

Fungal diversity of Ascomycota in China and Thailand: Descriptions of new taxa in honour of Kevin D. Hyde's 70th birthday

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Abstract

China and Thailand possess a rich fungal biodiversity. In this study, we introduce four novel genera-*Aquaguizhoumyces* (*Neohendersoniaceae*), *Biseriospora* (*Dactylosporaceae*), *Pseudocatenuliconidia* (*Vamsapriyaceae*), *Xenobactrodesmium* (*Savoryellaceae*)-alongside 47 new species and three new habitat or distributional records. All newly described taxa are comprehensively documented through morphological characterization and relationships analyzed based on multigene phylogenetic analyses. The new species include: *Acrogenospora hydei*, *A.*

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keviniana, *Acrohelicosporium hydei*, *Aquaguizhoumyces hydei*, *Berkleasium hydei*, *Biseriospora hydei*, *Brachiosphaera hydei*, *Conioscypha davidii*, *C. hydei*, *C. keviniana*, *Cylindromonium hydei*, *Cyphellophora hydeae*, *Distoseptispora davidii*, *D. keviniana*, *D. polyblasta*, *D. pseudoaquisubtropica*, *D. solitaria*, *D. vaginae*, *D. velvetica*, *Fusichalara hydei*, *Helicoma kevinianum*, *Longiappendispora keviniana*, *Melomastia hydeae*, *Menisporopsis hydei*, *Neogaeumannomyces hydei*, *N. kevinifiliformis*, *Neohelicomyces davidii*, *Ne. kevinianus*, *Neohelicosporium hydei*, *Neo. kevinianus*, *Neomassaria davidii*, *Neom. hydeae*, *Neom. keviniana*, *Paramonodictys hydei*, *Pararoussoella hydei*, *Pleopunctum hydei*, *Pseudocatenuliconidia hydei*, *Pseudodactylaria hydei*, *Pseudorobillarda hydeana*, *Setophoma hydei*, *Sporoschisma hydei*, *Trichoderma guangxiensis*, *T. mashanense*, *T. zhongshanense*, *Tubeufia hydei*, *Vikalpa hydei*, and *Xenobactrodesmium hydei*. Furthermore, we report two new habitat records for *Rhodoveronaea hyalina* and *Hermatomyces xizangensis*, as well as a new geographical and habitat record for *Polyplosphaeria appendiculata*. All taxa are supported by morphological and multigene phylogenetic analyses. This contribution is dedicated to Kevin D. Hyde in celebration of his 70th birthday, in recognition of his outstanding contributions to the field of mycology.

Keywords – 51 new taxa – *Dothideomycetes* – freshwater fungi – phylogeny, *Sordariomycetes* – taxonomy

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INTRODUCTION

Fungi play pivotal roles in ecosystems as decomposers, symbionts, and pathogens of both plants and animals (Blackwell 2011, De Silva et al. 2016, Hongsanan et al. 2020a, b, Hyde et al. 2020b, Senanayake et al. 2023, Liu et al. 2024b). They are ubiquitously distributed across diverse environments, including soil, water, living organisms, and organic remains, exhibiting an extraordinary degree of species diversity (Barron 1968, Jayawardena et al. 2020, Yang et al. 2023, Ren et al. 2024a, Shen et al. 2024b, Wanasinghe et al. 2025). Among these, saprobic fungi represent the largest functional group, primarily obtaining nutrients through the decomposition of organic materials such as dead plant and animal matter and feces (Richardson 2001, Hyde et al. 2023, Liu et al. 2024b, Ma et al. 2024b, Sun et al. 2025). Consequently, saprobic fungi play a critical role in global carbon cycling and sequestration (Lebreton et al. 2021). Furthermore, they serve as important sources of nutrients and bioactive compounds, with applications in food, nutraceuticals, cosmetics, medicine, pharmaceuticals, and various industrial processes (Šnajdr et al. 2011, Mortimer et al. 2012, Hyde et al. 2019b, Niego et al. 2021, Badalyan et al. 2022).

China and Thailand are among the countries with the highest recorded fungal diversity worldwide (Wang et al. 2021, Wang & Cai 2023). In 2020 alone, 2,905 new fungal species and infraspecific taxa were published globally. China led with the discovery of 663 new species, accounting for 23% of the global total, followed by Thailand with 10% (Wang et al. 2021). According to the international fungal database Species Fungorum (<https://speciesfungorum.org/names/names.asp>, accessed on 16 April 2025), over 160,000 fungal species have been described globally. Of these, more than 27,000 fungal species have been recorded in China (National Microbiology Data Center, <https://nmdc.cn/resource/db/chinadirectoriesitem>, accessed on 16 April 2025).

To commemorate the 70th birthday of Prof. Dr. Kevin D. Hyde and to honor his outstanding contributions to mycology, this study introduces four new genera, 47 new species, and three new records of geographical or habitat distribution. Detailed morphological descriptions, photo-plates, cultural characteristics, and multigene phylogenetic analyses are provided to document these fungi.

MATERIALS AND METHODS

Collection, examination and isolation

Decaying wood or leaves samples were collected from freshwater and terrestrial habitats in China and Thailand, following the method described by Senanayake et al. (2020). The samples were brought to the laboratory and incubated under moist conditions at room temperature for 3–5 days. After incubation, the samples were examined under a dissecting microscope, and the microscopic features of the fungi were studied and photographed. Measurements of the fungal fruiting bodies were taken using Tarosoft (R) Image Frame Work software (Liu et al. 2010). Photo-plates with selected images were prepared using Adobe Photoshop CC 2019 (Adobe Systems, USA). Pure cultures were obtained from single spore isolations on water agar (WA) or potato dextrose agar (PDA). Dried specimens were deposited in the herbarium of the Kunming Institute of Botany, Academia Sinica (HKAS), Kunming, China, the herbarium of the University of Electronic Science and Technology (UESTC), Chengdu, China, the herbarium of Guizhou Medical University (GMB), Guiyang, China, and the herbarium of the Guizhou Academy of Agriculture Sciences (GZAAS), Guiyang, China. Pure cultures were deposited in the China General Microbiological Culture Collection Center (CGMCC), Beijing, China, the University of Electronic Science and Technology Culture Collection (UESTCC), Chengdu, China, the Guizhou Medical University Culture Collection (GMBCC), Guiyang, China, and the Guizhou Culture Collection (GZCC), Guiyang, China. Facesoffungi (FoF) numbers were obtained as described by Jayasiri et al. (2015), and the names of new taxa were registered in Fungal Names (2025) or Index Fungorum (2025).

DNA extraction, PCR amplification and sequencing

Fungal colonies grown on PDA medium for 1–2 months at 25°C in an incubator or at room temperature were used for DNA extraction. Fresh mycelia were scraped and genomic DNA was extracted using a commercial kit (Sangon Biotech, Shanghai, P.R. China). Six primer pairs were selected in this study (not for every analysis): The primer pairs ITS5/ITS4 (White et al. 1990) for the internal transcribed spacer (ITS) region, LR0R/LR5 (Vilgalys & Hester 1990) for the large subunit ribosomal DNA (28S, LSU), NS1/NS4 (White et al. 1990) for the small subunit ribosomal DNA (18S, SSU), EF1-983F/EF1-2218R (Rehner & Buckley 2005) for the translation elongation factor 1- α (*tef1- α*) gene, Bt2a/Bt2b (Glass & Donaldson 1995) for the β -tubulin (*tub2*) gene, and fRPB2-5F/fRPB2-7cR (Liu et al. 1999) for the second largest subunit of RNA polymerase II (*rpb2*) gene were used for PCR amplification. Polymerase chain reactions (PCR) were performed following protocols described by Liu et al. (2019 a, b). PCR products were purified and sequenced by Sangon Biotech (Shanghai, P.R. China).

Phylogenetic analyses

Phylogenetic analyses were performed separately for new taxa to analyze their phylogenetic relationships. Sequence alignments were generated using the online MAFFT version 7 platform (<https://mafft.cbrc.jp/alignment/server/index.html>) with default settings. Ambiguous or uninformative regions were trimmed using Trimal v1.2 (Capella-Gutierrez et al. 2009) with the “gappyout” option. Multiple gene alignments were concatenated using SequenceMatrix 1.7.8 (Vaidya et al. 2011), and the combined datasets were checked and converted into various formats using AliView (Larsson 2014). Newly generated sequences were submitted to GenBank.

Maximum likelihood (ML) analyses were conducted using the IQ-TREE web server (Trifinopoulos et al. 2016) with 1,000 ultrafast bootstrap (BS) replicates, and the substitution model option was selected automatically. Bootstrap support values (ML-BS) equal or greater than 75% are indicated above or below each branch, respectively.

Bayesian inference (BI) analyses were performed using MrBayes v3.2.6 under the Markov chain Monte Carlo (MCMC) algorithm (Ronquist et al. 2012). The best-fit substitution model for each gene was determined using MrModeltest v2.3 (Nylander 2008) under the Akaike Information Criterion (AIC). Two parallel MCMC runs of four chains each were executed for 1,000,000 generations or until the average standard deviation of split frequencies dropped below 0.01 (stopval = 0.01). Trees were sampled every 1,000 generations, and the first 25% were discarded as burn-in. The remaining trees were used to calculate posterior probabilities (PP). PP values equal or greater than 0.95 are shown above or below the corresponding branches.

Phylogenetic trees were visualized and edited using FigTree v1.4.4 (<https://tree.bio.ed.ac.uk/software/figtree>), and the exports were edited using Adobe Illustrator CS6 software (Adobe Systems, USA).

TAXONOMY

In this paper, we adopt the classification scheme proposed by Hyde et al. (2024). The phylum Ascomycota and its subordinate taxonomic ranks are listed in alphabetical order.

Phylum Ascomycota Caval.-Sm.

Subphylum Pezizomycotina O.E. Erikss. & Winka

Class Dothideomycetes O.E. Erikss. & Winka

Subclass Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker

Dyfolomycetales K.L. Pang, K.D. Hyde & E.B.G. Jones

Pleurotremataceae Walt. Watson

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

Melomastia has a global distribution, and the majority of *Melomastia* species are saprobes

found in diverse habitats, such as terrestrial, freshwater, marine, and mangrove ecosystems (Li et al. 2022b, Kularathnage et al. 2023, Du et al. 2024). The sexual morph of *Melomastia* is characterized by globose to subglobose, coriaceous to carbonaceous, ostiolate ascomata, bitunicate, 8-spored, cylindrical asci, and fusiform to oblong, ovoid, or cylindrical, hyaline, septate ascospores with or without gelatinous sheath (Du et al. 2024, Ren et al. 2024a), while the asexual morph of *Melomastia* remains undetermined. Many *Melomastia* species, including the type species *M. mastoidea*, lack molecular data.

Melomastia hydeae Y.X. Yu & Jian K. Liu, sp. nov.

Fig. 1

Fungal Names number: FN 573022; Facesoffungi number: FoF 17825

Etymology – The specific epithet “hydeae” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 149986

Saprobic on dead branches of wood. Sexual morph: *Ascomata* 389–633 × 415–556 µm ($\bar{x}$ = 562 × 484 µm, n = 10), visible as numerous, black, cone-shaped structures on host surface, solitary, gregarious, semi-immersed, globose to compressed globose, carbonaceous, dark brown to black, rough-walled, ostiolate. *Ostioles* 124–268 × 137–189 µm ($\bar{x}$ = 170 × 161 µm, n = 15), neck crest-like, central, carbonaceous, dark brown to black, papillate, periphyses filling the ostiolar canal. *Peridium* 19–32 µm wide, two-layered, outer thick, carbonaceous and inner composed of 5–6 layers of hyaline cells of *textura angularis* to *textura prismatica*. *Hamathecium* 1.6–2.9 µm ($\bar{x}$ = 2 µm, n = 15), composed of numerous, dense, filiform, unbranched, septate, cellular pseudoparaphyses. *Asci* 106–168 × 7–10 µm ($\bar{x}$ = 145 × 8.9 µm, n = 30), 8-spored, bitunicate, cylindrical or subclavate, apically round, with a small ocular chamber. *Ascospores* 17–22 × 6–8 µm ($\bar{x}$ = 20 × 7 µm, n = 30), uniseriate, partial overlapping, ellipsoid with broad fusiform ends, 2(-3)-septate, constricted at the septa, hyaline glistening, with guttules in each cell, smooth-walled with mucilaginous sheaths. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h. Colonies growing well on PDA and reaching about 20 mm diam. after 2 weeks at 25 °C, circular, medium dense, flat to raised, margin entire, white from above, pale yellow to yellow from below.

Material examined – China, Sichuan Province, Mianyang City, Qiqu Mountain scenic spot, 31°40'23"N, 105°11'1"E, 560 m elevation, on dead wood in terrestrial habitat, 08 October 2023, Y.X. Yu, MY05A (HKAS 149986, holotype), ex-type culture CGMCC 3.29112 = UESTCC 25.0251; *ibid.*, MY05B (HUEST 25.0065, isotype), ex-isotype UESTCC 25.0252.

Notes – Phylogenetic analysis results showed that *Melomastia hydeae* clustered with *M. italica*, *M. rhizophorae* and *M. thailandica*, but represented a distinct clade with high support (98% ML, 1.00 BYPP) (Fig. 2). NCBI BLASTn searches of our collection, *M. guttata* showed 90.85% similarity to *M. septata* (MFLUCC 22-0112) in the ITS sequence, 98.70% similarity to *M. italica* (MFLUCC 15-0160) in the LSU sequence, and 99.18% similarity to *M. rhizophorae* (JK 5349A) in the SSU sequence. *Melomastia hydeae* share similar ascus and ascospore morphology with *M. italica*, *M. rhizophorae* and *M. thailandica*. However, *Melomastia hydeae* has larger (19.6×7 vs. 10.1–4 µm) and 2(-3)-septate ascospore when compared to *M. italica*. In addition, the ascospore ends of the *Melomastia hydeae* are usually pale pointed, which differs from *M. italica* as the latter's ascospore has round to acute ends (Norphanphoun et al. 2017). Additionally, *Melomastia hydeae* is easily differentiated from *M. rhizophorae* and *M. thailandica* by having the ellipsoid with broad fusiform ends, 2(-3)-septate, and smooth-walled ascospore (Hyde et al. 2016, Dayarathne et al. 2020). Therefore, *Melomastia hydeae* is introduced as a new species based on morphological characters and phylogenetic evidence.

Jahnulales K.L. Pang, Abdel-Wahab, El-Shar., E.B.G. Jones & Sivichai

Aliquandostipitaceae Inderb.

Brachiosphaera Nawawi, Transactions of the British Mycological Society 67 (2): 213 (1976)

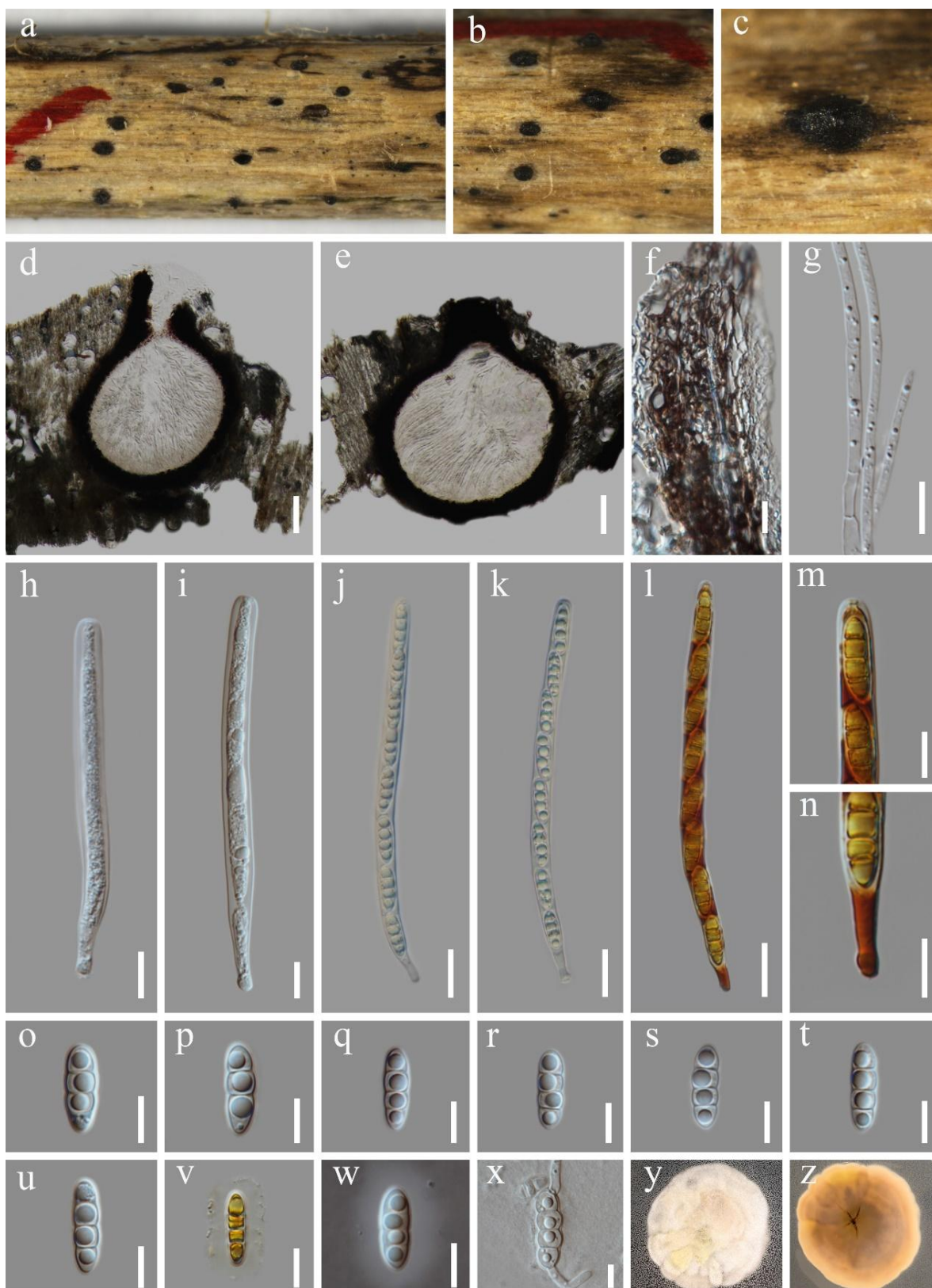


Figure 1 – *Melomastia hydeae* (HKAS 149986, holotype) a Habitat of the host surface. b, c Ascomata immersed in the host surface. d, e Vertical section through ascoma. f Vertical section of the peridium. g Hamathecium. h–l Asci(l) in Lugol's iodine. m ocular chamber in Lugol's iodine. (n) pedicel in Lugol's iodine. o–v Ascospores ((v) in Lugol's iodine). w Ascospore stained in Indian ink showing the mucilaginous sheath. x Germinating ascospore. y, z Colony on PDA above and below. Scale bars: d, e = 100 μ m, j–l = 20 μ m, f–i, m–n, o–x = 10 μ m.



Figure 2 – ML tree based on the combined LSU, SSU and *tef1-α* sequences, representing the genus *Melomastia* and *Dyfrolomyces*. Bootstrap support values for ML equal to or greater than 75% are placed above the branches and PP values equal to or greater than 0.90 are indicated in bold branches. The tree is rooted with *Anisomeridium phaeospermum* (MPN539) and *Anisomeridium ubianum* (MPN94). Ex-type strains are indicated in bold. The new taxon is indicated in red.

Brachiosphaera was introduced by Descals et al. (1976) based on the type species *Br. tropicalis*, along with a new combination *Br. jamaicensis* (= *Actinospora jamaicensis*). *Brachiosphaera* belongs to *Aliquandostipitaceae* (*Jahnulales*, *Dothideomycetes*). *Brachiosphaera* is characterized by hyaline, simple or branched conidiophores, monoblastic conidiogenous cells, and hyaline, globose to subglobose conidial body with radiating arms (Descals et al. 1976, Seifert

et al. 2011). To date, three species, viz., *Br. jamaicensis* (type species), *Br. radiaticonidiosa*, *Br. tropicalis*, are accepted in *Brachiosphaera* and all of them have been reported from freshwater habitats (Calabon et al. 2022, Xu et al. 2025).

Brachiosphaera hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 3

Fungal Names number: FN 572851; Facesoffungi number: FoF 17809

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – GZAAS 25-0534

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, grey, shiny. *Mycelium* immersed in the substratum, composed of branched, septate, hyaline to brown hyphae. *Conidiophores* 219–328 × 10–18 µm ($\bar{x}$ = 273 × 13 µm, n = 20), erect, flexuous, subcylindrical or sometimes moniliform, mostly simple, septate, subhyaline to brown, paler towards the apex, thick-walled. *Conidiogenous cells* 13–23 × 9–17 µm ($\bar{x}$ = 18.5 × 14 µm, n = 20), monoblastic, integrated, terminal, cylindrical to variously shaped, subhyaline to pale brown, smooth. *Conidia* 37–56 µm ($\bar{x}$ = 45 µm, n = 20) diam., globose to subglobose, filled with numerous small globose globules, hyaline, furnished with 4–8 radiating arms, hyaline, 0–4 septate, smooth, 21–69 × 5–10 µm ($\bar{x}$ = 40 × 8 µm, n = 30).

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes producing from conidial arms. Colonies reaching up to 32 mm diam. after 35 days of cultivation at 28°C, circular, medium dense, rough on the surface, with entire margin, greyish brown at center, dark brown at outer ring from above, sometimes with white mycelia grown on the surface; pale brown to dark brown; dark brown at center, yellowish brown at outer ring from below.

Material examined – China, Guizhou Province, Zunyi City, Tian E Bao Forest Park, N 28°31'59", E 106°1'59", elevation 941 m, on decaying wood from a freshwater stream, 28 July 2022, X.J. Xiao, TEB1 (GZAAS 25-0534, holotype), ex-type culture GZCC 25-0519.

Notes – Our collection differs from *Br. jamaicensis* by having smaller (37–56 µm vs. 55–66 µm) conidial body. Besides, our collection has less (4–8 vs. 10–14) conidial arms than those of *Br. jamaicensis* (Descals et al. 1976). In our phylogenetic tree (Fig. 13), our strain GZCC 25-0519 formed a sister clade to *Br. radiaticonidiosa* (KUNCC 24-17943) with 84% ML and 1 PP support. Although, *Br. hydei* and *Br. radiaticonidiosa* share similar morphology (Xu et al. 2025), ITS comparison shows there are 2.7% bp differences (14 out of 505 bp, without gaps). Therefore, we identify our collection as a distinct species based on recommendations outlined by Jeewon & Hyde (2016). Presently, five *Br. tropicalis* strains (SS2523, SS2724, SS2944, SS2522, E192-1) have been deposited in GenBank. In our phylogenetic analysis (Fig. 4), strain SS2523, SS2724 and SS2944 grouped together, and strain SS2522 and E192-1 formed a distinct, clade respectively. We infer these strains may represent three different species. Fresh collections are needed to resolve this issue.

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

Acrogenosporaceae Jayasiri & K.D. Hyde

Acrogenospora M.B. Ellis, Dematiaceae Hyphomycetes: 114 (1971)

Acrogenospora was introduced by Ellis (1971) with *A. sphaerocephala* as the type species. Sexual morph of *Acrogenospora* was linked to *Farlowiella*, which has pedicellate didymospores (Boehm et al. 2009). Asexual morph is characterized by macronematous, mononematous, erect conidiophores, blastic, terminal or intercalary, percurrent conidiogenous cells, and globose to obovoid, brown, aseptate conidia (Ellis 1971, Goh et al. 1998, Bao et al. 2020, Li et al. 2024). *Acrogenospora* is frequently reported from freshwater habitats (Goh et al. 1998, Bao et al. 2020, Li et al. 2024), but some species also occur on terrestrial habitats (Goh et al. 1998, Hyde et al. 2023). *Acrogenospora* presently comprises 27 species (Species Fungorum 2025).

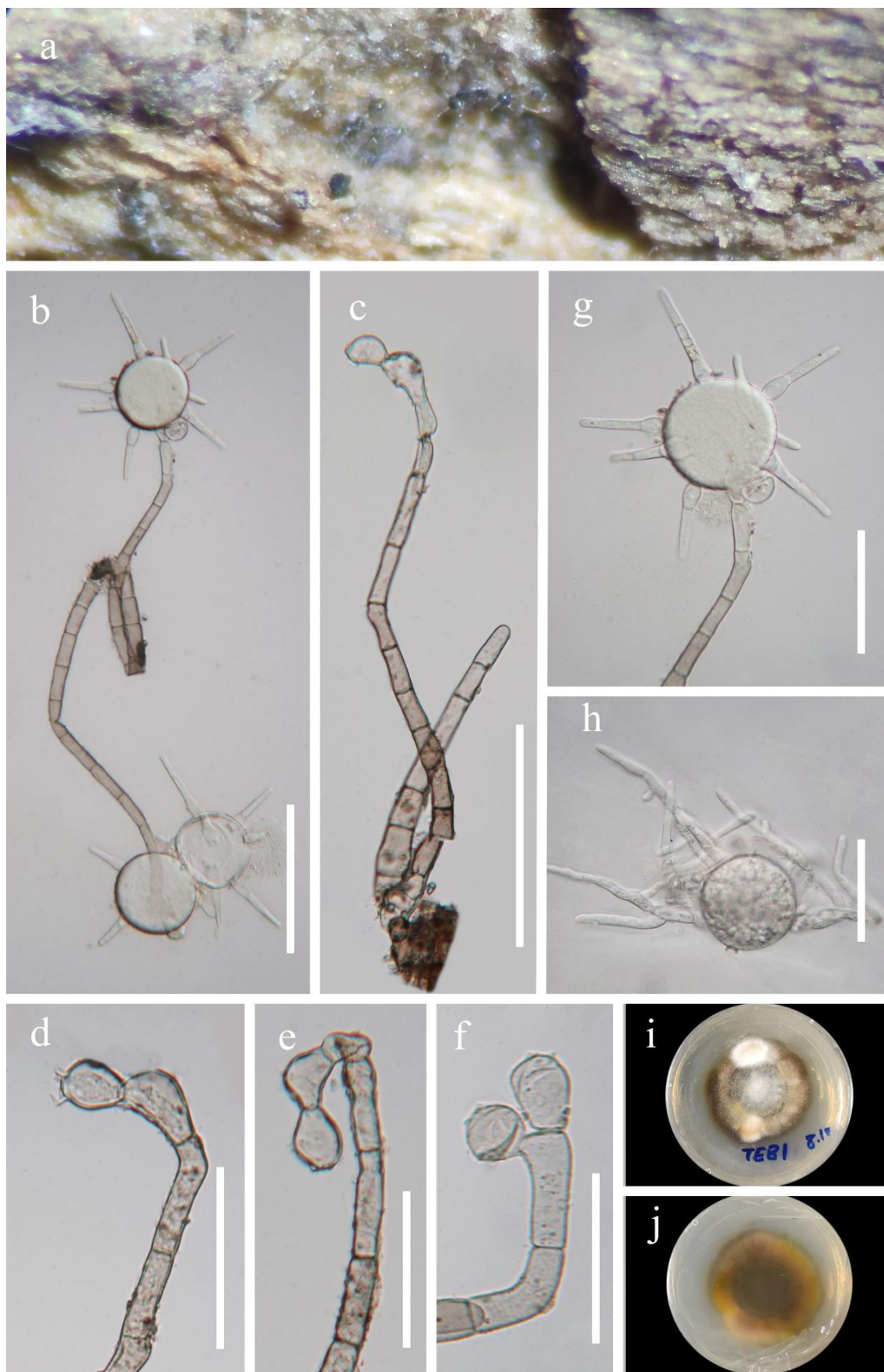


Figure 3 – *Brachiosphaera hydei* (GZAAS 25-0534, holotype). a Colonies on dead wood surface. b–g Conidiophores, conidiogenous cells and conidia. h Germinated conidium. i, j Colony on PDA (i from above, j from below). Scale bars: b, c = 100 μ m, d–h = 50 μ m.

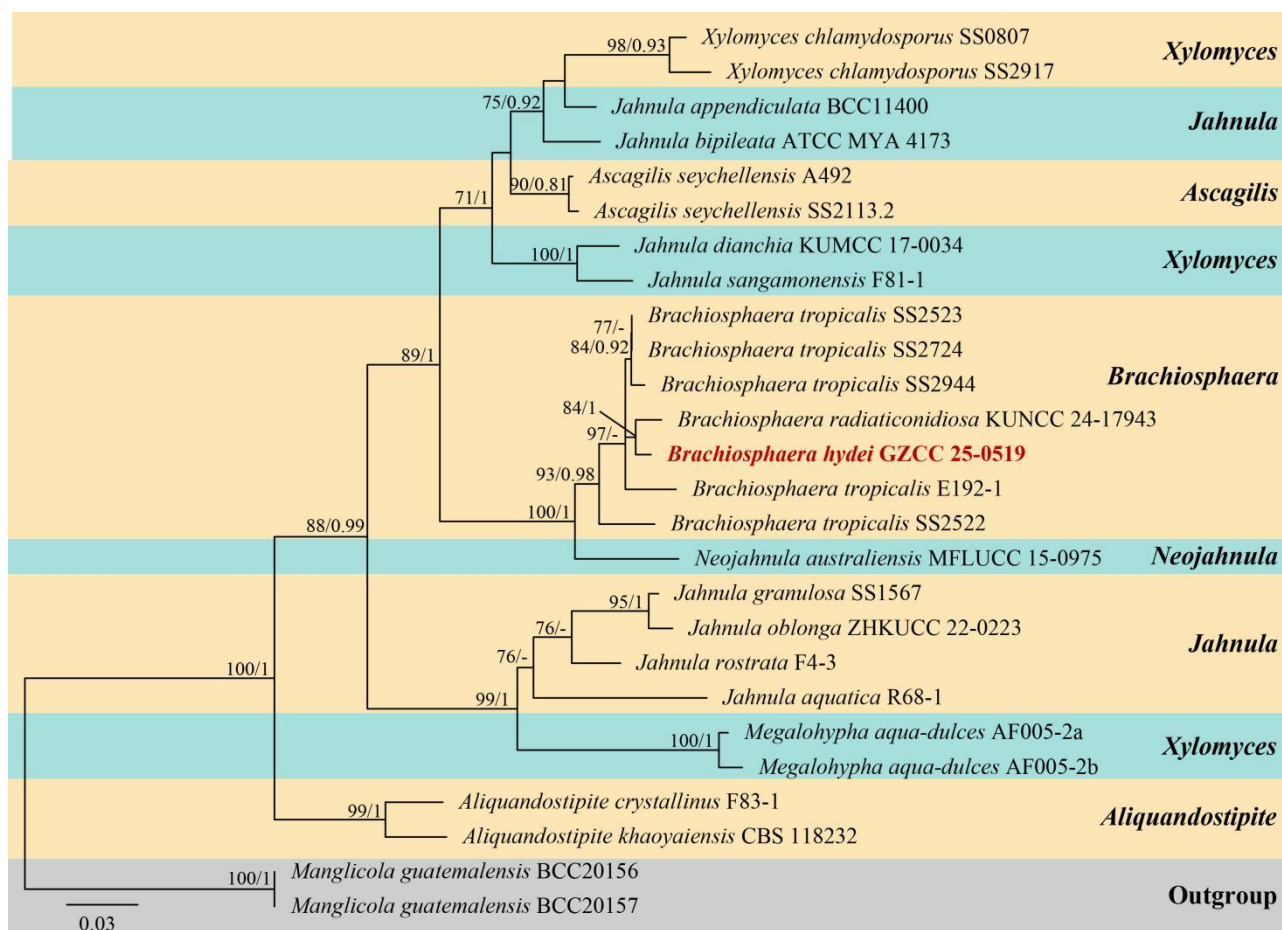


Figure 4 – ML tree based on the combined LSU and ITS sequences, representing the family *Aliquandostipitaceae*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Manglicola guatemalensis* (BCC20156 and BCC20157). The new taxon is indicated in bold and red.

Acrogenospora hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 5

Fungal Names number: FN 572843; Facesoffungi number: FoF 17802

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 132134

Saprobic on submerged rotting wood in a freshwater stream. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, dark brown, scattered, sparse. Mycelium immersed, composed of septate, branched, dark brown, smooth hyphae. Conidiophores 137–356 × 8–15 μm ($\bar{x}$ = 252 × 11.5 μm, n = 20), macronematous, mononematous, solitary, erect, long, straight or slightly flexuous, cylindrical, dark brown at base, paler towards apex, unbranched, septate, thick-walled. Conidiogenous cells monoblastic, integrated, terminal, brown, percurrent proliferating. Conidia 22–44 × 23–32 μm ($\bar{x}$ = 30 × 27 μm, n = 25), acrogenous, solitary, subglobose, ellipsoidal to pyriform, dark brown when mature, aseptate, verrucose.

Culture characteristics – Conidia germinating on PDA within 24 h and germ tubes produced from the basal end. Colonies reaching up to 25 mm diam. after 55 days, circular, surface rough, edge entire, medium dense, umbonate, initially pale brown, becoming brown at the outer margin, yellowish brown to dark brown with black center at the inner cycle, the outer margin and inner cycle delimited by a dark brown ring.

Material examined – China, Guizhou Province, Qiannan Prefecture, Weng'an County, Zhujiashan National Forest Park, N 26°58'8", E 107°37'5", elevation 958 m, on decaying wood

from a freshwater stream, 27 August 2023, X.J. Xiao, G2 (HKAS 132134, holotype), ex-type culture GZCC 24-0022.

Notes – In our phylogenetic tree (Fig. 7), our strains GZCC 24-0022 and GZCC 24-0108 grouped together and is sister to two strains of *Acrogenospora carmichaeliana* (FMR11021 and CBS 164.76) and three strains of *A. alticampestricola* (KUNCC 10428, KUNCC 24-18055 and KUNCC 24-18056). *Acrogenospora hydei* differs from *A. carmichaeliana* by having larger conidia ($22\text{--}44 \times 23\text{--}32\ \mu\text{m}$ vs. $19\text{--}32 \times 13\text{--}23.5\ \mu\text{m}$) (Goh et al. 1998). Besides, ITS comparison shows there are 5.1% (28 out of 551, including 4 gaps) differences with *A. carmichaeliana* (FMR11021). *Acrogenospora hydei* differs from *A. alticampestricola* by having much shorter conidiophores ($137\text{--}356\ \mu\text{m}$ vs. $318\text{--}589\ \mu\text{m}$) and ellipsoidal to pyriform, larger conidia ($22\text{--}44 \times 23\text{--}32\ \mu\text{m}$ vs. $21\text{--}30 \times 20\text{--}30\ \mu\text{m}$) (Xu et al. 2025). ITS comparison shows there are 4.6% (25 out of 544 bp, including 4 gaps) differences with the ex-type (KUNCC 10428) of *A. alticampestricola*. Therefore, we introduce a new species, *Acrogenospora hydei* to accommodate our collection.

Acrogenospora keviniana X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 6

Fungal Names number: FN 572844; Facesoffungi number: FoF 17860

Etymology – The specific epithet “keviniana” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 136241

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, dark brown, hairy. *Mycelium* immersed, composed of septate, branched, dark brown, smooth hyphae. *Conidiophores* $404\text{--}588 \times 8\text{--}15\ \mu\text{m}$ ($\bar{x} = 476 \times 11.6\ \mu\text{m}$, $n = 20$), macronematous, mononematous, solitary, erect, long, straight or slightly flexuous, cylindrical, dark brown at base, paler towards apex, unbranched, septate, thick-walled. *Conidiogenous cells* blastic, integrated, initially terminal, later becoming intercalary, percurrent proliferating brown. *Conidia* $22\text{--}37\ \mu\text{m}$ ($\bar{x} = 27.5\ \mu\text{m}$, $n = 25$) diam., acropleurogenous, solitary, globose, dark brown when mature, aseptate, smooth.

Culture characteristics – Conidia germinating on PDA within 24 h and germ tubes produced from the basal end. Colonies reaching up to 25 mm diam. after 55 days, circular, surface rough, edge entire, medium dense, umbonate, initially pale brown, becoming brown at the outer margin, yellowish brown to dark brown with black center at the inner cycle, the outer margin and inner cycle delimited by a dark brown ring.

Material examined – China, Guizhou Province, Qiannan Prefecture, Weng'an County, Zhujiashan National Forest Park, N $26^{\circ} 58' 8''$, E $107^{\circ} 37' 5''$, elevation 958 m, on decaying wood from a freshwater stream, 27 August 2023, X.J. Xiao, ZJ39 (HKAS 136241, holotype), ex-type culture GZCC 24-0108.

Notes – *Acrogenospora keviniana* (GZCC 24-0108) formed a sister clade with *A. hydei* (GZCC 24-0022) in our phylogenetic tree (Fig. 7). *Acrogenospora keviniana* differs from *A. hydei* by having longer conidiophores ($404\text{--}588\ \mu\text{m}$ vs. $137\text{--}356\ \mu\text{m}$). Besides, *Acrogenospora keviniana* only possesses globose conidia, while *A. hydei* has subglobose, ellipsoidal to pyriform conidia. ITS shows there are 4.04% differences (22 out of 545 bp, without gaps) between the strain GZCC 24-0022 and GZCC 24-0108. Therefore, we introduce the collection GZCC 24-0108 as a new species, namely *Acrogenospora keviniana*.

Pleosporales Luttr. ex M.E. Barr

Dictyosporiaceae Boonmee & K.D. Hyde

Vikalpa M.J. D'souza, Boonmee, Bhat & K.D. Hyde, Fungal Diversity, 80: 479 (2016)

Vikalpa was established by Boonmee et al. (2016) to accommodate a group of hyphomycetes with cheiroid conidia, with *V. australiensis* as the type species. The genus is characterized by superficial, punctiform or effuse, scattered, sporodochial conidiomata; micronematous, aseptate, hyaline to pale brown conidiophores; integrated, holoblastic, doliiform to cylindrical conidiogenous; and solitary, cheiroid, pale brown, euseptate or distoseptate conidia which consist of three rows of

cells that are in different planes, with or without appendages (Boonmee et al. 2016, Shen et al. 2022). Members of *Vikolpa* occur as saprobes on decaying wood substrates in terrestrial and freshwater habitats and are distributed in Australia, China, India, New Zealand, and the Federated States of Micronesia (Sutton 1985, McKenzie 2008, Boonmee et al. 2016, Shen et al. 2022, Liu et al. 2024c). Currently, seven species are accepted in the genus, of which only four from Yunnan Province, China, viz., *V. dujuanhuensis*, *V. grandispora*, *V. lignicola*, and *V. sphaerica*, are reported in freshwater habitats, and the remaining three are reported in terrestrial habitats.

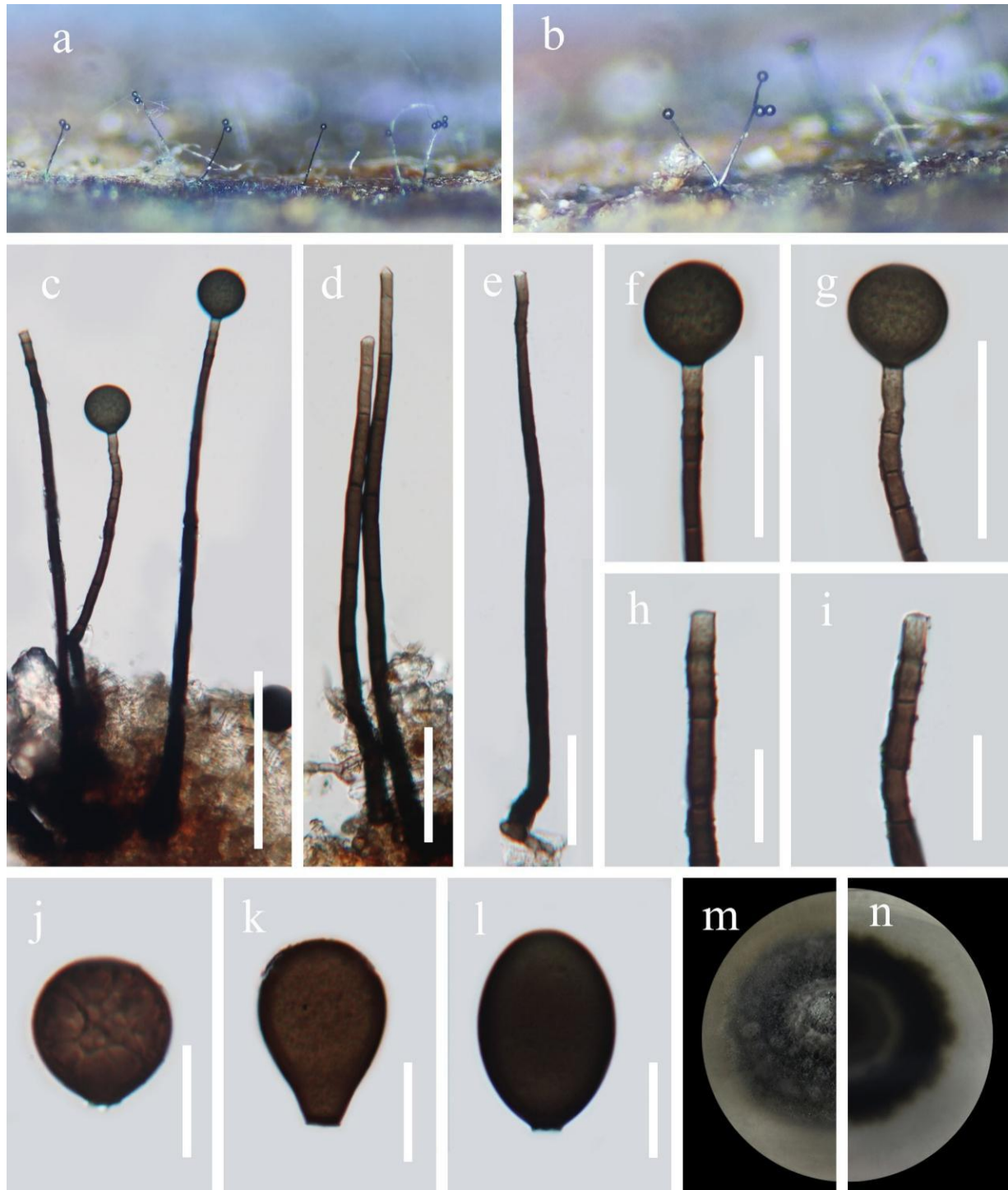


Figure 5 – *Acrogenospora hydei* (HKAS 132134, holotype). a, b Colonies on natural substrate. c–e Conidiophores and conidia. f–i Conidiogenous cells and conidia. j–l Conidia. m, n Colony on PDA (m from above, n from below). Scale bars: c, d = 100 μ m, e–i = 50 μ m, j–l = 20 μ m.

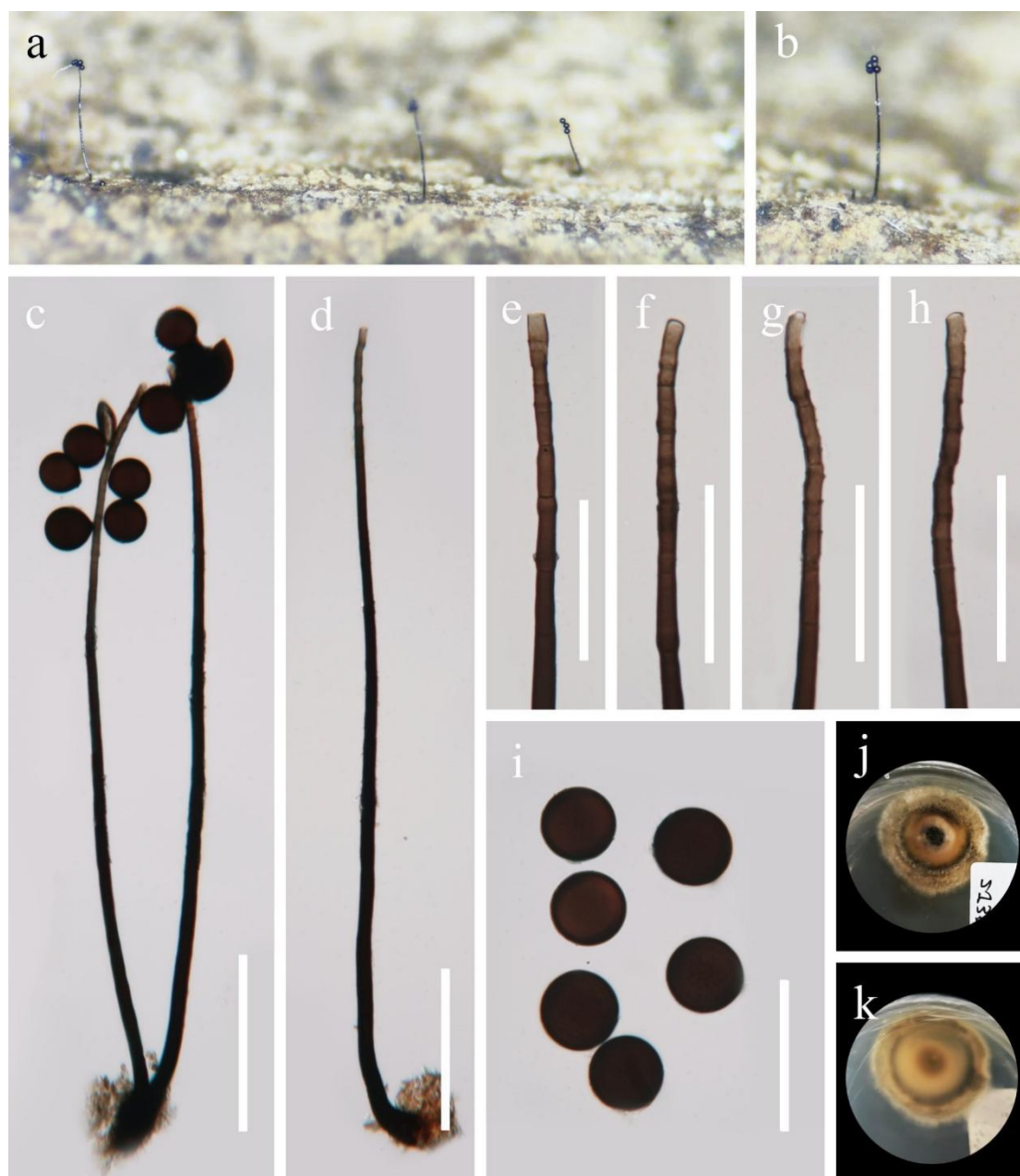


Figure 6 – *Acrogenospora keviniana* (HKAS 136241, holotype). a, b Colonies on natural substrate. c, d Conidiophores and conidia. e–h Conidiogenous cells. i Conidia. j, k Colony on PDA (j from above, k from below). Scale bars: c, d = 100 μ m, e–i = 50 μ m.

Vikalpa hydei H.W. Shen & Z.L. Luo, sp. nov.

Fig. 8

Fungal Names number: FN 573029; Facesoffungi number: FoF 17846

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday

Holotype – HKAS 145699

Saprobic on submerged decaying wood in a freshwater River. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate, punctiform, sporodochial, scattered, brown to dark brown. *Mycelium* composed of immersed or partly superficial, septate, branched, hyaline to pale brown hyphae. *Conidiophores* micronematous, mononematous, septate, cylindrical, unbranched, hyaline to pale brown, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 4–5.5(–6.5) $\times$ (3–)3.5–4 μ m ($\bar{x}$ = 4.5 $\times$ 4 μ m, n = 15) holoblastic, subcylindrical, subglobose, septate, hyaline to pale brown, smooth-walled. *Conidia* (44–)46–50(–52) $\times$ (13–)14–17(–19) μ m ($\bar{x}$ = 48 $\times$ 15 μ m, SD = 1.9 $\times$ 1.3, n = 50), solitary, cheiroid, pale brown

to brown, consisting of three rows of cells in different planes, 12–14 cells in each row, euseptate, irregular, constricted at the septa, guttulate, each row 6.5–8 µm wide, with globose to subglobose, gelatinous appendages, 6–10 µm diam.

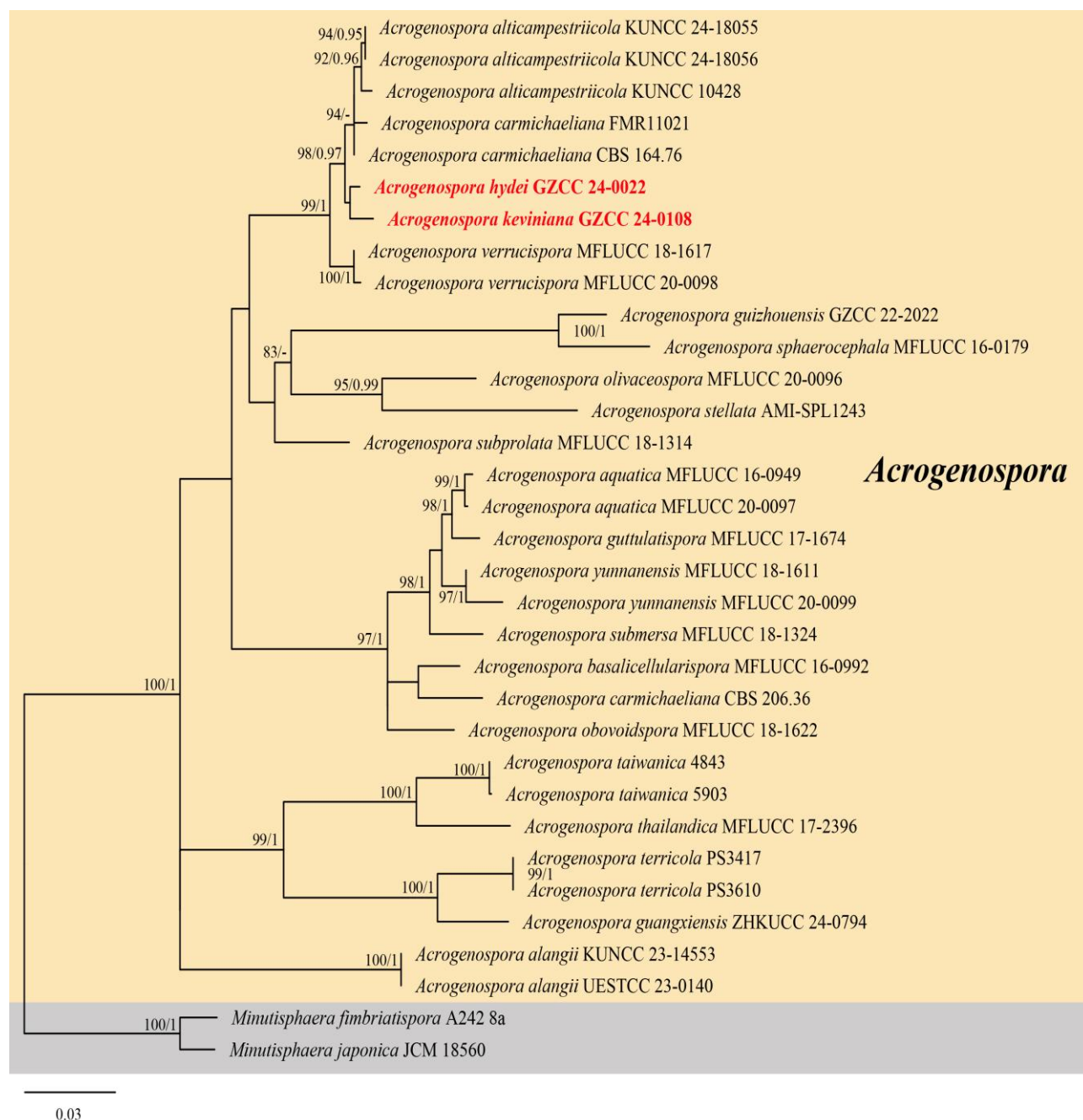


Figure 7 – ML tree based on the combined LSU, ITS, SSU, *rpb2*, and *tef1-α* sequences, representing the genus *Acrogenospora*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Minutisphaera fimbriatispora* (A242-8a) and *Minutisphaera japonica* (JCM 18560). The new taxa are indicated in bold and red.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes produced at ends. Colony growth on PDA; reaching about 1.5–2 cm in three weeks at room temperature. Mycelium papillary in the middle part, dense, creamy yellow, sparse, white at edge; brown to reddish-brown on the reverse side.

Material examined – China, Yunnan Province, Nujiang Prefecture, Fugong County,

27.260995°N, 98.881291°E (1300 m), on submerged decaying wood, 4 May 2023, Z.Q. Zhang, S4504 (HKAS 145699, holotype), ex-type culture DLUCC 4504.

Notes – Phylogenetic analysis showed that *Vikalpa hydei* clustered within *Vikalpa* clade with 100% ML and 1.00 PP support (Fig. 9). Morphologically, *V. hydei* conforms to the generic concept of *Vikalpa* in having superficial, punctiform or effuse, scattered, sporodochial conidiomata; micronematous, aseptate, hyaline to pale brown conidiophores; integrated, holoblastic, doliiform to cylindrical conidiogenous; and solitary, cheiroid, pale brown, euseptate or distoseptate conidia which consist of three rows of cells that are in different planes, with or without appendages (Boonmee et al. 2016, Shen et al. 2022). However, *V. hydei* can be distinguished by other *Vikalpa* species by longer conidia than *V. dujuanhensis* (38–49 µm), *V. grandispora* (38–49 µm), *V. australiensis* (36–43 µm), *V. freycinetiae* (31–43 µm), *V. lignicola* (25–40.5 µm), *V. micronesiaca* (20–30 µm) and *V. sphaerica* (26–30 µm) (Sutton 1985, McKenzie 2008, Boonmee et al. 2016, Shen et al. 2022, Liu et al. 2024c). In addition, *V. hydei* differs from *V. lignicola* and *V. micronesiaca* in having appendages, while *V. lignicola* and *V. micronesiaca* lack appendages (Boonmee et al. 2016). In a BLASTn search of NCBI, the closest matches of the LSU sequence of *V. hydei* (HKAS 145699) with 99% (819/824 bp, without gap) similarity, was to *V. sphaerica* (strain CGMCC, 3.20682, OP526649); the closest matches with the SSU sequence with 99% (1013/1016 bp, without gap) similarity, was to *Aquadictyospora lignicola* (voucher HUEST, 23.0213, PP925653); and the closest matches with the *tef1*-α sequences with 98% (915/937 bp, without gap) similarity, was to *V. sphaerica* (strain CGMCC 3.20682, OP542241). Therefore, based on morphological and sequence data, *V. hydei* is introduced as a new species from freshwater habitat.

Heratomycetaceae Locq. ex A. Hashim. & Kaz. Tanaka

Heratomyces Speg., Anal. Mus. nac. B. Aires, Ser. 3 13: 445 (1910)

Heratomyces was established by Spegazzini (1910) to accommodate *H. tucumanensis*. The genus is characterized by pulvinate, sporodochial conidiomata and dimorphic conidia (lenticular or cylindrical) arising from monoblastic, integrated, terminal, cylindrical conidiogenous cells. The lenticular conidia are globose to subglobose, ellipsoidal, muriform, with subhyaline to pale brown peripheral cells surrounding dark brown to black central cells; the cylindrical conidia are hyaline, cylindrical to subcylindrical or turbinate, consisting of 1–4 columns of 2–12 cells (Tibpromma et al. 2016, Hashimoto et al. 2017, Koukol et al. 2018, Ren et al. 2021). Species of *Heratomyces* are widely distributed and have been reported from both temperate and tropical regions, mainly from Thailand in Asia (Chang 1995, Tibpromma et al. 2016, Hashimoto et al. 2017, Koukol et al. 2018, Boonmee et al. 2021, Ren et al. 2021, Zhang et al. 2023). Thirty-five epithets of *Heratomyces* are listed in the Index Fungorum database, but only 27 species are recognized. *Heratomyces* species are primarily saprobes on dead plant debris in terrestrial habitats, with the exception of *H. hainanensis* and *H. hongheensis*, which have been reported from freshwater habitats (Tibpromma et al. 2016, Koukol et al. 2018, Ren et al. 2021, Zhang et al. 2023, Shen et al. 2024b).

Heratomyces xizangensis G.L. Zhao, N.G. Liu & Y.Z. Lu, Mycokeys (2025)

Fig. 10

Fungal Names number: FN 573046; Facesoffungi number: FoF 17658

Saprobic on decaying submerged wood in a freshwater river. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, superficial, scattered, conspicuous, glistening, flattened, brown to black. *Mycelium* mostly immersed, consisting of branched, septate, smooth, thin-walled, pale brown to brown hyphae. *Conidiophores* micronematous, mononematous, cylindrical, erect, pale brown to brown, unbranched, smooth, thick-walled. *Conidiogenous cells* holoblastic, short, cylindrical, hyaline, thick-walled, terminal, determinate, often arising directly on the superficial mycelium. *Conidia* (34–)40–45(–48) × (29–)32–36(–38) µm ($\bar{x}$ = 42 × 34 µm, SD = 2.3 × 1.9, n = 50), solitary, dry, subglobose to broad-ellipsoidal, muriform, slightly constricted at the septa, smooth, central cells dark brown to black, peripheral cells narrow and brown, flattened, subhyaline to pale brown, ellipsoidal in side view, middle cells dark brown to black.

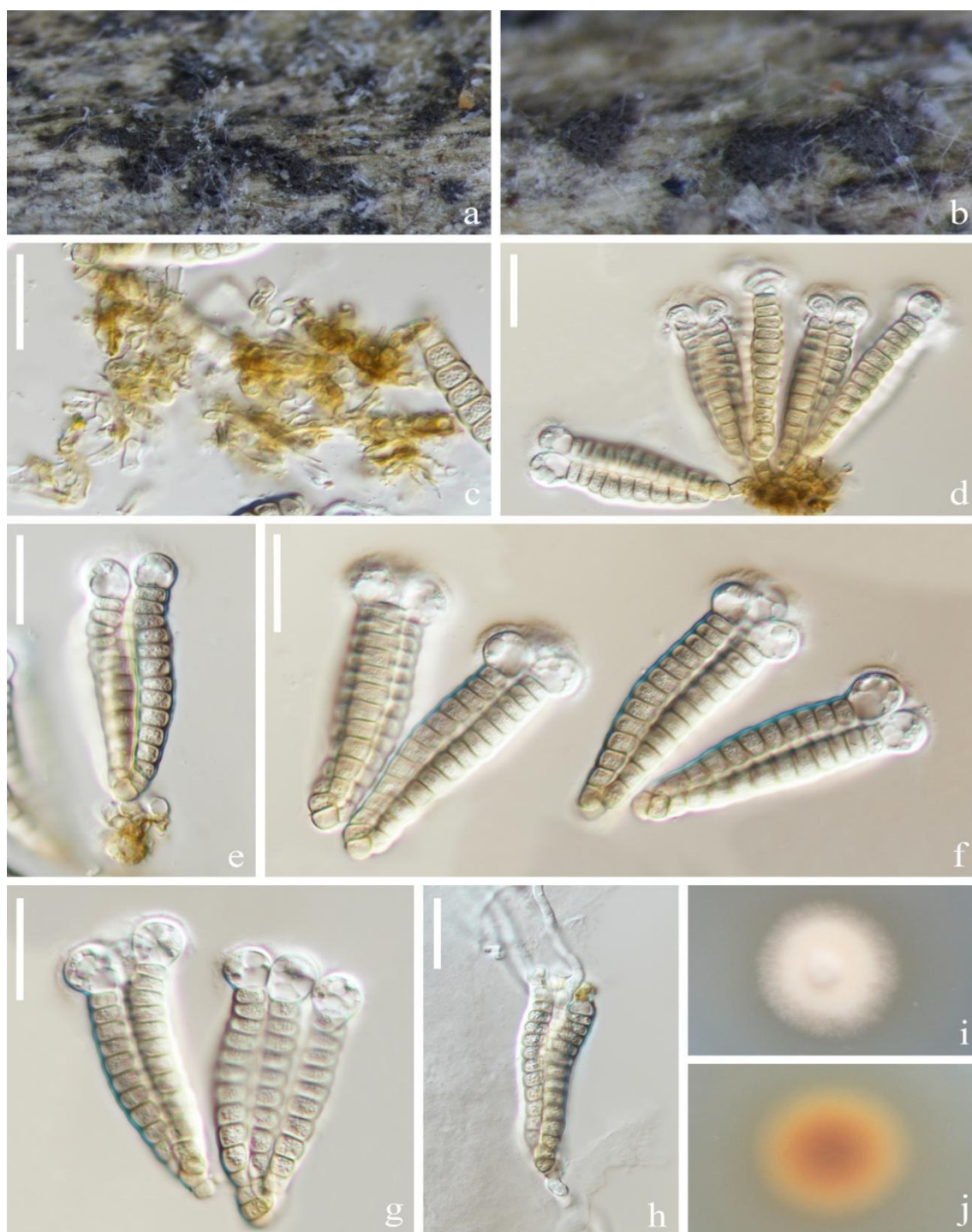


Figure 8 – *Vikalpa hydei* (HKAS 125817, holotype). a, b Colonies on the substratum. c–e Conidiophores, conidiogenous cells, and conidia. f, g Conidia with globose to subglobose, gelatinous appendages. h Germinated conidium. i, j Culture on PDA (from above and from below). Scale bars: c–h = 20 μ m.

Cultural characteristics – Conidia germinating on PDA and germ tubes produced from peripheral cells of conidium within 12 h. Colonies on PDA, reaching 1.5–2.5 cm after one month at room temperature, surface hyphae grey-brown, fluffy, flocculent; reverse side greyish brown to brown, dense, cracked in the middle.

Material examined – China, Yunnan Province, Nujiang Prefecture, Gongshan County, Dulong River, 28°02'29"N, 98°19'08"E, 1730 m; on submerged decaying wood, 1 May 2023, W.P. Wang, S4901 (HKAS 145709), living culture KUNCC 23-15937.

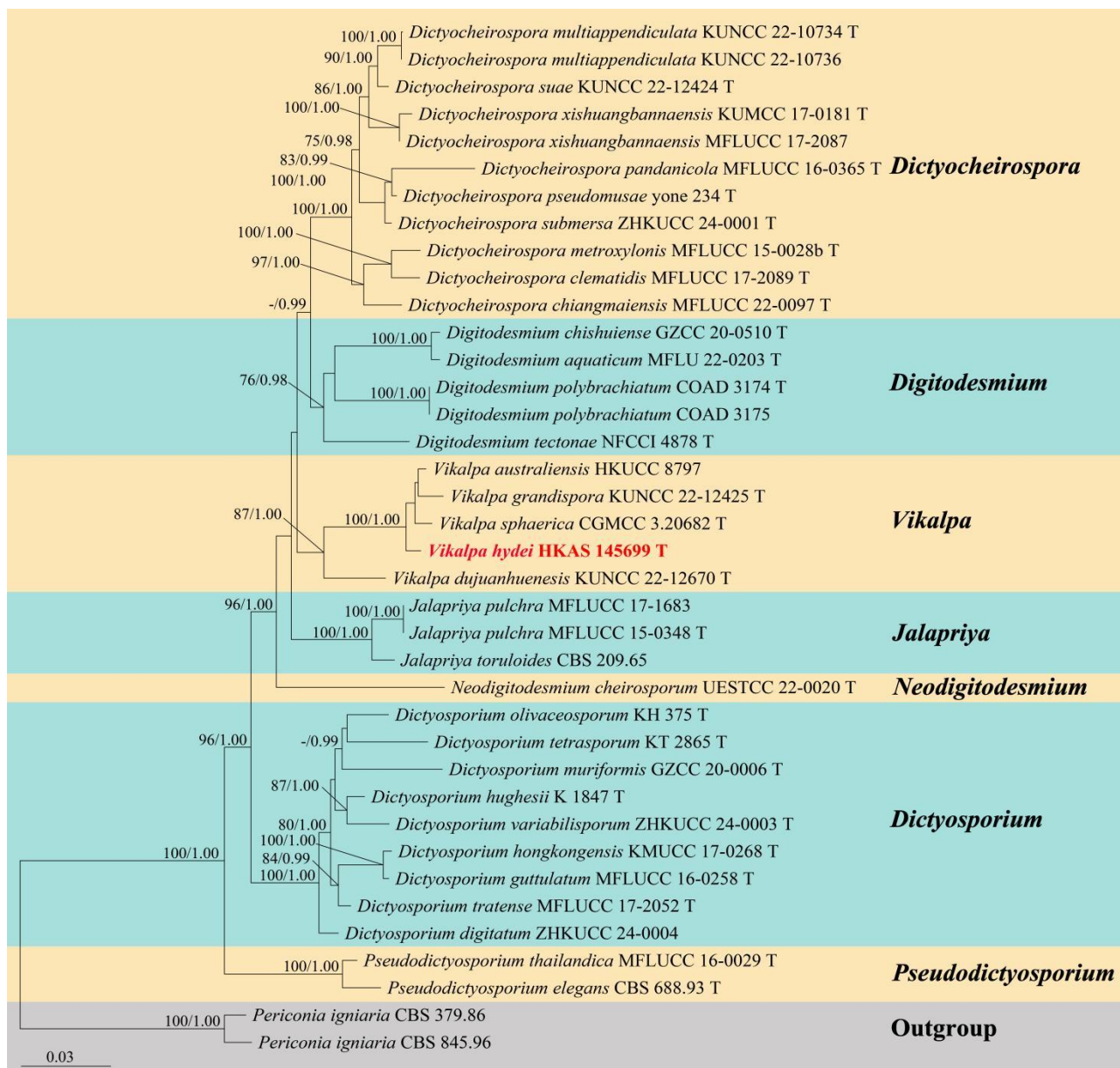


Figure 9 – ML tree based on the combined ITS, LSU, SSU and *tef1-α* sequences, representing the family Dictyosporiaceae. Bootstrap support values for ML equal to or greater than 65% and PP values equal to or greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Periconia igniaria* (CBS 379.86 and CBS 845.96). Ex-type strains are marked with “T”. The new taxon is indicated in bold and red.

Notes – *Hermatomyces xizangensis* was introduced by Zhao et al. (2025) on dead vines of *Pueraria* sp. from Xizang Autonomous Region, China. Morphologically, our collection resembles *He. xizangensis* (HKAS 149902) in having lenticular conidia with largely overlapping measurement (40–45 × 32–36 μm vs. 26–48 × 17–39 μm) (Zhao et al. 2025). Besides, ITS and *tef1-α* comparisons showed there are only one gap (797bp) and one bp (941bp) differences, respectively. Therefore, we identify our collection as *Hermatomyces xizangensis*, and report it from a freshwater habitat for the first time.

Neohendersoniaceae A. Giraldo & Crous

Aquaguizhoumyces X.J. Xiao, N.G. Liu & Y.Z. Lu, gen. nov.

Fungal Names number: FN 572846; Facesoffungi number: FoF 17804

Etymology – The specific epithet “Aqua” refers to aquatic habitat and “guizhoumyces” refers to the location where the fungus was collected.

Saprobic on submerged wood from a freshwater habitat. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, black, gregarious. *Mycelium* immersed, composed of light brown to brown, branched, smooth hyphae. *Conidiophores* semi-macronematous, mononematous, flexuous, simple or branched, pale brown to brown, septate, thick-walled. *Conidiogenous cells* monoblastic, integrated, terminal, pale brown to brown, smooth. *Conidia* solitary or catenate, oblong with obtuse ends, septate, olivaceous brown to dark brown, verrucose.

Type species – *Aquaguizhoumyces hydei* X.J. Xiao, N.G. Liu & Y.Z. Lu

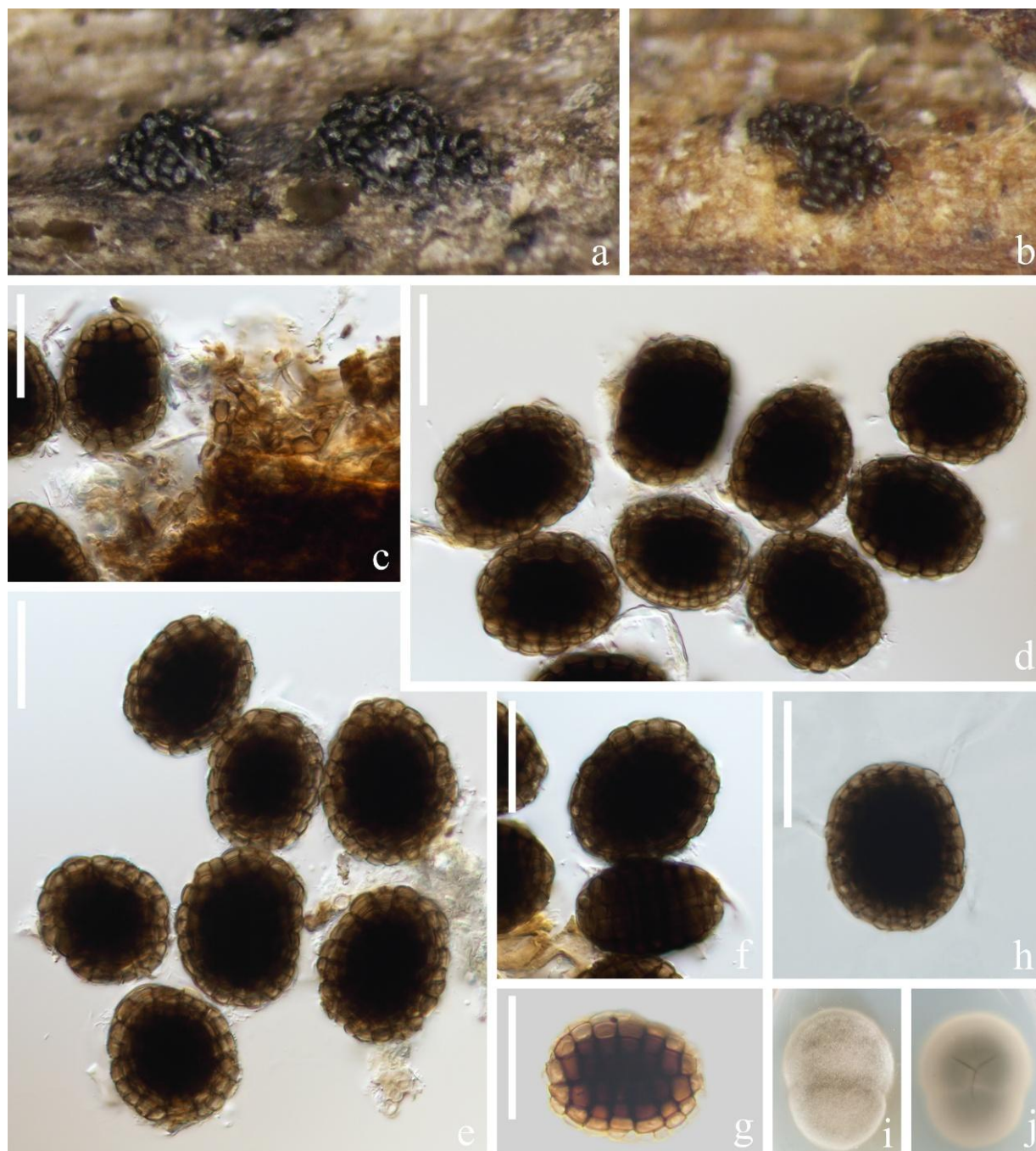


Figure 10 – *Hermatomyces xizangensis* (HKAS 145709). a, b Colonies on the natural substrate. c Conidiophores and conidium. d–g Conidia h Germinated conidium i, j Culture on PDA. Scale bars: c–h = 30 μ m.

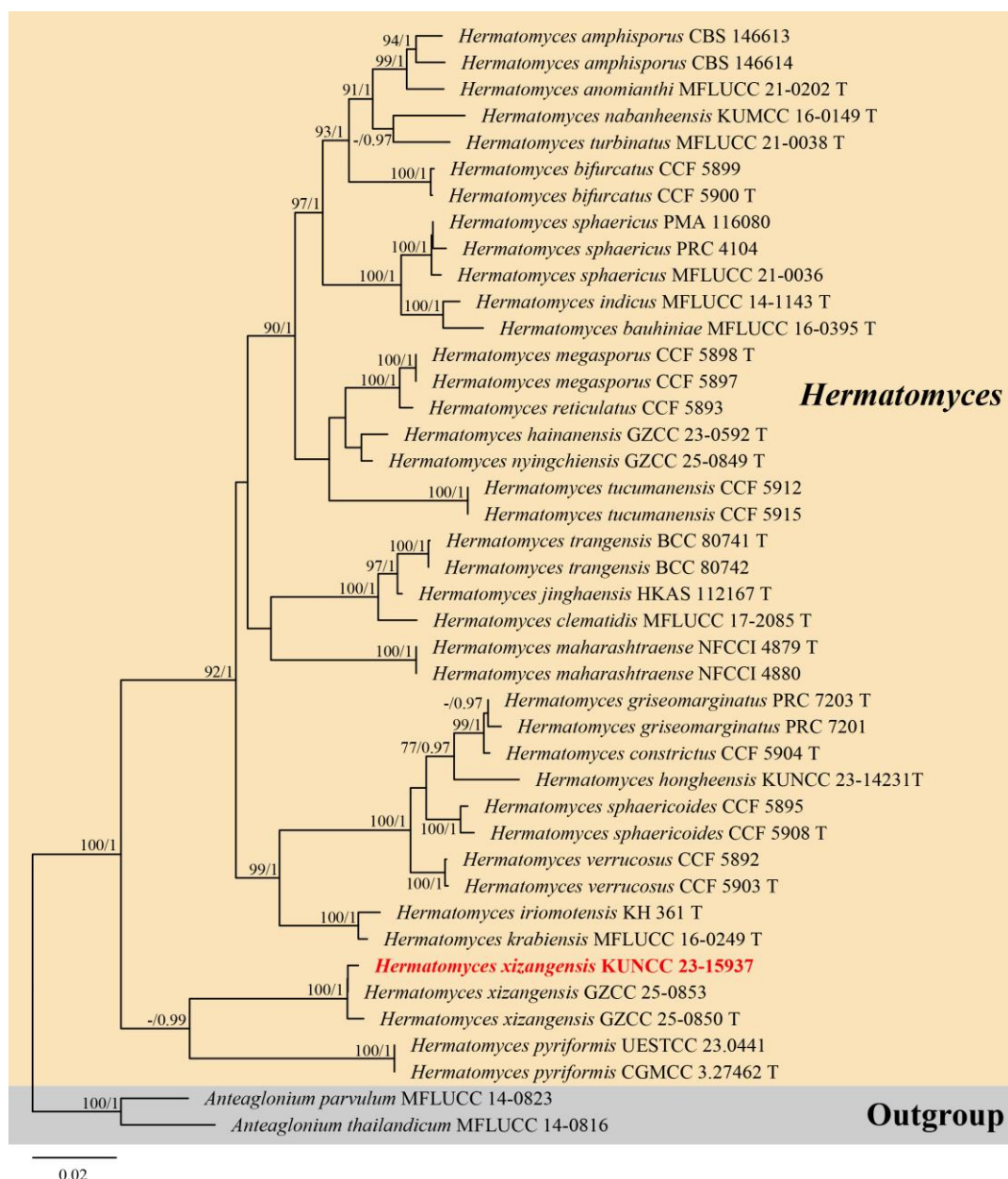


Figure 11 – ML tree based on the combined ITS, LSU, *tef1-α* and *rpb2* sequences, representing the family *Hermatomycetaceae*. Bootstrap support values for ML equal to or greater than 65% and PP values equal to or greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Cryptocoryneum akitaense* (MAFF 245365) and *Cryptocoryneum brevicondensatum* (MAFF 245366). The ex-type strains are marked with “T” and the new taxon is indicated in bold and red.

Aquaguizhoumyces hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 12

Fungal Names number: FN 572847; Facesoffungi number: FoF 17805

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 136240

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, black, gregarious. *Mycelium* immersed, composed of light brown to brown, branched, smooth hyphae. *Conidiophores* semi-macronematous, mononematous, flexuous, apex swollen, simple or branched, pale brown to brown, septate, thick-walled. *Conidiogenous cells* 8–28 × 3–5 μm ($\bar{x}$ = 14.5 × 4 μm, n = 25), monoblastic, integrated, terminal, pale brown to brown, smooth. *Conidia* 33–49 × 11–17 μm ($\bar{x}$ = 40 × 14 μm, n = 30),

solitary or formed in short chains, oblong with obtuse ends, 0–3-septate, olivaceous brown to dark brown, verrucose.

Culture characteristics – Conidia germinating on PDA within 48 h and germ tubes produced from basal end of conidia. Colonies reaching up to 22 mm diam. after 20 days on PDA media, medium dense, circular, flat, with entire edge, grey to dark grey at center, white at outer ring from above, brown at center, pale yellow at margin from below.

Material examined – China, Guizhou Province, Liupanshui City, Shuicheng County, Yushe National Forest Park, N 26°27'17", E 104°48'26", elevation 2232 m, on decaying wood from a freshwater stream, 27 February 2023, X.J. Xiao, YSS61 (HKAS 136240, holotype), ex-type culture GZCC 24-0084.

Notes – Eight genera are accommodated in *Neohendersoniaceae*. Among them, *Brevicollum*, *Neobrevicollum* and *Pseudoneohendersonia* only have sexual morphs (Tanaka et al. 2017, Li et al. 2023, Yang et al. 2024). Asexual morph of other six genera, i.e., *Amarenographium*, *Crassiparies*, *Medicopsis*, *Neohendersonia* and *Neomedicopsis* were reported as coelomycetous (De Gruyter et al. 2013, Wijayawardene et al. 2016, Giraldo et al. 2017, Tanaka et al. 2017, Crous et al. 2019a). *Aquaguizhoumyces* is the first hyphomycetous asexual morphic genus accommodated in *Neohendersoniaceae*.

***Neomassariaceae* Nitschke**

Neomassaria Mapook, Camporesi & K.D. Hyde, Fungal Diversity 80: 74 (2016)

Neomassaria was introduced by Hyde et al. (2016) based on *Neom. fabacearum*, and was originally classified in *Massariaceae* (*Pleosporales*, *Dothideomycetes*). Ariyawansa et al. (2018) described a second species *Neom. formosana* and established the family *Neomassariaceae* to accommodate *Neomassaria*. The sexual morph has immersed, globose to subglobose, brown to dark brown ascomata with a central ostiole, 8-spored, bitunicate, oblong to cylindrical asci, and ellipsoid to fusiform, hyaline, 1-septate ascospores with or without a gelatinous sheath (Hyde et al. 2016, Ariyawansa et al. 2018, De Silva et al. 2022, Lu et al. 2025). The asexual morph of *Neomassaria* is sporidesmium-like (Zhang et al. 2024, Sun et al. 2025). To date, ten species are accepted in *Neomassaria* and all of them are reported from China and Thailand.

Neomassaria davidii N.G. Liu & Jian K. Liu, sp. nov.

Fig. 14

Fungal Names number: FN 572894; Facesoffungi number: FoF 17834

Etymology – The specific epithet “davidii” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – GZAAS 25-0545

Saprobic on decaying wood in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on natural substrate effuse, olivaceous brown, velvety. Mycelium partly immersed, composed of pale brown, branched, septate, smooth, 1.5–3 µm wide hyphae. Conidiophores 39–96(–120) × 3–5 µm, macronematous, mononematous, erect, solitary or two or three aggregated at the base, straight or broadly curved, cylindrical, median brown, slightly taper towards the apex, unbranched, septate, thick-walled, percurrently proliferating 2–3 times. Conidiogenous cells 10–17.5 × 3.5–5.5 µm ($\bar{x}$ = 15 × 4.5 µm, n = 15), monoblastic, integrated, terminal, cylindrical, brown. Conidia 29–56 × 6–8.5 µm ($\bar{x}$ = 39.5 × 7.5 µm, n = 15), acrogenous, solitary, obclavate, rostrate, median brown, 3–7-septate, septa darkened, verruculose, with truncate, thickened and darkened base.

Culture characteristics – Conidia germinating on water agar within 24 h. Germ tubes produced from both apex and base. Colonies superficial, circular, umbonate, mycelium dense, with entire edge, brown in the center, with a green ring around, whitish brown to greyish brown in the outer ring from above, and dark brown, paler towards the edge from below

Material examined – Thailand, Chiang Rai Province, Wiang Chiang Rung District, on decaying wood in terrestrial habitat, 7 January 2020, N.G. Liu, CRJ5 (GZAAS 25-0545, holotype), ex-type culture GZCC 25-0531.

Notes – In our phylogenetic tree (Fig. 17), the strain GZCC 25-0531 formed a sister clade with *Neom. fibraureae* (HKAS 138718) with maximum statistical support. Morphologically, the conidia of our collection are smaller ($29\text{--}56 \times 6\text{--}8.5\ \mu\text{m}$ vs. $41\text{--}96 \times 5.5\text{--}12\ \mu\text{m}$) compared to those of *Neom. fibraureae* (Sun et al. 2025). Moreover, the phylogenetic analyses also suggest that our collection represents a previously undescribed species.

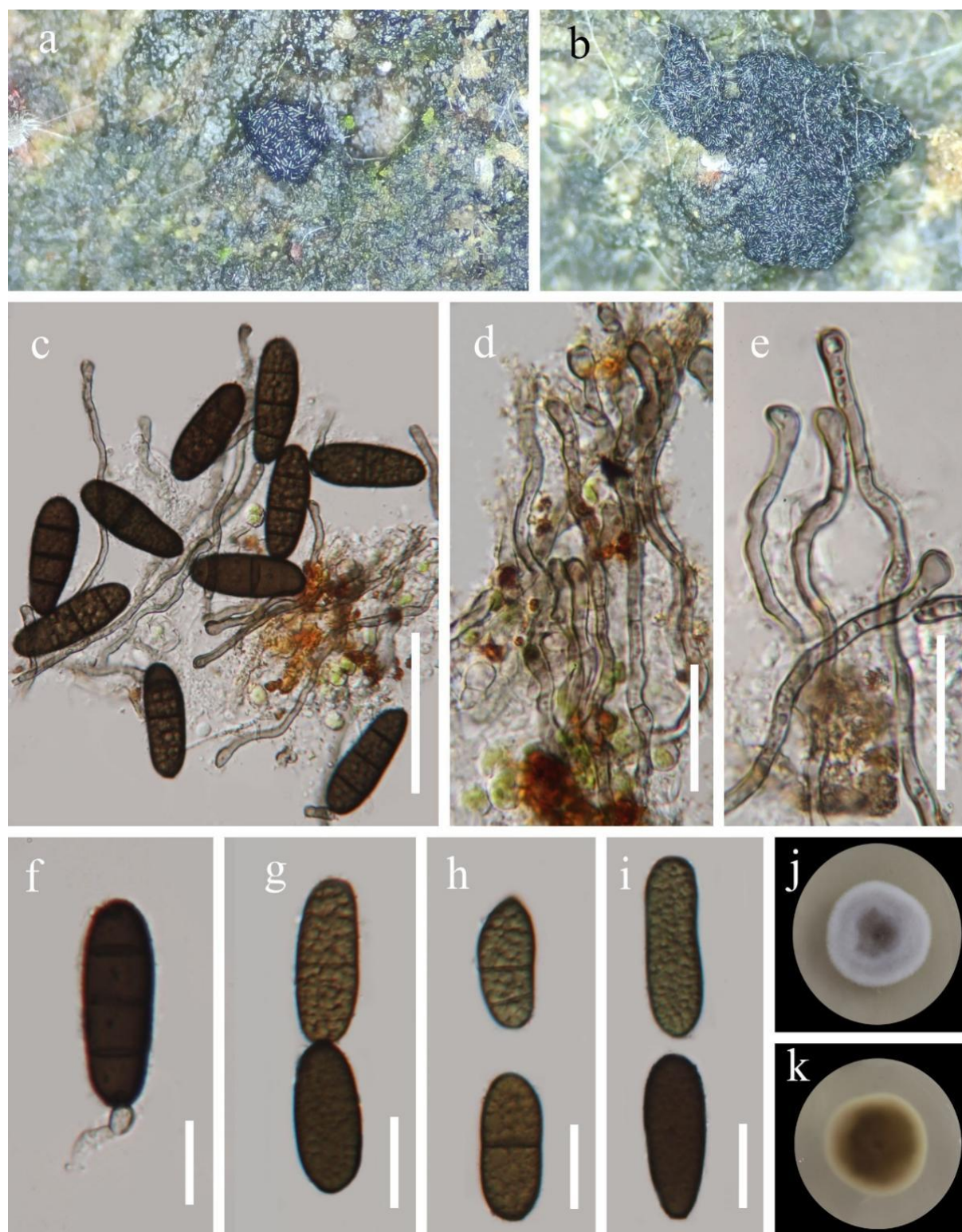


Figure 12 – *Aquaguizhoumyces hydei* (HKAS 136240, holotype). a, b Colonies on dead wood surface. c Conidiophores and conidia. d, e Conidiophores. f Conidiogenous cell and conidium. g–i Conidia. j, k Colony on PDA (j from above, k from below). Scale bars: c = 50 μm , d–i = 20 μm .

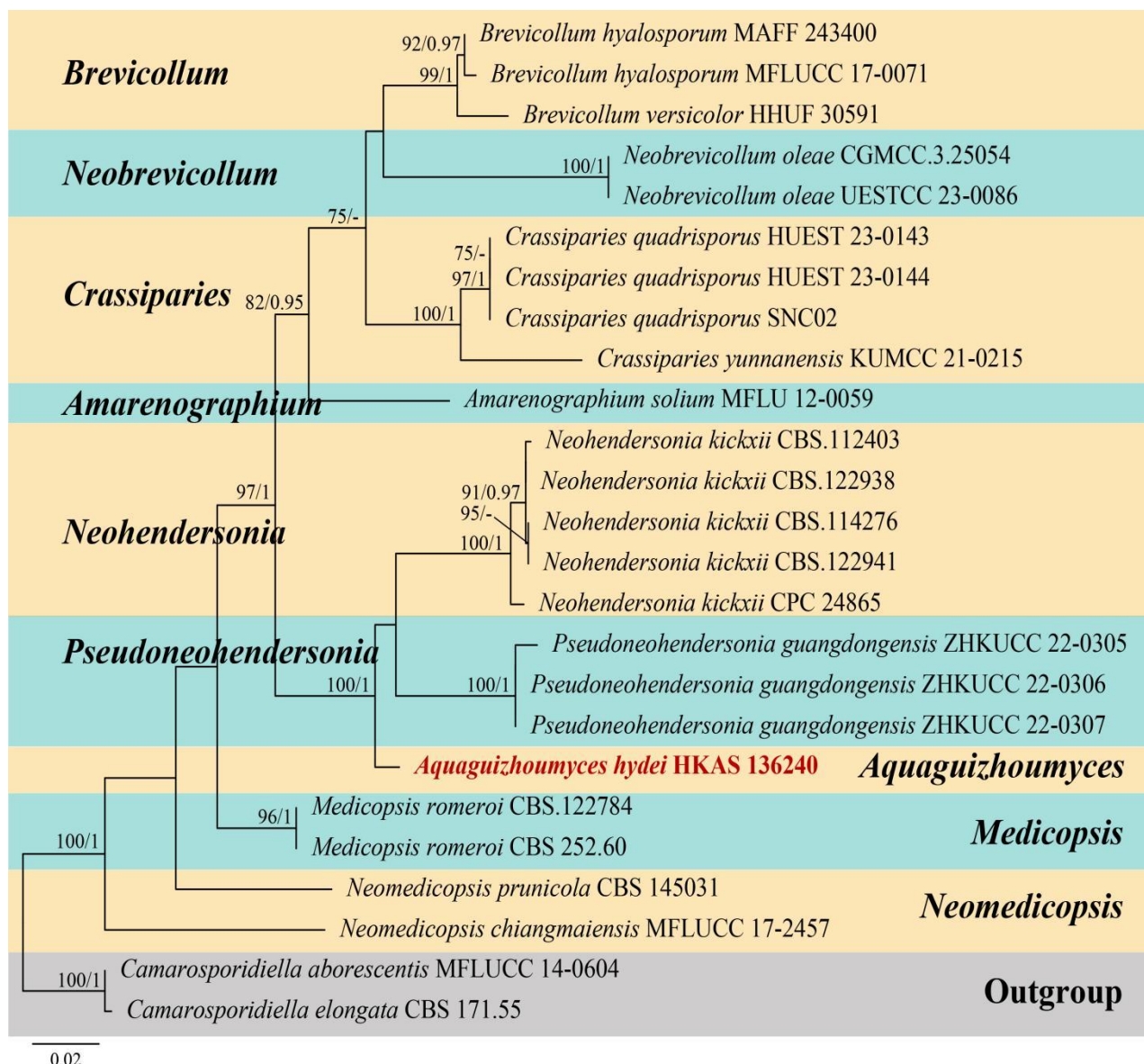


Figure 13 – ML tree based on the combined LSU and ITS sequences, representing the family *Neohendersoniaceae*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Camarosporidiella aborescentis* (MFLUCC 14-0604) and *Camarosporidiella elongata* (CBS 171.55). The new taxon is indicated in bold and red.

Neomassaria hydeae Y. Xiao & Jian K. Liu, sp. nov.

Fig. 15

Fungal Names number: FN 573023; Facesoffungi number: FoF 17833

Etymology – The specific epithet “hydeae” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 149996

Saprobic on dead branches of *Camellia sinensis*. Sexual morph: *Ascomata* 170–200 × 200–290 µm ($\bar{x}$ = 190 × 260 µm, n = 10), solitary or scattered, coriaceous, immersed to slightly erumpent, visible as black dots on the host surface, unilocular, globose to subglobose, brown to dark brown. *Ostiole* central. *Peridium* 10–20 µm wide, comprising light brown cells of *textura angularis*, inner cells hyaline, fusing at the outside indistinguishable from the host tissues. *Hamathecium* comprising 1–2 µm wide, cylindrical to filiform, septate, branched, pseudoparaphyses. *Asci* 80–125 × 12–25 µm ($\bar{x}$ = 95 × 19 µm, n = 20), 8-spored, bitunicate, oblong

to cylindrical, short pedicellate, with ocular chamber. *Ascospores* $20\text{--}30 \times 5\text{--}9 \mu\text{m}$ ($\bar{x} = 26 \times 8 \mu\text{m}$, $n = 30$), overlapping 1–2-seriate, hyaline to brown, ellipsoid to fusiform, 1-septate, with two oil globules at each end. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h and germ tubes produced from one or both ends. Colonies on PDA reaching 12 mm diam. after two weeks at 25 °C, flossy, circular, margin irregular, with four grey and light brown circles in the middle from above, dark brown at the center, yellow to light brown at margin from below.

Material examined – China, Sichuan Province, Chengdu City, Dujiangyan City, Chaxi Village, 31° 3' 60"N, 103° 41' 40"E, elevation 720 m, on dead branches of *Camellia sinensis*, 26 March 2024, Y. Xiao, X5 (HKAS 149996, holotype), ex-type culture CGMCC 3.29116 = UESTCC 25.0102; *ibid.*, 26 March 2024, X5-1 (HUEST 25.0082), UESTCC 25.0103.

Notes – *Neomassaria hydeae* is phylogenetically close to *Neom. thailandica* (MFLUCC 21-0193) and represents as a distinct lineage (Fig. 17). Additionally, the nucleotide base pair comparison between *Neom. thailandica* (ex-type strain, MFLUCC 21-0193) and *Neom. caffearius* (ex-type strain, UESTCC 25.0102) revealed 33/605 bp (5.5%, without gaps) of ITS, 36/996 bp (3.6% without gaps) of *rpb2* and 37/995 bp (3.7%, without gaps) of *tef1- α* differences. Furthermore, there are differences in the size of the ascomata, wall thickness, as well as the color and shape of the spores. The spores of *Neom. thailandica* are hyaline, lack oil globules (De Silva et al. 2022), while the spores of *Neom. hydeae* become hyaline to brown and contain two distinct oil globules. Therefore, *Neom. hydeae* is introduced as a new species with the justification of phylogenetic and morphological evidence.

Neomassaria keviniana N.G. Liu & Jian K. Liu, sp. nov.

Fig. 16

Fungal Names number: FN 572895; Facesoffungi number: FoF 17835

Etymology –The specific epithet “keviniana” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – GZAAS 25-0546

Saprobic on decaying wood in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown to black, velvety. *Mycelium* partly immersed, partly superficial, composed of pale brown, branched, septate, smooth, 2–3 μm wide hyphae. *Conidiophores* up to 660 μm long, main stipe 8–17 μm wide, branch 4–6 μm wide, macronematous, mononematous, erect, solitary or caespitose, straight or broadly curved, subcylindrical, slightly taper towards the apex, with a wide main stipe and thin branches, brown to dark brown, septate, thick-walled. *Conidiogenous cells* 10–19 $\times$ 3.5–5.5 μm ($\bar{x} = 14 \times 4.5 \mu\text{m}$, $n = 20$), monoblastic, terminal, integrated, cylindrical, brown. *Conidia* 49–82 μm ($\bar{x} = 59.5 \mu\text{m}$, $n = 20$) long, 8–12 μm ($\bar{x} = 9.5 \mu\text{m}$, $n = 20$) wide at the broadest, 2–5 μm ($\bar{x} = 3.5 \mu\text{m}$, $n = 20$) wide at base, acrogenous, solitary, obclavate, rostrate, olivaceous brown, up to 11-septate, slightly constricted at the darkened septa, verruculose.

Culture characteristics – Conidia germinating on water agar within 24 h. Germ tubes produced from both apex and base. Colonies superficial, circular, umbonate, mycelium dense, with entire edge, brown in the center, paler at the edge from above, and dark brown from below.

Material examined – China, Guizhou Province, Guizhou Academy of Agricultural Sciences, on decaying wood in terrestrial habitat, 18 July 2020, N.G. Liu, NKY006 (GZAAS 25-0546, holotype), ex-type, GZCC 25-0532.

Notes – In the phylogenetic tree (Fig. 17), our strain GZCC 25-0532 formed a distinct clade and clustered with *Neom. camelliae* (CGMCC 3.25585 and UESTCC 23.0154), *Neom. hydeae* (UESTCC 25.0102 and UESTCC 25.0103), *Neom. sichuanensis* (CGMCC 3.25586 and UESTCC 23-0158), and *Neom. thailandica* (MFLUCC 21-0193). Among them, *Neom. hydeae* and *Neom. thailandica* are only known from their sexual morphs, precluding a morphological comparison (De Silva et al. 2022, this study). Our collection differs from *Neom. camelliae* and *Neom. sichuanensis* by the distinct conidiophores. Moreover, our collection has smaller conidia (49–82 $\times$ 8–12 μm vs.

70–190 × 9–20 μm) than those of *Neom. sichuanensis* (Wu et al. 2025). Based on these morphological differences and the phylogenetic result, we propose our collection as a new species.

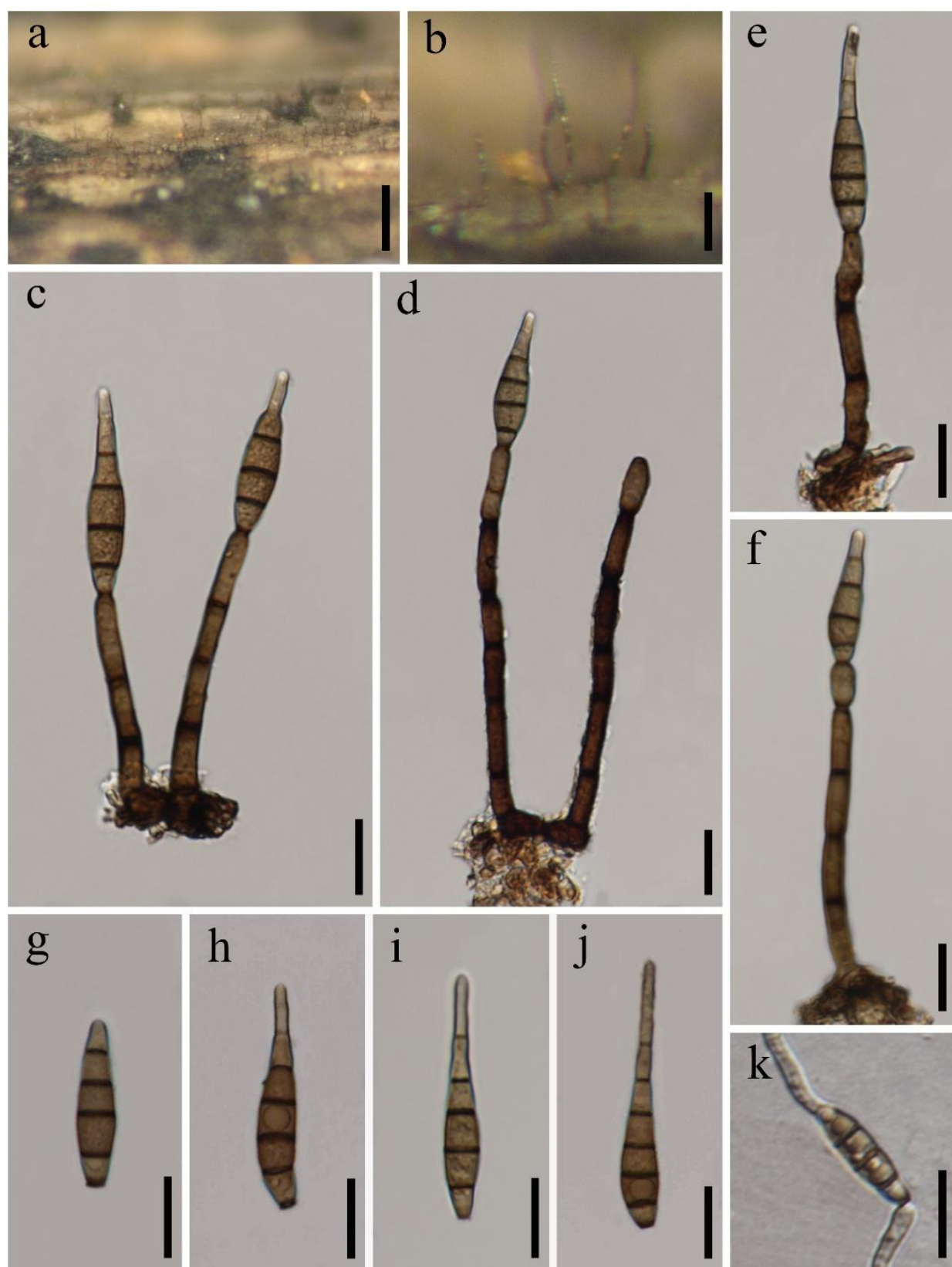


Figure 14 – *Neomassaria davidii* (GZAAS 25-0545, holotype). a, b Colonies on natural substrate. c–f Conidiophores and conidia. g–j Conidia. k Germinated conidium. Scale bars: a = 300 μm , b = 50 μm , c–l = 15 μm .



Figure 15 – *Neomassaria hydeae* (HKAS 149996, holotype) a–c appearance of ascomata on host surface. d vertical section through ascoma. e peridium. f hamathecium. g–k asci. l–o ascospores. p, q Colony on PDA (above and below). Scale bars: d = 80 μm , g–j = 20 μm , e, f, k–n = 10 μm .

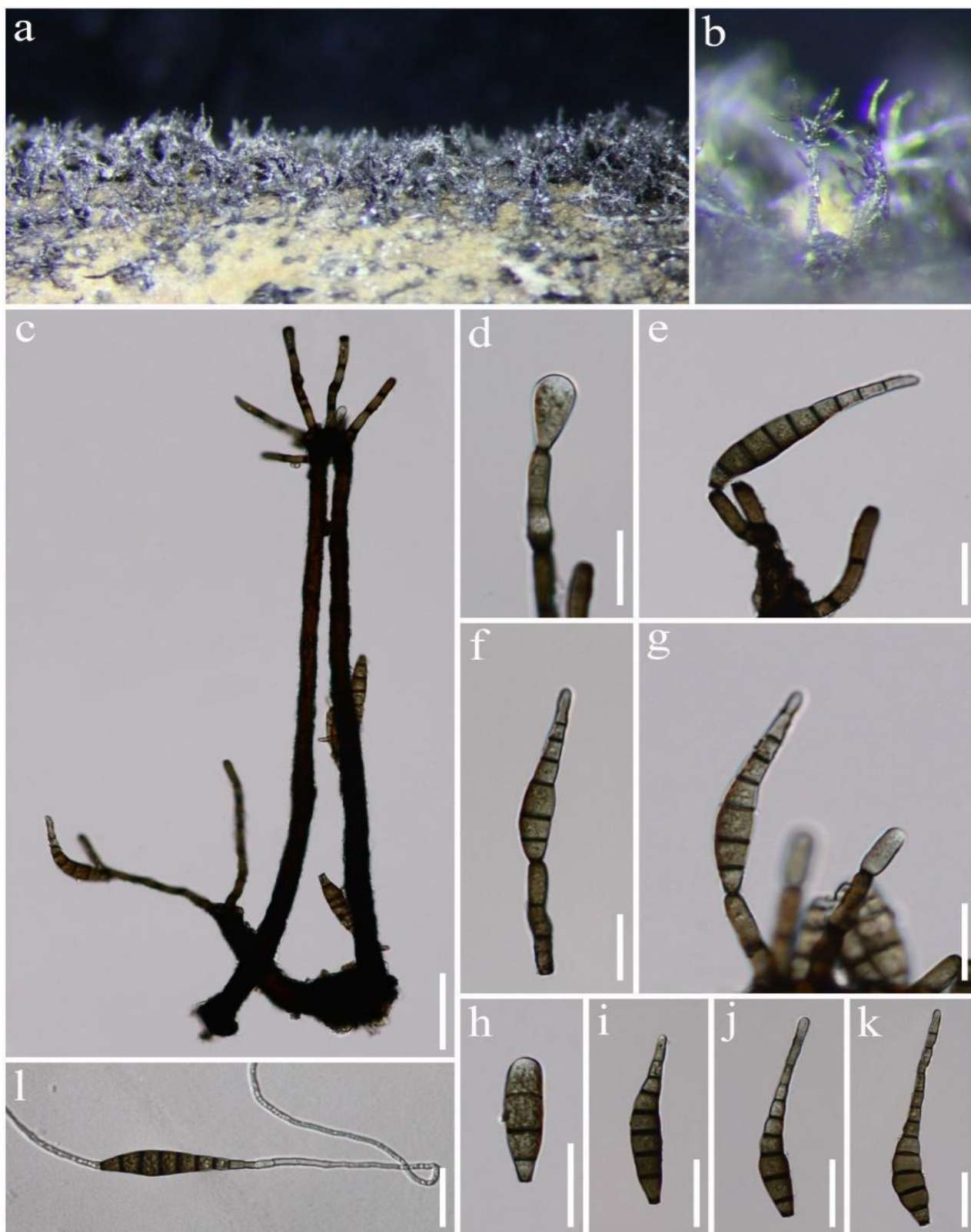


Figure 16 – *Neomassaria keviniana* (GZAAS 25-0546, holotype). a, b Colonies on natural substrate. c Conidiophores and conidia. d–g Conidiogenous cells and conidia. h–k Conidia. l Germinated conidium. Scale bars: c = 50 μ m, d–g = 20 μ m, h–l = 25 μ m.

Parabambusicolaceae Kaz. Tanaka & K. Hiray.

Paramonodictys N.G. Liu, K.D. Hyde & J.K. Liu, Fungal Diversity 100: 90 (2020)

Hyde et al. (2020a) introduced the monotypic genus *Paramonodictys* to accommodate a monodictys-like species, *P. solitaria*. Asexual morph of *Paramonodictys* has absent conidiophores and subglobose to obovoid, brown, muriform conidia (Hyde et al. 2020a, Yang et al. 2022, Li et al. 2023, Xu et al. 2023), and its sexual morph has not been observed. *Paramonodictys* occurs on both terrestrial and freshwater habitats, and all *Paramonodictys* species are reported from China to date.

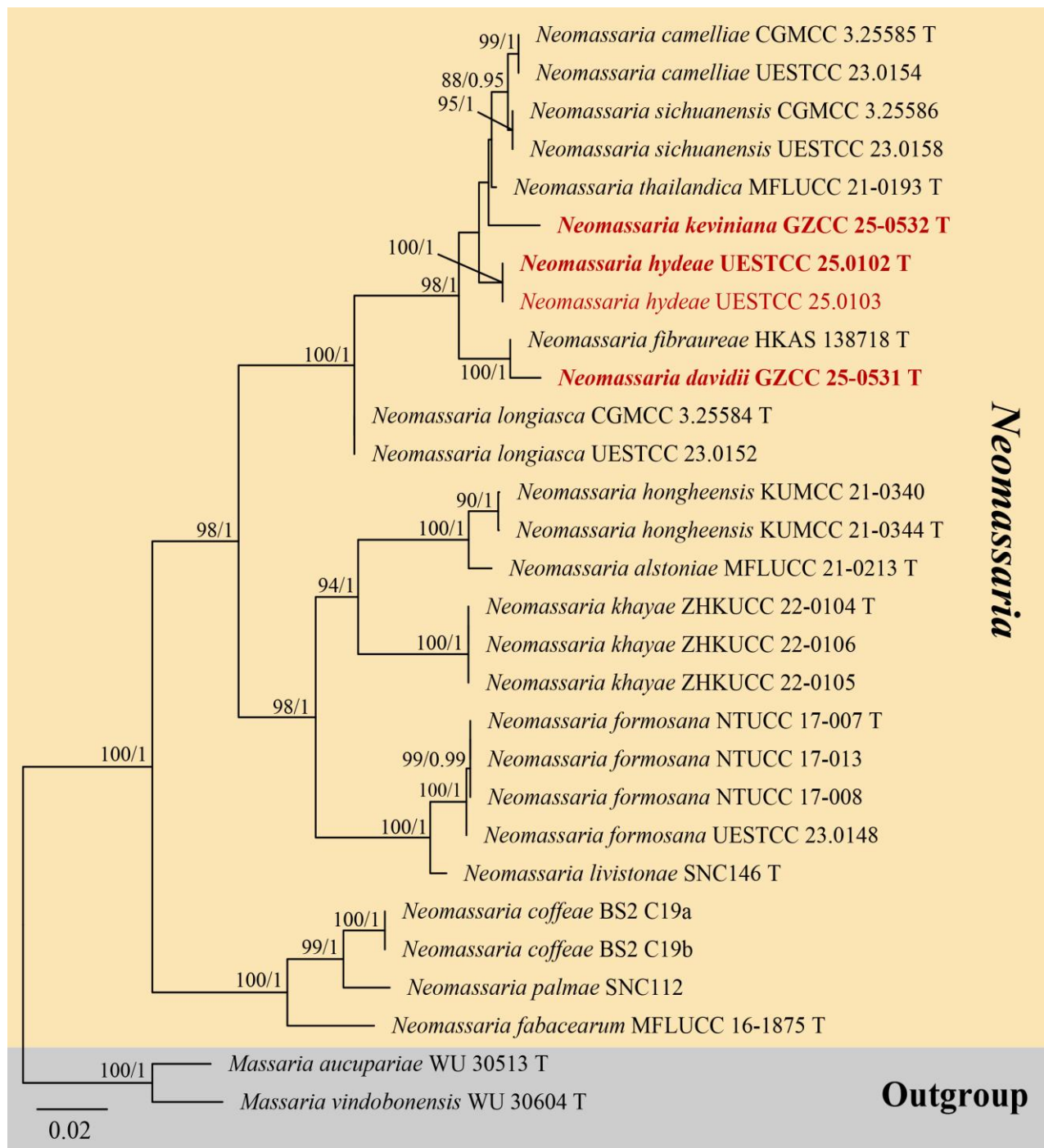


Figure 17 – ML tree based on the combined LSU, SSU, *tef1-α* and *rpb2* sequences. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Massaria aucupariae* (WU 30513) and *Massaria vindobonensis* (WU 30604). ex-type strains are marked with “T”. The new taxa are indicated in bold and red.

Paramonodictys hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.
Fungal Names number: FN 572896; Facesoffungi number: FoF 17836

Fig. 18

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 132140

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, black, gregarious. *Mycelium* immersed in the substratum. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* monoblastic, integrated. *Conidia* 60–117 × 45–77 µm ($\bar{x}$ = 88 × 60 µm, n = 30), solitary, subglobose, ellipsoidal, obovoid or irregular, olivaceous brown to dark brown, muriform, verrucose.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes produced from peripheral cells. Colonies reaching up to 8 mm diam. after 20 days, medium dense, circular, flat, edge entire, white at outer ring pale brown at the center from above, yellow at outer ring, darker at the center from below.

Material examined – China, Guizhou Province, Liupanshui City, Shuicheng County, Yushe National Forest Park, N 26°27'17", E 104°48'26", elevation 2232 m, on decaying wood from a freshwater stream, 27 February 2023, X.J. Xiao, YSS100 (HKAS 132140, holotype), ex-type culture GZCC 24-0079.

Notes – Six species have been described in *Paramonodictys* with morphological description and molecular evidence. In the phylogenetic analysis (Fig. 19), our strain GZCC 24-0079 formed an independent internal clade within *Paramonodictys* group, indicating it is a phylogenetically distinct species. Therefore, we introduce a new species *Paramonodictys hydei* to accommodate our collection.

Phaeoseptaceae S. Boonmee, Thambugala & K.D. Hyde

Pleopunctum N.G. Liu, K.D. Hyde & J.K. Liu, *Mycosphere* 10 (1): 767 (2019)

Pleopunctum was introduced by Liu et al. (2019b) to accommodate the type species *Pl. ellipsoideum*, along with *Pl. pseudoellipsoideum*. *Pleopunctum* is characterized by its asexual morph, which has sporodochial conidiomata, macronematous or micronematous conidiophores, monoblastic conidiogenous cells, and dimorphic conidia: 1) oval, ellipsoidal to oblong, brown, muriform, with 1–3 hyaline, basal cells (Liu et al. 2019b, Xu et al. 2023, Zhang et al. 2023, Ren et al. 2024b); 2) doliiform, broad clavate, hyaline, phragmosporous (Phukhamsakda et al. 2020). Its sexual morph has not been reported. *Pleopunctum* has been documented in both freshwater and terrestrial environments (Dong et al. 2020b, Boonmee et al. 2021, Liu et al. 2024a). To date, 11 species within *Pleopunctum* are recognized (Species Fungorum 2025), and sequence data are available for all of these species.

Pleopunctum hydei M.Y. Han, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 20

Index Fungorum number: IF904385; Facesoffungi number: FoF 17838

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – GMB-W1501

Saprobic on decaying wood in a terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, dark brown to black, gregarious, punctiform. *Mycelium* immersed, composed of pale brown, branched, septate, smooth hyphae. *Conidiophores* semi-macronematous to macronematous, mononematous, cylindrical, pale brown, unbranched, septate. *Conidiogenous cells* monoblastic, integrated, terminal, pale brown. *Conidia* 9–17 × 10–13 µm ($\bar{x}$ = 13 × 12 µm, n = 25), acrogenous, solitary, ellipsoidal, muriform, constricted at the septa, dark brown in the upper half, pale brown in the lower half, often with a hyaline to pale brown, cup-shaped basal cell, 3–9 × 6–11 µm ($\bar{x}$ = 6.5 × 8.5 µm, n = 25), smooth-walled.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes producing from the basal end. Colonies reaching up to 15 mm diam. after 31 days of cultivation at 28°C, medium dense, flat, circular, margin entire, dark brown from above and below.

Material examined – China, Yunnan Province, Honghe Hani and Yi Autonomous Prefecture, Honghe County, N 23°16'10", E 102°17'35", elevation 2000 m, on decaying wood in a terrestrial habitat, 18 July 2024, Meiyan Han, HHX30 (GMB-W1501, holotype), ex-type culture GMBCC2249.

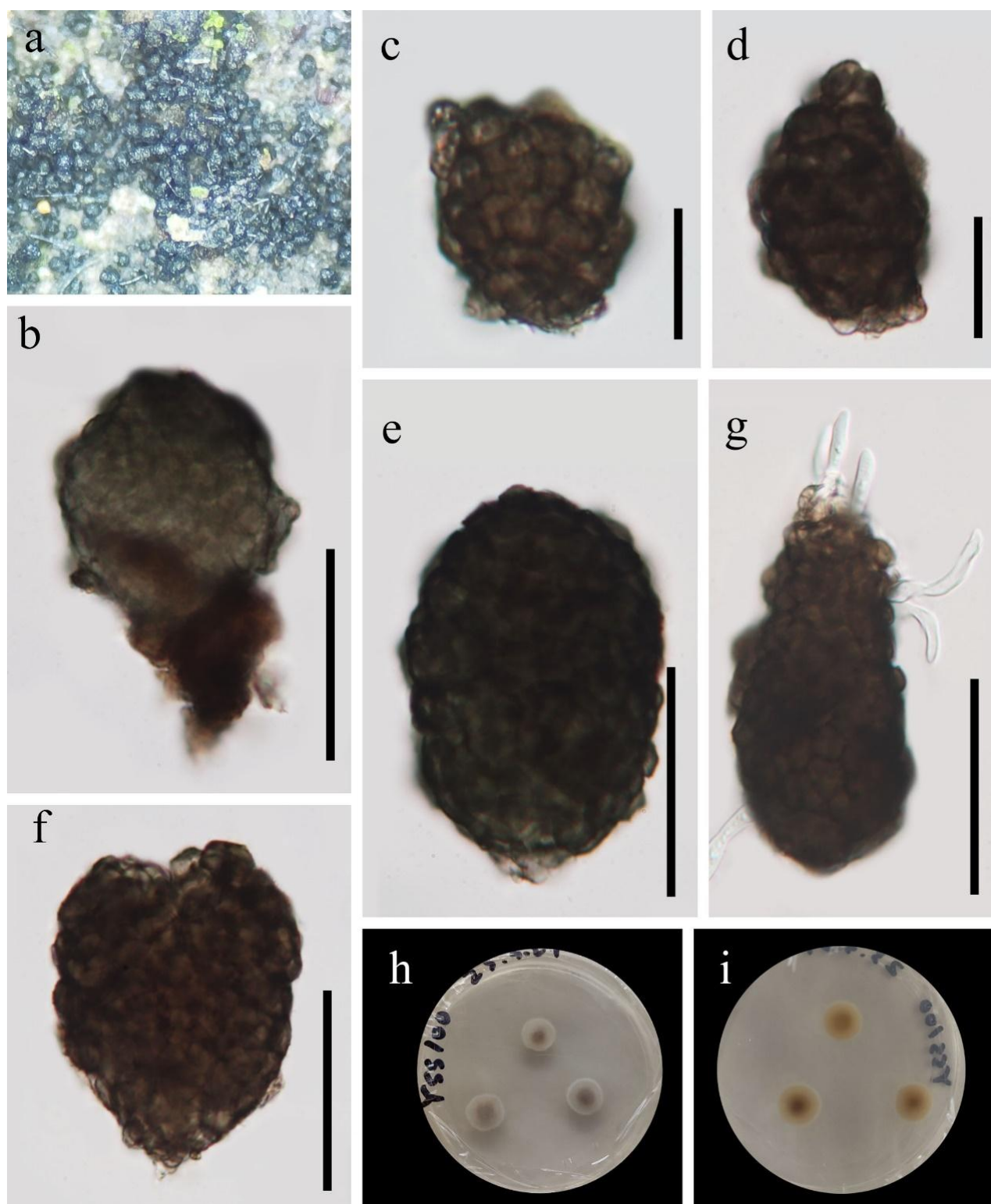


Figure 18 – *Paramonodictys hydei* (HKAS 132140, holotype). a Colonies on natural substrate. b–f conidia. g Germinated conidium. h, i Colonies on PDA (h from above, i from below). Scale bars: c, d = 20 μ m, b, e–g = 50 μ m.

Notes – Our collection aligns well with the generic concept of *Pleopunctum*, as it exhibits sporodochial conidiomata and ellipsoidal, muriform conidia with a hyaline to pale brown basal cell (Liu et al. 2019b, Liu et al. 2024a). Phylogenetic analysis (Fig. 21) reveals our strain GMBCC2249 formed a distinct clade basal to a group consisting of *Pl. menglaense* (KUMCC 21-0025 and KUMCC 21-0026), *Pl. guizhouense* (GZCC 23-0595), *Pl. megalosporum* (KUNCC 10442, KUNCC 10785 and KUNCC 21-0622), *Pl. multicellularum* (KUNCC 10781, KUNCC 10789 and KUNCC 10778), and *Pl. rotundatum* (KUNCC 10780 and KUNCC 10787). This strongly indicates that strain GMBCC2249 represents a phylogenetically distinct species. Given that sequence data are available for all known *Pleopunctum* species, we hereby propose our collection as a new species.

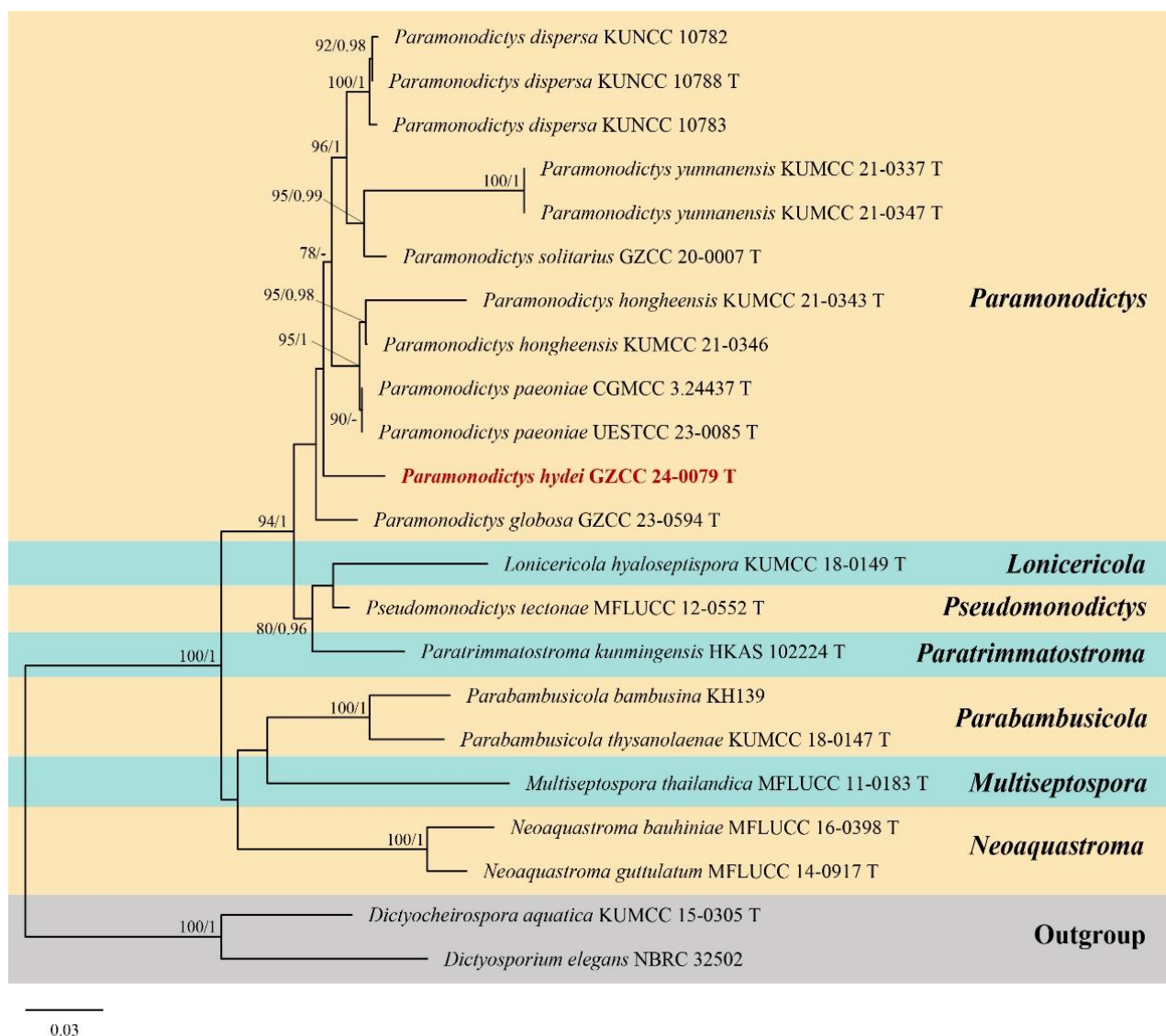


Figure 19 – ML tree based on the combined LSU, ITS and *rpb2* sequences. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Dictyocheiropsora aquatica* (KUMCC 15-0305) and *Dictyosporium elegans* (NBRC 32502). ex-type strains are marked with “T”. The new taxon is indicated in bold and red.

Phaeosphaeriaceae M.E. Barr

Setophoma Gruyter

De Gruyter et al. (2010) introduced *Setophoma* with *S. terrestris* as the type species. *Setophoma* species are characterized by setose, pycnidial conidiomata, phialidic conidiogenous cells, and ellipsoidal to subcylindrical, aseptate, guttulate conidia (De Gruyter et al. 2010,

Thambugala et al. 2017, Marin-Felix et al. 2019). *Setophoma* species are well-known pathogens or saprobic on important crops, including tea (Phookamsak et al. 2014, Marin-Felix et al. 2019). There are seventeen epithets listed in the Species Fungorum (2025), of which *S. cyperi* was transferred to *Wingfieldomyces* (Marin-Felix et al. 2019). Recent studies showed that the genus is polyphyletic and formed two distinct clades within *Phaeosphaeriaceae* (Tennakoon et al. 2020). Our phylogenetic analyses yielded similar results as Tennakoon et al. (2020); thus, the genus may need revision based on further phylogenetic analyses. In this study, we introduce a new species *Setophoma hydei*, which was isolated from *Oryza sativa* in Thailand.

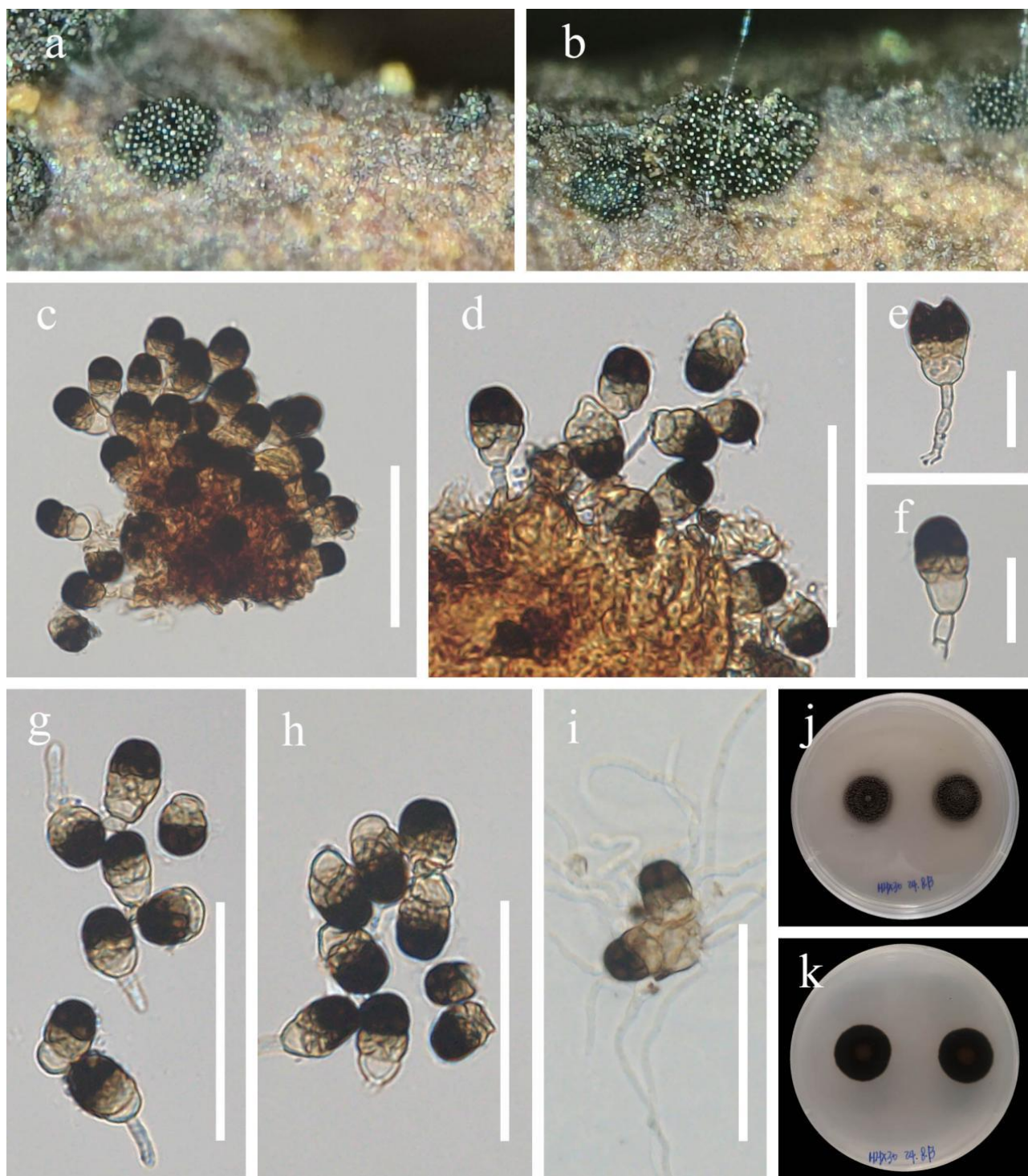


Figure 20 – *Pleopunctum hydei* (GMB-W1501, holotype). a, b Colonies on natural substrate. c, d Sporodochia. e–h Conidiogenous cells and conidia. i Germinated conidia. j, k Colony on PDA (j from above, k from below). Scale bars: c–d, g–i = 50 μ m, e–f = 20 μ m.

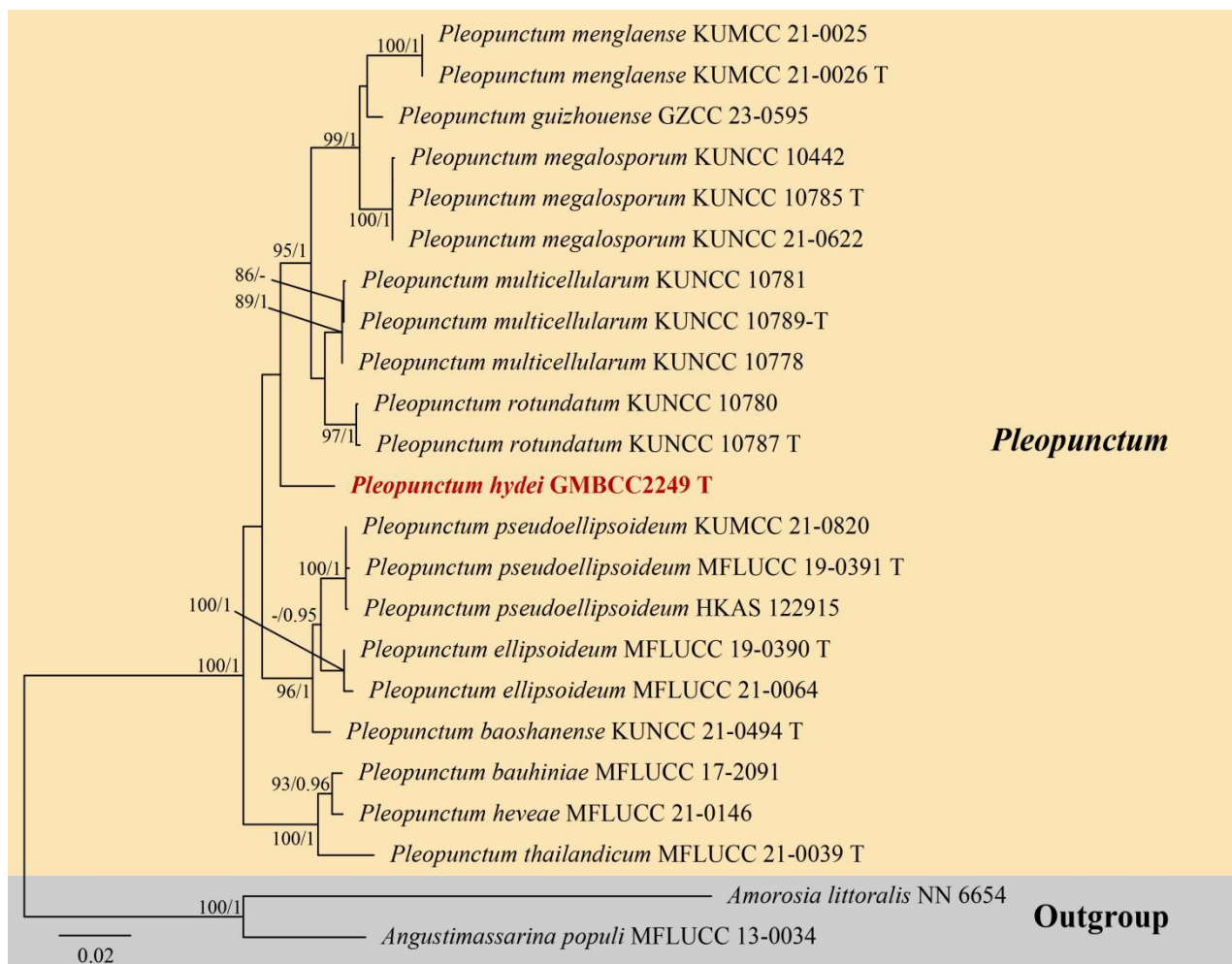


Figure 21 – ML tree based on the combined LSU, ITS and *tef1-α* sequences. Bootstrap support values for ML equal to or greater than 75% and PP values equal to or greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Amorisia littoralis* (NN 6654) and *Angustimassarina populi* (MFLUCC 13-0034). Ex-type strains are marked with “T”. The new taxon is indicated in bold and red.

***Setophoma hydei* X.G. Tian, sp. nov.**

Fig. 22

Fungal names number: FN900976, Facesoffungi number: FoF 17842

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – MFLU 23-0184

Saprobic on dead leaves of *Oryza sativa*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* up to 150 µm diam., pycnidial, immersed, solitary, scattered, visible as black spots and setose on host surface, globose to subglobose, black. *Conidiomatal setae* abundant, subulate to cylindrical, brown to black, septate, unbranched, smooth-walled. *Conidiomata wall* 9–15.5 µm wide, thin, composed of 2–4 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, monophialidic, phialidic, smooth, 3–4.5 µm long. *Conidia* 4.5–5.5 × 2–2.5 µm ($\bar{x}$ = 5 × 2 µm, n = 35), ellipsoidal to subcylindrical, hyaline, aseptate, 1–3-guttules, smooth.

Culture characteristics – Colonies on PDA reaching 15 mm diam. after two weeks at 25°C. Colonies on PDA filamentous at margins, flat, superficial, circular, smooth surface, white from above, pale brown from below.

Material examined – Thailand, Chiang Rai Province, Doi Pui, on dead leaves of *Oryza sativa*, 5 November 2020, X.G. Tian, r5-2 (MFLU 23-0184, holotype), ex-type culture MFLUCC 23-0168.

Notes – In the multi-loci phylogenetic tree (Fig. 23), our strain MFLUCC 23-0168 clustered as a sister taxon to *Setophoma poaceicola*. *Setophoma hydei* shares similar morphology to *S. poaceicola* in having setose pycnidia, phialidic conidiogenous cells, and hyaline, ellipsoidal to subcylindrical, aseptate conidia (Thambugala et al. 2017). However, the comparison of the ITS region between *S. hydei* and *S. poaceicola* revealed 10 bp (483 bp, 2%) differences. Phylogenetic analyses support *Setophoma hydei* as a distinct new species.

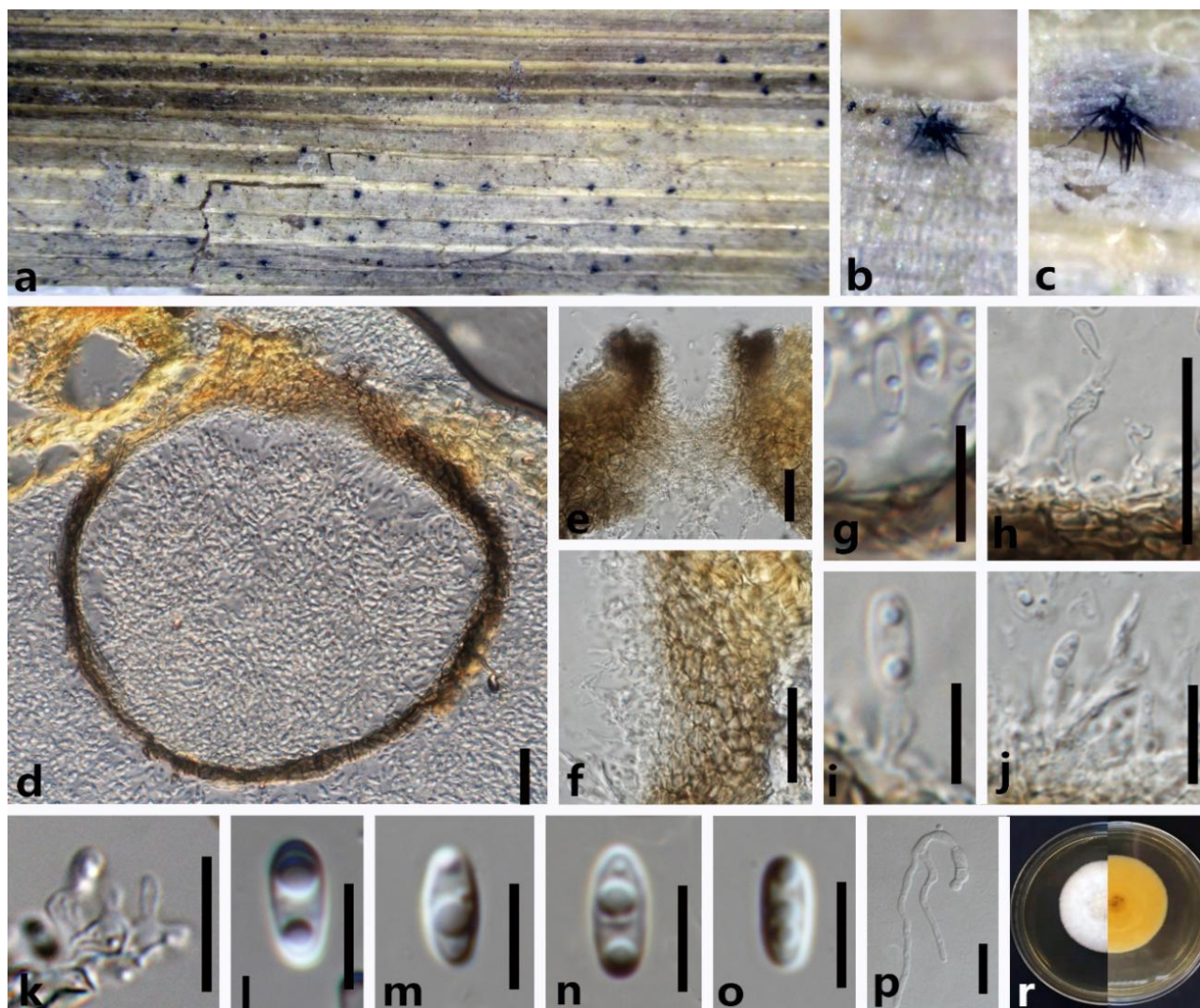


Figure 22 – *Setophoma hydei* (MFLU 23-0184, holotype) a–c Conidiomata on the leaves of *Oryza sativa*. d Vertical section of conidioma. e Ostiole. f Conidiomatal wall. g–k Conidiogenous cells with conidia. l–o Conidia. p Germinated conidium. r Colony on PDA from above and below. Scale bars: d = 50 μ m, e–g, o = 20 μ m, h–j = 10 μ m, k–n = 5 μ m.

Roussoellaceae Jian K. Liu, Phook., D.Q. Dai & K.D. Hyde

Pararoussoella Wanas., E.B.G. Jones & K.D. Hyde

Pararoussoella was introduced by Wanasinghe et al. (2018) to accommodate a sexual species, *Pa. rosarum*, from *Rosa* sp. (*Rosaceae*) of UK, based on morphological characteristics and multigene phylogenetic analysis. Subsequently, three new and two previously described species originally assigned to *Roussoella* were transferred to *Pararoussoella*, comprising three asexual species (*Pararoussoella juglandicola*, *Pa. lincangensis* and *Pa. quercina*) and two sexual species (*Pa. mangrovei* = *Roussoella mangrovei* and *Pa. mukdahanensis* = *Roussoella mukdahanensis*) (Crous et al. 2019a, 2020b, Phukhamsakda et al. 2020, Ren et al. 2024a). The sexual of *Pararoussoella* is similar to taxa of *Roussoella* and is characterized by immersed and globose

ascomata; cellular pseudoparaphyses; central, papillate, black ostioles; cylindrical to oblong asci; and uniseriate, brown to dark brown ascospores with irregular, longitudinal striations (Wanasinghe et al. 2018, Phukhamsakda et al. 2020). The asexual is characterized by erumpent, immersed, elliptical to ampulliform, globose, brown to dark brown conidiomata; conidiophores reduced to conidiogenous cells; conidiogenous cells enteroblastic, phialidic, hyaline, ampulliform to doliiform; and aseptate, subcylindrical, guttulate, hyaline becoming brown conidia (Crous et al. 2019a, 2020b, Ren et al. 2024a). Species of *Pararoussoella* occur on a variety of plant materials and are distributed in places such as China, Germany, Thailand, UK and Ukraine (Dai et al. 2017, Hyde et al. 2018, Wanasinghe et al. 2018, Crous et al. 2019a, 2020b, Ren et al. 2024a).

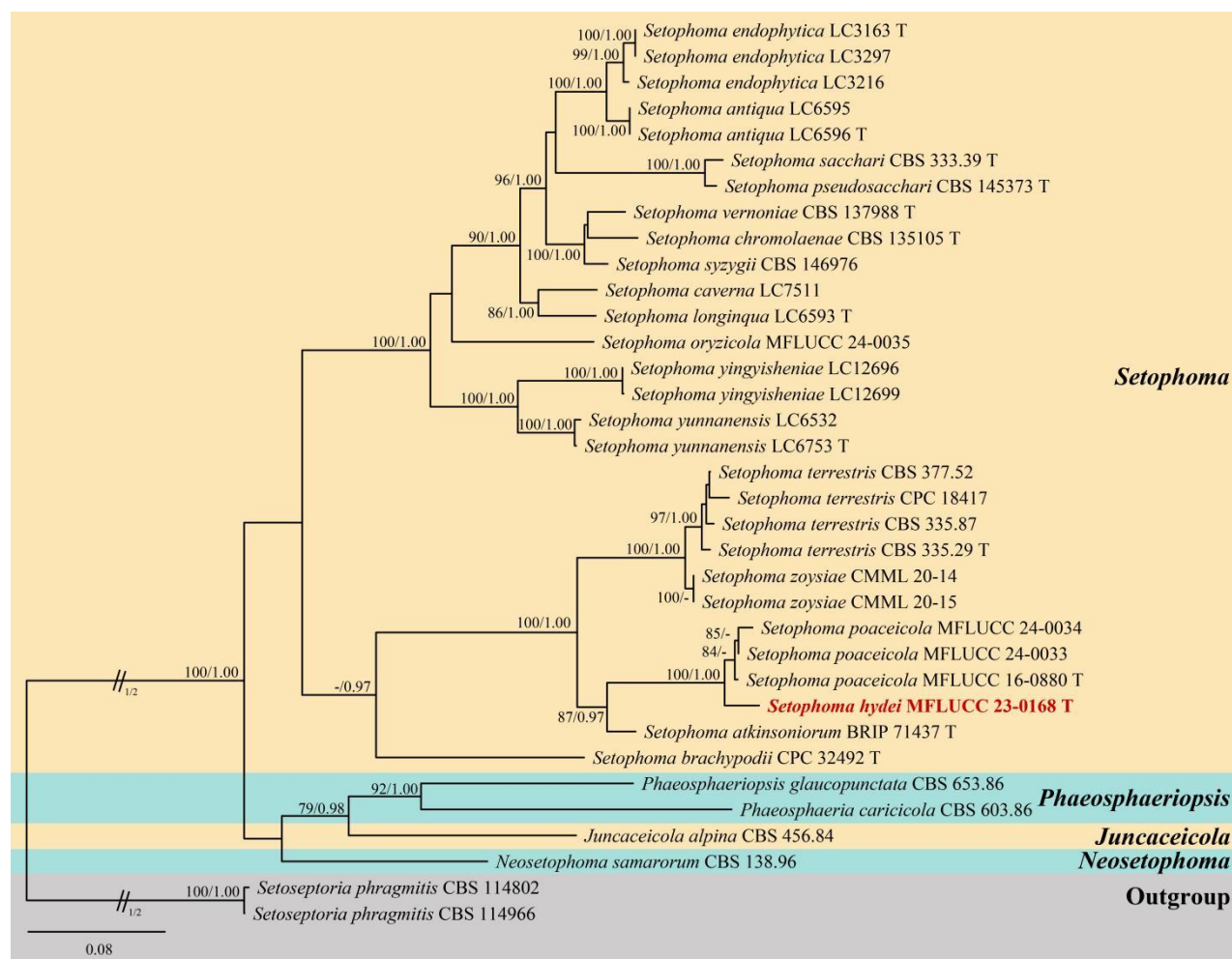


Figure 23 – ML tree based on the combined ITS, LSU, *tef1-α*, *rpb2*, and *tub2* sequences, representing *Setophoma*. Bootstrap support values for ML greater than 70% and PP greater than 0.90 are given near nodes as ML-BS/PP. The tree is rooted with *Setoseptoria phragmitis* (CBS 114802 and CBS 114966). Ex-type strains are marked with “T”. The new taxon is indicated in bold and red.

Pararoussoella hydei H.W. Shen & Z.L. Luo, sp. nov.

Fig. 24

Fungal Names number: FN 573028; Facesoffungi number: FoF 17837

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 145700

Saprobic on submerged decaying wood in freshwater river. Asexual morph: *Conidiomata* pycnidial, 430–490 μm high, 330–390 μm diam., superficial to semi-immersed, solitary or gregarious, globose to subglobose, uniloculate, brown to dark brown, ostiolate. *Ostiole* circular,

centrally located. *Conidiomatal wall* 25–65 μm wide, composed of several layers of thick, subhyaline to brown, irregular cells of *textura angularis*. *Conidiophores* reduced to *conidiogenous cells*. *Conidiogenous cells* arising from the inner wall cells of the conidiomata, enteroblastic, phialidic, determinate, ampulliform, hyaline, smooth-walled, $(4.7\text{--})6.4\text{--}10.4(-13) \times 4\text{--}6(-7) \mu\text{m}$ ($\bar{x} = 8.4 \times 5.2 \mu\text{m}$, $\text{SD} = 2.0 \times 0.8$, $n = 30$). *Conidia* $3.7\text{--}4.7 \times 2.5\text{--}3.2(-4) \mu\text{m}$ ($\bar{x} = 4 \times 3 \mu\text{m}$, $\text{SD} = 0.3 \times 0.3$, $n = 50$), acrogenous, ellipsoidal, hyaline becoming brown, aseptate, guttulate, rounded at both ends, smooth-walled. Sexual morph: Undetermined.

Culture characteristics – Conidia germinating on PDA medium and germ tubes produced from ends of conidium within 12 h. Colonies on PDA medium reaching around 4.5–5 cm diam. after one month at room temperature (around 25°C) in dark, circular, loose, smooth-edged, dense, pale gray to brown on the forward; circular, pale gray to brown, dense on the reverse.

Material examined – China, Yunnan Province, Nujiang Prefecture, Fugong County 27.260995° N, 98.881291° E, on submerged decaying wood, 4 May 2023, Y. Wang, S4621 (HKAS 145700, holotype), ex-type culture KUNCC 23-14357.

Notes – Phylogenetic analysis showed that *Pararoussoella hydei* clustered with the type strain of *Pa. lincangensis* and with 100% ML and 1.00 PP support (Fig. 25). *Pararoussoella hydei* resembles *Pa. lincangensis* in having globose to subglobose, brown to dark brown conidiomata; enteroblastic, phialidic, determinate, ampulliform, hyaline conidiogenous cells; and ellipsoidal, guttulate, aseptate, hyaline becoming brown, smooth conidia (Ren et al. 2024a). However, *Pa. hydei* can be distinguished from *Pa. lincangensis* by the larger conidiomata (430–490 μm high $\times$ 330–390 μm diam. vs. 75–140 μm high $\times$ 140–160 μm diam.), conidiogenous cells ($6.4\text{--}10.4 \times 4\text{--}6 \mu\text{m}$ vs. $4.4\text{--}5.4 \times 2.6\text{--}3.6 \mu\text{m}$) and conidia ($3.7\text{--}4.7 \times 2.5\text{--}3.2 \mu\text{m}$ vs. $3.1\text{--}3.8 \times 2\text{--}2.2 \mu\text{m}$). The ITS, LSU and *tef1- α* sequences between *Pa. hydei* and *Pa. lincangensis* (KUMCC 21-0619, ex-type) showed 10 bp (including one gap), 5 bp and 14 bp (including one gap) nucleotide base differences, respectively. Therefore, based on morphological characteristics and molecular evidence, we introduce *Pararoussoella hydei* as a new species.

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray.

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

Polyposphaeria was introduced by Tanaka et al. (2009). Asexual morph is tetraploa-like that has micronematous conidiophores, monoblastic conidiogenous cells, and globose to subglobose conidial body with several setose appendages (Tanaka et al. 2009, Tibpromma et al. 2018, Senanayake et al. 2023, Tang et al. 2023). Its sexual morph has globose, black to reddish brown ascomata, 8-spored, fissitunicate, clavate, short-stalked asci, and narrowly fusiform, hyaline to pale olive-brown, septate ascospores with entire sheath (Tanaka et al. 2009). Seven *Polyposphaeria* species are listed in Species Fungorum (2025).

Polyposphaeria appendiculata Y.R. Sun, N.G. Liu & K.D. Hyde, Fungal Diversity (2024)

Fig. 26

Index Fungorum number: IF902306; Facesoffungi number: FoF 17839

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, scattered, black. Mycelium immersed, composed of branched, septate, dark brown hyphae. Conidiophores absent. Conidiogenous cells monoblastic. Conidia $54\text{--}179 \times 45\text{--}77 \mu\text{m}$ ($\bar{x} = 48 \times 82 \mu\text{m}$, $n = 25$), solitary, subglobose to obovoid, or irregular, with thin peel-like outer wall of conidia, composed of numerous internal hyphae inside, brown to dark brown when mature. Appendages $27\text{--}64 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} = 46 \times 4 \mu\text{m}$, $n = 30$), cylindrical, unbranched, round at apex, brown, septate, thick-walled.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes producing from conidial body or appendages. Colonies reaching up to 14 mm diam. after 20 days, medium dense, circular, flat, edge entire, greyish brown at the center, white at the edge from above, brown at the center, paler at the edge from below.

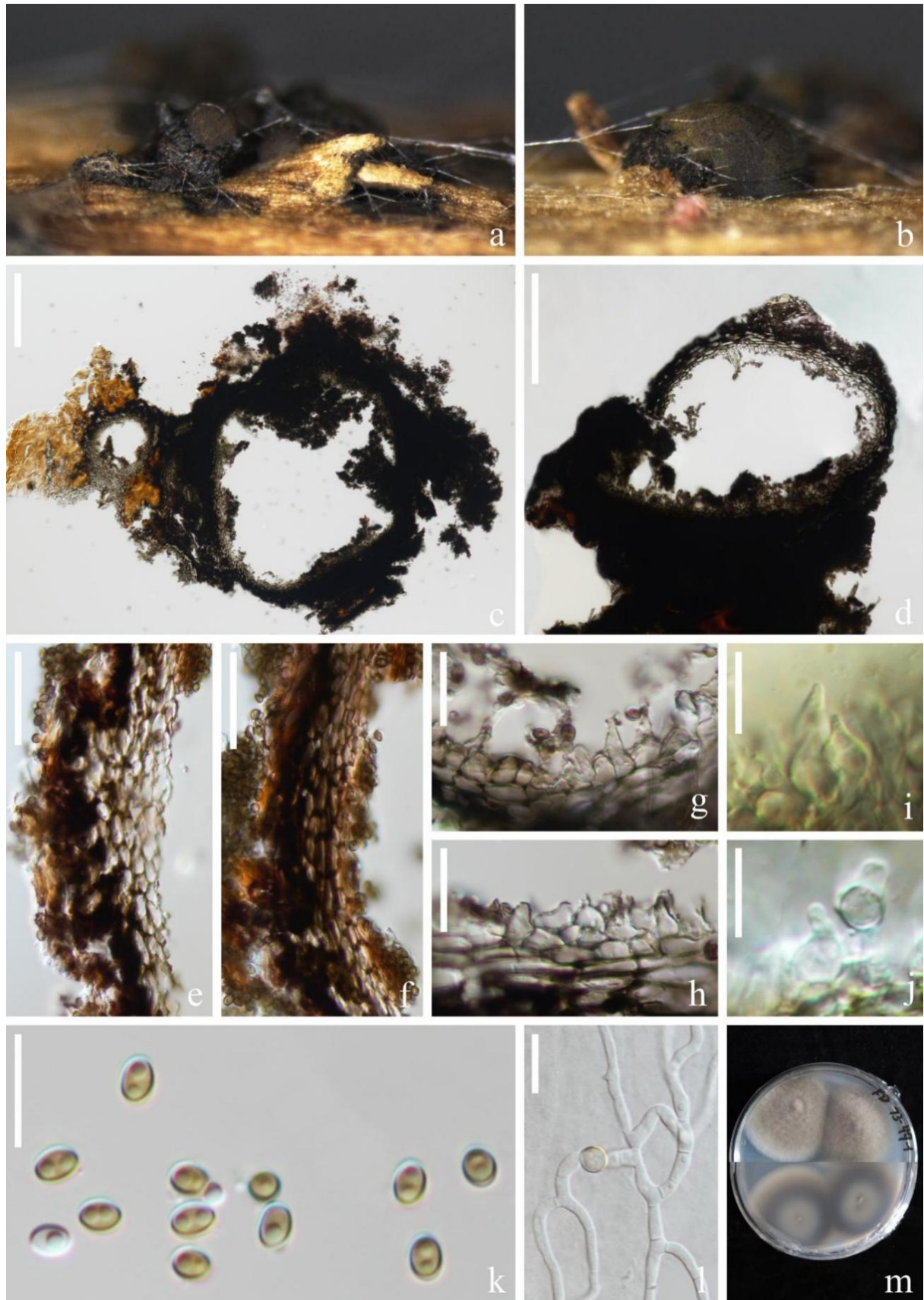


Figure 24 – *Pararoussoella hydei* (HKAS 145700, holotype). a, b Appearance of conidiomata on the host substrate. c, d Section of conidioma. e, f Conidioma wall. g–j Conidiogenous cells. k Conidia. l Germinated conidium. m Culture on PDA (upper from above and lower from below). Scale bars: c, d = 120 μm , e, f = 30 μm , g, h = 15, i–l = 10 μm .

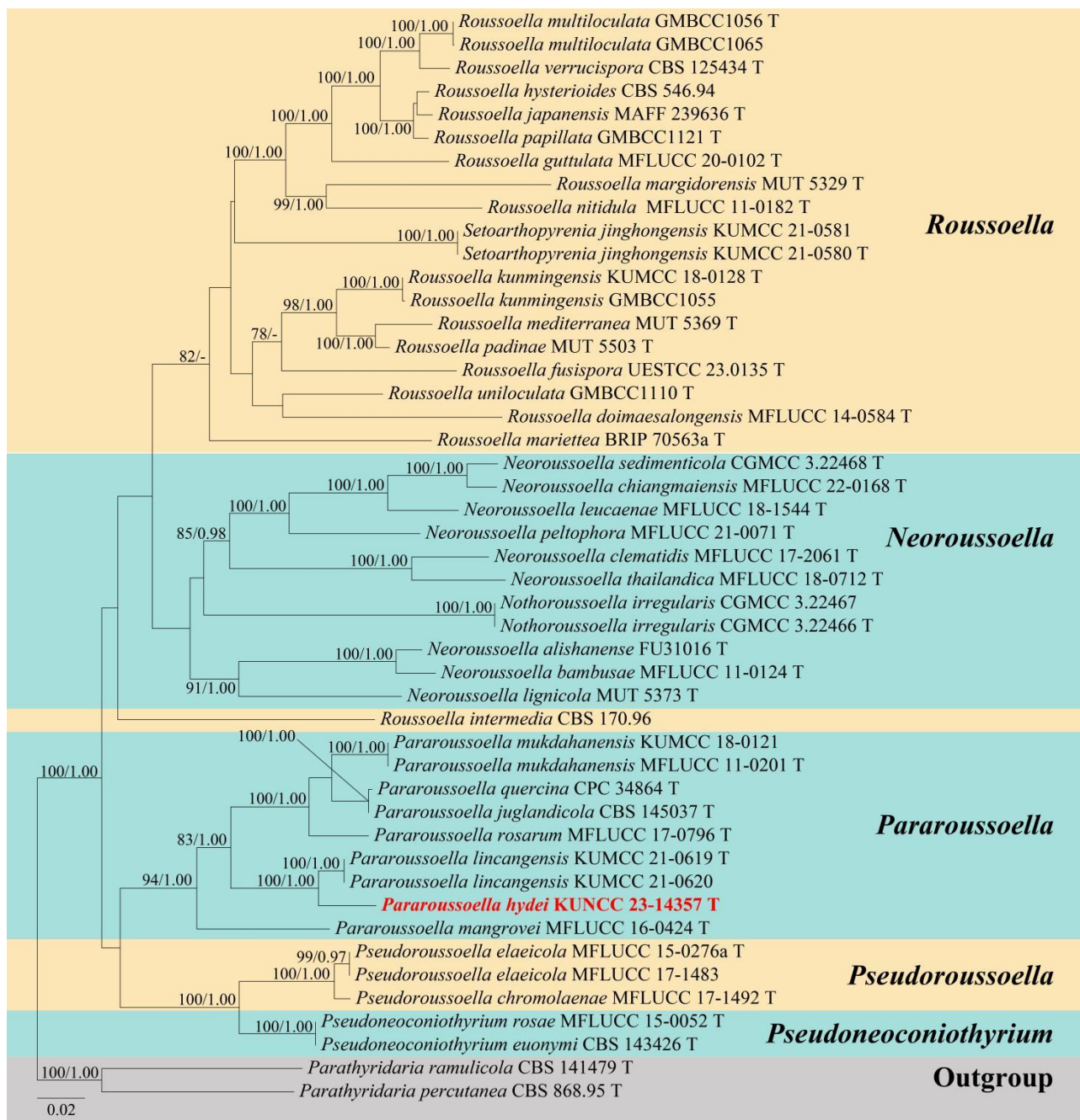


Figure 25 – ML tree of *Roussoellaceae* based on the combined LSU, ITS, *tef1-α* and *rpb2* sequences. Bootstrap support values for ML equal to or greater than 65% and PP values equal to or greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Parathyridaria percutanea* (CBS 868.95) and *P. ramulicola* (CBS 141479). Ex-type strains are marked with “T”. The new taxon is indicated in bold and red.

Material examined – China, Guizhou Province, Zunyi City, Xishui County, Sancha River Conservation Area, N 28°33'50", E 106°24'9", elevation 1133 m, on decaying wood from a freshwater stream, 3 October 2023, X.J. Xiao, SCS24 (HKAS 132144), living culture GZCC 24-0062.

Notes – In our phylogenetic tree (Fig. 27), the strain GZCC 24-0062 clustered with *Polyposphaeria appendiculata* (MFLUCC 24-0097) with 97% ML and 0.96 PP support. *Polyposphaeria appendiculata* was introduced by Liu et al. (2024a) in a terrestrial habitat from Thailand. Our collection morphologically resembles *Po. appendiculata* in not having conidiophores and subglobose to ellipsoidal or irregular conidia. However, the conidial sizes are larger (54–179 ×

45–77 μm vs. 67–100 $\times$ 63–89 μm) than those of *Po. appendiculata* (Liu et al. 2024a). ITS, *tef1*- α and *rpb2* comparisons show there are 13 bp (including 2 gaps, totally 716 bp), 23 bp (without gaps, totally 949 bp), and 14 bp (including 1 gap, totally 960 bp) differences, respectively, between GZCC 24-0062 and MFLUCC 24-0097 (ex-type strain). Therefore, we identify our collection as *Polyposphaeria appendiculata*. This is the first time *Polyposphaeria appendiculata* is reported from freshwater habitat in China.

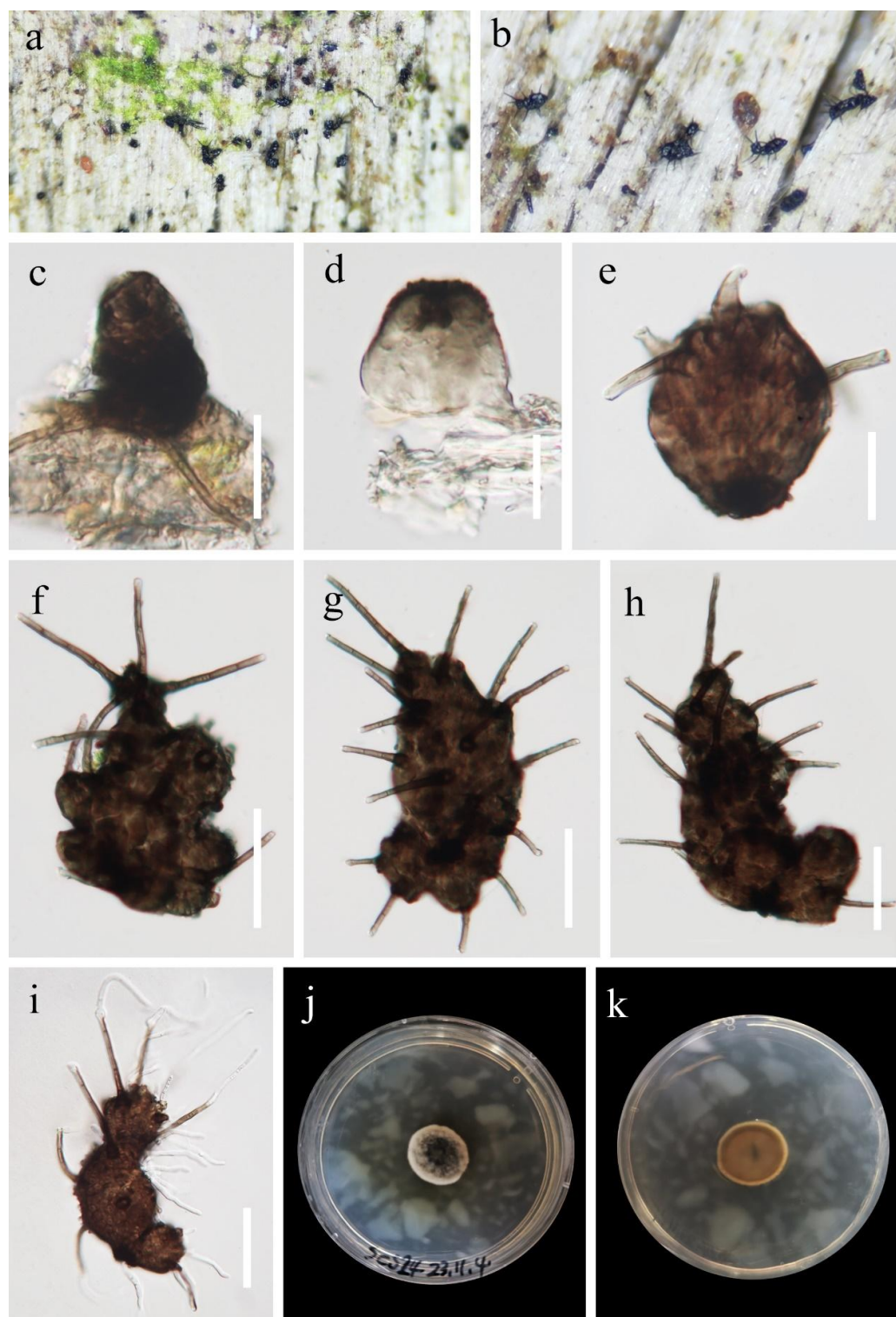


Figure 26 – *Polyposphaeria appendiculata* (HKAS 132144, new habitat and geographical record). a, b Colonies on dead wood surface. c–h Conidia. i Germinated conidium. j, k Colony on PDA (j from above, k from below). Scale bars: c–e = 20 μm , f–i = 50 μm .

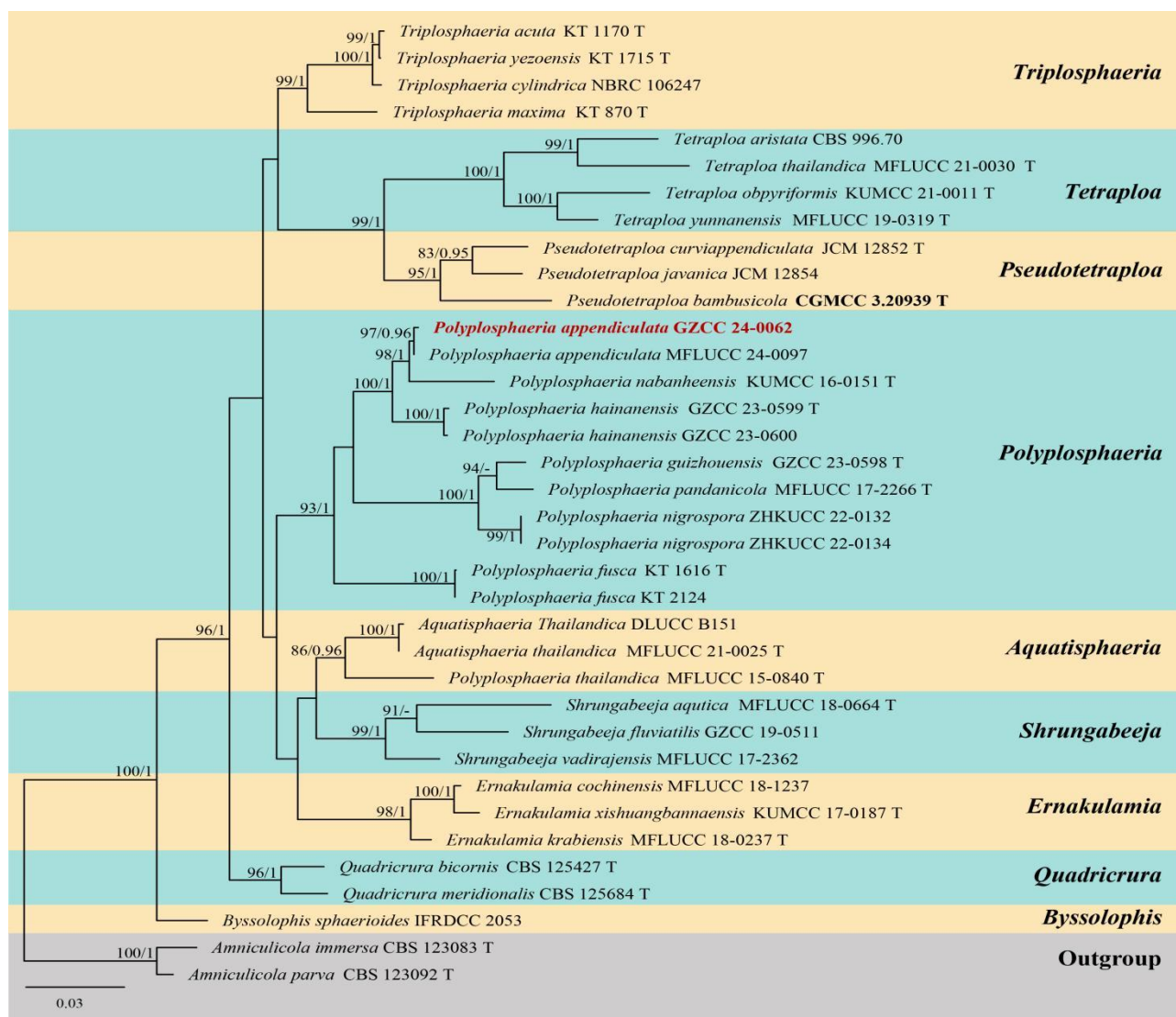


Figure 27 – ML tree based on the combined LSU, ITS, SSU and *tub* sequences. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Amniculicola immersa* (CBS 123083) and *Amniculicola parva* (CBS 123092). ex-type strains are marked with “T”. The new report is indicated in bold and red.

Tubeufiales Boonmee & K.D. Hyde

Tubeufiaceae M.E. Barr

Acrohelicosporium Jian Ma, K.D. Hyde & Y.Z. Lu, Fungal Diversity 129: 379 (2024)

Acrohelicosporium was recently introduced by Ma et al. (2024b) in Tubeufiaceae (Tubeufiales, Dothideomycetes) to accommodate four species *Ac. abundatum* (type species), *Ac. aquaticum*, *Ac. guizhouense*, and *Ac. viridisporum*, and an unidentified species, *Acrohelicosporium* sp. Among them, three species were reported from freshwater habitats, and one species (*Ac. abundatum*) was isolated from terrestrial habitat. *Acrohelicosporium* is characterized by macronematous, mononematous, simple conidiophores, blastic, integrated or discrete, terminal or intercalary, denticulate conidiogenous cells, and helicoid, hyaline, aseptate conidia (Ma et al. 2024b). The sexual morph of *Acrohelicosporium* is undetermined.

Acrohelicosporium hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 28

Fungal Names number: FN 572845; Facesoffungi number: FoF 17803

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 144600

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Unknown. Asexual morph: *Colonies* on natural substrate effuse, gregarious, white to brown, shiny. *Mycelium* immersed in the substratum, composed of branched, septate, pale brown to brown hyphae. *Conidiophores* 93–188 × 7–10 µm ($\bar{x}$ = 143 × 8 µm, n = 25), macronematous, mononematous, flexuous or straight, erect, unbranched, septate, hyaline to brown, thick-walled. *Conidiogenous cells* 9.5–17 × 4.5–8.5 µm ($\bar{x}$ = 14 × 6.5 µm, n = 25), monoblastic, or rarely polyblastic, integrated, lateral, pale brown to brown, with tooth-like protrusions, 2.5–6 × 1–3 µm. *Conidia* 28–34 µm diameter, filaments 285–388 × 4–7 µm ($\bar{x}$ = 353 × 5 µm, n = 30), loosely coiled 1–3½ times, pleurogenous, solitary, helicoid, rounded at base, becoming loosely coiled in water, hyaline to pale brown, septate, smooth.

Culture characteristics – Conidia on PDA within 24 h and germ tubes produced from spores. After 10 days of cultivation at 28 °C, the diameter of the colonies on PDA can reach up to 16 mm diam, medium dense, with a flat surface, regular, edge entire, from above: pale brown at the margin, brown to pale brown inner circular; from below: pale brown at the margin, dark brown inner circular.

Material examined – China, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Rongjiang County, Yueliang mountain, N 25°38'18", E 108°12'27", elevation 615 m, on decaying wood from a freshwater stream, 11 June 2023, X.J. Xiao, YLS15 (HKAS 144600, holotype), ex-type culture GZCC 24-0075.

Notes – In the phylogenetic tree, our strain GZCC 24-0075 is related to *Acrohelicosporium aquaticum* (CGMCC 3.25539) and *Acrohelicosporium* sp. (CBS 284.54) with weak support (Fig. 29). Morphologically, our collection differs from *Ac. aquaticum* by having larger conidial dimensions (28–34 µm diam. vs. 23–28 µm diam.). Moreover, our collection has much larger conidial filament than those of *Ac. aquaticum* (285–388 × 4–7 µm vs. 91–141.5 × 1.5–3 µm) (Ma et al. 2024b). Morphology of *Acrohelicosporium* sp. (CBS 284.54) has not been described, thus cannot be compared with. ITS comparison shows that there are 22 out of 436 bp (5.05%, including 4 bp gaps) differences between our strain GZCC 24-0075 and CBS 284.54. Therefore, we introduce our collection as a new species based on both morphology and phylogeny.

Berkleasmium Zobel, *Icones fungorum hucusque cognitorum* 6: 4 (1854)

Berkleasmium was introduced by Corda (1854) based on the type species *B. concinnum*. It is a cosmopolitan genus found in both terrestrial and freshwater habitats (Lu et al. 2018b, Ma et al. 2024b). Tanney & Miller (2017) linked the sexual and asexual morphs of *B. concinnum*. The sexual morph is characterized by subglobose to globose, dark brown to black, ostiolate, setose ascomata seated on a subiculum, 8-spored, bitunicate, cylindrical, pedicellate asci, and biseriate, fusiform, hyaline, multi-septate, guttulate ascospores. The asexual morph exhibits either sporodochial conidiomata with dictyoconidia or solitary conidiomata with helicoid conidia (Lu et al. 2018b). *Berkleasmium* is a polyphyletic genus (Pinnoi et al. 2007). Although 46 epithets are listed in *Species Fungorum* (2025), only nine species are accepted in Tubeufiaceae (Lu et al. 2018b, Ma et al. 2024b). Recently, a new lichenicolous species, *B. lichenicola* was introduced by Diederich & Etayo (2024). However, molecular data for this species are not yet available.

Berkleasmium hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 30

Fungal Names number: FN 572848; Facesoffungi number: FoF 17806

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – GZAAS 25-0536

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, white to green or brown, gregarious, glistening. *Mycelium* partly immersed, partly superficial, composed of pale brown to brown, branched, septate hyphae. *Conidiophores* 15–32 × 4–7 µm ($\bar{x}$ = 22 × 6 µm, n = 25),

macronematous, mononematous, arising from creeping hyphae, straight or broadly curved, erect, sometimes branched, pale brown to brown, septate, thick-walled. *Conidiogenous cells* $10\text{--}24 \times 3\text{--}7 \mu\text{m}$ ($\bar{x} = 14 \times 5 \mu\text{m}$, $n = 20$), holoblastic, monoblastic, integrated, terminal, pale brown to brown, smooth. *Conidia* $541\text{--}684 \times 8\text{--}13 \mu\text{m}$ ($\bar{x} = 608 \times 10 \mu\text{m}$, $n = 30$), $80\text{--}105 \mu\text{m}$ diameter, tightly coiled 2–3 times, acrogenous, solitary, helicoid, not becoming loosely coiled in water, pale brown to brown, septate, slightly constricted at the septa, smooth-walled.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies reaching up to 29 mm diam. after 3 months of cultivation at 28°C , medium dense, surface flat, irregular, edge undulate, unevenly brown from above and below.

Material examined – China, Guizhou Province, Xishui County, Guizhou Xishui National Nature Reserve, N $28^\circ33'34''$, E $106^\circ24'13''$, elevation 1186 m, on decaying wood from a freshwater stream, 31 May 2025, X.J. Xiao, XLS10 (GZAAS 25-0536, holotype), ex-type culture GZCC 25-0518.

Notes – Among the nine accepted *Berkleasium* species in *Tubeufiaceae*, only *B. macrofilamentosus* lacks molecular data. *Berkleasium macrofilamentosus* was initially described by Matsushima (1983) as *Helicomycetes macrofilamentosus*. Our collection differs from *B. macrofilamentosus* by larger conidiophores ($15\text{--}32 \times 4\text{--}7 \mu\text{m}$ vs. $7\text{--}20 \times 3\text{--}4 \mu\text{m}$), and much larger conidial diameter ($80\text{--}105 \mu\text{m}$ vs. $35\text{--}55 \mu\text{m}$). Given these distinct morphological differences, we consider our collection to represent a different species. In the phylogenetic tree (Fig. 31), our strain GZCC 25-0518 clustered with seven *B. aquaticum* strains and *B. hainanense* (CGMCC 3.25558) but formed a distinct clade, confirming its phylogenetic distinctness.

Helicoma Corda, *Icones fungorum hucusque cognitorum* 1: 15 (1837)

Helicoma was one of the three earliest described helicosporous hyphomycete genera introduced by Corda (1837). It belongs to *Tubeufiaceae* (*Tubeufiales*, *Dothideomycetes*) and is distributed worldwide in both freshwater and terrestrial habitats (Lu et al. 2018b, Liu et al. 2019c, Lu et al. 2023, Ma et al. 2024b). The sexual morph is characterized by subglobose, oval to obovoid, dark brown ascomata with a central ostiole, 8-spored, bitunicate, cylindrical, short-pedicellate asci, and 2–3-seriate, fusiform to clavate, hyaline, septate ascospores (Boonmee et al. 2014, Lu et al. 2018b). Five conidial types are recognized in its asexual morph (Matsushima 1983, Gao et al. 2016, Lu et al. 2018b, Ma et al. 2024b). Seventy species are accepted in *Helicoma* (Ma et al. 2024b).

Helicoma kevinianum X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 32

Fungal Names number: FN 572888; Facesoffungi number: FoF 17821

Etymology – The specific epithet “kevinianum” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 145873

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, white to pale brown, gregarious, glistening. *Mycelium* partly immersed, partly superficial, composed of pale brown to brown, branched, septate hyphae. *Conidiophores* $72\text{--}134 \times 5\text{--}9 \mu\text{m}$ ($\bar{x} = 112 \times 7 \mu\text{m}$, $n = 20$), macronematous, mononematous, erect, flexuous or straight, cylindrical, tapering towards the apex, upper half hyaline to subhyaline, lower half brown, simple or branched, septate, thick-walled. *Conidiogenous cells* $8.5\text{--}13 \times 6\text{--}7.5 \mu\text{m}$ ($\bar{x} = 11 \times 6.5 \mu\text{m}$, $n = 20$), polyblastic, integrated, intercalary, pale brown to brown, with tooth-like protrusions, smooth. *Conidia* $300\text{--}407 \times 5\text{--}7.5 \mu\text{m}$ ($\bar{x} = 354 \times 6 \mu\text{m}$, $n = 30$), pleurogenous, solitary, helicoid, loosely coiled 1–1¼ times, rounded at both ends, becoming loosely coiled in water, hyaline to pale brown, septate, smooth.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies reaching up to 6 cm diam. after 72 days of cultivation at 28°C , medium dense, flat, regular, margin filariform, dark brown from above and below.

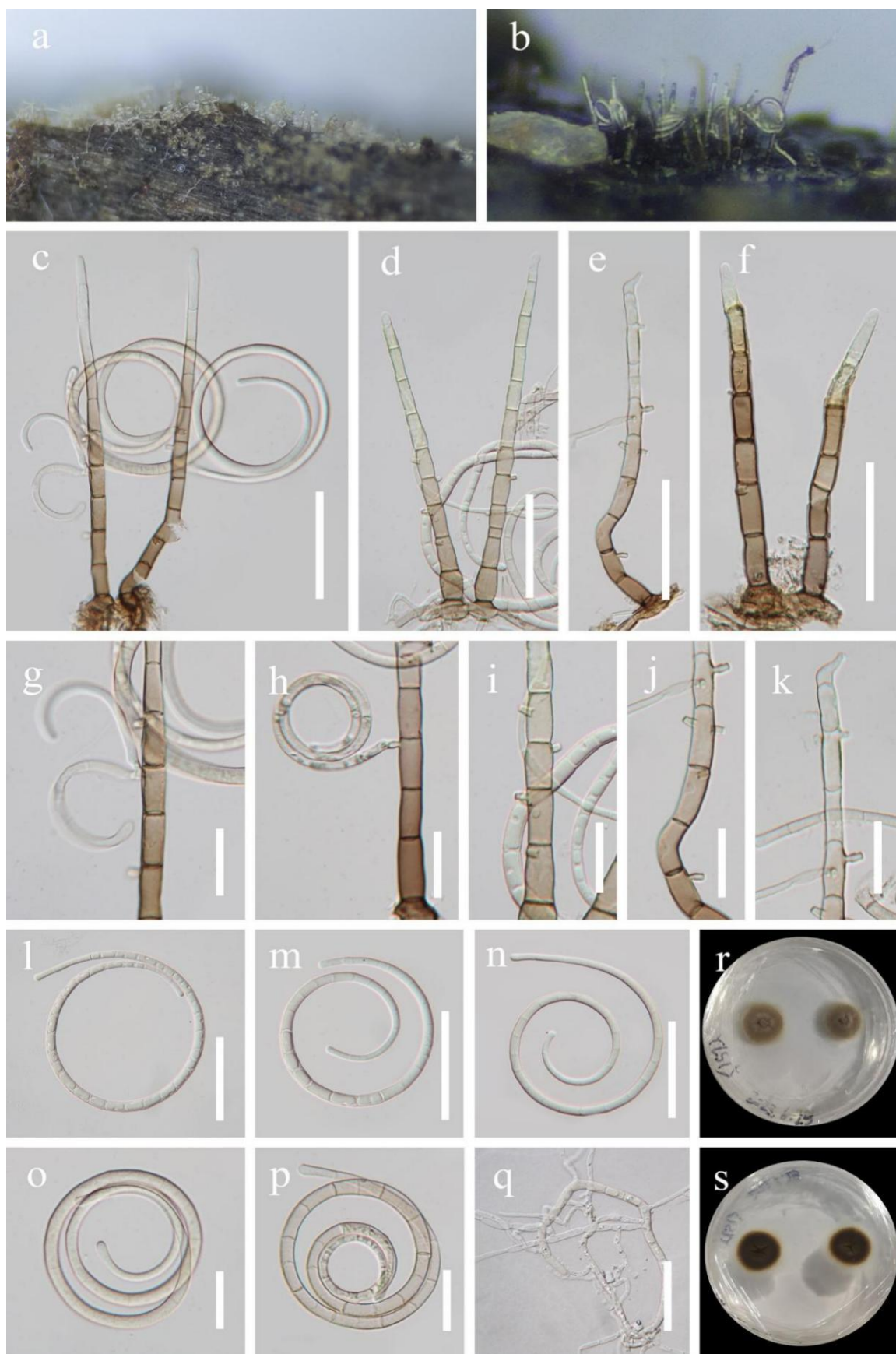


Figure 28 – *Acrohelicosporium hydei* (HKAS 144600, holotype). a, b Colonies on dead wood surface. c–f Conidiophores and conidia. g–k Conidiogenous cells and conidia. l–p Conidia. q Germinated conidium. r, s Colony on PDA (r from above, s from below). Scale bars: c–f, l–n = 50 μ m, g–k, o–q = 20 μ m.

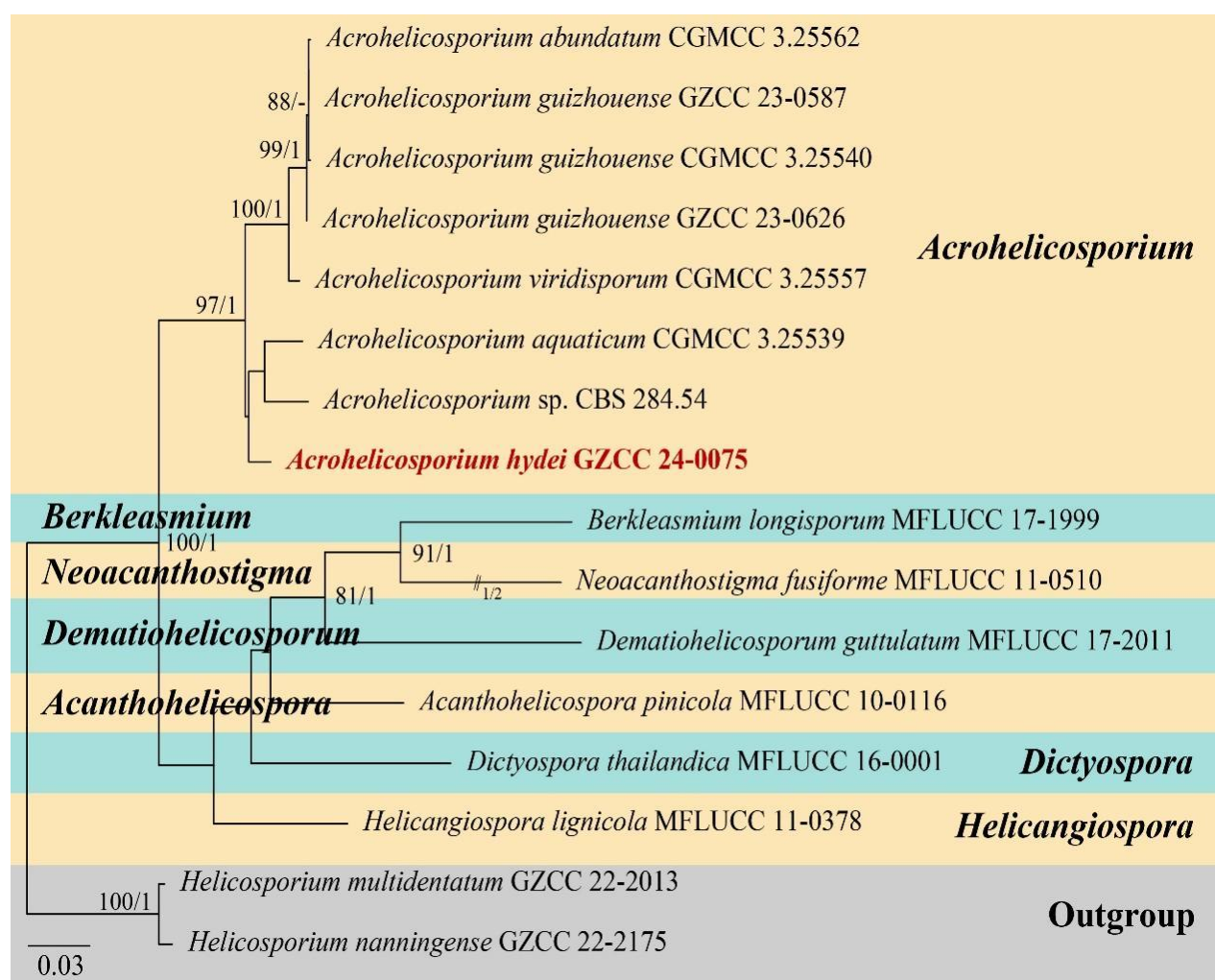


Figure 29 – ML tree based on the combined LSU, ITS, *rpb2* and *tef1-α* sequences, representing the genus *Acrohelicosporium*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Helicosporium multidentatum* (GZCC 22-2013) and *Helicosporium nanningense* (GZCC 22-2175). The new taxon is indicated in bold and red.

Material examined – China, Guizhou Province, Qiannan Prefecture, Weng'an County, Zhujiashan National Forest Park, N 26°57'55", E 107°36'25", elevation 1045 m, on decaying wood from a freshwater habitat, 24 June 2023, X.J. Xiao, ZJ58 (HKAS 145873, holotype), ex-type culture GZCC 24-0129, other living culture, GZCC 25-0517.

Notes – In the phylogenetic analysis (Fig. 33), our strain GZCC 24-0129 and GZCC 24-0517 clustered together with *Helicoma tropicum* (CGMCC 3.25574 and ZHKUCC 24-0099) and *H. yunnanense* (KUNCC 23-13501) with 79% ML and 0.6 PP support. Morphologically, our isolates share similarities with *H. tropicum* and *H. yunnanense* in possessing intercalary conidiogenous cells with tooth-like protrusions. However, our collection differs from *H. tropicum* in the dimorphic nature of its conidia (Ma et al. 2024b). Compared to *H. yunnanense*, our isolates feature larger conidia (300–407 × 5–7.5 μm vs. 132.5–239 × 3–4 μm) and fewer coils (1–1¼ times vs. 1½–3 times). Furthermore, phylogenetic analyses based on LSU, ITS, *tef1-α* and *rpb2* sequences showed our two strains formed a distinct clade, suggesting a hitherto undescribed species.

Neohelicomycetes Z.L. Luo, D.J. Bhat & K.D. Hyde, Cryptogamie, Mycologie 38 (1): 39 (2017)

Neohelicomycetes was introduced by Luo et al. (2017) for three new taxa, i.e., *Ne. aquaticus* (type species), *Ne. grandisporus*, and *Ne. submerses*. It is characterized by macronematous, mononematous, pale brown, simple or branched conidiophores, monoblastic, lateral, denticulate

conidiogenous cells, and helicoid, hyaline to pale brown conidia (Luo et al. 2017, Dong et al. 2020b, Lu et al. 2022, Yang et al. 2023, Ma et al. 2024a). Twenty-eight species are listed in Species Fungorum (2025) and all of them have DNA sequence data. *Neohelicomyces* species have been reported from both freshwater and terrestrial habitats with a worldwide distribution.

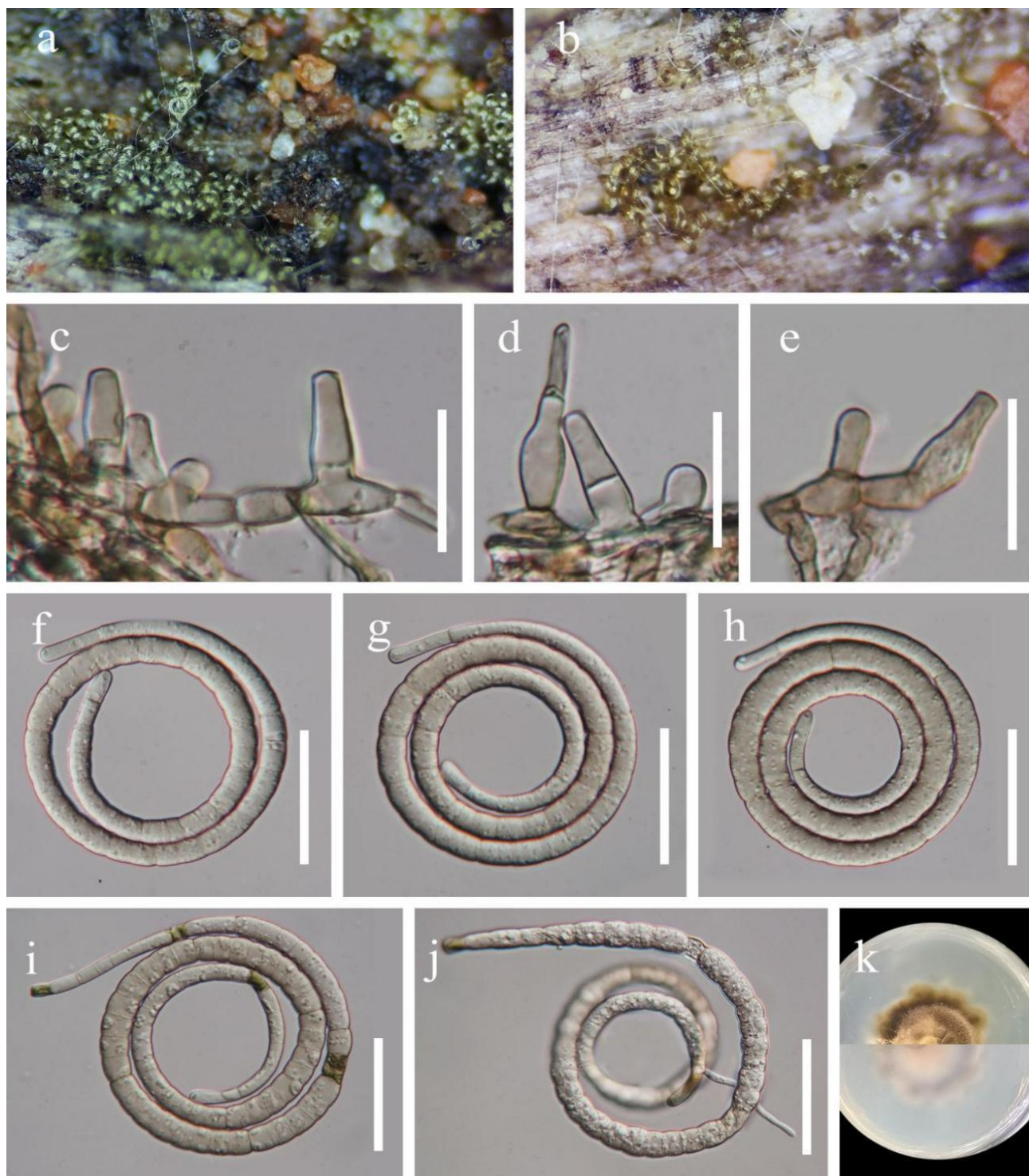


Figure 30 – *Berkleasmium hydei* (GZAAS 25-0536 holotype). a, b Colonies on dead wood surface. c–e Conidiophores and conidiogenous cells. f–i Conidia. j Germinated conidium. k Colony on PDA (upper and lower view). Scale bars: c–e = 20 μ m, f–j = 50 μ m.

Neohelicomyces davidii X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.
Fungal Names number: FN 572890; Facesoffungi number: FoF 17829

Fig. 34

Etymology – The specific epithet “davidii” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 145875

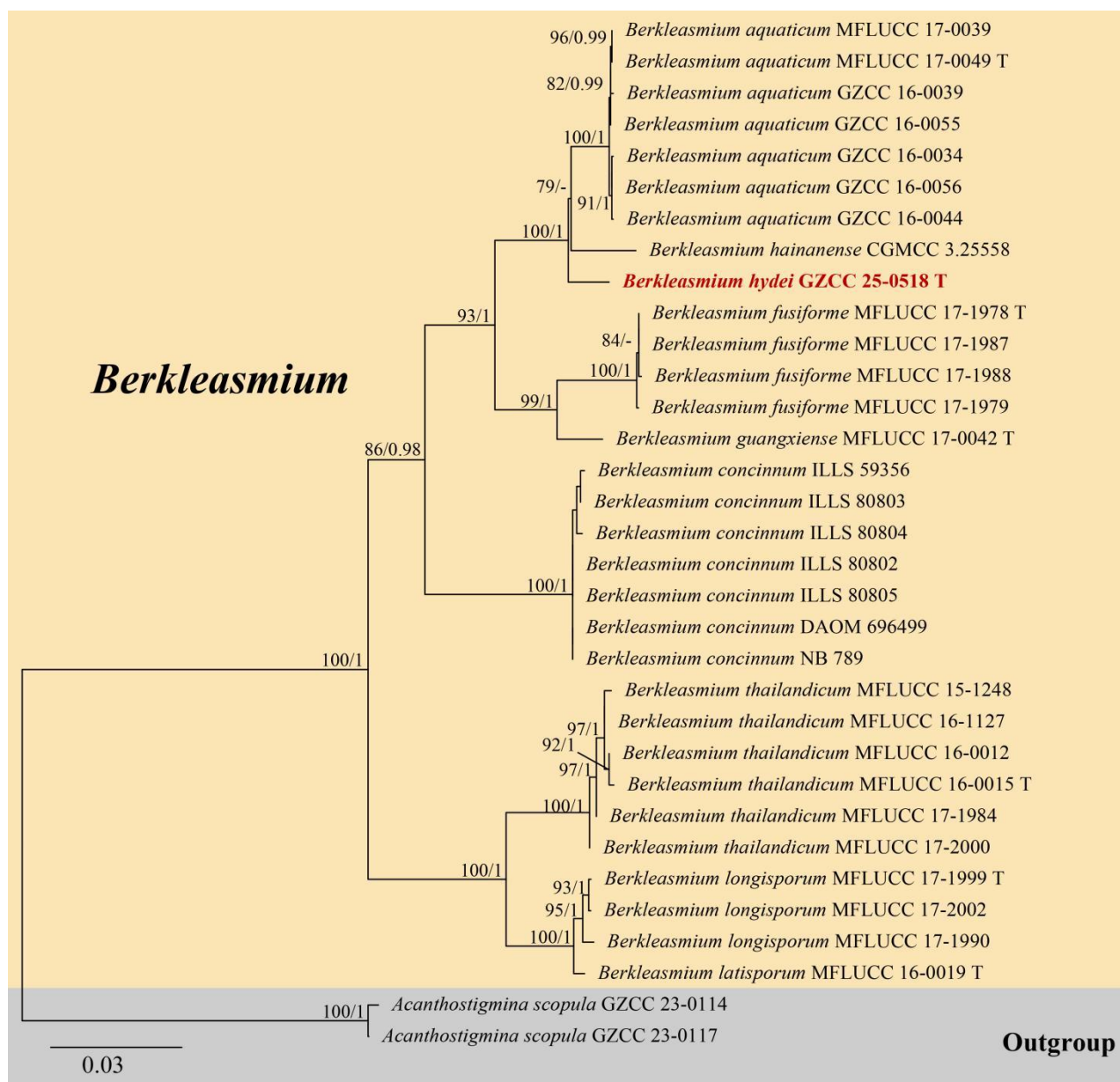


Figure 31 – ML tree based on the combined LSU, ITS, *rpb2* and *tef1-α* sequences, representing the genus *Berkleasmium*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Acanthostigmina scopula* (GZCC 23-0114) and *Acanthostigmina scopula* (GZCC 23-0117). Type strains are marked with “T”. The new taxon is indicated in bold and red.

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, white to pale pink, gregarious, glistening. *Mycelium* partly immersed, partly superficial, composed of brown, branched, septate hyphae. *Conidiophores* 52–169 × 4–7 μm ($\bar{x}$ = 114 × 5 μm, n = 20), macronematous, mononematous, erect, straight or slightly flexuous, pale brown to brown at base, paler towards the apex, unbranched, septate, thick-walled. *Conidiogenous cells* 9.5–18 × 2–6 μm ($\bar{x}$ = 15 × 4 μm, n = 25), holoblastic, mono- or polyblastic, integrated, terminal and intercalary, with lateral minute denticles, hyaline, smooth. *Conidia* 200–273 × 3–4 μm ($\bar{x}$ = 237 × 3.5 μm, n = 20), loosely coiled

1½–2⅓ times, acropleurogenous, solitary, helicoid, becoming loosely coiled in water, hyaline, indistinctly septate, guttulate, smooth-walled.



Figure 32 – *Helicoma kevinianum* (HKAS 145873, holotype). a Colonies on dead wood surface. b–d Conidiophores and conidiogenous cells. e–g Conidiogenous cells. h–l Conidia. m Germinated conidium. n Colony on PDA (upper and lower view). Scale bars: b–m = 50 μm.

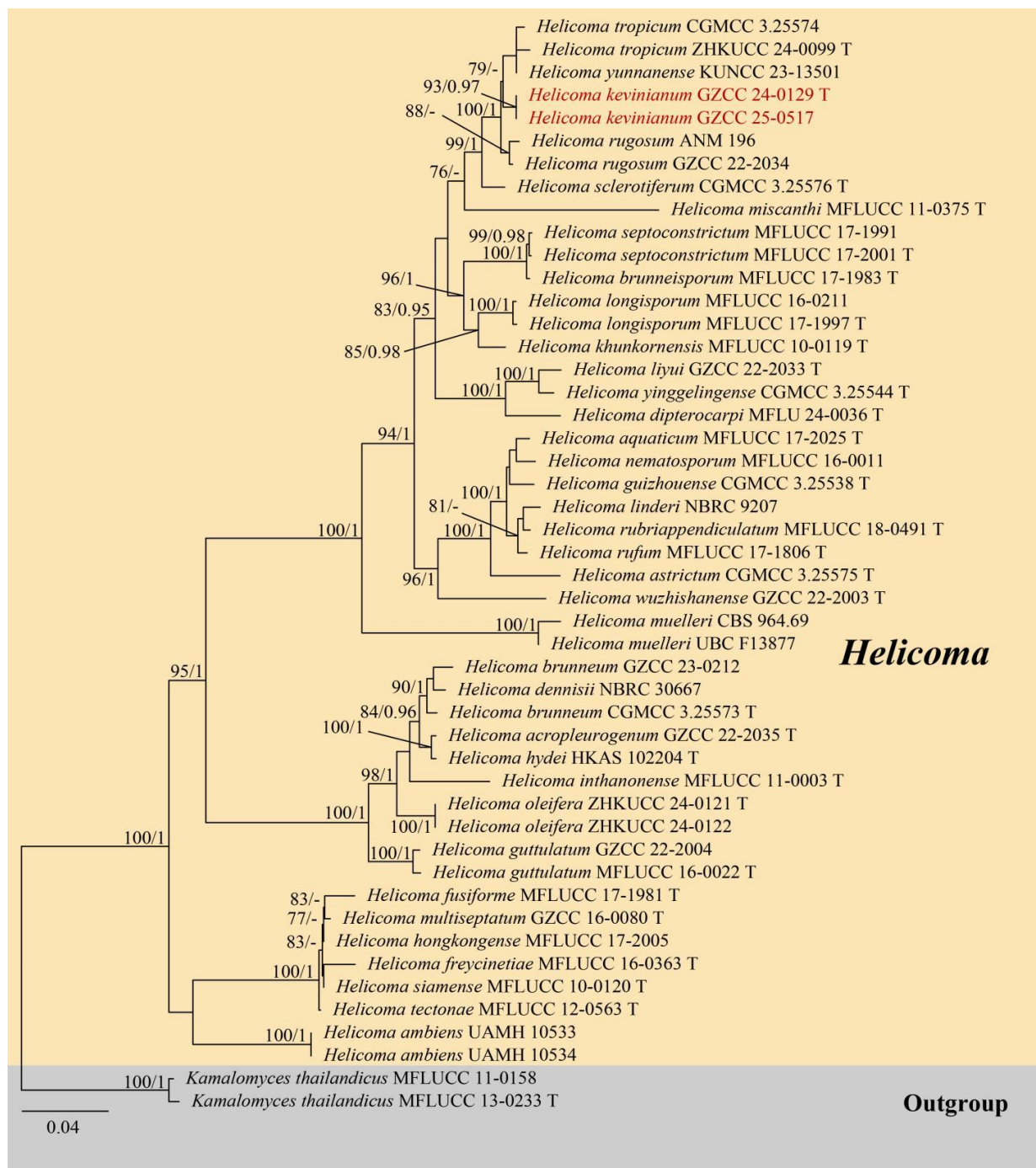


Figure 33 – ML tree based on the combined LSU, ITS, *tef1-α* and *rpb2* sequences, representing the genus *Helicoma*. Bootstrap support values for ML equal to or greater than 75% and PP values equal to or greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Kamalomyces thailandicus* (MFLUCC 11-0158) and *Kamalomyces thailandicus* (MFLUCC 13-0233). Ex-type strains are marked with “T”. The new taxon is indicated in red.

Culture characteristics – Conidia germinating on PDA media within 12 h. Colonies reaching up to 34 mm diam. after 30 days of cultivation at 28°C, medium dense, surface rough, irregular, edge undulate, dark brown at center, brown at the margin from above and below.

Material examined – China, Guizhou Province, An Shun City, Pu Ding County, Wujiangdu Reservoir, N 27.310155, E 106.683209, elevation 1203 m, on decaying wood from a freshwater river, 21 June 2024, X.J. Xiao, YLH21 (HKAS 145875, holotype), ex-type culture GZCC 24-0290.

Notes – Our strain GZCC 24-0290 is phylogenetically related to *Neohelicomyces guttulatus* (CGMCC 3.25550), *Ne. lignicola* (CGMCC 3.25551) and *Ne. macrosporus* (CGMCC 3.25552)

without significant support (Fig. 36). Morphologically, our collection closely resembles *Ne. guttulatus*. However, it can be differentiated from *Ne. lignicola* by its larger conidia ($200\text{--}273 \times 3\text{--}4 \mu\text{m}$ vs. $98\text{--}177 \times 2\text{--}4 \mu\text{m}$). In contrast with *N. macrosporus*, our collection features longer conidiophores ($52\text{--}169 \mu\text{m}$ vs. $35\text{--}86 \mu\text{m}$) and slightly smaller conidia ($200\text{--}273 \times 3\text{--}4 \mu\text{m}$ vs. $176.5\text{--}327.5 \times 4.5\text{--}7.5 \mu\text{m}$) (Ma et al. 2024b). Moreover, the ITS sequence comparison reveals distinct differences among these four isolates. Our strain GZCC 24-0290 exhibits 5.78% differences (29/502, 9 gaps), 10.6% differences (53/500, 7 gaps), and 8.28% differences (41/495, 18 gaps) to *Ne. guttulatus* (CGMCC 3.25550), *Ne. lignicola* (CGMCC 3.25551), and *Ne. macrosporus* (CGMCC 3.25552), respectively. Therefore, based on morphology and phylogeny, we introduce our collection as a new species.

Neohelicomyces kevinianus X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 35

Fungal Names number: FN 572891; Facesoffungi number: FoF 17830

Etymology – The specific epithet “kevinianus” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 136253

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, gregarious, white. Mycelium immersed in the substratum, composed of branched, septate, hyaline hyphae. Conidiophores $3.5\text{--}6 \mu\text{m}$ ($\bar{x} = 4.5 \mu\text{m}$, $n = 20$) wide, macronematous, mononematous, flexuous, erect, branched or unbranched, septate, hyaline to pale brown, smooth. Conidiogenous cells $8\text{--}25 \times 3\text{--}5.5 \mu\text{m}$ ($\bar{x} = 17 \times 4 \mu\text{m}$, $n = 25$), holoblastic, mono- or polyblastic, integrated, with lateral minute denticles, hyaline. Conidia $14\text{--}22 \mu\text{m}$ ($\bar{x} = 18 \mu\text{m}$, $n = 20$) diameter, conidial filament $101\text{--}147 \mu\text{m}$ ($\bar{x} = 18 \mu\text{m}$, $n = 20$) long, tightly coiled $2\frac{1}{2}\text{--}3\frac{2}{3}$ times, acropleurogenous, solitary, helicoid, becoming loosely coiled in water or not, hyaline, indistinctly septate, guttulate, smooth-walled.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies reaching up to 34 mm diam. after 30 days of cultivation at 28°C , medium dense, flat, circular, edge undulate, dark brown at center, olivaceous brown at margin from above and below.

Material examined – China, Guizhou Province, Bijie City, Weining Yi, Hui and Miao Autonomous County, Yingdong Village, N $26^{\circ}52'33''$, E $104^{\circ}22'18''$, elevation 2030 m, on decaying wood from a freshwater stream, 2 August 2023, X.J. Xiao, WJY26 (HKAS 136253, holotype), ex-type culture GZCC 24-0073.

Notes – In our phylogenetic tree (Fig. 36), the strain GZCC 24-0073 clustered together with *Neohelicomyces guizhouensis* (GZCC 23-0725) and *Ne. pallidus* (CBS 271.52 and CBS 962.69) without significant support. Morphologically, our collection bears a close resemblance to *Ne. guizhouensis*, with similar measurements for described morphological characters (Ma et al. 2024a). However, it can be distinguished from *Ne. pallidus* by the larger diameter of its coiled conidia ($200\text{--}273 \times 3\text{--}4 \mu\text{m}$ vs. $98\text{--}177 \times 2\text{--}4 \mu\text{m}$) (Linder 1929). Nevertheless, multi-gene phylogenetic analyses strongly suggest that strain GZCC 24-0073 represents a distinct species. Therefore, we introduce our collection as a new species based on both morphology and phylogeny.

Neohelicosporium Y.Z. Lu, J.C. Kang & K.D. Hyde, Mycol. Progr. 17 (5): 637 (2017)

Neohelicosporium was introduced by Lu et al. (2018a) to accommodate five species, including the type *Neo. parvisporum*. Subsequently, other 20 species were described in this genus. *Neohelicosporium* is characterized by macronematous, mononematous, simple or branched conidiophores, blastic, integrated, sympodial, denticulate conidiogenous cells and helicoid, hyaline conidia (Lu et al. 2018a, b, Dong et al. 2020b, Li et al. 2022a, Yang et al. 2023, Xiong et al. 2024). Four species, i.e., *Neo. aurantiellum*, *Neo. ellipsoideum*, *Neo. fusisporum*, and *Neo. ovoideum* have been linked to with their sexual morph (Promputtha & Miller 2010, Jayasiri et al. 2017, Lu et al. 2018b). *Neohelicosporium* species occur on both terrestrial and freshwater habitats and most species were isolated from China and Thailand.

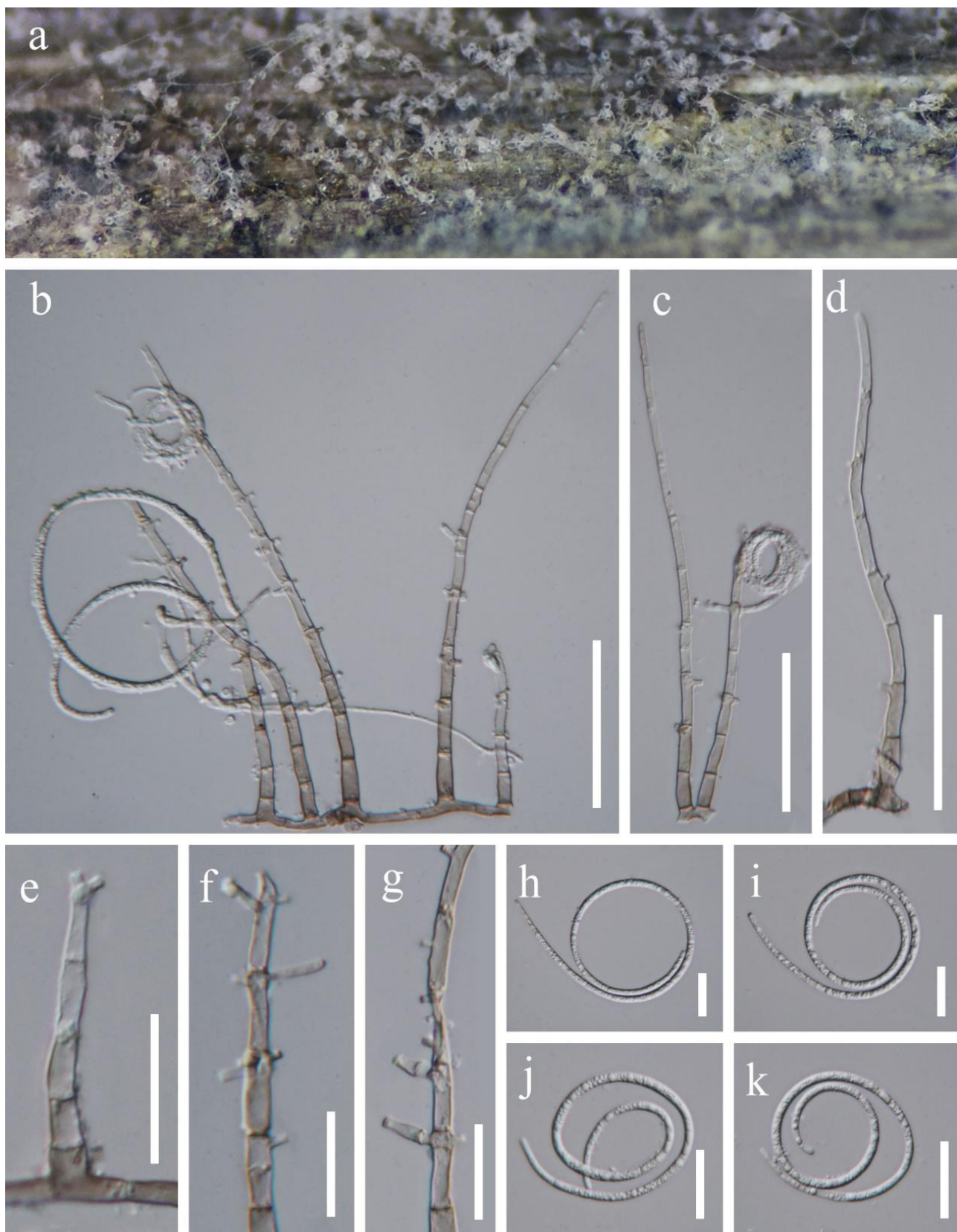


Figure 34 – *Neohelicomycetes davidii* (HKAS 145875, holotype). a Colonies on dead wood surface. b–d Conidiophores, conidiogenous cells and conidia. e–g Conidiogenous cells. h–k Conidia. Scale bars: b–d = 50 μ m, e–k = 20 μ m.

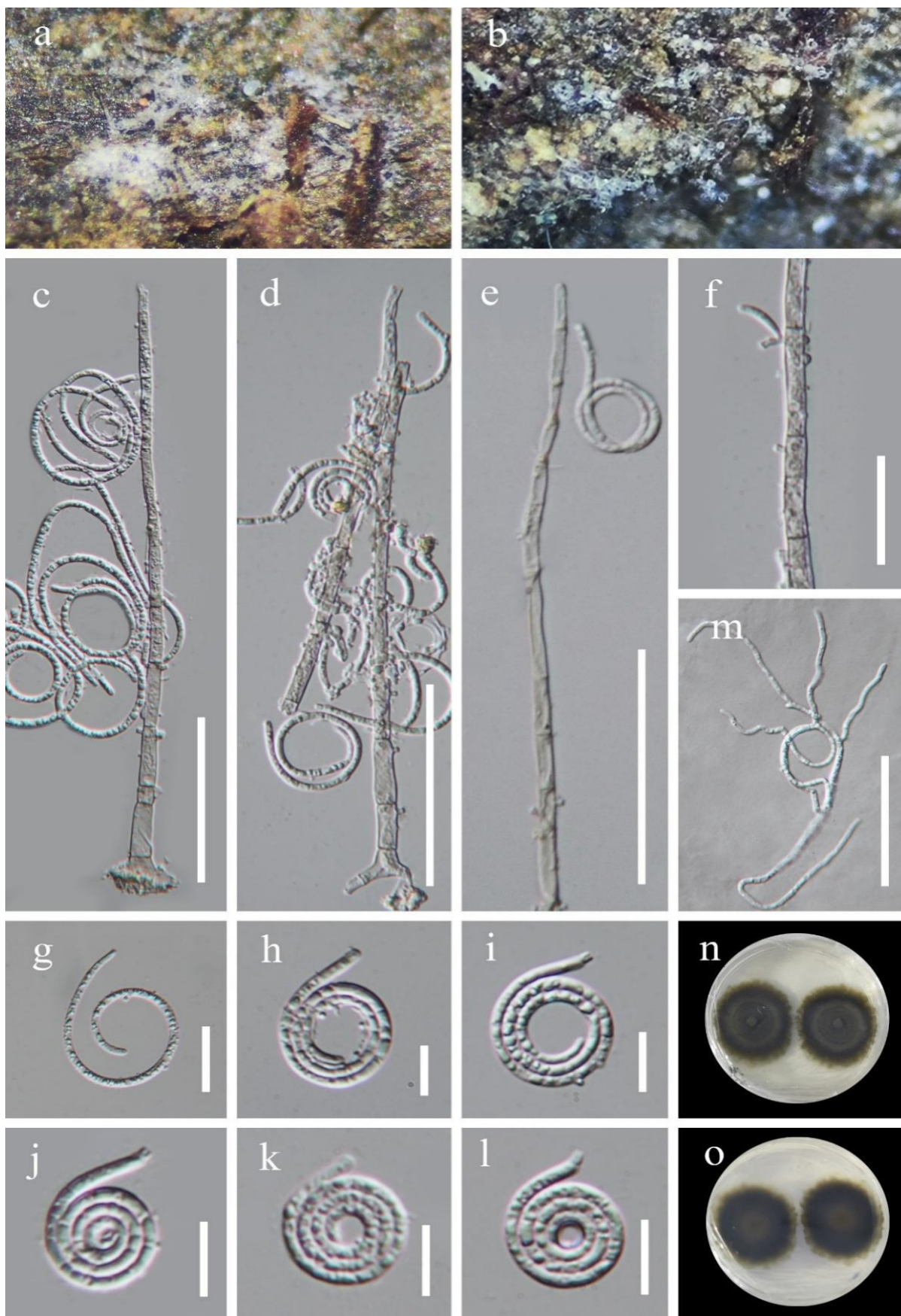


Figure 35 – *Neohelicomyces kevinianus* (HKAS 136253, holotype). a, b Colonies on dead wood surface. c–e Conidiophores, conidiogenous cells and conidia. f Conidiogenous cells. g–l Conidia. m Germinated ascospores. n, o Colony on PDA (upper and lower view). Scale bars: c= 50 μ m, d–k = 20 μ m.

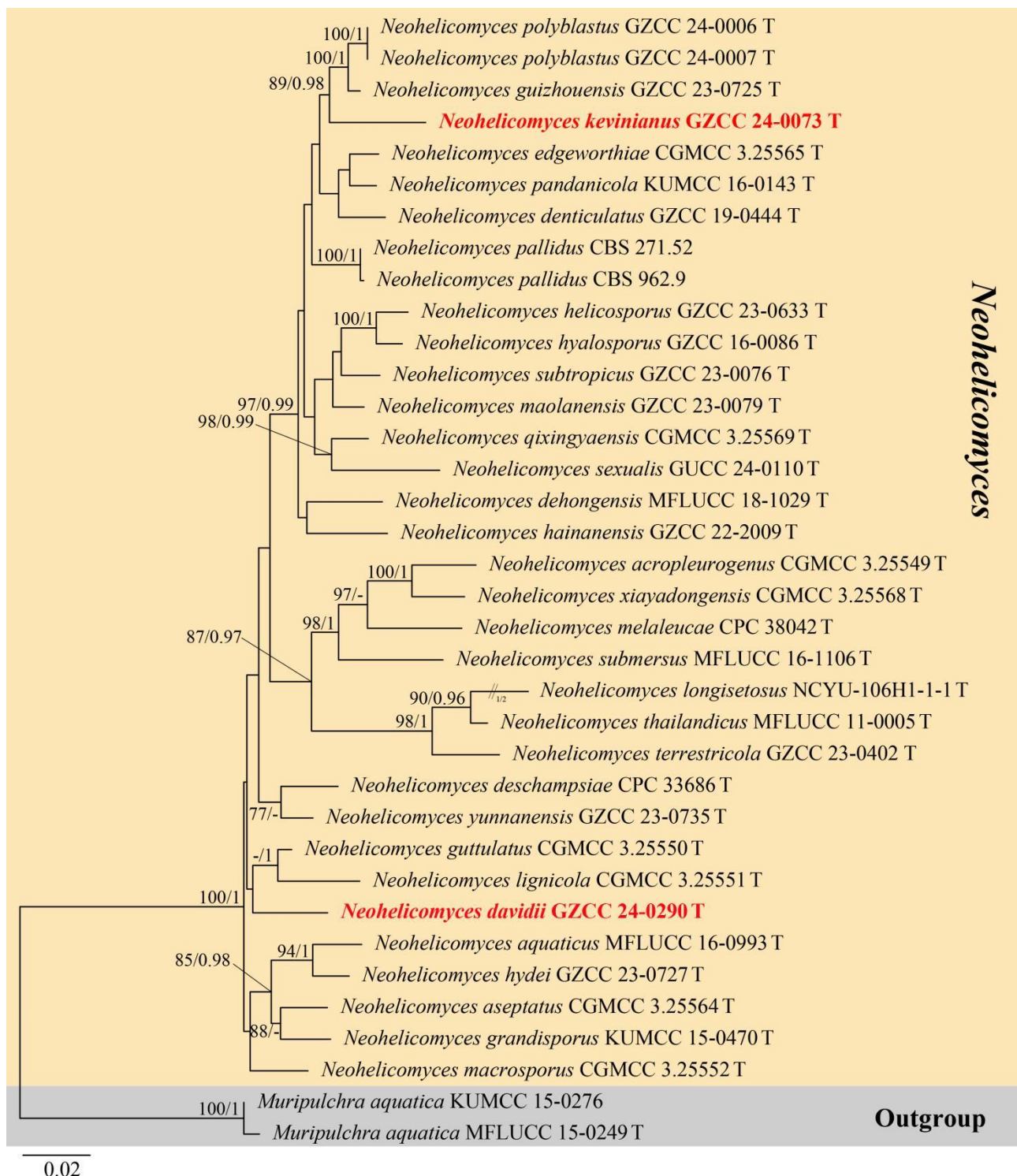


Figure 36 – ML tree based on the combined LSU, ITS, *rpb2* and *tef1*-α sequences, representing *Neohelicomyces*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Muripulchra aquatica* (KUMCC 15-0245) and *Muripulchra aquatica* (MFLUCC 15-0249). Ex-type strains are marked with “T”. The new taxa are indicated in bold and red.

Neohelicosporium hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 37

Fungal Names number: FN 572892; Facesoffungi number: FoF 17831

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 144611

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined.

Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, white to yellow, gregarious, glistening. *Mycelium* partly immersed, partly superficial, composed of brown, branched, septate hyphae. *Conidiophores* 114–200 × 6–11 µm ($\bar{x}$ = 162 × 86 µm, n = 20), macronematous, mononematous, arising from creeping hyphae, erect, flexuous, pale brown to brown, simple or branched, septate, slightly constricted at the septa, thick-walled. *Conidiogenous cells* 9–15 × 5–9 µm ($\bar{x}$ = 12 × 7 µm, n = 20), holoblastic, mono- or polyblastic, integrated, terminal and intercalary, with tooth-like or nipple-like protrusions, hyaline to subhyaline, smooth. *Conidia* 200–250 × 4–5.5 µm ($\bar{x}$ = 220 × 4.5 µm, n = 25), loosely coiled 1½–2½ times, acropleurogenous, solitary, helicoid, becoming loosely coiled in water, hyaline to pale brown, indistinctly septate, guttulate, smooth-walled.

Culture characteristics – *Conidia* germinating on PDA within 12 h. Colonies reaching up to 11 mm diam. after 15 days of cultivation at 28°C, circular, center slightly edge entire, dark brown at the center, paler at the margin from above and below.

Material examined – China, Guizhou Province, Xishui County, Guizhou Xishui National Nature Reserve, N 28°33'34", E 106°24'13", elevation 1186 m, on decaying wood from a freshwater stream, 31 May 2024, X.J. Xiao, X2S3 (HKAS 144611, holotype), ex-type culture GZCC 24-0277.

Notes – In the phylogenetic tree (Fig. 39), our strain GZCC 24-0277 formed a sister clade with *Neohelicosporium guangxiense* (CBS 257.59 and MFLUCC 17-1522). Morphologically, our isolate closely resembles *Neo. guangxiense*, but features shorter and wider conidiophores (114–200 × 6–11 µm vs. 125–290 × 4–6 µm) (Lu et al. 2018a). Both species were collected from freshwater habitats in China. However, comparison of the *tef1-α* sequences showed a 2.64% divergence (18/681 bp, without gaps), while comparison of the *rpb2* sequences indicated a 4.5% divergence (47/1045 bp, without gaps). For a morphological comparison with species lacking available sequence data, see Table 1. Based on the distinct morphology and phylogenetic placement, we introduce our collection as a new species.

Neohelicosporium kevinianus X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 38

Fungal Names number: FN 572893; Facesoffungi number: FoF 17832

Etymology – The specific epithet “kevinianus” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 144602

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, gregarious, white, shiny. *Mycelium* immersed in the substratum, composed of branched, septate, brown hyphae. *Conidiophores* 24–124 × 4–7 µm ($\bar{x}$ = 80 × 6 µm, n = 20), macronematous, mononematous, arising from creeping hyphae, flexuous or straight, erect, mostly unbranched, septate, pale brown to brown, paler towards the apex, smooth. *Conidiogenous cells* 10–19 × 3–7 µm ($\bar{x}$ = 14.5 × 5 µm, n = 20), holoblastic, polyblastic, integrated, terminal and intercalary, with distinct tooth-like or nipple-like protrusions, hyaline to brown, smooth. *Conidia* 22–27 µm diam., conidial filament 106–131 × 3.5–5.5 µm ($\bar{x}$ = 120 × 4.5 µm, n = 25), loosely coiled 1½–2½ times, acropleurogenous, solitary, helicoid, rounded at the tip, becoming loosely coiled in water, guttulate, hyaline to pale brown, septate, smooth.

Culture characteristics – *Conidia* germinating on PDA within 12 h and germ tubes produced from middle or ends of conidial filament. Colonies reaching up to 38 mm diam. after 68 days, medium dense, surface flat, circle, edge undulate, elm green from above and below.

Material examined – China, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Shibing County, Yuntaishan National Forest Park, N 27°6'56", E 108°6'44", elevation 1045 m, on decaying wood from a freshwater stream, 24 June 2023, X.J. Xiao, YTS2A (HKAS 144602, holotype), ex-type culture GZCC 24-0092.

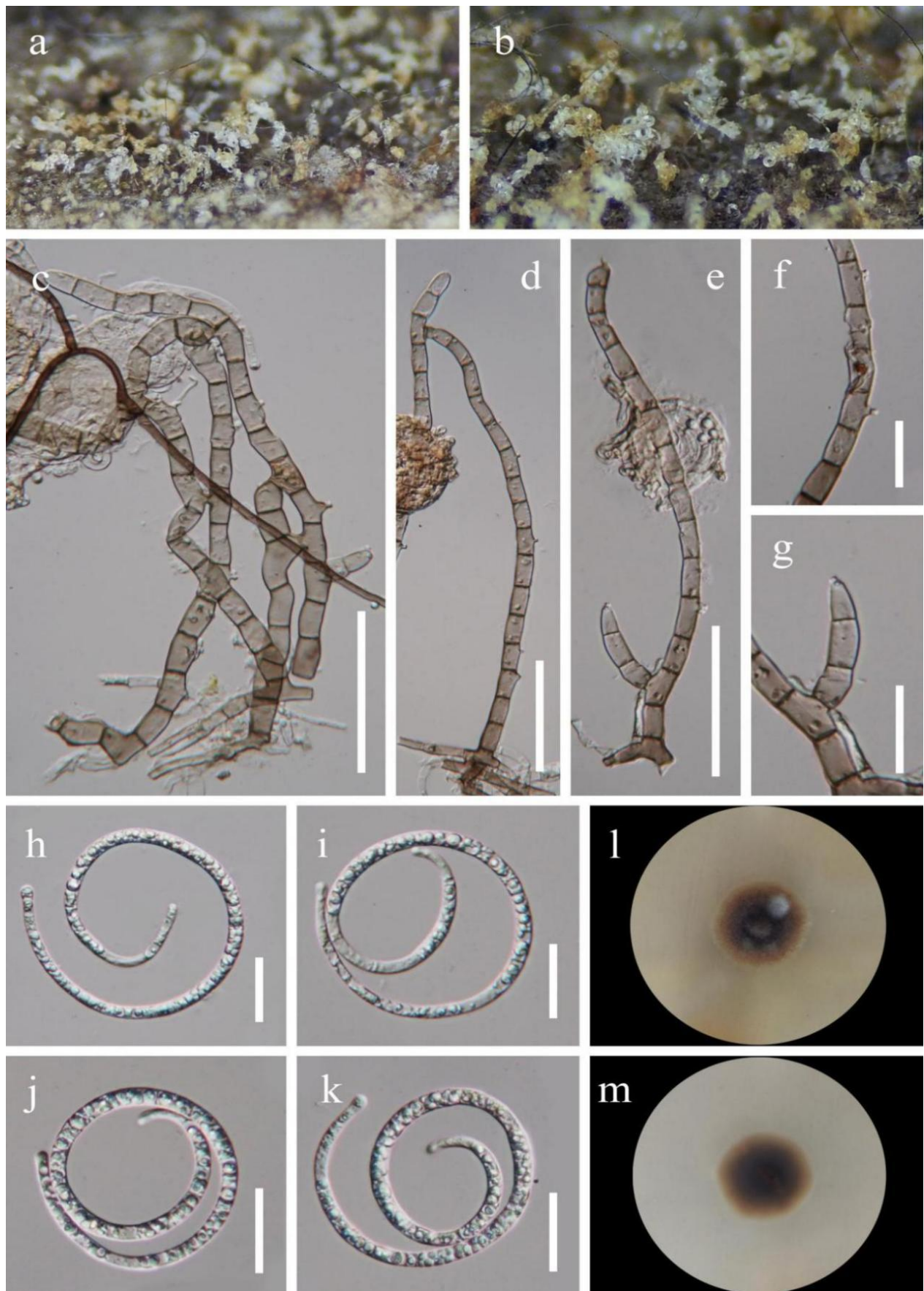


Figure 37 – *Neohelicosporium hydei* (HKAS 144611, holotype). a, b Colonies on dead wood surface. c–e Conidiophores and conidiogenous cells. f, g Conidiogenous cells. h–k Conidia. l, m Colony on PDA (upper and lower view). Scale bars: c–e = 50 μ m, f–k = 20 μ m.

Notes – Four species, i.e., *Neohelicosporium myrtacearum*, *Neo. nizamabadense*, *Neo. sympodiophorum* and *Neo. vesiculiferum*, lack sequence data in *Neohelicosporium*, thus, their phylogenetic affinities with other *Neohelicosporium* species cannot be inferred. We compare the detailed morphology of these four species with our collections (Table 1). Based on its distinct morphology, we regard that our species is not conspecific with any of these four species. In our phylogenetic tree (Fig. 39), the strain GZCC 24-0092 formed an independent clade, indicating that they represent a phylogenetically distinct species. Therefore, we introduce a new species, *Neohelicosporium kevinianus* to accommodate our collection.

***Tubeufia* Penz. & Sacc., Malpighia 11: 517 (1898)**

Tubeufia is the type genus of *Tubeufiaceae*. Members of *Tubeufia* are predominantly saprobic, thriving on decayed wood across tropical and temperate regions. They inhabit both terrestrial and freshwater environments (Boonmee et al. 2014, Luo et al. 2017, Lu et al. 2018b, Ma et al. 2024b). Sexual morph of *Tubeufia* is characterized by superficial, setose or non-setose, ostiolate ascomata seated on a subiculum, 8-spored, bitunicate asci, and filiform, fusiform or cylindrical, hyaline to pale brown, multi-septate ascospores (Chaiwan et al. 2017, Lu et al. 2018b), while its asexual morph presents a dimorphic nature, with either helicosporous or dictyosporous conidia (Lu et al. 2018b, Ma et al. 2024b). Currently, 83 species have been accommodated to *Tubeufia* (Ma et al. 2024b).

***Tubeufia hydei* X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.**

Fig. 40

Fungal Names number: FN 572898; Facesoffungi number: FoF 04387

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – CGMCC3.29053

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, white, gregarious, glistening. *Mycelium* partly immersed, partly superficial, composed of hyaline, branched, septate hyphae. *Conidiophores* 23–60 × 3–5 µm ($\bar{x}$ = 41 × 4 µm, n = 25), macronematous, mononematous, arising from creeping hyphae, straight or flexuous, cylindrical, geniculate, hyaline, branched or unbranched, septate. *Conidiogenous cells* 7–25 × 2–4 µm ($\bar{x}$ = 16 × 3 µm, n = 25), holoblastic, mono- or polyblastic, integrated, intercalary or terminal, repeatedly geniculate, hyaline, smooth. *Conidia* 246–329 × 5–7.5 µm ($\bar{x}$ = 295 × 6 µm, n = 25), loosely coiled 1½–2 times, acropleurogenous, solitary, helicoid, becoming loosely coiled in water, hyaline, septate, guttulate, smooth-walled.

Culture characteristics – Conidia germinating on PDA within 12 h. Colonies reaching up to 19 mm diam. after 10 days of cultivation at 28°C, medium dense, flat, irregularly circular, margin filariform, greyish brown at center, pale grey at margin from above, dark brown at center, pale grey at margin from below.

Material examined – China, Guizhou Province, Qiannan Prefecture, Weng'an County, Zhujiashan National Forest Park, N 26°58'8", E 107°37'5", elevation 958 m, on decaying wood from a freshwater habitat, 27 August 2023, X.J. Xiao, ZJ50 (HKAS 136245, holotype), ex-type culture GZCC 24-0116.

Notes – In the phylogenetic tree (Fig. 41), the strain GZCC 24-0116 was closely related to *Tubeufia longihelicospora* (MFLUCC 16-0753 and MFLUCC 21-0151). Morphologically, our collection closely resembles *Tu. longihelicospora*, exhibiting macronematous, hyaline, branched, geniculate conidiophores and loosely coiled, hyaline conidia, with largely overlapping measurements (Boonmee et al. 2021, Tian et al. 2022). However, comparison of the ITS sequences between GZCC 24-0116 and MFLUCC 16-0753 (ex-type strain of *Tu. longihelicospora*) shows a difference of 3.35% (17/508 bp, including 5 gaps), while the *tefl*-α sequence comparison reveals a 2.2% difference (20/911 bp, no gaps). In the phylogenetic tree, *Tubeufia hydei* (GZCC 24-0116) forms a distinct lineage, indicating a novel species.

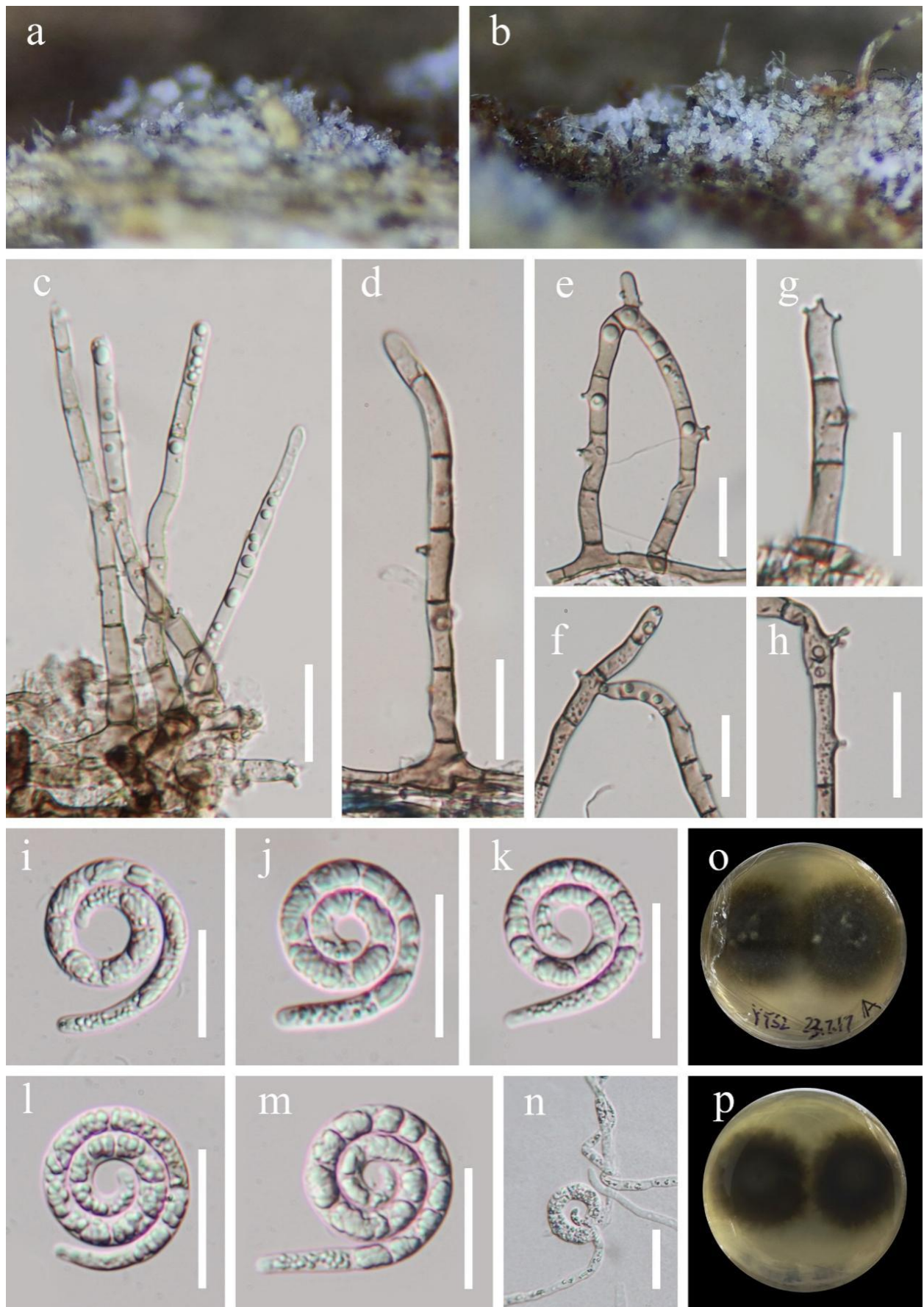


Figure 38 – *Neohelicosporium kevinianus* (HKAS 144602, holotype). a, b Colonies on dead wood surface. c–e Conidiophores. f–h Conidiogenous cells. i–m Conidia. n Germinated conidium. o, p Colony on PDA (o from above, p from below). Scale bars: c–n = 20 μ m.

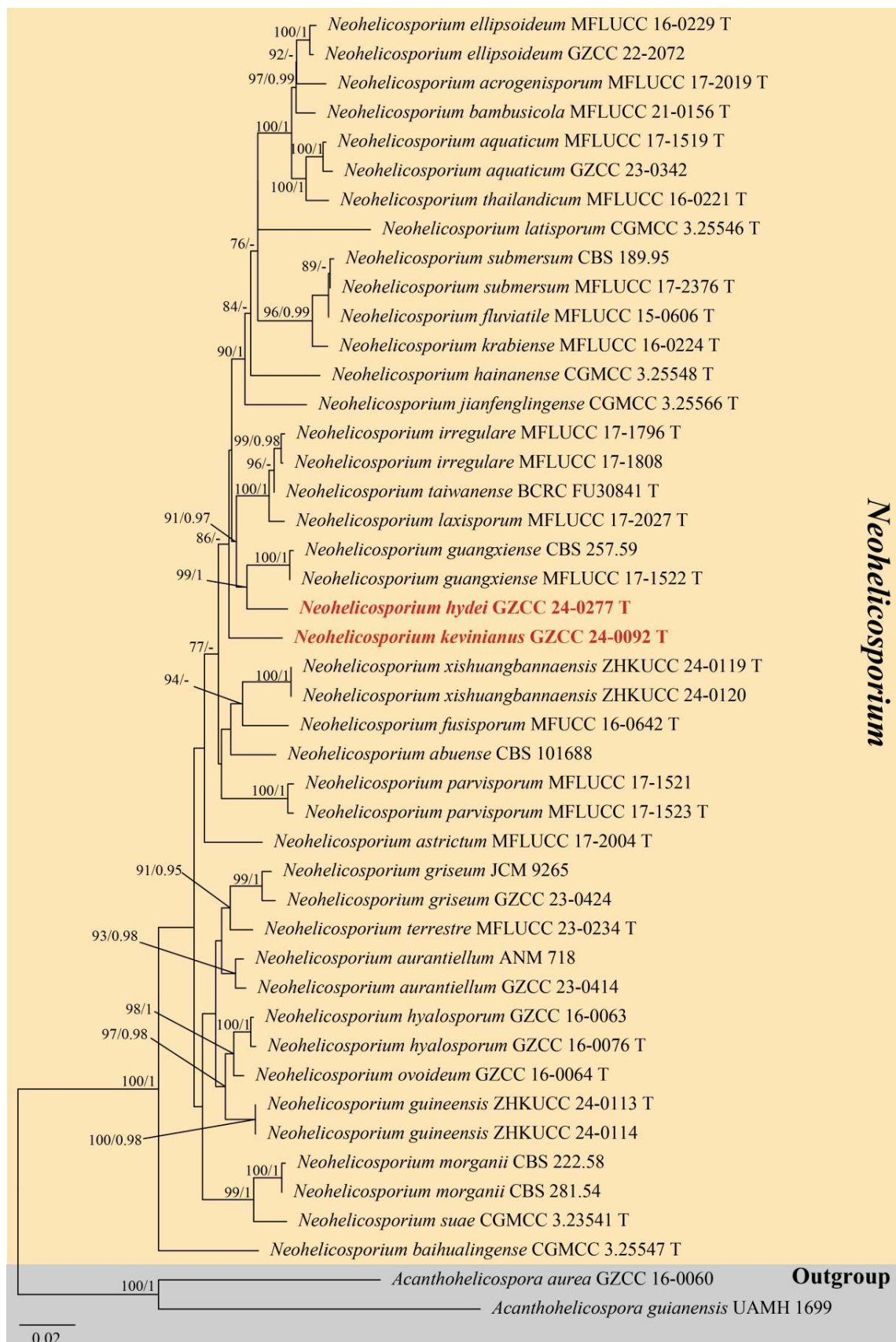


Figure 39 – ML tree based on the combined LSU, ITS, *rpb2* and *tef1-α* sequences, representing *Neohelicosporium*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Acanthohelicospora aurea* (GZCC 16-0060) and *Acanthohelicospora guianensis* (UAMH 1699). Ex-type strains are marked with “T”. The new taxa are indicated in bold and red.

Table 1 Morphology comparison between *Neohelicosporium hydei* and *Neo. kevinianus*, *Neo. myrtacearum*, *Neo. nizamabadense*, *Neo. sympodiophorum*, and *Neo. Vesiculiferum*.

Species	Conidiophores (μm)	Conidiogenous cells (μm)	Conidial dimensions (μm)	Conidial filaments (μm)	Coiled	References
<i>Neo. hydei</i>	114–200 × 6–11	9–15 × 5–9	/	200–250 × 4–5.5	1½–2½	This study
<i>Neo. kevinianus</i>	24–124 × 4–7	10–19 × 3–7	22–27	106–131 × 3.5–5.5	1½–2½	This study
<i>Neo. myrtacearum</i>	80–175 × 3.8–8	1.3–9.8 × 1.2–4.2	13–18.5	1.8–2 wide	2–2½	Singh & Singh (2016)
<i>Neo. nizamabadense</i>	57–198 × 2–5	/	18.2–28	1.4–2.2 wide	2–3½	Rao & Rao (1964)
<i>Neo. sympodiophorum</i>	up to 250 × 4.5–6.5	1.5–3 wide	27–36	2.5–4.5 wide	3½–4	Zhao et al. (2007)
<i>Neo. vesiculiferum</i>	32.5–155 × 3–7.5	/	11–18	1–1.5 wide	2–3½	Da Cruz et al. (2009)

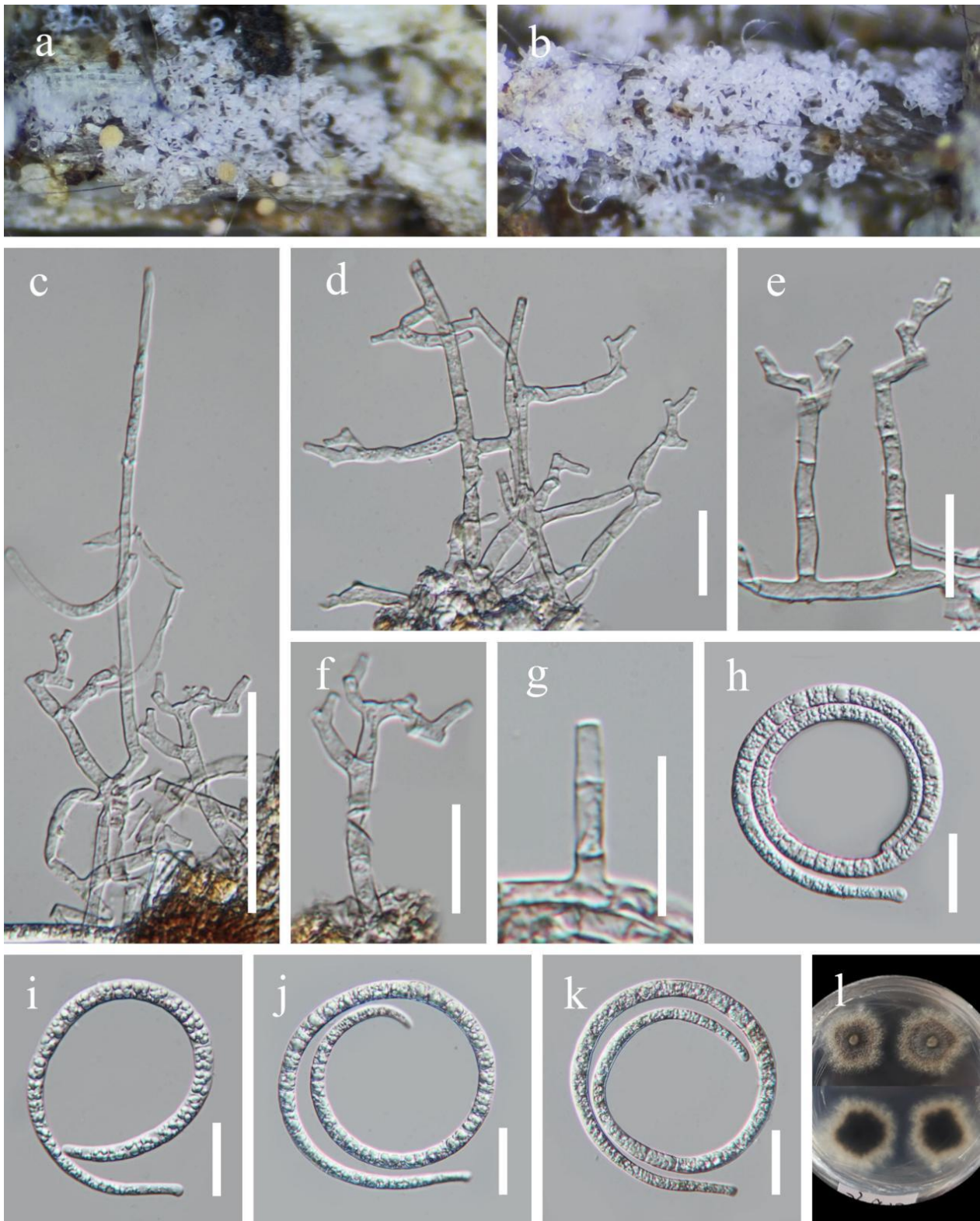


Figure 40 – *Tubeufia hydei* (HKAS 136245, holotype). a, b Colonies on dead wood surface. c–g Conidiophores and conidiogenous cells. h–k Conidia. l Colony on PDA (upper and lower view). Scale bars: c = 50 μ m, d–k = 20 μ m.

Dothideomycetes family *incertae sedis*

Pseudorobillardaceae Crous

Pseudorobillarda M. Morelet, Bull. Soc. Sci. Nat. Archéol. Toulon & Var 23 (175): 5 (1968)

Pseudorobillarda was introduced by Morelet (1968) to accommodate *Pse. phragmitis* and *Pse. muhlenbergiae*. *Pseudorobillarda* is represented by its coelomycetous asexual morph, which has

pycnidial, globose, unilocular conidiomata with central ostiole, hyaline, reduced conidiophores, and subcylindrical to fusiform, 0–4-septate conidia with appendages at one end (Crous et al. 2019a, Song et al. 2022, Wang et al. 2024). Species within the *Pseudorobillarda* exhibit a wide range of lifestyles and have a diverse array of hosts. They can be found in both freshwater and terrestrial habitats globally (Song et al. 2022). *Pseudorobillarda* is presently assigned in *Pseudorobillardaceae* (*Dothideomycetes* family *incertae sedis*), and 21 species are listed in Species Fungorum (2025).

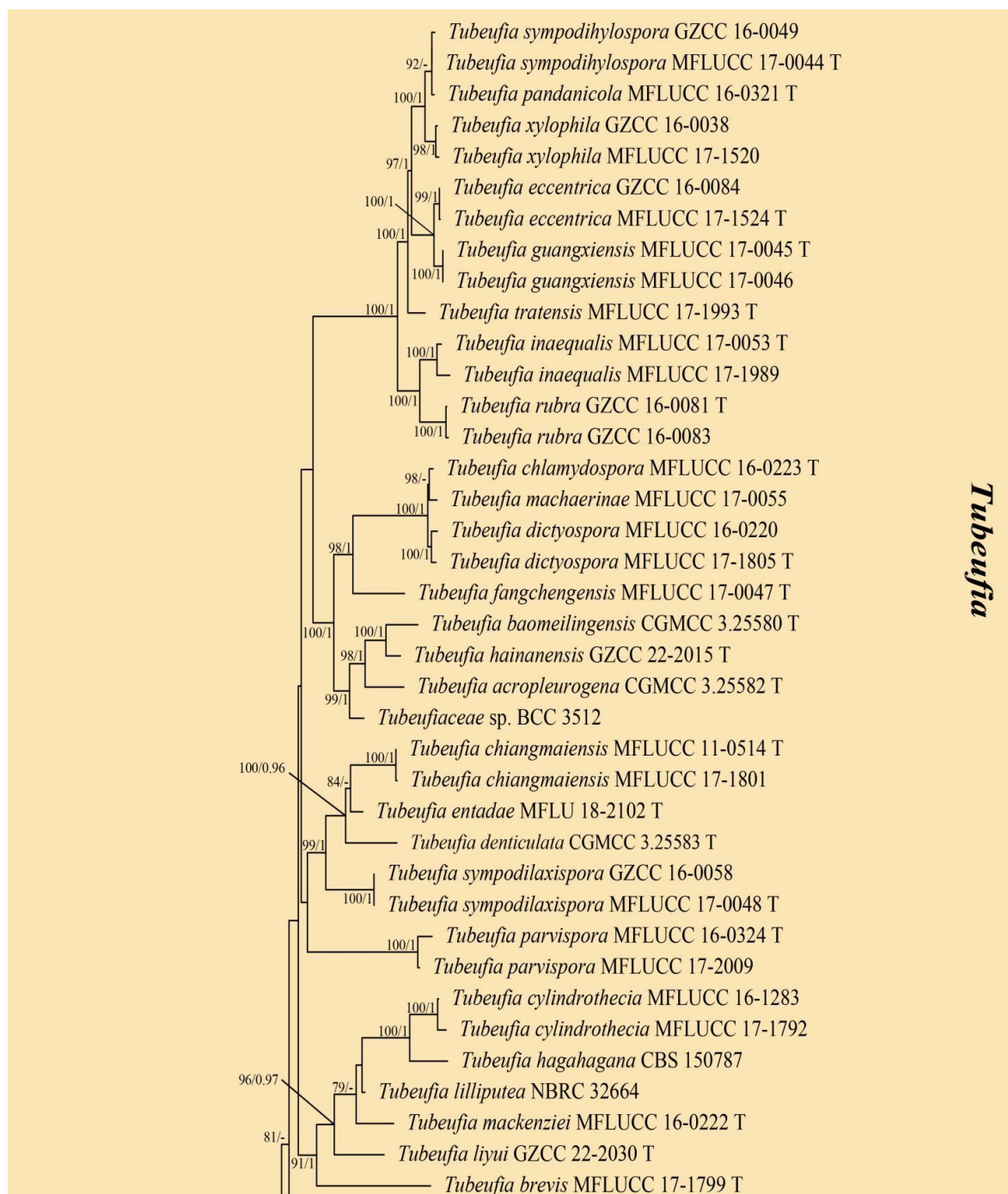


Figure 41 – ML tree based on the combined LSU, ITS, *tef1-α* and *rpb2* sequences, representing *Tubeufia*. Bootstrap support values for ML equal to or greater than 75% and PP values equal to or greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Acanthohelicospora aurea* (GZCC 16-0060) and *Acanthohelicospora guianensis* (UAMH 1699). Ex-type strains are marked with “T”. The new taxon is indicated in bold and red.

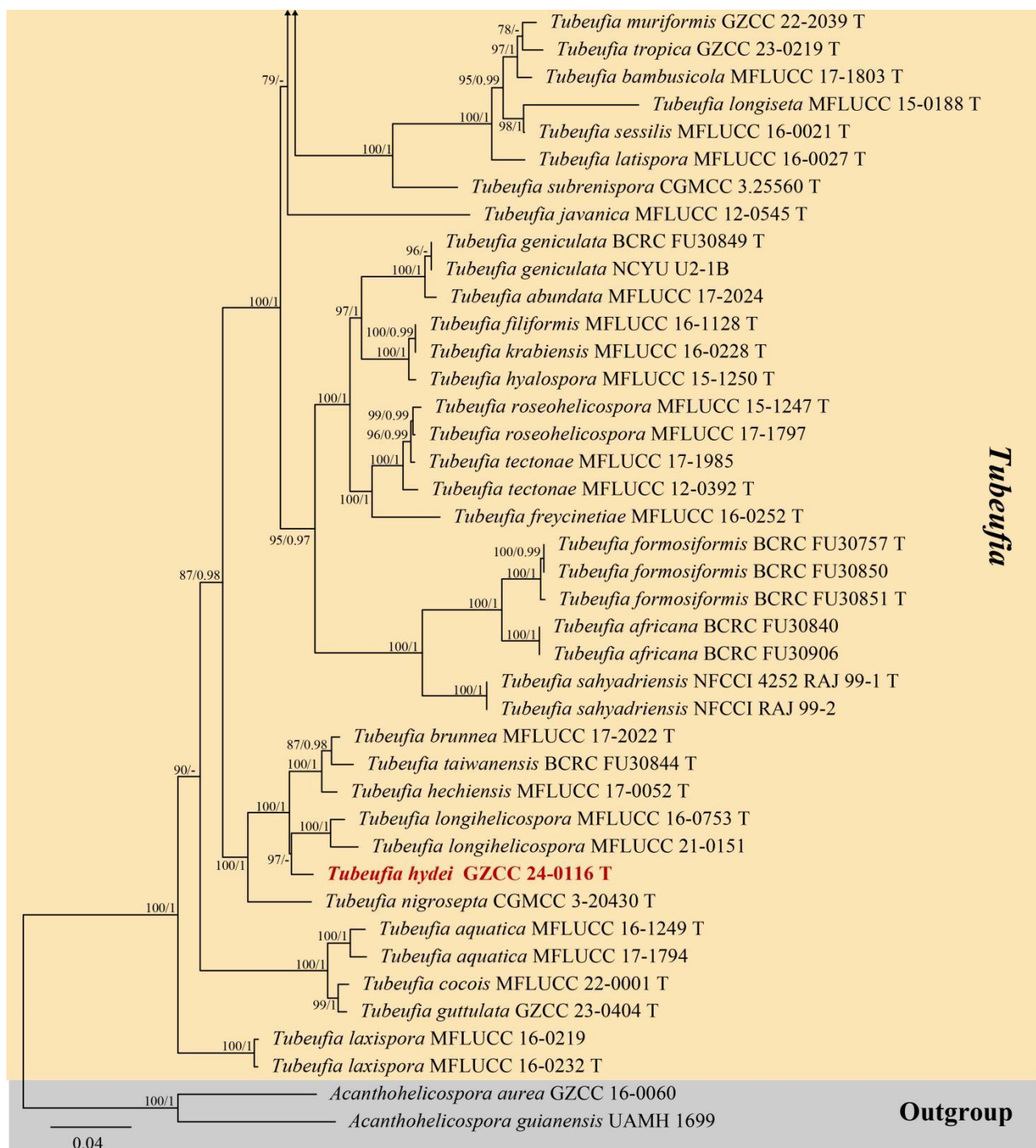


Figure 41 – Continued

Pseudorobillarda hydeana Y. Xiao & Jian K. Liu, sp. nov.

Fig. 42

Fungal Names number: FN 573026; Facesoffungi number: FoF 17841

Etymology – The specific epithet “hydeana” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 149997

Saprobic on dead branches of *Camellia sinensis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 453–503 μm $\times$ 368–402 μm ($\bar{x}$ = 487 $\times$ 382 μm , n = 10), with small black dot-like protrusions, scattered or aggregated, and partially buried in the matrix. *Conidiophores* erect, hyaline, branched, 19.8–21.4 μm long, 1–2 μm wide. *Conidiogenous cells* 4.6–5.8 $\times$ 2.4–4.1 μm ($\bar{x}$ = 5.7 $\times$ 2.7 μm , n = 30), hyaline and bottle-shaped spore-producing structures. *Conidia* 11.4–12.9 $\times$ 2.5–3.1 μm ($\bar{x}$ = 12.8 $\times$ 2.8 μm , n = 30), ellipsoid, straight or

slightly bent, smooth-walled, with fine granular content, bearing 2 unbranched, filiform apical appendages.

Culture characteristics – Ascospores germinated on PDA within 24 h and germ tubes produced from one or both ends. Colonies on PDA reached a 12 mm diameter after two weeks at 25 °C. Colonies from above: rough, dry, opaque, felty, flat, circular; white at first, becoming light yellow in the center with age, margin white and irregular.

Material examined – China, Sichuan Province, Leshan City, Muchuan County, 28° 54' 37"N, 103° 52' 12"E, elevation 550 m, on dead branches of *Camellia sinensis*, 24 October 2023, Y. Xiao, XP06 (HKAS 149997, holotype), ex-type culture UESTCC 25.0106; *ibid.*, XP06-1 (HUEST 25.0086, isotype), ex-isotype UESTCC 25.0107.

Notes – *Pseudorobillarda hydeana* (UESTCC 25.0106 and UESTCC 25.0107) is phylogenetically close to *Pse. camelliae-sinensis* (MFLU 21-0007) and represents as a distinct lineage (Fig. 43). The nucleotide base pair comparison between *Pse. hydeana* (ex-type strain, UESTCC 25.0106) and *Pse. camelliae-sinensis* (ex-type strain, MFLU 21-0007) revealed 3.7% (without gaps) of ITS differences. Morphologically, *Pse. hydeana* resembles *Pse. camelliae-sinensis* in producing subcylindrical conidia with distinct apical appendages. However, *Pse. hydeana* and *Pse. camelliae-sinensis* are distinguishable based on conidiomatal size (453–503 $\mu\text{m} \times$ 368–402 μm vs. 106–120 $\mu\text{m} \times$ 120–155 μm). Moreover, conidia of *Pse. camelliae-sinensis* are brown, fusiform with two septa, while the conidia of *Pse. hydeana* are hyaline, cylindrical, and aseptate (Rathanyaka et al. 2021). Therefore, with the justification of phylogenetic and morphological evidence, *Pseudorobillarda hydeana* is introduced as a new species.

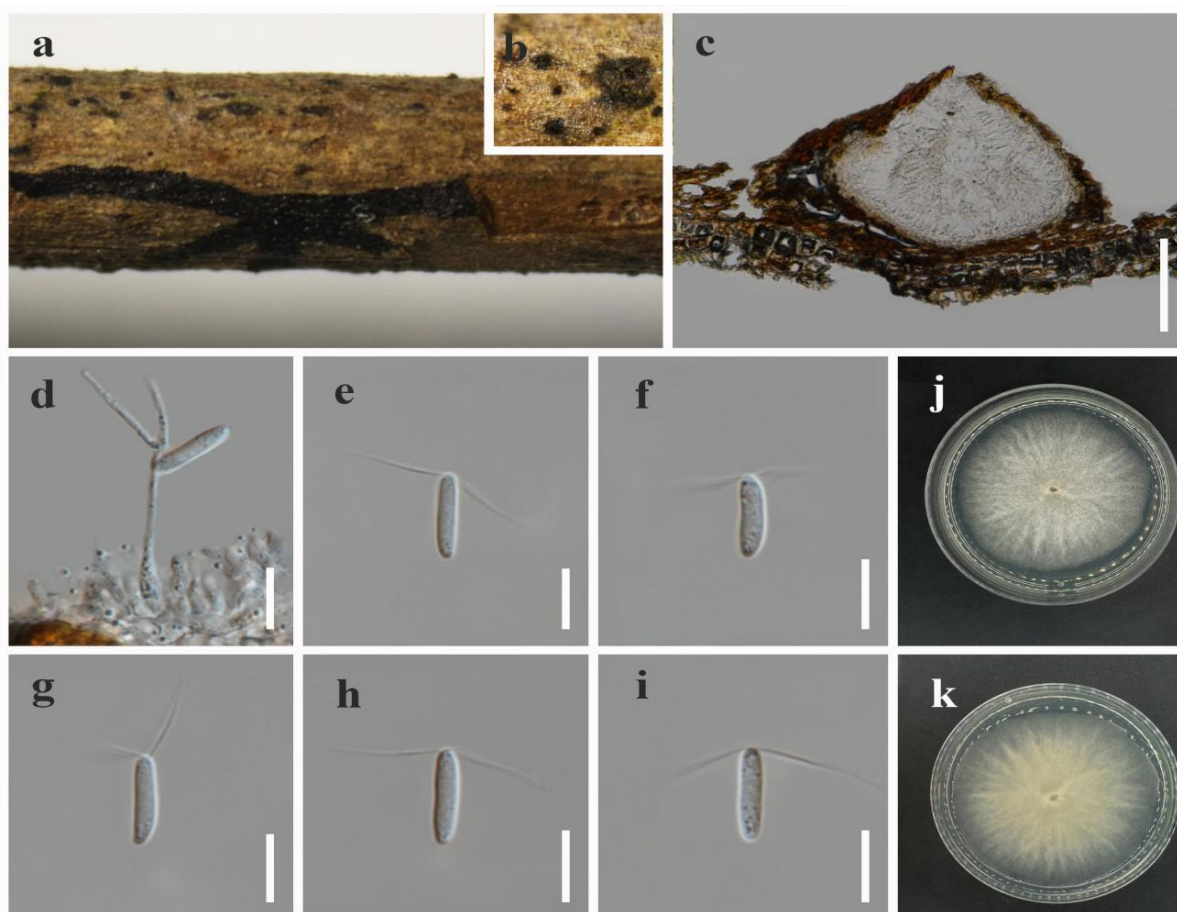


Figure 42 – *Pseudorobillarda hydeana* (HKAS 149997, holotype). a, b Appearance of conidiomata on substrate. c Vertical sections through conidiomata. d Conidiophore and conidiogenous cells. e–i Conidia. j, k Colony on PDA from above and below. Scale bars: c=50 μm ; d, e=50 μm ; f–j=10 μm .

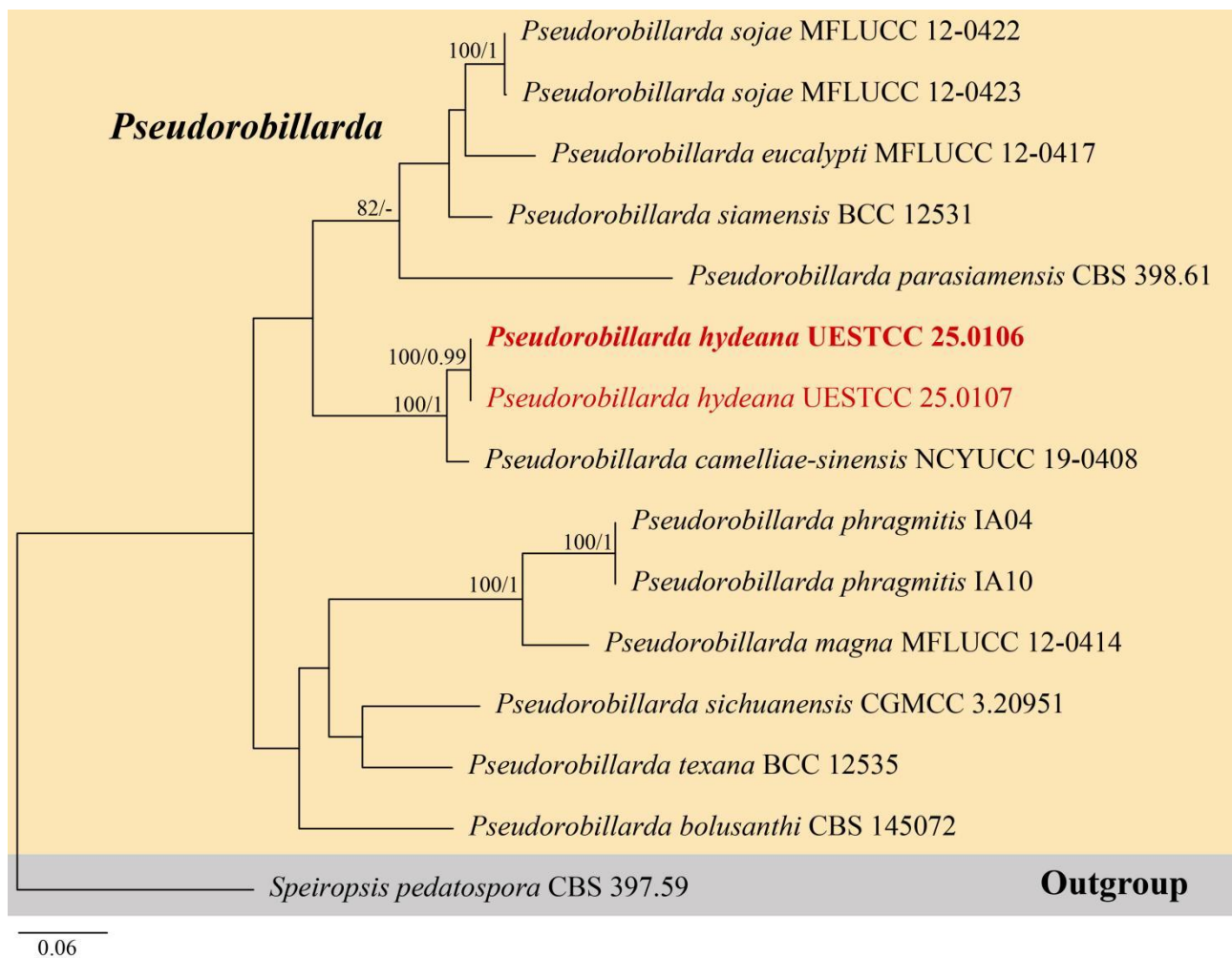


Figure 43 – ML tree based on the combined LSU, ITS and *rpb2* sequences, representing *Pseudorobillarda*. Bootstrap support values for ML equal to or greater than 75% are placed above the branches, and PP values equal to or greater than 0.90 are indicated in bold branches. The tree is rooted with *Speiropsis pedatospora* (CBS 397.59). The new taxon is indicated in red.

Class Eurotiomycetes O.E. Erikss. & Winka

Subclass Chaetothyriomycetidae Doweld

Chaetothyriales M.E. Barr

Cyphellophoraceae Réblová & Unter.

Cyphellophora G.A. De Vries, Mycopathol. Mycol. Appl. 16: 47 (1962)

Cyphellophora was introduced by De Vries (1962) based on the type species *Cyp. laciniata*. The asexual morph of *Cyphellophora* features micronematous or macronematous, simple or branched conidiophores, phialidic, hyaline to pale brown conidiogenous cells with collarettes, and solitary or catenate, cylindrical, ellipsoidal, fusoid, oblong-ovoid, or acicular, hyaline to brown, aseptate or septate conidia (De Vries 1962, Crous et al. 2016, Torres-Garcia et al. 2023). *Cyphellophora* species have a global distribution and occupy diverse ecological niches, including human and plant pathogens, and species associating with plant materials or non-biological substrates (Gao et al. 2015, Torres-Garcia et al. 2023, Crous et al. 2024). Currently, 40 species are listed in Species Fungorum (2025).

Cyphellophora hydeae Y.X. Yu & Jian K. Liu, sp. nov.

Fig. 44

Fungal Names number: FN 573020; Facesoffungi number: FoF 17814

Etymology – The specific epithet "hydeae" is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 149985

Saprobic on dead branches of *Magnolia officinalis* in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown, scattered. *Mycelium* immersed, composed of hyaline, branched, septate, smooth hyphae. *Conidiomata* 318–964 × 38–124 µm, synnematal, erect, rigid, cylindrical, pileate at the tip, dark brown at base, paler towards the apex, composed of compactly arranged conidiophores. *Conidiophores* 16–50 × 1.6–2.6 µm, macronematous, synnematos, filiform, subcylindrical, pale to brown, hyaline to subhyaline towards apex, branched, septate, thick-walled. *Conidiogenous cells* 12–16 × 1–2.5 µm, phialidic, terminal, subcylindrical, smooth, with flared collarete, 0.5–1.5 µm diam. *Conidia* 6.5–9 × 1.5–3 µm ($\bar{x}$ = 7.5 × 2.5 µm, n = 30), acrogenous, solitary, ellipsoid, apex obtuse, tapering toward a sub-truncate base, hyaline to pale brown, 1-septate, smooth.

Culture characteristics – Conidia germinating on PDA within 24 h, and germ tubes producing from basal cells. Colonies on PDA reaching 25 mm in diam. after one month at 25°C, flattened, floccose, medium dense, circular, edge entire, white at center, green at edge from above, greyish-green from below.

Material examined – China, Sichuan Province, Dujiangyan City, Longxi-Hongkou National Nature Reserve, 103°69'05"E, 31°13'66"N, elevation 1050 m, on dead branches of a medicinal plant *Magnolia officinalis* (Magnoliaceae), 20 March 2023, S36A (HKAS 149985, holotype); ex-type culture CGMCC 3.29111 = UESTCC 25.0249; *ibid.*, S36B (HUEST 25.0063, isotype), ex-isotype UESTCC 25.0250.

Notes – The multi-gene phylogeny indicated that *Cyphellophora hydeae* (UESTCC 25.0249 and UESTCC 25.0250) are nested within *Cyphellophora* and clustered with *C. clematidis* (CPC 33880) in a sister clade (Fig. 45). Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cyp. clematidis* (GenBank NR_163356.1; Identities = 306/328(93%), 10/328(3%)). Closest hits using the LSU sequence are *Cyp. clematidis* (GenBank NG_068614.1; Identities = 823/835 (99%), 1/835(0%)). Morphologically, *Cyp. houpoea* is comparable to *Cyp. clematidis* (Crous et al. 2019a). However, *Cyp. hydeae* can be distinguished from *Cyp. clematidis* by their hyaline to pale brown, 1-septate conidia. Besides, *Cyphellophora hydeae* is phylogenetically distinct from other species presently known based on their DNA sequences and is therefore introduced here as new to science.

Subclass Sclerococomycetidae Réblová, Unter. & W. Gams

Sclerococcales Réblová, Unter. & W. Gams

Dactylosporaceae Bellem. & Hafellner

Biseriospora X.J. Xiao, N.G. Liu & Y.Z. Lu, gen. nov.

Fungal Names number: FN 572849; Facesoffungi number: FoF 17807

Etymology – The genus name refers to its conidia consisting of two vertical columns.

Saprobic on submerged rotting wood from a freshwater stream. **Sexual morph:** Undetermined. **Asexual morph:** *Colonies* on natural substrate effuse, dark brown to black, punctiform. *Mycelium* immersed, composed of hyaline to pale brown, branched, septate, smooth hyphae. *Conidiophores* macronematous to semi-macronematous, mononematous, solitary, moniliform, pale brown, unbranched, septate, thin- to thick walled. *Conidiogenous cells* monoblastic, integrated, terminal, doliiform, pale brown. *Conidia* solitary, acrogenous, cheiroid, consisting of two vertical columns, straight or broadly curved, septate, brown, smooth or verruculose.

Type species – *Biseriospora hydei* X.J. Xiao, N.G. Liu & Y.Z. Lu

Notes – Six genera are recognized in *Dactylosporaceae*, viz., *Cylindroconidiis* (Yu et al. 2018), *Fusichalara* (Hughes & Nag Raj 1973, Kuo et al. 2024), *Gamsomyces* (= *Pseudobactrodesmium*) (Dong et al. 2020a, Yang et al. 2023, Liu et al. 2024a), *Rhopalophora* (Réblová et al. 2017), *Pseudosclerococcum* (Olariaga et al. 2019), *Sclerococcum* (Diederich 2015, Ma et al. 2024b). All of these genera generate hyphomycetous asexual morphs, yet none of them

have cheiroid conidia. *Biseriospora* is phylogenetically distinct within *Dactylosporaceae* (Fig. 47) and represents a new genus.

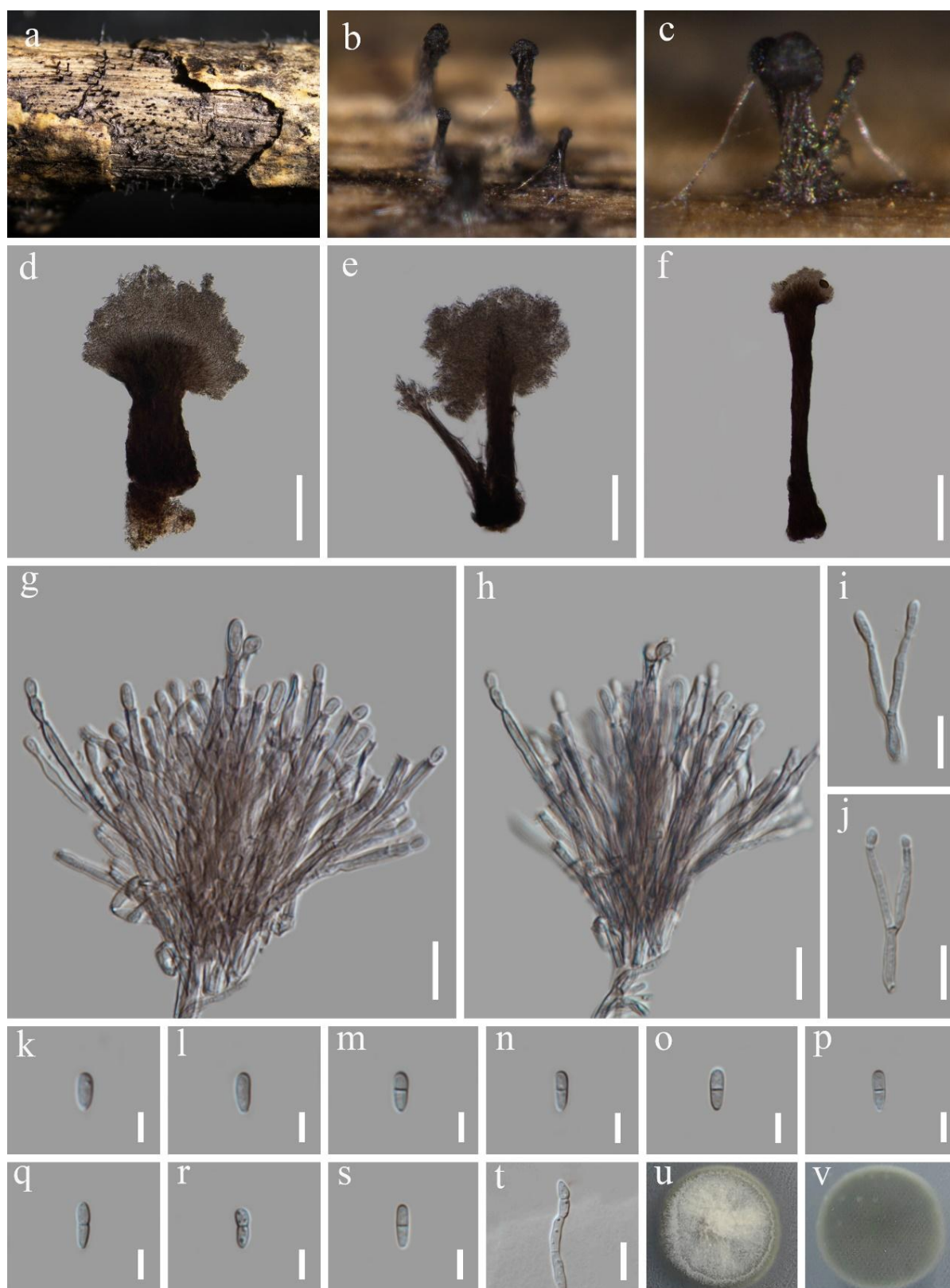


Figure 44 – *Cyphellophora hydeae* (HKAS 149985, holotype). a–c Colonies on natural substrate. d–f Fruiting bodies. g–j Conidiogenous cells and conidia. k–s Conidia. t Germinated conidium. u, v Colony on PDA (u from above and v from below). Scale bars: d–f = 100 μ m, g–j, t = 10 μ m, k–s = 5 μ m.

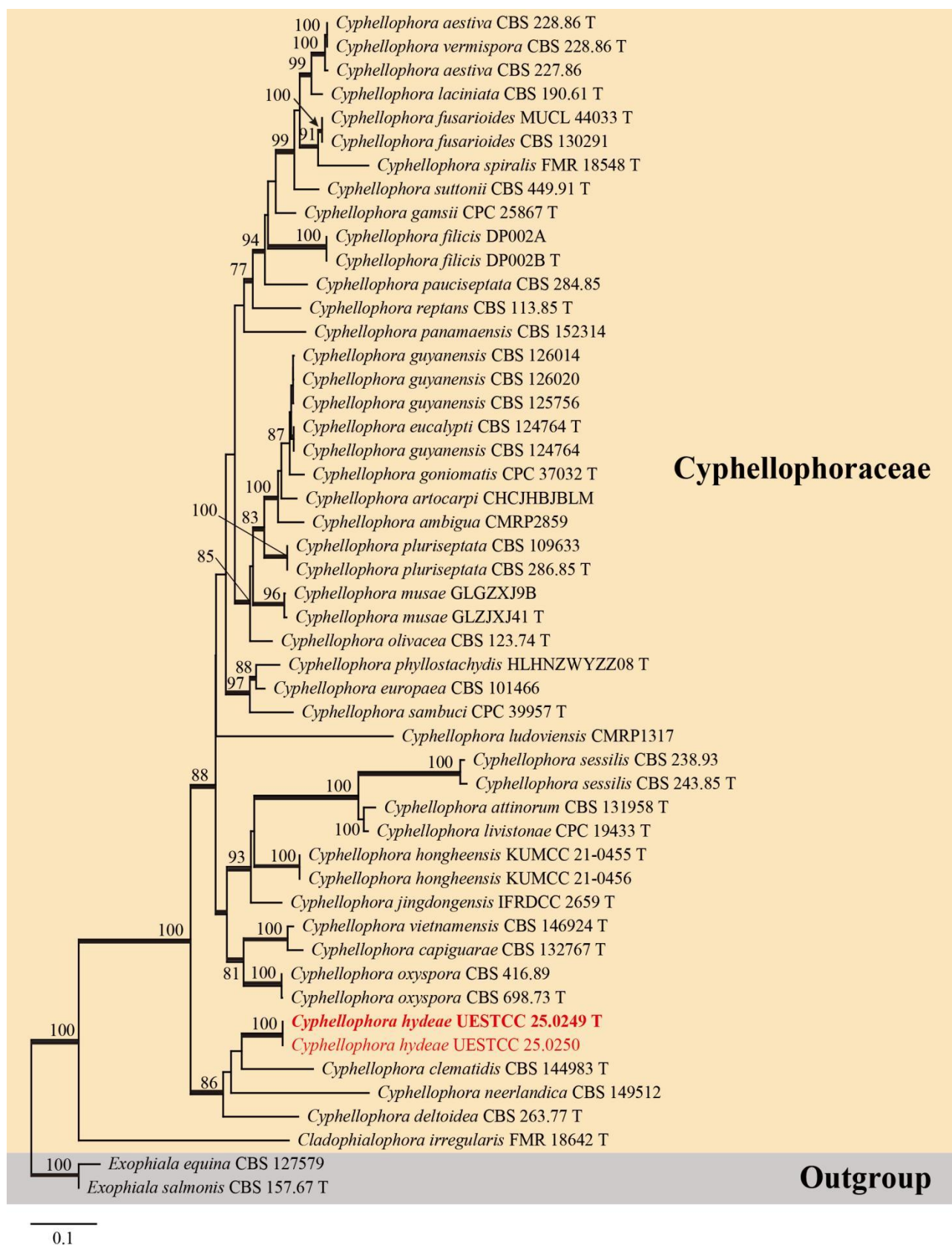


Figure 45 – ML tree based on the combined LSU, ITS, SSU, *rpb2* and *tub2* sequences, representing the family *Cyphellophoraceae*. Bootstrap support values for ML equal or greater than 75% are placed above the branches, and PP values equal or greater than 0.95 are indicated in bold branches. The tree is rooted with *Exophiala equina* (CBS 127579) and *Exophiala salmonis* (CBS 157.67). Ex-type strains are marked with “T”, and the new taxon is indicated in bold and red.

Biseriospora hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 46

Fungal Names number: FN 572850; Facesoffungi number: FoF 17808

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – GZAAS 25-0537

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, dark brown to black, punctiform. *Mycelium* immersed, composed of hyaline to pale brown, branched, septate, smooth hyphae. *Conidiophores* macronematous to semi-macronematous, mononematous, solitary, moniliform, pale brown, unbranched, septate, thin- to thick walled. *Conidiogenous cells* 3.5–5.5 × 3–4 µm ($\bar{x}$ = 4.5 × 3.5 µm, n = 20), monoblastic, integrated, terminal, doliiform, pale brown. *Conidia* 28–49 × 12–16 µm ($\bar{x}$ = 39 × 14 µm, n = 30), solitary, acrogenous, cheiroid, consisting of two vertical columns, each fusiform with obtuse ends, straight or broadly curved, 5–13-septate, thickened, darkened and constricted at the septa, brown to dark brown when mature, smooth or verruculose.

Culture characteristics – Conidia germinating on PDA media within 24 h and germ tubes producing from apex of the conidia. Colonies reaching up to 11 mm diam. after 30 days of cultivation at 28°C, medium dense, circular, flat, margin entire, white to pale brown from above, dark brown to black from below.

Material examined – China, Guizhou Province, Xishui County, Guizhou Xishui National Nature Reserve, 28°9'17" N, 105°55'50" E, elevation 640 m, on decaying wood from a freshwater stream, 2 October 2023, X.J. Xiao, NJS2 (GZAAS 25-0537, holotype), ex-type culture GZCC 24-0037.

Notes – The cheiroid conidia in our collections closely resemble those of cheirosporous genera within *Dictyosporiaceae* (Goh et al. 1999, Boonmee et al. 2016, Yang et al. 2018a, Shen et al. 2022, Liu et al. 2024a, Sun et al. 2025). Nevertheless, *Dictyosporiaceae* is classified under *Pleosporales* (*Dothideomycetes*), while our taxon belongs to *Dactylosporaceae* (*Sclerococcales*, *Eurotiomycetes*) (Fig. 47). These two lineages are phylogenetically distant.

Fusichalara S. Hughes & Nag Raj, New Zealand J. Bot. 11: 662 (1973)

Fusichalara was introduced by Hughes & Nag Raj (1973) based on the type species *F. dimorphospora*, along with *F. dingleyae* and *F. novae-zelandiae*, which were collected from freshwater or terrestrial habitats in New Zealand. This genus was characterized by its brown to dark brown, unbranched conidiophores that possess long phialides, and its conidia are cylindrical, elongate cuneiform, fusiform or slightly sigmoid, hyaline to brown, septate (Hughes & Nag Raj 1973, Kuo et al. 2024). *Fusichalara* is a polyphyletic genus placed in *Chaetosphaeriaceae* (*Chaetosphaeriales*, *Sordariomycetes*) (Réblová 2004) and *Dactylosporaceae* (*Sclerococcales*, *Eurotiomycetes*) (Réblová et al. 2017, Kuo et al. 2024). However, due to the absence of sequence data from the type species, its taxonomic position remains unresolved. Presently, seven species are accepted in *Fusichalara*.

Fusichalara hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 48

Fungal Names number: FN 572862; Facesoffungi number: FoF 17820

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 145869

Saprobic on submerged rotting wood from a freshwater river. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, black with apical hyaline conidial chains, hairy, gregarious. *Mycelium* partly immersed, partly superficial, composed of branched, hyaline, septate, smooth hyphae. *Conidiophores* 105–191 × 4–9 µm ($\bar{x}$ = 146 × 6 µm, n = 15), macronematous, mononematous, solitary, erect, straight or flexuous, cylindrical, brown to dark brown, septate, thick-walled. *Conidiogenous cells* 25–64 × 3–8 µm ($\bar{x}$ = 43 × 5.5 µm, n = 15), phialidic, integrated, terminal, subcylindrical, composed of slightly inflated venter and a tubular

collar, the point of transition from venter to collar slightly constricted, with pronounced wall-thickening of the inner wall; distal end of tubular collar bearing a conspicuous rim of ragged marginal frills at the opening, producing endogenous conidia successively which accumulate in a chain after emergence from the tubular collar. *Conidia* 16–22 × 1.5–2.5 µm ($\bar{x}$ = 19 × 2 µm, n = 30), catenate, elongated fusiform, hyaline to pale brown, 1–3-septate, smooth.

Culture characteristics – Conidia germinating on PDA media within 24 h and germ tubes produced from both ends. Colonies reaching up to 15 mm diam. after 20 days, medium dense, irregular circular, with raised center and undulate edge, white at center, yellow at outer ring from above, yellow at center, paler towards the edge from below.

Material examined – China, Guizhou Province, Zunyi City, Xishui County, Sancha River Conservation Area, N 28°33'50", E 106°24'9", elevation 1133 m, on decaying wood from a freshwater stream, 3 October 2023, X.J. Xiao, ZJ42 (HKAS 145869, holotype), ex-type culture GZCC 24-0112.

Notes – Four described *Fusichalara* species, i.e., *F. clavatispora*, *F. dimorphospora*, *F. goanensis*, and *F. novae-zelandiae* lack available sequence data. Kuo et al. (2024) presented a synopsis along with conidial illustrations of *Fusichalara* species. Our collection can be distinguished from these four species based on differences in conidial shape and size. In the phylogenetic analysis (Fig. 47), our strain formed a sister clade to *F. minuta* (CBS 709.88) with 86% ML and 0.96 pp support. *Fusichalara minuta* differs from our collection by having clavate, fusiform or fusiform-clavate conidia. Additionally, the conidia of our collection are larger (16–22 × 1.5–2.5 µm, compared to 10.5–15 × 2–2.5 µm in *F. minuta*) (Kuo et al. 2024). The ITS comparison reveals 45 bp (including 10 gaps) differences between our strain GZCC 24-0112 and CBS 709.88. Given these distinct morphological and molecular differences, we propose our collection as a new species.

Class Sordariomycetes O.E. Erikss. & Winka

Subclass Diaporthomycetidae Senan., Maharachch. & K.D. Hyde

Distoseptisporales Z.L. Luo, K.D. Hyde & H.Y. Su

Distoseptisporaceae K.D. Hyde & McKenzie

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

Distoseptispora is a sporidesmium-like genus introduced by Su et al. (2016) with *D. fluminicola* as the type species. *Distoseptispora* is commonly characterized by its hyphomycetous asexual morph, which has macronematous, mononematous, brown conidiophores, blastic conidiogenous cells, and mostly obclavate, disto- or euseptate conidia (Su et al. 2016, Luo et al. 2018, Sun et al. 2020, Li et al. 2021b, Yang et al. 2021, Shen et al. 2024a), while its sexual morph has perithecial, subglobose to ellipsoidal, dark brown, ostiolate ascomata with a short neck, cylindrical, 8-spored asci, and uniseriate, fusiform, hyaline, 0–3-septate ascospores with a mucilaginous sheath (Yang et al. 2021). *Distoseptispora* species can occur on both terrestrial and freshwater habitats, and most species are reported from China and Thailand. The placement of *Distoseptispora martini* is questionable in this genus (Yang et al. 2021, Zhang et al. 2022, Shen et al. 2024a), because its unique acrodictys-like morphology which has ellipsoid, oblate or subglobose and muriform conidia (Xia et al. 2017). Fresh collections are needed to confirm its placement in *Distoseptispora*.

Distoseptispora davidii X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 49

Fungal Names number: FN 572857; Facesoffungi number: FoF 17816

Etymology – The specific epithet “davidii” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 145866

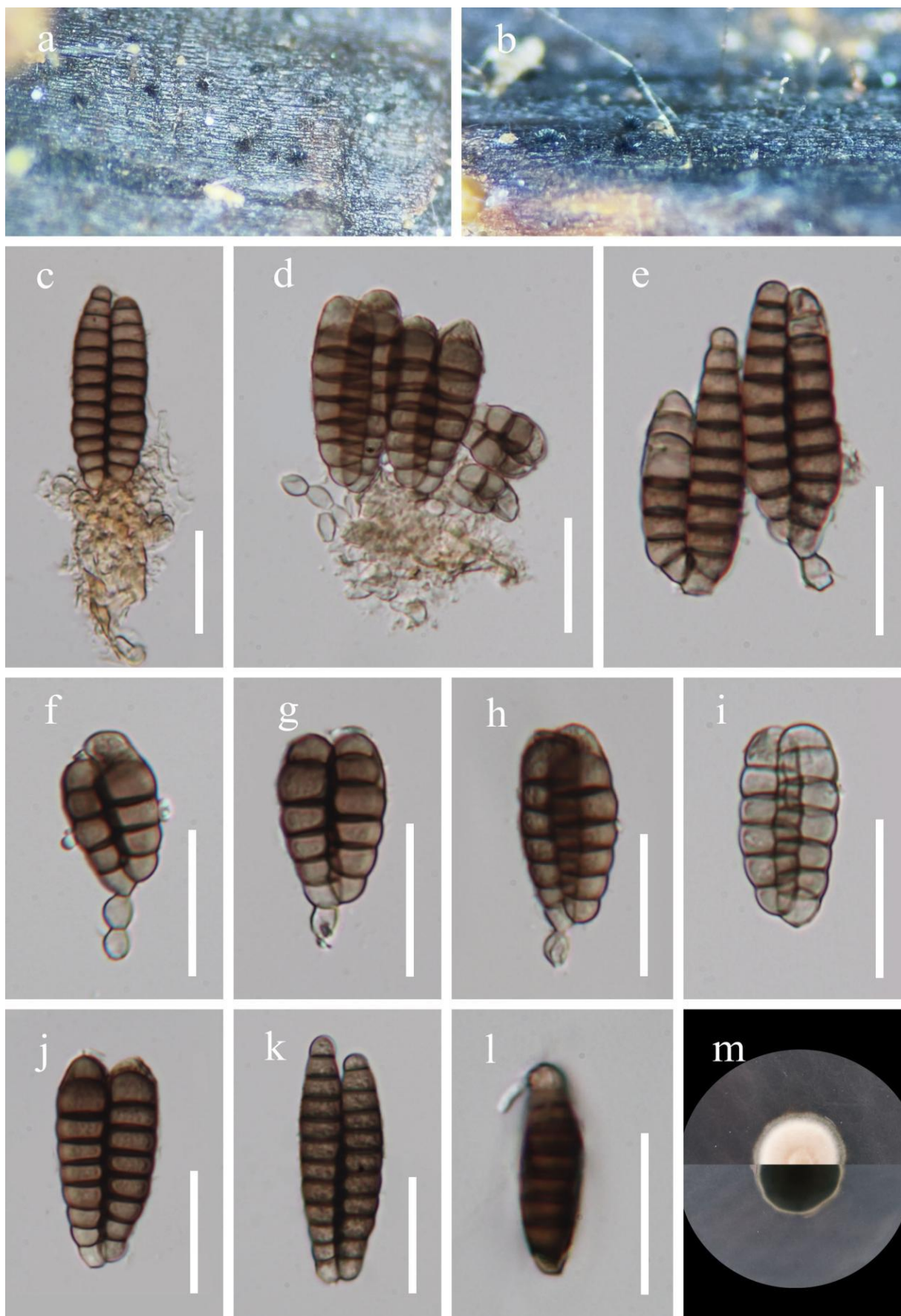


Figure 46 – *Biseriospora hydei* (GZAAS 25-0537, holotype). a, b Colonies on dead wood surface. c, d Synnemata. e–h Conidiogenous cells and conidia. i–k Conidia. l Germinated conidium. m Colony on PDA (upper and lower view). Scale bars: c–l = 20 μ m.

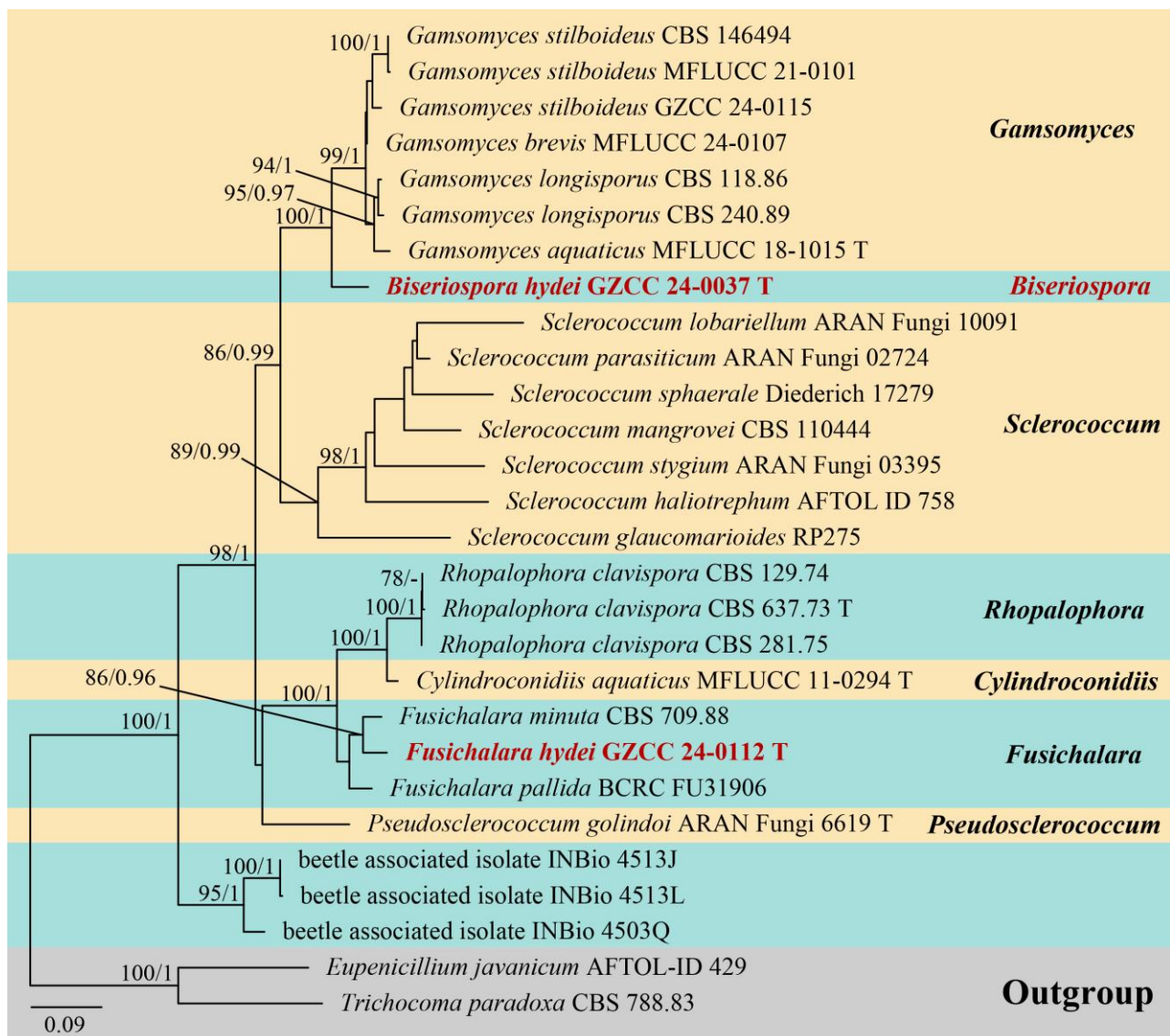


Figure 47 – ML tree based on the combined LSU, ITS and *rpb2* sequences, representing the family *Dactylosporaceae*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Eupenicillium javanicum* (AFTOL-ID 429) and *Trichocoma paradoxa* (CBS 788.83). Type strains are marked with “T”. The new taxa are indicated in bold and red.

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown to black, velvety. *Mycelium* partly immersed, partly superficial, composed of dark brown to black, branched, septate, smooth hyphae. *Conidiophores* 64–104 × 5–8 μm ($\bar{x}$ = 92 × 7 μm, n = 25), macronematous, mononematous, solitary, erect, curved, cylindrical, dark brown at base, slightly paler towards the apex, unbranched, septate, thick-walled. *Conidiogenous cells* 4–12 × 4–6 μm ($\bar{x}$ = 8 × 5 μm, n = 20), monoblastic, integrated, terminal, cylindrical, pale to dark brown, percurrent. *Conidia* 93–177 × 12–17 μm ($\bar{x}$ = 128 × 15 μm, n = 25), acrogenous, solitary, obclavate, rostrate, straight or curved, olivaceous brown, multi-distoseptate, smooth.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes producing from apex. Colonies reaching up to 33 mm diam. after 68 days of cultivation at 28°C, dense, circular, margin filiform, dark brown at the margin, grayish brown in the center from above, dark brown at the center and margin, paler at the middle ring from below.

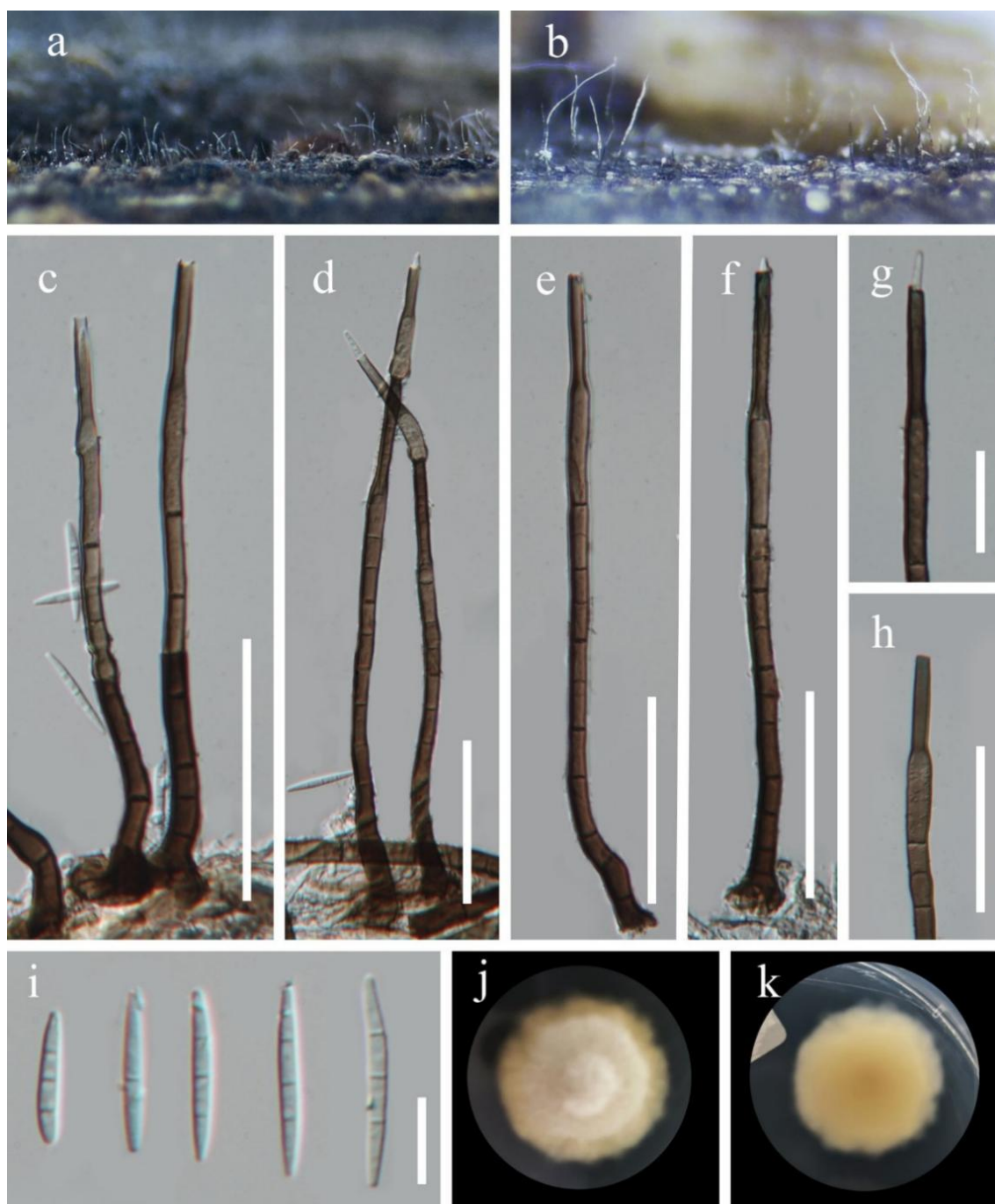


Figure 48 – *Fusichalara hydei* (HKAS 145869, holotype) a, b Colonies on natural substrate. c–h Conidiophores, conidiogenous cells and conidia. i Conidia. Scale bars: c–f, h = 50 μ m, g = 20 μ m, i = 10 μ m.

Material examined – China, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Shibing County, Yuntaishan National Forest Park, N 27°6'56", E 108°6'44", elevation 1045 m, on decaying wood from a freshwater habitat, 24 June 2023, X.J. Xiao, YTS14 (HKAS 145866, holotype), ex-type culture GZCC 24-0091.

Notes – Our collection is phylogenetically related to *Distoseptispora aquisubtropica* (GZCC 22-0075), *D. martini* (CGMCC 3.18651), *D. solitaria* (GZCC 24-0038) and *D. pseudoaquisubtropica* (GZCC 24-0061) (Fig. 56). We analyzed the morphological and base pair differences among these species, with the results presented in Tables 2 and 3. The observed genetic and phenotypic distinctions strongly support the introduction of our collection as a novel species.



Figure 49 – *Distoseptispora davidii* (HKAS 145866, holotype). a Colonies on dead wood surface. b–e Conidiophores, conidiogenous cells and conidia. f–i Conidiogenous cells. j–m Conidia. n Germinated conidium. o, p Colony on PDA (upper and lower view). Scale bars: b, j–n = 50 μ m, d–i = 20 μ m.

Distoseptispora keviniana X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 50

Fungal Names number: FN 572856; Facesoffungi number: FoF 17815

Etymology – The specific epithet “keviniana” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 145874

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, brown to dark brown, velvety. *Mycelium* immersed, composed of lime-green to dark brown, branched, septate, smooth hyphae. *Conidiophores* 55–120 × 4–8 µm ($\bar{x}$ = 83 × 6 µm, n = 20), macronematous, mononematous, solitary, erect, straight or broadly curved, cylindrical, olivaceous brown to dark brown, unbranched, septate, thick-walled. *Conidiogenous cells* 15–24 × 3.5–6 µm ($\bar{x}$ = 20 × 5 µm, n = 20), monoblastic, integrated, terminal, subcylindrical, pale brown to dark brown, smooth. *Conidia* 41–103 × 10–15 µm ($\bar{x}$ = 63 × 13 µm, n = 20), acrogenous, solitary, obclavate, rostrate, straight or slightly curved, olivaceous brown, up to 12-distoseptate, slightly constricted at the septa, smooth.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes producing from apex. Colonies reaching up to 18 mm diam. after 31 days of cultivation at 28°C, dense, circular, margin entire, olivaceous brown at the center, yellowish brown at the margin from above, dark olivaceous brown at the center, yellowish brown at the margin from below.

Material examined – China, Guizhou Province, Anshun City, Pu Ding County, Wujiangdu Reservoir, N 27.310155, E 106.683209, elevation 1203 m, on decaying wood from a freshwater river, 21 June 2024, X.J. Xiao, YLH9 (HKAS 145874, holotype), ex-type culture GZCC 24-0289.

Notes – In the NCBI BLASTn search based on ITS sequences, the closest match of GZCC 24-0289 was *Distoseptispora gasaensis* (HJAUP C2034) (GenBank no: OQ942896) with 96.09% similarity. Morphologically, the two species differ in that the former has olivaceous brown, up to 12-distoseptate conidia, shorter conidiophores (55–120 × 4–8 µm vs. 104–204 × 4–7.2 µm) (Hu et al. 2023). In the phylogenetic tree (Fig. 56), our strain GZCC 24-0289 formed a distinct clade in *Distoseptispora*, indicating it is a distinct species.

Distoseptispora polyblasta Y.R. Sun, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 51

Fungal Names number: FN 572907; Facesoffungi number: FoF 16060

Etymology – The specific epithet “polyblasta” refers to its polyblastic conidiogenous cells.

Holotype – GZAAS 25-0540

Saprobic on decaying bamboo culms in a freshwater habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown, velvety. *Mycelium* immersed, composed of pale to brown, branched, septate, smooth, 1–3.5 µm wide hyphae. *Conidiophores* up to 310 µm long, 3–6 µm wide, macronematous, mononematous, erect, solitary or two or three aggregated at the base, straight or slightly flexuous, cylindrical, brown to dark brown, paler towards the apex, unbranched, septate, thick-walled. *Conidiogenous cells* 17–24 × 3.5–5.5 µm ($\bar{x}$ = 20 × 4.5 µm, n = 15), polyblastic, integrated, terminal, cylindrical, brown. *Conidia* 47–85 µm ($\bar{x}$ = 64.5 µm, n = 30) long, 6–10.5 µm ($\bar{x}$ = 8 µm, n = 30) wide at the broadest, 1.5–3.5 µm ($\bar{x}$ = 2.5 µm, n = 30) wide at the base, acrogenous, solitary, obclavate, with truncate base, olivaceous brown to brown, 6–9-euseptate, verrucose.

Culture characteristics – Conidia germinating on water agar within 24 h and germ tubes producing from both apex and base. Colonies on PDA media superficial, circular, umbonate, mycelium dense, with entire edge, brown in the center, paler at the edge from above, and dark olivaceous brown from below.

Material examined – Thailand, Chiang Rai Province, Huai Kang Pla Waterfall Forest Park, on decaying bamboo submerged in a freshwater, 11 November 2020, Y.R. Sun, CR04 (GZAAS 25-0540, holotype), ex-type culture GZCC 25-0526.



Figure 50 – *Distoseptispora keviniana* (HKAS 145874, holotype). a Colonies on dead wood surface. b–c Conidiophores, conidiogenous cells and conidia. d–f Conidiophores. g–i Conidiogenous cells. j–l Conidia. m, n Colony on PDA (m from above, n from below). Scale bars: b = 50 μ m, c–l = 20 μ m.

Notes – *Distoseptispora polyblasta* clusters with *D. yunnanensis* in our phylogenetic tree (Fig. 56). Morphologically, *D. polyblasta* resembles *D. yunnanensis* in having obclavate, olivaceous to brown, euseptate conidia. However, it has shorter conidia (47–85 μm vs. 58–108 μm), longer and thinner conidiophores (up to $310 \times 3\text{--}6 \mu\text{m}$ vs. $131\text{--}175 \times 6\text{--}7 \mu\text{m}$) than those of *D. yunnanensis* (Li et al. 2021b). Moreover, the conidiogenous cells of *D. polyblasta* are polyblastic, while the latter is monoblastic (Li et al. 2021b). The ITS (549 bp) variability between *D. polyblasta* (GZCC 25-0526) and *D. yunnanensis* (MFLUCC 20-0153) shows there are 20 bp differences including 5 gaps. And for *tef1*- α (901 bp), there are 18 bp differences without gaps.

Distoseptispora pseudoaquisubtropica X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 52

Fungal Names number: FN 572858; Facesoffungi number: FoF 17817

Etymology – The specific epithet “pseudoaquisubtropica” refers to its morphological similarity to *Distoseptispora aquisubtropica*.

Holotype – HKAS 136251

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, brown, hairy. *Mycelium* immersed, composed of branched, lime-green to dark green, smooth hyphae. *Conidiophores* $31\text{--}50 \times 7.5\text{--}10 \mu\text{m}$ ($\bar{x} = 38.5 \times 8.5 \mu\text{m}$, $n = 20$), macronematous, mononematous, solitary, erect, short, flexuous or straight, unbranched, cylindrical, brown, 3–5-septate, thick-walled. *Conidiogenous cells* $6\text{--}10 \times 4.5\text{--}8 \mu\text{m}$ ($\bar{x} = 8 \times 7 \mu\text{m}$, $n = 20$), monoblastic, integrated, sub-cylindrical, dark brown to brown. *Conidia* $284\text{--}423 \times 12\text{--}19 \mu\text{m}$ ($\bar{x} = 354 \times 15.5 \mu\text{m}$, $n = 20$), acrogenous, straight or curved, long-obclavate, rarely branched, with truncate base, greenish brown, distoseptate, slightly constricted at the septa, smooth.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes produced from apex. Colonies reaching up to 6 mm diam. after 20 days, dense, circular, with a raised center and entire edge, greyish brown to dark brown at the center, brown at the outer ring from above, dark brown at the center with a pale brown ring at the edge from below.

Material examined – China, Guizhou Province, Zunyi City, Xishui County, Sancha River Conservation Area, N $28^{\circ}33'50''$, E $106^{\circ}24'9''$, elevation 1133 m, on decaying wood from a freshwater habitat, 3 October 2023, X.J. Xiao, SCS23B (HKAS 136251, holotype), ex-type culture GZCC 24-0061.

Notes – In the phylogenetic tree (Fig. 56), *Distoseptispora pseudoaquisubtropica* (GZCC 24-0061) clustered with *D. aquisubtropica* (GZCC 22-0075), *D. davidii* (GZCC 24-0091), *D. martinii* (CGMCC 3.18651) and *D. solitaria* (GZCC 24-0038). Morphological and molecular comparisons are shown in Table 2 and Table 3.

Distoseptispora solitaria X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 53

Fungal Names number: FN 572859; Facesoffungi number: FoF 17822

Etymology – The specific epithet “solitaria” refers its solitary conidia.

Holotype – HKAS 145916

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, brown to dark brown, velvety. *Mycelium* partly immersed, partly superficial, composed of brown to dark brown, branched, septate, smooth hyphae. *Conidiophores* $91\text{--}188 \times 5\text{--}9 \mu\text{m}$ ($\bar{x} = 134 \times 7 \mu\text{m}$, $n = 30$), macronematous, mononematous, solitary, erect, flexuous or straight, cylindrical, brown to dark brown at base, slightly paler towards the apex, unbranched, septate, thick-walled. *Conidiogenous cells* $8\text{--}16 \times 3\text{--}6 \mu\text{m}$ ($\bar{x} = 11 \times 4.5 \mu\text{m}$, $n = 25$), monoblastic, terminal, integrated, sub-cylindrical, pale brown to brown, smooth. *Conidia* $32\text{--}54 \times 8\text{--}11 \mu\text{m}$ ($\bar{x} = 43 \times 9 \mu\text{m}$, $n = 25$), acrogenous, obclavate, straight or slightly curved, olivaceous to dark brown, mostly 9-distoseptate when mature, smooth.



Figure 51 – *Distoseptispora polyblasta* (GZAAS 25-0540, holotype) a, b Colonies on natural substrate. c Conidiophores. d–f Conidiogenous cells and conidia. g–j Conidia. k Germinated conidium. Scale bars: a = 500 µm, b = 300 µm, c = 50 µm, d–k = 20 µm.



Figure 52 – *Distoseptispora pseudoaquisubtropica* (HKAS 136251, holotype). a Colonies on natural substrate. b, c Conidiophores. d–g Conidia. h, i Colony on PDA (h from above, i from below). Scale bars: b–c = 20 μ m, d–g = 100 μ m.

Table 2 Morphological comparisons of related *Distoseptispora* species.

Species	Holotype	Conidiophores	Conidiogenous cells	Conidia	References
<i>D. aquisubtropica</i>	HKAS 124023	16–83 × 5–11 µm, brown at the base, pale brown or subhyaline towards the apex	3–11 × 3–7 µm, pale brown or brown	43–278 × 11–19 µm, pale brown or dark brown, olivaceous, 16–31-distoseptate, obclavate or lanceolate	Ma et al. (2022)
<i>D. davidii</i>	HKAS 145866	64–104 × 5–8 µm, dark brown at base, slightly paler towards the apex	4–12 × 4–6 µm, pale to dark brown	93–177 × 12–17 µm, olivaceous brown, multi-distoseptate, obclavate, unbranched	This study
<i>D. martinii</i>	CGMCC3.18651	50–110 × 3.5–4.5 µm, dark brown	subhyaline to pale brown	15–20 × 11–16 µm, pale brown to brown, muriform	Xia et al. (2017)
<i>D. solitaria</i>	HKAS 145916	91–188 × 5–9 µm, brown to dark brown at base, slightly paler towards the apex	8–16 × 3–6 µm, pale brown to brown	32–54 × 8–11 µm, olivaceous to dark brown, mostly 9-distoseptate, obclavate, unbranched	This study
<i>D. pseudoaquisubtropica</i>	HKAS 136251	31–50 × 7.5–10 µm, brown	6–10 × 4.5–8 µm, dark brown to brown	284–423 × 12–19 µm, greenish brown, distoseptate, long-obclavate, rarely branched	This study

Table 3 Sequence comparisons of *D. davidii* with related *Distoseptispora* species.

Species	Strain	ITS	<i>tef1-α</i>	<i>rpb2</i>
<i>D. aquisubtropica</i>	GZCC 22-0075	6.50% (31/477)	4.81% (44/915)	6.61% (74/1120)
<i>D. martinii</i>	CGMCC3.18651	6.65% (30/451)	not available	not available
<i>D. solitaria</i>	GZCC 24-0038	6.46% (35/542)	not available	not available
<i>D. pseudoaquisubtropica</i>	GZCC 24-0061	5.71% (31/543)	4.83% (45/931)	not available

Note: ITS: Part of rDNA 18S (3' end), the first internal transcribed spacer (ITS1), the 5.8S rRNA gene, the second ITS region (ITS2) and part of the 28S rRNA (5' end); *tef1-α*: translation elongation factor 1-alpha gene; *rpb2*: RNA polymerase II second largest subunit

Culture characteristics – Conidia germinating on PDA within 24 h and germ tubes producing from basal end. Colonies reaching up to 13 mm diam. after 37 days of cultivation at 28°C on PDA, circular, margin entire, surface rough, velvety, pale brown at the margin, dark brown in the center from above, pale brown at the margin, dark brown in the center from below.

Material examined – China, Guizhou Province, Xishui County, Guizhou Xishui National Nature Reserve, 28°9'17" N, 105°55'50" E, elevation 640 m, on decaying wood from a freshwater stream, 2 October 2023, X.J. Xiao, NJS31 (HKAS 145916, holotype), ex-type culture GZCC 24-0038.

Notes – In our phylogenetic analysis (Fig. 56), our strain GZCC 24-0038 clustered together with *Distoseptispora aquisubtropica* (GZCC 22-0075) with 99% ML and 1 PP support. Morphologically, our collection has longer conidiophores (91–188 × 5–9 µm vs. 6–83 × 5–11 µm) and smaller conidia (32–54 × 8–11 µm vs. 43–278 × 11–19 µm). Besides, ITS comparison reveals that our collection exhibits 5.19% difference (25/482, 4 gaps) to *D. aquisubtropica* (GZCC 22-0075). Therefore, we introduce our collection as a new species based on both morphology and phylogeny.

Distoseptispora vaginae N.G. Liu & Jian K. Liu, sp. nov.

Fig. 54

Fungal Names number: FN 572860; Facesoffungi number: FoF 17818

Etymology – The specific epithet “vaginae” is derived from Latin vagina, meaning sheath, and refers to the apical sheath of the conidium.

Holotype– GZAAS 25-0541

Saprobic on decaying wood in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown, velvety. *Mycelium* immersed, composed of pale to brown, branched, septate, smooth, 1–3.5 µm wide hyphae. *Conidiophores* 90–130 × 3–7.5 µm, macronematous, mononematous, erect, solitary, straight or slightly flexuous, cylindrical, brown to dark brown, paler towards the apex, unbranched, septate, thick-walled. *Conidiogenous cells* 11–20 × 2.5–5.5 µm ($\bar{x}$ = 15 × 3.5 µm, n = 15), monoblastic, integrated, terminal, cylindrical, brown. *Conidia* 61–86 µm ($\bar{x}$ = 72.5 µm, n = 30) long, 13–19.5 µm ($\bar{x}$ = 16 µm, n = 30) wide at the broadest, 3–4.5 µm ($\bar{x}$ = 3.5 µm, n = 30) wide at the base, acrogenous, solitary, fusiform to fusiform-obclavate, with truncate base, dark green to greenish brown with hyaline apex, 7–16-distoseptate, smooth, with an apical, hyaline, mucilaginous sheath.

Culture characteristics – Conidia germinating on water agar within 24 h and germ tubes producing from both apex and base. Colonies on PDA media superficial, circular, mycelium dense, with entire edge, greyish brown in the center, paler towards outer ring from above, and dark olivaceous brown from below.

Material examined – Guizhou Province, Malinghe canyon, on decaying wood in terrestrial habitat, 18 July 2019, N.G. Liu, MLH8 (GZAAS 25-0541, holotype), ex-type culture GZCC 25-0527.

Notes – *Distoseptispora vaginae* resembles *D. appendiculata* in having hyaline sheath around the conidial tip, and they also have similar conidial measurement (Luo et al. 2019). But these two species are phylogenetically distinct (Fig. 56). *Distoseptispora vaginae* is sister to *D. fusiformis* in our phylogenetic tree. Although, they both have fusiform conidia, those of *D. vaginae* are longer (61–86 µm vs. 35–52 µm) than the latter. Besides, hyaline conidial tips and apical sheath are absent in *D. fusiformis* (Yang et al. 2021). The ITS (549 bp) variability between *D. vaginae* (GZCC 25-0527) and *D. fusiformis* (GZCC 20-0512) shows there are 33 bp differences including 7 gaps. And for *tef1-α* (901 bp), there are 38 bp differences without gaps. Therefore, we introduce our collection as a new species based on both morphology and phylogeny.

Distoseptispora velvetica X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 55

Fungal Names number: FN 572861; Facesoffungi number: FoF 17819

Etymology – The specific epithet “velvetica” refers to its velvety colonies on natural substrate.



Figure 53 – *Distoseptispora solitaria* (HKAS 145916, holotype). a Colonies on dead wood surface. b, c Conidiophores, conidiogenous cells and conidia. d, e Conidiogenous cells. f–j Conidia. Scale bars: b, c = 50 μ m, d–j = 20 μ m.

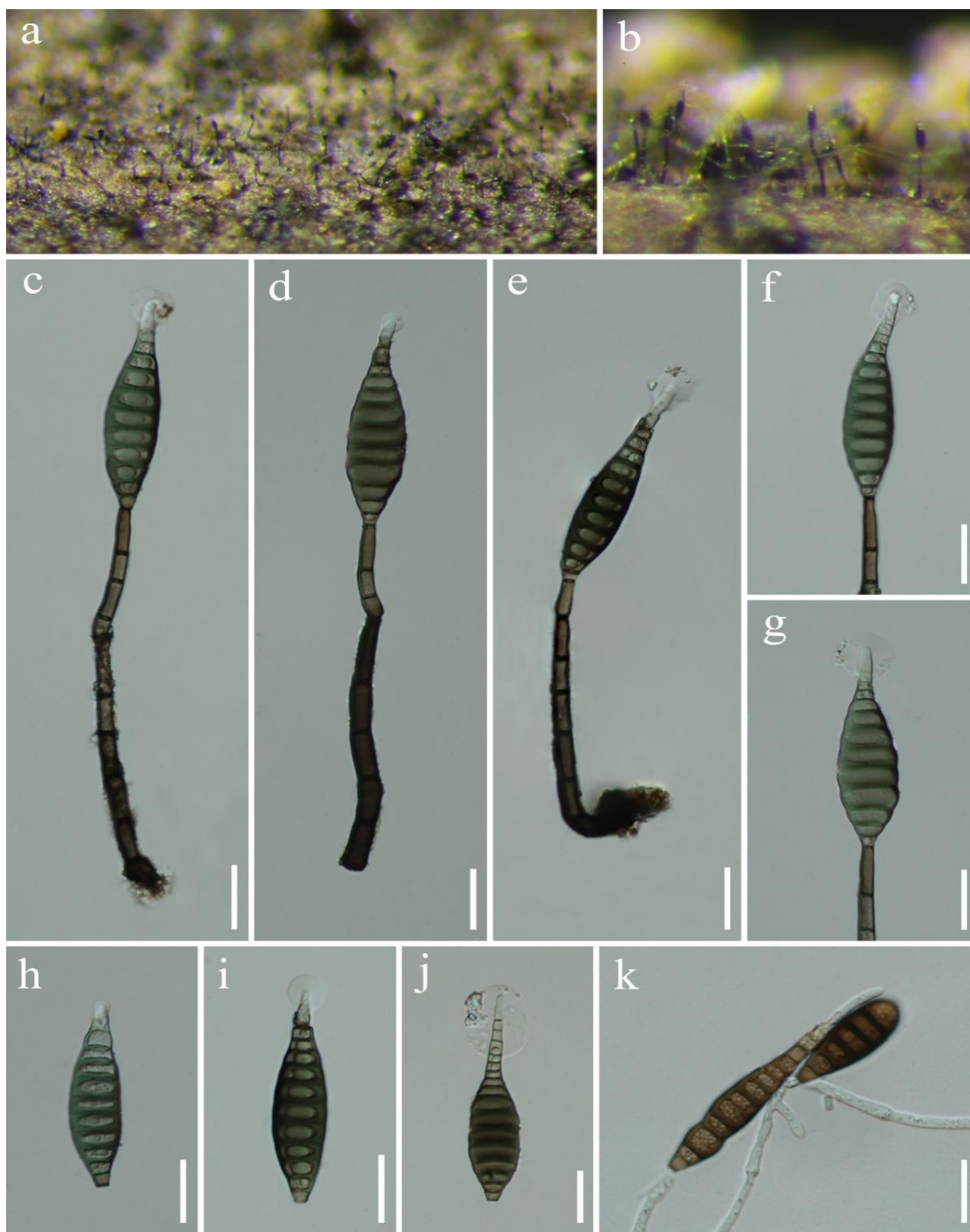


Figure 54 – *Distoseptispora vaginae* (GZAAS 25-0541, holotype) a, b Colonies on natural substrate. c–e Conidiophores and conidia. f, g Conidiogenous cells and conidia. h–j Conidia. k Germinated conidia. Scale bars: c–k 20 μ m.

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, brown to dark brown, velvety. *Mycelium* partly immersed, partly superficial, composed of hyaline to brown, branched, septate, smooth hyphae. *Conidiophores* 75–107 $\times$ 4–8 μ m ($\bar{x}$ = 88 $\times$ 6 μ m, n = 20), macronematous,

mononematous, erect, flexuous or straight, cylindrical, olivaceous or dark brown, unbranched, septate, thick-walled. *Conidiogenous cells* 11–17 × 4–6 µm ($\bar{x}$ = 15 × 5 µm, n = 20), monoblastic, integrated, terminal, sub-cylindrical, olivaceous to brown. *Conidia* 46–86 × 10–25 µm ($\bar{x}$ = 60 × 12 µm, n = 20), acrogenous, solitary, obclavate, rostrate, straight or slightly curved, olivaceous brown, multi-distoseptate, slightly constricted at the septa, smooth.

Culture characteristics – Conidia germinating on PDA within 24 h and germ tubes producing from the apex. Colonies reaching up to 31 mm diam. after 90 days of cultivation at 28°C, dense, circular, center raised, margin entire, brown in the center, and successively pale yellow, brown and white moving outwards from above, dark brown in the center, pale yellow in the margin from below.

Material examined – China, Guizhou Province, Du Shan County, N 25°58'33", E 107°41'15", elevation 697 m, on decaying wood from a freshwater stream, 18 June 2024, X.J. Xiao, DS27 (GZAAS 25-0535, holotype), ex-type culture GZCC 24-0286.

Notes – In the phylogenetic tree (Fig. 56), our strain GZCC 24-0286 formed a sister clade to *Distoseptispora muchuanensis* (CGMCC 3.27444). Morphologically, our collection has longer (75–107 µm vs. 40–75 µm) conidiophores and larger (46–86 × 10–25 µm vs. 40–60 × 10–13 µm) conidia than the holotype of *D. muchuanensis* (Yu et al. 2024). Additionally, ITS comparison reveals that our strain GZCC 24-0286 exhibits 3.55% difference (18/524, 1 gaps) to *D. muchuanensis* (CGMCC 3.27444). Therefore, based on both morphology and phylogeny, we introduce our collection as novel species.

Magnaporthales Thongk., Vijaykr. & K.D. Hyde

Magnaporthaceae P.F. Cannon

Neogaeumannomyces D.Q. Dai & K.D. Hyde, Fungal Diversity 72: 34 (2015)

Neogaeumannomyces was a monotypic genus introduced by Liu et al. (2015) based on the type species *N. bambusicola*, which was collected on dead culm of bamboo in Thailand. It is characterized by its sexual morph which has immersed, globose to subglobose, black, ostiolate ascomata, 8-spored, unitunicate, cylindrical asci with a short furcate pedicel and an apical ring, and curved to sigmoid, filiform to long fusiform, elongate, hyaline, septate ascospores (Liu et al. 2015). In this study, we report coelomycetous asexual morph of *Neogaeumannomyces* for the first time.

Neogaeumannomyces hydei X.D. Yu & Jian K. Liu, sp. nov.

Fig. 57

Fungal Names number: FN; Facesoffungi number: FoF 17827

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 150793

Saprobic on dead branches of bamboo. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 150–250 µm high, 350–600 µm diam., black, solitary, subglobose, immersed, thick-walled. *Conidiomatal wall* 20–40 µm wide, composed of thick-walled, brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 15–25 × 1.5–3.5 µm, holoblastic, hyaline, cylindrical to subcylindrical, determinate, terminal, smooth-walled. *Conidia* 70–80 × 4.5–6 µm ($\bar{x}$ = 78 × 5 µm; n = 50), filiform, curved to sigmoid, filiform to long fusiform, elongate, narrow and curved at the ends, guttulate, hyaline, smooth-walled.

Material examined – China, Sichuan Province, Chengdu City, Xinjin County, Banzhulin, 30°29'48"N, 103°48'47"E, 480m Elevation, on dead branches of bamboo in terrestrial habitat, 9 May 2022, X.D. Yu, C16 (HKAS 150793, holotype); ex-type culture CGMCC 3.29339 = UESTCC 25.0262.

Notes – Multi-gene phylogenetic analysis showed that our isolate belong to *Neogaeumannomyces* and are closely related to *N. bambusicola* (Fig. 59). However, we are not able to compare their morphology as the former species is only represented by a coelomycetous asexual morph (Liu et al. 2015). Nevertheless, *N. hydei* differs from *N. bambusicola* by 19 bp in its ITS (491 bp) region. Moreover, the two species are phylogenetically distinct (Fig. 59). Therefore,

Neogaeumannomyces hydei is introduced as a new species based on morphological characters and phylogenetic evidence.



Figure – 55 *Distoseptispora velvetica* (GZAAS 25-0535, holotype). a Colonies on dead wood surface. b–f Conidiophores and conidiogenous cells. g–i Conidia. j Germinated conidium. k, l Colony on PDA (upper and lower view). Scale bars: b–j = 20 μm.

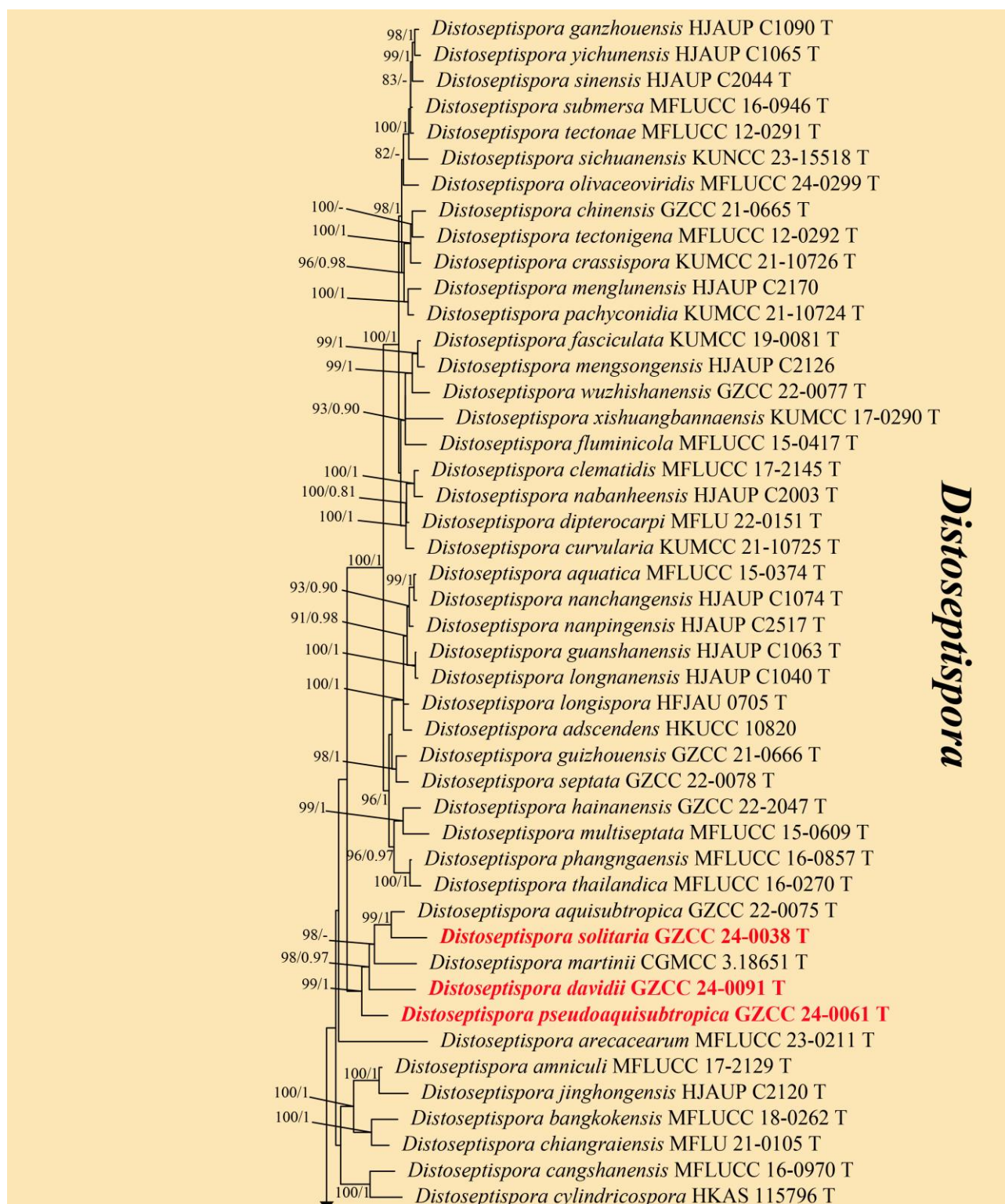


Figure 56 – ML tree based on the combined LSU, ITS, *tef1*- α and *rpb2* sequences, representing the genus *Distoseptispora*. Bootstrap support values for ML equal to or greater than 75% and PP values equal to or greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Aquapteridospora fusiformis* (MFLUCC 18-1606) and *Aquapteridospora lignicola* (MFLUCC 15-0377). ex-type strains are marked with “T”. The new taxa are indicated in bold and red.

Neogaeumannomyces kevinifiliiformis X.D. Yu & Jian K. Liu, sp. nov.

Fig. 58

Fungal Names number: FN 849144; Facesoffungi number: FoF 17828

Etymology – The specific epithet “kevinifiliiformis” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

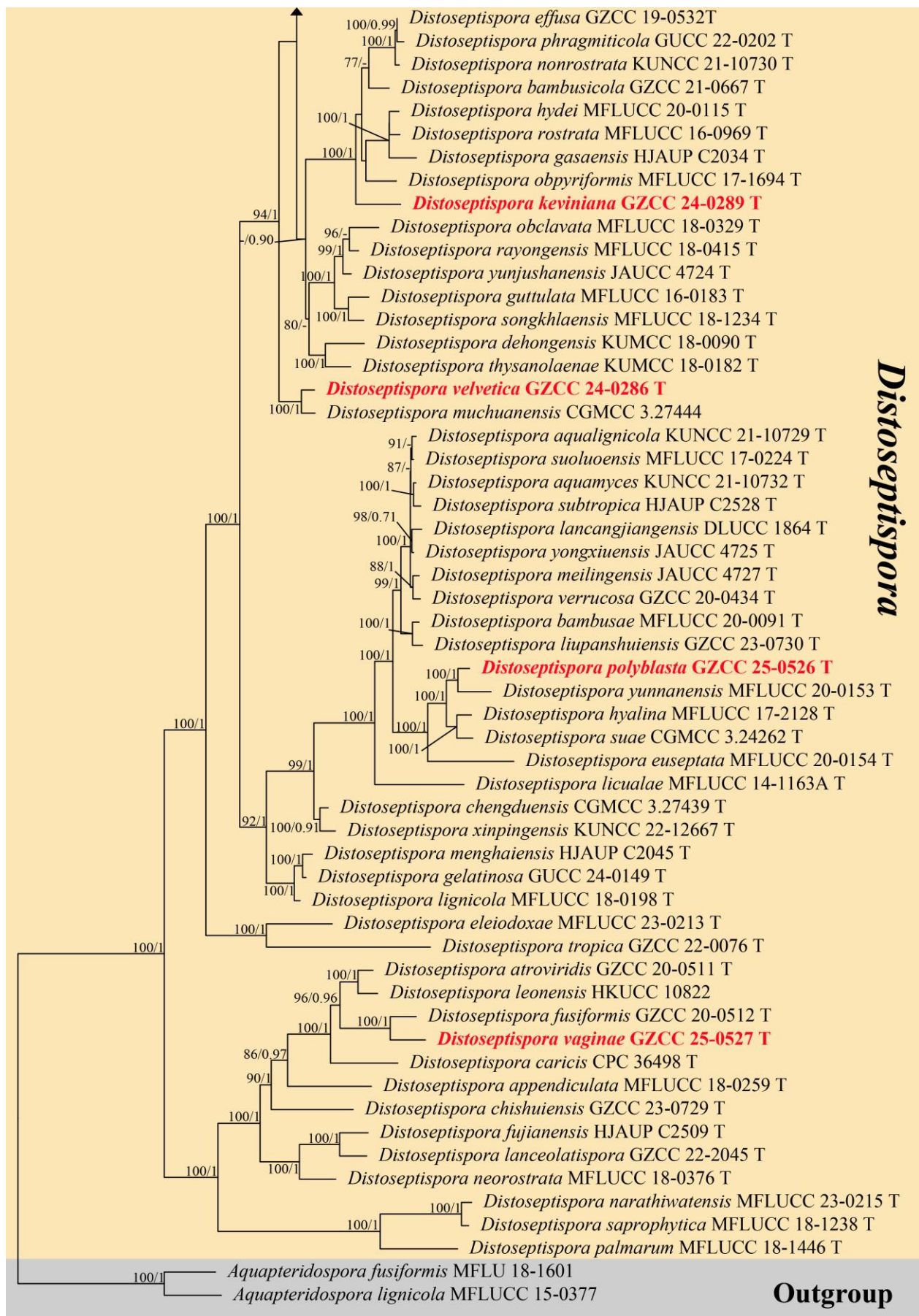


Figure 56 – Continued

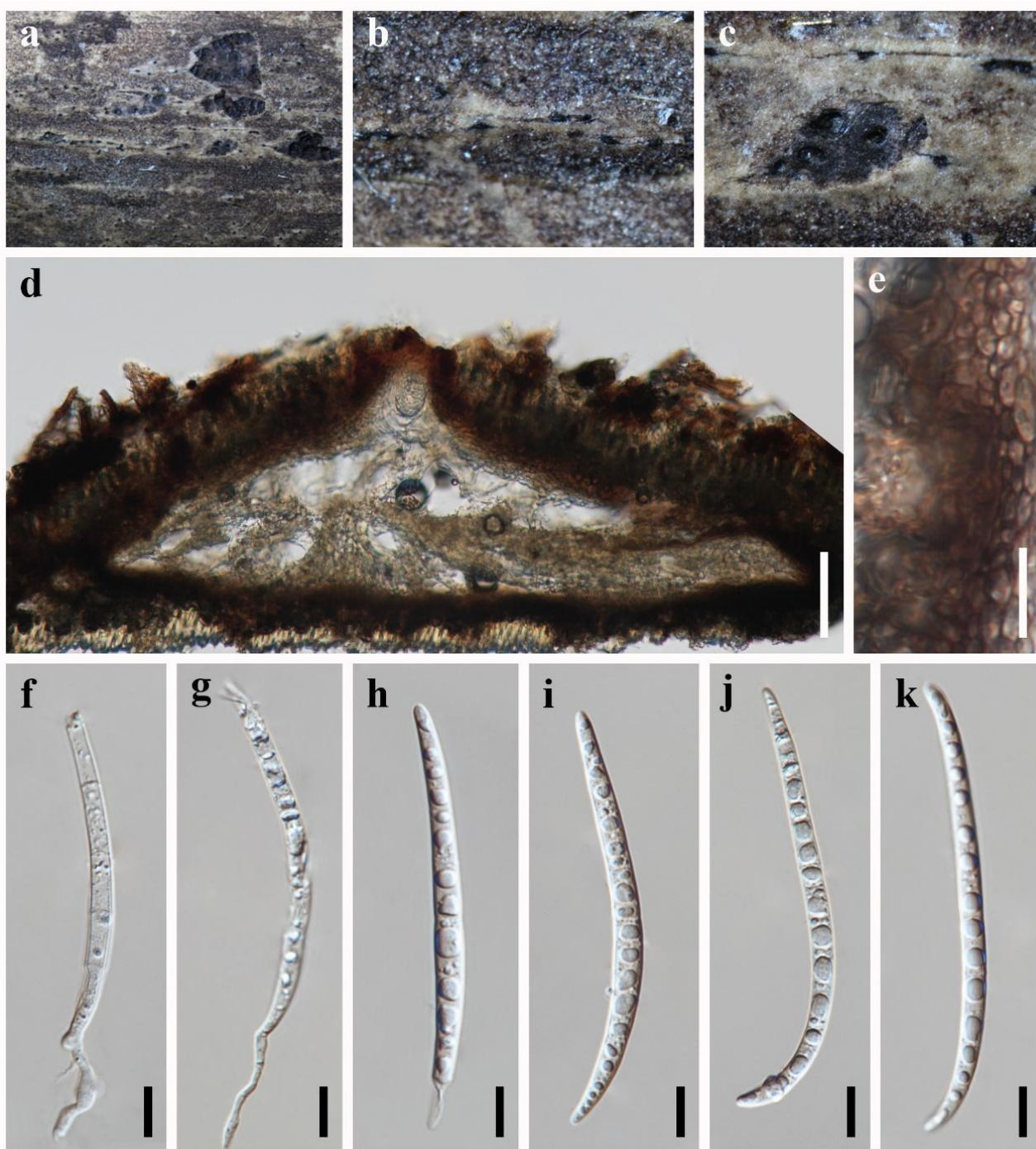


Figure 57 – *Neogaeumannomyces hydei* (HKAS 150793, holotype). a–c Conidiomata on surface of dead bamboo culms. d Vertical sections of conidiomata. e Wall of conidioma. f–g Conidiogenous cells bearing conidia. h–k Conidia. Scale bars: d = 50 μ m, e–k = 10 μ m.

Holotype – HKAS 150794

Saprobic on dead branches of bamboo. Sexual morph: *Ascomata* solitary to gregarious, immersed, visible as black domes on the substrate, in vertical section 250–300 μ m high, 350–650 μ m diam., subglobose, coriaceous, uni-loculate. *Peridium* 20–50 μ m wide, composed of several layers of hyaline to brown, thick-walled cells of *textura angularis*. *Hamathecium* 7–11 μ m wide, hyphae-like, septate paraphyses, unbranched, embedded in a gelatinous matrix. *Asci* 100–130 $\times$ 17–25 μ m ($\bar{x}$ = 115 $\times$ 21 μ m, n = 30), 8-spored, unitunicate, cylindrical, straight or slightly curved, short pedicellate, with an apical ring. *Ascospores* 90–100 $\times$ 5–6 μ m ($\bar{x}$ = 95 $\times$ 5.5 μ m, n = 50),

filiform, curved to sigmoid, filiform to long fusiform, elongate, narrow and curved at the ends, septate, guttulate, hyaline, smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Colonies growing well on PDA and reaching about 50–60 mm diam. after 3 months at 25 °C, circular, with dense mycelium on the surface, velvety, white from above, brown from below.

Material examined – China, Sichuan Province, Meishan City, Danling County, Jiulongshan Forest Park, 29°54'48"N, 103°35'13"E, 460m Elevation, on dead branches of bamboo in terrestrial habitat, 14 July 2022, X.D. Yu, D42 (HKAS 150794, holotype); ex-type culture CGMCC 3.29340 = UESTCC 25.0263.

Notes – *Neogaeumannomyces kevinifiliformis* resembles *N. bambusicola* in having 8-spored, cylindrical, short pedicellate asci, filiform to long fusiform, hyaline, guttulate ascospores (Liu et al. 2015). However, *N. kevinifiliformis* has larger asci ($100\text{--}130 \times 17\text{--}25 \mu\text{m}$ vs. $105\text{--}110 \times 10\text{--}20 \mu\text{m}$) and wider ascospores ($90\text{--}100 \times 5\text{--}6 \mu\text{m}$ vs. $85\text{--}105 \times 4\text{--}5.5 \mu\text{m}$) than *N. bambusicola* (Liu et al. 2015). The phylogenetic analyses (Fig. 59) indicated that *N. kevinifiliformis* is a phylogenetically distinct species. In addition, comparison of nucleotide differences between *N. kevinifiliformis* and *N. bambusicola* showed that there are 5% (25/527) differences in ITS gene regions, which also supports the introduction of *Neogaeumannomyces kevinifiliformis* as a new species.

Rhamphoriales K.D. Hyde & Hongshan

Rhamphoriaceae Réblová

Rhodoveronaea Arzanlou, W. Gams & Crous, Studies in Mycology 58: 89 (2007)

Rhodoveronaea was introduced by Arzanlou et al. (2007) with *R. varioseptata* as the type species. *Rhodoveronaea* has macronematous, brown conidiophores, polyblastic and sympodial conidiogenous cells with denticles bearing ellipsoidal to obovoid, pale brown, 0–multiseptated conidia with a protruding base and a marginal basal frill (Arzanlou et al. 2007). Sexual morph of *Rhodoveronaea* has not been reported. Six species are accommodated to *Rhodoveronaea*, of which two species, i.e., *R. aquatica* and *R. hainanensis*, are found from freshwater habitats.

Rhodoveronaea hyalina X.M. Chen & Karun., Phytotaxa 638 (1): 55 (2024)

Fig. 60

Fungal Names number: FN; Facesoffungi number: FoF 15232

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Colonies on natural substrate effuse, brown, shiny. Mycelium partly immersed, partly superficial, composed of branched, septate, dark brown hyphae. Conidiophores $123\text{--}200 \times 4.5\text{--}7.5 \mu\text{m}$ ($\bar{x} = 168 \times 6 \mu\text{m}$, $n = 20$), macronematous, mononematous, slightly flexuous or straight, unbranched, septate, dark brown at base, paler towards the apex, thick-walled. Conidiogenous cells $32\text{--}75 \times 4\text{--}7 \mu\text{m}$ ($\bar{x} = 55 \times 5 \mu\text{m}$, $n = 20$), polyblastic, integrated, terminal, pale to brown, sympodial. Conidia $11.5\text{--}23 \times 4\text{--}6 \mu\text{m}$ ($\bar{x} = 18.5 \times 5 \mu\text{m}$, $n = 30$), acropleurogenous, cylindrical to fusiform, subhyaline to pale brown, 1–3-septate, verrucose.

Culture characteristics – Conidia germinating on PDA within 48 h and germ tubes produced from both ends of the conidia. Colonies reaching up to 15 mm diam. after 150 days, irregular, center umbonate, edge undulate, greyish dark brown from above, dark brown from below.

Material examined – China, Guizhou Province, Liupanshui City, Shuicheng County, Yushe National Forest Park, N 26°27'17", E 104°48'26", elevation 2232 m, on decaying wood from a freshwater stream, 27 February 2023, X.J. Xiao, YSS31 (HKAS 136239), living culture GZCC 24-0082.

Notes – *Rhodoveronaea hyalina* was introduced by Chen et al. (2024) from decaying wood in a terrestrial habitat in Yushe National Forest Park, Guizhou province, China. Our collection was collected from the same location but in a freshwater habitat. Morphologically, our collection has longer conidiophores ($123\text{--}200 \mu\text{m}$ vs. $95\text{--}165 \mu\text{m}$) than those of the terrestrial sample. Their conidial sizes largely overlap ($11.5\text{--}23 \times 4\text{--}6 \mu\text{m}$ vs. $14\text{--}18 \times 4.5\text{--}8 \mu\text{m}$) (Chen et al. 2024). Besides, ITS, *tefl-α* and *rpb2* comparisons show there are only 8 bp (without gaps, totally 511 bp), 9 bp (with 1 gap, totally 899 bp) and 21 bp (without gap, totally 993 bp) differences between our

strain GZCC 24-0082 and the ex-type (GZCC 23-0622) of *R. hyalina*, respectively. We identify our collection as *Rhodoveronaea hyalina*. This is the first report of this species from freshwater habitat.

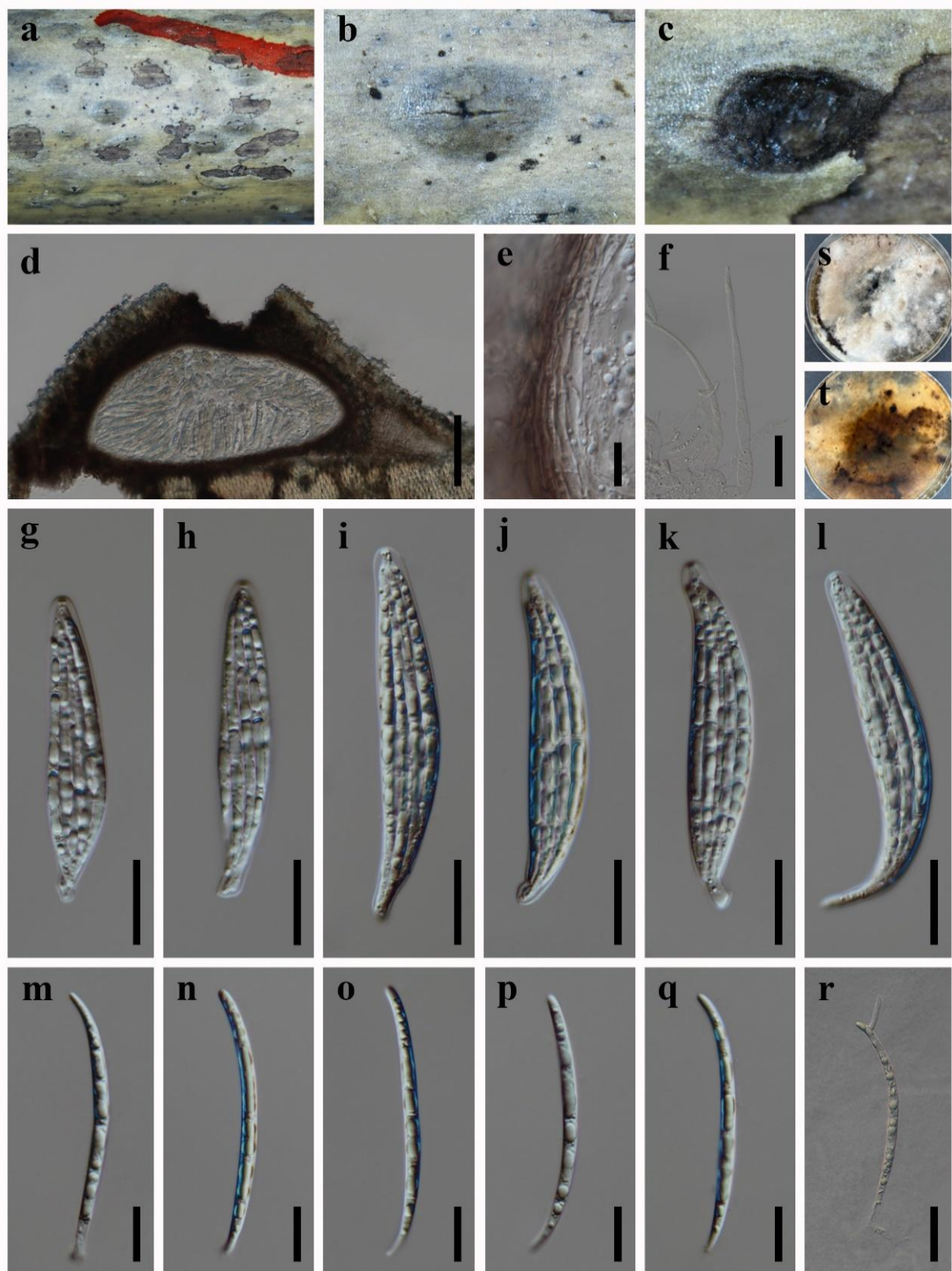


Figure 58 – *Neogaeumannomyces kevinifiliformis* (HKAS 150794, holotype). a–c Ascomata on host substrate. d Vertical sections of ascomata. e Structure of peridium. f Paraphyses. g–l Asci. m–q Ascospores. r Germinated ascospore. s, t Colony on PDA from above and below. Scale bars: d = 100 μ m, f–l, r = 30 μ m, m–q = 20 μ m, e = 10 μ m.

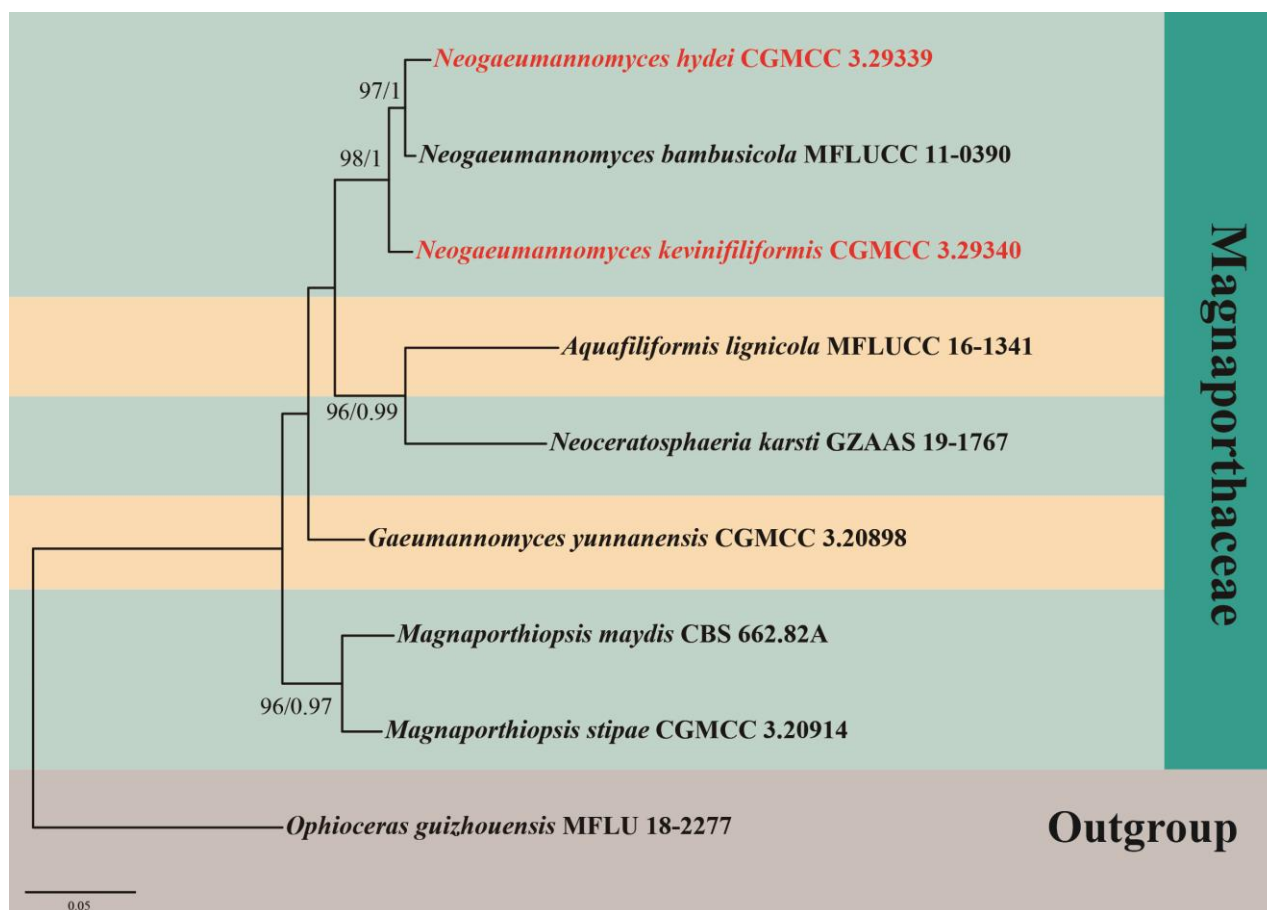


Figure 59 – ML tree based on the combined LSU and ITS sequences, representing the family *Magnaporthaceae*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Ophioceras guizhouensis* (MFLU 18-2277). Ex-type strains are indicated in bold. The new taxa are indicated in bold and red.

Subclass *Hypocreomycetidae* O.E. Erikss. & Winka

Hypocreales Lindau

Hypocreaceae De Not.

Trichoderma Pers. Neues Magazin für die Botanik 1: 92 (1794)

Persoon (1794) introduced the genus *Trichoderma* to accommodate a tree-like conidiophores forming species, *T. viride*, placed it in *Hypocreaceae* (*Hypocreales*, *Sordariomycetes*). Sexual morph of *Trichoderma* was linked with *Hypocrea*, which characterized by having 16 ascospores. Despite *Hypocrea* typifies the family *Hypocreaceae* and order *Hypocreales*, *Trichoderma* has priority over *Hypocrea* according the Art. 11 of The International Code of Nomenclature for algae, fungi and plants (ICN) (Rossman et al. 2013). *Trichoderma* species are widely distributed in a diversity of ecosystems, such as soli, wood and fiber materials, and even mushroom fruiting body (Gu et al. 2020). Consideration of the production of enzymes including cellulase, chitinase, etc. and numerous peptaibols (Degenkolb et al. 2015, Sun et al. 2016), these species have been exhaustive explored and greatly applied on and enzyme industry and plant disease management (Chaverri et al. 2015, Bunbury-Blanchette & Walker 2019, Gu et al. 2020).

Trichoderma guangxiensis Jing Z. Sun & H.W. Liu, sp. nov.

Fig. 62

Fungal Names number: FN 573030; Facesoffungi number: FoF 17844

Etymology –The specific epithet “guangxiensis” refers to the location where the fungus was collected.

Holotype – CGMCC 3.29049

Saprobia, isolated from a field soil of sugarcane. Sexual morph: Undetermined. Asexual morph: *Conidiophores* pyramidal with opposing branches, less frequently solitary, closely-spaced branches, each branch, and the main axis terminating in 2–3 cruciately to nearly verticillately disposed phialides (Fig. 62D). *Phialides* elongate-ampulliform and constricted at the base, hyaline, $(5.0\text{--})6.0\text{--}7.5\text{--}(10) \times (1.5\text{--})1.8\text{--}2.5\text{--}(3.0) \mu\text{m}$ ($\bar{x} = 6.5 \times 2.5 \mu\text{m}$, $\text{SD} = 1.3 \times 0.3$, $n = 50$), length/width ratio $(2.0\text{--})2.5\text{--}5.0\text{--}(6.0) \mu\text{m}$ ($\bar{x} = 3.0$, $n = 50$), base $1.4\text{--}2.0 \mu\text{m}$ ($\bar{x} = 1.6 \mu\text{m}$, $n = 50$) (Fig. 62E–H). *Conidia* subglobose to globose, smooth, hyaline $(1.8\text{--})2.0\text{--}2.5\text{--}(3.2) \times (1.6\text{--})1.8\text{--}2.8\text{--}(3.0) \mu\text{m}$ ($\bar{x} = 2.3 \times 2.0 \mu\text{m}$, $\text{SD} = 0.21 \times 0.17$, $n = 50$), length/width ratio $1.0\text{--}1.3\text{--}(1.7) \mu\text{m}$ ($\bar{x} = 1.1$, $n = 50$) (Fig. 62H). *Chlamydospores* unobserved. No odor; no diffusing pigment observed.

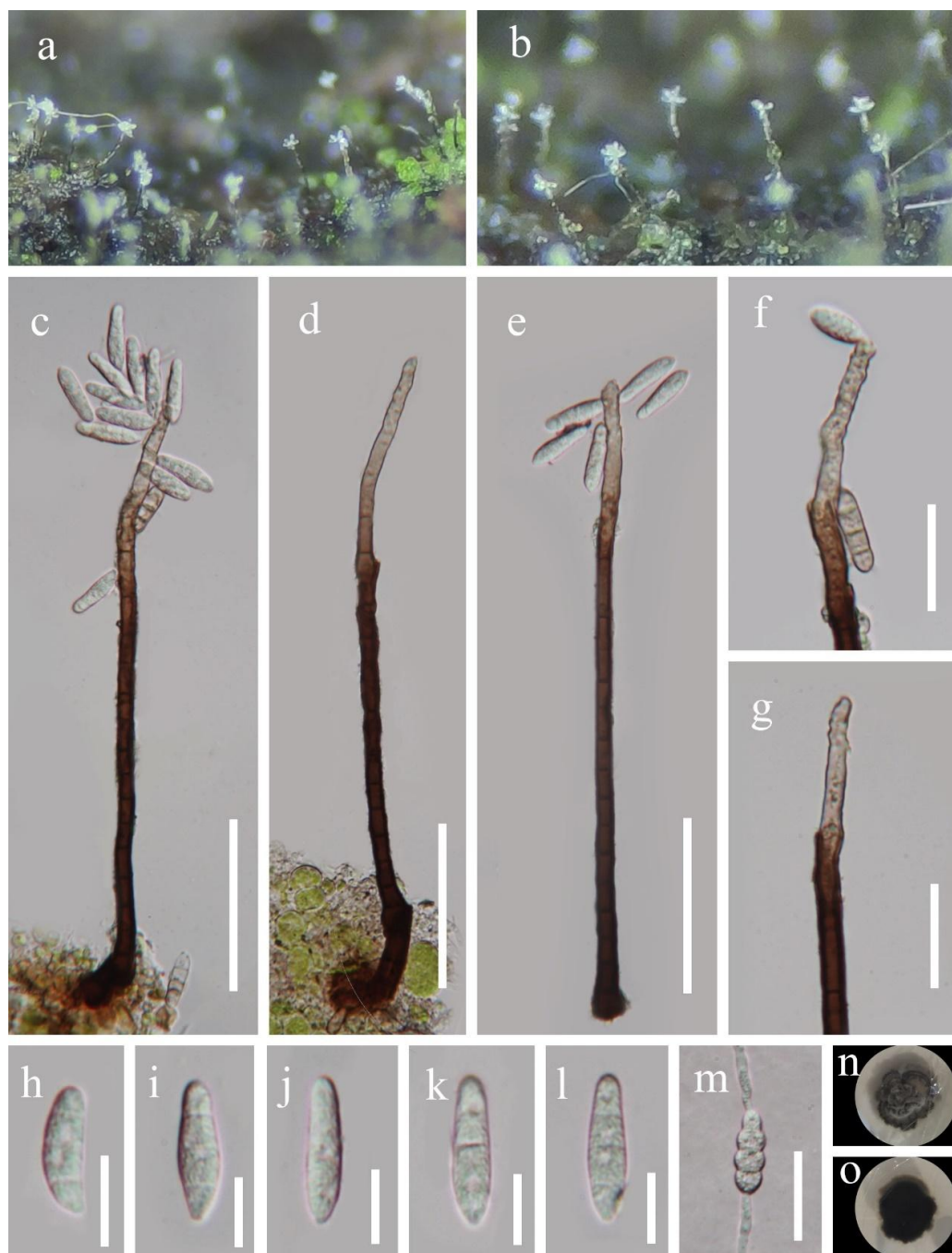


Figure 60 – *Rhodoveronea hyalina* (HKAS 136239). a, b Colonies on natural substrate. c–e Conidiophores and conidia. f, g Conidiogenous cells and conidia. h–l Conidia. m Germinated conidium. n, o Colony on PDA (n from above, o from below). Scale bars: c–e = 50 μm , f–g, m = 20 μm , h–l = 10 μm .

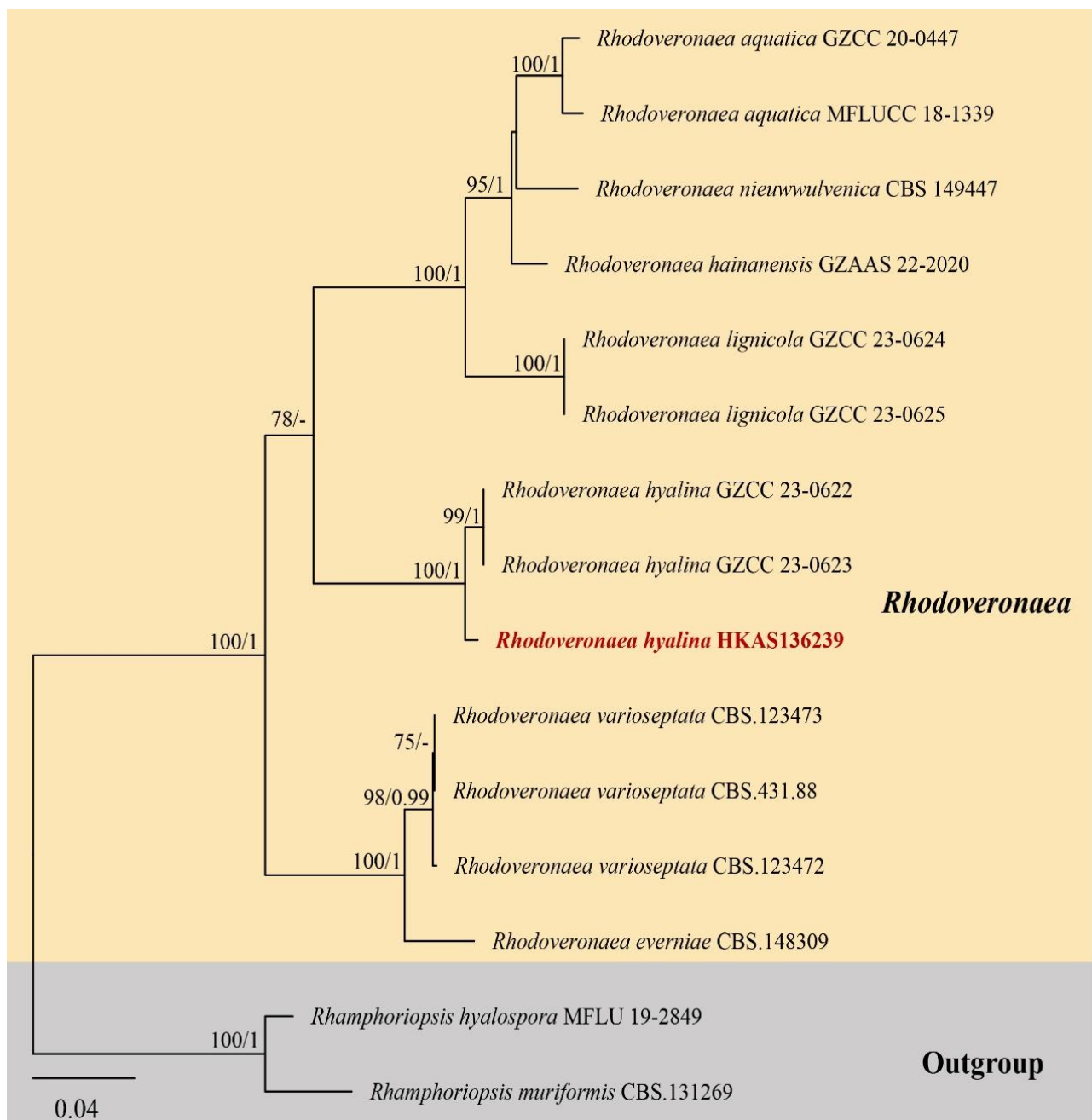


Figure 61 – ML tree based on the combined LSU, ITS and *rpb2* sequences. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Rhamphoriopsis hyalospora* (MFLU 19-2849) and *Rhamphoriopsis muriformis* (CBS 131269). The new taxon is indicated in bold and red.

Culture characteristics – On PDA after 72 h, colony covering the plate at 25°C. Colony white; mycelium dense and radial. Aerial hyphae conspicuous. No diffusing pigment, not distinct odor (Fig. 62A). Conidial production noted after 5 days, starting around the original inoculum, effuse in the aerial hyphae, first white, turning grass-green after 7 d. Chlamydospores unobserved; On CMD after 72 h, covering the plate at 25°C. Colony white to yellowish, mycelia loose. Aerial hyphae short, inconspicuous. No diffusing pigment, not distinct odor (Fig. 62B). Conidial production noted after 3 days, effuse in aerial hyphae, becoming yellow-green after 3 days. Chlamydospores unobserved; On SNA after 72 h, colony covering the plate 25°C. Colony white to yellowish; mycelium loose, especially at the margin. Aerial hyphae short. No diffusing pigment, not distinct odor (Fig. 62C). Conidial production noted after 2 days, starting at the margin, effuse in the aerial

hyphae. Small pustules formed around the inoculum, first white, turning green after 3 d, with hairs protruding beyond the surface.

Material examined – China, Guangxi Zhuang Autonomous Region, He Pu, Bei Hai, 21°47'28"N, 108°59'21"E, ca. 5.6 m elev., from a soil of sugarcane, 12 July 2024, ex-type culture CGMCC3.29049; China, Guangxi Zhuang Autonomous Region, He Pu, Bei Hai, 21°47'28", 108°59'21", ca. 5.6 m elev., from a soil of sugarcane, 12 July 2024, living culture CGMCC3.29050.

Notes – Multi-locus molecular phylogeny based on ITS, *tefl-α*, and *rpb2* genes enables rapid and accurate identification of *Trichoderma* species, resulting in numerous new *Trichoderma* species (Chaverri et al. 2015, Gu et al. 2020). In our phylogenetic tree, our isolates CGMCC3.29051 and CGMCC3.29052 grouped together with *T. afroharzianum* and *T. atrobrunneum*; Our isolates CGMCC3.29054, CGMCC3.29055 and CGMCC3.29053 were sister to *T. yunnanense* and *T. kunmingense*; Our isolates CGMCC3.29049 and CGMCC3.29050 clustered with *T. anisoharzianum*, *T. kunmingense*, *T. yunnanense* and the CGMCC3.29054, CGMCC3.29055, CGMCC3.29053 clade (Fig. 65).

The three new species were characterized by tree-like conidiophores, verticillate or in whorls of 2–4, however, their phialides and conidia differ each other and their phylogenetic close relatives. *Trichoderma mashanense* having ampulliform to lageniform phialides ($7.0\text{--}12.0 \times 2.0\text{--}2.5 \mu\text{m}$), subglobose to globose conidia ($2.0\text{--}3.0 \times 2.0\text{--}2.5 \mu\text{m}$) (Fig. 63). It differs from *T. afroharzianum* by longer and slender phialides ($8.6\text{--}9.5 \times 3.0\text{--}3.1 \mu\text{m}$) and smaller conidia ($3.1\text{--}3.3 \times 2.8\text{--}2.9 \mu\text{m}$); It differs from *T. atrobrunneum* by longer and slender phialides ($6.3\text{--}7.3 \times 3.3\text{--}3.5 \mu\text{m}$) (Chaverri et al. 2015). *Trichoderma zhongshanense* also producing elongate-ampulliform and constricted at the base ($4.0\text{--}6.5 \times 3.0\text{--}3.5 \mu\text{m}$), ovoid to subglobose conidia ($1.8\text{--}2.4 \times 1.5\text{--}2.0 \mu\text{m}$) (Fig. 64). It differs from *T. anisoharzianum* and *T. kunmingense* by shorter and wider phialides and smaller conidia. The phialides and conidia of type strain of *T. anisoharzianum*, *T. kunmingense* *T. yunnanense* are ($7.1\text{--}13.9 \times 2.4\text{--}3.2 \mu\text{m}$) and ($3.2\text{--}4.2 \times 2.3\text{--}3.0 \mu\text{m}$) (Zheng et al. 2021) and ($6.0\text{--}9.0 \times 2.5\text{--}4.5 \mu\text{m}$) and ($3.4\text{--}4.4 \times 2.7\text{--}3.4 \mu\text{m}$) (Qiao et al. 2018); *Trichoderma zhongshanense* differs from *T. yunnanense* by smaller conidia ($3.0\text{--}3.5 \times 2.8\text{--}3.2 \mu\text{m}$) (Yu et al. 2007). *Trichoderma guangxiensis* producing elongate-ampulliform and constricted at the base ($6.0\text{--}7.5 \times 1.8\text{--}2.5 \mu\text{m}$), ovoid to subglobose conidia ($2.0\text{--}2.5 \times 1.8\text{--}2.8 \mu\text{m}$) (Fig. 62). It differs from *T. anisoharzianum*, *T. kunmingense*, *T. yunnanense* by distinctly zonate forming on PDA, CMD and SNA media and mature conidia forming a head at the apex of phialides (Yu et al. 2007, Qiao et al. 2018, Zheng et al. 2021).

Trichoderma guangxiensis, *T. mashanense*, *T. zhongshanense* were encountered from the field soil of sugarcane in Guang Xi Zhuang Autonomous Region. The phylogenetic result presents these species belong to *Harzianum* clade. Species in the *Harzianum* clade are the most well-known *Trichoderma* species, due to its antifungal properties and effective bio-control ability, used to suppress soil-borne plant pathogens (Chaverri et al. 2015, Degenkolb et al. 2015, Bunbury-Blanchette & Walker 2019).

***Trichoderma mashanense* Jing Z. Sun & H.W. Liu, sp. nov.**

Fig. 63

Fungal Names number: FN 573031; Facesoffungi number: FoF 17763

Etymology – The specific epithet “mashanense” refers to the location where the fungus was isolated.

Holotype – CGMCC3.29051

Saprobic, isolated from a field soil of sugarcane. Sexual morph: Undetermined. Asexual morph: *Conidiophores* pyramidal with opposing branches, less frequently solitary, closely-spaced branches, each branch, and the main axis terminating in 2–5 cruciately to nearly verticillately disposed phialides (Fig. 63D). *Phialides* elongate-ampulliform and attenuated at the base, hyaline, ($5.5\text{--}7.0\text{--}12.0\text{--}12.5 \times (1.5\text{--}2.0\text{--}2.5\text{--}3.0) \mu\text{m}$) ($\bar{x} = 10.0 \times 2.0 \mu\text{m}$, SD = 2.1×0.4 , n = 50), length/width ratio ($3.5\text{--}4.0\text{--}5.0\text{--}6.0$) ($\bar{x} = 2.0$, n = 50), base $1.0\text{--}2.5 \mu\text{m}$ ($\bar{x} = 1.5 \mu\text{m}$), tip $0.5\text{--}1.0 \mu\text{m}$ ($\bar{x} = 0.6 \mu\text{m}$) (Fig. 63F, H). Mature conidia forming a head at the apex of phialides, hyaline, smooth-walled, unicellular, subglobose to globose and mostly $(1.5\text{--}2.0\text{--}3.0\text{--}3.5) \times (1.5\text{--}2.0\text{--}$

2.5(–3.0) μm ($\bar{x} = 2.5 \times 2.0 \mu\text{m}$, $\text{SD} = 0.15 \times 0.14$, $n = 50$), length/width ratio (1.0–)1.1–1.4 (–1.5) ($\bar{x} = 1.2$, $n = 50$) (Fig. 63I).

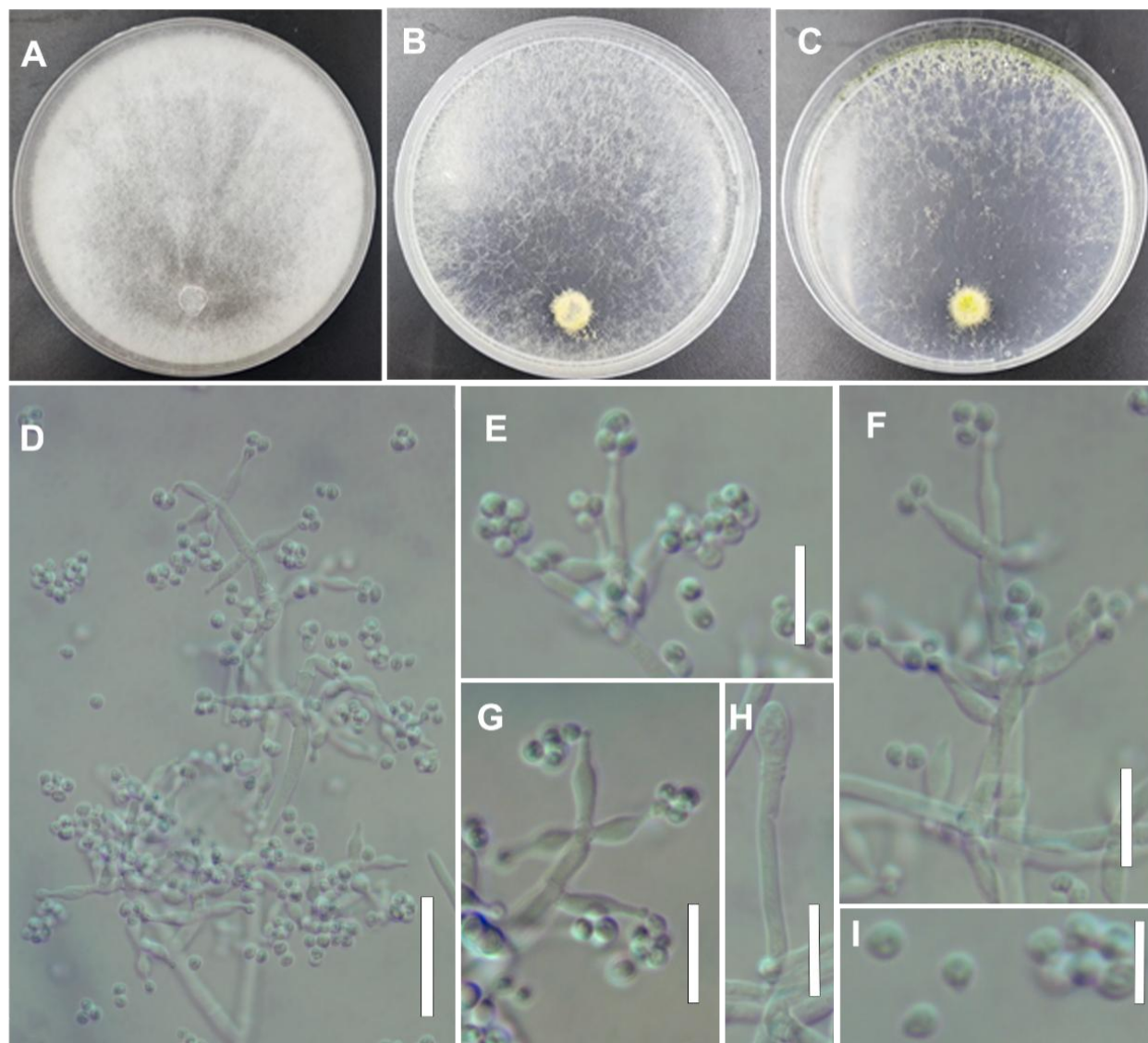


Figure 62 – *Trichoderma guangxiensis* (CGMCC3.29049, ex-type). Cultures at 25 °C after 3 days (A on PDA, B on CMD, C on SNA) D conidiophores E, F, G conidiophores and phialides. H. chlamydospores I conidia. Scale bars: d = 20 μm , e–h = 10 μm . i = 5 μm .

Culture characteristics – On PDA after 72 h, colony radius 56–58 mm at 25°C. Colony white to yellowish-white, regularly circular, indistinctly zonate; mycelium dense and radial. No diffusing pigment, not distinct odor (Fig. 63A). Conidial production noted after 3 days, starting around the original inoculum, effuse in the aerial hyphae, first white, turning yellow-green after 3 d. Chlamydospore not observed. On CMD after 72 h, colony radius 37–38 mm at 25°C. Colony white to yellowish-white, weak, indistinctly radial. Aerial hyphae short, inconspicuous. No diffusing pigment noted, odor indistinct (Fig. 63B). Conidial production noted after 3 days, scant, effuse in aerial hyphae, becoming yellow-green after 3 days. On SNA after 72 h, colony radius 51–52 mm at 25°C. Colony yellowish-white, indistinctly zonate; mycelium loose, especially at the margin. Aerial hyphae loose. No diffusing pigment, not distinct odor (Fig. 63C). Conidial production noted after 5 days, starting around the inoculum, effuse in the aerial hyphae. Small pustules formed around the inoculum, first white, turning green after 5 d, with hairs protruding beyond the surface.

Material examined – China, Guangxi Zhuang Autonomous Region, Ma Shan, 23°35'11"N, 108°1'33"E, ca. 400 m elev., from a field soil of sugarcane, 12 July 2024, ex-type culture CGMCC3.29051. Zhong Shan, Guangxi Zhuang Autonomous Region, 24°28'39"N, 111°11'22"E, ca. 375 m elev., from a soil of sugarcane, 11 Aug 2024, *ibid.* living culture CGMCC3.29052.

Notes – See notes of *Trichoderma guangxiensis*.

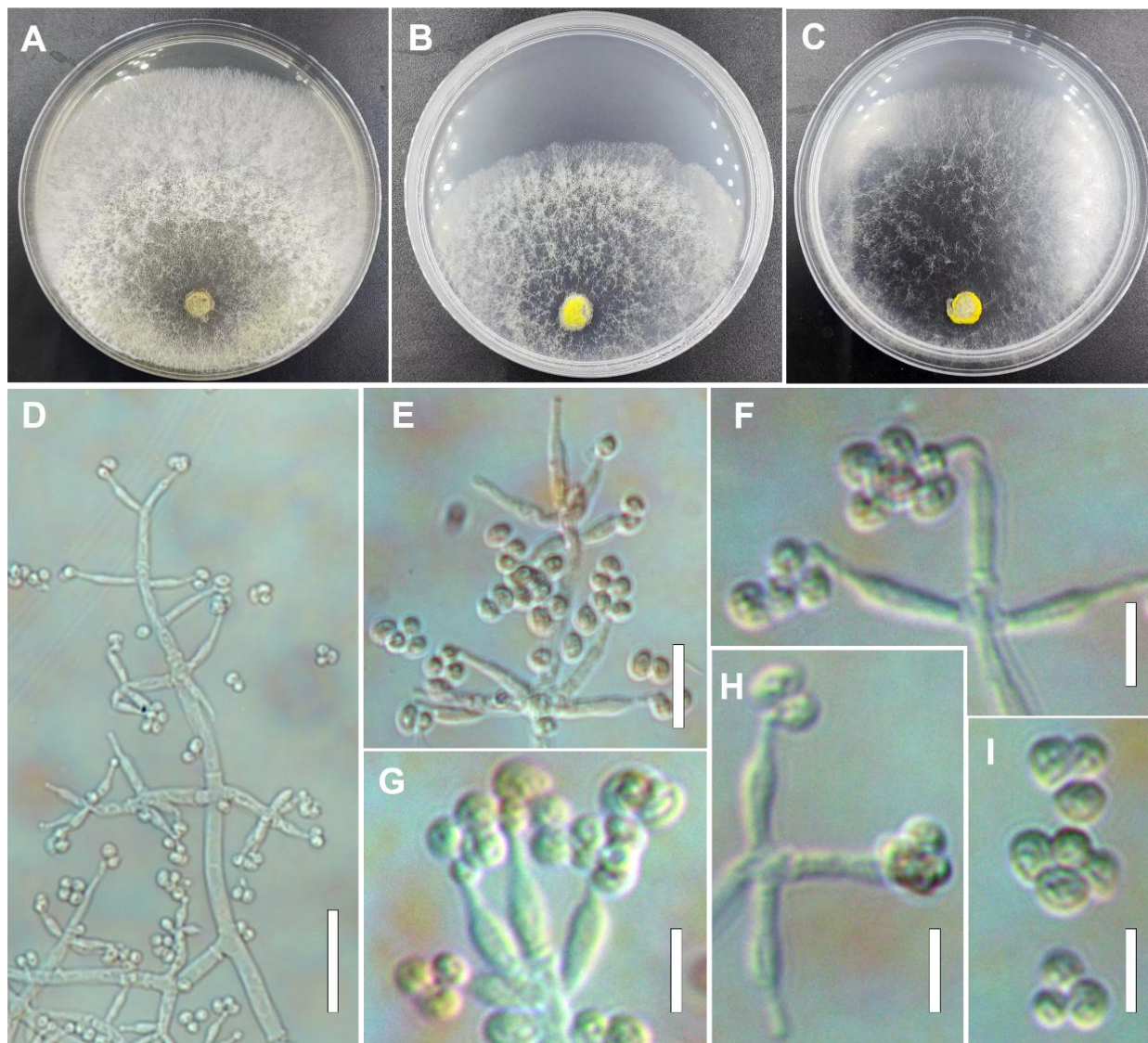


Figure 63 – *Trichoderma mashanense* (CGMCC3.29051, type strain). A–C Cultures at 25°C after 3 days (A on PDA B on CMD C on SNA) D conidiophores E, F, G conidiophores and phialides. H. chlamydospores I conidia. Scale bars: d = 20 μ m, e–h = 10 μ m. i = 5 μ m.

Trichoderma zhongshanense Jing Z. Sun & H.W. Liu, sp. nov.

Fig. 64

Fungal Names number: FN 573032; Facesoffungi number: FoF 17845

Etymology –The specific epithet “zhongshanense” refers to the location where the fungus was isolated.

Holotype – CGMCC3.29053

Saprobic, isolated from a field soil of sugarcane. Sexual morph: Undetermined. Asexual morph: *Conidiophores* pyramidal with opposing branches, the distance between branches relatively large, each branch terminating in a whorl of 2–3 phialides (Fig. 64D), phialides whorls typically cruciate, but often nearly verticillate (Fig. 64E–H). *Phialides* elongate-ampulliform and constricted at the base, hyaline, (3.0–)4.0–6.5(–10.0) $\times$ (2.5–)3.0–3.5(–3.6) μ m ($\bar{x}$ = 6.0 $\times$ 3.0 μ m, SD = 0.8 $\times$

0.5, $n = 50$), length/width ratio (1.2–)1.5–3.0(–4) ($\bar{x} = 2.0$, $n = 50$), base 1.0–1.5 μm ($\bar{x} = 1.2$ μm), tip 0.5–0.8 μm ($\bar{x} = 0.6$ μm) (Fig. 64E–H). *Conidia* ovoid to subglobose, smooth, hyaline (1.5–)1.8–2.4(–2.5) $\times$ (1.3–)1.5–2.0(–2.3) μm ($\bar{x} = 2.2 \times 1.8$ μm , $\text{SD} = 0.2 \times 0.1$, $n = 50$), length/width ratio (1.1–)1.2–1.4(–1.7) ($\bar{x} = 1.2$, $n = 50$) (Fig. 64I). *Chlamydospores* unobserved. No odor; no diffusing pigment observed.

Culture characteristics – On PDA after 72 h, colony radius 55–58 mm at 25°C. Colony white-green to bright green, regularly circular, distinctly zonate; mycelium dense and radial. Aerial hyphae short, inconspicuous. No diffusing pigment, not distinct odor. Conidial production noted after 2 days, starting around the inoculum, effuse in the aerial hyphae, first white, turning green after 2 d (Fig. 64A). *Chlamydospores* unobserved; On CMD after 72 h, colony radius 43–45 mm at 25°C. Colony white to yellowish, irregularly circular, distinctly zonate; mycelium loose. Aerial hyphae short, inconspicuous. No diffusing pigment, not distinct odor. Conidial production noted after 3 days, starting around the inoculum (Fig. 64B). Small pustules formed at the colony margin, first white, turning blue-green after 7 d, with hairs protruding beyond the surface. *Chlamydospores* unobserved; On SNA after 72 h, colony radius 48–50 mm at 25°C, 51–52 mm at 30°C, 3–4 mm at 35°C. Colony yellowish-white, regularly circular, distinctly zonate; mycelium loose, especially at the margin. Aerial hyphae short, inconspicuous. No diffusing pigment, not distinct odor. Conidial production noted after 2 days, starting around the inoculum, effuse in the aerial hyphae. Small pustules formed along with one concentric ring, first white, turning yellow-green after 5 d, with hairs protruding beyond the surface (Fig. 64C).

Material examined – China, Guangxi Zhuang Autonomous Region, Zhong Shan, 24°28'39"N, 111°11'22"E, ca. 375 m elev., from a soil of sugarcane, 11 Aug 2024, ex-type culture CGMCC3.29053; Zhong Shan, Guangxi Zhuang Autonomous Region, 24°28'39"N, 111°11'22"E, ca. 375 m elev., from a soil of sugarcane, 11 Aug 2024, living culture CGMCC3.29054. Zhong Shan, Guangxi Zhuang Autonomous Region, 24°28'39"N, 111°11'22"E, ca. 375 m elev., from a soil of sugarcane, 11 Aug 2024, living culture CGMCC3.29055.

Notes – See notes of *Trichoderma guangxiensis*.

Nectriaceae Tul. & C. Tul.

Cylindromonium Crous, Persoonia 43: 313 (2019)

Crous et al. (2019b) introduced *Cylindromonium* in *Nectriaceae* (*Hypocreales*, *Sordariomycetes*) to accommodate *Cyl. eugeniicola* (type species), *Cyl. lichenicola* ($\equiv$ *Acremonium lichenicola*), and *Cyl. rhabdosporum* ($\equiv$ *Acremonium rhabdosporum*). Subsequently, four species were accommodated to *Cylindromonium* (Crous et al. 2020a, 2021, 2023, Ohmaki et al. 2023). *Cylindromonium* species are lichenicolous, mycophilic or saprophytic with a cosmopolitan distribution (Crous et al. 2019b, 2020a, 2021, 2023, Ohmaki et al. 2023). Asexual morph of *Cylindromonium* has hyaline conidiophores, phialidic conidiogenous cells, and hyaline, septate or aseptate conidia (Crous et al. 2019b, 2020a, 2021, 2023). While its sexual morph was recently reported by Ohmaki et al. (2023), which has perithecial and globose ascomata occurred on host lichen thallus, unitunicate, 8-spored, broadly cylindrical to clavate, non-stipitate asci, and biseriate, ellipsoid, hyaline, 1-septate ascospores.

Cylindromonium hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 66

Fungal Names number: FN 572855; Facesoffungi number: FoF 17813

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 136242

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, hyaline, hairy, glistening. *Mycelium* immersed, composed of branched, hyaline, smooth hyphae. *Conidiophores* 95–137 $\times$ 3–6 μm ($\bar{x} = 117 \times 4$ μm , $n = 20$), semi-macronematous, mononematous, solitary, erect, arising from creeping hyphae, straight or slightly flexuous, sub-cylindrical, hyaline, unbranched, 1–3-septate, smooth.

Conidiogenous cells 48–131 × 2–4.5 μm ($\bar{x}$ = 108 × 3.5 μm, n = 20), phialidic, integrated, apex with periclinal thickening, collarete inconspicuous, hyaline. *Conidia* 30–42 × 3.5–5.5 μm ($\bar{x}$ = 36 × 4.5 μm, n = 25), aggregating in transparent heads, falcate, hyaline, aseptate, verrucose.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes produced from both ends. Colonies reaching up to 20 mm diam. after 10 days, mycelia dense, circular, flat, margin undulate, white at the outer ring, pale brown at the center from above, yellow with slightly darker at the center from below.

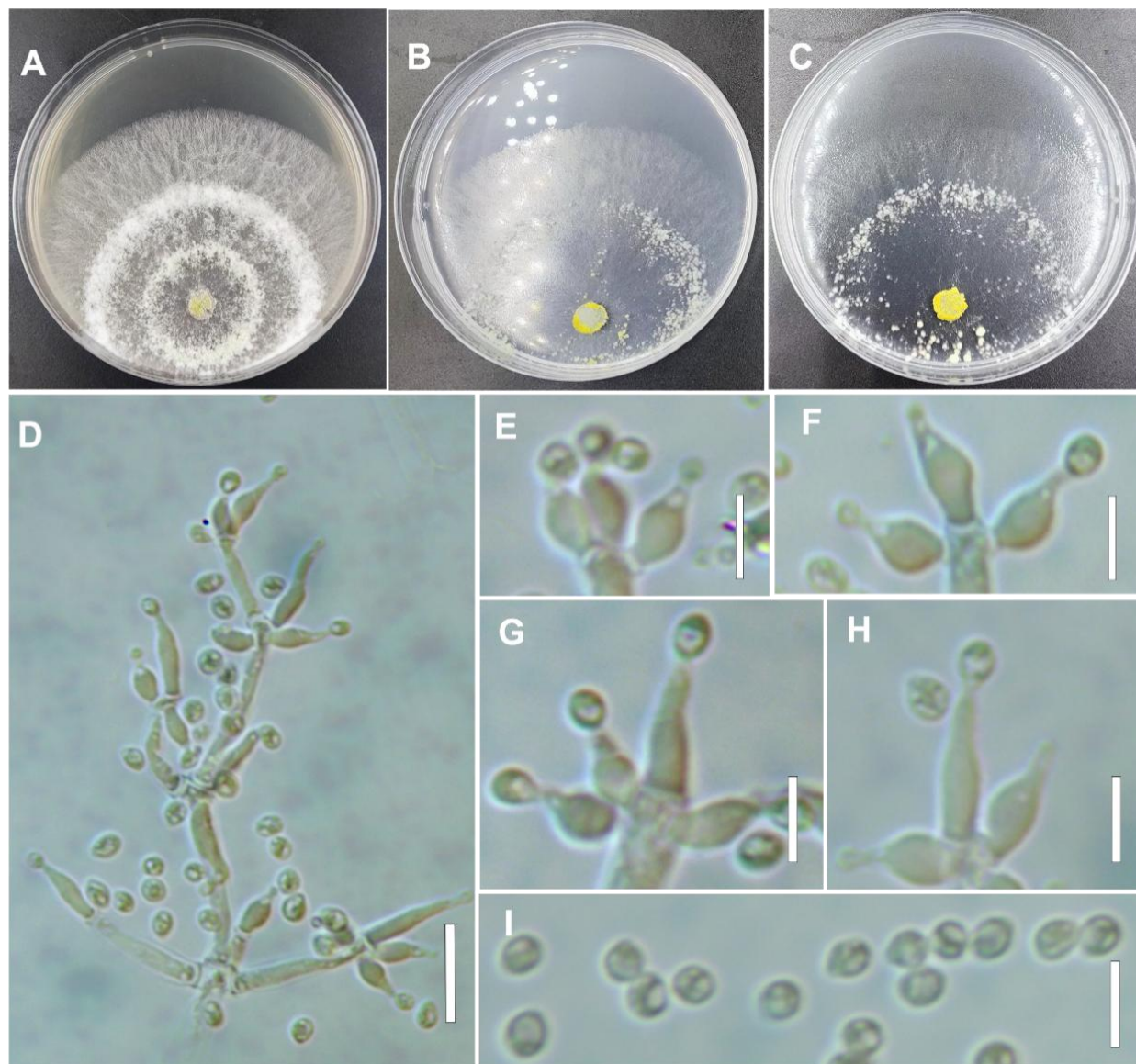


Figure 64 – *Trichoderma zhongshanense* (CGMCC3.29053, type strain). A–C Cultures at 25°C after 3 days (A on PDA B on CMD C on SNA) D conidiophores E–H conidiophores and phialides. I conidia. Scale bars: d = 10 μm, e–i = 5 μm.

Material examined – China, Guizhou Province, Qiannan Prefecture, Weng'an County, Zhujiashan National Forest Park, N 26°58'8", E 107°37'5", elevation 958 m, on decaying wood from a freshwater stream, 27 August 2023, X.J. Xiao, ZJ3 (HKAS 136242, holotype), ex-type culture GZCC 24-0105.

Notes – To date, eight species are accommodated to *Cylindromonium* and all species have available sequence data. In the phylogenetic tree (Fig. 67), our strain GZCC 24-0105 grouped with *Cyl. eugeniicola* with 90% ML and 0.96 PP support. Our collection differs from *Cyl. eugeniicola* by

having falcate and aseptate conidia, while the latter has cylindrical and 1-septate conidia. Microstructure measurements of *Cyl. eugenicola* were not provided (Crous et al. 2019b). ITS comparison shows there are 61 bp (including 12 gaps, totally 568 bp) differences between GZCC 24-0105 and the ex-type strain (CBS 146075) of *Cyl. eugenicola*. Therefore, based on morphology and phylogeny, we identify our collection as a new species.

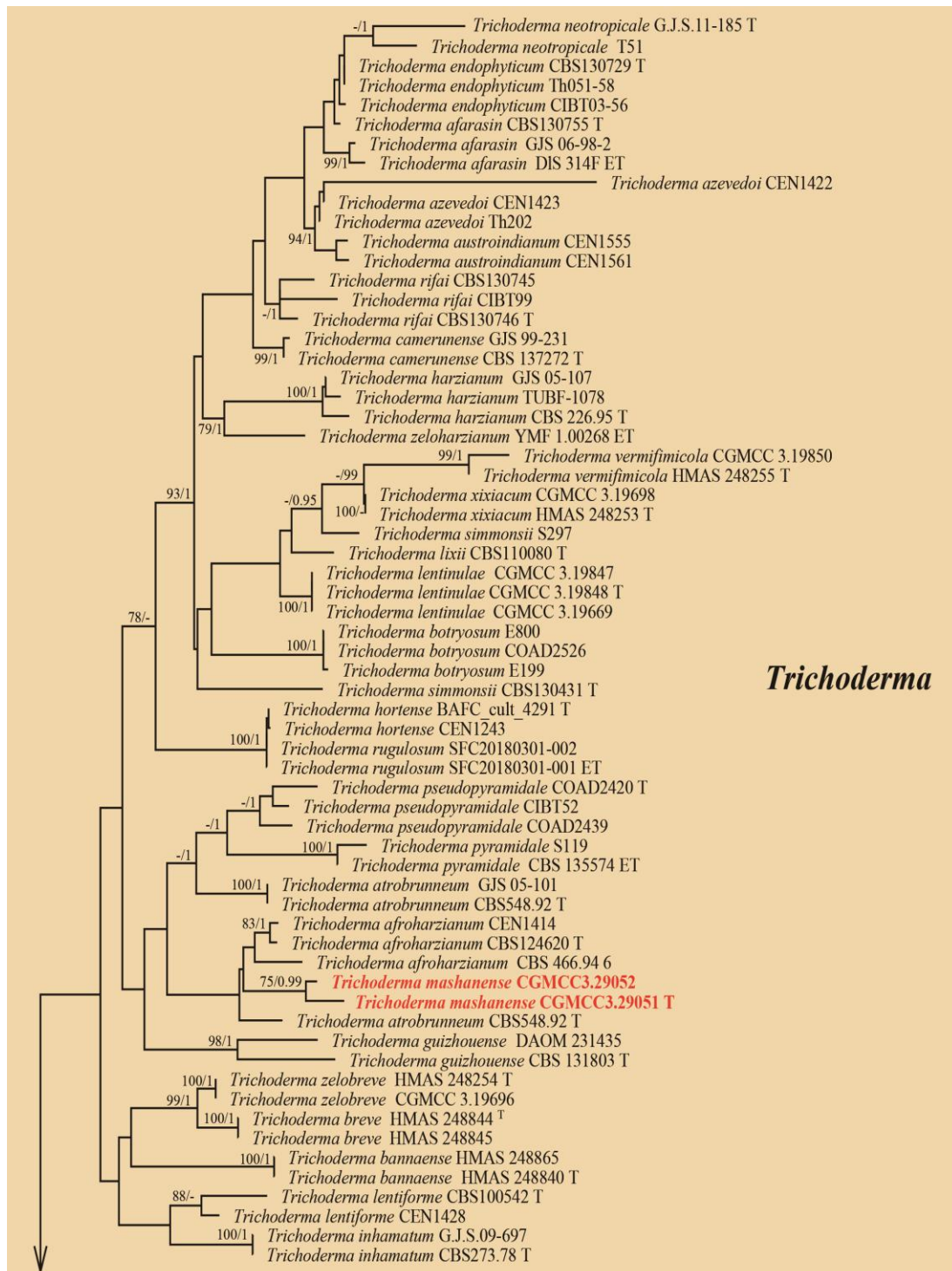


Figure 65 – ML tree based on the combined ITS, *rpb2* and *tefla* sequences, representing *Trichoderma*. Bootstrap support values for ML equal to or greater than 50% and PP values equal to or greater than 0.95 are placed above the branches. The tree is rooted with *Trichoderma estonicum*, *Trichoderma parastinicum*, *Trichoderma ceramicum*. ex-type and ex-epitype strains are marked with “T” and “ET”, respectively. The new taxa are indicated in bold and red.

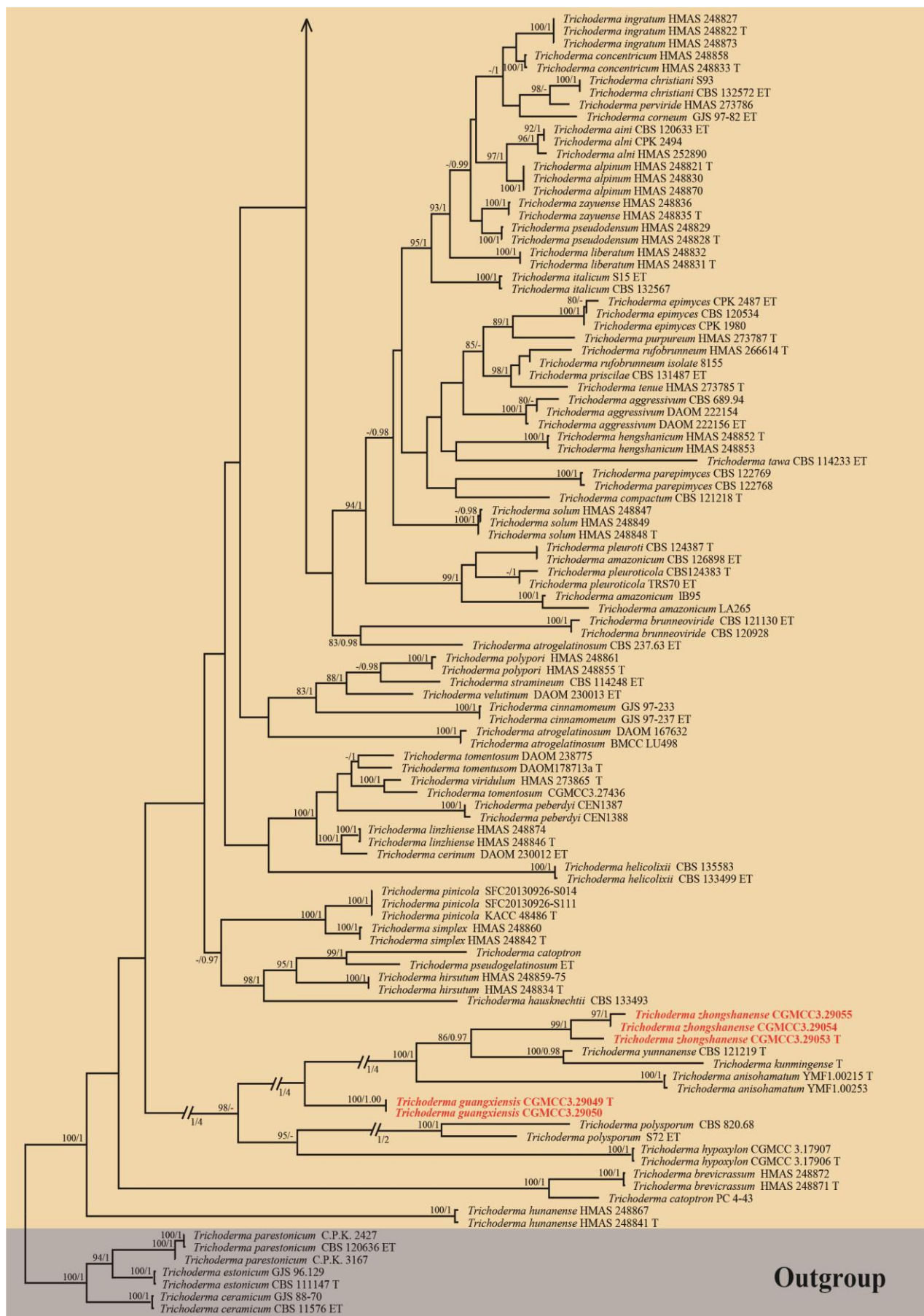


Figure 65 – Continued.

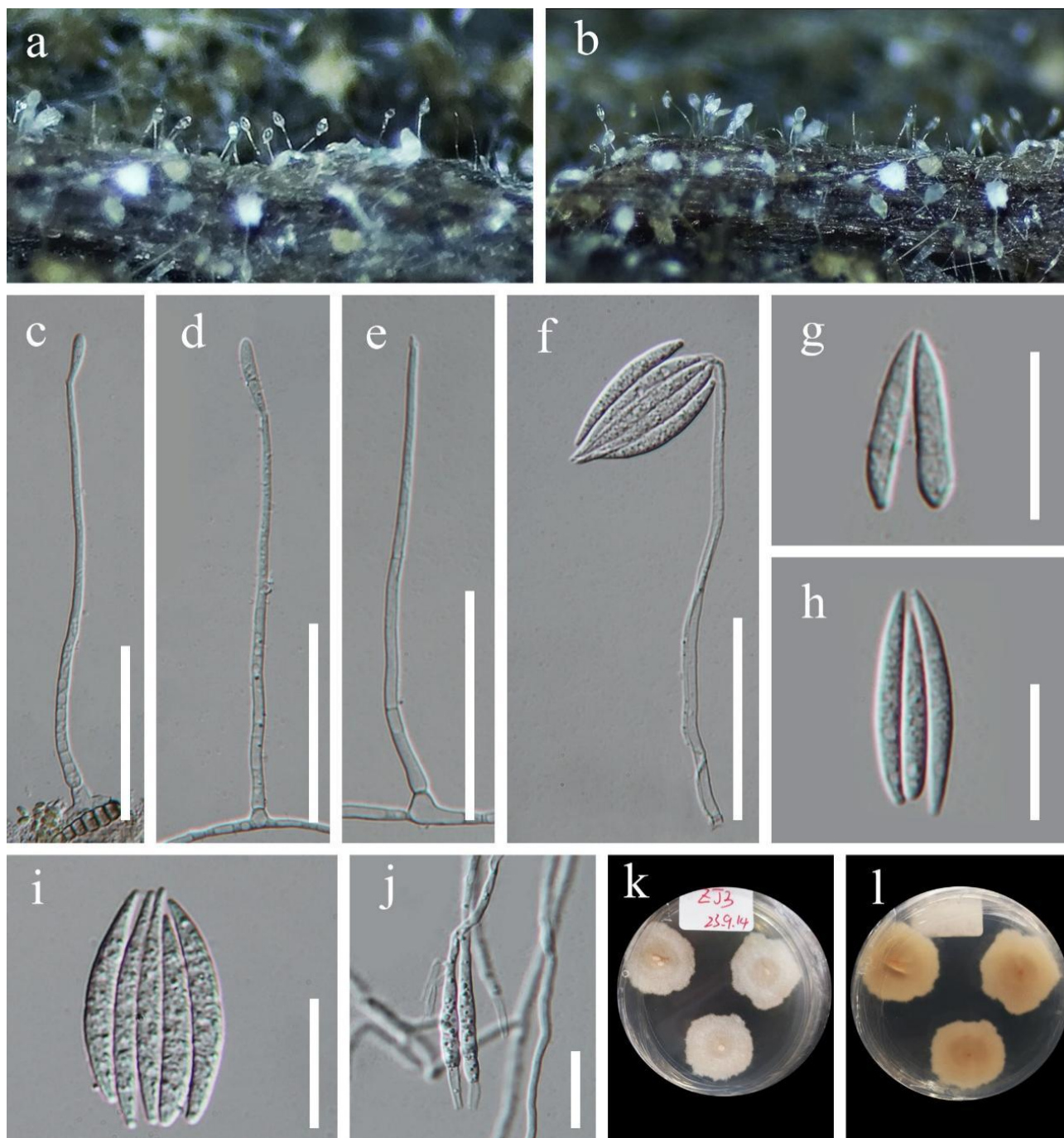


Figure 66 – *Cyldromonium hydei* (HKAS 136242, holotype). a, b Colonies on natural substrate. c–f Conidiophores and conidia. g–i Conidia. j Germinated conidia. k, l Colonies on PDA (k from above, l from below). Scale bars: c–f = 50 µm, g–j = 20 µm.

Subclass *Savoryellomycetidae* Hongsanan, K.D. Hyde & Maharachch.

Conioscyphales Réblová & Seifert

Conioscyphaceae Réblová & Seifert

Conioscypha Höhn., Ann. Mycol. 2 (1): 58 (1904)

Conioscypha was introduced by von Höhnelt (1904) with *C. lignicola* as the type species. Asexual morphs of *Conioscypha* are trimorphic. The typical hyphomycetous asexual morph is characterized by phialidic, cup-like conidiogenous cells which have one to several collaretted phialide, formed by layers of ruptured walls in the process of conidial production (Shearer 1973). Sun et al. (2025) transferred three *Vanakripta* species to *Conioscypha* which has sporodochial conidiomata and blastic conidiogenous cells bearing ellipsoidal to obovoid conidia (Bhat &

Kendrick 1993, Tsui et al. 2003, Liu et al. 2024a). Most *Conioscypha* species have micronematous, mononematous conidiophores, except for *C. synnemata* which has synnematus conidiophores (Sun et al. 2025). Sexual morph of *Conioscypha* has inconspicuous, ostiolate, subhyaline to pale orange ascomata, 8-spored, unitunicate, hyaline asci with a refractive J- apical annulus, and fusiform, 3–7-septate ascospores (Réblová & Seifert 2004). *Conioscypha* species have a cosmopolitan distribution colonizing on both terrestrial and freshwater habitats (Liu et al. 2019a).

Conioscypha davidii X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 68

Fungal Names number: FN 572854; Facesoffungi number: FoF 17812

Etymology – The specific epithet “davidii” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 144597

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, black, gregarious, glistening. *Mycelium* immersed, composed of hyaline, branched, septate, smooth hyphae. *Conidiophores* arising directly from the hyphae, and reduced to conidiogenous cells, hyaline. *Conidiogenous cells* phialidic, integrated, sessile or on micronematous conidiophores, percurrently proliferating, with cup-shaped multi-collarete, hyaline, smooth. *Conidia* 13–19 × 12–17 µm ($\bar{x}$ = 16 × 14 µm, n = 30), solitary, globose to subglobose, obovoid, olivaceous when young, dark brown when mature, aseptate, smooth or verrucose. Conidia formed by percurrent regeneration of the apex of the conidiogenous cell at the same level.

Culture characteristics – Conidia germinating on PDA within 48 h and germ tubes producing from the conidial base. Colonies reaching up to 32 mm diam. after 130 days of cultivation at 28°C, medium dense, flat, circular, center wrinkled, margin entire, pale yellow from above and below.

Material examined – China, Guizhou Province, Dushan County, N 25°58'33", E 107°41'15", elevation 697 m, on decaying wood from a freshwater stream, 18 June 2024, X.J. Xiao, DS23 (HKAS 144597, holotype), ex-type culture GZCC 24-0282.

Notes – In the phylogenetic tree (Fig. 71), our strain GZCC 24-0282 formed a sister clade to *Conioscypha pleiomorpha* (FMR 13134) and *C. verrucosa* (MFLUCC 18-0419) with weak support. Morphologically, our collection closely resembles *C. pleiomorpha*, including the conidial measurement size (13–19 × 12–17 µm vs. 13–18 × 12–14 µm) (Hernández-Restrepo et al. 2017). However, it differs from *C. verrucosa*, which exhibits macronematous, moniliform conidiophores with globose to subglobose, ellipsoidal or clavate cells (Hyde et al. 2020a). Additionally, ITS comparison reveals that our strain GZCC 24-0282 exhibits 8.2% difference (44/536, 13 gaps) and 9% difference (45/500, 16 gaps) to *C. pleiomorpha* (FMR 13134) and *C. verrucosa* (MFLUCC 18-0419), respectively. Therefore, we introduce our collection as a new species.

Conioscypha hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 69

Fungal Names number: FN 572852; Facesoffungi number: FoF 17810

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 144599

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, black, gregarious, glistening. *Mycelium* immersed, composed of hyaline, branched, septate, smooth hyphae. *Conidiophores* arising directly from the hyphae, and reduced to conidiogenous cells, hyaline. *Conidiogenous cells* phialidic, integrated, sessile or on micronematous conidiophores, percurrently proliferating, with cup-shaped multi-collarete, hyaline, smooth. *Conidia* 13–26 µm ($\bar{x}$ = 17.5 µm, n = 30) diam., solitary, globose to subglobose, hyaline when young, dark brown when mature, aseptate, smooth. Conidia formed by percurrent regeneration of the apex of the conidiogenous cell at the same level.

Culture characteristics – Conidia germinating on PDA media within 24 h and germ tubes producing from the conidial periphery. Colonies reaching up to 35 mm diam. after 4 months of

cultivation at 28°C on PDA media, medium dense, circular, margin filiform, white to pale brown from above and below.

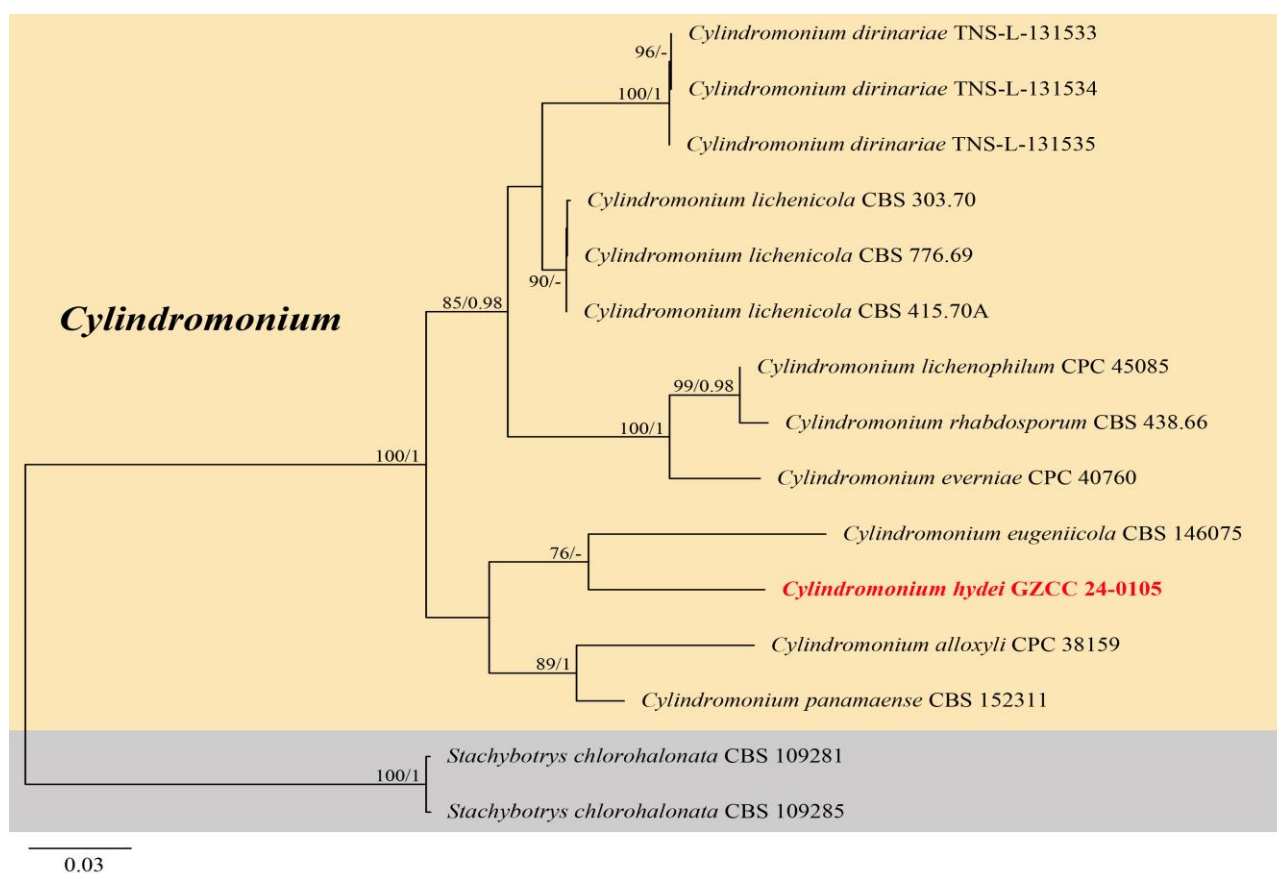


Figure 67 – ML tree based on the combined LSU, ITS and *rpb2* sequences, representing the genus *Cyindromonium*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Stachybotrys chlorohalonata* (CBS 109281 and CBS 109285). The new taxon is indicated in bold and red.

Material examined – China, Guizhou Province, Du Shan County, N 25°58'33", E 107°41'15", elevation 697 m, on decaying wood from a freshwater stream, 18 June 2024, X.J. Xiao, DS33 (HKAS 144599, holotype), ex-type culture GZCC 24-0284.

Notes – Our strain GZCC 24-0284 exhibited a close phylogenetic relationship with *Conioscypha japonica* (CBS 387.84) based on multigene analyses (Fig. 71). However, it can be distinguished from *C. japonica* by the morphology of its conidia, which are globose to subglobose, whereas *C. japonica* produces obpyriform, subglobose, and ellipsoidal conidia (Udagawa & Toyazaki 1983). Furthermore, our conidia are larger than those of *C. japonica* (13–26 µm diam. vs. 9–13 × 5–10 µm or 10–14 × 4.5–7 µm) (Udagawa & Toyazaki 1983). In addition, ITS sequence data are unavailable for *C. japonica*, but *rpb2* sequence comparison reveals a 6.08% difference (65 out of 1069 bp, without gaps).

Conioscypha keviniana X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 70

Fungal Names number: FN 572853; Facesoffungi number: FoF 17811

Etymology – The specific epithet “keviniana” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 144601

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* immersed, composed of hyaline, branched, septate, smooth hyphae. *Conidiophores* micronematous, hyaline. *Conidiogenous cells* phialidic, cup-shaped

multi-collarette not observed. *Conidia* 7–14 × 5–10 μm ($\bar{x}$ = 10 × 7.5 μm, n = 30), solitary, ellipsoidal to obovoid, pale brown to brown, aseptate, guttulate.

Culture characteristics – Conidia germinating on PDA media within 24 h and germ tubes producing from the basal end. Colonies reaching up to 35 mm diam. after 4 months of cultivation at 28°C on PDA media, irregular, smooth, margin entire, white to pale yellow from above and below.

Material examined – China, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Shibing County, Yuntaishan National Forest Park, N 25°58'33", E 107°41'15", elevation 697 m, on decaying wood from a freshwater stream, 18 June 2024, X.J. Xiao, YTS1 (HKAS 144601, holotype), ex-type culture GZCC 24-0090.

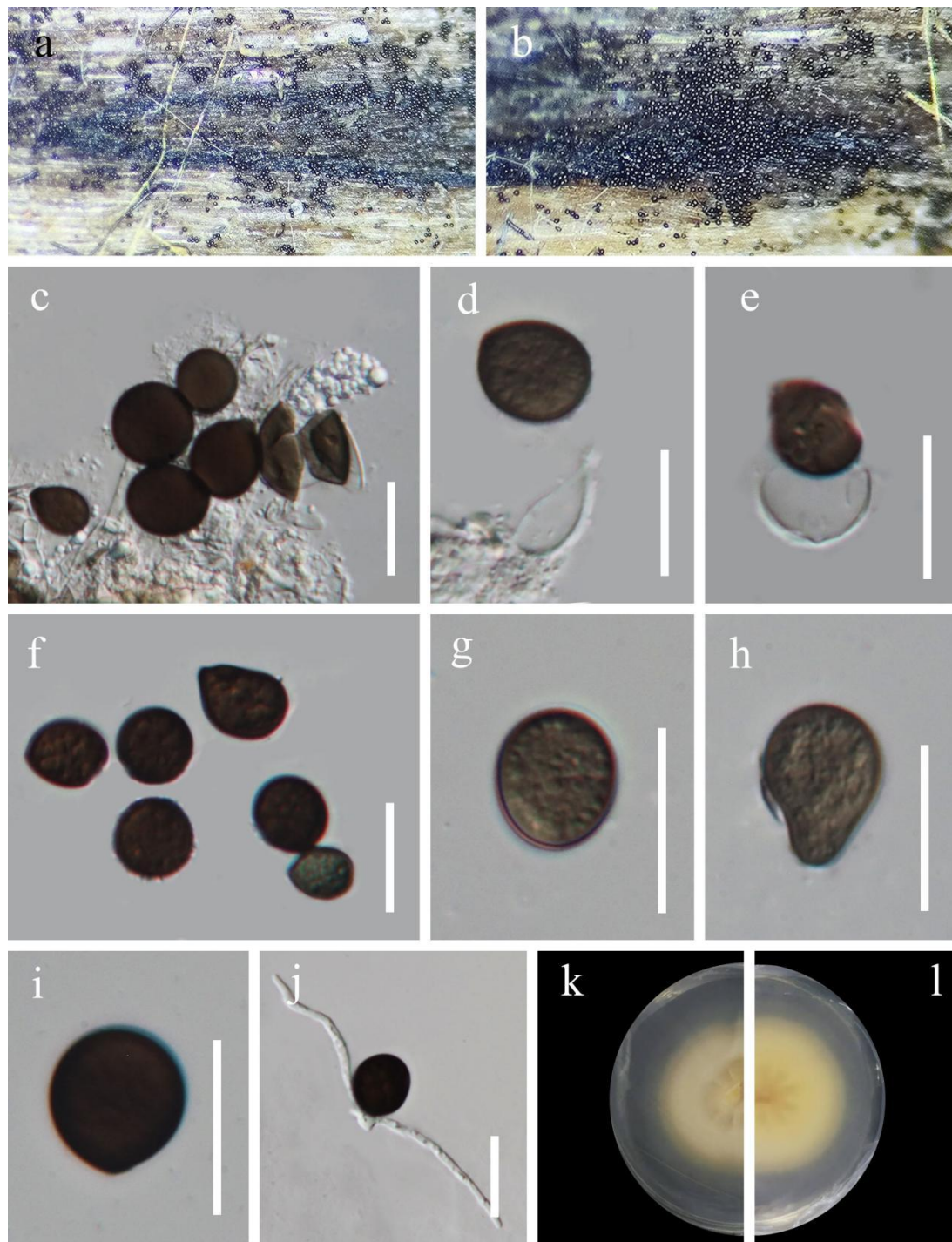


Figure 68 – *Conioscypha davidii* (HKAS 144597, holotype). a, b Colonies on dead wood surface. c–e Conidiogenous cell and conidia. f–i Conidia. j Germinated conidium. k, l Colony on PDA (upper and lower view). Scale bars: c–j = 20 μm.

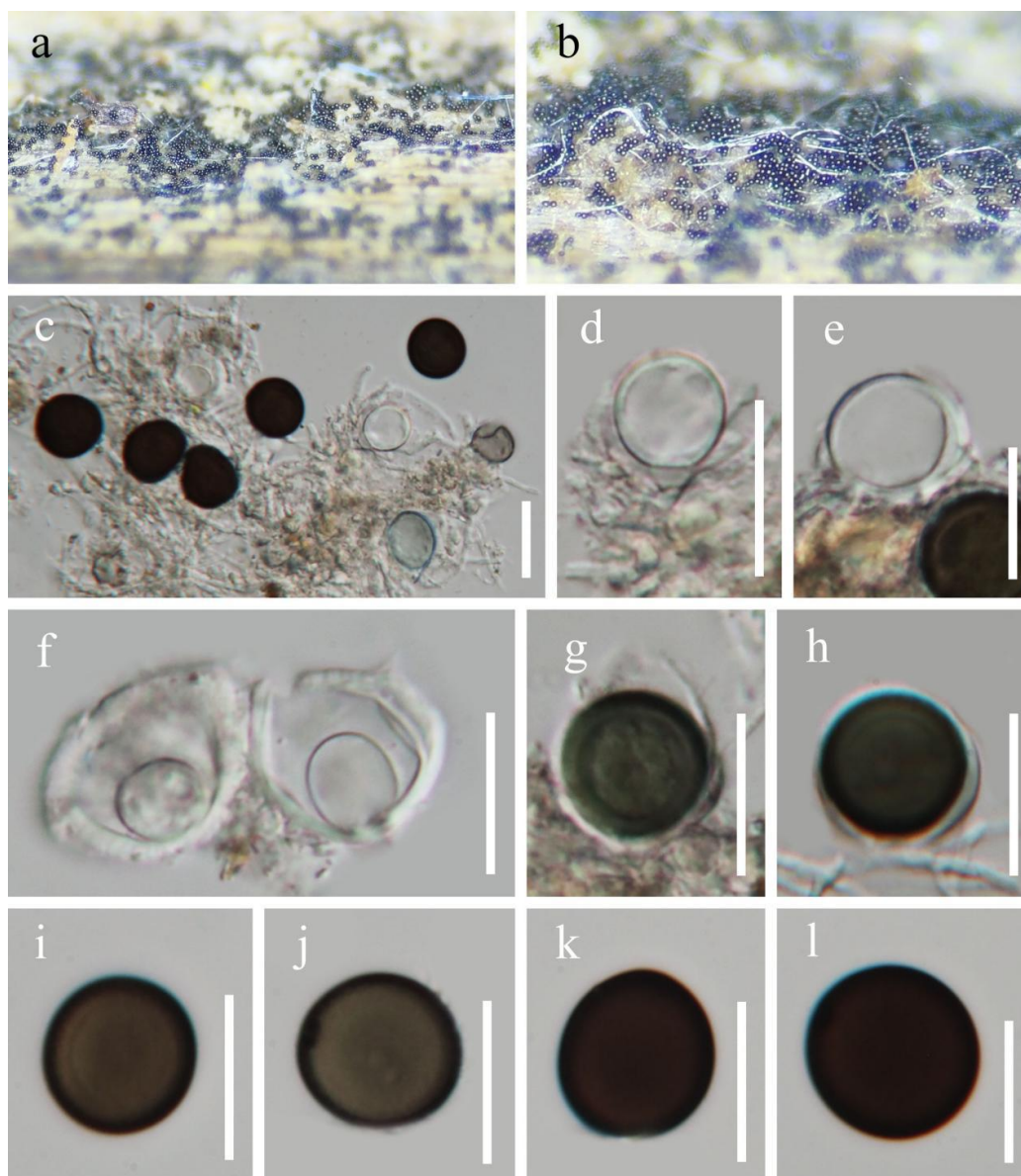


Figure 69 – *Conioscypha hydei* (HKAS 144599, holotype). a, b Colonies on dead wood surface. c Conidiogenous cells bearing conidia. d–h Conidiogenous cell attached with conidia. i–l Conidia. Scale bars: d = 10 μm c, e–l = 20 μm.

Notes – Based on a megablast search of NCBI's GenBank nucleotide database, the ITS sequence of our strain GZCC 24-0090 showed distant and partial similarity to *Vanakripa minutiellipsoidea* (strain MFLU 17-1724, GenBank MN513033.1; Identities = 390/446(87%), 23 gaps (5%)), and closest hits using the *rpb2* sequence had highest similarity to *C. varia* (strain CBS 113653, GenBank JQ429261.1; Identities = 851/1056 (81%), 19 gaps (1%)). Our collection differs from *Vanakripa minutiellipsoidea* by the presence of “separating cells” and blastic conidiogenous cells (Pinnoi et al. 2003), and differs from *C. varia* by its morphologically variable conidia (Shearer 1973). In our phylogenetic analyses of combined LSU-ITS-*rpb2* sequence data (Fig. 71), the strain GZCC 24-0090 formed a separate lineage, indicating it is a phylogenetically distinct species.

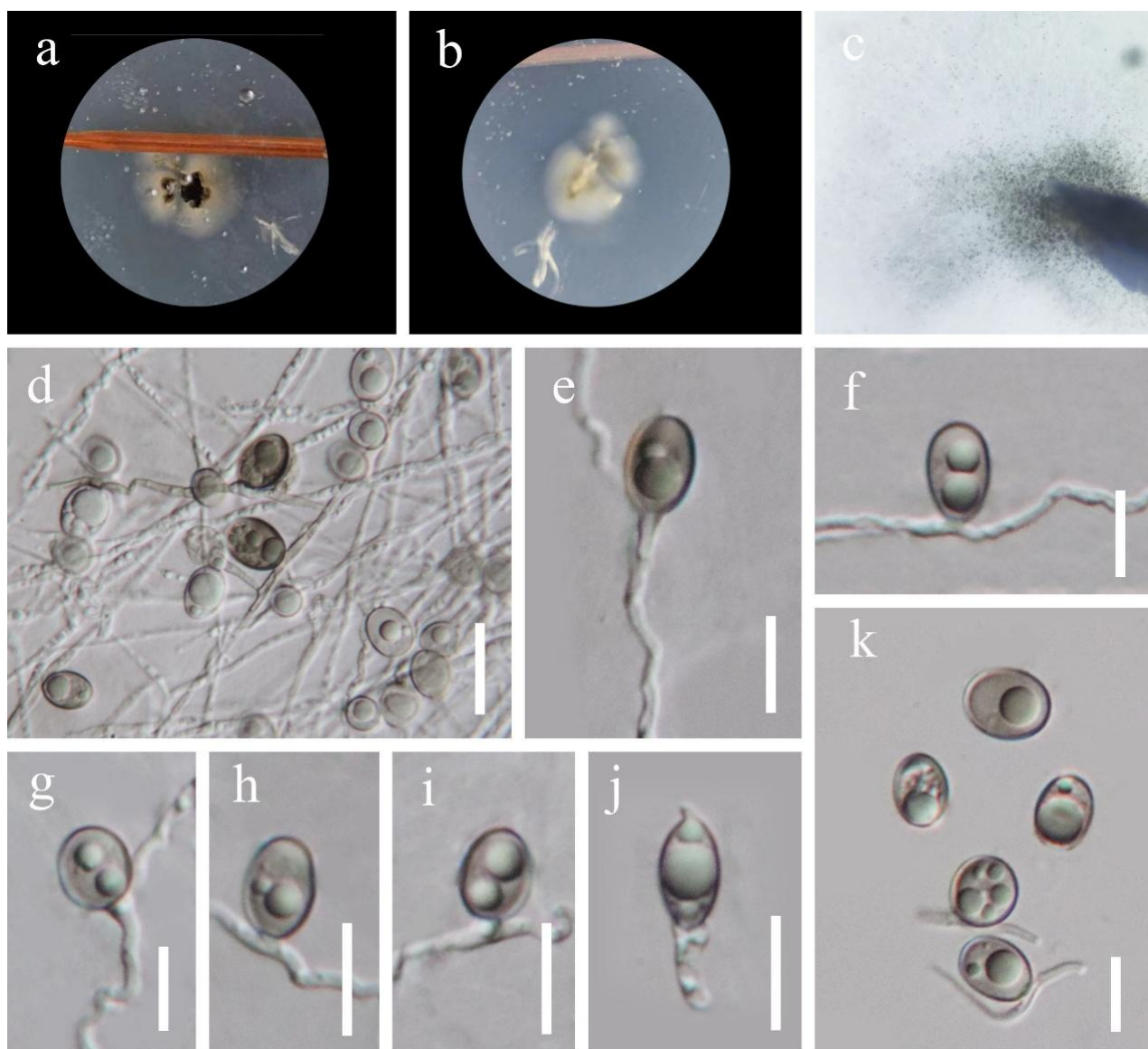


Figure 70 – *Conioscypha keviniana* (HKAS 144601, holotype). a, b Colonies on PDA media. d–k Sporulation on PDA media in 20 days. Scale bars: d–k = 20 μm.

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

Savoryellaceae Jaklitsch & Réblová

Xenobactrodesmium X.J. Xiao, N.G. Liu & Y.Z. Lu, gen. nov.

Fungal Names number: FN 572899; Facesoffungi number: FoF 17847

Etymology – The specific epithet “*Xenobactrodesmium*” refers to its morphological resemblance to *Bactrodesmium*.

Saprobic on submerged rotting wood from a freshwater habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, black, punctiform, glistening. *Mycelium* immersed, composed of branched, brown to dark brown, smooth hyphae. *Conidiophores* micronematous to semi-macronematous, mononematous, flexuous or straight, unbranched, hyaline to pale brown, septate, thick- or thin-walled. *Conidiogenous cells* monoblastic, holoblastic, terminal, integrated, borne directly on hyphae or on short conidiophores, hyaline to pale brown, smooth. *Conidia* solitary, dry, acrogenous, obclavate to obpyriform, straight or slightly curved, euseptate, thickened and darkened at the septa, olivaceous to dark brown, smooth.

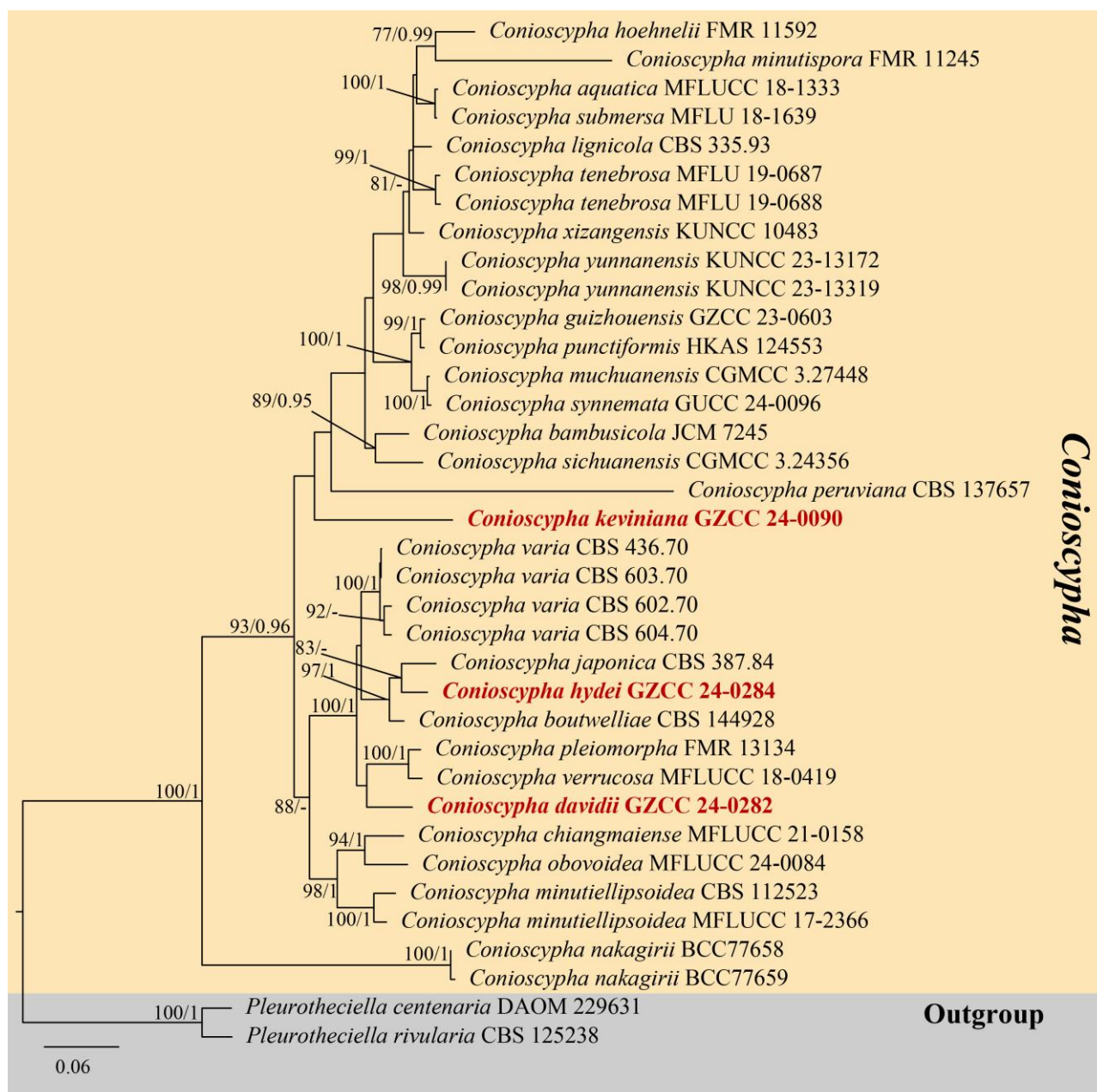


Figure 71 – ML tree based on the combined LSU, ITS and *rpb2* sequences, representing the genus *Conioscypha*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Pleurotheciella centenaria* (DAOM 229631) and *Pleurotheciella rivularia* (CBS 125238). The new taxa are indicated in bold and red.

Type species: *Xenobactrodesmium hydei* X.J. Xiao, N.G. Liu & Y.Z. Lu

Notes: *Xenobactrodesmium* morphologically resembles *Bactrodesmium* in having sporodochial conidiomata, micronematous to semi-macronematous conidiophores. However, the conidial shape of *Bactrodesmium* varies and can be subglobose, clavate, pyriform, ellipsoidal, obovoid, fusiform or cylindrical (Réblová et al. 2020). In contrast, our collection features obclavate to obpyriform conidia. Apart from the difference in morphology, the monophyly of *Bactrodesmium* and our collection is also not well supported. In the present phylogenetic tree (Fig. 73), our strain formed a distinct clade sister to *Bactrodesmium* group with 38% ML and 0.55 PP value. Additionally, in a broader taxa sampling (data not shown), which includes taxa from *Pleurotheciales*, *Conioscyphales* and *Fuscosporellales*, our collection was not closely related to *Bactrodesmium*. Therefore, we propose a new genus *Xenobactrodesmium* in *Savoryellaceae* to accommodate our collection.

Xenobactrodesmium hydei X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.

Fig. 72

Fungal Names number: FN 572900; Facesoffungi number: FoF 17848

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 144609

Saprobic on submerged rotting wood from a freshwater habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, black, punctiform, glistening. *Mycelium* immersed, composed of branched, brown to dark brown, septate, smooth hyphae. *Conidiophores* micronematous to semi-macronematous, mononematous, arising from hyphae, flexuous or straight, mostly simple, hyaline to pale brown, septate, smooth. *Conidiogenous cells* monoblastic, holoblastic, terminal, integrated, borne directly on immersed hyphae or on short conidiophores, pale brown or hyaline, smooth. *Conidia* 41–58 × 15–20 µm ($\bar{x}$ = 49 × 18 µm, n = 30), solitary, acrogenous, obclavate to obpyriform, straight or slightly curved, 5–8-septate, olivaceous to dark brown, smooth.

Culture characteristics – Conidia germinating on PDA within 48 h and germ tubes producing from the basal end of the conidia. Colonies reaching up to 12 mm diam. after 4 months of cultivation at 28°C, irregular, dense, margin undulate, brown to dark brown from above and below.

Material examined – China, Guizhou Province, Zunyi City, Xishui County, Sancha River, N 28°33'50", E 106°24'9", elevation 1133 m, on decaying wood from a freshwater habitat, 3 October 2023, X.J. Xiao, SCS17 (HKAS 144609, holotype), ex-type culture GZCC 24-0271.

Notes – Except for *Bactrodesmium*, *Xenobactrodesmium hydei* morphologically resembles the recently introduced genus *Gohteikhimyces* in having sporodochial conidiomata and micronematous to semi-macronematous conidiophores (Ou et al. 2024). However, *Gohteikhimyces* produces ellipsoidal, broadly cymbiform, or mitriform conidia (Ou et al. 2024), whereas *Xenobactrodesmium* has obclavate conidia. Phylogenetically, *Gohteikhimyces* is placed in *Savoryellomycetidae* genera *incertae sedis*, while *Xenobactrodesmium* belongs to *Savoryellaceae*.

Subclass *Sordariomycetidae* O.E. Erikss. & Winka

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

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Menisporopsis S. Hughes, Mycol. Pap. 48: 59 (1952)

Menisporopsis was introduced by Hughes (1952) with *Me. theobromae* as the type species. *Menisporopsis* is commonly characterized by its hyphomycetous asexual morph, which has dark brown, septate setae surrounded by synnematus conidiophores, phialidic conidiogenous cells, and lunate to falcate, hyaline, aseptate or septate, appendiculate conidia aggregated in slimy heads (Da Cruz et al. 2014, Wu & Diao 2022). Sexual morph is reported only for *Me. kobensis* (Matsushima 2001). Species of *Menisporopsis* are saprobic in both terrestrial and freshwater habitats (Tsui et al. 1999, Da Cruz et al. 2014, Chen et al. 2022). Sixteen species are currently accepted in *Menisporopsis* (Species Fungorum, 2024).

Menisporopsis hydei X.J. Xiao, J.W. Liu & Y.Z. Lu, sp. nov.

Fig. 74

Fungal Names number: FN 572889; Facesoffungi number: FoF 17826

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 136249

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, white, shiny. *Mycelium* immersed, composed of branched, brown, smooth hyphae. *Setae* 152–278 × 3–6.5 µm ($\bar{x}$ = 217 × 5 µm, n = 20), central, erect, broadly curved or straight, brown, unbranched, septate, thick-walled, lower part encased tightly by compact conidiophores and obviously wider than each conidiophore. *Synnemata* 59–92 µm long, 2.5–5 µm wide. *Conidiophores* 58–72 × 3–5 µm ($\bar{x}$ = 65 × 4 µm, n = 25), macronematous, synnematus, unbranched, pale brown to brown, smooth. *Conidiogenous cells* monophialidic,

integrated, terminal, subcylindrical, pale to brown, with collarettes, smooth. *Conidia* 17–23 × 2.5–4.5 µm ($\bar{x}$ = 19 × 3.5 µm, n = 30), aggregated in slimy masses at the apex of the synnemata, acrogenous, fusiform, curved, hyaline, aseptate, verruculose, with two single, hyaline, unbranched, hair-like setulae at each end, 4–6 µm long.

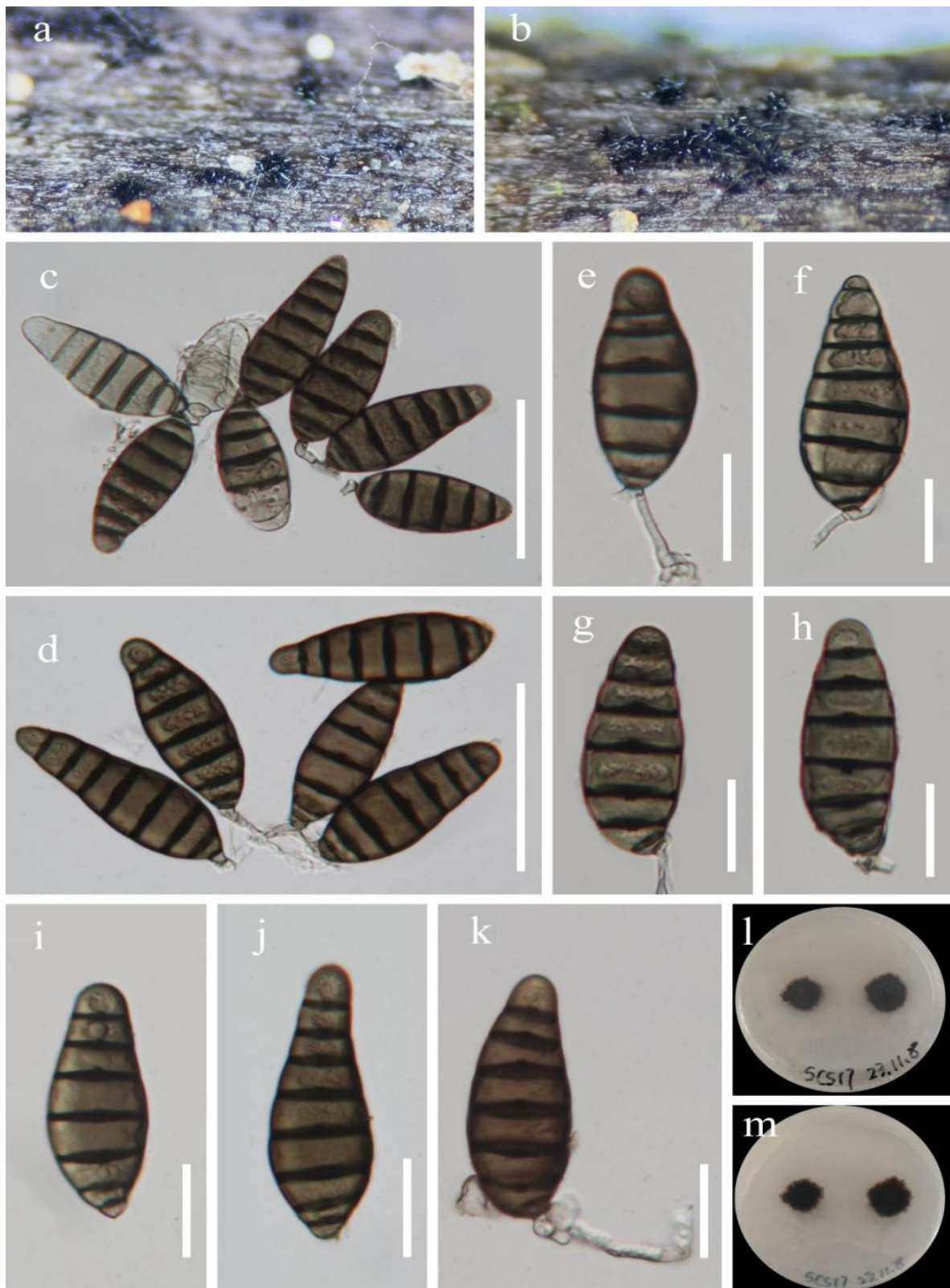


Figure 72 – *Xenobactrodesmium hydei* (HKAS 144609, holotype) a, b Colonies on natural substrate. c–j Conidiophores and conidia. k Germinated conidium. l, m Colonies on PDA media (l from above, m from below).

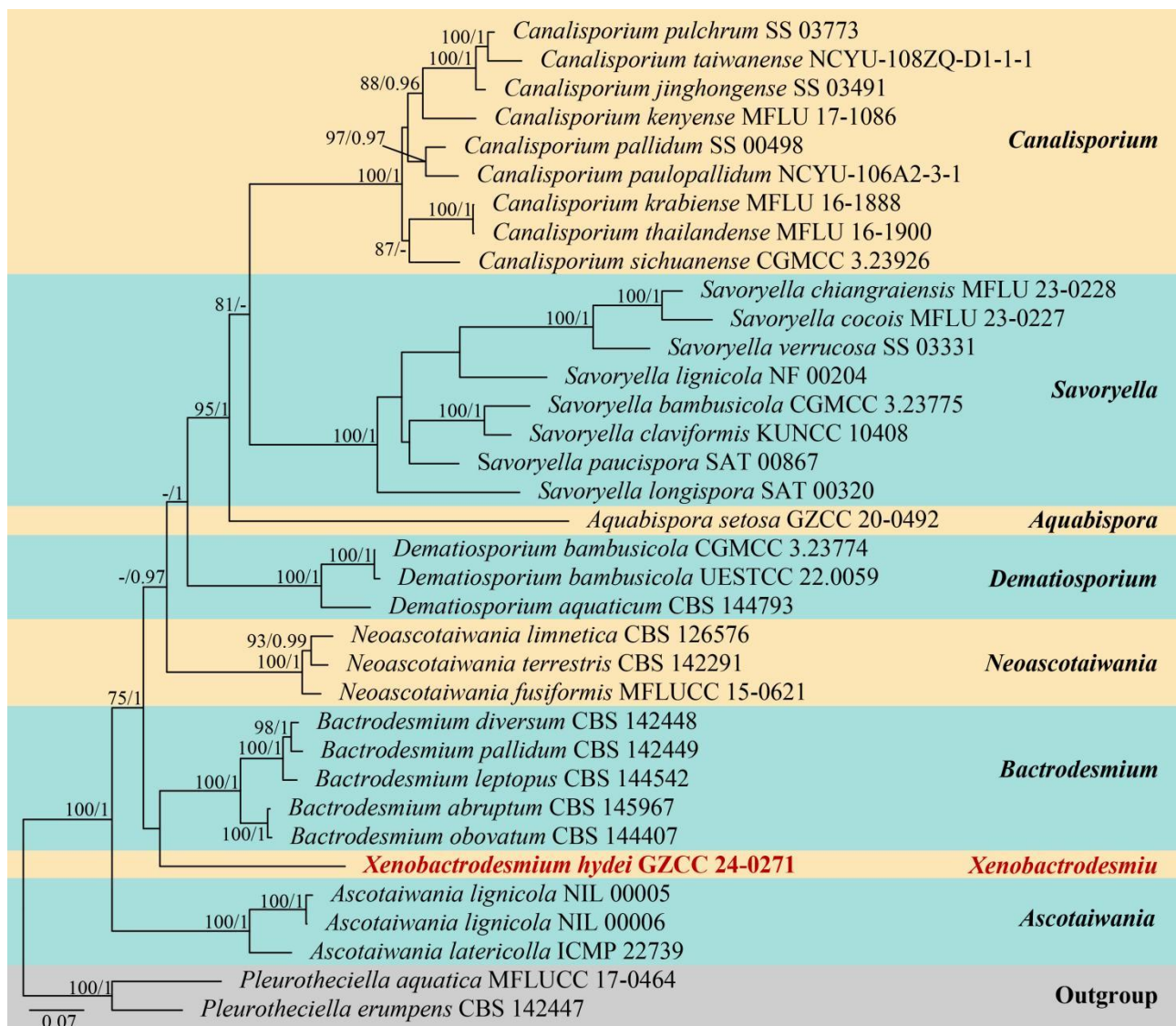


Figure 73 – ML tree based on the combined LSU, ITS and *rpb2* sequences, representing the family *Savoryellaceae*. Bootstrap support values for ML equal to or greater than 75% and PP values equal to or greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Pleurotheciella aquatica* (MFLUCC 17-0464) and *Pleurotheciella erumpens* (CBS 142447). The new taxon is indicated in bold and red.

Culture characteristics – Conidia germinating on PDA within 24 h and germ tubes produced from both ends of conidia. Colonies reaching up to 32 mm diam. after 60 days on PDA media, medium dense, surface rough, circular, edge undulate, blackish brown at center, pale greyish brown at outer ring from above, black at center, pale yellow at outer ring from below.

Material examined – China, Guizhou Province, Qiandongnan Miao and Dong Autonomous Prefecture, Zhenyuan County, Gaoguo River, N 27°14'40", E 108°18'30", elevation 777 m, on decaying wood from a freshwater stream, 27 June 2023, X.J. Xiao, G3 (HKAS 136249, holotype), ex-type culture GZCC 24-0025.

Notes – Sixteen *Menisporopsis* species are listed in Species Fungorum (July 2025). Among them, *Me. ludoviciana*, *Me. kobensis*, *Me. multisetulata*, *Me. pleioetosa*, *Me. profuse* and *Me. trisetulosa* were described without molecular data. *Menisporopsis ludoviciana* has morphological resemblance with *Cryptophialoidea* rather than *Menisporopsis* (Kirk 1985, Kirk & Sutton 1985, Kuthubutheen & Sutton 1985, Yang et al. 2018b). *Menisporopsis kobensis* has longer conidiophores (75–90 µm), larger conidia (22.5–30 × 4–5 µm) and longer setulae (6–10 µm) than our collection. Our collection has longer conidia (17–23 µm) than those of *Me. multisetulata* (12–

18 μm), *Me. pleioetosa* (12–18 μm) and *Me. profusa* (12–15 μm). Besides, conidia of *Me. multisetulata* and *Me. pleioetosa* both have more than 2 setulae on each end (Tsui et al. 1999). Comparing with *Me. trisetulosa*, our collection has much shorter conidiophores ($58\text{--}72 \times 3\text{--}5 \mu\text{m}$ vs. $120\text{--}175 \times 2\text{--}4 \mu\text{m}$). Moreover, *Me. trisetulosa* has 3 setulae, while our collection has 2 setulae (Siboe et al. 1999).

In the phylogenetic tree (Fig. 75), our strain GZCC 24-0025 formed an independent internal clade which is sister to *Menisporopsis anisospora* (CBS 109475), *Me. dinemasporioides* (CGMCC 3.20711) and *Menisporopsis* sp. (LCM1078), indicating it is a phylogenetically distinct species. Therefore, we introduce our collection as a new species.

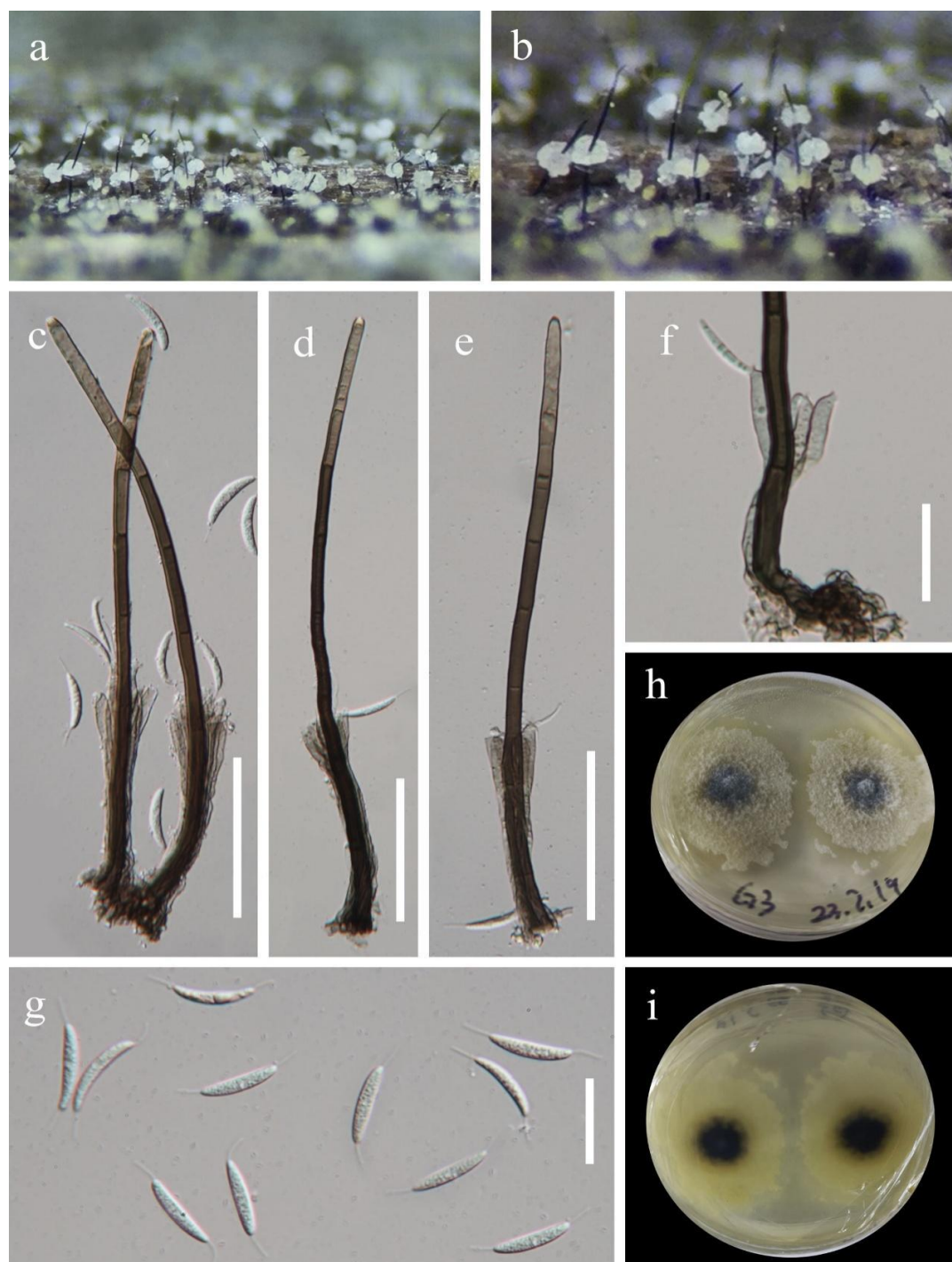


Figure 74 – *Menisporopsis hydei* (HKAS 136249, holotype). a, b Colonies on dead wood surface. c–e Fruiting bodies. f Conidiogenous cells and conidium. g Conidia. h, i Colonies on PDA (h from above, i from below). Scale bars: c–e = 50 μm , f–g = 20 μm .

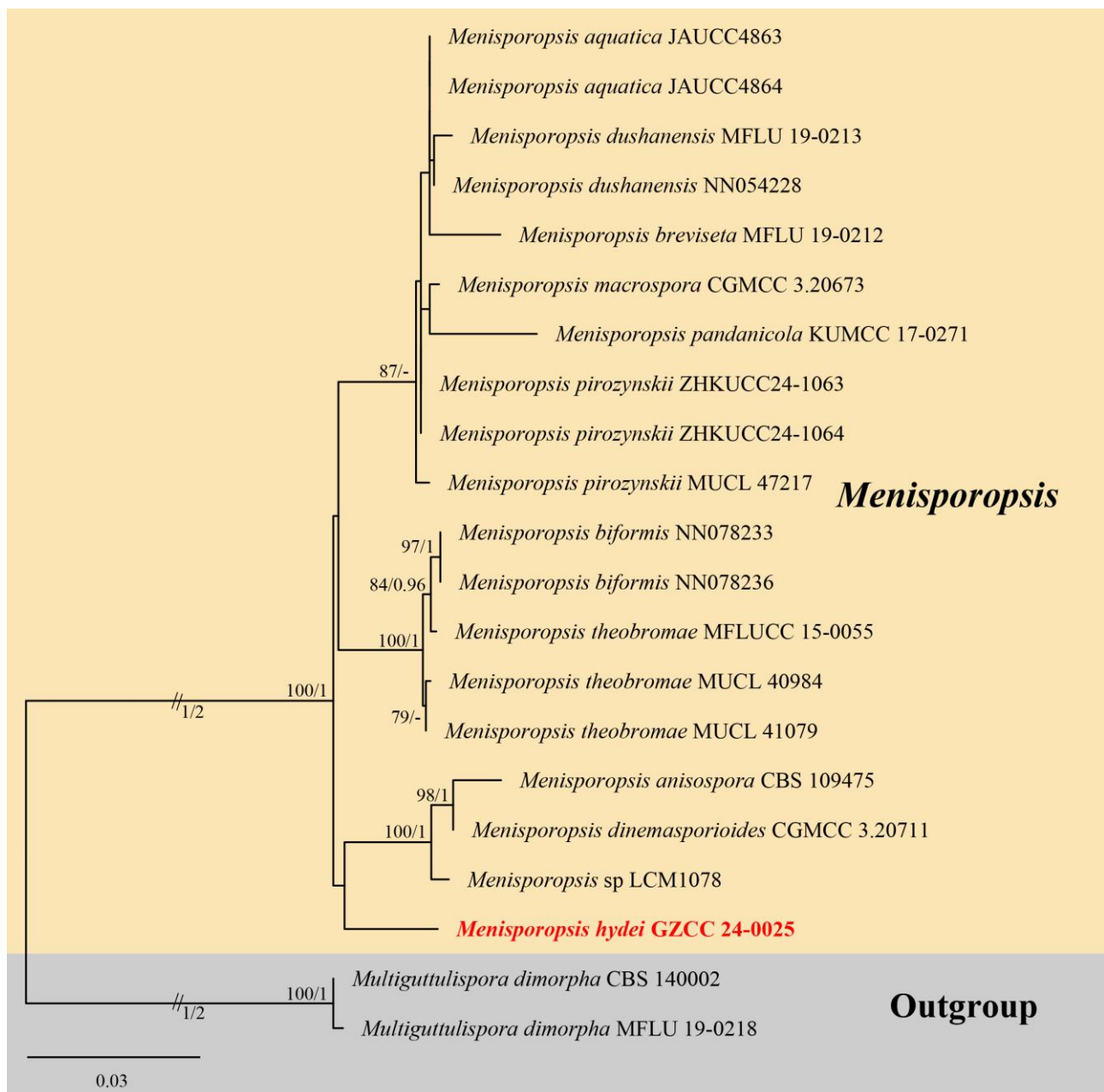


Figure 75 – ML tree based on the combined LSU and ITS sequences. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Multiguttulispora dimorpha* (CBS 140002 and MFLU 19-0218). The new taxon is indicated in bold and red.

Sporoschisma Berk. & Broome, Gard. Chron. 1847 (33): 540 (1847)

Sporoschisma species predominantly found in freshwater habitats (Luo et al. 2016, Yang et al. 2016, Hyde et al. 2019a). Asexual morph of *Sporoschisma* was characterized by macronematous, mononematous, dark brown, unbranched conidiophores composed of a cylindrical stipe and a swollen venter with a long cylindrical neck, present or absent setae, monophialidic conidiogenous cells, and catenate, mostly cylindrical, dematiaceous, septate conidia formed endogenously in basipetal chains (Goh et al. 1997, Sivichai et al. 2000, Luo et al. 2016, Yang et al. 2016, Liu et al. 2024a), while its sexual morph features broadly pyriform ascomata covered with setae, unitunicate, 8-spored, cylindrical to narrow clavate asci, and fusiform, curved, pigmented, septate ascospores (Wu & Diao 2022). Twenty-four records of *Sporoschisma* are listed in Species Fungorum (2025).

***Sporoschisma hydei* X.D. Yu & Jian K. Liu, sp. nov.**

Fig. 76

Fungal Names number: FN; Facesoffungi number: FoF 17843

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 150792

Saprobic on dead branches of bamboo in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: *Colonies* effuse, black, hairy, with glistening conidia in chains. *Setae* 120–370 × 4–7 µm ($\bar{x}$ = 230 × 6 µm, n = 10), arising from the bulbous base, often with 1–3 at the side of conidiophores, capitate, 1–2-septate, smooth-walled, brown, becoming paler towards the apex, straight or slightly flexuous. *Conidiophores* 150–350 × 10–20 µm ($\bar{x}$ = 200 × 15 µm, n = 10), macronematous, mononematous, erect, straight or slightly flexuous, solitary or aggregated in small groups, dark brown to black, composed of a cylindrical stipe, a swollen venter and a phialide stalk. *Conidiogenous cells* monophialidic, integrated, terminal, determinate, dark brown. *Conidia* 30–40 × 10–12 µm ($\bar{x}$ = 35 × 11 µm, n = 30), emerging in a chain inside the tubular collarette, develop basipetally, cylindrical, often truncate and sometimes slightly rounded at both ends, terminal conidia usually rounded at the apex, 3-euseptate, darkened at the septa, dark olivaceous brown to dark brown.

Culture characteristics – Conidia germinating on PDA within 24 h. Colonies reaching about 20 mm diam. after 3 months at 25°C, irregular, raised to umbonate, dense, edge undulate, black from above and below.

Material examined – China, Sichuan Province, Zigong City, Rong County, Hualonggou Bamboo Sea, 29°28'52"N, 104°17'20"E, 625m Elevation, on dead branches of bamboo in terrestrial habitat, 3 November 2022, X.D. Yu, H1 (HKAS 150792, holotype); ex-type culture UESTCC 01.0424.

Notes – The phylogenetic analyses based on ITS, LSU and *tef1-α* sequence data showed that the new collection *Sporoschisma hydei* nested within *Sporoschisma* and formed a distinct lineage (Fig. 77). *Sporoschisma hydei* resembles *Sp. mirabile* in having catenate, cylindrical, 3-septate conidia (Luo et al. 2016). In addition, the conidial size is also similar (30–40 × 10–12 µm vs. 31.5–40.5 × 10.5–11.5 µm) (Luo et al. 2016). However, *Sp. hydei* differs in having dark olivaceous brown to dark brown conidia. Therefore, establishment of the new species is justified by morphology and phylogenetic evidence.

***Pseudodactylariales* Crous**

***Pseudodactylariaceae* Crous**

***Pseudodactylaria* Crous, Persoonia 39: 421 (2017)**

Pseudodactylaria was introduced by Crous et al. (2017) to accommodate the type species *P. xanthorrhoeae*. It is characterized by macronematous, hyaline or brown conidiophores, polyblastic conidiogenous cells with numerous aggregated cylindrical denticles, and cylindrical, fusiform, fusoid-ellipsoid, hyaline, septate or aseptate conidia with or without appendages (Crous et al. 2017, Lin et al. 2018, Hyde et al. 2020a, Lu et al. 2020, Bao et al. 2021, Yang et al. 2023). Ten species are accepted in *Pseudodactylaria* (Species Fungorum 2024), and most of them were reported from freshwater habitats.

***Pseudodactylaria hydei* X.J. Xiao, N.G. Liu & Y.Z. Lu, sp. nov.**

Fig. 78

Fungal Names number: FN 572897; Facesoffungi number: FoF 17840

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 136238

Saprobic on submerged rotting wood from a freshwater stream. Sexual morph: Undetermined. Asexual morph: *Colonies* on natural substrate effuse, yellow to golden brown, shiny. *Mycelium* immersed in the substratum, composed of branched, septate, hyaline hyphae. *Conidiophores* 28–60 × 3–6 µm ($\bar{x}$ = 47.5 × 5 µm, n = 20), macronematous, mononematous, arising from creeping

hyphae, erect, solitary, flexuous, simple or branched, septate, hyaline, filled with numerous small globose globules, thick-walled. *Conidiogenous cells* 11.5–45 × 3–5.5 µm ($\bar{x}$ = 27 × 4.3 µm, n = 20), polyblastic, integrated, terminal, sympodial, apical part forming a rachis with numerous, cylindrical denticles, hyaline. *Conidia* 20–26 × 2.5–4 µm ($\bar{x}$ = 23 × 3.5 µm, n = 30), acropleurogenous, solitary, fusiform, hyaline, with an indistinct median septum, smooth.



Figure 76 – *Sporoschisma hydei* (HKAS 150792, holotype). a–c Colonies on natural substratum. d–h Conidiophores and conidia. i–j Conidia. k, l Colony on PDA from above and below. Scale bars: g = 50 µm, d–f, h–j = 30 µm.

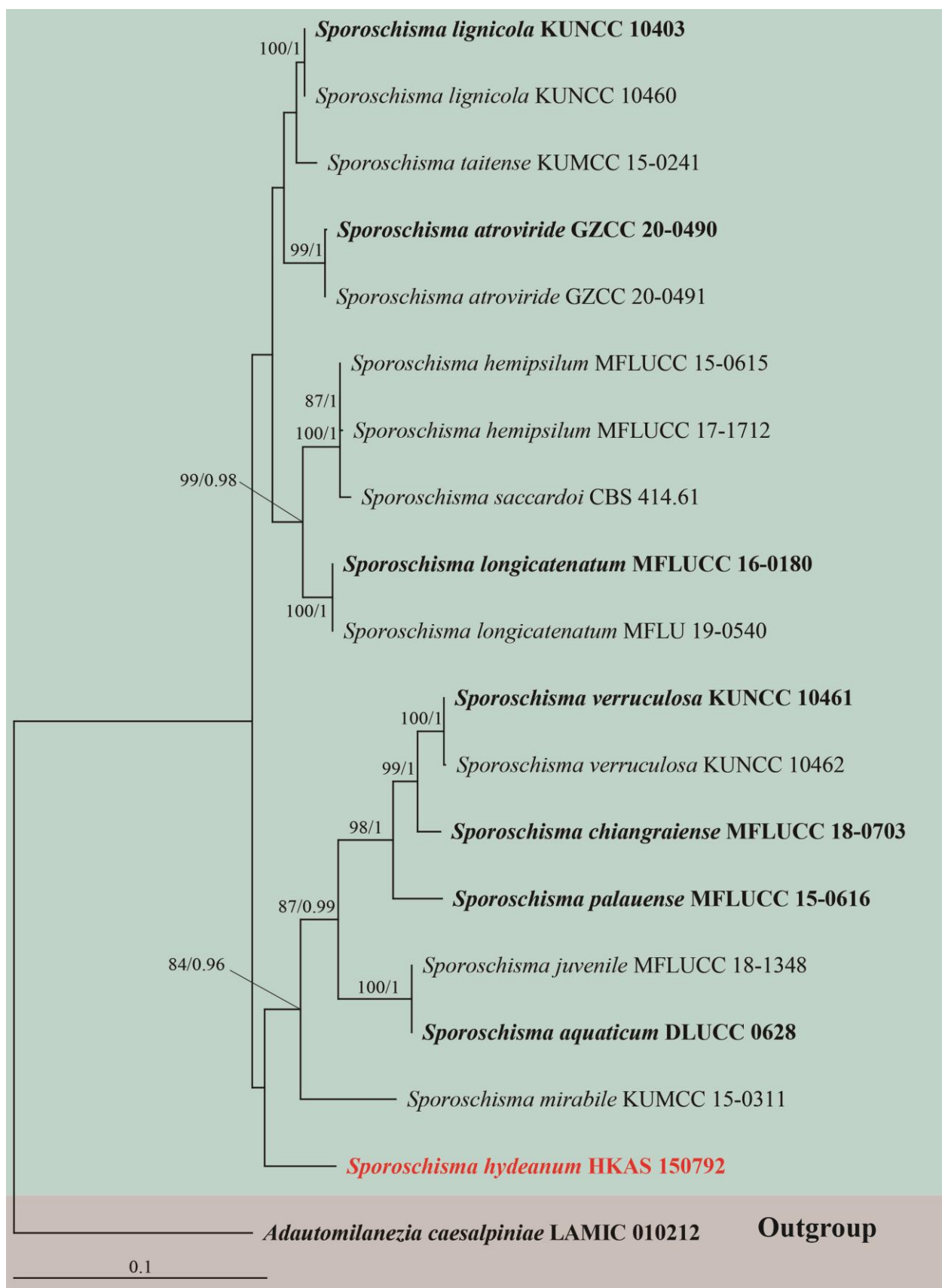


Figure 77 – ML tree based on the combined LSU, ITS and *tef1-α* sequences, representing *Sporoschisma*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Adautomilanezia caesalpiniae* (LAMIC 010212). Ex-type strains are indicated in bold. The new taxon is indicated in bold and red.

Culture characteristics – Conidia germinating on PDA within 12 h and germ tubes produced from both ends of the conidia. Colonies reaching up to 22 mm diam. after 28 days, medium dense, flat, circular, edge entire, dark to blackish brown at the center, paler at the outer ring from above, dark to blackish brown at the outer ring, paler at the center from below.

Material examined – Material examined – China, Guizhou Province, Qiannan Buyi and Miao Autonomous Prefecture, Duyun County, N 26°23'4", E 107°21'7", elevation 1245 m, on decaying wood from a freshwater stream, 5 October 2023, X.J. Xiao, DPS12 (HKAS 136238, holotype), ex-type culture GZCC 24-0012.

Notes – Ten accepted species in *Pseudodactylaria* and all have DNA sequence data. In our phylogenetic tree (Fig. 79), the strain GZCC 24-0012 grouped together with *Ps. hyalotunicata* (HKUCC2593) and *Ps. xanthorrhoeae* (CBS 143414) with weak support. Crous et al. (2017) transferred *Dactylaria hyalotunicata* (Tsui et al. 1997) to *Pseudodactylaria* as *Ps. hyalotunicata* based on LSU phylogeny. Our collection has similar morphology with *Ps. hyalotunicata* and *Ps. xanthorrhoeae* including in size of conidiophores ($28\text{--}60 \times 3\text{--}6 \mu\text{m}$ vs. $30\text{--}60 \times 4\text{--}5 \mu\text{m}$ vs. $20\text{--}50 \times 4\text{--}5 \mu\text{m}$) and conidia ($20\text{--}26 \times 2.5\text{--}4 \mu\text{m}$ vs. $20\text{--}25 \times 2.5\text{--}3 \mu\text{m}$ vs. $22\text{--}27 \times 3.5 \mu\text{m}$). However, *Ps. hyalotunicata* and *Ps. xanthorrhoeae* have a hyaline, gelatinous conidial sheath, which is absent in our collection (Tsui et al. 1997, Crous et al. 2017). In addition, there are 11 bp (including 2 gaps, totally 816 bp) and 6 bp (without gaps) differences for LSU sequences between HKUCC2593, CBS 143414 and our strain, respectively. ITS sequence is lacking for *Ps. hyalotunicata*. Therefore, we introduce our collection as a new species mainly based on its distinct phylogenetic placement.

Subclass Xylariomycetidae O.E. Erikss & Winka

Xylariales Nannf.

Cainiaceae J.C. Krug

Longiappendispora Mapook & K.D. Hyde, Fungal Diversity 101: 139 (2020)

Longiappendispora is a monotypic genus introduced by Mapook et al. (2020) based on the type *L. chromolaenae*, which was isolated from dead stems of *Chromolaena odorata* in Thailand. *Longiappendispora* is represented by its sexual morph and features immersed, unilocular, globose to subglobose, coriaceous, ostiolate ascomata, 8-spored, unitunicate, cylindrical to broadly filiform, short-pedicellate asci, and uniseriate, ellipsoid to broadly fusiform, brown to dark brown, 1-septate, guttulate ascospores with polar appendages (Mapook et al. 2020). *Longiappendispora* is classified in *Cainiaceae* (*Xylariales*, *Sordariomycetes*). In this study, we introduce a second species of *Longiappendispora*.

Longiappendispora keviniana Y.X. Yu & Jian K. Liu, sp. nov.

Fig. 80

Fungal Names number: FN573021; Facesoffungi number: FoF 17824

Etymology – The specific epithet “keviniana” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 149987

Saprobic on dead stems of *Saccharum arundinaceum*, forming black round spots. Sexual morph: *Ascomata* 200–438 μm high, 250–483 μm diam. ($\bar{x} = 352 \times 399 \mu\text{m}$, $n = 10$), immersed beneath clypeus, unilocular, globose to subglobose, coriaceous, solitary or scattered, sometimes gregarious. *Ostiole* central. *Peridium* 14–25 μm wide, composed of thick-walled, hyaline to brown cells, *texture angularis*. *Hamathecium* 2.9–4.2 μm ($\bar{x} = 3.8 \mu\text{m}$, $n = 20$), hyaline, numerous, filamentous, branched, septate, cellular pseudoparaphyses. *Asci* 149–225 $\times$ 11–14 μm ($\bar{x} = 195 \times 12 \mu\text{m}$, $n = 30$), 8-spored, unitunicate, long-cylindrical, short-pedicellate, with a J+, trapezoidal shape apical ring, bluing in Melzer’s reagent. *Ascospores* 20–28.5 $\times$ 7–9 μm ($\bar{x} = 23 \times 8 \mu\text{m}$, $n = 30$), uniseriate, ellipsoid to broadly fusiform, tapering towards narrow ends, hyaline when immature, becoming brown to dark brown when mature, 1-septate, with a guttule in each cell, sometimes slightly constricted septum, tapering at the ends with a hyaline appendage, smooth-walled. Asexual morph: Undetermined.

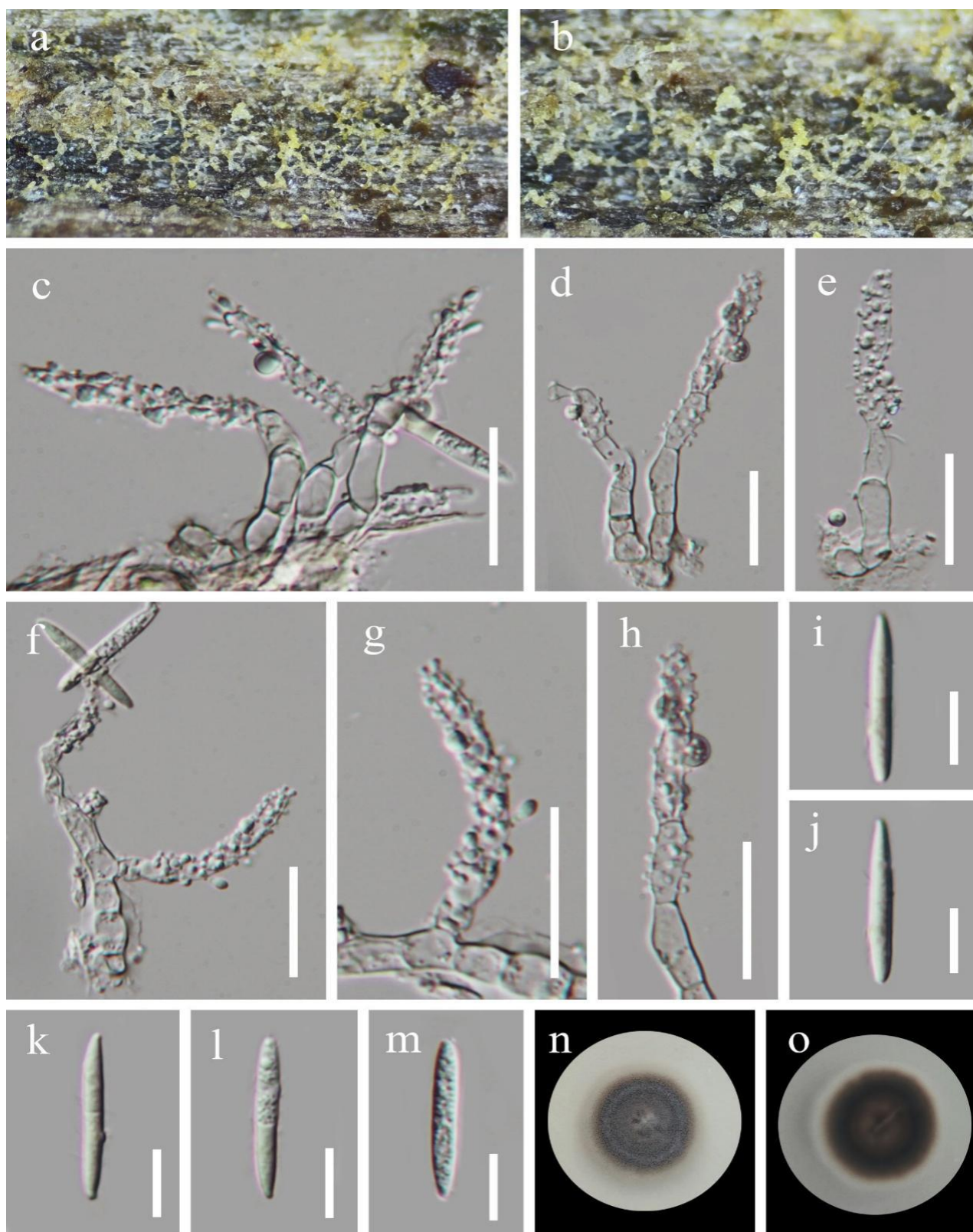


Figure 78 – *Pseudodactylaria hydei* (HKAS 136238, holotype). a, b Colonies on dead wood surface. c–h Conidiophores and conidiogenous cells. i–m Conidia. n, o Colony on PDA (n from above, o from below). Scale bars: c–h = 20 μ m, i–m = 10 μ m.

Culture characteristics – Ascospores germinating on PDA within 24 h. Colonies growing well on PDA and attaining a diameter about 50 mm after 7 d at 25 °C, circular, medium dense, flat to raised, margin entire, white to pale yellow from above and below.

Material examined – China, Sichuan Province, Mianyang City, Qiqu Mountain scenic spot, 31°40'23"N, 105°11'1"E, 560 m elevation, on dead stems of *Saccharum arundinaceum* in terrestrial habitat, 08 October 2023, Y.X. Yu, MY14A (HKAS 149987, holotype), ex-type culture CGMCC 3.29113 = UESTCC 25.0253; *ibid.*, MY14B (HUEST 25.0067, isotype), ex-isotype UESTCC 25.0254.

Figure 79 – ML tree based on the combined LSU and ITS sequences, representing *Pseudodactylaria*. Bootstrap support values for ML greater than 75% and PP greater than 0.95 are given near nodes as ML-BS/PP. The tree is rooted with *Neoschizothecium curvisporum* (CBS 507.50) and *Zopfiella tardifaciens* (CBS 670.82). The new taxon is indicated in bold and red.

Vamsapriyaceae Y.R. Sun, Yong Wang bis & K.D. Hyde
Pseudocatenuliconidia Y.X. Yu & Jian K. Liu, gen. nov.

Fungal Names number: FN 573024

Etymology – The specific epithet “Pseudo” refers to its morphological similarity with *Catenuliconidia*.



Figure 80 – *Longiappendispora keviniana* (HKAS 149987, holotype). a Habitat of the host surface. b, c Ascomata immersed in the host surface. d, e Vertical section through ascoma. f Vertical section of the peridium. g Hamathecium. h–l Asci((l) with J+, wedge-shaped rings (Stained in Melzer’s reagent)). m–u Ascospores. v Germinating ascospore. w, x Colony on PDA above and below. Scale bars: d, e = 100 μ m, h–l = 20 μ m, f–g, m–v = 10 μ m.



Figure 81 – *Pseudocatenuliconidia hydei* (HKAS 149988, holotype). a–c Colonies on natural substrate. d, e Conidiophore and conidia. f–j Conidiogenous cells and developing conidia. k–o Conidia. p Germinated conidium. Scale bars: d–e, i–j = 20 μ m, f–h, k–p = 10 μ m.

Saprobic in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on natural substrate effuse, dark brown to black, velvety. Mycelium immersed, composed of hyaline, branched, septate, smooth hyphae. Conidiophores macronematous, mononematous, fasciculate, erect, cylindrical, dark brown, septate, thick-walled. Conidiogenous cells monoblastic,

integrated, terminal, truncated the apex, clavate, brown to dark brown. *Conidia* acrogenous, catenate, ellipsoid to cylindrical, rounded or subtruncate at the apex, truncate at the base, dark brown, 1-septate at the middle, septa thickened and darkened, slightly constricted at the septa, with a globule in each cell, verrucose.

Type species – *Pseudocatenuliconidia hydei* Y.X. Yu & Jian K. Liu

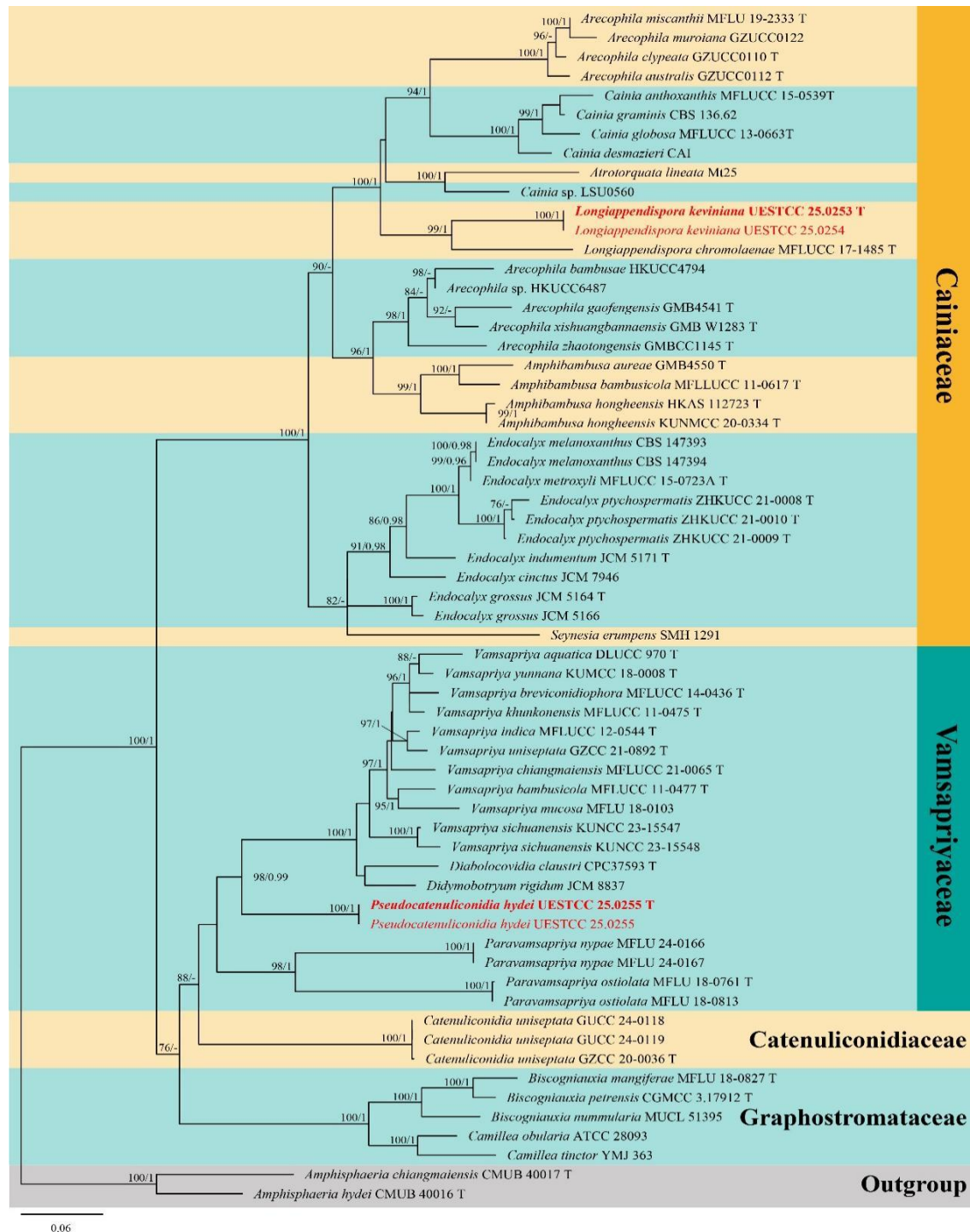


Figure 82 – ML tree based on the combined ITS, LSU, *rpb2* and *tub2* sequences, representing the families *Barrmaeliaceae*, *Cainiaceae* and *Vamsapriyaceae*. Bootstrap support values for ML equal to or greater than 70% are placed above the branches, and PP values equal to or greater than 0.95 are indicated in bold branches. The tree is rooted with *Amphisphaeria chiangmaiensis* (CMUB 40017) and *Amphisphaeria hydei* (CMUB 40016). Ex-type strains are marked with “T”. The new taxa are indicated in red.

Pseudocatenuliconidia hydei Y.X. Yu & Jian K. Liu, sp. nov.

Fig. 81

Fungal Names number: FN 573025

Etymology – The specific epithet “hydei” is in honor of Kevin D. Hyde for his great contributions to mycology and in celebration of his 70th birthday.

Holotype – HKAS 149988

Saprobic on dead stems of *Cinnamomum camphora* in terrestrial habitat. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown to black, velvety. *Mycelium* immersed, composed of hyaline, branched, septate, smooth hyphae. *Conidiophores* 73–170 × 7–9 µm, macronematous, mononematous, fasciculate, erect, cylindrical, dark brown, septate, thick-walled. *Conidiogenous cells* 28–47 × 6.5–9 µm ($\bar{x}$ = 37 × 8 µm, n = 30), monoblastic, integrated, terminal, truncated the apex, clavate, brown to dark brown. *Conidia* 21–37 × 7–9.8 µm ($\bar{x}$ = 29 × 8 µm, n = 30), acrogenous, catenate, formed in acropetal chains, ellipsoid to cylindrical, rounded or subtruncate at the apex, truncate at the base, 2.3–5.8 µm wide, dark brown, 1-septate at the middle, septa thickened and darkened, slightly constricted at the septa, with a globule in each cell, verrucose.

Culture characteristics – Conidia germinating on PDA within 24 h. Colonies reaching about 30 mm diam. after 7 d at 25 °C, circular, medium dense, flat or center raised, margin entire, white from above, pale yellow from below.

Material examined – China, Sichuan Province, Mianyang City, Qiqu Mountain scenic spot, 31°40'23"N, 105°11'1"E, 560 m elevation, on dead stems *Cinnamomum camphora* in terrestrial habitat, 08 October 2023, Y.X. Yu, MY39A (HKAS 149988, holotype), ex-type culture CGMCC 3.29114 = UESTCC 25.0255; *ibid.*, MY39B (HUEST 25.0069, isotype), ex-isotype culture UESTCC 25.0256.

Notes – *Pseudocatenuliconidia* closely resembles *Catenuliconidia* morphologically, as both possess fasciculate conidiophores, monoblastic conidiogenous cells, and catenate, ellipsoid to cylindrical, 1-septate conidia with darkened and thickened septum (Yuan et al. 2020, Sun et al. 2025). However, despite these morphological similarities, *Catenuliconidia* and *Pseudocatenuliconidia* are phylogenetically distinct. *Catenuliconidia* is classified within *Catenuliconidiaceae* (Sun et al. 2025), whereas *Pseudocatenuliconidia* is a member of *Vamsapriyaceae* (Fig. 82).

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DECLARATION ON CONFLICT OF INTEREST

This manuscript includes co-authors who are members of the editorial board of Mycosphere. These authors were not involved in the peer review process or in the editorial decision-making related to this manuscript. The authors declare that there are no other conflicts of interest regarding the publication of this work.

REFERENCES

Ariyawansa HA, Jaklitsch WM, Voglmayr H. 2018 – Additions to Taiwan fungal flora 1: *Neomassariaceae* fam. nov. *Cryptogamie, Mycologie* 39, 359–372.

- Arzanlou M, Groenewald JZ, Gams W, Braun U et al. 2007 – Phylogenetic and morphotaxonomic revision of *Ramichloridium* and allied genera. *Studies in Mycology* 58, 57–93.
- Badalyan SM, Barkhudaryan A, Rapior S. 2022 – Medicinal macrofungi as cosmeceuticals: a review. *International Journal of Medicinal Mushrooms* 24, 1–13.
- Bao DF, Hyde KD, McKenzie EHC, Jeewon R et al. 2021 – Biodiversity of lignicolous freshwater hyphomycetes from China and Thailand and description of sixteen species. *Journal of Fungi* 7(8), 669.
- Bao DF, McKenzie EHC, Bhat DJ, Hyde KD et al. 2020 – *Acrogenospora* (Acrogenosporaceae, Minutisphaerales) appears to be a very diverse genus. *Frontiers in Microbiology* 11, 1606.
- Barron GL. 1968 – The genera of hyphomycetes from soil. Williams & Wilkins, Baltimore, USA.
- Bhat DJ, Kendrick B. 1993 – Twenty-five new conidial fungi from the Western Ghats and the Andaman Islands (India). *Mycotaxon* 49, 19–90.
- Blackwell M. 2011 – The fungi: 1, 2, 3 ... 5.1 million species? *American Journal of Botany* 98, 426–438.
- Boehm EWA, Mugambi GK, Miller AN, Huhndorf SM et al. 2009 – A molecular phylogenetic reappraisal of the Hysteriaceae, Mytiliniaceae and Gloniaceae (Pleosporomycetidae, Dothideomycetes) with keys to world species. *Studies in Mycology* 64, 49–83.
- Boonmee S, D'souza MJ, Luo ZL, Pinruan U et al. 2016 – Dictyosporiaceae fam. nov. *Fungal Diversity* 80, 457–482.
- Boonmee S, Rossman AY, Liu JK, Li WJ et al. 2014 – Tubeufiales, ord. nov., integrating sexual and asexual generic names. *Fungal Diversity* 68, 239–298.
- Boonmee S, Wanasinghe DN, Calabon MS, Huanraluek N et al. 2021 – Fungal diversity notes 1387–1511: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 111, 1–335.
- Bunbury-Blanchette AL, Walker AK. 2019 – *Trichoderma* species show biocontrol potential in dual culture and greenhouse bioassays against Fusarium basal rot of onion. *Biological Control* 130, 127–135.
- Calabon MS, Hyde KD, Jones EBG, Luo ZL et al. 2022 – Freshwater fungal numbers. *Fungal Diversity* 114, 3–235.
- Capella-Gutierrez S, Silla-Martinez JM, Gabaldon T. 2009 – trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics* 25, 1972–1973.
- Chaiwan N, Lu YZ, Tibpromma S, Bhat DJ et al. 2017 – *Neotubeufia* gen. nov. and *Tubeufia guangxiensis* sp. nov. (Tubeufiaceae) from freshwater habitats. *Mycosphere* 8, 1443–1456.
- Chang HS. 1995 – Notes on Taiwan dematiaceous hyphomycetes, some species of the genera *Exserticlava*, *Craspedodidymum* and *Hermatomyces*. *Botanical bulletin of Academia Sinica* 36, 243–246.
- Chaverri P, Fabiano BR, Walter J, Romina G et al. 2015 – Systematics of the *Trichoderma harzianum* species complex and the re-identification of commercial biocontrol strains. *Mycologia* 107, 558–590.
- Chen JH, Hu DM, Song HY, Zhai ZJ et al. 2022 – *Menisporopsis aquatica* sp. nov. (Sordariomycetes, Chaetosphaeriales, Chaetosphaeriaceae), from freshwater habitat in China. *Biodiversity Data Journal* 10, e91008.
- Chen XM, Tang X, Du TY, Lu YZ et al. 2024 – Two new species of *Rhodoveronaea* (Rhamphoriales, Ascomycota) from terrestrial habitats in China. *Phytotaxa* 638, 49–60.
- Corda ACJ. 1837 – Icones fungorum hucusque cognitorum. 1, 1–32.
- Corda ACJ. 1854 – Icones fungorum hucusque cognitorum. 6, 1–91.
- Crous PW, Costa MM, Kandemir H, Vermaas M et al. 2023 – Fungal Planet description sheets: 1550–1613. *Persoonia* 51, 280–417.
- Crous PW, Cowan DA, Maggs-Kölling G, Yilmaz N et al. 2020a – Fungal Planet description sheets: 1112–1181. *Persoonia* 45, 251–409.
- Crous PW, Osieck ER, Jurjević Ž, Boers J et al. 2021 – Fungal Planet description sheets: 1284–1382. *Persoonia* 47, 178–374.

- Crous PW, Schumacher RK, Akulov A, Thangavel R et al. 2019a – New and interesting fungi. 2. Fungal Systematics and Evolution 3, 57–134.
- Crous PW, Wingfield MJ, Burgess TI, Carnegie AJ et al. 2017 – Fungal Planet description sheets: 625–715. Persoonia 39, 270–467.
- Crous PW, Wingfield MJ, Jurjevic Z, Balashov S et al. 2024 – Fungal Planet description sheets: 1697–1780. Fungal Systematics and Evolution 14, 325–577.
- Crous PW, Wingfield MJ, Lombard L, Roets F et al. 2019b – Fungal Planet description sheets: 951–1041. Persoonia 43, 223–425.
- Crous PW, Wingfield MJ, Richardson DM, Le Roux JJ et al. 2016 – Fungal Planet description sheets: 400–468. Persoonia 36, 316–458.
- Crous PW, Wingfield MJ, Schumacher RK, Akulov A et al. 2020b – New and Interesting Fungi. 3. Fungal Systematics and Evolution 6, 157–231.
- Da Cruz ACR, dos Santos Santa Izabel T, Leão-Ferreira SM, Gusmão LFP. 2009 – Conidial fungi from the semi-arid Caatinga biome of Brazil. New species and new records of *Helicosporium*. Mycotaxon 110, 53–64.
- Da Cruz ACR, Marques MFO, Gusmão LFP 2014 – Conidial fungi from the semi-arid Caatinga biome of Brazil. The genus *Menisporopsis*. Acta Botanica Brasilica 28, 339–345.
- Dai DQ, Phookamsak R, Wijayawardene NN, Li WJ et al. 2017 – Bambusicolous fungi. Fungal Diversity 82, 1–105.
- Dayarathne MC, Jones EBG, Maharachchikumbura SSN, Devadatha B et al. 2020 – Morpho-molecular characterization of microfungi associated with marine based habitats. Mycosphere 11, 1–188.
- De Gruyter J, Woudenberg JH, Aveskamp MM, Verkley GJ et al. 2013 – Redisposition of phoma-like anamorphs in Pleosporales. Studies in Mycology 75, 1–36.
- De Gruyter J, Woudenberg JHC, Aveskamp MM, Verkley GJM et al. 2010 – Systematic reappraisal of species in *Phoma* section *Paraphoma*, *Pyrenochaeta* and *Pleurophoma*. Mycologia 102, 1066–1081.
- De Silva NI, Hyde KD, Lumyong S, Phillips AJL et al. 2022 – Morphology, phylogeny, host association and geography of fungi associated with plants of Annonaceae, Apocynaceae and Magnoliaceae. Mycosphere 13, 955–1076.
- De Silva NI, Lumyong S, Hyde KD, Bulgakov T et al. 2016 – Mycosphere Essays 9: Defining biotrophs and hemibiotrophs. Mycosphere 7, 545–559.
- De Vries GA. 1962 – *Cyphellophora laciniata* nov. gen., nov. sp. and *Dactylium fusarioides* Fragoso et Ciferri. Mycopathologia et Mycologia Applicata 16, 47–54.
- Degenkolb T, Fog Nielsen K, Dieckmann R, Branco-Rocha F et al. 2015 – Peptaibol, secondary-metabolite, and hydrophobin pattern of commercial biocontrol agents formulated with species of the *Trichoderma harzianum* complex. Chemistry Biodiversity 12, 662–684.
- Descals E, Nawawi A, Webster J. 1976 – Developmental studies in *Actinospora* and three similar aquatic hyphomycetes. Transactions of the British Mycological Society 67, 207–222.
- Diederich P, Etayo J. 2024 – *Berkleasmium*. Flora of Lichenicolous Fungi 2, 90–92.
- Diederich P. 2015 – Two new lichenicolous species of *Sclerococcum* (asexual Ascomycetes) growing on Graphidaceae. Bulletin de la Société des naturalistes luxembourgeois 117, 35–42.
- Dong W, Hyde KD, Doilom M, Yu XD et al. 2020a – *Pseudobactrodesmium* (Dactylosporaceae, Eurotiomycetes, Fungi) a novel lignicolous genus. Frontiers in Microbiology 11, 456.
- Dong W, Wang B, Hyde KD, McKenzie EHC et al. 2020b – Freshwater Dothideomycetes. Fungal Diversity 105, 319–575.
- Du TY, Karunarathna SC, Tibpromma S, Hyde KD et al. 2024 – *Melomastia* (Dothideomycetes, Ascomycota) species associated with Chinese *Aquilaria* spp. MycoKeys 111, 65–86.
- Ellis MB. 1971 – Dematiaceous hyphomycetes. Commonwealth Mycological Institute, Kew, Surrey, England.
- Gao JM, Yang CL, Wang JY, Xia JW et al. 2016 – *Helicoma jianfenglingense* sp. nov. and *Cubasina* and *Endophragmiella* species new to China. Mycotaxon 131, 351–356.

- Gao L, Ma Y, Zhao W, Wei Z et al. 2015 – Three new species of *Cyphellophora* (Chaetothyriales) associated with sooty blotch and flyspeck. PLoS One 10, e0136857.
- Giraldo A, Crous PW, Schumacher RK, Cheewangkoon R et al. 2017 – The Genera of Fungi—G3: *Aleurocystis*, *Blastacervulus*, *Clypeophysalospora*, *Licrostroma*, *Neohendersonia* and *Spumatoria*. Mycological Progress 16, 325–348.
- Glass NL, Donaldson GC. 1995 – Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. Applied and Environmental Microbiology 61, 1323 – 1330.
- Goh TK, Ho WH, Hyde KD, Umali TE. 1997 – New records and species of *Sporoschisma* and *Sporoschismopsis* from submerged wood in the tropics. Mycological Research 101, 1295–1307.
- Goh TK, Hyde KD, Ho WH. 1999 – A revision of the genus *Dictyosporium*, with descriptions of three new species. Fungal Diversity 2, 65–100.
- Goh TK, Hyde KD, Tsui KM. 1998 – The hyphomycete genus *Acrogenospora*, with two new species and two new combinations. Mycological Research 102, 1309–1315.
- Gu X, Wang R, Sun Q, Wu B et al. 2020 – Four new species of *Trichoderma* in the *Harzianum* clade from northern China. MycoKeys 73, 109–132.
- Hashimoto A, Matsumura M, Hirayama K, Tanaka K. 2017 – Revision of Lophiotremataceae (*Pleosporales*, *Dothideomycetes*): *Aquasubmersaceae*, *Cryptocoryneaceae*, and *Hermatomycetaceae* fam. nov. Persoonia 39, 51–73.
- Hernández-Restrepo M, Gené J, Castañeda-Ruiz RF, Mena-Portales J et al. 2017 – Phylogeny of saprobic microfungi from Southern Europe. Studies in Mycology 86, 53–97.
- Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN et al. 2020a – Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. Mycosphere 11, 1553–2107.
- Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN et al. 2020b – Refined families of Dothideomycetes: orders and families incertae sedis in Dothideomycetes. Fungal Diversity 105, 17–318.
- Hu YF, Liu JW, Luo XX, Xu ZH et al. 2023 – Multi-locus phylogenetic analyses reveal eight novel species of *Distoseptispora* from southern China. Microbiology Spectrum 11, e02468-23.
- Hughes SJ, Nag Raj TR. 1973 – New Zealand fungi. 20. *Fusichalara* gen. nov. New Zealand Journal of Botany 11, 661–671.
- Hughes SJ. 1952 – Fungi from the Gold Coast. I. Mycological Papers 48, 1–91.
- Hyde KD, Chaiwan N, Norphanphoun C, Boonmee S et al. 2018 – Mycosphere notes 169–224. Mycosphere 9, 271–430.
- Hyde KD, Dong Y, Phookamsak R, Jeewon R et al. 2020a – Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 100, 5–277.
- Hyde KD, Hongsanan S, Jeewon R, Bhat DJ et al. 2016 – Fungal diversity notes 367–490: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 80, 1–270.
- Hyde KD, Noorabadi MT, Thiyagaraja V, He MQ et al. 2024 – The 2024 Outline of Fungi and fungus-like taxa. Mycosphere 15, 5146–6239.
- Hyde KD, Norphanphoun C, Ma J, Yang HD et al. 2023 – Mycosphere notes 387–412 – novel species of fungal taxa from around the world. Mycosphere 14, 663–744.
- Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ et al. 2020b – Refined families of Sordariomycetes. Mycosphere 11, 305–1059.
- Hyde KD, Tennakoon DS, Jeewon R, Bhat DJ et al. 2019a – Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 96, 1–242.
- Hyde KD, Xu JC, Rapior S, Jeewon R et al. 2019b – The amazing potential of fungi: 50 ways we can exploit fungi industrially. Fungal Diversity 97, 1–136.
- Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J et al. 2015 – The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74, 3–18.

- Jayasiri SC, Hyde KD, Jones EBG, Lu YZ. 2017 – *Neohelicosporium fusisporum* sp. nov. (*Tubeufiaceae*) and a first record of a sexual morph within *Neohelicosporium*. *Studies in Fungi* 2, 210–217.
- Jayawardena RS, Hyde KD, Chen YJ, Papp V et al. 2020 – One stop shop IV: taxonomic update with molecular phylogeny for important phytopathogenic genera: 76–100 (2020). *Fungal Diversity* 103, 87–218.
- Jeewon R, Hyde KD. 2016 – Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. *Mycosphere* 7, 1669–1677.
- Kirk PM, Sutton BC. 1985 – A reassessment of the anamorph genus *Chaetopsina* (*Hyphomycetes*). *Transactions of the British Mycological Society* 85, 709–717.
- Kirk PM. 1985 – New or interesting microfungi XIV. Dematiaceous hyphomycetes from Mt Kenya. *Mycotaxon* 23, 305–352.
- Koukol O, Delgado G, Hofmann TA, Piepenbring M. 2018 – Panama, a hot spot for *Hermatomyces* (*Hermatomycetaceae*, *Pleosporales*) with five new species, and a critical synopsis of the genus. *IMA Fungus* 9, 107–141.
- Kularathnage ND, Tennakoon DS, Zhu X, Zhou J et al. 2023 – Reinstating *Dyfrulomyces* and introducing *Melomastia pyriformis* sp. nov. (*Pleurotremataceae*, *Dyfrulomycetales*) from Guangdong Province, China. *Current Research in Environmental & Applied Mycology* 13, 426–438.
- Kuo CH, Hsieh SY, Goh TK. 2024 – A new species of *Fusichalara* (*Sclerococcaceae*, *Eurotiomycetes*) from Taiwan. *Mycoscience* 65, 199–207.
- Kuthubutheen AJ, Sutton BC. 1985 – *Cryptophiale* from Malaysia. *Transactions of the British Mycological Society* 84, 303–306.
- Larsson A. 2014 – AliView: a fast and lightweight alignment viewer and editor for large datasets. *Bioinformatics* 30, 3276–3278.
- Lebreton A, Zeng Q, Miyauchi S, Kohler A et al. 2021 – Evolution of the mode of nutrition in symbiotic and saprotrophic fungi in forest ecosystems. *Annual Review of Ecology, Evolution, and Systematics* 52, 385–404.
- Li L, Du HZ, Thiyagaraja V, Bhat DJ et al. 2024 – Two novel freshwater hyphomycetes, in *Acrogenospora* (*Minutisphaerales*, *Dothideomycetes*) and *Conioscypha* (*Conioscyphales*, *Sordariomycetes*) from Southwestern China. *Mycoskeys* 101, 249–273.
- Li LL, Shen HW, Bao DF, Wanasinghe DN et al. 2022a – The plethora of *Tubeufiaceae* in lakes of the northwestern Yunnan plateau, China. *Frontiers in Microbiology* 13, 1056669.
- Li WL, Liang RR, Dissanayake AJ, Liu JK. 2023 – *Mycosphere* notes 413–448: *Dothideomycetes* associated with woody oil plants in China. *Mycosphere* 14, 1436–1529.
- Li WL, Liu ZP, Zhang T, Dissanayake AJ et al. 2021b – Additions to *Distoseptispora* (*Distoseptisporaceae*) associated with submerged decaying wood in China. *Phytotaxa* 520, 75–86.
- Li WL, Maharachchikumbura SSN, Cheewangkoon R, Liu JK. 2022b – Reassessment of *Dyfrulomyces* and four new species of *Melomastia* from Olive (*Olea europaea*) in Sichuan Province, China. *Journal of Fungi* 8, 76.
- Lin CG, McKenzie EHC, Bhat DJ, Liu JK et al. 2018 – *Pseudodactylaria brevis* sp. nov. from Thailand confirms the status of *Pseudodactylariaceae*. *Phytotaxa* 369, 241–250.
- Linder DH. 1929 – A monograph of the helicosporous fungi imperfecti. *Annals of the Missouri Botanical Garden* 16, 227–388.
- Liu JK, Chomnunti P, Cai L, Phookamsak R et al. 2010 – Phylogeny and morphology of *Neodeightonia palmicola* sp. nov. from palms. *Sydowia* 62, 261–276.
- Liu JK, Hyde KD, Jones EBG, Ariyawansa HA et al. 2015 – Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity* 72, 1–197.
- Liu NG, Bhat DJ, Hyde KD, Liu JK. 2019a – *Conioscypha tenebrosa* sp. nov. (*Conioscyphaceae*) from China and notes on *Conioscypha* species. *Phytotaxa* 413, 159–171.

- Liu NG, Hyde KD, Bhat DJ, Jumpathong J et al. 2019b – Morphological and phylogenetic studies of *Pleopunctum* gen. nov. (*Phaeoseptaceae*, *Pleosporales*) from China. *Mycosphere* 10, 757–775.
- Liu NG, Hyde KD, Sun YR, Bhat DJ et al. 2024a – Notes, outline, taxonomy and phylogeny of brown-spored hyphomycetes. *Fungal Diversity* 129, 1–281.
- Liu NG, Lu YZ, Bhat DJ, McKenzie EHC et al. 2019c – *Kevinhydea brevistipitata* gen. et sp. nov. and *Helicoma hydei* sp. nov., (*Tubeufiaceae*) from decaying wood habitats. *Mycological Progress* 18, 671–682.
- Liu SL, Wang XW, Li GJ, Deng CY et al. 2024b – Fungal diversity notes 1717–1817: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 124, 1–216.
- Liu SL, Zhao P, Cai L, Shen S et al. 2024c – Catalogue of fungi in China 1. New taxa of plant-inhabiting fungi. *Mycology*, 1–58.
- Liu YJ, Whelen S, Hall BD. 1999 – Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. *Molecular Biology and Evolution* 16, 1799–1808.
- Lu L, Karunarathna SC, Rajeshkumar KC, Elgorban AM et al. 2025 – Unveiling fungal diversity associated with coffee trees in China using a polyphasic approach and a global review of coffee saprobic fungi. *IMA Fungus* 16, e144874.
- Lu YZ, Boonmee S, Liu JK, Hyde KD et al. 2018a – Multi-gene phylogenetic analyses reveals *Neohelicosporium* gen. nov. and five new species of helicosporous hyphomycetes from aquatic habitats. *Mycological Progress* 17, 631–646.
- Lu YZ, Liu JK, Hyde KD, Jeewon R et al. 2018b – A taxonomic reassessment of the *Tubeufiales* based on multi-locus phylogeny and morphology. *Fungal Diversity* 92, 131–344.
- Lu YZ, Ma J, Xiao XJ, Zhang LJ et al. 2022 – Four new species and three new records of helicosporous hyphomycetes from China and their multi-gene phylogenies. *Frontiers in Microbiology* 13, 1–23.
- Lu YZ, Ma J, Xiao XJ, Zhang LJ et al. 2023 – Two novel species and one new record of *Helicoma* from tropical China. *Mycosystema* 42, 263–277.
- Lu YZ, Zhang JY, Lin CG, Luo ZL et al. 2020 – *Pseudodactylaria fusiformis* sp. nov. from freshwater habitat in China. *Phytotaxa* 446, 95–102.
- Luo ZL, Bao DF, Bhat DJ, Yang J et al. 2016 – *Sporoschisma* from submerged wood in Yunnan, China. *Mycological Progress* 15, 1145–1155.
- Luo ZL, Bhat DJ, Jeewon R, Boonmee S et al. 2017 – Molecular phylogeny and morphological characterization of asexual fungi (*Tubeufiaceae*) from freshwater habitats in Yunnan, China. *Cryptogamie, Mycologie* 38, 27–53.
- Luo ZL, Hyde KD, Liu JK, Bhat DJ et al. 2018 – Lignicolous freshwater fungi from China II: Novel *Distoseptispora* (*Distoseptisporaceae*) species from northwestern Yunnan Province and a suggested unified method for studying lignicolous freshwater fungi. *Mycosphere* 9, 444–461.
- Luo ZL, Hyde KD, Liu JK, Maharachchikumbura SSN et al. 2019 – Freshwater *Sordariomycetes*. *Fungal Diversity* 99, 451–660.
- Ma J, Gomdola D, Boonmee S, Shen HW et al. 2024a – Three new species of *Neohelicomyces* (*Tubeufiales*, *Tubeufiaceae*) from freshwater and terrestrial habitats in China. *MycoKeys* 105, 317–336.
- Ma J, Hyde KD, Tibpromma S, Gomdola D et al. 2024b – Taxonomy and systematics of lignicolous helicosporous hyphomycetes. *Fungal Diversity* 129, 365–653.
- Ma J, Zhang JY, Xiao XJ, Xiao YP et al. 2022 – Multi-gene phylogenetic analyses revealed five new species and two new records of *Distoseptisporales* from China. *Journal of Fungi* 8, 1202.
- Mapook A, Hyde KD, McKenzie EHC, Jones EBG et al. 2020 – Taxonomic and phylogenetic contributions to fungi associated with the invasive weed *Chromolaena odorata* (Siam weed). *Fungal Diversity* 101, 1–175.

- Marin-Felix Y, Hernández-Restrepo M, Iturrieta-González I, García D et al. 2019 – Genera of phytopathogenic fungi: GOPHY 3. *Studies in Mycology* 94, 1–124.
- Matsushima T. 1983 – Matsushima Mycological Memoirs No. 3. Published by the author.
- Matsushima T. 2001 – Matsushima Mycological Memoirs 10. Published by the author.
- McKenzie EHC. 2008 – Two new dictyosporous hyphomycetes on *Pandanaceae*. *Mycotaxon* 104, 23–28.
- Morelet M. 1968 – De Aliquibus in *Mycologia Novitatibus*. *Bulletin de la Société des Sciences Naturelles et d'Archéologie de Toulon et du Var* 23, 5–6.
- Mortimer PE, Karunarathna SC, Li QH, Gui H et al. 2012 – Prized edible Asian mushrooms: ecology, conservation and sustainability. *Fungal Diversity* 56, 31–47.
- Niego AG, Rapior S, Thongklang N, Raspé O et al. 2021 – Macrofungi as a nutraceutical source: promising bioactive compounds and market value. *Journal of Fungi* 7, 397.
- Norphanphoun C, Jeewon R, McKenzie EHC, Wen TC et al. 2017 – Taxonomic position of *Melomastia italica* sp. nov. and phylogenetic reappraisal of Dyfrolomycetales. *Cryptogamie, Mycologie* 38, 507–525.
- Nylander JAA. 2008 – MrModeltest 2.3. Uppsala, Department of Systematic Zoology, Uppsala University.
- Ohmaki A, Okane I, Crous PW, Verkley GJM. 2023 – *Cylindromonium dirinariae* sp. nov. (*Ascomycota*, *Hypocreales*), a new nectrioid lichenicolous species on *Dirinaria applanata* in Japan. *Fungal Systematics and Evolution* 11, 1–10.
- Olariaga I, Teres J, Martín JM, Prieto M et al. 2019 – *Pseudosclerococcum golindoi* gen. et sp. nov., a new taxon with apothecial ascomata and a Chalara-like anamorph within the *Sclerococcales* (*Eurotiomycetes*). *Mycological Progress* 18, 895–905.
- Ou JH, Hsieh SY, Kuo CH. 2024 – *Gohteikhimycetes*, a novel hyphomycete genus from submerged wood, based on three collections in Taiwan. *Mycological Progress* 23, 46.
- Persoon CH. 1794 – Neuer Versuch einer systematischen Eintheilung der Schwämme. *Neues Magazin für die Botanik in ihrem ganzen Umfange* 1, 63–80.
- Phookamsak R, Liu JK, Manamgoda DS, Chukeatirote E et al. 2014 – The sexual state of *Setophoma*. *Phytotaxa* 176, 260–269.
- Phukhamsakda C, McKenzie EHC, Phillips AJL, Jones EBG et al. 2020 – Microfungi associated with *Clematis* (*Ranunculaceae*) with an integrated approach to delimiting species boundaries. *Fungal Diversity* 102, 1–203.
- Pinnoi A, Jeewon R, Sakayaroj J, Hyde KD et al. 2007 – *Berkleasium crunisia* sp. nov. and its teleomorphic affinities to the *Pleosporales* based on 18S, 28S and ITS-5.8S rDNA sequence analyses. *Mycologia* 99, 378–384.
- Pinnoi A, McKenzie EHC, Jones EBG, Hyde KD. 2003 – Palm fungi from Thailand: *Custingophora undulatistipes* sp. nov. and *Vanakripa minutiellipsoidea* sp. nov. *Nova Hedwigia* 77, 213–219.
- Promptutha I, Miller AN. 2010 – Three new species of *Acanthostigma* (*Tubeufiaceae*, *Dothideomycetes*) from Great Smoky Mountains National Park. *Mycologia* 102, 574–587.
- Qiao M, Du X, Zhang Z, Xu JP et al. 2018 – Three new species of soil-inhabiting *Trichoderma* from southwest China. *Myckeys* 44, 63–80.
- Rao PR, Rao D. 1964 – Some helicospores from Hyderabad—II. *Mycopathologia et Mycologia Applicata* 24, 27–34.
- Rathanyaka AR, Chethana KWT, Tennakoon DS, Lumyong S et al. 2021 – Additions to the microfungi in Taiwan: introducing *Pseudorobillarda camelliae-sinensis* sp. nov., (*Pseudorobillardaceae*) and new host records of pleosporalean taxa in mountainous habitats. *Phytotaxa* 516, 115–139.
- Réblová M, Hernández-Restrepo M, Fournier J, Nekvindová J. 2020 – New insights into the systematics of *Bactrodesmium* and its allies and introducing new genera, species and morphological patterns in the *Pleurotheciales* and *Savoryellales* (*Sordariomycetes*). *Studies in Mycology* 95, 415–466.

- Réblová M, Seifert KA. 2004 – *Conioscyphascus*, a new ascomycetous genus for holomorphs with *Conioscypha* anamorphs. *Studies in Mycology* 50, 95–108.
- Réblová M, Untereiner WA, Štěpánek V, Gams W. 2017 – Disentangling *Phialophora* section *Catenulatae*: disposition of taxa with pigmented conidiophores and recognition of a new subclass, *Sclerococcomycetidae* (*Eurotiomycetes*). *Mycological Progress* 16, 27–46.
- Réblová M. 2004 – Four new species of *Chaetosphaeria* from New Zealand and redescription of *Dictyochaeta fuegian*. *Studies in Mycology* 50, 171–186.
- Rehner SA, Buckley E. 2005 – A *Beauveria* phylogeny inferred from nuclear ITS and EF1- α sequences: evidence for cryptic diversification and links to *Cordyceps teleomorphs*. *Mycologia* 97, 84–98.
- Ren GC, Jayasiri SC, Tibpromma S, de Farias ARG et al. 2024a – Saprobiic ascomycetes associated with woody litter from the Greater Mekong Subregion (Southwestern China and Northern Thailand). *Mycosphere* 15, 954–1082.
- Ren GC, Tibpromma S, Dong KX, Gao CX et al. 2024b – Unveiling fungi associated with *Castanopsis* woody litter in Yunnan Province, China: Insights into *Pleosporales* (*Dothideomycetes*) species. *MycoKeys* 108, 15–45.
- Ren GC, Wanasinghe DN, Monkai J, Mortimer PE et al. 2021 – Novel saprobic *Hermatomyces* species (*Hermatomycetaceae*, *Pleosporales*) from China (Yunnan Province) and Thailand. *MycoKeys* 82, 57–79.
- Richardson MJ. 2001 – Diversity and occurrence of coprophilous fungi. *Mycological Research* 105, 387–402.
- Ronquist F, Teslenko M, van Der Mark P, Ayres DL et al. 2012 – MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61, 539–542.
- Rossmann AY, Seifert KA, Samuels GJ, Minnis AM et al. 2013 – Genera in *Bionectriaceae*, *Hypocreaceae*, and *Nectriaceae* (*Hypocreales*) proposed for acceptance or rejection. *IMA Fungus* 4, 41–51.
- Seifert K, Morgan-Jones G, Gams W, Kendrick B. 2011 – The genera of Hyphomycetes. CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands.
- Senanayake I, Rathnayaka AR, Marasinghe DS, Calabon MS et al. 2020 – Morphological approaches in studying fungi: collection, examination, isolation, sporulation and preservation. *Mycosphere* 11, 2678–2754.
- Senanayake IC, Rossi W, Leonardi M, Weir A et al. 2023 – Fungal diversity notes 1611–1716: taxonomic and phylogenetic contributions on fungal genera and species emphasis in south China. *Fungal Diversity* 122, 161–403.
- Shearer CA. 1973 – Fungi of the Chesapeake Bay and its tributaries II. The genus *Conioscypha*. *Mycologia* 65, 128–136.
- Shen HW, Bao DF, Boonmee S, Lu YZ et al. 2024a – Diversity of *Distoseptispora* (*Distoseptisporaceae*) taxa on submerged decaying wood from the Red River in Yunnan, China. *MycoKeys* 102, 1–28.
- Shen HW, Bao DF, Wanasinghe DN, Boonmee S et al. 2022 – Novel species and records of *Dictyosporiaceae* from freshwater habitats in China and Thailand. *Journal of Fungi* 8, 1200.
- Shen HW, Luo ZL, Bao DF, Luan S et al. 2024b – Lignicolous freshwater fungi from China IV: Morphology and phylogeny reveal new species of *Pleosporales* from plateau lakes in Yunnan Province, China. *Mycosphere* 15, 6439–6524.
- Siboe GM, Kirk PM, Cannon PF. 1999 – New dematiaceous hyphomycetes from Kenyan rare plants. *Mycotaxon* 73, 283–302.
- Singh P, Singh S. 2016 – Additions to helicoid fungi from India. *Current Research in Environmental & Applied Mycology* 6, 248–255.
- Sivichai S, Hywel-Jones NL, Somrithipol S. 2000 – Lignicolous freshwater Ascomycota from Thailand: *Melanochaeta* and *Sporoschisma* anamorphs. *Mycological Research* 104, 478–485.

- Šnajdr J, Dobiášová P, Větrovský T, Valášková V et al. 2011 – Saprotrophic basidiomycete mycelia and their interspecific interactions affect the spatial distribution of extracellular enzymes in soil. *FEMS Microbiology Ecology* 78, 80–90.
- Song JY, Tian Q, Liu JK. 2022 – *Pseudorobillarda sichuanensis* sp. nov. associated with *Bambusa* sp. from Sichuan province, China. *Phytotaxa* 561, 256–266.
- Spegazzini C. 1910 – *Mycetes Argentinenses* (Series V). *Anales del Museo Nacional de Historia Natural Buenos Aires* ser 3 13, 329–467.
- Su HY, Hyde KD, Maharachchikumbura SSN, Ariyawansa HA et al. 2016 – The families *Distoseptisporaceae* fam. nov., *Kirschsteiniotheliaceae*, *Sporormiaceae* and *Torulaceae*, with new species from freshwater in Yunnan Province, China. *Fungal Diversity* 80, 375–409.
- Sun JZ, Pei YF, Li EW, Li W et al. 2016 – A new species of *Trichoderma hypoxylon* harbours abundant secondary metabolites. *Scientific Reports* 6, 37369.
- Sun YR, Goonasekara ID, Thambugala KM, Jayawardena RS et al. 2020 – *Distoseptispora bambusae* sp. nov. (Distoseptisporaceae) on bamboo from China and Thailand. *Biodiversity Data Journal* 8, e53678.
- Sun YR, Hyde KD, Liu NG, Jayawardena RS et al. 2025 – Micro-fungi in southern China and northern Thailand: emphasis on medicinal plants. *Fungal Diversity* 131, 99–299.
- Sutton BC. 1985 – Notes on some deuteromycete genera with cheiroid or digitate brown conidia. *Proceedings / Indian Academy of Sciences* 94, 229–244.
- Tanaka K, Hashimoto A, Matsumura M, Sato T. 2017 – *Brevicollum*, a new genus in *Neohendersoniaceae*, *Pleosporales*. *Mycologia* 109, 608–619.
- Tanaka K, Hirayama K, Yonezawa H, Hatakeyama S et al. 2009 – Molecular taxonomy of bambusicolous fungi: *Tetraplospira* fam. nov., a new pleosporalean family with Tetraploa-like anamorphs. *Studies in Mycology* 64, 175–209.
- Tang X, Jeewon R, Lu YZ, Alrefaei AF et al. 2023 – Morphophylogenetic evidence reveals four new fungal species within *Tetraplospira* (Pleosporales, Ascomycota) from tropical and subtropical forest in China. *Mycology* 100, 171–204.
- Tanney J, Miller AN. 2017 – Asexual-sexual morph connection in the type species of *Berkleasmium*. *IMA Fungus* 8, 99–105.
- Tennakoon DS, Thambugala KM, Wanasinghe DN, Gentekaki E et al. 2020 – Additions to Phaeosphaeriaceae (Pleosporales): *Elongaticollum* gen. nov., *Ophiosphaerella taiwanensis* sp. nov., *Phaeosphaeriopsis beaucarnea* sp. nov. and a new host record of *Neosetophoma poaceicola* from Musaceae. *Mycology* 70, 59–88.
- Thambugala KM, Wanasinghe DN, Phillips AJL, Camporesi E et al. 2017 – Mycosphere notes 1–50: grass (*Poaceae*) inhabiting *Dothideomycetes*. *Mycosphere* 8, 697–796.
- Tian XG, Karunarathna SC, Xu RJ, Lu YZ et al. 2022 – Three new species, two new records and four new collections of Tubeufiaceae from Thailand and China. *Journal of Fungi* 8, 206.
- Tibpromma S, Bhat J, Doilom M, Lumyong S et al. 2016 – Three new *Hermatomyces* species (*Lophiotremataceae*) on *Pandanus odorifer* from Southern Thailand. *Phytotaxa* 275, 127–139.
- Tibpromma S, Hyde KD, McKenzie EHC, Bhat DJ et al. 2018 – Fungal diversity notes 840–928: micro-fungi associated with *Pandanaceae*. *Fungal Diversity* 93, 1–160.
- Torres-Garcia D, Garcia D, Reblova M, Jurjevic Z et al. 2023 – Diversity and novel lineages of black yeasts in *Chaetothyriales* from freshwater sediments in Spain. *Persoonia* 51, 194–228.
- Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ. 2016 – W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research* 44, W232–W235.
- Tsui CKM, Goh TK, Hyde KD. 2003 – Reflections on the genus *Vanakripa*, and a description of *V. ellipsoidea* sp. nov. *Mycologia* 95, 124–127.
- Tsui KM, Goh TK, Hyde KD, Hodgkiss IJ. 1999 – Reflections on *Menisporopsis*, with the addition of *M. multisetulata* sp. nov. from submerged wood in Hong Kong. *Mycological Research* 103, 148–152.

- Tsui KM, Goh TK, Hyde KD. 1997 – A new species of *Dactylaria* from Hong Kong. *Sydowia* 49, 182–186.
- Udagawa SI, Toyazaki N. 1983 – A new species of *Conioscypha*. *Mycotaxon* 18, 131–137.
- Vaidya G, Lohman DJ, Meier R. 2011 – SequenceMatrix: concatenation software for the fast assembly of multi-gene datasets with character set and codon information. *Cladistics* 27, 171–180.
- Vilgalys R, Hester M. 1990 – Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172, 4238–4246.
- Von Höhnelt F. 1904 – Mycologische Fragmente. *Mycologische Fragmente* 2, 38–60.
- Wanasinghe DN, Phookamsak R, Dissanayake LS, Xu J 2025 – Unexplored microfungi diversity from dead woody litter in the dry-hot valleys of Honghe (Yunnan, China). *Studies in Fungi* 10: e017.
- Wanasinghe DN, Phukhamsakda C, Hyde KD, Jeewon R et al. 2018 – Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on Rosaceae. *Fungal Diversity* 89, 1–236.
- Wang K, Cai L, Yao Y. 2021 – Overview of nomenclature novelties of fungi in the world and China (2020). *Biodiversity Science* 29, 1064–1072.
- Wang K, Cai L. 2023 – Overview of the historical and current status of fungal taxonomy and diversity in China. *Mycosystema* 42, 50–62.
- Wang WP, Hyde KD, Bao DF, Wanasinghe DN et al. 2024 – Lignicolous freshwater fungi from karst landscapes in Yunnan Province, China. *Mycosphere* 15, 6525–6640.
- White TJ, Bruns T, Lee S, Taylor J. 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (eds) *PCR protocols: A guide to methods and applications*. Academic Press, San Diego, pp 315–322.
- Wijayawardene NN, Hyde KD, Wanasinghe DN, Papizadeh M et al. 2016 – Taxonomy and phylogeny of dematiaceous coelomycetes. *Fungal Diversity* 77, 1–316.
- Wu N, Lu YH, Chethana KWT, Cheewangkoon R et al. 2025 – Morpho-phylogenetic evidence reveals novel species and new record of *Neomassaria* (Neomassariaceae) associated with *Camellia sinensis* in Southwestern China. *Myckeys* (in press).
- Wu WP, Diao YZ. 2022 – Anamorphic chaetosphaeriaceous fungi from China. *Fungal Diversity* 116, 1–546.
- Xia JW, Ma YR, Li Z, Zhang XG. 2017 – Acrodictys-like wood decay fungi from southern China, with two new families *Acrodictiaceae* and *Junewangiaceae*. *Scientific Reports* 7, 7888.
- Xiong YR, Hyde KD, Lu L, Harishchandra DL et al. 2024 – Novel *Helicoma* and *Neohelicosporium* (*Tubeufiaceae*, *Tubeufiales*) species and two new host records of *Helicoma* on tropical palms (*Arecaceae*) from China. *MycKeys* 108, 287–315.
- Xu RJ, Hyde KD, Li JN, Boonmee S et al. 2025 – Lignicolous freshwater fungi of the pan Qinghai-Xizang Plateau, China. *Fungal Diversity* 133, 23–234.
- Xu RJ, Zhu YA, Liu NG, Boonmee S et al. 2023 – Taxonomy and phylogeny of hyphomycetous muriform conidial taxa from the Tibetan Plateau, China. *Journal of Fungi* 9, 560.
- Yang EF, Tibpromma S, Karunarathna SC, Phookamsak R et al. 2022 – Taxonomy and phylogeny of novel and extant taxa in Pleosporales associated with *Mangifera indica* from Yunnan, China (Series I). *Journal of Fungi* 8, 152.
- Yang J, Liu JK, Hyde KD, Bhat DJ et al. 2016 – New species of *Sporoschisma* (*Chaetosphaeriaceae*) from aquatic habitats in Thailand. *Phytotaxa* 289, 147–157.
- Yang J, Liu JK, Hyde KD, Jones EBG et al. 2018a – New species in *Dictyosporium*, new combinations in *Dictyocheirospora* and an updated backbone tree for *Dictyosporiaceae*. *MycKeys* 36, 83–105.
- Yang J, Liu LL, Jones EBG, Hyde KD et al. 2023 – Freshwater fungi from karst landscapes in China and Thailand. *Fungal Diversity* 119, 1–212.

- Yang J, Liu LL, Jones EBG, Li WL et al. 2021 – Morphological variety in *Distoseptispora* and introduction of six novel species. *Journal of Fungi* 7, 945.
- Yang J, Liu NG, Liu JK, Hyde KD et al. 2018b – Phylogenetic placement of *Cryptophiale*, *Cryptophialoidea*, *Nawawia*, *Neonawawia* gen. nov. and *Phialosporostilbe*. *Mycosphere* 9, 1132–1150.
- Yang YH, Manawasinghe IS, Wanasinghe, DN, de Farias, ARG et al. 2024 – A novel genus and new records of *Dothideomycetes* associated with *Litchi chinensis* litter from Guangdong Province, China. *New Zealand Journal of Botany* 62, 216–238.
- Yu XD, Dong W, Bhat DJ, Boonmee S et al. 2018 – *Cylindroconidiis aquaticus* gen. et sp. nov., a new lineage of aquatic hyphomycetes in *Sclerococcaceae* (*Eurotiomycetes*). *Phytotaxa* 372, 79–87.
- Yu XD, Zhang SN, Liang XD, Zhu JT et al. 2024 – Bambusicolous fungi from Southwestern China. *Mycosphere* 15, 5038–5145.
- Yu ZF, Qiao M, Zhang Y, Zhang KQ 2007 – Two new species of *Trichoderma* from Yunnan, China. *Antonie van Leeuwenhoek* 92, 101–108.
- Yuan HS, Lu X, Dai YC, Hyde KD et al. 2020 – Fungal diversity notes 1277–1386: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 104, 1–266.
- Zhang H, Zhu R, Qing Y, Yang H et al. 2022 – Polyphasic identification of *Distoseptispora* with six new species from fresh water. *Journal of Fungi* 8, 1063.
- Zhang SN, Hyde KD, Jones EBG, Yu XD et al. 2024 – Current insights into palm fungi with emphasis on taxonomy and phylogeny. *Fungal Diversity* 127, 55–301.
- Zhang YZ, Chen QL, Ma J, Lu YZ et al. 2023 – Morphological and multi-gene phylogenetic analyses reveal five new hyphomycetes from freshwater habitats. *Frontiers in Microbiology* 14, 1253239.
- Zhao G, Liu X, Wu W. 2007 – *Helicosporous hyphomycetes* from China. *Fungal Diversity* 26, 313–524.
- Zhao GL, Lu YZ, Xiao XJ, Liu Y et al. 2025 – Morphological and phylogenetic analyses reveal three new species associated with *Pueraria* from Xizang Autonomous Region, China. *Mycocokeys* (in press).
- Zheng H, Qiao M, Lv Y, Du X et al. 2021 – New species of *Trichoderma* isolated as endophytes and saprobes from southwest China. *Journal of Fungi* 7, 467.