

Diversity and taxonomy of hyphomycetous Fungi in Southwestern China

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Abstract

This study explores the diversity of hyphomycetous fungi associated with decaying plant material in freshwater habitats of Southwestern China. Approximately 100 specimens were analyzed using combined morphological and multi-locus phylogenetic approaches. The ITS, SSU, LSU, *rpb2*, *tub2*, and *tef1-α* loci were employed for phylogenetic analyses of the treated taxa. This study has identified 36 taxa, including a new genus, *Bulbocatenulomyces*, 28 new species, and 8 new geographical records. Most of these, 24 species belong to *Sordariomycetes*, followed by *Dothideomycetes* (11 species) and *Orbiliomycetes* (1 species). The new species include *Acremonium nigrobrunneum*, *Bactrodesmium wumengense*, *Bulbocatenulomyces nigricans*, *Chloridium tongrense*, *Conlarium phaeoconidium*, *Distoseptispora longissima*, *D. quinqueseptata*, *D. tongrensis*, *Helminthosporium dichoramosum*, *H. undecimseptatum*, *Hawksworthiomyces cylindroconidius*, *Mariannaea alba*, *Memnoniella anliuensis*, *Xenopleopunctum muriformis*, *Phragmocephala wuliangshanensis*, *Polyplosphaeria chinensis*, *Protocreopsis alba*, *Pyricularia puerensis*, *Rhaphoriopsis globularis*, *R. yunnanensis*, *R. zhaotongensis*, *Rostriconidium fuscum*, *R. yunnanense*, *Sarocladium bambusicola*, *Torula puerensis*, *Triplosphaeria irregularis*, *Tubeufia chinensis*, and *Xylolentia yibinensis*. The new geographical records are *Chloridium chlamydosporum*, *C. fuscum*, *Dictyocheiropsora chiangmaiensis*, *Nectriella rusci*, *Orbilium ellipsospora*, *Parasympodiella cryptomeriae*, *Pleurothecium lignicola*, and *Volutella minutissima*. In addition, *Pseudolophiotrema* is synonymized under *Clematidis*, with its species recombined as *C. elymicola* comb. nov. These findings significantly enhance the understanding of hyphomycetous fungal diversity in Southwestern China. The discovery of numerous novel species highlights the

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presence of many undescribed taxa, especially in freshwater habitats, presenting compelling opportunities for further mycological research.

Keywords – anamorphic fungi – Ascomycota – biodiversity – karst ecosystem – new taxa

INTRODUCTION

Hyphomycetes represent a morphologically diverse and ecologically significant assemblage of fungi, primarily known for their anamorph (Seifert et al. 2011, He et al. 2019, Liu et al. 2024). Traditionally defined as fungi that produce conidia on exposed hyphae or conidiophores without enclosing fruiting bodies (Seifert et al. 2011, Kirk et al. 2008). Hyphomycetes encompass a broad range of anamorphic fungi predominantly within the phyla *Ascomycota*, and, to a lesser extent, *Basidiomycota* (Seifert et al. 2011, He et al. 2019, Wijayawardene et al. 2020, 2022). In contrast to coelomycetes, which develop conidia in closed structures such as pycnidia or acervuli, hyphomycetous fungi form conidia openly on conidiophores, a key distinguishing trait in classical fungal taxonomy (Seifert et al. 2011). Although the group “Hyphomycetes” is not monophyletic and does not represent a natural taxonomic unit, it continues to be used informally, and practically to describe anamorphic fungi with exposed conidiogenesis (Seifert et al. 2011, He et al. 2019).

Morphologically, hyphomycetes are highly variable, exhibiting a wide array of conidial forms, sizes, septation patterns, pigmentation, and modes of development. Conidia can be unicellular or multicellular, hyaline or pigmented, smooth or ornamented, and may be produced solitarily or in chains, acrogenous or pleurogenous, dry or wet, smooth or verruculose, thin- or thick-walled, smooth or rough-walled, aseptate or septate, constricted or unconstricted at septa, with or without appendages (Ellis 1971, 1976, Seifert et al. 2011). Setae are present in some genera (Iturriaga et al. 2013, Lin et al. 2017, Wu & Diao 2022). The development of conidiogenous cells, whether phialides (bottle-shaped cells producing conidia in basipetal succession), annellides (conidiogenous cells that leave ring-like scars), and tretic (where conidia emerge through small pores) is a foundational feature in their identification and classification (Bhat 2010, Seifert et al. 2011).

Hyphomycetes-like morphs have long been recognized as a distinct group of anamorphic fungi (Hooke 1665, van Leeuwenhoek 1680). Formal classification begins with Persoon (1801), who placed them under *Nematothecii*. The term “Hyphomycetes” was first introduced by von Martius (1817) and later adopted by Fries (1836), forming a foundation for modern fungal taxonomy. Subsequently, the term “Fungi Imperfecti” was coined by Fuckel (1869) to categorize fungi that reproduce exclusively by anamorph stage, lacking a known teleomorphic stage. Ainsworth (1963) subdivided the group into four orders (*Sphaeropsidales*, *Melanconiales*, *Moniliales*, and *Mycelia Sterilia*) based on the morphological structures involved in conidial production, such as pycnidia, acervuli, conidiophores, or the absence of conidia. Saccardo (1899) contributed further to this artificial system by introducing the term *Deuteromycetae* to describe fungi known only in their anamorphic form. Within this framework, hyphomycetes were placed as an artificial class under *Deuteromycetae*. To bring order to this diverse group, Hawksworth et al. (1983) proposed a classification of hyphomycetes into four orders *Agonomycetales*, *Hyphomycetales*, *Stilbellales*, and *Tuberculariales* based on the presence or absence of conidia and the degree of conidiophore aggregation into synnemata or sporodochia. However, it became evident that such morphological systems were insufficient to reflect true phylogenetic relationships. With the emergence of molecular systematics, particularly multigene phylogenetic analyses, these artificial groupings were gradually abandoned. Studies by Seifert et al. (2011) and Crous et al. (2007, 2015) showed that hyphomycetous genera are widely dispersed across unrelated lineages within *Ascomycota* (e.g., *Pleosporales*, *Hypocreales*, *Eurotiales*) and, to a lesser extent, *Basidiomycota*. The implementation of the “One Fungus = One Name” policy under the International Code of Nomenclature (McNeill et al. 2012) further unified taxonomic practices by eliminating the dual naming of teleomorphic and anamorphic forms.

Recent studies reaffirm the critical role of morphological traits in hyphomycete identification. According to Liu et al. (2024) and Lin et al. (2025), features such as conidial shape, conidiophore structure, and conidiogenous cell morphology including variations in size and pigmentation are essential for species delineation and should not be overlooked. Molecular systematics has revolutionized hyphomycete taxonomy, enabling accurate phylogenetic placement of previously ambiguous taxa. DNA sequencing of ribosomal (ITS, LSU, SSU) and protein-coding genes (e.g., *tefl-α*, *tub2*, *rpb1*, *rpb2*) has clarified relationships between anamorphic and teleomorphic forms, revealing the polyphyletic nature of many traditional genera (Jeewon & Hyde 2016, Li et al. 2022). Integrative taxonomy combining molecular, morphological, and ecological data now forms the basis for classification, aligning nomenclature with evolutionary relationships and resolving longstanding ambiguities in fungal systematics (McNeill et al. 2012, Hyde et al. 2023, 2024).

This study focuses on freshwater hyphomycetes, an ecological group of fungi that inhabit and depend upon freshwater environments for all or part of their life cycle (Thomas 1996). They are commonly divided into four biological groups: aero-aquatic hyphomycetes, terrestrial-aquatic hyphomycetes, submerged-aquatic (amphibious) hyphomycetes, and Ingoldian fungi (Goh & Hyde 1996, Jones et al. 2014, Raja et al. 2018, Da Silva et al. 2019). Ingoldian fungi (aquatic hyphomycetes sensu stricto) are specifically associated with decaying leaves in flowing water. They sporulate on decaying leaves and plant debris in flowing water, produce characteristic conidial shapes that facilitate attachment and dispersal, and are often recovered from stream foam and detrital films (Chan et al. 2000, Descals 2005, Fiuza & Gusmão 2013, Calabon et al. 2023). Freshwater hyphomycetes are commonly reported on decaying wood submerged in various freshwater habitats, and they are also regarded as wood decay fungi or lignicolous fungi (Calabon et al. 2023). Recent studies have significantly expanded the known diversity of freshwater hyphomycetes, with numerous new taxa being reported (Bao et al. 2021, Hyde et al. 2021, Calabon et al. 2022, 2023, Li et al. 2024). Recent compilations by Calabon et al. (2022, 2023) reported 3,880 freshwater fungal species, the majority belonging to *Ascomycota* (2,968 species), with *Sordariomycetes* (823 species) and *Dothideomycetes* (677 species) as the most species-rich classes. Despite this remarkable diversity, many freshwater taxa remain of uncertain classification due to the absence of living cultures and DNA from type specimens, highlighting the need for integrated taxonomic, molecular, and ecological investigations to clarify their diversity and ecological significance (Calabon et al. 2023).

More than 2265 genera and 13,800 hyphomycetous species have been described worldwide (Seifert et al. 2011, Wijayawardene et al. 2022), including many molds of agricultural (Jayawardena et al. 2019, 2020, 2024), medical, and industrial importance (Hyde et al. 2017, Jones et al. 2019). Hyphomycetes occupy diverse habitats, commonly found in terrestrial ecosystems such as forest litter, decaying wood, soil, and plant surfaces. Many also inhabit freshwater and marine environments, where they play key roles in organic matter decomposition (Hyde et al. 2017, Jones et al. 2019). As saprobes, they contribute to nutrient cycling by breaking down plant material. Others live as endophytes, colonizing living plant tissues without symptoms and potentially enhancing drought tolerance or disease resistance (Yuan et al. 2020). Some are mycoparasitic, infecting other fungi, while many are pathogens of plants, animals, and humans. Notable pathogenic genera include *Fusarium* spp., causing vascular wilts and root-rots in plants; *Aspergillus* spp., implicated in human respiratory infections (Chen et al. 2020). Hyphomycetes are of significant biotechnological and medical importance. *Trichoderma harzianum* is widely applied in biocontrol due to its antagonism against plant pathogens, while *Penicillium chrysogenum* remains pivotal as the original source of penicillin (Mayer et al. 2011). Several species produce enzymes and secondary metabolites with pharmaceutical and industrial applications, though some, such as *Aspergillus fumigatus*, act as opportunistic pathogens in immune-compromised individuals (Latgé & Chamilos 2019). Genera like *Helicoma*, *Helicosporium*, *Helicomycetes*, *Zalerion*, and *Tubeufia* yield diverse bioactive compounds, including antitumor agents (e.g., trapoxins A and B), antifungals (e.g., pneumocandins A0 and B0), and MDR-reversing metabolites (Schmatz et al. 1992, Fan et al. 2019, Zeng et al. 2022, Qian et al. 2023). Recent studies have also identified

cytotoxic and antibacterial polyketides from *Neohelicomycetes* and *Neohelicosporium* species (Zhang et al. 2023, Zheng et al. 2023, Zhang et al. 2024). Despite this, hyphomycete taxonomy remains challenging, especially due to the complexity of morphological characteristics and the lack of comprehensive molecular data for many species. Nevertheless, only several genera have been comprehensively studied to understand the generic boundaries and species complexes (e. g. *Alternaria fide*, *Stachybotrys fide* Wang et al. 2015).

Although hyphomycetes are not monophyletic, their ecological importance, morphological diversity, and applied value sustain ongoing mycological interest. In this study, we investigate the diversity of saprobic hyphomycetes from decaying wood, primarily in freshwater habitats, across southwestern China. We report a new genus, 28 new species and a novel combination supported by morphological characteristics and multi-locus phylogenetic analyses using ITS, SSU, LSU, *rpb2*, *tub2*, and *tef1- α* regions.

MATERIALS AND METHODS

Samples collection

Submerged dead twigs and decaying wood materials were collected from freshwater habitats (rivers, lakes, waterfalls, streams, and ponds) across southern China, including Guizhou, Sichuan, and Yunnan provinces, and the Guangxi Zhuang Autonomous Region, between June and October 2024, following the collection protocol of Luo et al. (2018). All relevant habitat information was recorded. Samples were transported in sterile containers and incubated at 20°C in sealed boxes with maintained humidity.

Plastic boxes (24 cm $\times$ 16 cm $\times$ 6 cm) were prepared for sample incubation. The interior of each box was first rinsed with sterile water and subsequently wiped with 75% ethanol to ensure sterility. After drying, two layers of sterilized tissue paper were placed at the bottom of the box. Three sterilized straws were then laid on top of the tissues to prevent the samples from coming into direct contact with the moist surface. An appropriate amount of sterile water was added so that the tissues were moistened but no excess water accumulated at the bottom. The processed samples were then arranged horizontally on the straws. Each box was clearly labeled and placed on a culture rack for incubation at room temperature for one week. Afterwards, the specimens were subjected to morphological analysis and isolation. After finalizing the observation and isolation, the specimens were deposited at the Herbarium of Guizhou Medical University (GMB) and the Herbarium of Cryptogams, Kunming Institute of Botany, Chinese Academy of Sciences (KUN-HKAS). Living cultures were deposited at the Guizhou Medical University Culture Collection (GMBC). All scientific names of fungi follow the entries in MycoBank and Index Fungorum, hence no authorities and years of publications are given in the text apart from the taxonomic entries.

Morphological studies and isolation

Macroscopic characteristics were examined under an Olympus SZ61 stereomicroscope (Japan) and photographed with a Canon 700D digital camera (Canon, Tokyo, Japan). The samples were mounted in water for microscopic examination. The Tarosoft (R) Image Frame Work (v 0.9.7) program and Adobe Photoshop CS6 software (Adobe Systems, USA) were used for measuring and processing images. Pure cultures were obtained via single-spore isolation following Shen et al. (2023). Conidia were suspended in sterile water, spread on water agar (WA), and incubated at 25°C for 12–24 hours. The single germinated conidia were transferred to fresh potato dextrose agar (PDA) medium and incubated at room temperature. A few of the remaining germinated spores in the media plate were separated along with agar using a needle and transferred onto water-mounted glass slides for photographs to capture the germination position of the germ tubes. Germinated conidia were then transferred to PDA plates under sterile conditions maintained pure cultures.

DNA extraction, PCR amplification and sequencing

Mycelium was scraped from pure culture plates using a sterilized scalpel for DNA extraction by using the commercially available BIOMIGA fungus genomic DNA extraction kit (Biomiga, San Diego, USA). All DNA samples were kept at -20°C until analysed. Small subunit (SSU), internal transcribed spacers (ITS), large subunit (LSU), translation elongation factor (*tef1- α*), *tub2* (*β -tubulin*), and RNA polymerase II second largest subunit (*rpb2*) were amplified by PCR with primers NS1/NS4, ITS1/ITS4 (White et al. 1990, Gardes & Bruns 1993), LR0R/LR5 (Vilgalys & Hester 1990), EF1-983F/EF1-2218R (Rehner & Samuels 1994), T1/T22 (O'Donnell & Cigelnik 1997), and *rpb2*-5F/*rpb2*-7cR (Liu et al. 1999), respectively. The PCR mixture (25 μL) was composed as follows: 9.5 μL of double distilled water, 12.5 μL of PCR Master Mix, 1 μL of each primer, and 1 μL of template DNA. The PCR amplification was conducted as reported by Samarakoon et al. (2022). PCR products were checked through 1.5 % agarose gel electrophoresis stained with GoldenView (Habib et al. 2025), and were sent to Sangon Co., China, for sequencing.

Sequence alignments and phylogenetic analyses

All assembled sequences were compared with each other and all known sequences in GenBank using the BLAST algorithm for precise identification (<https://ncbi.nlm.nih.gov>) (Altschul et al. 1990). The reference sequences retrieved from open databases originated from recently published data and BLASTn results of close matches. Sequences were aligned using the MAFFT v.7.110 online program (Katoh et al. 2019) with the default settings. The alignments were adjusted manually using BioEdit v.7.0.5.3 (Hall 1999) where necessary. The maximum likelihood (ML) analyses were implemented in RAxML v.8.2.12 using the GTRGAMMA substitution model with 1,000 bootstrap replicates (Stamatakis 2014). The phylogenetic analyses were also performed for Bayesian inference in MrBayes v. 3.2.2 (Ronquist et al. 2012) online. The Markov chain Monte Carlo (MCMC) sampling in MrBayes v.3.2.2 (Ronquist et al. 2012) was used to determine the posterior probabilities (PP). Six simultaneous Markov chains were run for 1,000,000 generations, and trees were sampled every 1,000th generation. The first 25 % of the trees were discarded as burn-ins. The remainder was used to calculate the posterior probabilities (PPs) for individual branches. The same settings were applied for all the phylogenetic analyses. The phylogenetic tree was visualized in FIGTREE v.1.4.3 (Rambaut 2012). All analyses were run on the CIPRES Science Gateway v 3.3 webportal (Miller et al. 2012). All the obtained sequences were deposited in GenBank (Table 1). The outgroups and loci used in phylogenetic analyses, tailored to specific families and genera including ITS, SSU, LSU, *rpb2*, *tub2*, and *tef1- α* , were chosen based on published literature. The best-scoring RAxML tree is presented in the phylogenetic figures, and the phylogenetic placement of isolated strains is detailed in the notes section of each respective taxon.

Arrangement of taxa

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

Dothideomycetes order *incertae sedis*

Tubeufiales Boonmee & K.D. Hyde, Fungal Diversity 68 (1): 245 (2014).

Tubeufiaceae M.E. Barr, Mycologia 71: 948 (1979).

Tubeufia chinensis Q.F. Zhang, K. Habib & Q.R. Li, *sp. nov.*

Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker, Mycologia 98 (6): 1048 (2007).

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

Dictyosporiaceae Boonmee & K.D. Hyde, Fungal Diversity 80: 462 (2016).

Dictyocheiropora chiangmaiensis H.W. Shen, Boonmee & Z.L. Luo (new geographic record)

Massarinaceae Munk, Friesia 5 (3-5): 305 (1956).

Helminthosporium dichoramosum L.L. Liu, K. Habib, Q. F. Zhang & Q.R. Li, *sp. nov.*

Helminthosporium undecimseptatum Q.F. Zhang, K. Habib & Q.R. Li, *sp. nov.*

Pseudolophiotremataceae K.D. Hyde & Hongsanan, Phytotaxa 383 (1): 97 (2018).

Bulbocatenulomyces L.L. Liu, K. Habib & Q.R. Li, *gen. nov.*

Bulbocatenuromyces nigricans L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Clematidis elymicola (A. Hashim. & Kaz. Tanaka) K. Habib & Q.R. Li, *comb. nov.*
Xenoploepunctum J.Y. Zhang, Y.Z. Lu & K.D. Hyde
Xenoploepunctum muriformis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

Torulaceae Corda, Deutschlands Flora, Abt. III. Die Pilze Deutschlands 2: 71 (1829).
Rostriconidium fuscum L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Rostriconidium yunnanensis Q.F. Zhang, K. Habib & Q.R. Li, *sp. nov.*
Torula puerensis L.L. Liu, K. Habib, K. Habib & Q.R. Li, *sp. nov.*

Tetraplospheariaceae Kaz. Tanaka & K. Hiray., Stud. Mycol. 64: 177 (2009).
Polypliosphaeria chinensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Triplospheeria irregularis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

Orbiliomycetes O.E. Erikss. & Baral, Myconet 9: 96 (2003).
Orbiliales Baral, O.E. Erikss., G. Marson & E. Weber, Myconet 9: 96 (2003).
Orbiliaceae Nannf., Nova Acta Regiae Soc. Sci. Upsal. Ser. 4, 8 (2): 250 (1932).
Orbilium ellipsospora (Preuss) Bin Liu, E. Weber & Baral (new geographic record).

Sordariomycetes O.E. Erikss. & Winka, Myconet 1: 10 (1997).
Diaporthomycetidae Senan., Maharachch. & K.D. Hyde, Fungal Diversity 72: 208 (2015).
Conlariales K.D. Hyde & Hongsanan, Fungal Diversity 107: 94 (2021)
Conlariaceae Huang Zhang, K.D. Hyde & Maharachch., Fungal Diversity 85: 90 (2017)
Conlarium phaeoconidium L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

Distoseptisporales Z.L. Luo, H.Y. Su & K.D. Hyde, Fungal Diversity 99: 482 (2019).
Distoseptisporaceae K.D. Hyde & McKenzie, Fungal Diversity 80:375–409 (2016).
Distoseptispora longissima L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Distoseptispora quinqueseptata L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Distoseptispora tongrensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

Hypocreomycetidae O.E. Erikss. & Winka, Myconet 1: 6 (1997).
Hypocreales Lindau, Die Natürlichsten Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1 (1): 343 (1897).
Bionectriaceae Samuels & Rossman, Stud. Mycol. 42: 15 (1999).
Acremonium nigrobrunneum W.M. Li, K. Habib & Q.R. Li, *sp. nov.*
Nectriella rusci Lechat, Lowen & Gardiennet (new geographic record in China).
Protocreopsis alba L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

Nectriaceae Tul. & C. Tul., Selecta Nectriei- Phacidiei- Pezizei 3: 3 (1865).
Mariannaea alba L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Volutella minutissima Lechat & J. Fourn. (new geographic record).

Sarocladiaceae L. Lombard, Persoonia 41: 343 (2018).
Sarocladium bambusicola L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

Stachybotryaceae L. Lombard & Crous, Persoonia 32: 283 (2014)
Memnoniella anliuensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

Parasymphodiellales Hern.-Rest., Gené, R.F. Castañeda & Crous, Stud. Mycol. 86: 87 (2017).
Parasymphodiellaceae Hern.-Rest., Gené, Guarro & Crous, Stud. Mycol. 86: 87 (2017).
Parasymphodiella cryptomeriae W.H. Tian, K.D. Hyde & Maharachch. (new geographic record).

- Pleurotheciales* Réblová & Seifert, *Persoonia* 37: 63 (2015).
Pleurotheciaceae Réblová & Seifert, *Persoonia* 37: 63 (2015).
Pleurothecium lignicola C.Y. Xu, H.Y. Song & D.M. Hu (new geographic record).
Savoryellomycetidae Hongsanan, K.D. Hyde & Maharachch, *Fungal Diversity* 84: 35 (2017).
Pleurotheciales Réblová & Seifert, *Persoonia* 37: 63 (2015).
Pleurotheciaceae Réblová & Seifert, *Persoonia* 37: 63 (2015).
Phragmocephala wuliangshanensis Q.F. Zhang, K. Habib, Q.R. Li, *sp. nov.*
Savoryellales Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones, *Mycologia* 103 (6): 1368 (2011).
Savoryellaceae Jaklitsch & Réblová, in Jaklitsch, *Index Fungorum* 209: 1 (2015)
Bactrodesmium wumengense L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Sordariomycetidae O.E. Erikss. & Winka, *Myconet* 1: 10 (1997).
Chaetosphaeriales Huhndorf, Mill. & Fernández, *Mycol. Res.* 108 (12): 378 (2004).
Chaetosphaeriaceae Réblová, M.E. Barr & Samuels, *Sydowia* 51: 56 (1999).
Chloridium chlamydosporum (J.F.H. Beyma) S. Hughes (new geographic record).
Chloridium fuscum (Corda) Réblová & Hern.-Restr. (new geographic record in China).
Chloridium tongrense L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Magnaporthales Thongk., Vijaykr. & K.D. Hyde, *Fungal Diversity* 34: 168 (2009)
Pyriculariaceae Klaubauf, M.-H. Lebrun & Crous, *Stud. Mycol.* 79: 104 (2014).
Pyricularia puerensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Ophiostomatales Benny & Kimbr., *Mycotaxon* 12 (1): 48 (1980).
Ophiostomataceae Nannf., *Nova Acta Regiae Soc. Sci. Upsal. Ser. 4, 8* (2): 30 (1932).
Hawksworthiomyces cylindroconidius L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Rhamphoriales K.D. Hyde & Hongsanan, *Fungal Diversity* 107: 94 (2021)
Rhamphoriaceae Réblová, *Mycologia* 11 (4): 754 (2018).
Rhamphoriopsis globularis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*
Rhamphoriopsis yunnanensis W.M. Li, K. Habib & Q.R. Li, *sp. nov.*
Rhamphoriopsis zhaotongensis W.M. Li, K. Habib & Q.R. Li, *sp. nov.*
Xylolentia yibinensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

RESULTS

Taxonomy

- Ascomycota* Caval. Sm., *Biol. Rev. Cambridge Philos. Soc.* 73: 247 (1998)
Dothideomycetes O.E. Erikss. & Winka, *Myconet* 1: 5 (1997).
Tubeufiales Boonmee & K.D. Hyde, *Fungal Diversity* 68 (1): 245 (2014).
Tubeufiaceae M.E. Barr, *Mycologia* 71: 948 (1979).
Tubeufia Penz. & Sacc., *Malpighia* 11: 517 (1898).

Notes – *Tubeufia* was introduced by Penzig & Saccardo (1898) with *T. javanica* as the type species. Species of the genus are widely distributed across tropical and temperate regions, thriving in both freshwater and terrestrial habitats, and are primarily found on well-rotted wood (Ma et al. 2024). The genus is characterized by both helicosporous and dictyosporous anamorphs. The helicosporous anamorphic forms of the genus show considerable variation in shape, with some species having abundant, elongated conidiophores, while others have very short conidiophores. According to Species Fungorum (accessed 29 June 2025), the genus currently comprises 83 accepted species.

Table 1 GenBank accession numbers obtained in this study.

Taxon	Source	Status	GenBank accession number					
			ITS	LSU	SSU	<i>tef1-α</i>	<i>rpb2</i>	<i>tub2</i>
<i>Acremonium nigrobrunneum</i>	GMBC6915	ET	PV939402	PV939430	N/A	N/A	N/A	N/A
<i>Acremonium nigrobrunneum</i>	GMBC6916		PV939403	PV939431	N/A	N/A	N/A	N/A
<i>Bactrodesmium wumengense</i>	GMBC5329	ET	PV932955	PV932974	PV932993	PX392319	PX373376	N/A
<i>Bactrodesmium wumengense</i>	GMBC5330		PV932956	PV932975	PV932994	PX392320	PX373377	N/A
<i>Bulbocatenuulomyces nigricans</i>	GMBC5316	ET	PV951775	PV951769	PV961433	PX392372	PX373345	N/A
<i>Bulbocatenuulomyces nigricans</i>	GMBC5317		PV951776	PV951770	PV961434	PX392373	PX373346	N/A
<i>Chloridium chlamydosporum</i>	GMBC5326		PV932959	PV932978	PV932997	PX392321	N/A	PX373402
<i>Chloridium chlamydosporum</i>	GMBC5331		PV932960	PV932979	PV932998	PX392322	N/A	PX373403
<i>Chloridium fuscum</i>	GMBC5325		PV932961	PV932980	PV932999	PX392323	PX373378	N/A
<i>Chloridium fuscum</i>	GMBC5332		PV932962	PV932981	PV933000	PX392324	PX373379	N/A
<i>Chloridium tongrense</i>	GMBC5335	ET	PV932957	PV932976	PV932995	PX049182	PX373380	PX373404
<i>Chloridium tongrense</i>	GMBC5336		PV932958	PV932977	PV932996	N/A	PX373381	PX373405
<i>Conlarium phaeoconidium</i>	GMBC5337	ET	PV932963	PV932982	PV933001	PX392325	N/A	N/A
<i>Conlarium phaeoconidium</i>	GMBC5338		PV932964	PV932983	PV933002	PX392326	N/A	N/A
<i>Dictyocheiropsora Chiangmaiensis</i>	GMBC5324		PV932965	PV932984	PV933003	PX392327	PX373340	N/A
<i>Distoseptispora longissima</i>	GMBC5339	ET	PV932968	PV932987	PV933006	PX392330	PX373356	N/A

Taxon	Source	Status	GenBank accession number					
			ITS	LSU	SSU	<i>tef1-a</i>	<i>rpb2</i>	<i>tub2</i>
<i>Distoseptispora longissima</i>	GMBC5340		PV932969	PV932988	PV933007	PX392331	PX373357	N/A
<i>Distoseptispora quinqueseptata</i>	GMBC5341	ET	PV932966	PV932985	PV933004	PX392328	PX373358	N/A
<i>Distoseptispora quinqueseptata</i>	GMBC5342		PV932967	PV932986	PV933005	PX392329	PX373359	N/A
<i>Distoseptispora tongrensis</i>	GMBC5343	ET	PV932970	PV932989	PV933008	N/A	PX373360	N/A
<i>Distoseptispora tongrensis</i>	GMBC5344		PV932971	PV932990	PV933009	N/A	PX373361	N/A
<i>Hawksworthiomyces cylindroconidius</i>	GMBC5345	ET	PV932972	PV932991	PV933010	N/A	N/A	N/A
<i>Hawksworthiomyces cylindroconidius</i>	GMBC5346		PV932973	PV932992	PV933011	N/A	N/A	N/A
<i>Helminthosporium dichoramosum</i>	GMBC5347	ET	PV933607	PV933625	PV933643	PX392332	PX373341	N/A
<i>Helminthosporium dichoramosum</i>	GMBC5348		PV933608	PV933626	PV933644	PX392333	PX373342	N/A
<i>Helminthosporium undecimseptatum</i>	GMBC5136	ET	PV939400	PV939428	PV939454	N/A	PX373343	N/A
<i>Helminthosporium undecimseptatum</i>	GMBC5142		PV939401	PV939429	PV939455	N/A	PX373344	N/A
<i>Mariannaea alba</i>	GMBC5351	ET	PV933609	PV933627	PV933645	PX392334	PX373364	PX373398
<i>Mariannaea alba</i>	GMBC5352		PV933610	PV933628	PV933646	PX392335	PX373365	PX373399
<i>Memnoniella anliuensis</i>	GMBC5323	ET	PV933613	PV933631	PV933649	PX392338	PX373370	N/A
<i>Memnoniella anliuensis</i>	GMBC5334		PV933614	PV933632	PV933650	PX392339	PX373371	N/A
<i>Nectriella rusci</i>	GMBC5310		PV933615	PV933633		PX392340		N/A
<i>Orbilia ellipsospora</i>	GMBC5315		PV933616	PV933634	PV933651	PX392341	PX373355	N/A
<i>Parasymphodiella</i>	GMBC5312		PV933617	PV933635	PV933652	PX392342	PX373372	N/A

Taxon	Source	Status	GenBank accession number					
			ITS	LSU	SSU	<i>tef1-a</i>	<i>rpb2</i>	<i>tub2</i>
<i>cryptomeriae</i>								
<i>Parasympodiella</i>	GMBC5321		PV933618	PV933636	PV933653	PX392343	PX373373	N/A
<i>cryptomeriae</i>								
<i>Phragmocephala</i>	GMBC5134	ET	PV939396	PV939424	PV939450	PX392362	N/A	N/A
<i>wuliangshanensis</i>								
<i>Phragmocephala</i>	GMBC5135		PV939397	PV939425	PV939451	PX392363	N/A	N/A
<i>wuliangshanensis</i>								
<i>Pleurothecium lignicola</i>	GMBC5137		PV939410	PV939438	PV939462	N/A	PX373374	N/A
<i>Pleurothecium lignicola</i>	GMBC5143		PV939411	PV939439	PV939463	N/A	PX373375	N/A
<i>Polyplosphaeria</i>	GMBC5319	ET	PV939392	PV939420	PV939448	PX392358	N/A	N/A
<i>chinensis</i>								
<i>Polyplosphaeria</i>	GMBC5320		PV939393	PV939421	PV939449	PX392359	N/A	N/A
<i>chinensis</i>								
<i>Protocreopsis alba</i>	GMBC5357	ET	PV933619	PV933637	PV933654	PX392344	PX373362	PX373396
<i>Protocreopsis alba</i>	GMBC5358		PV933620	PV933638	PV933655	PX392345	PX373363	PX373397
<i>Pyricularia puerensis</i>	GMBC5359	ET	PV933621	PV933639	PV933656	PX392346	PX373384	N/A
<i>Pyricularia puerensis</i>	GMBC5360		PV933622	PV933640	PV933657	PX392347	PX373385	N/A
<i>Rhamphoriopsis</i>	GMBC5313	ET	PV933623	PV933641	PV933658	PX392348	PX373386	N/A
<i>globularis</i>								
<i>Rhamphoriopsis</i>	GMBC5314		PV933624	PV933642	PV933659	PX392349	PX373387	N/A
<i>globularis</i>								
<i>Rhamphoriopsis</i>	GMBC6917	ET	PV939404	PV939432	PV939456	PX392366	PX373388	N/A
<i>yunnanensis</i>								
<i>Rhamphoriopsis</i>	GMBC6919		PV939405	PV939433	PV939457	PX392367	PX373389	N/A
<i>yunnanensis</i>								
<i>Rhamphoriopsis</i>	GMBC6918	ET	PV939406	PV939434	PV939458	PX392368	PX373390	N/A
<i>zhaotongensis</i>								
<i>Rhamphoriopsis</i>	GMBC6920		PV939407	PV939435	PV939459	PX392369	PX373391	N/A
<i>zhaotongensis</i>								

Taxon	Source	Status	GenBank accession number					
			ITS	LSU	SSU	<i>tef1-α</i>	<i>rpb2</i>	<i>tub2</i>
<i>Rostriconidium fuscum</i>	GMBC5361	ET	PV939386	PV939414	PV939442	PX392352	PX373349	N/A
<i>Rostriconidium fuscum</i>	GMBC5362		PV939387	PV939415	PV939443	PX392353	PX373350	N/A
<i>Rostriconidium yunnanensis</i>	GMBC5140	ET	PV939398	PV939426	PV939452	PX392364	N/A	N/A
<i>Rostriconidium yunnanensis</i>	GMBC5141		PV939399	PV939427	PV939453	PX392365	N/A	N/A
<i>Sarocladium bambusicola</i>	GMBC5327	ET	PV939388	PV939416	PV939444	PX392354	PX373368	N/A
<i>Sarocladium bambusicola</i>	GMBC5328		PV939389	PV939417	PV939445	PX392355	PX373369	N/A
<i>Torula puerensis</i>	GMBC5363	ET	PV939384	PV939412	PV939440	PX392350	PX373351	N/A
<i>Torula puerensis</i>	GMBC5364		PV939385	PV939413	PV939441	PX392351	PX373352	N/A
<i>Triplosphaeria irregularis</i>	GMBC5365	ET	PV939390	PV939418	PV939446	PX392356	PX373353	N/A
<i>Triplosphaeria irregularis</i>	GMBC5366		PV939391	PV939419	PV939447	PX392357	PX373354	N/A
<i>Tubeufia chinensis</i>	GMBC5132	ET	PV939394	PV939422	N/A	PX392360	PX373338	N/A
<i>Tubeufia chinensis</i>	GMBC5138		PV939395	PV939423	N/A	PX392361	PX373339	N/A
<i>Volutella minutissima</i>	GMBC5311		PV939408	PV939436	PV939460	PX392370	PX373366	PX373400
<i>Volutella minutissima</i>	GMBC5318		PV939409	PV939437	PV939461	PX392371	PX373367	PX373401
<i>Xenopleopunctum muriformis</i>	GMBC5349	ET	PV951779	PV951773	PV961437	PX392376	PX373347	N/A
<i>Xenopleopunctum muriformis</i>	GMBC5350		PV951780	PV951774	PV961438	PX392377	PX373348	N/A
<i>Xylolentia yibinensis</i>	GMBC5367	ET	PV951777	PV951771	PV961435	PX392374	PX373392	N/A
<i>Xylolentia yibinensis</i>	GMBC5368		PV951778	PV951772	PV961436	PX392375	PX373393	N/A

Note: ET indicates Ex-type, NA indicates sequence not available, ITS: Internal transcribed spacer region, LSU: Large Subunit of Ribosomal RNA, SSU: Small Subunit of ribosomal RNA, *tef1-α*: Translation elongation factor, *tub2*: β-tubulin, *rpb2*: RNA polymerase II second largest subunit.

Tubeufia chinensis Q.F Zhang, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 2)

Mycobank No.: MB859998

Etymology – The epithet refers to China, where the holotype was collected.

Description – *Saprobic* on submerged rotten wood along the pond. Teleomorph: undetermined. Anamorph: hyphomycetous. *Colonies* on natural substrate black, thinly effused; seen under a dissecting microscope as a loose network of straight, dark brown hyphae bearing sparse, scattered, ovoid, shiny black conidia. *Mycelia* mostly immersed, partly superficial, composed of dark brown, septate and branched hyphae. *Conidiophores* 40–95 × 4–10 µm ($\bar{x}$ = 58.7 × 7.5 µm, n = 30), arising laterally from the superficial repent hyphae, erect, straight or curved, at first thin-walled and pale yellow-brown, becoming thick-walled and olive-brown; the apical portion remains thin-walled. *Conidiogenous cells* undetermined. *Conidia* 85–168 × 43–76 µm ($\bar{x}$ = 132.9 × 60.3 µm, n = 30), straightly or obliquely borne on the tips of conidiophores, single, broad ellipsoid to ovoid spherical to obclavate, muriform, dark brown except for the pale-colored basal cell; the conidium usually surrounded by a 1-cell deep cortical layer composed of flattened, thin-walled, subhyaline cells.

Culture characteristics – Conidia germinated within 12 hours on PDA. Colonies on PDA reaching 20–30 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface white to light brown, with densely mycelium, circular, smooth edges, raised and radial cracking at the center; reverse brown.

Material examined – China Yunnan Province, Wuliangshan National Nature Reserve, 24°25'33.66"N, 101°23'55.67"E, altitude 1455 m, on submerged dead branches of an unknown tree along the pond, collected on 2 August 2024, Qin-Fang Zhang, 2024WLSY70-2 (GMB5132, **holotype**); ex-type culture, GMBC5132; *ibid.*, KUN-HKAS 150431 isotype

Additional specimens examined – China Yunnan Province, Wuliangshan National Nature Reserve, 24°35'56.42"N, 100°25'55.85"E, altitude 2180 m, on submerged dead branches of an unknown tree along the pond, collected on 2 August 2024, Qin-Fang Zhang, 2024WLSY151 (GMB5138, GMBC5138).

Notes – In the phylogenetic analysis (Fig. 1), *Tubeufia chinensis* appears as a sister clade to *T. africana*. Morphologically, they are closely related but differ significantly in the dimensions of their conidiophores and conidia. *Tubeufia chinensis* has significantly larger conidiophores (40–95 × 4–10 µm vs. 15–45 × 3.5–5 µm) and conidia (85–168 × 43–76 µm vs. 55–95 × 38–70 µm). Additionally, secondary conidia, which are commonly observed in *T. africana* (typically 3–5 muriform, globose structures clustered at the conidial apex), were not found in *Tubeufia chinensis* (Deighton & Pirozynski 1966, Zhao et al. 2007). Comparative analysis of nucleotide base pairs showed that *T. chinensis* differs from *T. africana* (J11-1-1) by 1.7% (8/483) in the ITS locus, 0.7% (6/808) in the *tefl-α* gene, and 1.1% (11/970) in the *rpb2* gene.

Tubeufia chinensis is also similar to *Tubeufia formosiformis* in terms of conidia and conidiophore morphology. However, it differs by having much smaller conidiophores (30–40 × 5–7 µm) and smaller conidia [92–118 × 43–51(–65) µm] with secondary conidia (Ma et al. 2024).

Tubeufia subrenispora, which has larger conidia, differs from *T. chinensis* in having smaller conidiophores (18–54 × 5.5–10.5 µm) and curved to subreniform conidia (89–205 × 59–127 µm) with the upper part tapering into an incurved, hook-like shape (Ma et al. 2024).

Based on these clear morphological distinctions and phylogeny, we introduce *Tubeufia chinensis* as a new species.

Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker, Mycologia 98 (6): 1048 (2007).

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

Dictyosporiaceae Boonmee & K.D. Hyde, Fungal Diversity 80: 462 (2016).

Dictyocheiropsora M.J. D'souza, Boonmee & K.D. Hyde, Fungal Diversity 80: 465 (2016),

Notes – *Dictyocheiropsora* was established by Boonmee et al. (2016) with *D. rotunda* as the type species. The genus is characterized by dark, sporodochial colonies that produce aeroaquatic, cheiroid, non-complanate, or cylindrical conidia, mostly with conidial arms that are closely

gathered at the apex (Boonmee et al. 2016). The genus is closely related to *Dictyosporium*, but *Dictyocheiropsora* differs in having conidia arms are on different planes and closely located at the apex. According to Species Fungorum (accessed 28 June 2025), the genus currently comprises 25 accepted species.

Dictyocheiropsora chiangmaiensis H.W. Shen, Boonmee & Z.L. Luo, J. Fungi 8 (11, no. 1200): 8 (2022). (Fig. 4)

Description – *Saprobic* on decaying wood in a freshwater lake habitat. Teleomorph: Undetermined. Anamorph: Hyphomycetous. *Colonies* punctiform, sporodochial, scattered, black, shiny. *Mycelium* partially immersed, pale brown to brown, septate, smooth, branched, hyphae 2.5–4.5 μm wide. *Conidiophores* micronematous, mononematous, septate, cylindrical to sub-cylindrical, pale-brown to brown, smooth, thin-walled. *Conidiogenous cells* 5–8.5 $\times$ 3.5–6.5 μm ($\bar{x}$ = 6.6 $\times$ 4.8 μm , n = 30), holoblastic, cylindrical, septate, hyaline, smooth and thin-walled. *Conidia* 32.5–66.4 $\times$ 13.5–25.5 μm ($\bar{x}$ = 52.3 $\times$ 17.5 μm , n = 30), solitary, cheiroid, cylindrical, dark brown, composed of 3–6 rows of cells, euseptate, combined, each row with 8–10 cells, slightly bent inward at the apex. *Conidial secession* schizolytic.

Culture characteristics – Conidia germinated and formed germ tubes on WA medium within 12 hours. Colonies on PDA reaching 15–20 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface white, flocculent, smooth-edged; reverse pale brown.

Material examined – China, Sichuan Province, Leshan City, Jiazhou lùxin park, 29°34′44.07″ N, 103°42′26.26″ E, altitude 390 m, on a decaying wood near a lake, 15 October 2024, L.L. Liu, 2024LXGY2 (GMB5324, GMBC5324).

Notes – Phylogenetically (Fig. 3), the sequence of our collections clustered with the ex-type strain of *Dictyocheiropsora chiangmaiensis* (MFLUCC 22-0097), shows 100% sequence similarity in ITS, LSU, SSU and *tef1- α* loci. Despite this molecular identity, there is a significant difference in conidial size between our collection and the holotype. The holotype description reports conidia (40–)42–46(–48) $\times$ (–14)16–18(–20) μm (Shen et al. 2022), whereas the conidia in our collection are considerably larger (32.5–66.4 $\times$ 13.5–25.5 μm). This discrepancy suggests that the morphological variability of the species may be broader than previously recognized, or it may indicate the need for re-examination of the holotype material.

The species was previously reported only from Thailand (Shen et al. 2022), and our study represents the first record of *D. chiangmaiensis* for China

Culture characteristics – Conidia germinated and formed germ tubes on WA medium within 12 hours. Colonies on PDA reaching 15–20 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface white, flocculent, smooth-edged; reverse pale brown.

Material examined – China, Sichuan Province, Leshan City, Jiazhou lùxin park, 29°34′44.07″ N, 103°42′26.26″ E, altitude 390 m, on a decaying wood near a lake, 15 October 2024, L.L. Liu, 2024LXGY2 (GMB5324, GMBC5324).

Notes – Phylogenetically (Fig. 3), the sequence of our collections clustered with the ex-type strain of *Dictyocheiropsora chiangmaiensis* (MFLUCC 22-0097), shows 100% sequence similarity in ITS, LSU, SSU and *tef1- α* loci. Despite this molecular identity, there is a significant difference in conidial size between our collection and the holotype. The holotype description reports conidia (40–)42–46(–48) $\times$ (–14)16–18(–20) μm (Shen et al. 2022), whereas the conidia in our collection are considerably larger (32.5–66.4 $\times$ 13.5–25.5 μm). This discrepancy suggests that the morphological variability of the species may be broader than previously recognized, or it may indicate the need for re-examination of the holotype material.

The species was previously reported only from Thailand (Shen et al. 2022), and our study represents the first record of *D. chiangmaiensis* for China.

Massarinaceae Munk, Friesia 5 (3-5): 305 (1956).

Helminthosporium Link, Mag. Neuesten Entdeck. Gesammten Naturk. Ges. Naturf. Freunde Berlin 3 (1): 10 (1809).

Notes – *Helminthosporium* is a species-rich genus established by Link (1809), with *H. velutinum* as the type species. Species of *Helminthosporium* are characterized by septate and erect conidiophores, acro-pleurogenous and distoseptate conidia, which have a ring-shaped scar at the base. Members of the genus are commonly found on leaves and decaying wood in terrestrial habitats, rarely reported in freshwater habitats (Chen et al. 2022). According to Species Fungorum (accessed 29 June 2025), the genus currently comprises 334 accepted species. In this study, we report two new hyphomycetous species of the genus found in a freshwater habitat.

Helminthosporium dichoramosum L.L. Liu, K. Habib, Q. F. Zhang & Q.R. Li, *sp. nov.* (Fig. 6)

MycoBank No.: MB859980

Etymology – The epithet refers to its dichotomously branched conidia.

Description – *Saprobic* on decaying twigs in a river. Teleomorph: Undetermined. Anamorph: Hyphomycetous. *Colony* on natural substrate effuse, dark brown to black, scattered, hairy. *Mycelium* superficial and mostly immersed in the substratum, towards the surface forming stroma-like aggregations of light to brown pseudoparenchymatous cells. *Conidiophores* 479.5–720.5 × 13–17.5 µm ($\bar{x}$ = 613.0 × 15.3 µm, *n* = 20), macronematous, mononematous, arising solitarily or in fascicles from the stroma cells, erect, simple, septate, straight or flexuous, thick-walled, subcylindrical, smooth, brown to dark brown, paler near the apex, with well-defined small pores at the apex. *Conidiogenous cells* 30.6–56.8 × 9.4–13.7 µm ($\bar{x}$ = 42.5 × 12.1 µm, *n* = 30), enteroblastic, cylindrical, integrated, terminal and intercalary, pale brown to brown. *Conidia* 51.6–120.2 × 11.2–15.4 µm ($\bar{x}$ = 81.1 × 13.3 µm, *n* = 30), tapering to 3–6 µm ($\bar{x}$ = 4.3, *n* = 30) at the distal end, often with dichotomously branched rostrate, obpyriform to lageniform, straight, flexuous, thin-walled, verruculose, schizolytic, grey-white to pale brown, 5–17-distoseptate (*n* = 35), with angular lumina.

Culture characteristics – Conidia germinated and formed germ tubes on WA medium within 36 hours. Colonies on PDA reaching 15–25 mm diam., after 2 weeks at 24–27°C on PDA. Colony surface white to cream, circular, umbonate, fluffy, margins smooth; reverse lemon yellow.

Material examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'21.77" N, 104°00'19.12" E, altitude: 1419 m, on decaying twigs of an unknown tree in a river, 11 October 2024, L.L. Liu, 2024WMS232 (GMB5347, **holotype**); ex-type culture, GMBC5347; *ibid.*, KUN-HKAS 150436, isotype.

Additional specimens examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'29.79" N, 104°00'05.54" E, altitude: 1371m, on decaying twigs of an unknown tree in a river, 11 October 2024, L.L. Liu, 2024WMS257 (GMB5348, GMBC5348).

Notes – In the phylogram (Fig. 5), *Helminthosporium dichoramosum* is closely related to *H. austriacum*, *H. camelliae-sinensis* and *H. yunnanense*. However, these species can be easily distinguished by differences in the size of the conidiophore and conidia, as well as the number of conidial septa in *H. dichoramosum* has longer conidiophores (480–720 × 13–17.5 µm vs. 275–700 × 11.5–19 µm) and much larger conidia (51–120 × 11–15 µm vs. 35–48 × 13.7–16.5 µm), with more conidial distoseptate (5–17 distoseptate vs. 5–7 distoseptate) (Voglmayr & Jaklitsch 2017) compared to *H. austriacum*. Furthermore, the conidia of *H. dichoramosum* possess dichotomously branched arms at the apex, a feature not reported in *H. austriacum* (Voglmayr & Jaklitsch 2017). Molecular comparisons also support their separation. Comparative analysis of nucleotide base pairs showed that *H. dichoramosum* differs from *H. austriacum* (CBS 139924) by 4.7 % (23/485) in the ITS locus, 0.1% (1/1042) in the SSU locus, 1.8 % (14/773) in the *tefl-a* gene, and 1.5 % (16/1035) in the *rpb2* gene.

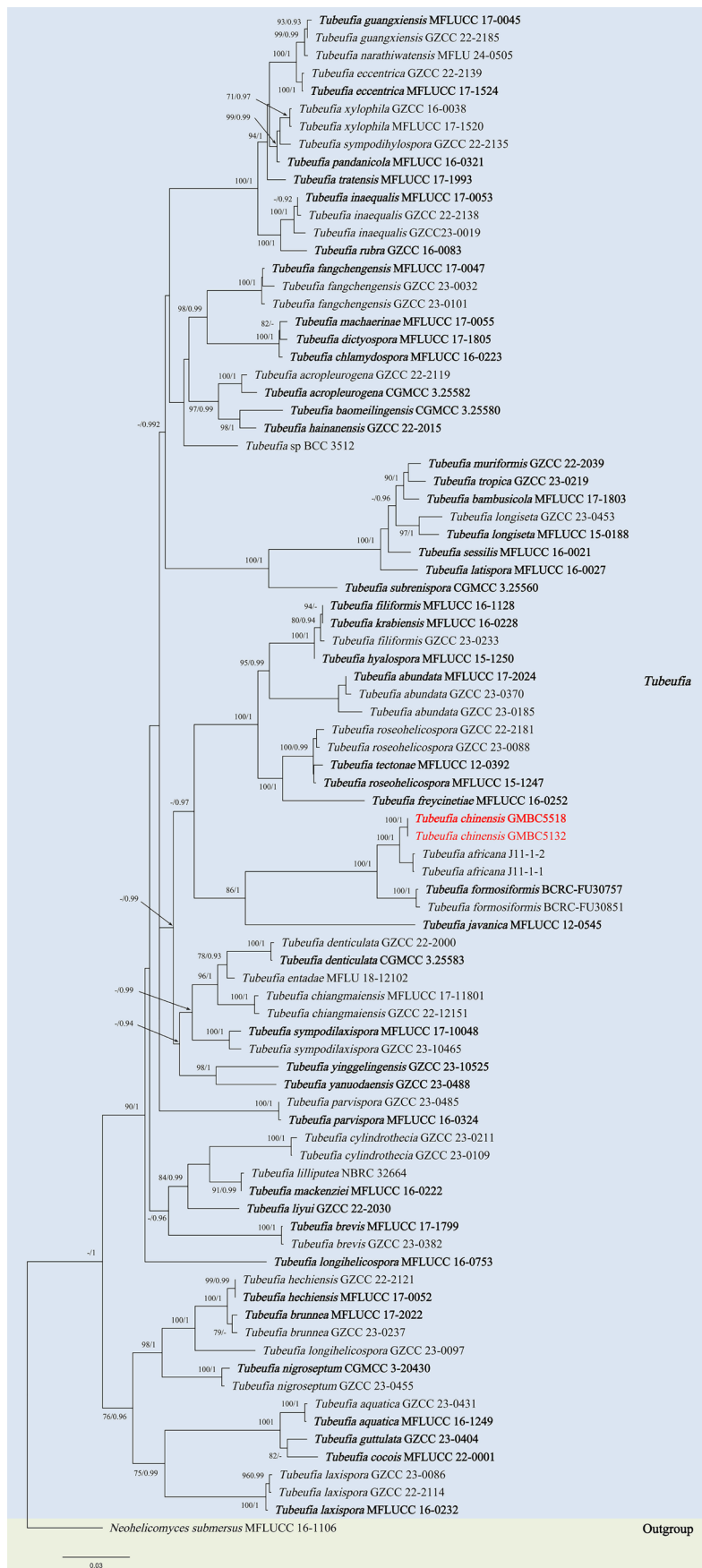


Figure 1 – ML tree of *Tubeufia* and related taxa based on ITS, LSU, *tef1-α* and *rpb2* loci. The alignment for this tree includes 3325 bp (ITS: 1–523 bp; LSU: 524–1368 bp; *tef1-α*: 1369–2280 bp; *rpb2*: 2281–3325 bp). *Neohelicomycetes submersus* (MFLUCC 16-1106) was selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$

are shown on the branches. Newly generated sequences are indicated in red and type strains or specimen are in bold.

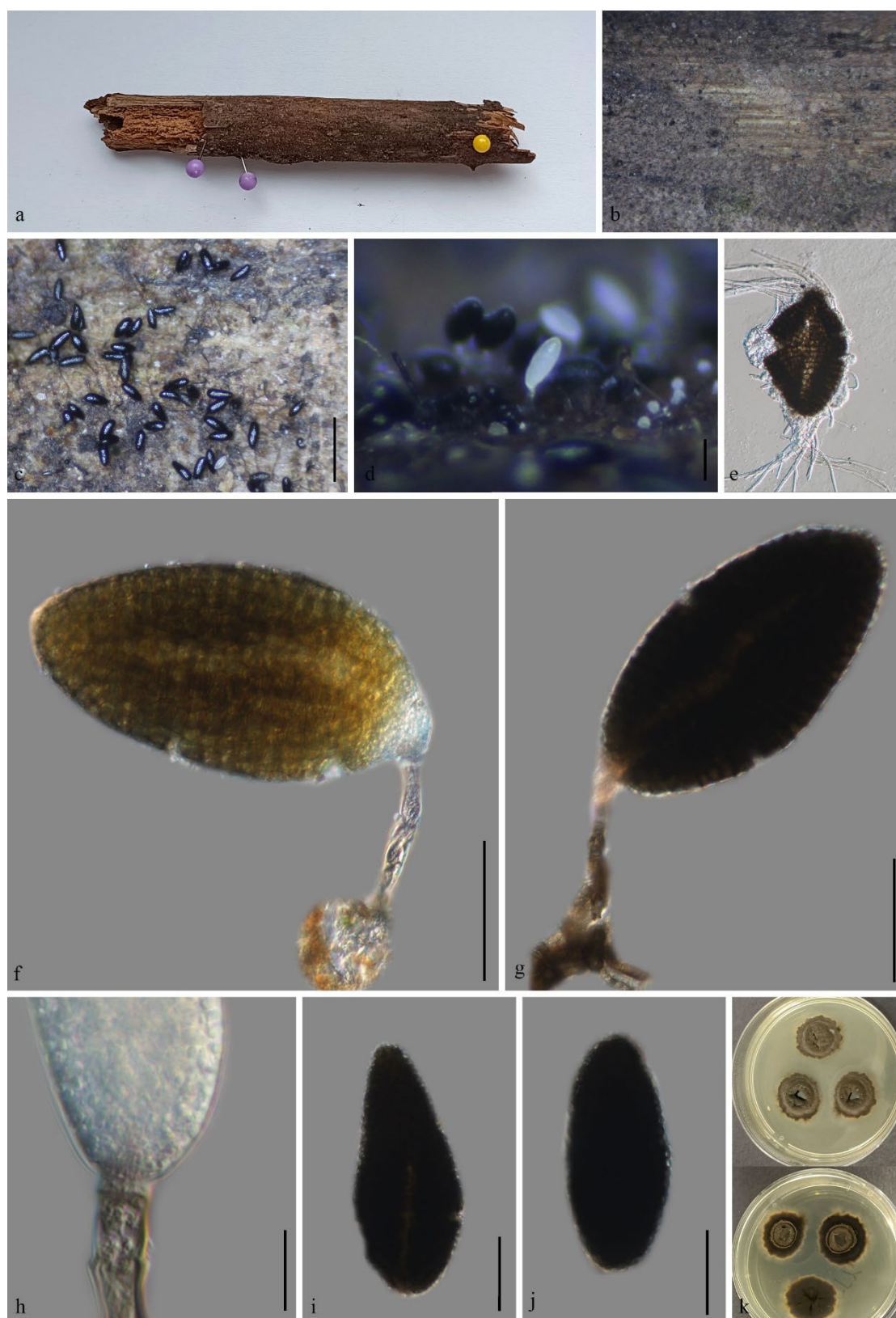


Figure 2 – *Tubeufia chinensis* (GMB5132, holotype) a–d Conidiophores and conidia on natural substratum. e Germinating conidium. f, g Conidiophores and conidia. h. Conidiogenous cells. i, j Conidia. k Surface and reverse view of culture on PDA. Scale bars: b = 1 mm, c = 0.5 mm, d = 0.1 mm, h = 10 μ m; e–g, i–j = 50 μ m.

0.2 % (1/552) in the 28S gene, 1.3 % (6/468) in the 18S gene, 0.5 % (5/926) in the *tef1- α* gene, and 1.6% (16/1031) in the *rpb2* gene.

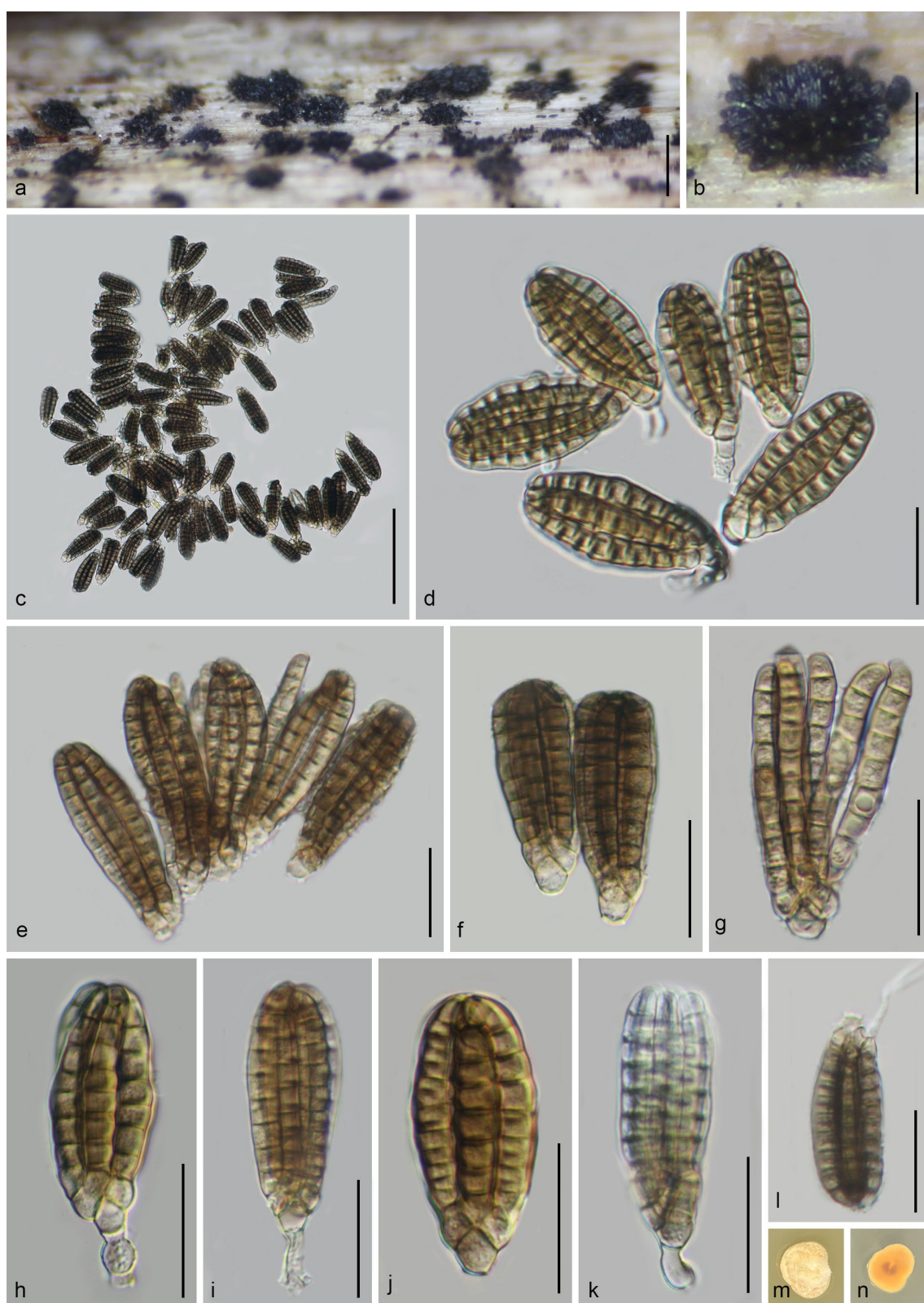


Figure 4 – *Dictyocheirospora Chiangmaiensis* (GMB5324) a–b Colonies on substratum. c–k Conidia (h, l, k with conidiogenous cells). l Germinating conidium. m Surface view of culture on PDA. n Reverse view of culture on PDA. Scale bars: a = 0.5 mm, b = 0.2 mm, c = 100 μ m, d–l = 25 μ m.

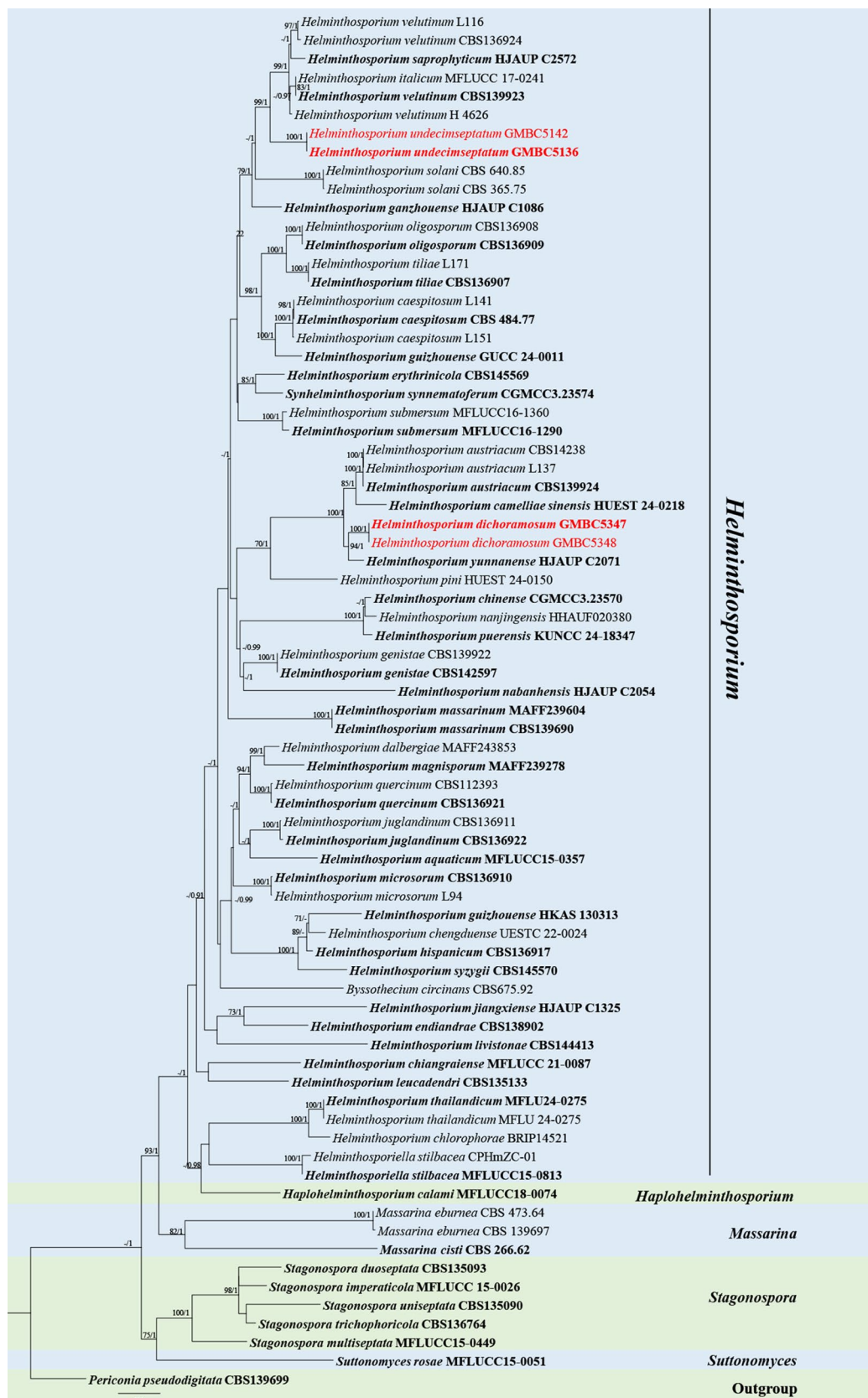


Figure 5 – RAxML tree based on analysis of a combined ITS, LSU, SSU, *tef1-α*, and *rpb2* sequences for *Helminthosporium*. The alignment for this tree includes 4361 bp (ITS:1–511; LSU: 512–1383; SSU: 1384–2410; *tef1-α*: 2411–3274; *rpb2*: 3275–4361). *Periconia pseudodigitata* (CBS139699) was selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly described species are marked red in bold. Ex-types are indicated in black bold.

Helminthosporium camelliae-sinensis can be distinguished from *H. dichoramosum* by its smaller conidia ($33\text{--}77 \times 8\text{--}15 \mu\text{m}$ vs. $51.6\text{--}120.2 \times 11.2\text{--}15.4 \mu\text{m}$) and fewer distosepta ($5\text{--}8$ vs. $5\text{--}17$) (Chi et al. 2025).

Helminthosporium dichoramosum is distinctive due to its dichotomously branched conidia. Based on these morphological and molecular differences, as well as the phylogenetic analysis, we introduce *H. dichoramosum* as a new species.

Helminthosporium undecimseptatum Q.F. Zhang, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 7)

Mycobank No.: MB859981

Etymology – The epithet refers to its up to 11-septate conidia.

Description – *Saprobic* on submerged decaying wood along the riverbank. Teleomorph: undetermined. Anamorph: Colonies dark brown, effuse, velvety. Mycelium immersed, composed of branched, septate, thick-walled hyphae. Conidiophores $420\text{--}985 \times 13\text{--}23 \mu\text{m}$ ($\bar{x} = 582.6 \times 15.8 \mu\text{m}$, $n = 30$), mononematous, macronematous, mostly unbranched, proliferating, dark brown, 17–23-septate, erect or flexuous, tapering towards apex, bulbous at base with cells near apex of conidiophore guttulate and fertile. Conidiogenous cells polytretic integrated, intercalary and terminal. Conidia $56\text{--}72 \times 13\text{--}16 \mu\text{m}$ ($\bar{x} = 64.5 \times 14.5 \mu\text{m}$, $n = 30$), single, obclavate, pale brown to brown, 7–11-distoseptate, smooth, straight or curved, base slightly truncate, cicatrized and wider than apex, dark brown, apical cell paler than other cells, rounded at apex, guttulate when young, non-guttulate at maturity. Conidial secession schizolytic.



Figure 6 – *Helminthosporium dichoramosum* (GMB5347, holotype). a, b Colony on wood. c Conidiophores and conidia. d Conidiogenous cells. e–i Conidia. j Germinated conidium.

k Surface view of culture on PDA. l Reverse view of culture on PDA. Scale bars: a, b=0.5 mm, c=50 μ m, d–j= 20 μ m.

Culture characteristics – Conidia germinated within 12 hours on WA. Colonies on PDA reaching 30–40 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface dirty white to light brown, with densely mycelium, cottony, slightly elevated, edge entire, emission at margin; reverse dark brown to black with margin pale brown.

Material examined – China Yunnan Province, Wuliangshan National Nature Reserve, 24°25'33.66"N, 101°23'55.67"E, altitude 1455 m, on submerged dead branches of an unknown tree along the riverbank, collected on 2 August, 2024, Qin-Fang Zhang, 2024WLSY98 (GMB5136, **holotype**); ex-type culture, GMBC5136; *ibid.*, KUN-HKAS 150434, isotype

Additional material examined – China Yunnan Province, Wuliangshan National Nature Reserve 24°35'56.42"N, 100°25'55.21"E, altitude 2180 m, on submerged dead branches of an unknown tree along the riverbank, collected on 2 August 2024, Qin-Fang Zhang, 2024WLSY135 (GMB5142, GMBC5142).

Notes – In the phylogenetic analysis (Fig. 5), *Helminthosporium undecimseptatum* forms a well-supported sister clade to *H. velutinum*. *Helminthosporium undecimseptatum* can be distinguished from *H. velutinum* by its longer conidiophores (420–985 $\times$ 13–23 μ m vs. 340–698 $\times$ 14–26 μ m) and smaller conidia (56–72 $\times$ 13–16 μ m vs. 56–89 $\times$ 14.3–18.5 μ m) with lesser septa (7–11 distoseptate vs. 6–18 distoseptate) (Voglmayr & Jaklitsch 2017). Comparative analysis of nucleotide base pairs showed that *H. undecimseptatum* differs from *H. velutinum* (CBS 136924) by 2.9 % (15/520) in the ITS locus, 0.4 % (3/857) in the LSU locus, and 4.6 % (50/1085) in the *rpb2* gene.

Helminthosporium undecimseptatum is also phylogenetically closely related to *H. italicum* (Fig. 5). However, *H. undecimseptatum* morphologically differs in having longer conidiophores (420–985 $\times$ 13–23 μ m vs. 330–600 $\times$ 16–18 μ m) and slightly smaller, narrower conidia (56–72 $\times$ 13–16 μ m vs. 58–78 $\times$ 15–23 μ m) (Tian et al. 2018). Molecular comparisons of ITS, LSU, and *tef1- α* sequences between *H. undecimseptatum* and *H. italicum* (MLUCC 17-0241) showed 98.1 %, 99.6 % and 96.9 %, respectively.

Morphologically, *H. undecimseptatum* and *H. aquaticum* share a similar conidial shape and comparable size, but *H. aquaticum* has smaller conidiophores (410–580 $\times$ 13–17 μ m) and slightly larger conidia (70–80 $\times$ 16–18 μ m), with 8–10 distoseptate conidia (Zhu et al. 2016).

Given these morphological and molecular differences, along with the phylogenetic analysis, we introduce *Helminthosporium undecimseptatum* as a new species.

Pseudolophiotremataceae K.D. Hyde & Hongsanan, Phytotaxa 383 (1): 97 (2018).

Bulbocatenulomyces L.L. Liu, K. Habib & Q.R. Li, *gen. nov.*

MycoBank No.: MB860082

Typification – *Bulbocatenulomyces nigricans* L.L. Liu, K. Habib & Q.R. Li

Etymology – *Bulbo* refers to the bulbous conidiogenous cells; *catenul* refers to the small chain-like arrangement of 1–3 conidiogenous cells; *-myces*, a standard fungal suffix.

Description –Teleomorph: undetermined. Anamorph: *Colonies* on natural substratum, superficial, sporodochial, scattered, compact, black and shining. *Mycelium* immersed, branched, septate, hyaline to pale-brown. *Conidiophores* micronematous, hyaline, reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, determinate, terminal, with bulbous to ampulliform cells forming chain-like appearance, guttulate, constricted at septa. *Conidia* acrogenous, solitary, dark brown to black, broadly ellipsoid to ovoid, usually with conidiogenous cell attached.

Bulbocatenulomyces nigricans L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 9)

MycoBank No.: MB860083

Etymology – The epithet refers to its black, shining colonies on the substratum.

Description – *Saprobic* on decaying wood in a lake. Teleomorph: undetermined. Anamorph: *Colonies* on natural substratum, superficial, sporodochial, scattered, compact, black and shining, irregular shaped. *Mycelium* immersed, branched, septate, hyaline to pale-brown. *Conidiophores* micronematous, micronematous, hyaline, reduced to conidiogenous cells. *Conidiogenous cells* 9–25 × 8–16 µm ($\bar{x}$ = 16.9 × 10.6 µm, n = 30), monoblastic, determinate, terminal, with 1 to 3 bulbous to ampulliform cells, forming a chain-like appearance, guttulate, constricted at septa. *Conidia* 31–39.5 × 17–21.5 µm ($\bar{x}$ = 34.8 × 19 µm, n = 30), solitary, dark brown to black, hyaline to light brown at base, broadly ellipsoid to ovoid, usually with conidiogenous cell attached.



Figure 7 – *Helminthosporium undecimseptatum* (GMB5136, holotype). a. Substratum. b–d Conidiophores and conidia on natural substratum. e Germinating conidium. f–h Conidiophores

and Conidia. i Conidiogenous cells. j, k Conidia. l Surface view of culture on PDA. Scale bars: b = 1 mm, c, d = 0.5 mm, e–h = 50 µm, i = 10 µm, j, k = 30 µm.

Culture characteristics – Conidia germinated and formed germ tubes on WA medium within 24 hours. Colonies on PDA reaching 10–20 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface white to creamy with dull greenish tinge, with densely mycelium, velvety; reverse dark brown with green tinge.

Material examined – China, Guangxi Zhuang Autonomous Region, Nanning City, Daming Mountain National Nature Reserve, 23°47'3.42"N, 108°42'33.53"E, altitude 1560 m, on submerged decaying wood in a lake, 11 August 2023, L.L. Liu, 2023DMS21 (GMB5316, **holotype**); ex-type culture, GMBC5316; *ibid.*, KUN-HKAS 150408 isotype.

Additional specimens examined – China, Guangxi Zhuang Autonomous Region, Nanning City, Daming Mountain National Nature Reserve, 23°47'25.67"N 108°42'42.07"E, altitude 1510 m, on a decaying wood, on submerged decaying wood in a lake, 11 August 2023, L.L. Liu, 2023DMS68 (GMB5317, GMBC5317).

Notes – Phylogenetically (Fig. 8), *Bulbocatenulomyces nigricans* clusters within a clade containing *Clematidis elymicola* (= *Pseudolophiotrema elymicola*) and *C. italica*, both of which are known only for their teleomorphs (Li et al. 2016, Hashimoto et al. 2017). However, *Bulbocatenulomyces nigricans* forms a distinct branch that clearly differentiates it from these two species. Comparative analysis of nucleotide base pairs showed that *Bulbocatenulomyces nigricans* differs from *C. italica* (MFLUCC 150084) by 12.1 % (59/486) in the ITS locus, 4.3 % (37/856) in the LSU locus, and 28.9 % (395/1369, having 26.7 % gaps in the middle of sequence) in the SSU locus. In comparison to *Clematidis elymicola* (HHUF 28984), *Bulbocatenulomyces nigricans* differed by 10.9 % (52/479 bp) in the ITS locus, 3.3 % (28/838 bp) in the LSU locus, 35.2 % (477/1354 bp, having 32.7 % gaps in the middle of sequence) in the SSU locus, 8.6 % (82/958 bp) in the *tef1-α* gene, and 19.1 % (193/1009 bp) in the *rpb2* gene.

Bulbocatenulomyces nigricans resembles *Aquadictyospora* and *Pseudoberkleasium*, but it is not phylogenetically related to either genus. Morphologically, *Bulbocatenulomyces nigricans* is characterized by dark brown to black conidia with faint, barely visible muriform septation and conidiogenous cells that consist of 1–3 sequentially arranged bulbous to ampulliform cells (forming a chain), whereas *Aquadictyospora* and *Pseudoberkleasium* produce brown to olivaceous conidia with conspicuous muriform septation and single, globose conidiogenous cells (Li et al. 2017, Tibpromma et al. 2018).

In the absence of an anamorph in its closest teleomorph relatives and given both its distinctive conidiogenous structure and its clear phylogenetic separation from morphologically similar genera, we establish *Bulbocatenulomyces* gen. nov. to accommodate *B. nigricans*.

Clematidis Tibpromma, Camporesi & K.D. Hyde, Fungal Diversity 78: 59 (2016).

Synonym: *Pseudolophiotrema* A. Hashim. & Kaz. Tanaka

Notes – *Clematidis* was introduced by Li et al. (2016), with *Clematidis italica* as the type species, which was found as a saprobe on *Clematis vitalba*. The genus is characterized by superficial, globose to subglobose ascomata, scattered on the host surface, with an ostiole at the center, asci 8-spored, bitunicate, cylindrical to cylindric-clavate, short pedicellate or sessile and ascospores hyaline, fusiform, 1-septate at the center, swollen, with guttules in each cell, with or without mucilaginous sheath (Li et al. 2016). The anamorph of the genus remains unknown.

Hashimoto et al. (2017) proposed the monotypic genus *Pseudolophiotrema* to accommodate *P. elymicola*, a species that align with the generic characteristics of *Clematidis*. However, they did not include *Clematidis italica* in their phylogenetic analysis, resulting in the establishment of *Pseudolophiotrema* as a distinct genus. Both *Clematidis* and *Pseudolophiotrema* are monotypic. Our multigene phylogenetic analyses (Fig. 8) have demonstrated that *Clematidis italica* and *Pseudolophiotrema elymicola* are sister species. Given that *Clematidis* was established prior to *Pseudolophiotrema*, and based on their close phylogenetic relationship and morphological

similarity, we propose transferring *Pseudolophiotrema elymicola* to the genus *Clematidis* as *Clematidis elymicola* comb. nov., thereby synonymizing *Pseudolophiotrema* with *Clematidis*.

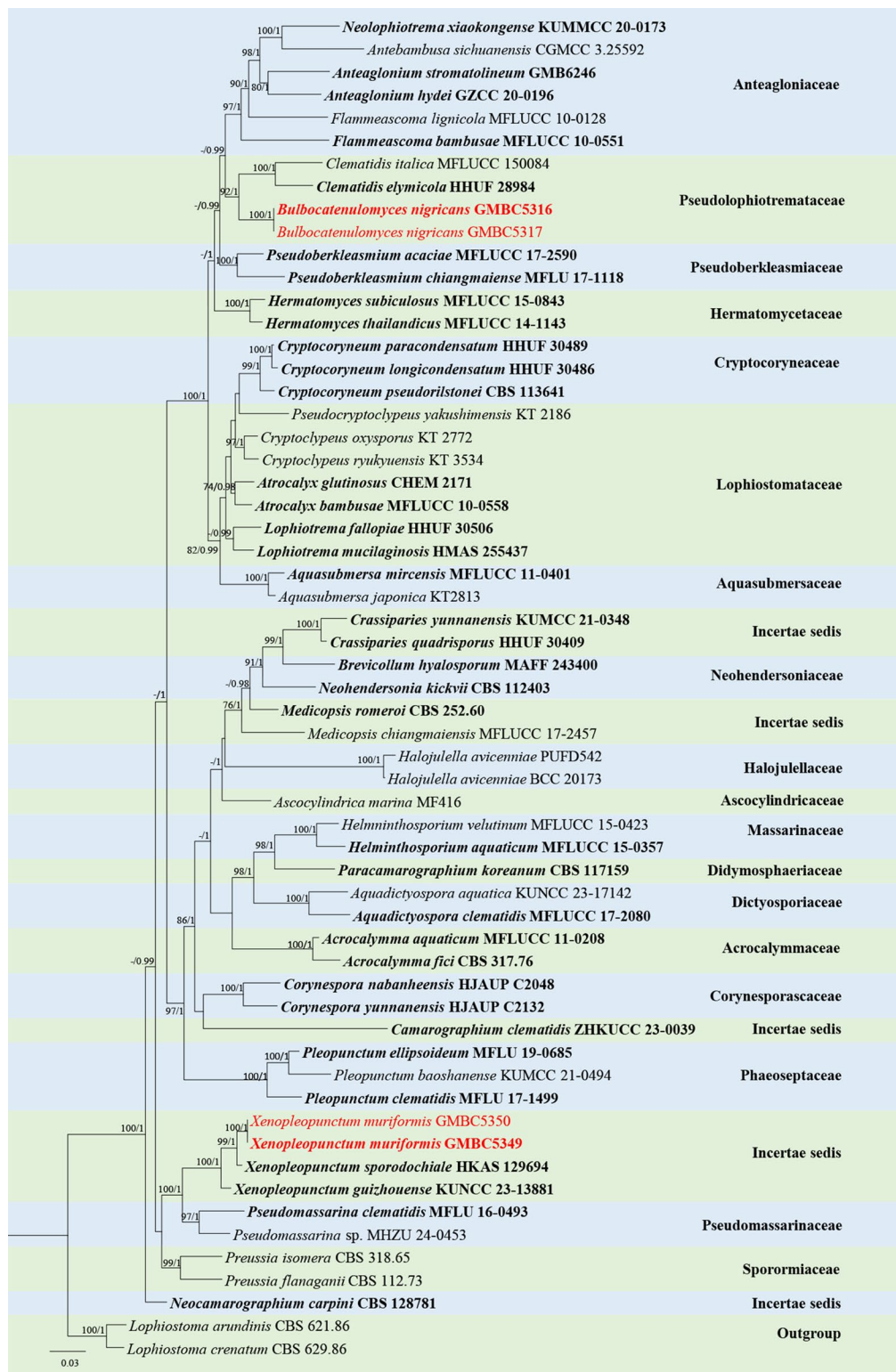


Figure 8 – ML tree of selected *Pleosporales* based on ITS-LSU-SSU-*tef1-α* dataset. The alignment for this tree includes 3228 bp (ITS:1–481; LSU: 482–1308; SSU: 1309–2324; *tef1-α*: 2325–3228). *Lophiostoma crenatum* (CBS 629.86) and *L. arundinis* (CBS 621.86) were selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAXML $\geq 70\%$ are shown on the branches. The newly described species are marked red in bold. Ex-type/type strains are indicated in black bold.

Clematidis elymicola (A. Hashim. & Kaz. Tanaka) K. Habib & Q.R. Li, **comb. nov.**

Mycobank No.: MB860000

Basionym: *Pseudolophiotrema elymicola* A. Hashim. & Kaz. Tanaka, *Persoonia* 39: 70 (2017).

Holotype detail (Hashimoto et al. 2017): Japan, Hokkaido, Yufutsu, on dead leaves of *Leymus mollis*, 1 Sept. 2003, Y. Harada, KT 1450 (HHUF 28984 holotype, ex-holotype culture JCM 13090 = MAFF 239600).

Description – Refer Hashimoto et al. (2017)

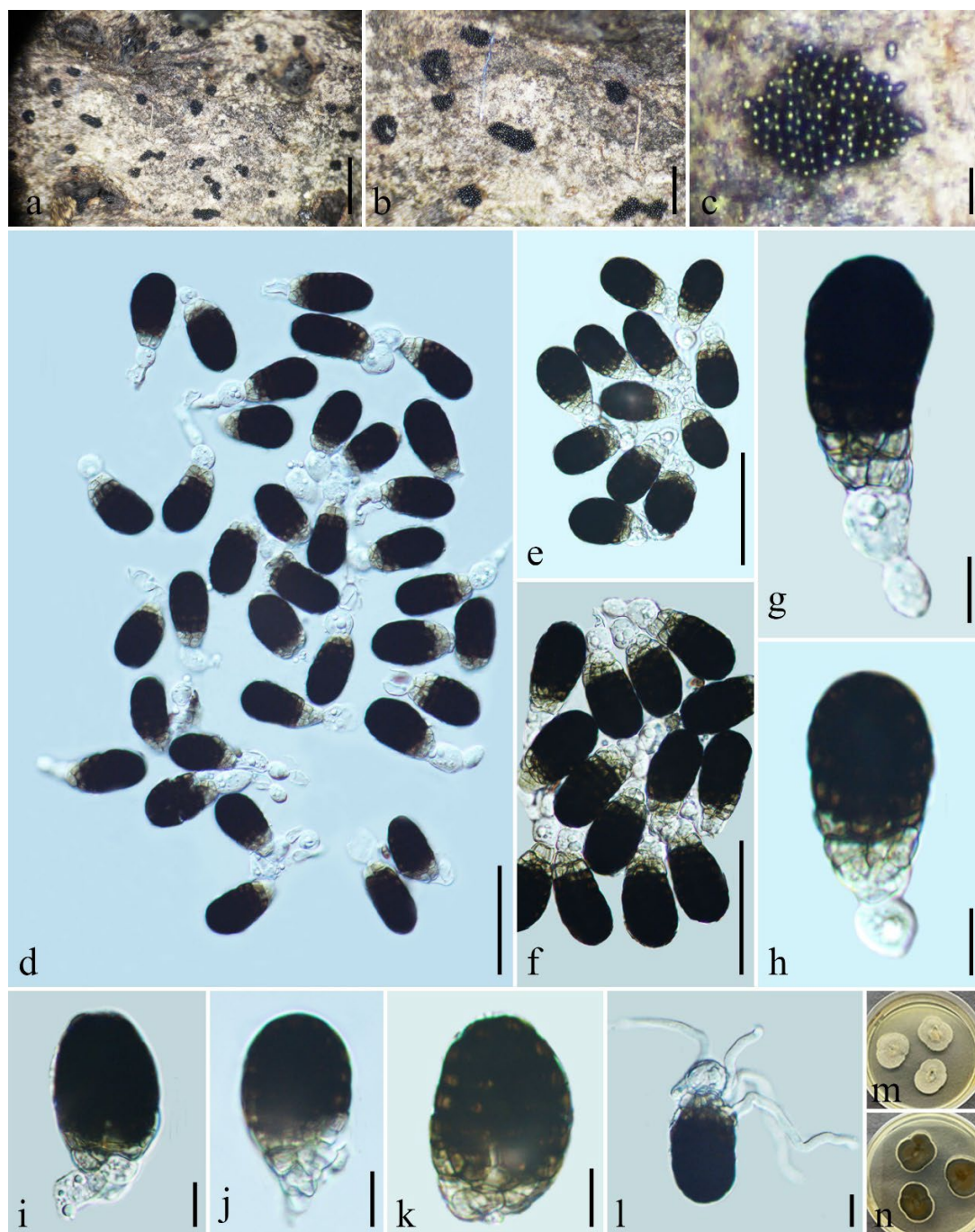


Figure 9 – *Bulbocatenulomyces nigricans* (GMB5316, holotype). a–c Colonies on the host substrate, d–k Conidia. l Germinated conidium, m Surface view of culture on PDA. n Reverse view of culture on PDA. Scale bars: a = 1 mm, b = 0.5 mm, c = 0.1 mm, d–f = 50 µm, g–l = 10 µm.

Xenopleopunctum J.Y. Zhang, Y.Z. Lu & K.D. Hyde, IMA Fungus 16, e167717 (2025).

Index Fungorum number. IF904147

Notes – *Xenopleopunctum* has been recently established as a new genus, with *X. guizhouense* designated as the type species (Zhang et al. 2025). The genus is characterized by effuse, superficial, brown to black colonies, scattered to aggregated; conidiophores cylindrical, brown, sometimes reduced to conidiogenous cells; conidiogenous cells monoblastic, terminal, thick-walled, brown and conidia acrogenous, ranging from ellipsoidal to muriform, brown to dark brown, darker at the septa, paler at the base, with hyaline basal cell. Currently, the genus is represented by *X. guizhouense* and *X. sporodochiale*. In this study, we introduce the third species, *X. muriformis*.

Xenopleopunctum muriformis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 10)

Mycobank No: MB860085

Etymology – The epithet refers to its muriform conidia.

Description – *Saprobic* on decaying twigs of an unknown plant. Teleomorph: Undetermined. Anamorph: hyphomycetous. *Colonies* on natural substratum sporodochial, superficial, scattered or aggregated in small groups, with an irregular outline, appearing as dark, beady to velvety masses composed of dense conidiophores and conidia. *Mycelium* immersed in the substrate, composed of branched, septate, smooth, hyaline hyphae. *Conidiophores* micronematous, hyaline, reduced to conidiogenous cells. *Conidiogenous cells* 28.9–33.2 × 2.1–2.5 µm ($\bar{x}$ = 31.3 × 2.3 µm, n = 30), holoblastic, monoblastic, integrated, terminal, cylindrical, hyaline, smooth-walled. *Conidia* 33.3–60.2 × 23.8–32.1 µm ($\bar{x}$ = 52.4 × 27.9 µm, n = 30), solitary, dry, dictyosporous, broadly ellipsoidal to ovate, obovoid, broadly rounded at apex and tapering toward the base, septate longitudinally and transversely forming a muriform pattern, young conidia hyaline, becoming brown to dark brown at maturity, usually with conidiogenous cell attached 10–20 × 10–17 µm ($\bar{x}$ = 14.8 × 13.4 µm, n = 30).

Culture characteristics – Conidia germinated within 12 hours on WA. Colonies on PDA reaching 10–15 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface initially white becoming yellowish to pale brown with age, with densely mycelium, circular, entire, velvety, center raised; reverse pale yellow to buff.

Material examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, on a decaying wood, 24°25′47.75″ N, 100°54′49.37″ E, altitude: 2106 m, 13 October 2024, L.L. Liu, 2024WLSY60 (GMB5349, **holotype**); ex-type culture, GMBC5349; *ibid.*, KUN-HKAS 150429 isotype.

Additional specimens examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°20′22.31″N, 100°48′36.41″E, altitude: 2202 m, on a decaying wood, 15 September 2024, L.L. Liu, 2024WLSY93 (GMB5350; GMBC5350).

Notes – Phylogenetically (Fig. 8), *Xenopleopunctum muriformis* forms a well-supported sister clade with *X. sporodochiale* (ML/B1 = 99/1). Comparative analysis of nucleotide base pairs showed that *X. muriformis* differs from *X. sporodochiale* (HKAS 129694) by 1.8 % (9/489) in the ITS locus, 0.4 % (2/514) in the SSU locus, 3.4 % (27/805) in the LSU locus. Morphologically, *X. muriformis* differs from *X. sporodochiale* in having longer conidiogenous cells (28.9–33.2 × 2.1–2.5 µm vs. 3.0–6.2 × 2.5–3.1 µm) and larger conidia (33.3–60.2 × 23.8–32.1 µm vs. 35.0–47.8 × 18.3–25.5 µm), with a larger basal cell (10–20 × 10–17 µm vs. 7.5–12 × 7.3–12 µm). In addition, the muriform conidial cells of *X. muriformis* are distinctly smaller and occur in greater numbers than those observed in *X. sporodochiale*.

The type species, *X. guizhouense*, forms a distinct clade from *X. muriformis* and is morphologically characterized by significantly smaller conidiogenous cells (4–6.5 µm diam. vs. 28.9–33.2 × 2.1–2.5 µm) and slightly larger conidia (46.5–66.5 × 22.0–32.5 µm vs. 33.3–60.2 µm long) (Zhang et al. 2025).

Torulaceae Corda, Deutschlands Flora, Abt. III. Die Pilze Deutschlands 2: 71 (1829).

Rostriconidium Z.L. Luo, K.D. Hyde & H.Y. Su, Mycol. Progr. 17 (5): 536 (2018).

Notes – *Rostriconidium* was established by Su et al. (2018) and typified by *R. aquaticum*, which was collected from a freshwater habitat in Yunnan Province, China. The genus is characterized by long conidiophores, monotretic or polytretic, dark brown to black conidiogenous cells, and multi-septate, pyriform to rostrate conidia, with or without a subhyaline apex and an especially dark structure at the base with a light-colored cell above conidia (Su et al. 2018). According to Species Fungorum (accessed 28 June 2025), the genus currently comprises three accepted species. Herein, we introduce two new species of *Rostriconidium*, both found on submerged decaying wood in freshwater habitats.

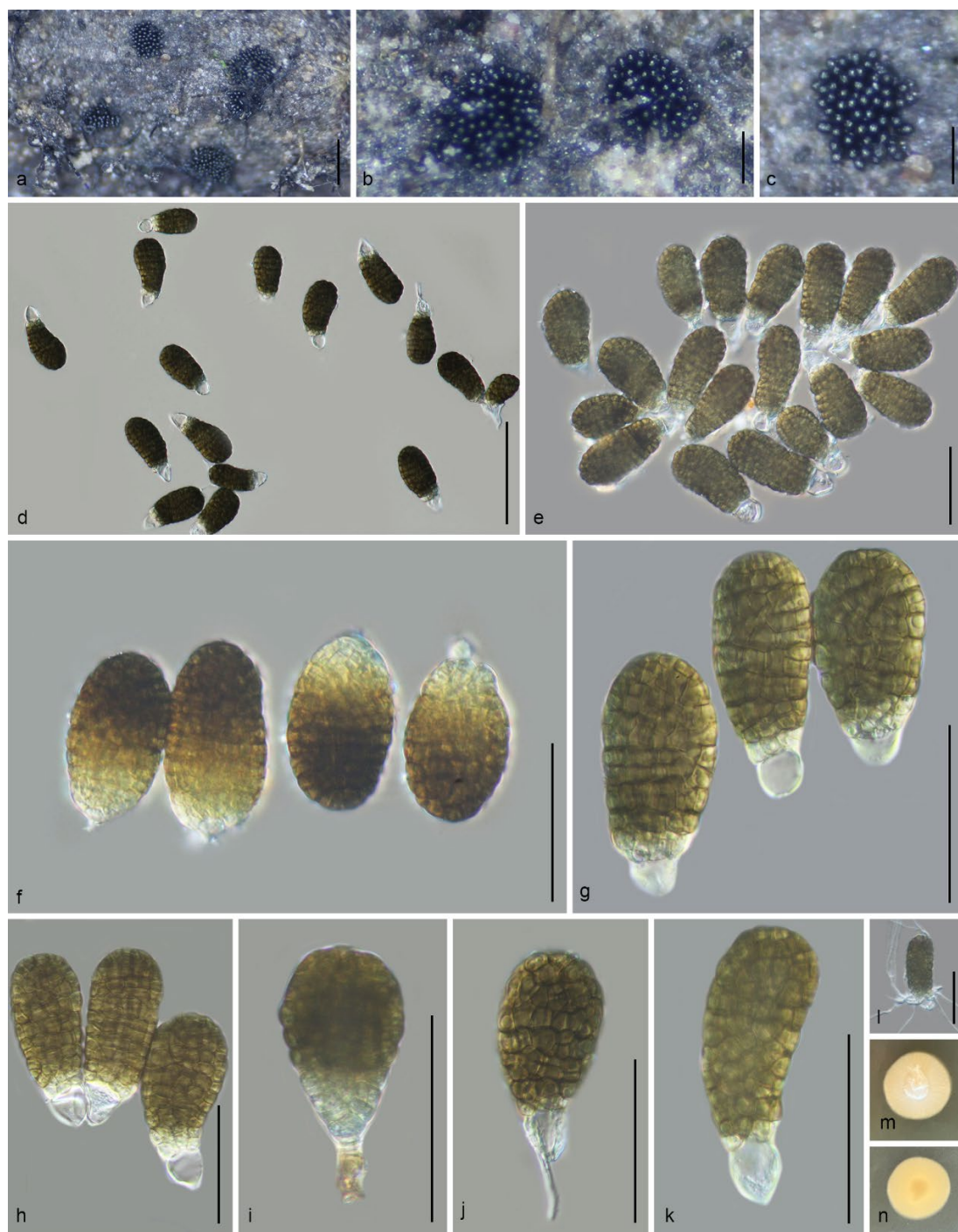


Figure 10 – *Xenopleopunctum muriformis* (GMB5350, holotype) a–c Colony on wood. d–k Conidia. l Germinating conidium. m, n Surface and reverse view of culture on PDA. Scale bars: a = 0.5 mm, b, c = 0.2 mm, d = 100 μ m, e–l = 50 μ m.



Figure 11 – ML tree of *Torula* and *Rostriconidium* and related taxa based on ITS, LSU, *rpb2*, SSU and *tef1-α* loci. The alignment for this tree includes 4619 bp (ITS:1–552 bp; LSU: 553–1590 bp; *rpb2*: 1591–2632 bp; SSU: 2633–3694 bp; *tef1-α*: 2634–4619 bp). *Roussoellopsis macrospora* (MFLUCC 12-0005) and *Roussoellopsis tosaensis* (KT 1659) were selected as the outgroup taxa. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML ≥ 70 % are shown on the branches. The newly described species are marked red. Ex-type/type strains are indicated in black bold.

Rostriconidium fuscum L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 12)

Mycobank No.: MB859993

Etymology – The epithet refers to its dark-brown conidia.

Description – *Saprobic* on submerged decaying wood along the waterfall. Teleomorph: Undetermined. Anamorph: *Colonies* effuse on natural substratum, erect, scattered, hairy, dark brown to black. *Mycelium* immersed in the substratum, composed of pale brown to brown, septate, unbranched hyphal elements. *Conidiophores* $265\text{--}491 \times 11\text{--}17.5\ \mu\text{m}$ ($\bar{x} = 358.2 \times 14.5\ \mu\text{m}$, $n = 20$), macronematous, mononematous, solitary, erect, septate, smooth, straight to flexuous, subcylindrical, dark brown to black, pale yellowish pigment observed at apex. *Conidiogenous cells* $32.5\text{--}66 \times 11.2\text{--}18.5\ \mu\text{m}$ ($\bar{x} = 52 \times 13.7\ \mu\text{m}$, $n = 20$), monotretic or sometimes polytretic, sympodial, integrated, terminal, roughly cylindrical and flexuous, dark brown to almost black. *Conidia* $98\text{--}137 \times 20.5\text{--}26\ \mu\text{m}$ ($\bar{x} = 116.2 \times 23\ \mu\text{m}$, $n = 20$), solitary, fusiform to pyriform, rostrate at maturity, dark brown, 5–8-septate, with guttulate cells, a thick and black truncate scar at the base, pale yellowish pigmented cell just above the black scar, broader from the center, apex narrowly cylindrical, obtuse, hyaline, sometimes with hyaline sheath at apex or near apex.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 20–30 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface creamy white with reddish brown tinge, with densely mycelium, circular, smooth edges; reverse brown from the center to reddish brown ring towards the margin, margins creamy brown.

Material examined – China, Guizhou Province, Qingzhen City, Anliu Town, Yangpidong Scenic Area, 26°20′29.667″N, 106°21′15.26″E, altitude 707 m, on a decaying wood along the waterfall, 23 October 2024, L.L. Liu, 2024YPD6 (GMB5361, **holotype**); ex-type culture, GMBC536; *ibid.*, KUN-HKAS 150442 isotype.

Additional specimens examined – China, Guizhou Province, Qingzhen City, Anliu Town, Yangpidong Scenic Area, 26°20′29.672″N, 106°21′15.35″E, altitude 707 m, on a decaying wood along the waterfall, 23 October 2024, L.L. Liu, 2024YPD18 (GMB5362, GMBC5362).

Notes – *Rostriconidium fuscum* aligns well with the generic concept of *Rostriconidium*, characterized by erect, septate conidiophores, terminal cylindrical conidiogenous cells, and rostrate, septate conidia with a subhyaline base. Phylogenetic analysis (Fig. 11) shows that *R. fuscum* forms a well-supported sister relationship with *R. aquaticum*. Morphologically, *R. aquaticum* has longer conidiophores ($370\text{--}590 \times 13\text{--}17\ \mu\text{m}$) and much larger, 8–9-septate conidia ($134\text{--}180 \times 22\text{--}26\ \mu\text{m}$) compared to *R. fuscum*, which has conidiophores measuring $265\text{--}491 \times 11\text{--}17.5\ \mu\text{m}$ and smaller, 5–8-septate conidia ($98\text{--}137 \times 20.5\text{--}26\ \mu\text{m}$) (Su et al. 2018). Comparative analysis of nucleotide base pairs showed that *R. fuscum* differs from *R. aquaticum* (MFLU 17-1415) by 2.6% (13/494) in the ITS locus, 0.4% (3/809) in the LSU locus, 2.2% (18/822) in the *tef1- α* gene, and 2.1% (17/827) in the *rpb2* gene.

Morphologically, *Rostriconidium fuscum* is closely related to *R. cangshanense* and *R. pandanicola*. *Rostriconidium cangshanense* differs by having larger conidiophores ($279\text{--}528 \times 12\text{--}14\ \mu\text{m}$) and smaller conidia ($94\text{--}109 \times 21\text{--}24\ \mu\text{m}$) (Shen et al. 2021). *Rostriconidium pandanicola* has slightly narrower conidiophores ($171\text{--}485 \times 10\text{--}13\ \mu\text{m}$) and smaller, 4–7-septate conidia ($55\text{--}111 \times 18\text{--}26\ \mu\text{m}$) (Tibpromma et al. 2018). Given these morphological differences and phylogenetic analysis, we introduce *Rostriconidium fuscum* as a new species.

Rostriconidium yunnanensis Q.F. Zhang, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 13)

Mycobank No.: MB859994

Etymology – The epithet refers to Yunnan Province, where the holotype was collected.

Description – *Saprobic* on submerged dead branches along the riverbank. Teleomorph: undetermined. Anamorph: *Colonies* on the natural substrate, scattered, erect, hairy, dark, dry. *Mycelium* is partly immersed in the substrate and partly on the surface, septate, branched, brown. *Conidiophores* $274\text{--}845 \times 11\text{--}19\ \mu\text{m}$ ($\bar{x} = 485.6 \times 14.5\ \mu\text{m}$, $n = 30$), macronematous, mononematous, single, septate, dark brown to black, smooth or rough-walled, unbranched, straight or slightly flexuous, light-color at the apex. *Conidiogenous cells* monoblastic, enteroblastic,

integrated, terminal, cylindrical, smooth, dark brown, with black circle-peak shape conidiogenous scars. *Conidia* 116–208 × 27–35 µm ($\bar{x}$ = 152.1 × 30.7 µm, n = 30), dry, solitary, pyriform, fusiform to obclavate, rostrate, dark brown to black, 6–8-septate, slightly constricted at some septa, with black truncate, dark structure at the base with a light-colored cell above it, straight or slightly flexuous, smooth-walled. Teleomorph: Undetermined.

Culture characteristics – *Conidia* germinated with 12 hours on PDA. Colonies on PDA reaching 25–35 mm diam., after 4 weeks at 24–27 °C on PDA. Colony surface initially white-grey, later become dark brown, with densely mycelium, circular, entire edges; reverse reddish brown at center to light brown toward edges.

Material examined – China Yunnan Province, Wuliangshan National Nature Reserve, 24°25'33.66"N, 101°23'55.67"E, altitude 1455 m, on submerged dead branches of an unknown tree along the riverbank, collected on 2 August, 2024, Qin-Fang Zhang 2024 WLSY96-2 (GMB5140, **holotype**); ex-type culture, GMBC5140; *ibid.*, KUN-HKAS 150433, isotype.

Additional material examined – China, Yunnan Province, Wuliangshan National Nature Reserve, 24°35'56.42"N, 100°25'55.73"E, altitude 1520 m, on submerged dead branches of an unknown tree along the riverbank, collected on 2 August, 2024, Qin-Fang Zhang 2024 WLSY165 (GMB5141, GMBC5141).

Notes – Phylogenetically (Fig. 11), *Rostriconidium yunnanensis* forms a clade in sister relationship with *R. cangshanense*. However, *R. yunnanensis* can be readily distinguished by its longer conidiophores compared to *R. cangshanense* (274–845 × 11–19 µm vs. 279–528 × 12–14 µm) and its much larger conidia (116–208 × 27–35 µm vs. 94–109 × 21–24 µm) (Shen et al. 2021). Additionally, *R. cangshanense* possesses polyblastic conidiogenous cells and a hyaline sheath at the conidial apex, while *R. yunnanensis* lacks a conidial sheath and has monoblastic conidiogenous cells (Shen et al. 2021). Comparative analysis of nucleotide base pairs showed that *R. yunnanensis* differs from *R. cangshanense* (MFLUCC 20-0147) by 1.9 % (10/520) in the ITS locus and 0.3 % (2/788) in the LSU locus.

The other two species of the genus also differ significantly in conidiophore and conidia dimensions. *Rostriconidium aquaticum* has smaller conidiophores (370–590 × 13–17 µm) and smaller, 8–9-septate conidia (134–180 × 22–26 µm) (Su et al. 2018), compared to *R. yunnanensis*, which has conidiophores measuring 274–845 × 11–19 µm and larger, 5–8-septate conidia (116–208 × 27–35 µm). *Rostriconidium pandanicola* also has smaller conidiophores (171–485 × 10–13 µm) and smaller, 4–7-septate conidia (55–111 × 18–26 µm) (Tibpromma et al. 2018).

Based on these morphological differences and the results of phylogenetic analysis, we propose *Rostriconidium yunnanensis* as a new species.

Torula Pers., Ann. Bot. (Usteri) 15: 25 (1794).

Notes – *Torula* is a hyphomycetous genus, established by Persoon (1795) with *T. monilis* as the type species. The genus is characterized by dark brown to black, discrete, velvety colonies, with one supporting cell of conidiophores, or reduced to the conidiogenous cells, mono- to polyblastic, brown, doliiform to ellipsoidal or clavate, smooth to verruculose conidiogenous cells, frequently collapsing and becoming coronate, and acrogenous, phragmosporous, brown, smooth to verrucose, globose to subglobose celled conidia, that are frequently in branched chains and constricted at the septa (Tian et al. 2023, Li et al. 2024). *Torula* species are generally saprophytic. They have a worldwide distribution and abound in humid or freshwater habitats (Tian et al. 2023). According to Species Fungorum (accessed 28 June 2025), the genus currently comprises 204 accepted species.

Torula puerensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 14)

Mycobank No.: MB859992

Etymology – The epithet refers to Puer City, where the holotype was collected.

Description – *Saprobic* on decaying wood submerged in a freshwater swamp. Teleomorph: Undetermined. Anamorph: Colonies on natural substrate effuse, scattered, gregarious, black and powdery. Mycelium immersed or partially immersed, composed of septate, branched, dark brown to

blackish hyphal elements. *Conidiophores* 1.4–2 μm ($\bar{x}$ = 1.8 μm , n = 20), macronematous to semi-macronematous, septate, smooth, thin-walled, straight or slightly flexuous, dark brown, with 1–2 doliiform to subglobose cells. *Conidiogenous cells* polyblastic, terminal, dark brown to black, doliiform to subglobose, smooth to minutely verruculose and thick-walled. *Conidia* 12–25 $\times$ 5–9 μm ($\bar{x}$ = 16.5 $\times$ 7.2 μm , n = 30), catenulate, acrogenous, simple, phragmosporous, dark brown to black, minutely verruculose, 2–4 septate, rounded at both ends, composed of subglobose cells, often smaller at the apex (1–2 cells subhyaline at the base and black at the apex), slightly constricted at some septa and chiefly subcylindrical. Conidial secession schizolytic.



Figure 12 – *Rostriconidium fuscum* (GMB5361, holotype). a–b Colony on wood. c–d Conidiophores and conidia. e–f Conidiogenous cells and conidia. g–k Conidia. l Germinated conidium. m Surface view of culture on PDA. n Reverse view of culture on PDA. Scale bars: a, b = 0.5 mm, c, d = 100 μm , e–l = 50 μm .

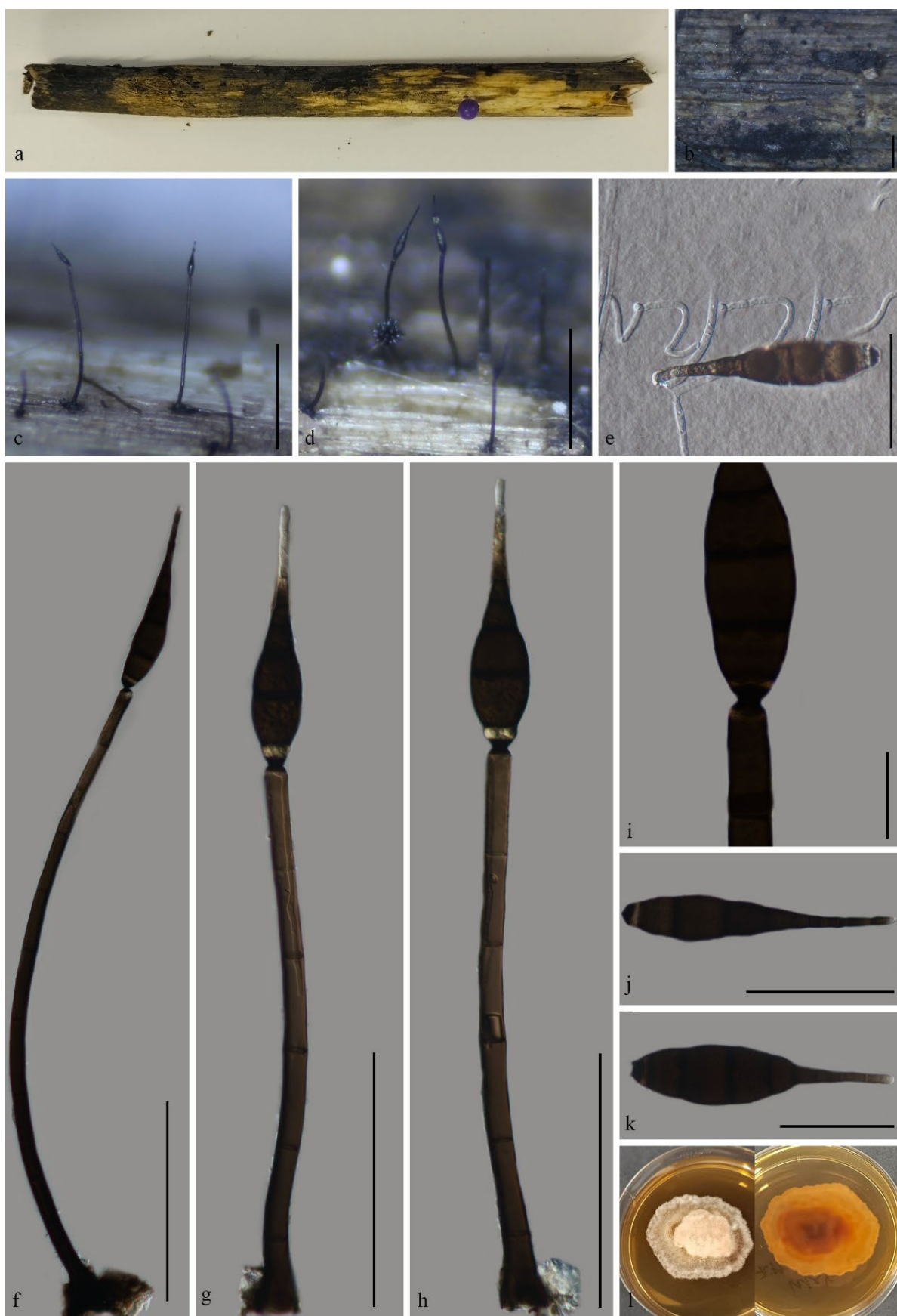


Figure 13 – *Rostriconidium yunnanensis* (GMB5140, holotype). a–d Conidiophores and conidia on natural substratum. e Germinating conidium. f–h Conidiophores and conidia. i Conidiogenous cells. j, k Conidia. l Surface and reverse view of culture on PDA. Scale bars: b= 1mm, c, d = 0.5 mm, e = 100 μ m, f–h = 200 μ m, I = 40 μ m, j, k = 100 μ m.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 10–15 mm diam., after 3 weeks at 24–27 °C on PDA. Colony surface white to pale yellow, with densely mycelium, velvety, roughly circular; reverse light yellow.

Material examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°20′22.31″N, 100°48′36.41″E, altitude 2202 m, on decaying wood submerged in a swamp, 13 October 2024, L.L. Liu, 2024WLSY30 (GMB5363, **holotype**); ex-type culture, GMBC5363; *ibid.*, KUN-HKAS 150428, isotype.

Additional specimens examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°25′47.75″N, 100°54′49.37″E, altitude 2106 m, on a decaying wood submerged in a swamp, 13 October 2024, L.L. Liu, 2024WLSY89 (GMB5364, GMBC5364).

Notes – Phylogenetically (Fig. 11), *Torula puerensis* forms a clade in a sister relationship with a *Torula* sp. (strains KUNCC 23-13949, KUNCC 23-13912, KUNCC 23-13999, KUNCC 23-13941). Nucleotide comparisons revealed that *T. puerensis* shares 97.8% similarity in ITS, 97.3% in *tef1-a*, and 95.1% in *rpb2* with *Torula* sp. (KUNCC 23-13912). These isolates remain undescribed.

Morphologically, *Torula puerensis* shares brown, verruculose conidia with the phylogenetically closely related *T. fici* and *T. hydei*. However, *T. fici* can be distinguished by its larger conidiophores (up to 13 µm tall vs. 1.4–2 µm) and smaller 2–3-septate conidia (17–19 × 5–6 µm vs. 1–4-septate, 12–25 × 5–9 µm) (Crous et al. 2015). *Torula hydei* can be distinguished by its 2–3-septate, much smaller conidia (7.5–14 µm long × 2–4 µm wide) (Li et al. 2020). *Torula submersa*, which has 1–4-septate conidia, differs in having smaller conidia (6–20 × 4–8 µm) and is phylogenetically distantly related (Tian et al. 2023).

Based on these distinct morphological differences and phylogenetic analysis, we describe *Torula puerensis* as a new species.

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray., Stud. Mycol. 64: 177 (2009).

Polyposphaeria Kaz. Tanaka & K. Hiray., Stud. Mycol. 64: 192 (2009).

Notes – *Polyposphaeria* was established by Tanaka et al. (2009) and typified by *P. fusca*, based on combined SSU and LSU DNA sequence data. The genus is characterized by micronematous conidiophores, monoblastic conidiogenous cells, and globose to subglobose, brown to dark brown conidia containing numerous internal hyphae (Tanaka et al. 2009, Tibpromma et al. 2018). All members of *Polyposphaeria* are reported as saprobes on various plant hosts. The genus is distributed across Japan, China, and Thailand in terrestrial habitats (Tanaka et al. 2009, Li et al. 2016, Tibpromma et al. 2018). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises seven accepted species.

Polyposphaeria chinensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 16)

MycoBank No.: MB859997

Etymology – The epithet refers to China, where the holotype was collected.

Description – *Saprobic* on a decaying wood in a freshwater swamp. Teleomorph: not observed. Anamorph: Hyphomycetous. *Colonies* effuse, scattered, and gregarious on host substrate, brown to blackish brown, glistening. *Mycelium* semi-immersed or immersed, dark brown, branched, septate. *Conidiophores* absent. *Conidiogenous cells* indistinguishable from creeping hyphal elements, monoblastic, integrated, determinate. *Conidia* 60–176 × 47–80.5 µm ($\bar{x}$ = 79.4 × 59.1 µm, *n* = 30), variable conidial shape, globose to subglobose, sometimes obconical, broadly ellipsoidal to broadly pyriform, sometimes with thin peel on the outer wall of conidia, internally filled with a mass of hyaline, solitary, brown to dark brown, smooth appendages. *Appendages* 20.5–69 × 2.5–5 µm ($\bar{x}$ = 45.3 × 3.9 µm, *n* = 30). cylindrical, solitary, straight or flexuous, unbranched and almost hyaline towards the apex, 0–6-septa observed, smooth, thin-walled, rounded at apex, persistent.

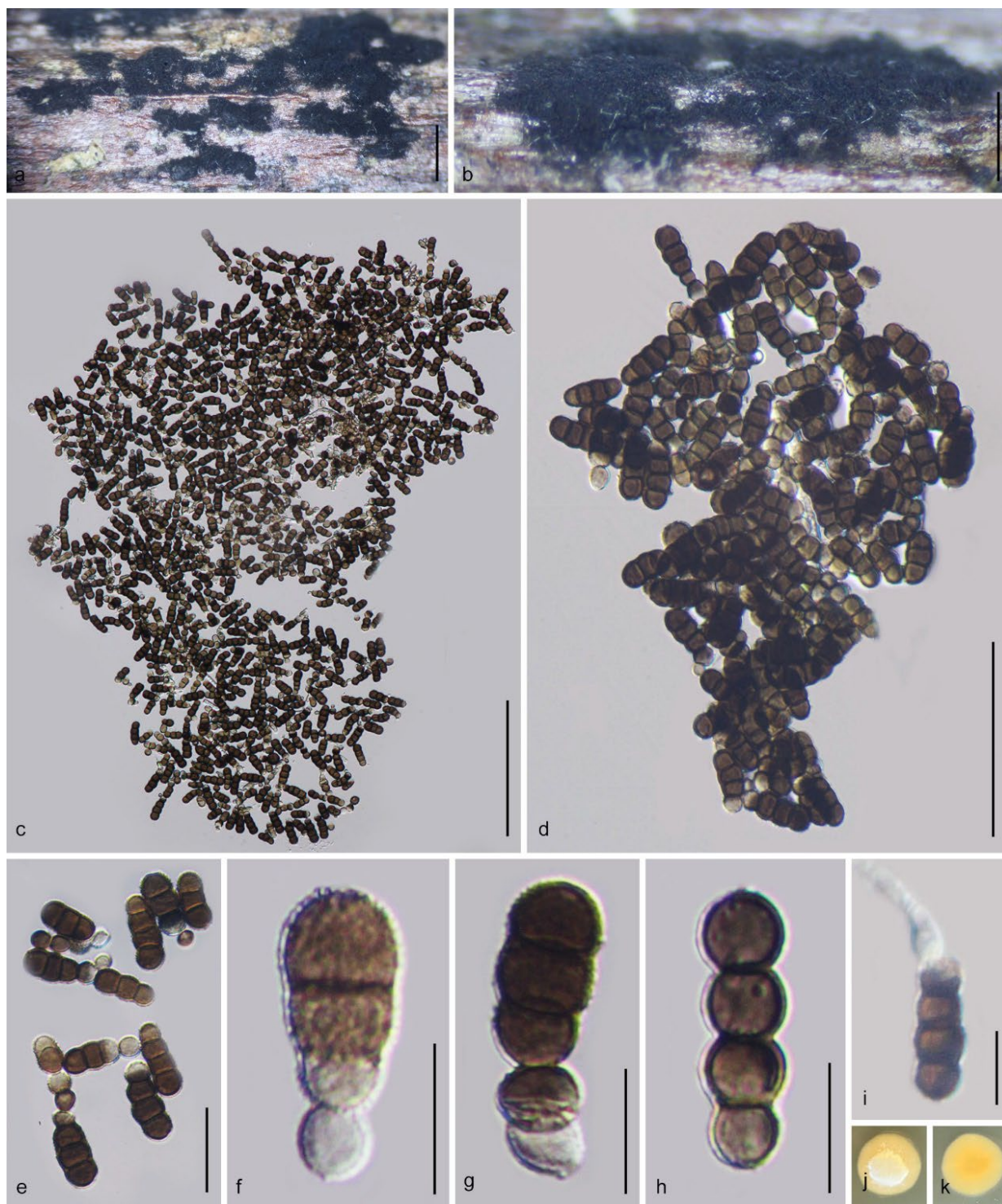


Figure 14 – *Torula puerensis* (GMB5363, holotype). a, b Colony on wood. c–h Conidia. i Germinated conidium. j Surface view of culture on PDA. k Reverse view of culture on PDA. Scale bars: a = 1 mm, b = 0.5 mm, c = 100 μ m, d = 50 μ m, e = 20 μ m, f–i = 10 μ m.

Culture characteristics – Conidia germinated and formed germ tubes with 12 hours on WA. Colonies on PDA reaching 15–25 mm diam., after 2 weeks at 24–27°C on PDA. Colony surface dirty white with grey tinge, with densely mycelium, roughly circular, cottony, flat; reverse dark grey.

Material examined – China, Sichuan Province, Leshan City, Heizhugou National Forest Park, 28°59'10.95 "N, 103°2'12.60" E, altitude 1751 m, on a decaying wood in a freshwater swamp, 26

October 2024, L.L. Liu, 2024HZG88 (GMB5319, **holotype**); ex-type culture, GMBC5319; *ibid.*, KUN-HKAS 150417, isotype.

Additional specimens examined – China, Sichuan Province, Leshan City, Heizhugou National Forest Park, 28°59′30.08 "N, 103°2′43.70" E altitude 1790m, on a decaying wood in a freshwater swamp, 26 October. 2024, L.L. Liu, 2024HZG121 (GMB5320, GMBC5320).

Notes – Phylogenetically (Fig. 15), *Polyposphaeria chinensis* is closely related to *P. appendiculata*. Morphologically, *P. chinensis* shares variable shaped brown conidia with thin outer walls and unbranched, cylindrical, septate appendages with *P. appendiculata*. However, *P. chinensis* differs in having significantly larger conidia (60–176 × 47–80.5 µm vs. 67–100 × 63–89 µm), lacking verrucose conidial ornamentation, and lacking conidiophores (present in *P. appendiculata*) (Liu et al. 2024). Comparative analysis of nucleotide base pairs showed that *P. chinensis* differs from *P. appendiculata* (mrcs8) by 1.1% (5/466) in the ITS locus, 0.2% (2/826) in the LSU locus, 0.1% (1/990) in the SSU locus, and 2.8% (27/950) in the *tef1-a* gene.

Polyposphaeria nabanheensis is also phylogenetically close to *P. chinensis*, but differs by being found on dead leaves of *Pandanus* sp., having smaller conidia (110–150 × 75–88 µm), the presence of conidiophores, and long 3–9-septate appendages (60–125 × 4–6 µm, compared to 20.5–69 × 2.5–5 µm, 0–6-septate in *P. chinensis*) (Tibpromma et al. 2018).

Polyposphaeria hainanensis differs from *P. chinensis* by having smaller conidiophores (49–134.5 × 52–90.5 µm) with 0–4-septate appendages (36–58 × 3–5.5 µm) (Tang et al. 2023). *Polyposphaeria guizhouensis* differs in having smaller conidia (34–61 × 41–63 µm) with 0–3-septate, short appendages (13–38 × 2.5–6 µm) (Tang et al. 2023). The type species of the genus, *P. fusca*, has smaller, globose to subglobose conidia (43–100(–125) µm), and *P. thailandica* and *P. pandanicola* have smaller conidia (20.5–43 × 17.5–54 µm and 36–70 × 40–75 µm, respectively) (Tibpromma et al. 2018). Based on these morphological and phylogenetic differences, we introduce *Polyposphaeria chinensis* as a new species.

Triplosphaeria Kaz. Tanaka & K. Hiray., Stud. Mycol. 64: 186 (2009).

Tanaka et al. (2009) established *Triplosphaeria* to accommodate fungi with a *Massarina*-like teleomorph and a tetraploa-like anamorph. The teleomorph is characterized by subglobose ascomata with none to short beak, fissitunicate, cylindrical to clavate, 8-spored, short-stalked asci, and fusiform, hyaline, 1-septate, ascospores with entire sheaths. Its anamorph is characterized by micronematous conidiophores, monoblastic conidiogenous cells, and ovoid to obpyriform, brown conidia with 3 setose appendages and conidia composed of 3 columns with distosepta (Tanaka et al. 2009). According to Species Fungorum (accessed 20 July 2025), the genus currently comprises 8 accepted species. Herein, we describe a new species of the genus found on dead culms of bamboo.

Triplosphaeria irregularis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 17)

MycoBank No.: MB859996

Etymology – The epithet refers to its irregular shaped conidia.

Description – *Saprobic* on dead bamboo stems in a freshwater wetland. Teleomorph: Undetermined. Anamorph: *Colonies* on natural substrate effuse, compact, scattered, subglobose to oval, black. Mycelium superficial. *Conidiophores* absent. *Conidiogenous cells* monoblastic, integrated, usually indistinguishable from superficial hyphae. *Conidia* 19.6–49 × 17.8–32.5 µm ($\bar{x}$ = 37.5 × 21.7 µm, n = 30), solitary, irregular in shape, subcylindrical to ellipsoidal or subglobose or amygdaliform, dark brown to black, distoseptate, consisting of 2–5 columns of cells, 5–8-septate in each column, with 1–6 appendages. *Appendages* 2.5–9.2 × 2.4–4.6 µm ($\bar{x}$ = 4.8 × 3.2 µm, n = 30), 0–1-septate, hyaline, smooth, unbranched, straight or curved.

Culture characteristics – Conidia germinated and formed germ tubes within 36 hours on WA. Colonies on PDA reaching 15–25 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface white to light brown, circular, velvety, flat, center raised; reverse center white, dark brown at side, margin sienna.

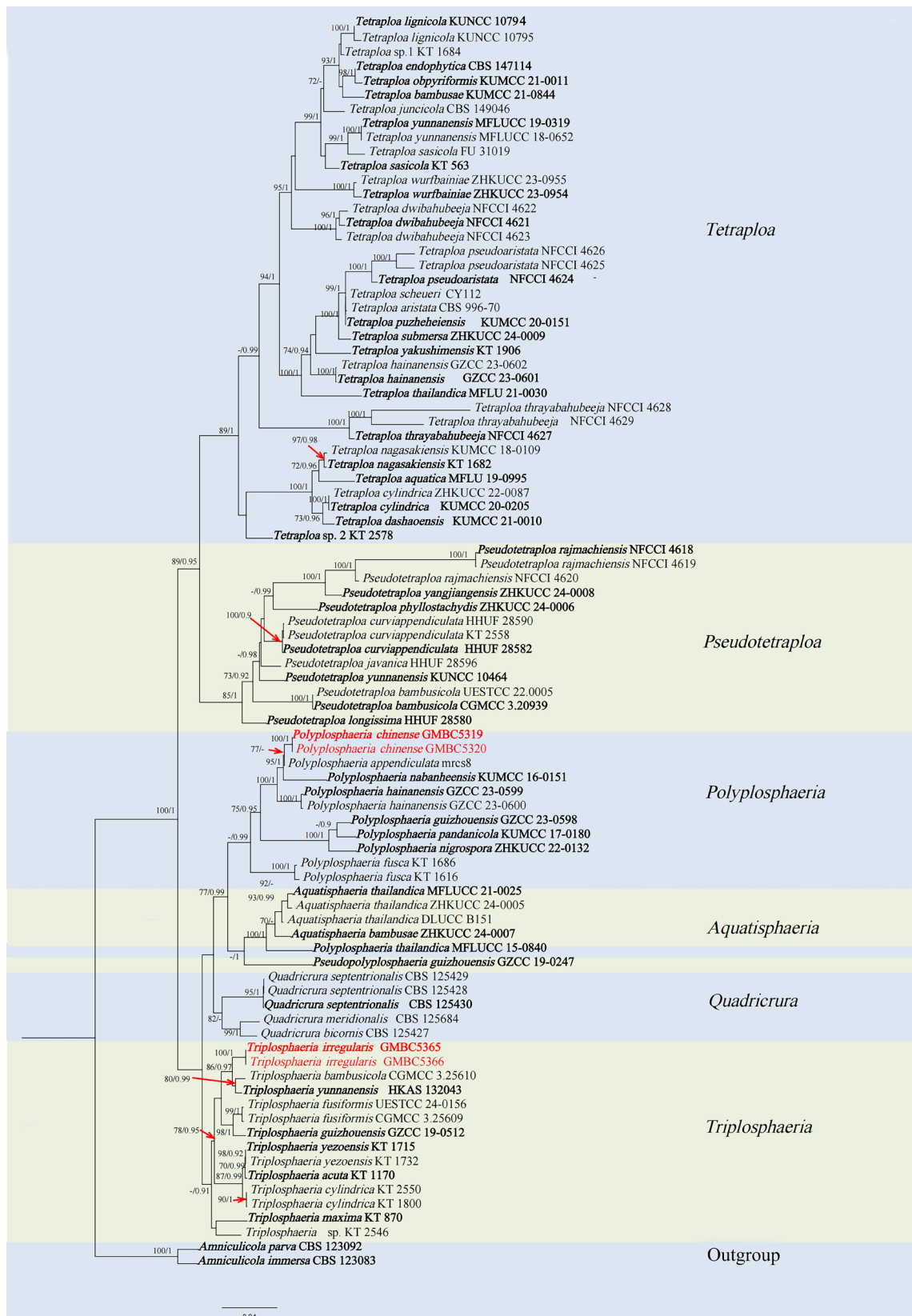


Figure 15 – ML tree of *Polyplosphaeria* and *Triplosphaeria* and related taxa based on LSU, ITS, SSU, *tub2*, and *rpb2* loci. The alignment for this tree includes 4632 bp (LSU:1–1314 bp; ITS: 1315–1867 bp; SSU: 1868–2889 bp; *tub2*: 2890–3534 bp; *rpb2*: 3535–4632 bp). *Amniculicola parva* (CBS 123092) and *Amniculicola immersa* (CBS 123083) were selected as the outgroup taxa. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly described species sequences are marked red in bold. Ex-type/type strains are indicated in black bold.

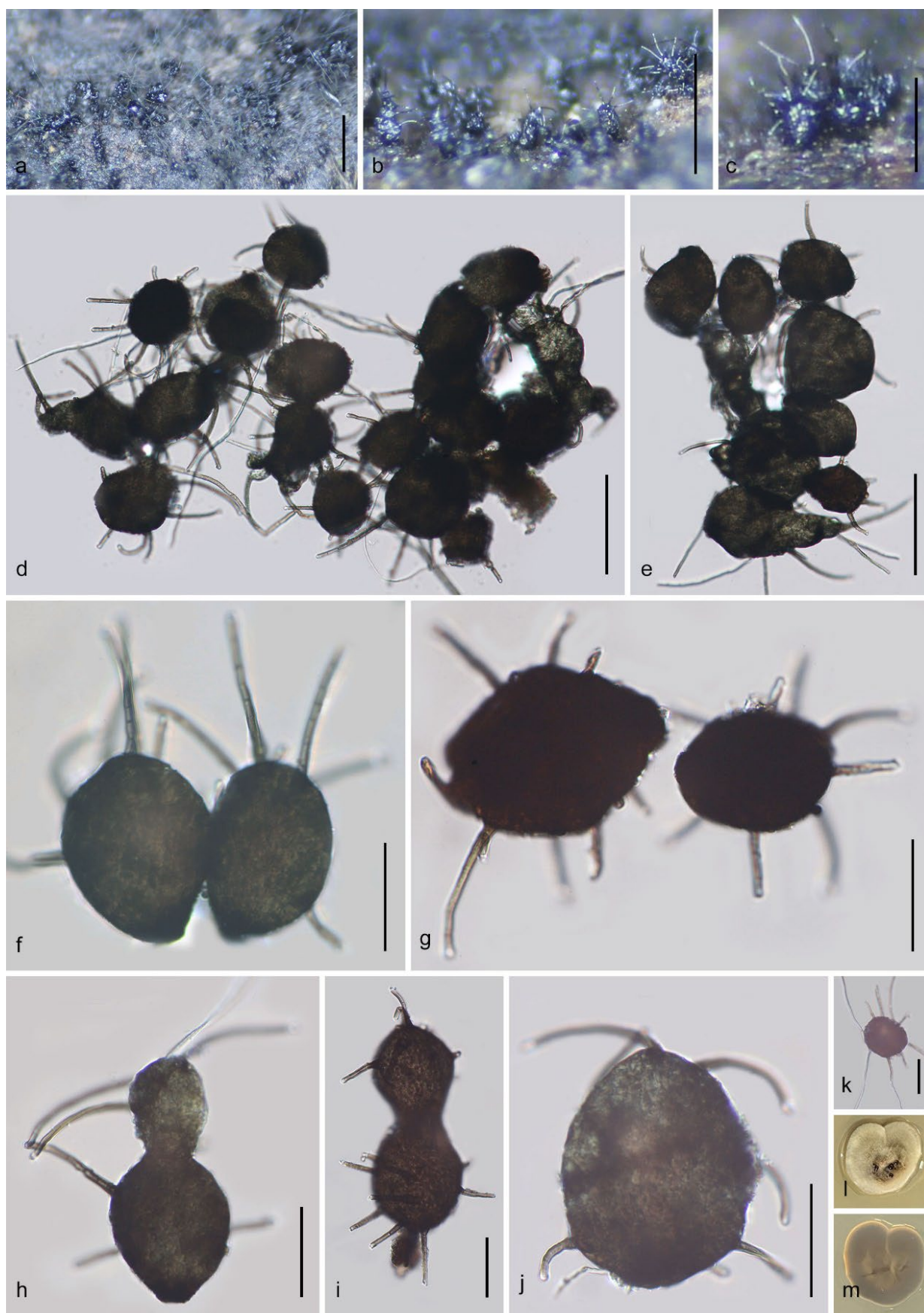


Figure 16 – *Polyposphaeria chinensis* (GMB5319) a–c Colony on wood. d–j Conidia. k Germinated conidium. l Surface view of culture on PDA. m Reverse view of culture on PDA. Scale bars: a, b = 0.5 mm, c = 0.2 mm. d, e = 100 μ m, f–k = 50 μ m.

Material examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'21.770"N, 104°00'19.121"E, altitude 1419 m, on the dead bamboo stems in a wetland, 12 October 2024, L.L. Liu, 2024WMS245 (GMB5365, **holotype**); ex-type culture, GMBC5365; *ibid.*, KUN-HKAS 150438, isotype.

Additional specimens examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'29.79"N, 104°00'05.548" E, altitude 1371 m, on the dead bamboo stems in a wetland, 12 October 2024, L.L. Liu, 2024WMS293 (GMB5366, GMBC5366).

Notes – *Triplosphaeria* is represented by eight species worldwide, all of which have molecular data available and have been used in phylogenetic studies (Fig. 15) that clearly distinguish the *Triplosphaeria* known species from *T. irregularis*. Phylogenetically, *T. irregularis* is closely related to *T. bambusicola* and *T. yunnanensis*.

Triplosphaeria bambusicola can be distinguished by its larger conidia (45–85 × 20–30 µm, compared to 19.6–49 × 17.8–32.5 µm in *T. irregularis*), with dark brown, 0–2-septate appendages (vs. hyaline, 0–1-septate appendages in *T. irregularis*) (Yu et al. 2024). *Triplosphaeria yunnanensis* differs by having larger conidia (54–76 × 20–28 µm), with 3–4 pale brown to brown appendages (vs. 1–6 hyaline appendages in *T. irregularis*) (Shen et al. 2024b). Comparative analysis of nucleotide base pairs showed that *T. irregularis* differs from the type isolate of *T. bambusicola* (CGMCC 3.25610) by 2.8% (13/459) in the ITS and 0.1% (1/863) in the LSU locus. In comparison to the type isolate of *T. yunnanensis* (HKAS 144527) differs by 8.0% (41/511) in the ITS locus, 0.5% (4/861) in the LSU locus, and 14.2% (123/864) in the *tef1-α* gene.

Based on these morphological and phylogenetic differences, we introduce *Triplosphaeria irregularis* as a new species.

Orbiliomycetes O.E. Erikss. & Baral, Myconet 9: 96 (2003).

Orbiliales Baral, O.E. Erikss., G. Marson & E. Weber, Myconet 9: 96 (2003).

Orbiliaceae Nannf., Nova Acta Regiae Soc. Sci. Upsal. Ser. 4, 8 (2): 250 (1932).

Orbilium Fr., Fl. Scan.: 343 (1836).

Notes – *Orbilium* was introduced by Fries (1836), initially encompassing two species: *O. leucostigma* and *O. xanthostigma*. Over time, *Orbilium* has evolved into a large and complex genus, now comprising 512 species according to the Species Fungorum database (accessed July 2, 2025). It is the most diverse genus within the *Orbiliomycetes* (Baral et al. 2020). Species of *Orbilium* are found in a wide range of ecosystems, from humid to arid and from subarctic to tropical climates. They thrive on various substrates, including wood, bark, leaves, and dung, and can be found in diverse environmental conditions, such as xeric, hygic, and aquatic habitats (Baral et al. 2020). In this study, we report *Orbilium ellipsospora* as new record for China.

Orbilium ellipsospora (Preuss) Bin Liu, E. Weber & Baral, *Orbiliomycetes*: 1603 (2020). (Fig. 19)

Description – *Saprobic* on decaying wood in a freshwater wetland. Teleomorph: undetermined. Anamorph: Hyphomycetous. *Colonies* on natural substratum effuse, erect, hairy, white, scattered, mostly solitary, sometimes in small groups. *Mycelium* composed of hyaline, multiseptate hyphae, branched. *Conidiophores* 121.5–309.2 × 2.4–4.3 µm ($\bar{x}$ = 249.2 × 3.3 µm, n = 15), micronematous, mononematous, erect, sometimes flexuous, subcylindrical, hyaline towards apex paler brown towards base, smooth, unbranched. *Conidiogenous cells* 37.3–68.5 × 1.5–2.5 µm ($\bar{x}$ = 46.3 × 1.9 µm, n = 15), terminal, integrated, monoblastic, subcylindrical to cylindrical, giving rise to clusters of conidia. *Conidia* 29–52.5 × 10.5–15.5 µm ($\bar{x}$ = 46.5 × 13.2 µm, n = 20), hyaline, smooth, guttulate, 2–4 septate, ellipsoid to spindle-shaped to obconical, sometimes cuneate.

Culture characteristics – Conidia germinated and formed germ tubes within 24 hours on WA. Colonies on PDA reaching 30–40 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface pale yellowish-brown with creamy margin, spreading with sparse to moderate aerial mycelium, hairy; reverse creamy white to light brown towards center.



Figure 17 – *Triplosphaeria irregularis* (GMB5365, holotype). a–b Colony on bamboo substrate. c–k Conidia. l Germinated conidium. m Surface view of culture on PDA. n Reverse view of culture on PDA. Scale bars: a, b = 0.5 mm, c–k = 20 μ m.

Material examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°20'22.31"N, 100°48'36.41"E, altitude 2202 m, on a decaying wood in a wetland, 12 October 2024, L.L. Liu, 2024WLSY02 (GMB5315, GMBC5315).

Notes – The sequence of our collection, GMB5315, shows a 100% similarity with *Orbilia ellipsospora* isolates. This species was initially described as *Menispora ellipsospora*, collected from rotten needles of *Pinus* in Germany. Scholler et al. (1999) reclassified it as *Dactylellina ellipsospora* based on phylogenetic analyses. Baral et al. (2020) revisited the classification, revising it once again to *Orbilia ellipsospora* following both morphological and phylogenetic reassessment.

Morphologically, our collection GMB5315, is consistent with the characteristics of *Orbilia ellipsospora* (Scholler et al. 1999, Baral et al. 2020). This study represents the first report of *O. ellipsospora* in China, expanding its known geographical range.

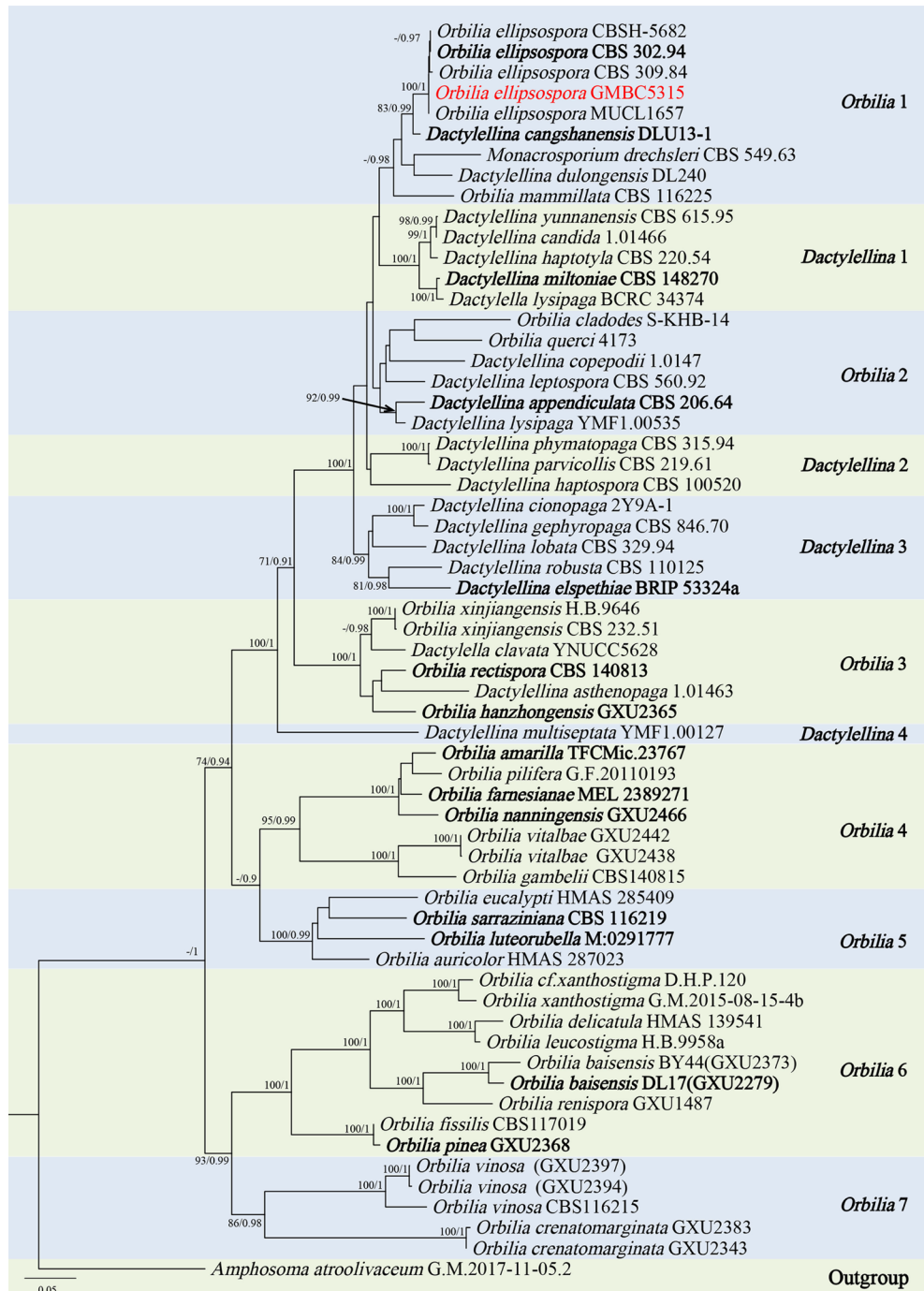


Figure 18 – ML tree of *Orbilia* and related taxa based on ITS and LSU loci. The alignment for this tree includes 1492 bp (ITS:1–587 bp; LSU: 588–1492 bp). *Amphosoma atroolivaceum* (G.M.2017-11-05.2) was selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAXML ≥ 70 % are shown on the branches. Newly generated sequences are indicated in red and type strains are in bold.

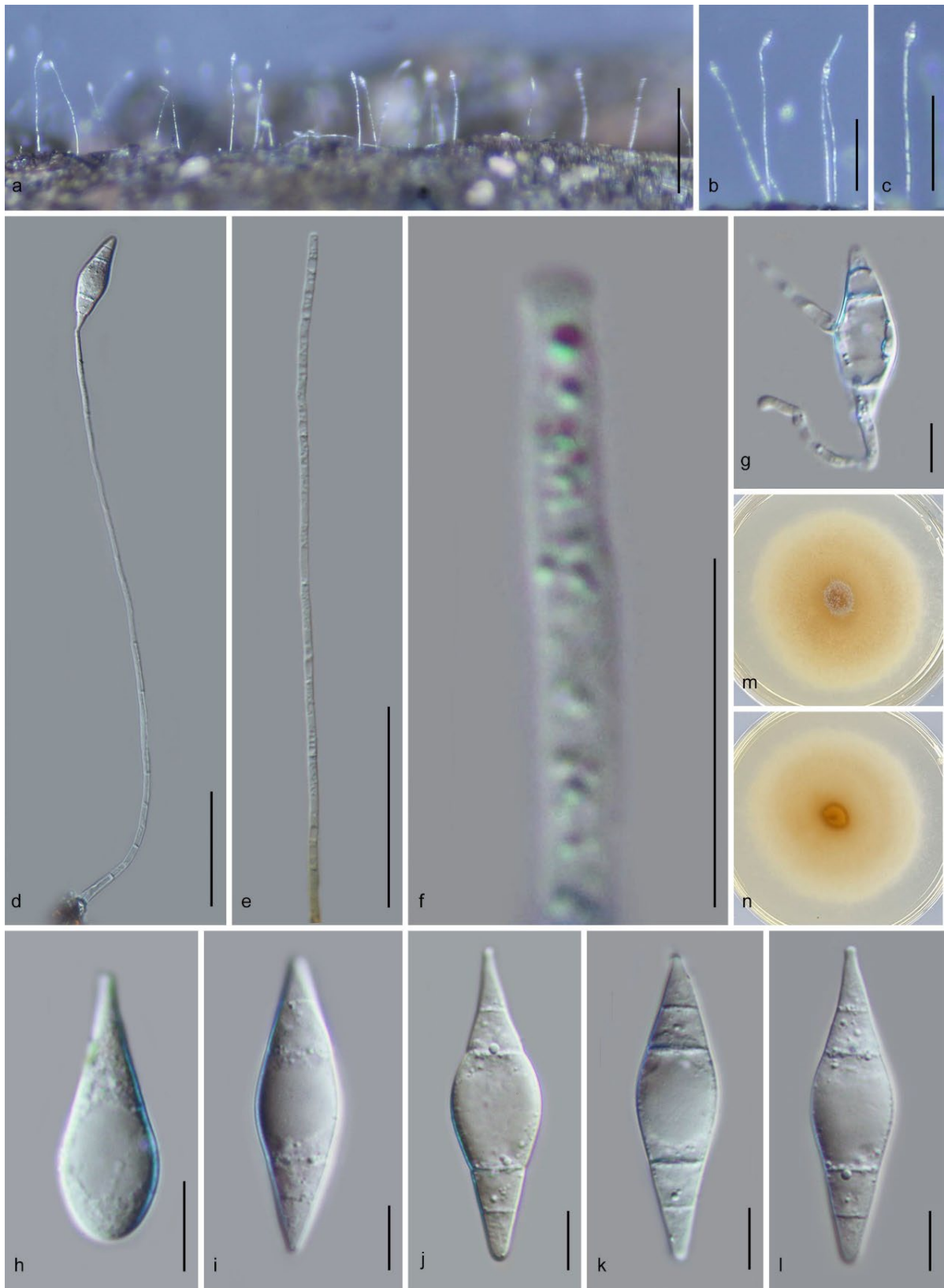


Figure 19 – *Orbilia ellipsospora* (GMB5315). a–c Colony on wood. d Conidiophores and conidia. e Conidiophores f Conidiogenous cells. g Germinated conidium. h Immature conidia. i–l Mature conidia. m Surface view of culture on PDA. n Reverse view of culture on PDA. Scale bars: a = 0.5 mm, b, c = 0.2 mm, d, e = 50 μ m, g–l = 10 μ m.

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

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

Conlarium F. Liu & L. Cai, Mycologia 104(5): 1180 (2012).

Phylogenetic tree showing relationships within Conlariaceae and related families. The tree is rooted with *Wongia aquatica* (MFLUCC 18-1607) as the outgroup. The main clade is Conlariaceae, which includes several genera: *Conlarium*, *Dictyosporella*, *Junewangia*, *Sporidesmiella*, *Pseudoproboscispora*, *Atractospora*, *Annulusmagnus*, *Cancellidium*, and *Sporidesmium*. The tree is color-coded by family: Conlariaceae (yellow), Junewangiaceae (light blue), Pseudoproboscisporaceae (light green), Atractosporaceae (light blue), Annulatascaceae (light blue), Cancellidiaceae (light blue), Sporidesmiaceae (light blue), and Outgroup (light green). Bootstrap values are shown at the nodes. The tree is labeled with the following taxa and their accession numbers: *Conlarium dupliciascosporum* CGMCC 3.14939, *Conlarium dupliciascosporum* CGMCC 3.14938, *Conlarium dupliciascosporum* CGMCC 3.14940, *Conlarium nanningense* HMAS 247075, *Conlarium nanningense* HMAS_247985, *Conlarium baiseense* HMAS 247298, *Conlarium baiseense* HMAS 247986, *Conlarium muriforme* GZCC 20-0442, *Conlarium bambusae* CGMCC 3.27447, *Conlarium sacchari* HMAS 247301, *Conlarium sacchari* HMAS 247300, *Conlarium sacchari* HMAS 247299, *Conlarium sichuanense* UESTCC 21.0015, *Conlarium sichuanense* CGMCC 3.20406, *Conlarium guizhouense* GZCC 22-2028, *Conlarium guizhouense* CGMCC 3.24357, *Conlarium multiseptatum* KUNCC 23-14310, *Conlarium yunnanense* DLUCC2131, *Conlarium thailandense* MFLUCC 17-2349, *Conlarium aquaticum* MFLUCC 15-0992, *Conlarium metasequoiae* HMAS 131281, *Riomyces rotundus* AF303-1, *Conlarium subglobosum* MFLU 17-1728, *Conlarium indicum* NFCCI 4841, *Conlarium phaeoconidium* GMBC5337, *Conlarium phaeoconidium* GMBC5338, *Dictyosporella thailandensis* MFLUCC 15-0985, *Dictyosporella Chiangmaiensis* MFLUCC 17-2345, *Dictyosporella guizhouensis* MFLU 18-1505, *Junewangia globulosa* CBS126093, *Junewangia lamma* HMAS 44438, *Sporidesmiella hyalosperma* MFLUCC 18-1013, *Sporidesmiella aquatica* MFLU 18-1602, *Pseudoproboscispora thailandensis* MFLUCC 15-0989, *Neodiluvicola aquatica* MFLUCC 15-0986, *Atractospora aquatica* MFLU 18-2322, *Atractospora aquatica* S-1297, *Annulusmagnus triseptatus* CBS 127688, *Cancellidium griseonigrum* MFLUCC 17-2117, *Sporidesmium Chiangmaiense* MFLUCC 18-0999, *Sporidesmium thailandense* MFLUCC 15-0964, and *Wongia aquatica* MFLUCC 18-1607.

Conlarium phaeoconidium L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 21)

Mycobank No.: MB859975

Etymology – The epithet refers to its dark-brown conidia.

Description – *Saprobic* on submerged dead wood in a freshwater swamp. Teleomorph: Undetermined. Anamorph: Hyphomycetous. *Colonies* on natural substrate superficial, gregarious, effuse, sporodochial, punctiform, dark. *Mycelium* mostly immersed on substratum, partly superficial, septate, brown, branched hyphae. *Conidiophores* absent or reduced to *conidiogenous cells*. *Conidiogenous cells* up to 12.5 µm wide, monoblastic, integrated, cylindrical, brown. *Conidia* 70–177 × 60–100 µm ($\bar{x}$ = 122.9 × 79.2 µm, n = 20), acrogenous, solitary, ellipsoidal or mostly irregular in shape, muriform, dark blackish-brown, with transversely septate and longitudinally septate, rough, thin-walled, protruding basal cell.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 10–15 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface grayish-white, gray at margin, circular, floccose, center raised; reverse black to gray.

Material examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°25′47.75″N, 100°54′49.37″E, altitude: 2106 m, on submerged dead wood in a swamp, 13 October 2024, L.L. Liu, 2024WLSY106 (GMB5337, **holotype**); ex-type culture, GMBC5337; *ibid.*, KUN-HKAS 150427, isotype.

Additional specimens examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°20′22.31″N, 100°48′36.41″E, altitude 2202 m, on submerged dead wood in a swamp, 13 October 2024, L.L. Liu, 2024WLSY135 (GMB5338, GMBC5338).

Notes – Phylogenetically (Fig. 20), *Conlarium phaeoconidium* forms an independent clade (ML/B1=100/1) at the basal of *Conlarium* genus. Morphologically, *C. phaeoconidium* can be distinguished from all other species in the genus by its much larger (70–177 × 60–100 µm), dark-colored conidia, in which septation cannot be observed. BLAST analysis of the LSU sequence showed the highest similarity (98.6%) with *C. subglobosum*, which is easily distinguished by its smaller conidia (14.5–24 µm diam). Comparative analysis of nucleotide base pairs of ITS sequence showed that *Conlarium phaeoconidium* differs from *C. subglobosum* (MFLU 17-1728) by 12.7% (67/528). All other species of the genus have conidia smaller than 105 µm, with a brown color and clear septation visible. The conidial sizes in other species of *Conlarium* are 15.5–35 × 11–26.5 µm in *C. duplumascosporum*, 45–70 × 20–57 µm in *C. aquaticum*, 25–45 × 17–33 µm in *C. thailandense*, 21–35 × 7–12 µm in *C. baiseense*, 11–21 × 9–21 µm in *C. nanningense*, 14–19 × 13–22 µm in *C. sacchari*, 14.5–24 µm in *C. subglobosum*, and 60–103 × 39–88 µm in *C. indicum* (Liu et al. 2012, Phookamsak et al. 2019, Dong et al. 2021).

Based on these morphological differences and phylogeny, we introduce *Conlarium phaeoconidium* as a new species.

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

Distoseptisporaceae K.D. Hyde & McKenzie, Fungal Diversity 80:375–409 (2016).

Distoseptispora K.D. Hyde, McKenzie & Maharachch., Fungal Diversity 80:375–409 (2016).

Notes – Members of *Distoseptispora* are primarily saprophytic fungi found on woody substrates in freshwater habitats, mainly in China and Thailand, with some species also reported from terrestrial environments (Hyde et al. 2016, Luo et al. 2018, 2019, Dong et al. 2021, Ma et al. 2022, Shen et al. 2024a). The genus is typified by *Distoseptispora fluminicola*, and characterized by acrogenous, solitary, distoseptate conidia that separate schizolytically from monoblastic, integrated, terminal, determinate conidiogenous cells, borne on macronematous, unbranched, septate conidiophores. *Distoseptispora* species are commonly isolated from decaying leaves, wood, and twigs in humid environments (Zhang et al. 2022, Shen et al. 2024a). According to Species Fungorum (accessed 30 June 2025), the genus currently comprises 104 accepted species. Herein, we describe three new species of the genus found on submerged decaying wood in freshwater habitats.

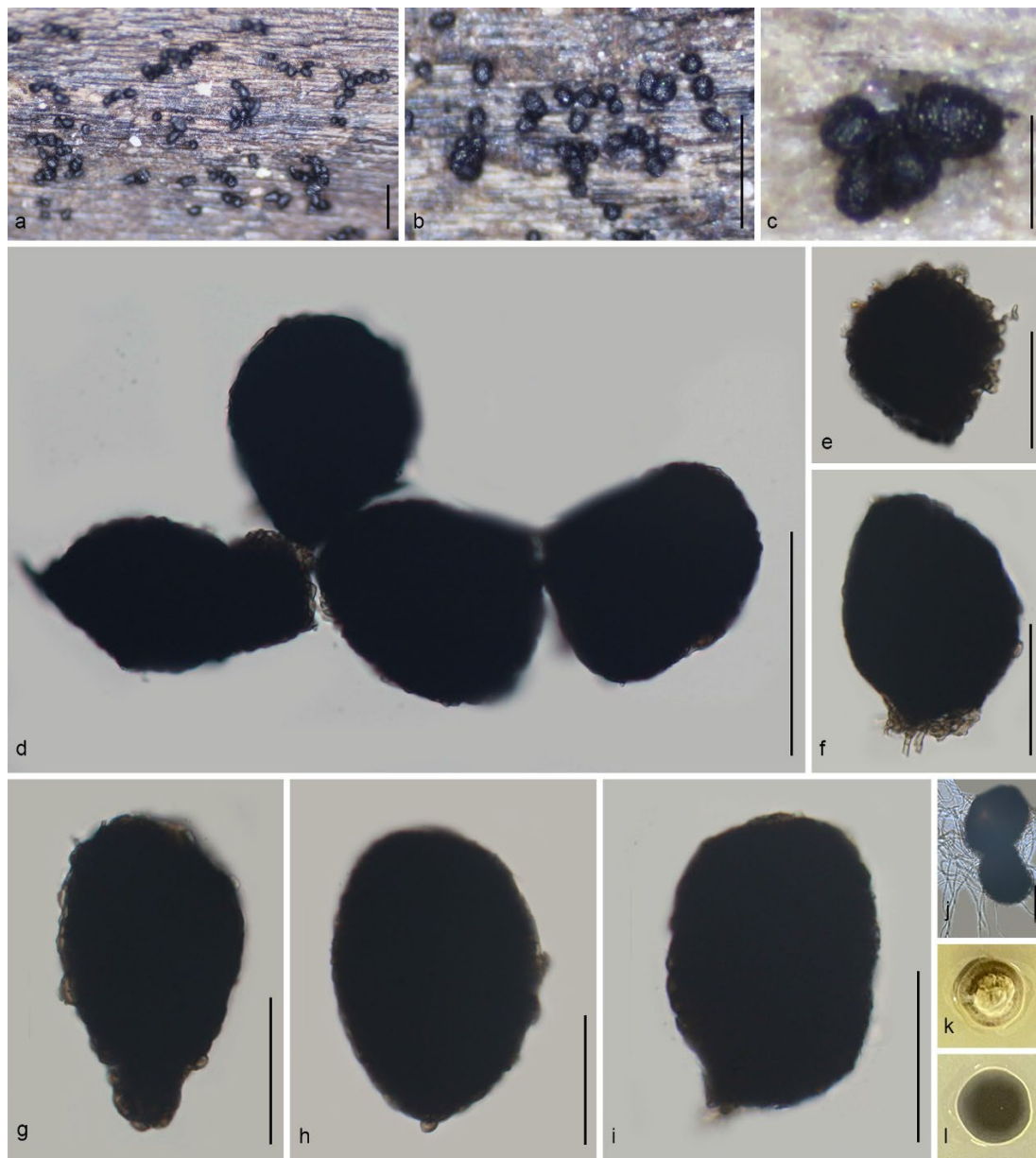


Figure 21 – *Conlarium phaeoconidium* (GMB5337, holotype). a–c Colony on wood. d–i Conidia. j Germinated conidium. k, l Surface and reverse view of culture on PDA. Scale bars: a, b = 0.5 mm, c = 0.2 mm, d = 100 μ m, e–j = 50 μ m.

Distoseptispora longissima L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 23)

MycoBank No.: MB859977

Etymology – The epithet refers to its longer conidia.

Description – *Saprobic* on submerged decaying wood in a freshwater wetland. Teleomorph: undetermined. Anamorph: Hyphomycetous. *Colonies* on the substratum superficial, effuse, hairy, black-brown. *Mycelium* mostly immersed, composed of branched, septate, smooth, pale-brown hyphae. *Conidiophores* 204–332 $\times$ 5–8.5 μ m ($\bar{x}$ = 258.9 $\times$ 7.0 μ m, n = 20), macronematous, mononematous, unbranched, 10–17 septate, single, cylindrical, straight or slightly flexuous, smooth, pale-brown, robust at the base. *Conidiogenous cells* 5–13.5 $\times$ 3.2–6.1 μ m ($\bar{x}$ = 9.5 $\times$ 5.1 μ m, n = 20), monoblastic or polyblastic, integrated, determinate, terminal, cylindrical, pale-brown, smooth. *Conidia* 45–167 $\times$ 6.5–10 μ m ($\bar{x}$ = 117.3 $\times$ 7.7 μ m, n = 25), 2.6–3.9 μ m wide at the apex ($\bar{x}$ = 3.1 μ m, n = 25), acrogenous, solitary, obclavate, rostrate, curved, 6–24-euseptate, rounded at the apex, truncate at the base, tapering towards apex, smooth, thin-walled, pale green to pale brown.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 20–30 mm diam., after 4 weeks at 24–27 °C on PDA. Colony surface off-white to dirty white, velvety, subcircular, convex; reverse black.

Material examined – China, Guangxi Zhuang Autonomous Region, Fangchenggang City, Shangsi County, Shiwan Mountain National Nature Reserve, 21°57′12.34" N, 108°2′31.58" E, altitude 300 m, on a submerged decaying wood in a wetland, 17 September 2024, L.L. Liu, 2024SWS64 (GMB5339, **holotype**); ex-type culture, GMBC5339; *ibid.*, KUN-HKAS 150421, isotype.

Additional specimens examined – China, Guangxi Zhuang Autonomous Region, Fangchenggang City, Shangsi County, Shiwan Mountain National Nature Reserve, 21°57′27.22"N, 108°5′25.84"E, altitude 270 m, on a submerged decaying wood in a wetland, 17 September 2024, L.L. Liu, 2024SWS112 (GMB5340; GMBC5340).

Notes – In the phylogenetic tree (Fig. 22), *Distoseptispora longissima* is closely related to *D. palmarum*, but the two species can be easily distinguished by conidiophores and conidia size. *Distoseptispora longissima* has longer conidiophores ($204\text{--}332 \times 5\text{--}8.5\ \mu\text{m}$ vs. $90\text{--}165 \times 4\text{--}7\ \mu\text{m}$) and smaller conidia ($45\text{--}167 \times 6.5\text{--}10\ \mu\text{m}$ vs. $35\text{--}180 \times 7\text{--}11\ \mu\text{m}$) with fewer eusepta 6–24 (vs. 7–27 distoseptate) (Hyde et al. 2019). Comparative analysis of nucleotide base pairs showed that *D. longissima* differs from *D. palmarum* (MFLU 18-0588) by 11.4% (58/508) in the ITS locus, 0.5% (4/833) in the LSU locus, 0.4% (4/1017) in the SSU locus, 5.8% (52/901) in the *tefl- α* gene, and 15.0% (160/1070) in the *rpb2* gene.

Distoseptispora rostrata has conidia of comparable size but differs in having shorter conidiophores ($82\text{--}126 \times 5\text{--}7\ \mu\text{m}$) and slightly shorter conidia ($115\text{--}155 \times 9\text{--}11\ \mu\text{m}$) with 15–23 distoseptate (Luo et al. 2018, Zhai et al. 2022). Other species of the genus can be easily distinguished by conidiophore and conidia size, as well as the number of septa (see Table in Zhai et al. 2022). Based on these differences and the phylogenetic analysis, we introduce *D. longissima* as a new species.

Distoseptispora quinquesepata L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 24)

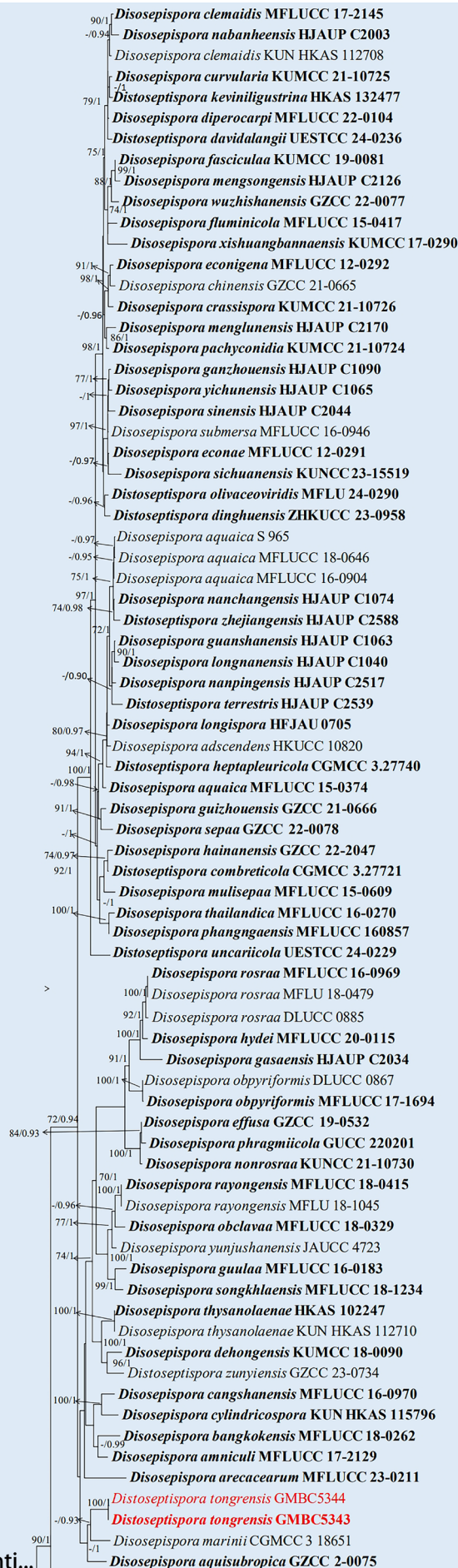
Mycobank No.: MB859976

Etymology – The epithet refers to its five-septate conidia.

Description – *Saprobic* on submerged dead wood in a wetland. Teleomorph: Undetermined. Anamorph: Hyphomycetous. Colonies superficial, effuse, hairy, gregarious, brown. Mycelium immersed to superficial, composed of septate, branched, pale brown hyphae. Conidiophores $173\text{--}311\ \mu\text{m} \times 5.8\text{--}9\ \mu\text{m}$ ($\bar{x} = 256.1 \times 7.3\ \mu\text{m}$, $n = 20$), macronematous, mononematous, cylindrical, straight or flexuous, 13–17 septate, unbranched, brown, smooth, thin-walled, often containing inflated or constricted cells at the apex or middle. Conidiogenous cells $7.1\text{--}10.6 \times 3.9\text{--}5.5\ \mu\text{m}$ ($\bar{x} = 9.3 \times 4.6\ \mu\text{m}$, $n = 25$), holoblastic, mono- to polyblastic, integrated, determinate, terminal and intercalary, subcylindrical, brown, smooth. Conidia $11\text{--}39.5 \times 4.5\text{--}8\ \mu\text{m}$ ($\bar{x} = 25.9 \times 6.4\ \mu\text{m}$, $n = 30$), secession schizolytic, solitary or occasionally catenate, dry, smooth, thin-walled, subcylindrical or obclavate, straight or curved, 2–5-distoseptate, mostly 5-septate slightly constricted at septa, olivaceous to brown, apex rounded.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 10–15 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface whitish gray, with densely mycelium, circular, entire, floccose, center raised; reverse black.

Material examined – China, Guangxi Zhuang Autonomous Region, Fangchenggang City, Shangsi County, Shiwan Mountain National Nature Reserve, 21°57′12.34" N, 108°2′31.58" E, altitude 300 m, on a submerged decaying wood in a wetland, 17 September 2024, L.L. Liu, 2024SWS65 (GMB5341, **holotype**); ex-type culture, GMBC5341; *ibid.*, KUN-HKAS 150424, isotype.



Disosepispora

Conti...

Figure 22 – RAxML tree based on analysis of a combined ITS, LSU, *tef1-α*, and *rpb2* sequences for *Distoseptispora*. The alignment for this tree includes 3354 bp (ITS:1–522; LSU: 523–14271392; *tef1-α*: 393–2311; *rpb2*: 2312–3354). *Myrmecridium schulzeri* (CBS 100.54) and *M. banksiae* (CPC 19852) were selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly described species are marked red in bold. Ex-type/type strains are indicated in black bold.

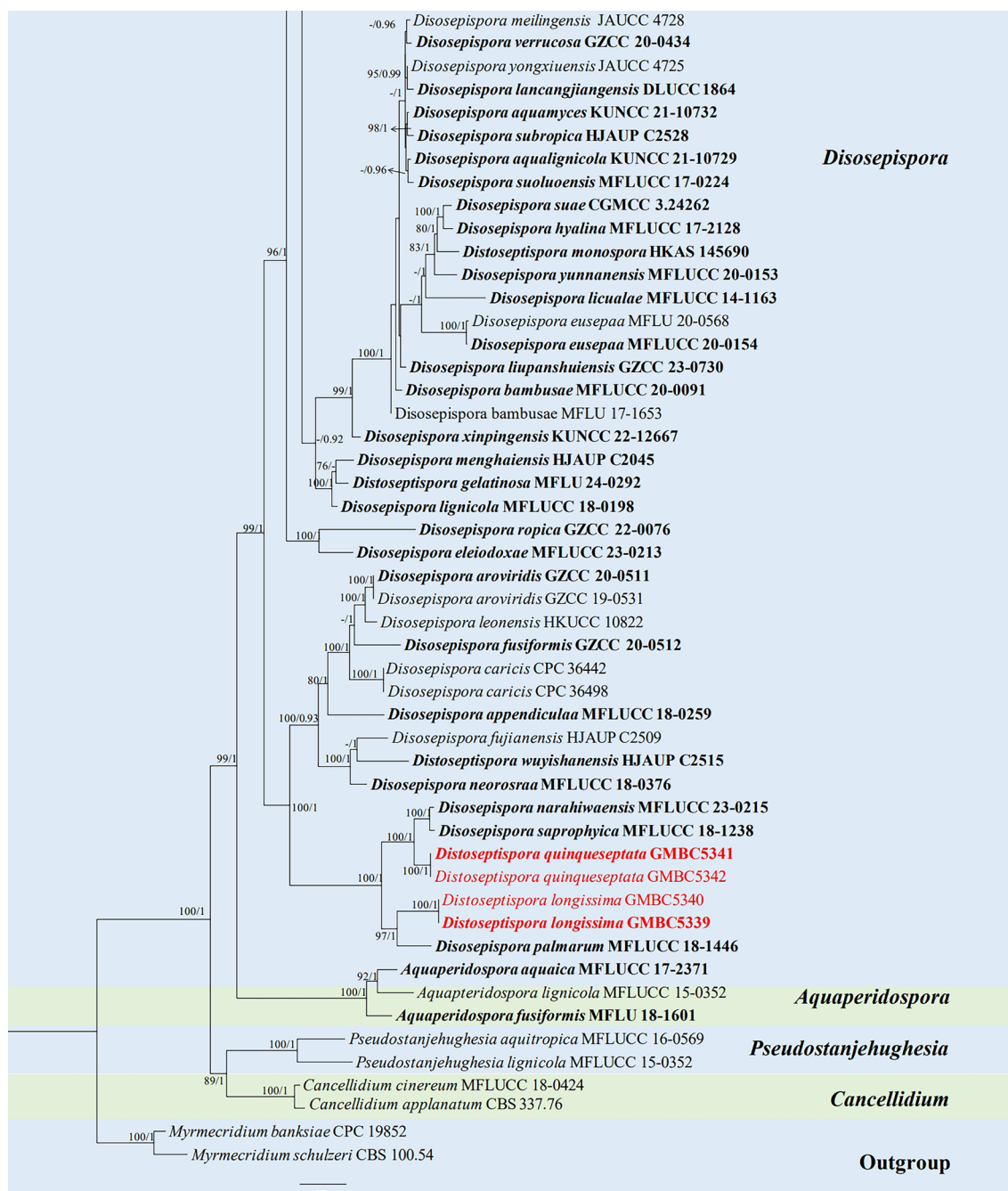


Figure 22 - Continued

Additional specimens examined – China, Guangxi Zhuang Autonomous Region, Fangchenggang City, Shangsi County, Shiwan Mountain National Nature Reserve, 21°57'27.22"N, 108°5'25.84"E, altitude 270 m, on a submerged decaying wood in a wetland, 17 September 2024, L.L. Liu, 2024SWS98 (GMB5342, GMB5342).

Notes – In the phylogram (Fig. 22), *Distoseptispora quinqueseptata* is closely related to *D. saprophytica* and *D. narathiwatensis*. However, *D. quinqueseptata* and *D. saprophytica* can be

easily distinguished based on conidiophore and conidial size. *Distoseptispora saprophytica* has shorter conidiophores ($50\text{--}140 \times 3.2\text{--}4.2\ \mu\text{m}$ vs. $173\text{--}311 \times 5.8\text{--}9\ \mu\text{m}$) and smaller conidia ($14.5\text{--}30 \times 4.5\text{--}7.5\ \mu\text{m}$ with 2–6 distoseptate vs. $11\text{--}39.5 \times 4.5\text{--}8\ \mu\text{m}$ with 2–5 distoseptate) (Dong et al. 2021). Comparative analysis of nucleotide base pairs showed that *D. quinqueseptata* differs from *D. saprophytica* (MFLUCC 18-1238) by 13.7% (72/527) in the ITS locus, 2.0% (13/656) in the LSU locus, 6.5% (57/875) in the *tef1- α* gene, and 19.2% (168/876) in the *rpb2* gene.



Figure 23 – *Distoseptispora longissima* (GMB5339, holotype). a–c Colony on wood. d–e Conidiophores and conidia. f Conidiogenous cells. j, k Conidia. l Surface view of culture on PDA. m Reverse view of culture on PDA. Scale bars: a, b = 0.5 mm, c = 0.3 mm, d, e = 100 μ m, f–k = 20 μ m.

Compared to *Distoseptispora narathiwatensis*, *D. quinqueseptata* has longer conidiophores (173–311 μ m $\times$ 5.8–9 μ m vs. 27–155 $\times$ 3–6.5 μ m), shorter conidiogenous cells (7.1–10.6 μ m length vs. 7–17 μ m length), and fewer septa in conidia (2–5 vs. 1–7). Additionally, the conidiophore cells of *D. narathiwatensis* are often inflated or constricted at the apex or middle, which is not observed in *D. quinqueseptata* (Karimi et al. 2024). The ITS, LSU, *rpb2*, and *tef1- α* sequences of *D. quinqueseptata* and *D. narathiwatensis* show similarities of 96.8%, 98.5%, 91.3%, and 96.4%, respectively.

Morphologically, *Distoseptispora quinqueseptata* resembles *D. dehongensis* in having five distoseptate conidia. However, it can be distinguished from *D. dehongensis* by its longer conidiophores (173.1–311 $\times$ 5.8–9 μ m vs. 47–128 $\times$ 3–5.5 μ m) and smaller conidia (11–39.5 $\times$ 4.5–8 μ m vs. 17–30 $\times$ 7.5–10 μ m) (Hyde et al. 2019).

Based on these morphological differences and phylogenetic analysis, we introduce *Distoseptispora quinqueseptata* as a new species.

Distoseptispora tongrensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 25)

Mycobank No.: MB859978

Etymology – The epithet refers to Tongren City, where the holotype was collected.

Description – *Saprobic* on submerged decaying wood in a wetland. Teleomorph: undetermined. Anamorph: hyphomycetous. *Colonies* on the substratum superficial, effuse, rounded, scattered, hairy. *Mycelium* partially superficial, partially immersed, composed of branched, septate, smooth, hyaline to pale-brown hyphae. *Conidiophores* 29–54 $\times$ 4.2–5.2 μ m ($\bar{x}$ = 41.5 $\times$ 4.6 μ m, n = 20), macronematous, mononematous, unbranched, 3–5 septate, solitary or caespitose, erect, cylindrical, smooth, light olivaceous, tapering towards upper side, slightly robust at the base, flat at the apex. *Conidiogenous cells* 9–12 $\times$ 3–5 μ m ($\bar{x}$ = 10.5 $\times$ 3.9 μ m, n = 20), monoblastic, determinate, olivaceous to light brown, cylindrical but slightly tapering towards apex. *Conidia* 23–37 $\times$ 6.5–10.2 μ m ($\bar{x}$ = 32.4 $\times$ 7.8 μ m, n = 20), acrogenous, solitary, dry, obclavate to clavate sometimes fusiformis, straight or slightly curved, truncate at the base, mostly 5–9 distoseptate, light brown with bluish-green tinge, paler towards the apex, thick-walled.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 10–15 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface creamy white, with densely mycelium, circular, smooth edges; reverse dark greyish black, with creamy white margin.

Material examined – China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°19'40.64" N, 108°8'37.63" E, altitude 701 m, on a submerged decaying wood in a wetland, 13 August 2024, L.L. Liu, 2024FDSZNF34 (GMB5343, **holotype**); ex-type culture, GMBC5343; *ibid.*, KUN-HKAS 150414, isotype.

Additional specimen examined – Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°19'46.72" N, 108°8'11.55" E, altitude 874 m, on a submerged decaying wood in a wetland, 13 August 2024, L.L. Liu, 2024FDSZNF50 (GMB5344; GMBC5344).

Notes – In the phylogenetic tree (Fig. 22), *Distoseptispora tongrensis* is closely related to *D. aquisubtropica*. However, *D. tongrensis* can be distinguished by its shorter conidiophores (29–54 $\times$ 4.2–5.2 μ m) and much smaller conidia (23–37 $\times$ 6.5–10.2 μ m) compared to those of *D. aquisubtropica*, which has conidiophores of 15.6–83 $\times$ 4.8–11 μ m and conidia of 42.5–278 $\times$ 11.1–19 μ m. Additionally, the conidia of *D. tongrensis* have fewer septa (5–9) compared to *D. aquisubtropica* (16–31) (Ma et al. 2022). Comparative analysis of nucleotide base pairs showed that *D. tongrensis* differs from *D. aquisubtropica* (GZCC 22-0075) by 7.3% (37/509) in the ITS locus, 1.4% (12/859) in the LSU locus, 9.2% (85/926) in the *tef1- α* gene, and 8.6 % (92/1073) in the *rpb2* gene.



Figure 24 – *Distoseptispora quinqueseptata* (GMB5341 holotype). a, b Colony on wood. c, d Conidiophores and conidia. e, f Conidiogenous cells. g Germinated conidium. h–m Conidia. n Surface view of culture on PDA. o Reverse view of culture on PDA. Scale bars: a = 0.5 mm, b = 0.1 mm, c, d = 100 μ m, e–g = 20 μ m, h–m = 10 μ m.

In terms of conidial septation, *D. tongrensis* is comparable to *D. yongxiuensis* and *D. hydei*. However, *D. yongxiuense* can be differentiated by its much longer conidiophores (112–253 $\times$ 4–9 μ m) and longer conidia (46–86 $\times$ 10–16 μ m), while *D. hydei* is distinguishable by its larger conidiophores (87–145 $\times$ 3–7 μ m) and larger conidia (32–58 $\times$ 10–15 μ m) (Zhai et al. 2022).

Based on these differences and phylogenetic analysis, we introduce *Distoseptispora tongrensis* as a new species.

Hypocreomycetidae O.E. Erikss. & Winka, Myconet 1: 6 (1997).

Hypocreales Lindau, Die Natürlichen Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1 (1): 343 (1897).

Bionectriaceae Samuels & Rossman, Stud. Mycol. 42: 15 (1999).

Acremonium Link, Mag. Neuesten Entdeck. Gesammten Naturk. Ges. Naturf. Freunde Berlin 3 (1): 15 (1809).

Notes – *Acremonium* was described by Link (1809) based on a species thought to produce single spores terminally on fertile cells. However, Gams (1971) re-examined herbarium material of Link (1809) and determined that the type species, *A. alternatum*, produces conidia in chains from thin, tapering phialides. *Acremonium* species are characterized by septate hyphae that give rise to narrow, mostly lateral phialides bearing unicellular conidia either in mucoid heads or in unbranched chains, and conidiophores with or without verticillate branching. The genus is highly ubiquitous, comprising saprophytic, parasitic, or endophytic fungi found in diverse environments (Gams 1971, Summerbell et al. 2011, Hou et al. 2023). According to Species Fungorum (accessed 28 June 2025), the genus currently comprises 109 accepted species.

Acremonium nigrobrunneum W.M. Li, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 27)

MycoBank No.: MB859972

Etymology – The epithet refers to its blackish-brown colonies on the substrate.

Description – On dead wood in a freshwater wetland. Teleomorph: Undetermined. Anamorph: *Colonies* on natural substratum velvety, superficial, blackish-brown. *Conidiophores* mononematous, arising laterally from superficial hyphae, simple to branched, rarely septate, pale brown to brown, becoming paler or subhyaline towards the apex, slightly verrucose, cylindrical to ampulliform, straight to slightly flexuous. *Conidiogenous cells* polyblastic, discrete, straight, tapering gradually toward the tip, hyaline to pale brown, slightly verrucose, $27\text{--}44 \times 3\text{--}7\ \mu\text{m}$ ($\bar{x} = 35.06 \times 5.9\ \mu\text{m}$, $n = 30$). *Conidia* holoblastic, acrogenous, catenate, 1–3 short acropetal, golden-brown to dark brown, verrucose, aseptate, globose, $7\text{--}10 \times 6\text{--}9\ \mu\text{m}$ ($\bar{x} = 8.6 \times 7.2\ \mu\text{m}$, $n = 30$) diam., conidial secession schizolytic.

Culture characteristics – Conidia germinated within 12 hours on WA. Colonies on PDA reaching 15–20 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface cream white, with densely mycelium, circular, smooth edges, raised center; reverse olive brown with light brown margin.

Material examined – China, Guizhou Province, Guiyang City, Yunmanhu Campus of Guizhou Medical University, 26°39'50.78"N, 106°46'20.39"E, elevation 1264 m, on dead wood in a wetland, 26 June 2024, Wen-Mei Li, 2024GYHSY24-1 (GMB6915, **holotype**); ex-type culture, GMBC6915; *ibid.*, KUN-HKAS 150415, isotype.

Additional material examined – China, Guizhou Province, Guiyang City, Yunmanhu Campus of Guizhou Medical University, 26°39'49.76"N, 106°46'20.72"E, elevation 1264 m, on dead wood in a wetland, 26 June 2024, Wen-Mei Li, 2024GYHSY43 (GMB6916, GMBC6916).

Notes – In phylogenetic analysis (Fig. 26), *Acremonium nigrobrunneum* forms a well-supported clade (99% ML/0.99 PP) sister to the type strain of *A. cavaraeae* (CBS 101149). Morphologically, *A. nigrobrunneum* resembles *A. cavaraeae* in producing acrogenous, catenate conidia. However, the two species are readily distinguishable by ecology and conidial morphology. *Acremonium cavaraeae* is an endophytic species known only from culture-based descriptions and has been isolated from diverse substrate, including the outer wall of a wooden house, *Cocos nucifera*, and the parasitic fungus *Shiraia bambusicola* (Ito et al. 2000, Xu et al. 2017). In contrast, *A. nigrobrunneum* produces velvety, superficial, blackish-brown colonies on decaying wood. Comparative analysis of nucleotide base pairs showed that *A. nigrobrunneum* differs from

A. cavaraeum (CBS 101149) by 1.9% (9/477) in the ITS locus and 0.7% (3/461) in the LSU locus.

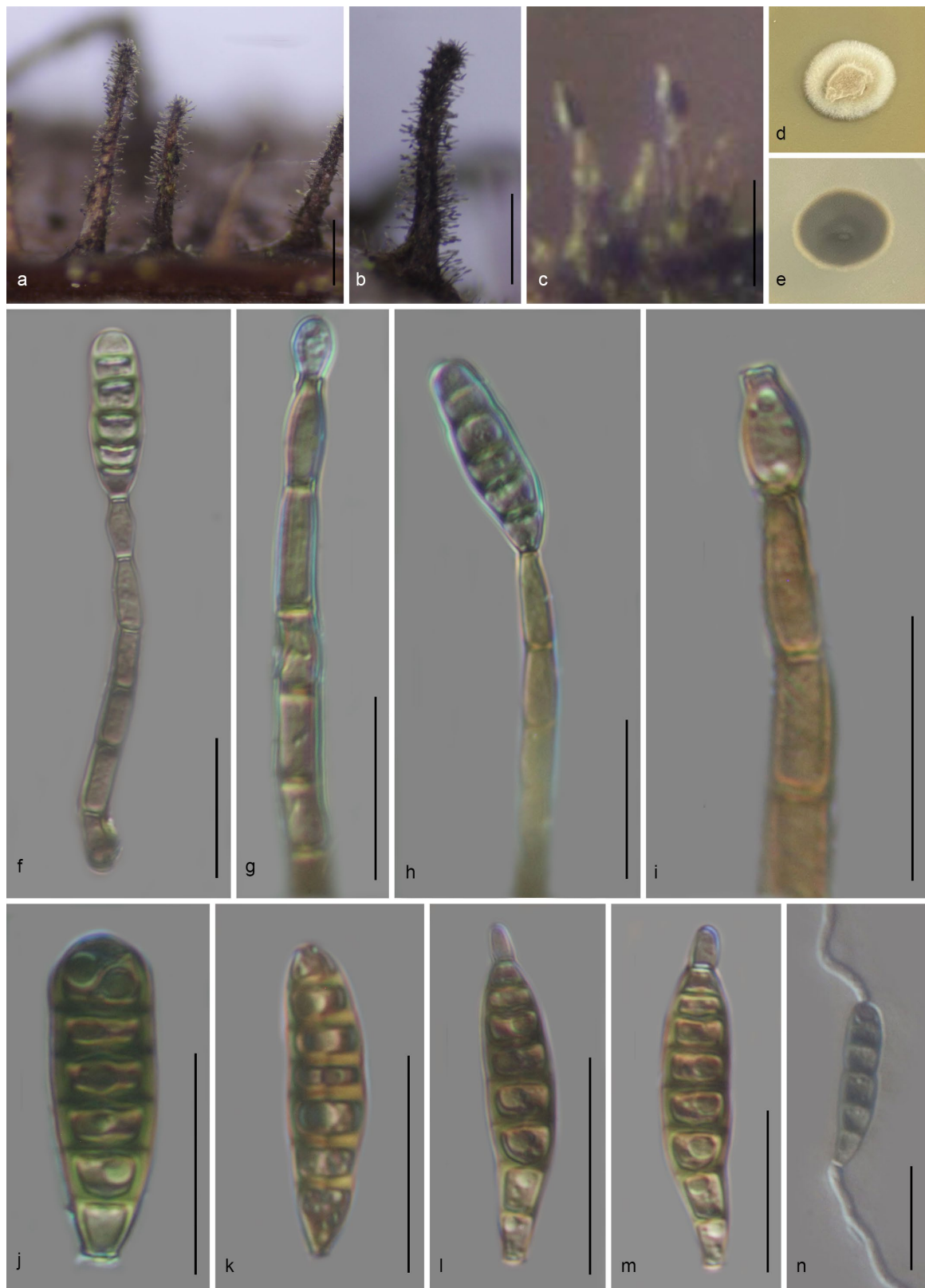


Figure 25 – *Distoseptispora tongrensis* (GMB5343, holotype). a–c Colony on wood. d, e Surface and reverse view of culture on PDA. f, g Conidiophores and conidia. h Conidiogenous cells and conidia. i Conidiogenous cells. j–m Conidia. n Germinated conidium. Scale bars: a = 0.5 mm, b = 0.1 mm, f–m = 20 μm.

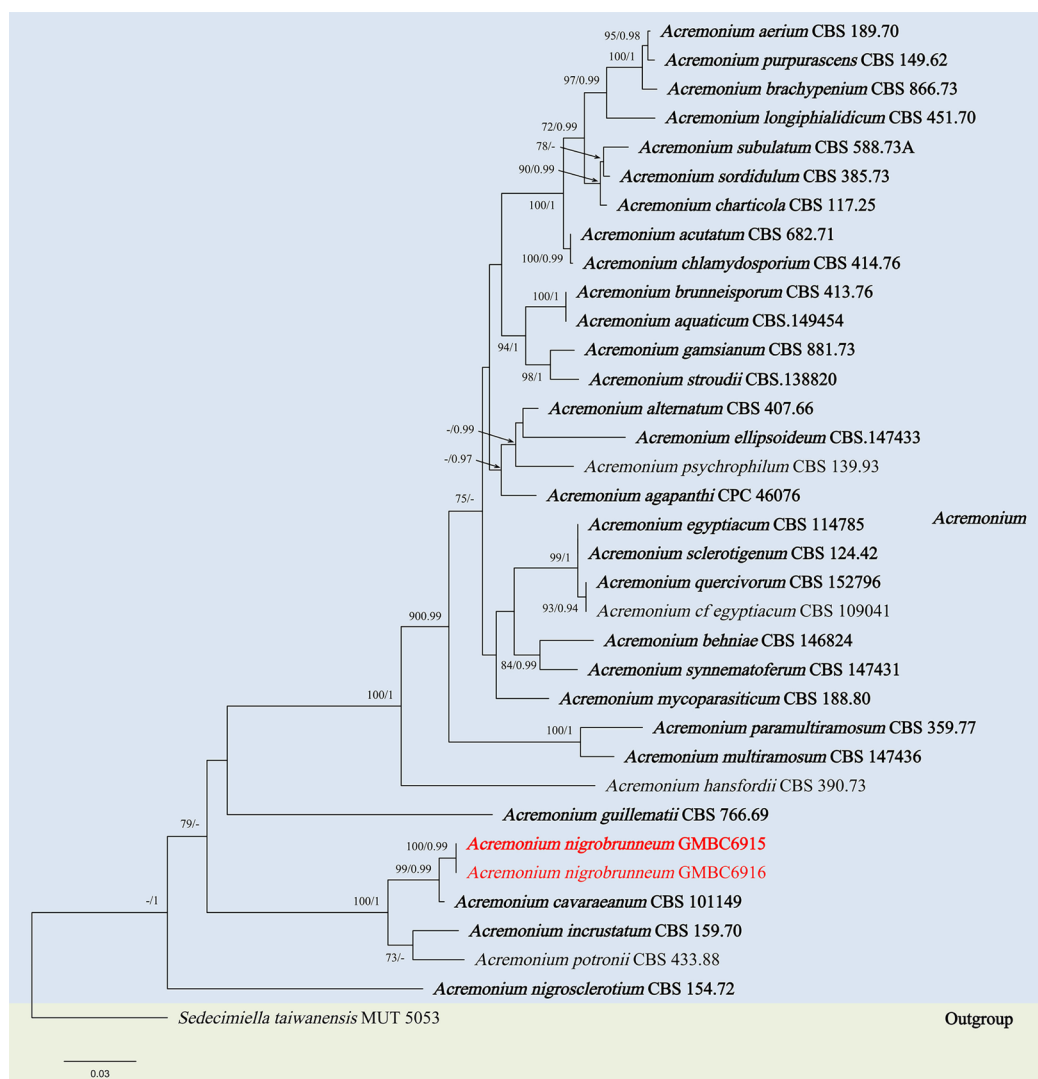


Figure 26 – ML tree of *Acremonium* and related taxa based on ITS and LSU loci. The alignment for this tree includes 1283 bp (ITS: 1–506 bp; LSU: 507–1283 bp). *Sedecimiella taiwanensis* (MUT 5053) was selected as an outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAXML $\geq 70\%$ are shown on the branches. Newly generated sequences are indicated in red and Type strains or specimens are in bold.

Morphologically, *Acremonium nigrobrunneum* produces larger, globose, golden-brown to dark brown conidia ($7\text{--}10 \times 6\text{--}9 \mu\text{m}$), whereas *A. cavaraeanum* has smaller ($3.2\text{--}4.5 \times 1.2\text{--}2.5 \mu\text{m}$), hyaline, fusiform to ellipsoid conidia with minutely truncate ends. The ITS sequence similarity between the two strains is 97.83 %, with five nucleotide differences.

Based on these morphological differences and phylogenetic distinctness, we introduce *A. nigrobrunneum* as a novel species.

Nectriella Nitschke ex Fuckel, Jahrb. Nassauischen Vereins Naturk. 23-24: 175 (1870).

Notes – The genus *Nectriella* was established by Fuckel (1870) and is typified by *Nectriella fuckelii*. The genus is characterized by white to pale yellow or pale brown ascomatal perithecia, which are often immersed, and ellipsoid to fusoid, 1-septate, hyaline ascospores that are smooth to faintly spinulose or striate. When cultured, species of *Nectriella* typically produce kutilakesa-like sporodochia and acremonium-like anamorphs (Alfieri & Samuels 1979, Rossman et al. 1999). Most *Nectriella* species are found on dead wood and herbaceous substrates and are not considered plant pathogens (Rossman et al. 1999). According to Species Fungorum (accessed 30 June 2025), the

genus currently comprises 65 accepted species. In this study, we describe a species that represents a new record for China.

Nectriella rusci Lechat, Lowen & Gardiennet, Persoonia 25: 118 (2010). (Fig. 29)

Description – *Saprobic* on decaying twigs in a freshwater lake. Teleomorph: Undetermined. Anamorph: Hyphomycetous. *Colonies* on natural substratum effuse, erect, hairy, white, scattered, solitary. *Mycelium* composed of hyaline, multiseptate hyphae, branched. *Conidiophores* 57.8–110.9 $\times$ 1.9–2.5 μm ($\bar{x}$ = 92.4 $\times$ 2.2 μm , n = 20), macronematous, solitarily, conidiophores reduced to conidiogenous cells, arising singly from superficial hyphae, erect, flexuous, subcylindrical to subulate, with apical taper, thick-walled in lower region, with non-flared cylindrical apical collarette. *Conidia* 4.7–10.8 $\times$ 2.9–3.8 μm ($\bar{x}$ = 8.4 $\times$ 3.3 μm , n = 30), adhering to slimy heads, subcylindrical with subobtuse apices, aseptate, hyaline, smooth- and thin-walled, guttulate, verruculose.

Culture characteristics – *Conidia* germinated and formed germ tubes within 36 hrs on WA. Colonies on PDA reaching 10–15 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface white to cream, irregular, spreading with moderate aerial mycelium, leathery, center raised, smooth lobate edges, lobate margins; reverse lemon yellow.

Material examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'21.770"N, 104°00'19.121"E, altitude: 1419 m, on a decaying submerged wood in a freshwater lake, 28 October 2024, L.L. Liu, 2024WMS254 (GMB5310, GMBC5310).

Notes – The sequence of our collection, GMB5310, showed 100% similarity in the ITS and LSU loci with the holotype of *Nectriella rusci* (CBS 126457) and cluster together phylogenetically (Fig. 28). The original anamorph description of *N. rusci* was based on culture characteristics, which share the same conidiophore length but has larger conidia (4.5–) 5–12 (–18) $\times$ 2.5–4.8 (–5.2) μm (Lechat et al. 2010), compared to our collection, which has conidia of 4.7–10.8 $\times$ 2.9–3.8 μm . Based on the 100% sequence similarity and the lack of an anamorphic characterization from natural substrates, we identify our collection as *Nectriella rusci*.

This species was previously reported in France (Lechat et al. 2010). Its anamorph is now observed on a natural substrate for the first time and represent a new record for China.

Protocreopsis Yoshim. Doi, Bull. natn. Sci. Mus., Tokyo, B 2(4): 129 (1977)

Notes – The genus was established by Doi (1977) (typified by *P. fusigera*) to accommodate *Nectria*-like fungi characterized by pale ascomata, typically surrounded by white to tan hyphae, and the production of striate ascospores. The anamorph of the genus is characterized by monophialidic conidiophores that are typically unbranched, septate, and either smooth or spinulose. Conidia are ellipsoid, fusiform, (sub)cylindrical, or oblong, aseptate, hyaline, and smooth-walled (Doi 1977, Rossman et al. 1999, Hou et al. 2023). Species of the genus occur on decaying plant material in tropical and subtropical regions, commonly colonizing decaying monocotyledonous leaves, often on palms or *Musaceae* (Rossman et al. 1999, Crous et al. 2024). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 18 accepted species.

Protocreopsis alba L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 31)

Mycobank No.: MB859987

Etymology – The epithet refers to its white colonies on the substratum.

Description – *Saprobic* on decaying wood along the riverbank. Teleomorph: undetermined. Anamorph: *Colonies* effuse, erect, scattered on natural substratum, white to transparent, shiny, solitary or mostly forming groups. *Conidiophores* 21.4–80.3 $\times$ 1.4–5.6 μm ($\bar{x}$ = 44.4 $\times$ 3.2 μm , n = 30), erect, simple, cylindrical, minutely tapering towards apex, hyaline, smooth, thin-walled, edges truncate. adelophialides and schizophialides not observed. *Conidiogenous cells* phialidic solitary, straight or slightly flexuous, hyaline, subcylindrical, monoblastic. *Conidia* 3.5–7.8 $\times$ 2–3.6 μm ($\bar{x}$ = 5.5 $\times$ 2.8 μm , n = 30), grouped at tip of phialide to form a mucous head, unicellular, ellipsoidal to subcylindrical, hyaline, smooth, thin-walled, arranged in slimy heads.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 10–20 mm diam., after 2 weeks at 24–27 °C on PDA. Colony surface creamy white to pale brown, with densely mycelium, circular, smooth edges; reverse bright yellow.

Material examined – China, Sichuan Province, Leshan City, Heizhugou National Forest Park, 28°59'10.95" N, 103°2'12.60" E, altitude: 1751 m, on a decaying wood along the riverbank, 23 October 2024, L.L. Liu, 2024HZG65 (GMB5357, **holotype**); ex-type culture, GMBC5357; *ibid.*, KUN-HKAS 150416, isotype.

Additional specimens examined – China, Sichuan Province, Leshan City, Heizhugou National Forest Park, 28°59'30.08" N, 103°2'43.70" E, altitude: 1790 m, on a decaying wood along the riverbank, 23 October 2024, L.L. Liu, 2024HZG103 (GMB5358, GMBC5358).

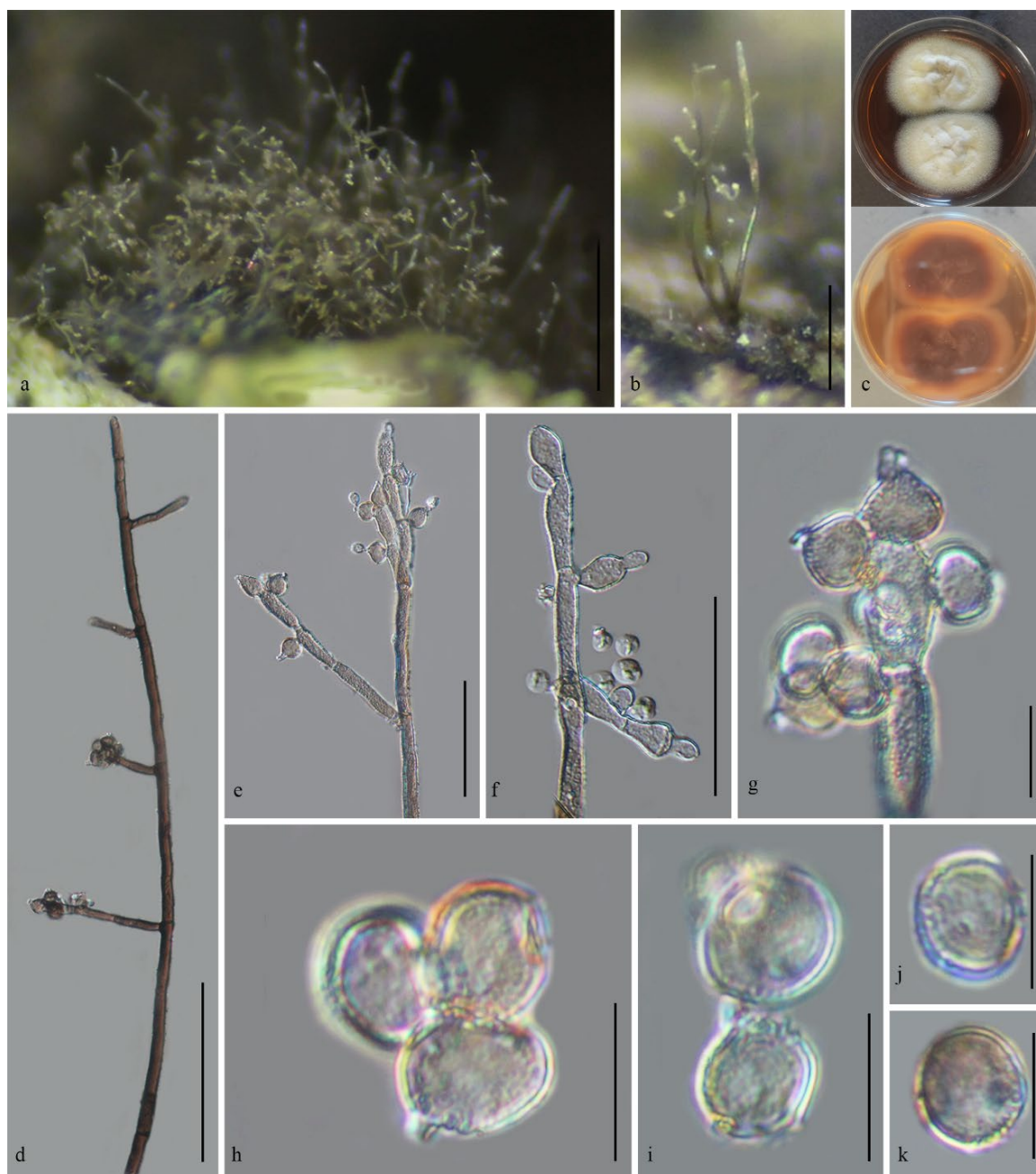


Figure 27 – *Acremonium nigrobrunneum* (GMB6915 holotype). a–b Colonies on natural substratum. c Surface and reverse view of culture on PDA. d–f Conidiophores and conidia. g Conidiogenous cells with conidia. h–k Conidia. Scale bars: a = 0.5 mm, b = 0.2 mm, d = 100 μm, e, f = 50 μm, g–k = 10 μm.

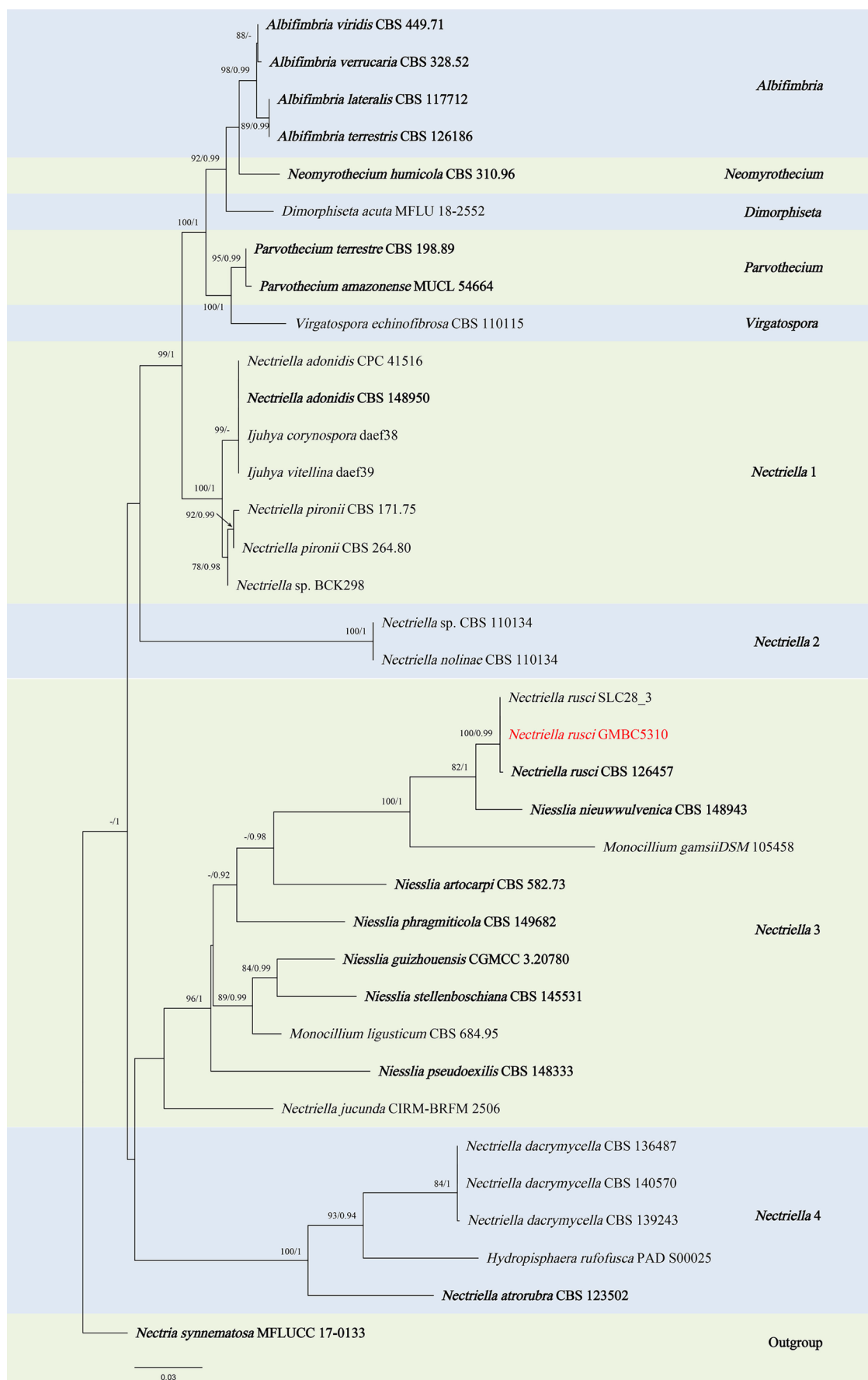


Figure 28 – ML tree of *Nectriella* and related taxa based on ITS and LSU loci. The alignment for this tree includes 1370 bp (ITS: 1–541 bp; LSU: 542–1370 bp). *Nectria synnematos* (MFLUCC 17-0133) was selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap

support values of RAxML ≥ 70 % are shown on the branches. Newly generated sequences are indicated in red and holotype strains are in bold.

Notes – Phylogenetically (Fig. 30), *Protocreopsis alba* forms an independent clade, strongly supporting its recognition as a distinct species. Morphologically, our collection aligns with the generic diagnosis of *Protocreopsis*. Most described species in the genus are based on teleomorph or cultured anamorph characteristics whereas the anamorph of *P. alba* is readily observed forming persistent white colonies directly on its natural substrate. The type species of the genus *P. fusigera* differs from *P. alba* in having larger conidiophores ($150\text{--}210 \times 4.5\text{--}6.5\text{ }\mu\text{m}$ vs. $21.4\text{--}80.3 \times 1.4\text{--}5.6\text{ }\mu\text{m}$ in *P. alba*) and much longer conidia ($40\text{--}55 \times 11\text{--}13\text{ }\mu\text{m}$ vs. $3.5\text{--}7.8 \times 2\text{--}3.6\text{ }\mu\text{m}$ in *P. alba*) (Rossman et al. 1999). In the BLAST search for ITS and SSU regions, the closest hits were *Protocreopsis rutila* (JCM 23088), with sequence identities of 87.5% and 97.8%, respectively. Most of species in this genus have been reported on leaf material, with no anamorphs described from natural substrates. The conidia of most species in *Protocreopsis* are similar in size and shape, typically $7\text{--}8\text{ }\mu\text{m}$ long, which does not provide sufficient differentiation for species identification (Rossman et al. 1999, Lechat et al. 2016, Hou et al. 2023). However, based on its independent phylogenetic position, which clearly distinguishes it from other species and the anamorphs found on natural substrates within the genus, we recognize *P. alba* as a new species.

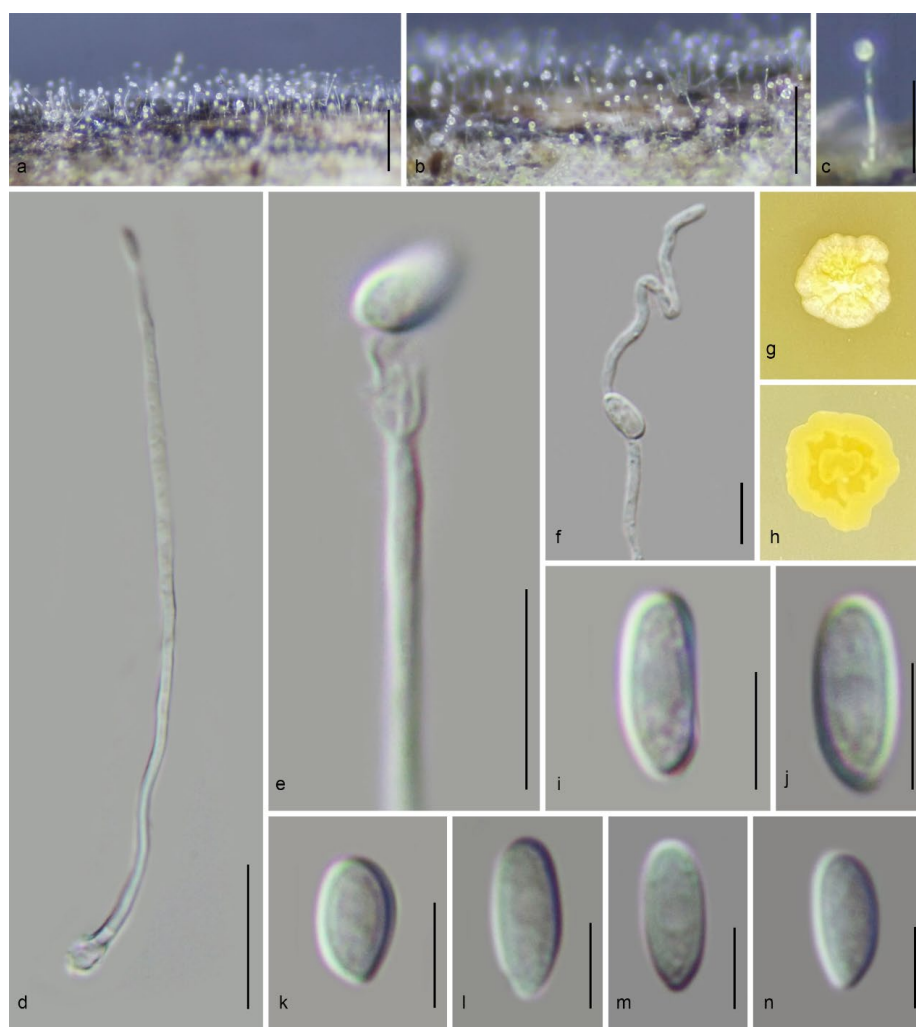


Figure 29 – *Nectriella rusci* (GMB5310) a–c Colony on wood. d Conidiophores and conidia. e Conidiogenous cells and conidia. f Germinated conidium. g Surface view of culture on PDA. h Reverse view of culture on PDA. i–n Conidia. Scale bars: a, b = 0.3 mm, c = 0.1 mm, d = 20 μm , e, f = 10 μm , i–n = 5 μm .



Figure 30 – ML tree of *Protocreopsis* and related taxa based on ITS and LSU loci. The alignment for this tree includes 1342 bp (ITS: 1–566 bp; LSU: 567–1342 bp). *Lasionectriopsis dentifera* (CBS 574.76) and *Lasionectriopsis germanica* (CBS 143538) were selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. Newly generated sequences are indicated in red and type strains are in bold.

Nectriaceae Tul. & C. Tul., Selecta Nectriei- Phacidiei- Pezizei 3: 3 (1865).

Mariannaea G. Arnaud ex Samson, Stud. Mycol. 6: 74 (1974).

Notes – The genus *Mariannaea* was reestablished by Samson (1974) to accommodate *M. camptospora*. It was assigned to *Nectriaceae* by Samuels & Seifert (1991). Molecular phylogenetic studies (Cai et al. 2010, Lombard et al. 2015, Hu et al. 2016) have confirmed the placement of *Mariannaea* within the *Nectriaceae* and supported the monophyly of this family.

Samson (1974) originally characterized *Mariannaea* by the production of one-celled conidia formed in sticky heads from flask-shaped phialides. However, later reports described species producing straight chains of two-celled, one-septate conidia (Samuels 1989, Matsushima 1995). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 23 accepted species. Members of this genus are predominantly found in terrestrial and freshwater habitats (Samuels 1989, Samson & Bigg 1988, Matsushima 1995, Cai et al. 2010, Gräfenhan et al. 2011, Nonaka et al. 2015).



Figure 31 – *Protocreopsis alba* (GMB5357 holotype). a–c Colony on wood. d Conidiophores and conidia. e Conidiophores. f Conidiogenous cells and conidia. g Germinating conidium. h–n Conidia. o Surface view of culture on PDA. p Reverse view of culture on PDA. Scale bars: a, b = 0.2 mm, c = 0.1 mm. d–h = 20 μ m, i–n = 5 μ m.

Mariannaea alba L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 33)

Mycobank No.: MB859982

Etymology – The epithet refers to its white colonies on substratum.

Description – *Saprobic* on decaying wood in a freshwater wetland. Teleomorph: Undetermined. Anamorph: Hyphomycetous. *Colonies* effuse, scattered, hairy, erect, white.

Mycelium hyaline to pale brown, smooth. *Conidiophores* 290–421 × 2.3–4.5 μm ($\bar{x}$ = 377.5 × 3.2 μm, n = 15), 5–9 septate, macronematous, mononematous, erect, multiseptate, hyaline, bearing short branches with phialides or whorls of phialides in verticils along the main stalk. *Conidiogenous cells* 16–24 × 1.2–2 μm ($\bar{x}$ = 19.2 × 1.6 μm, n = 15), phialades, slightly wide from the base 2.4–3.5 μm, monoblastic, terminal becoming intercalary, cylindrical slightly tapering apically, hyaline. *Conidia* 4–7 × 2.2–4 μm ($\bar{x}$ = 5.4 × 3.2 μm, n = 30), ellipsoid, broader from center, tapering towards both ends, hyaline, smooth, thin-walled, forming imbricate chains.

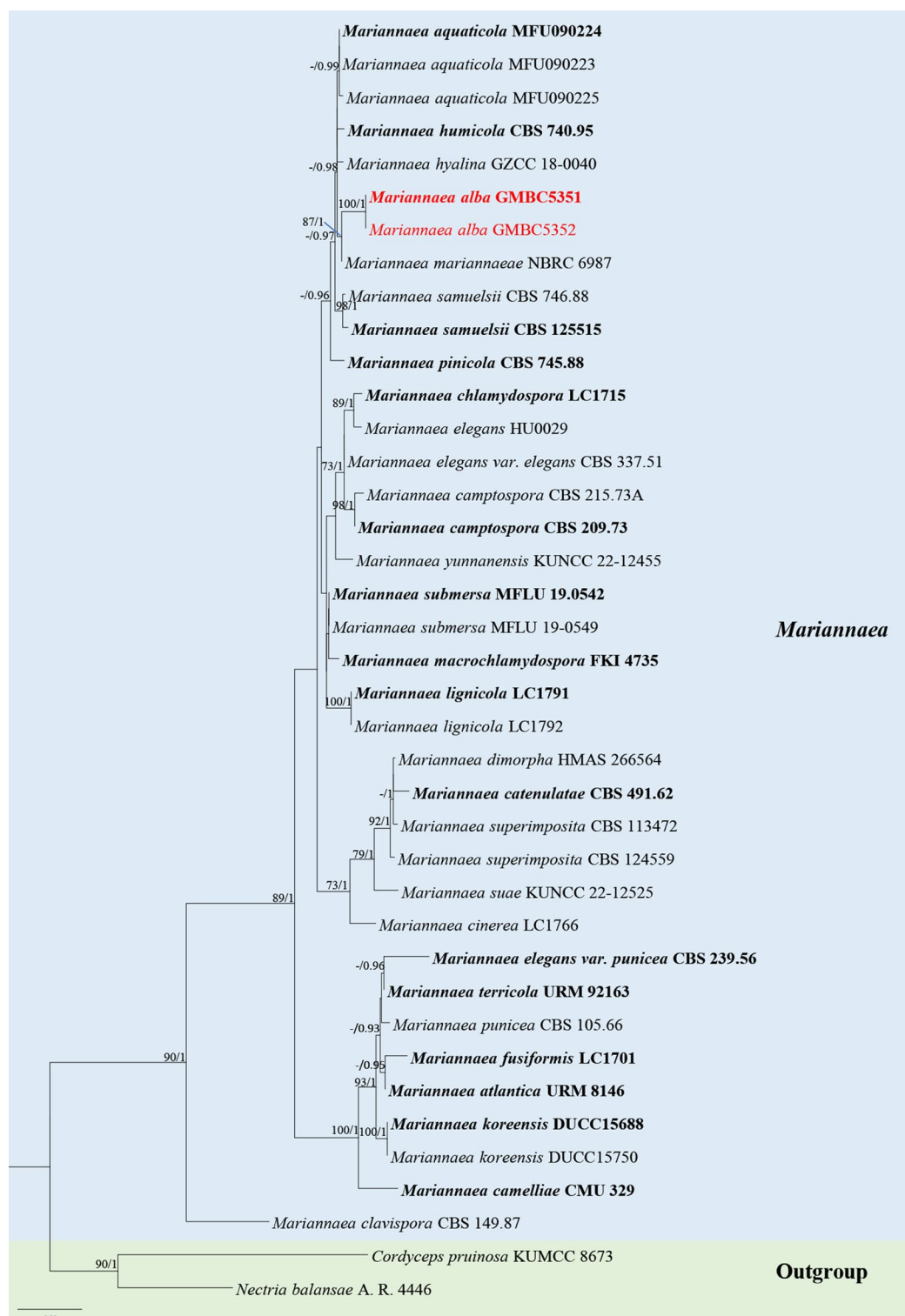


Figure 32 – ML tree of *Mariannaea* genus based on ITS, LSU and *tub2* loci. The alignment for this tree includes 1957 bp (ITS:1–552 bp; LSU:553–1408 bp; *tub2*:1409–1957 bp). *Nectria balansae*

(A.R. 4446) and *Cordyceps pruinose* (KUMCC 8673) were selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly described species is marked red in bold. Ex-type/type strains are indicated in black bold.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 20–30 mm diam., after 2 weeks at 24–27 °C on PDA. Colony surface creamy with yellowish tinge, with densely mycelium, circular, floccose, smooth edges, raised and radial cracking; reverse brown, with bright yellow margins.

Material examined – China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°23′0.43″N, 108°7′30.36″ E, altitude 1115 m, on a decaying wood in a freshwater wetland, 23 August 2024, L.L. Liu, 2024FDSLL57 (GMB5351, **holotype**); ex-type culture, GMBC5351; *ibid.*, KUN-HKAS 150411, isotype.

Additional specimens examined – China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°23′5.41″N, 108°7′41.91″E, altitude 1179 m, on a decaying wood in a freshwater wetland, 23 August 2024, L.L. Liu, 2024FDSLL89 (GMB5352, GMBC5352).

Notes – In the phylogenetic tree (Fig. 32), *Mariannaea alba* clusters closely with *M. pinicola* and *M. humicola*. *Mariannaea humicola* has been isolated from rhizosphere soil and decaying wood from an unknown tree and was described based on its culture characteristics. In contrast, the new species, *M. alba*, produces white colonies on decaying wood and is described based on its natural substrate. Morphologically, the two species differ in conidiophore size, with *M. alba* having larger conidiophores (290–421 $\times$ 2.3–4.5 μm vs. 80–100 $\times$ 3–7 μm) and slightly larger conidia (4–7 $\times$ 2.2–4 μm vs. 3–6 $\times$ 2–3 μm) (Lombard et al. 2015). *Mariannaea pinicola* has been described based on both its teleomorphic and its culture-based anamorphic morphology, with conidiophores size 80–400 μm tall and fusoid conidia that are larger (5–17 $\times$ 2–4.5 μm vs. ellipsoid conidia 4–7 $\times$ 2.2–4 μm in *M. alba*) (Samuels & Seifert 1991). Comparative analysis of nucleotide base pairs showed that *M. alba* differs from type isolate of *M. pinicola* (CBS 745.88) by 1.3% (6/470) in the ITS locus, 0.1% (8/702) in the LSU locus, and 3.5% (10/285) in the *tub2* gene.

Mariannaea koreensis shares similar conidiophore and conidia sizes with *M. alba*. However, phylogenetically, it is distant from the new species and was isolated from swamp soil (Noh & Kim 2025). Based on these morphological differences and phylogenetic analysis, we propose *Mariannaea alba* as a new species.

Volutella Fr., Systema Mycologicum 3 (2): 458, 466 (1832).

Notes – *Volutella* was introduced by Fries (1832), with *V. ciliata* as the type species. The genus is characterized by conidiophores sporodochial or synnematal, unbranched, setose, synnemata determinate, pale, composed of a stipe and a divergent capitulum of conidiophores with conidial mass, stipe comprising of parallel hyphae, conidiogenous cells are monophialidic, subulate, mostly with a conspicuous periclinal thickening, and conidia are ellipsoidal, ovate or oblong, aseptate, hyaline, occur in slimy white, yellow, orange or pink masses (Gräfenhan et al. 2011, Lombard et al. 2015, Perera et al. 2023). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 90 accepted species.

Volutella minutissima Lechat & J. Fourn., Ascomycete.org 14(3): 90 (2022). (Fig. 35)

Description – *Saprobic* on decaying wood in a freshwater lake. Teleomorph: Undetermined. Anamorph: Colonies scattered on natural substratum, solitary, *Synnemata* 600–1100 μm high and 180–300 μm wide at the widest point, superficial, base partially immersed in the substrate, abopyriform to subglobose, white, rounded at the apex and tapering gradually toward the base, glabrous; sometimes the apex appears shiny. *Synnemata* surrounded by several conspicuous, hyaline, rigid, long setae. *Setae* 29.8–46.7 $\times$ 1.0–2.6 μm ($\bar{x}$ = 340.1 $\times$ 2.0 μm , n = 30) long, hyaline, smooth-walled, rigid, tapering toward the apex. *Conidiophores* 29.8–46.7 $\times$ 1.0–2.6 μm ($\bar{x}$ = 37.4 $\times$ 2 μm , n = 30), macronematous, *synnemata* composed of parallel hyphae, with septate elements, pale-colored, erect or curved, subcylindrical to cylindrical, hyaline towards apex, paler

towards the base, unbranched. *Conidiogenous cells* terminal, hyaline, smooth, integrated, giving rise to a cluster of conidia. Conidia $2.9\text{--}6.5 \times 1.8\text{--}3 \mu\text{m}$ ($\bar{x} = 5 \times 2.3 \mu\text{m}$, $n = 30$), broadly ellipsoid to oblong, hyaline.

Culture characteristics – Conidia germinated and formed germ tubes within 24 hrs on WA. Colonies on PDA reaching 30–40 mm diam., after 2 weeks at 24–27°C on PDA. Colony surface white to pale-yellow, hairy, circular, partially immersed in medium, smooth edges; reverse pale yellow.

Material examined – China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°19'40.64"N, 108°8'37.63"E, altitude 701 m, on a decaying wood in a freshwater lake, 23 August 2024, L.L. Liu, 2024 FDSDCY10 (GMB5311, GMBC5311); China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°19'46.72"N, 108°8'11.55"E altitude 874 m, on a decaying wood in a freshwater lake, 23 August 2024, L.L. Liu, 2024FDSDCY19 (GMB5318, GMBC5318).



Figure 33 – *Mariannaea alba* (GMB5351 holotype). a–c Colony on wood. d–f Conidiophores and conidia. g Conidiogenous cells and conidia. h Germinated conidium. i Surface view of culture on PDA. j Reverse view of culture on PDA. k–m Conidia. Scale bars: a, b = 0.5 mm, c = 0.2 mm. d, e, f = 50 μ m, h = 20 μ m, g, k–l = 10 μ m, m = 5 μ m.

Notes – Phylogenetically (Fig. 34), our collections GMB5311 and GMB5318 cluster with *Volutella minutissima*, a species previously described based on its teleomorph and culture-based anamorph. Sequence comparison revealed a 99.8% similarity in the ITS region with the holotype isolate of *V. minutissima*. Morphological characters and the dimensions of the conidiophore and conidia are consistent with the holotype description (Lechat et al. 2022). We report GMB5311 as an anamorph of *V. minutissima* found on a natural substrate. It was previously reported from French Guiana (Lechat et al. 2022), this study presents it as a new record for China.

Sarocladiaceae L. Lombard, Persoonia 41: 343 (2018).

Sarocladium W. Gams & D. Hawksw., Kavaka 3: 57 (1976) [1975].

Notes – *Sarocladium*, the type genus of *Sarocladiaceae*, it is a morphologically and ecologically diverse genus (Crous et al. 2018). The genus was established by Gams & Hawksworth (1975) and its taxonomy was later reviewed by Summerbell et al. (2011), with *S. oryzae* designated as the type species. Morphologically, members of *Sarocladium* are characterized by cylindrical, erect, phialidic conidiogenous cells and elongated phialides rising solitary on vegetative hyphae or on conidiophores that are sparsely or repeatedly branched, and the production of cylindrical conidia (Summerbell et al. 2011, Ou et al. 2020). Ecologically, *Sarocladium* species occupy a wide range of niches. They have been reported as plant pathogens, endophytes, mycoparasites, and saprobes, with some species also acting as opportunistic human pathogens (Giraldo et al. 2015, Yeh & Kirschner 2014, Liu et al. 2017, Crous et al. 2018, Ou et al. 2020). The genus is globally distributed, with records from various regions including China, Egypt, Germany, India, Kenya, the Solomon Islands, and Sri Lanka (Summerbell et al. 2011, Liu et al. 2017). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 38 accepted species. In this study, we report a new species of the genus found on decaying bamboo culm along a stream.

Sarocladium bambusicola L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 37)

Mycobank No.: MB859995

Etymology – The epithet refers to its host, bamboo.

Description – *Saprobic* on decaying bamboo culm along a stream. Teleomorph: Undetermined. Anamorph: Colonies white with black glistening heads on natural substratum, Mycelium partly immersed, composed of branched, septate, hyaline to pale brown, smooth, thin-walled hyphae. *Conidiophores* 200–600 $\times$ 2.5–5.5 μ m ($\bar{x}$ = 389.9 $\times$ 3.9 μ m, n = 30), macronematous, synnematus, erect, unbranched, light brown, subhyaline towards apex, smooth, gregarious, straight or slightly flexuous, 6–10 septate. *Conidiogenous cells* 7–14.7 $\times$ 2.5–4.1 μ m ($\bar{x}$ = 11.6 $\times$ 3.3 μ m, n = 30), polyphialidic, hyaline, integrated, ampulliform or cylindrical thin toward apex, compactly grouped, acropetally proliferating. *Conidia* 4–7 $\times$ 1.8–3.3 μ m ($\bar{x}$ = 5.3 $\times$ 2.5 μ m, n = 30), unicellular, cylindrical with rounded ends, hyaline, smooth.

Culture characteristics – Colonies on PDA reaching 30–40 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface pale yellowish to greyish white, circular, flat, smooth edges; reverse light yellow.

Material examined – China, Sichuan Province, Yibin City, Shulan Bamboo Sea Resort, 28°28'27.40" N, 104°57'03.64" E, altitude 610 m, on a decaying bamboo along a stream, 20 September 2024, L.L. Liu, 2024SNZ31 (GMB5327, **holotype**); ex-type culture, GMBC5327; *ibid.*, KUN-HKAS 150423, isotype.

Additional specimens examined – China, Sichuan Province, Yibin City, Shulan Bamboo Sea Resort, 28°27'30.25" N, 104°58'10.35" E, altitude 659 m, on a decaying bamboo along a stream, 22 September 2024, L.L. Liu, 2024SNZ69 (GMB5328, GMBC5328).

Notes – Phylogenetically (Fig. 36), *Sarocladium bambusicola* forms a well-supported clade in a sister relationship with *S. pseudokiliense*. The latter, described only from culture, produces narrower cylindrical conidia (3–6 × 1–1.5 µm) (Masigol et al. 2022). Comparative analysis of nucleotide base pairs showed that *S. bambusicola* differs from *S. pseudokiliense* (IRAN 3649C) by 2.3% (11/487) in the ITS locus, 0.7% (4/573) in the LSU locus, and 2.1% (9/426) in the *tef1-α* gene.

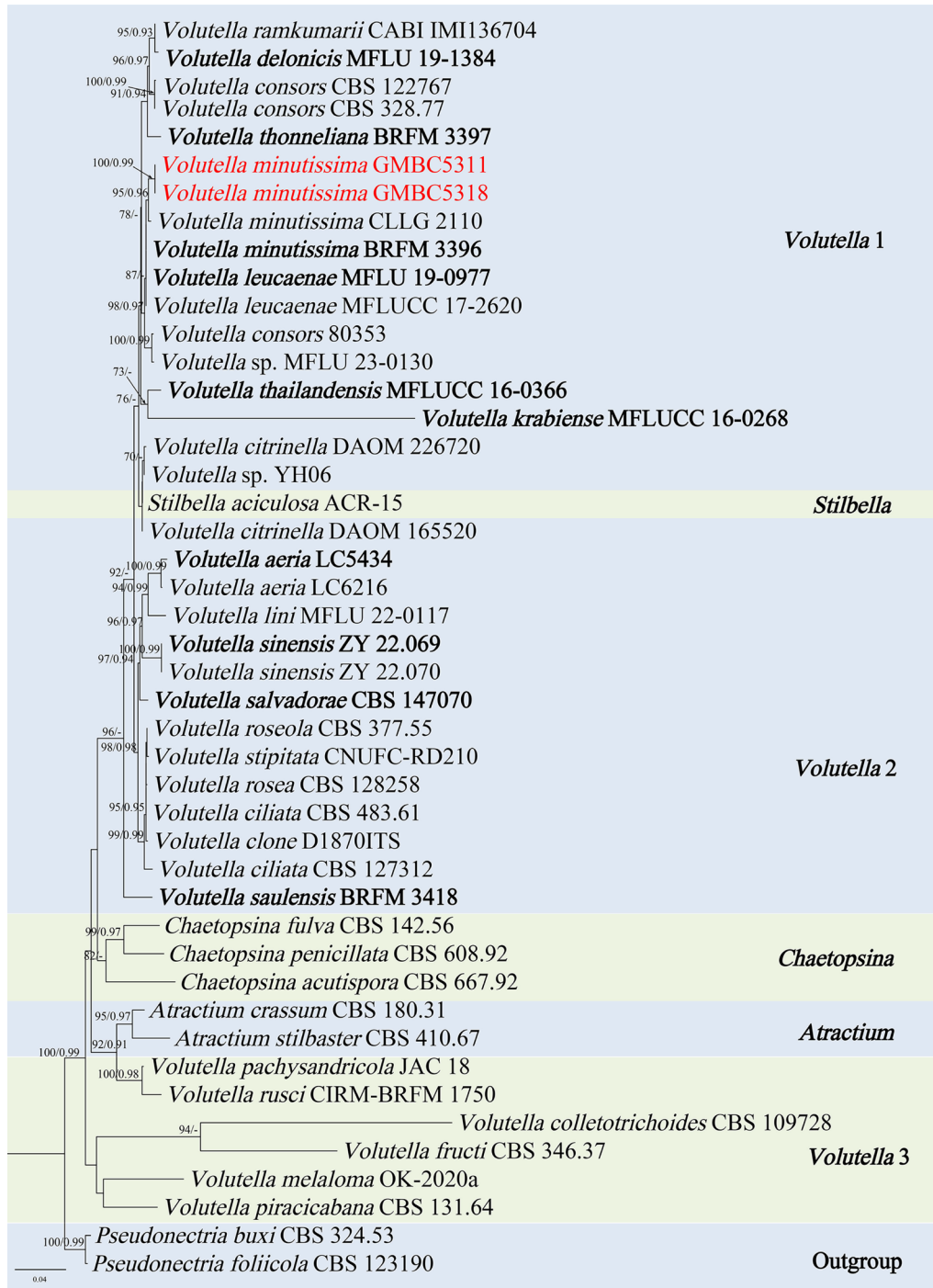


Figure 34 – ML tree of *Volutella* species based on ITS and LSU loci. The alignment for this tree includes 1401bp (ITS: 1–530bp; LSU: 535–1401bp). *Pseudonectria buxi* and *P. foliicola* were selected as the outgroup taxa. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAXML ≥ 70 % are shown on the branches. The newly generated sequences are marked red in bold. Ex-type/type strains are indicated in black bold.

Morphological characters of species of *Sarocladium* have mainly been reported from culture, except *S. clematidis*, which has been documented on natural substrate (*Clematis patens*). *Sarocladium clematidis* differs by its dark brown colonies (vs. white with black glistening heads), shorter conidiophores ($85\text{--}320 \times 12\text{--}19\ \mu\text{m}$ vs. $200\text{--}600 \times 2.5\text{--}5.5\ \mu\text{m}$), and slight larger, fusiform to broadly fusiform conidia ($4\text{--}9 \times 2\text{--}4\ \mu\text{m}$ vs. $4\text{--}7 \times 1.8\text{--}3.3\ \mu\text{m}$) (Phukhamsakda et al. 2020). Based on these difference and phylogeny we introduce *S. bambusicola* as a new species.

Stachybotryaceae L. Lombard & Crous, Persoonia 32: 283 (2014).

Memnoniella Höhn., Zentralbl. Bakteriол. 2. Abt. 60 (1/6): 16 (1923).

Notes – *Memnoniella* was established by von Höhnelt (1923), with *M. echinata* as the type species. The genus comprises saprobic microfungi commonly found in both outdoor and indoor environments (Wang et al. 2015). The genus is characterized by macronematous, unbranched conidiophores, phialidic conidiogenous cells with conspicuous collarettes, and unicellular, aseptate, smooth to verrucose conidia, which are typically arranged in dry chains. According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 24 accepted species. In this study we introduce a new species of the genus found on submerged decaying wood in freshwater habitat.

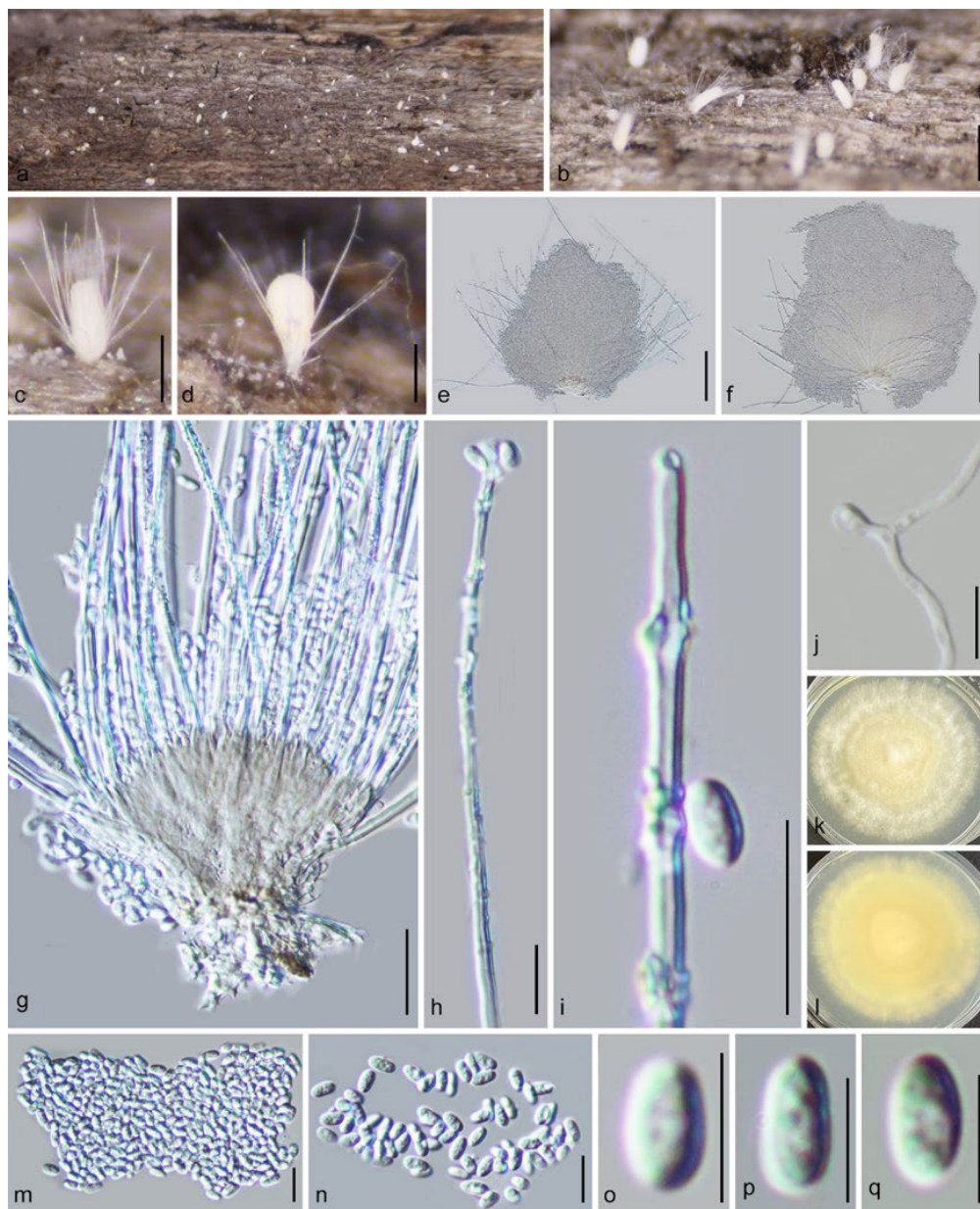


Figure 35 – *Volutella minutissima* (GMB5311). a–d Colony on wood. e–g Conidiophores and conidia. h, i Conidiogenous cells and conidia. j Germinated conidium. k Surface view of culture on PDA. l Reverse view of culture on PDA. m–q Conidia. Scale bars: b = 0.5 mm, c, d = 0.2 mm, e, f = 100 μ m, g = 20 μ m, h–j, m, n = 10 μ m. o–q = 5 μ m.

Memnoniella anliuensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 39)

MycoBank No.: MB859984

Etymology – The epithet refers to Anliu Town, where the holotype was collected.

Description – *Saprobic* on a dead wood along the edge of a waterfall. Teleomorph: undetermined. Anamorph: *Colonies* superficial, gregarious, scattered, black, mass or bouquet. *Conidiophores* 80.5–255 $\times$ 4–6.5 μ m ($\bar{x}$ = 200 $\times$ 4.8 μ m, n = 20), macronematous, slightly swollen at the apex, straight to flexuous, unbranched, containing a crown of phialides, minutely verrucose predominantly towards the upper part, thick-walled, dark brown to blackish stipe, paler towards the base, verrucose, rough, cylindrical. *Conidiogenous cells* 9.7–13 $\times$ 3.5–6.5 μ m ($\bar{x}$ = 11 $\times$ 5.1 μ m, n = 30), phialidic, subhyaline to brown, clavate, ampulliform, broadly fusiform. Conidial heads arising from conidiogenous cells, convex, round at the apex, blackish brown. *Conidia* 6.5–9.6 $\times$ 6.2–9.4 μ m ($\bar{x}$ = 7.8 $\times$ 7.6 μ m, n = 30), spherical, verrucose, brown to dark olivaceous brown, guttulated.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 30–40 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface white with brown margin, irregular in shape, smooth edges, raised at the center; reverse light brown with yellowish-orange tinge.

Material examined – China, Guizhou Province, Qingzhen City, Anliu Town, Yangpidong Scenic Area, 26°20'29.67" N, 106°21'15.26" E, altitude 707 m, on a decaying wood along the edge of a waterfall, 25 October 2024, L.L. Liu, 2024YPD4 (GMB5323, **holotype**); ex-type culture, GMBC5323; *ibid.*, KUN-HKAS 150441, isotype.

Additional specimens examined – China, Guizhou Province, Qingzhen City, Anliu Town, Yangpidong Scenic Area, 26°18'21.07" N, 106°19'19.77" E, altitude 765 m, on a decaying wood along the edge of a waterfall, 25 October 2024, L.L. Liu, 2024 YPD15 (GMB5334, GMBC5334).

Notes – In the phylogram (Fig. 38), *Memnoniella anliuensis* forms a clade in a sister relationship with *M. oblongispora*. The two species can be easily distinguished based on habitat, conidiophores and conidia size, and shape. *Memnoniella oblongispora* has been reported on decaying *Quercus* sp. leaves, with smaller, smooth conidiophores (85–180 μ m $\times$ 6.5–12 μ m) and smaller oblong-shaped conidia (8.5–12 $\times$ 4.5–7 μ m) (Lin et al. 2016). In contrast, *Memnoniella anliuensis* has been isolated from decaying wood and feature larger, verrucose conidiophores (80.5–255 $\times$ 4–6.5 μ m) and spherical conidia (6.5–9.6 $\times$ 6.2–9.4 μ m). Additionally, the conidiophores of *M. oblongispora* are hyaline at the base and olive grey at the apex, while *M. anliuensis* has conidiophores dark brown to blackish, becoming paler toward the base. Comparative analysis of nucleotide base pairs showed that *M. anliuensis* differs from *M. oblongispora* (MFLUCC 17-2064) by 1.2% (6/513) in the ITS locus, 2.2% (17/782) in the LSU locus, 0.1% (1/887) in the SSU locus, 0.8% (5/658) in the *tef1- α* gene, and 1.5% (11/752) in the *rpb2* gene.

Morphologically, *Memnoniella anliuensis* resembles *M. pseudonilagirica* and *M. chrysanthemi* in conidial shape. However, *M. pseudonilagirica* is distinguishable by its larger conidiophores (150–300 $\times$ 9–15 μ m) compared to those of *M. anliuensis* (80.5–255 $\times$ 4–6.5 μ m), larger and wider conidiogenous cells (13–20 $\times$ 6–11 μ m vs. 9.7–13 $\times$ 3.5–6.5 μ m for *M. anliuensis*) and larger conidia (14–23 $\times$ 12–22 μ m vs. 6.5–9.6 $\times$ 6.2–9.4 μ m for *M. anliuensis*) (Lombard et al. 2016). *Memnoniella chrysanthemi* differs by having shorter conidiophores (130–175 $\times$ 10–18 μ m) with smooth stipes hyaline at the base and dark brown to blackish at the apex and larger conidia 12–18 μ m in diameter (Habib et al. 2025).

Based on these morphological differences and the phylogeny, we introduce *Memnoniella anliuensis* as a new species.

Parasympodiellales Hern.-Rest., Gené, R.F. Castañeda & Crous, Stud. Mycol. 86: 87 (2017).

Parasympodiellaceae Hern.-Rest., Gené, Guarro & Crous, Stud. Mycol. 86: 87 (2017).

Parasympodiella Ponnappa, Trans. Br. mycol. Soc. 64(2): 344 (1975).

Notes – *Parasympodiella* was established by Ponnappa (1975), with *P. laxa* as the type species. The genus is characterized by single conidiophores that bear terminal and intercalary, integrated, indeterminate, sympodially extending conidiogenous cells. These cells produce catenate, cylindrical, thallic conidia through the disarticulation of the fertile hyaline branches (Ponnappa 1975, Li et al. 2014). Species of *Parasympodiella* are primarily saprobic, found on leaves, wood, and twigs. According to Species Fungorum (accessed 2 July 2025), the genus currently comprises 11 accepted species.

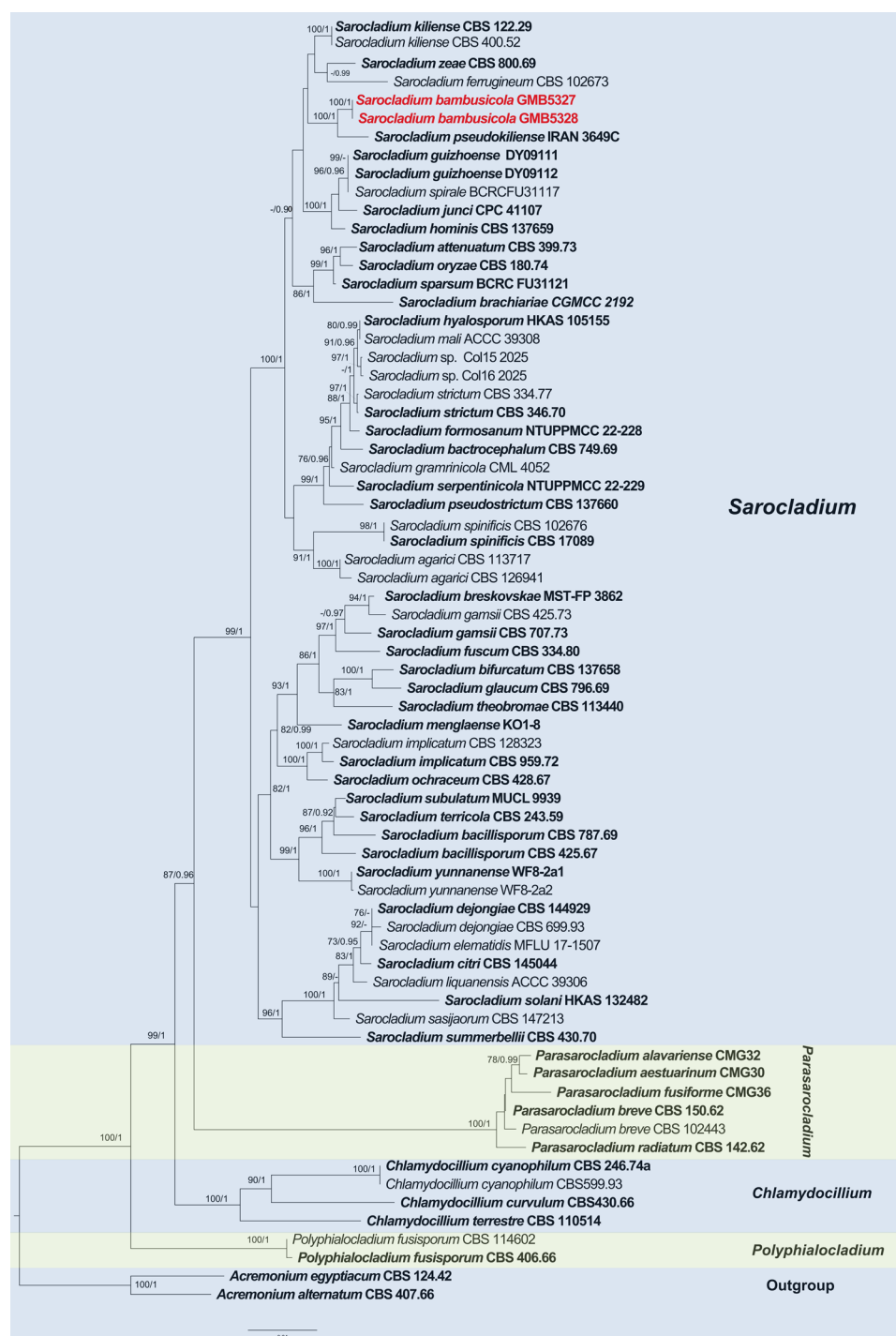


Figure 36 – ML tree of genus *Sarocladium* and related taxa based on ITS, LSU and *tef1-α* loci. The alignment for this tree includes 2080 bp (ITS:1–489; LSU: 490–1272; *tef1-α*: 1273–2080).

Acremonium egyptiacum (CBS 124.42) and *A. alternatum* (CBS 407.66) were selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly described species is marked red in bold. Ex-type/type strains are indicated in black bold.



Figure 37 – *Sarocladium bambusicola* (GMB5327, holotype). a–c Colonies on bamboo. d–f Conidiophores and conidia. g Conidiogenous cells and conidia. h Germinated conidium.

i–m Conidia. n Surface view of culture on PDA. o Reverse view of culture on PDA. Scale bars: a, b = 0.5 mm, c = 0.2 mm, d, e = 100 µm, f–h = 20 µm, i–m = 5 µm.

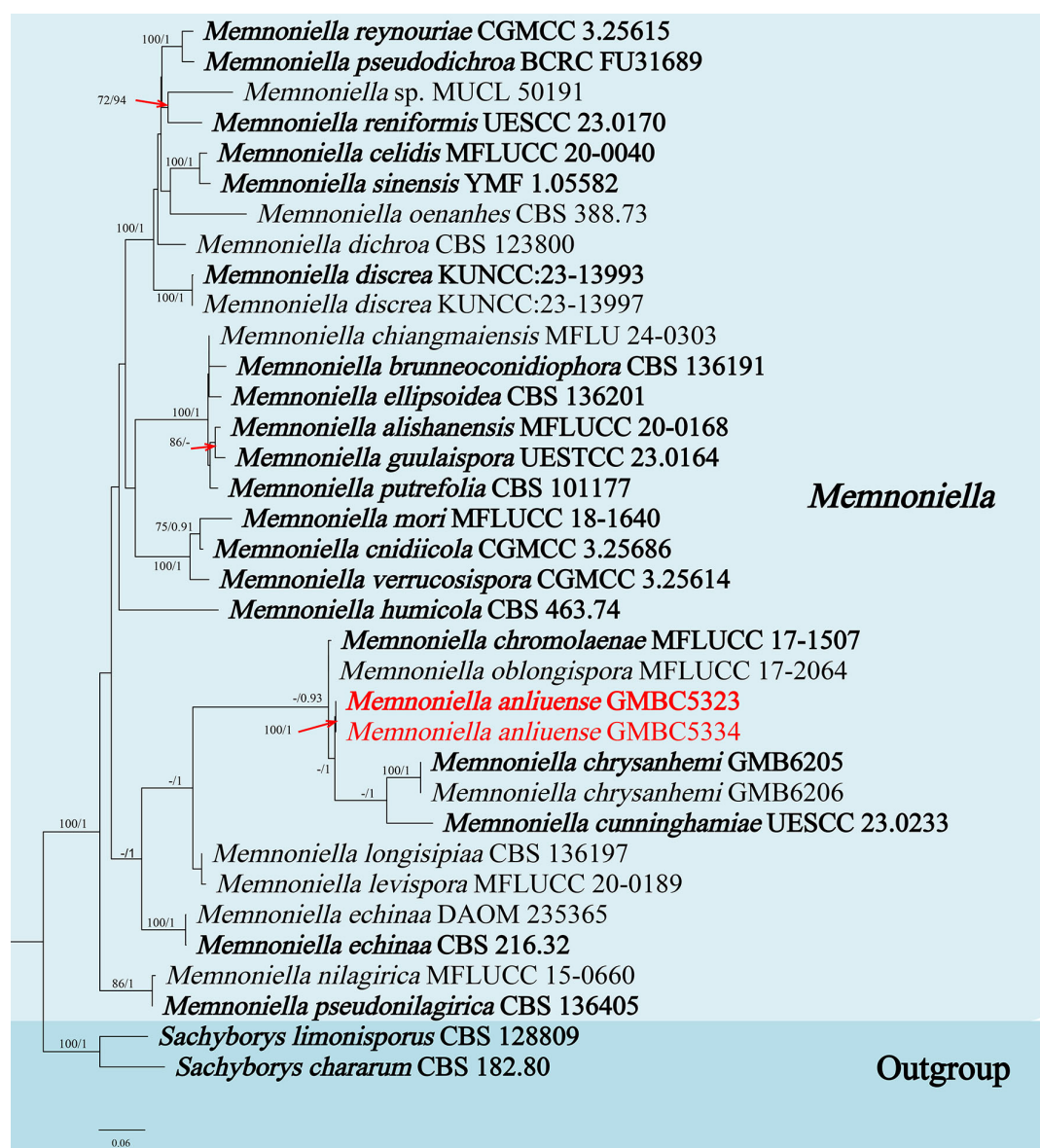


Figure 38 – ML tree of *Memnoniella* species based on ITS, *rpb2*, *tef1-a* and *tub2* loci. The alignment for this tree includes 2139 bp (ITS:1–590 bp; *rpb2*: 595–1315 bp; *tef1-a*: 1320–1787 bp; *tub2*: 1792–2139 bp). *Stachybotrys limonisorus* (CBS 128809) and *S. chartarum* (CBS 182.80) was selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly described species are marked red in bold. Ex- type/type strains are indicated in black bold.

Parasymphodiella cryptomeriae W.H. Tian, K.D. Hyde & Maharachch., Mycosphere 15(1): 1794–1900 (2024). (Fig. 41)

Description – *Saprobic* on decaying wood in a freshwater wetland. Teleomorph: Undetermined. Anamorph: Hyphomycetous. Mycelium consisting of branched, septate, smooth, hyaline to dark brown. *Conidiophores* 113.3–410.2 $\times$ 4.9–10.1 µm ($\bar{x}$ = 313.6 $\times$ 7.2 µm, n = 25), macronematous, mononematous, erect, solitary, scattered, unbranched, cylindrical, septate; sterile part dark brown to black, thick-walled, 7–15 septa; fertile part brown, becoming paler toward the apex. *Conidiogenous cells* 43.5–56.0 $\times$ 5.0–8.6 µm ($\bar{x}$ = 49.1 $\times$ 6.7 µm, n = 25), holoblastic, terminal and intercalary, integrated, indeterminate, sympodial proliferation, smooth, pale brown to

brown, becoming hyaline toward the apex, between conidiogenous loci. *Conidia* $26.8\text{--}56.1 \times 4.9\text{--}8.6\ \mu\text{m}$ ($\bar{x} = 45.2 \times 7.8\ \mu\text{m}$, $n = 30$), hyaline, dry, smooth, thallic-arthric, forming in loose unbranched chains, becoming verruculose with age, guttulate, thin-walled, cylindrical, 0–4-septate, apex and base of intercalary conidia truncate, apical conidia with obtuse or rounded apex, occurring in unbranched conidial chains.

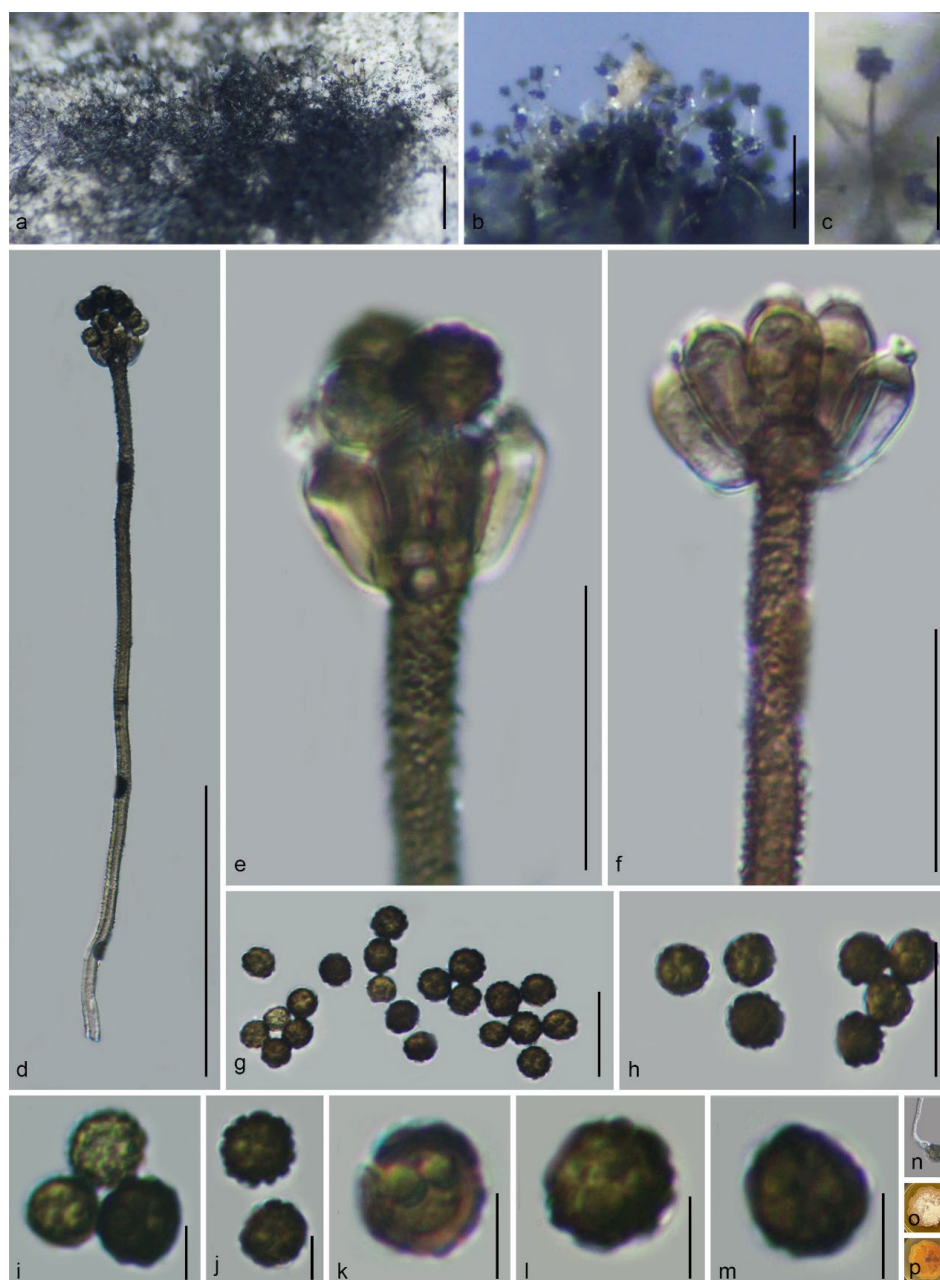


Figure 39 – *Memnoniella anliuensis* (GMB5323, holotype). a-c Colony on wood. d Conidiophores and conidia. e, f Conidiogenous cells and conidia. g-m Conidia. n Germinated conidium. o Surface view of culture on PDA. p Reverse view of culture on PDA. Scale bars: a = 0.5 mm, b = 0.2 mm, c = 0.1 mm, d = 50 μm , e-h = 20 μm , i-n = 5 μm .

Culture characteristics – Conidia germinated and formed germ tubes within 36 hrs on WA. Colonies on PDA reaching 40–50 mm diam., after 2 weeks at 24–27°C on PDA. Colony surface white, velvety, fluffy; reverse dark.

Materials examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'21.770"N, 104°00'19.121"E, altitude 1419 m, on a decaying wood in a freshwater wetland, 12 October 2024, L.L. Liu, 2024WMS238 (GMB5312, GMBC5312).

Additional specimens examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'29.79"N, 104°00'05.548"E, altitude 1371 m, on a decaying wood in a freshwater wetland, 12 October 2024, L.L. Liu, 2024WMS279 (GMB5321, GMBC5321).

Notes – Phylogenetically (Fig. 40), our isolates (GMBC5312, GMBC5321), cluster with *Parasymphodiella cryptomeriae*. Morphology of our collection also aligns with the original description of *P. cryptomeriae* (Tian et al. 2024). This species was previously reported on the leaves of *Cryptomeria japonica*, but in our study, it was found growing on twigs in a freshwater habitat. Given the morphological similarity to the original taxon, we identify our collection as *P. cryptomeriae* (Tian et al. 2024). This finding represents a new record for Yunnan Province, China, and documents a new substrate for the species, suggesting a wider geographical and ecological distribution than previously known.

Pleurotheciales Réblová & Seifert, Persoonia 37: 63 (2015).

Pleurotheciaceae Réblová & Seifert, Persoonia 37: 63 (2015).

Pleurothecium Höhn., Ber. dt. bot. Ges. 37: 154 (1918) (1919).

Notes – *Pleurothecium* is a genus of terrestrial and freshwater fungi, typified by *Pleurothecium recurvatum* (Fernández et al. 1999, Réblová et al. 2016, Long et al. 2023). The genus was first introduced by Höhnelt (1919) to accommodate *P. recurvatum* (Morgan) Höhn (Goos 1969). Fernández et al. (1999) introduced the teleomorphic genus *Carpoligna* and linked it to *Pleurothecium*. However, Réblová et al. (2016) recommended using *Pleurothecium* instead of *Carpoligna*, citing its priority and greater species diversity. According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 18 accepted species.

Pleurothecium lignicola C.Y. Xu, H.Y. Song & D.M. Hu, Mycosphere 16(2): 225–234 (2025). (Fig. 43)

Description – *Saprobic* on submerged decaying wood in a freshwater wetland. Teleomorph: undetermined. Anamorph: *Colonies* on the decaying wood superficial, effuse, solitary, black, with white conidial masses aggregated at apex. *Mycelium* partly immersed, partly superficial, consist of branched, septate, smooth-walled, brown hyphae. *Conidiophores* 216–496 × 3–11 µm ($\bar{x}$ = 368.5 × 4.5 µm, n = 30), macronematous, mononematous, erect, straight or slightly sinuous, mostly unbranched, rarely branched, septate, smooth, cylindrical, dark brown, becoming pale brown to subhyaline towards the apex. *Conidiogenous cells* holoblastic, polyblastic, terminal, integrated, smooth-walled, cylindrical to tapered, pale brown to subhyaline, sympodial, with narrow, cylindrical denticles, denticles, 1.0–2.6 × 0.8–1.9 µm ($\bar{x}$ = 1.8 × 1.3 µm, n = 30), *Conidia* 17–22 × 5–7 µm ($\bar{x}$ = 20.5 × 6.5 µm, n = 30), acrogenous, solitary, straight or slightly sinuous, ellipsoidal to clavate, rounded at apex, obtuse to tapered towards base, 3-septate, hyaline, guttulate.

Culture characteristics – Conidia germinated within 12 hours on PDA. Colonies on PDA reaching 1–2.5 cm diam., after 4 weeks at 24–27°C on PDA. Colony surface blackish-brown, light brown at margin, circular, arc-shaped edges, raised at the center; reverse blackish at center to whitish grey toward edges.

Material examined – China, Guangxi Zhuang Autonomous Region, Cenwang Laoshan National Nature Reserve, 24°17'5.04"N, 106°13'51.25"E, altitude 1583 m, on dead branches of an unknown plant in a freshwater wetland, collected on 2 August, 2024, Qin-Fang Zhang 2024 CWLS47 (GMB5137, GMBC5137); China, Guangxi Zhuang Autonomous Region, Cenwang Laoshan National Nature Reserve, 24°17'0.66"N, 106°13'54.58"E, altitude 1699 m, on dead branches of an unknown plant in a freshwater wetland, collected on 2 August, 2024, Qin-Fang Zhang 2024 CWLS89 (GMB5143, GMBC5143).

Notes – The isolate from our collection, GMB5137, shows 99.9% similarity to the type isolates of *Pleurothecium lignicola*. Morphologically, it aligns with the original description and ecological characteristics of *P. lignicola*, except for the longer conidiophores observed in our collection (216–496 µm compared to 154–280 µm) (Xu et al. 2025). It has previously been reported

from Yunnan Province, China, this is the second report of this taxon from a new locality in Guangxi Zhuang Autonomous Region, extending its known geographical distribution.

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

Pleurotheciales Réblová & Seifert, *Persoonia* 37: 63 (2015).

Pleurotheciaceae Réblová & Seifert, *Persoonia* 37: 63 (2015).

Phragmocephala E.W. Mason & S. Hughes, Naturalist (Hull), ser. 3, 1951: 97 (1951).

Notes – The hyphomycetous genus *Phragmocephala* is typified by *P. elliptica* (basionym: *Monotospora elliptica*), originally described from dead herbaceous substrates (Mason & Hughes 1951). The taxonomic position of this genus remains unresolved. Initially, Su et al. (2015) placed it in the family *Melanommataceae* (*Dothideomycetes*), but more recently in a fungal outline, Hyde et al. (2024) classified it within the *Pleurotheciaceae* (*Pleurotheciales*, *Savoryellomycetidae*). Its diagnostic characters include macronematous, mononematous, erect and typically straight conidiophores terminating in a single, integrated holoblastic conidiogenous cell (Whitton et al. 2012). The phragmo conidia are typically ellipsoidal, blastic, solitary, 3–6 septate, seceding with a portion of conidiogenous cell by rupture of the wall, immediately below the base of the conidium (Mason & Hughes 1951). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 10 accepted species. However, molecular sequence data is not available for most taxa. Herein, we introduce a new species of *Phragmocephala* discovered on submerged decaying wood in a freshwater habitat.

Phragmocephala wuliangshanensis Q.F. Zhang, K. Habib & Q.R. Li, *sp. nov.* (Fig. 45)

Mycobank No.: MB859986

Etymology – The epithet refers to Wuliangshan National Nature Reserve, where the holotype was collected.

Description – *Saprobic* on submerged decaying wood along the stream. Teleomorph: undetermined. Anamorph: *Mycelium* partly immersed, composed of septate, dark brown, branched, smooth, 2.8–4.2 μm wide *hyphae*. *Conidiophores* 92–152 $\times$ 3–7 μm ($\bar{x}$ = 112 $\times$ 4.6 μm , n = 30), synnematos, macronematous, septate, erect, in fascicles, unbranched, dark brown at the base, pale brown at fertile, flared apex, sometimes proliferating, 7–12-septate. *Conidiogenous cells* 18–41 $\times$ 4–8 μm ($\bar{x}$ = 30.3 $\times$ 5.8 μm , n = 30), monoblastic, terminal, integrated, pale brown. *Conidia* 27–33 $\times$ 14–17 μm ($\bar{x}$ = 30.7 $\times$ 15.8 μm , n = 30), 3–4-septate, ellipsoidal to subglobose, middle cells dark brown to black, pale brown at apical and basal cells, with a thick dark band on the central septum; smooth, rounded at apex, truncate at base; conidial secession schizolytic.

Culture characteristics – Conidia germinate within 12 WA. Colonies on PDA reaching 20–30 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface pale white, pale brown at edges, with dense mycelium, irregular, flat; reverse dark brown to black.

Material examined – China, Yunnan Province, Wuliangshan National Nature Reserve, 24°12'48.12"N, 101°13'28.44"E, altitude 1800 m, on submerged dead wood along the stream, collected on 2 August, 2024, Qin-Fang Zhang 2024 WLSY96-1 (GMB5134, **holotype**); ex-type culture, GMBC5134; *ibid.*, KUN-HKAS 150432, isotype.

Additional specimens examined – China, Yunnan Province, Wuliangshan National Nature Reserve, 24°12'45.92"N, 101°13'24.32"E, altitude 1832 m, on submerged dead wood along the stream, collected on 2 August 2024, Qin-Fang Zhang 2024 WLSY906B (GMB5135; GMBC5135).

Notes – *Phragmocephala wuliangshanensis* is characterized by 7–12-septate conidiophores (92–152 $\times$ 3–7 μm) and smaller conidia (27–33 $\times$ 14–17 μm) with 3–4 septa. Morphologically, *P. wuliangshanensis* resembles *P. agapanthi*, *P. atra*, and *P. garethjonesii* in conidiophore and conidial morphology. However, it is readily distinguished from these species by differences in conidial and conidiophore dimensions, and number of septa.

Phragmocephala agapanthi differs from *P. wuliangshanensis* by having been found on dead flower stalks of *Agapanthus praecox*, shorter conidiophores (40–80 $\times$ 6–8 μm vs. 92–152 $\times$ 3–7 μm) with 3–6 septa and slight smaller conidia (25–30 $\times$ 15–18 μm vs. 27–33 $\times$ 14–17 μm) with 3–

5 septa (Crous et al. 2024). *Phragmocephala atra* is distinguished by its slightly longer conidiophores (128–157 µm) with 4–8-septa, and 4-septate, slight larger conidia (30–35 × 15–18 µm) (Su et al. 2015). In the BLAST search, the ITS region showed the closest match to *Phragmocephala atra* (LCGS09) with 93.8% similarity, while the LSU region showed 98.9% similarity to the same strain. *Phragmocephala garethjonesii* differs through its larger conidiophores (163.5–199.5 µm) with 4–6-septa and broader conidia (28–35 × 16.5–20.5 µm) with 5–6 septa (Su et al. 2015).

The type species, *P. elliptica*, differs by occurring on dead herbaceous hosts and producing larger conidia (36–41 × 18–21.5 µm). Its conidia contain two or more longitudinally arranged pale brown to hyaline cells, absent in *P. wuliangshanensis* (Su et al. 2015).

Phylogenetically (Fig. 44), *P. wuliangshanensis* also forms an independent clade, indicates clear molecular differences, strongly supporting its recognition as an undescribed species. Therefore, we introduce *P. wuliangshanensis* as a new species in the genus *Phragmocephala*.

Savoryellales Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones, Mycologia 103 (6): 1368 (2011).

Savoryellaceae Jaklitsch & Réblová, in Jaklitsch, Index Fungorum 209: 1 (2015).

Bactrodesmium Cooke, Grevillea 12(no. 61): 35 (1883).

Notes – The hyphomycetous genus *Bactrodesmium* was proposed by Cooke (1883) to accommodate *Sporidesmium abruptum* and *S. spilomeum*, although Cooke did not formally make the nomenclatural combinations. Hughes (1958) later designated *B. abruptum* as the lectotype species and introduced new combinations. Saccardo (1886) attempted to reduce *Bactrodesmium* to synonym under *Clasterosporium*, but this was not accepted by subsequent mycologists like Ellis (1959) and Zhang et al. (2016). Species of *Bactrodesmium* occur mostly on decaying wood and bark, though some are found on living (*B. mastigophorum*) or fallen leaves (*B. peruvianum*, *B. novaegeronense*) or unusual substrates like paper (*B. papyricola*) (Réblová et al. 2020). Morphologically, the genus is characterized by brown to black sporodochial conidiomata, often appearing as small, shiny, spiky piles. Conidiophores are macronematous or semi-macronematous and mononematous (rarely synnematous). Conidia are produced holoblastically, phragmosporous or dictyosporous, euseptate or distoseptate (sometimes with bands or pores at the septa), range in colour from subhyaline to golden, brown, olive brown, or black, and show highly variable shapes (subglobose, pyriform, clavate, obovoid, ellipsoidal, fusiform, cylindrical). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 45 accepted species. In this study, we introduce a new species of the genus found on a decaying wood in a freshwater lake.

Bactrodesmium wumengense L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 47)

MycoBank No.: MB859973

Etymology – The epithet refers to Wumeng Mountain National Nature Reserve, where the holotype was collected.

Description – On dead wood in a freshwater lake. Teleomorph: unknown. Anamorph: Colonies on natural substrate effuse, sporodochial, 0.1–0.4 mm diam., black, shiny, scattered, superficial, black, pulvinate, punctiform. Mycelium immersed in the substrate, septate, hyaline to brown. Hyphae 2.5–4.3 µm wide. Conidiophores, macronematous, fasciculate, arising from basal hyphae, septate, hyaline to brown, branched, 2.9–5 µm wide near the base. Conidiogenous cells 3.9–12.5 × 2.5–8.6 µm ($\bar{x}$ = 7.2 × 5.2 µm, n = 30), terminal, hyaline, integrated, monoblastic, cylindrical, slightly broadening towards the apex, thin-walled. Conidia 26–64.5 × 14.5–19.5 µm ($\bar{x}$ = 46.8 × 16.9 µm, n = 30), clavate or ellipsoidal-clavate, rounded to narrowed at the apex, truncate at the base, 3–6-septate, smooth, with a conspicuous blackish central pore at the septa and a large guttule at each cell, brown to dark brown, paler towards the base, basal cell subhyaline to pale brown.

Culture characteristics – Conidia germinated and formed germ tubes within 36 hours on WA. Colonies on PDA reaching 5–10 mm diam., after 8 weeks at 24–27°C on PDA. Colony surface

gray, with densely mycelium, circular, thick, entire, velvety, smooth edges, raised at the center; reverse black.

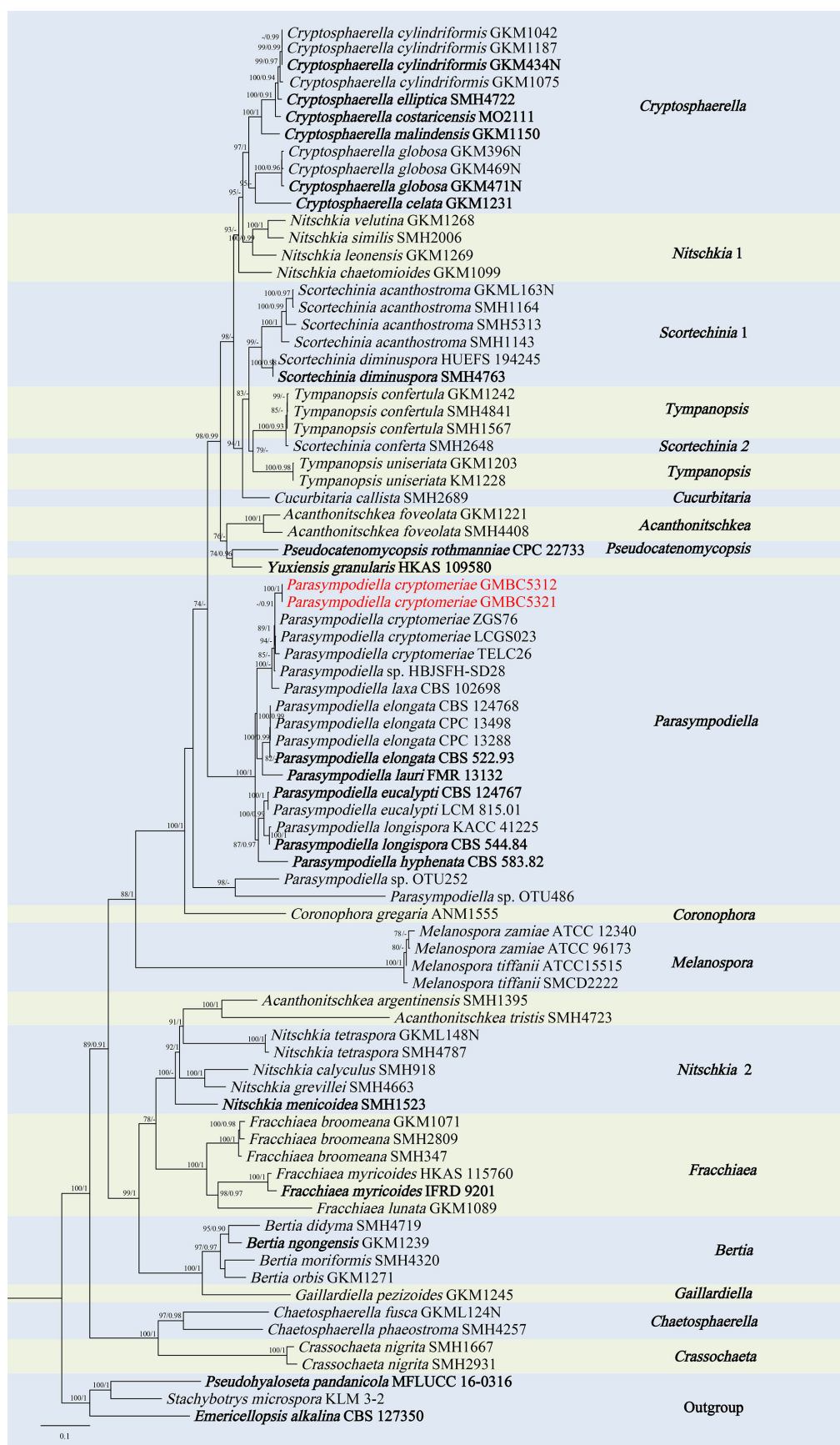


Figure 40 – ML tree of *Parasymphodiella* and related taxa based on ITS, LSU, *tef1-α* and *rpb2* loci. The alignment for this tree includes 3427 bp (ITS:1–539 bp; LSU:544–1572 bp; *tef1-α*:1577–2313 bp; *rpb2*:2318–3427 bp). Of these characters. *Emericellopsis alkaline* (CBS 127350), *Pseudohyaloseta pandanicola* (MFLUCC 16-0316) and *Stachybotrys microspore* (KLM 3-2) were selected as the outgroup taxa. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly generated sequences are marked red. Ex-types are indicated in black bold.



Figure 41 – *Parasymphodiella cryptomeriae* (GMB5321). a, b Colonies on wood. c–e Conidiophores and conidia. f Conidiogenous cells and conidia. g–k Conidia. l Germinated conidium. m Surface view of culture on PDA. n Reverse view of culture on PDA. Scale bars: a, b = 0.5 mm, c–e = 100 μ m, f = 50 μ m, g–l = 20 μ m.

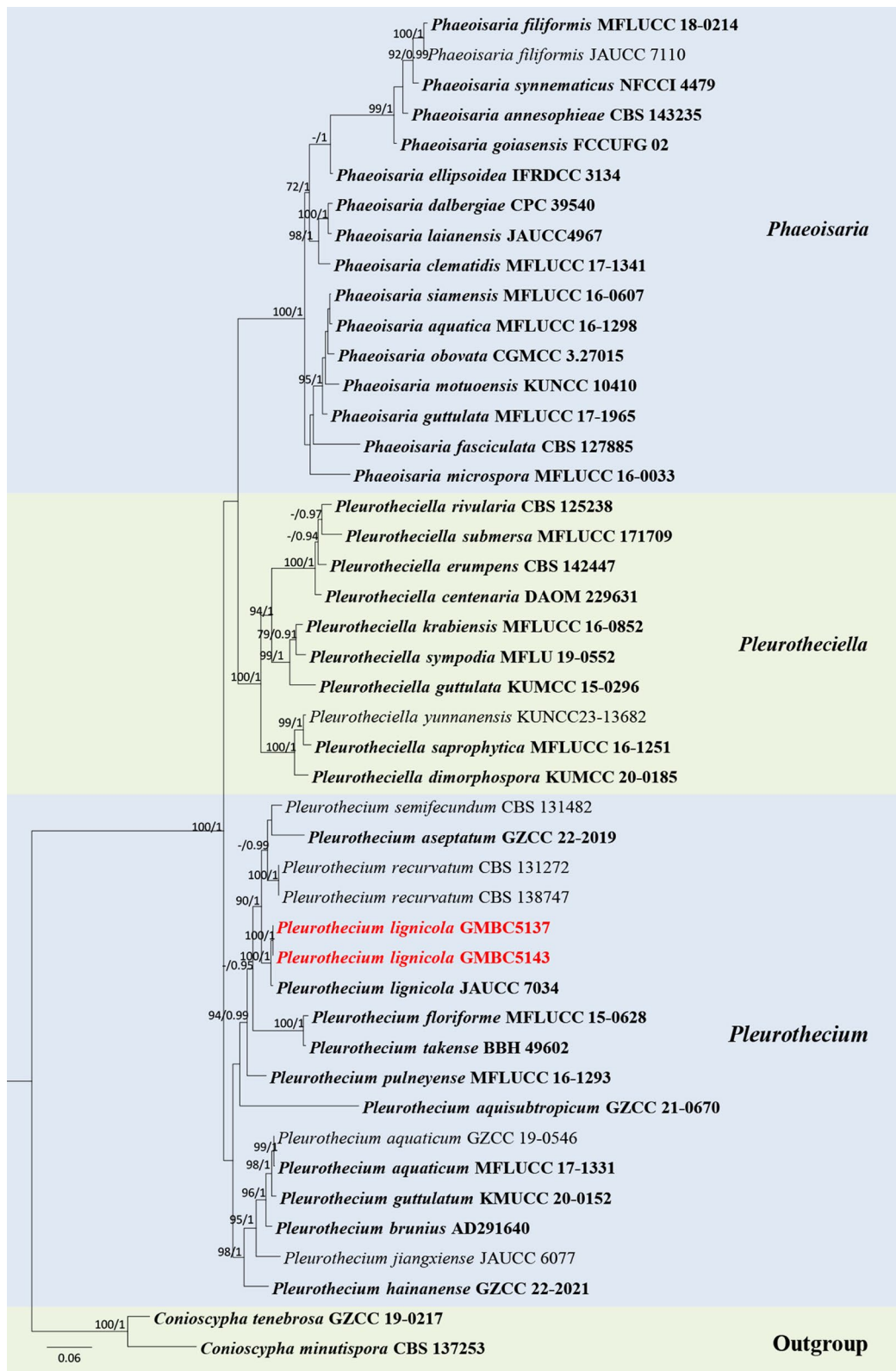


Figure 42 – ML tree of genus *Pleurothecium* and related taxa based on ITS, LSU, SSU and *rpb2* loci. The alignment for this tree includes 3353 bp (ITS:1–510; LSU: 511–1359; SSU: 1360–2324; *rpb2*: 2325–3353). *Conioscypha minutispora* (CBS 137253) and *C. tenebrosa* (GZCC 19-0217) were selected as the outgroup taxa. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly generated sequences are marked red. Ex-type/type strains are indicated in black bold.

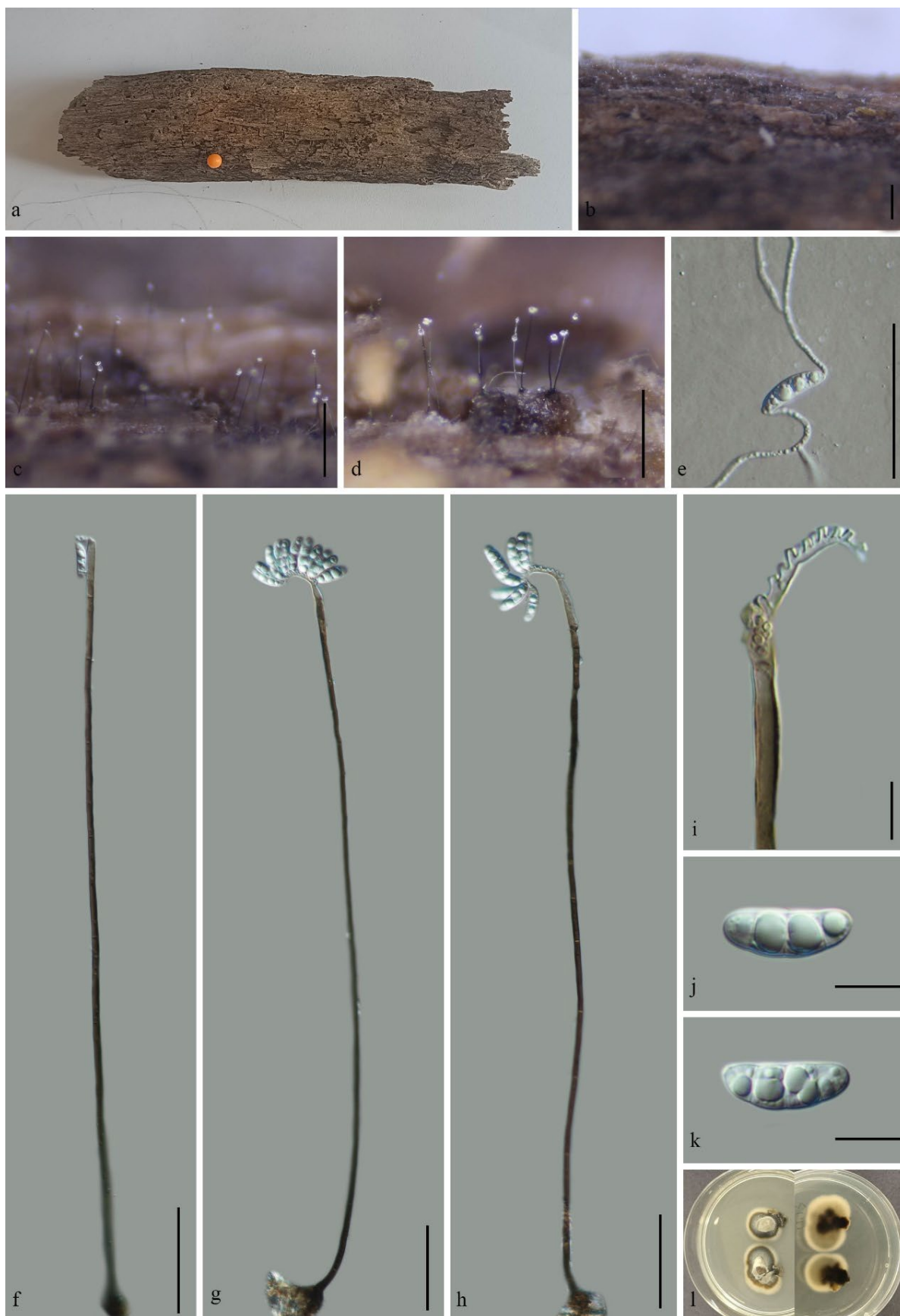


Figure 43 – *Pleurothecium lignicola* (GMB5137). a–d Colony on on natural substratum. e Germinating conidium. f–h Conidiophores and Conidia. i Conidiogenous cells. j–k Conidia. l Surface and reverse view of culture on PDA. Scale bar: b = 1 mm, c, d = 0.5 mm, e–h = 50 μ m, i–k = 10 μ m.

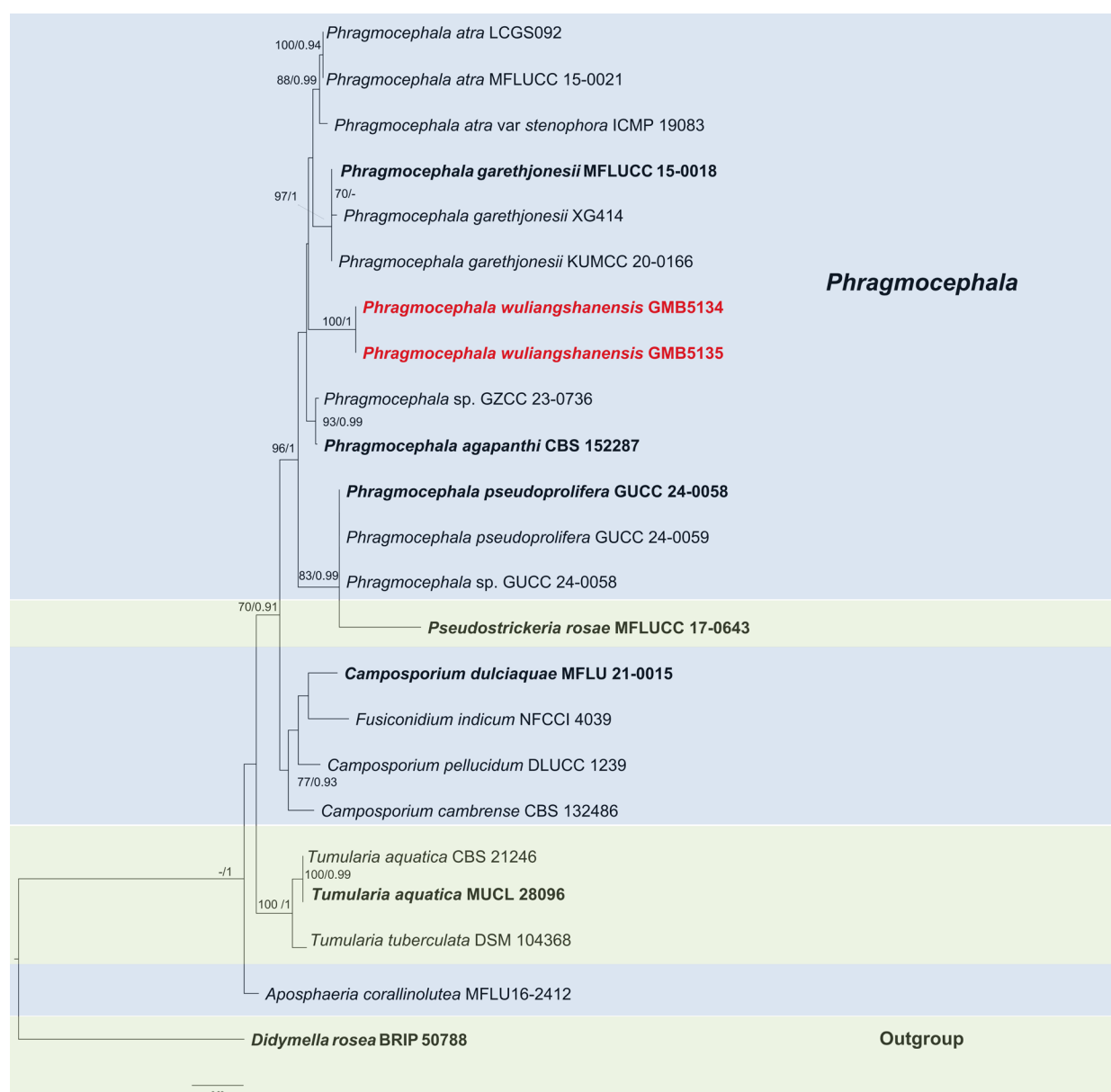


Figure 44 – ML tree of genus *Phragmocephala* and related taxa based on ITS and LSU loci. The alignment for this tree includes 1294 bp (ITS:1–461; LSU: 462–1294). *Didymella rosea* (BRIP 50788) was selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAXML $\geq 70\%$ are shown on the branches. The newly generated sequences are marked red in bold. Ex-type/type strains are indicated in black bold.

Material examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'21.770"N, 104°00'19.121"E, altitude 1419 m, on a decaying wood in a lake, 12 October 2024, L.L. Liu, 2024WMS256 (GMB5329, **holotype**); ex-type culture, GMBC5329; *ibid.*, KUN-HKAS 150440, isotype.

Additional specimens examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19'21.235"N, 104°00'19.132"E, altitude 1414 m, on a decaying wood in a lake, 15 October 2024, L.L. Liu, 2024WMS272 (GMB5330; GMBC5330).

Notes – Morphologically and phylogenetically (Fig. 46), *Bactrodesmium wumengense* is closely related to *B. leptopus*, both share similar conidia and conidiophore shapes. However, *B. leptopus* can be distinguished from *B. wumengense* by its smaller conidia with less septa. According to the original description by Saccardo (1886), *B. leptopus* has the conidia of 30–40 $\times$ 15–20 μm with 3–5 septa. Hughes & White (1983), who examined the holotype material in different stages, reported distinct conidial measurements corresponding to their septation, 23.4–

29.7 × 11.7–16.2 µm for 3-septate conidia, 23.4–41.5 × 10.8–18 µm for 4-septate conidia, and 32–47 × 11.7–16.2 µm for 5-septate conidia. Réblová et al. (2020) described *B. leptopus* with slightly smaller conidia (25.5–36 × 9–12.5 µm) that possess also 3–5-septate. In contrast, the new species, *B. wumengense*, has larger conidia (26–64.5 × 14.5–19.5 µm) with 3–6 septa. Comparative analysis of nucleotide base pairs showed that *B. wumengense* differs from *B. leptopus* (CBS 144542) by 9.0% (49/545) in the ITS locus, 0.5% (4/885) in the LSU locus, 5.4% (52/961) in the *tef1-α* gene, and 15.5% (177/1142) in the *rpb2* gene.



Figure 45 – *Phragmocephala wuliangshanensis* (GMB5134 holotype). a Host. b–d Colonies on host surface. e Germinating conidium. f–h Conidiophores and conidia. i Conidiogenous cells with conidia. j–k Conidia. l Surface and reverse view of culture on PDA. Scale bars: b = 1 mm, c, d = 0.5 mm, e, i–k = 10 µm, f–h = 50 µm.

In the key provided by Réblová et al. (2020), *Bactrodesmium wumengense* keys out closer to *B. diversum*, *B. pallidum*, *B. spilomeum*, and *B. nothofagi*. However, these taxa differ in conidial dimensions and septation. *Bactrodesmium diversum* possesses smaller conidia ($27\text{--}52.5 \times 14\text{--}20.5 \mu\text{m}$) with 3–5 septa. *Bactrodesmium pallidum* has 4–6-septate conidia ($29\text{--}57 \times 9\text{--}13 \mu\text{m}$) which taper toward the apex. *Bactrodesmium spilomeum* is characterized by 3–5-septate conidia, $24\text{--}43 \times 8.5\text{--}11 \mu\text{m}$ in size, with a rounded apex. *Bactrodesmium nothofagi* produces larger conidia ($47\text{--}55 \times 18\text{--}25 \mu\text{m}$) with 5–8 septa. Phylogenetically also, *B. diversum* and *B. pallidum* cluster distantly from *B. wumengense*. Based on these morphological differences and phylogeny, we propose *B. wumengense* as a new species.

Chaetosphaeriales Huhndorf, Mill. & Fernández, Mycol. Res. 108 (12): 378 (2004).

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels, Sydowia 51: 56 (1999).

Chloridium Link, Mag. Neuesten Entdeck. Gesamten Naturk. Ges. Naturf. Freunde Berlin 3 (1): 13 (1809).

Notes – *Chloridium* is a genus of dematiaceous hyphomycetes inhabiting soil and wood. Link (1809) introduced the genus with the single species *Chloridium viride*, characterized by pigmented, unbranched, erect, caespitose conidiophores bearing aseptate, hyaline, globose conidia that adhere in a green mass at the tip (Réblová et al. 2022). Traditionally, *Chloridium* species were considered primarily wood-inhabiting fungi, typically found on wood in later stages of decay or on other plant debris (Gams & Holubová-Jechová 1976). However, culture studies (Domsch et al. 2007) revealed their common presence in soil. Data mining studies by Réblová et al. (2022) revealed that over 87% of *Chloridium* samples originated from various soil types, including bulk, top, and rhizosphere soils. They reported that 55.4% of all samples in GlobalFungi were sourced from these soils, suggesting that *Chloridium* can be classified as a soilborne fungus. According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 59 accepted species. In this study, we report a new species of the genus, found growing on decaying twigs in a freshwater environment.

Chloridium chlamydosporum (J.F.H. Beyma) S. Hughes, Canad. J. Bot. 36(6): 748 (1958). (Fig. 49)

Description – *Saprobic* on decaying wood in a freshwater wetland. Teleomorph: undetermined. Anamorph: *Colonies* composed of light-colored conidial heads, hairy, white to transparent heads, brown in mass, solitary or in groups of 2–5. *Conidiophores* $144.5\text{--}260.5 \times 2.7\text{--}6.2 \mu\text{m}$ ($\bar{x} = 216 \times 4.6 \mu\text{m}$, $n = 20$), macronemtous, multiseptate, dark brown slightly paler towards apex, sub-cylindrical to cylindrical, slightly bulbous or lobate base, erect, straight or slightly flexuous, unbranched. *Conidiogenous cells* $5.5\text{--}9.5 \times 1.3\text{--}2.5 \mu\text{m}$ ($\bar{x} = 6.6 \times 1.8 \mu\text{m}$, $n = 20$), monophialidic with one or two conidiogenous loci, integrated, terminal, extending percurrently sometimes sympodial, cylindrical to subcylindrical, pale brown to subhyaline, slightly funnel-shaped. *Conidia* $3\text{--}4.5 \times 1.4\text{--}2.5 \mu\text{m}$ ($\bar{x} = 3.8 \times 1.9 \mu\text{m}$, $n = 20$), obovate to ellipsoidal-obovate, pale brown upon ageing, aseptate, smooth, accumulating in slimy whitish heads, sometimes slightly tapering and truncate at the base, hyaline, thin-walled.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 20–30 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface light brown to greyish white, circular, smooth edges, raised at the center; reverse grayish-brown.

Material examined – China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19′21.770″N, 104°00′19.121″E, altitude 1419 m, on a decaying wood in a freshwater wetland, 7 October 2024, L.L. Liu, 2024WMS106 (GMB5326, GMBC5326); China, Yunnan Province, Zhaotong City, Wumeng Mountain National Nature Reserve, 28°19′29.79″N, 104°00′05.548″E, altitude 1371 m, on a decaying wood in a freshwater wetland, 7 October 2024, L.L. Liu, 2024WMS137 (GMB5331, GMBC5331).

Note – Phylogenetically (Fig. 48), the sequence of our collection clustered with *Chloridium chlamydosporum* (ML/B1 = 100 %/1). This species primarily inhabits soil but has also been

documented on decaying wood of *Quercus petraea*, and other unidentified hosts, as well as on the needles of *Abies firma* (Réblová et al. 2022). *Chloridium chlamydosporum* is characterized by solitary, brown, unbranched conidiophores that form a single layer, obovate to ellipsoidal-obovate conidia accumulating in slimy whitish heads, and mostly lateral, sessile, globose chlamydospores (Réblová et al. 2022). The morphological characteristics of our collections agree with those of *C. chlamydosporum* as described by Hughes (1958). This study reports it as a new record for China.

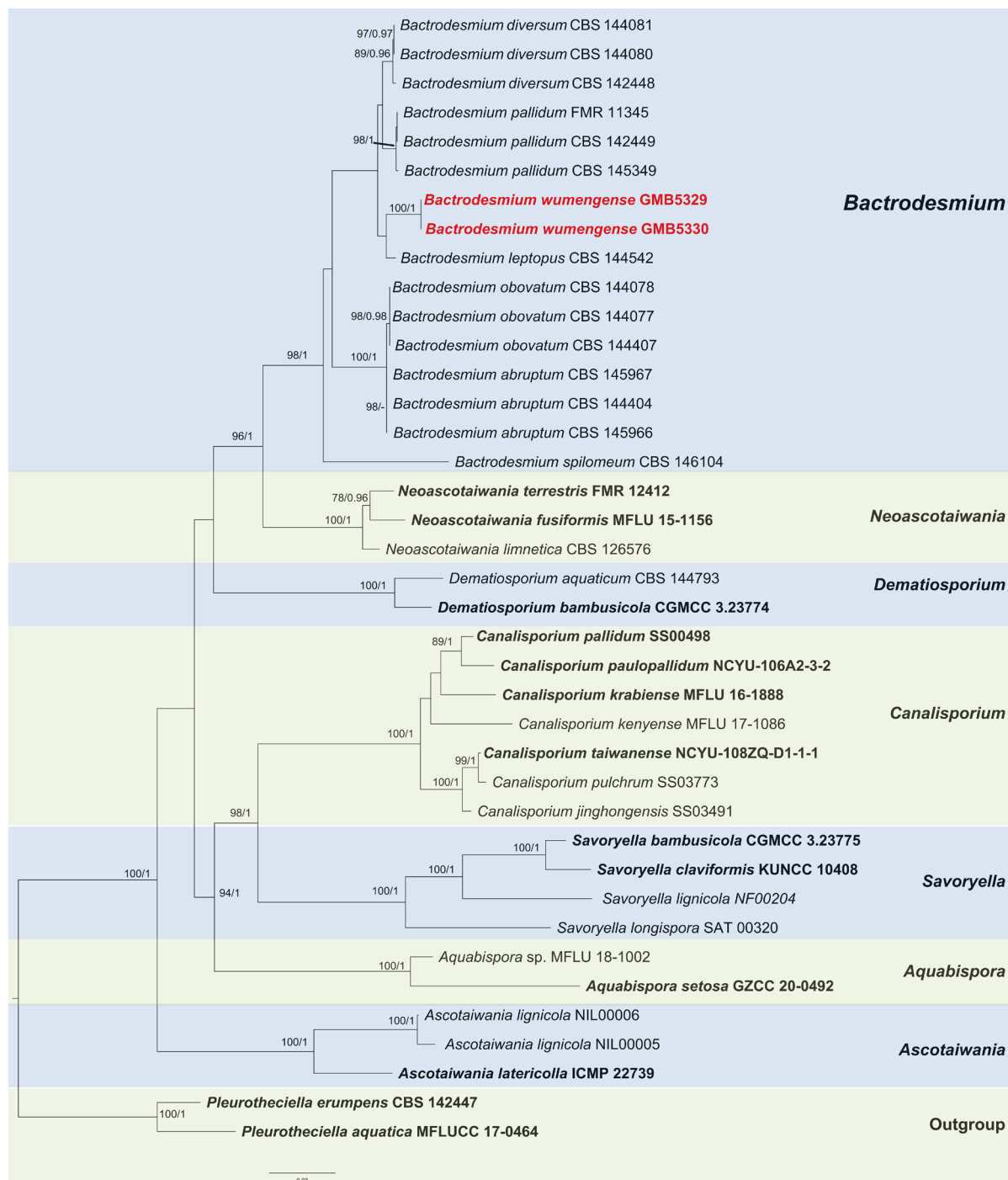


Figure 46 – RAxML tree based on analysis of a combined LSU, SSU, and ITS sequences for *Savoryellaceae*. The alignment for this tree includes 2599 bp (ITS:1–497; LSU: 498–1641; SSU: 1642–2599). *Pleurotheciella aquatica* (MFLUCC 17-0464) and *P. erumpens* (CBS 142447) were selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly described species are marked red in bold. Ex-type/type strains or specimen are indicated in black bold.



Figure 47 – *Bactrodesmium wumengense* (GMB5329, holotype). a–c Colonies on wood. d–g Conidiophores and conidia. h Conidiogenous cells and conidia. i–n Conidia. o Germinate conidium. p, q Surface and reverse view of culture on PDA. Scale bars: a = 0.5 mm, b, c = 0.2 mm, d, e = 50 μ m, f–o = 20 μ m.

Chloridium fuscum (Corda) Réblová & Hern.-Restr., in Réblová, Hernández-Restrepo, Sklenář, Nekvindová, Réblová & Kolařík, Stud. Mycol. 103: 176 (2022). (Fig. 50)

Description – *Saprobic* on decaying wood in a freshwater wetland. Teleomorph: Undetermined. Anamorph: *Colonies* on natural substratum effuse, pale-brown to brown, hairy. *Mycelium* mostly immersed. vegetative hyphae hyaline to light brown. *Conidiophores* 195.7–310.3 $\times$ 3.9–5.1 μ m ($\bar{x}$ = 261.2 $\times$ 4.6 μ m, n = 20), micronematous, subulate, crowded, arising singly, consisting of a straight erect stipe, hyaline to pale brown, smooth-walled, unbranched. *Collar-like hyphae (or short basal cells)* formed just underneath the septum, arising from the lower half of the conidiophore stipe, short, irregularly curved, slightly pigmented, giving rise to a succession of 2-5

phialides. Internodes 20.5–28.9 μm ($\bar{x}$ = 24.2 μm , n = 20) long, repeatedly septate. *Phialides* lightly pigmented, subulate, with a tapering tip, 9.5–18.9 $\times$ 3.9–5.1 μm ($\bar{x}$ = 15.4 $\times$ 3.8 μm , n = 30), collarette conspicuous, occasionally proliferation percurrently. *Conidia* 3.1–4.9 $\times$ 2.1–3.7 μm ($\bar{x}$ = 3.9 $\times$ 2.8 μm , n = 30) formed on a protruding meristematic tip from multiple conidiogenous loci, accumulating in slimy heads, ellipsoidal to oval, colorless or pale brown, smooth, usually 1-guttulate) lightly apiculate at the base. Chlamydospores absent. Sterile lateral setae in the upper part of the conidiophores absent.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA medium. Colonies on PDA reaching 20–25 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface creamy, white, center raised, thick, small, irregular, entire, waxy; reverse cream.

Material examined – China, Sichuan Province, Leshan City, Jiazhou lùxin park, 29°35'18.23"N, 103°43'29.4" E, altitude 400 m, on a decaying wood in a wetland, 19 October 2024, L.L. Liu, 2024LXGY65 (GMB5325, GMBC5325).

Additional specimens examined – China, Sichuan Province, Leshan City, Jiazhou Lùxin park, 29°34'44.07"N, 103°42'26.26"E altitude 425 m, on a decaying wood in a wetland, 19 October 2024, L.L. Liu, 2024LXGY79 (GMB5332, GMBC5332).

Note – Phylogenetically (Fig. 48), the sequence of our collection clustered with *Gonytrichum macrocladum*, confirming the identity of our taxon as *G. macrocladum*. Recently, this species has been reclassified as a combination under the name *Chloridium fuscum* (Réblová et al. 2022). Morphological characteristics of our collections align with the description of *C. fuscum* by Réblová et al. (2022). This saprobic species occupies diverse terrestrial and freshwater habitats, frequently isolated from soil and commonly colonizing plant debris, particularly decaying wood and bark buried in damp soil associated with *Cenchrus purpureus*, *Pinus* spp., *Platanus occidentalis*, *Quercus* spp., *Sambucus* spp., bamboo, and other unidentified hosts (Réblová et al. 2022). This study establishes the first record of *Chloridium fuscum* in southwestern China.

Chloridium tongrense L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 51)

MycoBank No.: MB 859974

Etymology – The epithet refers to Tongren City, where the holotype was collected.

Description – *Saprobic* on decaying wood in a freshwater wetland. Teleomorph: Undetermined. Anamorph: Colonies effuse, brown, hairy. Mycelium mostly immersed in the substrate, composed of brown, septate, subhyaline to pale brown, smooth, hyphae. *Conidiophores* 90–205 $\times$ 2.3–4.6 μm ($\bar{x}$ = 134.3 $\times$ 3.4 μm , n = 20), in group with a septate, cylindrical, erect, unbranched, straight or flexuous, 2–7-septate, pale brown to brown, dark brown at the base, becoming paler towards the apex, smooth, thin-walled. *Conidiogenous cells* 23–37 $\times$ 2.4–3.6 μm ($\bar{x}$ = 29.4 $\times$ 3.0 μm , n = 20), monophialidic, integrated, terminal, pale brown to brown, becoming paler towards the apex, smooth, apex subhyaline; collarettes 1.9–4.5 μm ($\bar{x}$ = 3.1 μm , n = 20) μm wide, 1.4–2.8 μm ($\bar{x}$ = 2.0 μm , n = 20) μm deep, with multispore-producing loci within the collarettes. *Conidia* 2.9–4.6 $\times$ 2.2–3.5 μm ($\bar{x}$ = 3.8 $\times$ 2.9 μm , n = 35) produced singly within the collarette and aggregated in cirrhi on top of the conidiogenous cell, globose to subglobose, ellipsoidal, uniguttulate, smooth-walled, aseptate, hyaline.

Culture characteristics – Conidia germinated and formed germ tubes within 24 hours on WA. Colonies on PDA reaching 10–15 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface cream-white, small, irregular, entire, waxy, center raised, thick; reverse cream.

Material examined – China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°23'0.43"N, 108°7'30.36"E, altitude 1115 m, on a decaying wood in a wetland, 23 August 2024, L.L. Liu, 2024 FDSZNF15 (GMB5335, **holotype**); ex-type culture, GMBC5335; *ibid.*, KUN-HKAS 150412, isotype.

Additional specimens examined – China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°23'5.41" N, 108°7'41.91"E, altitude 1179 m, on a decaying wood in a wetland, 15 September 2024, L.L. Liu, 2024 FDSZNF29 (GMB5336, GMBC5336).

Notes – BLASTn results of ITS, *tub2*, and *tef1-α* sequences of *Chloridium tongrense* showed the highest similarity to *C. guttiferum* and placed it as phylogenetically closely related (Fig. 48). However, the two species can be distinguished by their habitat and measurements of the conidiophore, conidiogenous cells, and conidia. *Chloridium guttiferum* has been isolated from soil, whereas *C. tongrense* is a saprobe found on decaying wood and twigs in freshwater environments. Comparative analysis of nucleotide base pairs showed that *C. tongrense* differs from *C. guttiferum* (CBS 126073) by 2.2% (11/510) in the ITS locus, 2% (19/950) in the *tef1-α* gene, and 10.6% (49/462) in the *tub2* gene.

Chloridium tongrense has a shorter conidiophore (90–205 × 2.3–4.6 μm) compared to *C. guttiferum* (80–377 × 2.5–3.5 μm), larger and wider conidiogenous cells (23–37 × 2.4–3.6 μm vs. 15.5–27 × 2.5–3 μm), and slight larger conidia (2.9–4.6 × 2.2–3.5 μm vs. 3.5–4.5 × 2.5–3 μm) (Réblová et al. 2022). The ITS sequence similarity between *C. tongrense* and *C. guttiferum* was 97.7%, the *tub2* 89.9%, and the *tef1-α* similarity was 98.1%. Other closely related species, *C. bellum* var. *bellum* and *C. bellum* var. *luteum*, were also described based on culture characteristics and are saprobes found in soil. Based on these differences and phylogeny, we propose *Chloridium tongrense* as a new species.

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

Pyriculariaceae Klaubauf, M.-H. Lebrun & Crous, Stud. Mycol. 79: 104 (2014).

Pyricularia (Sacc.) Sacc., Syll. Fung. 4: 217 (1886).

Notes – The genus *Pyricularia* was described by Saccardo (1886) for a single species, *P. grisea* found on grasses. The genus is characterized by the formation of conidia on cylindrical denticles produced from usually slender, thin-walled conidiophores. The conidiogenous cells are terminal, sometimes becoming intercalary through sympodial extension of the conidiogenous cell and formation of new cross walls. The conidia are often 1- or 2-septate, and obpyriform, obturbinate or obclavate in shape (Ellis 1971). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 45 accepted species.

Pyricularia puerensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 53)

MycoBank No.: MB859988

Etymology – The epithet refers to Puer City, where the holotype was collected.

Description – *Saprobic* on decaying wood in a freshwater lake. Teleomorph: Undetermined. Anamorph: *Colonies* on natural substratum scattered, gregarious, erect, white, branched, glistening. *Mycelium* consisting of smooth, hyaline to blackish grey, branched, septate hyphae, 3–4 μm in diameter. *Conidiophores* 95.5–190 × 3.8–7.5 μm ($\bar{x}$ = 137 × 5.4 μm, n = 20), forming from hyphae or microsclerotia, macronematous, solitary, erect, straight to curved, unbranched, greyish brown, hyaline towards apex, thick-walled, smooth, subcylindrical tapering slightly towards apex, 5–6-septate, bulbous at the base, lacking rhizoids. *Conidiogenous cells* 29–80 × 4–7.2 μm ($\bar{x}$ = 60.5 × 5.4 μm, n = 30), integrated, terminal, subhyaline to greyish brown, smooth, forming a rachis with numerous protruding denticles, a minute marginal frill due to rhexolytic secession. *Conidia* 22–36 × 5.3–7.5 μm ($\bar{x}$ = 30.3 × 6.2 μm, n = 30), obclavate to acuminate with subacutely rounded upper edge, tapering towards the base, mostly with elongated apical cell forming a neck-like structure, smooth, guttulated, 2–3-septate, hyaline to subhyaline; hilum truncate, slightly protruding, unthicken, not darkened.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 25–35 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface white to creamy white, with densely mycelium, circular, cottony, smooth edges, raised at the center; reverse light yellowish.

Material examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°20′22.31″N, 100°48′36.41″E, altitude 2202 m, on a decaying wood in a freshwater lake, 13 October 2024, L.L. Liu, 2024WLSY65, (GMB5359, **holotype**); ex-type culture, GMBC5359; *ibid.*, KUN-HKAS 150430, isotype.

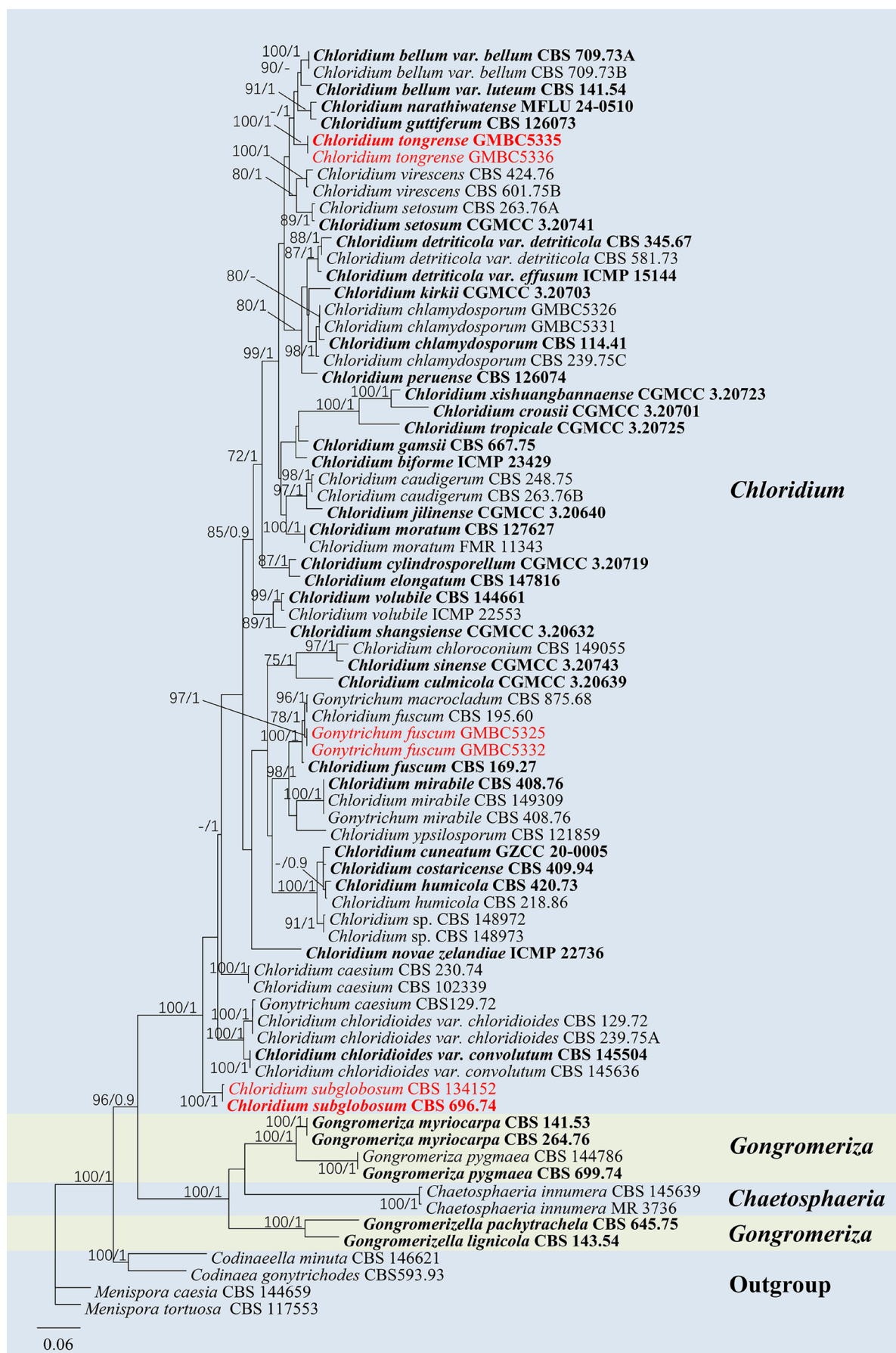


Figure 48 – ML tree of *Chloridium* and related taxa based on ITS, LSU, *tef1- α -1* and *tub2* loci. The alignment for this tree includes 3143 bp (ITS:1–595bp; LSU: 596–1600; *tef1- α* : 1601–2605; *tub2*: 2606–3143). *Menispora tortuosa* (CBS 117553); *Menispora caesia* (CBS 144659); *Codinaea*

gonytrichodes (CBS593.93); *Codinaeella minuta* (CBS 146621) were selected as the outgroup taxa. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly described species are marked red in bold. Ex-type/type strains or specimen are indicated in black bold.



Figure 49 – *Chloridium chlamydosporum* (GMB5326). a–c Colony on wood. d, e Conidiophores and conidia. f–h Conidiogenous cells and conidia. i–m Conidia. n Germinating conidium. o Surface view of culture on PDA. p Reverse view of culture on PDA. Scale bars: a = 0.5 mm, b, c = 0.2 mm, d–f = 50 µm, g, n = 10 µm, h–m = 2 µm.

Additional specimens examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°25'47.75"N, 100°54'49.37"E, altitude: 2106 m, on a decaying wood in a freshwater lake, 13 October 2024, L.L. Liu, 2024WLSY798, (GMB5360, GMBC5360).

Notes – In the phylogenetic analysis (Fig. 52), *Pyricularia puerensis* forms a well-supported, independent clade, distinguishing it from other known species within the genus.

Morphologically, *P. puerensis* resembles *P. oryzae* in its obclavate conidia with 2–3 septa and a truncate hilum. However, *P. puerensis* can be distinguished from *P. oryzae* by its larger conidiophores ($95.5\text{--}190 \times 3.8\text{--}7.5\ \mu\text{m}$ vs. up to $130 \times 3\text{--}4\ \mu\text{m}$ in *P. oryzae*), larger conidia ($22\text{--}36 \times 5.3\text{--}7.5\ \mu\text{m}$ vs. $17\text{--}23 \times 8\text{--}11\ \mu\text{m}$), and larger conidiogenous cells ($29\text{--}80 \times 4\text{--}7.2\ \mu\text{m}$ vs. $10\text{--}20 \times \text{ca. } 5\ \mu\text{m}$ in *P. oryzae*). Additionally, the conidiogenous cells of *P. puerensis* are terminal and form a distinct rachis bearing numerous denticles with a marginal frill due to rhexolytic secession, whereas those of *P. oryzae* are sympodial and smooth, lacking such ornamentation (Ellis 1971, Klaubauf et al. 2014).

The BLASTn results of ITS sequence revealed the highest similarity to *P. urashimae*. *Pyricularia urashimae* can be distinguished by pale brown, 2-septate smaller conidia ($18\text{--}27 \times 7\text{--}9\ \mu\text{m}$) (Crous et al. 2016). Comparative analysis of nucleotide base pairs showed that *P. puerensis* differs from *P. urashimae* (CPC 29414) by 4.4% (21/477) in the ITS and 0.5% (4/826) in the LSU loci.

Based on these morphological differences and the phylogenetic analysis, we introduce *Pyricularia puerensis* as a new species.

Ophiostomatales Benny & Kimbr., Mycotaxon 12 (1): 48 (1980).

Ophiostomataceae Nannf., Nova Acta Regiae Soc. Sci. Upsal. Ser. 4, 8 (2): 30 (1932).

Hawksworthiomyces Z.W. de Beer, Marinc. & M.J. Wingf., Fungal Biol. 120 (11): 1329 (2016).

Notes – The genus *Hawksworthiomyces* was introduced by De Beer et al. (2016) to include *Hawksworthiomyces lignivorus*. Currently, the genus contains seven species, listed in Species Fungorum (accessed June 29, 2025). Members of *Hawksworthiomyces* are characterized by mononematous, micronematous or macronematous; conidiogenous cells polyblastic, integrated or discrete, terminal or intercalary, apical part bearing denticles; conidia hyaline, nonseptate, ellipsoidal to cylindrical, secondary conidia occasionally produced (De Beer et al. 2016). The teleomorph has not yet been determined (De Beer et al. 2016). In this study, we describe a new species isolated from submerged wood in a freshwater lake.

Hawksworthiomyces cylindroconidius L.L. Liu, K. Habib & Q.R. Li, *sp. nov.* (Fig. 55)

Mycobank No.: MB859979

Etymology – The epithet refers to Tongren City, where the holotype was collected.

Description – *Saprobic* on submerged decaying wood in a freshwater lake. Teleomorph: Undetermined. Anamorph: Colonies scattered on wood, erect, white, glistening, crystal-like, subglobose to globose, neck white, cylindrical, straight or slightly curved. Conidiophores micronematous, mononematous, synnemata, $94.5\text{--}131.5 \times 11\text{--}20.5\ \mu\text{m}$ ($\bar{x} = 103.5 \times 16.7\ \mu\text{m}$, $n = 10$), hyaline, upright or prone, base simple or rhizoid-like in appearance. Conidiogenous cells $15.5\text{--}36.5 \times 1.1\text{--}1.5\ \mu\text{m}$ ($\bar{x} = 25.8 \times 1.3\ \mu\text{m}$, $n = 15$), monoblastic, hyaline, sub-cylindrical to cylindrical. Conidia $2.3\text{--}5.2 \times 1\text{--}1.5\ \mu\text{m}$ ($\bar{x} = 4.5 \times 1.2\ \mu\text{m}$, $n = 30$), hyaline, 1-celled, elongated, rectangular, slightly rounded apex.

Culture characteristics – Conidia germinated and formed germ tubes within 24 hrs on WA. Colonies on PDA reaching 10–15 mm diam., after 3 weeks at 24–27 °C on PDA. Colony surface bright yellow, with densely mycelium, cottony, circular, smooth edges, raised at the center; reverse pale-yellow with creamy margins.

Material examined – China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°23'0.43" N, 108°7'30.36" E, 1115 m, on a submerged decaying

wood in a freshwater lake, 5 September 2024, L.L. Liu, 2024FDSZNF16 (GMB5345, **holotype**); ex-type culture, GMBC5345; *ibid.*, KUN-HKAS 150413, isotype.

Additional specimens examined – China, Guizhou Province, Tongren City, Shiqian County, Foding Mountain Nature Reserve, 27°23′5.41″ N, 108°7′41.91″ E, altitude: 1179 m, on a submerged decaying wood in a freshwater lake, 5 September 2024, L.L. Liu, 2024FDSZNF54 (GMB5346, GMBC5346).

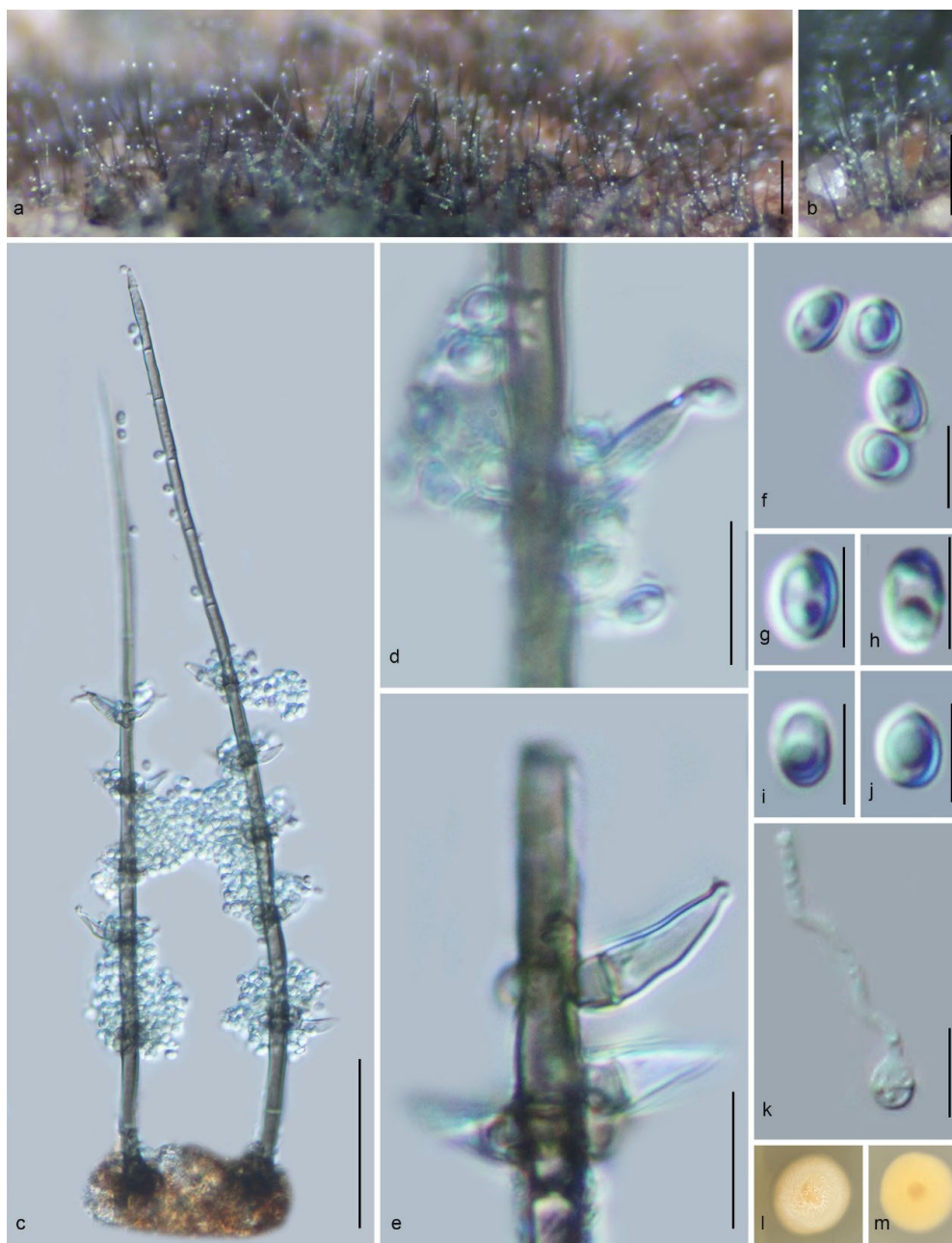


Figure 50 – *Chloridium fuscum* (GMB5325). a, b Colony on wood. c Conidiophores and conidia. d, e Conidiogenous cells and conidia. f–j Conidia. k Germinated conidium. l Surface view of culture on PDA. m Reverse view of culture on PDA. Scale bars: a, b = 0.2 mm, c = 50 μ m, d, e = 10 μ m, f–k = 5 μ m.

Notes – In the phylogenetic tree (Fig. 54), *Hawksworthiomyces cylindroconidius* is closely related to *H. crousii* and *H. sequentia*. However, *H. cylindroconidius* can be easily distinguished based on its characterization on natural substrata, with long, glistening, unbranched conidiophores (94.5–131.5 $\times$ 11–20.5 μ m) with a globose head, and smaller monoblastic conidiogenous cells

($15.5\text{--}36.5 \times 1.1\text{--}1.5 \mu\text{m}$) as well as smaller conidia ($2.3\text{--}5.2 \times 1\text{--}1.5 \mu\text{m}$). In contrast, *H. crousii* has been described based on culture characteristics, with branched, upright conidiophores that are often reduced to conidiogenous cells ($6\text{--}69 \times 1\text{--}2 \mu\text{m}$), polyblastic conidiogenous cells ($5\text{--}22 \mu\text{m}$ long), and slight larger conidia ($3\text{--}6.5 \times 1.5\text{--}3.5 \mu\text{m}$) (De Beer et al. 2016). Comparative analysis of nucleotide base pairs showed that *H. cylindroconidius* differs from *H. crousii* (CMW37531) by 5.7% (28/491) in the ITS gene and 0.9% (7/806) in the LSU gene. *Hawksworthiomyces sequentia* is known only from its DNA sequences, with a sequence obtained as an uncultured fungal DNA clone extracted from decaying conifer wood. The ITS similarity to *H. sequentia* was found to be 93%.

Based on these morphological and molecular differences, as well as the phylogenetic analysis, we introduce *Hawksworthiomyces cylindroconidius* as a new species.



Figure 51 – *Chloridium tongrense* (GMB5335 holotype) a–c Colony on wood. d–f Conidiophores. g–i Conidiogenous cells and conidia. j–o Conidia. p Germinated conidium. q Surface view of culture on PDA. r Reverse view of culture on PDA. Scale bars: a = 0.5 mm, b, c = 0.2 mm. d–f = 50 μm , g–j, p = 10 μm , k–o = 5 μm .

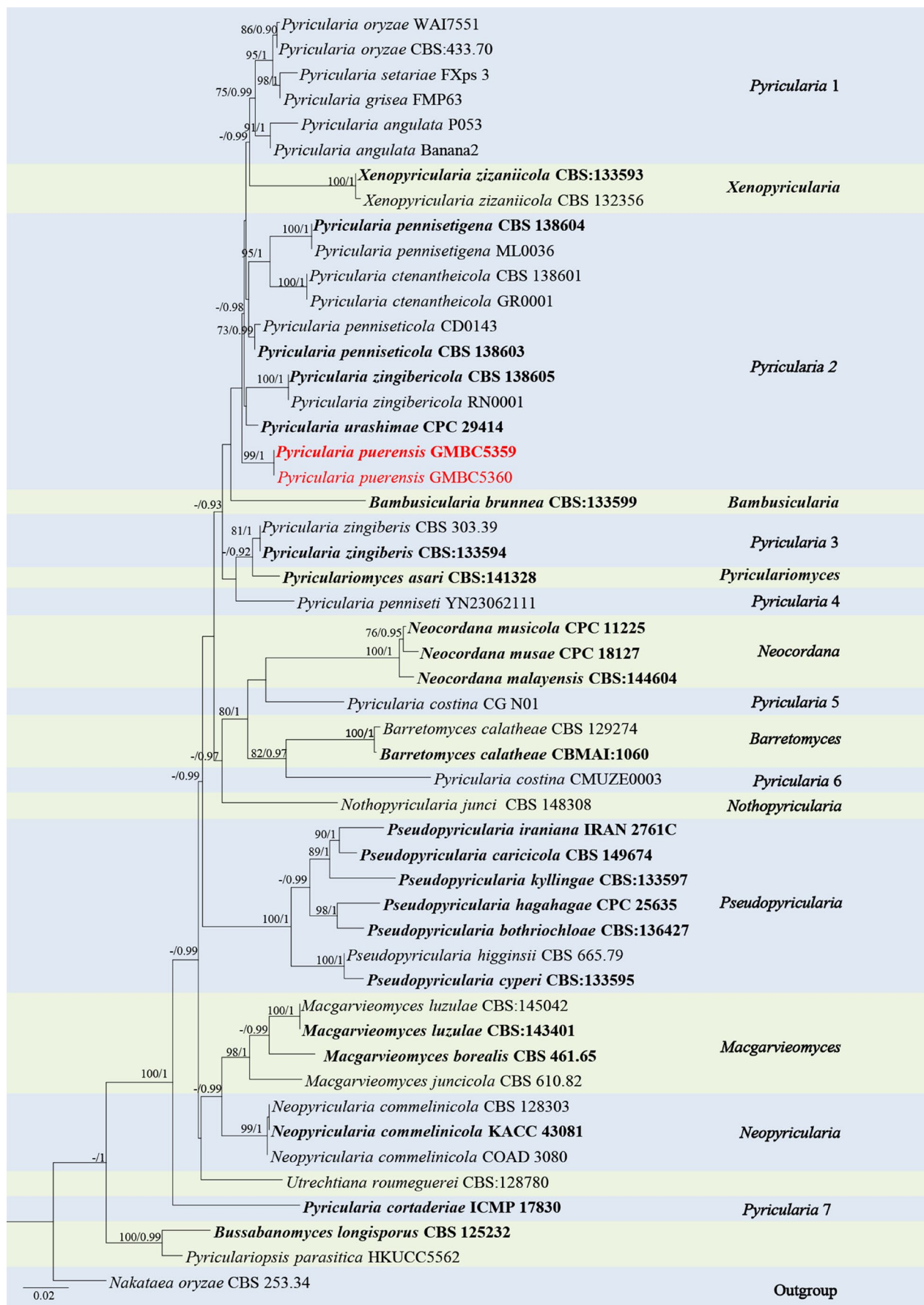


Figure 52 – ML tree of genus *Pyricularia* and related taxa based on ITS and LSU loci. The alignment for this tree includes 1336 bp (ITS:1–494; LSU: 495–1336). *Nakataea oryzae* (CBS 253.34) was selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support

values of RAxML $\geq 70\%$ are shown on the branches. The newly generated sequences are marked red in bold. Ex-type/type strains are indicated in black bold.

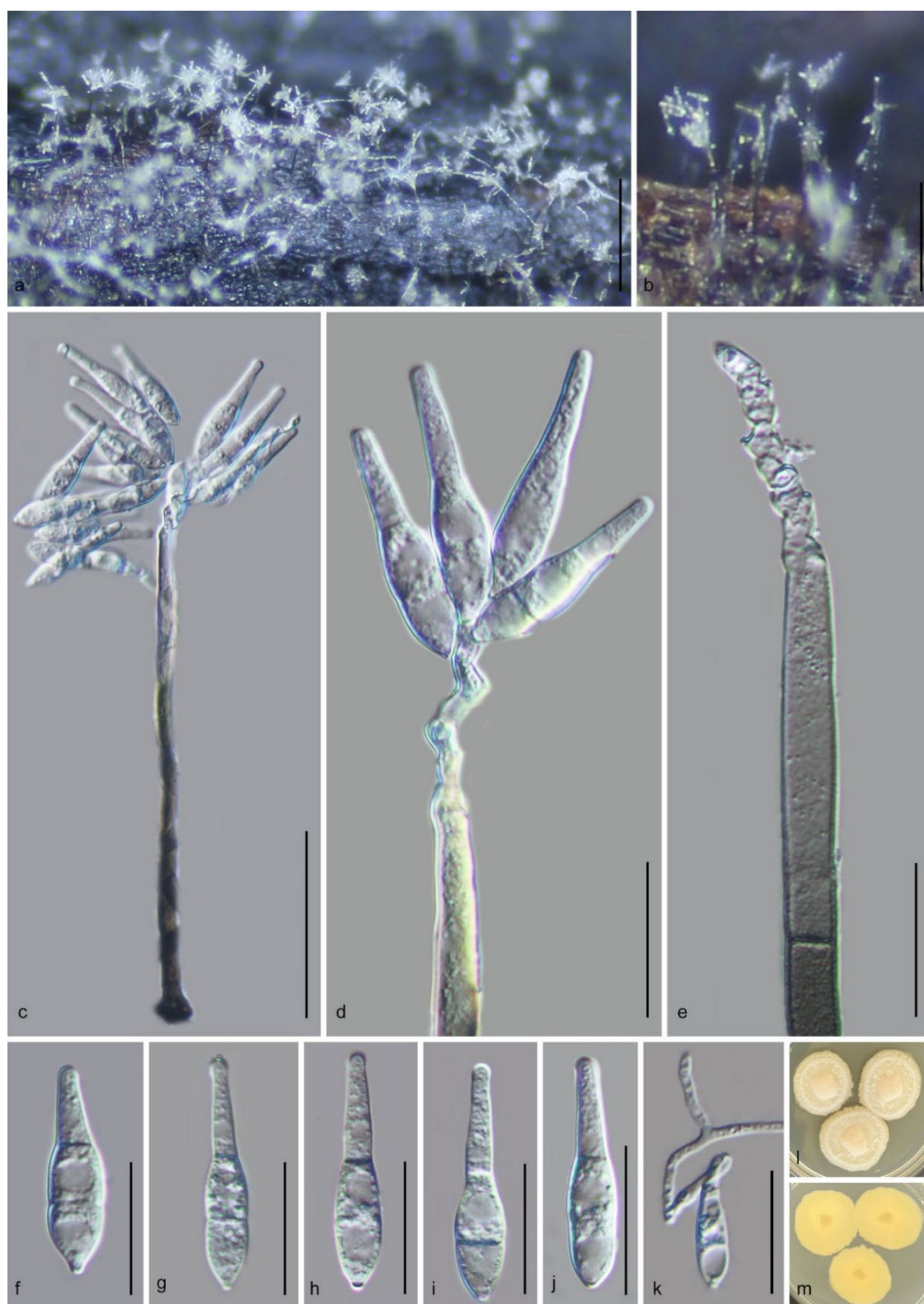


Figure 53 – *Pyricularia puerensis* (GMB5359 holotype). a, b Colony on wood. c Conidiophores and conidia. d, e Conidiogenous cells and conidia. f–j Conidia. k Germinating conidium. l Surface view of culture on PDA. m Reverse view of culture on PDA. Scale bars: a = 0.5 mm, b = 0.2 mm, c = 50 μ m, d–k = 20 μ m.

Rhamphoriales K.D. Hyde & Hongnan, Fungal Diversity 107: 94 (2021).

Rhamphoriaceae Réblová, Mycologia 11 (4): 754 (2018).

Rhamphoriopsis Réblová & Gardiennet, Mycologia 11 (4): 755 (2018).

Notes – *Rhamphoriopsis* was introduced by Réblová & Štěpánek (2018), with the type species *R. muriformis*, isolated from decaying wood of *Buxus sempervivens* in France. The genus is characterized by perithecial, nonstromatic, immersed ascomata with cylindrical necks; unitunicate, 8-spored asci with a distinct non-amyloid apical and ellipsoidal to fusiform, smooth-walled ascospores. The anamorph of *Rhamphoriopsis* is characterized by macronematous, mononematous conidiophores, which may form loose fascicles, conidiogenous cells integrated, terminal, cylindrical, tapering apically, polyblastic, produce numerous denticles and conidia ellipsoidal to obovoid, hyaline, aseptate (Réblová & Štěpánek 2018). According to Species Fungorum (accessed 3 July 2025), the genus currently comprises 6 accepted species. In this study, we describe three new species of the genus, all isolated from decaying wood along the river.

Rhamphoriopsis globularis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 57)

Mycobank No.: MB859989

Etymology – The epithet refers to its globose conidia.

Description – *Saprobic* on decaying wood along the riverbank. Teleomorph: Undetermined. Anamorph: *Colonies* on natural substratum effuse, scattered or in small groups, hairy, visible as solitary, brown to dark brown conidiophores with white conidial masses at the apex. *Mycelium* partially superficial and partially immersed, composed of hyaline to fade olivaceous, smooth-walled, septate hyphae. *Conidiophores* synnematus, 200–450 × 21–41 µm ($\bar{x}$ = 316.5 × 31.3 µm, n = 15), macronematous in loose tufts of hyphae, subcylindrical to cylindrical, brown towards the base paler towards apex, smooth, aseptate to septate, thin-walled, with terminal cells giving rise to clusters of conidiogenous cells. *Conidiogenous cells* polyblastic, integrated, terminal, pale brown near the base, becoming hyaline towards the apex, smooth-walled, sympodially extending with numerous denticles. *Conidia* 2.5–4.2 × 2–3.7 µm ($\bar{x}$ = 3.2 × 2.8 µm, n = 30), solitary, acropleurogenous, smooth, thin-walled, aseptate, hyaline, globose to ovoid.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 10–15 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface light brown, with irregular margins, compact, slightly appressed, irregular, raised at the center; reverse light brown.

Material examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°20′22.31″N, 100°48′36.41″E, altitude 2202 m, on dead twig of unidentified tree along the riverbank, 12 October 2024, L.L. Liu, 2024WLSY08 (GMB5313, **holotype**); ex-type culture, GMBC5313; *ibid.*, KUN-HKAS 150426, isotype.

Additional specimens examined – China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Wuliangshan National Nature Reserve, 24°25′47.75″N, 100°54′49.37″E, altitude 2126 m, on dead twig of unidentified tree along the riverbank, 12 October 2024, L.L. Liu, 2024WLSY19 (GMB5314, GMBC5314).

Notes – Phylogenetically (Fig. 56), *Rhamphoriopsis globularis* forms an independent clade, differentiating it from all six known species in the genus. Morphologically, it is closely related to *R. aquimicrospora* sharing synnematus, erect, cylindrical, brown conidiophores. However, *R. aquimicrospora* can be distinguished by its smaller synnemata (135–178 × 5–11 µm vs. 200–450 × 21–41 µm in *R. globularis*) and smaller ellipsoidal conidia (2–3.2 × 1.3–2 µm vs. globose to ovoid conidia 2.5–4.2 × 2–3.7 µm) (Yang et al. 2023). *Rhamphoriopsis hyalospora* has smaller non-synnematus conidiophores 40–145 µm long, and smaller conidia, 2.0–3.7 × 1.8–2.6 µm (Lin et al. 2023).

The type species, *R. muriformis*, differs in having smaller, non-synnematus conidiophores (40–66 µm long), and narrower conidia (3.5–5.5 × 1.5–2 µm) (Réblová & Štěpánek 2018). *Rhamphoriopsis sympodialis* also has non-synnematus conidiophores (14–45 µm) and smaller ellipsoidal to obovoid conidia (1.9–4 × 1.4–2.2 µm) (Hyde et al. 2020). *Rhamphoriopsis glauca* is

described based on its culture anamorph, with guttuliform to ellipsoidal conidia, smaller in size ($2.5\text{--}3.5 \times 1.6\text{--}2.2 \mu\text{m}$) with pointed base, occasionally becoming inflated and giving rise to secondary conidia or short secondary conidiophores (Yang et al. 2023). The BLASTn results of ITS and LSU sequences showed the highest similarity to *R. synnematos*. Comparative analysis of nucleotide base pairs showed that *R. globularis* differs from *R. synnematos* (CPC 45231) by 7.2% (37/515) in the ITS locus, 1.0% (8/841) in the LSU locus, and 11.6% (100/859) in the *rpb2* gene. Morphologically, *R. synnematos* differs through smaller synnemata ($70\text{--}300 \times 10\text{--}30 \mu\text{m}$) and smaller conidia ($2.5\text{--}3 \times 1.5\text{--}2 \mu\text{m}$) (Crous et al. 2023).

The recently described new species *Rhamphoriopsis cuprea* (sequence data not yet released in NCBI) can be distinguished by its mononematous conidiophores ($30\text{--}90 \times 2\text{--}3.5 \mu\text{m}$) and comparatively larger conidia ($4\text{--}6.5 \times 1.5\text{--}2 \mu\text{m}$) (Réblová et al. 2025).

Based on these morphological differences and phylogeny, we introduce *R. globularis* as a new species.

Rhamphoriopsis yunnanensis W.M. Li, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 58)

Mycobank No.: MB859990

Etymology – The epithet refers to Yunnan Province, where the holotype was collected.

Description – *Saprobic* on decaying submerged wood along the riverbank. Teleomorph: Undetermined. Anamorph: Colonies effuse, scattered or in small groups, hairy, visible as solitary, dark brown to black conidiophores with white conidial masses at the apex. *Mycelium* partially superficial, partially immersed, composed of septate, smooth-walled, pale brown to hyaline hyphae. *Conidiophores* macronematous, synnematos, erect, smooth-walled, septate, cylindrical, reddish brown, paler towards the apex, compact parallelly forming synnemata $100\text{--}255 \times 5\text{--}15 \mu\text{m}$ at middle part, $15\text{--}33 \mu\text{m}$ wide near the base, with terminal of conidiophores splaying out as a fared head. *Conidiogenous cells* polyblastic, integrated, terminal, pale brown near the base, becoming hyaline towards the apex, smooth-walled, sympodially extending with numerous denticles. *Conidia* $2\text{--}3 \times 1.5\text{--}2.2 \mu\text{m}$ ($\bar{x} = 2.5 \times 1.8 \mu\text{m}$, $n = 30$), ellipsoidal, aseptate, smooth-walled, hyaline.

Culture characteristics – Conidia germinated within 12 hours on WA. Colonies on PDA reaching 10–15 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface cream, small, circular, margin undulate, velvety, raised at the center; reverse cream yellow.

Material examined – China, Yunnan Province, Zhaotong City, Wumengshan National Nature Reserve, 25°23'15.05"N, 103°15'05.90"E, elevation: 2300 m, on decaying submerged wood along the riverbank, 25 October 2024, Wen-Mei Li, 2024WMS155-2 (GMB6917, **holotype**); ex-type culture, GMBC6917; *ibid.*, KUN-HKAS 150408, isotype.

Additional specimens examined – China, Yunnan Province, Zhaotong City, Wumengshan National Nature Reserve, 25°23'15.10"N, 103°15'06.38"E, elevation: 2546 m, on decaying submerged wood along the riverbank, 25 October 2024, Wen-Mei Li, 2024WMS176 (GMB6919, GMBC6919).

Notes – Phylogenetically (Fig. 56), *Rhamphoriopsis yunnanensis* is closely related to *R. aquimicrospora*, and both species sharing synnematos, erect, cylindrical, brown conidiophores, and hyaline, aseptate, ellipsoidal conidia of similar size (Yang et al. 2023). However, *R. aquimicrospora* can be distinguished by its smaller synnemata ($135\text{--}178 \mu\text{m} \times 5\text{--}11 \mu\text{m}$ vs. $100\text{--}255 \mu\text{m} \times 5\text{--}15 \mu\text{m}$ in *R. yunnanensis*) (Yang et al. 2023). Comparative analysis of nucleotide base pairs showed that *R. yunnanensis* differs from *R. aquimicrospora* (GZCC:20-0515) by 7.8% (39/501) in the ITS locus, 1.6% (13/822) in the LSU locus, 12.0% (118/984) in the *rpb2* gene, and 6.1% (55/908) in the *tef1- α* gene. *Rhamphoriopsis synnematos*, which also has synnematos conidiophores, differs by having larger synnemata ($70\text{--}300 \mu\text{m} \times 10\text{--}30 \mu\text{m}$) (Crous et al. 2023). Molecular comparison of *R. yunnanensis* sequences with *R. synnematos* (CPC 45231) showed similarities of ITS 94.1%, LSU 99.6%, and *rpb2* 89.0%, respectively.

The recently described new species *Rhamphoriopsis cuprea* (sequence data not yet released in NCBI) can be distinguished by its mononematous conidiophores ($30\text{--}90 \times 2\text{--}3.5 \mu\text{m}$) and larger conidia ($4\text{--}6.5 \times 1.5\text{--}2 \mu\text{m}$) (Réblová et al. 2025).

Given these molecular and morphological differences, we describe *Rhamphoriopsis yunnanensis* as a new species.

Rhamphoriopsis zhaotongensis W.M. Li, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 59)

Mycobank No.: MB859991

Etymology – The epithet refers to Zhaotong City, where the holotype was collected.

Description – *Saprobic* on decaying submerged wood along the riverbank. Teleomorph: Undetermined. Anamorph: *Colonies* effuse, scattered or in small groups, hairy, visible as solitary, brown to black conidiophores with white conidial masses at the apex. *Mycelium* partially superficial, partially immersed, composed of septate, smooth-walled, pale brown to hyaline hyphae. *Conidiophores* macronematous, synnematos, erect, smooth-walled, septate, cylindrical, reddish brown, paler towards the apex, compact parallelly forming synnemata which are 150–340 µm long, 9–17 µm wide at middle part, 18–45 µm wide near the base, with terminal of conidiophores splaying out as a fared head. *Conidiogenous cells* polyblastic, integrated, terminal, pale brown near the base, becoming hyaline towards the apex, smooth-walled, sympodially extending with numerous denticles. *Conidia* $1.9\text{--}2.8 \times 1.4\text{--}1.9$ µm ($\bar{x} = 2.45 \times 1.7$ µm, $n = 30$) ellipsoidal, aseptate, smooth-walled, hyaline.

Culture characteristics – Conidia germinated within 24 hours on WA. Colonies on PDA reaching 10–20 mm diam., after 3 weeks at 24–27°C on PDA. Colony surface cream, small, irregular, margin undulate, floccose, raised at the center; reverse olive at center, cream yellow toward margins.

Material examined – China, Yunnan Province, Zhaotong City, Wumengshan National Nature Reserve, 25°23'15.05"N, 103°15'05.90"E, elevation 2300 m, on decaying submerged wood along the riverbank, 25 October 2024, Wen-Mei Li, 2024WMS160-1 (GMB6918, **holotype**); ex-type culture, GMBC6918; *ibid.*, KUN-HKAS 150444, isotype.

Additional specimens examined – China, Yunnan Province, Zhaotong City, Wumengshan National Nature Reserve, 25°23'15.10"N, 103°15'06.38"E, elevation 2546 m, on decaying submerged wood along the riverbank, 25 October 2024, Wen-Mei Li, 2024WMS179 (GMB6920, GMBC6920).

Notes – In the phylogenetic tree (Fig. 56), *Rhamphoriopsis zhaotongensis* appears as a sister taxon to *R. synnematos*. Morphologically, the two species are closely related, sharing synnematos, erect, brown conidiophores, and hyaline, aseptate, ellipsoidal conidia (Crous et al. 2023). However, *R. synnematos* can be distinguished by having smaller synnemata (70–300 µm tall $\times$ 10–30 µm wide at the base vs. 150–340 µm tall $\times$ 18–45 µm wide at the base in *R. zhaotongensis*), and slightly larger conidia $2.5\text{--}3 \times 1.5\text{--}2$ µm (vs. $1.9\text{--}2.8 \times 1.4\text{--}1.9$ µm) (Crous et al. 2023). Comparative analysis of nucleotide base pairs showed that *R. zhaotongensis* differs from *R. synnematos* (CPC 45231) by 4.6% (24/518) in the ITS locus, 1.0% (8/840) in the LSU locus, and 9.3% (80/857) in the *rpb2* gene.

Rhamphoriopsis aquimicrospora also has synnematos conidiophores, can be distinguished by its smaller synnemata (135–178 µm long, 5–11 µm wide at the middle, and 8.5–20 µm wide near the base) and slightly larger conidia ($2\text{--}3.2 \times 1.3\text{--}2$ µm) (Yang et al. 2023). All other species in the genus can be readily distinguished by having non-synnematos conidiophores.

Based on both phylogenetic analyses and morphological distinctions, *Rhamphoriopsis zhaotongensis* is introduced here as a novel species in the genus *Rhamphoriopsis*.

Xylolentia Réblová, Mycologia 11 (4): 759 (2018).

Notes – *Xylolentia* was established by Réblová & Štěpánek (2018) to accommodate the holomorphic species *X. brunneola*. Its teleomorph produces black ascomata with a cylindrical neck, unitunicate, cylindric-clavate, long pedicellate asci bearing a distinct, inamyloid apical ring, and ellipsoidal to obovoid, brown, septate ascospores (Réblová & Štěpánek 2018). The anamorph is characterized by macronematous, mononematous, unbranched, septate conidiophores, polyblastic conidiogenous cells, and ellipsoidal to obovoid or subglobose, aseptate conidia that are initially

hyaline, or becoming brown and with age (Réblová & Štěpánek 2018, Zhao et al. 2025). According to Species Fungorum (accessed 14 July 2025), the genus currently comprises 7 species. Here, we describe a new hyphomycetous species of *Xylolentia* isolated from a freshwater habitat.

Xylolentia yibinensis L.L. Liu, K. Habib & Q.R. Li, *sp. nov.*

(Fig. 60)

MycoBank No.: MB860081

Etymology – The epithet refers to Yibin City, where the holotype was collected.

Description – *Saprobic* on decaying wood in a freshwater wetland. Teleomorph: Undetermined. Anamorph: *Colonies* on the natural substrate effused, scattered, hairy, white, glistening like pearls. *Mycelium* partially superficial, partially immersed in the substratum. *Conidiophores* 41–70.5 × 2.7–4.5 µm ($\bar{x}$ = 55.5 × 3.3 µm, n = 30), macronematous, mononematous, scattered, erect, 3–5 septate, simple, straight or slightly flexuous, smooth, thick-walled, septate, cylindrical to subcylindrical, with acute apex, dark brown at the base, paler towards the apex almost hyaline, thick at the base, slightly swollen just below the conidiogenous cells. *Conidiogenous cells* 13.5–25.8 × 2.5–4.5 µm ($\bar{x}$ = 22.5 × 3.3 µm, n = 30), polyblastic, integrated, terminal, sympodial, cylindrical with acute apex, subhyaline, guttulate, 22–25.5 µm thick in the broadest part. *Conidia* 2.5–5 × 2–4 µm ($\bar{x}$ = 3.8 × 3 µm, n = 30), aggregated in slimy mass, acropleurogenous, simple, smooth, aseptate, subglobose to oval, hyaline to pale olivaceous, guttulated.

Culture characteristics – Conidia germinated and formed germ tubes within 12 hours on WA. Colonies on PDA reaching 15–25 mm diam., after 4 weeks at 24–27°C on PDA. Colony surface light yellowish, with densely mycelium, roughly circular, raised at the center; reverse pale yellow.

Material examined – China, Sichuan Province, Yibin City, Shulan Bamboo Sea Resort, 28°28'27.40 "N, 104°57'03.64" E, altitude: 610 m, on a decaying wood in a freshwater wetland, 21 September 2024, L.L. Liu, 2024SNZ33 (GMB5367, **holotype**); ex-type culture, GMBC5367; *ibid.*, KUN-HKAS 150422, isotype.

Additional specimen examined – China, Sichuan Province, Yibin City, Shulan Bamboo Sea Resort, 28°27'30.25 "N, 104°58'10.35" E, altitude 659 m, on a decaying wood in a freshwater wetland, 21 September 2024, L.L. Liu, 2024SNZ45 (GMB5368, GMBC5368).

Notes – Phylogenetically (Fig. 56), *Xylolentia yibinensis* forms an independent clade within *Xylolentia* clade. In BLASTn searches, it shows highest similarity to *X. aseptata*. Morphologically, *X. yibinensis* resembles *X. aseptata* in having polyblastic conidiogenous cells and hyaline, guttulate conidia aggregated in slimy masses. However, *X. aseptata* can be distinguished by its much larger conidiophores (95–215 µm vs. 41–70.5 µm) and narrower, ellipsoidal to reniform conidia (2.8–5.3 × 1.8–3 µm), compared to the subglobose to oval conidia (2.5–5 × 2–4 µm) of *X. yibinensis* (Yang et al. 2023). Comparative analysis of nucleotide base pairs showed that *X. yibinensis* differs from *X. aseptata* (GZCC 20-0424) by 2.0% (11/540) in the ITS locus, 0.1% (1/884) in the LSU locus, 0.1 % (1/1000) in the SSU locus, 6.2% (61/989) in the *rpb2* gene, and 1.5% (14/905) in the *tef1-α* gene.

Morphologically, *X. yibinensis* also resembles *Xylolentia bambusae*, but the latter differs by having larger conidiophores (57–95 × 2.5–4 µm), smaller conidiogenous cells (16.5–20 × 2.5–3 µm), and smaller conidia (3.6–4.8 × 2.1–3.3 µm) (Zhao et al. 2025). The type species *Xylolentia brunneola* also possesses subglobose to obovoid conidia of similar size (4–5.5 × 3–4 µm) to *X. yibinensis*, but differs in having an anamorph described from culture with pale brown conidia, larger conidiophores (55–120 × 4.5–5.5 µm), and a phylogenetically distant position (Réblová & Štěpánek 2018).

Given these morphological and molecular differences, along with clear phylogenetic distinction, we propose *Xylolentia yibinensis* as a new species.

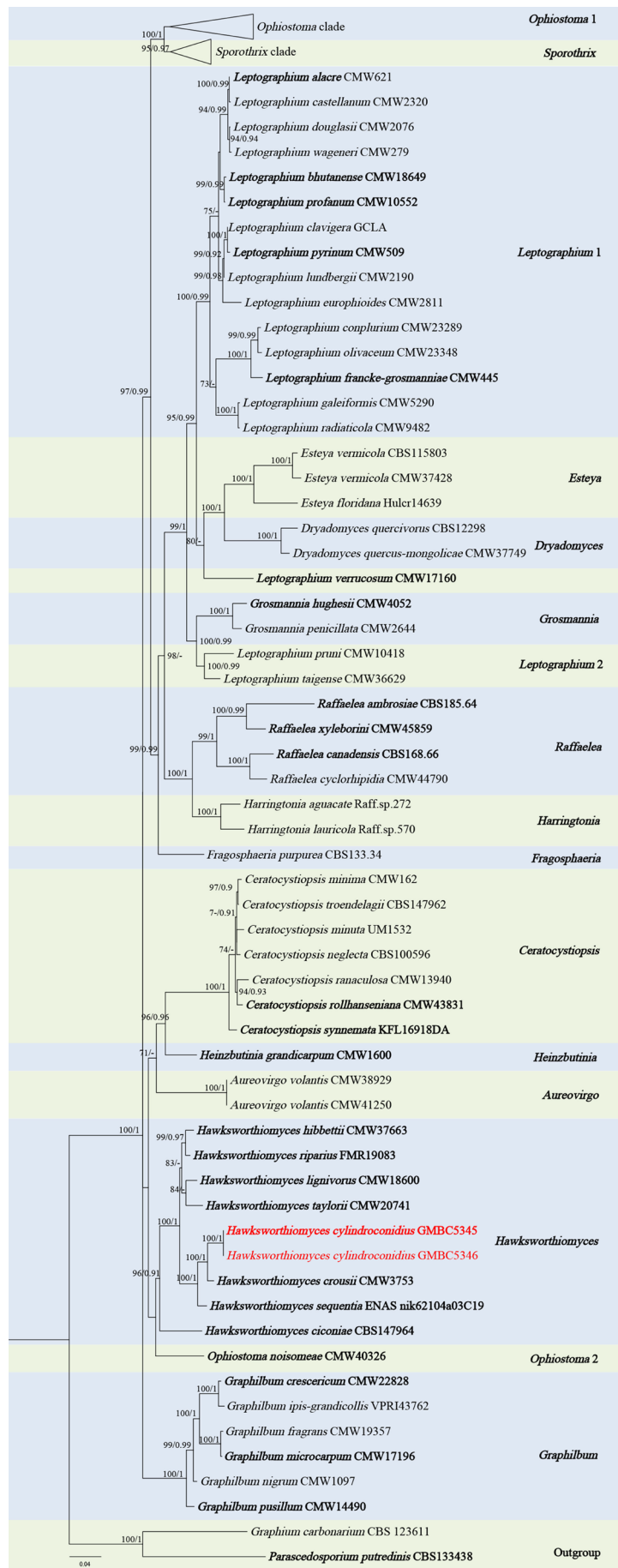


Figure 54 – ML tree of *Hawksworthiomyces* and related taxa based on ITS and LSU loci. The alignment for this tree includes 1340 bp (ITS:1–498 bp; LSU:499–1340 bp). *Graphium*

carbonarium (CBS 123611) and *Parascedosporium putredinis* (CBS 133438) was selected as the outgroup taxa. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly generated strains are marked red in bold. Ex-type/holotype strain are marked bold.

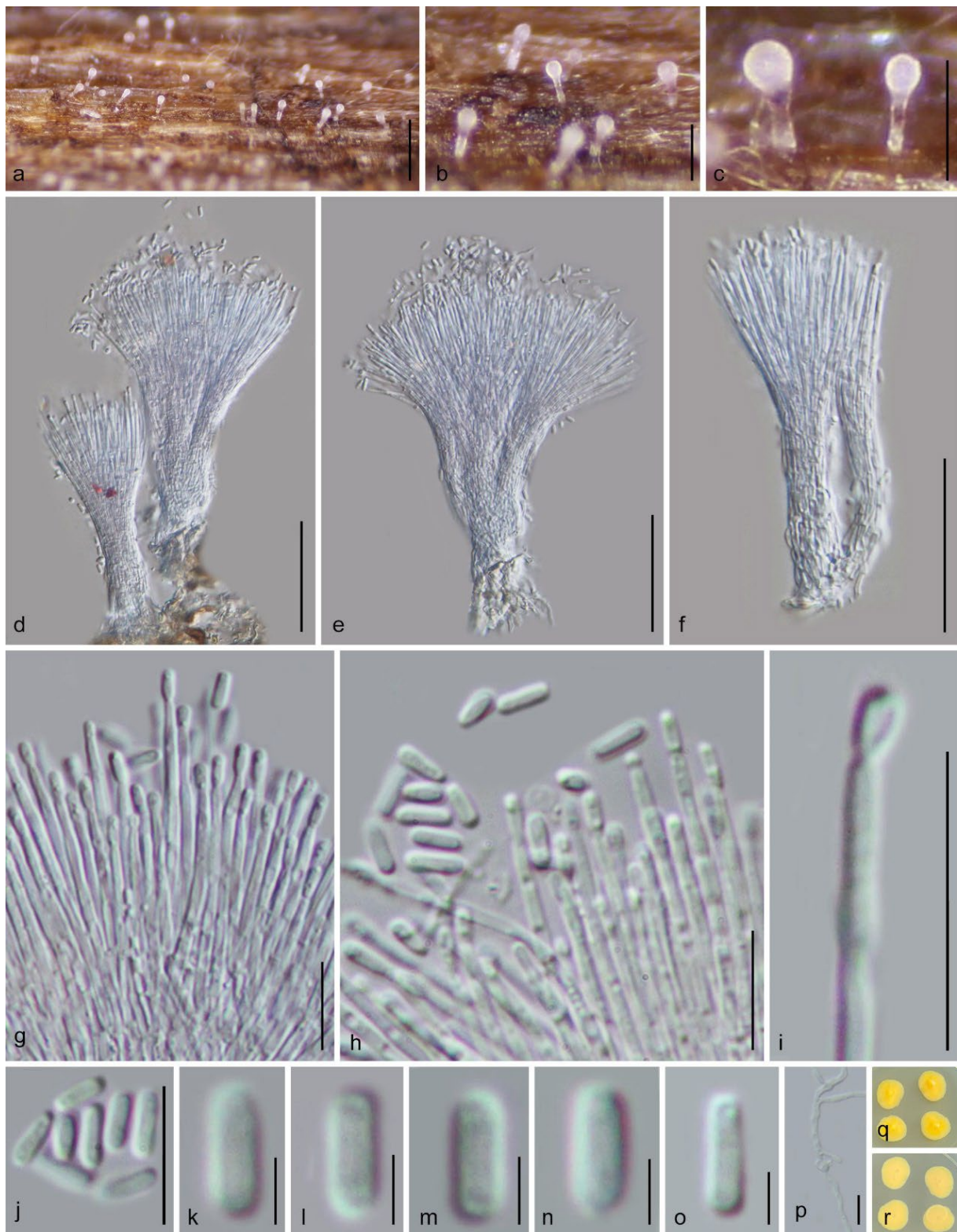


Figure 55 – *Hawksworthiomyces cylindroconidius* (GMB5345 holotype). a–c Colonies on wood. d–f Conidiophores and conidia. g–i Conidiogenous cells and conidia. j–o Conidia. p: Germinated conidium. q Surface view of culture on PDA. r Reverse view of culture on PDA. Scale bars: a = 0.5 mm, b, c = 0.2 mm, d–f = 50 µm, g–j, p = 10 µm, k–o = 2 µm.

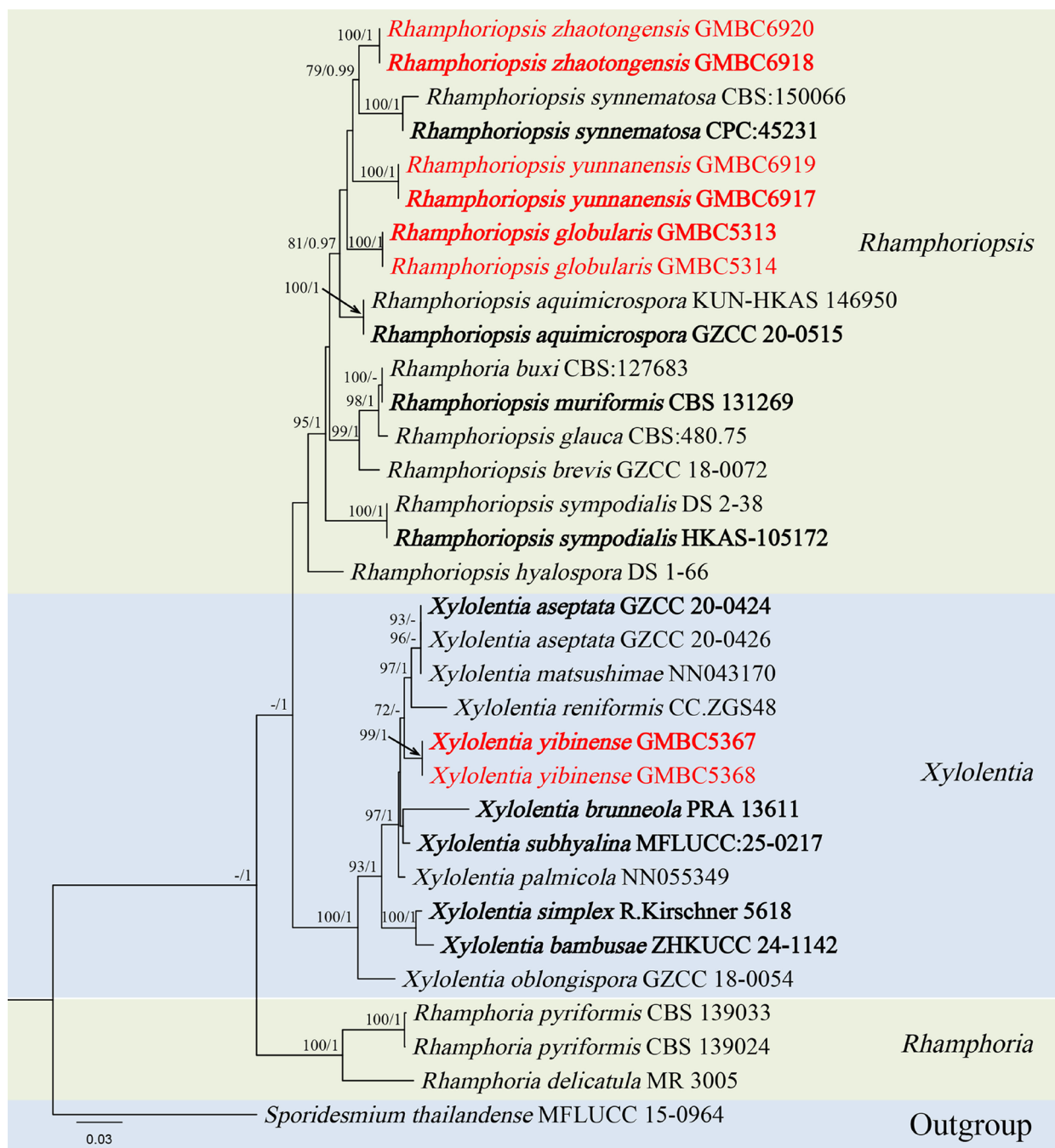


Figure 56 – ML tree of *Rhamphoriopsis*, *Xylolentia* and related taxa based on ITS-LSU-SSU-*rpb2* loci. The alignment for this tree includes 3373 bp (ITS:1–496bp; LSU: 497–1350 bp; SSU: 1351–2328 bp; *rpb2*: 2329–3373 bp). *Sporidesmium thailandense* (MFLUCC 15-0964) was selected as the outgroup taxon. Values of the Bayesian PP ≥ 0.90 and bootstrap support values of RAxML $\geq 70\%$ are shown on the branches. The newly generated sequences are marked red in bold. Ex-type/type strains are indicated in black bold.

DISCUSSION

China, with its vast and diverse landscapes, is recognized as a global hotspot for fungal diversity. This is particularly true for its southwestern regions, including Guizhou, Sichuan, Xizang, and Yunnan Provinces. The country has contributed nearly 7 % of all newly described fungal taxa worldwide, making it the second-largest contributor globally (Wang & Cai 2023). The highest proportion of these newly described fungal taxa within China originate from its southwestern provinces, highlighting their exceptional biodiversity (Wang & Cai 2023). Southwestern China is

characterized by hilly and mountainous terrains, high vegetation coverage, mild climates, and abundant rainfall, provide ideal conditions for fungal growth (Dai et al. 2021, Wijayawardene et al. 2021, Habib et al. 2025).

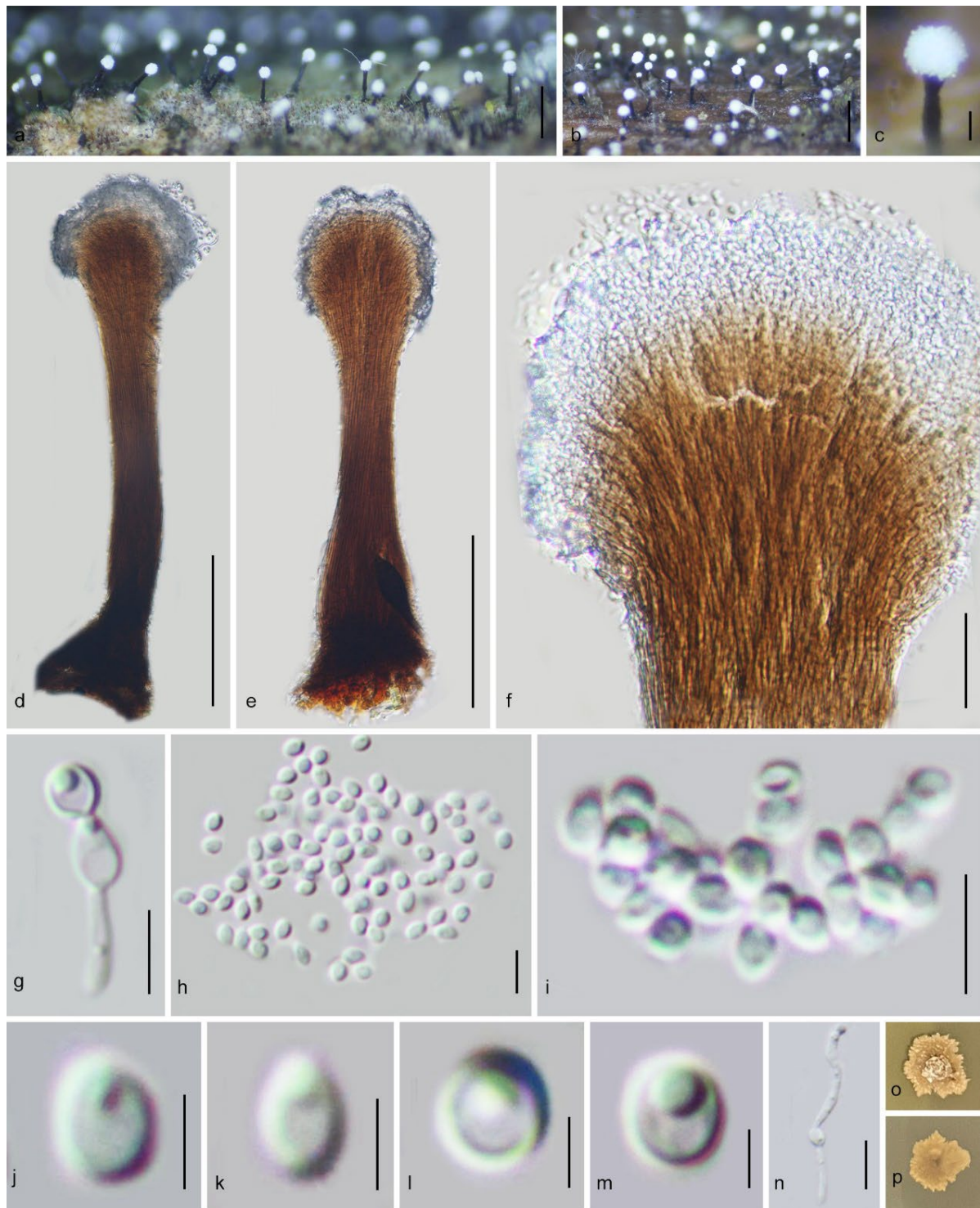


Figure 57 – *Rhamphoriopsis globularis* (GMB5313, holotype) a–c Colony on wood. d–f Conidiophores and conidia. g Conidiogenous cells and conidia. h–m Conidia. n Germinating conidium. o Surface view of culture on PDA. p Reverse view of culture on PDA. Scale bars: a, b = 0.5 mm, c = 0.1 mm. d, e = 100 μ m, f = 20 μ m, g–i = 5 μ m, j–m = 2 μ m, n = 10 μ m.

The diversity of hyphomycetous fungi in Southwestern China is currently being studied. In the current study, we introduce 29 new hyphomycetous species from this region. The discovery of

such a large number of new hyphomycetous species in a single study underscores the remarkable fungal diversity of Southwestern China and reinforces its status as a critical region for mycological research.

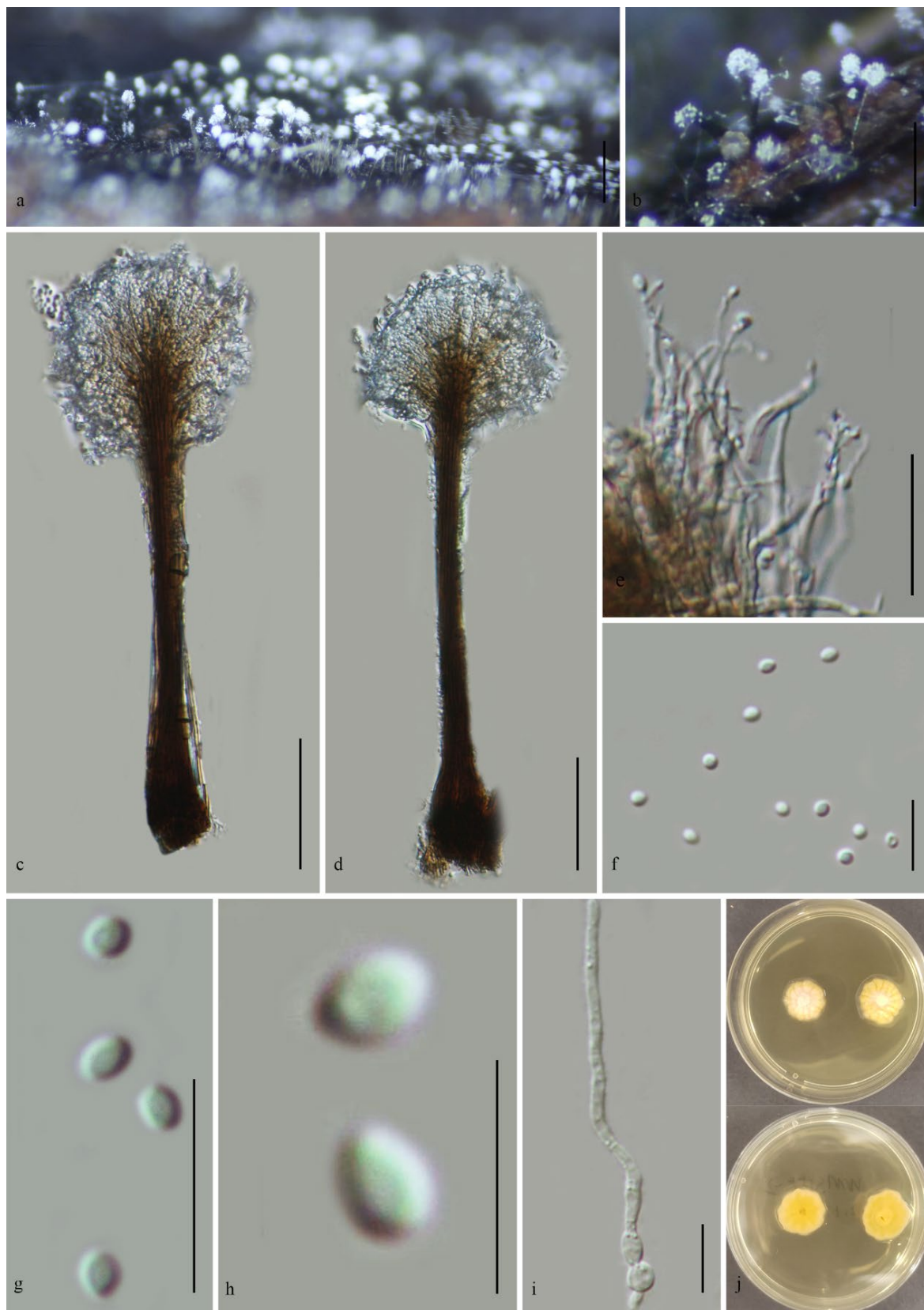


Figure 58 – *Rhamphoriopsis yunnanensis* (GMB6917, holotype) a–b Conidiophores and conidia on natural substratum. c–d Conidiophores and conidia. e Conidiogenous cells. f–h Conidia.

i Germinating conidia. j Surface and reverse view of culture on PDA. Scale bars: a = 0.5 mm, b = 0.2 mm, c–d = 50 μ m, e = 20 μ m, f–g, i = 10 μ m, h = 5 μ m.

Globally, Hyphomycetes comprise over 2,265 genera and 13,800 species (Ellis 1971, 1976, Seifert et al. 2011, Wijayawardene et al. 2022) yet estimates suggest that between 540,000 and 860,000 anamorphic fungi remain undiscovered (Wijayawardene et al. 2022). Our study identified 36 hyphomycetous fungi belonging to 21 families and 28 genera. Among these species, 28 are new to science and 8 are new records for the region, represent a substantial contribution to this group. Hyphomycetes include fungi of agricultural, medical, and industrial importance (Hyde et al. 2017, Jones et al. 2014), highlighting the broader implications of our work beyond taxonomy.

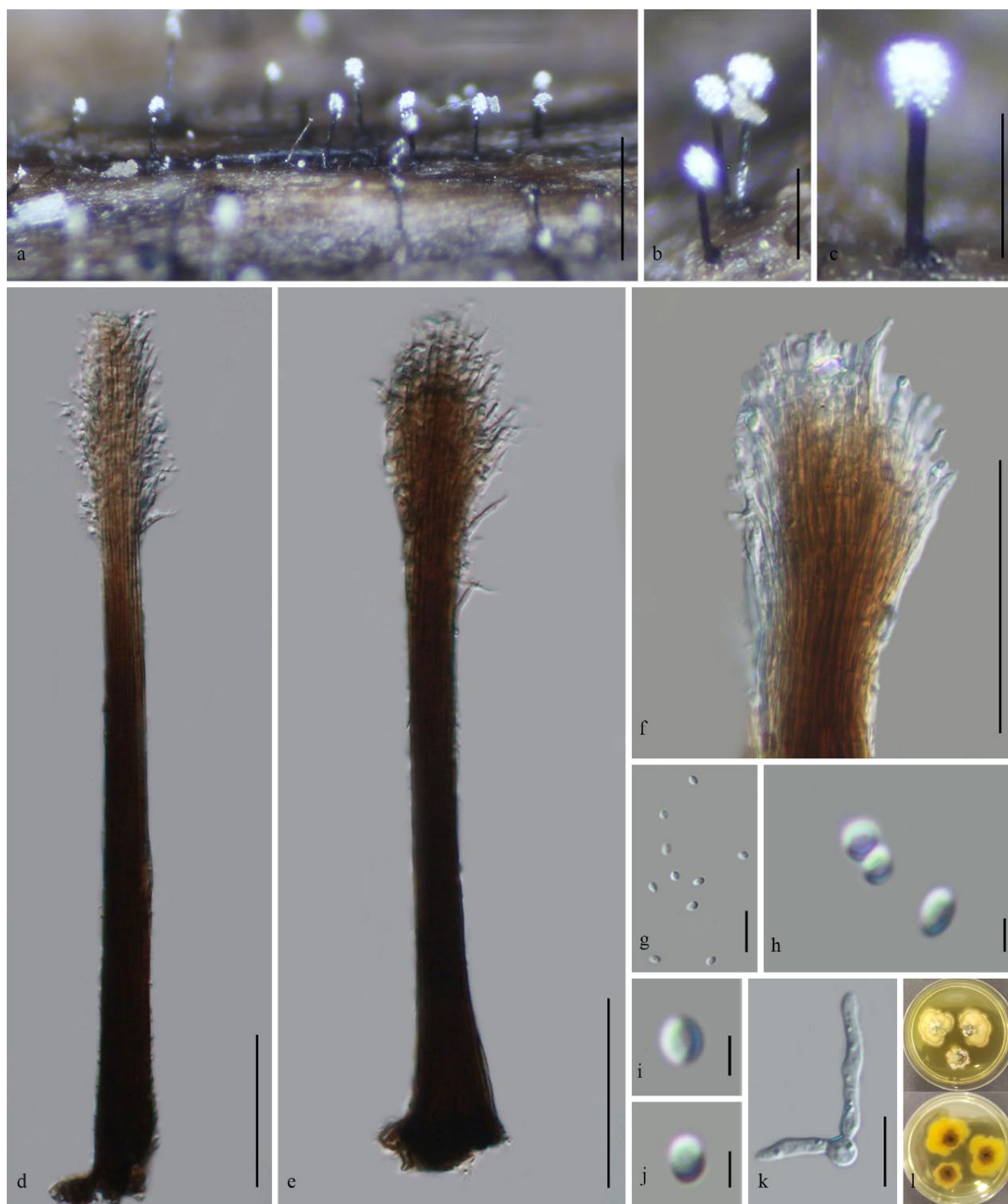


Figure 59 – *Rhamphoriopsis zhaotongensis* (GMB6918, holotype) a–c Conidiophores natural substratum. d, e Conidiophores and conidia. f Conidiogenous cells. g–j Conidia. k Germinating

conidia. l Surface and reverse view of culture on PDA. Scale bars: a = 0.5 mm, b, c = 0.2 mm, d–f = 50 μ m, g, k = 10 μ m, h–j = 2 μ m.

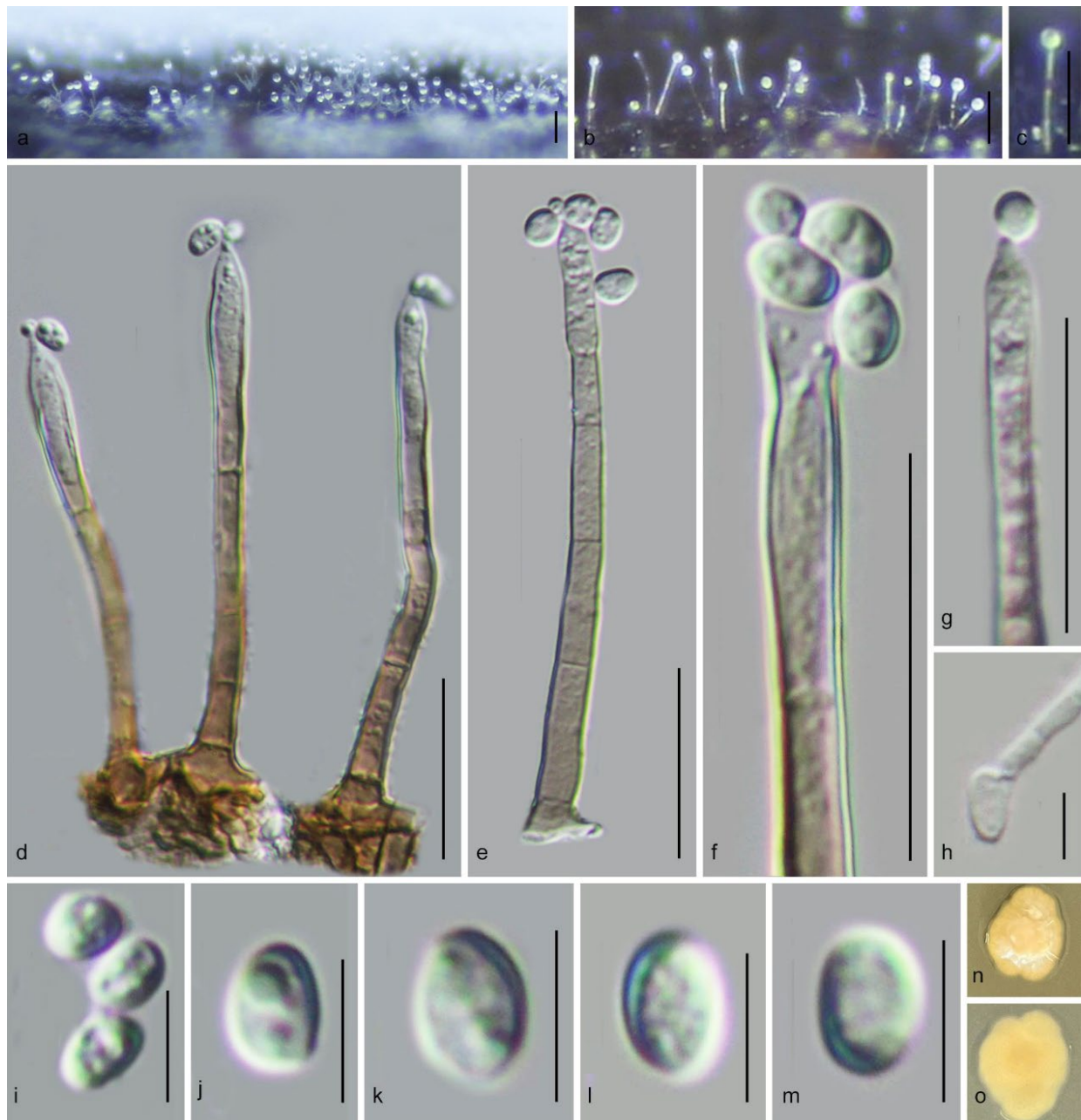


Figure 60 – *Xylolentia yibinensis* (GMB5367, holotype) a–c Colony on wood. d–f Conidiophores and conidia. g Conidiogenous cells and conidia. h Germinating conidium. i–m Conidia. n Surface view of culture on PDA. o Reverse view of culture on PDA. Scale bars: a–c = 0.1 mm, d–g = 20 μ m, h–m = 5 μ m.

Our findings are based on comprehensive molecular phylogenetic analyses and comparative morphological examinations. Our study encountered several taxonomic challenges that reflect broader issues in hyphomycetes research. For example, some phylogenetically closely related species were previously described solely based on culture characteristics, complicating comparisons with our specimens collected from natural substrates. Our statistical analysis revealed that conidial size alone is an unreliable criterion for species delimitation in some hyphomycetes. Species with small conidia and ellipsoidal or ovoid shapes proved difficult to distinguish morphologically, whereas those with larger conidia showed greater variation in size, shape, and

color, offering more reliable differentiation. This limitation was particularly evident in genera like *Protocreopsis* where most species have been described based on teleomorphic stages or culture-based anamorphs, with conidia typically measuring 7–8 μm in length (Rossman et al. 1999, Lechat et al. 2016, Hou et al. 2023). In our study, *Protocreopsis alba* formed an independent clade in the phylogenetic analysis, yet their conidial dimensions on natural substrates showed no variation from previously described species with anamorph based on culture characteristic. This underscores the necessity of multi-locus molecular analyses, which provide greater resolution for distinguishing closely related taxa, especially when morphological markers are ambiguous.

The complexity of pleomorphic fungi also complicates taxonomic efforts. Some Hyphomycetes have both teleomorphic and anamorphic morphs, sometimes in the same host at the same time or only one morph at a time, while others produce multiple anamorphs (synanamorphs e.g., *Chloridium*, *Tubeufia*) (Thiyagaraja et al. 2025). Similarly, fungi described solely based on culture-based characteristics are often difficult to distinguish. For example, *Volutella minutissima*, previously described based on its teleomorph and culture-based anamorph, was here introduced with its anamorph from natural substrates.

Phylogenetically, the newly described genus *Bulbocatenuomyces* clusters closely with the genus *Clematidis*, which is primarily known for its teleomorphic states. However, as the anamorphic states of *Clematidis* remain undescribed and phylogenetically *Clematidis* form a distinct clade, we cannot confidently assign our isolates as its anamorphs. Therefore, we proposed the new genus *Bulbocatenuomyces*. This ambiguity likely stems from several factors including insufficient collection and study of Hyphomycetes in natural habitats, geographically or host-substrate restricted sampling efforts, and the potential for some species to express their anamorphic phase on different hosts or during different seasons than their teleomorphic phase. Resolving these taxonomic uncertainties requires significantly expanded, systematic sampling across diverse hosts, substrates, seasons, and geographical regions, coupled with integrated morphological and molecular study.

The identification of new Hyphomycetes species in this study is likely just the tip of the iceberg for the fungal diversity of southwestern China. The unique combination of topographic complexity, climatic suitability, and ecological diversity of the region suggests that many more undescribed taxa await discovery, particularly in freshwater and other understudied habitats. Future research should prioritize polyphasic approaches, combining advanced molecular techniques with detailed morphological and ecological observations, to uncover the full extent of Hyphomycetes diversity.

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DECLARATION ON CONFLICT OF INTEREST

The authors have declared that no competing interests exist.

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