MYCOSPHERE 15(1): 6439–6524 (2024) www.mycosphere.org ISSN 2077 7019
Doi 10.5943/mycosphere/15/1/28

ARTICLE

Lignicolous freshwater fungi from China IV: Morphology and phylogeny reveal new species of *Pleosporales* from plateau lakes in Yunnan Province, China

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Citation – Shen HW, Luo ZL, Bao DF, Luan S, Bhat DJ, Boonmee S, Wang WP, Su XJ, Li YX, Al-Otibi F, Lu YZ, Yang LQ, Hyde KD 2024 – Lignicolous freshwater fungi from China IV: Morphology and phylogeny reveal new species of *Pleosporales* from plateau lakes in Yunnan Province, China. Mycosphere 15(1), 6439–6524, Doi 10.5943/mycosphere/15/1/28

Abstract

This paper is the fourth in a series focused on lignicolous freshwater fungi from China. Yunnan Province is one of the hotspots for fungal research in China, with particularly remarkable fungal diversity, but there is still a significant knowledge gap in our understanding of lignicolous freshwater fungi in lentic habitats (such as lakes and ponds) compared to lotic habitats. As part of our ongoing research on the diversity of lignicolous freshwater fungi in Yunnan plateau lakes, 35 collections of *Pleosporales* (*Dothideomycetes*) were collected and discovered. Based on morphological characteristics and multigene concatenation datasets, these collections were identified as 21 species, including 18 new species, *viz.*, *Aquimassariosphaeria aquatica*, *Astrosphaeriella yunnanensis*, *Beverwykella grandispora*, *Cryptocoryneum sinense*, *Floricola aquatica*, *Hermatomyces hongheensis*, *Hongkongmyces cylindricisporus*, *H. guttulatus*, *H. hongheensis*, *H. yunnanensis*, *Lindgomyces yunnanensis*, *Lolia fusiformispora*, *Periconia dujuanhuensis*, *P. hongheensis*, *P. yunnanensis*, *Pseudotetraploa aquatica*, *Roussoella dujuanhuensis* and *Triplosphaeria yunnanensis*, one new geographical record for China, *Setoseptoria phragmitis* and two new records for freshwater habitats, *Lonicericola qujingensis* and *Occultibambusa jonesii*. Detailed descriptions, illustrations, and notes are provided for these species. The genus *Paralentithecium* and the species *P. aquaticum* and *P. suae* are also validated here. The study increases the number of lignicolous freshwater fungi in Yunnan Plateau lakes and enhances our understanding of the freshwater fungal diversity in lentic freshwater habitats.

Keywords – 18 new species – *Dothideomycetes* – multi-gene phylogeny – Plateau lakes – taxonomy

Submitted: 7 June 2024; **Accepted:** 21 November 2024; **Published:** 9 December 2024
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Accepted by: Mingkwan Doilom

INTRODUCTION

Lignicolous freshwater fungi are a special ecological group, referring to those taxa that occur on woody debris submerged in freshwater habitats (Hyde et al. 2016a, Calabon et al. 2023). They are widely distributed in lotic (such as lakes, ponds, reservoirs), lentic (such as rivers, and streams) and artificial freshwater habitats (such as water cooling towers) (Luo et al. 2004). Lignicolous freshwater fungi play a key role in the decomposition of submerged wood in freshwater habitats, breaking down lignocelluloses and releasing nutrients, and all of these are important in ecosystem functioning (Yuen et al. 1998, Bucher et al. 2004, Hyde et al. 2016a). Lignicolous freshwater fungi have been well-studied in Asia over the past decade, with particular emphasis on China and Thailand. Some new species and higher-level classifications have been introduced, based on morphological and phylogenetic analyses (Hyde et al. 2016a, 2023a, b, Luo et al. 2016, 2018a, b, 2019, Bao et al. 2018, 2021a, 2022, 2023, Yang et al. 2019, 2021, 2023, Calabon et al. 2021a, Dong et al. 2020, 2021, Manawasinghe et al. 2022, Shen et al. 2022a, Zhang et al. 2022). In recent years, Yunnan has been one of the hot spots for research on lignicolous freshwater fungi, with more than 280 species already reported (Bao et al. 2019, 2020, 2021a, 2023, Luo et al. 2019, Dong et al. 2020, 2021, Shen et al. 2022a). However, these species were mainly reported from lotic habitats, with only a few species form lentic habitats (plateau lakes) (Cai et al. 2002, Luo et al. 2004). A comprehensive study on the diversity and distribution pattern of lignicolous freshwater fungi in lakes from Yunnan Plateau is ongoing and several studies have been published (Luo et al. 2018a, Huang et al. 2022, Li et al. 2022, Shen et al. 2022b, 2023, Bao et al. 2023, Luan et al. 2023). Even though these investigations have increased the number of lignicolous freshwater fungi from plateau lakes in Yunnan, there are still significant knowledge gaps in our understanding of these fungi in the lakes in the region relative to lignicolous freshwater fungi in lotic freshwater habitats.

Pleosporales, the largest order in the *Dothideomycetes*, was formally established by Barr (1987) to accommodate species characterized by: ascomata with narrowly or broadly cellular pseudoparaphyses, asci in a basal layer, peridium usually pseudoparenchymatous, and ascospores that exhibit bipolar asymmetry (Barr 1987). Currently, *Pleosporales* comprises 91 families and 614 genera, the members have been reported as epiphytes, saprobes, endophytes or parasites, pathogens, hyperparasites on fungi or insects and or as lichenized fungi on a variety of substrates in terrestrial and aquatic habitats (Zhang et al. 2012, Hyde et al. 2013, Wanasinghe et al. 2018, Hongsanan et al. 2020a, Mapook et al. 2020, Wijayawardene et al. 2022a). Freshwater fungi in *Pleosporales* are highly diverse with more than 30 families including lignicolous freshwater fungi, and most of which are distributed in *Astrosphaeriellaceae*, *Dictyosporiaceae*, *Distoseptisporaceae*, *Lentitheciaceae*, *Lindgomycetaceae*, *Lophiostomataceae, etc.* (Cai et al. 2008, Tanaka et al. 2015, Boonmee et al. 2016, Su et al. 2016, Hyde et al. 2016b, 2017, 2020a, 2021, Luo et al. 2018b, Bao et al. 2019, Dong et al. 2020, 2021, Calabon et al. 2021b, 2022, Yang et al. 2021, Shen et al. 2022b, Zhai et al. 2022, Zhang et al. 2022, Hu et al. 2023).

We have been systematically studying lignicolous freshwater fungi in Yunnan plateau lakes and several new taxa have been introduced (Huang et al. 2022, Li et al. 2022, Bao et al. 2023, Luan et al. 2023, Shen et al. 2023). The present study is part of our ongoing research on lignicolous freshwater fungi in Yunnan plateau lakes. Specimens of decaying wood were collected from several plateau lakes (including, Cibihu, Dianchi, Dujuanhu, Fuxianhu, Luguhu, Qiluhu, Xihu, Xingyunhu, Yangzonghai and Yilonghu lakes) and Mofanghe Reservoir in Yunnan Province. Through morphological examination and molecular phylogenetic analysis, we identified and determined the phylogenetic placement of the novel lignicolous freshwater fungi. Based on unique morphology and multigene phylogeny, eighteen new species, a new geographical record in China, and two new records of freshwater habitats, are described in detail and illustrated.

MATERIALS AND METHODS

Specimen collection, examination and isolation

The specimens of submerged decaying wood were collected from plateau lakes in Yunnan

Province between 2021 to 2023, including, Cibihu, Dianchi, Dujuanhu, Fuxianhu, Luguhu, Qiluhu, Xihu, Xingyunhu, Yangzonghai and Yilonghu lakes. Samples collection, processing, incubation, observation and isolation were conducted according to Luo et al. (2018b) and Shen et al. (2023). Specimens were deposited in the Cryptogamic Herbarium of Kunming Institute of Botany, Chinese Academy of Sciences (HKAS), Kunming, China. The pure cultures were deposited with the China General Microbiological Culture Collection Center (CGMCC), and Kunming Institute of Botany Culture Collection (KUNCC). Facesoffungi numbers and Index Fungorum number were obtained as described in (Jayasiri et al. 2015) and Index Fungorum number (https://indexfungorum.org/names; accessed on 20 June 2024).

DNA extraction, PCR amplification and sequencing

DNA extraction, PCR amplification, sequencing, and phylogenetic analysis were done following the methods of Senanayake et al. (2020). Mycelia for DNA extraction from each isolate was grown on PDA for 3–4 weeks at 24℃. Total genomic DNA was extracted from 100–300 mg axenic mycelium, scraped from the edges of the growing culture, using a sterile scalpel and transferred to 1.5 mL microcentrifuge tube using sterilized inoculum needles. Mycelium was ground to a fine powder with liquid nitrogen or quartz sand to break the cells for DNA extraction. DNA was extracted with the Trelief^{TM} Plant Genomic DNA Kit (TSP101) following manufacturer guidelines.

Six gene regions, ITS, LSU, SSU, *tef*1-α, *rpb*2 and *tub*2 were amplified using ITS5/ITS4 (White et al. 1990), LR0R/LR5 (Vilgalys & Hester 1990), NS1/NS4 (Liu et al. 1999), EF1-983F/EF1-2218R (Liu et al. 1999), RPB2-5F/RPB2-7cR (Liu et al. 1999) and T1/BT2b (Glass & Donaldson 1995) primer pairs, respectively. Primer sequences are available in the WASABI database on the AFTOL website (aftol.org). The PCR mixture contained 12.5 μL of 2× GS Taq PCR MasterMix (mixture of DNA Polymerase, dNTPs, Mg^{2+} and optimized buffer; Genesand Biotech, Beijing, China), 1 μL of each primer including forward primer and reverse primer (10 μM), 1 μL template DNA extract and 9.5 μL double-distilled water (Luo et al. 2018b). The PCR thermal cycling conditions of ITS were: 94 ℃ for 3 min, followed by 35 cycles of denaturation at 94℃ for 30 s, annealing at 56 ℃ for 50 s, elongation at 72 ℃ for 1 min, and a final extension at 72 ℃ for 10 min; LSU and *tef*1-α were: 94 ℃ for 3 min, followed by 35 cycles of denaturation at 94 ℃ for 30 s, annealing at 55 ℃ for 50 s, elongation at 72 ℃ for 1 min, and a final extension at 72 ℃ for 10 min. *rpb*2 were: 95 ℃ for 5 min, followed by 40 cycles of denaturation at 95 ℃ for 1 min, annealing at 52 ℃ for 90 s, elongation at 72 ℃ for 92 s, and a final extension at 72 ℃ for 10 min. PCR products were then purified using minicolumns, purification resin and buffer according to the manufacturer's protocols. The sequences were carried out at Beijing Tsingke Biological Engineering Technology and Services Co., Ltd (Beijing P.R. China).

Phylogenetic analyses

BLAST searches using the BLASTn algorithm were performed to retrieve similar sequences from GenBank (http://ncbi.nlm.nih.gov, accessed on 14 June 2024). The sequences were aligned using MAFFT online service: multiple alignment program MAFFT v.7 (Kuraku et al. 2013, Katoh et al. 2019, http://mafft.cbrc.jp/ alignment/server/index.html, accessed on 14 June 2024), and sequence trimming was performed with trimAl v.1.2 with default parameters (http://trimal.cgenomics.org for specific operation steps, Capella-Gutiérrez et al. 2009). The sequence dataset was combined using SquenceMatrix v.1.7.8 (Vaidya et al. 2011). FASTA alignment formats were changed to PHYLIP and NEXUS formats by the website: ALignment Transformation EnviRonment (ALTER) (http://sing.ei.uvigo.es/ALTER/, accessed on 14 June 2024).

Maximum likelihood (ML) analysis was performed setting RAxML-HPC2 on XSEDE (8.2.12) (Stamatakis 2006, Stamatakis et al. 2008) in CIPRES Science Gateway (Miller et al. 2010, http://phylo.org/portal2, accessed on 25 June 2024), using the GTR+GAMMA model with 1000 bootstrap repetitions. Bayesian analyses were performed in MrBayes 3.2.6 (Ronquist et al. 2012)

and the best-fit model of sequences evolution was estimated via MrModeltest 2.2 (Guindon & Gascuel 2003, Darriba et al. 2012). The Markov Chain Monte Carlo (MCMC) sampling approach was used to calculate posterior probabilities (PP) (Rannala & Yang 1996). Bayesian analyses of six simultaneous Markov chains were run for 1M generations and trees were sampled every thousand generation. Phylogenetic trees were visualized using FigTree v1.4.0 (http://tree.bio.ed.ac.uk /software/figtree/), editing and typesetting using Adobe Illustrator (AI) (Adobe Systems Inc., San Jose, CA, USA). The new sequences were submitted in GenBank and the strain information used in this paper are provided in Supplementary Table 1.

RESULTS

Taxonomy

Astrosphaeriellaceae Phookamsak & K.D. Hyde, Fungal Diversity 74: 161 (2015).

Astrosphaeriellaceae was introduced to accommodate species of *Astrosphaeriella* sensu stricto and *Pteridiospora* with erumpent, carbonaceous ascostromata. Additionally, *Astrosphaeriella* was designated as the type genus by Phookamsak et al. (2015a). In their study, a new genus *Astrosphaeriellopsis* was introduced to accommodate *A. bakeriana*, which previously belonged to *Astrosphaeriella*, though the genus was excluded from *Astrosphaeriellaceae* (Phookamsak et al. 2015a). However, based on multi-gene phylogenetic analysis, Wanasinghe et al. (2018) assigned *Astrosphaeriellopsis* to *Astrosphaeriellaceae* and accepted four genera, *Astrosphaeriella*, *Astrosphaeriellopsis*, *Pteridiospora*, and *Pithomyces* in this family (Wanasinghe et al. 2018). In subsequent studies, *Acrocordiopsis*, *Aquatospora*, *Caryospora*, *Javaria*, *Mycopepon*, *Quercicola*, *Triseptatospora* and *Xenoastrosphaeriella* were accepted in *Astrosphaeriellaceae* based on morphological and phylogenetic studies (Jayasiri et al. 2019, Wijayawardene et al. 2022a, Konta et al. 2023). Currently, eleven genera *viz.*, *Aquatospora*, *Astrosphaeriella*, *Astrosphaeriellopsis*, *Caryospora*, *Javaria*, *Mycopepon*, *Pithomyces*, *Pteridiospora*, *Quercicola*, *Triseptatospora*, *and Xenoastrosphaeriella* are accepted in *Astrosphaeriellaceae*. *Astrosphaeriellaceae* is widespread in distribution and its members are usually saprobic or parasitic on bamboo, palms, or stout grasses (Liu et al. 2011, Phookamsak et al. 2015a, Hongsanan et al. 2020a, Konta et al. 2023).

Astrosphaeriella Syd. & P. Syd., Annls mycol. 11(3): 260 (1913)

Astrosphaeriella was introduced by Sydow & Sydow (1913) with *A. fusispora* as the type species. *Astrosphaeriella* species are mainly known in their sexual morph and are characterized by carbonaceous, conical to mammiform ascomata, with ruptured, reflexed, stellate, host remnants around the base and pale brown to brown, fusiform ascospores produced in bitunicate, cylindrical to cylindric-clavate asci (Sydow & Sydow 1913, Hawksworth 1981, Yue & Eriksson 1986, Barr 1990, Hyde 1992, 1994a, b, Aptroot 1995, Frölich & Hyde 1995, Hyde & Fröhlich 1998, Tanaka & Harada 2005, Tanaka et al. 2009, Liu et al. 2011, Phookamsak et al. 2015a). *Astrosphaeriella* species can also be recognized by their unique trabeculate pseudoparaphyses (Liew et al. 2000). *Astrosphaeriella* is a morphologically well-studied genus, species in the genus are reported as saprobes or pathogens from aquatic and terrestrial habitats (Hyde & Fröhlich 1998, Liu et al. 2011, Phookamsak et al. 2015a). *Astrosphaeriella* has been revised several times based on its morphology, Hawksworth (1981) circumscribed *Astrosphaeriella* as an exclusively tropical genus occurring on bamboo or palm plants, and accepted four species in *Astrosphaeriella* (Hawksworth 1981). Hyde & Fröhlich (1998) reviewed the genus and accepted 31 species (including 10 newly described species). Hyde et al. (2000) expanded the concept of *Astrosphaeriella* to include species with slit-like ostioles. Currently, 52 species are listed in the Species Fungorum database, although only approximately ten species are accepted by Wijayawardene et al. (2022a). These species occur as saprobes on bamboos, palms and stout grasses from terrestrial habitats (Hawksworth 1981, Hyde & Fröhlich 1998, Hyde et al. 2000, Liu et al. 2011, Phookamsak et al. 2015a), whereas a few

species have been reported in freshwater habitats (Hyde & Fröhlich 1998, Cai et al. 2003, Ren et al. 2013, Dong et al. 2020).

Astrosphaeriella yunnanensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 1

Index Fungorum number: IF571997; Facesoffungi number: FoF15477

Etymology – The name refers to Yunnan Province, where the type specimen of this fungus was collected.

Holotype – HKAS 131656.

Saprobic on decaying submerged wood in freshwater. Sexual morph: *Ascomata* 600–900 µm high, 530–910 µm diam., erumpent to superficial, solitary to gregarious, conical, with ruptured, reflexed, stellate, carbonaceous, host remnants around the base, uni-loculate, carbonaceous, breakable, ostiolate. *Ostioles* short, centrally located. *Peridium* uneven in thickness, 30–50 µm wide at the base, 70–110 µm wide on sides, composed of several layers of thick, dark brown to black, melanized, irregular cells of *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, 1–2 µm wide, filiform, trabeculate pseudoparaphyses, anastomosing among the asci, embedded in a hyaline, gelatinous matrix. *Asci* 169–194(–205) × 9–11 µm ($\bar{x}$ = 181 × 10 µm, n = 25), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, shortly pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 33–40 × 4–5 µm ($\bar{x}$ = 36 × 4 µm, n = 40), overlapping 2–3-seriate, elongate, narrow fusiform, straight or slightly curved, 1(–3)-septate, constricted at the central septum, hyaline to pale brown, guttulate, smooth-walled, surrounded by entire mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 12 h and germ tubes produced from ends of ascospore. Colonies on PDA reaching 1.5–2 cm diam. after two months at room temperature, colony circular, smooth edge, surface hyphae pale brown, flocculent, dense, sparse and thin at the edge, bulge at middle; reverse side pale brown to dark brown, smooth, cracked at the middle.

Material examined – China, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'15.6" N, 100°1'30.00" E, 2500 m; on a rotten bamboo branch submerged in water, 21 February 2022, H.W. Shen, S2820 (HKAS 131656, holotype), ex-type culture KUNCC 23–16916.

GenBank numbers – LSU: PQ436668, SSU: PQ435251, *tef*1-α: PQ456944.

Notes – *Astrosphaeriella yunnanensis* conforms to the generic concept of *Astrosphaeriella* in having carbonaceous, conical ascomata, with ruptured, reflexed, stellate, host remnants around the base; fusiform ascospores produced in bitunicate, cylindrical to cylindric-clavate asci (Liu et al. 2011, Phookamsak et al. 2015a). It is similar to *A. angustispora* and *A. mauritiae* in having superficial and carbonaceous ascomata, elongate-fusiform, hyaline, septate ascospores with a mucilaginous sheath. However, *Astrosphaeriella yunnanensis* has larger ascospores than *A. angustispora* (33–40 × 4–5 µm *vs.* 25–30 × 2.3–2.8 µm), and the ascospore surrounded by an entire mucilaginous sheath, while the sheath of *A. angustispora* is flame-like at both ends (Hyde & Fröhlich 1998). *Astrosphaeriella yunnanensis* has longer ascospores (33–40 × 4–5 µm *vs.* 25–28.8 × 4–5.3 µm) with more septa (1–3 *vs.* 1) than *A. mauritiae*. In the multi-gene phylogenetic analysis, *Astrosphaeriella yunnanensis* basal to *Astrosphaeriella* with 100% ML and 1.00 BYPP support (Fig. 2). Following the guidelines of Pem et al. (2021) and based on morphological differences and phylogenetic analysis, we introduce *Astrosphaeriella yunnanensis* as a new species.

Cryptocoryneaceae A. Hashim. & Kaz. Tanaka, Persoonia 39: 56 (2017)

Cryptocoryneaceae was introduced by Hashimoto et al. (2017) to accommodate the single genus *Cryptocoryneum*, based on morphological and multi-locus phylogeny results (Hashimoto et al. 2017), and belongs in *Dothideomycetes* (Wijayawardene et al. 2022). *Cryptocoryneaceae* is known only by its asexual morphs, with most members acting as saprobes on plant debris in terrestrial habitats. No *Cryptocoryneaceae* species have been collected from freshwater habitats (Kirk 1983, Hashimoto et al. 2016, Boonmee et al. 2021).

Cryptocoryneum Fuckel, Jb. nassau. Ver. Naturk. 23-24: 372 (1870)

Cryptocoryneum, a monophyletic genus in *Cryptocoryneaceae*, was established by Fuckel (1865) to accommodate *C. fasciculatum* (= *C. hysterioides*) (Fuckel 1865, Hashimoto et al. 2016). *Cryptocoryneum* is characterized by stromatic sporodochia, cheiroid conidia, and conidial arms developed upwards from the cap cells (Fuckel 1865, Hashimoto et al. 2016, 2017). Hashimoto et al. (2016) carried out a taxonomic reassessment of the species in *Cryptocoryneum*, based on the morphological observations and molecular analysis, and proposed that conidial size, number of conidial arms and conidial septa are important characteristics for species delimitation (Hashimoto et al. 2016). In their study, seven new species were introduced, and a key was provided for 13 accepted species, based on detailed morphological characteristics. Subsequently, a new species, *C. rosae*, was introduced from Uzbekistan on the wood of *Rosa* sp. (Boonmee et al. 2021). Currently, 14 *Cryptocoryneum* species have been described worldwide, and most of them occur on dead wood, a few species reported from leaf litter or on arthropod dung (Talbot 1952, Kirk 1983, Hashimoto et al. 2016, Boonmee et al. 2021).

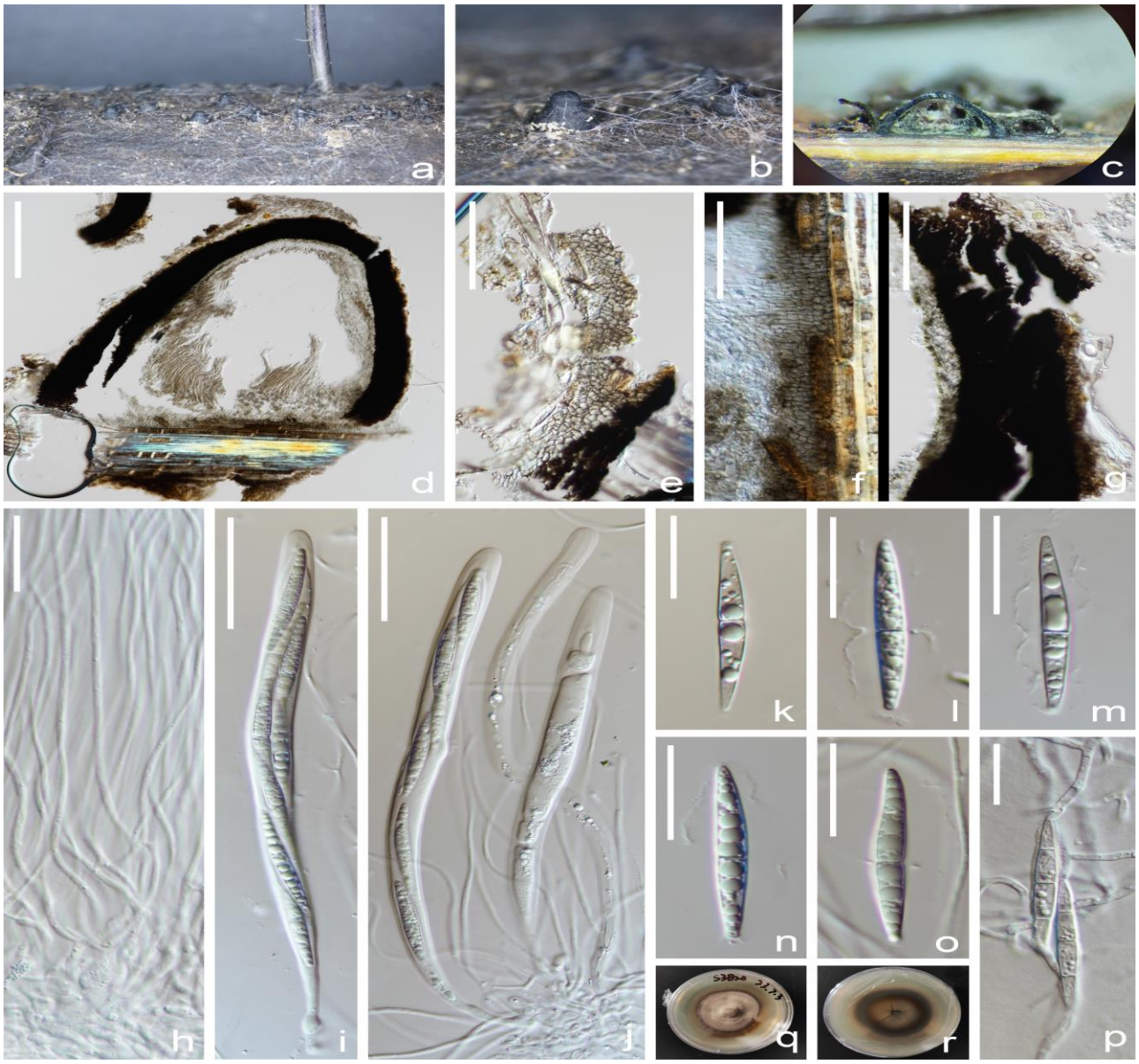

Figure 1 – *Astrosphaeriella yunnanensis* (HKAS 131656, holotype). a, b Appearance of ascomata on host substrate. c, d Sections of ascomata. e–g Peridium. h Pseudoparaphyses. h, j Asci. k–o Ascospores. p Germinated ascospore. q, r Colony on PDA. Scale bars: d = 200 µm, e–g = 70 µm, h, k–p = 20 µm, i, j = 40 µm.

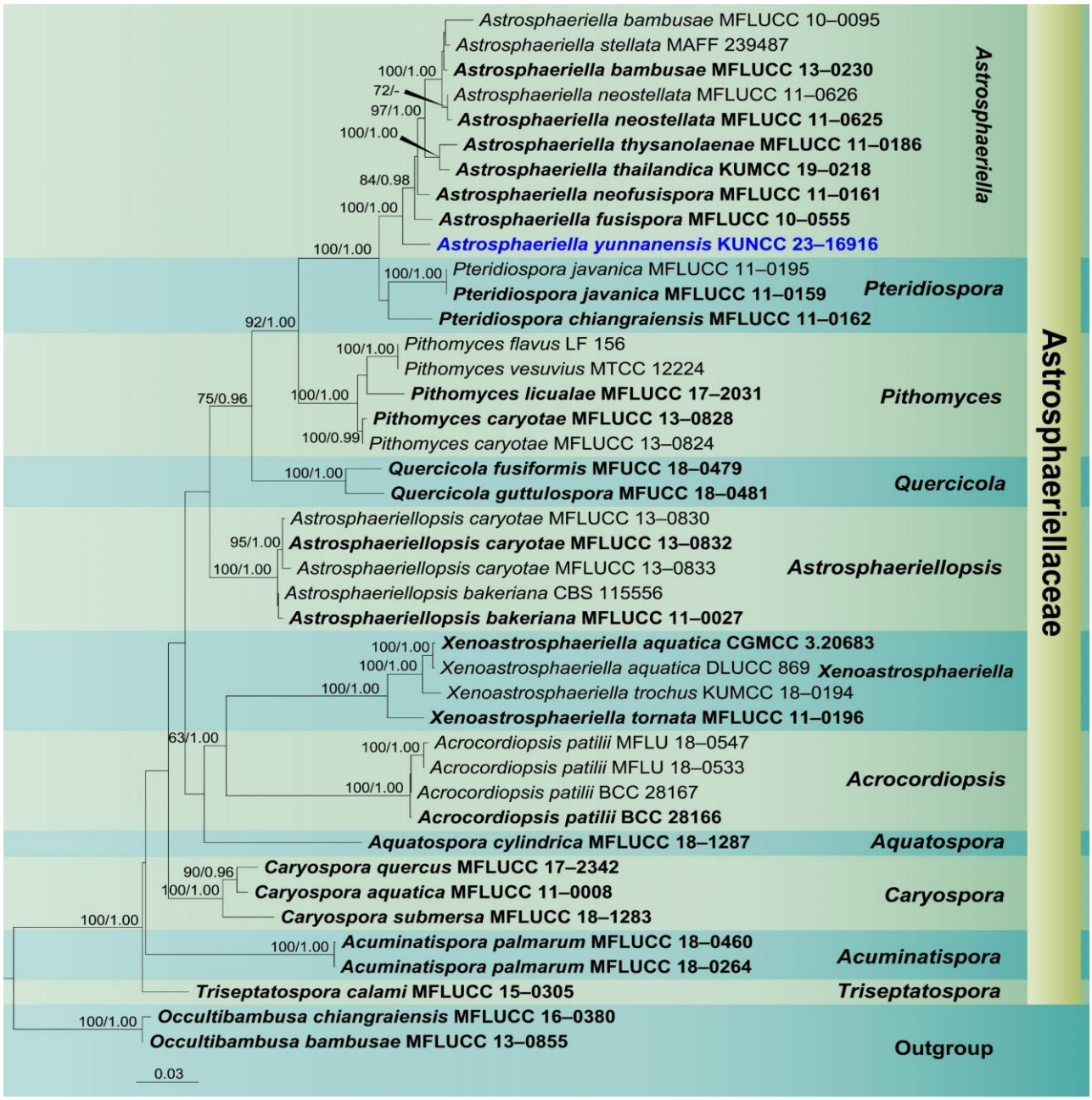

Figure 2 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, *tef*1-α and *rpb*2 sequence dataset representing *Astrosphaeriellaceae*. Forty-two strains are included in the combined analyses which comprise 4682 characters including gaps (1322 characters for LSU, 1409 characters for SSU, 853 characters for *tef*1-α, 1044 characters for *rpb*2). *Occultibambusa chiangraiensis* (MFLUCC 16–0380) and *O. bambusae* (MFLUCC 13–0855) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best-scoring RAxML tree with a final likelihood value of -18969.103671 is presented. The matrix had 1310 distinct alignment patterns, with 39.07% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.250901, C = 0.242761, G = 0.279531, T = 0.226807; substitution rates AC = 1.355592, AG = 3.863968, AT = 1.201855, CG = 1.109714, CT = 10.015154, GT = 1.000000; Tree-Length = 1.107489; gamma distribution shape parameter α = 0.165350. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains indicated are in bold and newly generated sequence are shown in blue.

Cryptocoryneum sinense H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 3

Index Fungorum number: IF571860; Facesoffungi number: FoF15478

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

Holotype – HKAS 131841.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Sporodochia* on natural substrate effuse, superficial, conspicuous, glistening, flattened, pulvinate, often confluent, dark brown to black. *Conidiophores* arising from the stromatic cells, straight, simple, septate, hyaline to pale brown, smooth. *Conidiogenous cells* monoblastic, cylindrical to oblong, terminal, determinate, hyaline to pale brown. *Conidia* (26–)31–41(–49) × 19–28(–37) μm ($\bar{x}$ = 36 × 24 μm, n = 40), solitary, dry, acrogenous, branched, cheiroid, with brown cap cells firmly united together, 7–16 arms (mostly 11 arms); basal cells brown, cuneiform, smooth, thin-walled; arms (22–)30–38(–42) × 4–5 μm ($\bar{x}$ = 34 × 5 μm, n = 40), cylindrical, hyaline to pale brown, branched at base, smooth, 7–9(–11)-septate. Sexual morph: Undetermined.

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 two months at room temperature, colony circular or Irregular, smooth edge, surface hyphae pale brown, fluffy, flocculent; reverse side pale brown to brown, dense, cracked in the middle.

Material examined – China, Yunnan Province, Yuxi City, Mofanghe Reservoir, 23°40'36" N, 101°44'08" E; 2213 m; on submerged decaying wood, 23 February 2023, W. Ying, on submerged, H.W. Shen, FD 46–10–1 (HKAS 131841, holotype), ex-type culture KUNCC 23–14279.

GenBank numbers – ITS: PQ340459, LSU: PP189895, SSU: PQ435255, *tef*1-α: PQ456946, *rpb*2: PQ348599.

Notes – *Cryptocoryneum sinense* is similar to other *Cryptocoryneum* in having cheiroid, septate conidia, and conidial arms developed upwards from the cap cells (Fuckel 1865, Hashimoto et al. 2016, Hashimoto et al. 2017, Boonmee et al. 2021). Based on the key to species of *Cryptocoryneum* provided by Hashimoto et al. (2016), *C. sinense* can be distinguished from other *Cryptocoryneum* species. In the phylogenetic analysis, *C. sinense* clustered with *C. rosae* with 100% ML and 1.00 BYPP support (Fig. 4). The comparison of ITS, LSU, SSU *tef*1-α and *rpb*2 sequences between *C. sinense* and *C. rosae* shows that ITS, *tef*1-α and *rpb*2 have 1% (5/477 bp), 2.3% (20/884 bp), and 2.3% (23/989 bp) differences respectively, while there are not any base pair differences between LSU and SSU sequences. Using the guidelines of Chethana et al. (2021), and based on morphological and phylogenetic evidence, we introduce *C. sinense* as a new species, which is the first species of *Cryptocoryneum* discovered from freshwater habitats.

Hermatomycetaceae Locq. ex A. Hashim. & Kaz. Tanaka, Persoonia 39: 56 (2017).

Hermatomycetaceae was informally proposed as a provisional name by Locquin (1984) which was later confirmed by Hashimoto et al. (2017) and reintroduced to accommodate the single genus *Hermatomyces*, based on phylogenetic analysis (Hashimoto et al. 2017). Only asexual morphs have been reported, and are characterized by dimorphic conidia (lenticular or cylindrical) arising from sporodochial conidiomata (Chang 1995, Tibpromma et al. 2016, Hashimoto et al. 2017, Koukol et al. 2018, Ren et al. 2021).

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

Hermatomyces was established by Spegazzini (1910) to accommodate *H. tucumanensis*. It 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). *Hermatomyces* species are widely distributed and have been reported from both temperate and tropical regions, mainly from Thailand in Asia (Doilom et al. 2017, Tibpromma et al. 2016, Hashimoto et al. 2017, Koukol et al.

2018, Boonmee et al. 2021, Ren et al. 2021, de Silva et al. 2022). Although Index Fungorum lists 34 records of *Hermatomyces*, only 26 species are recognized, and these members are saprobic on dead plant debris in terrestrial habitats, and there have been no reports from freshwater habitats (Koukol et al. 2018, Ren et al. 2021, Wijayawardene et al. 2021, de Silva et al. 2022).

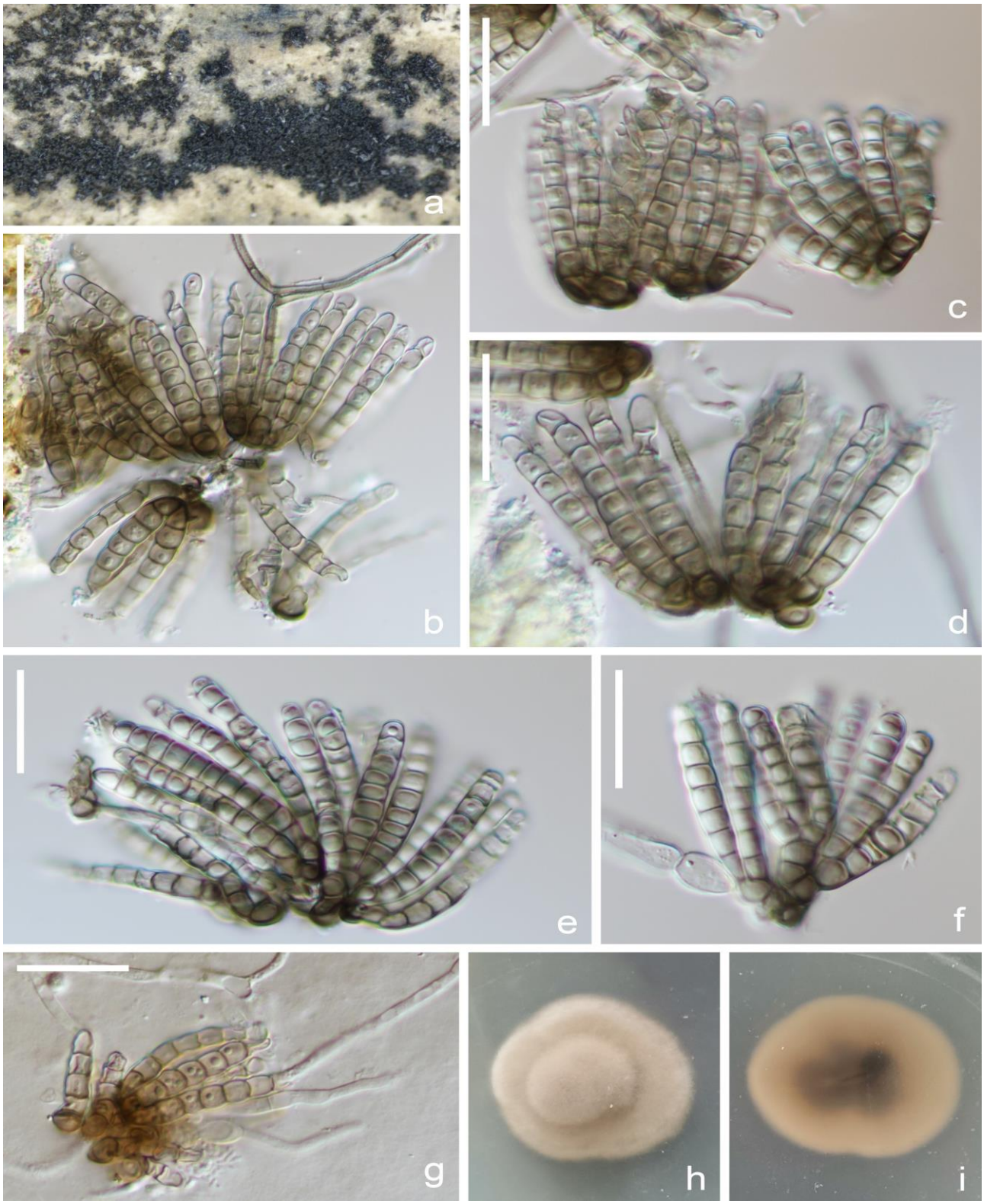

Figure 3 – *Cryptocoryneum sinense* (HKAS 131841, holotype). a Colonies on the natural substrate. b–f Conidia. g Germinated conidium. h, i Culture on PDA. Scale bars: b–g = 20 μm.

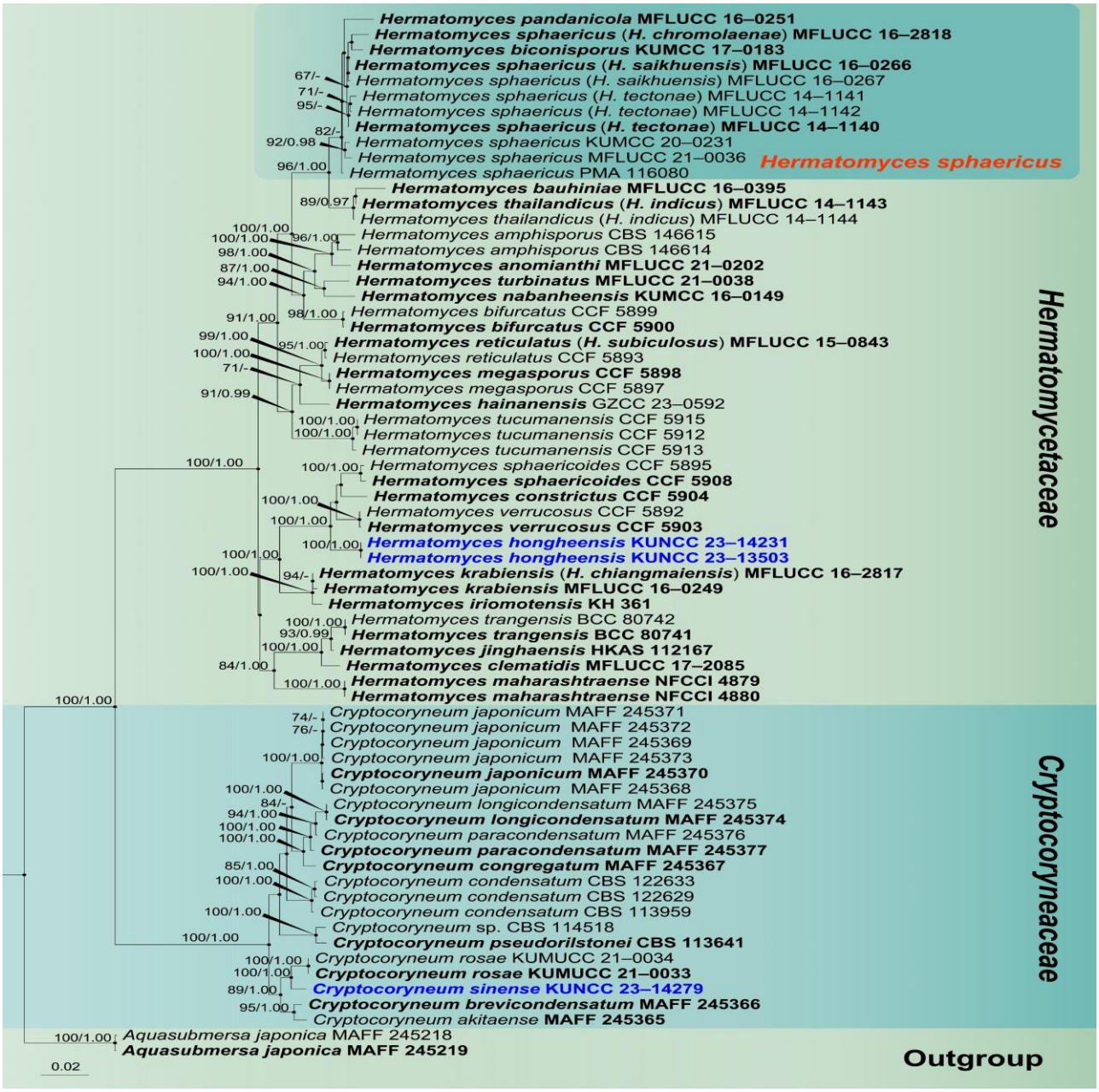

Figure 4 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef*1-α and *rpb*2 sequence dataset representing *Hermatomycetaceae* and *Cryptocoryneaceae*. Sixty-eight strains are included in the combined analyses which comprise 4233 characters including gaps (518 characters for ITS, 868 characters for LSU, 1024 characters for SSU, 839 characters for *tef*1-α, 984 characters for *rpb*2). *Aquasubmersa japonica* (MAFF 24218 and MAFF 24219) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best-scoring RAxML tree with a final likelihood value of -17718.344312 is presented. The matrix had 1076 distinct alignment patterns, with 19.20% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248854, C = 0.254130, G = 0.264427, T = 0.232589; substitution rates AC = 1.098813, AG = 4.478906, AT = 1.236894, CG = 0.937373, CT = 9.866685, GT = 1.000000; Tree-Length = 0.749179; gamma distribution shape parameter α = 0.118053. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Hermatomyces hongheensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 5

Index Fungorum number: IF571861; Facesoffungi number: FoF15479

Etymology – The name refers to Honghe Prefecture, Yunnan Province, where the holotype was collected.

Holotype – HKAS 132064

Saprobic on decaying submerged wood in freshwater. 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, subhyaline or pale brown, unbranched, smooth, thick-walled. *Conidiogenous cells* holoblastic, short, cylindrical, hyaline, thick-walled, terminal, determinate, often arising directly on the superficial mycelium. *Conidia* 32–38(–47) × (19–)25–31(–35) µm ($\bar{x}$ = 35 × 28 µm, n = 40), 17–20 µm thick, solitary, dry, lenticular, subglobose to ellipsoidal, muriform, sometimes slightly constricted at the septa, smooth, central cells dark brown to black, peripheral cells narrow and brown, flattened, subhyaline to pale brown, obovoid or oblong in side view, consisting of two rows, each row with 4–5 cells, middle cells dark brown to black, end cells pale brown to dark brown. Sexual morph: Undetermined.

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, colony circular, smooth edge, surface hyphae grey-brown, fluffy, flocculent; reverse side grey-brown to brown, dense, cracked in the middle.

Material examined – China, Yunnan Province, Honghe City, Yilonghu Lake, 23°40'56.4" N, 101°43'46.8" E, 1400 m; on submerged decaying wood, 23 February 2023, H.W. Shen, FD 45-23-2 (HKAS 132064, holotype), ex-type cultures KUNCC 23–13503 = KUNCC 23–14231.

GenBank numbers – KUNCC 23–13503, ITS: PQ340461, LSU: PP189897, SSU: PQ435257, *tef*1-α: PQ456948, *rpb*2: PQ348601; KUNCC 23–14231, ITS: PQ340462, LSU: PP189898, *tef*1-α: PQ456949.

Notes – In the phylogenetic analysis, *Hermatomyces hongheensis* clustered with *H. sphaericoides*, *H. verrucosus* and *H. constrictus* in a distinct clade within *Hermatomyces* (Fig. 4). Except for *H. constrictus*, the other two species of this lineage only produce lenticular conidia (Koukol et al. 2018). *Hermatomyces hongheensis* can be distinguished from *H. constrictus* by its larger conidia (32–38(–47) × (19–)25–31(–35) µm *vs.* (22−)25.5–29.5(−32) × 19–23.5(−27.5)), in addition *H. constrictus* has cylindrical conidia, in contrast, the conidia of *H. hongheensis* are subglobose to ellipsoidal (Koukol et al. 2018). *Hermatomyces sphaericoides* differs from *H. hongheensis* in having smaller conidia ((20.5−) 24.5–28(−31) × (20−)23–26(−29) µm *vs.* 32–38(–47) × (19–)25–31(–35) µm). *Hermatomyces hongheensis* has larger conidia than *H. verrucosus* (32–38(–47) × (19–)25–31(–35) µm *vs.* 23–30(−39) × 21–29.5 µm). We therefore describe *H. hongheensis* as a new species, which is the first report of *Hermatomyces* species in a freshwater habitat.

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

Lentitheciaceae was introduced by Zhang et al. (2009a) to accommodate those lentitheciaceous taxa that have narrow peridia, fusiform to broadly cylindrical pseudoparaphyses, hyaline ascospores with 1–3-transverse septa and containing refractive globules, surrounded by a mucilaginous sheath or extended appendage-like sheaths and asexual morphs producing stagonospora-like or dendrophoma-like asexual morphs (Zhang et al. 2012, Hyde et al. 2013, Wanasinghe et al. 2014, Calabon et al. 2021b). Currently, the family comprises 19 genera with more than 100 species on various substrates from different environments have been accepted to *Lentitheciaceae* (Höhnel 1919, Tanaka & Harada 2005, de Gruyter et al. 2009, Zhang et al. 2009a, Hirayama et al. 2010, Quaedvlieg et al. 2013, Wanasinghe et al. 2014, Crous et al. 2015a, Knapp et al. 2015, Phookamsak et al. 2015b, Tanaka et al. 2015, Wijayawardene et al. 2015, Li et al. 2016,

Dayarathne et al. 2018, Hyde et al. 2020a, 2021, Liu et al. 2021, Yang et al. 2022a, Rajeshkumar et al. 2023, Shen et al. 2023). *Halobyssothecium*, *Lentithecium*, *Setoseptoria* and *Tingoldiago* accommodates mostly freshwater (Tanaka et al. 2005, 2015, Zhang et al. 2009a, b, Quaedvlieg et al. 2013, Calabon et al. 2021b, Shen et al. 2023, Yang et al. 2023).

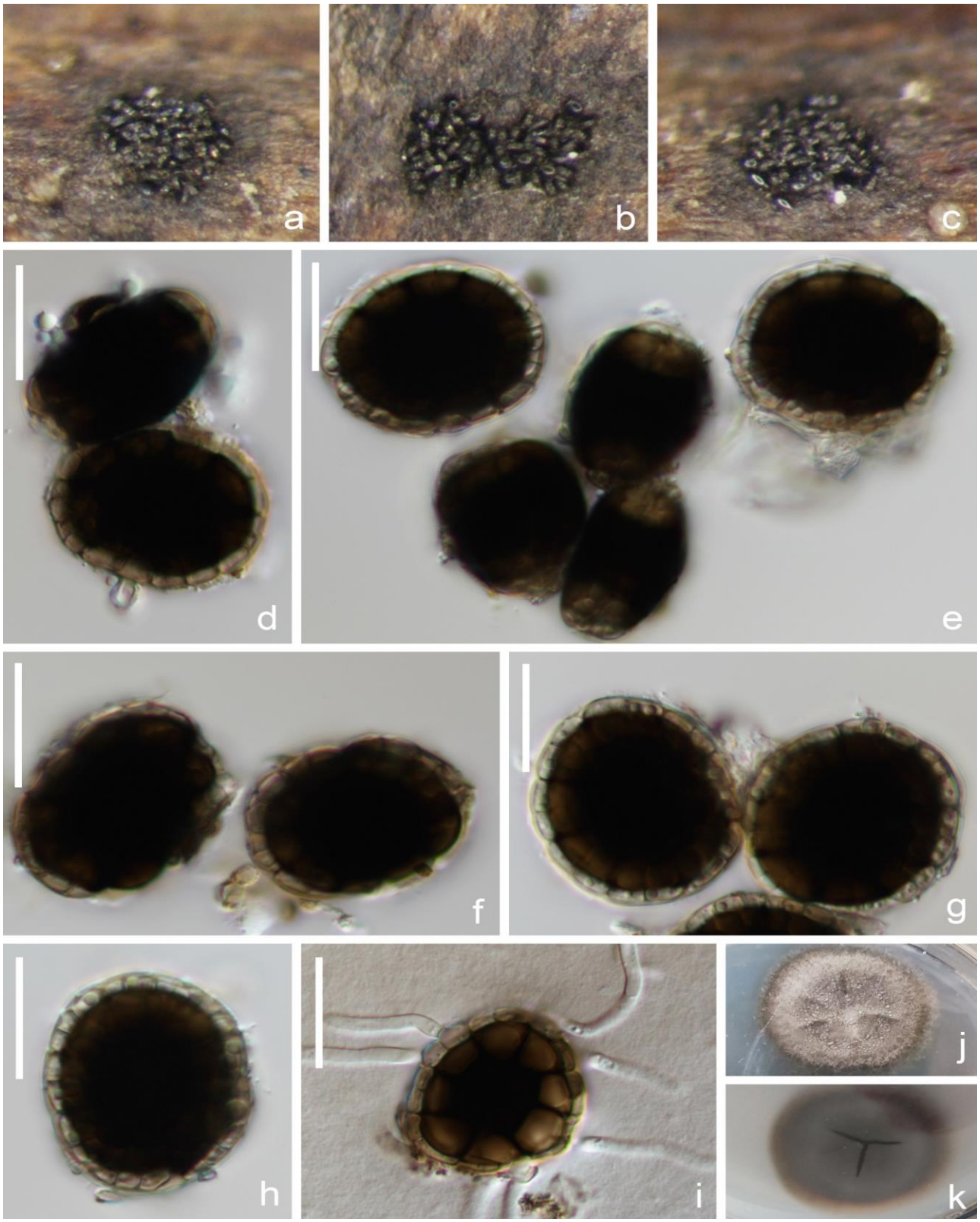

Figure 5 – *Hermatomyces hongheensis* (HKAS 132064, holotype). a–c Colonies on the natural substrate. d Conidiogenous cell and conidia. e–h Conidia. i Germinated conidium. j, k Culture on PDA. Scale bars: d–i = 20 μm.

Setoseptoria Quaedvl., Verkley & Crous, Stud. Mycol. 75: 382 (2013)

Setoseptoria was introduced by Quaedvlieg et al. (2013) and is typified by *S. phragmitis*. It was established to accommodate septoria-like coelomycetes having subcylindrical, (1–)3-septate hyaline conidia. The sexual morph of *Setoseptoria* is characterized by superficial to semi-immersed, gregarious, subglobose to globose ascomata, septate, filamentous pseudoparaphyses, ascospores are fusiform to cylindrical or ellipsoidal-fusiform, with a submediant primary septum, constricted at the septum, hyaline, asymmetrical, with a mucilaginous sheath. Only *S. phragmitis* and *S. suae* are known with asexual morphs, characterized by immersed, globose conidiomata, subcylindrical to doliiform, hyaline, smooth, conidiogenous cells and subcylindrical, (1–)3-septate, straight to slightly curved, hyaline, smooth, conidia (Quaedvlieg et al. 2013, Tanaka et al. 2015, Wanasinghe et al. 2018, Shen et al. 2023). Currently, 12 species are listed in Index Fungorum (http://www.indexfungorum.org/Names/Names.asp; accessed on 20 June 2024); members of *Setoseptoria* are saprobic on herbaceous plants, especially *Phragmites* (*Poaceae*) (Quaedvlieg et al. 2013, Tanaka et al. 2015, Hyde et al. 2016b, Wanasinghe et al. 2018, Shen et al. 2023). Most species of *Setoseptoria* are reported from terrestrial habitats, with only *S. arundinacea*, *S. baiyunensis*, *S. bambusae*, *S. magniarundinacea* and *S. suae* collected from freshwater habitats (Tanaka et al. 2015, Senanayake et al. 2023, Shen et al. 2023, Yang et al. 2023).

Setoseptoria phragmitis Quaedvl., Verkley & Crous, Stud. Mycol. 75: 383 (2013) Fig. 6

Saprobic on submerged decaying wood in freshwater. Asexual morph: *Conidiomata* 200–290 µm high, 190–200 µm diam., solitary, scattered, semi-immersed to immersed in the host, pycnidial, subglobose to ellipsoidal, flattened, unilocular, pale brown to dark brown, ostiolate, papillate. *Ostiole* centrally located, short. *Peridium* 25–40 µm wide, thickening at the upper zone, thick-walled, composed of several layers, outermost layer heavily, pigmented, thick-walled, comprising pale brown to dark brown cells of *textura angularis*, inner layer composed of pale brown to hyaline, flattened, thin-walled cells of *textura angularis* to *textura prismatica*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–11(–15) × 3–4 µm ($\bar{x}$ = 8 × 3 µm, n = 35), arising from the inner layers of conidiomata, hyaline, enteroblastic, phialidic, determinate, ampuliform, subcylindrical to lageniform. *Conidia* (40–)56–82(–105) × 4–5 µm ($\bar{x}$ = 69 × 4 µm, n = 35), cylindrical to subcylindrical, with obtuse to subobtuse ends, straight or slightly curved, hyaline, (3–)5–7(–10)-septate, euseptate, guttulate, slightly constricted at the septum, smooth-walled. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA within 12 h and germ tubes produced from around of conidium. Colonies on PDA reaching 2–3 cm diam. after two months at room temperature, colony circular, smooth edge, surface hyphae pale brown to brown, flocculent, dense; reverse side pale brown to brown.

Material examined – CHINA, Yunnan Province, Kunming City, Yangzonghai Lake, 24°54'43.70" N, 103°1'3.64" E, 1770 m; on submerged decaying culm of *Phragmites* (*Poaceae*), 20 February 2023, C.C. Ao, FD 29-7-2 (HKAS 131588), living culture KUNCC 23–13107; *ibid*, Dali City, Eryuan county, Cibihu Lake, 26°09' N, 99°57' E, 2052 m; on submerged decaying culm of *Phragmites* (*Poaceae*), 21 July 2021, S.P. Huang, CBH 1-27-1 (HKAS 131634).

GenBank numbers – KUNCC 23–13107, ITS: PQ340472, LSU: PP189910, SSU: PQ435267, *tef*1-α: PQ456962; HKAS 131634, ITS: PQ571252, LSU: PP189926, SSU: PQ341573.

Notes – Two strains collected from freshwater plateau lakes of Yunnan Province were identified as *Setoseptoria phragmitis* based on morphological and phylogenetic studies. Morphological examination showed that these two collections fit well with the description of *S. phragmitis* in having enteroblastic, phialidic, determinate, ampuliform, subcylindrical to lageniform conidiogenous cells and cylindrical to subcylindrical, hyaline, euseptate, guttulate conidia with obtuse to subobtuse ends (Quaedvlieg et al. 2013). Multigene phylogenetic analysis showed that our collections cluster with two strains of *S. phragmitis* (CBS 114802 and CBS 144966) (Fig. 7). Comparison of ITS, LSU, and SSU gene loci between the two newly obtained strains and the type strain of *S. phragmitis* revealed only a few base pair differences. The *Setoseptoria* species appear to

have a host-specificity for *Phragmites* sp. (*Poaceae*), with almost previously reported species were isolated from *Phragmites* sp. (*Poaceae*) (Quaedvlieg et al. 2013, Tanaka et al. 2015, Wanasinghe et al. 2018, Shen et al. 2023). *Setoseptoria phragmitis* has so far been reported in terrestrial and marine habitats (Quaedvlieg et al. 2013, Tibell et al. 2020), and in this study, *S. phragmitis* was reported from a freshwater habitat for the first time.

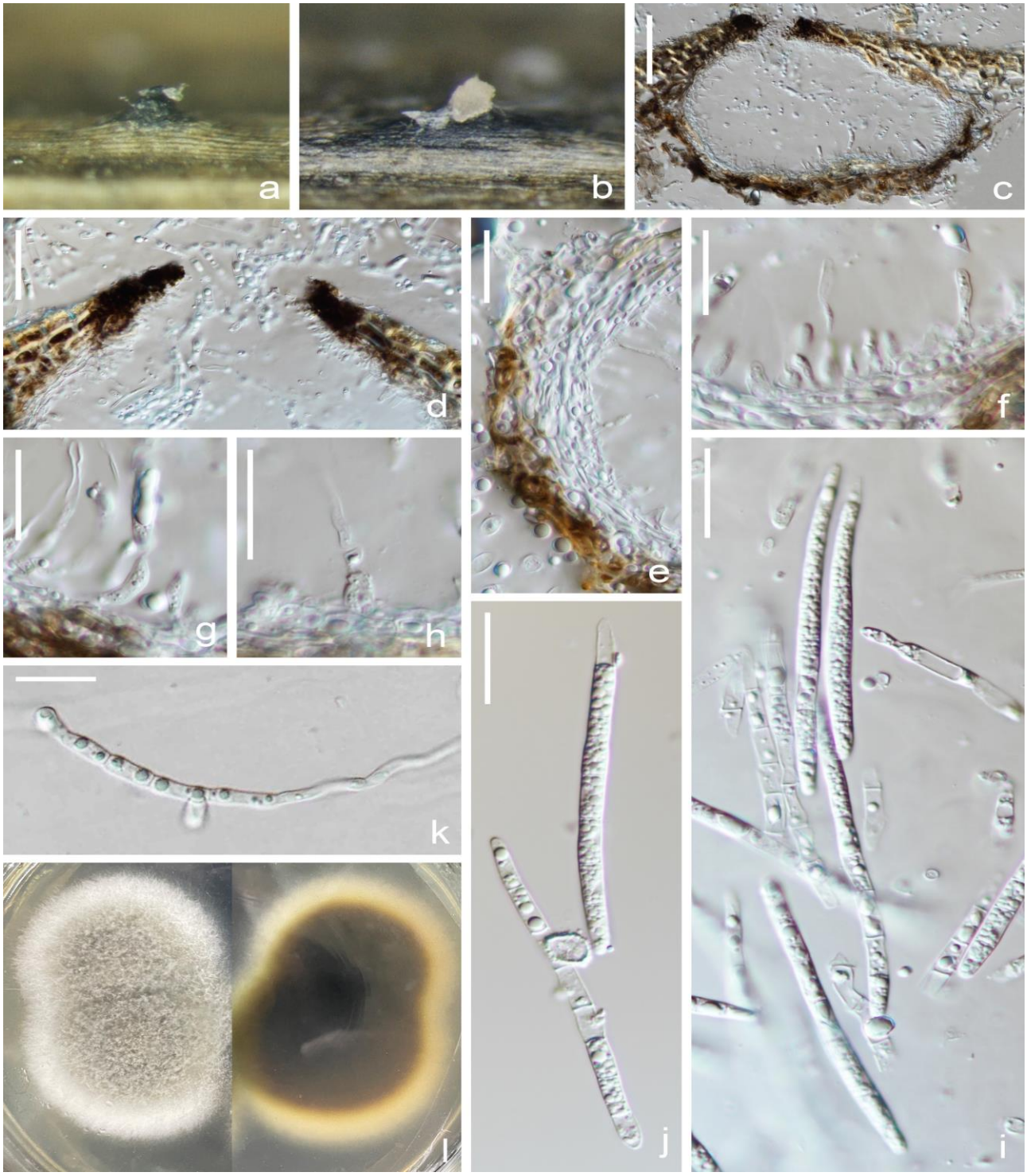

Figure 6 – *Setoseptoria phragmitis* (HKAS 131634, new habitat records). a, b Appearance of coniodiomata on substrate. c Section of conidiomata. d Ostiole. e Setae on peridium. f–h Conidiogenous cells and developing conidia. i, j Conidia. k Germinating conidium. l Colony on PDA. Scale bars: c = 70 µm, d = 40 µm, e–k = 20 µm.

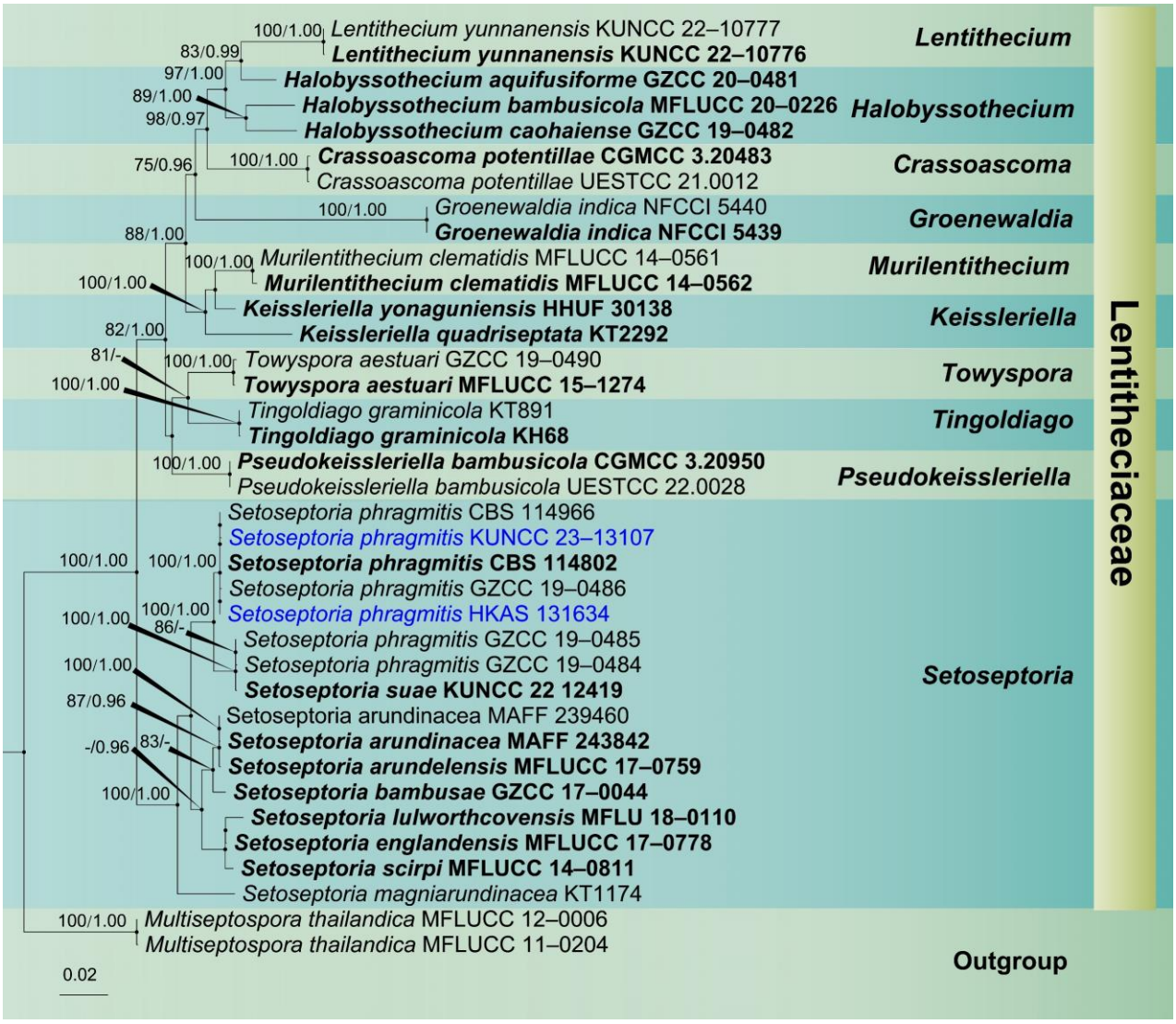

Figure 7 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU and *tef*1-α sequence dataset representing *Lentitheciaceae*. Thirty-seven strains are included in the combined analyses which comprise 3800 characters including gaps (1321 characters for LSU, 512 characters for ITS, 1013 characters for SSU, 945 characters for *tef*1-α). *Multiseptospora thailandica* (MFLUCC 12–0006 and MFLUCC 11–0204) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best-scoring RAxML tree with a final likelihood value of -13223.809207 is presented. The matrix had 826 distinct alignment patterns, with 20.67% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.250901, C = 0.250273, G = 0.270788, T = 0.239954; substitution rates AC = 0.238985, AG = 1.838146, AT = 1.378727, CG = 1.367292, CT = 6.917654, GT = 1.000000; Tree-Length = 0.634713; gamma distribution shape parameter α = 0.129684. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Lindgomycetaceae K. Hiray., Kaz. Tanaka & Shearer, Mycologia 102(3): 733 (2010).

The aquatic family *Lindgomycetaceae* was introduced to accommodate *Lindgomyces* and its sister taxon *Massariosphaeria typhicola*, based on morphological and molecular phylogenetic analysis (Hirayama et al. 2010). Thereafter, a previously described genus, *Clohesyomyces*, and six

new genera *viz. Aquimassariosphaeria* (Dong et al. 2020), *Arundellina* (Hyde et al. 2016b), *Hongkongmyces* (Tsang et al. 2014), *Ocellisimilis* (Yang et al. 2023), *Lolia* (Abdel-Aziz & Abdel-Wahab 2010) and *Neolindgomyces* (Jayasiri et al. 2019) were placed in *Lindgomycetaceae* based on phylogenetic and morphological data. Species of *Lindgomycetaceae* usually grow on woody debris as saprobes in aquatic habitats (Jayasiri et al. 2019, Dong et al. 2020, Yang et al. 2023). Several species have been reported as human pathogens from terrestrial habitats (Tsang et al. 2014, Hyde et al. 2016b, 2017). Currently, 34 species are placed in this family, 20 of which are reported from freshwater habitats (https://indexfungorum.org/, accessed on 20 June 2024).

Aquimassariosphaeria W. Dong & Doilom, Fungal Diversity 105: 424 (2020).

Aquimassariosphaeria was established by Dong et al. (2020) to accommodate *A. kunmingensis* (type) and *A. typhicola* (*Massariosphaeria typhicola* (P. Karst.) Leuchtm.), based on morphological and phylogenetic analyses (Dong et al. 2020). *Aquimassariosphaeria* is only known by the sexual morphs which is characterized by immersed, erumpent to superficial ascomata, sometimes staining substrate purple, and narrowly fusiform or vermiform, brown, transversely septate ascospores (Dong et al. 2020). Currently, three sexual species are accepted in *Aquimassariosphaeria*, all of these species are saprobic on decaying plant debris submerged in freshwater habitats (Dong et al. 2020, Yang et al. 2023).

Aquimassariosphaeria aquatica H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 8

Index Fungorum number: IF571862; Facesoffungi number: FoF15480

Etymology – The name refers to the aquatic habitat where the holotype was collected.

Holotype – HKAS 131666.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Colonies* on natural substrate effuse, hairy, surface, conspicuous, brown to dark brown. *Mycelium* mostly immersed, partly superficial, consisting of branched, septate, smooth, pale brown to brown hyphae. *Conidiophores* micronematous, reduced to a hyphal cell that extends laterally to form a conidium, unbranched, hyaline to pale brown. *Conidiogenous cells* integrated, monoblastic, cylindrical, pale brown to brown, smooth-walled. *Conidia* 494–592 × 6–8 μm ($\bar{x}$ = 540 × 7 μm, n = 35), usually more than 500 μm long, solitary, filamentous, filiform, straight or slightly curved, unbranched, septate, smooth-walled, constricted at some septum, brown to dark brown, guttulate, proliferative apically. Sexual morph: Undetermined.

Material examined – China, Yunnan Province, Yuxi City, Qiluhu Lake, 24°10'29" N, 102°46'40" E; 1796 m; on submerged decaying wood, 12 July 2021, Y.K. Jiang, QLH 2-16-1 (HKAS 131666, holotype); *ibid*, Honghe Prefecture, Yilonghu Lake, 23°41'49.2" N, 102°30'52.2" E; 1400m; on submerged decaying wood, 23 February 2023, H.W. Shen, FD 44-8-2 (HKAS 131715, paratype), ex-paratype culture KUNCC 23–13472; *ibid*, Yuxi City, Xingyunhu Lake, 24°23'05" N, 102°48'22" E; 1722m; on submerged decaying wood, 10 July 2021, H.W. Shen, XYH 1-5-1 (HKAS 131807); *ibid*, Qiluhu Lake, on submerged decaying wood, 10 July 2021, Q.X. Yang, QLH 5-27-2 (HKAS 132075), living culture KUNCC 23–16137.

GenBank numbers – HKAS 131666, LSU: PP189914, SSU: PQ341572, *tef*1-α: PQ456964; HKAS 131807, LSU: PP189913, SSU: PQ341571, *tef*1-α: PQ456963; KUNCC 23–13472, LSU: PP189892, SSU: PQ435250, *tef*1-α: PQ456943; KUNCC 23–16137, LSU: PP189891, SSU: PQ435249.

Notes – In our phylogenetic analysis, species of *Aquimassariosphaeria*, *Clohesyomyces*, and *Lolia*, as well as our four new collections, clustered in an unstable lineage (Fig. 9). Three verified strains of *Clohesyomyces aquaticus* (MLUCC 11–0092, MLUCC 15–0979 and MLUCC 18–1037) clustered with *Trematosphaeria hydrela* (CBS 880.70) at the base of the clade, while the endophyte *Clohesyomyces symbioticus* (DM01444, DM0177 and DM0192) and two unnamed strains of *Clohesyomyces* sp. (KUNCC 23–12906 and KUNCC 23–13013) clustered in *Aquimassariosphaeria* clade, while species of *Lolia* clustered between these two clades. Currently, only sexual morphs have been discovered in *Aquimassariosphaeria*, and are characterized by

narrowly fusiform or vermiform, brown, transversely septate ascospores (Dong et al. 2020, Yang et al. 2023). However, only the asexual morph (Coelomycetous) has been reported in *Clohesyomyces symbioticus*, and so whether *C. symbioticus* is related to *Aquimassariosphaeria* requires further research. Our four asexual collections with filiform conidia are related to *Aquimassariosphaeria* in the phylogenetic analysis (Fig. 9), but morphological comparisons were impossible. Based on current morphological and molecular data, we conservatively consider our four collections to be asexual stages of *Aquimassariosphaeria* until more evidence emerges that they are distinct taxa. We therefore introduce *A. aquatica* as a new species.

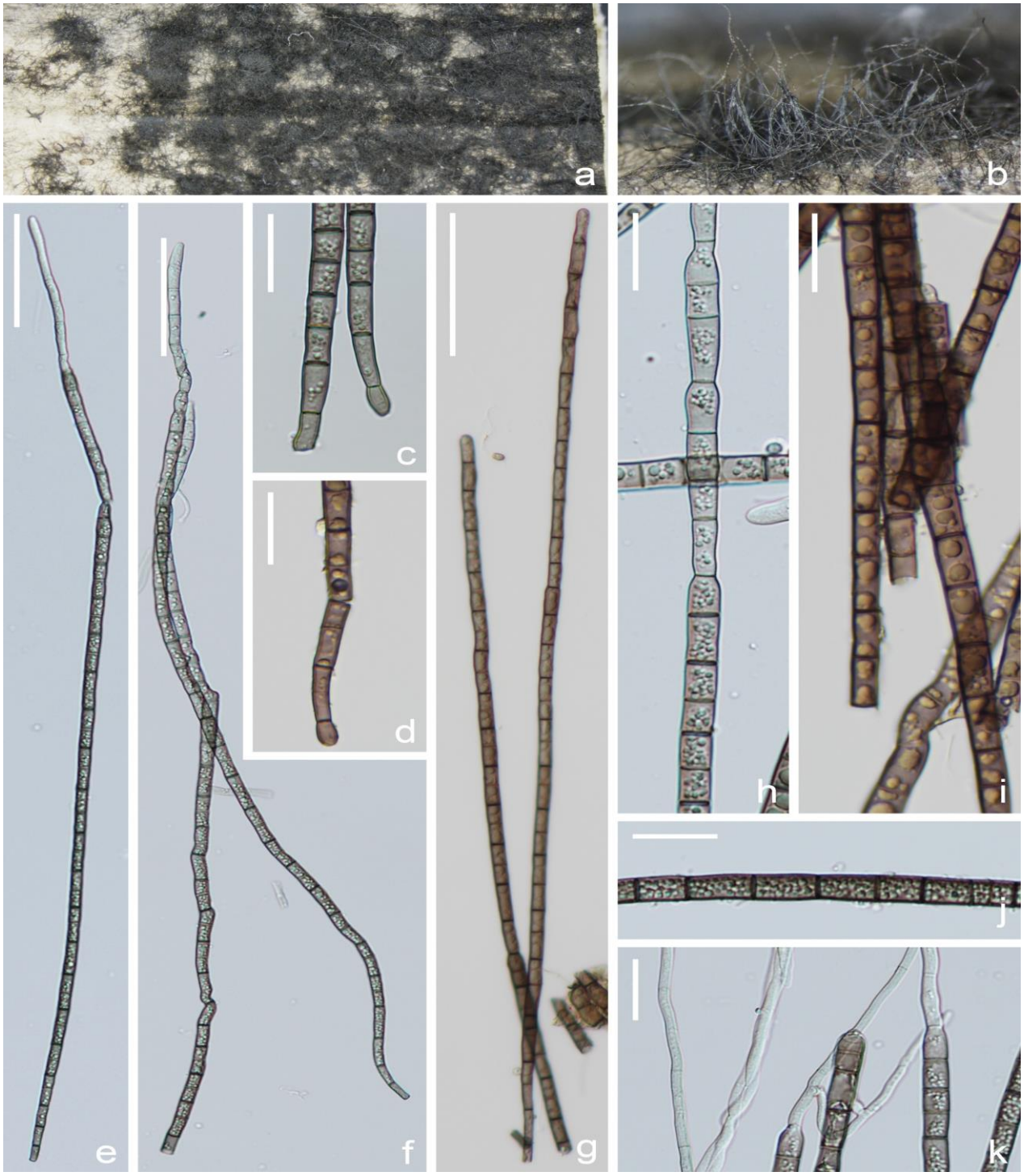

Figure 8 – *Aquimassariosphaeria aquatica* (HKAS 131666, holotype). a, b Colonies on substrate. c, d Base of conidia. e–g Conidia. h Proliferating conidia. i, j Part of conidia. k Conidia germinated on natural substrate. Scale bars: c = 70 µm, d = 40 µm, e–k = 20 µm.

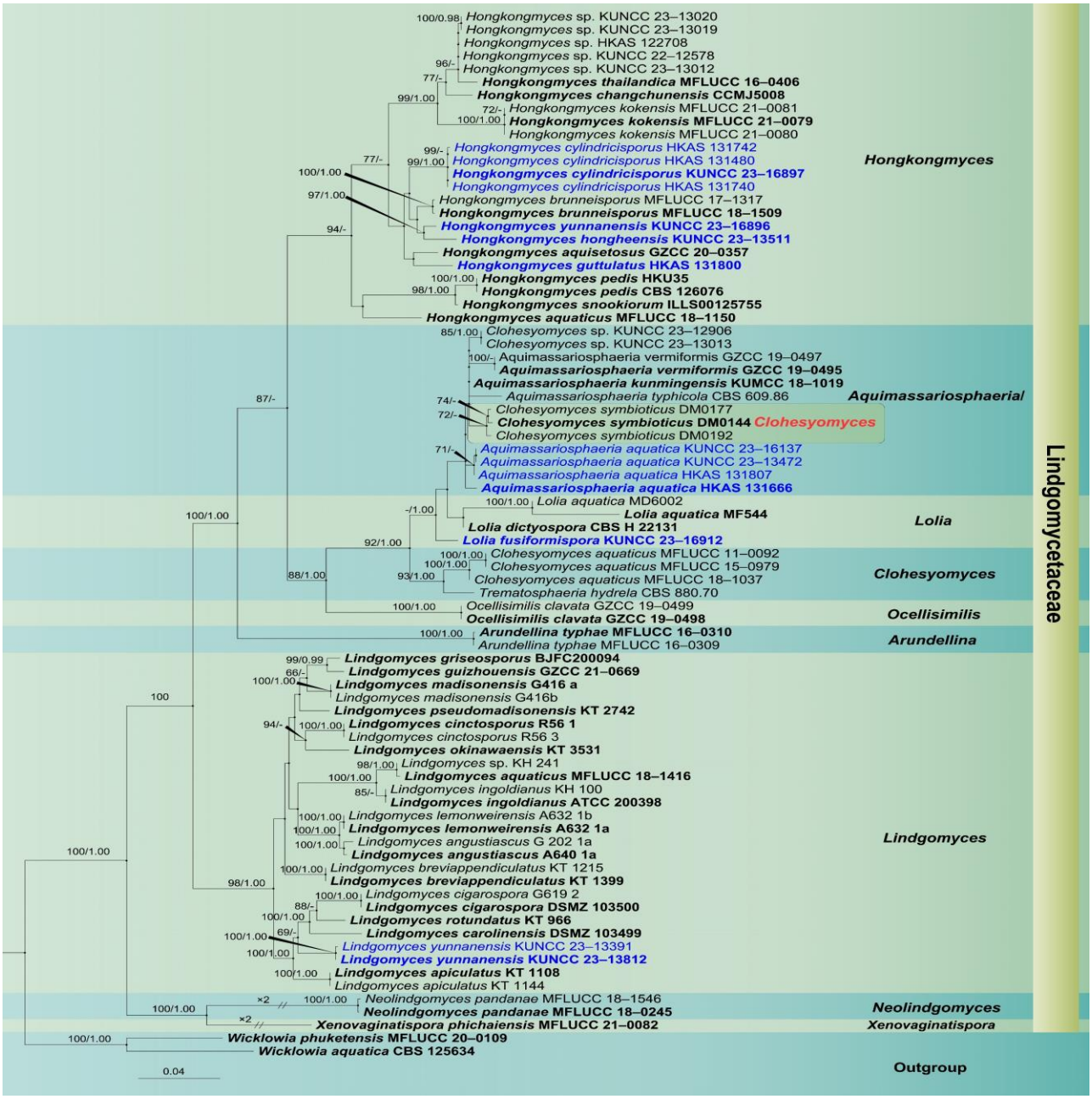

Figure 9 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef*1-α sequence dataset representing *Lindgomycetaceae*. Eighty strains are included in the combined analyses which comprise 3259 characters including gaps (1004 characters for LSU, 941 characters for SSU, 430 characters for ITS, 883 characters for *tef*1-α). *Wicklowia aquatica* (MFLUCC 20–0109) and *M. phuketensis* (CBS 125634) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best-scoring RAxML tree with a final likelihood value of -23952.766047 is presented. The matrix had 796 distinct alignment patterns, with 29.80% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248623, C = 0.233217, G = 0.274440, T = 0.243720; substitution rates AC = 1.039009, AG = 2.894433, AT = 1.657722, CG = 1.323879, CT = 9.302401, GT = 1.000000; Tree-Length = 0.971424; gamma distribution shape parameter α = 0.125625. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Hongkongmyces C.C. Tsang, J.F.W. Chan, N.J. Trendell-Smith, A.H.Y. Ngan, I.W.H. Ling, S.K.P. Lau & P.C.Y. Woo, Med. Mycol. 52 (7): 740 (2014).

Hongkongmyces was introduced by Tsang et al. (2014) to accommodate *H. pedis*, which was isolated from a human foot with a suppurative granulomatous infection. Subsequently, six freshwater species *viz. H. aquaticus*, *H. aquisetosus*, *H. brunneisporus*, *H. changchunensis*, *H. kokensis*, *H. snookiorum*, and one new terrestrial species, *H. thailandicus* have been reported (Hyde et al. 2017, Dong et al. 2020, Bao et al. 2021b, Boonmee et al. 2021, Jayawardena et al. 2022, Yang et al. 2023). Except for *H. pedis* and *H. snookiorum*, all other species grow saprobically on decaying plant debris. Both the sexual and asexual morphs of *Hongkongmyces* have been reported. The sexual morph is characterized by subglobose, dark brown to black ascomata; filiform, hyaline, septate, branched pseudoparaphyses; hyaline, reddish-brown to dark brown, yellowish-green, septate, fusiform ascospores which are surrounded with a mucilaginous sheath (Hyde et al. 2017, Bao et al. 2021b, Yang et al. 2023). The asexual morph is characterized by globose to ampulliform or ellipsoidal, pycnidial conidiomata; hyaline, solitary, ellipsoid to obovoid, globose, subglobose, irregular, aseptate conidia (Crous et al. 2018, Dong et al. 2020, Boonmee et al. 2021, Jayawardena et al. 2022). Currently, eight species have been included in *Hongkongmyces*, including three sexual species, *viz. H. aquisetosus*, *H. brunneisporus* and *H. thailandica* (Hyde et al. 2017, Bao et al. 2021b, Jayawardena et al. 2022, Yang et al. 2023).

Hongkongmyces cylindricisporus H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 10

Index Fungorum number: IF571863; Facesoffungi number: FoF15481

Etymology – The name refers to the cylindrical to subcylindrical conidia of this species.

Holotype – HKAS 131741.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Conidiomata* 211–272 µm high, 239–320 µm diam., pycnidial, black, scattered, solitary to gregarious, semi-immersed or superficial, globose to subglobose, uni-loculate, ostiolate. *Ostioles* central, papillate. *Peridium* 19–32 µm wide, composed of brown to dark brown, irregular, thick-walled cells arranged in a *textura angularis*. *Conidiophores* reduced. *Conidiogenous cells* 7–9 × 3–4 µm ($\bar{x}$ = 8 × 4 µm, n = 20), phialidic, determinate, cylindrical to subcylindrical, hyaline, thin-walled. *Conidia* (24–)30–37(–43) × 6–7 µm ($\bar{x}$ = 34 × 6 µm, n = 60), hyaline, ellipsoidal, cylindrical to subcylindrical, rounded at both ends, straight or slightly curved, (2–)3-septate, slightly constricted at septum, smooth-walled, guttulate. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA within 12 h and germ tubes produced from ends of conidium. Colonies on PDA reaching 2–3 cm diam. after two months at room temperature, colony circular, smooth edge, surface hyphae reddish brown to dark brown, flocculent, dense; reverse side dark brown, smooth, dense, cracked at the middle zone.

Material examined – China, Yunnan Province, Lijiang City, Luguhu Lake; 27°44'13.59" N, 100°49'04.72"E, 2690 m, on submerged decaying wood, 3 March 2021, Y. Tao, LGH 6-25-2 (HKAS 131739, holotype), ex-type culture KUNCC 23–16897; *ibid*, on submerged decaying wood, 3 March 2021, S. Luan, LGH 6-2-1 (HKAS 131740, paratype); *ibid*, on submerged decaying wood, 3 March 2021, Z.Q. Zhang, LGH 6-16-1 (HKAS 131742); *ibid*, 27°40'51.08" N, 100°51'04.08" E, 2690 m, on submerged decaying wood, 4 March 2021, Z.Q. Zhang, LGH 9-45-1 (HKAS 131480).

GenBank numbers – HKAS 131739, ITS: PQ607751, LSU: PP189921, SSU: PQ435258; HKAS 131740, ITS: PQ607754, LSU: PP189920; HKAS 131742, ITS: PQ607755, LSU: PP189919, SSU: PQ341575, *tef*1-α: PQ456965; HKAS 131480, ITS: PQ607753, LSU: PP189922, SSU: PQ341576, *tef*1-α: PQ456966.

Notes – In our phylogenetic analysis, the four strains of *Hongkongmyces cylindricisporus* clustered in an independent lineage (Fig. 9). *Hongkongmyces cylindricisporus* can be distinguished from other species by its cylindrical to subcylindrical conidia, whereas conidia of the other species are mainly ellipsoid to obovoid, globose, or subglobose (Crous et al. 2018, Dong et al. 2020, Boonmee et al. 2021, Jayawardena et al. 2022). *Hongkongmyces cylindricisporus* resembles *H. guttulatus* in having hyaline, septate, guttulate, ellipsoidal, cylindrical to subcylindrical, irregular

conidia, however, *H. cylindricisporus* has larger conidia (30–37 × 6–7 µm *vs.* 20–26 × 6–7 µm) than *H. guttulatus*. According to the guidelines of Pem et al. (2021) and based on unique morphological and phylogenetic evidence, we introduce *H. cylindricisporus* as a new species.

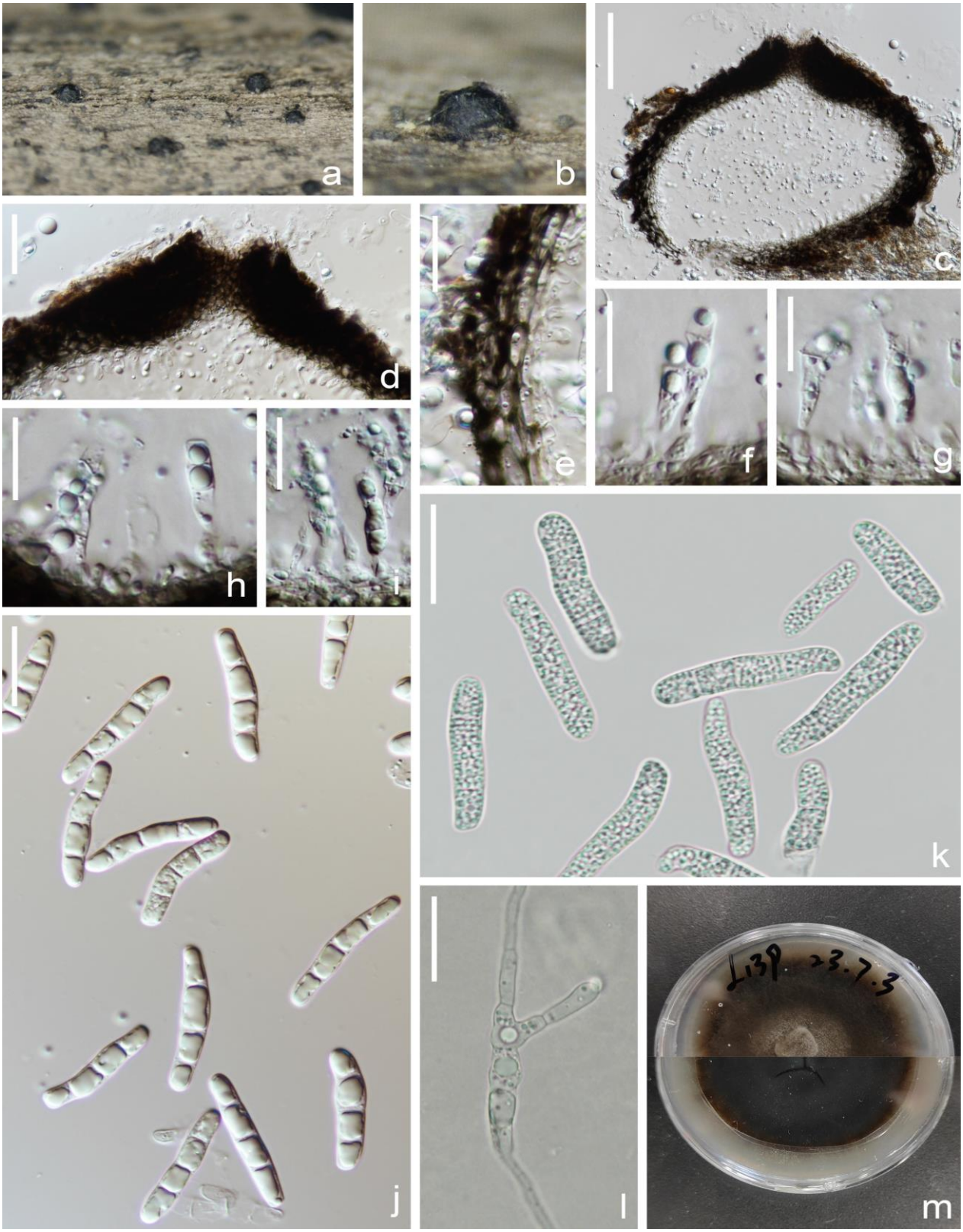

Figure 10 – *Hongkongmyces cylindricisporus* (HKAS 131739, holotype). a, b Appearance of conidiomata on substrate. c Section of conidiomata. d Ostiole. e Peridium. f–i Conidiogenous cells and developing conidia. j, k Conidia. l Germinating conidium. m Colony on PDA. Scale bars: c = 70 µm, d = 30 µm, e–l = 20 µm.

Hongkongmyces guttulatus H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 11

Index Fungorum number: IF571996; Facesoffungi number: FoF15482

Etymology – The name refers to the guttulate conidia of this species.

Holotype – HKAS 131800.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Conidiomata* 185–232 µm high, 272–305 µm diam., pycnidial, black, scattered, solitary to gregarious, semi-immersed or superficial, globose to subglobose, uni-loculate, ostiolate. *Ostioles* central, single, papillate. *Peridium* 20–27 µm wide, composed of brown to dark brown, irregular, thick-walled cells arranged in a *textura angularis*. *Conidiophores* reduced. *Conidiogenous cells* 8–15(–20) × 4–6 µm ($\bar{x}$ = 12 × 5 µm, n = 25), phialidic, determinate, cylindrical to subcylindrical, hyaline, thin-walled. *Conidia* 20–26 × 6–7 µm ($\bar{x}$ = 23 × 6 µm, n = 30), hyaline, ellipsoidal, cylindrical to subcylindrical, rounded at both ends, straight or slightly curved, (1–)2–3-septate, mostly 3-septate, slightly constricted at septum, smooth-walled, guttulate. Sexual morph: Undetermined.

Material examined – China, Yunnan Province, Dali City, Xihu Lake; 26°00'32.83" N, 100°03'35.43" E, 1970 m, on submerged decaying wood, 8 May 2021, S.P. Huang, XH 2-16-3 (HKAS 131800, holotype).

GenBank numbers – ITS: PQ571256, LSU: PP189918, SSU: PQ341574, *tef*1-α: PQ456967.

Notes – *Hongkongmyces guttulatus* can be distinguished from other species of *Hongkongmyces* by its unique morphology. *Hongkongmyces guttulatus* resembles *H. cylindricisporus*, however, they can be distinguished by conidial morphology (see notes of *Hongkongmyces cylindricisporus*). Multigene analysis showed that *H. guttulatus* clusters with *H. aquisetosus* (Fig. 9), comparison of the LSU, SSU, and *tef*1-α gene between *H. guttulatus* and *H. aquisetosus* revealed 0.5% (4/861 bp), 0% (0/989 bp), and 2.4% (22/908 bp) base differences, respectively. According to the guidelines of Pem et al. (2021) and based on unique morphological characteristics and phylogenetic analysis, we introduce *H. guttulatus* as a new species.

Hongkongmyces hongheensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 12.

Index Fungorum number: IF571998; Facesoffungi number: FoF15483

Etymology – The name refers to Honghe Prefecture, Yunnan Province, where the holotype was collected.

Holotype – HKAS 131785.

Saprobic on decaying submerged wood in freshwater. Sexual morph: *Ascomata* 121–135 µm high, 117–156 µm diam., black, scattered, solitary to gregarious, immersed or semi-immersed, globose to subglobose, uni-loculate, ostiolate, papillate. *Ostioles* centrally located. *Peridium* 17–24 µm wide, thick, composed of several layers, outermost layer heavily pigmented, thick-walled, comprising pale brown to dark brown cells of *textura angularis*, inner layer composed of pale brown to hyaline, cells towards the inner-side lighter, with flattened, thin-walled cells of *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, 2–3 µm wide, filamentous, septate, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* (54–)77–113(–134) × (9–)11–13 µm ($\bar{x}$ = 95 × 12 µm, n = 45), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apex rounded with a minute ocular chamber. *Ascospores* overlapping 2–3-seriate, reddish brown to brown, fusiform, enlarged at the 3rd cell from apex, (16–)20–24 × 5–7 µm ($\bar{x}$ = 22 × 6 µm, n = 80), 5(–6)-septate, constricted at septa, straight or slightly curved, smooth-walled, guttulate, surrounded by an entire mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 12 h and germ tubes produced from around ascospore. Colonies on PDA reaching 1–2.5 cm diam. after two months at the room temperature, colony circular, smooth edge, surface hyphae grey-light brown, flocculent, bulge at middle; reverse side brown to dark brown, crack in the middle.

Material examined – China, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°40'28.95" N, 102°36'30.00" E; 1400 m; on submerged decaying wood, 22 February 2023, H.W. Shen, FD 43-37-1 (HKAS 131785, holotype), ex-type culture KUNCC 23–13511.

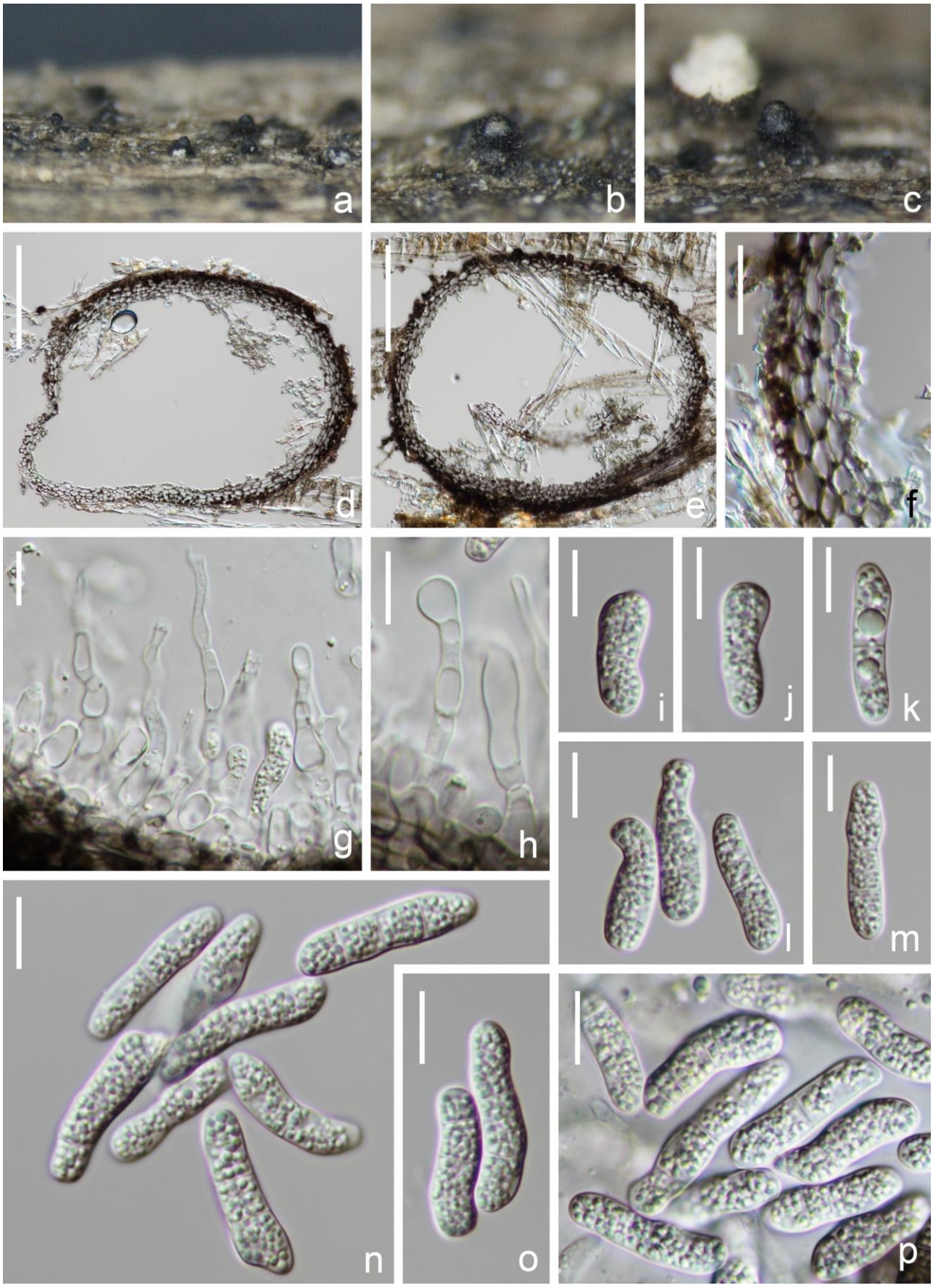

Figure 11 – *Hongkongmyces guttulatus* (HKAS 131800, holotype). a–c Appearance of conidiomata on substrate. d, e Section of conidiomata. f Peridium. g, h Conidiogenous cells and developing conidia. i–p Conidia. Scale bars: d, e = 90 µm, f = 20 µm, g–p = 10 µm.

GenBank numbers – ITS: PQ607752, LSU: PP189899, SSU: PQ435259, *tef*1-α: PQ456950.

Notes – *Hongkongmyces hongheensis* fits well with the generic concept of the sexual morph of *Hongkongmyces* in having reddish-brown to brown, fusiform ascospores, surrounded with a mucilaginous sheath. Morphological comparison with the sexual species of *Hongkongmyces* (*H. aquisetosus*, *H. brunneisporus*, *H. thailandica* and *H. yunnanensis*), *Hongkongmyces hongheensis* has smaller asci (77–113 × 11–13 μm *vs.* 135–170 × 12.5–15 μm) and ascospores (20–24 × 5–7 μm *vs.* 26–34 × 6–9 μm) than *H. aquisetosus* (Yang et al. 2023). Likewise, *H. brunneisporus* has larger asci (104–125 × 19–23 μm *vs.* 77–113 × 11–13 μm) and ascospores (37–44 × 9–11 μm *vs.* 20–24 × 5–7 μm) than *H. hongheensis* (Bao et al. 2021b). *Hongkongmyces hongheensis* is distinct from *H. thailandica* by reddish-brown to brown, smaller ascospores (20–24 × 5–7 μm *vs.* 45–60 × 8–18 μm), and with more septate (5(–6)-septate *vs.* 1-septate) (Hyde et al. 2017). *Hongkongmyces hongheensis* can be distinguished from *H. yunnanensis* by smaller asci (77–113 × 11–13 μm *vs.* 103–123 × 15–17 μm) and ascospores (20–24 × 5–7 μm *vs.* 26–31 × 7–9 μm), and less septa (5(–6)-septate *vs.* 6–7-septate). Phylogenetic analysis showed that *H. hongheensis* clustered *H. yunnanensis* with 100% ML and 1.00 BYPP support (Fig. 9). Nucleotide comparison between *H. hongheensis* and *H. yunnanensis* shows 0.5% (4/798, one gap), 0.2% (2/876), 2.0% (19/936) base difference for LSU, SSU and *tef*1-α sequence respectively. Following the guidelines of Pem et al. (2021) and based on morphological characteristics and phylogenetic analysis, we introduce *H. hongheensis* as a new species.

Hongkongmyces yunnanensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 13

Index Fungorum number: IF571999; Facesoffungi number: FoF15484

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

Holotype – HKAS 131741.

Saprobic on decaying submerged wood in freshwater. Sexual morph: *Ascomata* 163–230 μm high, 159–232 μm diam., black, scattered, solitary to gregarious, immersed or semi-immersed, globose to subglobose, uni-loculate, ostiolate, papillate. *Ostioles* central, papillate. *Peridium* 23–34 μm wide, thick, composed of several layers, outermost layer heavily pigmented, thick-walled, comprising brown to dark brown cells of *textura angularis*, inner layer composed of hyaline to pale brown, cells towards the inner-side lighter, flattened, thin-walled cells of *textura angularis*. *Hamathecium* composed of numerous, 2 μm wide, filamentous, septate, anastomosed pseudoparaphyses. *Asci* (88–)103–123(–134) × (13–)15–17 μm ($\bar{x}$ = 113 × 16 μm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, slightly curved, subsessile to short pedicellate, apex rounded with a minute ocular chamber. *Ascospores* overlapping 2-seriate, reddish-brown to brown, fusiform, enlarged at the 3rd or 4th cell from the apex, (21–)26–31 × 7–9 μm ($\bar{x}$ = 28 × 8 μm, n = 60, 6–7-septate, constricted at the septa, straight or slightly curved, smooth-walled, guttulate, without mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 12 h and germ tubes produced from ends of ascospore. Colonies on PDA reaching 2–3 cm diam. after two months at the room temperature, colony circular, smooth edge, surface hyphae reddish brown to brown, flocculent, bulge at the middle; reverse side three layers, the outermost layer reddish brown, the middle layer dark brown, and the inner layer pale brown.

Material examined – China, Yunnan Province, Lijiang City, Luguhu Lake; 27°44'13.59" N, 100°49'04.72" E, 2690 m; on submerged decaying wood, 3 March 2021, S. Luan, LGH A 6-25-1 (HKAS 131741, holotype), ex-type culture KUNCC 23–16896.

GenBank numbers – ITS: PQ607753, LSU: PP189917, SSU: PQ435260, *tef*1-α: PQ456951.

Notes – Multigene phylogenetic analysis showed that *H. yunnanensis* clustered with *H. hongheensis* with 97% ML and 1.00 PP support (Fig. 9). However, *H. yunnanensis* can be distinguished from *H. hongheensis* by its lager asci (103–123 × 15–17 μm *vs.* 77–113 × 11–13 μm) and ascospores (26–31 × 7–9 μm *vs.* 20–24 × 5–7 μm) (see notes of *Hongkongmyces hongheensis*). Based on morphological and molecular evidence (Pem et al. 2021), we introduce *H. yunnanensis* as

a new species from freshwater plateau lakes in Yunnan Province, China, and is the fifth sexual morph species of the genus *Hongkongmyces*.

Figure 12 – *Hongkongmyces hongheensis* (HKAS 131785, holotype). a, b Appearance of ascomata on substrate. c, d Section of ascoma. e–g Peridium. h Pseudoparaphyses. i–k Asci. l–p Ascospores. q Ascospore stained with Indian ink. r Germinated ascospore. s Colony on PDA. Scale bars: c = 50 µm, d = 40 µm, e–k = 20 µm, l–r = 10 µm.

Figure 13 – *Hongkongmyces yunnanensis* (HKAS 131741, holotype). a, b Appearance of ascomata on substrate. c Section of ascomata. d, e Peridium. f Setae on peridium. g Pseudoparaphyses. h Asci. i Ascospores. j Ascospore stained with Indian ink. k Germinating ascospore. l Colony on PDA. Scale bars: c = 70 µm, d–h = 20 µm, i–k = 40 µm.

Lindgomyces K. Hiray., Kaz. Tanaka & Shearer, Mycologia 102(3): 733 (2010).

Lindgomyces was established by Hirayama et al. (2010) to accommodate freshwater fungi characterized by globose to subglobose ascomata, fissitunicate, clavate to cylindrical asci that are rounded at the apex, and septate, hyaline ascospores with a gelatinous sheath, which sometimes extends to form bipolar mucilaginous appendages. Senescent ascospores are brown, >3-septate (Hirayama et al. 2010, Dong et al. 2020). *Lindgomyces* was typified by *L. ingoldianus* (Shearer & K.D. Hyde) K. Hiray., Kaz. Tanaka & Shearer (Hirayama et al. 2010). Currently, 15 species are accepted in *Lindgomyces*, all of which have been reported from freshwater habitats, and as saprobic on decaying plant substrates (Dong et al. 2020, Jayawardena et al. 2022).

Lindgomyces yunnanensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 14

Index Fungorum number: IF572000; Facesoffungi number: FoF15485

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

Holotype – HKAS 131833.

Saprobic on decaying submerged wood in freshwater. Sexual morph: *Ascomata* 188–264 µm high, 153–190 µm diam., black, scattered, solitary to gregarious, semi-immersed, flattened globose, subglobose, uni-loculate, ostiolate, papillate. *Ostioles* centrally located, short. *Peridium* 38–57 µm wide, thick, composed of several layers, outermost layer heavily pigmented, thick-walled, irregular, comprising pale brown to dark brown cells of *textura angularis*, inner layer composed of pale brown to hyaline, cells towards the inside lighter, flattened, irregular, thin-walled cells of *textura angularis*. *Hamathecium* composed of numerous, 2–3 µm wide, filamentous, septate, anastomosed pseudoparaphyses. *Asci* (78–)89–121(–164) × 21–27(–35) µm ($\bar{x}$ = 105 × 24 µm, n = 30), 8-spored, bitunicate, fissitunicate, broad cylindrical to cylindric-clavate, short pedicellate, slightly or slightly curved, apex rounded with a thin ocular chamber. *Ascospores* overlapping 2–3-seriate, (25–)29–32 × 10–11(–14) µm ($\bar{x}$ = 31 × 10 µm, n = 60), hyaline, broad-fusiform with acute ends, 1-septate, constricted at the septum, straight or slightly curved, asymmetrical, with a broad upper cell 10–11 µm wide, lower cell 9–10 µm wide, with two prominent large guttules on both sides of the septum and two smaller ones, surrounded by a thin gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 12 h and germ tubes produced from ends of ascospore. Colonies on PDA reaching 1–2.5 cm diam. after one month at the room temperature, colony circular, smooth edge, surface hyphae pale brown to brown, flocculent, dense, bulge at middle; reverse side pale brown to brown.

Material examined – China, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'30.44" N, 101°1'39.51" E, 2500 m; on submerged decaying wood, 23 February 2023, H.W. Shen, FD 48-27-1 (HKAS 131833, holotype), ex-type culture KUNCC 23–13812; *ibid*, 24°32'22.76 N, 101°1'6.85" E; 2500 m; on submerged decaying wood, 23 February 2023, H.W. Shen, FD 50-37-1 (HKAS 131443, paratype), ex-paratype culture KUNCC 23–13391.

GenBank numbers – KUNCC 23–13812, ITS: PQ340463, LSU: PP189900, SSU: PQ435261, *tef*1-α: PQ456952; KUNCC 23–13391, ITS: PQ340464, LSU: PP189901, SSU: PQ435262, *tef*1-α: PQ456953.

Notes – *Lindgomyces yunnanensis* conforms to the generic concept of *Lindgomyces* with globose to subglobose ascomata; fissitunicate, clavate to cylindrical asci; and septate, hyaline, fusiform ascospores with a gelatinous sheath, which sometimes extends to form bipolar mucilaginous appendages (Hirayama et al. 2010, Dong et al. 2020). Based on the taxonomic key of *Lindgomyces* provided by Dong et al. (2020), *L. yunnanensis* is easily distinguished from other members by the smaller ascospore (Dong et al. 2020). Phylogenetic analysis results showed that *L. yunanensis* clustered with *L. carolinensis*, *L. cigarospora* and *L. rotundatus* with low support (Fig. 9). Based on unique morphological characteristics, we, therefore, introduce *L. yunnanensis* as an additional new species from freshwater habitats.

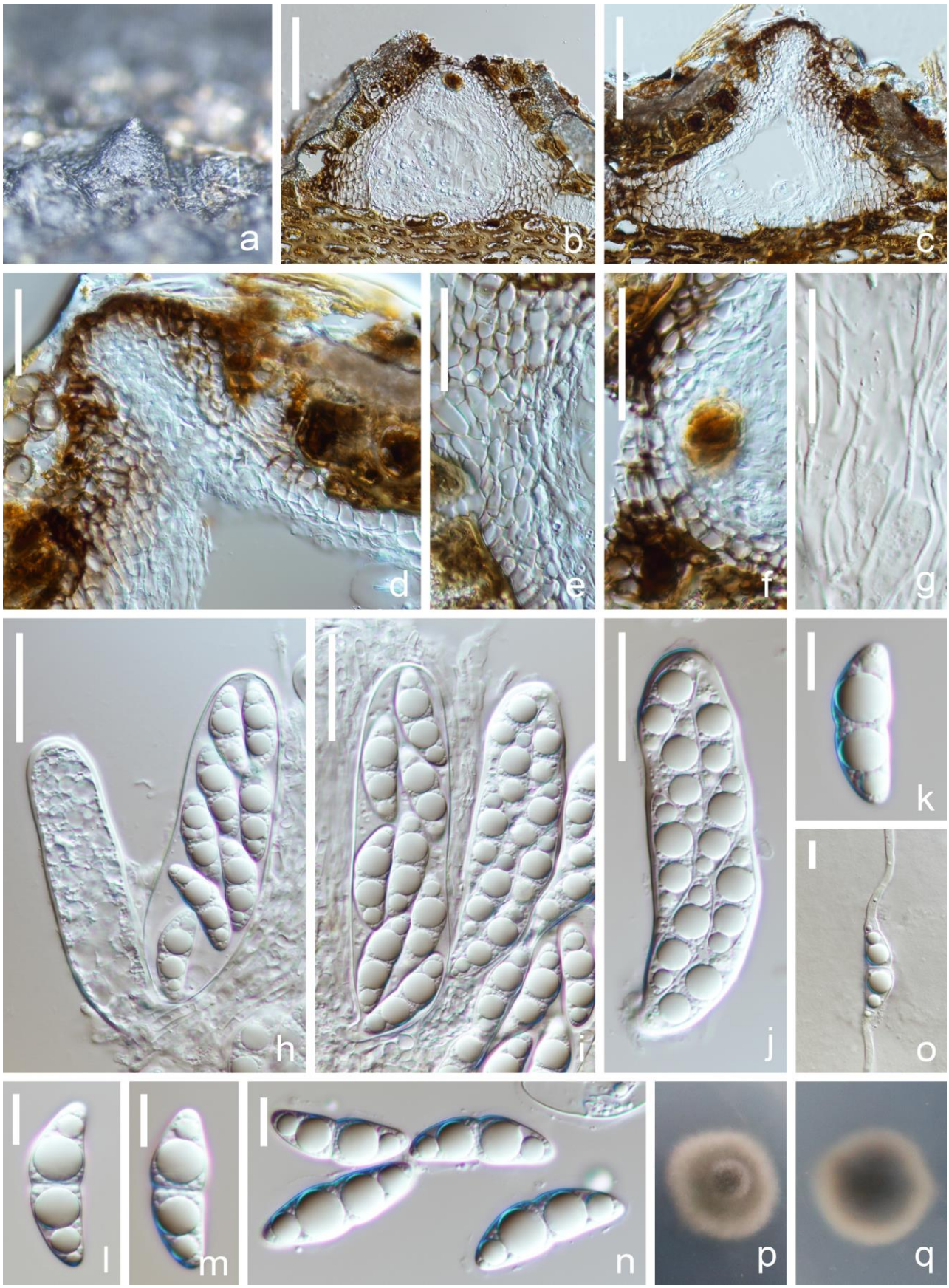

Figure 14 – *Lindgomyces yunnanensis* (HKAS 131833, holotype). a Appearance of ascomata on substrate. b, c Sections of ascomata. d Ostioles. e, f Peridium. g Pseudoparaphyses. h–j Asci. k–n Ascospores. o Germinating ascospore. p, q Colony on PDA. Scale bars: b, c = 80 µm, d–j = 30 µm, k–o = 10 µm.

Lolia Abdel-Aziz & Abdel-Wahab, Mycotaxon 114: 36 (2011)

Lolia was introduced by Abdel-Aziz & Abdel-Wahab (2010) to accommodate the asexual species *L. aquatica*, which was collected from submerged decayed stem of *Phragmites australis* in a freshwater river in Egypt (Abdel-Aziz & Abdel-Wahab 2010). Both asexual and sexual morphs of *L. aquatica* have been reported (Abdel-Aziz & Abdel-Wahab 2010, Abdel-Aziz 2016). The asexual morph of *Lolia* is characterized by acervular conidiomata, clavate, ellipsoidal, cylindrical conidia with apical, sub-apical and basal appendages (Abdel-Aziz & Abdel-Wahab 2010). The sexual morph of *Lolia* is characterized by immersed to erumpent, globose to subglobose ascomata; fissitunicate, cylindric-clavate asci; fusiform, yellow to dark-brown, septate ascospores, surrounded with a gelatinous sheath (Abdel-Aziz 2016). Currently, two species of the genus *Lolia*, *viz.*, *L. aquatica* and *L. dictyospora*, are collected from submerged decaying wood in freshwater habitats in Egypt (Abdel-Aziz & Abdel-Wahab 2010).

Lolia fusiformispora H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 15

Index Fungorum number: IF572001; Facesoffungi number: FoF15486

Etymology – The name refers to the fusiform ascospores of this species.

Holotype – HKAS 131465.

Saprobic on decaying submerged wood in freshwater. Sexual morph: *Ascomata* 160–280 µm high, 265–320 µm diam., solitary, scattered, immersed to semi-immersed, globose to subglobose with flattened base, papillate, ostiolate, dark-brown to black. *Ostioles* centrally located. *Peridium* 23–38 µm wide, composed of pale brown to dark brown, flattened, irregular cells of *textura angularis*, outermost layer heavily pigmented. *Hamathecium* composed of numerous, 1.5–2 µm wide, thin, filamentous, branched, septate, anastomosed pseudoparaphyses. *Asci* (90–)99–121 (–139) × 11–13(–15) µm ($\bar{x}$ = 110 × 12 µm, n = 50), 8-spored, bitunicate, fissitunicate, short pedicellate, cylindrical to cylindric-clavate, slightly or slightly curved, apex rounded with a minute ocular chamber. *Ascospores* (23–)26–32(–38) × 5–7 µm ($\bar{x}$ = 29 × 6 µm, n = 50), overlapping 2–3-seriate, pale brown to brown when mature, fusiform with acute ends, enlarged at the 3rd or 4th cell from the apex, 4–6-septate, constricted at the septum, straight or slightly curved, guttulate, smooth or delicately verruculose, surrounded by prominent gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 12 h and germ tube produced from one end of ascospore. Colonies on PDA reaching 4–5 cm diam. after two months at the room temperature, colony circular, smooth edge, surface hyphae pale brown to brown, flocculent, dense, bulge at middle; reverse side pale brown to brown.

Material examined – China, Yunnan Province, Dali City, Cibihu Lake, 26°08'49.05" N, 99°56'56.51" E, 2060 m; on submerged decaying wood, 21 July 2021, L.L. Li, CBH 2-15-1 (HKAS 131465, holotype), ex-type culture KUNCC 23–16912.

GenBank numbers – LSU: PP189923, SSU: PQ435263, *tef*1-α: PQ456954.

Notes – Phylogenetic analyses showed that *Lolia fusiformispora* clustered with *L. dictyospora* and *L. aquatica* (Fig. 9). Comparison of LSU sequence between *L. fusiformispora* and *L. aquatica* revealed a 1.9% (15/905 bp, including 3 gaps) base difference while the LSU sequence between *L. fusiformispora* and *L. dictyospora* showed a 1.0% (8/805 bp) base difference. *Lolia fusiformispora* is similar to *L. aquatica* in having fusiform, yellow to dark-brown, septate, verruculose ascospores and surrounded with a gelatinous sheath (Abdel-Aziz 2016). However, it can be distinguished from *L. aquatica* by smaller asci (99–121 × 11–13 µm *vs.* 109–145 × 17–26 µm) and ascospores (26–32 × 5–7 µm *vs.* 26–37 × 6–9 µm). *Lolia dictyospora* differs from *L. fusiformispora* in having smaller ascospores (14–19 × 4–7 µm *vs.* 26–32 × 5–7 µm), in addition, it has longitudinal and transverse septate, while *L. fusiformispora* has only transverse septa (Abdel-Aziz 2016). According to the guidelines of Pem et al. (2021) and based on morphological and phylogenetic evidence, we introduce *L. fusiformispora* as a new species. Currently, all three *Lolia* species have been reported from freshwater habitats.

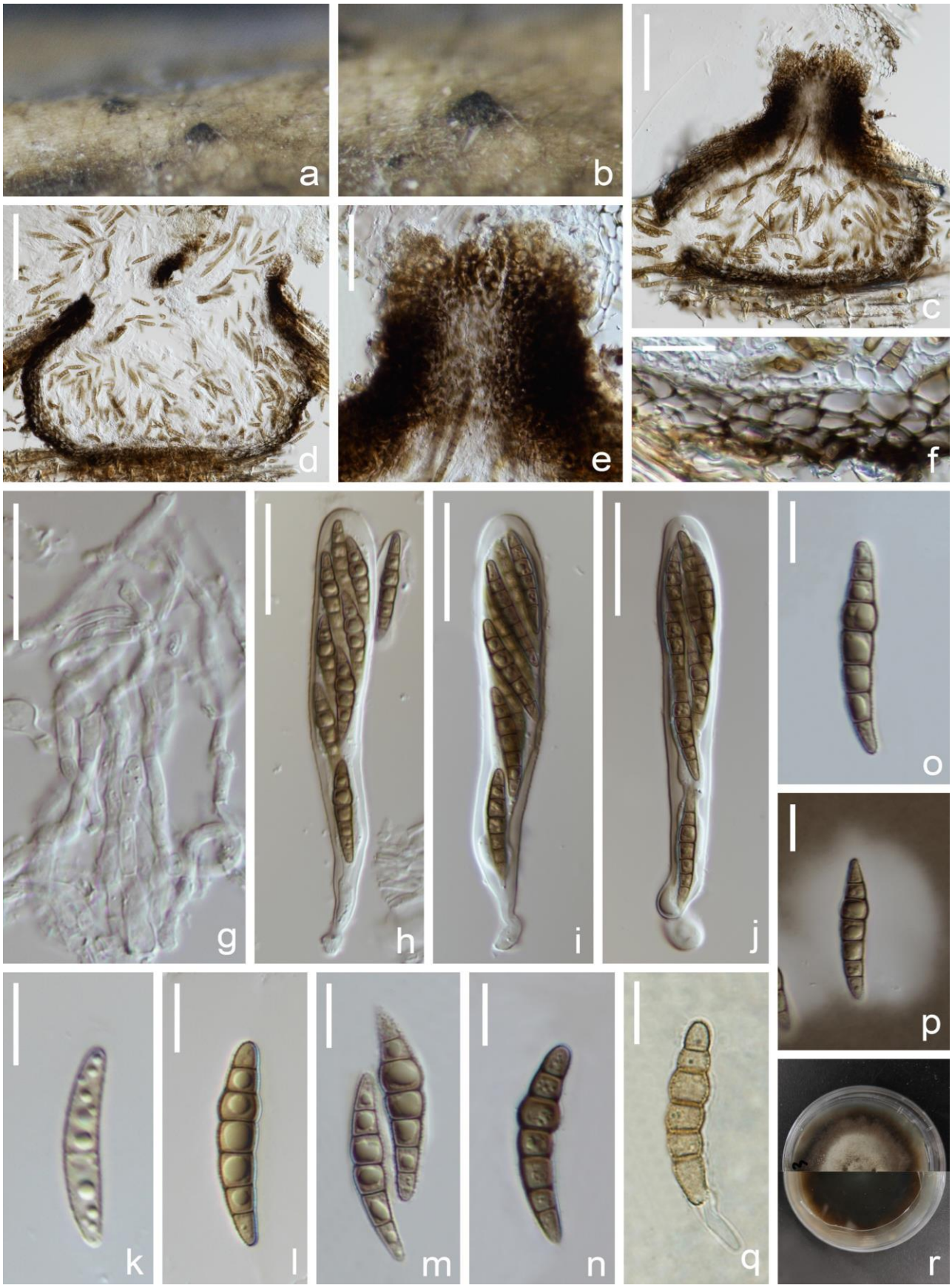

Figure 15 – *Lolia fusiformispora* (HKAS 131465, holotype). a, b Appearance of ascomata on substrate. c, d Sections of ascomata. e Ostioles. f Peridium. g Pseudoparaphyses. h–j Asci. k–o Ascospores. p Ascospore stained with Indian ink. q Germinating ascospore. r Colony on PDA. Scale bars: c, d = 90 µm, e = 40 µm, f, g = 20 µm, h–j = 30 µm, k–q = 10 µm.

Occultibambusaceae D.Q. Dai & K.D. Hyde, Fungal Diversity 82: 25 (2017)

Occultibambusaceae was established by Dai et al. (2017) to accommodate *Neooccultibambusa* (Doilom et al. 2017), *Occultibambusa* (Dai et al. 2017), *Seriascoma* (Dai et al. 2017), and *Versicolorisporium* (Hatakeyama et al. 2008), with *Occultibambusa* as the type genus. Subsequently, a new genus *Brunneofusispora* introduced to *Occultibambusaceae* based on morphological and phylogenetic analyses (Phookamsak et al. 2019). Currently, 27 species in five genera are accommodated in *Occultibambusaceae*. These species are commonly found as saprobes on monocotyledons, such as bamboo, but have also been found on other plant debris such as *Ammophila* sp. (Jayasiri et al. 2016), *Clematis* sp. (Phukhamsakda et al. 2020), *Pandanus* sp. (Hyde et al. 2018, Tibpromma et al. 2018), and *Tectona* sp. (Doilom et al. 2017). Additionally, a few have been reported from leaf spot of *Senna tora* (Tan et al. 2021).

Occultibambusa D.Q. Dai & K.D. Hyde, Fungal Diversity 82: 26 (2016)

Occultibambusa is typified by *O. bambusae* and was introduced by Dai et al. (2017) to accommodate species characterized by immersed, dark, ascostromata with periphysate ostioles, broad cylindrical to clavate asci, and dark brown, fusiform, 1-septate ascospores; and the asexual morph with oblong, hyaline to pale brown, aseptate conidia (Dai et al. 2017). *Occultibambusa* species typically grow saprobically on dead bamboo culms in terrestrial habitats (Dai et al. 2017, Zhang et al. 2017, Jiang et al. 2021a, Yu et al. 2021); only *O. aquatica*, *O. kunmingensis* and *O. pustula* are from freshwater habitats (Hyde et al. 2016b, Dai et al. 2017, Dong et al. 2020).

Occultibambusa jonesii J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, Mycosphere 8(4): 553 (2017) Fig. 16

Saprobic on decaying submerged wood in freshwater. Sexual morph: *Ascomata* 225–310 µm high, 230–265 µm diam., solitary to gregarious, semi-immersed or superficial, flattened globose, subglobose, uni-loculate, ostiolate, papillate. *Ostioles* short, centrally located, 75–95 µm wide, 32–40 µm thick. *Peridium* 27–40 µm wide at the sides, 12–16 µm wide at the base, composed of several layers, outer layer heavily pigmented, thick-walled, irregular, comprising pale brown to dark brown cells of *textura angularis*, inner layer composed of pale brown to hyaline, flattened, thin-walled cells of *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, 3–4 µm wide, filamentous, septate, anastomosed pseudoparaphyses, embedded in a gelatinous matrix. *Asci* (64–)77–108(–128) × 13–16 µm ($\bar{x}$ = 92 × 15 µm, n = 40), 8-spored, bitunicate, fissitunicate, broadly cylindrical to clavate, straight or slightly curved, shortly pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 30–34(–39) × 7–8 µm ($\bar{x}$ = 32 × 7 µm, n = 45), overlapping 2–3-seriate, fusiform, straight to somewhat curved, 1-septate, with a broad upper cell 7–8 µm wide, under cell 6–7 µm wide, constricted at the septum, hyaline when young and becoming brown to greyish when mature, guttulate, smooth-walled, without mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 12 h and germ tubes produced from ends of ascospore. Colonies on PDA reaching 1–1.5 cm diam. after two weeks at the room temperature in dark, colony circular, smooth edge, surface hyphae pale brown, flocculent, dense, sparse, bulge at middle; reverse side pale brown to brown, smooth.

Material examined – China, Yunnan Province, Kunming City, Dianchi Lake, 23°39'18.95" N, 102°32'57.19" E, 1400 m; on submerged decaying wood, 22 February 2023, H.W. Shen, FD 40-35-1 (HKAS 131779), living culture KUNCC 23–13523.

GenBank numbers – ITS: PQ607754, LSU: PP189903, SSU: PQ435265, *tef*1-α: PQ456956, *rpb2*: PQ348602.

Notes – Multigene phylogenetic analysis showed that our new collection clustered with *Occultibambusa aquatica* and *O. jonesii* without significant phylogenetic distance (Fig. 17). Comparison of the LSU, SSU, *tef*1-α and *rpb*2 molecular sequences between the new collection and *O. jonesii* (GZCC 16–0117) revealed 0.4% (3/831 bp), 0.9% (8/915 bp), 1.1% (10/948 bp), and 0% (0/997 bp) base pair differences, respectively. Morphologically, our new collection conforms to the

characteristics of *O. jonesii* in having fissitunicate, broadly cylindrical to clavate asci, fusiform, brown to greyish, 2-celled ascospores with a broad upper cell, and without sheath (Zhang et al. 2017). However, asci and ascospores of *O. aquatica* are smaller than both specimens of *O. jonesii* (GZAAS 16-0161 and HKAS 131785) (Zhang et al. 2017). Based on the similar morphological and molecular data, we identified the collection as *O. jonesii*, which was reported from freshwater habitats for the first time.

Figure 16 – *Occultibambusa jonesii* (HKAS 131785, new habitat records). a Appearance of ascomata on substrate. b, c Sections of ascomata. d Ostioles. e–g Peridium. h Pseudoparaphyses. i–k Asci. l–o Ascospores. p Germinating ascospore. q Colony on PDA. Scale bars: b, c = 100 µm, d = 50 µm, e–h = 30 µm, i–k = 20 µm, l–p = 10 µm.

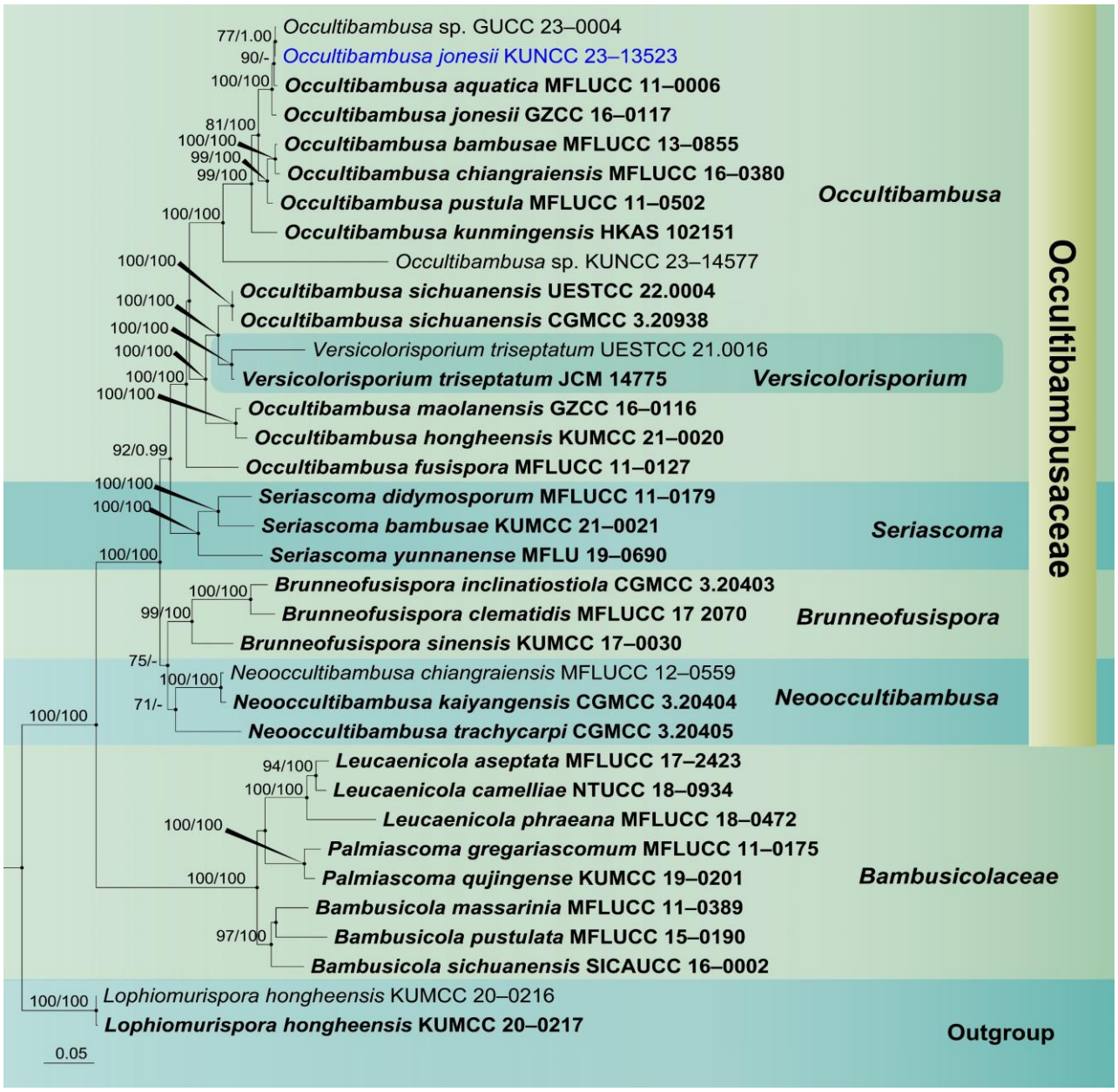

Figure 17 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, *tef*1-α and *rpb*2 sequence dataset representing *Occultibambusaceae* and *Bambusicolaceae*. Thirty-five strains are included in the combined analyses which comprise 4300 characters including gaps (845 characters for LSU, 1013 characters for SSU, 499 characters for ITS, 943 characters for *tef*1-α, 1000 characters for *rpb*2). *Lophiomurispora hongheensis* (KUMCC 20–0216 and KUMCC 20–0217) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best-scoring RAxML tree with a final likelihood value of -25088.365163 is presented. The matrix had 1508 distinct alignment patterns, with 18.26% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.245596, C = 0.253522, G = 0.269919, T = 0.230963; substitution rates AC = 1.677479, AG = 3.323698, AT = 1.310281, CG = 1.120426, CT = 7.245754, GT = 1.000000; Tree-Length = 1.775792; gamma distribution shape parameter α = 0.205768. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Parabambusicolaceae Kaz. Tanaka & K. Hiray., Stud. Mycol. 82: 115 (2015)

Parabambusicolaceae was proposed by Tanaka et al. (2015) to accommodate *Multiseptospora* and two novel genera, *Aquastroma* and *Parabambusicola*, as well as two unnamed *Monodictys* species (Tanaka et al. 2015). Subsequently, eleven new genera, *Kevinia* (Senanayake et al. 2023), *Lonicericola* (Phookamsak et al. 2019), *Multilocularia* (Li et al. 2016), *Neoaquastroma* (Samarakoon et al. 2019), *Neomultiseptospora* (Xie et al. 2022), *Paramonodictys* (Hyde et al. 2020a), *Paratrimmatostroma* (Phookamsak et al. 2019), *Paramultiseptospora* (Phookamsak et al. 2022), *Pseudomonodictys* (Ariyawansa et al. 2015), *Pseudomultiseptospora* (Senanayake et al. 2023), and *Scolecohyalosporium* (Xie et al. 2022) were introduced to *Parabambusicolaceae*. *Parabambusicolaceae* is characterised by pseudothecioid ascomata with or without surrounding stromatic tissues, papillate to epapillate ostioles, clavate to fusiform asci and hyaline or brown multi-septate, clavate to fusiform, hyaline ascospores (Liu et al. 2015, Tanaka et al. 2015, Li et al. 2016), and the asexual morphs are monodictys-like, trimmatostroma-like hyphomycetes (Ariyawansa et al. 2015, Tanaka et al. 2015). Currently, 30 species in 14 genera are included in *Parabambusicolaceae*, these species are usually saprobes occur on various dead or decaying plant culms, branches and leaves of plants in terrestrial habitats, as well as a pteridophyte (Ariyawansa et al. 2015, Phukhamsakda et al. 2018, Phookamsak et al. 2019, 2022, Wijayawardene et al. 2022b, Yang et al. 2022b, Li et al. 2023). A few species are also reported from aquatic habitats (Tanaka et al. 2015, Dong et al. 2020, Xie et al. 2022, Xu et al. 2023).

Lonicericola Phookamsak, Jayasiri & K.D. Hyde, Fungal Diversity 95: 39 (2019)

Lonicericola is a monotypic genus introduced by Phookamsak et al. (2019) to accommodate *L. hyaloseptispora* (type species) based on morphological and phylogenetic evidences. *Lonicericola hyaloseptispora* is a saprobe from dead branches of *Lonicera maackii* in Yunnan Province, China (Phookamsak et al. 2019). Subsequently, two new species, *L. fuyuanensis* and *L. qujingensis* have been introduced and two new species were collected on dead branches of *Caprifoliaceae* and *Magnolia grandiflora*, respectively (Yasanthika et al. 2020, Wijayawardene et al. 2022b). Currently, three species are accepted in the genus and all the three species were reported from terrestrial habitats in Yunnan, China (Phookamsak et al. 2019, Yasanthika et al. 2020, Wijayawardene et al. 2022b). In this study, *L. qujingensis* was collected from submerged decaying wood in freshwater habitats.

Lonicericola qujingensis D.Q. Dai, Wanas. & Wijayaw., Frontiers in Microbiology 13: 17 (2022), Fig. 18

Saprobic on decaying submerged wood in freshwater. Sexual morph: *Ascomata* 171–245 µm high, 131–154 µm diam., black, scattered, solitary to gregarious, immersed or semi-immersed, globose to subglobose, uni-loculate, glabrous, ostiolate, papillate. *Ostioles* centrally located, oblong. *Peridium* 22–28 µm wide, thick, composed of several layers, outermost layer heavily pigmented, thick-walled, comprising pale brown to dark brown cells of textura angularis, inner layer composed of pale brown to hyaline, cells towards the inside lighter, flattened, thick-walled cells of *textura angularis* to *textura prismatica*. *Hamathecium* composed of numerous, 2–3 µm wide, thick-walled, filamentous, septate pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* (101–)110–160(–182) × (21–)25–31(–33) µm ($\bar{x}$ = 135 × 28 µm, n = 20), 8-spored, bitunicate, fissitunicate, broadly cylindrical to cylindric-clavate, subsessile to short pedicellate, apex rounded with a thin ocular chamber. *Ascospores* (41–)44–51(–55) × 10–12(–14) µm ($\bar{x}$ = 47 × 11 µm, n = 50), overlapping 2–3-seriate, hyaline, fusiform to vermiform, enlarged at the 3rd or 4th cell from the apex, (7–)8(–9)-septate, constricted at septa, smooth-walled, with small guttules, surrounded by entire mucilaginous sheath (15–21 µm diam.). Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on PDA within 12 h and germ tubes produced from around ascospore. Colonies on PDA reaching 1–2.5 cm diam. after 2 two months at the room temperature, colony circular, smooth edge, surface hyphae grey-light brown, flocculent, bulge at middle; reverse side brown to dark brown, crack in the middle.

Material examined – China, Yunnan Province, Kunming City, Yangzonghai Lake, 24°53'39.31" N, 102°58'58.82" E; 1770 m; on submerged decaying wood, 19 February 2023, Z.Q. Zhang, FD 26-34-1 (HKAS 131545), living culture KUNCC 23–13439.

GenBank numbers – ITS: PQ340465, LSU: PP189902, SSU: PQ435264, *tef*1-α: PQ456955.

Notes – Our new collection, HKAS 131545, collected from Yangzonghai Lake in Yunnan Province, is similar to *Lonicericola hyaloseptispora* and *L. qujingensis* in having broadly cylindrical to cylindric-clavate asci; and hyaline, fusiform to vermiform, septate, smooth-walled, guttulate ascospores, enlarged at the 3rd or 4th cell from the apex, and surrounded by a mucilaginous sheath (Wijayawardene et al. 2022b). Ascospore and asci characteristics can be used to distinguish species of *Lonicericola* (Wijayawardene et al. 2022b). Based on the key to *Lonicericola* species provided by Wijayawardene et al. (2022b) , morphology of our new collection is consistent with *L. qujingensis*. Phylogenetic analysis shows that our new collection clusters with the holotype of *L. qujingensis* with 100% ML support (Fig. 19). In addition, the nucleotides comparison of ITS, LSU, SSU and *tef*1-α genes between our strain, KUNCC 23–13439 and type strain, GMBCC1178 showed that our collection has extremely high base similarity with *L. qujingensis* (only ITS has a 22 base pair difference, including 21 gaps), so we identified our new collection as *L. qujingensis*, which was first reported in freshwater environments.

Pleomassariaceae M.E. Barr, Mycologia 71(5): 949 (1979)

Pleomassariaceae was established by Barr (1979) to accommodate *Asteromassaria*, *Pleomassaria* and *Splanchnonema*, with *Pleomassaria* as the type. Later, Barr (1993a) treated *Pleomassaria* as a synonym for *Splanchnonema* based on similar morphology, except for ascospore septation, and accepted *Asteromassaria*, *Eopyrenula*, *Kirschsteiniothelia*, *Macrovalsaria*, and *Splanchnonema* in *Pleomassariaceae* based on morphological characteristics and host (Hawksworth 1985, Barr 1993a). Based on phylogenetic analysis, Zhang et al. (2009a) treated *Pleomassariaceae* as a synonym of *Melanommataceae*. Subsequently, *Pleomassariaceae* was reinstated as a separate family based on the distinct morphology and phylogenetic analysis (Zhang et al. 2012). Lumbsch & Huhndorf (2010) accepted *Asteromassaria*, *Lichenopyrenis*, *Peridiothelia*, *Pleomassaria* and *Splanchnonema* in *Pleomassariaceae*, however, the *Asteromassaria* was excluded by Hyde et al. (2013). Currently, six genera are accepted in *Pleomassariaceae viz. Beverwykella*, *Lichenopyrenis*, *Myxocyclus*, *Peridiothelia*, *Prosthemium* and *Splanchnonema*, with approximately 50 species (Wijayawardene et al. 2022a). Most members of *Pleomassariaceae* occur on branches, stems, twigs, and leaves as saprobes in terrestrial habitats (Tilak & Kale 1970, Barr 1982, 1993a, b, Ramaley 1995), whereas a few are endophytes and lichenized fungi (Kowalski & Kehr 1992, Calatayud et al. 2001, Aptroot & Moon 2014). In addition, several fungi have been reported from freshwater habitats (Van Beverwijk 1954, Nawawi & Kuthubutheen 1988, Voglmayr & Delgado-Rodriguez 2003).

Beverwykella Tubaki, Trans. Mycol. Soc. Japan 16(2): 138 (1975)

Beverwykella was introduced by Tubaki (1975) with *B. pulmonaria* (*Papulaspora pulmonaria*) (Beverw.) Tubaki as type species. *Beverwykella* is characterized by lenticular, black, multicellular conidia and a vertical main branch and a series of mainly opposite side branches (Van Beverwijk 1954, Nawawi & Kuthubutheen 1988, Voglmayr & Delgado-Rodriguez 2003). Tian et al. (2015) placed *Beverwykella* in *Pleomassariaceae*, based on phylogenetic analysis. Currently, three species are accepted in *Beverwykella*, *viz. Beverwykella cerebriformis*, *B. clathrata*, and *B. pulmonaria*. All of these species were collected from leaves submerged in water in Asia, Europe and North America (Van Beverwijk 1954, Nawawi & Kuthubutheen 1988, Voglmayr & Delgado-Rodriguez 2003).

Beverwykella grandispora H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 20

Index Fungorum number: IF572002; Facesoffungi number: FoF15490

Etymology – The name refers to the large conidia of this species.

Holotype – HKAS 131498.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Colonies* effuse, brown, conspicuous. *Mycelium* partly superficial, partly immersed in the substratum, composed of smooth, branched, septate, brown hyphae. *Conidiophores* macronematous, mononematous, mostly hyaline, sometimes light brown, septate, erect, straight to slightly flexuous, unbranched, 5–8 µm wide. *Conidiogenous cells* 20–22 × 5–7 µm ($\bar{x}$ = 21 × 6 µm), integrated, monoblastic, terminal, hyaline. *Conidia* (94–)102–123(–137) × (85–)92–114(–120) µm ($\bar{x}$ = 113 × 103 µm), hyaline when young, brown to dark brown when mature, lenticular, orbicular, with mature conidia composed of two layers of cells with different textures; the outer layer of cells closely laid, thin-walled, and mainly composed of important branches and gaps. Sexual morph: Undetermined.

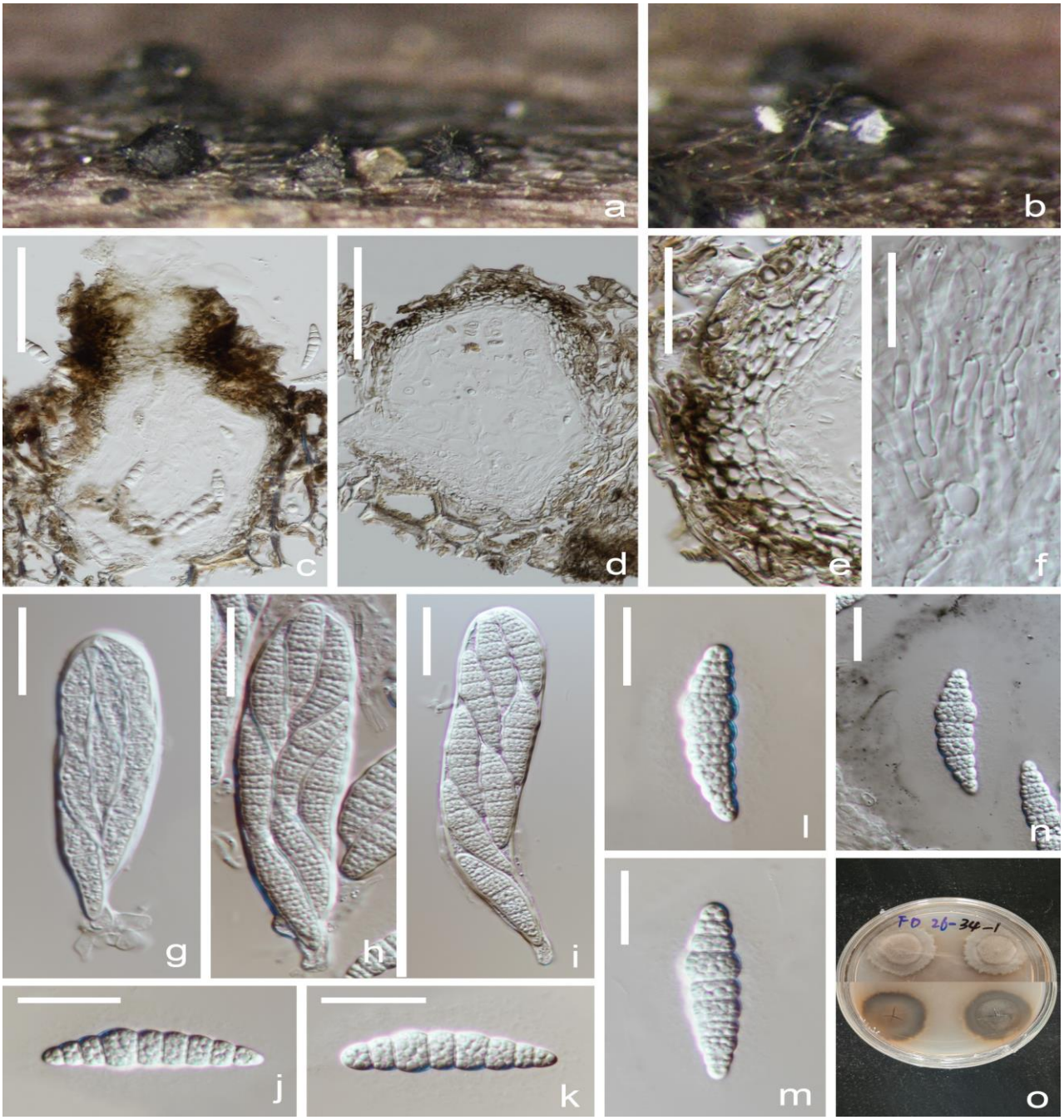

Figure 18 – *Lonicericola qujingensis* (HKAS 131545, new habitat records). a, b Appearance of ascomata on host substrate. c, d Sections of ascomata. e Peridium. f Pseudoparaphyses. g–i Asci. j–m Ascospores. n Ascospore stained with Indian ink. o Colony on PDA. Scale bars: c, d = 80 µm, e, g–i = 30 µm, f, j–n = 20 µm.

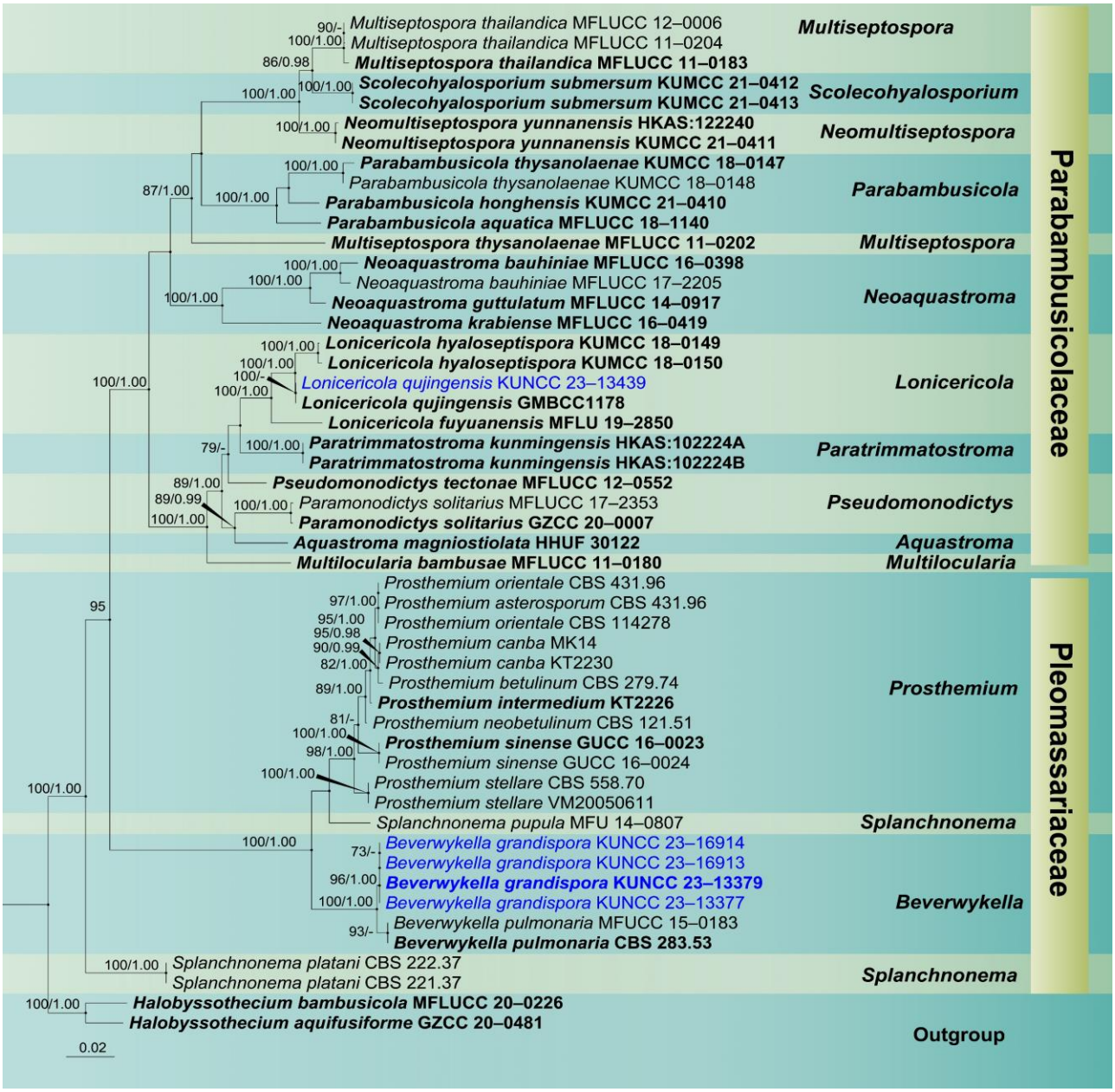

Figure 19 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef*1-α sequence dataset representing *Parabambusicolaceae* and *Pleomassariaceae*. Fifty-one strains are included in the combined analyses which comprise 3701 characters including gaps (1269 characters for LSU, 1021 characters for SSU, 498 characters for ITS, 913 characters for *tef*1-α). *Halobyssothecium bambusicola* (MFLUCC 20–0226) and *H. aquifusiforme* (GZCC 20–0481) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best-scoring RAxML tree with a final likelihood value of -15871.807282 is presented. The matrix had 1001 distinct alignment patterns, with 30.18% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.240090, C = 0.247530, G = 0.273401, T = 0.238979; substitution rates AC = 1.120341, AG = 2.248194, AT = 1.258642, CG = 1.417375, CT = 6.752943, GT = 1.000000; Tree-Length = 0.922735; gamma distribution shape parameter α = 0.167002. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Culture characteristics – Conidia germinating on PDA and germ tubes produced from around conidium within 12 h. Colonies on PDA, reaching 2 cm in diameter after one month at room temperature, colony circular, smooth edge, surface hyphae white to gray-brown, flocculent; reverse side brown to dark brown.

Material examined – China, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'22.76" N, 101°1'6.85" E; 2500 m, on submerged decaying wood, 24 February 2023, H.W. Shen, FD 50-25-1 (HKAS 131498, holotype), ex-type culture KUNCC 23–13379; *ibid*, on submerged decaying wood, 25 February 2022, H.W. Shen, YJ 30-53-1 (HKAS 131662, paratype), ex-paratype culture KUNCC 23–16913; *ibid*, on submerged decaying wood, 24 February 2023, H.W. Shen, FD 50-39-1 (HKAS 131495), living culture KUNCC 23–13377; *ibid*, on submerged decaying wood, 25 February 2022, H.W. Shen, YJ 30-30-1 (HKAS 131661), living culture KUNCC 23–16914.

GenBank numbers – KUNCC 23–13379, ITS: PQ340457, LSU: PP189893, SSU: PQ435252, *tef*1-α: PQ456945; KUNCC 23–16913, ITS: PQ607756, LSU: PP189915, SSU: PQ435253; KUNCC 23–13377, ITS: PQ340458, LSU: PP189894; KUNCC 23–16914, ITS: PQ607757, LSU: PP189916, SSU: PQ435254.

Notes – Phylogenetic analysis showed that *Beverwykella grandispora* clustered with the type species *B. pulmonaria* in an independent lineage within *Pleomassariaceae* (Fig. 19). Comparison of ITS, LSU, SSU and *rpb*2 gene between *B. grandispora* (KUNCC 23–13379) and *B. pulmonaria* (CBS 283.53) revealed 2.23% (11/493 bp, including 6 gaps), 0.24% (3/1254 bp, including 2 gaps), 1.27% (17/1340 bp, including 7 gaps), 2.31% (19/824 bp) base pair difference, respectively. In addition, morphological examination showed that *B. grandispora* fits well with the morphological concept of *Beverwykella* in having lenticular, black, multicellular conidia and a vertical main branch and a series of mainly opposite side branches (Van Beverwijk 1954, Nawawi & Kuthubutheen 1988, Voglmayr & Delgado-Rodriguez 2003). *Beverwykella grandispora* can be distinguished from the known species of *Beverwykella* by a maximum conidial size (102–123 × 92–114 μm) compared to *B. cerebriformis* (42–65 × 30–35 μm), *B. clathrata* (25–28 × 40–60 μm), and *B. pulmonaria* (62–110 × 57–103 μm). According to the guidelines for introducing new species (Pem et al. 2021) and based on molecular sequence data and morphological characteristics, we introduce *Beverwykella grandispora* as a new species. This is the second species of *Beverwykella* reported from freshwater habitats.

Periconiaceae Nann., Repert. mic. uomo: 482 (1934)

Periconiaceae was introduced by Nannizzi (1934) and typified by *Periconia* Tode. This family was initially proposed to accommodate *Periconia* and *Stachybotrys* (Nannizzi 1934). Later, *Stachybotrys* was transferred to a new family, *Stachybotryaceae*, based on phylogenetic and morphological studies (Crous et al. 2014). Tanaka et al. (2015) resurrected *Periconiaceae*, and accepted *Bambusistroma* (Adamčík et al. 2015), *Flavomyces* (Knapp et al. 2015), *Periconia* (Tode 1971) and *Noosia* (Crous et al. 2011) in this family, based on molecular data coupled with morphological (sexual-asexual morph) characteristics (Tanaka et al. 2015). Yang et al. (2022c) treated *Bambusistroma* and *Noosia* as synonyms of *Periconia* based on morphological and phylogenetic evidence. Currently, 225 epithets are known in this family (http://indexfungorum.org/Names/Names.asp, accessed on 20 June 2024), which are commonly found as saprobes on various substrates from terrestrial habitats in worldwide (Dong et al. 2020, Hongsanan et al. 2020b).

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

Periconia was introduced by Tode (1971), with *P. lichenoides* as the type species. *Periconia* species are mainly known as asexual morph, with only a few species exhibiting sexual morphs (Tanaka et al. 2015, Yang et al. 2022c, Su et al. 2023). The asexual morph is characterized by macronematous, mononematous, branched or unbranched, and pale to dark brown conidiophores; monoblastic to polyblastic conidiogenous cells; globose to ellipsoidal, catenate or solitary, smooth or verrucose conidia (Tanaka et al. 2015, Yang et al. 2022c). The sexual morph is characterized by

scattered or grouped, globose ascomata with a central ostiole, hyaline periphyses, 8-spored asci, and broadly fusiform, 1-septate, hyaline and smooth ascospores with an entire sheath (Adamčík et al. 2015, Tanaka et al. 2015, Yang et al. 2022c). Members of *Periconia* mainly grow saprobically on various plant detritus in terrestrial habitats with a few from freshwater habitats (Dong et al. 2020). Several species have also been reported as endophytes and pathogens (Tanaka et al. 2015, Sarkar et al. 2019, Yang et al. 2022c, Su et al. 2023, Liao et al. 2024). In this study, we introduced three new species, *viz*., *Periconia dujuanhuensis*, *P. hongheensis* and *P. yunnanensis*.

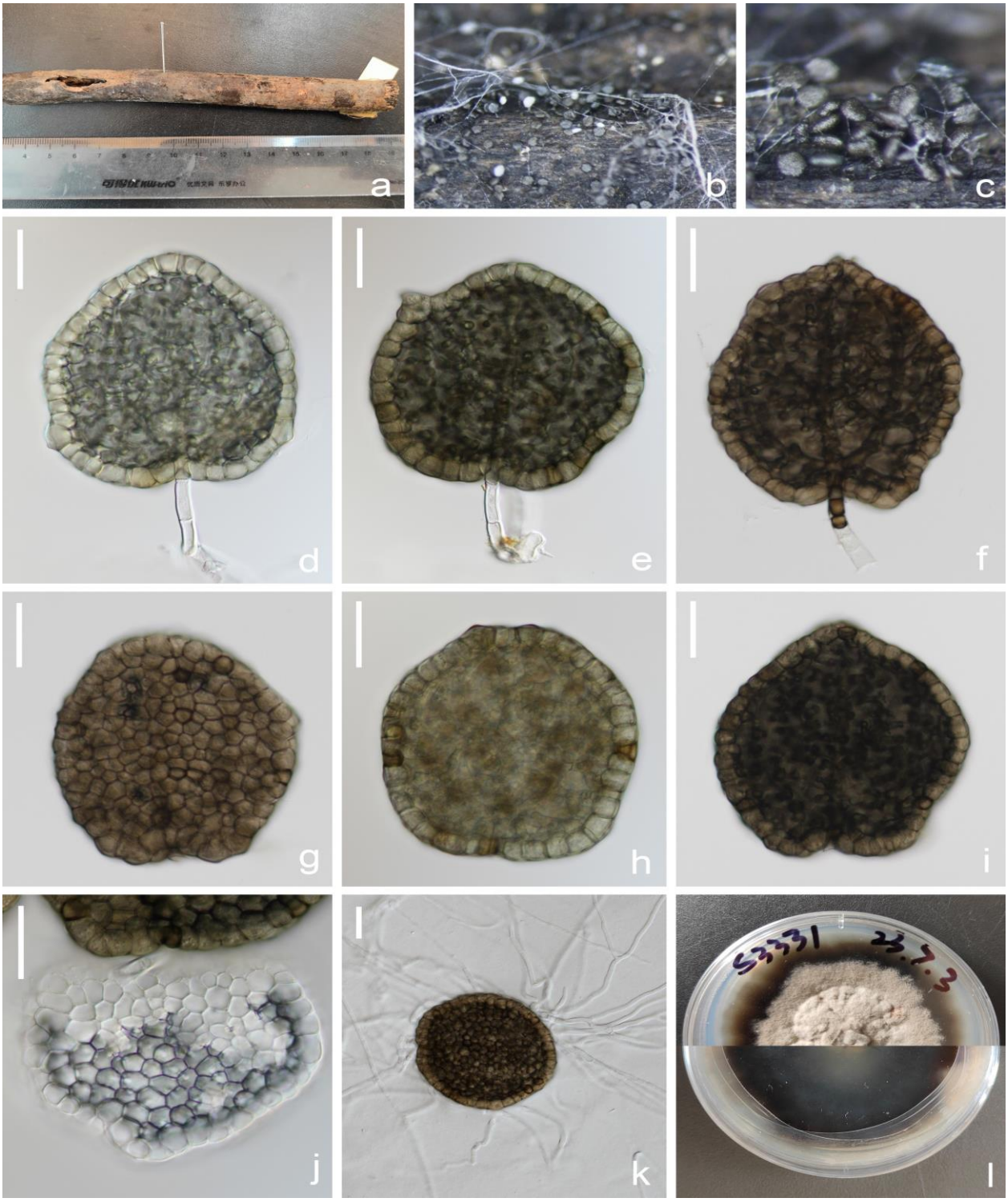

Figure 20 – *Beverwykella grandispora* (HKAS 131498, holotype). a Natural substrate. b, c Colonies on natural substrate. d–f Conidiophores, conidiogenous cells and conidia. g–j Conidia. k Germinating conidium. l Colony on PDA. Scale bars: d–k = 40 μm.

Periconia dujuanhuensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 21

Index Fungorum number: IF572003; Facesoffungi number: FoF15487

Etymology – The name refers to Dujuanhu Lake, Yunnan Province, where this species was collected.

Holotype – HKAS 131782.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Colonies* on natural substrate superficial, effuse, brown to dark brown, hairy. *Mycelium* mostly immersed, septate, smooth, brown. *Conidiophores* (322–)333–390(–423) × 5–8(–10) μm ($\bar{x}$ = 361 × 7 μm, n = 15), macronematous, mononematous, erect, straight or slightly curved, solitary, broader at base, septate, unbranched below, branched at apices, dark brown to black, smooth-walled. *Conidiogenous cells* 4–9(–11) × 3–8 μm ($\bar{x}$ = 6 × 6 μm, n = 25) terminal, mono- to polyblastic, subglobose, brown, smooth. *Conidia* 10–11(–14) × (9–)10–11(–12) μm ($\bar{x}$ = 11 × 11 μm, n = 70), solitary, globose, light olive green, pale brown to dark brown, aseptate, with a big guttule, verrucose. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA within 12 h and germ tube produced from around of conidium. Colonies on PDA reaching 1–2 cm diam. after one months at the room temperature, colony circular, smooth edge, surface hyphae flocculent, dense, white; reverse side white, dense, smooth.

Material examined – China, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'30.44" N, 101°1'39.51" E, 2500 m; on submerged decaying wood, 24 February 2023, H.W. Shen, FD 48-42-1 (HKAS 131781, holotype), ex-type culture KUNCC 23–13482.

GenBank numbers – ITS: PQ340469, LSU: PP189907, *tef*1-α: PQ456957.

Notes – Phylogenetic analysis showed that *Periconia dujuanhuensis* clustered as a sister clade to *P. didymosporum* with stable support (100% ML and 1.00 PP, Fig. 22). *Periconia didymosporum* is the only known sexual species, it was transferred from *Bambusistroma* based on morphological characteristics and phylogenetic analysis (Yang et al. 2022c). *Periconia didymosporum* is characterized by solitary or grouped ascomata, immersed in a clypeus-like basal stroma, 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate asci, with well-developed ocular chamber, embedded in anastomosed, cellular pseudoparaphyses, and hyaline, fusiform, 1-septate ascospores, with an entire sheath (Adamčík et al. 2015, Yang et al. 2022a). *Periconia dujuanhuensis* is only reported from its asexual morph, we are unable to compare the morphology between *P. dujuanhuensis* and *P. didymosporum*. However, our new collection fits well with the generic concept of the *Periconia*. In addition, comparison of the ITS, LSU, SSU, and *tef*1-α gene between *P. dujuanhuensis* and *P. didymosporum* revealed 8.2% (38/465 bp, including 3 gaps), 1.63% (13/799 bp, including 2 gaps), 0.42% (4/961 bp, including one gap), and 3.72% (33/887 bp, including one gap) base differences, respectively. Based on the significant differences in molecular data, we introduce *P. dujuanhuensis* as a new species from freshwater habitats.

Periconia hongheensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 23

Index Fungorum number: IF572004; Facesoffungi number: FoF15488

Etymology – The name refers to Honghe Prefecture, Yunnan Province, where this species was collected.

Holotype – HKAS 131670.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Colonies* on natural substrate superficial, effuse, brown to dark brown, hairy. *Mycelium* mostly immersed, septate, smooth, brown. *Conidiophores* (303–)328–476(–530) × 7–8 μm ($\bar{x}$ = 402 × 8 μm, n = 20), macronematous, mononematous, erect, straight or slightly curved, solitary, broader at base, septate, branched at the apices, pale brown to dark brown, smooth-walled. *Conidiogenous cells* 5–10(–15) × 3–7(–10) μm ($\bar{x}$ = 7 × 5 μm, n = 20) mono- to polyblastic, ovoid to subglobose, terminal, pale brown, smooth or verrucose. *Conidia* 4–5 × 4(–5) μm (x= 4 × 4 μm, n = 70), catenulate, globose, initially pale brown, light golden to brown when mature, aseptate, verruculose. Sexual morph: Undetermined.

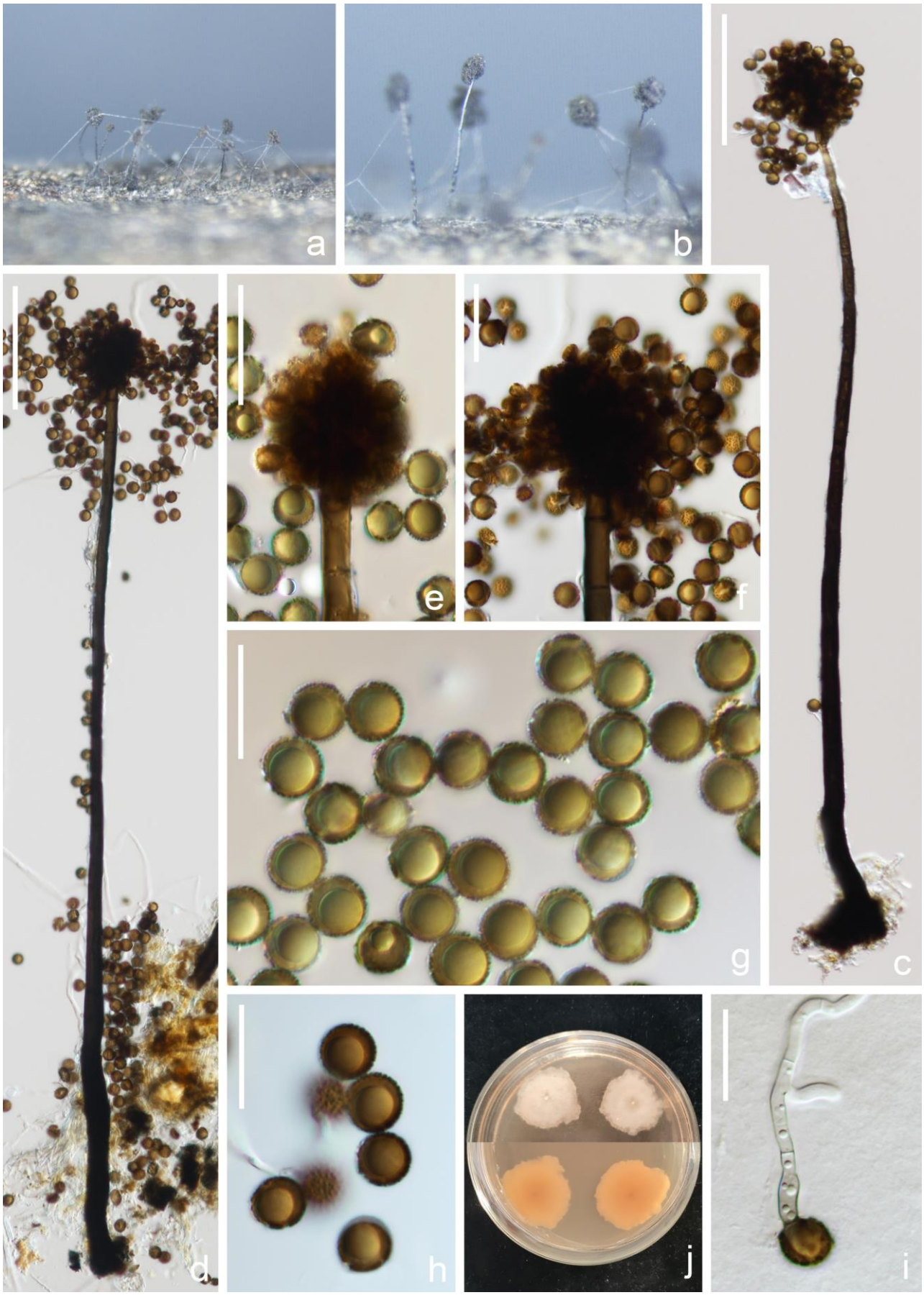

Figure 21 – *Periconia dujuanhuensis* (HKAS 131782, holotype). a, b Colonies on substrate. c, d Conidiophore with conidia. e, f Conidiogenous cells and developing conidia. g, h Conidia. i Germinated conidium. j Colony on PDA. Scale bars: c, d = 100 μm, e, f = 30 μm, g–i = 20 μm.

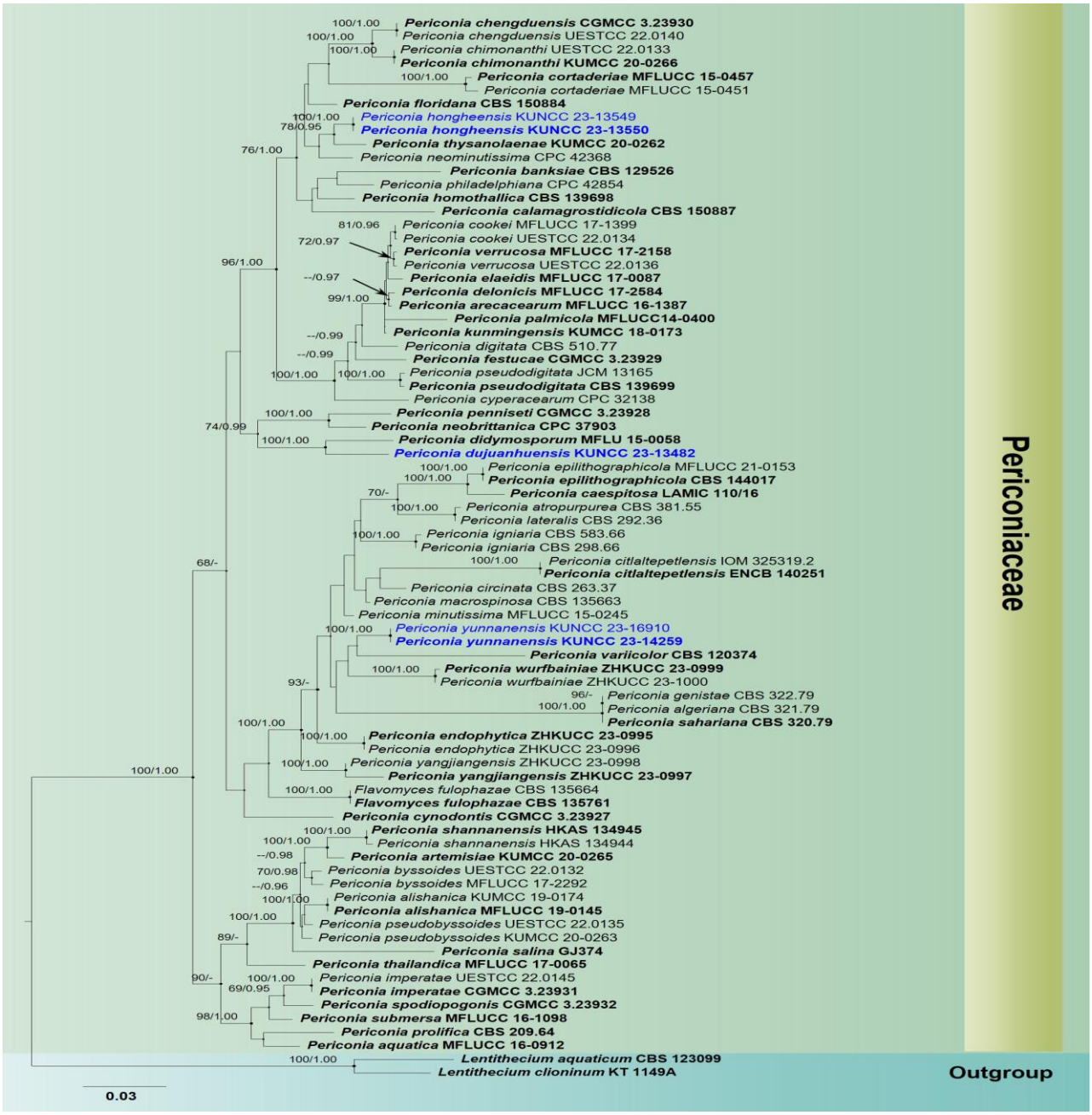

Figure 22 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef*1-α sequence dataset representing *Periconiaceae*. Seventy-nine strains are included in the combined analyses which comprise 3280 characters including gaps (846 characters for LSU, 545 characters for ITS, 1019 characters for SSU, 870 characters for *tef*1-α). *Lentithecium aquaticum* (CBS 123099) and *L. clioninum* (KT 1149A) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best scoring RAxML tree with a final likelihood value of -17280.841261 is presented. The matrix had 986 distinct alignment patterns, with 25.12% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.236949, C = 0.257364, G = 0.269635, T = 0.236053; substitution rates AC = 1.878188, AG = 2.836794, AT = 1.858848, CG = 1.429180, CT = 11.126250, GT = 1.000000; Tree-Length = 1.675084; gamma distribution shape parameter α = 0.178709. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains indicated are in bold and newly generated sequence are shown in blue.

Culture characteristics – Conidia germinated on PDA within 12 h and germ tube produced from around of conidium. Colonies on PDA reaching 1–2 cm diam. after one months at the room temperature, colony circular, smooth edge, surface hyphae flocculent, dense, white; reverse side white at the edges and middle area brown to dark brown, dense, smooth.

Material examined – China, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°41'13.38" N, 102°34'29.37" E, 1400 m; on submerged decaying wood, 22 February 2023, Z.Q. Zhang, FD 42-10-1 (HKAS 131670, holotype), ex-type culture KUNCC 23–13550; *ibid*, on submerged decaying wood, 22 February 2023, Z.Q. Zhang, FD 42-18-1 (HKAS 131673, paratype), ex-paratype culture KUNCC 23–13549.

GenBank numbers – KUNCC 23–13550, ITS: PQ340467, LSU: PP189905, *tef*1-α: PQ456958; KUNCC 23–13549, ITS: PQ340466, LSU: PP189904.

Notes – Based on a megablast search of NCBIs GenBank nucleotide database, the best matching result of the ITS sequence is *Periconia macrospinosa* (strain BRPET25, sequence ID: MT658103; similarities: 507/508 (99%), 1 gap). The best matching result of LSU sequence is *P. digitata* (strain CBS 510.77, sequence ID: AB807561; similarities: 1253/1267 (99%), 2 gaps). The best matching result of *tef*1-α sequence is *P. thysanolaenae* (strain KUMCC 20–0262, sequence ID: MW460896; similarities: 866/891 (97%), no gap). Phylogenetic analysis showed that *P. hongheensis* formed an independent lineage in the *Periconia* clade and sister to *P. thysanolaenae*, with 78% ML and 0.95 BYPP support (Fig. 22). *Periconia hongheensis* is similar to *P. thysanolaenae* in having macronematous, mononematous conidiophores that are branched at the apex, with polyblastic, ovoid to subglobose conidiogenous cells, and producing catenulate, globose, and verrucous conidia (Yang et al. 2022c). However, *P. hongheensis* can be distinguished from *P. thysanolaenae* by the smaller conidia (4–5 × 4(–5) μm *vs.* 4.5–6 × 4–6 μm). Based on the unique morphological characteristics combined with phylogenetic analysis (Pem et al. 2021), we introduce *Periconia hongheensis* as a new species.

Periconia yunnanensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 24

Index Fungorum number: IF572005; Facesoffungi number: FoF15489

Etymology – The name refers to Yunnan Province, where this species was collected.

Holotype – HKAS 131727.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Colonies* on natural substrate superficial, effuse, brown to dark brown, hairy. *Mycelium* mostly immersed, septate, smooth, brown. *Conidiophores* (457–)474–583(–693) μm long ($\bar{x}$ = 528, n = 20), 5–7 μm ($\bar{x}$ = 6 μm, n = 20) wide at the apex, 11–15 μm ($\bar{x}$ = 13 μm, n = 20) wide at the base, macronematous, mononematous, erect, mostly curved, solitary, broader at the base, unbranched, septate, dark brown, smooth-walled. *Conidiogenous cells* 8–10 × 6–8 μm ($\bar{x}$ = 9 × 7 μm, n = 20), polyblastic, subglobose, terminal, proliferous, pale brown to brown, smooth. *Conidia* 11–14 × (9–)11–13(–15) μm ($\bar{x}$ = 12 × 12 μm, n = 60), solitary, globose, brown to dark brown, aseptate, obviously verruculose. Sexual morph: Undetermined.

Culture characteristics – Conidia germinated on PDA within 12 h and germ tubes produced from around of conidium. Colonies on PDA reaching 2–2.5 cm diam. after one months at the room temperature, colony circular, smooth edge, surface hyphae flocculent, dense, reddish-brown at the edge, dark brown in centre zoon, sparse and thin at the edge; reverse side pale brown to dark brown, smooth.

Material examined – China, Yunnan Province, Kunming City, Dianchi Lake, 24°53'50.48" N, 102°45'44.51" E, 1894 m; on submerged decaying wood, 19 February 2023, S. Luan, FD 38-14-2 (HKAS 131727, holotype), ex-type culture KUNCC 23–14259; *ibid*, Yangzonghai Lake, 24°51'34.01" N, 102°59'30.53" E; 1770m; on submerged decaying wood, 19 February 2023, H.W. Shen, FD 25-26-1 (HKAS131424, paratype), ex-paratype culture KUNCC 23–16910.

GenBank numbers – KUNCC 23–14259, ITS: PQ340468, LSU: PP189906, *tef*1-α: PQ456960; KUNCC 23–16910, ITS: PQ607755, LSU: PP189925, *tef*1-α: PQ456959.

Figure 23 – *Periconia hongheensis* (HKAS 131670, holotype). a Colonies on substrate. b, c Conidiophore with conidia. d, e Conidiogenous cells and developing conidia. f, g Conidia chains with young conidia. h, i Conidia. j Germinated conidium. k Colony on PDA. Scale bars: b, c = 70 μm, d, e = 20 μm, f–j = 5 μm.

Notes – Phylogenetic analysis showed that *Periconia yunnanensis* clusters with *P. variicolor* with low support (Fig. 22). Comparison of the ITS gene between *P. yunnanensis* and *P. variicolor* revealed 5.8% (35/484 bp, including 7 gaps) base pair differences. In addition, *P. yunnanensis* is similar to *P. variicolor* which has globose, brown to dark brown, aseptate, verrucose conidia (Cantrell et al. 2007). However, *P. yunnanensis* has longer conidiophores (474–583 μm *vs.* 20–271 μm) and larger conidia (11–13 μm *vs.* 7.5–9.5 μm) than *P. variicolor*. We therefore, introduce *P. yunnanensis* as a new species, based on morphological characters and phylogenetic analysis (Pem et al. 2021).

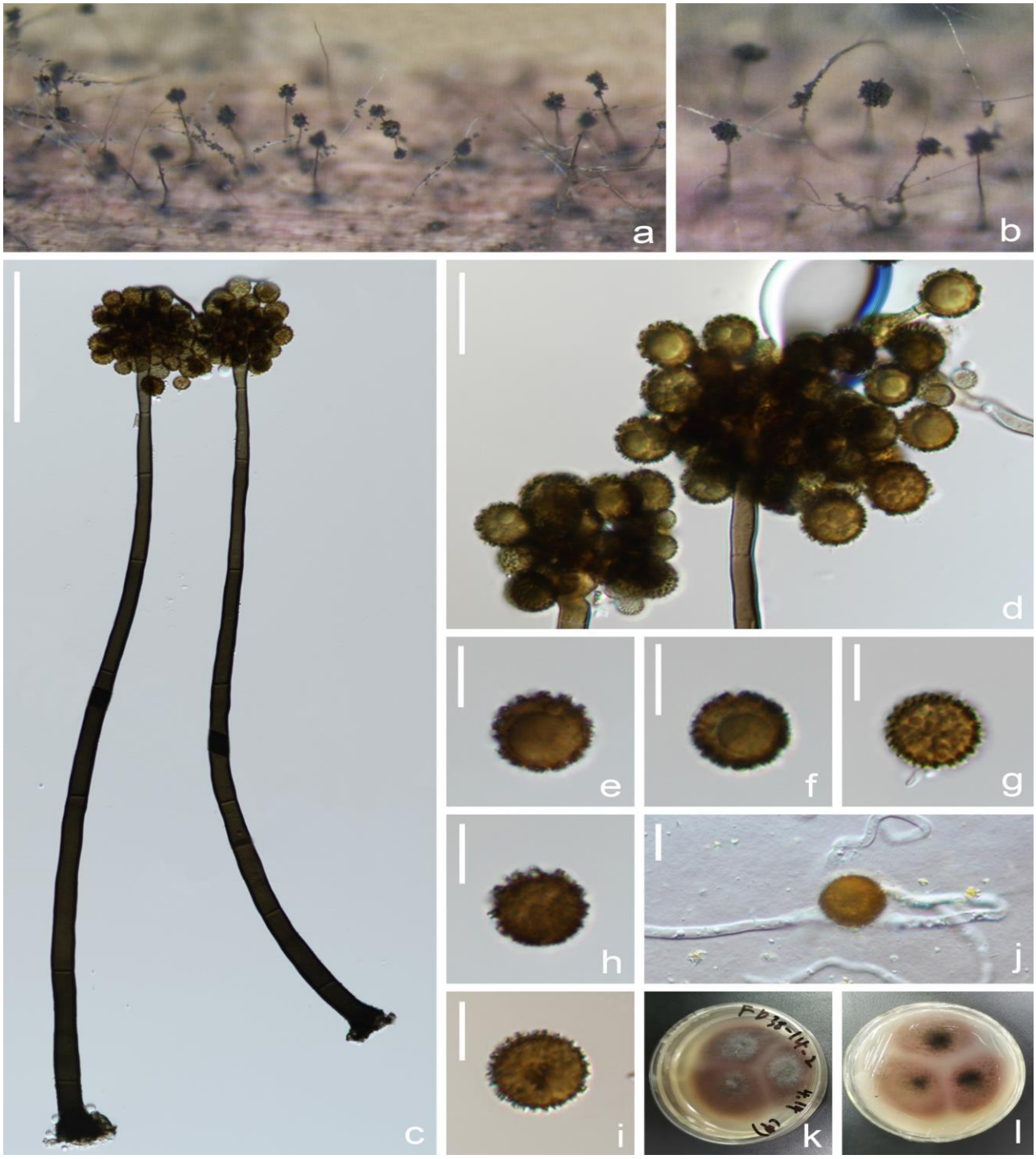

Figure 24 – *Periconia yunnanensis* (HKAS 131727, holotype). a, b Colonies on substrate. c Conidiophore with conidia. d Conidiogenous cells and developing conidia. e–i Conidia. j Germinated conidium. k, l Colony on PDA. Scale bars: c = 100 μm, d = 20 μm, e–j = 10 μm.

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

Roussoellaceae was introduced by Liu et al. (2014) to accommodate three genera, *Neoroussoella*, *Roussoella* (type) and *Roussoellopsis*. According to the updated "Outline of Fungi and fungus-like taxa – 2021" by Wijayawardene et al. (2022a), twelve genera are included in *Roussoellaceae*. Subsequent studies have transferred *Immotthia* to *Dictyosporiaceae* based on morphological and phylogenetic analyses (Jiang et al. 2021b). Currently the family contains eleven genera *viz.*, *Appendispora*, *Cytoplea*, *Elongatopedicellata*, *Neoroussoella*, *Pararoussoella*, *Pseudoneoconiothyrium*, *Pseudoroussoella*, *Roussoella*, *Roussoellopsis*, *Setoarthopyrenia* and *Xenoroussoella* (Jiang et al. 2021b, Wijayawardene et al. 2022a).

Roussoella Sacc., Atti dell'Istituto Veneto Scienze, 6: 410 (1888)

Roussoella, the type genus of *Roussoellaceae*, was introduced by Saccardo and Paoletti (1888) with *R. nitidula* as the type species. The asexual morphs of *Roussoella* has been linked to *Cytoplea* (Liu et al. 2014). The sexual morph of the genus is characterized by immersed, large, and loculate ascostromata, cylindrical and bitunicate asci, brown, fusiform to ellipsoidal, ornamented, and two-celled ascospores surrounded by a sheath (Liu et al. 2014, Dai et al. 2017, 2022). The pseudoparaphyses appear to be trabeculate (Liew et al. 2000). The asexual morph is characterized by superficial or semi-immersed, subglobose, multilocular conidiomata; holo- or entero-blastic, hyaline, cylindrical to ellipsoidal, ampulliform conidiogenous cells and oblong, ellipsoidal, globose, obovoid, aseptate conidia (Liu et al. 2014, Dai et al. 2017, Hyde et al. 2020b, Dai et al. 2022). *Roussoella* species are primarily saprobic in terrestrial habitats and most are associated with bamboo (Liu et al. 2014, Dai et al. 2017, Jiang et al. 2019, Dai et al. 2022), several species have also been reported from palm petioles (Hyde 1997, Hyde et al. 1999), stems of *Solanum mauritianum* (Crous et al. 2016), and leaf spots of *Coffea arabica* (Crous et al. 2015b). *Roussoella aquatica*, *R. intermedia* and *R. minutella* were reported from freshwater habitats (Dong et al. 2020). *Roussoella solani* has been reported as a human pathogen (Mochizuki et al. 2017). The phylogenetic placement of *Roussoella* species is well-resolved, except for *R. aequatoriensis*, *R. alveolata*, *R. angustispora*, *R. bambusae*, *R. calamicola*, *R. chilensis*, *R. donacicola*, *R. palmicola*, *R. saltuensis*, *R. serrulata* and *R. verruculosa*, for which molecular sequences are currently unavailable (Dai et al. 2022).

Roussoella dujuanhuensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 25

Index Fungorum number: IF572006; Facesoffungi number: FoF15491

Etymology – The name refers to Dujuanhu Lake, where the species was collected.

Holotype – HKAS 131782.

Saprobic on decaying submerged wood in freshwater. Sexual morph: *Ascomata* 180–230 μm high, 270–330 μm diam., solitary, scattered to gregarious, immersed under an epidermis, erumpent to semi-immersed, raised on host surface, dark brown to black, ampulliform, uni-loculate, ostiolate. *Peridium* 12–30 μm thick, comprising of several layers, outer layer thick-walled, comprising pale brown to dark brown cells of *textura angularis*; inner layer comprising hyaline, thick-walled cells of *textura angularis*. *Hamathecium* 1–2 μm wide, dense, branched, septate, thick-walled, filiform, hyaline, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* (59–)72–89(–111) × 4–5 μm ($\bar{x}$ = 80 × 5 μm, n = 40), 8-spored, bitunicate, cylindrical, straight or slightly curved, short to long pedicellate with furcate ends, apically rounded with an ocular chamber. *Ascospores* (6–)8–10 × 3–4 μm ($\bar{x}$ = 9 × 3 μm, n = 60), partially overlapping 1-seriate, ellipsoid to fusiform, 1-septate, constricted at the septum, with a broad upper cell, straight to slightly curved, pale brown to yellowish when young, brown to grey brown when mature, guttulate, verrucose, with longitudinally striate surface, surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA and germ tubes produced from end of ascospore within 12 h. Colonies on PDA, reaching 2-3 cm in diameter after one month at room temperature in dark, colony circular, smooth edge, surface hyphae pale to light-brown, flocculent; reverse side brown.

Material examined – China, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'30.44" N, 101°1'39.51" E; 2500m, on submerged decaying culm of bamboo, 24 February 2023, H.W. Shen, FD 48-42-2 (HKAS 131782, holotype), ex-holotype KUNCC 23–13483.

GenBank numbers – ITS: PQ340471, LSU: PP189909, SSU: PQ435266, *tef*1-α: PQ456961, *rpb*2: PQ348603.

Notes – Phylogenetic analysis showed that *Roussoella dujuanhuensis* clustered with *R. kunmingensis* with 92% ML and 1.00 BYPP support (Fig. 26). A comparison of ITS, LSU, *tef*1-α and *rpb*2 sequence data between *R. dujuanhuensis* and *R kunmingensis* showed 7.2% (26/361 bp, including 5 gaps), 0.25% (2/796 bp), 2.2% (19/883 bp), 6.1% (53/873 bp) base pair differences, respectively. *Roussoella dujuanhuensis* is similar to *R. kunmingensis* in the shape and size of the asci and ascospores, but the ascomata of *R. kunmingensis* are wider (395–440 μm *vs.* 270–330 μm). In addition, the ascospores of *R. dujuanhuensis* are surrounded by a mucilaginous sheath, which are lacking in the ascospores of *R. kunmingensis* (Jiang et al. 2019). Based on phylogenetic analysis and unique morphological characteristics (Pem et al. 2021), we introduce *Roussoella dujuanhuensis* as a new species.

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

Teichosporaceae was established by Barr (2002) to accommodate eight genera, *Bertiella*, *Byssothecium*, *Chaetomastia*, *Immotthia*, *Loculohypoxylon*, *Moristroma*, *Sinodidymella*, and *Teichospora* (type genus) based on trophic states, peridium and ascus structure (Barr 2002, Jaklitsch et al. 2016). Based on phylogenetic analysis, *Moristroma*, *Byssothecium* and *Bertiella* have been transferred to Chaetothyriomycetidae, *Massarinaceae* and *Melanommataceae*, respectively (Nordén et al. 2005, Mugambi & Huhndorf 2009, Schoch et al. 2009). Based on morphological and molecular phylogenetic evidence, Jaklitsch et al. (2016) applied a broad generic concept in *Teichosporaceae*, and also treated the *Floricolaceae* as a synonym of *Teichosporaceae*, and all genera under *Floricolaceae* were synonymous with *Teichospora* (Jaklitsch et al. 2016). Tennakoon et al. (2021) dismissed this broad generic concept of *Teichospora* proposed by Jaklitsch et al. (2016) based on morphological dissimilarities and the monophyletic status of the established genera, and accepted *Asymmetrispora*, *Aurantiascoma*, *Floricola*, *Magnibotryascoma*, *Misturatosphaeria*, *Pseudoaurantiascoma*, *Pseudomisturatosphaeria*, *Ramusculicola* and *Teichospora* in *Teichosporaceae* (Tennakoon et al. 2021). According to the recent outline classification of Wijayawardene et al. (2022a), 17 genera are accepted in *Teichosporaceae*.

Floricola Kohlm. & Volkm.-Kohlm., Bot. Mar. 43(4): 385 (2000)

Floricola was introduced by Kohlmeyer & Volkmann-Kohlmeyer (2000) with *F. striata* (coelomycetous) as the type species. Thambugala et al. (2015) proposed a new family, *Floricolaceae*, to accommodate *Floricola*, *Misturatosphaeria* and seven new genera, with *Floricola* as the type genus, based on morphological and phylogenetic analyses. Jaklitsch et al. (2016) adopted a broad generic concept for *Teichospora*, and treated nine genera, *viz.*, *Asymmetrispora*, *Aurantiascoma*, *Floricola*, *Magnibotryascoma*, *Misturatosphaeria*, *Neocurreya*, *Pseudoaurantiascoma*, *Pseudomisturatosphaeria*, and *Ramusculicola* as synonyms of *Teichospora*, and *Floricolaceae* as synonymous with *Teichosporaceae*. However, subsequent studies did not accept this treatment, *Floricola* and other eight genera were reinstated (Boonmee et al. 2019, Tennakoon et al. 2021, Wijayawardene et al. 2022a). Both the sexual and asexual morphs of *Floricola* have been reported, but only *F. festucae* has been reported by the sexual morph (Tennakoon et al. 2021). Presently, *Floricola* comprises six species, *viz.*, *Floricola clematidis*, *F. festucae*, *F. juncicola*, *F. striata*, *F. sulcata* (*Sclerostagonospora sulcata*), and *F. viticola*, these species grow saprobically on culms, stems, leaves and inflorescences a variety of hosts from terrestrial habitats (Kohlmeyer & Volkmann-Kohlmeyer 2000, Ariyawansa et al. 2015, Phukhamsakda et al. 2020, Tennakoon et al. 2021, Crous et al. 2022).

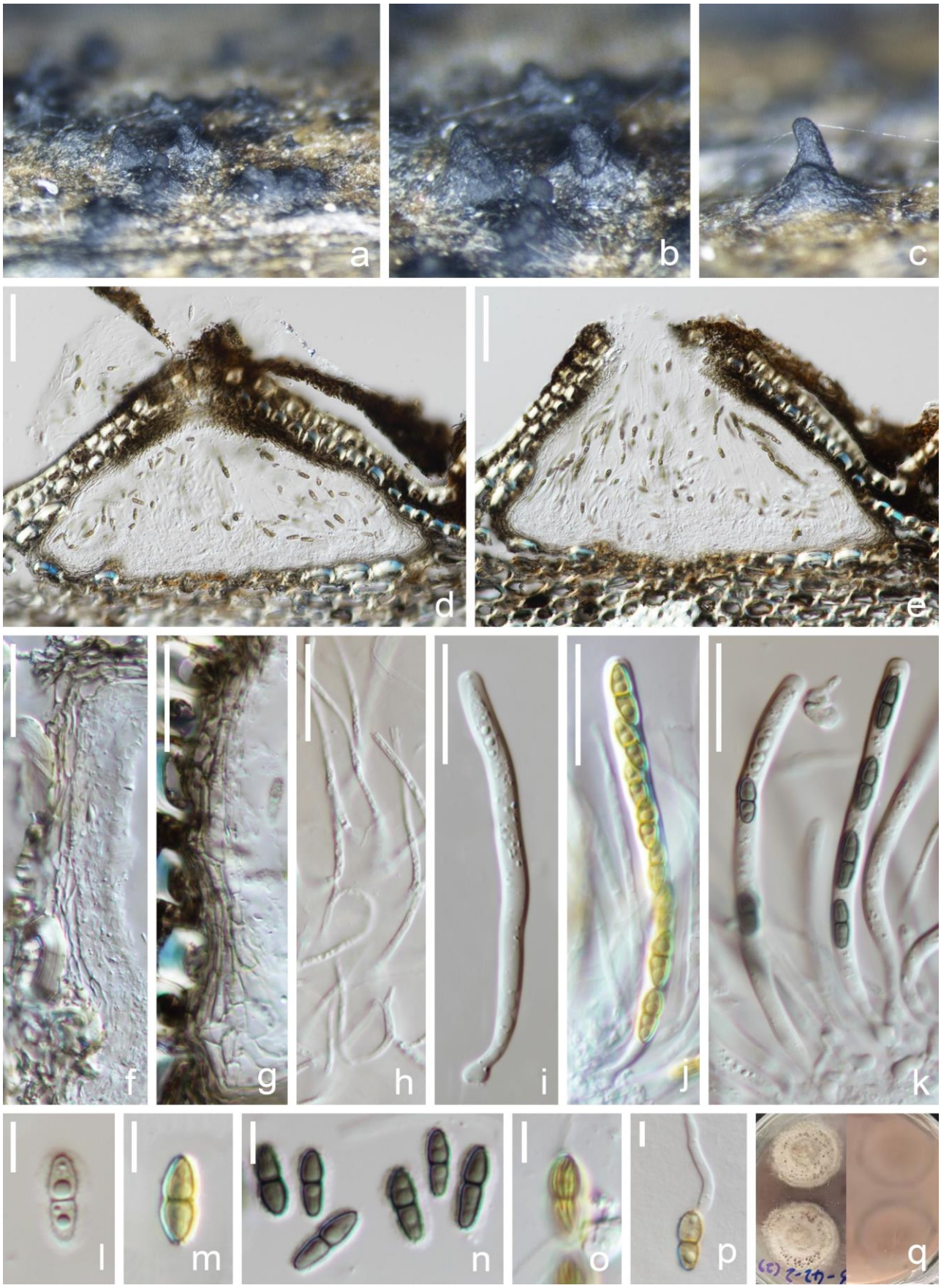

Figure 25 – *Roussoella dujuanhuensis* (HKAS 131782, holotype). a–c Appearance of ascomata on host substrate. d, e Sections of ascomata. f, g Peridium. h Trabeculate pseudoparaphyses. i–k Asci. l–n Ascospores. o Ascospore striated longitudinally. p Germinating ascospore. q Colony on PDA. Scale bars: d, e = 50 µm, f–k = 20 µm, l–p = 5 µm.

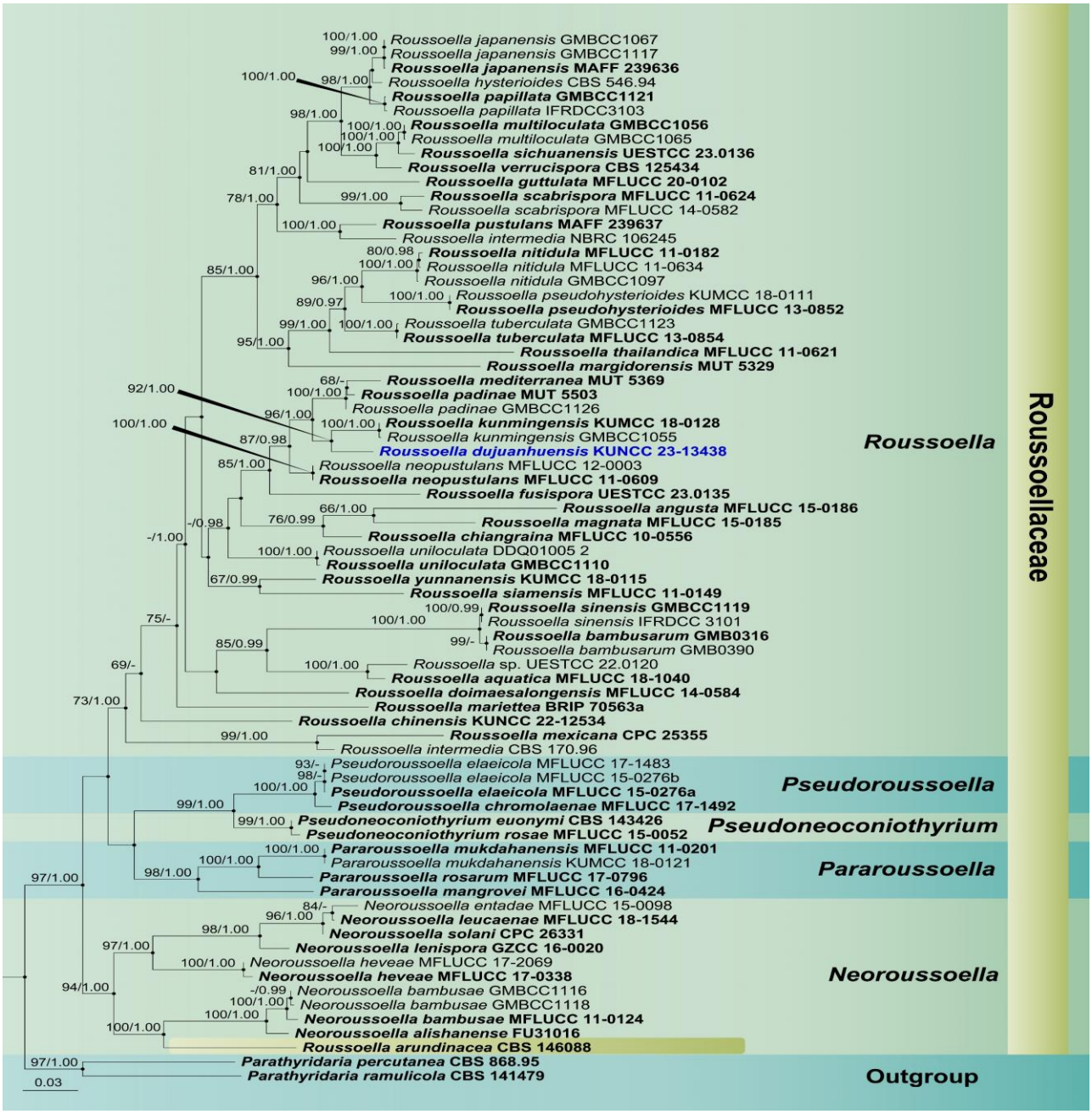

Figure 26 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *tef*1-α and *rpb*2 sequence dataset representing *Roussoellaceae*. Seventy-four strains are included in the combined analyses which comprise 3376 characters including gaps (871 characters for LSU, 559 characters for ITS, 890 characters for *tef*1-α, 1056 characters for *rpb*2). *Parathyridaria percutanea* (CBS 868.95) and *P. ramulicola* (CBS 141479) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best scoring RAxML tree with a final likelihood value of -26688.813040 is presented. The matrix had 1362 distinct alignment patterns, with 24.65% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.243049, C = 0.264574, G = 0.269631, T = 0.222746; substitution rates AC = 1.708159, AG = 4.907600, AT = 1.798346, CG = 1.113555, CT = 8.434843, GT = 1.000000; Tree-Length = 3.223791; gamma distribution shape parameter α = 0.168350. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains indicated are in bold and newly generated sequence are shown in blue.

Floricola aquatica H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 27

Index Fungorum number: IF572007; Facesoffungi number: FoF15492

Etymology – The name refers to the aquatic habitat, where the holotype of this species was collected.

Holotype – HKAS 131717.

Saprobic on decaying submerged wood in a freshwater Lake. Sexual morph: *Ascomata* 230–270 μm diam., 230–300 μm high, semi-immersed to immersed, solitary, scattered, globose to subglobose, brown to dark brown, ostiolate, papilla erumpent through host surface. *Ostioles* short, centrally located. *Peridium* 20–30 μm wide at the base, 40–70 μm wide in sides, comprising several layers of thick-walled, brown to lightly pigmented cells of *textura angularis*, inner layers of hyaline, somewhat flattened cells. *Hamathecium* composed of 2–3 μm wide, septate, guttulate pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 96–137(–160) × 8–10 μm ($\bar{x}$ = 117 × 9 μm, n = 25), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* (21–)23–27(–30) × 5–6 μm ($\bar{x}$ = 25 × 5 μm, n = 50), overlapping, uniseriate, hyaline to yellowish when young, yellowish brown when mature, cylindric-fusiform, 5–7-septate, tapering towards rounded ends, straight to slightly curved, slightly constricted at the septum, guttulate, smooth-walled, surrounded by entire mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospore germinated on PDA within 12 h and germ tubes produced from ends of ascospore. Colonies on PDA reaching 5 cm diam. after one months at the room temperature, colony circular, smooth edge, surface hyphae brown, flocculent, dense, sparse and thin at the edge; reverse side pale brown to dark brown, smooth.

Material examined – China, Yunnan Province, Kunming City, Dianchi Lake, 24°53'50.48" N, 102°45'44.51" E, 1894 m; on unknown submerged decaying wood, 19 February 2023, S. Luan, FD 38-30-2 (HKAS 131717, holotype), ex-type culture KUNCC 23–14239.

GenBank numbers – ITS: PQ340460, LSU: PP189896, SSU: PQ435256, *tef*1-α: PQ456947, *rpb*2: PQ348600.

Notes – Phylogenetic analysis showed that *Floricola aquatica* clustered together with the sexual species, *F. festucae*, with 99% ML and 1.00 BYPP support (Fig. 28). A nucleotides comparison of ITS, LSU, SSU and *tef*1-α sequence data between *F. aquatica* and *F. festucae* revealed 5.06% (27/533 bp, including 7 gaps), 0.37% (3/812 bp, including 1 gaps), 0.31% (3/972 bp, including 1 gaps), 2.21% (19/860 bp) differences, respectively. *Floricola aquatica* is similar to *F. festucae* in having semi-immersed to immersed, globose to subglobose ascomata, and cylindric-fusiform, septate, guttulate ascospores (Tennakoon et al. 2021). All known *Floricola* species are sexual except *F. festucae*. Thus, we only compare the morphology of our new collection with *F. festucae*. *Floricola aquatica* can be distinguished from *F. festucae* by the larger ((21–)23–27(–30) × 5–6 μm *vs.* 20–25 × 5–6 μm) and more septa (5–6-septate *vs.* 5–7-septate) ascospores. In addition, ascospores of *F. festucae* lacks a mucilaginous sheath, while ascospores of *F. aquatica* are surrounded by an entire mucilaginous sheath. Therefore, based on morphological and phylogenetic analyses (Pem et al. 2021), we introduce *F. aquatica* as a new species, which is the first species of *Floricola* discovered in freshwater habitats.

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

Tetraplosphaeriaceae was established by Tanaka et al. (2009) to accommodate five new genera with tetraploa-like asexual morphs, with *Tetraplosphaeria* Kaz. Tanaka & K. Hiray. as type genus. Subsequently, Hyde et al. (2013) treated the type genus, *Tetraplosphaeria* as a synonym of *Tetraploa* according to nomenclatural priority. Later, a new genus, *Aquatisphaeria*, and three previously described genera were placed in *Tetraplosphaeriaceae* based on morphological and phylogenetic analyses (Ariyawansa et al. 2015, Delgado et al. 2017, Pem et al. 2019, Dong et al. 2020, Li et al. 2021). *Tetraplosphaeriaceae* is known for its tetraploa-like asexual morphs, where the conidia are globose to long obpyriform, composed of 3–8 columns or internal hyphal structure, with 2–8 appendages arising from apical or/and basal part (Tanaka et al. 2009, Hyde et al. 2013,

Dong et al. 2020, Hongsanan et al. 2020b, Li et al. 2021). The sexual morphs of *Tetraplosphaeriaceae* are massarina-like with narrowly fusiform to broadly cylindrical, hyaline to pale brown and 1(–3)-septate ascospores, usually with mucilaginous sheath or appendage-like sheath (Tanaka et al. 2009, Hyde et al. 2013, Hongsanan et al. 2020b). Most members of *Tetraplosphaeriaceae* occur as saprobes on the branches, culms, leaves, and stems of various hosts in terrestrial habitats (Tanaka et al. 2009, Tibpromma et al. 2018, Jayawardena et al. 2022, Senanayake et al. 2023), also occur on the spathes of coconuts (Hyde et al. 2020a), and a few also reported as endophytic (Crous et al. 2021). A few species of *Tetraplosphaeriaceae* are also found in freshwater habitats and also known as fossils (Tanaka et al. 2009, Dong et al. 2020, Li et al. 2020, Bao et al. 2021a, Li et al. 2021, Nuñez Otaño et al. 2022, Liu et al. 2023, Yang et al. 2023).

Figure 27 – *Floricola aquatica* (HKAS 131717, holotype). a Appearance of ascomata on natural substrate. b Section of ascomata. c Peridium. d Pseudoparaphyses. e, f Asci. g, h Ascospores with mucilaginous sheath. g, i–k Ascospores. l Ascospore stained with Indian ink. m Germinating ascospore. n, o Colony on PDA. Scale bars: b = 80 µm, c–f = 20 µm, g–m = 10 µm.

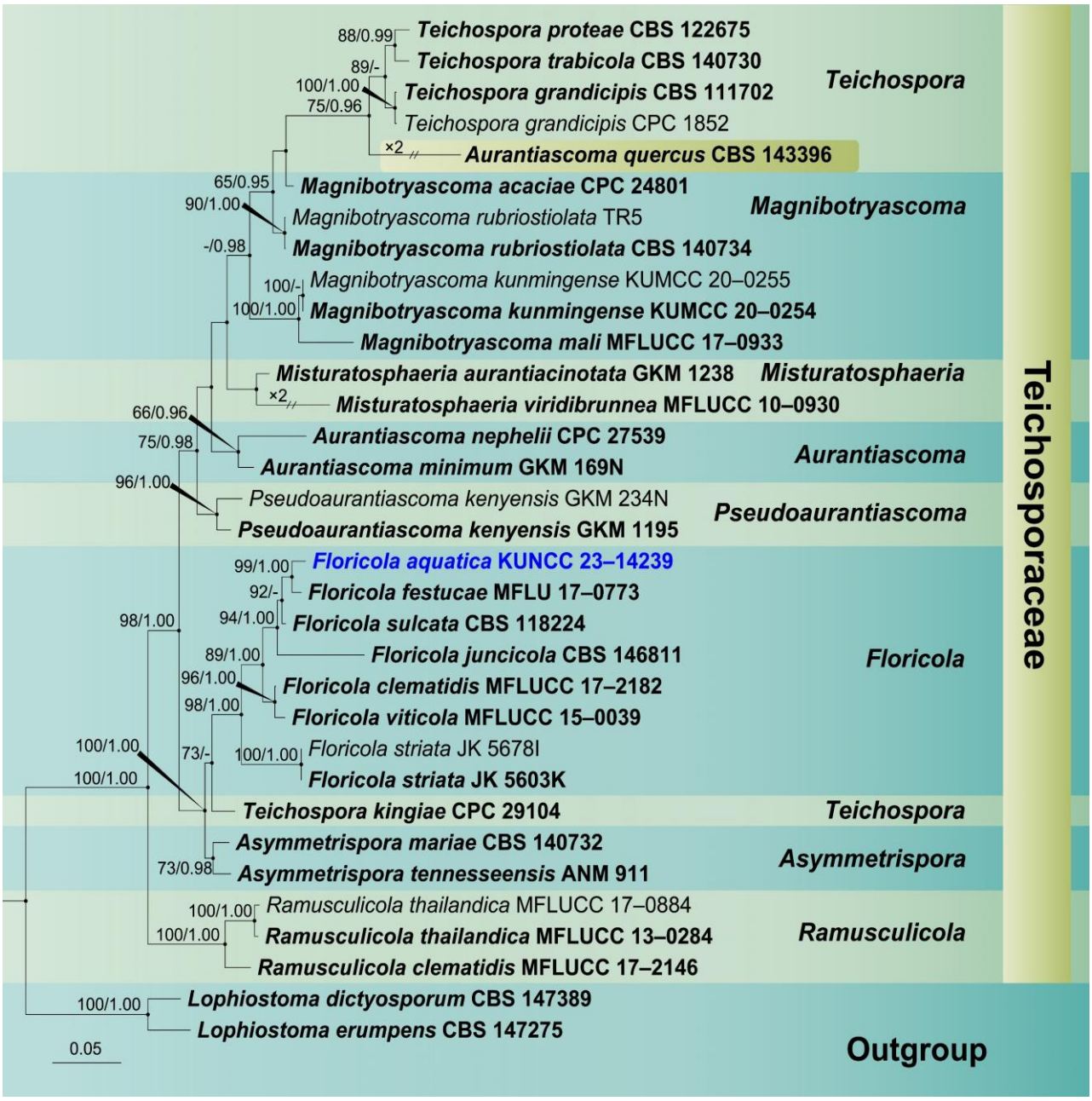

Figure 28 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *tef*1-α, *rpb*2 and SSU sequence dataset representing *Teichosporaceae*. Thirty-three strains are included in the combined analyses which comprise 4156 characters including gaps (875 characters for LSU, 535 characters for ITS, 718 characters for *tef*1-α, 1057 characters for *rpb*2, 971 characters for SSU). *Lophiostoma dictyosporum* (CBS 147389) and *L. erumpens* (CBS 147275) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best scoring RAxML tree with a final likelihood value of -18268.844974 is presented. The matrix had 1132 distinct alignment patterns, with 41.14% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.243381, C = 0.254886, G = 0.279282, T = 0.222451; substitution rates AC = 1.301800, AG = 2.664461, AT = 1.286557, CG = 1.108042, CT = 7.986513, GT = 1.000000; Tree-Length = 1.311535; gamma distribution shape parameter α = 0.254422. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains are indicated in bold and newly generated sequence are shown in blue.

Pseudotetraploa Kaz. Tanaka & K. Hiray., in Tanaka, Stud. Mycol. 64: 193 (2009)

Pseudotetraploa, proposed for three tetraploa-like species, is characterized by conidia composed of 4 to 8 columns, which are obpyriform to long obpyriform, pseudoseptate, with 4 (rarely 6 to 8) appendages, and with *Pseudotetraploa curviappendiculata*. as the type species (Tanaka et al. 2009, Hyde et al. 2013). *Pseudotetraploa* species are saprobes associated with bamboo and currently comprises six species, *viz.*, *P. bambusicola*, *P. curviappendiculata* (*Tetraploa curviappendiculata*), *P. javanica* (*T. javanica*), *P. longissima* (*T. longissima*), *P. rajmachiensis* and *P. yunnanensis*, and from terrestrial habitats (Tanaka et al. 2009, Hyde et al. 2020a, Yu et al. 2022, Tang et al. 2023).

Pseudotetraploa aquatica H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 29

Index Fungorum number: IF572008; Facesoffungi number: FoF15493

Etymology – The name refers to the aquatic habitat, where the holotype was collected.

Holotype – HKAS 131574.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Colonies* on natural substrate effuse, surface, conspicuous, black, glistening. *Mycelium* immersed, partly superficial, consisting of branched, septate, smooth, pale brown to brown hyphae. *Conidiophores* absent. *Conidiogenous cells* monoblastic, usually indistinguishable from the superficial hyphae. *Conidia* solitary, straight or slightly curved, brown to dark brown, pseudoseptate, of two types: ovoid to obclavate or pyriform conidia (56–)98–131(–145) μm ($\bar{x}$ = 144 μm, n = 25) long, 10–16 μm wide at the apex, (22–)30–56(–63) μm wide at the widest part, composed of 3–4 inconspicuous columns of cells, each column being closely integrated; cheiroid conidia (96–)104–124(–135) μm ($\bar{x}$ = 144 μm, n = 15) long, 77–104(–124) μm wide at the widest part, composed of 2–5 rows divergent from the base or middle part, each row consisting of 1–4 inconspicuous columns of cells, conidia without appendages at the apex, germinating easily, with germ tubes emerging from the basal cells or the apical cells. Sexual morph: Undetermined.

Material examined – China, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'30.44" N, 101°1'39.51" E; 2500 m, on submerged decaying wood, 24 February 2023, H.W. Shen, FD 48-4-1 (HKAS 131574, holotype), ex-type culture KUNCC 23–13375.

GenBank numbers – ITS: PQ340470, LSU: PP189908, *tub*2: PQ456973.

Notes – Multigene phylogenetic analysis showed that *Pseudotetraploa aquatica* formed an independent lineage basal to other *Pseudotetraploa* with 79% ML and 1.00 BYPP support (Fig. 30). Based on a megablast search of NCBIs GenBank nucleotide database, the best matching ITS sequence is *Quadricrura meridionalis* (strain CBS 125684, sequence ID: MH863636; similarities: 451/483 (93%), 5 gaps). The best matching result of the LSU sequence is *Pseudotetraploa javanica* (strain HC 4934, sequence ID: AB524611; similarities: 1250/1268 (99%), one gap). The best matching result of *tub*2 sequence is *P. longissima* (strain HC 4933, sequence ID: AB524858; similarities: 500/568 (88%), 7 gaps). *Pseudotetraploa aquatica* can be distinguished from other *Pseudotetraploa* species by several unique features; lacking appendages, cheiroid conidia composed of 2–5 rows divergent from the base or middle part, each row consisting of 1–4 inconspicuous columns of cells (Tanaka et al. 2009). Based on molecular and unique morphological data (Pem et al. 2021), we introduce *P. aquatica* as a new species, which is the first species of this genus reported from freshwater habitats.

Triplosphaeria Kaz. Tanaka & K. Hiray., Stud. Mycol. 64: 185 (2009)

Triplosphaeria was introduced by Tanaka et al. (2009) to accommodate massarina-like taxa with tetraploa-like asexual morphs. The sexual morphs are characterized by hyaline, 1-septate, fusiform ascospores with an entire sheath. The asexual morph is tetraploa-like with ovoid to obpyriform conidia composed of 3 columns, with 3 appendages at the apex. *Triplosphaeria* is similar to *Tetraploa* but differs by its hemispherical ascomata with a flattened base, conidia composed of 3 columns, ovoid to obpyriform, with 3 setae appendages (Tanaka et al. 2009, Hyde et al. 2013). Currently, the genus contains five species, as saprobes and probably prefer to bamboo.

Triplosphaeria acuta and *T. guizhouensis* were collected from freshwater habitats (Tanaka et al. 2009, Liu et al. 2023).

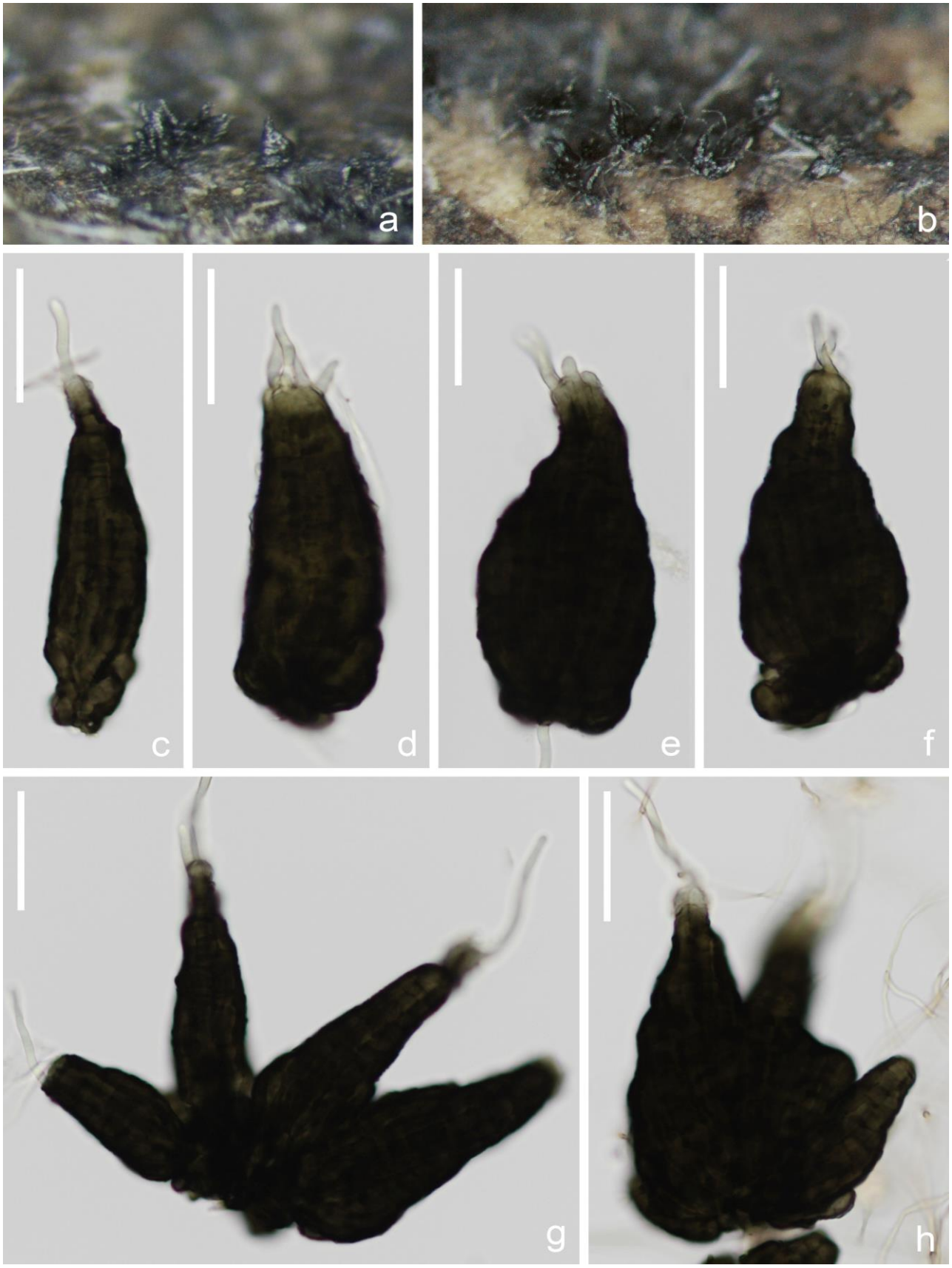

Figure 29 – *Pseudotetraploa aquatica* (HKAS 131574, holotype). a, b Colonies on natural substrate. c–h Conidia and germ tubes germinate from the apex. Scale bars: c–h = 20 μm.

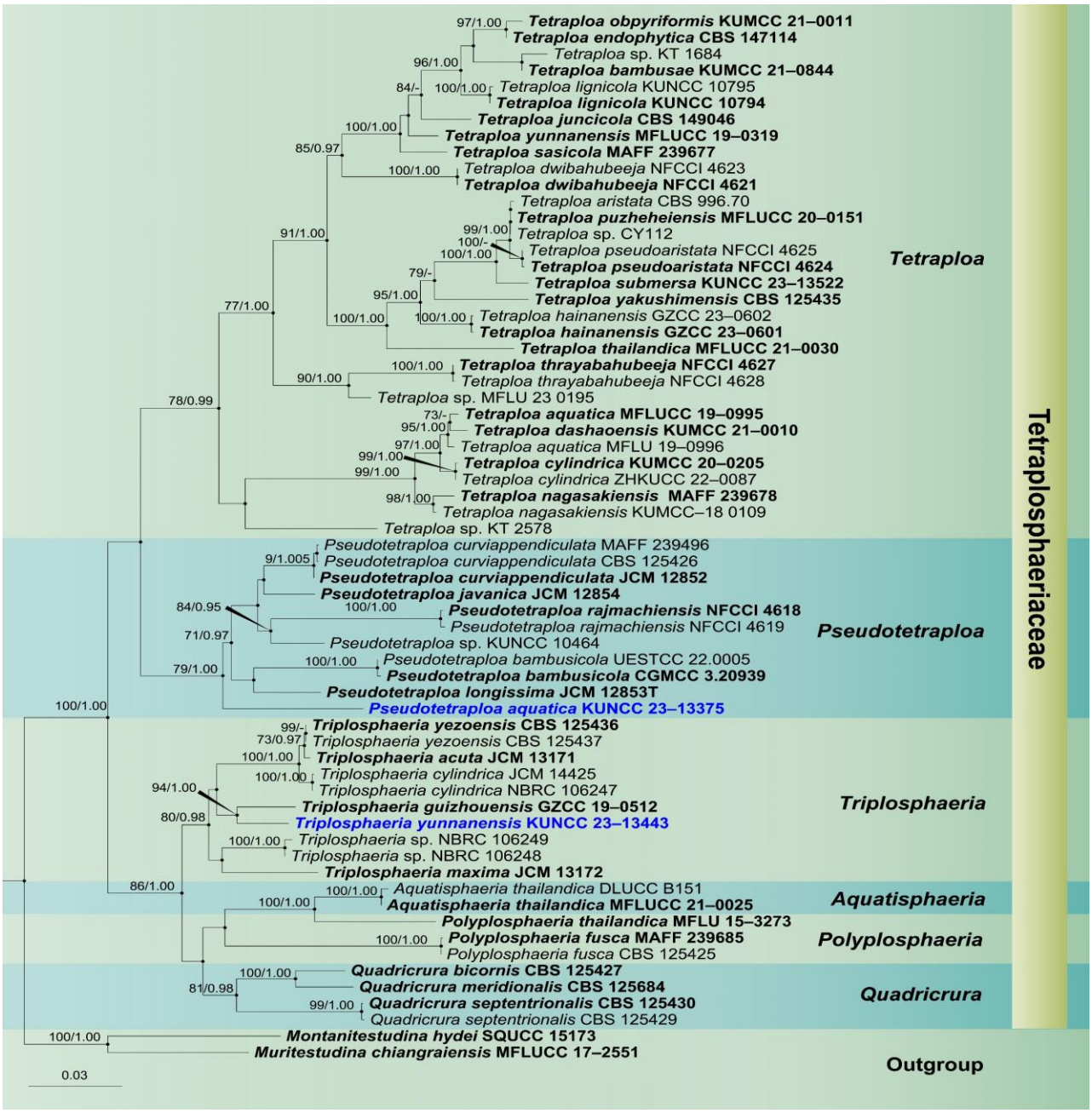

Figure 30 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU and *tub*2 sequence dataset representing *Tetraplosphaeriaceae*. Sixty-four strains are included in the combined analyses which comprise 3067 characters including gaps (913 characters for LSU, 530 characters for ITS, 991 characters for SSU, 633 characters for *tub*2). *Montanitestudina hydei* (SQUCC 1517) and *Muritestudina chiangraiensis* (MFLUCC 17–2551) were selected as the outgroup taxa. Phylogenetic trees generated from maximum likelihood and Bayesian inference analyses were similar in overall topologies. The best scoring RAxML tree with a final likelihood value of -15642.876263 is presented. The matrix had 898 distinct alignment patterns, with 20.28% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.244595, C = 0.248308, G = 0.274184, T = 0.232913; substitution rates AC = 3.041900, AG = 4.424457, AT = 2.119221, CG = 1.334891, CT = 10.779290, GT = 1.000000; Tree-Length = 1.492221; gamma distribution shape parameter α = 0.133548. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (BYPP) greater than 0.95 are defined above the nodes as ML/BYPP. The type strains are indicated in bold and newly generated sequence are shown in blue.

Triplosphaeria yunnanensis H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov. Fig. 31

Index Fungorum number: IF572009; Facesoffungi number: FoF15494

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

Holotype – HKAS 132043.

Saprobic on decaying submerged wood in freshwater. Asexual morph: *Colonies* on natural substrate effuse, surface conspicuous, brown to black. *Mycelium* mostly immersed, consisting of branched, septate, smooth, pale brown to brown hyphae. *Conidiophores* absent. *Conidiogenous cells* monoblastic, usually indistinguishable from the superficial hyphae. *Conidia* (54–)59–72(–76) μm ($\bar{x}$ = 66 μm, n = 20) long, 20–28 μm ($\bar{x}$ = 16 μm, n = 20) wide at the base, (11–)13–19(–21) μm ($\bar{x}$ = 24 μm, n = 20) wide at the apex, solitary, straight or slightly curved, ovoid to obclavate or pyriform, composed of 2–4 columns of cells, 9–10-septate in each column, sometimes divided into 3–4 separate columns from the base and middle part, guttulate, smooth-walled or sometimes verrucose on the base cell, with 3–4 appendages. *Appendages* (10–)13–21(–29) × 3 μm, divergent, pale brown to brown, (1–)2-septate, straight or slightly flexuous, smooth-walled. Sexual morph: Undetermined.

Cultural characteristics: Conidia germinating on PDA and germ tubes produced from appendages within 12 h. Colonies on PDA, reaching 1–1.5 cm after one month at room temperature, colony circular, smooth edge, surface hyphae white to grey-brown, floccose; reverse side grey to brown.

Material examined – China, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'22.76" N, 101°1'6.85" E; 2500 m, on submerged decaying wood, 24 February 2023, H.W. Shen, FD 50-74-3 (HKAS 132043, holotype), ex-type culture KUNCC 23–13443.

GenBank numbers – ITS: PQ340474, LSU: PP189912, SSU: PQ435268, *tub*2: PQ456974.

Notes – In the phylogenetic analysis *Triplosphaeria yunnanensis* clustered with *T. guizhouensis* with 94% ML and 1.00 BYPP support (Fig. 30). *Triplosphaeria guizhouensis* is an asexual species collected on submerged decaying wood from a stream in Guizhou Province. The conidia comprises three or four columns, and are guttulate, sometimes verrucose at the base cell, with 3–4 appendages, distinguishing it from other *Triplosphaeria* species (Liu et al. 2023). *Triplosphaeria yunnanensis* is also an asexual species found on submerged decaying wood in freshwater habitats from Dujuanhu Lake, a plateau lake in Yunnan. *Triplosphaeria yunnanensis* is similar to *T. guizhouensis* in having conidia with 3–4 columns and 3–4 appendages (Liu et al. 2023). However, *T. yunnanensis* can be distinguished from *T. guizhouensis* by its longer ((54–)59–72(–76) μm *vs.* 18.9–23 μm), ovoid to obclavate or pyriform conidia with more septa (9–10 *vs.* 5–7). Furthermore, sometimes the conidia of *T. yunnanensis* are divided into 3–4 separate columns from the base and middle. Nucleotide comparison of the ITS, LSU, SSU and *tef*1-α between *T. yunnanensis* and *T. guizhouensis* revealed 3.49% (17/487 bp, including 1 gap), 0.97% (7/719 bp), and 8.11% (46/567 bp, including 3 gaps) differences, respectively. Based on morphological characters and phylogenetic analysis (Pem et al. 2021), *T. yunnanensis* is introduced as a new species from freshwater habitats.

Triplosphaeria sp. (NBRC 106248 and NBRC 106249) forms a separate lineage in the *Triplosphaeria* clade in our phylogenetic analysis (Fig. 30). Since the sexual morphs of NBRC 106248 and NBRC 106249 were not found, and the conidial morphology observed on natural host plants was significantly different from those produced on the rice straw agar (RSA) medium, Tanaka et al. (2009) treated them as *Triplosphaeria* sp.

Validation of names

Notes – *Lentithecium* is a polyphyletic group, with some species having been transferred to closely related genera based on morphological and phylogenetic analyses (Dong et al. 2020, Calabon et al. 2021b). Our previous molecular phylogenetic and morphological studies have demonstrated that *Lentithecium aquaticum* is distinct from other *Lentithecium* species, leading to its reassignment to the new genus *Paralentithecium* (Shen et al. 2023). Unfortunately, the name *Paralentithecium* (MB 849738) has not been validly published according to current nomenclature

rules (Turland et al. 2018), because the holotype of the previously described species *L. aquaticum* was not cited. This makes not only the genus name invalidly described, but also the species recognized in the genus, *Paralentithecium suae*. Additionally, *Paralentithecium aquaticum* remains invalidly published because no new identifier has been registered for it in the MycoBank, Index Fungorum, or Fungal Names databases. Below, we validate *Paralentithecium* and its related species names.

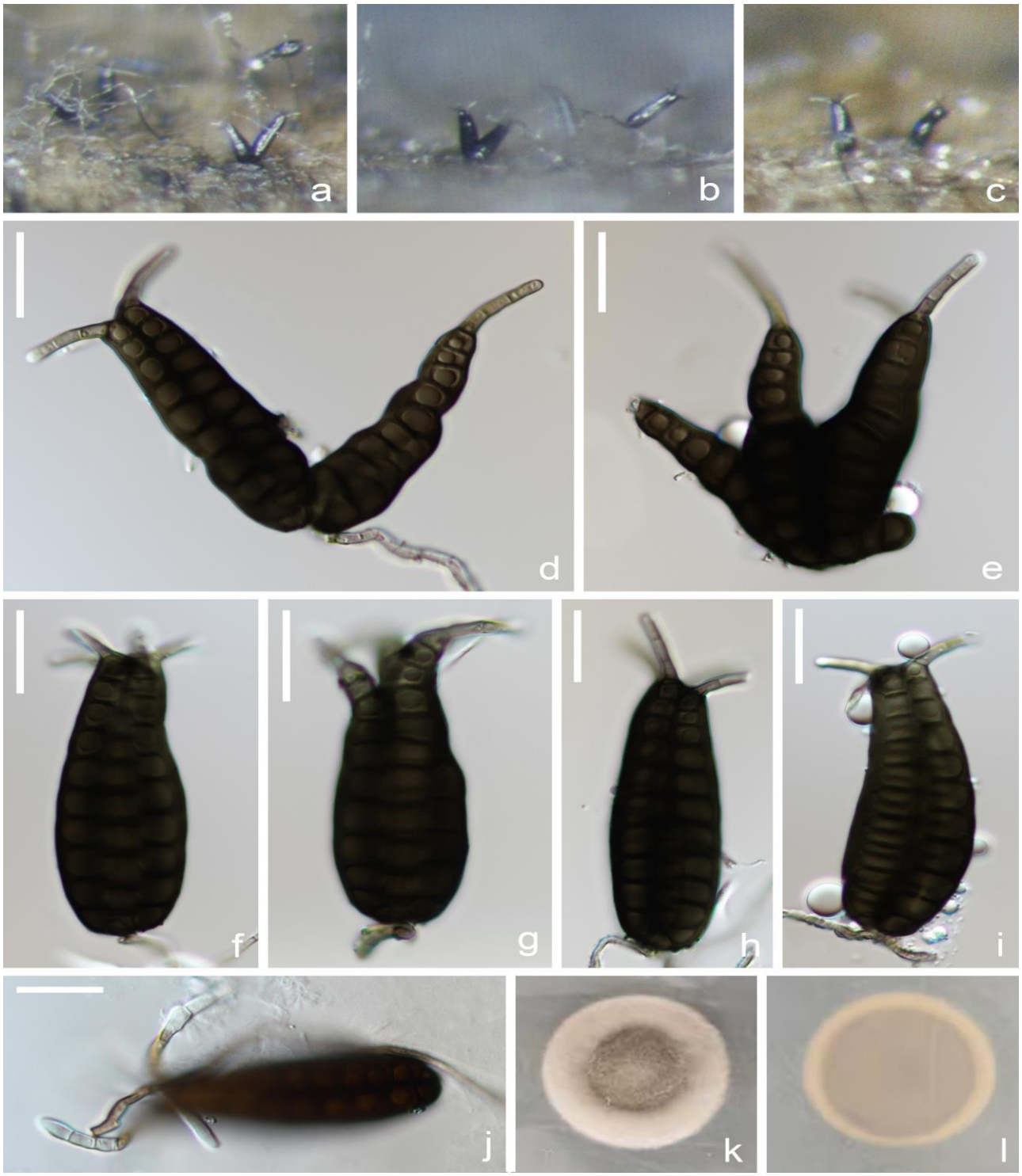

Figure 31 – *Triplosphaeria yunnanensis* (HKAS 132043, holotype). a–c Colonies on natural substrate. d, f–i Conidia with the appendages and inconspicuous conidiogenous cells. e Conidium. j Germinating conidium. k, l Colony on PDA (k from above, l from below). Scale bars: d–j = 20 μm.

Paralentithecium H.W. Shen, K.D. Hyde & Z.L. Luo, gen. nov.

Index Fungorum number: IF902572

Synonym – *Paralentithecium* H.W. Shen, K.D. Hyde & Z.L. Luo, Journal of Fungi 9(10, no. 962): 17 (2023), *nom. inval.*, Art. 40.1, see Arts 40.3 and Arts 6.3, 12.1 (Shenzhen).

Etymology – referring to the comparable morphological characters to that of *Lentithecium*.

Description – see Shen et al. (2023).

Type species – *Paralentithecium aquaticum* (Ying Zhang, J. Fourn. & K.D. Hyde) H.W. Shen & Z.L. Luo (see below).

Paralentithecium aquaticum (Yin. Zhang, J. Fourn. & K.D. Hyde) H.W. Shen & Z.L. Luo, comb. nov.

Index Fungorum number: IF902622

Basionym – *Lentithecium aquaticum* Yin. Zhang, J. Fourn. & K.D. Hyde, Fungal Diversity 38: 234 (2009).

Synonyms – *Paralentithecium aquaticum* (Ying Zhang, J. Fourn. & K.D. Hyde) H.W. Shen & Z.L. Luo, Journal of Fungi 9(10, no. 962): 17 (2023), *nom. inval.*, Art. F.5.1 (Shenzhen).

Holotype – France, Ariège, Rimont, Peyrau, on submerged wood of *Fraxinus excelsior*, 400 m, 09 Octber 2006, leg., det. J. Fournier (CBS H-20220), preserved in the Culture Collection of the Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands (CBS) (Zhang et al. 2009a).

Paralentithecium suae H.W. Shen, K.D. Hyde & Z.L. Luo, sp. nov.

Index Fungorum number: IF902621

Synonym – *Paralentithecium suae* H.W. Shen, K.D. Hyde & Z.L. Luo, Journal of Fungi 9(10, no. 962): 17 (2023), *nom. inval.*, Art. 35.1 (Shenzhen).

Etymology – "suae" (Lat.) in memory of the Chinese mycologist Prof. Hong-Yan Su (4 April 1967–3 May 2022).

Holotype – China, Yunnan Province, Lijiang City, Ninglang County, Luguhu Lake, 27°44'15" N, 100°45'16" E (2700 m), on unknown submerged decaying wood, 5 March 2021, Z.Q. Zhang and L. Sha (KUN-HKAS 124587), preserved in the herbarium of Kunming Institute of Botany, Academia Sinica (KUN-HKAS). Ex-type culture (CGMCC 3.24265) is deposited at the China General Microbiological Culture Collection Center (CGMCC).

Description – see Shen et al. (2023).

DISCUSSION

Freshwater fungi have been studied along a north-south gradient in Asia (Hyde et al. 2016a) and their ecology and function have recently been reviewed (Calabon et al. 2023). However there have been fewer studies on fungi in lakes compared to lentic habitats (Hyde & Goh 1998, Calabon et al. 2023). Since the beginning of 21st century, initial studies were carried out to understand the species diversity and community structure of lignicolous freshwater fungi in the plateau lakes of Yunnan Province, China. These studies have reported a diverse array of intriguing and newly discovered species of lignicolous freshwater fungi (Cai et al. 2002, Luo et al. 2004). Subsequent studies introduced several new species from different lakes in Yunnan Plateau and a few habitat records were also reported based on morphological and multi-gene phylogenetic evidence (Luo et al. 2017, 2018a, 2019, Su et al. 2018, Huang et al. 2022, Li et al. 2022, Shen et al. 2022b, 2023, Bao et al. 2023, Luan et al. 2023). Although these newly described species have increased the number of lignicolous freshwater fungi known in Yunnan Plateau lakes, our knowledge is still limited as compared to the lotic freshwater habitats. Therefore, to further understand these habitats, we systematically collected submerged specimens from plateau lakes in Yunnan Province during past two years and carefully introduced several new species, including new habitat and geographical records (Huang et al. 2022, Li et al. 2022, Luan et al. 2023, Shen et al. 2023). This study was an extension of previous research on the taxonomy and phylogenetic placement of the *Pleosporales* species obtained through morphological and phylogenetic analyses. Thirty-five

collections were collected from submerged decaying wood in several plateau lakes. Based on morphological characteristics and multi-gene phylogenetic analysis, 21 species were identified, including 18 new species, one new geographical record for China and two new records for freshwater habitats. These species not only contributed to the addition of species of *Pleosporales*, but also further enriched the number of lignicolous freshwater fungi known in the lakes of the Yunnan Plateau, allowing us to understand their diversity.

ACKNOWLEDGEMENTS

We would like to thank the National Natural Science Foundation of China (Project ID: 32060005, U2002203), National Science and Technology Fundamental Resources Investigation Program of China (2021FY100900), and the Yunnan Fundamental Research Project (202201AW070001) for financial support. This work was also supported by the High-Level Talents Program of Yunnan Province (YNQR-QNRC-2020-113) and Foundation of Yunnan Province Science and Technology Department (202305AM070003). Hong-Wei Shen thanks Qiu-Xia Yang, Yi-Kang Jiang and Zheng-Quan Zhang for their help with the sample collection, DNA extraction and PCR amplification. Thanks to Rong-Ju Xu for his help with the specimen and culture preservation. The authors extend their appreciation to the Researchers Supporting Project number (RSP2024R114), King Saud University, Riyadh, Saudi Arabia. Dan-Feng Bao thanks financial support by the Postdoctoral Fellowship Program of CPSF (GZC20240346).

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Supplementary Table 1 Taxa used in the phylogenetic analyses and their corresponding GenBank accession numbers. The ex-type strains are indicated using "T" after strain numbers; newly generated sequences are indicated in bold. "–" stands for no sequence data in GenBank.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	LSU	SSU	*tef*1-α
Astrosphaeriellaceae					
Acrocordiopsis patilii	BCC 28166 T	GU479772	GU479736	–	GU479811
Acrocordiopsis patilii	BCC 28167	GU479773	GU479737	–	GU479812
Acrocordiopsis patilii	MFLU 18–0533	MN017850	MN017916	–	–
Acrocordiopsis patilii	MFLU 18–0547	MN017849	MN017915	MN077067	MN077078
Acuminatispora palmarum	MFLUCC 18–0264 T	MH390437	MH390401	MH399248	–
Acuminatispora palmarum	MFLUCC 18–0460	MH390438	MH390402	MH399249	MH399252
Aquatospora cylindrica	MFLUCC 18–1287	MN913715	MT864327	MT954375	MT878460
Astrosphaeriella bambusae	MFLUCC 10–0095	JN846720	JN846741	–	–
Astrosphaeriella bambusae	MFLUCC 13–0230	KT955461	–	KT955424	KT955408
Astrosphaeriella fusispora	MFLUCC 10–0555	KT955462	KT955443	KT955425	KT955413
Astrosphaeriella neofusispora	MFLUCC 11–0161	KT955463	KT955444	KT955426	KT955418
Astrosphaeriella neostellata	KUMCC 19–0218	MN629351	MN629353	MN635787	MN639599
Astrosphaeriella neostellata	MFLUCC 11–0625	KT955464	–	–	–
Astrosphaeriella stellata	MAFF 239487	AB524592	AB524451	–	–
Astrosphaeriella thailandica	MFLUCC 11–0191	KT955465	KT955445	KT955427	KT955404
Astrosphaeriella thysanolaenae	MFLUCC 11–0186	KT955466	KT955446	KT955428	KT955422
Astrosphaeriella vesuvius	MTCC 12224	KP814136	KP814137	–	KP814139
Astrosphaeriellopsis bakeriana	CBS 115556	GU301801		GU349015	–
Astrosphaeriellopsis bakeriana	MFLUCC 11–0027 T	JN846730	JN846740	–	–
Astrosphaeriellopsis caryotae	MFLUCC 13–0830	MF588990	MF588980	–	–
Astrosphaeriellopsis caryotae	MFLUCC 13–0832 T	MF588991	MF588981	MF588974	–
Astrosphaeriellopsis caryotae	MFLUCC 13–0833	MF588992	MF588982	–	–
Astrosphaeriella yunnanensis	**KUNCC 23–16916 T**	**–**	**PQ436668**	**PQ435251**	**PQ456944**
Caryospora aquatica	MFLUCC 11–0008 T	MH057847	MH057850	–	–
Caryospora quercus	MFLU 18–2151 T	MK347979	MK347869	–	–
Caryospora submersa	MFLUCC 18–1283	MN913720	–	–	–
Occultibambusa bambusae	MFLUCC 13–0855 T	KU863112	KU872116	KU940193	KU940170
Occultibambusa chiangraiensis	MFLUCC 16–0380 T	KX655546	KX655551	KX655561	KX655566
Pithomyces caryotae	MFLUCC 13–0824	MF588998	MF588988	–	–

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number				
		ITS	**LSU**	**SSU**	***tef*1-α**	
Pithomyces caryotae	MFLUCC 13–0828 T	MF588999	MF588989	MF588978	–	
Pithomyces flavus	LF–156	KP814133	KP814134	–	KP814138	
Pithomyces licualae	MFLUCC 17–2031 T	MF588995	MF588985	–	–	
Pteridiospora chiangraiensis	MFLUCC 11–0162	KT955480	KT955459	KT955442	KT955419	
Pteridiospora javanica	MFLUCC 11–0159	KJ742940	KJ739607	KJ739605	–	
Pteridiospora javanica	MFLUCC 11–0195	KJ742941	KT955460	KJ739606	–	
Quercicola fusiformis	MFUCC 18 0479 T	MK348009	MK347898	MK360085	MK434864	
Quercicola guttulospora	MFUCC 18 0481 T	MK348010	MK347899	MK360086	–	
Triseptatospora calami	MFLUCC 15–0305	ON650710	ON650705	ON734018		
Xenoastrosphaeriella aquatica	DLUCC 1525	MZ420753	MZ420755	MZ442701	MZ442703	
Xenoastrosphaeriella aquatica	DLUCC 869	MZ420752	MZ420754	MZ442700	MZ442702	
Xenoastrosphaeriella tornata	MFLUCC 11–0196	KT955467	KT955447	KT955429	KT955405	
Xenoastrosphaeriella trochus	KUMCC 18–0194	MT659668	MT659669	MT653597	MT653598	
		ITS	**LSU**	**SSU**	***tef*1-α**	***rpb*2**
Hermatomycetaceae* and *Cryptocoryneaceae						
Aquasubmersa japonica	MAFF 245218	LC061591	LC061586	LC061581	LC194383	LC194420
Aquasubmersa japonica	MAFF 245219 T	LC061592	LC061587	LC061582	LC194384	LC194421
Cryptocoryneum akitaense	MAFF 245365 T	LC096154	LC194348	LC194306	LC096136	LC194430
Cryptocoryneum brevicondensatum	MAFF 245366 T	LC096155	LC194349	LC194307	LC096137	LC194431
Cryptocoryneum condensatum	CBS 113959	LC096156	LC194350	LC194308	LC096138	LC194432
Cryptocoryneum condensatum	CBS 122629	LC096157	LC194351	LC194309	LC096139	LC194433
Cryptocoryneum condensatum	CBS 122633	LC096158	LC194352	LC194310	LC096140	LC194434
Cryptocoryneum congregatum	MAFF 245367 T	LC096159	LC194353	LC194311	LC096141	LC194435
Cryptocoryneum japonicum	MAFF 245368	LC096160	LC194354	LC194312	LC096142	LC194436
Cryptocoryneum japonicum	MAFF 245369	LC096161	LC194355	LC194313	LC096143	LC194437
Cryptocoryneum japonicum	MAFF 245370 T	LC096162	LC194356	LC194314	LC096144	LC194438
Cryptocoryneum japonicum	MAFF 245371	LC096163	LC194357	LC194315	LC096145	LC194439
Cryptocoryneum japonicum	MAFF 245372	LC096164	LC194358	LC194316	LC096146	LC194440
Cryptocoryneum japonicum	MAFF 245373	LC096165	LC194359	LC194317	LC096147	LC194441
Cryptocoryneum longicondensatum	MAFF 245374 T	LC096166	LC194360	LC194318	LC096148	LC194442
Cryptocoryneum longicondensatum	MAFF 245375	LC096167	LC194361	LC194319	LC096149	LC194443
Cryptocoryneum paracondensatum	MAFF 245376	LC096168	LC194362	LC194320	LC096150	LC194444

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number				
		ITS	**LSU**	**SSU**	***tef*1-α**	***rpb*2**
Cryptocoryneum paracondensatum	MAFF 245377 T	LC096169	LC194363	LC194321	LC096151	LC194445
Cryptocoryneum pseudorilstonei	CBS 113641 T	LC096170	LC194364	LC194322	LC096152	LC194446
Cryptocoryneum rosae	KUMUCC 21–0033 T	MZ493300	MZ493314	MZ493286	MZ508409	MZ508418
Cryptocoryneum rosae	KUMUCC 21–0034	MZ493301	MZ493315	MZ493287	MZ508410	MZ508419
Cryptocoryneum sinense	**KUNCC 23–14279 T**	**PQ340459**	**PP189895**	**PQ435255**	**PQ456946**	**PQ348599**
Cryptocoryneum sp.	CBS 114518	LC096171	LC194365	LC194323	LC096153	LC194447
Hermatomyces amphisporus	CBS 146614	LR812666	LR812666	–	LR812660	LR812671
Hermatomyces amphisporus	CBS 146615	LR812667	LR812667	–	LR812661	LR812672
Hermatomyces anomianthi	MFLUCC 21–0202	OL413437	OK655817	–	OM117546	–
Hermatomyces bauhiniae	MFLUCC 16–0395 T	MK443382	MK443378	–	MK443384	MK443386
Hermatomyces biconisporus	KUMCC 17–0183 T	MH275063	MH260296	MK443380	MH412771	MH412755
Hermatomyces bifurcatus	CCF 5899	LS398262	LS398262	–	LS398416	LS398343
Hermatomyces bifurcatus	CCF 5900 T	LS398263	LS398263	–	LS398417	LS398344
Hermatomyces clematidis	MFLUCC 17–2085T	MT310603	MT214556	MT226673	MT394735	MT394684
Hermatomyces constrictus	CCF 5904 T	LS398264	LS398264	–	LS398418	LS398345
Hermatomyces hainanensis	GZCC 23–0592	OR098708	OR091329	–	–	–
Hermatomyces hongheensis	**KUNCC 23–13503 T**	**PQ340461**	**PP189897**	**PQ435257**	**PQ456948**	**PQ348601**
Hermatomyces hongheensis	**KUNCC 23–14231 T**	**PQ340462**	**PP189898**	**–**	**PQ456949**	**–**
Hermatomyces indicus	MFLUCC 14–1143T1	KU144920	KU764692	KU712468	KU872754	KU712488
Hermatomyces indicus	MFLUCC 14–1144	KU144921	KU764693	KU712469	KU872755	KU712489
Hermatomyces iriomotensis	KH 361T	LC194483	LC194367	LC194325	LC194394	LC194449
Hermatomyces jinghaensis	HKAS 112167 T	MW989495	MW989519	–	MZ042642	–
Hermatomyces krabiensis	MFLUCC 16–0249 T	KX525750	KX525742	KX525746	KX525758	KX525754
Hermatomyces krabiensis	MFLUCC 16–2817 T	–	KY559394	–	–	–
Hermatomyces maharashtraense	NFCCI 4879	MZ147016	MZ099917	–	MZ130659	MZ130660
Hermatomyces maharashtraense	NFCCI 4880	MZ147019	MZ147042	–	MZ130661	MZ130662
Hermatomyces megasporus	CCF 5897	LS398265	–	–	LS398419	LS398346
Hermatomyces megasporus	CCF 5898T	LS398266	LS398266	–	LS398420	–
Hermatomyces nabanheensis	KUMCC 16–0149 T	KY766058	KY766059	KY766060	KY766061	–
Hermatomyces pandanicola	MFLUCC 16–0251 T	KX525751	KX525743	KX525747	KX525759	KX525755
Hermatomyces reticulatus	CCF 5893	LS398267	LS398267	–	LS398421	LS398347
Hermatomyces reticulatus	MFLUCC 15–0843 T	KX259521	KX259523	KX259525	KX259527	KX259529

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number				
		ITS	**LSU**	**SSU**	***tef*1-α**	***rpb*2**
Hermatomyces sphaericoides	CCF 5908T	LS398273	LS398273	–	LS398427	LS398352
Hermatomyces sphaericoides	CCF 5895	LS398270	LS398270	–	LS398424	LS398350
Hermatomyces sphaericus	PMA 116080	LS398281	LS398281	–	LS398431	LS398356
Hermatomyces sphaericus	MFLUCC 21–0036	MW989492	MW989516	–	MZ042639	MZ042636
Hermatomyces sphaericus	KUMCC 20–0231	MW989493	MW989517	–	MZ042640	MZ042637
Hermatomyces sphaericus	MFLUCC 16–2818 T	–	KY559393	–	–	–
Hermatomyces sphaericus	MFLUCC 16–0266 T	KX525748	KX525740	KX525744	KX525756	KX525752
Hermatomyces sphaericus	MFLUCC 16–0267	KX525749	KX525741	KX525745	KX525757	KX525753
Hermatomyces sphaericus	MFLUCC 14–1140 T	KU144917	KU764695	KU712465	KU872757	KU712486
Hermatomyces sphaericus	MFLUCC 14–1141	KU144918	KU764696	KU712466	KU872758	–
Hermatomyces sphaericus	MFLUCC 14–1142	KU144919	KU764697	KU712467	–	KU712487
Hermatomyces trangensis	BCC 80741T	KY790598	KY790600	KY790602	KY790606	KY790604
Hermatomyces trangensis	BCC 80742	KY790599	KY790601	KY790603	KY790607	KY790605
Hermatomyces tucumanensis	CCF 5912	LS398288	LS398288	–	LS398435	LS398360
Hermatomyces tucumanensis	CCF 5913	LS398289	LS398289	–	LS398436	LS398361
Hermatomyces tucumanensis	CCF 5915	LS398290	LS398290	–	LS398437	LS398362
Hermatomyces turbinatus	MFLUCC 21–0038 T	MW989494	MW989518	–	MZ042641	MZ042638
Hermatomyces verrucosus	CCF 5903 T	LS398292	LS398292	–	LS398439	LS398364
Hermatomyces verrucosus	CCF 5892	LS398291	LS398291	–	LS398438	LS398363
		ITS	**LSU**	**SSU**	***tef*1-α**	
Lentitheciaceae						
Crassoascoma potentillae	UESTCC 21.0012	OK161239	OK161256	OK161235	OK181167	
Crassoascoma potentillae	CGMCC 3.20483 T	OK161240	OK161257	OK161236	OK181168	
Groenewaldia indica	NFCCI 5439T	OQ379185	OQ379187	OQ379189	OQ361689	
Groenewaldia indica	NFCCI 5440	OQ379186	OQ379188	OQ379190	OQ361690	
Halobyssothecium aquifusiforme	GZCC 20–0481 T	OP377825	OP377925	OP378010	OP473005	
Halobyssothecium bambusicola	MFLUCC 20–0226 T	MN833419	MT068489	MT068494	MT477868	
Halobyssothecium caohaiense	GZCC 19–0482 T	OP377841	MW133831	MW134611	OP473019	
Keissleriella quadriseptata	KT2292 T	AB811456	AB807593	AB797303	AB808572	
Keissleriella yonaguniensis	HHUF 30138 T	NR_155212	NG_059402	NG_064856	AB808573	
Lentithecium yunnanensis	KUNCC 22–10776 T	ON227126	ON227127	ON227123	ON228074	
Lentithecium yunnanensis	KUNCC 22–10777	ON227125	ON227124	ON227122	ON228075	

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	**LSU**	**SSU**	***tef*1-α**
Multiseptospora thailandica	MFLUCC 11–0204	KU693447	KU693440	KU693444	KU705659
Multiseptospora thailandica	MFLUCC 12–0006	KU693448	KU693441	KU693445	KU705660
Murilentithecium clematidis	MFLUCC 14–0561	KM408756	KM408758	KM408760	KM454444
Murilentithecium clematidis	MFLUCC 14–0562 T	KM408757	KM408759	KM408761	KM454445
Pseudokeissleriella bambusicola	CGMCC 3.20950 T	ON614135	ON614138	ON614096	ON639623
Pseudokeissleriella bambusicola	UESTCC 22.0028	ON614134	ON614137	ON614095	ON639622
Setoseptoria arundelensis	MFLUCC 17–0759 T	MG828962	MG829073	MG829173	–
Setoseptoria arundinacea	MAFF 239460	LC014594	AB807574	AB797284	AB808550
Setoseptoria arundinacea	MAFF 243842 T	LC014595	AB807575	AB797285	AB808551
Setoseptoria bambusae	GZCC 17–0044	OP377820	OP377919	OP378004	OP472999
Setoseptoria englandensis	MFLUCC 17–0778 T	MG828963	MG829074	MG829174	–
Setoseptoria lulworthcovensis	MFLU 18–0110 T	–	MG829075	MG829175	–
Setoseptoria magniarundinacea	KT1174	LC014596	AB807576	AB797286	AB808552
Setoseptoria phragmitis	CBS 114802 T	KF251249	KF251752	–	–
Setoseptoria phragmitis	CBS 114966	KF251250	KF251753	–	–
Setoseptoria phragmitis	GZCC 19–0484	OM692195	MW133833	MW134613	–
Setoseptoria phragmitis	GZCC 19-0485	OM692196	MW133834	MW134614	–
Setoseptoria phragmitis	GZCC 19-0486	OM692197	MW133835	MW134615	–
Setoseptoria phragmitis	**KUNCC 23–13107**	**PQ340472**	**PP189910**	**PQ435267**	**PQ456962**
Setoseptoria phragmitis	**HKAS 131634**	**PQ571252**	**PP189926**	**PQ341573**	**–**
Setoseptoria scirpi	MFLUCC 14–0811 T	MF939637	KY770982	KY770980	KY770981
Setoseptoria suae	KUNCC 22–12419	OQ874973	OQ732684	OQ875041	OR367673
Tingoldiago graminicola	KH68 T	LC014598	AB521743	AB521726	AB808561
Tingoldiago graminicola	KT891	LC014600	AB521744	AB521727	AB808563
Towyspora aestuari	MFLUCC 15–1274 T	NR_148095	KU248852	KU248853	–
Towyspora aestuari	GZCC 19–0490	OP377848	MW133839	MW134618	–
		ITS	**LSU**	**SSU**	***tef*1-α**
Lindgomycetaceae					
Aquimassariosphaeria aquatica	**HKAS 131666 T**	**–**	**PP189914**	**PQ341572**	**PQ456964**
Aquimassariosphaeria aquatica	**HKAS 131807**	**–**	**PP189913**	**PQ341571**	**PQ456963**
Aquimassariosphaeria aquatica	**KUNCC 23–13472**	**–**	**PP189892**	**PQ435250**	**PQ456943**
Aquimassariosphaeria aquatica	**KUNCC 23–16137**	**–**	**PP189891**	**PQ435249**	**–**

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	**LSU**	**SSU**	***tef*1-α**
Aquimassariosphaeria kunmingensis	KUMCC 18–1019 T	–	MT627661	MT864312	–
Aquimassariosphaeria typhicola	CBS 609.86	–	EF165033	EF165037	–
Aquimassariosphaeria vermiformis	GZCC 19–0495 T	–	MW133798	MW134586	OP473025
Aquimassariosphaeria vermiformis	GZCC 19–0497	–	MW133800	MW134588	OP473026
Arundellina typhae	MFLUCC 16–0309	KX274245	KX274252	KX274256	–
Arundellina typhae	MFLUCC 16–0310 T	KX274246	KX274251	KX274257	–
Clohesyomyces aquaticus	MFLUCC 11–0092	JX276948	JX276950	JX276949	–
Clohesyomyces aquaticus	MFLUCC 15–0979	MT627678	MN913686	MT864307	–
Clohesyomyces aquaticus	MFLUCC 18–1037	MT627725	MN913713	MT864329	MT954388
Clohesyomyces sp.	KUNCC23–13013	–	OQ857280	OQ857279	–
Clohesyomyces sp.	KUNCC23–12906	–	OQ851889	OQ851891	–
Clohesyomyces symbioticus	DM0144 T	OK139670	OK135170	OK139667	OK094526
Clohesyomyces symbioticus	DM0177	OK139671	OK135171	OK139668	OK094527
Clohesyomyces symbioticus	DM0192	OK139672	OK135172	OK139669	OK094528
Hongkongmyces aquaticus	MFLUCC 18–1150 T	–	MN913694	MT864302	MT954379
Hongkongmyces aquisetosus	GZCC 20–0357 T	–	OP377921	OP378006	OP473001
Hongkongmyces brunneisporus	MFLUCC 18–1509 T	–	MW004643	MW004647	MW018837
Hongkongmyces brunneisporus	MFLUCC 17–1317	–	MW004645	MW004649	MW018839
Hongkongmyces changchunensis	CCMJ5008 T	OL996122	OL897173	OL891809	OL944603
Hongkongmyces cylindricisporus	**HKAS 131480**	**PQ571253**	**PP189922**	**PQ341576**	**PQ456966**
Hongkongmyces cylindricisporus	**HKAS 131740**	**PQ571254**	**PP189920**	**–**	**–**
Hongkongmyces cylindricisporus	**HKAS 131742**	**PQ571255**	**PP189919**	**PQ341575**	**PQ456965**
Hongkongmyces cylindricisporus	**KUNCC 23–16897 T**	**PQ607751**	**PP189921**	**PQ435258**	**–**
Hongkongmyces guttulatus	**HKAS 131800 T**	**PQ571256**	**PP189918**	**PQ341574**	**PQ456967**
Hongkongmyces hongheensis	**KUNCC 23–13511 T**	**PQ607752**	**PP189899**	**PQ435259**	**PQ456950**
Hongkongmyces kokensis	MFLUCC 21–0079 T	MZ538506	MZ538540	–	MZ567084
Hongkongmyces kokensis	MFLUCC 21–0080	MZ538507	MZ538541	–	MZ567085
Hongkongmyces kokensis	MFLUCC 21–0081	MZ538508	MZ538542	–	MZ567086
Hongkongmyces pedis	HKU35 T	JQ435790	KF314111	KF314117	–
Hongkongmyces pedis	CBS 126076 T	NR149338	–	–	–
Hongkongmyces snookiorum	ILLS00125755 T	MH161189	–	–	MH161190
Hongkongmyces sp.	KUNCC23–13012	OQ852927	–	OQ857281	–

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	**LSU**	**SSU**	***tef*1-α**
Hongkongmyces sp.	KUNCC22–12578	OQ851521	–	OQ851886	–
Hongkongmyces sp.	KUNCC23–13019	OQ852926	OQ851898	OQ857283	–
Hongkongmyces sp.	KUNCC23–13020	OQ852928	OQ857278	OQ857282	–
Hongkongmyces sp.	HKAS 122708	OQ158938	OQ170860	OQ168214	–
Hongkongmyces thailandica	MFLUCC 16–0406 T	KY771325	KY771321	KY771323	KY771327
Hongkongmyces yunnanensis	**KUNCC 23–16896 T**	**PQ607753**	**PP189917**	**PQ435260**	**PQ456951**
Lindgomyces angustiascus	A640-1a T	JX508281	JX508279	JX508280	–
Lindgomyces angustiascus	G 202-1a	JX508286	JX508285	JX508287	–
Lindgomyces apiculatus	KT 1108 T	JF419892	JF419884	JF419886	KF314134
Lindgomyces apiculatus	KT 1144	JF419893	JF419885	JF419887	–
Lindgomyces aquaticus	MFLUCC 18–1416	MT627692	MN913727	MT864317	–
Lindgomyces breviappendiculatus	KT 1399 T	JF419897	AB521749	AB521734	KF314133
Lindgomyces breviappendiculatus	KT 1215	–	AB521748	AB521733	–
Lindgomyces carolinensis	DSMZ 103499 T	KX655793	KX655800	KX655801	–
Lindgomyces cigarospora	DSMZ 103500 T	KX655794	KX655804	KX655805	–
Lindgomyces cigarospora	G619-2	KX655798	KX655806	KX655807	–
Lindgomyces cinctosporus	R56-1 T	JF419905	AB522431	AB522430	–
Lindgomyces cinctosporus	R56-3	–	GU266245	GU266238	–
Lindgomyces griseosporus	BJFC200094 T	KC954093	KC769693	–	–
Lindgomyces guizhouensis	GZCC 21–0669 T	OM339435	OM339432	–	–
Lindgomyces ingoldianus	ATCC 200398 T	JF419898	AB521736	AB521719	–
Lindgomyces ingoldianus	KH 100	–	AB521737	AB521720	–
Lindgomyces lemonweirensis	A632-1a T	JF419894	JF419888	JF419890	–
Lindgomyces lemonweirensis	A632-1b	JF419895	JF419889	JF419891	–
Lindgomyces madisonensis	G416-a T	KT207818	KT207820	KT207822	–
Lindgomyces madisonensis	G416b	KT207819	KT207821	KT207823	–
Lindgomyces okinawaensis	KT 3531 T	LC100022	LC100027	LC100019	–
Lindgomyces pseudomadisonensis	KT 2742 T	LC149914	LC149916	LC149912	–
Lindgomyces rotundatus	KT 966 T	JF419901	AB521739	AB521722	–
Lindgomyces sp.	KH 241	JF419900	AB521738	AB521721	–
Lindgomyces yunnanensis	**KUNCC 23–13391**	**PQ340464**	**PP189901**	**PQ435262**	**PQ456953**
Lindgomyces yunnanensis	**KUNCC 23–13812 T**	**PQ340463**	**PP189900**	**PQ435261**	**PQ456952**

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number				
		ITS	**LSU**	**SSU**	***tef*1-α**	
Lolia aquatica	MD6002	–	KU726001	–	–	
Lolia aquatica	MF644 T	–	HM367732	–	–	
Lolia dictyospora	CBS H-22131 T	–	NG067306	NG063064	–	
Lolia fusiformispora	**KUNCC 23–16912 T**	**–**	**PP189923**	**PQ435263**	**PQ456954**	
Neolindgomyces pandanae	MFLUCC 18–0245 T	MK347768	MK347985	MK347875	MK360062	
Neolindgomyces pandanae	MFLUCC 18–1546	MK347778	MK347995	MK347885	MK360064	
Ocellisimilis clavata	GZCC 19–0498 T	OP377835	MW133801	MW134589	OP473013	
Ocellisimilis clavata	GZCC 19–0499	OP377837	MW133802	MW134590	OP473015	
Trematosphaeria hydrela	CBS 880.70	JQ435796	KF314116	KF314123	LC382203	
Wicklowia aquatica	CBS 125634 TO	OM322822	MH875044	NG_061099	–	
Wicklowia phuketensis	MFLUCC 20–0109 T	–	MT068484	MT068490	–	
Xenovaginatispora phichaiensis	MFLUCC 21–0082 T	MZ538534	MZ538569	MZ538577	MZ567110	
		ITS	**LSU**	**SSU**	***tef*1-α**	***rpb*2**
Occultibambusaceae						
Bambusicola massarinia	MFLUCC 11-0389 T	JX442033	JX442037	JX442041	KP761725	KP761716
Bambusicola pustulata	MFLUCC 15-0190 T	KU940118	KU863107	KU872112	KU940190	KU940165
Bambusicola sichuanensis	SICAUCC 16-0002 T	MK253473	MK253532	MK253528	MK262828	MK262830
Brunneofusispora clematidis	MFLUCC 17-2070 T	MT310615	MT214570	MT226685	MT394629	MT394692
Brunneofusispora inclinatiostiola	CGMCC 3.20403 T	MZ964866	MZ964875	MZ964884	OK061069	OK061075
Brunneofusispora sinensis	KUMCC 17-0030 T	MH393558	MH393557	MH393556	MH395329	–
Leucaenicola aseptata	MFLUCC 17-2423 T	MK347746	MK347963	MK347853	MK360059	MK434891
Leucaenicola camelliae	NTUCC 18-093-4 T	MT112302	MT071278	MT071229	MT374091	MT743283
Leucaenicola phraeana	MFLUCC 18-0472 T	MK347785	MK348003	MK347892	MK360060	MK434867
Lophiomurispora hongheensis	KUMCC 20-0216	MW264218	MW264197	MW264227	MW256819	MW256810
Lophiomurispora hongheensis	KUMCC 20-0217 T	MW264216	MW264195	MW264225	MW256817	MW256808
Neooccultibambusa chiangraiensis	MFLUCC 12-0559	KU712442	KU764699	KU712458	KU872761	–
Neooccultibambusa kaiyangensis	CGMCC 3.20404 T	MZ964868	MZ964877	MZ964886	OK061071	OK061077
Neooccultibambusa trachycarpi	CGMCC 3.20405 T	MZ964870	MZ964879	MZ964888	OK061073	OK061079
Occultibambusa aquatica	MFLUCC 11-0006 T	KX698114	KX698110	KX698112	–	–
Occultibambusa bambusae	MFLUCC 13-0855 T	KU940123	KU863112	KU872116	KU940193	KU940170
Occultibambusa chiangraiensis	MFLUCC 16-0380 T	–	KX655546	KX655551	KX655561	KX655566
Occultibambusa fusispora	MFLUCC 11-0127 T	KU940125	KU863114	–	KU940195	KU940172

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number				
		ITS	**LSU**	**SSU**	***tef*1-α**	***rpb*2**
Occultibambusa hongheensis	KUMCC 21-0020 T	MZ329037	MZ329033	MZ329029	MZ325467	–
Occultibambusa jonesii	GZCC 16-0117 T	–	KY628322	KY628324	KY814756	KY814758
Occultibambusa jonesii	**KUNCC 23–13523**	**PQ607754**	**PP189903**	**PQ435265**	**PQ456956**	**PQ348602**
Occultibambusa kunmingensis	HKAS 102151 T	MT627716	MN913733	MT864342	MT954407	MT878453
Occultibambusa maolanensis	GZCC 16-0116 T	–	KY628323	KY628325	KY814757	KY814759
Occultibambusa pustula	MFLUCC 11-0502 T	KU940126	KU863115	KU872118	–	–
Occultibambusa sichuanensis	CGMCC 3.20938 T	ON332913	ON332931	–	ON381181	ON383989
Occultibambusa sichuanensis	UESTCC 22.0004 T	ON332914	ON332932	–	ON381182	ON383990
Occultibambusa sp.	GUCC 23-0004	OR392463	OR392460	OR392457	OR396952	OR396950
Occultibambusa sp.	KUNCC 23-14577	OR589312	OR600960	OR743208	OR739171	–
Palmiascoma gregariascomum	MFLUCC 11-0175 T	KP744452	KP744495	KP753958	–	KP998466
Palmiascoma qujingense	KUMCC 19-0201 T	MT477183	MT477185	MT477186	–	MT495782
Seriascoma bambusae	KUMCC 21-0021 T	MZ329039	MZ329035	MZ329031	MZ325468	MZ325470
Seriascoma didymosporum	MFLUCC 11-0179 T	KU940127	KU863116	KU872119	KU940196	KU940173
Seriascoma yunnanense	MFLU 19-0690 T	–	MN174695	MN174694	MN381858	MN210324
Versicolorisporium triseptatum	JCM 14775 T	AB365596	AB330081	AB524501	–	–
Versicolorisporium triseptatum	UESTCC 21.0016	OL741378	OL741318	OL741381	–	–
		ITS	**LSU**	**SSU**	***tef*1-α**	
Periconiaceae						
Flavomyces fulophazae	CBS 135664	KP184000	KP184039	KP184081	–	
Flavomyces fulophazae	CBS 135761 T	NR_137960	NG_058131	NG_061191	–	
Lentithecium aquaticum	CBS 123099 TO	NR_160229	NG_064211	NG_016507	GU349068	
Lentithecium clioninum	KT 1149A O	LC014566	AB807540	AB797250	AB808515	
Periconia algeriana	CBS 321.79	MH861212	MH872979	–	–	
Periconia alishanica	KUMCC 19–0174	MW063167	MW063231	–	MW183792	
Periconia alishanica	MFLUCC 19–0145 T	MW063165	MW063229	–	MW183790	
Periconia aquatica	MFLUCC 16–0912 T	KY794701	KY794705	–	KY814760	
Periconia artemisiae	KUMCC 20–0265 T	MW448657	MW448571	MW448658	MW460898	
Periconia arecacearum	MFLUCC 16-1387 T	PP592462	PP621090	PP828795	PP639222	
Periconia atropurpurea	CBS 381.55	MH857524	MH869061	–	–	
Periconia banksiae	CBS 129526 T	JF951147	NG_064279	–	–	
Periconia byssoides	MFLUCC 17–2292	MK347751	MK347968	MK347858	MK360069	

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	LSU	SSU	*tef*1-α
Periconia byssoides	UESTCC 22.0132	OP955985	OP956010	OP956054	OP961451
Periconia caespitosa	LAMIC 110/16 T	MH051906	MH051907	–	–
Periconia calamagrostidicola	CBS 150887 T	PP791432	PP791460	PP780620	–
Periconia chengduensis	CGMCC 3.23930 T	OP955987	OP956012	OP956056	OP961453
Periconia chengduensis	UESTCC 22.0140	OP955977	OP956002	OP956046	OP961443
Periconia chimonanthi	KUMCC 20–0266 T	NR_176752	MW448572	MW448656	MW460897
Periconia chimonanthi	UESTCC 22.0133	OP955964	OP955989	OP956033	OP961430
Periconia circinata	CBS 263.37	MW810265	MH867413	–	MW735660
Periconia citlaltepetlensis	ENCB 140251 T	MH890645	MT625978	–	–
Periconia citlaltepetlensis	IOM 325319.2	MT649221	MT649216	–	–
Periconia cookei	MFLUCC 17–1399	MG333490	MG333493	–	MG438279
Periconia cookei	UESTCC 22.0134	OP955968	OP955993	OP956037	–
Periconia cortaderiae	MFLUCC 15–0451	KX965734	KX954403	KX986346	KY429208
Periconia cortaderiae	MFLUCC 15–0457 T	KX965732	KX954401	KX986345	KY310703
Periconia cynodontis	CGMCC 3.23927 T	OP909925	OP909921	OP909920	OP961434
Periconia cyperacearum	CPC 32138	MH327815	MH327851	–	–
Periconia delonicis	MFLUCC 17–2584 T	–	MK347941	MK347832	MK360071
Periconia didymosporum	MFLU 15–0058 T	KP761734	KP761731	KP761738	KP761728
Periconia digitata	CBS 510.77	LC014584	AB807561	AB797271	AB808537
Periconia dujuanhuensis	**KUNCC 23–13482 T**	**PQ340469**	**PP189907**	**–**	**PQ456957**
Periconia elaeidis	MFLUCC 17–0087 T	MG742713	MH108552	MH108551	–
Periconia endophytica	ZHKUCC 23–0995 T	OR995582	OR995588	PP277722	PP025968
Periconia endophytica	ZHKUCC 23–0996	OR995583	OR995589	PP277723	PP025969
Periconia epilithographicola	CBS 144017 T	NR_157477	–	–	–
Periconia epilithographicola	MFLUCC 21–0153	OL753687	OL606155	OL606144	OL912948
Periconia festucae	CGMCC 3.23929 T	OP955973	OP955998	OP956042	OP961439
Periconia genistae	CBS 322.79	MH861213	MH872980	–	–
Periconia homothallica	CBS 139698 T	AB809645	NG_059397	AB797275	AB808541
Periconia hongheensis	**KUNCC 23–13549**	**PQ340466**	**PP189904**	**–**	**–**
Periconia hongheensis	**KUNCC 23–13550 T**	**PQ340467**	**PP189905**	**–**	**PQ456958**
Periconia igniaria	CBS 298.66	MH858798	MH870438	–	–
Periconia igniaria	CBS 583.66	MH858888	MH870553	–	–
Periconia imperatae	CGMCC 3.23931 T	OP955984	OP956009	OP956053	OP961450

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	**LSU**	**SSU**	***tef*1-α**
Periconia imperatae	UESTCC 22.0145	OP955979	OP956004	OP956048	OP961445
Periconia lateralis	CBS 292.36	MH855804	MH867311	–	–
Periconia macrospinosa	CBS 135663	KP183999	KP184038	KP184080	–
Periconia minutissima	MFLUCC 15–0245	KY794703	KY794707	–	–
Periconia neobrittanica	CPC 37903 T	MN562149	MN567656	–	–
Periconia neominutissima	CPC 42368	OQ628478	OQ629060	–	–
Periconia palmicola	MFLUCC14–0400 T	–	MN648327	MN648319	MN821070
Periconia penniseti	CGMCC 3.23928 T	OP955971	OP955996	OP956040	OP961437
Periconia philadelphiana	CPC 42854	OQ628486	OQ629068	–	–
Periconia prolifica	CBS 209.64 T	NR_160097	MH870050	–	–
Periconia pseudobyssoides	KUMCC 20–0263	MW444851	MW444852	MW444853	MW460894
Periconia pseudobyssoides	UESTCC 22.0135	OP955965	OP955990	OP956034	OP961431
Periconia pseudodigitata	CBS 139699 T	LC014591	AB807564	AB797274	AB808540
Periconia pseudodigitata	JCM 13165	LC014590	AB807563	AB797273	AB808539
Periconia sahariana	CBS 320.79 T	MH861211	MH872978	–	–
Periconia salina	GJ374 T	MN047086	MN017846	MN017912	–
Periconia spodiopogonis	CGMCC 3.23932 T	OP955963	OP955988	OP956032	OP961429
Periconia submersa	MFLUCC 16–1098 T	KY794702	KY794706	–	KY814761
Periconia thailandica	MFLUCC 17–0065 T	KY753887	KY753888	KY753889	–
Periconia thysanolaenae	KUMCC 20–0262 T	MW442967	MW444850	NG_081407	MW460896
Periconia variicolor	CBS 120374 T	DQ336713	–	–	–
Periconia verrucosa	MFLUCC 17–2158 T	MT310617	MT214572	MT226686	MT394631
Periconia verrucosa	UESTCC 22.0136	OP955966	OP955991	OP956035	OP961432
Periconia wurfbainiae	ZHKUCC 23–0999 T	OR995586	OR995592	PP277726	PP025972
Periconia wurfbainiae	ZHKUCC 23–1000	OR995587	OR995593	PP277727	PP025973
Periconia yangjiangensis	ZHKUCC 23–0997 T	OR995584	OR995590	PP277724	PP025970
Periconia yangjiangensis	ZHKUCC 23-0998	OR995585	OR995591	PP277725	PP025971
Periconia yunnanensis	**KUNCC 23–14259 T**	**PQ340468**	**PP189906**	**–**	**PQ456960**
Periconia yunnanensis	**KUNCC 23–16910**	**PQ607755**	**PP189925**	**–**	**PQ456959**
		ITS	**LSU**	**SSU**	***tef*1-α**
Parabambusicolaceae* and *Pleomassariaceae					
Aquastroma magniostiolata	HHUF 30122 T	NR_153583	NG_056936	NG_061000	AB808486

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	LSU	SSU	*tef*1-α
Beverwykella grandispora	**KUNCC 23–13377**	**PQ340458**	**PP189894**	**–**	**–**
Beverwykella grandispora	**KUNCC 23–13379 T**	**PQ340457**	**PP189893**	**PQ435252**	**PQ456945**
Beverwykella grandispora	**KUNCC 23–16913**	**PQ607756**	**PP189915**	**PQ435253**	**–**
Beverwykella grandispora	**KUNCC 23–16914**	**PQ607757**	**PP189916**	**PQ435254**	**–**
Beverwykella pulmonaria	CBS 283.53 T	MH857201	MH868739	NG_061258	–
Beverwykella pulmonaria	MFUCC 15–0183	–	KT934251	–	–
Halobyssothecium aquifusiforme	GZCC 20–0481 TO	OP377825	OP377925	OP378010	OP473005
Halobyssothecium bambusicola	MFLUCC 20–0226 TO	MN833419	MT068489	MT068494	MT477868
Lonicericola fuyuanensis	MFLU 19–2850 T	NR_172419	NG_073809	NG_070329	MN938324
Lonicericola hyaloseptispora	KUMCC 18–0149 T	NR_164294	NG_066434	NG_067680	–
Lonicericola hyaloseptispora	KUMCC 18–0150 T	MK098194	MK098200	MK098206	MK098210
Lonicericola qujingensis	GMBCC1178 T	OM855593	OM855602	OM855616	OM857556
Lonicericola qujingensis	**KUNCC 23–13439**	**PQ340465**	**PP189902**	**PQ435264**	**PQ456955**
Multilocularia bambusae	MFLUCC 11–0180 T	NR_148099	NG_059654	NG_061229	KU705656
Multiseptospora thailandica	MFLUCC 11–0204	KU693447	KU693440	KU693444	KU705659
Multiseptospora thailandica	MFLUCC 12–0006	KU693448	KU693441	KU693445	KU705660
Multiseptospora thailandica	MFLUCC 11–0183 T	NR_148080	NG_059554	KP753955	KU705657
Multiseptospora thysanolaenae	MFLUCC 11–0202 T	–	NG_059655	NG_063600	KU705658
Neoaquastroma bauhiniae	MFLUCC 17–2205	MH025953	MH023320	MH023316	MH028248
Neoaquastroma bauhiniae	MFLUCC 16–0398 T	NR_165217	NG_067814	NG_070696	MH028247
Neoaquastroma guttulatum	MFLUCC 14–0917 T	KX949739	KX949740	KX949741	KX949742
Neoaquastroma krabiense	MFLUCC 16–0419 T	NR_165218	NG_067815	NG_067670	MH028249
Neomultiseptospora yunnanensis	KUMCC 21–0411 T	OL898884	OL898925	OL898890	OL964282
Neomultiseptospora yunnanensis	HKAS 122240 T	OL898885	OL898926	OL898891	OL964283
Parabambusicola aquatica	MFLUCC 18–1140 T	NR_171877	NG_073791	–	–
Parabambusicola honghensis	KUMCC 21–0410 T	OL898880	OL898921	OL898886	–
Parabambusicola thysanolaenae	KUMCC 18–0147 T	NR_164044	NG_066435	NG_067681	MK098209
Parabambusicola thysanolaenae	KUMCC 18–0148	MK098193	MK098198	MK098202	MK098211
Paramonodictys solitarius	MFLUCC 17–2353	MT627707	MN913703	MT864299	MT954397
Paramonodictys solitarius	GZCC 20–0007 T	MN901152	MN897835	MN901118	MT023012
Paratrimmatostroma kunmingensis	HKAS 102224A T	MK098192	MK098196	MK098204	MK098208
Paratrimmatostroma kunmingensis	HKAS 102224B T	MK098195	MK098201	MK098207	–
Prosthemium intermedium	KT2226 T	NR_119409	NG_042333	–	–

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	**LSU**	**SSU**	***tef*1-α**
Prosthemium neobetulinum	CBS 121.51	AB554078	AB553747	AB553640	–
Prosthemium asterosporum	CBS 431.96	MH862584	MH874210	–	–
Prosthemium betulinum	CBS 279.74	AB554089	AB553759	–	–
Prosthemium canba	MK14	AB554098	AB553768	–	–
Prosthemium canba	KT2230	AB554096	AB553766	–	–
Prosthemium orientale	CBS 431.96	AB554083	AB553752	–	–
Prosthemium orientale	CBS 114278	AB554084	AB553753	–	–
Prosthemium sinense	GAAS–100–01	KX687764	KX687761	–	–
Prosthemium sinense	GAAS–100–02	KX687765	KX687762	–	–
Prosthemium stellare	CBS 558.70	AB554112	AB553782	–	–
Prosthemium stellare	VM20050611	AB554111	AB553781	AB553650	–
Pseudomonodictys tectonae	MFLUCC 12–0552 T	–	NG_059590	NG_061213	KT285571
Scolecohyalosporium submersum	KUMCC 21–0412 T	OL898883	OL898924	OL898889	OL964281
Scolecohyalosporium submersum	KUMCC 21–0413 T	OL898881	OL898922	OL898887	OL964279
Splanchnonema platani	CBS 221.37	MH855894	MH867404	–	–
Splanchnonema platani	CBS 222.37	KR909311	KR909316	KR909318	KR909319
Splanchnonema pupula	MFLU 14–0807	KP659196	KP659197	–	–
		ITS	**LSU**	***tef*1-α**	***rpb*2**
Roussoellaceae					
Neoroussoella alishanense	FU31016 T	MK503816	MK503822	MK336181	MN037756
Neoroussoella bambusae	MFLUCC 11–0124 T	KJ474827	KJ474839	KJ474848	KJ474856
Neoroussoella bambusae	GMBCC1116	OM891810	OM884022	ON098358	ON098377
Neoroussoella bambusae	GMBCC1118	OM891812	OM801294	ON098359	ON098376
Neoroussoella entadae	MFLUCC 15–0098	MH275075	MH260309	–	–
Neoroussoella heveae	MFLUCC 17–0338 T	MH590693	MH590689	–	–
Neoroussoella heveae	MFLUCC 17–2069	MT310634	MT214589	MT394647	MT394703
Neoroussoella lenispora	GZCC 16–0020 T	–	KX791431	–	–
Neoroussoella leucaenae	MFLUCC 18–1544 T	MK347767	MK347984	MK360067	MK434876
Neoroussoella solani	CPC 26331 T	KX228261	KX228312	–	–
Pararoussoella mangrovei	MFLUCC 16–0424 T	MH025951	MH023318	MH028246	MH028250
Pararoussoella mukdahanensis	KUMCC 18–0121	MH453489	MH453485	MH453478	MH453482
Pararoussoella mukdahanensis	MFLUCC 11–0201 T	KU940129	KU863118	–	–

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	**LSU**	***tef*1-α**	***rpb*2**
Pararoussoella rosarum	MFLUCC 17–0796 T	NR_157529	NG059872	MG829224	–
Parathyridaria percutanea	CBS 868.95 TO	KF322118	KF366449	KF407987	KF366452
Parathyridaria ramulicola	CBS 141479 TO	KX650565	KX650565	KX650536	KX650584
Pseudoneoconiothyrium euonymi	CBS 143426 T	MH107915	MH107961	–	MH108007
Pseudoneoconiothyrium rosae	MFLUCC 15–0052 T	NR_157523	NG059868	–	–
Pseudoroussoella chromolaenae	MFLUCC 17–1492 T	MT214345	MT214439	MT235769	–
Pseudoroussoella elaeicola	MFLUCC 17–1483	MT214348	MT214442	MT235772	MT235808
Pseudoroussoella elaeicola	MFLUCC 15–0276b	MH742330	MH742327	–	–
Pseudoroussoella elaeicola	MFLUCC 15–0276a T	MH742329	MH742326	–	–
Roussoella angusta	MFLUCC 15–0186 T	–	KT281979	–	–
Roussoella aquatica	MFLUCC 18–1040 T	NR_171975	NG_073797	–	–
Roussoella arundinacea	CBS 146088 T	MT223838	MT223928	–	MT223699
Roussoella bambusarum	GMB0316 T	ON479891	ON479892	–	–
Roussoella bambusarum	GMB0390	ON505055	ON505051	–	–
Roussoella chiangraina	MFLUCC 10–0556 T	KJ474828	KJ474840	KJ474849	KJ474857
Roussoella chinensis	KUNCC 22–12534 T	OP555451	OP555449	–	–
Roussoella doimaesalongensis	MFLUCC 14–0584 T	KY026584	KY000659	KY651249	KY678394
Roussoella dujuanhuensis	**KUNCC 23–13438 T**	**PQ340471**	**PP189909**	**PQ456961**	**PQ348603**
Roussoella fusispora	UESTCC 23.0135 T	OR141720	OR142438	OR161835	OR161837
Roussoella guttulata	MFLUCC 20–0102 T	NR_172428	NG_075383	MW022188	MW022187
Roussoella hysterioides	CBS 546.94	KF443405	KF443381	KF443399	KF443392
Roussoella intermedia	NBRC 106245	KJ474831	AB524624	–	–
Roussoella intermedia	CBS 170.96	KF443407	KF443382	KF443398	KF443394
Roussoella japanensis	MAFF 239636 T	KJ474829	AB524621	AB539114	AB539101
Roussoella japanensis	GMBCC1067	OM891802	OM884018	ON098344	ON098381
Roussoella japanensis	GMBCC1117	OM891811	OM884023	ON098345	ON098382
Roussoella kunmingensis	KUMCC 18–0128 T	MH453491	MH453487	MH453480	MH453484
Roussoella kunmingensis	GMBCC1055	OM891797	OM884013	ON098353	ON098385
Roussoella magnata	MFLUCC 15–0185 T	–	KT281980	–	–
Roussoella margidorensis	MUT 5329 T	KU314944	MN556322	MN605897	MN605917
Roussoella mariettea	BRIP 70563a T	OM417291	OM333605	ON624200	ON624228
Roussoella mediterranea	MUT 5369 T	KU314947	MN556324	MN605899	MN605919
Roussoella mexicana	CPC 25355 T	KT950848	KT950862	–	–

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number				
		ITS	**LSU**	***tef*1-α**	***rpb*2**	
Roussoella multiloculata	GMBCC1056 T	OM891799	OM884015	ON098343	ON098369	
Roussoella multiloculata	GMBCC1065	OM891800	OM884016	ON098338	ON098364	
Roussoella neopustulans	MFLUCC 11–0609 T	KJ474833	KJ474841	KJ474850	–	
Roussoella neopustulans	MFLUCC 12–0003	KU940130	KU863119	–	–	
Roussoella nitidula	MFLUCC 11–0182 T	KJ474835	KJ474843	KJ474852	KJ474859	
Roussoella nitidula	MFLUCC 11–0634	KJ474834	KJ474842	KJ474851	KJ474858	
Roussoella nitidula	GMBCC1097	OM891805	OM884020	ON098351	ON098384	
Roussoella padinae	MUT 5503 T	KU158170	MN556327	MN605902	MN605922	
Roussoella padinae	GMBCC1126	OM891816	OM884025	ON098356	ON098383	
Roussoella papillata	GMBCC1121 T	OM891814	OM755608	ON098346	ON098378	
Roussoella papillata	IFRDCC3103	ON228188	ON228184	ON244452	ON244450	
Roussoella pseudohysterioides	MFLUCC 13–0852 T	KU940131	KU863120	KU940198	–	
Roussoella pseudohysterioides	KUMCC 18–0111	MH453490	MH453486	MH453479	MH453483	
Roussoella pustulans	MAFF 239637 T	KJ474830	AB524623	AB539116	AB539103	
Roussoella scabrispora	MFLUCC 11–0624 T	KJ474836	KJ474844	KJ474853	KJ474860	
Roussoella scabrispora	MFLUCC 14–0582	KY026583	KY000660	–	–	
Roussoella siamensis	MFLUCC 11–0149 T	KJ474837	KJ474845	KJ474854	KJ474861	
Roussoella sichuanensis	UESTCC 23.0136 T	OR141721	OR142439	OR161836	OR161838	
Roussoella sinensis	GMBCC1119 T	OM891813	OM884024	ON098357	ON098379	
Roussoella sinensis	IFRDCC 3101	ON228187	ON228183	ON244453	ON244451	
Roussoella sp.	UESTCC 22.0120	OR762065	OR762066	OR763024	–	
Roussoella thailandica	MFLUCC 11–0621 T	KJ474838	KJ474846	–	–	
Roussoella tuberculata	MFLUCC 13–0854 T	KU940132	KU863121	KU940199	–	
Roussoella tuberculata	GMBCC1123	OM891815	OM755613	ON098352	ON098380	
Roussoella uniloculata	GMBCC1110 T	OM891809	OM801286	ON098360	ON098374	
Roussoella uniloculata	DDQ01005–2	OM891817	OM884026	ON098361	ON098375	
Roussoella verrucispora	CBS 125434 T	KJ474832	AB524622	AB539115	AB539102	
Roussoella yunnanensis	KUMCC 18–0115 T	MH453492	MH453488	MH453481	–	
Roussoella yunnanensis	KUMCC 18–0115 T	MH453492	MH453488	–		
		ITS	**LSU**	**SSU**	***tef*1-α**	***rpb*2**
Teichosporaceae						
Asymmetrispora mariae	CBS 140732 T	KU601580	KU601580	–	KU601614	–

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number				
		ITS	**LSU**	**SSU**	***tef*1-α**	***rpb*2**
Asymmetrispora tennesseensis	ANM 911 T	–	GU385207	–	GU327769	–
Aurantiascoma minimum	GKM 169 T	–	GU385165	–	GU327768	–
Aurantiascoma nephelii	CPC 27539 T	KY173469	KY173558	–	–	–
Aurantiascoma quercus	CBS 143396 T	MH107920	MH107966	–	MH108030	MH108010
Floricola aquatica	**KUNCC 23–14239 T**	**PQ340460**	**PP189896**	**PQ435256**	**PQ456947**	**PQ348600**
Floricola clematidis	MFLUCC 17–2182 T	MT310638	MT214594	MT226706	MT394651	–
Floricola festucae	MFLU 17–0773 T	MW587280	MW587275	MW587277	MW590256	–
Floricola juncicola	CBS 146811 T	MW883419	MW883813	–	MW890108	MW890063
Floricola striata	JK 5603 T	–	GU479785	GU479751	–	–
Floricola striata	JK 5678I	–	GU301813	GU296149	GU479852	GU371758
Floricola sulcata	CBS 118224 T	JX517284	JX517293	–	–	–
Floricola viticola	MFLUCC 15–0039 T	KT305997	KT305993	KT305995	–	–
Lophiostoma dictyosporum	CBS 147389 O	MW759251	MW750379	–	MW752411	MW752388
Lophiostoma erumpens	CBS 147275 O	MW759262	MW750381	–	MW752409	MW752386
Magnibotryascoma acaciae	CPC 24801T	KR611877	KR611898	–	–	–
Magnibotryascoma kunmingense	KUMCC 20–0254 T	MW424769	MW424784	MW424799	MW430105	MW430112
Magnibotryascoma kunmingense	KUMCC 20–0255	MW424770	MW424785	MW424800	MW430106	MW430113
Magnibotryascoma mali	MFLUCC 17–0933 T	MF173433	MF173429	MF173431	MF173435	MF173437
Magnibotryascoma rubriostiolata	TR5	KU601589	KU601589		KU601606	KU601598
Magnibotryascoma rubriostiolata	CBS 140734 T	KU601590	KU601590	–	KU601609	KU601599
Misturatosphaeria aurantiacinotata	GKM 1238 T	–	GU385173	–	GU327761	–
Misturatosphaeria viridibrunnea	MFLUCC 10–0930 T	MH940251	MH940252	–	–	–
Pseudoaurantiascoma kenyensis	GKM 1195 T	–	GU385194	–	GU327767	–
Pseudoaurantiascoma kenyensis	GKM 234N	–	GU385188	–	GU327765	–
Ramusculicola clematidis	MFLUCC 17–2146	MT310640	MT214596	MT226707	MT394652	MT394707
Ramusculicola thailandica	MFLUCC 17–0884	MW587279	MW587274	MW587276	MW590255	–
Ramusculicola thailandica	MFLUCC 13–0284 T	KP899141	KP888647	KP899131	KR075167	–
Teichospora grandicipis	CPC 1852	JN712456	JN712520	–	–	–
Teichospora grandicipis	CBS 111702 T	JN712457	JN712521	–	–	–
Teichospora kingiae	CPC 29104 T	KY173468	KY173557	–	–	–
Teichospora proteae	CBS 122675 T	EU552117	EU552117	–	–	–
Teichospora trabicola	CBS 140730 T	KU601591	KU601591	–	–	KU601600

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	**LSU**	**SSU**	***tub*2**
Tetraplosphaeriaceae					
Aquatisphaeria thailandica	MFLUCC 21–0025	MW890969	MW890763	MW890967	–
Aquatisphaeria thailandica	DLUCC B151	–	MW890764	MW890968	–
Montanitestudina hydei	SQUCC 15173 O	MW077149	MW077158	MW077165	–
Muritestudina chiangraiensis	MFLUCC 17–2551 TO	MG602247	MG602248	MG602249	–
Polyplosphaeria fusca	KT2124	AB524791	AB524607	AB524466	AB524853
Polyplosphaeria fusca	KT1616	AB524789	AB524604	AB524463	AB524851
Polyplosphaeria thailandica	MFLU 15–3273	KU248766	KU248767	–	–
Pseudotetraploa aquatica	**KUNCC 23–13375 T**	**PQ340470**	**PP189908**	**–**	**PQ456973**
Pseudotetraploa bambusicola	CGMCC 3.20939 T	ON332915	ON332933	ON332923	–
Pseudotetraploa bambusicola	UESTCC 22.0005	ON332916	ON332934	ON332924	–
Pseudotetraploa curviappendiculata	JCM 12852T	AB524792	AB524608	AB524467	AB524854
Pseudotetraploa curviappendiculata	MAFF 239496	AB524793	AB524609	AB524468	AB524855
Pseudotetraploa curviappendiculata	CBS 125426	AB524794	AB524610	AB524469	AB524856
Pseudotetraploa javanica	JCM 12854	AB524795	AB524611	AB524470	AB524857
Pseudotetraploa longissima	JCM 12853 T	AB524796	AB524612	AB524471	AB524858
Pseudotetraploa rajmachiensis	NFCCI 4618 T	MN937222	MN937204	–	MN938305
Pseudotetraploa rajmachiensis	NFCCI 4619	MN937221	MN937203	–	MN938304
Pseudotetraploa yunnanensis	KUNCC 10464 T	OR449073	OR438891	–	–
Quadricrura bicornis	CBS 125427	AB524797	AB524613	AB524472	AB524859
Quadricrura meridionalis	CBS 125684	AB524798	AB524614	AB524473	AB524860
Quadricrura septentrionalis	CBS 125429	AB524799	AB524615	AB524474	AB524861
Quadricrura septentrionalis	CBS 125430	AB524800	AB524616	AB524475	AB524862
Tetraploa aquatica	MFLU 19–0996	MT530449	MT530453	MT530454	–
Tetraploa aquatica	MFLUCC 19–0995 T	MT530448	MT530452	–	–
Tetraploa aristata	CBS 996.70	AB524805	AB524627	AB524486	AB524867
Tetraploa bambusae	KUMCC 21–0844 T	ON077078	ON077067	ON077073	ON075065
Tetraploa cylindrica	KUMCC 20–0205 T	MT893205	MT893204	MT893203	MT899417
Tetraploa cylindrica	ZHKUCC 22–0087	ON555689	ON555688	ON555690	ON564477
Tetraploa dashaoensis	KUMCC 21–0010 T	OL473549	OL473555	OL473556	OL505601
Tetraploa dwibahubeeja	NFCCI 4621 T	MN937225	MN937207	–	MN938308
Tetraploa dwibahubeeja	NFCCI 4623	MN937226	MN937208	–	MN938309
Tetraploa endophytica	CBS 147114T	KT270279	MW659165	–	–

Supplementary Table 1 Continued.

Taxon	Voucher/Strain Number	GenBank Accession Number			
		ITS	**LSU**	**SSU**	***tub*2**
Tetraploa hainanensis	GZCC 23–0601 T	OR427325	OR438892	OR438286	OR449116
Tetraploa hainanensis	GZCC 23–0602	OR427326	OR438893	–	OR449117
Tetraploa juncicola	CBS 149046	ON603780	ON603800	–	–
Tetraploa lignicola	KUNCC 10794	ON422286	ON422294	ON422300	–
Tetraploa lignicola	KUNCC 10795	ON422287	ON422295	ON422301	–
Tetraploa nagasakiensis	KUMCC 18–0109	MK079890	MK079891	MK079888	–
Tetraploa nagasakiensis	KT 1682 T	AB524806	AB524630	AB524489	AB524868
Tetraploa obpyriformis	KUMCC 21–0011 T	OL473558	OL473554	OL473557	OL505600
Tetraploa pseudoaristata	NFCCI 4624 T	MN937232	MN937214	–	MN938315
Tetraploa pseudoaristata	NFCCI 4625	MN937230	MN937212	–	MN938313
Tetraploa puzheheiensis	MFLUCC 20–0151 T	MT627744	MT627655	–	–
Tetraploa sasicola	KT 563 T	AB524807	AB524631	AB524490	AB524869
Tetraploa thailandica	MFLUCC 21–0030 T	MZ412518	MZ412530	MZ413274	–
Tetraploa thrayabahubeeja	NFCCI 4627 T	MN937235	MN937217	–	MN938318
Tetraploa thrayabahubeeja	NFCCI 4628	MN937233	MN937215	–	MN938316
Tetraploa yakushimensis	KT 1906T	AB524808	AB524632	AB524491	AB524870
Tetraploa yunnanensis	MFLUCC 19–0319 T	MT627743	MN913735	MT864341	–
Tetraploa sp.	KT 1684	–	AB524628	AB524487	–
Tetraploa sp.	KT 2578	–	AB524629	AB524488	–
Tetraploa sp.	CY112	HQ607964	–	–	–
Tetraploa sp.	MFLU 23–0195	OR438372	OR438842	OR458353	–
Triplosphaeria acuta	JCM 13171 T	AB524809	AB524633	AB524492	AB524871
Triplosphaeria cylindrica	JCM 14425	AB524810	AB524635	AB524494	AB524872
Triplosphaeria cylindrica	NBRC 106247	AB524811	AB524636	AB524495	AB524873
Triplosphaeria guizhouensis	GZCC 19 0512 T	OQ646060	MW133854	MW134632	OQ659019
Triplosphaeria maxima	JCM 13172 T	AB524812	AB524637	AB524496	AB524874
Triplosphaeria sp.	NBRC 106248	AB524815	AB524640	AB524499	AB524877
Triplosphaeria sp.	NBRC 106249	AB524816	AB524641	AB524500	AB524878
Triplosphaeria yezoensis	CBS 125436 T	AB524813	AB524638	AB524497	AB524875
Triplosphaeria yezoensis	CBS 125437	AB524814	AB524639	AB524498	AB524876
Triplosphaeria yezoensis	CBS 125437	AB524814	AB524639	AB524498	
Triplosphaeria yunnanensis	**KUNCC 23–13443 T**	**PQ340474**	**PP189912**	**PQ435268**	**PQ456974**