*, highlights the region's potential as a reservoir of unexplored fungal diversity.

The pathogenicity of fungi is a topic of significant interest, particularly in the context of plant and animal health. While many fungi are benign or beneficial, some can cause diseases in plants, animals, or humans. In this study, the pathogenic potential of newly identified species was assessed, with particular attention given to those that may impact agriculture or natural ecosystems. For example, *Fusarium altiplanum*, *F. rubellum* and *Corynespora xinjiangensis* are known for their pathogenicity in plants,

which could have implications for local agriculture and plant conservation efforts. Understanding the pathogenicity of these fungi is crucial for developing strategies to manage and mitigate their impacts. The newly identified fungi from this study exhibit a range of ecological types, including saprophytic, parasitic, and symbiotic relationships. Saprobic fungi, such as *Trichoderma habaense* and *T. xinpingense*, play a vital role in decomposing organic matter, thereby contributing to nutrient cycling within their ecosystems.

The classification and taxonomy of fungi are continually evolving fields, driven by advances in molecular biology and phylogenetic analyses. This study utilized robust phylogenetic analyses to confirm the taxonomic placements of the newly described species within the established fungal classification framework. These analyses not only validated the morphological assessments but also provided insights into the evolutionary relationships between different fungal taxa. Future studies could focus on the ecological roles of fungi in nutrient cycling and ecosystem functioning, the potential applications of fungi in biotechnology and medicine, and the impacts of climate change on fungal diversity and distribution. Additionally, there is a need for continued documentation and conservation efforts to protect the unique fungal communities of this region.

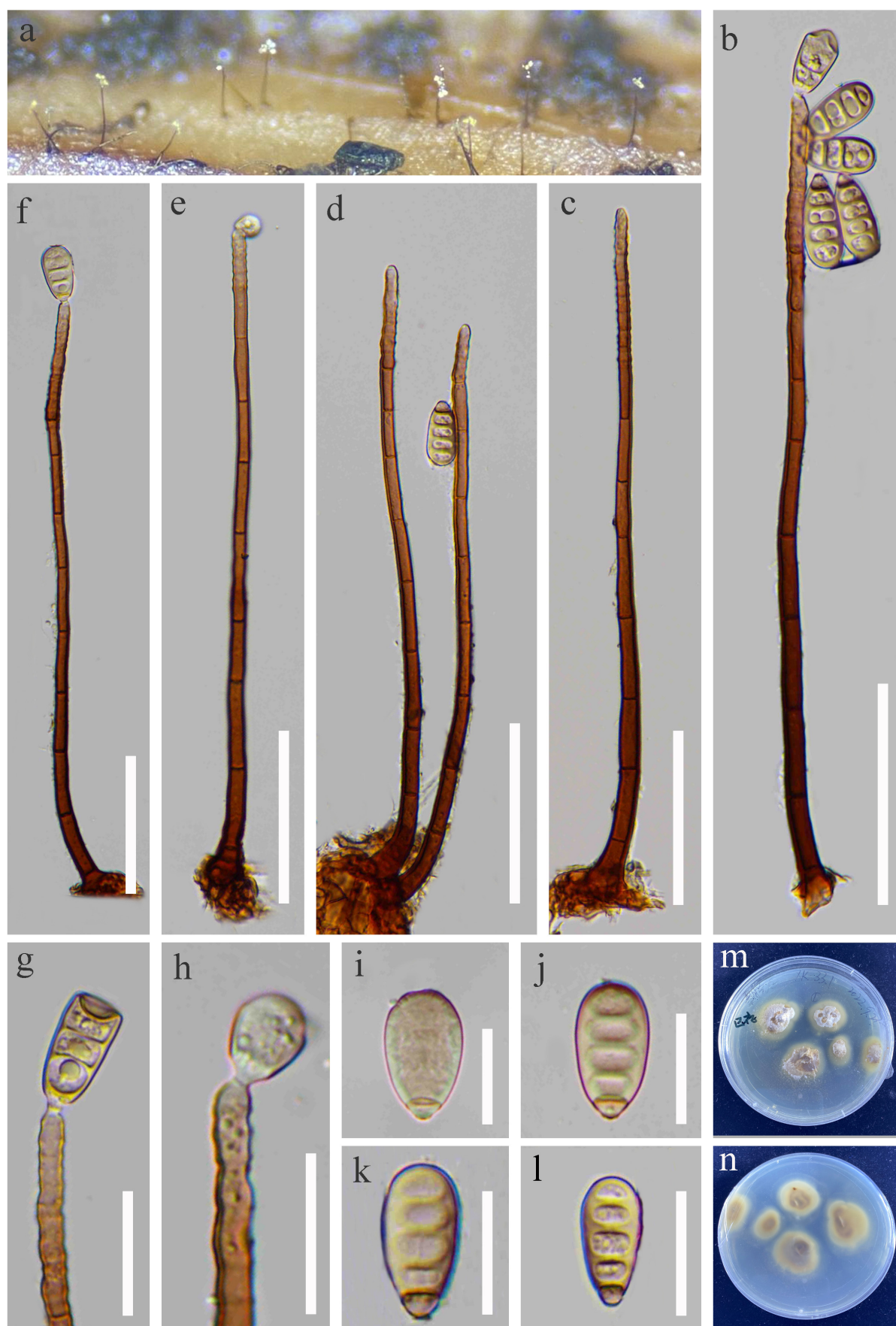


Fig. 112 *Sporidesmiella gezaensis* (HKAS 136093, holotype) a Colony on natural substrates. b–f Conidiophores with conidia. g, h conidiogenous cells with conidia. i–l Conidia. m, n Culture on PDA medium, m from above, n from below. Scale bars: b–f = 50 µm, g–l = 20 µm.

Acknowledgments

The whole work was funded by the Second Tibetan Plateau Scientific Expedition and Research Program (Grant No. 2024QZKK02010303), the National Natural Science Foundation of China (32470015, U2202205, 32060007), the Key project at central government level: the ability establishment of sustainable use for valuable Chinese medicine resources (2060302), the Major Science and Technology Special Project of Yunnan Province (202502AE090044), the Yunnan Basic Research Special Project (202401AS070030), the Technological Innovation Talent Cultivation Project Zhao Qi of Yunnan Province (202405AD350054), the Innovation Guidance and Technology-Based Enterprise Cultivation Program of Yunnan Province Science and Technology Department (No. 202504BI090008), the Yunnan Province Zhao Qi Expert Workstation (Yunnan Bofan Biotechnology Co., Ltd.), and the Yunnan Province Zhao Qi Expert Workstation (Chengjiang Green Field Agricultural Technology Service Co., Ltd.). Kevin D Hyde and Fatima Al-Otibi extend their appreciation to the ongoing Research Funding Program (ORF-2026-114), King Saud University, Riyadh, Saudi Arabia. We thank Mr. Peng Gao, Mr. Xue-Hua Zhang (Lasa, Xizang), Mr. Jia-Xi Pan (Shantou, Guangdong) for helping with the field trips in Xizang and Xinjiang, China.

Author contributions

Conceptualization, Xu RJ, Wang YB, Chen BZ and Zhao Q; methodology, Xu RJ, Wang YB, Chen BZ and Li JN; formal analysis, Hyde KD, Zhao Q and Yang ZL; resources, Xu RJ, Wang YB, Chen BZ, Li JN, He SC, Shen HW, Luo ZL, Lu YZ, Ma J, Xiao YP, Li Y, Yang HD, Zhao YW, Fan Q, Liao HF, Wei CY, Tang M, Wang XM and Al-Otibi F; data curation, Xu RJ, Wang YB, Chen BZ and Li JN; writing—original draft preparation, Xu RJ, Wang YB, Chen BZ and Zhao Q; writing—review and editing, Zhao Q, Wang YB, Hyde KD and Yang ZL; supervision, Zhao Q, Wang YB, Hyde KD and Yang ZL; project administration, Zhao Q, Hyde KD and Wang YB; funding acquisition, Zhao Q, Hyde KD and Wang YB. All authors have read and agreed to the published version of the manuscript.

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Conflict of interest statement

The author list includes members of the Editorial Board of Fungal Diversity. They were not involved in the journal's review of, or decisions related to, this manuscript. The authors declare no competing interests.

Data availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Supplementary Information

The online version contains supplemental information available at <https://doi.org/10.65390/fdiv.2026.136012>.

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