TAXONOMY AND PHYLOGENY OF FRESHWATER FUNGI FROM PLATEAU LAKES IN YUNNAN, CHINA

HONGWEI SHEN

DOCTOR OF PHILOSOPHY
IN
BIOLOGICAL SCIENCE

SCHOOL OF SCIENCE
MAE FAH LUANG UNIVERSITY
2024

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Hongwei Shen

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Author	Hongwei Shen
Degree	Doctoral of Philosophy (Biological Science)
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ABSTRACT

Lignicolous freshwater fungi are a special ecological group, referring to those fungal taxa that occur on woody debris submerged in freshwater habitats. They are widely distributed in lotic and lentic habitats, and play a key role in the decomposition of submerged wood in freshwater habitats, breaking down lignocelluloses and releasing nutrients, all of which are important for ecosystem functioning. Yunnan Province is one of the hot spots 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 compared with lotic freshwater habitats. This study collected submerged wood specimens from several plateau lakes in Yunnan Province, China. Based on morphological and phylogenetic analyses, more than 180 lignicolous freshwater fungi species were identified. The species diversity, community composition, and possible influencing factors of lignicolous freshwater fungi in Yunnan plateau lakes were explored. The lignicolous freshwater fungi recorded in this study were primarily distributed in *Dothideomycetes* and *Sordariomycetes*, with several species reported in *Eurotiomycetes* and *Leotiomycetes*. 82 lignicolous freshwater fungal species in *Dothideomycetes* and *Sordariomycetes* were described and illustrated in detail, belonging to twelve genera, ten families, and nine orders. Based on molecular evidence and morphological characteristics,

a new genus *Paralentithecium* was established to accommodate *P. aquaticum* and the new species *P. suae*; 50 new species, *viz.*, *Apiospora fuxianhuensis*, *A. hongheensis*, *Aquimassariosphaeria aquatica*, *Astrosphaeriella yunnanensis*, *Beverwykella grandispora*, *Chloridium guttulatum*, *C. yunnanense*, *Cryptocoryneum sinense*, *Dematiosporium hydei*, *D. muriforme*, *Dictyocheirospora multiappendiculata*, *D. suae*, *Floricola aquatica*, *Fuscocatenula guttulata*, *Hermatomyces hongheensis*, *Hongkongmyces cylindricisporus*, *H. guttulatus*, *H. hongheensis*, *H. yunnanensis*, *Kirschsteiniothelia dujuanhuensis*, *Lindgomyces yunnanensis*, *Lolia fusiformispora*, *Obliquifusoideum sinense*, *Paralentithecium suae*, *Paramirandina guttulata*, *Periconia dujuanhuensis*, *P. hongheensis*, *P. yunnanensis*, *Pseudodactylaria guttulata*, *Pseudostanjehughesia tripospora*, *P. verrucosa*, *Pseudotetraploa aquatica*, *Roussoella dujuanhuensis*, *Setoseptoria suae*, *Sporidesmiella dujuanhuensis*, *S. guttulata*, *S. hongheensis*, *S. hydei*, *Sporidesmium dianchiense*, *Sp. distoseptatum*, *Sp. guttulatum*, *Sp. hongheense*, *Sp. hydei*, *Sp. kunmingense*, *Sp. yangzonghaiense*, *Sp. yunnanense*, *Triplosphaeria yunnanensis*, *Vikalpa dujuanhuensis*, *V. sphaerica*, *Xylolentia aquatica* are introduced. Nine species *viz.*, *A. guangdongensis*, *A. marii*, *C. chlamydosporum*, *Lentithecium yunnanensis*, *Lonicericola qujingensis*, *Multiguttulispora dimorpha*, *Occultibambusa jonesii*, *Tainosphaeria phialogeniculata*, and *Thozetella wenyingiae* were reported for the first time from freshwater habitats. Five species, *viz.*, *Codinaea paniculata*, *Dematipyriforma nilotica*, *Halobyssothecium phragmitis*, *Ha. unicellulare* and *Setoseptoria phragmitis* were reported in China for the first time. 18 known species were rediscovered and reported. The composition analysis of the lignicolous freshwater fungi community in Dianchi Lake, Yangzonghai Lake, Xingyunhu Lake, and Dujuanhu Lake showed that each lake contains endemic species, which can be used as indicators for assessing ecosystem health and water quality. At present, there is limited knowledge about lignicolous freshwater fungi in the Plateau lakes of the Yunnan Province. The knowledge about the community structure, species composition, diversity, and distribution characteristics of lignicolous freshwater fungi in this region is limited. The study of

lignicolous freshwater fungi in plateau lakes is of great significance for understanding the occurrence and evolution of lignicolous freshwater fungal species, biodiversity, ecological functions, and scientific research.

Keywords: 51 new taxa, Lignicolous freshwater fungi, Taxonomy, Phylogeny, *Dothideomycetes*, *Sordariomycetes*, Yunnan Plateau Lakes

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ABBREVIATIONS AND SYMBOLS

diam.	diameter
et al.,	and others
h	hour
gen.	genus/genera
ibid.	ibidem
i.e.	that is
min	millimetre
mm	novum (Latin for new thing)
nov.	novum (Latin for new thing)
s	second
sp.	species
vs.	versus
$\bar{x}$	average
°C	degree centigrade
µm	micrometer
µL	microliter
%	percent

CHAPTER 1

INTRODUCTION

1.1 Definition of Lignicolous Freshwater Fungi

Lignicolous freshwater fungi are a special group of fungi that grow on submerged woody debris in freshwater habitats (Wong et al., 1998; Luo et al., 2004; Pinnoi et al., 2006; Hu et al., 2010; Hyde, Fryar et al., 2016; Luo et al., 2019; Dong et al., 2020). Initially, they were collectively referred to as freshwater fungi until Hyde, Fryar et al. (2016) proposed the concept of "lignicolous freshwater fungi". Lignicolous freshwater fungi are distributed worldwide, but research has focused on tropical, subtropical, and temperate regions of Asia, particularly China and Thailand (Hyde, Fryar et al., 2016; Luo et al., 2019; Dong et al., 2020; Calabon et al., 2022, 2023; Bao et al., 2023; Yang et al., 2023). Professor Ingold was the first to recognize the lignicolous freshwater *Ascomycota*, and published a series of papers about fungi on submerged substrates in the Lake District, England (Ingold, 1951, 1955). Since then and until the end of the 19th century, relevant papers have been reported around the world, but the main research was concentrated in Australia, the UK and the USA (Shearer, 1993). However, from the early 20th century onwards, research on lignicolous freshwater fungi has been concentrated in Asia, particularly in regions such as Hong Kong, Guizhou Province, Yunnan Province of China, and Thailand (Zhang et al., 2011; Hyde, Fryar et al., 2016; Luo et al., 2019; Dong et al., 2020; Bao, Hyde et al., 2021; Calabon, Jones et al., 2021; Dong, Hyde et al., 2021; Shen, Bao, Wanasinghe et al., 2022; Bao et al., 2023; Yang et al., 2023).

Lignicolous freshwater fungi inhabit a variety of freshwater habitats, including streams, rivers, ponds, lakes, swamps, dams, and even tree holes (Wong et al., 1998; Luo et al., 2004, 2019; Pinnoi et al., 2006; Hu et al., 2010; Hyde, Fryar et al., 2016; Dong et al., 2020). Lignicolous freshwater fungi play an important role in nutrient and

carbon cycling, biological diversity, and ecosystem functioning of freshwater ecosystems with their ability to decompose lignocellulose in woody litter, softening the wood and releasing nutrients (Palmer et al., 1997; Wong et al., 1998; Yuen et al., 1998; Bucher et al., 2004; Vijaykrishna et al., 2006; Hyde, Fryar et al., 2016).

1.2 Habitats of Lignicolous Freshwater Fungi

The freshwater habitats provide a unique habitat for lignicolous freshwater fungi. Freshwater environments can be divided into three types: (1) lentic comprises any natural aquatic environment lacking a continuous flow of water; lakes and ponds are typical lentic habitats that provide calm environments in which fungi can develop; (2) lotic comprises continuous flowing water bodies, such as rivers, streams, creeks and brooks. (3) artificial freshwater environments, such as water-cooling towers (Wong et al., 1998; Hyde, Fryar et al., 2016).

1.3 Sexual and Asexual Morphs of Lignicolous Freshwater Fungi

According to the morphological characteristics of the fruiting bodies, lignicolous freshwater fungi can be divided into three groups, (1) ascomycetes: ascospores are produced by asci in ascomata; (2) hyphomycetes: the conidia are produced by the conidiogenous cells on conidiophores without conidiomata; (3) coelomycetes: the conidia are produced by the conidiogenous cell in conidiomata (Shearer, 1993). Among them, hyphomycetes and coelomycetes are asexual stages, ascomycetes are sexual stages. Studies documenting sexual-asexual connections have also revealed many links between the sexual morphs and freshwater hyphomycetes (Sivichai & Jones, 2003; Hu et al., 2014; Abdel-Aziz, 2016a; Sati & Pathak, 2016; Tanney & Miller 2017; Luo et al., 2019; Yang et al., 2023). Hu et al. (2014) listed 77 hyphomycetes that have been linked to sexual morphs. As of 2016, there were over 300 species of extant aquatic hyphomycetes and 15% of them were linked to their sexual morphs (Sati & Pathak, 2016).

1.4 Classification of Lignicolous Freshwater Fungi

The traditional identification and classification of freshwater fungi are based primarily on their morphological characteristics, such as fruit bodies and spores (Shearer, 1993; Cai et al., 2002; Luo et al., 2004). These traditional tools were challenged and became highly subjective, especially among species complexes, non-sporulating fungi and cryptic species (Su et al., 2016). The classifications have been significantly improved with the utilization of molecular data. Hibbett et al. (2007) list six phyla in the kingdom fungi, of which four have freshwater representatives: *Ascomycota*, *Basidiomycota*, *Blastocladiomycota* and *Chytridiomycota*. The most specious phylum is the *Ascomycota* with freshwater representatives in 33 orders, 622 species excluding ascomycetous yeasts, while other taxa remain to be referred to orders. Lignicolous freshwater ascomycetes are composed of *Arthoniomycetes, Chaetothyriomycetes*, *Dothideomycetes*, *Eurotiomycetes*, *Laboulbeniomycetes*, *Lecanoromycetes*, *Lecanoromycetes*, *Leotiomycetes*, *Lichinomycetes*, *Sordariomycetes*, and *Pezizomycetes* (Jones et al., 2014). Calabon et al. (2022) comprehensive review of published data of biodiversity studies and single or multispecies taxonomic studies resulted in an updated classification of freshwater fungi under 17 phyla (45 classes). A total of 3,870 freshwater fungal species from freshwater habitats are distributed in *Ascomycota*, *Chytridiomycota*, *Rozellomycota*, Basidiomycota, *Blastocladiomycota*, *Monoblepharomycota*, *Mucoromycota*, *Aphelidiomycota*, *Entomophthoromycota*, *Mortierellomycota*, *Olpidiomycota*, and *Zoopagomycota*. *Sordariomycetes* and *Dothideomycetes* are the two largest classes of *Ascomycota*, which have the highest number of lignicolous freshwater fungi (Luo et al., 2019; Dong et al., 2020; Bao, Hyde et al., 2021; Dong, Hyde et al., 2021; Calabon et al., 2022; Bao et al., 2023; Yang et al., 2023). The latest classification and morphological study of freshwater *Dothideomycetes* and *Sordariomycetes* were by Luo et al. (2019) and Dong et al. (2020). Luo et al. (2019) provided a comprehensive monograph of lignicolous freshwater fungi in *Sordariomycetes* and introduced one new order, two new families, three new genera, and 47 new species. Dong et al. (2020) listed all the freshwater species belonging to six orders, 43 families, and 145 genera in *Dothideomycetes* and reviewed all genera with the description, illustration, distribution and the key.

1.5 Role and Importance of Lignicolous Freshwater Fungi in Habitats

Lignicolous freshwater fungi play an important role in the material and energy cycle of freshwater ecosystems, and they can degrade the cellulose and lignocellulose of woody debris in the freshwater to form a soft rot (Koske & Duncan, 1973; Zare-Maivan & Shearer 1988; Duarte et al., 2013). The degree of wood decay can be expressed in terms of weight loss, the number of soft rot cavities, and the reduction in compressive strength (Yuen et al., 1998). Leightley and Eaton (1977) studied fungi on submerged wood in streams and cooling towers that can also degrade wood and found that produce soft rot holes in the wood test block in the laboratory. Although the role and importance of lignicolous freshwater fungi are unclear, it is an indisputable fact that they can decompose the extremely indigestible lignocellulose in submerged wood and release nutrients into the water (Yuen et al., 1998; Abdel-Raheem & Shearer, 2002; Bucher et al., 2004).

1.6 Studies on Lignicolous Freshwater Fungi in China

Since the beginning of the 20th century, research on lignicolous freshwater fungi in Asia has dominated globally, with China and Thailand contributing the most to the discovery of lignicolous freshwater fungal species (Calabon, Jones et al., 2021). Zhang et al. (2011) listed 173 species belonging to 112 genera recorded from freshwater habitats in Thailand. Hu et al. (2013) reported 782 species of freshwater fungi in China. Subsequently, China has described many additional new taxa (Liu, Udayanga et al., 2015; Su et al., 2016; Luo et al., 2017, 2019; Bao et al., 2018, 2020, 2023; Luo, Hyde, Bhat et al., 2018; Luo, Hyde, Liu et al., 2018; Dong et al., 2020; Dong, Hyde et al., 2021; Xu et al., 2023, 2024; Yang et al., 2023), making it one of the countries with the richest diversity of freshwater fungi today. Studies of lignicolous freshwater fungi in China were first documented in 1988 with *Vibrissea truncorum* (Alb. and Schwein.) from submerged wood in Guizhou Province (He, 1988). Later, several mycologists carried out research on freshwater fungi from Guizhou, Hong Kong, Taiwan and Yunnan, provinces and many new taxa have been reported (Goh & Hyde, 1999; Tsui

et al., 2000; Ho & Hodgkiss, 2001; Cai et al., 2002; Luo et al., 2004). Guizhou and Yunnan Provinces (Yungui Plateau) are biodiversity hotspots with high floral, faunal and microbial diversity (Xu et al., 2017). In recent years, a large number of lignicolous freshwater fungi have been reported in Yunnan Province (Su et al., 2016; Bao et al., 2018, 2023; Luo et al., 2019; Dong et al., 2020; Dong, Hyde et al., 2021; Shen et al., 2023, 2024).

1.7 Studies on Lignicolous Freshwater Fungi in Yunnan Province, China

The study of freshwater fungi in Yunnan Province began in the 1980s (Yang et al., 1985; Yang & Ding, 1986), and based on the traditional classification method, a taxonomic survey of fungi on sediments, water bodies and floating objects (litter, fallen leaves, flowers, fruits, protozoa, algae, dead aquatic animals and plants) of several plateau freshwater lakes was conducted (Yang et al., 1985; Yang & Ding 1986; Yang, 1992; Cai et al., 2002; Luo et al., 2004). Subsequent studies focused on the discovery and description of new species, new geographic records, and new habitat records in lotic habitats (Luo et al., 2004, 2017, 2019; Cai et al., 2008; Liu, Udayanga et al., 2015; Su et al., 2016, 2018; Bao et al., 2018, 2020, 2023; Luo, Hyde, Bhat et al., 2018; Luo, Hyde, Liu et al., 2018; Li et al., 2022; Li, Wang et al., 2023; Shen et al., 2023, 2024; Wang et al., 2024). Several studies also discuss the impact of seasons, water pollution and hosts on freshwater fungal diversity (Luo et al., 2004). Compared with the lotic freshwater habitats, there are fewer studies on lignicolous freshwater fungi in lentic habitats. Cai et al. (2002) conducted a systematic study of lignicolous freshwater fungi in Fuxian Lake, documenting 65 known species. This research sparked a series of subsequent studies on lignicolous freshwater fungi in Yunnan Province. Luo et al. (2004) studied lignicolous freshwater fungi on submerged wood and grasses in Dianchi Lake, reported 97 lignicolous freshwater fungi, and also discussed the influence of seasons, water pollution and hosts on the diversity of these fung. Later, several studies reported lignicolous freshwater fungi from lotic habitats (streams and rivers) in Yunnan Province (Liu, Udayanga et al., 2015; Su et al., 2016). Shen, Bao, Bhat et al. (2022)

reviewed the lignicolous freshwater fungi reported in Yunnan Province from 1986 to 2021 to be 281 species mainly distributed in *Dothideomycetes* and *Sordariomycetes*, and a few in *Eurotiomycetes* and *Leotiomycetes* and rarely in *Orbiliomycetes* and *Pezizomycetes*. These species were mainly reported in lotic habitats (rivers, streams), with only 53 (19%) species from lentic habitats.

1.8 Objectives

1.8.1 To study taxonomy and phylogeny of lignicolous freshwater fungi from plateau lakes in Yunnan, China.

1.8.2 To introduce new taxa of lignicolous freshwater fungi.

1.8.3 To analyzing species composition and influencing factors of lignicolous freshwater fungi in plateau lakes.

1.9 Expected Outcomes

1.9.1 Phylogenetic relationships of ascomycetes associated with submerged wood decay from plateau lakes in Yunnan.

1.9.2 Identification of lignicolous freshwater fungi species from plateau lakes in Yunnan, and describe and introduce new species.

1.9.3 Explore their species composition from Dianchi, Dujuanhu, Yangzonghai and Yilonghu Lakes in Yunnan Province, China, and providing the specieslist for each lake.

1.10 Thesis Outline

This thesis comprises six chapters.

Chapter 1 is a general introduction, including the definition, and habitats, historical background, ecological role, and classification of freshwater fungi. Studies on Lignicolous Freshwater Fungi in China and Studies on Lignicolous Freshwater

Fungi in Yunnan Province, China briefly reviewed. The research objectives, expected outcome and thesis outline are listed.

Chapter 2 provides research methodology, including the collection, examination, isolation, and deposition of specimens; DNA extraction, PCR amplification, and sequencing; and phylogenetic analyses.

Chapter 3 presents morphological and phylogenetic analyses of 35 lignicolous freshwater fungi in the class *Dothideomycetes* collected from lakes in Yunnan Province, clarifying the phylogenetic placement of these species. Based on morphological and phylogenetic analyses, they were identified as 26 new species, three new geographical records, three new freshwater habitats records, and three new collections. Detailed morphological descriptions and illustrations are provided.

Chapter 4 presents morphological and phylogenetic analyses of 47 lignicolous freshwater fungi in the class *Sordariomycetes* collected from lakes in Yunnan Province, clarifying the phylogenetic placement of these species. Based on morphological and phylogenetic analyses, they were identified as 24 new species, two new geographical records, six new freshwater habitats records, and eighteen new collections. Detailed morphological descriptions and illustrations are provided.

Chapter 5 analyzes the species composition of lignicolous freshwater fungi from Dianchi lake, Dujuanhu lake, Yangzonghai lake, and Yilong lake in Yunnan Province, China and compares them with relevant studies, and discusses the problems and challenges in current research.

Chapter 6 provides an overall conclusion, the research advantages, and future work.

CHAPTER 2

MATERIALS AND METHODS

2.1 Collecting Area and Sample Collection

Lignicolous freshwater specimens were collected from nine major plateau lakes (Luguhu lake, Chenghai lake, Erhai lake, Yangzonghai lake, Dianchi lake, Fuxianhu lake, Xinyunhu lake, Qiluhu lake and Yilonghu lake) and other small lakes in Yunnan Province (Figure 2.1). Submerged wood samples were collected, including tree trunks, branches, and twigs that are variable in size, length, colour, texture and stage of decomposition. Samples were placed in plastic zip lock bags and brought to the laboratory for studies.

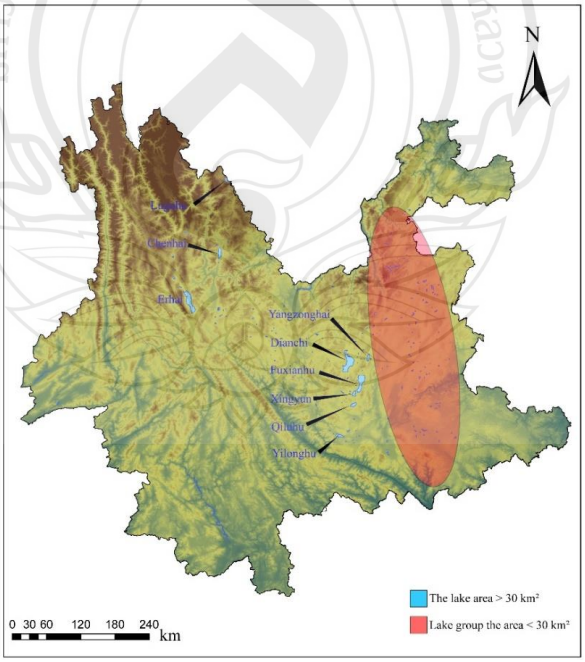
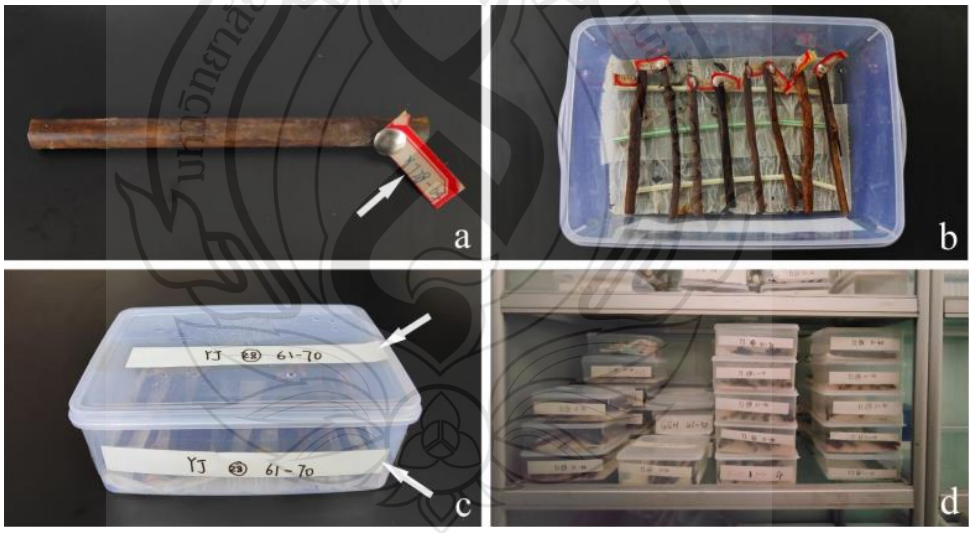


Figure 2.1 Map of specimen collections in Yunnan Province

2.2 Sample Processing and Incubation

The samples were brought to the laboratory in ziplock bags to avoid moisture loss and then trimmed to 15 cm long with pruning scissors. Each sample with a label number that is attached to the end of the sample with a thumbtack (Figure 2.2 a). In addition, plastic boxes with the size of 24 cm × 16 cm × 6 cm were prepared. First, rinse the inside of the plastic box with sterile water, then wipe the entire plastic box with 75% alcohol. After drying, put two layers of sterilized tissues on the bottom of the box, lay three sterilized straws on the tissues to prevent the sample from directly touching the sterilized tissues, and add an appropriate amount of sterile water (the water soaks sterile tissues, but accumulates at the bottom), and then arrange the processed samples horizontally on the straw, ten samples in each plastic box, and label the boxes in obvious places (Figure 2.2 b, c). The samples were placed on a culture rack and incubated at room temperature for one week (Figure 2.2 d).



Note a Sample with a label (arrow indicates sample number). b Samples in the plastic box. c Plastic box with labels (arrows indicate labels documenting detailed sampling sites and sample order). d the samples were incubated on the culture rack.

Figure 2.2 Sample processing and incubation

2.3 Morphological Studies and Isolation

The samples were be incubated in plastic containers with moistened sterilized tissue paper at room temperature for one week. Macromorphological characters of samples were observed using the Optec SZ 760 compound stereomicroscope and photographed using the Nikon SMZ1000 stereo zoom microscope. Micromorphology was examined from hand-sectioned structures using the Nikon ECLIPSE Ni-U compound stereomicroscope. Sexual morph (ascomycetes) structures (i.e., ascomata, ostiole, peridium, hamathecium, asci and ascospores), and asexual morph structures: (1) coelomycetes (i.e., conidiomata, ostiole, conidiomata wall, hamathecium, conidiogenous cells, conidiophores and conidia), (2) hyphomycetes (i.e. conidiophores, conidiogenous cells and conidia) were photographed by immersing sections in water mounted clean glass slides by hand sectioning of the fruiting bodies. Indian ink was used to reveal the presence of a gelatinous sheath around the ascospores or conidia. The measurements of photomicrographs were obtained using Tarosoft (R) Image Frame Work version 0.9.7. Images were edited with Adobe Photoshop CS5 Extended version 12.0.0.0 software (Adobe Systems, San Jose, California).

Single-spore isolation was carried out as described by Luo, Hyde, Liu et al. (2018). Fruiting bodies were cut horizontally looking through a stereomicroscope and the contents were transferred to a drop of sterile water on a flamed microscope slide. The spore suspension was spread over a few square centimeters of a petri plate containing potato dextrose agar (PDA) or water agar (WA) and was incubated at room temperature overnight. Germinated spores were aseptically transferred into fresh potato dextrose agar medium (PDA). Culture plates were incubated at room temperature for four-six weeks and inspected every week. Few of the remaining germinated spores in the media plate were separated with agar by using a needle and transferred into a water-mounted glass slide and photographs were taken to understand the origin of germ tubes. After obtaining pure cultures by isolation of fungal sexual morph, the sterile toothpicks (made from Bamboo) or pine needles were transferred into pure culture PDA media and the plates were incubated at room temperature for three months to obtain the asexual morph. After 2–3 months, cultures, toothpicks and pine needles on PDA were

examined for asexual structures. The living cultures were deposited in the China General Microbiological Culture Collection Center (CGMCC) and Kunming Institute of Botany Culture Collection (KUNCC). Facesoffungi numbers and Index Fungorum numbers were obtained as detailed in Jayasiri et al. (2015) and Index Fungorum (2022), respectively. After finalizing the observation and isolation, the herbarium specimens were deposited in the Kunming Institute of Botany, Academia Sinica herbarium (HKAS).

2.4 DNA Extraction, PCR Amplification and Sequencing

DNA extraction, PCR amplification, sequencing, and phylogenetic analysis were carried out following the methods described by Luo, Hyde, Liu et al. (2018). Mycelia used for DNA extraction were cultivated on PDA for 3–4 weeks at 24 ℃. From each isolate, total genomic DNA was extracted from 100–150 mg of axenic mycelium, which was carefully scraped from the edges of the growing culture with a sterile scalpel. This material was transferred to a 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 (Beijing Tsingke Biological Engineering Technology and Services Co., Ltd, Beijing, P.R. China).

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 at the WASABI database at the AFTOL website (aftol.org). The PCR mixture contained 12.5 μL of 2 × GS Taq PCR MasterMix (mixture of DNA Polymerase, dNTPs, Mg2+ and optimized buffer; Genes and 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, Hyde, Liu et al., 2018). The PCR thermal cycling conditions were performed as presented in Table 2.1. PCR products were purified using mini-columns, purification resin and buffer according to

the manufacturer's protocols. The PCR sequences were carried out at Beijing Tsingke Biological Engineering Technology and Services Co., Ltd (Beijing, P.R. China).

Table 2.1 Partial gene regions, primers and PCR amplification conditions used in this study

Genes	Initial denaturation		Denaturation		Annealing		Extension		No. of cycles	Final extension	
	Temp (℃)	Time (min)	Temp (℃)	Time (s)	Temp (℃)	Time (s)	Temp (℃)	Time (s)		Temp (℃)	Time (min)
ITS	94	3	94	30	56	50	72	60	30	72	10
LSU, *tef*1-α	94	3	94	50	55	60	72	60	30	72	10
*rpb*2	94	5	94	60	52	90	72	90	38	72	10
*tub*2	94	3	94	30	53	30	72	60	35	72	10

2.5 Phylogenetic Analyses

Preliminary identification of genes from fresh strains was performed using the GenBank database. ITS, LSU, SSU, *tef*1-α, *rpb*2 and *tub*2 were used for phylogenetic analysis based on the preliminary identification results and the related publications. The sequences were aligned using MAFFT online service: multiple alignment program MAFFT v.7 (Katoh et al., 2019) (http://mafft.cbrc.jp/ alignment/server/index.html), and sequence trimming was performed with trimAl v1.2 for Windows, and all parameters set by default (http://trimal.cgenomics.org for specific operation steps) (Capella-Gutierrez 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/).

Phylogenetic analyses of combined datasets were obtained based on Maximum-likelihood (ML) and Bayesian criteria (BI). ML tree and BI tree were run on the CIPRES Science Gateway portal (Stamatakis et al., 2008; Miller et al., 2010; Ronquist et al., 2012). MrModeltest v. 2.3 was run under the AIC (Akaike Information Criterion)

implemented in PAUP v. 4.0b10. to evaluate the best-fit model in both ML and BI analyses. ML analyses for the datasets were performed with RAxML-HPC2 on XSEDE v. 8.2.10 (Stamatakis et al., 2008) using the determined best fit substitution model with 1000 bootstrap iterations. The BI analysis was computed with MrBayes v. 3.2.6 (Ronquist et al., 2012). Six simultaneous Markov chains were run with suitable number of generations, and trees were sampled every 100th generation, ending the run automatically when standard deviation of split frequencies dropped below 0.01. Alignment gaps were treated as missing characters in the analysis of the combined data set, where they occurred in relatively conserved regions. Trees were inferred using the heuristic search option with 1000 random sequence additions, with maxtrees set at 1000. Phylogenetic trees were visualized using FigTree v1.4.0 (http://tree.bio.ed.ac.uk /software/figtree/), editing and typesetting were doneusing Adobe Illustrator (AI) (Adobe Systems Inc., the United States). The finalized alignment and tree were deposited in TreeBASE.

CHAPTER 3

LIGNICOLOUS FRESHWATER DOTHIDEOMYCETES FROM PLATEAU LAKES IN YUNNAN

This chapter is extracted from the following publications. I declare that my contribution to this chapter is 95 %.

Shen, H. W., Bao, D. F., Na, W., Luo, Z. L., & Hyde, K. D. (2024) *Paramirandina guttulata*, a new lignicolous freshwater fungi from a plateau Lake in Yunnan Province, China. *Biodiversity Data Journal*, submitted.

Shen, H. W., Luo, Z. L., Bao, D. F., Luan, S., Boonmee, S., Bhat, D. J., Wang, W. P., Su, X. J., Li, Y. X., Yang, L. Q., & Hyde, K. D. Lignicolous freshwater fungi from China IV: Morphology and phylogeny reveal new species of *Pleosporales* from plateau lakes in Yunnan Province, China. *Mycosphere*, submitted.

Liu, S. L., Zhao, P., Cai, L., Shen, S., Wei, H. W., Na, Q., Han, M. H., Wei, R. X., Ge, Y.P., Ma, H. X., Karunarathna, S. C., Tibprommab, S., Zhang, B., Dai, D., Lin, L., Fan, X. L., Luo, Z. L., Shen, H. W., Lu, L., Lu, W. H., Xu, R. F., Tohtirjap, A., Wu, F., & Zhou, L. W. (2024). Catalogue of fungi in China 1. New taxa of plant-inhabiting fungi. *Mycology*, 1–58. https://doi.org/10.1080/21501203.2024.2316066

Shen, H. W., Bao, D. F., Boonmee, S., Su, X. J., Tian, X. G., Hyde, K. D., & Luo, Z. L. (2023). Lignicolous freshwater fungi from plateau lakes in China (I): Morphological and phylogenetic analyses reveal eight species of Lentitheciaceae, including new genus, new species and new records. *Journal of Fungi*, 9(10), 962. https://doi.org/10.3390/jof9100962

Shen, H., Bao, D., Wanasinghe, D. N., Boonmee, S., Liu, J., & Luo, Z. (2022). Novel species and records of Dictyosporiaceae from freshwater habitats in China and Thailand. *Journal of Fungi*, 8(11), 1200. https://doi.org/10.3390/jof8111200

3.1 Introduction

Dothideomycetes is one of the largest class within the *Ascomycota*, comprising highly diverse fungi with over 19,000 known species (Schoch, Sung et al., 2009; Hyde et al., 2013). Species in this class are characterized by bitunicate asci (asci with two wall layers) with fissitunicate dehiscence property, a thick extensible inner layer (endotunica), a thin inextensible outer layer (ectotunica) and ascolocular ascoma development (Schoch, Sung et al., 2009; Hyde et al., 2013). Members of *Dothideomycetes* are cosmopolitan in distribution and occur in a wide variety of habitats including terrestrial, freshwater, marine and extreme habitats (Suetrong et al., 2009; Hyde et al., 2013; Dayarathne et al., 2020; Dong et al., 2020). Freshwater *Dothideomycetes* occurs primarily as saprophytes on a variety of decaying wood in freshwater habitats and are commonly found in freshwater lakes, streams, rivers (Luo et al., 2017; Bao et al., 2018; Lu et al., 2018; Luo, Hyde, Bhat et al., 2018; Yang, Liu et al., 2018; Dong et al., 2020; Lu, Pan et al., 2022; Shen, Bao, Wanasinghe et al., 2022; Shen et al., 2023; Yang et al., 2023). Dong et al. (2020) provides a key reference for a comprehensive taxonomic account of freshwater *Dothideomycetes*, including morphological descriptions, multi-locus phylogenetic analysis, notes with dichotomous keys of taxa, and mapped freshwater distributions with references for each species. *Pleosporales* is the most significant order of freshwater *Dothideomycetes*, encompassing most of the lignicolous freshwater fungi, followed by *Tubeufiales* and *Jahnulales*. Few taxa are reported in *Minutisphaerales*, *Capnodiales*, and *Kirschsteiniotheliales* (Dong et al., 2020; Calabon et al., 2022).

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. We introduced one new genus, *Paralentithecium*, 26 new species, *viz. Aquimassariosphaeria aquatica*, *Astrosphaeriella yunnanensis*, *Beverwykella grandispora*, *Cryptocoryneum sinense*, *Dictyocheirospora multiappendiculata*, *D. suae*, *Floricola aquatica*, *Hermatomyces hongheensis*, *Hongkongmyces cylindricisporus*, *Ho. guttulatus*, *Ho. hongheensis*, *Ho. yunnanensis*, *Kirschsteiniothelia dujuanhuensis*, *Lindgomyces yunnanensis*, *Lolia fusiformispora*, *Paralentithecium suae*, *Paramirandina guttulata*, *Periconia dujuanhuensis*, *P. hongheensis*, *P. yunnanensis*, *Pseudotetraploa aquatica*, *Roussoella dujuanhuensis*, *Setoseptoria suae*, *Triplosphaeria yunnanensis*, *Vikalpa dujuanhuensis*, *V. sphaerica*. Discovered three new geographical record in China, *viz.*, *Halobyssothecium phragmitis*, *Ha. unicellulare* and *S. phragmitis*, and three new freshwater habitat records, *viz.*, *Lentithecium yunnanensis*, *Lonicericola qujingensis*, *Occultibambusa jonesii*, and three known species *viz. Ha. Aquifusiforme*, *Le. Pseudoclioninum* and *S. bambusae*. Detailed descriptions, illustrations, and notes are provided for these species.

3.2 Materials and Methods

Sample collection, processing and cultivation; morphological studies and isolation; DNA extraction, PCR amplification and sequencing; phylogenetic analyses are carried out according to the steps in chapter 2. The new sequences were submitted in GenBank.

3.3 Taxonomy and Phylogeny

Dothideomycetes

Microthyriales

Microthyriaceae Sacc.

Notes: *Microthyriaceae* was introduced by Saccardo (1883) with *Microthyrium* as the type genus. Based on morphological examination of the generic type species, Wu et al. (2010; 2011; 2014) conducted several reappraises of *Microthyriaceae*, excluded many genera, and seven genera of *Microthyriaceae* were accepted. Wijayawardene et al.

(2018) accepted nine genera in this family, and later 11 genera were accepted by Hongsanan et al. (2020). In the latest "Outline of Fungi and fungus-like taxa", 12 genera were accepted in the *Microthyriaceae* (Wijayawardene, Hyde et al., 2022). Subsequently, several new genera were successively introduced into *Microthyriaceae* based on morphology and phylogeny (Qiao et al., 2021; Zheng et al., 2022; Liu, Yang et al., 2023). Currently, 18 genera are included in *Microthyriaceae*, including ten asexual genera (Liu, Yang et al., 2023).

Paramirandina L.L. Liu & Z.Y. Liu

Notes: *Paramirandina* is a freshwater genus introduced by Liu, Yang et al. (2023) to accommodate two lignicolous freshwater fungi from lotic habitats in Guizhou Province, with *P. aquatica* as the type species. *Paramirandina* is morphologically similar to *Heliocephala* and *Mirandina* but can be distinguished from them by the morphology of conidia and conidiogenous cells and differences in molecular sequence (Liu, Yang et al., 2023). *Paramirandina* is characterized by macronematous, mononematous, unbranched, erect, cylindrical, septate conidiophores with subhyaline apex; polyblastic, cylindrical to lageniform, pale brown to subhyaline, sometimes elongating percurrently conidiogenous cells; solitary or gathered in chains, fusiform, cymbiform or narrowly lunate, hyaline, septate conidia (Liu, Yang et al., 2023). The sexual morphs of *Paramirandina* have not yet been discovered, and two asexual species, *P. aquatica* and *P. cymbiformis*, are currently reported from lotic freshwater habitats in Giuzhou Province, China (Liu, Yang et al., 2023).

Paramirandina guttulata H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572010; Figure. 3.1

Etymology: "guttulata" refers to guttulate conidia of the species.

Holotype: HKAS 131771.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: Colonies on natural substrates effuse, hairy, mostly in small groups, sometimes scattered, dark brown, with glistening conidial masses at the apex. *Mycelium* mostly immersed, composed of branched, septate, hyaline to brown, smooth-walled hyphae. *Conidiophores* (230–)264–310(–330) × 4.5–5(–6) µm ($\bar{x}$ = 287 × 5 µm, n = 35), macronematous, mononematous, erect, gregarious, unbranched, cylindrical, straight to flexuous, septate, gradually tapering from the base to the apex, with the base transitioning from dark brown to hyaline towards the apex. *Conidiogenous cells* (31–)40–

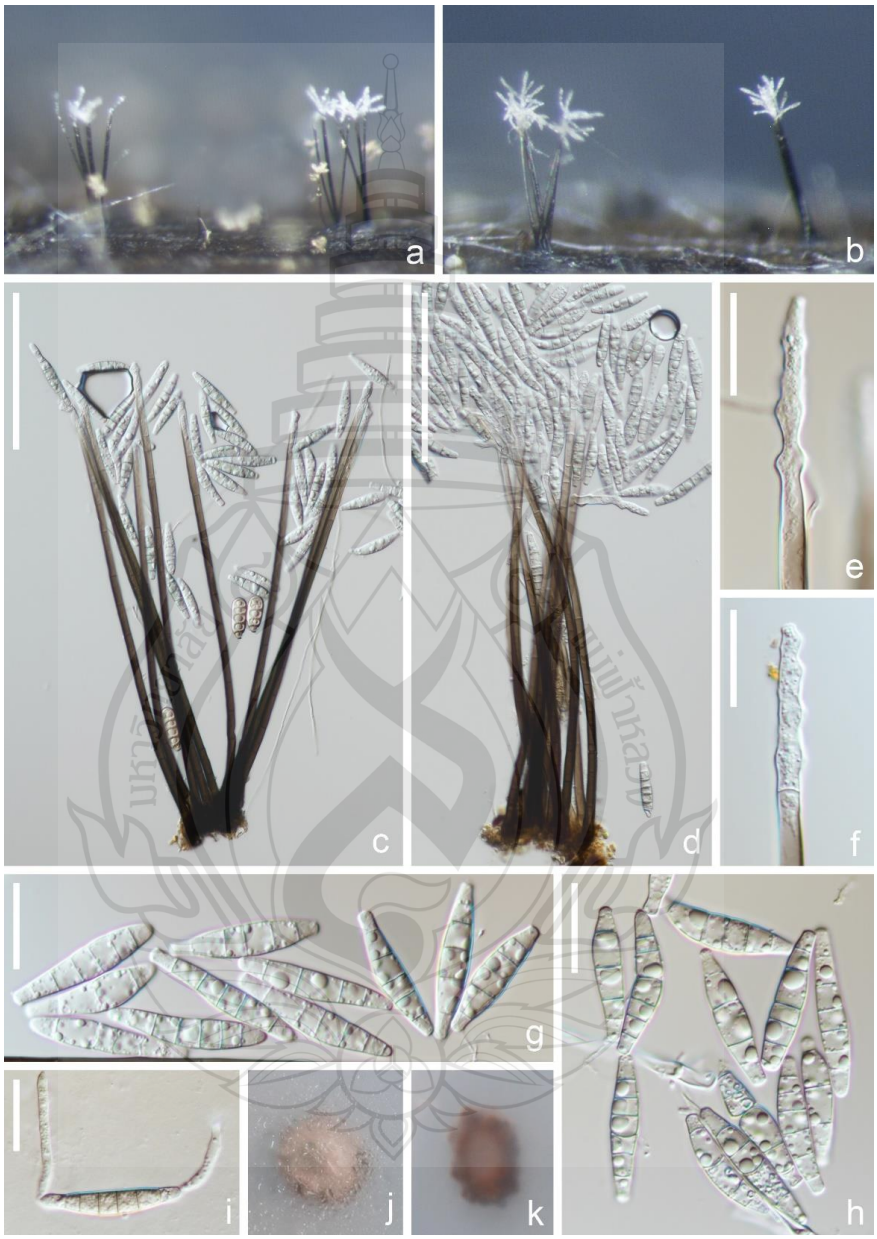
60(–70) × 4–5 µm ($\bar{x}$ = 50 × 5 µm, n = 20), polyblastic, integrated, terminal, determinate, sympodial, cylindrical, pale brown to hyaline, smooth. *Conidia* (31–)33–38(–44) × 6–7.5 µm ($\bar{x}$ = 35 × 7 µm, n = 40), acropleurogenous, solitary or in chains, fusiform, cymbiform, straight or slightly curved, truncate at the base, obtuse at the apex, hyaline, 4–6-septate, smooth, guttulate, sometimes bearing a new conidium at the apex.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium reaching 1-1.5 cm diam. after one month at room temperature (around 25 °C) in dark, circular, with dense, velvety, pale brown to brown mycelium from above, brown from below.

Material examined: CHINA, Yunnan Province, Pu'er City, Jingdong Yi Autonomous County, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on unknown decaying wood submerged in Dujuanhu Lake, Shen H.W., 24 February 2023, L2204 (HKAS 131771, holotype), ex-type living culture DLUCC 2204.

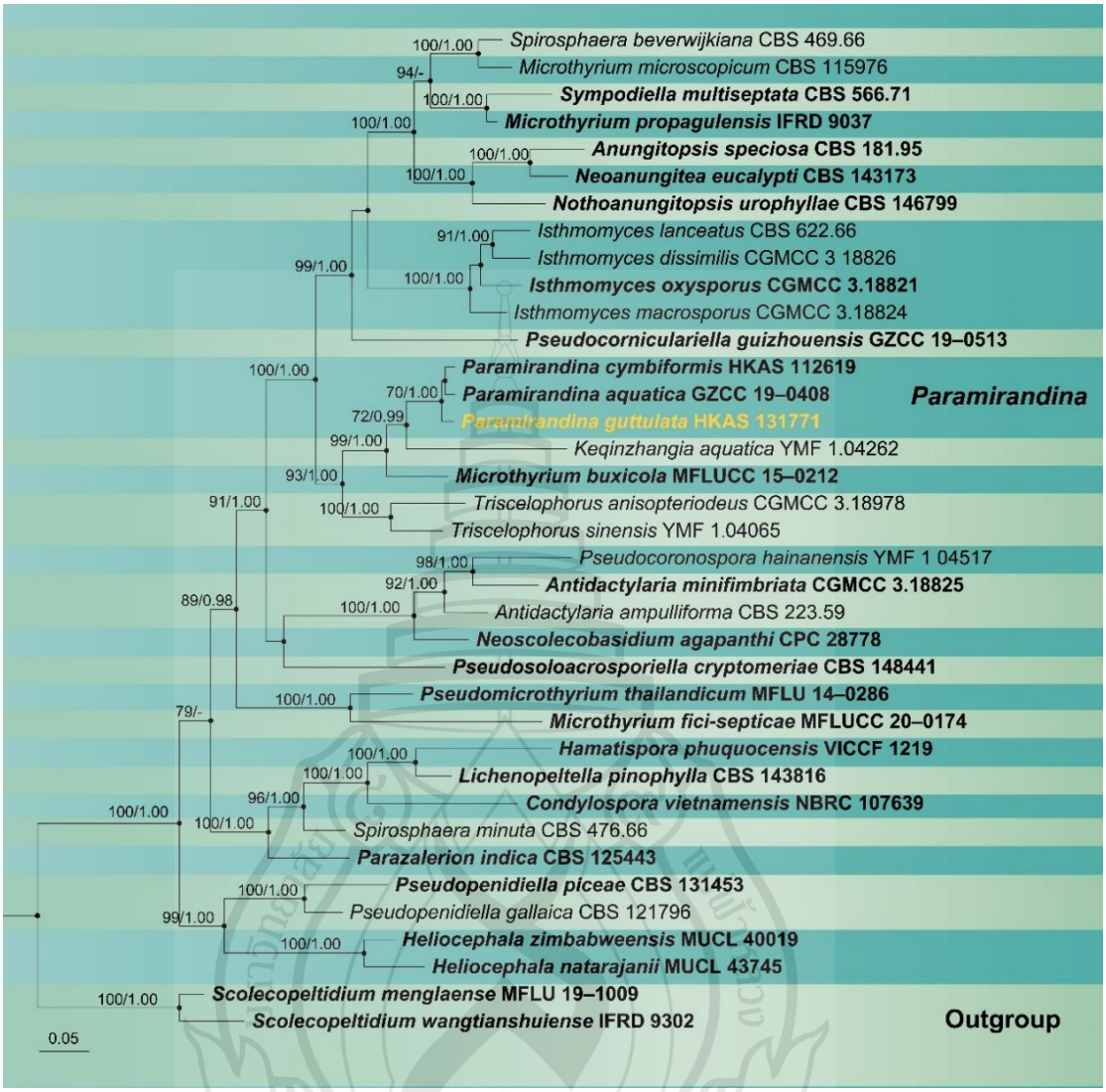
Notes: *Paramirandina* is an intriguing group whose members are notable for their conspicuous macro-morphology on the substrate, characterized by macronematous, mononematous, single or in small groups, unbranched, cylindrical, septate, dark brown conidiophores; terminal, integrated, polyblastic, sympodial, cylindrical to lageniform, pale brown to subhyaline, conidiogenous cells; fusiform, cymbiform or narrowly lunate, septate, hyaline conidia solitary or in chains, with truncate base (Liu, Yang et al., 2023). The morphological characteristics of *P. guttulata* fit the generic concept of *Paramirandina*, and closely resemble those of *P. aquatica* and *P. cymbiformis* (Liu, Yang et al., 2023). However, they can be distinguished from each other by several key morphological characteristics. *P. guttulata* can be distinguished from *P. aquatica* by the gregarious, longer conidiophores (264–310 × 4.5–5 µm vs. 138–200 × 4.5–8 µm) and slightly larger conidia (33–38 × 6–7.5 µm vs. 23–34 × 4–7.5 µm) (Liu, Yang et al., 2023). *P. guttulate* differs from *P. cymbiformis* in having gregarious conidiophores and larger conidia (33–38 × 6–7.5 µm vs. 24–30 × 5–6.5 µm) (Liu et al., 2023). Phylogenetic analysis showed that *P. guttulata* clustered with the other two *Paramirandina* species, and formed a basal lineage with 70% ML and 1.00 PP support (Figure 3.2). Compared the nucleotide base differences of ITS and LSU sequence data between *P. guttulata* and *P. aquatica* showed 7.5% (51/531 bp, including 11 gaps), and 1.6% (13/813 bp) differences, respectively. The LSU sequences between *P. guttulata* and *P. cymbiformis* showed 1.6% (12/768 bp)

nucleotide base differences. Therefore, based on unique morphological characters and phylogenetic analysis, *P. guttulata* was introduced as a new species from the plateau lakes in Yunnan Province, China.



Note a, b Colony on natural substrate. c, d Conidiophores with conidia. e, f Conidiogenous cells. g, h Conidia with sheath. i Germinated conidium. j, k Culture on PDA medium. Scale bars: c, d = 100 μm, e–1 = 20 μm.

Figure 3.1 *Paramirandina guttulata* (HKAS 131771, holotype)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *tef*1-α and *rpb*2 sequence dataset representing *Microthyriales*. Thirty-seven strains are included in the combined analyses which comprise 1356 characters including gaps (860 characters for LSU, 496 characters for ITS). *Scolecopeltidium menglaense* (MFLU 19–1009) and *S. wangtianshuiense* (IFRD 9302) were selected as the outgroup taxa. Bootstrap support values with a ML greater than 65%, and Bayesian posterior probabilities (PP) greater than 0.95 are given above the nodes, shown as "ML/PP". New species are indicated in yellow and type strains are in bold.

Figure 3.2 Phylogenetic tree of *Microthyriales*

Kirschsteiniotheliales Hern.-Restr., R.F. Castañeda, Gené & Crous

Kirschsteiniotheliaceae Boonmee & K.D. Hyde

Notes: *Kirschsteiniotheliaceae* was introduced by Boonmee et al. (2012) to accommodate taxa grouping with *K. aethiops* (Sacc.) D. Hawksw. (type species). Based on morphological data and phylogenetic analysis, *K. elaterascus* and *K. maritima* were transferred to *Morosphaeriaceae* and *Mytilinidiaceae*, respectively (Boonmee et al., 2012). *Kirschsteiniotheliaceae* currently contains only a single genus, *Kirschsteiniothelia*, and more than 40 species have been reported from terrestrial and freshwater habitats (Jayawardena et al., 2022; Zhang, Chen, Ma et al., 2023; de Farias et al., 2024).

Kirschsteiniothelia D. Hawksw.

Notes: *Kirschsteiniothelia* is the single genus in *Kirschsteiniotheliaceae* (*Kirschsteiniotheliales*, *Dothideomycetes*), introduced by Hawksworth (1985) to accommodate six species close to *Microfhelia incrusfans*, with *K. aethiops* (Berk. & Curtis) D. Hawksw. as the type. *Kirschsteiniothelia* was initially placed in *Pleosporaceae*, but subsequent multigene phylogenetic studies showed that *K. aethiops* was not closely related to *Pleosporaceae* (Hawksworth, 1985; Schoch et al., 2006). *K. elaterascus* Shearer and *K. maritma* (Linder) D. Hawksw. clustered with *Morosphaeriaceae* and *Mytiliniadiacea* respectively (Schoch, Crous et al., 2009). Based on morphological data and phylogenetic analysis, Boonmee et al. (2012) introduced *Kirschsteiniotheliaceae* to accommodate species grouping with *K. aethiops* (Sacc.) D. Hawksw., as well as transferred *K. elaterascus* and *K. maritime* to *Morosphaeriaceae* and *Mytilinidiaceae*, respectively. The sexual morph of *Kirschsteiniothelia* is by superficial, erumpent, globose to subglobose, membranaceous, scattered or loosely aggregated ascomata with or without central papilla; bitunicate, fissitunicate, cylindricalclavate asci; ellipsoidal, slightly curved, septate ascospores with or without a distinct gelatinous sheath (Boonmee et al., 2012; Mehrabi et al., 2017). The asexual morphs of *Kirschsteiniothelia* include dendryphiopsis-like and sporidesmium-like (Boonmee et al., 2012; Su et al., 2016; Bao et al., 2018; Jayawardena et al., 2022). More than 40 species are currently described in *Kirschsteiniothelia*, which typically grow saprophytically on woody substrates in terrestrial and freshwater habitats (Boonmee et al., 2012; Su et al., 2016; Bao et al., 2018; Jayawardena et al., 2022; de Farias et al., 2024). Ten species, *viz.*, *Kirschsteiniothelia aquatica*, *K. atra*, *K. aethiops*, *K. cangshanensis*, *K. crustacea*, *K. fluminicola*, *K. ramus*, *K. rostrata* and *K. submersa* have been reported

from freshwater habitats (Dong et al., 2020; Jayawardena et al., 2022; Yang et al., 2023; Zhang, Chen, Ma et al., 2023).

Kirschsteiniothelia dujuanhuensis H.W. Shen & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 571745; Figure. 3.3

Etymology: Name reflects the location from which it was collected, Dujuanhu Lake, Yunnan Province, China.

Holotype: HKAS 129177.

Saprobic on unknown submerged wood in a freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: Hyphomycetous. *Colonies* scattered, effuse, brown to dark brown, glistening, hairy on natural substrate. *Mycelium* mostly immersed, composed of branched, septate, subhyaline to brown, smooth-walled hyphae. *Conidiophores* 29–74(–119) × 9–11 μm ($\bar{x}$ = 51 × 10 μm, n = 15), macronematous, mononematous, dark brown to dark, solitary, erect, cylindrical, straight or slightly curved, slightly narrower towards the apex, unbranched, septate. *Conidiogenous cells* 8–10 × 7–8 μm ($\bar{x}$ = 9 × 7 μm, n = 15), monoblastic, cylindrical, integrated, terminal, brown to dark brown. *Conidia* (114–)122–155(–170) × 10–13(–16) μm ($\bar{x}$ = 138 × 12 μm, n = 15), brown to dark brown, obclavate, subcylindrical, solitary, straight, acrogenous, 6–15-septate, constricted at septum, truncate at base, tapering towards apex, smooth-walled, with a spherical transparent mucilaginous sheath at the apex.

Culture characteristics: Conidia germinated on PDA within 24 hours from single-spore isolation, germ tubes from both ends. Colony on PDA reaching 2.6 cm after 10 days at room temperature in dark, circular, borwn on the surface rough, with dense, velvety mycelium, brown to dark brown from below.

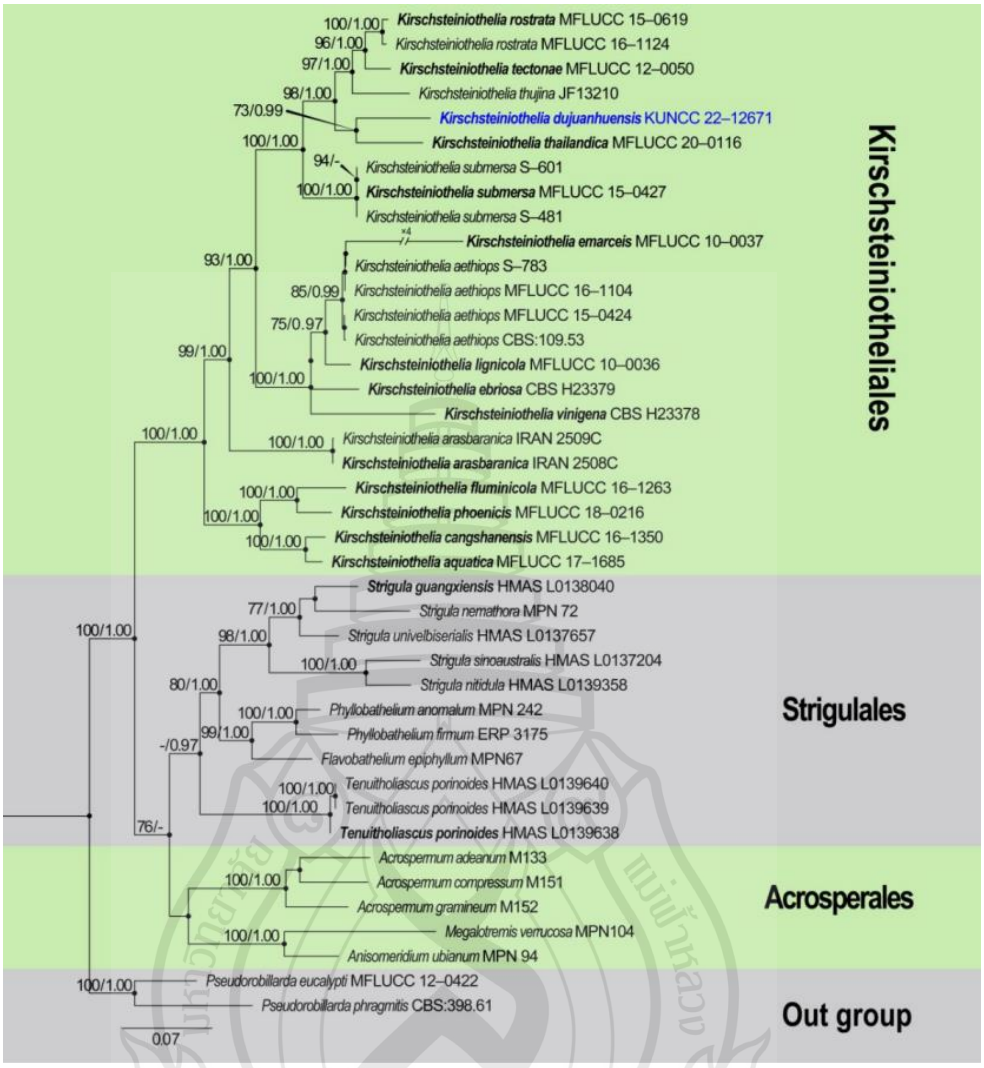
Material examined: CHINA, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Dujuanhu Lake, 24°32.53′ N, 101°1.63′ E, on submerged decaying wood, 25 February 2022, H.W. Shen, YJ 30-51-1 (KHAS 129177, holotype), ex-type living culture, KUNCC 22–12671.

Notes: Phylogenetic analysis combining LSU, SSU and ITS sequence data shows that *Kirschsteiniothelia dujuanhuensis* clustered as a sister clad with *K. thailandica* (MFLUCC 20-0116) with 73% ML and 0.99 PP support (Figure 3.4). In a BLASTn search of NCBI GenBank, the closest matches of the ITS sequence of *K. dujuanhuensis* (KUNCC 22–12671, ex-type) with 85.96% similarity, was to

Kirschsteiniothelia sp. (isolate 7020611638, MZ380314). The closest matches with the LSU sequence with 92.76 % similarity, was to *K. aethiops* (strain CBS 109.53, AY016361), and the closest matches with the SSU sequences with 96.91% similarity, was to *Kirschsteiniothelia* sp. (strain ZHKUCC 22–0220, OP289564). Morphologically, *K. dujuanhuensis* differs from *K. thailandica* in having longer conidia (122–155 µm vs. 74–110 µm) but shorter conidiophores (29–74 µm *vs.* 55–93 µm) (Sun et al., 2021). We therefore introduced *K. dujuanhuensis* as a new species of *Kirschsteiniothelia*, based on morphological and phylogenetic evidence.

Note a, b Colonies on natural substrates. c–e, i Conidiophores with conidia. f, g Conidiogenous cells with conidia and sheath. h Conidia with sheath. h Germinated conidium. k, l Culture (k from above, l from reverse). Scale bars: c–e, h, i = 30 µm, f, g = 20 µm, j = 40 µm.

Figure 3.3 *Kirschsteiniothelia dujuanhuensis* (HKAS 129177, holotype)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence dataset representing *Kirschsteiniotheliales* and other related families. Forty-one strains are included in the combined analyses which comprise 2175 characters including gaps (814 characters for LSU, 874 characters for SSU, 487 characters for ITS). *Pseudorobillarda phragmitis* (CBS 398.61) and *P. eucalypti* (MFLUCC 12–0422) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains are indicated in bold and newly generated sequence are shown in blue.

Figure 3.4 Phylogenetic tree of *Kirschsteiniotheliales*

Pleosporales Luttrell ex M.E. Barr

Astrosphaeriellaceae Phook. & K.D. Hyde

Notes: *Astrosphaeriellaceae* was introduced to accommodate species of *Astrosphaeriella* sensu stricto and *Pteridiospora* with erumpent, carbonaceous ascostromata, and *Astrosphaeriella* was designated as the type genus by Phookamsak, Norphanphoun et al. (2015b). 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, Norphanphoun et al., 2015). 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, Hyde et al., 2022; 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, Norphanphoun et al., 2015; Hongsanan et al., 2020; Konta et al., 2023).

Astrosphaeriella Syd. & P. Syd.

Notes: *Astrosphaeriella* was introduced by Sydow and Sydow (1913) with *A. fusispora* as the type species. *Astrosphaeriella* species are mainly known as the sexual morph and it is characterized by carbonaceous, conical to mammiform ascomata, with ruptured, reflexed, stellate, host remnants around the base; pale brown to brown, fusiform ascospores produced in bitunicate, cylindrical to cylindric-clavate asci (Hawksworth, 1981; Yue & Eriksson, 1986; Fröhlich & Hyde, 1995; Hyde & Fröhlich, 1998; Tanaka & Harada, 2005; Tanaka et al., 2009; Liu et al., 2011; Phookamsak, Norphanphoun et al., 2015). *Astrosphaeriella* is a morphologically well-studied genus, species in the genus are reported as saprobes or parasites from aquatic and terrestrial habitats (Hyde & Fröhlich, 1998; Liu et al., 2011; Phookamsak, Norphanphoun et al.,

2015). *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 and 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, Dai et al. (2022). These species occur as saprophytes on bamboos, palms and stout grasses from terrestrial habitats (Hawksworth, 1981; Hyde & Fröhlich, 1998; Hyde et al., 2000; Liu et al., 2011; Phookamsak, Norphanphoun et al., 2015), whereas a few species have been reported in freshwater habitats (Hyde & Fröhlich, 1998; Ren et al., 2013; Dong et al., 2020).

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

Fungal Names number: FN571997; Figure 3.5

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

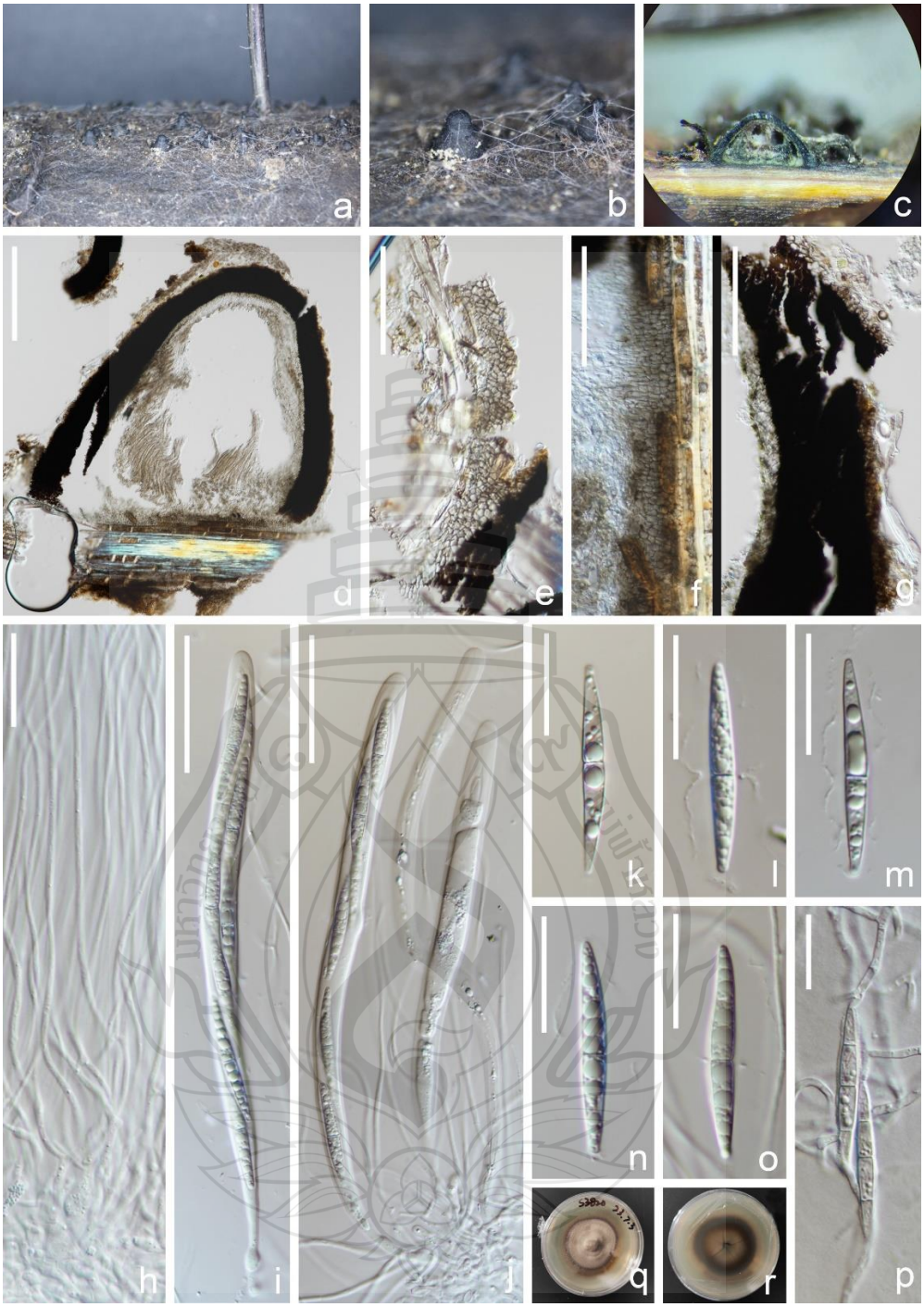
Holotype: HKAS 131656.

Saprobic on decaying submerged wood in freshwater habitat. **Asexual morph**: Undetermined. **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.

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.

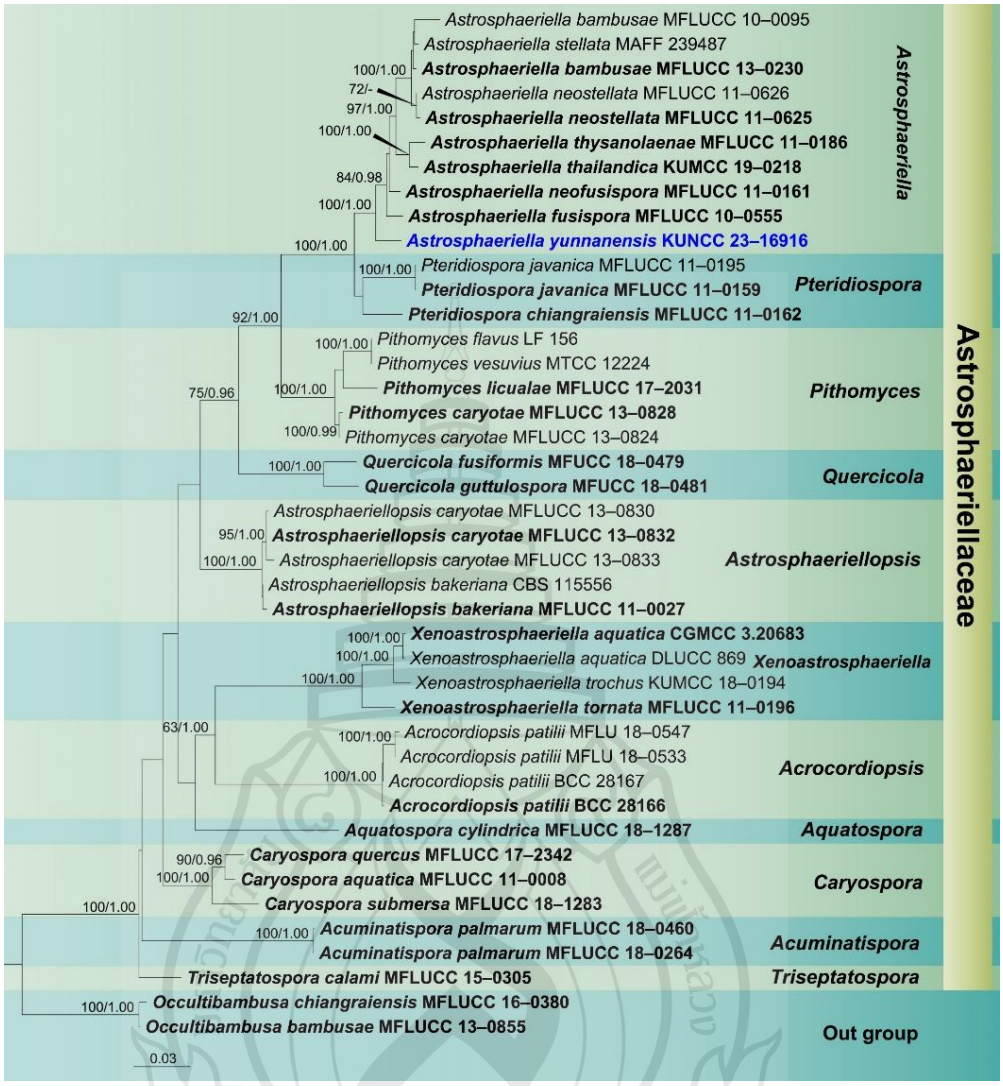
Material examined: CHINA, Yunnan Province, Puer City, Dujuanhu Lake, 24°32'15.6" N, 100°1′30.00″ E, 2500 m; on a rotten bamboo branch submerged in water, 21 February 2022, H.W. Shen, S2820 (HKAS 131656, holotype), ex-type culture KUNCC 23–16916.

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, Norphanphoun et al., 2015). It is morphologically similar to *A. angustispora* and *A. mauritiae* in having superficial and carbonaceous ascomata, elongate-fusiform, hyaline, septate ascospores with a mucilaginous sheath. However, *A. 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 and Fröhlich 1998). *Astrosphaeriella yunnanensis* has longer ascospores (33–40 × 4–5 µm *vs.* 25–28.8 × 4–5.3 µm) with more septate (1–3 *vs.* 1) than than *A. mauritiae*. In the multi-gene phylogenetic analysis, *A. yunnanensis* basal to *Astrosphaeriella* with 100% ML and 1.00 PP support (Figure 3.6). Based on the morphological differences and phylogenetic analysis results, we introduce *A. yunnanensis* as a new species.



Note a, b Appearance of ascomata on host substrate. c, d Section 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 3.5 *Astrosphaeriella yunnanensis* (HKAS 131656, holotype)



Note 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. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and newly generated sequence are shown in blue.

Figure 3.6 Phylogenetic tree of *Astrosphaeriellaceae*

Cryptocoryneaceae A. Hashim. & Kaz. Tanaka

Notes: *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). *Cryptocoryneaceae* is only known by the asexual morphs, sexual morphs are still undetermined, and most members of this family are saprophytes on plant debris in terrestrial habitats, there are no *Cryptocoryneaceae* species collected from freshwater habitats so far (Hashimoto et al., 2016; Boonmee et al., 2021).

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

Notes: *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 the presence of stromatic sporodochia, cheiroid conidia, and conidial arms developed downward from the cap cells (Fuckel, 1865; Hashimoto et al., 2016). Hashimoto et al. (2016) carried out a taxonomic reassessment of the species in *Cryptocoryneum*, based on the morphological observations and molecular phylogenetic analysis, and proposed that conidial size, number of conidial arms and conidial septa are important characteristics for species delimitation within *Cryptocoryneum* (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).

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

Fungal Names number: FN571860; Figure 3.7

Etymology: The name refers to the country where the holotype was collected: China.

Holotype: HKAS 131841.

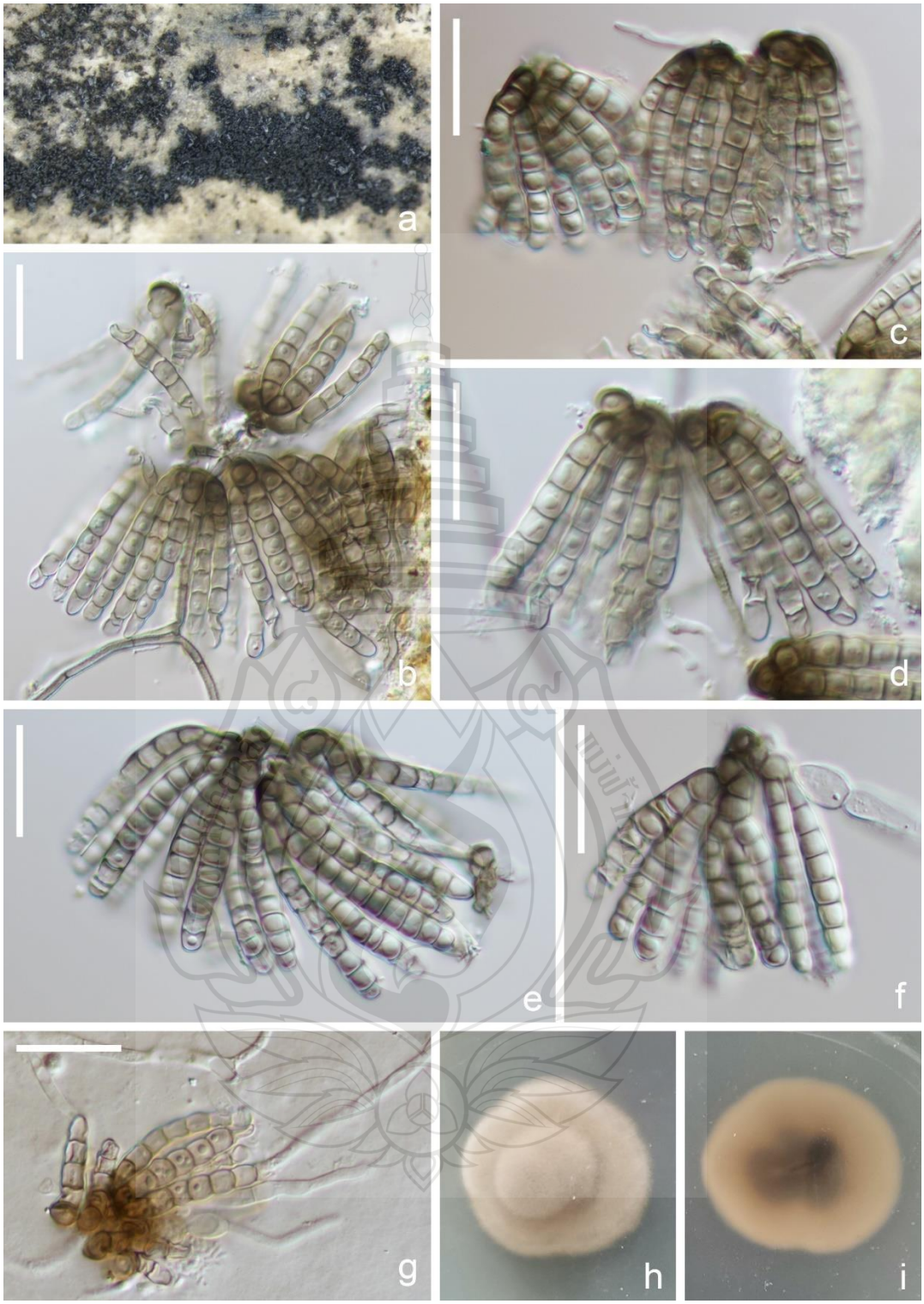
Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **Asexual morph**: *Sporodochia* on natural substrate effuse, superficial,

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.

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.

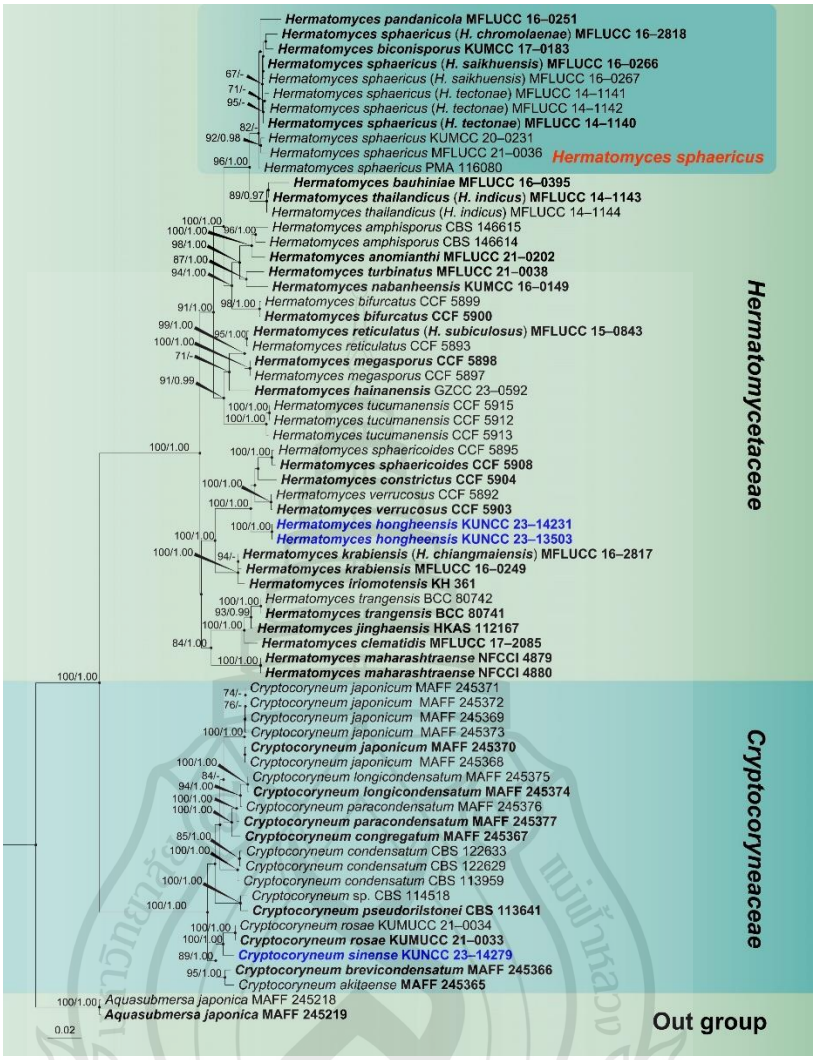
Material examined: CHINA, Yunnan Province, Yuxi City, Mofanghe Reservoir, 23°40′36" N, 101°44'08″ E; 2213 m; on submerged decaying wood, 23 February 2023, W. Ying, on submerged decaying wood, 23 February 2023, H.W. Shen, FD 46–10–1 (HKAS 131841, holotype), ex-type culture KUNCC 23–14279.

Notes: *Cryptocoryneum* sinense is morphologically similar to the members of *Cryptocoryneum* in having cheiroid, septate conidia, and conidial arms developed downward from the cap cells (Talbot, 1952; Kirk, 1983; Hashimoto et al., 2016; Boonmee et al., 2021). Based on the key to species of *Cryptocoryneum* provided by Hashimoto et al. (2016), *C. sinense* is easily distinguished from other *Cryptocoryneum* species. In the phylogenetic analysis, *C. sinense* clustered with *C. rosae* with 100% ML and 1.00 PP support (Figure 3.8). 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 rpb2 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. Based on morphological and phylogenetic evidence, we introduce *C. sinense* as a new species, which is the first species of *Cryptocoryneum* discovered from freshwater habitat.



Note a Colonies on the natural substrate. b–f Conidia. g Germinated conidium. h, i Culture on PDA. Scale bars: b–g = 20 μm.

Figure 3.7 *Cryptocoryneum sinense* (HKAS 131841, holotype)



Note 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 rpb2). *Aquasubmersa japonica* (MAFF 24218 and MAFF 24219) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Figure 3.8 Phylogenetic tree of *Hermatomycetaceae* and *Cryptocoryneaceae*

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

Notes: *Hermatomycetaceae* was first 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). So far, only asexual morphs have been reported, and they 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)

Notes: *Hermatomyces* was established by Spegazzini (1910) to accommodate *H. tucumanensis*. It's 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 countries, mainly from Thailand in Asia (Doilom et al., 2016; 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 the 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; de Silva et al., 2022).

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

Fungal Names number: FN 571861; Figure 3.9

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

Holotype: HKAS 132064.

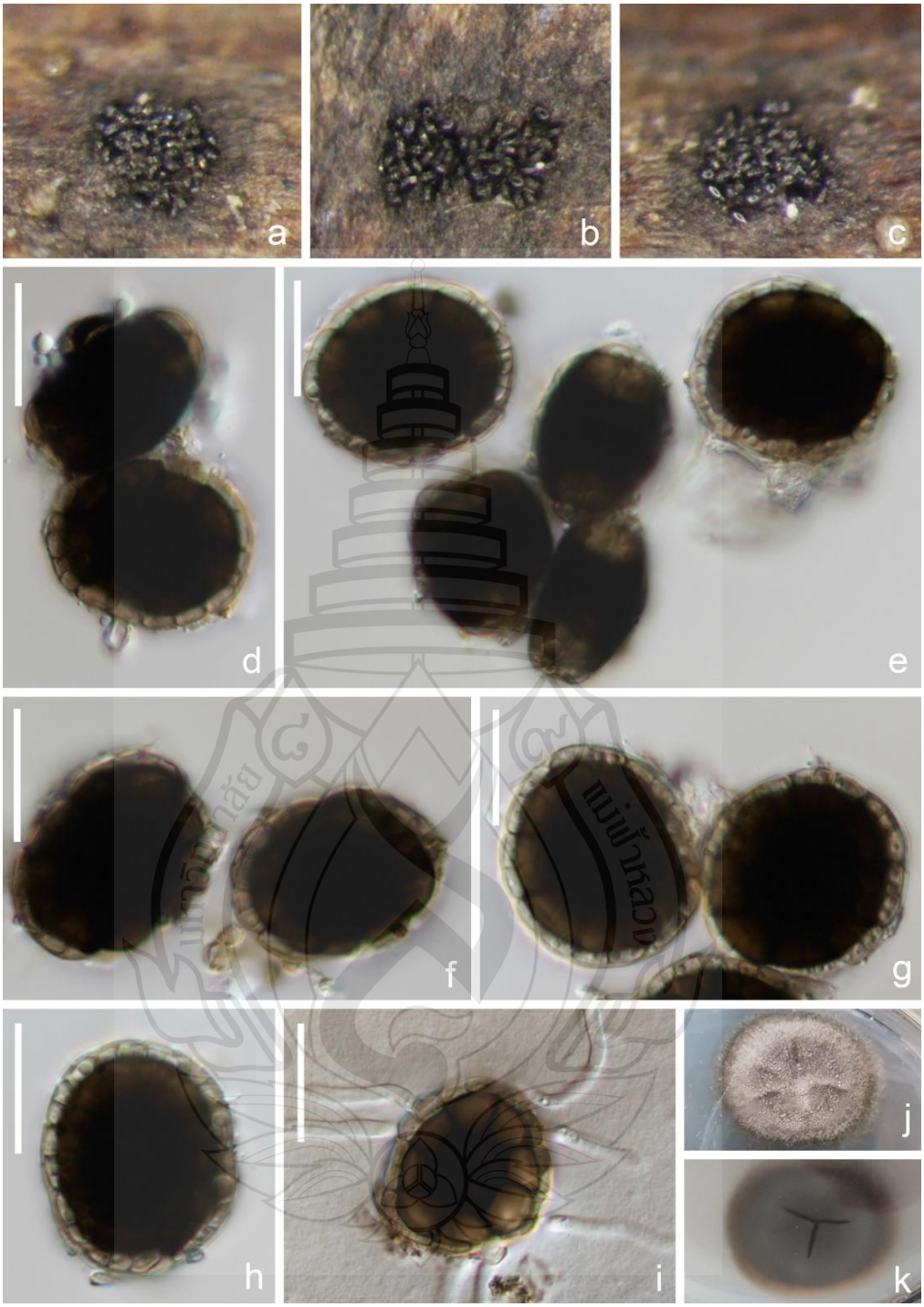
Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, superficial, scattered, conspicuous, glistening, flattened, brown to black. *Mycelium* mostly

immersed, consisting of branched, septate, smooth, thin-walled, pale brown to brown hyphae. *Conidiophores* micronematous, mononematous, cylindrical, erect, 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.

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 gray-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.

Notes: In the phylogenetic analysis, *Hermatomyces hongheensis* clustered with *H. sphaericoides*, *H. verrucosus* and *H. constrictus* in a distinct clade within *Hermatomyces* (Figure 3.10). 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 candida 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.



Note 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.

Figure 3.9 *Hermatomyces hongheensis* (HKAS 132064, holotype)

Dictyosporiaceae Boonmee & K.D. Hyde

Notes: *Dictyosporiaceae* was established by Boonmee et al. (2016) to accommodate a monophyletic group with cheiroid or digitate conidia, based on morphological and multigene phylogenetic evidence. Members of *Dictyosporiaceae* grow primarily as saprophytes on decaying wood and plant debris in terrestrial and freshwater habitats (Boonmee et al., 2016). *Dictyosporiaceae* is mainly known as the asexual morphs, which is mainly characterized by cheiroid, digitate, multi-septate, palmate, and/or dictyosporous conidia with or without appendages (Abdel-Aziz 2016b; Boonmee et al., 2016; Yang, Liu et al., 2018; Shen, Bao, Wanasinghe et al., 2022; Tian et al., 2022; Tennakoon et al., 2023). In less than five years, five new genera have been established in *Dictyosporiaceae* based on morphological and molecular sequence data, including two cheirosporous genera, *Paradictyocheirospora* and *Neodigitodesmium* (Crous et al., 2019; Piątek et al., 2020; Atienza et al., 2021; Rajeshkumar et al., 2021; Tian et al., 2022). A recent phylogenetic analysis by Tian et al. (2022) showed that *Paradictyocheirospora* clustered in the *Digitodesmium* clade, and combined with morphological data, Paradictyocheirospora was reduced to a synonym under the *Digitodesmium*. Currently, more than 150 species in 20 genera are accepted in *Dictyosporiaceae*, with more than 1/5 of these species reported from freshwater habitats (Tennakoon et al., 2023).

Dictyocheirospora M.J. D'souza, Boonmee & K.D. Hyde

Notes: *Dictyocheirospora* was established by Boonmee et al. (2016) to accommodate species that produce cheiroid, non-complanate, cylindrical conidia, mostly with conidial arms closely gathered together at the apex, with *D. rotunda* as the type species. At the same time, three new species and four species transferred from *Dictyosporium* and Cattanea were accepted into *Dictyocheirospora* (Boonmee et al., 2016). Subsequently, based on morphological and phylogenetic analyses, 21 species were added to *Dictyocheirospora*, including 17 new species and four species transferred from *Dictyosporium* (Wang et al., 2016; Tibpromma et al., 2018; Yang, Liu et al., 2018; Shen, Bao, Wanasinghe et al., 2022). Currently, 29 species are placed in *Dictyocheirospora*, and these species commonly occur as saprophytes and are reported on plant litter in terrestrial and freshwater habitats, 18 of which have been reported in

freshwater habitats (Boonmee et al., 2016; Wang et al., 2016; Yang, Liu et al., 2018; Shen, Bao, Wanasinghe et al., 2022; Tennakoon et al., 2023; Shu et al., 2024).

Dictyocheirospora multiappendiculata H.W. Shen & Z.L. Luo, ***sp. nov.***

MycoBank number: MB 846014; Figure 3.10

Etymology: "multiappendiculata" refers to the conidia of this species containing multiple appendages.

Holotype: HKAS 122866.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate punctiform, sporodochial, scattered, brown. Mycelium composed immersed or partly superficial, pale brown, septate, smooth, thin-walled, branched hyphae. *Conidiophores* micronematous, mononematous, septate, cylindrical, pale brown, smooth, thin-walled. *Conidiogenous cells* (10–)11–18(–20) × (–3)4–8(–10) ($\bar{x}$ = 14 × 6 μm, n = 20) μm holoblastic, cylindrical to subglobose, hyaline to pale brown, smooth, thin-walled, easy to break. *Conidia* (50–)55–62(–68) × (–16)19–22(–24) μm ($\bar{x}$ = 59 × 20 μm, n = 50), solitary, cheiroid, cylindrical, pale brown, non-complanate, smooth, closely appressed, composed of (5–)7 rows of cells, euseptate, each row with 9–13 cells, slightly bent inward at the apex, straight or slightly curved arms are inserted in different planes, with 1–5(–6) hyaline, globose to subglobose subapical appendages, appendages thin, easy to rupture and shrink. Conidial secession schizolytic.

Culture characteristics: Conidia germinating on PDA within 12 h and germ tubes produced at the basal cell. Colonies on PDA, reaching about 4 cm in 1 month at room temperature. Mycelium loose, flocculent, smooth-edged, white to light yellow on the surface, in reverse pale brown to brown.

Material examined: China, Yunnan Province, Yuxi City, on submerged decaying wood in Fuxian lake, 24°30′33" N, 102°54′36" E, (1700 m), 10 July 2021, H.W. Shen and Q.X. Yang, L-963 (HKAS 122866, holotype), ex-type culture (KUNCC 22-10734); *ibid.*, 24°37′14" N 102°51′03" E, (1700 m), 12 July 2021, Y.K. Jiang and S. Luan, L-987 (HKAS 122870), living culture (KUNCC 22–10736).

Notes: *Dictyocheirospora multiappendiculata* shares similar morphological characters to other *Dictyocheirospora* species in having cheiroid, cylindrical, euseptate, non-complanate conidia, and densely clustered at the apex. The globose to subglobose

apical or subapical appendages are similar to *D. hydei*, *D. indica*, *D. musae*, *D. nabanheensis*, *D. pseudomusae*, *D. suae* and *D. tetraploides*. However, *D. multiappendiculata* is distinguished from these species by the numbers of appendages. In the phylogenetic analysis, *D. multiappendiculata* and *D. suae* formed a sister lineage with 95% ML and 1.00 PP, support (Figure 3.11). The nucleotide comparison of ITS genes of *D. multiappendiculata* and D. suae revealed 11 bp (11/469 bp, 2.35%) nucleotide differences. Following Jeewon and Hyde (2016) recommendations in establishing species boundaries and new taxa among fungi, we introduce *D. multiappendiculata* as a new species.

Note a–c Colonies on the substratum. d Conidiomata and conidia. e Conidiophores with conidiogenous cells. f–h Conidiogenous cells, conidia and appendages. i, j Conidia with appendages. k Germinating conidium. l, m Culture colonies on PDA. Scale bars: d = 30 μm, e–k = 20 μm, l,m = 1 cm.

Figure 3.10 *Dictyocheirospora multiappendiculata* (HKAS 122866, holotype)

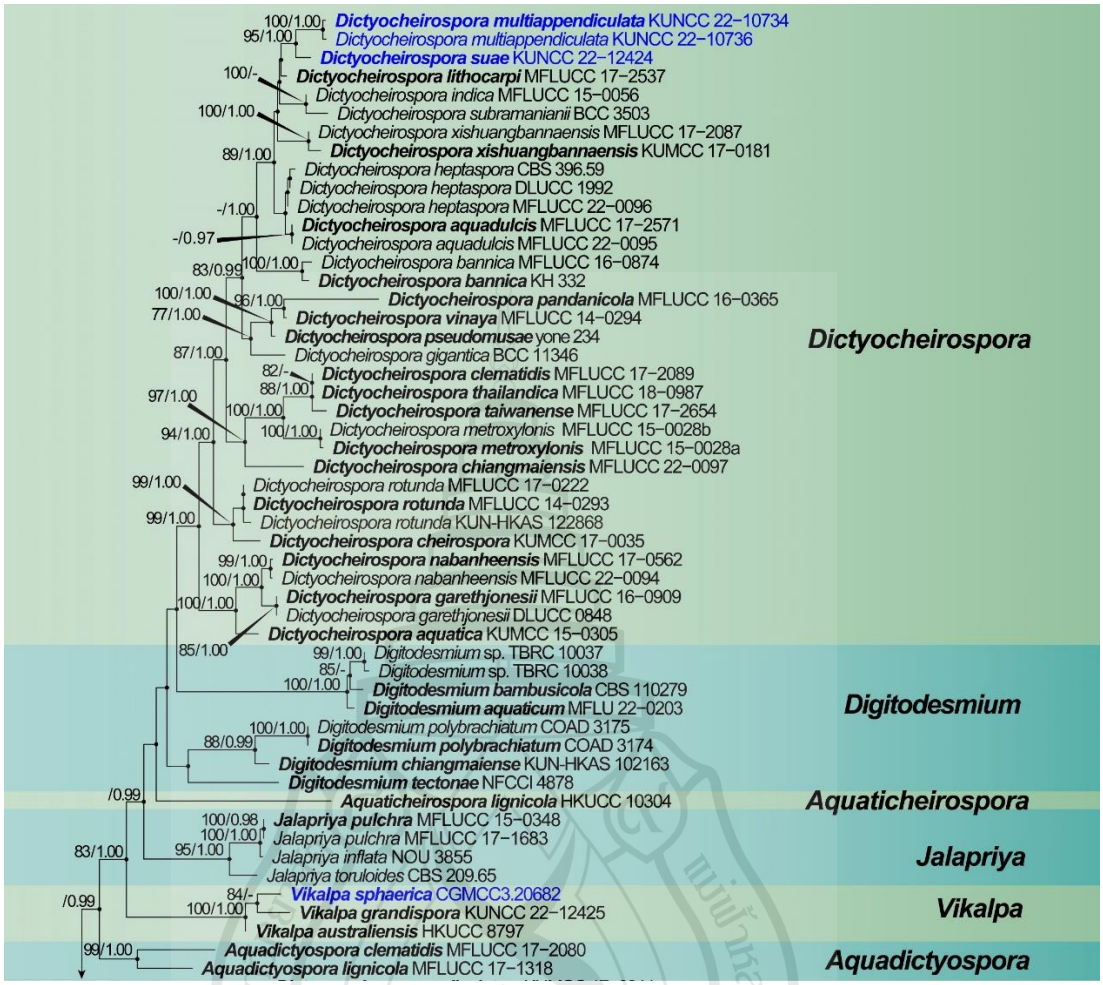
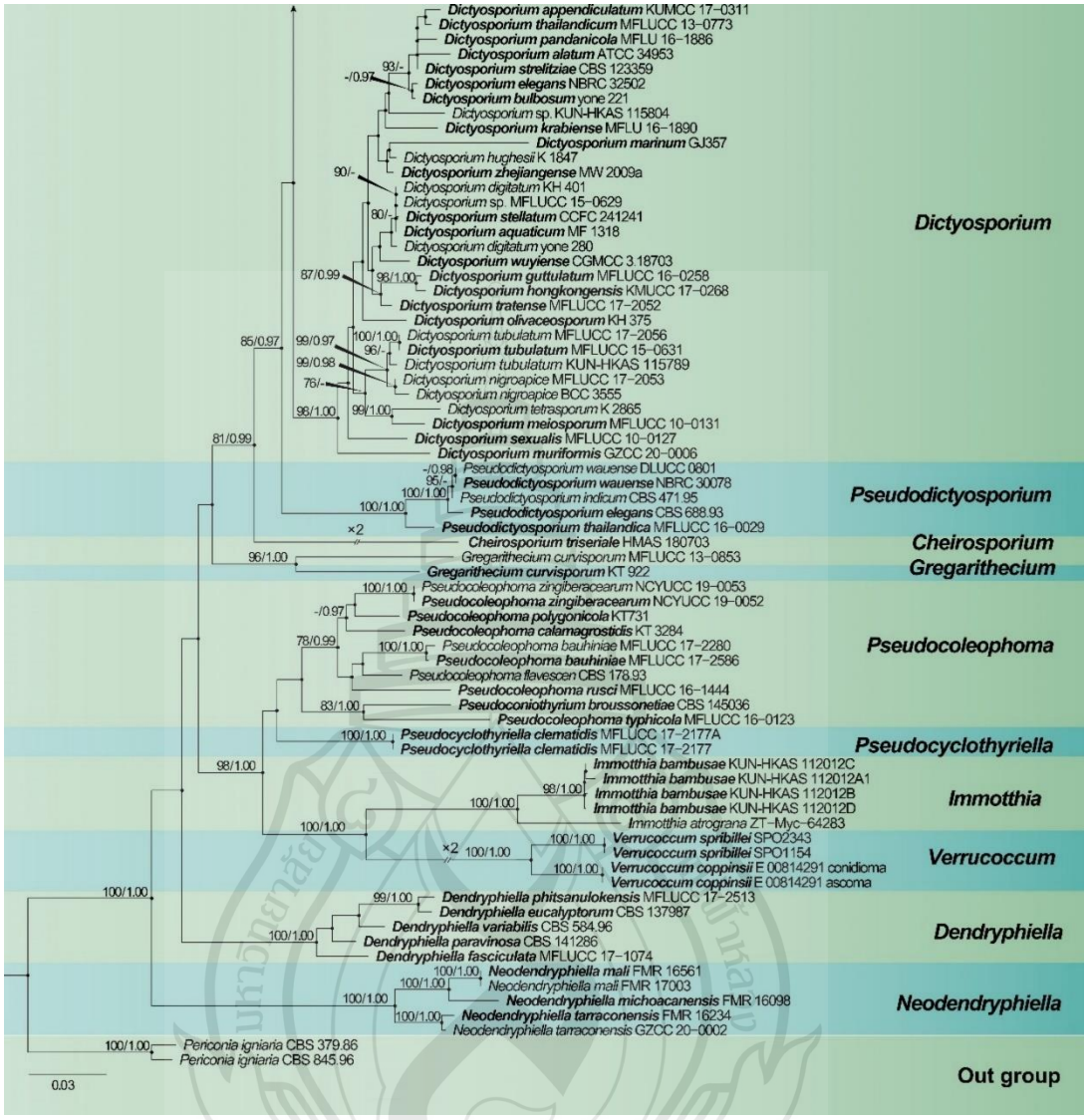


Figure 3.11 Phylogenetic tree of *Dictyosporiaceae*



Note Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef*1-αsequence dataset representing *Dictyosporiaceae*. 124 strains are included in the combined analyses which comprise 4041 characters including gaps. *Periconia igniaria* (CBS 379.86 and CBS 845.96) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Figure 3.11 (continued)

Dictyocheirospora suae H.W. Shen & Z.L. Luo, ***sp. nov.***

MycoBank number: MB 846010; Figure 3.12

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

Holotype: HKAS 121703.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate punctiform, sporodochial, scattered, brown. *Mycelium* composed immersed or partly superficial, brown to dark brown, septate, smooth, thin-walled, branched hyphae. *Conidiophores* micronematous, mononematous, septate, cylindrical, pale brown, smooth, thin-walled. *Conidiogenous cells* holoblastic, cylindrical, septate, hyaline to pale brown, smooth, thin-walled, sometimes lack conidiogenous cells. *Conidia* (65–)72–79 × (17–)20–25(–29) μm ($\bar{x}$ = 76 × 23 μm, n = 30), solitary, cheiroid, ellipsoid to cylindrical, not complanate, brown, composed of 5–7 rows of cells, unseparated, euseptate, tightly clustered at the apex of rows, each row with 12–15 cells, with globose to subglobose apical appendages. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA within 12 h and germ tubes produced at the base of cells. Colonies on PDA, reaching about 4 cm in one month at room temperature. Mycelium loose, flocculent, white with flaxen spots on the forward.

Material examined: China, Yunnan Province, Dali City, Erhai Lake, 25°49'04" N, 100°08'46" E, (1790 m), on submerged decaying wood, 1 April 2021, S.P. Huang, 3EH GSC 8-6-2 (HKAS 121703, holotype), ex-type culture (KUNCC 22–12424).

Notes: Phylogenetic analysis showed that *Dictyocheirospora* suae clusters as a sister taxon to *D. multiappendiculata* with 95% ML and 1.00 PP support (Figure 3.11). *Dictyocheirospora suae* and *D. multiappendiculata* shares similar morphology in having solitary, cheiroid, ellipsoid to cylindrical, not complanate conidia with apical appendages. However, *D. suae* has larger conidia (72–79 × 20–25 μm *vs.* 36–46 × 13–18 μm), and more cells in each row (12–15 *vs.* 9–13). In addition, the conidia of *D. multiappendiculata* have more appendages than *D. suae*. Comparison of the ITS sequences of *D. suae* and *D. multiappendiculata* showed 2.35% (11/469 bp) nucleotide differences.

Note a, b Colonies on the substratum. c Conidiomata. d, e Conidiophores and conidiogenous cells. f Conidia. g Conidiogenous cells with conidia. h Conidia with appendages. i Germinating conidium. j Culture colonies on PDA from above and from below. Scale bars: a = 200 μm, b = 100 μm, c = 30 μm, d–i = 20 μm, j = 2 cm.

Figure 3.12 *Dictyocheirospora suae* (HKAS 121703, holotype)

Vikalpa D'souza, Boonmee, Bhat & K.D. Hyde

Notes: *Vikalpa* was introduced by Boonmee et al. (2016) based on morphological characteristics and multi-gene phylogenetic analysis, with *Vikalpa* australiensis (B. Sutton) D'souza, Boonmee & K.D. Hyde as the type species (Boonmee et al., 2016). *Vikalpa* is a special group of cheirosporous hyphomycete, mainly characterized by euseptate conidia, with three rows of cells in different planes (Boonmee et al., 2016). Based on specific morphological and phylogenetic evidence, *Vikalpa australiensis* (*Dictyosporium australiense*), *V. freycinetiae* (*D. freycinetiae*) and *V. micronesiaca* (*D. micronesiacum*) were transferred from *Dictyosporium* to *Vikalpa* by Boonmee et al. (2016). Currently, the genus includes six species that are saprophytic on wood and decaying leaves from freshwater and terrestrial habitats (Boonmee et al., 2016).

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

MycoBank number: MB 846016; Figure 3.13

Etymology: "sphaerica" refers to the spherical appendages.

Holotype: HKAS 115805.

Saprobic on submerged decaying wood in freshwater habitat. **Sexual morph**: Undetermined. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate, punctiform, sporodochial, scattered, dark brown. Mycelium composed of immersed or partly superficial, septate, branched, hyaline to pale brown hyphae. *Conidiophores* micronematous, mononematous, septate, cylindrical, unbranched, hyaline to pale brown, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous* cells 4–7(–9) × (2–)3–4(–5) ($\bar{x}$ = 5 × 4 μm, n = 15), holoblastic, cylindrical, sometimes flat at the base, septate, hyaline to pale brown, smooth-walled. *Conidia* (23–)26–30(–34) × (11–)16–19(–20) μm ($\bar{x}$ = 28 × 17 μm, n = 50), solitary, cheiroid, pale brown to brown, not complanate, usually composed of 3–4 rows, rarely with 3 rows, rows separated from each other, 5–9 cells in each row, euseptate, irregular, constricted at the septa, guttulate, with hyaline, globose to subglobose appendages (6–)7–8(–9) × (5–)7–8(–9) μm ($\bar{x}$ = 8 × 8 μm, n = 50) at the apical cells, a few rows have either no appendages or fallen off. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA within 12 h and germ tubes produced at both ends. Colony growth on PDA; growth is slow, reaching about

4 cm in 1 month at room temperature. Mycelium loose, flocculent, smooth edged, brownish-red on the forward, orange on the edge and gray in the middle on the reverse side.

Material examined: China, Yunnan Province, Lijiang City, Luguhu Lake, 27°42′11″ N, 100°48′18″ E (2700 m), on submerged decaying wood in a small stream, 04 March 2021, Z.Q. Zhang and L. Sha, L185 (HKAS 115805, holotype), ex-type cultures (CGMCC 3.20682 = KUNCC 21–10711).

Notes: Phylogenetic analysis placed our new taxon, *Vikalpa sphaerica* (CGMCC 3.20682) close to *V. grandispora* with 84% ML support (Figure 3.11). Morphologically, *V. sphaerica* resembles *V. grandispora*, *V. australiensis* and *V. freycinetiae* in having solitary, cheiroid conidia with apical appendages (Sutton, 1985). However, *V. grandispora* have longer conidia (38–49 *vs.* 26–30) and more cells in each row (9–12 *vs.* 5–9). The rows of *V sphaerica* are separated from each other, and have less cells in each row than *V. australiensis* (5–9 *vs.* 7–11), *V. freycinetiae* have a greater number of cells (9–13 *vs.* 5–9) that are larger (31–43 μm *vs.* 26–30 μm) than *V. sphaerica* (McKenzie, 2008). Therefore, *V. sphaerica* is introduced as a new species, based on morphological and phylogenetic analysis.

Note a, b Colonies on the substratum. c, d Conidiophores and conidiogenous cells. e Conidia. f–l Conidia with appendages. m Germinating conidium. n Culture colonies on PDA. Scale bars: a, b = 200 μm, c–m = 10 μm, n = 1 cm.

Figure 3.13 *Vikalpa sphaerica* (HKAS 115805, holotype)

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

Fungal Names number: FN 571593; Figure 3.14

Etymology: "dujuanhuensis" refers to Dujuanhu Lake, in Yunnan Province, where this fungus was collected.

Holotype: HKAS 125817.

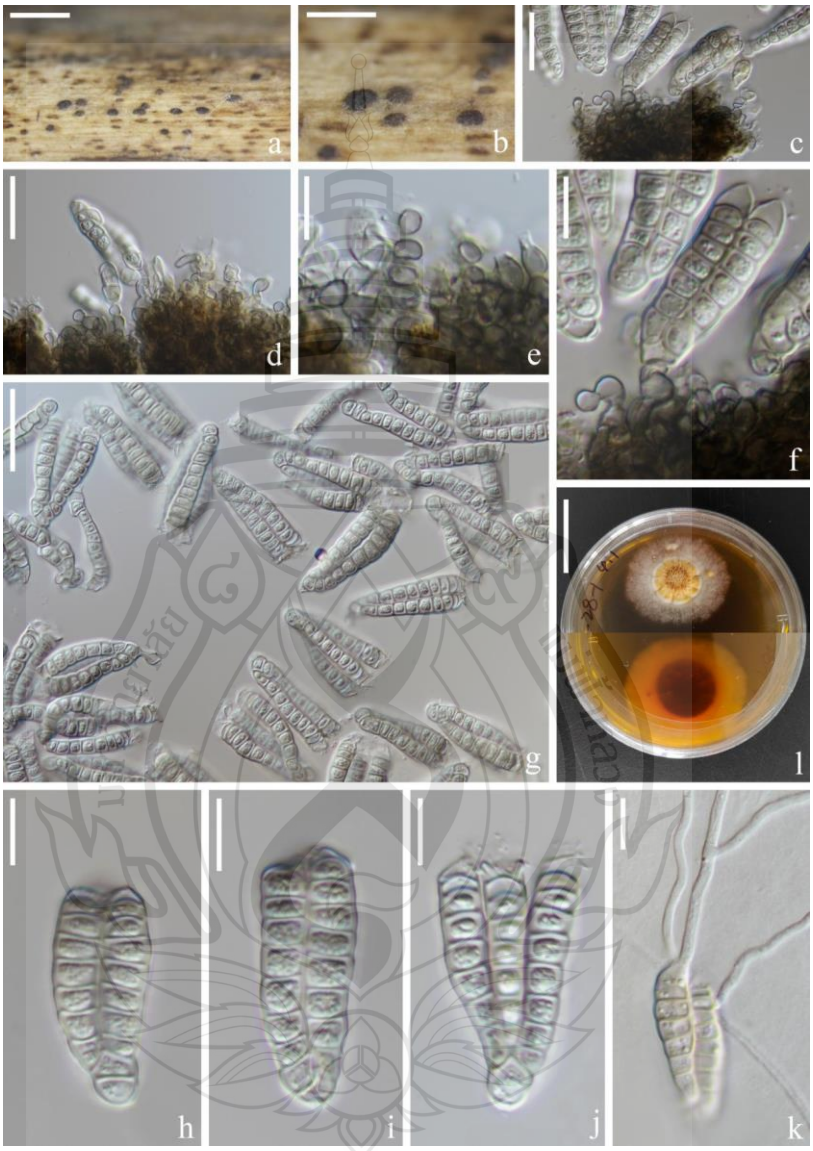
Saprobic on submerged decaying wood in a plateau freshwater lake habitat. **Sexual morph**: Undetermined. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate, punctiform, sporodochial, scattered, dark brown. *Mycelium* composed of immersed or partly superficial, septate, branched, hyaline to pale brown hyphae. *Conidiophores* micronematous, mononematous, septate, cylindrical, unbranched, hyaline to pale brown, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, cylindrical, subglobose, sometimes flat at the base, septate, hyaline to pale brown, smooth-walled. *Conidia* (30–)34–41(–43) × (11–)12–16(–20) μm ($\bar{x}$ = 38 × 14 μm, n = 50), solitary, cheiroid, pale brown to brown, consisting of three rows of cells in different planes, 8–10 cells in each row, euseptate, irregular, constricted at the septa, guttulate, each row 6–8(–9) μm ($\bar{x}$ = 7 μm, n = 50) wide, with or without transparent thin gelatinous appendages.

Culture characteristics: Conidia germinating on PDA within 12 h and germ tubes produced at ends. Colony growth on PDA; reaching about 2.5–3 cm in 45 days at room temperature. Mycelium papillary in the middle part, dense, creamy yellow, brown to reddish-brown, sparse, white at edge; pale cream yellow on the edge and dark reddish brown in the middle on the reverse side.

Material examined: China, Yunnan Province, Puer City, Jingdong Yi Autonomous County, Dujuan Lake, 24°32′32″ N, 101°01′38″ E, on submerged decaying wood, 25 February 2022, H.W. Shen, YJ 26-28-1 (HKAS 125817, holotype), ex-type living cultures (CGMCC 3.24268 = KUNCC 22–12670).

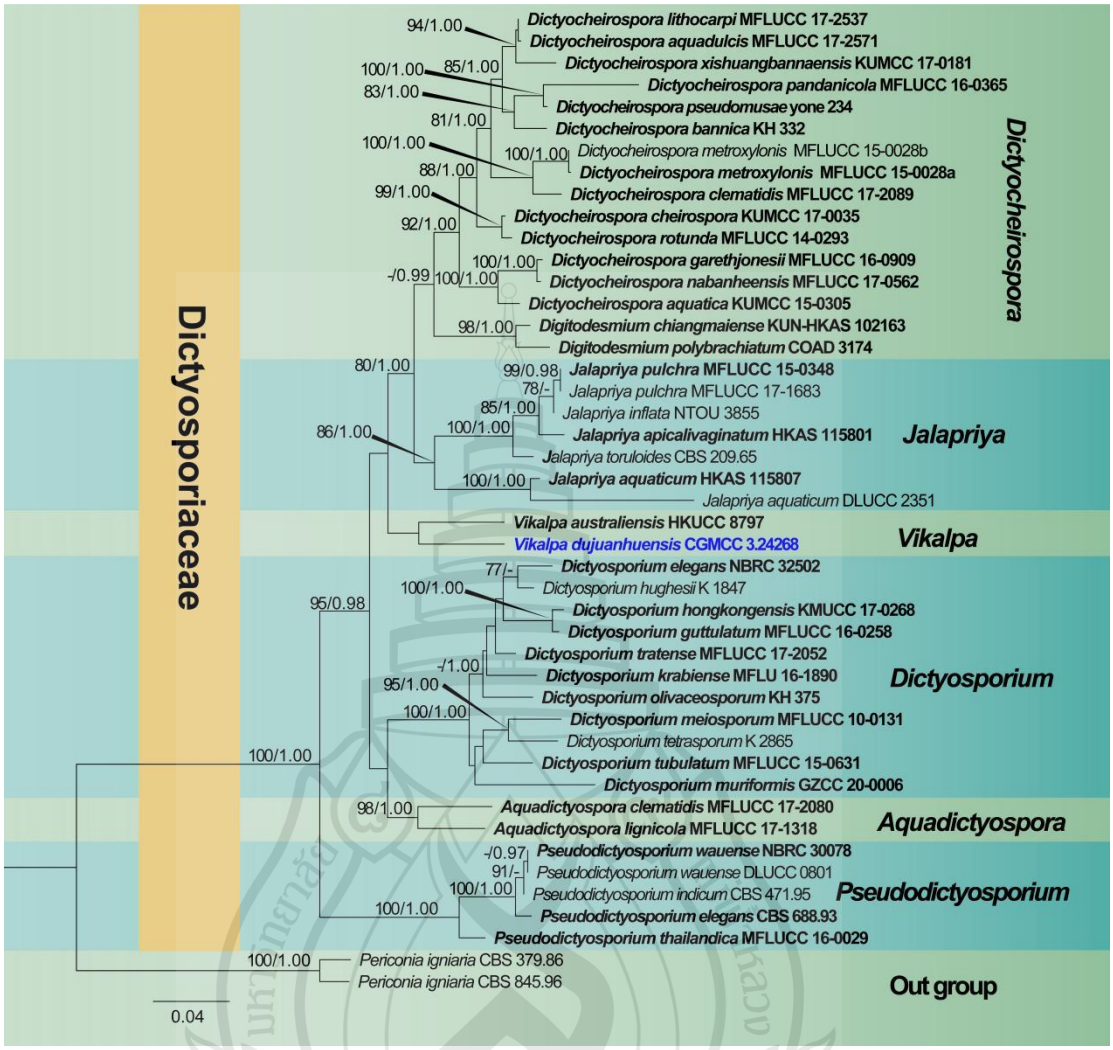
Notes: Phylogenetic analysis showed that *Vikalpa dujuanhuensis* cluster with *V. australiensis* with low support (Figure 3.15). Morphologically, *V. dujuanhuensis* fit with *Vikalpa* species in having euseptate conidia, with three rows of cells in different planes. However, *V. dujuanhuensis* have longer conidia than *V. lignicola* (34–41 μm *vs.* 25–40.5 μm) and *V. micronesiaca* (34–41 μm *vs.* 20–30 μm) (Boonmee et al., 2016). *V. dujuanhuensis* can be distinguished from *V. freycinetiae* by having lower number of

cells per row (8–10 cells *vs.* 9–13 cells) (McKenzie, 2008). Therefore, *V. dujuanhuensis* is introduced as a new species from freshwater habitat, based on morphological and phylogenetic analysis.



Note a, b Colonies on the substratum. c, d Conidiophores, conidiogenous cells and conidia. e Conidiogenous cells. f Conidiogenous cells with conidia. g–j Conidia. k Germinating conidium. l Culture on PDA. Scale bars: a = 1000 μm; b = 500 μm, c, d = 20 μm, g = 30 μm, e, f, h–k = 10 μm; l = 2 cm.

Figure 3.14 *Vikalpa dujuanhuensis* (HKAS 125817, holotype)



Note Phylogenetic tree based on RAxML analyses of combined ITS, LSU, SSU, and TEF sequence data. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Figure 3.15 Phylogenetic tree for *Vikalpa*

Lentitheciaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde

Notes: *Lentitheciaceae* was introduced by Zhang, Schoch et al. (2009) to accommodate those lentitheciaceous taxa, based on morphological characters and molecular phylogenetic analysis. *Lentitheciaceae* contains a highly diverse group of

species with diverse ascospore morphologies, such as: narrow to broad fusiform, muriform, ellipsoidal, filiform, and fasciculate, as well as varying ascospore colours (Wanasinghe et al., 2014; Knapp et al., 2015; Phookamsak, Manamgoda et al., 2015; Calabon, Jones, Hyde et al., 2021; Liu et al., 2021; Yang, Zhang et al., 2022; Shen et al., 2023; Yang et al., 2023). Based on specific morphological characteristics combined with molecular sequence data, 19 genera were established into *Lentitheciaceae* to accommodate these species, with most of the species reported in freshwater habitats concentrated in *Halobyssothecium*, *Lentithecium*, *Paralentithecium*, *Setoseptoria*, and *Tingoldiago* (Shen et al., 2023).

Halobyssothecium Dayar., E.B.G. Jones & K.D. Hyde

Notes: *Halobyssothecium* was introduced by Dayarathne et al. (2018) with *H. obiones* (M.E. Barr) Dayarathne, E.B.G. Jones & K.D. Hyde as the type species, this genus is proposed to accommodate taxa are saprobic on salt marsh halophytes and submerged decaying wood in aquatic habitats (Dayarathne et al., 2018). This genus includes both sexual and asexual morph, the sexual morph are characterized by globose to subglobose or ellipsoidal, carbonaceous, dark brown to black, ostiolate ascomata, pseudoparaphyses septate, branched, ascospores overlapping uniseriate to biseriately, clavate, ellipsoid, versicolored, end cells hyaline, central cells brown to dark brown, 1–3-septate, constricted at the septa, guttulate, slightly curved, lacking gelatinous sheath or appendages (Dayarathne et al., 2018; Devadatha et al., 2020; Calabon, Jones, Hyde et al., 2021). Calabon, Jones, Hyde et al. (2021) revision the taxa of *Halobyssothecium* and *Lentithecium* based multi-gene phylogenetic analyses of the combined LSU, SSU, ITS and *tef*1-α, five *Lentithecium* species were placed in *Halobyssothecium*. Subsequently, two additional new species from freshwater habitats were introduced, and currently thirteen species have been accepted into *Halobyssothecium*, ten of which have been reported in freshwater habitats (Calabon, Jones, Hyde et al., 2021; Shen et al., 2023; Yang et al., 2023).

Halobyssothecium aquifusiforme J. Yang, Jian K. Liu & K.D. Hyde, Fungal Diversity 119: 39 (2023).

I*ndex Fungorum number*: IF559450; *Facesoffungi number*: FoF12783; Figure 3.16

Saprobic on submerged decaying wood in a freshwater lake. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 354–382 μm high, 328–366 μm wide, immersed, clustered, sometimes solitary, scattered, subglobose or ellipsoidal, dark brown to black, carbonaceous, uniloculate, ostiolate. *Ostiolar* neck central, 86–114 μm long, 138–168 μm wide, papillate, rounded, short, dark brown, composed of several layers of pseudoparenchymatous cells. *Peridium* 22–35 μm thick, composed of several layers of pseudoparenchymatous cells, an outer layer composed of black cells, arranged in a textura angularis, inner layer composed of hyaline, flattened cells, arranged in a textura angularis. *Pseudoparaphyses* about 2 μm wide, branched, septate, hyaline, filamentous, anastomosing above the asci. *Asci* 97–129 × 13–16 μm ($\bar{x}$ = 113 × 14 μm, n = 20) μm, 8-spored, clavate to subcylindrical, bitunicate, fissitunicate, apex rounded, short pedicellate, with an ocular chamber. *Ascospores* (20–) 24–27 × 7–8 μm ($\bar{x}$ = 25 × 8 μm, n = 40), overlapping, uniseriate to biseriate, central cells are brown to dark brown, 1-septate when young, 3-septate when mature, constricted at the septa, slightly curved, fusiform, guttulate, conical and narrowly rounded at the ends, one cell on the central septum side is swollen, lacking gelatinous sheaths or appendages.

Culture characteristics: Ascospore germinating on PDA within 12 h. Colonies on PDA reaching 3 cm diameter in 6 weeks at room temperature. Mycelium superficial, initially white, later becoming brown to black, with pale brown dense aerial mycelium on the surface, mastoid, marginal mycelium smooth, sparse, brown to black; from below, light brown at the center, dark brown at the margin.

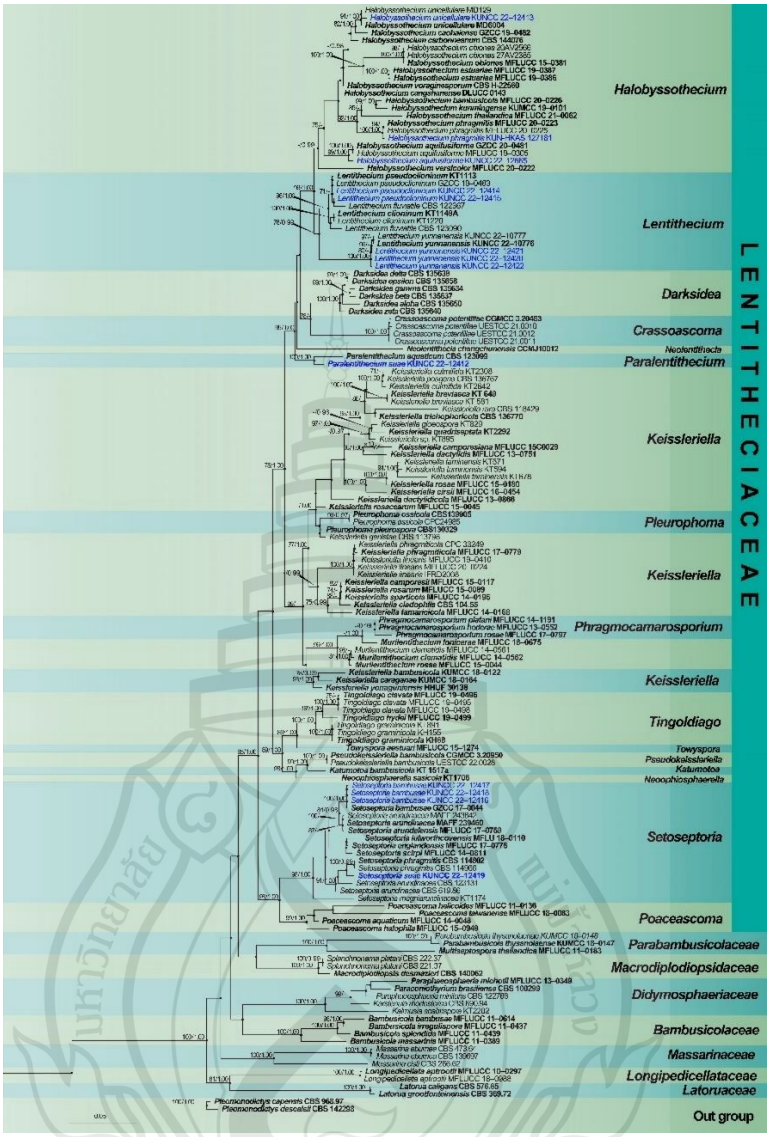
Material examined: China, Yunnan Province, Dali City, Eryuan County, Cibihu Lake, 26°09′59″ N, 99°55′27″ E (2050 m), on unknown submerged decaying wood, 21 July 2021, S.P. Huang and L.L. Li, L788 (HKAS 124599), living cultures (KUNCC 22–12665).

Notes: The phylogenetic analysis showed that our new strain, KUNCC 22–12665 clustered sister to *Halobyssothecium aquifusiforme* (GZCC 20–0481 and MFLUCC 19–0305) with 99% ML and 1.00 PP supports (Figure 3.17). Our species is similar to *H. aquifusiforme* in having immersed, subglobose ascomata, and fusiform, guttulate, septate ascospores which are constricted at the septum (Yang et al., 2023). We, therefore, identified our new collection as *H. aquifusiforme* and provided detailed descriptions and illustrations for it. *Halobyssothecium aquifusiforme* is an aquatic

species that was collected on submerged decaying wood in a freshwater stream in Guizhou, China. Our two new collections were collected from a plateau lake in Yunnan.

Note a, b Appearance of ascomata on the host. c, d Sections of ascomata. e Ostiole. f, g Section of peridium. h Pseudoparaphyses. i–n Asci. o–u Ascospores. v Germinated conidium. w, x Colony on MEA. Scale bar: c, d = 150 μm, e, i–n = 30 μm, f–h = 20 μm, o–v = 10 μm.

Figure 3.16 *Halobyssothecium aquifusiforme* (HKAS 1124599)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, and *tef*1-α sequence dataset representing *Lentitheciaceae*. 147 strains are included in the combined analyses which comprise 3777 characters (LSU: 1285 bp; SSU: 1021 bp; ITS: 539 bp; *tef*1-α: 932 bp, including gaps). The tree is rooted to *Pleomonodictys capensis* (CBS 968.97) and *P. descalsii* (CBS 142298). Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. New species are indicated in red bold, new strains are indicated in blue, and type strains are in black bold.

Figure 3.17 Phylogenetic tree for *Lentitheciaceae*

Halobyssothecium phragmitis M.S. Calabon, E.B.G. Jones, S. Tibell & K.D. Hyde, Mycological Progress 20: 711 (2021)

Index Fungorum number: IF558090; *Facesoffungi number*: FoF 09431; Figure 3.18

Saprobic on submerged decaying wood in a freshwater lake. **Asexual morph**: Coelomycetes (Calabon et al., 2021). **Sexual morph**: *Ascomata* 529–566 μm high, 545–691 μm wide, immersed or semi-immersed, solitary to gregarious, scattered, subglobose or ellipsoidal, dark brown, subcarbonaceous or coriaceous, uniloculate, with indistinct ostiolate. *Ostiolar* neck 172–265 μm high, 184–320 μm wide, central, papillate, rounded, short, dark brown, composed of several layers of pseudoparenchymatous cells. *Peridium* 26–77 μm thick, composed of several layers of pseudoparenchymatous cells, an outer layer composed of brown cells, arranged in a textura angularis and textura globulosa, and an inner layer composed of hyaline, flattened cells, arranged in a textura angularis. *Pseudoparaphyses* 2–3 μm wide, septate, hyaline, filiform, branched, anastomosing above the asci. *Asci* (102–)111–130(–137) × 10–12 μm ($\bar{x}$ = 121 × 11 μm, n = 30), 8-spored, clavate to subcylindrical, bitunicate, fissitunicate, short pedicellate with an ocular chamber. *Ascospores* 22–27 × 5–6 μm ($\bar{x}$ = 25 × 6 μm, n = 40), overlapping, uniseriate to biseriate, fusiform with narrow ends, cells swollen nearly central septum and gradually narrow toward ends, slightly curved, pale brown to dark brown and lightening from central cells to the end cells, 1-septate when young, 5-septate when mature, and constricted at the septa, lacking gelatinous sheaths or appendages.

Material examined: China, Yunnan Province, Dali City, Eryuan County, Xihu Lake, 26°00′33″ N, 100°03′35″ E (1970 m), on unknown submerged decaying wood, 8 May 2021, S.P. Huang and L.L. Li, L783 (HKAS 127181).

Notes: *Halobyssothecium phragmitis* was introduced by Calabon et al. (2021), and only the asexual morph is known. This species was collected on *Phragmites* (*Poaceae*) culm in Europe. Phylogenetic analysis combined with ITS, LSU, SSU, and *tef*1-α sequence data showed that our new collection (HKAS 127181) clustered with two strains of *H. phragmitis* (MFLUCC 20–0223 and MFLUCC 20–0225). The comparison of ITS, LSU, SSU, and t*ef*1-α sequences between our new collection (HKAS 127181) and the ex-type of *H. phragmitis* (MFLUCC 20–0226) showed 8 bp,

1 bp, 3 bp, and 3 bp differences, respectively. Morphologically, our new collection is similar to other sexual members of *Halobyssothecium* in having immersed or semi-immersed, subglobose or ellipsoidal, dark brown, subcarbonaceous or coriaceous ascomata, clavate to subcylindrical, bitunicate asci and 3-septate, fusiform ascospores (Dayarathne et al., 2018; Devadatha et al., 2020; Calabon, Jones, Hyde et al., 2021; Yang et al., 2023). Based on phylogenetic analysis and morphological evidence, we identified our new collection as *H. phragmitis*, and described its asexual morph. This is the first report of this species in China (Calabon, Jones, Hyde et al., 2021).

Note a, b Appearance of ascomata on the host. c, d Sections of ascomata. e, f Section of peridium, g Pseudoparaphyses. h, i Asci. j–n Ascospores. Scale bar: c, d = 200 µm, e–g = 20 µm, h, i = 40 µm, j–n = 10 µm.

Figure 3.18 *Halobyssothecium phragmitis* (HKAS 124600, new geographic record)

Halobyssothecium unicellulare (Abdel-Aziz) M.S. Calabon, K.D. Hyde & E.B.G. Jones, Mycological Progress 20: 715 (2021)

Index Fungorum number: IF558094; *Facesoffungi number*: FoF 09437; Figure 3.19

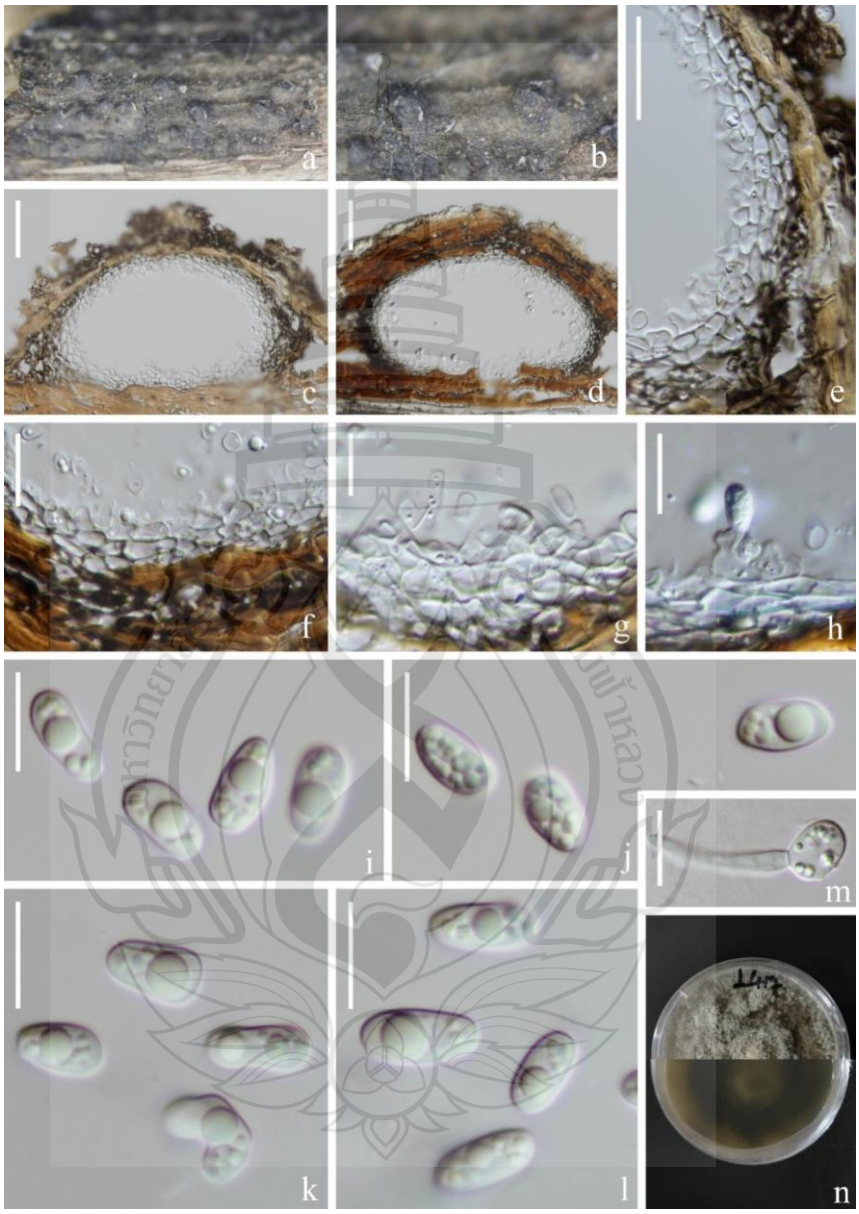
Saprobic on submerged decaying wood in a freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetes. *Conidiomata* 135–178 μm high, 205–242 μm wide, immersed to semi-immersed, most immersed, clustered, sometimes solitary, scattered, subglobose or ellipsoidal, uniloculate, dark brown to black, carbonaceous, short ostiolate, papillate, rounded. *Conidiomatal* walls 14–31 μm thick, composed of several layers of hyaline to black–brown cells of textura angularis. *Conidiophores* are reduced to conidiogenous cells. *Conidiogenous cells* 5–12 × 3–5 μm ($\bar{x}$ = 8 × 4 μm, n = 30), hyaline, thin-walled, holoblastic, smooth, subglobose to pear-shaped, swollen at the base, sometimes one conidiogenous cell producing two conidia. *Conidia* 9–11 × 4–5 μm ($\bar{x}$ = 10 × 5 μm, n = 60), subglobose, ovate, clavate, ellipsoid, allantoid or irregular, hyaline, aseptate, several small to one big guttulate, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 12 h and germ tubes produced from one end of the conidia. Colonies on PDA, circular, reaching 5 cm in one month at room temperature, flat surface, pale brown to brown in PDA medium. Mycelium superficial, white to brown, hairy, effuse with wavy edge, dense, circular, raised, undulate to filiform with age; reverse light brown in the middle, with a dark brown deposit on the outside.

Material examined: China, Yunnan Province, Dali City, Eryuan County, Xihu Lake, 26°00′33″ N, 100°03′35″ E (1970 m), on unknown submerged decaying wood, 8 May 2021, S.P. Huang and L.L. Li, L412 (HKAS 124589), living culture, KUNCC 22–12413.

Notes: The multigene phylogenetic analysis showed that our new collection (KUNCC 22–12413) clustered with the ex-type strain of *Halobyssothecium unicellulare* (MD 6004) with 91% ML and 1.00 PP support (Figure 3.17). Morphologically, our new collection fits well with the original description of *H. unicellulare*. The nucleotide comparison of LSU and SSU sequence data between our new collection (KUNCC 22–12413) and *H. unicellulare* (MD 6004) revealed 2 bp

(including one gap) and 1 bp (including one gap) differences, respectively. We therefore identified it as *H. unicellulare* and it was reported from China for the first time.



Note a, b Appearance of conidiomata on the host. c, d Sections of conidiomata. e, f Conidiomatal wall. g, h Developing conidia attach to conidiogenous cells. i–l Conidia. m Germinated conidium. n Colony on PDA. Scale bar: c, d = 40 μm, e, f = 20 μm, g–m = 10 μm.

Figure 3.19 *Halobyssothecium unicellulare* (HKAS 124589, new geographic record)

Lentithecium K.D. Hyde, J. Fourn. & Ying Zhang

Notes: *Lentithecium* was introduced by Zhang, Wang et al. (2009) to accommodate lignicolous species that havaing immersed to semi-immersed, globose to subglobose ascomata, a thin peridium, cellular pseudoparaphyses, short pedicellate asci and fusoid or filiform, subglobose, hyaline, brown, uni- to multi-septate ascospores, usually surrounded by a sheath (Zhang, Wang et al., 2009). Zhang, Wang et al. (2009) introduced one new species (*Lentithecium aquaticum*) and three new combinations in *Lentithecium* based on morphological characters and molecular phylogenetic analysis combined LSU, SSU and *rpb*2 gene. In recent studies, five taxa were transferred to *Halobyssothecium*, and one new species, *L. yunnanense* was introduced in *Lentithecium* (Calabon, Jones, Hyde et al., 2021; Lu, Dai et al., 2022). The genus currently contains five accepted species, three reported on submerged wood in freswater habitats (Tanaka et al., 2015; Shen et al., 2023; Yang et al., 2023).

Lentithecium pseudoclioninum Kaz. Tanaka & K. Hiray, Studies in Mycology 82: 99 (2015)

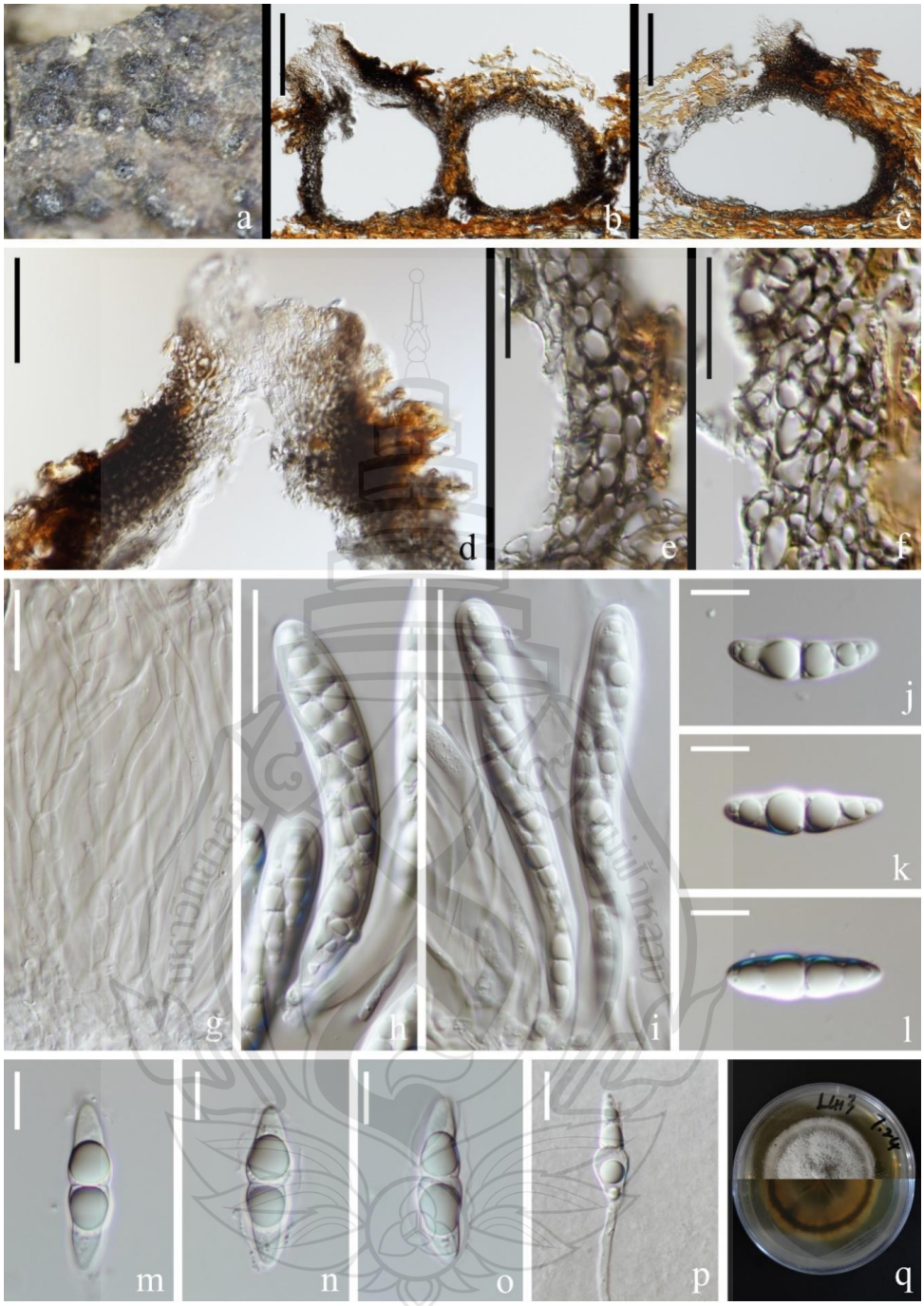
Index Fungorum number: IF811309; *Facesoffungi number*: FoF12785; Figure 3.20

Saprobic on submerged decaying wood in a freshwater lake. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 201–310 μm high, 227–274 μm wide, black, semi-immersed, gregarious, erumpent, globose or subglobose, uniloculate, ostiolate. *Ostiolar* neck central, papillate, 92–110 μm long, 100–107 μm wide. *Peridium* 20–32 μm, thick-walled, brown to dark brown cells, composing several layers of pseudoparenchymatous cells of textura angularis, outer layers heavily pigmented, inner layers hyaline to pale brown, flattened. *Pseudoparaphyses* 2–3 μm wide, filamentous, branched septate. *Asci* 98–118 × 14–16 μm ($\bar{x}$ = 108 × 15 μm, n = 30), 8-spored, bitunicate, fissitunicate, cylindric-clavate, slightly curved, pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 28–32 × 8–10 μm ($\bar{x}$ = 30 × 9 μm, n = 30), overlapping uni- to biseriate, narrowly fusiform, with a nearly median primary septum, constricted at the septum, hyaline, guttulate, usually with 2–4 larger guttules, broadly fusiform, narrowly rounded at the ends, with a mucilaginous sheath.

Culture characteristics: Ascospore germinating on PDA within 12 h and germ tubes produced from the ends of the spore. Colonies on PDA, circular, reaching 5 cm in one month at room temperature, smooth surface, papillae, brown to dark brown. Mycelium superficial, hairy, smooth, circular, reverse grayish; reverse pale to brown, crack at the middle, flocculent at the edge.

Material examined: China, Yunnan Province, Dali City, Eryuan County, Xihu Lake, 26°00′33″ N, 100°03′35″ E (1970 m), on unknown submerged decaying wood, 8 May 2021, S.P. Huang and L.L Li, L413 (HKAS 124590), living cultures (KUNCC 22–12414); *ibid.*, Erhai Lake, 26°00′32″ N, 100°03′35″ E (1970 m), on unknown submerged decaying wood, 01 April 2021, Z.Q. Zhang, L445 (HKAS 124593), living cultures (KUNCC 22–12415)

Notes: Our two new collections are morphologically consistent with the holotype of *Lentithecium pseudoclioninum* (Tanaka et al., 2015). In addition, phylogenetic analysis revealed that these two collections clustered with *L. pseudoclioninum* (Figure 3.17). Based on morphological and phylogenetic evidence, we identified our new collection as *L. pseudoclioninum*. *Lentithecium pseudoclioninum* has been collected on submerged twigs of woody plants in China and Japan (Tanaka et al., 2015; Yang et al., 2023). Our two specimens were collected from a freshwater plateau lake in Yunnan, China.



Note a Appearance of ascomata on the host. b, c Sections of ascomata; d Ostiole. e, f Section of peridium. g Pseudoparaphyses. h, i Asci j–o Ascospores. p Germinated conidium. q Colony on PDA. Scale bar: b, c = 100 µm, d = 50 µm, e–g = 20 µm, h, i = 30 µm, j–p = 10 µm.

Figure 3.20 *Lentithecium pseudoclioninum* (HKAS 124590)

Lentithecium yunnanensis W.H. Lu, Karun. & Tibpromma, Phytotaxa 554: 108 (2022)

Index Fungorum number: IF559622; *Facesoffungi number*: FoF 10778. Figure 3.21

Saprobic on submerged decaying wood in a freshwater lake. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 246–285 μm high, 179–229 μm wide, immersed to semi-immersed, clustered, sometimes solitary, scattered, subglobose or ellipsoidal, dark brown to black, carbonaceous, uni- to bi-loculate, with indistinct ostiolate. *Ostiolar* neck central, papillate, 127–156 μm long, 96–110 μm wide. *Peridium* 11–21 μm thick, composed of several layers of pseudoparenchymatous cells, outer layer composed of back brown to brown cells, arranged in textura angularis, inner layer composed of hyaline cells, arranged in textura angularis. *Pseudoparaphyses* about 2 μm wide, hyaline, filamentous, branched, septate, globose to subglobose swollen at the apex, sometimes swollen at the septum, anastomosing at the apex, embedded in a hyaline gelatinous matrix. *Asci* 98–117 × 14–15 μm ($\bar{x}$ = 108 × 15 μm, n = 15), 8-spored, clavate to subcylindrical, bitunicate, apex rounded, short pedicellate with an ocular chamber. *Ascospores* 27–30 × 5 ‒ 6 μm ($\bar{x}$ = 28 × 6 μm, n = 30), overlapping, uniseriate to biseriate, hyaline, 1-septate, smooth, constricted at the septa, slightly curved, guttulate, lacking gelatinous sheaths or appendages.

Culture characteristics: Ascospore germinating on PDA within 12 h and germ tubes produced from both ends of the spore. Colonies on PDA, circular, reaching 6 cm in 45 days at room temperature, smooth surface, papillae, brown in PDA medium. Mycelium superficial, brown to dark brown, hairy, smooth, circular; reverse brown to dark brown, crack at the middle, flocculent at the edge.

Material examined: China, Yunnan Province, Dali City, Eryuan County, Xihu Lake, 26°17′37″ N, 99°58′33″ E (2100 m), on unknown submerged decaying wood, 22 July 2021, L.L. Li, L680 (HKAS 124598), living culture (KUNCC 22–12420 = KUNCC 22–12422); *ibid.*, 26°17′24″ N, 99°57′56″ E (2100 m), on unknown submerged decaying wood, 22 July 2021, X.J. Yuan, L679 (HKAS 124597), living culture (KUNCC 22–12421).

Notes: *Lentithecium yunnanensis* is a terrestrial species introduced by Lu, Dai et al. (2022) that occurs on dead culms of *Artemisia* sp. near humid places. We collected

two lentithecium-like collections from decaying wood submerged in Xihu Lake, Dali, Yunnan Province. Phylogenetic analysis showed that our two new collections clustered with two strains of *L. yunnanensis* (KUNCC 22–10776 and KUNCC 22–10776). In addition, the morphology of our two collections is similar to the holotype of *L. yunnanensis* in having semi-immersed to immersed, subglobose to globose ascomata with short ostioles, and hyaline, clavate to fusiform, septate ascospores. Therefore, the two new collections were identified as *L. yunnanensis*, which was reported from the freshwater habitat for the first time.

Note a–c Appearance of ascomata on the host. d, e Sections of ascomata. f Section of peridium. g Pseudoparaphyses. h Ascomata wall with hypha. i–k Asci. l–p Ascospores. q Germinated conidium. r Colony on PDA. Scale bar: d, e = 100 μm, f, g = 20 μm, i–k = 30 μm, h, l–q = 10 μm.

Figure 3.21 *Lentithecium yunnanensis* (HKAS 124597, new habitat record)

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

MycoBank number: 849738.

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

Saprobic on submerged decaying wood in a freshwater lake. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* immersed to semi-immersed, clustered, sometimes solitary, scattered, subglobose or ellipsoidal, dark brown to black, carbonaceous, uni- to bi-loculate, with indistinct ostiolate. *Peridium* thick, composed of several layers of pseudoparenchymatous cells, an outer layer com-posed of back brown to brown cells, arranged in textura angularis, and an inner layer composed of hyaline cells, arranged in textura angularis. *Pseudoparaphyses* thick, hyaline, filamentous, branched, septate, globose to subglobose swollen at the apex, sometimes swollen at the septum, anastomosing at the apex, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, clavate to subcylindrical, bitunicate, apex rounded, short pedicellate with an ocular chamber. *Ascospores* overlapping, uniseriate to biseriate, hyaline, 1-septate, smooth, constricted at the septa, slightly curved, with gelatinous sheaths.

Type species: *Paralentithecium aquaticum* (Yin. Zhang, J. Fourn. & K.D. Hyde) H.W. Shen & Z.L. Luo.

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

MycoBank number: MB 512791.

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

Notes: *Lentithecium aquaticum* was introduced by Zhang, Wang et al. (2009) based on phylo-genetic analysis and morphological characteristics. The placement of this species was not stable and has been changed by several studies (Crous et al., 2018; Dayarathne et al., 2018; Dong et al., 2020). Previous phylogenetic analyses indicated that *Lentithecium aquaticum* did not cluster with other *Lentithecium* species, and it formed an individual lineage basal to *Darksidea*, *Halobyssothecium* and *Lentithecium*. Furthermore, phylogenetic studies of Dayarathne et al. (2018) and Devadatha et al. (2020) showed that *L. aquaticum* clustered within *Setoseptoria*. Several other studies

excluded *L. aquaticum* from *Lentithecium* (Crous et al., 2018; Dong et al., 2020). The latest phylogenetic analysis based on combined ITS, LSU, SSU, and *tef*1-α genes showed that *L. aquaticum* formed a separate lineage outside of *Lentithecium* (Calabon, Jones, Hyde et al., 2021). Our phylogenetic analysis shows that *L. aquaticum* clusters with our new collection KUNCC 22–12412 and forms a distinct lineage within *Lentitheciaceae* with 100 ML and 1.00 PP support (Figure 3.17). Therefore, we propose a new genus, *Paralentithecium* to accommodate *Paralentithecium aquaticum* (*Lentithecium aquaticum*) and a new species *P. suae*.

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

MycoBank number: 849739; *Facesoffungi number*: FoF 14876; Figure 3.22

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

Holotype: HKAS 124587.

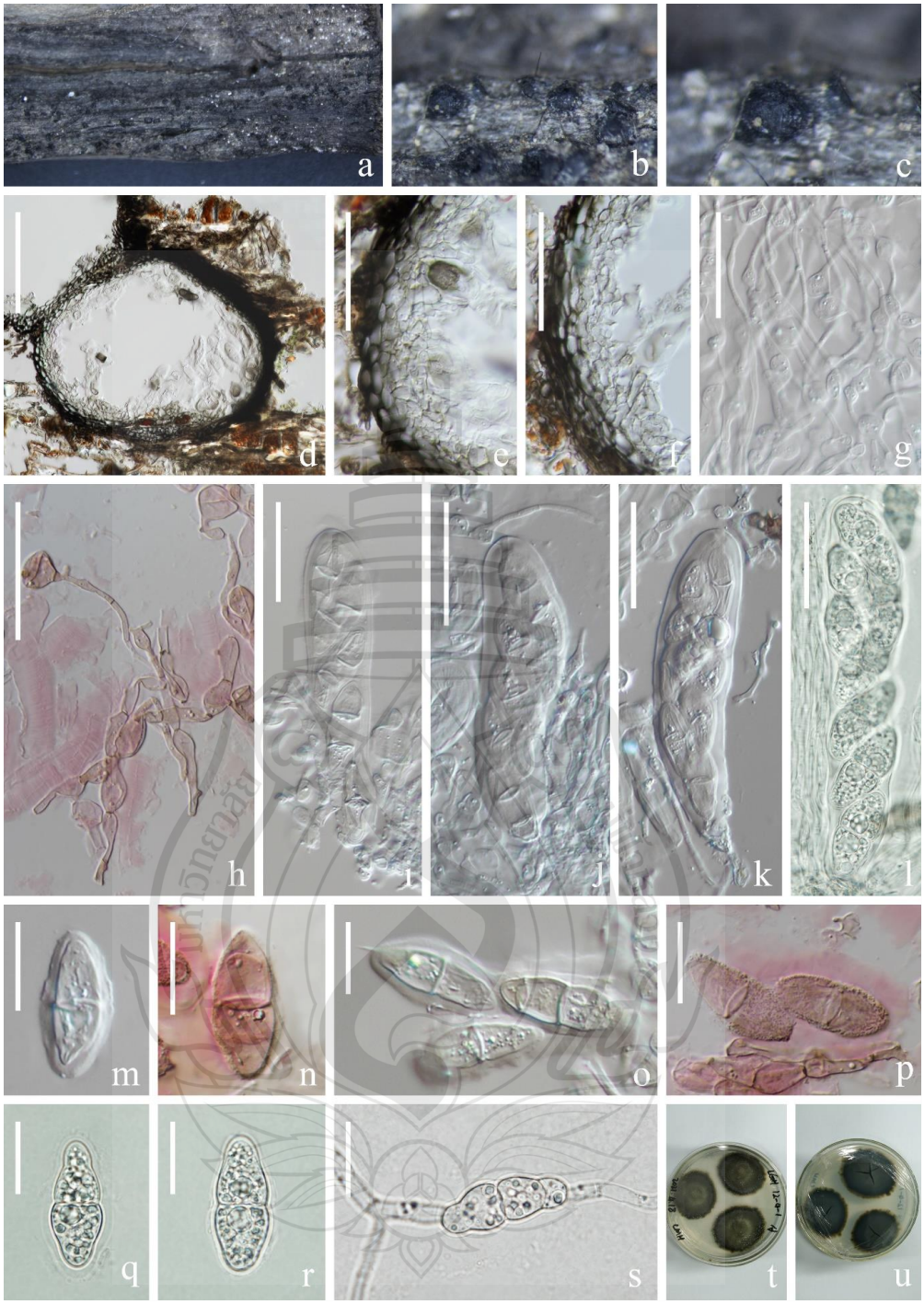
Saprobic on submerged decaying wood in a freshwater lake. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 212–253 μm high, 175–204 μm wide, immersed to semi-immersed, clustered, sometimes solitary, scattered, subglobose or ellipsoidal, dark brown to black, carbonaceous, uni- to bi-loculate, with indistinct ostiolate. *Peridium* 17–32 μm thick, composed of several layers of pseudoparenchymatous cells, outer layer composed of bark brown to brown cells, arranged in textura angularis, inner layer composed of hyaline cells, arranged in textura angularis. *Pseudoparaphyses* 2–3 μm wide, hyaline, filamentous, branched, septate, globose to subglobose swollen at the apex, sometimes swollen at the septum (6–10 μm wide), anastomosing at the apex, embedded in a hyaline gelatinous matrix. *Asci* 104–134 × 24–28 μm ($\bar{x}$ = 119 × 26 μm, n = 25), 8-spored, clavate to subcylindrical, bitunicate, apex rounded, short pedicellate with an ocular chamber. *Ascospores* 28–34 × 11–14 μm ($\bar{x}$ = 31 × 13 μm, n = 40), overlapping, uniseriate to biseriate, hyaline, 1-septate, broadly fusiform, smooth, constricted at the septa, slightly curved, guttulate, with gelatinous sheaths.

Culture characteristics: Ascospore germinating on PDA within 12 h and germ tubes produced from both ends of the spore. Colonies on PDA, circular, reaching 4–5 cm in one month at room temperature, smooth surface, papillae, brown to dark brown, olive green in PDA medium. Mycelium superficial, brown to dark brown, hairy, smooth,

circular; reverse dark brown, crack at the middle, flocculent at the edge, dark brown with greenish.

Material examined: 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, L184 (HKAS 124587, holotype), ex-type living cultures (CGMCC 3.24265 = KUNCC 22–12412).

Notes: In our phylogenetic analysis, *Paralentithecium suae* clustered with *P. aquaticum* with 100% ML and 1.00 PP support (Figure 3.17). Comparison of ITS, LSU, SSU, and *tef*1-α sequences between *P.* suae and *P. aquaticum* revealed 11 bp, 4 bp, 4 bp, and 22 bp differences, respectively. *Paralentithecium suae* resembles *P. aquaticum* in having hyaline, 1-septate, broadly fusiform ascospores with gelatinous sheaths (Zhang, Wang et al., 2009). However, *P. suae* is distinct from *P. aquaticum* in having globose to subglobose pseudoparaphyses that are swollen at the apex and sometimes swollen at the septum. In contrast, the pseudoparaphyses of *P. aquaticum* are not swollen. In addition, ascospores of *P. aquaticum* contain four refractive globules, while *P. suae* has ascospores with many small guttules (Zhang, Wang et al., 2009). Therefore, we introduce *P. suae* as a new species.



Note a–c Appearance of ascomata on the host. d Sections of ascomata. e, f Section of peridium. g, h Pseudoparaphyses. i–l Asci. m–r Ascospores. s Germinated conidium. t, u Colony on PDA. Scale bar: d = 100 μm, e–l = 40 μm; m–s = 20 μm.

Figure 3.22 *Paralentithecium suae* (HKAS 124587, holotype)

Setoseptoria Quaedvl., Verkley & Crous

Notes: *Setoseptoria* was introduced by Quaedvlieg et al. (2013) to accommodata septoria-like coelomycetes having subcylindrical, (1–)3-septate hyaline conidia, with *S. phragmitis* as type species. Both sexual and asexual morphs of *Setoseptoria* have been discovered. The sexual morph is characterized by superficial to semi-immersed, gregarious, subglobose to globose ascomata; ascospores fusiform to cylindrical or ellipsoidal-fusiform, with a submedian primary septum, constricted at the septum, hyaline, asymmetrical, with a mucilaginous sheath (Quaedvlieg et al., 2013; Tanaka et al., 2015; Yang et al., 2023). Only *S. phragmitis* and *S. suae* are known as asexual morph, characterized by immersed, globose conidiomata, conidiogenous cells hyaline, smooth, subcylindrical to doliiform, conidia hyaline, smooth, subcylindrical, (1–)3-septate, straight to slightly curved (Quaedvlieg et al., 2013; Shen et al., 2023). Members of *Setoseptoria* are saprophytic on herbaceous plants, especially *Phragmites* (*Poaceae*) (Quaedvlieg et al., 2013; Tanaka et al., 2015; Shen et al., 2023; Yang et al., 2023). Currently ten species are listed in Index Fungorum, five of which have been reported in freshwater habitats (Tanaka et al., 2015; Senanayake et al., 2023; Shen et al., 2023; Yang et al., 2023).

Setoseptoria bambusae J. Yang, J.K. Liu & K.D. Hyde, Fungal Diversity 119: 44 (2022)

Index Fungorum number: IF559452; *Facesoffungi number*: FoF12786; Figure 3.23

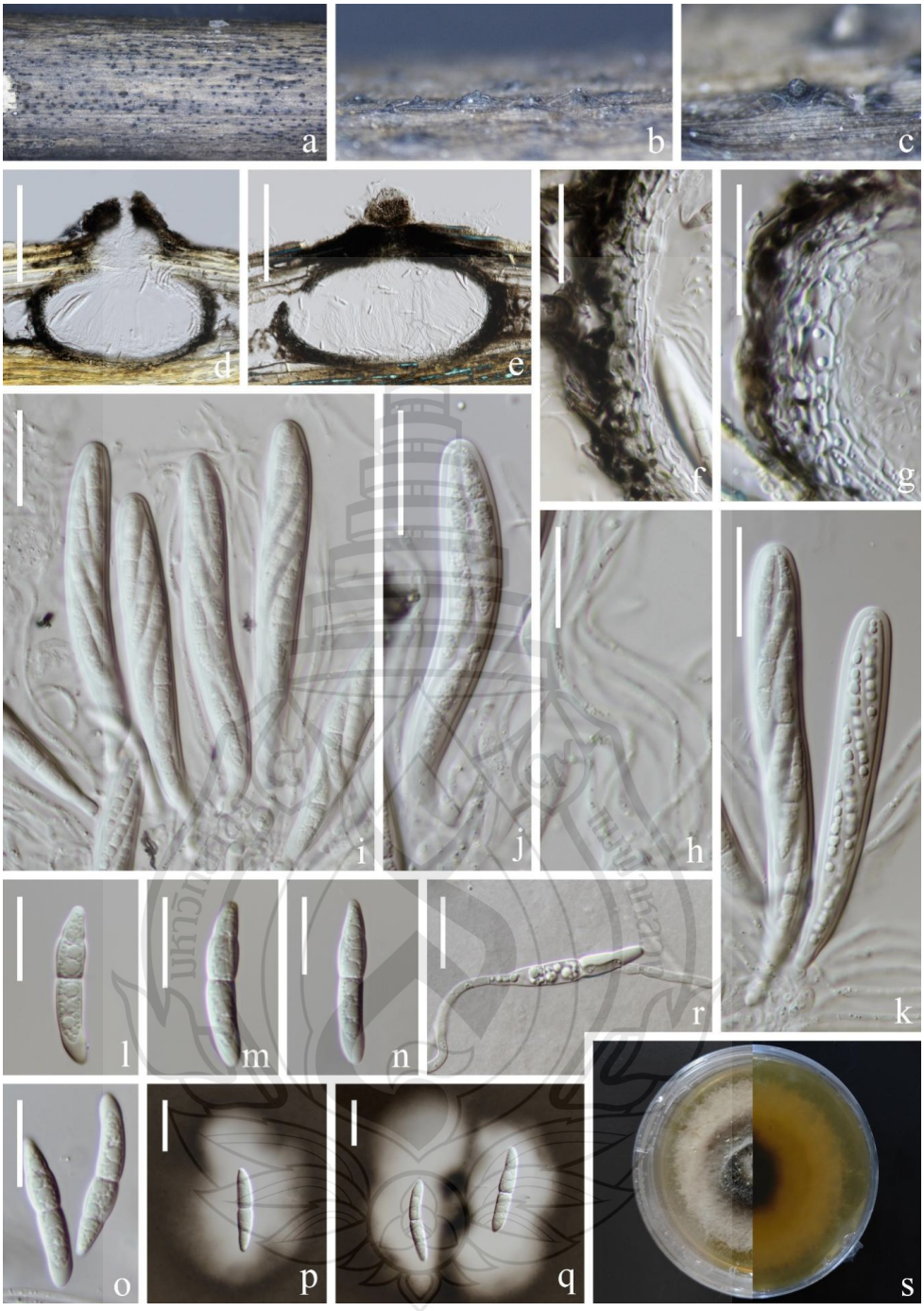
Saprobic on submerged decaying wood in a freshwater lake. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 245–375 μm high, 194–296 μm wide, black, superficial to semi-immersed, gregarious, fully or partly erumpent, globose, uniloculate, ostiolate. *Peridium* 26–39 μm wide, thick, multi-layered, outer layer most heavily pigmented, comprising blackish to dark brown amorphous layer, middle layer heavily pigmented, inner layer, pale brown to hyaline, cells towards the inside lighter, flattened, thick-walled. *Pseudoparaphyses* 2–3 μm wide, filamentous, branched septate. *Asci* 113–128 × 15–19 μm ($\bar{x}$ = 120 × 17 μm, n = 30), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 32–40 × 6–8 μm ($\bar{x}$ = 36 × 7 μm, n = 20), overlapping uni- to biseriate,

narrowly fusiform, with a nearly median primary septum, deeply constricted at the septum, hyaline, guttulate, asymmetrical, conical, and narrowly rounded at the ends.

Culture characteristics: Ascospore germinating on PDA within 12 h and germ tubes produced from one end of the spore. Colonies on PDA, circular, reaching 6 cm in 45 days at room temperature, smooth surface, papillae, pale brown in PDA medium. Mycelium superficial, grayish-brown to brown, hairy, smooth, circular; reverse pale brown at the edges, dark brown in the middle, flocculent at the edge.

Material examined: China, Yunnan Province, Yuxi City, Jiangchuan District, Xingyunhu Lake, 24°23′05″ N, 102°48′22″ E (1720 m), on unknown submerged decaying wood, 10 July 2021, H.W. Shen, L511 (HKAS 124592), living culture (KUNCC 22–12417); *ibid.*, 24° 23′05″ N, 102°48′22″ E (1720 m), on the submerged stem of *Phragmites* sp. (*Poaceae*), 10 July 2021, S. Luan, L579 (HKAS 124596), living culture (KUNCC 22–12418); *ibid.*, on submerged stem of *Phragmites* sp. (*Poaceae*), 10 July 2021, Y.K. Jiang, L474 (HKAS 124591), living culture (KUNCC 22–12416).

Notes: *Setoseptoria bambusae* was introduced by Yang et al. (2023) to accommodate two collections, GZCC 17–0044 (ex-type strain) and IFRD500-013 (previously identified as *S. arundinaceae*, without description). In this study, our four new collections clustered with the ex-type strain of *S. bambusae* with 100% ML and 1.00 PP support (Figure 3.17). Furthermore, our collections fit the morphological characteristics of *S. bambusae* except for the size of asci and ascospores, our isolate has shorter asci (113–128 *vs.* 130–180 μm) and longer ascospores (32–40 *vs.* 28–37 μm). Therefore, we identified them as *S. bambusae*. Our four new collections were collected from lentic freshwater habitats, while the holotype was collected from lotic habitats.



Note a–c Appearance of ascomata on the host. d, e Sections of ascomata. f, g Section of peridium. h Pseudoparaphyses. i–k Asci. l–o Ascospores. p, q Ascospore stained in Indian ink. r Germinated conidium. s Colony on PDA. Scale bar: d, e = 150 μm, f–k = 30 μm, h, i = 30 μm, l–r = 20 μm.

Figure 3.23 *Setoseptoria bambusae* (HKAS 124592)

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

MycoBank number: MB849740; *Facesoffungi number*: FoF14877; Figure 3.24

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

Holotype: HKAS 124595.

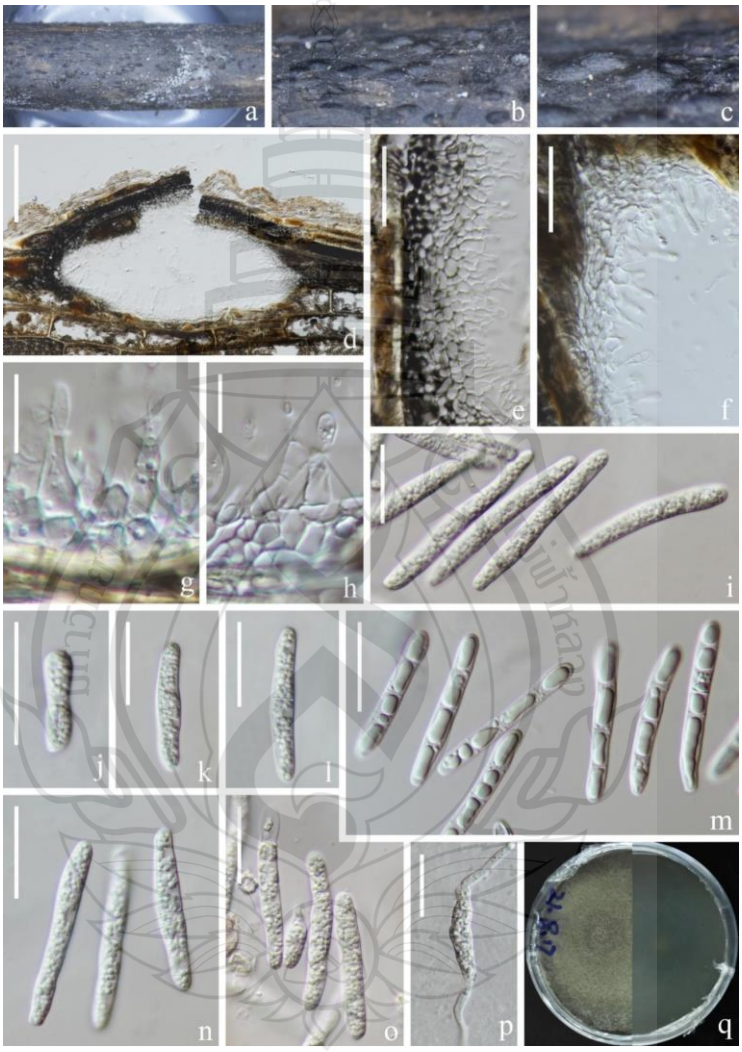
Saprobic on submerged decaying wood in a freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 383–512 μm high, 173–196 μm wide, solitary, scattered, semi-immersed to immersed in the host, pycnidial, subglobose to ellipsoidal, unilocular, black, ostiolate, apapillate. *Ostiole* short, centrally located. *Conidiomatal wall* 33–55 μm wide, thickening at the upper zone, thick-walled, composed of several layers of textura angularis, an outer layer comprising brown to dark brown cells, pigmented; inner layer comprising hyaline cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (4–)7–15(–26) × 4–6 μm ($\bar{x}$ = 11 × 5 μm, n = 25), arising from the inner layers of conidiomata, hyaline, enteroblastic, phialidic, determinate, ampuliform, subcylindrical to lageniform. *Conidia* 33–43 × 4–6 μm ($\bar{x}$ = 38 × 5 μm, n = 50), subcylindrical, with obtuse to subobtuse ends, straight or slightly curved, hyaline, (1–)3-septate, euseptate, mostly with one large central guttule per cell when young, with many small guttules in each cell at maturity, slightly constricted at the septum, smooth-walled.

Culture characteristics: Conidia germinated on PDA within 12 h and germ tubes produced from the ends of the spore. Colonies on PDA, circular, reaching 6 cm in one month at room temperature, brown to dark brown. Mycelium superficial, brown to dark brown, hairy, smooth, circular; dark brown from below.

Material examined: China, Yunnan Province, Yuxi City, Tonghai County, Qiluhu Lake, 24°08′37″ N, 102°46′24″ E, on submerged stem of *Phragmites* sp. (*Poaceae*), 11 July 2021, H.W. Shen, L570 (HKAS 124595, holotype), ex-type living cultures (CGMCC 3.24266 = KUNCC 22–12419).

Notes: Phylogenetic analysis showed that *Setoseptoria suae* clustered with *S. phragmitis* with 100% ML and 0.99 PP support (Figure 3.17). The comparison of ITS and LSU sequences between *S. suae* and *S. phragmitis* shows that the similarities are 96.9% (538/555 bp) and 99.9% (826/827 bp), respectively. *Setoseptoria suae* resembles *S. phragmitis* in having immersed, globose conidiomata, hyaline,

subcylindrical, smooth, guttulate, (1–)3-septate conidia (Quaedvlieg et al., 2013). However, *S. suae* can be distinguished from *S. phragmitis* by its larger conidia [33–43 × 4–6 µm *vs.* (19–)25–35(–38) × (3.5–)4 µm]. In addition, the conidia of *S. phragmitis* mostly have one large central guttule per cell, while *S. suae* has conidia with many small guttules in each cell. We, therefore, introduce *S. suae* as a new species.



Note a–c Appearance of conidiomata on the host. d Sections of conidiomata. e, f Section of peridium. g, h Conidiomata and conidiogenous cells. i–o Conidia. p Germinated conidium. q Colony on PDA. Scale bar: d = 100 µm, e, f = 30 µm, g, h = 10 µm, h, i = 30 µm, i–p = 10 µm.

Figure 3.24 *Setoseptoria suae* (HKAS 124595, holotype)

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

Fungal Names number: FN 804463; Figure 3.25

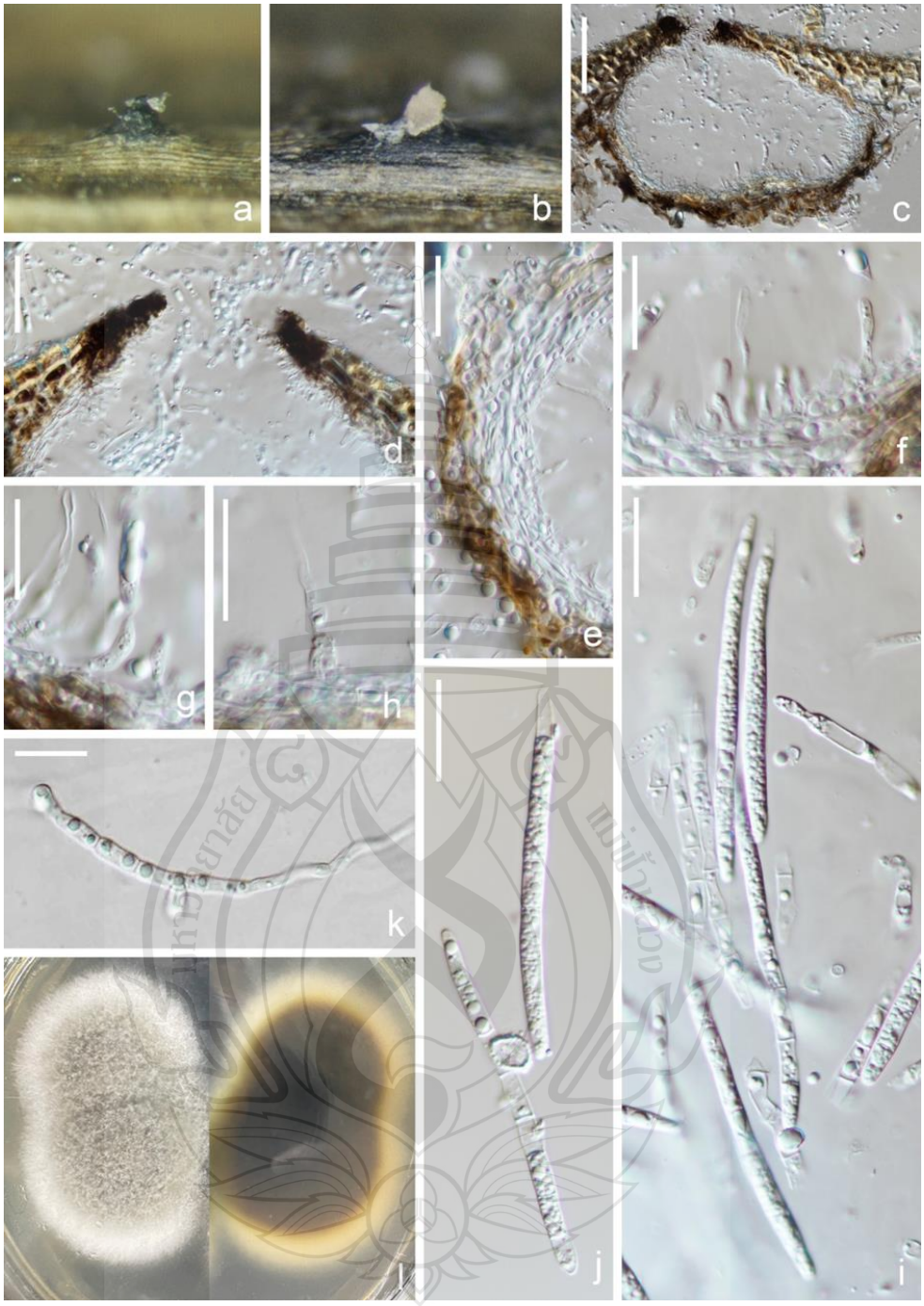
Saprobic on submerged decaying wood in freshwater habitat. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 200–290 μm high, 190–200 μm diam., solitary, scattered, semi-immersed to immersed in the host, pycnidial, subglobose to ellipsoidal, flattened, unilocular, pale brown to dark brown, ostiolate, apapillate. *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.

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* sp. (*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* sp. (*Poaceae*), 21 July 2021, S.P. Huang, CBH 1-27-1 (HKAS 131634).

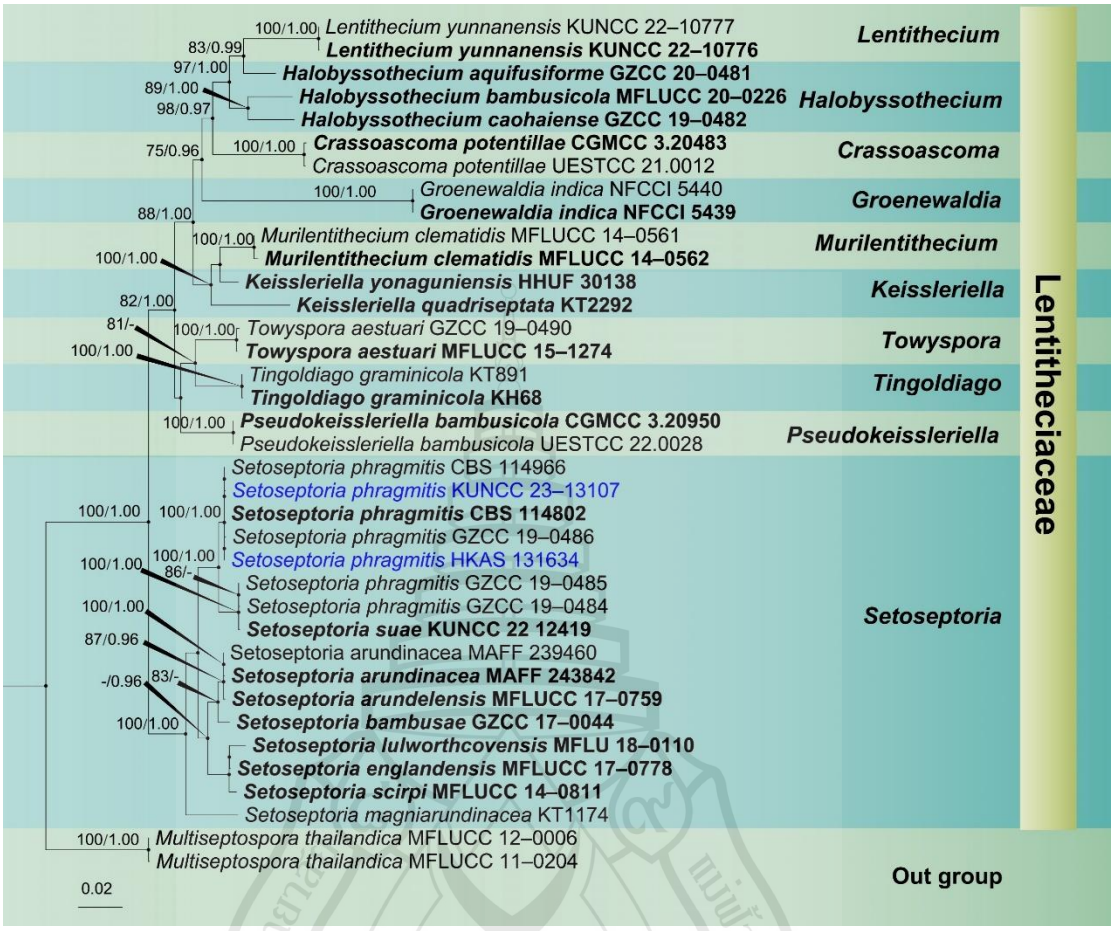
Notes: Two strains collected from freshwater plateau lakes of Yunnan Province were identified as *Setoseptoria phragmitis* based on morphological and phylogenetic studies. Morphological examination showed that these two collections fit well with the description of *S. phragmitis* in having enteroblastic, 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) (Figure 3.26). Comparison of ITS, LSU, and SSU gene loci between the two newly obtained strains and the type strain of *S. phragmitis* showed that there were only 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; 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 freshwater habitat for the first time.



Note a, b Appearance of coniodiomata on substrate. c Section of coniodiomata. 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 3.25 *Setoseptoria phragmitis* (HKAS 131634, new habitat records)



Note 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. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Figure 3.26 Phylogenetic tree for *Setoseptoria phragmitis*

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

Notes: 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, Hongsanan et al., 2016), *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 saprobic 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; Deng et al., 2020). Currently, 34 species are placed in this family, 20 of which are reported from freshwater habitats.

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

Notes: *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 are 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.***

Fungal Names number: FN 571862; Figure 3.27

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

Holotype: HKAS 131666.

Saprobic on decaying submerged wood in freshwater habitat. 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. *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.

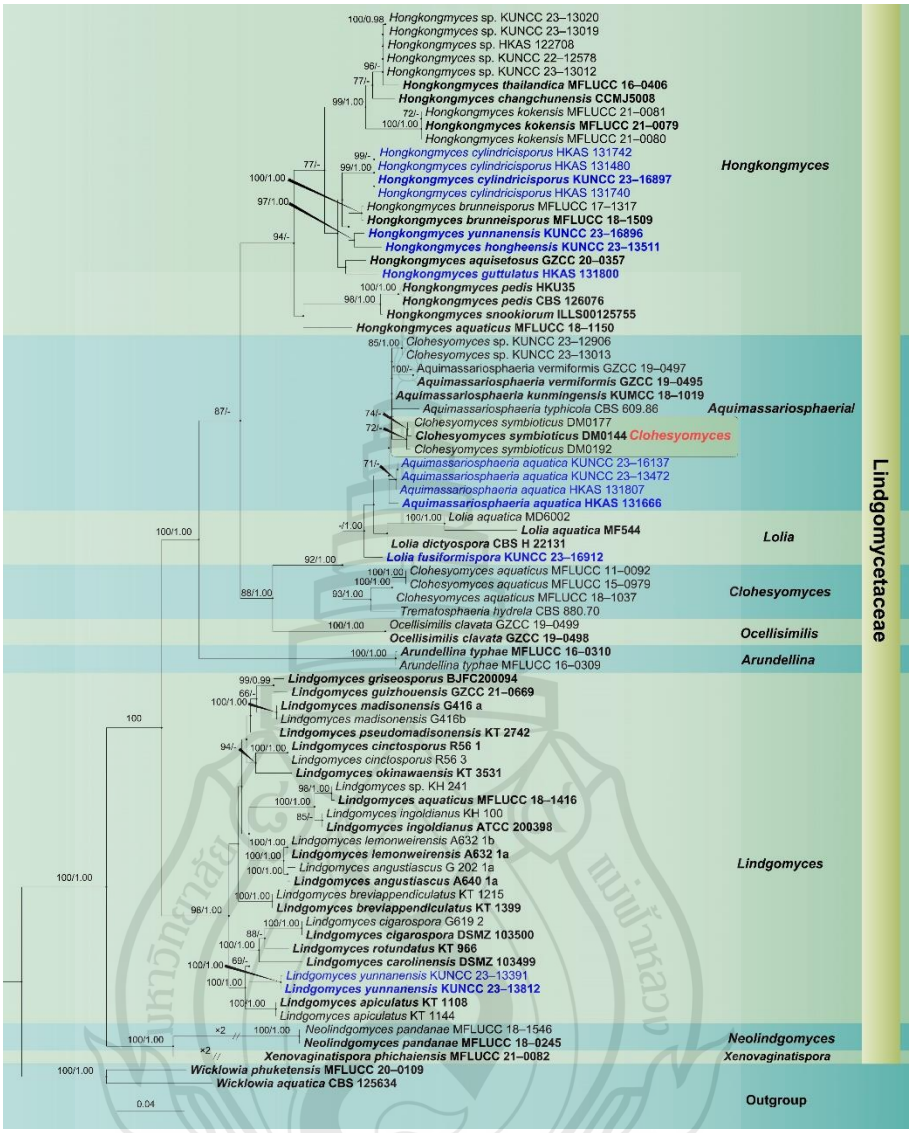
Material examined: CHINA, Yunnan Province, Yuxi City, Qiluhu Lake, 24°10′29" N, 102°46′40" E; 1796 m; on submerged decaying wood, 12 July 2021, Y.K. Jiang, QLH 2-16-1 (HKAS 131666, holotype); *ibid.*, Honghe Prefecture, Yilonghu Lake, 23°41′49.2" N, 102°30'52.2″ E; 1400m; on submerged decaying wood, 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.

Notes: In our phylogenetic analysis, species of *Aquimassariosphaeria*, *Clohesyomyces*, and *Lolia*, as well as our four new collections, are clustered in an unstable lineage (Figure 3.28). 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 *C. symbioticus* (DM01444, DM0177 and DM0192) and two unnamed strains *Clohesyomyces* sp. (KUNCC 23–12906 and KUNCC 23–13013) clustered in *Aquimassariosphaeria* clade, while species of *Lolia* were between these two clades. Currently, *Aquimassariosphaeria*, only sexual morphs have been discovered, and they are characterized by narrowly fusiform or vermiform, brown, transversely septate ascospores (Dong et al., 2020; Yang et al., 2023). However, *Clohesyomyces symbioticus*, only the asexual morph (Coelomycetous) has been reported, it is characterized by so whether *C. symbioticus* is related to *Aquimassariosphaeria* requires more research to clarify. Our four asexual collections with filiform conidia are related to *Aquimassariosphaeria* in phylogenetic analysis (Figure 3.28), 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.

Note a, b Colonies on substrate. c, d Base of conidia. e–g Conidia. h Proliferating conidia. i, j Part of conidia. Conidia germinate on natural substrate. Scale bars: c = 70 µm, d = 40 µm, e–k = 20 µm.

Figure 3.27 *Aquimassariosphaeria aquatica* (HKAS 131666, holotype)



Note 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. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Figure 3.28 Phylogenetic tree of *Lindgomycetaceae*

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).

Notes: Hongkongmyces was proposed by Tsang et al. (2014) to accommodate *H. pedis* which was isolated from a human foot with suppurative granulomatous fungal infection. Subsequently, six new 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 (Dong et al., 2020; Bao, Luo et al., 2021; Boonmee et al., 2021; Jayawardena et al., 2022; Yang et al., 2023). Except for *H. pedis* and *H. snookiorum*, all other species grow saprophytically on decaying plant debris. Both 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 and surrounded with a mucilaginous sheath (Hyde et al., 2017; Bao, Luo et al., 2021; 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, Luo et al., 2021; Jayawardena et al., 2022; Yang et al., 2023).

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

Fungal Names number: FN 571863; Figure 3.29

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

Holotype: HKAS 131741.

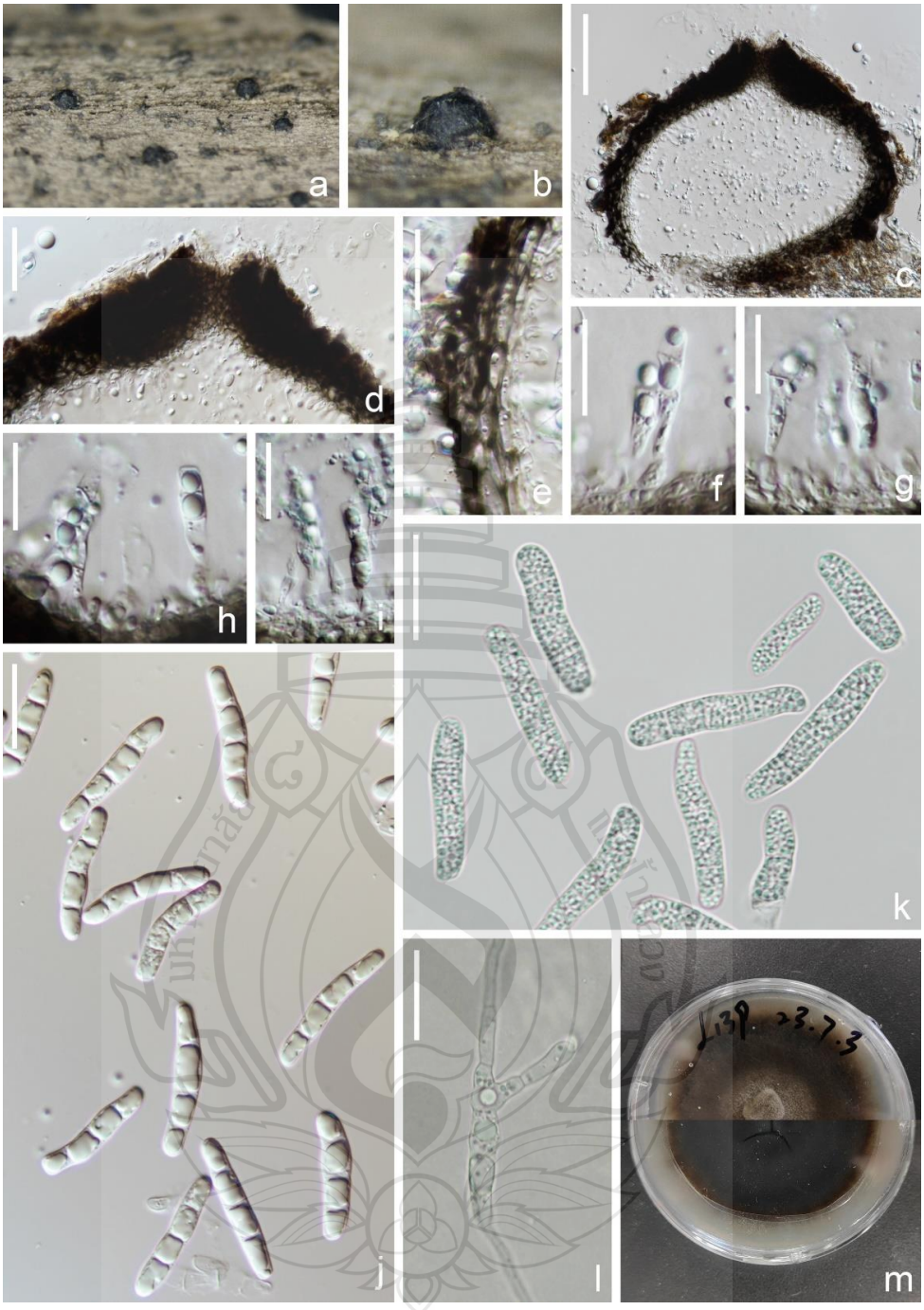
Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 211–272 µm high, 239–320 µm diam., pycnidial, black, scattered, solitary to gregarious, semi-immersed or superficial, globose to subglobose, uni-loculate, ostiolate. *Ostioles* 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.

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).

Notes: In our phylogenetic analysis, the four strains of *Hongkongmyces cylindricisporus* clustered in an independent lineage (Figure 3.28). *Hongkongmyces cylindricisporus* can be distinguished from previous species by cylindrical to subcylindrical conidia, whereas the conidia of the previous species are mainly ellipsoid to obovoid, globose, and 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*. Based on unique morphological and phylogenetic analysis evidence, we introduce *H. cylindricisporus* as a new species.



Note a, b Appearance of coniodiomata on substrate. c Section of coniodiomata. 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.

Figure 3.29 *Hongkongmyces cylindricisporus* (HKAS 131739, holotype)

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

Fungal Names number: FN 571996; Figure 3.30

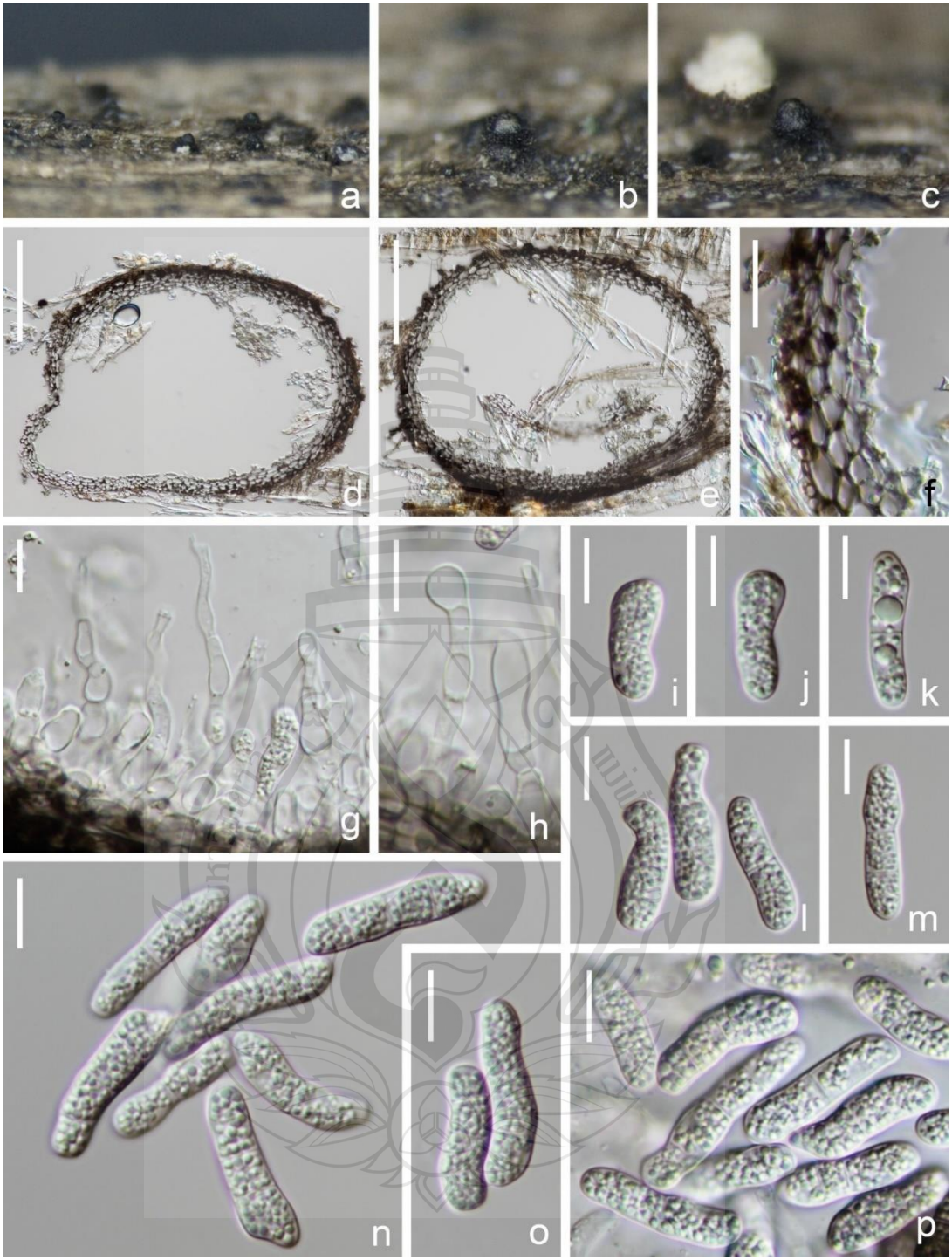
Etymology: The name refers to the guttulate conidia of this species.

Holotype: HKAS 131800.

Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **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.

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).

Notes: *Hongkongmyces guttulatus* can be distinguished from other species of *Hongkongmyces* by its unique morphology. *Hongkongmyces guttulatus* morphologically resembles *H. cylindricisporus*, however, they can be distinguished by conidial morphology (see notes of *H. cylindricisporus*). Multigene phylogenetic analysis showed that *H. guttulatus* clusters with *H. aquisetosus* (Figure 3.29), 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. Based on unique morphological characteristics and phylogenetic analysis, we introduce *H. guttulatus* as a new species.



Note a–c Appearance of coniodiomata on substrate. d, e Section of coniodiomata. f Peridium. g, h Conidiogenous cells and developing conidia. i–p Conidia. Scale bars: d, e = 90 µm, f = 20 µm, g–m = 10 µm.

Figure 3.30 *Hongkongmyces guttulatus* (HKAS 131800, holotype)

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

Fungal Names number: FN 571998; Figure 3.31

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

Holotype: HKAS 131785.

Saprobic on decaying submerged wood in freshwater habitat. **Asexual morph**: Undetermined. **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.

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.

Notes: Morphological studies show that *Hongkongmyces hongheensis* fits well with the generic concept of the sexual morph of *Hongkongmyces* in having reddish brown to brown, fusiform ascospores, and surrounded with a mucilaginous sheath.

Morphological comparison with the sexual species of *Hongkongmyces* (*H. aquisetosus*, *H. brunneisporus*, *H. thailandica* and *H. yunnanensis*), *H. 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, Luo et al., 2021). *H. 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). *H. 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 septate (5(–6)-septate *vs.* 6–7-septate). Phylogenetic analysis showed that *H. hongheensis* clustered *H. yunnanensis* with 100% ML and 1.00 PP support (Figure 3.28). Nucleotide comparison between *H. hongheensis* and *H. yunnanensis* shows 3.7% (27/728, 7 gaps), 0.5% (4/798, one gap), 0.2% (2/876), 2.0% (19/936) base difference for ITS, LSU, SSU and *tef*1-α sequence respectively. Based on morphological characteristics and phylogenetic analysis, we introduce *H. hongheensis* as a new species.

Note 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 3.31 *Hongkongmyces hongheensis* (HKAS 131785, holotype)

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

Fungal Names number: FN571999; Figure 3.32

Etymology: The name refers to the place where the holotype was collected: Yunnan Province.

Holotype: HKAS 131741.

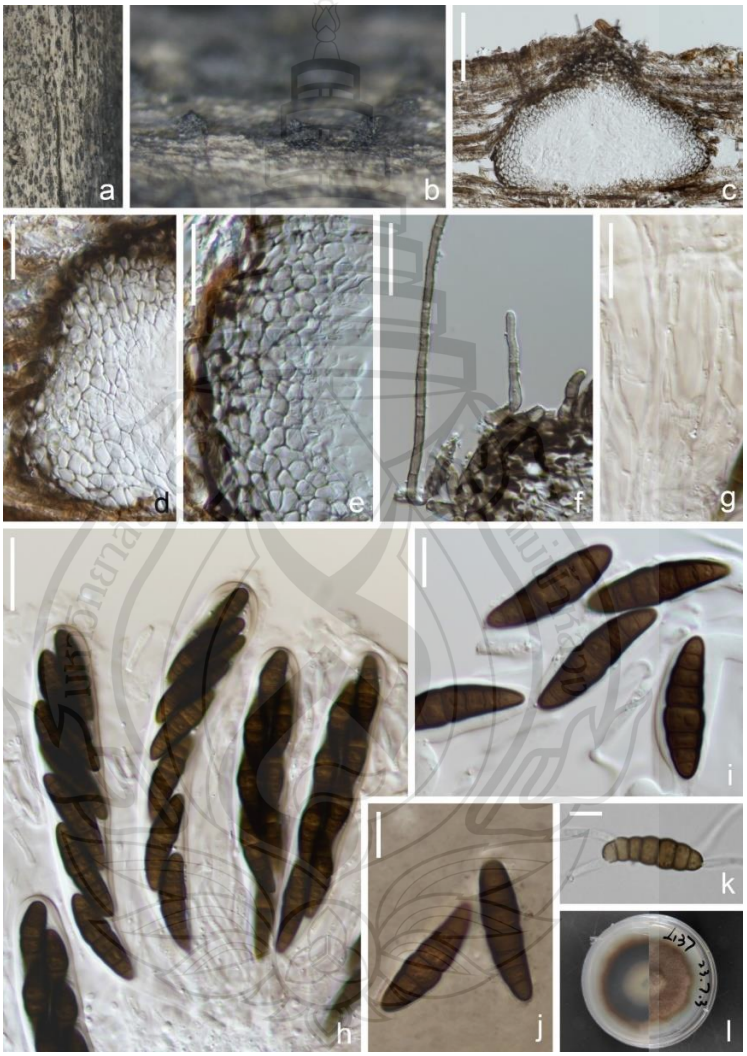
Saprobic on decaying submerged wood in freshwater habitat. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 163–230 µm high, 159–232 µm diam., black, scattered, solitary to gregarious, immersed or semi-immersed, globose to subglobose, uni-loculate, ostiolate, papillate. *Ostioles* central, 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.

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.

Notes: Multigene phylogenetic analysis showed that *H. yunnanensis* clustered with *H. hongheensis* with strong 97% ML and 1.00 PP support (Figure 3.28). However,

H. yunnanensis can be distinguished from *H. hongheensis* by its asci and ascospores (See notes of *H. hongheensis*). Based on morphological and molecular evidence, we therefore 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*.



Note 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.

Figure 3.32 *Hongkongmyces yunnanensis* (HKAS 131741, holotype)

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 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.***

Fungal Names number: FN 572000; Figure 3.33

Etymology: The name refers to the place where the holotype was collected: Yunnan Province.

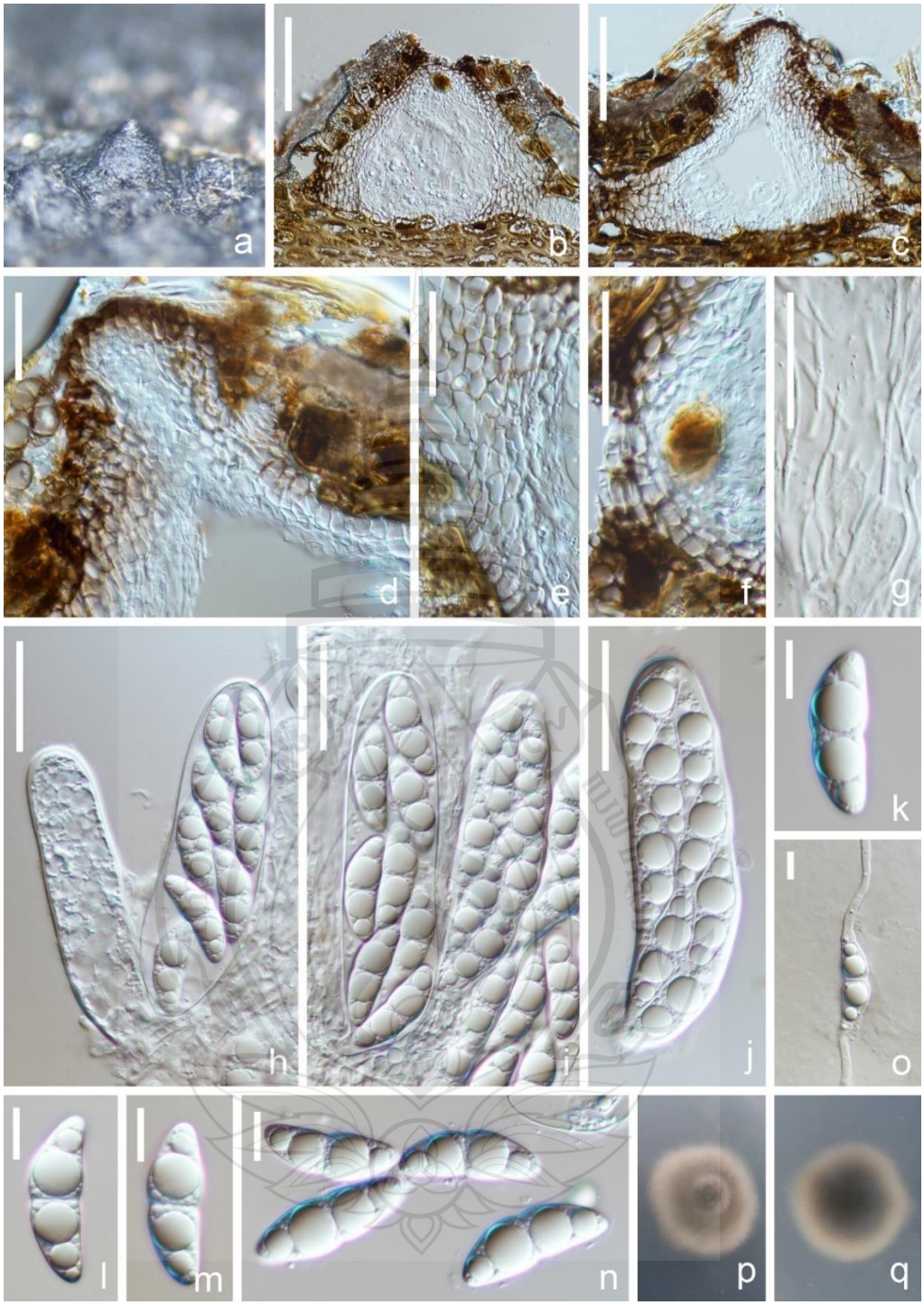
Holotype: HKAS 131833.

Saprobic on decaying submerged wood in freshwater habitat. **Asexual morph**: Undetermined. **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 big guttules on both sides of the septum and two smaller ones be side, surrounded by a thin gelatinous sheath.

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.

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 (Figure 3.28). Based on unique morphological characteristics, we, therefore, introduce *L. yunnanensis* as an additional new species from freshwater habitats.



Note a Appearance of ascomata on substrate. b, c Section 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.

Figure 3.33 *Lindgomyces yunnanensis* (HKAS 131833, holotype)

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

Notes: *Lolia* was introduced by Abdel-Aziz & Abdel-Wahab (2010) to accommodate the asexual species *L. aquatica* collected submerged decayed stem of *Phragmites australis* from 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, 2016a), however, the link between asexual and sexual morphs is not based on the same type specimen, so it does not conform to the "one fungus = one name" (Dong et al., 2020). 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). Its 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, 2016a). 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.***

Fungal Names number: FN 572001; Figure 3.34

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

Holotype: HKAS 131465.

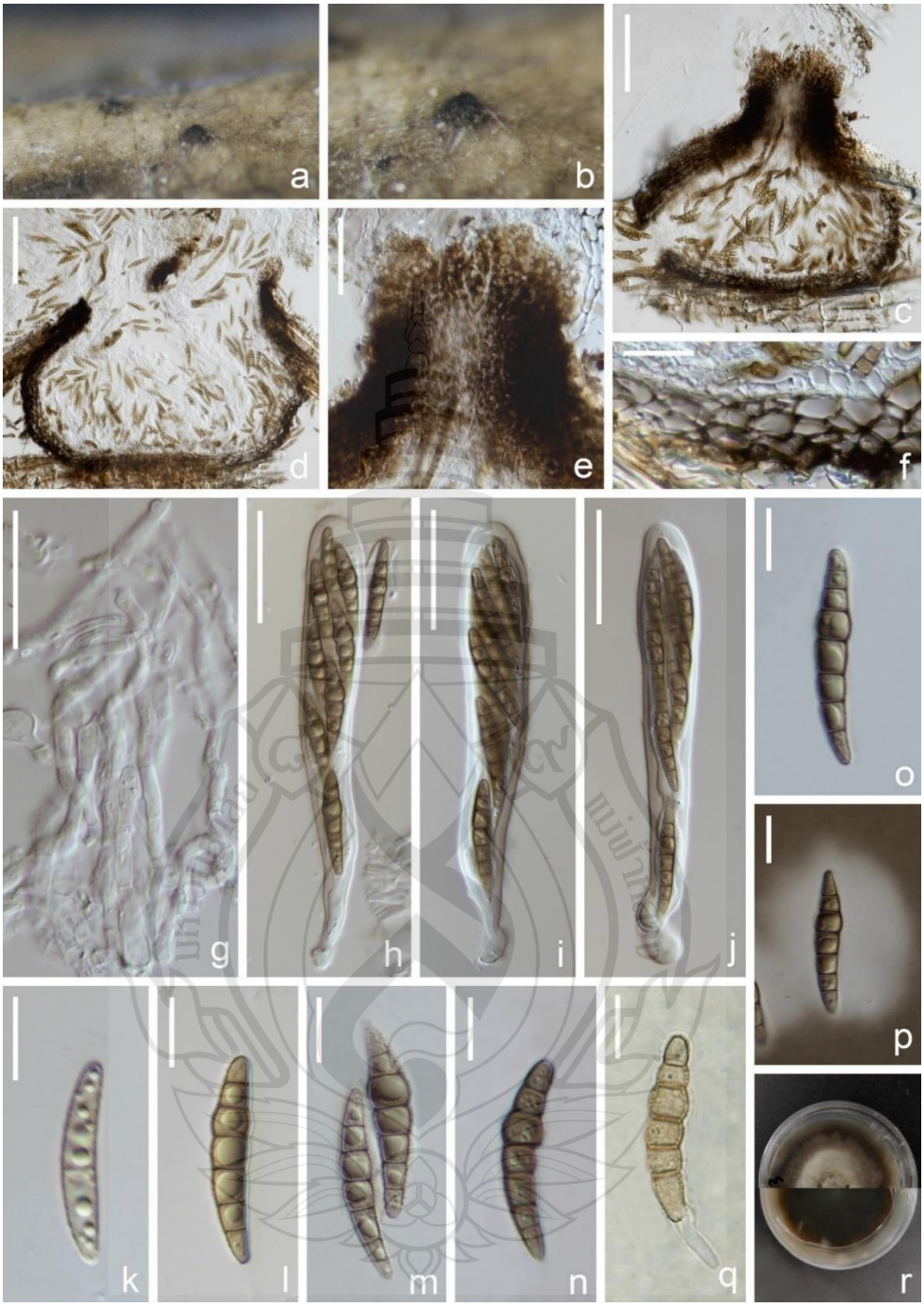
Saprobic on decaying submerged wood in freshwater habitat. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 160–280 µm high, 265–320 µm diam., solitary, scattered, immersed to semi-immersed, globose to subglobose with flattened base, papillate, ostiolate, dark-brown to black. *Ostioles* 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.

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.

Notes: Phylogenetic results showed that *Lolia fusiformispora* clustered with other two *Lolia* species, *L. dictyospora* and *L. aquatica* (Figure 3.28). Comparison of LSU sequence base pair differences between *L. fusiformispora* and *L. aquatica* showed a 1.9% (15/905 bp, including 3 gaps) difference; nucleotides differences of LSU sequence between *L. fusiformispora* and *L. dictyospora* is 1.0% (8/805 bp). Morphologically, *L. fusiformispora* is similar to *L. aquatica* in having fusiform, yellow to dark-brown, septate, verruculose ascospores and surrounded with a gelatinous sheath (Abdel-Aziz, 2016a). 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). *L. 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 septate (Abdel-Aziz, 2016a). Based on morphological and phylogenetic evidence, we introduce *L. fusiformispora* as a new species. Currently, all three *Lolia* species were reported from freshwater habitats.



Note a, b Appearance of ascomata on substrate. c, d Section 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.

Figure 3.34 *Lolia fusiformispora* (HKAS 131465, holotype)

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

Notes: *Occultibambusaceae* was established by Dai et al. (2017) to accommodate *Neooccultibambusa* Doilom & K.D. Hyde (Doilom et al., 2016), *Occultibambusa* D.Q. Dai & K.D. Hyde (Dai et al., 2017), *Seriascoma* Phookamsak, D.Q. Dai & K.D. Hyde (Dai et al., 2017), and *Versicolorisporium* Sat. Hatak., Kaz. Tanaka & Y. Harada (Hatakeyama et al., 2008), with *Occultibambusa* D.Q. Dai & K.D. Hyde as the type genus. Subsequently, a new genus *Brunneofusispora* S.K. Huang & K.D. Hyde 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., 2016). 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)

Notes: *Occultibambusa* is typified by *O. bambusae* D.Q. Dai & K.D. Hyde was introduced by Dai et al. (2017) to accommodate species characterized by immersed, dark coloured, 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 saprophytically on dead bamboo culms in terrestrial habitats (Dai et al., 2017; Zhang, Liu et al., 2017; Jiang, Phookamsak et al., 2021; Yu et al., 2021); only *O. aquatica*, *O. kunmingensis* and *O. pustula* are from freshwater habitats (Hyde, Hongsanan et al., 2016; 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)

Fungal Names number: FN 552743; Figure 3.35

Saprobic on decaying submerged wood in freshwater habitat. **Asexual morph**: Undetermined. **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 grayish when mature, guttulate, smooth-walled, without mucilaginous sheath.

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.

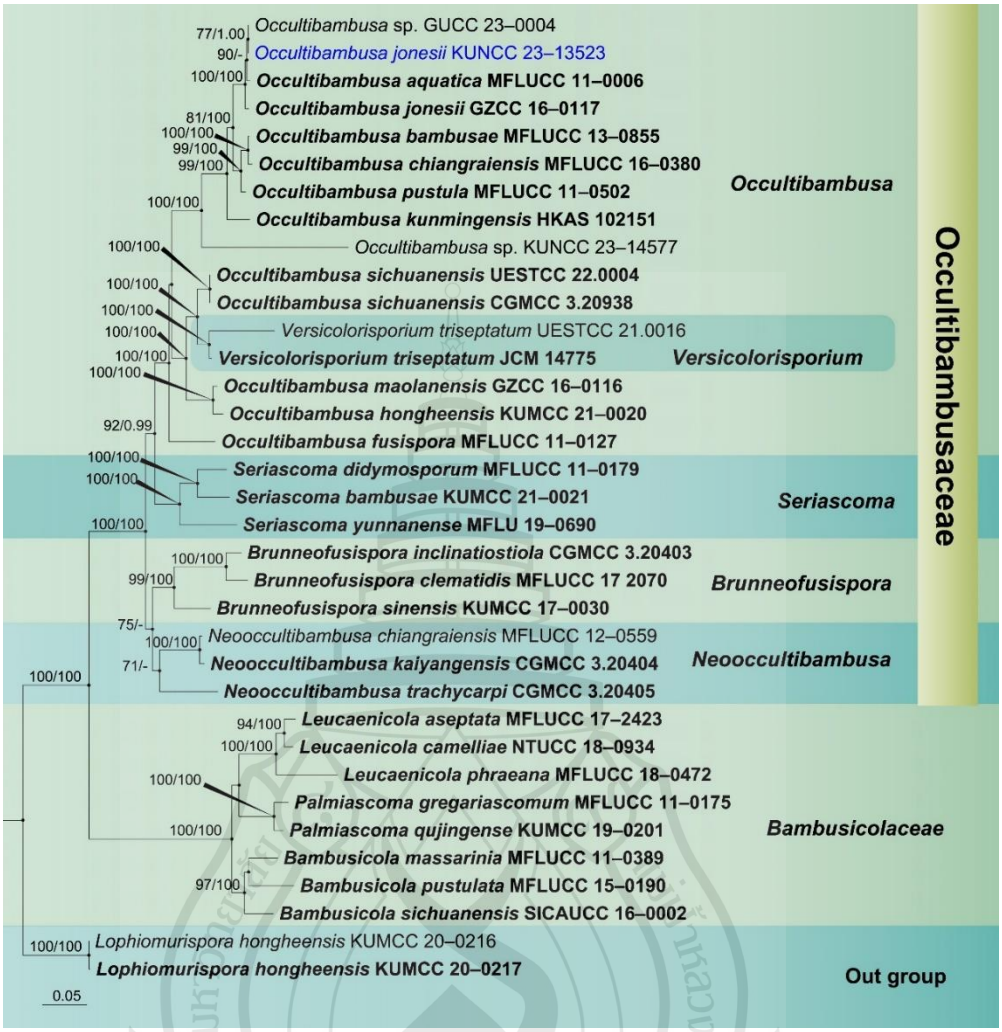
Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 23°39′18.95″ N, 102°32′57.19″ E, 1400 m; on submerged decaying wood, 22 February 2023, H.W. Shen, FD 40-35-1 (HKAS 131785), living culture KUNCC 23–13511.

Notes: Multigene phylogenetic analysis showed that our new collection clustered with *Occultibambusa aquatica* and *O. jonesii* without significant phylogenetic distance (Figure 3.36). 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 grayish, 2-celled ascospores with a broad upper cell, and without sheath (Zhang, Liu 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, Liu et al., 2017). Based on the similar morphological and molecular data,

we identified it as *O. jonesii*, which was reported from lentic freshwater habitats for the first time.

Note a Appearance of ascomata on substrate. b, c Section 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 3.35 *Occultibambusa jonesii* (HKAS 131785, new habitat record)



Note 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. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Figure 3.36 Phylogenetic tree of *Occultibambusaceae* and *Bambusicolaceae*

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

Notes: *Parabambusicolaceae* is 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, de Silva et al., 2020), *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 apapillate ostioles, clavate to fusiform asci and hyaline or brown multi-septate, clavate to fusiform, hyaline ascospores (Liu, Hyde et al., 2015; Tanaka et al., 2015; Li et al., 2016), and the asexual morphs are sporodochial or monodictys-like (Ariyawansa et al., 2015; Tanaka et al., 2015). Currently, 30 species in 14 genera are included in *Parabambusicolaceae*, these species are usually saprophytes occur on various dead or decaying plant culms, branches and leaves of plants in terrestrial habitats, as well as pteridophyte (Ariyawansa et al., 2015; Phukhamsakda et al., 2018; Phookamsak et al., 2019; Wijayawardene, Dai et al., 2022; Li, Liang 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)

Notes: *Lonicericola* is a monotypic genus introduced by Phookamsak et al. (2019) to accommodate *L. hyaloseptispora* (type species) based on morphological and phylogenetic evidences. *L. hyaloseptispora* is a saprophyte 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* member and *Magnolia grandiflora*, respectively (Yasanthika et al., 2020; Wijayawardene, Dai et al., 2022). Currently, three species are accepted in the genus and all the three species were reported

from terrestrial habitats in Yunnan, China (Yasanthika et al., 2020; Wijayawardene, Dai et al., 2022). In this study, *L. qujingensis* were collected from submerged decaying wood in freshwater habitat.

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

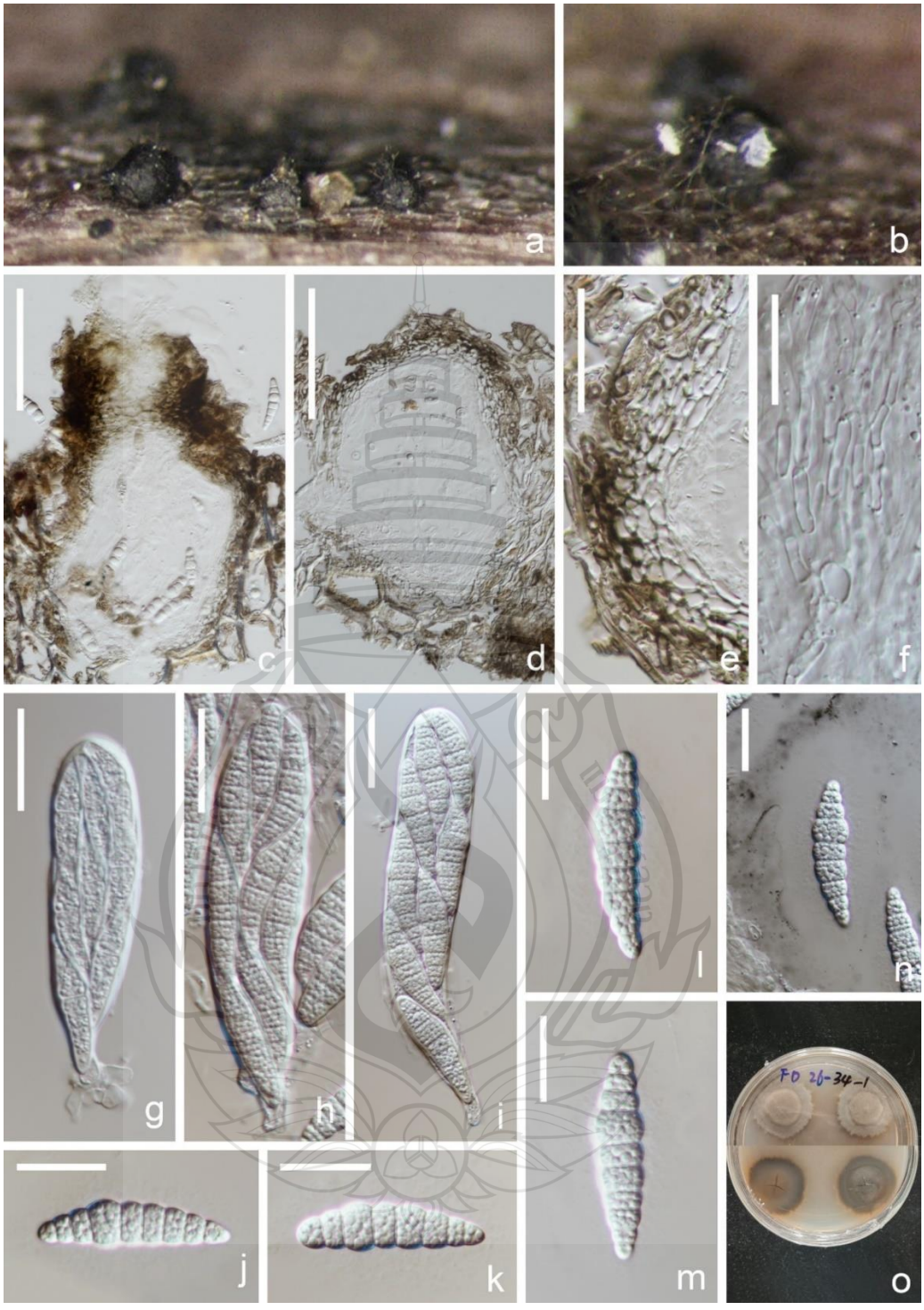
Fungal Names number: FN555252; Figure 3.37

Saprobic on decaying submerged wood in freshwater habitat. **Asexual morph**: Undetermined. **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, anastomosed 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.).

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.

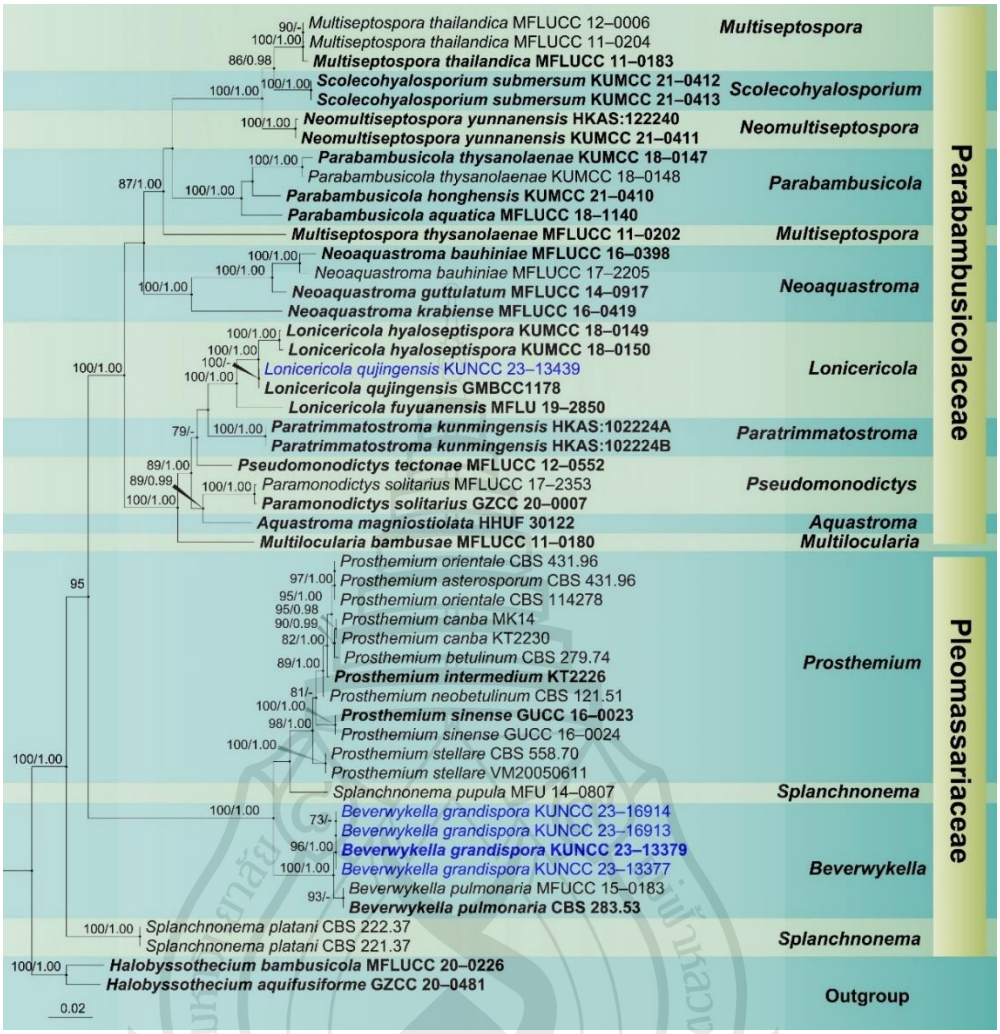
Material examined: CHINA, Yunnan Province, Kunming City, Yangzonghai Lake, 24°53′39.31″ N, 102°58′58.82″ E; 1770 m; on submerged decaying wood, 19 February 2023, Z.Q. Zhang, FD 26-34-1 (HKAS 131545), living culture KUNCC 23–13439.

Notes: Our new collection, HKAS 131545, collected from Yangzonghai Lake in Yunnan Province, it is morphologically similar to *Lonicericola hyaloseptispora* and *L. qujingensis* in having broadly cylindrical to cylindric-clavate asci; and hyaline, fusiform to vermiform, septate, smooth, guttulate ascospores, enlarged at the 3rd or 4th cell from the apex, and surrounded by a mucilaginous sheath (Wijayawardene, Dai et al., 2022). Ascospore and asci morphological characteristics can be used to distinguish species of *Lonicericola* (Wijayawardene, Dai et al., 2022). Based on the key to *Lonicericola* species provided by Wijayawardene, Dai et al. (2022), morphology of our new collection is consistent with *L. qujingensis*. Phylogenetic analysis results show that our new collection clusters with the holotype of *L. qujingensis* with 100% ML support (Figure 3.38). 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 22 base pair difference, but including 21 gaps), so we identified our new collection as *L. qujingensis,* which was first reported in freshwater habitat.



Note a, b Appearance of ascomata on host substrate. c, d Section 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 3.37 *Lonicericola qujingensis* (HKAS 131545, new habitat record)



Note 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. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and the newly generated sequence are shown in blue.

Figure 3.38 Phylogenetic tree of *Parabambusicolaceae* and *Pleomassariaceae*

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

Notes: *Pleomassariaceae* was established by Barr (1979) to accommodate *Pleomassaria*, *Splanchnonema* and *Asteromassaria*, 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, Schoch et al. (2009) 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 and 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 53 species (Wijayawardene, Hyde et al., 2022). Most members of *Pleomassariaceae* occur on branches, stems, twigs, and leaves as saprobes in terrestrial habitats (Tilak & Kale, 1970; Barr, 1982, 1993a, 1993b; 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)

Notes: *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 which 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.***

Fungal Names number: FN 572002; Figure 3.39

Etymology: The name refers to the large conidia.

Holotype: HKAS 131498.

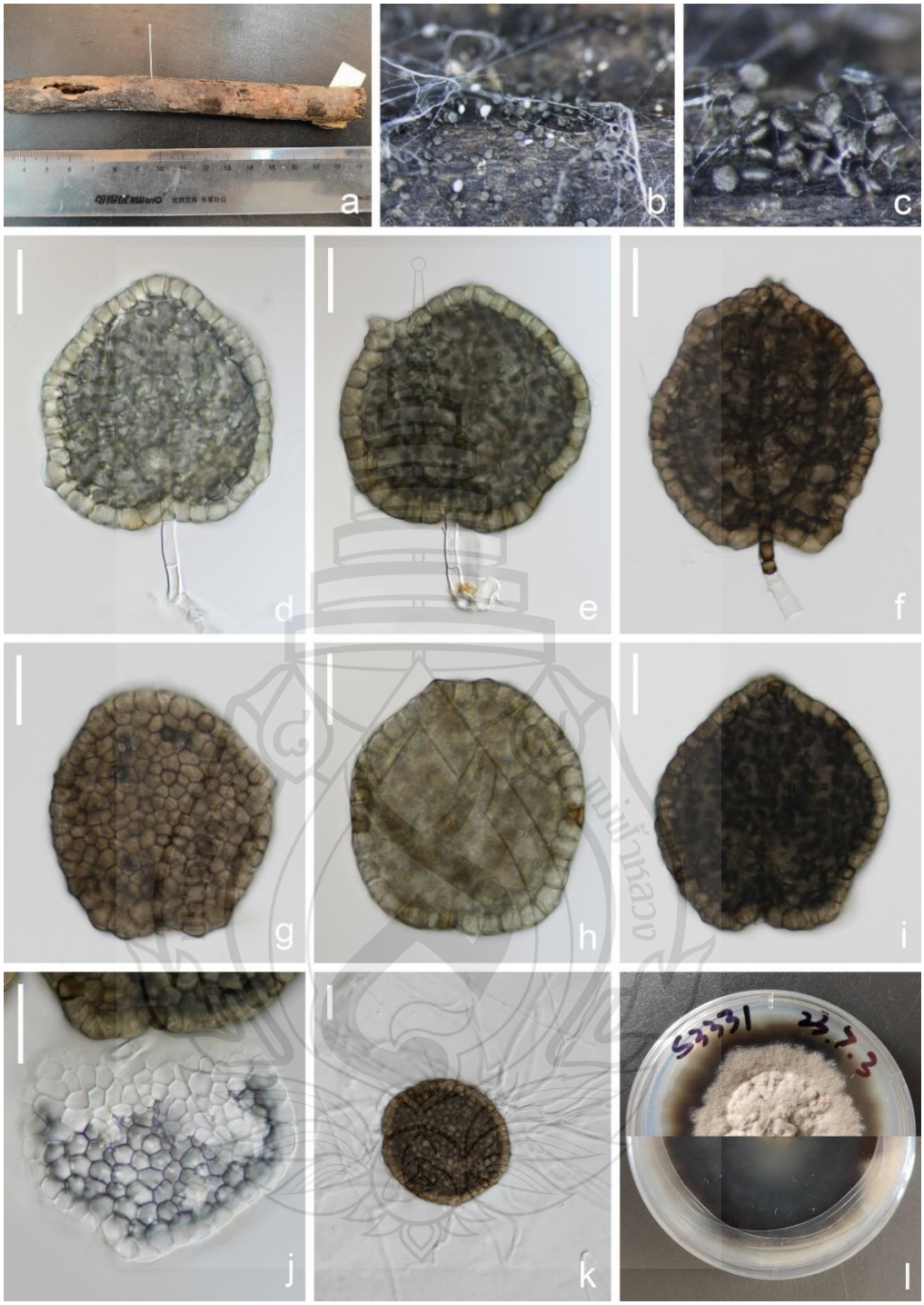
Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* effuse, brown, conspicuous. *Mycelium* partly superficial, partly immersed in the substratum, composed of smooth, branched, septate, brown hyphae. *Conidiophores* macronematous, mononematous, 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.

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 (HKAS131495), 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.

Notes: Phylogenetic analysis showed that *Beverwykella grandispora* clustered with the type species *B. pulmonaria* in an independent lineage within *Pleomassariaceae* (Figure 3.38). 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). *B. 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). Based on molecular sequence data and morphological characteristics, we introduce *B. grandispora* as a new species, it is the second species of *Beverwykella* reported from freshwater habitats.



Note 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.

Figure 3.39 *Beverwykella grandispora* (HKAS 131498, holotype)

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

Notes: *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, *Stachybotriaceae*, 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, 1791) and *Noosia* (Crous et al., 2011) in this family, based on molecular data coupled with morphological (sexual-asexual morphs) characteristics (Tanaka et al., 2015). In a recent research, Yang, Phookamsak et al. (2022) treated *Bambusistroma* and *Noosia* as synonyms of *Periconia* based on morphological and phylogenetic evidence. Currently, 225 epithets are known in this family (http://www.indexfungorum.org/Names/Names.asp; accessed on 20 Jun 2024), which subsist commonly found as saprobes on various substrates from terrestrial habitats in worldwide (Dong et al., 2020).

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

Notes: *Periconia* was introduced by Tode (1791), with *P. lichenoides* as the type species. *Periconia* species are mainly known as the asexual morph, only a few species are sexual morphs (Tanaka et al., 2015; Yang, Phookamsak et al., 2022; Su et al., 2023). The asexual morphs are 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, Phookamsak et al., 2022). And the sexual morphs are 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, Phookamsak et al., 2022). Members of *Periconia* mainly grow saprophytically 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, Phookamsak et al., 2022; Su et al., 2023). In this study, we introduced three new species, *viz*., *Periconia dujuanhuensis*, *P. hongheensis* and *P. yunnanensis*.

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

Fungal Names number: FN 572003; Figure 3.40

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

Holotype: HKAS 131782.

Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **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, verruculose.

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.

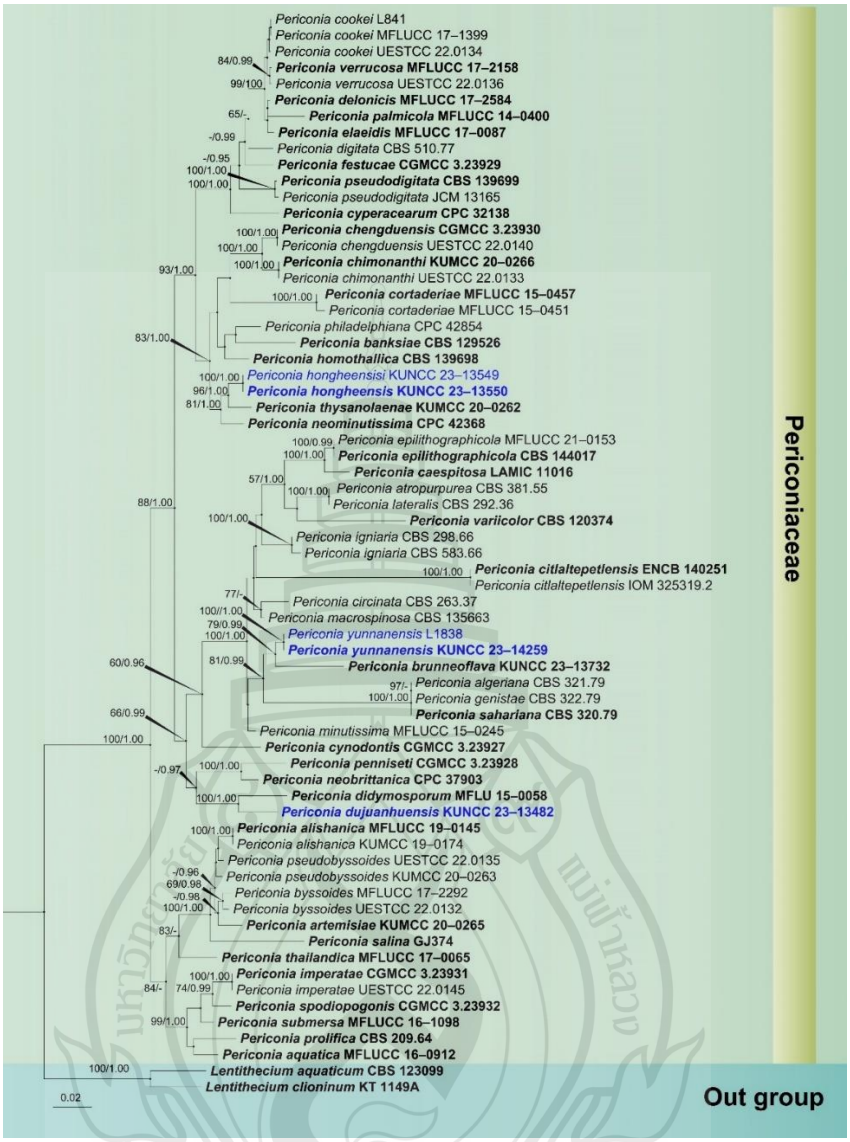
Material examined: CHINA, Yunnan Province, Puer City, Dujuanhu Lake, 24°32′30.44" N, 101°1′39.51″ E, 2500 m; on submerged decaying wood, 24 February 2023, H.W. Shen, FD 48-42-1 (HKAS 131782, holotype), ex-type culture KUNCC 23–13438.

Notes: Phylogenetic analysis showed that *Periconia dujuanhuensis* clustered as a sister clade with *P. didymosporum* with 100% ML and 1.00 PP support (Figure 3.41). *P. didymosporum* only sexual morph are known, it was transferred from the *Bambusistroma* based on morphological characteristics and phylogenetic analysis (Yang, Phookamsak et al., 2022). *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, Phookamsak et al., 2022).

Periconia dujuanhuensis only reported by the asexual morphs, we are unable to compare the morphology between *P. dujuanhuensis* and *P. didymosporum*, but our new collection is morphologically fit 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 habitat.

Note 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 3.40 *Periconia dujuanhuensis* (HKAS 131782, holotype)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef*1-α sequence dataset representing *Periconiaceae*. Sixty-seven strains are included in the combined analyses which comprise 3220 characters including gaps (860 characters for LSU, 542 characters for ITS, 937 characters for SSU, 881 characters for *tef*1-α). *Lentithecium aquaticum* (CBS 123099) and *L. clioninum* (KT 1149A) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and newly generated sequence are shown in blue.

Figure 3.41 Phylogenetic tree of *Periconiaceae*

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

Fungal Names number: FN 572004; Figure 3.42

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

Holotype: HKAS 131670.

Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **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.

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 is 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.

Notes: Based on a megablast search of NCBIs GenBank nucleotide database, the best matching result of ITS sequence is *Periconia macrospinosa* (strain BRPET25, sequence ID: MT658103; identities: 507/508 (99%), 1 gap). The best matching result of LSU sequence is *P. digitata* (strain CBS 510.77, sequence ID: AB807561; identities: 1253/1267 (99%), 2 gaps). The best matching result of *tef*1-α sequence is *P. thysanolaenae* (strain KUMCC 20–0262, sequence ID: MW460896; identities: 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 96%

ML and 1.00 PP support (Figure 3.41). *Periconia hongheensis* is similar to *P. thysanolaenae* in having macronematous, mononematous conidiophores that are branched at the apex, polyblastic, ovoid to subglobose conidiogenous cells, and catenulate, globose, and verrucous conidia (Yang, Phookamsak et al., 2022). 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, we introduce *P. hongheensis* as a new species.

Note 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.

Figure 3.42 *Periconia hongheensis* (HKAS 131670, holotype)

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

Fungal Names number: FN 572005; *Facesoffungi number*: ****; Figure 3.43

Etymology: The name refers to the location where this species was collected, Yunnan Province.

Holotype: HKAS 131727.

Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **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, monstly 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.

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 middle 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 (HKAS 131424, paratype), ex-paratype culture KUNCC 23–16910.

Note: Phylogenetic analysis showed that *Periconia yunnanensis* clusters with *P. brunneoflava* with 79% ML and 0.99 PP support (Figure 3.41). Comparison of the ITS, LSU, and *tef*1-α gene between *P. yunnanensis* and *P. brunneoflava* revealed 0.6% (3/479 bp), 6.2% (79/1268 bp), and 0.6% (4/718 bp, one gap) base pair differences, respectively. In addition, *P. yunnanensis* is morphologically similar to *P. brunneoflava* with globose, brown to dark brown, aseptate, verrucose conidia. However, *Periconia*

yunnanensis has longer conidiophores (474–583 μm vs. 150–240 μm) than *P. brunneoflava*. We therefore, introduce *P. yunnanensis* as a new species, based on morphological characters and phylogenetic analysis.

Note 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.

Figure 3.43 *Periconia yunnanensis* (HKAS 131727, holotype)

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

Notes: *Roussoellaceae* was introduced by Liu et al. (2014) to accommodate three genera, *Neoroussoella*, *Roussoella* (type genus) and *Roussoellopsis*. According to the updated "Outline of Fungi and fungus-like taxa – 2021" by Wijayawardene, Hyde et al. (2022) twelve genera are included in *Roussoellaceae*. Subsequent studies have transferred *Immotthia* to *Dictyosporiaceae* based on morphological and phylogenetic analyses (Jiang et al., 2019). Currently the family contains eleven genera *viz.*, *Appendispora, Elongatopedicellata, Neoroussoella, Pararoussoella, Pseudoneoconiothyrium, Pseudoroussoella, Roussoella, Roussoellopsis, Setoarthopyrenia* and *Xenoroussoella* (Jiang et al., 2019; Wijayawardene, Hyde et al., 2022).

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

Notes: *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 asexual morph is characterized by superficial or semi-immersed, subglobose, multilocular conidiomata; holo- or entero-blastic, hyaline, cylindrical to ellipsoidal, ampulliform conidiogenous cells; oblong, ellipsoidal, globose, obovoid, aseptate conidia (Liu et al., 2014; Dai et al., 2022). *Roussoella* species are primarily saprophytic in terrestrial habitats and most are associated with bamboo), 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., 2015). *R. aquatica*, *R. intermedia* and *R. minutella* were reported from freshwater habitats (Dong et al., 2020). *R. 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 missing (Dai et al., 2022).

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

Fungal Names number: FN 572006; Figure 3.44

Etymology: The name refers to the location where this species was collected, Dujuanhu Lake.

Holotype: HKAS 131782.

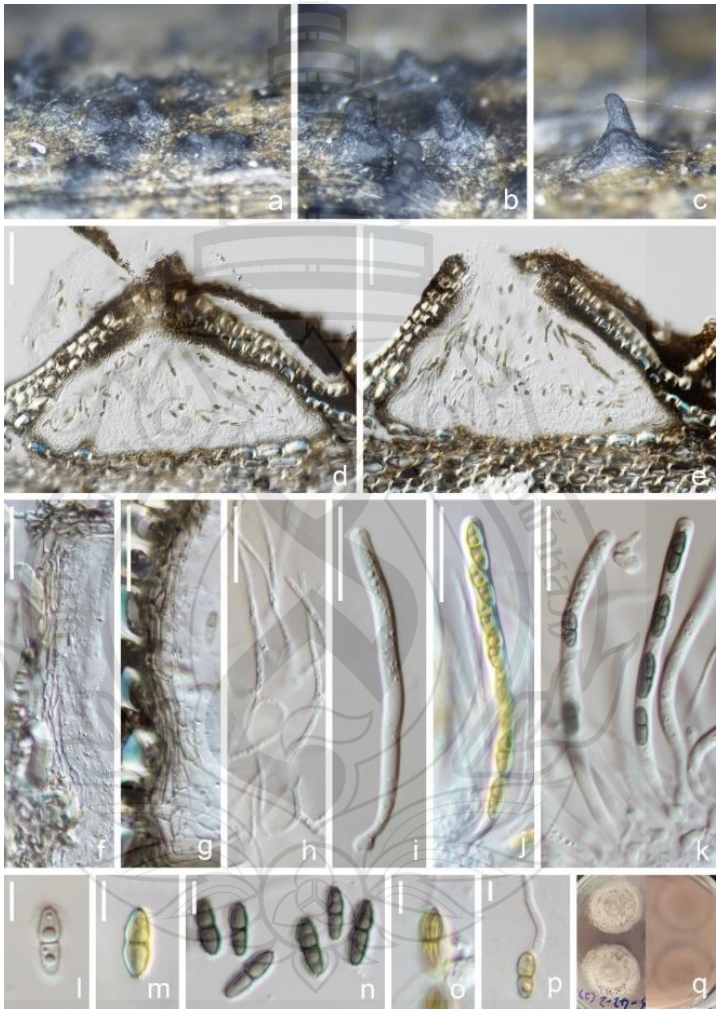
Saprobic on decaying submerged wood in freshwater habitat. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 180–230 μm high, 270–330 μm diam., solitary, scattered to gregarious, immersed under an epidermis, erumpent to semi-immersed, visible as raised on host surface, dark brown to black, 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 gray brown when mature, guttulate, verrucose, with longitudinally striated surface, surrounded by a mucilaginous sheath.

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, on submerged decaying culm of bamboo, 24 February 2023, H.W. Shen, FD 48-42-2 (HKAS 131782, holotype), ex-type KUNCC 23–13438.

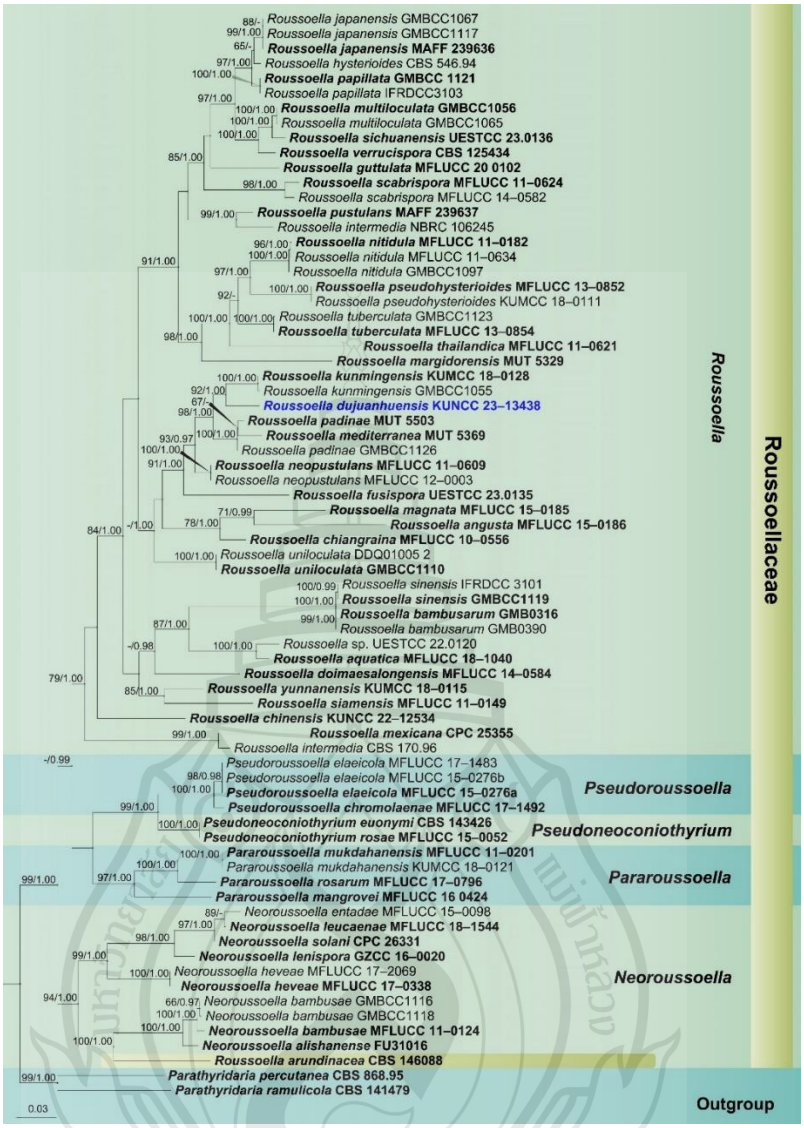
Notes: Phylogenetic analysis showed that *Roussoella dujuanhuensis* clustered with *R kunmingensis* with 92% ML and 1.00 PP support (Figure 3.45). A comparison of ITS, LSU, *tef*1-α and *rpb*2 sequence data between *R. dujuanhuensis* and *R kunmingensis* showed 7.2% (26/361 bp, including 5 gaps), 0.25% (2/796 bp), 2.2% (19/883 bp), 6. 1% (53/873 bp) base pair differences, respectively. Morphologically,

R. 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 *R. kunmingensis* (Jiang et al., 2019). Based on phylogenetic analysis and unique morphological characteristics, we introduced *R. dujuanhuensis* as a new species.



Note a–c Appearance of ascomata on host substrate. d, e Section of ascomata. f, g Peridium. h 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 3.44 *Roussoella dujuanhuensis* (HKAS 131782, holotype)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *tef*1-α and *rpb*2 sequence dataset representing *Roussoellaceae*. Seventy-three strains are included in the combined analyses which comprise 3274 characters including gaps (853 characters for LSU, 495 characters for ITS, 890 characters for *tef*1-α, 1036 characters for *rpb*2). *Parathyridaria percutanea* (CBS 868.95) and *P. ramulicola* (CBS 141479) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and newly generated sequence are shown in blue.

Figure 3.45 Phylogenetic tree for *Roussoellaceae*

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

Notes: *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). Later, 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, Crous et al., 2009). Based on morphological and molecular phylogenetic evidence, Jaklitsch et al. (2016) applied a broad generic concept in *Teichosporaceae*, and 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, Hyde et al. (2022) 17 genera are accepted in *Teichosporaceae*.

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

Notes: *Floricola* was introduced by Kohlmeyer and Volkmann-Kohlmeyer (2000) with *F. striata* Kohlm. & Volkm.-Kohlm. (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. Later, Jaklitsch et al. (2016) applied a broad generic concept in *Teichosporaceae*, and treated *Floricola* and *Misturatosphaeria*, and the seven newly introduced genera as synonymous with *Teichospora*, and *Floricolaceae* as a synonym of *Teichosporaceae*. However, subsequent studies were not accepted this treatment, *Floricola* and other eight genera were reinstated (Boonmee et al., 2019; Tennakoon et al., 2021). 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 clematidi*, *F. festucae*, *F. juncicola*, *F. striata*, *F. sulcata* (*Sclerostagonospora sulcata*), and *F. viticola*, these species grow saprophytically 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, Begoude et al., 2022).

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

Fungal Names number: FN 572007; Figure 3.46

Etymology: The name refers to the aquatic habitat in which the type of this species was collected.

Holotype: HKAS 131717.

Saprobic on decaying submerged wood in a freshwater Lake. **Asexual morph**: Undetermined. **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 hyaline, somewhat flattened cells. *Hamathecium* composed of 2–3 μm wide, septate, guttulate, trabeculate 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 an entire mucilaginous sheath.

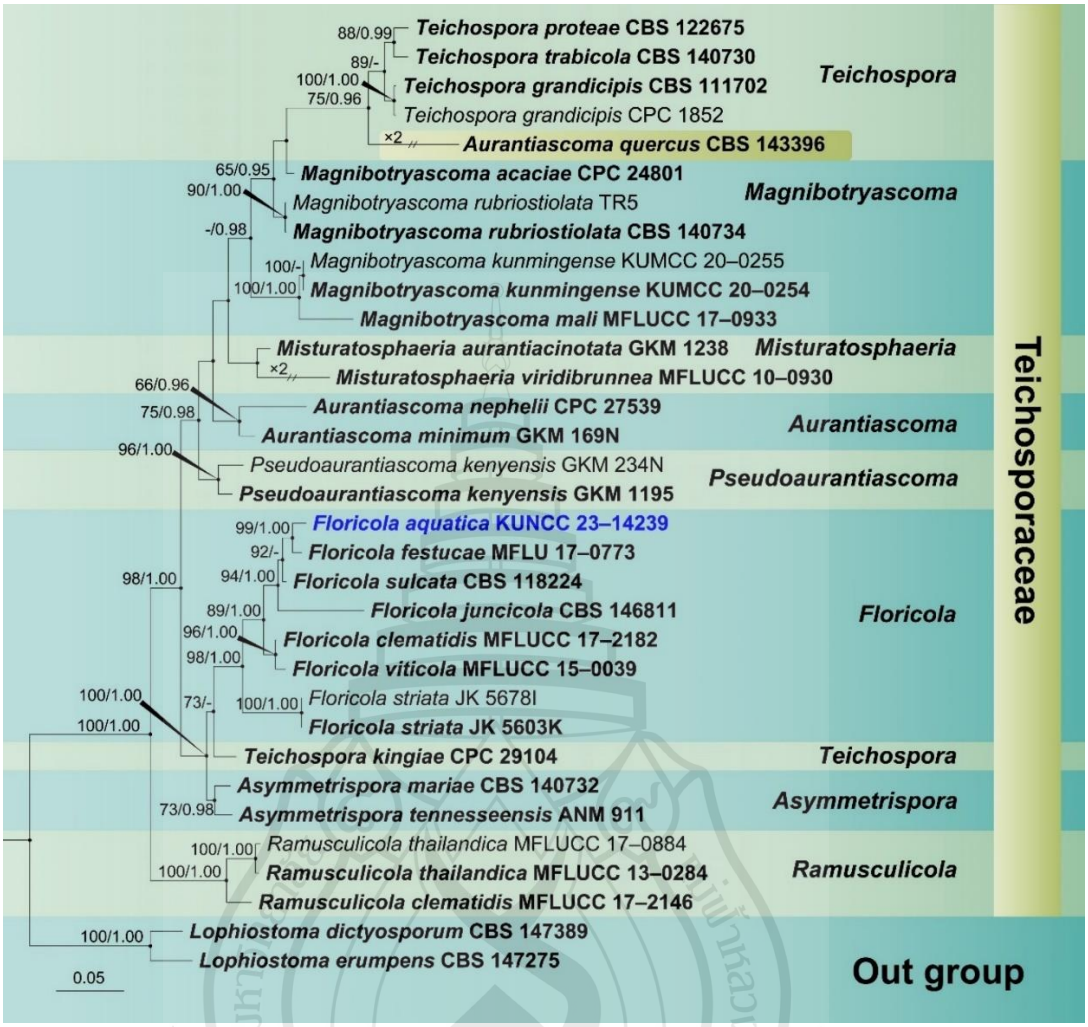
Culture characteristics: Ascospore germinated on PDA within 12 h and germ tubes produced from ends of ascospore. Colonies on PDA reaching 5 cm diam. after one months at the room temperature, colony circular, smooth edge, surface hyphae brown, flocculent, dense, sparse and thin at the edge; reverse side 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; on unknown submerged decaying wood, 19 February 2023, S. Luan, FD 38-30-2 (HKAS 131717, holotype), ex-type culture KUNCC 23–14239.

Notes: Phylogenetic analysis showed that *Floricola aquatica* clustered together with the sexual species, *F. festucae*, with 99% ML and 1.00 PP support (Figure 3.47). A nucleotides comparison of ITS, LSU, SSU and *tef*1-α gene 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) diferrences, respectively. *Floricola aquatica* is morphologically similar to *F. festucae* in having semi-immersed to immersed, globose to subglobose ascomata, cylindric-fusiform, septate, guttulate ascospores (Tennakoon et al., 2021). Since all *Floricola* members are sexual species 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 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 entire mucilaginous sheath. Therefore, based on morphological and phylogenetic analyses, we introduce *F. aquatica* as a new species, which is the first species of *Floricola* discovered in freshwater habitat.

Note 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 3.46 *Floricola aquatica* (HKAS 131717, holotype)



Note 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. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and newly generated sequence are shown in blue.

Figure 3.47 Phylogenetic tree for *Teichosporaceae*

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

Notes: *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, Bao et al., 2021). *Tetraplosphaeriaceae* is mainly known for the tetraploa-like asexual morph wherein, the conidia are globose to long obpyriform, composed of 3–8 columns or internal hyphal structure, with 2–8 setose appendages arising from apical or/and basal part (Tanaka et al., 2009; Hyde et al., 2013; Dong et al., 2020; Li, Bao 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., 2020). Most members of *Tetraplosphaeriaceae* occur as saprophytes 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, Dong et al., 2020), and a few also reported as endophytic (Crous, Cowan et al., 2021). A few species of *Tetraplosphaeriaceae* are also found in freshwater habitats and fossils (Tanaka et al., 2009; Dong et al., 2020; Li et al., 2020; Li, Bao et al., 2021; Liu, Feng et al., 2023; Zhao et al., 2024).

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

Notes: *Pseudotetraploa*, proposed for three tetraploa-like species, is characterized by conidia composed of 4 to 8 columns, obpyriform to long obpyriform, pseudoseptate, with 4 (rarely 6 to 8) setose appendages, and with *P. curviappendiculata* (Sat. Hatak., Kaz. Tanaka & Y. Harada) Kaz. Tanaka & K. Hiray. as the type species (Tanaka et al., 2009; Hyde et al., 2013). *Pseudotetraploa* species as saprobes appear to be associated with bamboo and currently contain six species, *viz.*, *P. bambusicola*, *P. curviappendiculata* (*Tetraploa curviappendiculata*), *P. javanica* (*T. javanica*), *P. longissima* (*T. longissima*), *P. rajmachiensis* and *P. yunnanensis*, and all of them

from terrestrial habitats (Tanaka et al., 2009; Hyde, Dong et al., 2020; Yu et al., 2022; Tang et al., 2023).

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

Fungal Names number: FN 572008; Figure 3.48

Etymology: The name refers to the aquatic habitat in which the type of this species was collected.

Holotype: HKAS 131574.

Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **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 undistinguishable from superficial hyphae. *Conidia* solitary, straight or slightly curved, brown to dark brown, pseudoseptate, 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 are 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, and germinate easily, with germ tubes emerging from the basal cells or the apical cells.

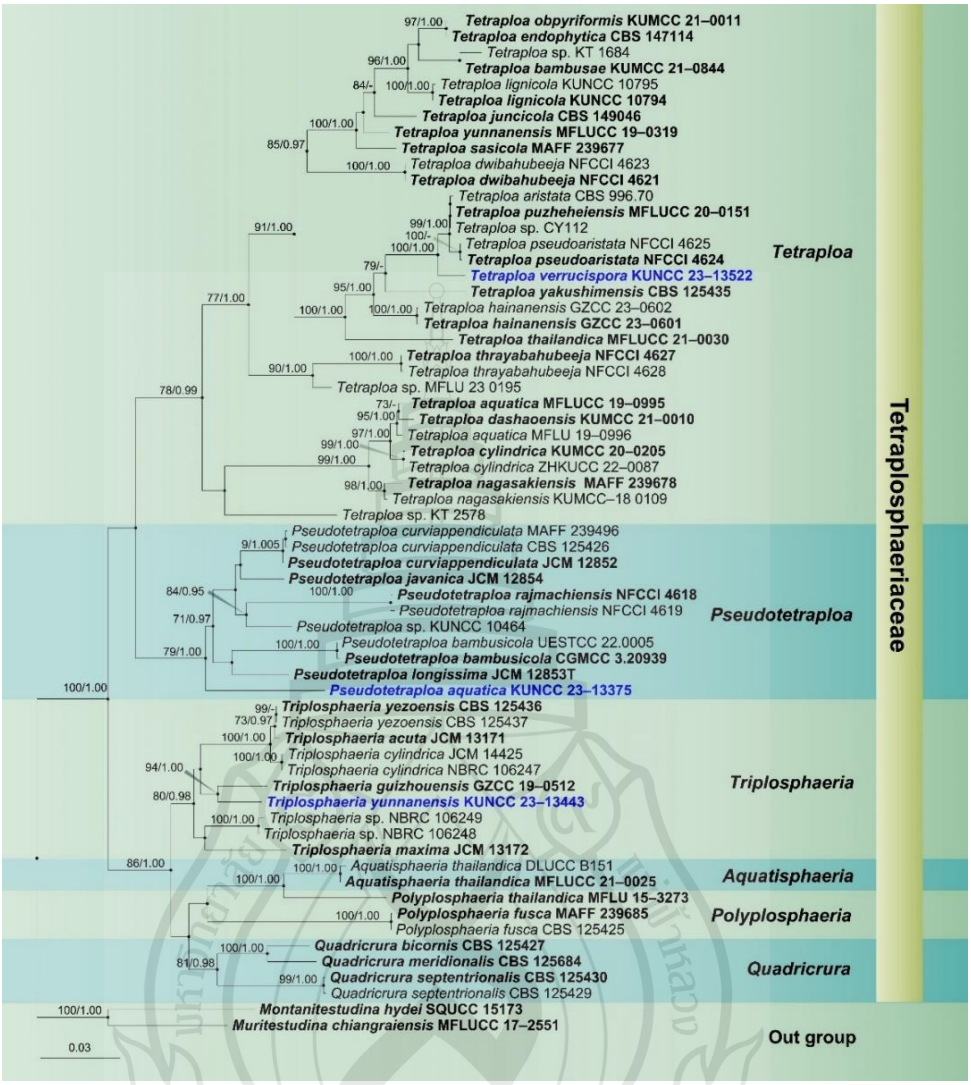
Material examined: CHINA, Yunnan Province, Puer City, Dujuanhu Lake, 24°32′30.44" N, 101°1′39.51″ E; 2500 m, on submerged decaying wood, 24 February 2023, H.W. Shen, FD 48-4-1 (HKAS 131574, holotype), ex-type culture KUNCC 23–13375.

Notes: Multigene phylogenetic analysis showed that *Pseudotetraploa aquatica* formed an independent lineage basal to *Pseudotetraploa* with 79% ML and 1.00 PP support (Figure 3.49). Based on a megablast search of NCBIs GenBank nucleotide database, the best matching result of ITS sequence is *Quadricrura meridionalis* (strain CBS 125684, sequence ID: MH863636; identities: 451/483(93%), 5 gaps). The best matching result of LSU sequence is *Pseudotetraploa javanica* (strain HC 4934, sequence ID: AB524611; identities: 1250/1268(99%), one gap). The best matching

result of *β-tubulin* sequence is *P. longissima* (strain HC 4933, sequence ID: AB524858; identities: 500/568(88%), 7 gaps). Morphologically, *P. aquatica* can be distinguished from other *Pseudotetraploa* species by several unique features, such as, lacks 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, we introduce *P. aquatica* as a new species, which is the first species of this genus reported from freshwater habitats.

Note a, b Colonies on natural substrate. c–h Conidia and germ tubes germinate from the apex. Scale bars: c–h = 20 μm.

Figure 3.48 *Pseudotetraploa aquatica* (HKAS 131574, holotype)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU and *β-tubulin* 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 *β-tubulin*). *Montanitestudina hydei* (SQUCC 1517) and *Muritestudina chiangraiensis* (MFLUCC 17–2551) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. The type strains indicated are in bold and newly generated sequence are shown in blue.

Figure 3.49 Phylogenetic tree for *Tetraplosphaeriaceae*

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

Notes: *Triplosphaeria* was introduced by Tanaka et al. (2009) to accommodate massarina-like ascomycetes with tetraploa-like asexual morphs. The sexual morphs are characterized by hyaline, 1-septate, fusiform ascospore with an entire sheath. The asexual morph is tetraploa-like with ovoid to obpyriform conidia composed of 3 columns, with 3 setae appendages at the apex. *Triplosphaeria* is similar to *Tetraploa* but differs by its hemispherical ascomata with 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 all of them are saprophytes and probably related to bamboo. *Triplosphaeria acuta* and *T. guizhouensis* were collected from freshwater habitats (Tanaka et al., 2009; Liu, Feng et al., 2023).

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

Fungal Names number: FN 572009; Figure 3.50

Etymology: The name refers to the location where this species was collected, Yunnan Province.

Holotype: HKAS 132043.

Saprobic on decaying submerged wood in freshwater habitat. **Sexual morph**: Undetermined. **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 undistinguishable from 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, sometimes divided into 3–4 separate columns from the base and middle. composed of 2–4 columns of cells, 9–10-septate in each column, guttulate, smooth-walled or sometimes verrucose on the base cell, with 3–4 setose appendages. Appendages (10–)13–21(–29) × 3 μm, divergent, pale brown to brown, (1–)2-septate, straight or slightly flexuous, smooth-walled.

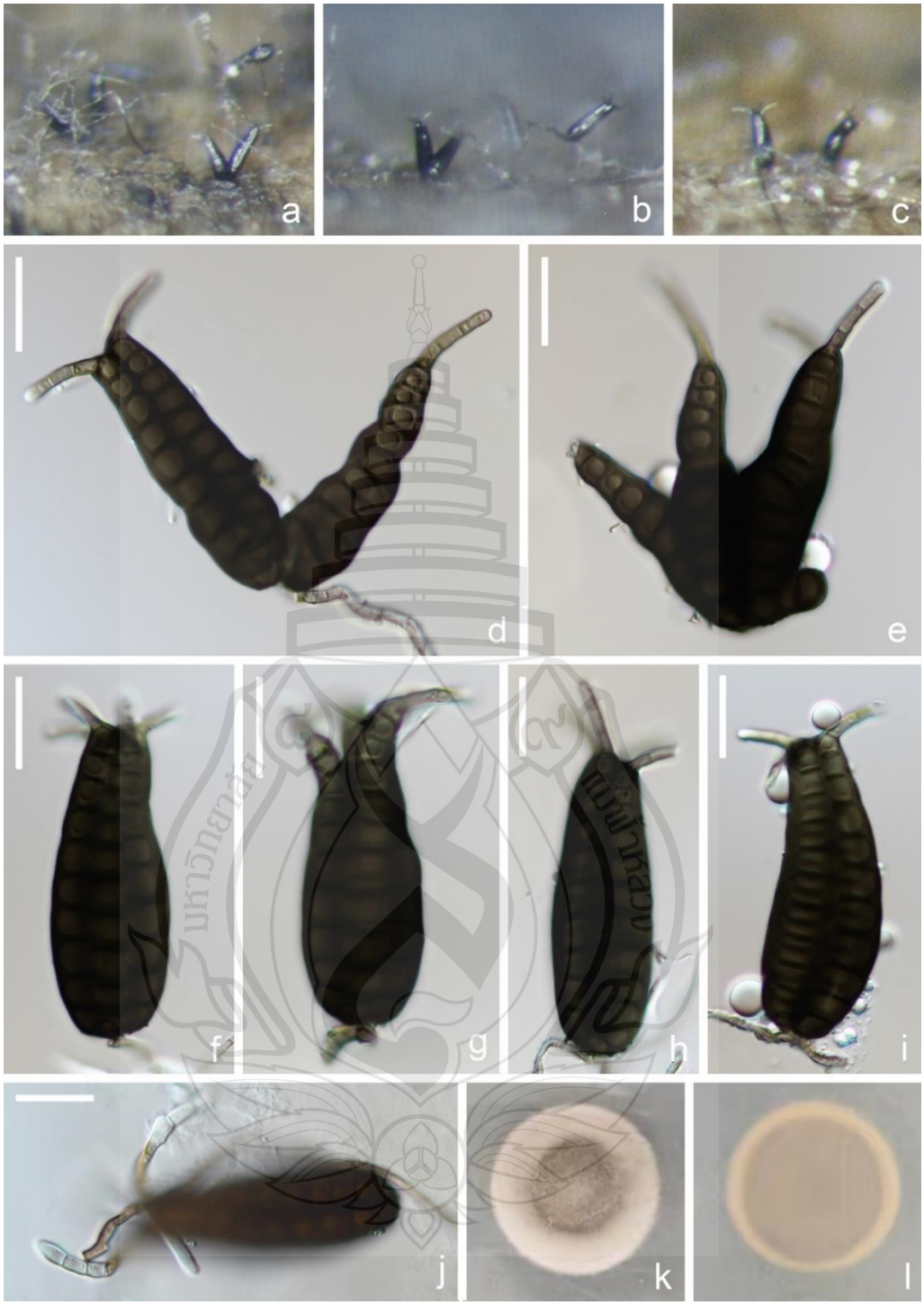
Cultural characteristics: Conidia germinating on PDA and germ tubes produced from appendages within 12 h. Colonies on PDA, reaching 1–1.5 cm after one month at room temperature, colony circular, smooth edge, surface hyphae white to gray-brown, flocculent; reverse side gray to brown.

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.

Notes: Phylogenetic analysis showed that *Triplosphaeria yunnanensis* clustered with *T. guizhouensis* with 94% ML and 1.00 PP support (Figure 3.49). *Triplosphaeria guizhouensis* is asexual species collected on submerged decaying wood from a stream in Guizhou Province, China, the conidia composed of three or four columns, guttulate, sometimes verrucose on the base cell, with 3–4 setae appendages. *Triplosphaeria yunnanensis* is also an asexual species found on submerged decaying wood in freshwater habitats, collected from Dujuanhu Lake, a plateau lake in Yunnan. Morphologically, *T. yunnanensis* is similar to *T. guizhouensis* with conidia having 3–4 columns and 3–4 setose appendages (Liu, Feng 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. Nucleotides comparison of the ITS, LSU, SSU and *tub* gene 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, *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 (Figure 3.49). 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 RSA medium, Tanaka et al. (2009) treated them as *Triplosphaeria* sp.. The conidia observed on the host plant are different from those produced on medium, and this has also been found in some previous studies (Boonmee et al., 2021; Yang et al., 2023). At the same time, there are significant morphological differences in the conidia produced in different media, such as *Fusarium* spp. (Souza et al., 2017). Except for *T. guizhouensis* and *T. yunnanensis*, asexual morphs of other *Triplosphaeria* species are observed from cultured on RSA medium (Tanaka et al., 2009). These species can

be distinguished from each other by the characteristics of the conidia (including *Triplosphaeria* sp.) (Tanaka et al., 2009). Although, *T. guizhouensis*, *T. yunnanensis* and *Triplosphaeria* sp. lack sexual morphs, they can still be easily distinguished based on the morphological characteristics of conidia (shape, size, septa and appendage characteristics) and molecular data. Based on the morphological differences of asexual types and phylogenetic analysis results, *Triplosphaeria* sp. should be regarded as a new species of *Triplosphaeria*. Since Tanaka et al. (2009) did not provide a description, and we did not examine the specimens, it will remain as *Triplosphaeria* sp. here.



Note a–c Colonies on natural substrate. d, f–i Conidia with the appendages and unconspicuous conidiogenous cells. e conidium. j Germinating conidium. k, l Colony on PDA (k from above, l from below). Scale bars: d–j = 20 μm.

Figure 3.50 *Triplosphaeria yunnanensis* (HKAS 132043, holotype)

3.4 Discussion

Research on lignicolous freshwater fungi in China has developed rapidly since the beginning of the 20th century. Several studies have been carried out to understand the species diversity and community structure of lignicolous freshwater fungi in the plateau lakes of Yunnan Province, China, and reported a large number of fungi including several interesting species and new species (Cai et al., 2002; Luo et al., 2004). Subsequent studies, introduced several new species from different lakes in Yunnan Plateau and reported also a few habitat records, based on morphological and multi-gene phylogenetic evidence (Luo et al., 2017, 2019; Luo, Hyde, Liu et al., 2018; Huang et al., 2022; Li et al., 2022; Shen, Bao, Wanasinghe et al., 2022; Bao et al., 2023; Luan et al., 2023; Shen et al., 2023). Although these newly described species have increased the number of lignicolous freshwater fungi in Yunnan Plateau lakes, our knowledge of freshwater fungi in Yunnan Plateau lakes is still limited compared to the lotic freshwater habitats. Therefore, to further understand the lignicolous freshwater fungi from plateau lakes, we systematically collected submerged specimens from plateau lakes in Yunnan Province during past two years, carefully investigated them and introduced several new species, which included new habitat and geographical records (Huang et al., 2022; Li et al., 2022; Luan et al., 2023; Shen et al., 2023).

This chapter is part of the study on lignicolous freshwater fungi in Yunnan. We collected submerged wood specimens from several plateau lakes (including, Cibihu, Dianchi, Dujuanhu, Erhai, Fuxianhu, Luguhu, Qiluhu, Xihu, Xingyunhu, Yangzonghai and Yilonghu Lakes) and studied the lignicolous freshwater fungi based on morphological and phylogenetic analyses. Through this study, we discovered some interesting and novel lignicolous freshwater fungi. Based on preliminary identification results, we conducted a comprehensive morphological and phylogenetic study on 55 collections belonging to *Dothideomycetes*. The results revealed 35 species, 26 of which were novel and 9 were known. These 35 species were assigned to 23 genera in 15 families of *Kirschsteiniotheliales*, *Microthyriales*, and *Pleosporales*. The *Pleosporales* contained the most species, 33 in total, while *Kirschsteiniotheliales* and *Microthyriales* contained one each.

CHAPTER 4

LIGNICOLOUS FRESHWATER SORDARIOMYCETES FROM PLATEAU LAKES IN YUNNAN

4.1 Introduction

Sordariomycetes is one of the largest classes of *Ascomycota* was introduced by Eriksson and Winka (1997) for taxa with perithecial ascomata, paraphysate hamathecium, periphysate ostioles and unitunicate or pseudoprotunicate asci. The class *Sordariomycetes* comprises a highly diverse range of fungi characterized mainly by perithecial ascomata and inoperculate unitunicate asci (Luo et al., 2019; Hyde, Norphanphoun et al., 2020). Members of the *Sordariomycetes* have a cosmopolitan distribution and accommodates mostly terrestrial taxa, some species are also found in aquatic habitats (Luo et al., 2019; Bao et al., 2023; Yang et al., 2023). Freshwater *Sordariomycetes* is one of the major and important fungal groups with a vital role in ecosystems (Hyde, Fryar et al., 2016; Luo et al., 2019). The latest systematic study of lignicolous freshwater *Sordariomycetes* was carried out by Luo et al. (2019) with taxonomic accounts for each genus. The study by Luo et al. (2019) documented *Sordariomycetes* species inhabiting freshwater habitats, including six subclasses, 30 orders, 56 families and 160 genera. Hyde et al. (2021) conducted an evolutionary analysis of the subclass *Diaporthomycetidae* under the class *Sordariomycetes*, proposing five new orders and six new families, and provided evidence of phylogeny, divergence estimates, and unique morphology. Bao et al. (2023) performed a phylogenetic and evolutionary analysis of the subclass *Hypocreomycetidae*, introducing new species and new families, and analyzed the ancestral character state of *Hypocreomycetidae* species in different habitats (including freshwater, marine and terrestrial habitats). The results indicated that freshwater and marine taxa evolved from terrestrial ancestors.

This chapter covers lignicolous freshwater *Sordariomycetes* species from plateau lakes in the Yunnan Province, China. Through morphological examination and

molecular phylogenetic analysis, we identified and determined the phylogenetic placement of the novel lignicolous freshwater fungi. We introduced one new genus, *Paralentithecium*, 24 new species, *viz. Apiospora fuxianhuensis, A. hongheensis, Chloridium guttulatum, C. yunnanense, Dematiosporium hydei, D. muriforme, Fuscocatenula guttulata, Obliquifusoideum sinense, Pseudodactylaria guttulata, Pseudostanjehughesia tripospora, P. verrucosa, Sporidesmium dianchiense, S. distoseptatum, S. guttulatum, S. hongheense, S. hydei, S. kunmingense, S. yangzonghaiense, S. yunnanense, Sporidesmiella dujuanhuensis, Sp. gattulata, Sp. hongheensis, Sp. hydei, Xylolentia aquatica*. Discovered three two geographical records in China, *viz.*, *Codinaea paniculata, Dematipyriforma nilotica*, and six new freshwater habitat records, *viz.*, *A. guangdongensis*, *A. marii*, *C. chlamydosporum*, *Multiguttulispora dimorpha*, *Tainosphaeria phialogeniculata*, *Thozetella wenyingiae*. Detailed descriptions, illustrations, and notes are provided for these species.

4.2 Materials and Methods

Sample collection, processing and cultivation; morphological studies and isolation; DNA extraction, PCR amplification and sequencing; phylogenetic analyses are carried out according to the steps in chapter 2.

4.3 Taxonomy and Phylogeny

Sordariomycetes

Amphisphaeriales

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr

Notes: *Apiosporaceae* was introduced by Hyde et al. (1998) to accommodate *Apiospora* Sacc., based on unique morphological characteristics. Currently, *Apiosporaceae* is placed in *Amphisphaeriales* and contains three genera, *viz. Apiospora* Sacc., *Arthrinium* Kunze and *Nigrospora* Zimm. (Samarakoon et al., 2020; Pintos and Alvarado 2021). *Apiosporaceae* species are saprobic, pathogenic or endophytic on plant tissues, lichens, and marine algae in terrestrial and freshwater habitats, occasionally infecting humans (Luo et al., 2019; Hyde, Norphanphoun et al., 2020).

Apiospora Sacc.

Notes: *Apiospora* was introduced by Saccardo (1875) with *A. montagnei* Sacc. as the type species. The sexual morphs of *Apiospora* are characterized by multi-locular perithecial stromata with hyaline ascospores surrounded by a thick gelatinous sheath (Dai et al., 2017; Pintos & Alvarado, 2021). The asexual morphs are characterized by basauxic, cylindrical, flexuous, unbranched conidiophores; conidiogenous cells ampulliform to cylindrical, with tiny denticles, hyaline; conidia in face view clavate, oval, elliptical, globose, subglobose, ellipsoid, subcylindrical, lobed, dentate or polygonal; in side view lenticular, with a pale equatorial slit (Pintos & Alvarado, 2021). The asexual morphs of *Apiospora* are similar to *Arthrinium*, so for a long time Apiospora was considered to be the asexual stage of *Arthrinium* (Crous & Groenewald, 2013; Pintos et al., 2019; Senanayake et al., 2020; Feng et al., 2021; Pintos & Alvarado, 2021). Crous and Groenewald (2013) re-evaluated the phylogeny of *Arthrinium* based on sequence data-sets and reduced *Apiospora* to a synonym of *Arthrinium* based on principle of nomenclatural priority. Based on morphological, sequence and ecological data, Pintos and Alvarado (2021) suggested that *Arthrinium* and *Apiospora* should be separated as two independent genera, although *Arthrinium* and *Apiospora* have no clear diagnostic characteristics. The study was generally accepted (Monkai et al., 2022; Pintos & Alvarado, 2022; Li, Peng et al., 2023; Liao et al., 2023; Liu, Li et al., 2023; Zhang, Chen, Boonmee et al., 2023), and subsequent genomic analysis confirmed the taxonomic decisions of the study (Sorensen et al., 2022). Species of *Apiospora* are distributed worldwide, and they have been reported as saprobes, endophytes, and pathogens of humans and plants (Hyde, Norphanphoun et al., 2020; Liao et al., 2023; Zhang, Chen, Boonmee et al., 2023).

Apiospora aquatica (Z.L. Luo, K.D. Hyde & H.Y. Su) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 205 (2021)

Fungal Names number: FN 837741, *Facesoffungi number*: FoF 07988; Figure 4.1

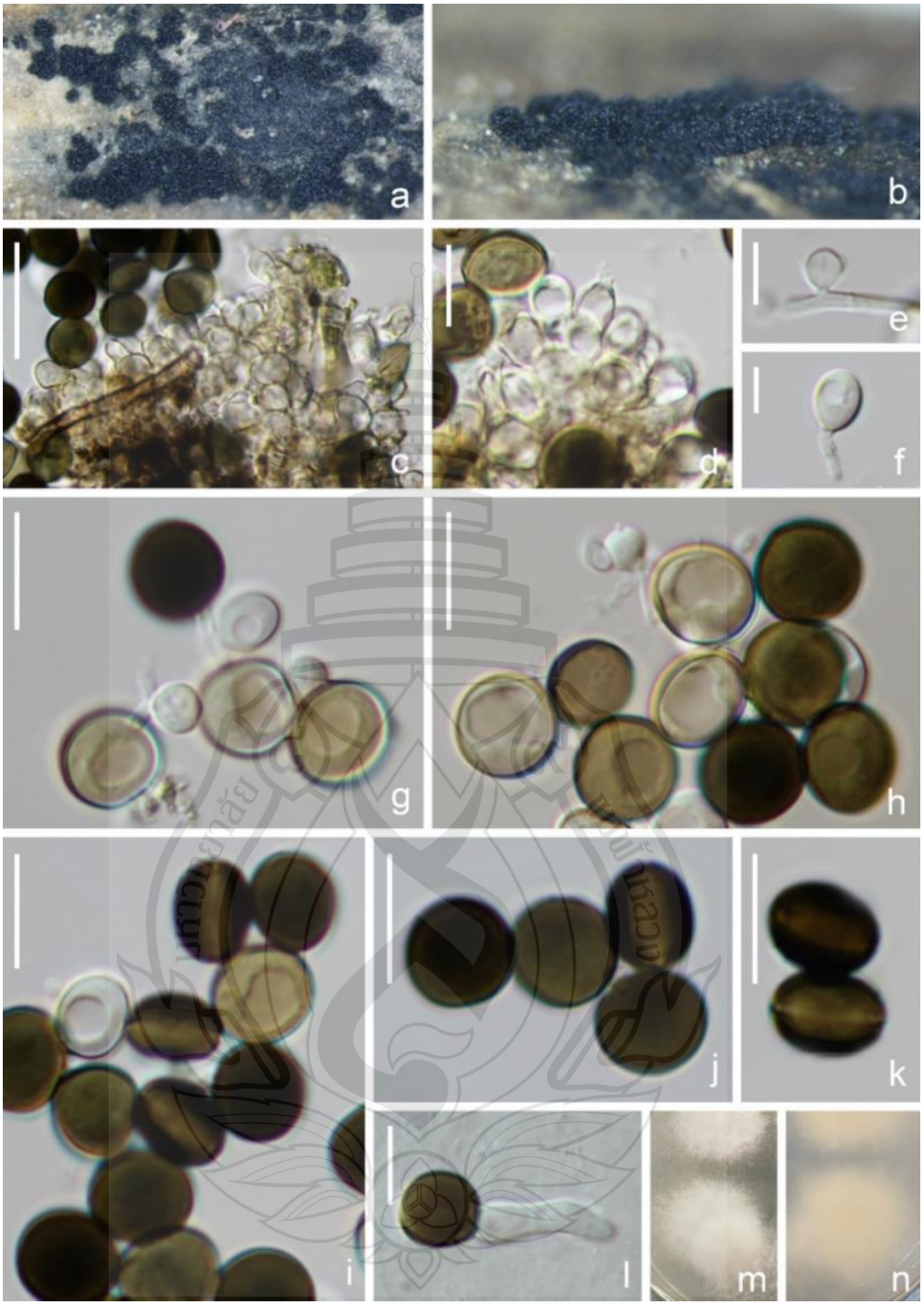
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: undetermined. **Asexual morph**: *Colonies* on natural substrate, sporodochia, superficial, gregarious, dark brown to black, glistening. *Mycelium* mostly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* arising from basal cells, reduced to conidiogenous cells, hyaline,

unbranched, smooth. *Conidiogenous cells* 5–8(–10) × 4–5 µm ($\bar{x}$ = 7 × 4 µm, n = 25), monoblastic, terminal, doliiform to ampulliform, hyaline to pale brown, smooth-walled. *Conidia* acrogenous, solitary, globose to subglobose, aseptate, pale brown to dark brown with olive-green tinge, 9–10 × 7–9 µm ($\bar{x}$ = 9 × 8 µm, n = 50) in in face view; lenticular, with pale equatorial slit and central scar, 5–7 µm wide in surface view.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from the surface of conidium within 12 h. Colonies grows rapidly on PDA medium reaching 4-4.5 cm diam. after two weeks at room temperature (around 25 °C) in dark, loose, flocculent, mastoid at the middle, grayish white on the forward, pale, irregular, dense, smooth-edged in reverse.

Material examined: CHINA, Yunnan Province, Lijaing City, Luguhu Lake, 27°41′ 41" N, 100°45′11" E, on submerged decaying wood, 23 October 2021, H.W. Shen, L999 (HKAS 131475), living culture, KUNCC 23–16117; *ibid.*, on submerged decaying wood, 21 October 2021, L.L. Li, L1128 (HKAS 131571).

Notes: In phylogenetic analysis, *Apiospora aquatica* (KUNCC 23–16117) cluster together with *A. aquatica* (S-642) with 76% ML and 0.96 PP support (Figure 4.2). Morphological, the strain KUNCC 23–16117 resemble with *A. aquatica* (S-642) in having hyaline to pale brown, smooth-walled conidiogenous cells and globose to subglobose, olivaceous to brown conidia. Hence, we propose KUNCC 23–16117 as *A. aquatica* based on morphological and phylogenetical analysis.



Note a, b Colony on natural substrate. c, d Conidiogenous cells and conidia. e, f Developing conidia. g–k Conidia in face view and side view. l Germinated conidium. m, n Culture on PDA medium. Scale bars: c = 20 μm, d, g–l = 10 μm, e, f = 5 μm.

Figure 4.1 *Apiospora aquatica* (HKAS 131475)

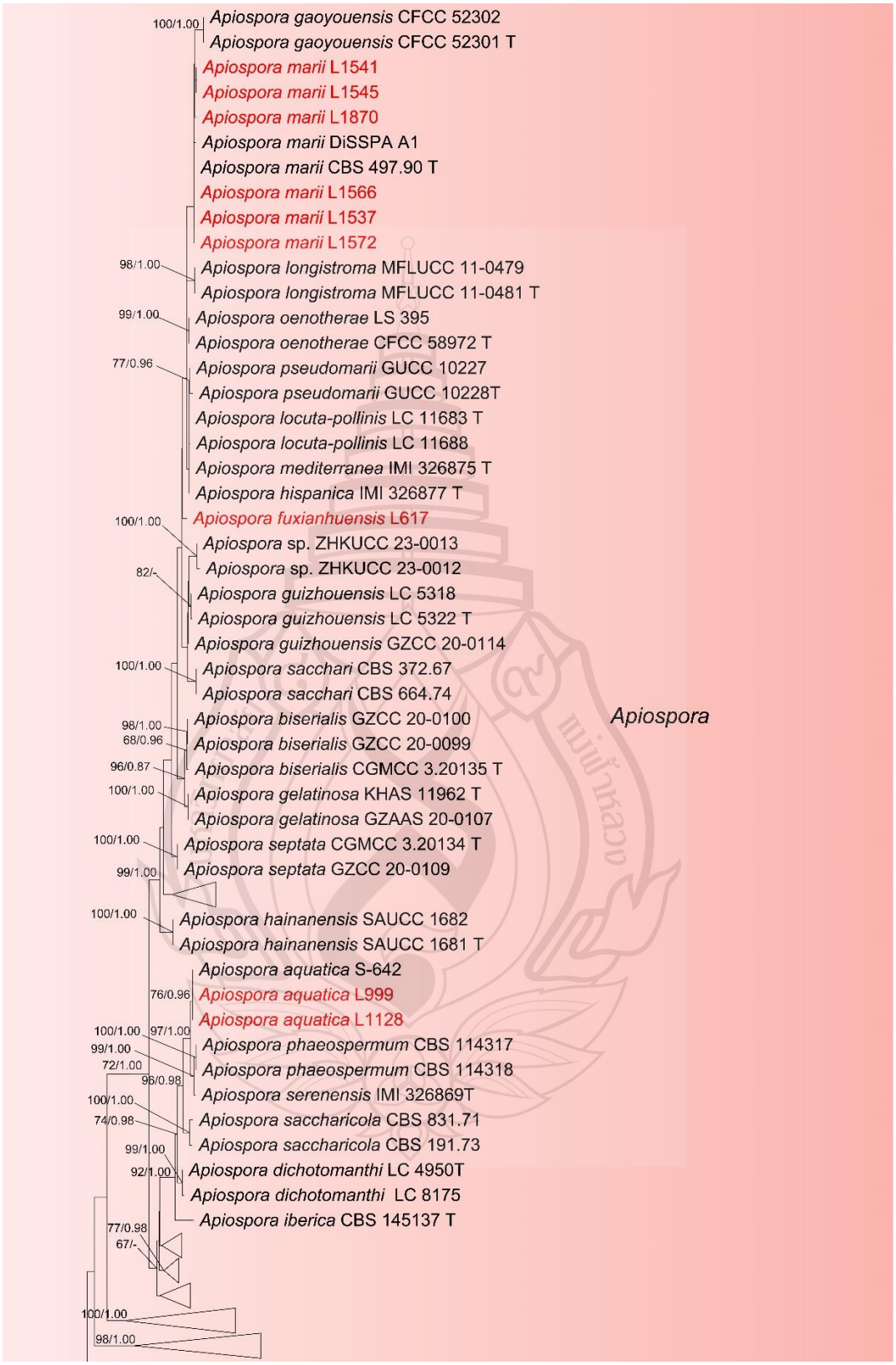
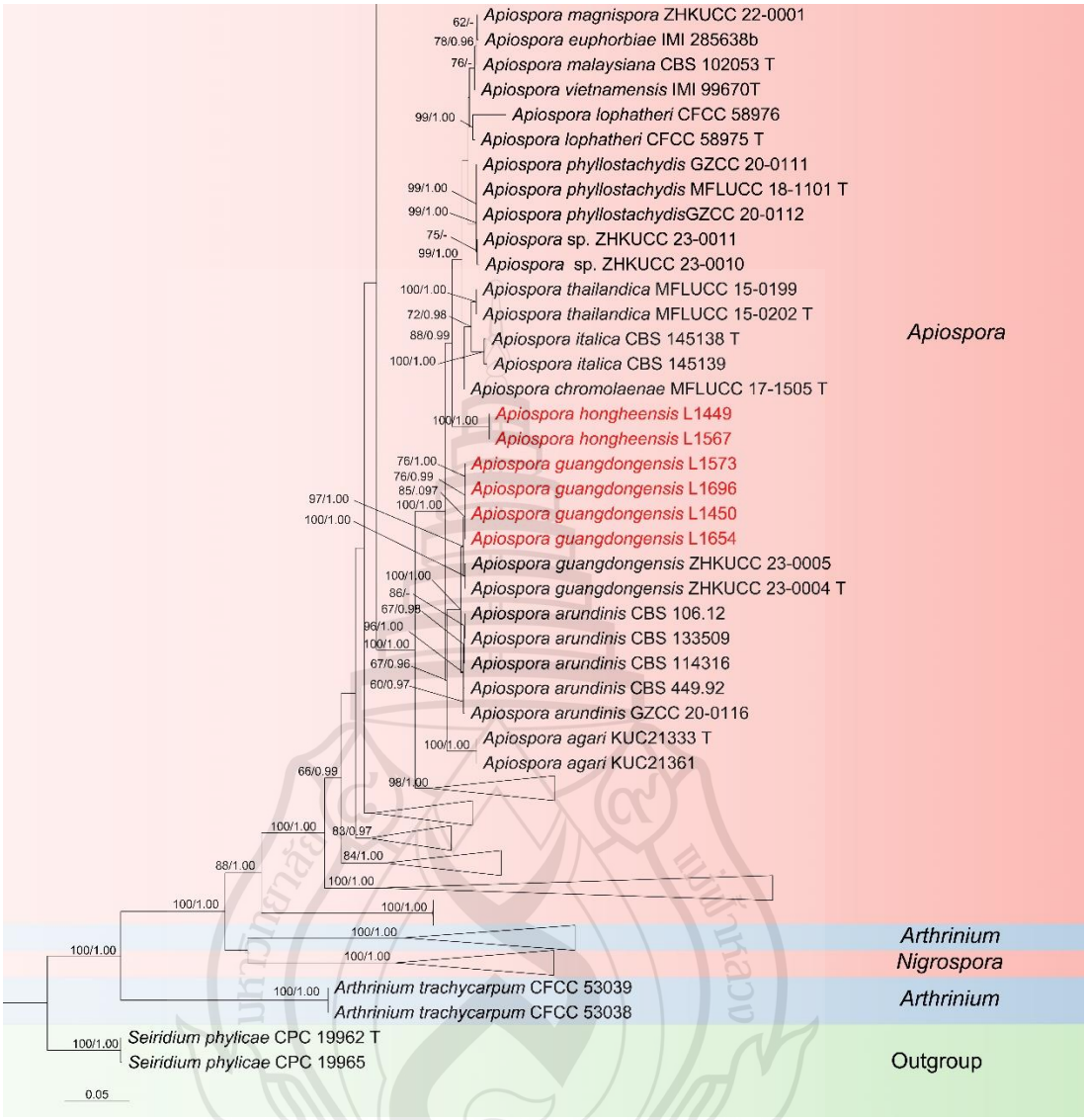


Figure 4.2 Phylogenetic tree for *Apiosporaceae*



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *tub*2 and *tef*1-α sequence dataset representing *Apiosporaceae*. 237 strains are included in the combined analyses which comprise 2143 characters including gaps (771 characters for LSU, 528 characters for ITS, 450 characters for *tub*2, 392 characters for *tef*1-α). *Seiridium phylicae* (CPC 19962 and CPC 19965) were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (ML) greater than 65% and Bayesian posterior probabilities (PP) greater than 0.95 are defined above the nodes as ML/PP. New species are indicated in red and type strains are indicated by a "T" after the strain number.

Figure 4.2 (continued)

Apiospora fuxianhuensis H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 571679; Figure 4.3

Etymology: "fuxianhuensis" refers to the place where this species was collected, Fuxianhu Lake.

Holotype: HKAS 131474.

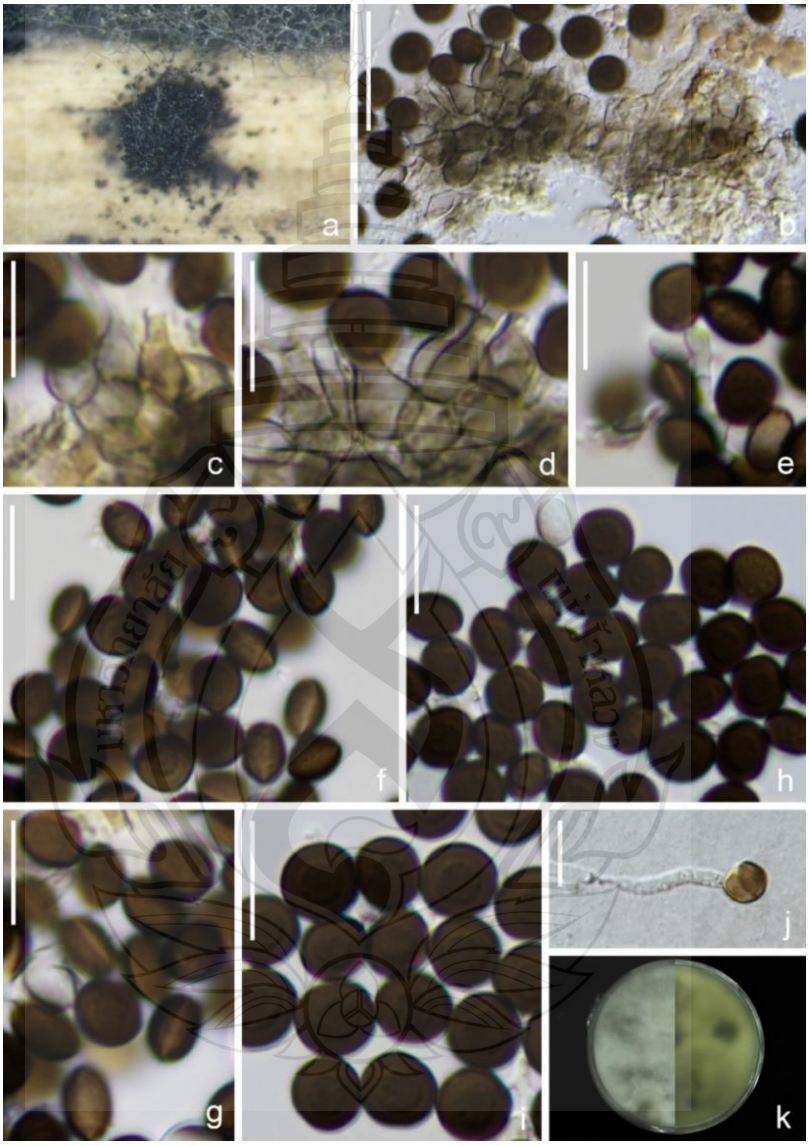
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: undetermined. **Asexual morph**: *Colonies* on natural substrate, sporodochia, superficial, scattered, punctiform, dark brown to black, glistening. *Mycelium* superficial and immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* micronematous, mononematous, erect, subcylindrical, unbranched, subhyaline to pale brown, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 5–9(–13) × 3–4 µm ($\bar{x}$= 7 × 4 µm, n = 35), monoblastic, terminal, doliiform to ampulliform, subhyaline to pale brown, septate, smooth-walled. *Conidia* acrogenous, solitary, globose to subglobose, ellipsoidal, aseptate, brown to dark brown, 6–7 × 6–7 µm ($\bar{x}$ = 7 × 7 µm, n = 50) in face view; lenticular, with pale equatorial slit and a central scar, 4–5 µm wide in surface view.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from the surface of conidium within 12 h. Colonies grows rapidly on PDA medium reaching 4.5-5 cm diam. after two weeks at room temperature (around 25 °C) in dark, loose, flocculent, pale to grayish white on the forward, pale to grayish, irregular, dense, smooth-edged in reverse.

Material examined: CHINA, Yunnan Province, Yuxi City, Fuxianhu Lake, 24°33′39" N, 102°56′49″ E, on submerged decaying wood, 10 July 2021, Y.K. Jiang, L617 (HKAS 131474, holotype), ex-type living culture, KUNCC 23–16114.

Notes: In phylogenetic analysis *Apiospora fuxianhuensis* (KUNCC 23–16114) formed an independent lineage within the *Apiospora* clade (Figure 4.2). In a BLASTn search of NCBI GenBank, the closest matches of the LSU sequence of *A. fuxianhuensis* (KUNCC 23–16114) with 100% similarity, was to *A. guizhouensis* (strain LC5318, KY494784); the closest matches with the ITS sequence with 100 % similarity, was to *A. marii* (strain CBS 497.90, NR_166043), the closest matches with the *tub* sequences with 721/730 (99%, no gap) similarity, was to *A. locuta-pollinis* (Sequence ID: OP289564), and the closest matches with the *tef*1-α sequences with 100% similarity,

was to *A. locuta-pollinis* (strain KUNCC 22–12408, OP381090). Morphologically, *A. fuxianhuensis* can easily distinguish with *A. hispanica* in having the conidiogenous cell of *A. fuxianhuensis* doliiform to ampulliform, septate while they are globose to subglobose and aseptate. So, we introduced *A. fuxianhuensis* as a novel species.



Note a Colony on natural substrate. b–e Conidiogenous cells and conidia. f, g Conidia in side view. h, i Conidia in face view. j Germinated conidium. k Culture on PDA medium. Scale bars: b = 20 μm, c–j = 10 μm.

Figure 4.3 *Apiospora fuxianhuensis* (HKAS 131589, holotype)

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

Fungal Names number: FN 900357, *Facesoffungi number*: FoF 14659; Figure 4.4

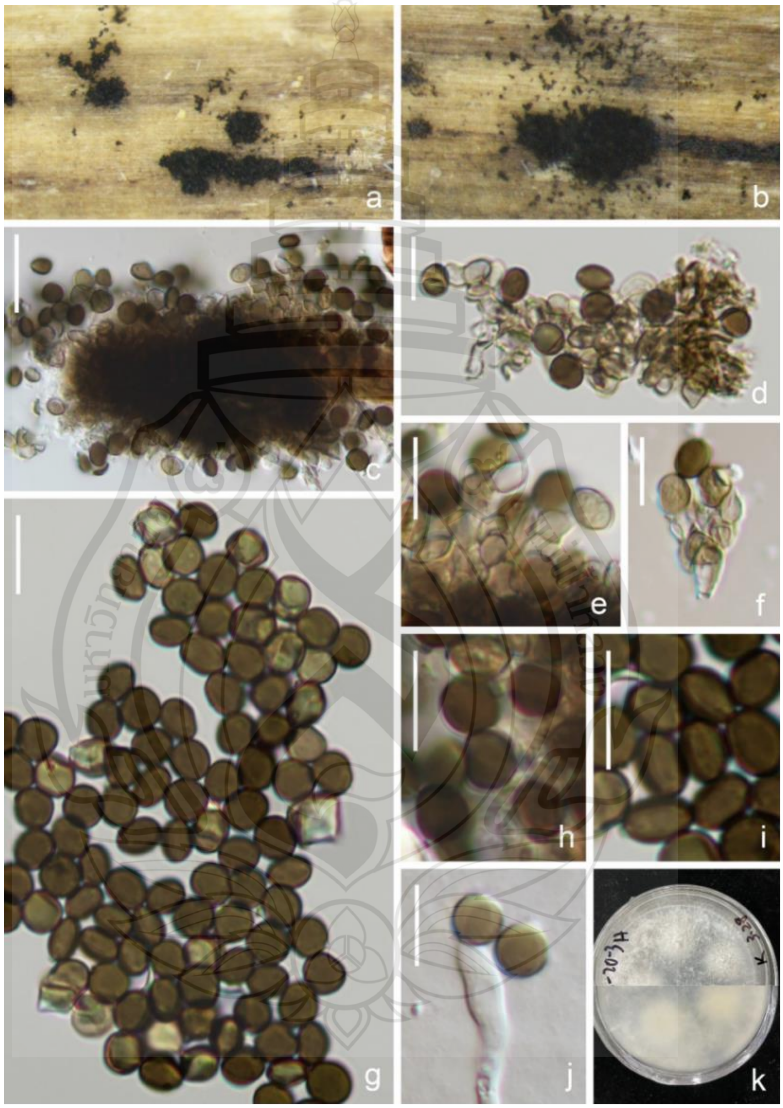
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: undetermined. **Asexual morph**: *Colonies* on natural substrate, sporodochia, superficial, gregarious, punctiform, dark brown to black. *Mycelium* mostly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* arising from basal cells, sometimes reduced to conidiogenous cells, subhyaline to brown, unbranched, smooth. *Conidiogenous cells* 4–6(–8) × 3–4 µm ($\bar{x}$= 5 × 4 µm, n = 20), monoblastic, terminal, subglobose, doliiform to ampulliform, subhyaline to pale brown, smooth-walled. *Conidia* acrogenous, solitary, globose to subglobose, ellipsoidal, aseptate, pale brown to dark brown with olive-green tinge, 5–6 × 5–6 µm ($\bar{x}$= 6 × 5 µm, n = 50) in face view; lenticular, with pale equatorial slit, 3–4 µm wide in surface view.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from the surface of conidium within 12 h. Colonies grows rapidly on PDA medium reaching 4-4.5 cm diam. after two weeks at room temperature (around 25 °C) in dark, loose, flocculent, mastoid at the middle, grayish white on the forward, pale, irregular, dense, smooth-edged in reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Yangzonghai Lake, 24°54′43.70″ N, 103°1′3.64″ E, on submerged decaying wood, 20 February 2023, C.C. Ao, L1450 (HKAS 131416), living culture, KUNCC 23–13032; *ibid.*, Dianchi Lake, 24°46′24.49″ N, 102°43′42.26″ E, on submerged decaying wood, 18 February 2023, Z.Q. Zhang, L1654 (HKAS 131523), living culture, KUNCC 23–13117; *ibid.*, on submerged decaying wood, 18 February 2023, Z.Q. Zhang, L1696 (HKAS 131538), living culture, KUNCC 23–13150; *ibid.*, Honghe Prefecture, Yilonghu Lake, 23°40′28.95″ N, 102°36′30.00″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L1573 (HKAS 131587), living culture, KUNCC 23–13100.

Notes: Phylogenetic analysis showed that our four isolates (KUNCC 23–13100, KUNCC 23–13117, KUNCC 23–13032, KUNCC 23–13150) were formed a sister clade with *Apiospora guangdongensis* with 97% ML and 1.00 PP support (Figure 4.2). Morphological, these collections resemble *A. guangdongensis* in having subcylindrical,

unbranched conidiophores; doliiform to ampulliform conidiogenous cell; and globose to ellipsoidal conidia (Liao et al., 2023). Additionally, the size of conidiogenous cell (4–6(–8) × 3–4 µm *vs.* 4–9 × 2–5 µm) and conidia (5–6 × 5–6 µm *vs.* 6–9 × 5–9 µm) also similar with *A. guangdongensis.* Therefore, we identified these collections as *A. guangdongensis*, representing the first report of this species from a freshwater habitat.



Note a, b Colony on natural substrate. c Conidiomata. d–f Conidiogenous cells and conidia. g, h Conidia in face view. i Conidia in side view. j Germinated conidium. k Culture on PDA medium. Scale bars: c = 20 µm, d–j = 10 µm.

Figure 4.4 *Apiospora guangdongensis* (HKAS 131587, new habitat record)

Apiospora hongheensis H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 571680; Figure 4.5

Etymology: "hongheensis" refers to the place where this species was collected, Honghe Prefecture.

Holotype: HKAS 131590.

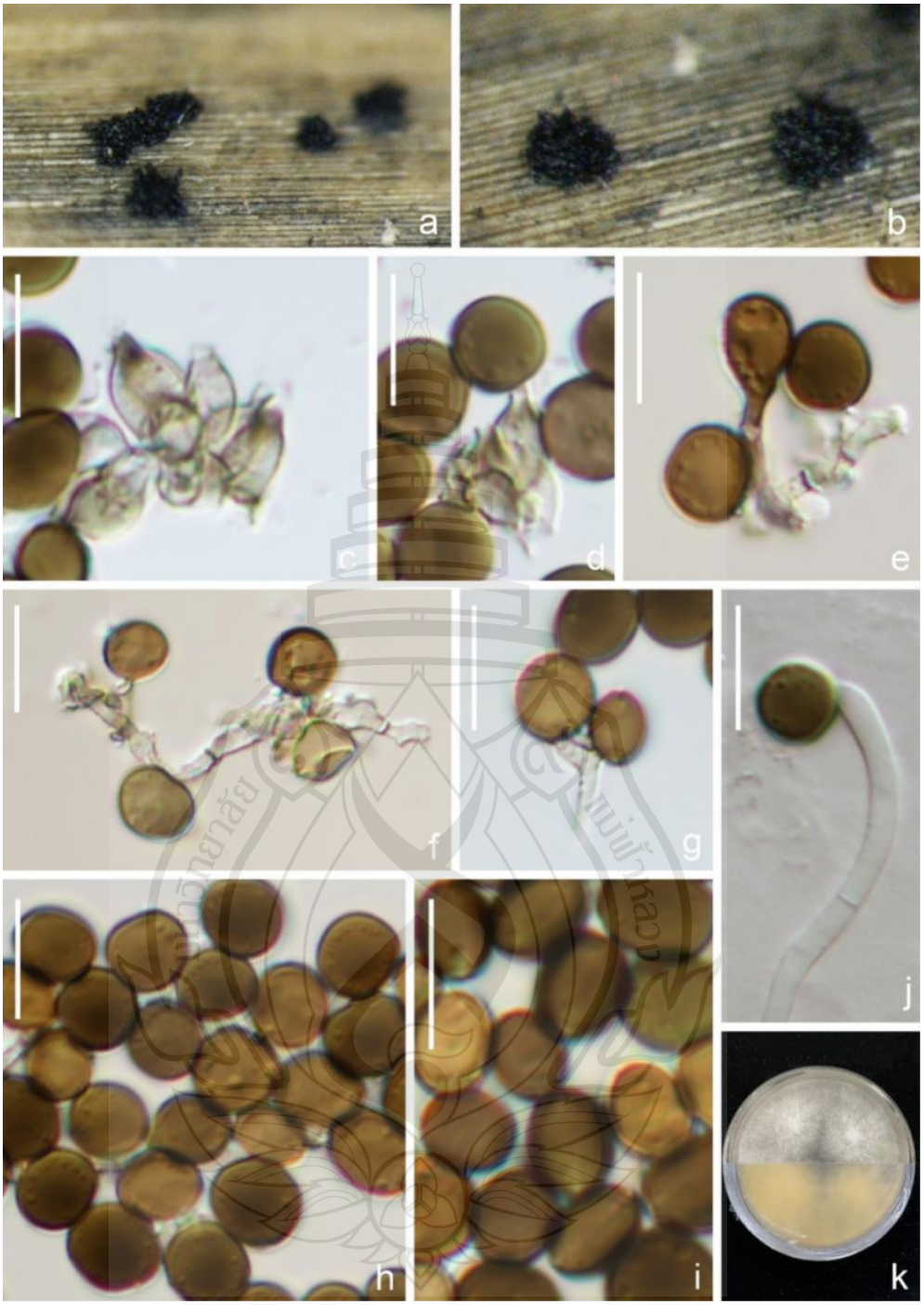
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: undetermined. **Asexual morph**: *Colonies* on natural substrate, sporodochia, superficial, scattered, punctiform, dark brown to black, glistening. *Mycelium* superficial and immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* micronematous, mononematous, erect, subcylindrical, unbranched, subhyaline to pale brown, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 5–8 × 3–5 µm ($\bar{x}$= 7 × 4 µm, n = 20), monoblastic, terminal, flask-shaped, ampulliform, urn-shaped, subcylindrical, subhyaline to pale brown with olive-green tinge, smooth, thin-walled. *Conidia* acrogenous, solitary, globose to subglobose, aseptate, brown to dark brown with olive-green tinge, 7–8 × 6–8 µm ($\bar{x}$= 7 × 7 µm, n = 50) in face view; lenticular to ellipsoidal, with pale equatorial slit, 5–6 µm wide in surface view.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from the surface of conidium within 12 h. Colonies grows rapidly on PDA medium reaching 4-5cm diam. after two weeks at room temperature (around 25 °C) in dark, loose, flocculent, pale to grayish white on the forward, pale to grayish, irregular, dense, smooth-edged in reverse.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°39′18.95″ N, 102°32′57.19″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L1567 (HKAS 131590, holotype), ex-holotype living culture, KUNCC 23–13103; *ibid.*, 23°40′28.95″ N, 102°36′30.00″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L1449 (HKAS 131405, paratype), ex-paratype living culture, KUNCC 23–13031.

Notes: Phylogenetic analysis showed that our two strains (KUNCC 23–13103 and KUNCC 23–13031) of *Apiospora hongheensis* clustered together and forming a distinct lineage within the *Apiospora* clade with 88% ML and 0.99 PP support (Figure 4.8). In a BLASTn search of NCBI GenBank, the closest matches of the ITS sequence

of *A. hongheensis* (KUNCC 23–13103, ex-type) with 100% similarity, was to *A. malaysiana* (isolate LF8, KX510120), the closest matches with the LSU sequence with 99 % similarity, was to *A. arundinis* (culture MUT<ITA>:3035, MG980403), and the closest matches with the *tub* sequences with 640/703(91%) similarity, was to *Apiospora* sp. (strain SAUCC 1981, OQ613289). Morphologically, our strain can distinguish with *A. chromolaenae* by the smaller conidiogenous cell (5–8 × 3–5 µm *vs.* 6.5–12 × 1–2 µm). Furthermore, the conidiogenous cell of *A. hongheensis* are flask-shaped, ampulliform, urn-shaped, subcylindrical, subhyaline to pale brown with olive-green tinge, but *A. chromolaenae* are elongated, broadly fliform to ampulliform, hyaline. Additionally, the conidia of are *A. hongheensis* globose to subglobose, but the they are irregular arrangement in pseudo-chains. Hence, we introduced *A. hongheensis* as a novel species.



Note a, b Colony on natural substrate. c–g Conidiogenous cells and conidia. h Conidia in face view. i Conidia in side view. j Germinated conidium. k Culture on PDA medium. Scale bars: c–j = 10 μm.

Figure 4.5 *Apiospora hongheensis* (HKAS 131590, holotype)

Apiospora marii (Larrondo & Calvo) Pintos & P. Alvarado, Fungal Systematics and Evolution 7: 206 (2021)

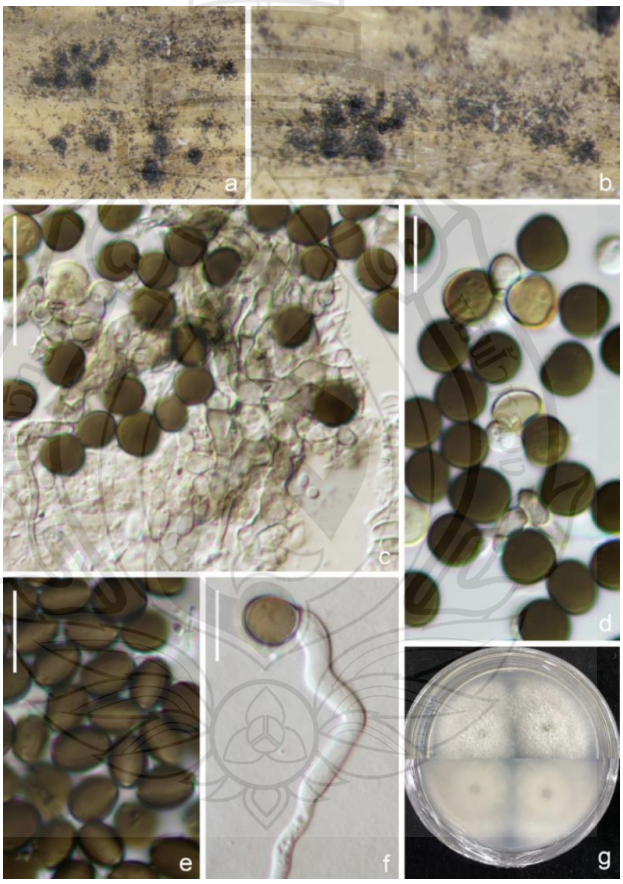
Fungal Names number: FN 837685; Figure 4.6

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: see Pintos et al. (2019). **Asexual morph**: *Colonies* on natural substrate, sporodochia, superficial, scattered, punctiform, dark brown to black. *Mycelium* partly superficial, partly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* micronematous, mononematous, erect, subcylindrical, branched or unbranched, straight or flexuous, subhyaline to pale brown, smooth-walled, sometimes reduced to conidiogenous cells. *Conidiogenous cells* 5–9(–11) × 3–4 µm ($\bar{x}$= 6 × 4 µm, n = 35), monoblastic, terminal, subglobose, doliiform to ampulliform, subcylindrical, subhyaline to pale brown, smooth-walled. *Conidia* acrogenous, solitary, globose to subglobose, ellipsoidal, aseptate, pale brown to dark brown with olive-green tinge, 7–8 × 6–7 µm ($\bar{x}$= 7 × 6 µm, n = 50) in face view; lenticular, with pale equatorial slit and and a central scar, 4–5 µm wide in surface view.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from the surface of conidium within 12 h. Colonies grows rapidly on PDA medium reaching 4-4.5 cm diam. after two weeks at room temperature (around 25 °C) in dark, loose, flocculent, mastoid at the middle, grayish white on the forward, pale, irregular, dense, smooth-edged in reverse.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°39′18.95″ N, 102°32′57.19″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L1537 (HKAS 131610), living culture, KUNCC 23–13094; *ibid.*, on submerged decaying wood, 22 February 2023, H.W. Shen, L1541 (HKAS 131589), living culture, KUNCC 23–13095; *ibid.*, on submerged decaying wood, 22 February 2023, H.W. Shen, L1545 (HKAS 131613), living culture, KUNCC 23–13096; *ibid.*, on submerged decaying wood, 22 February 2023, H.W. Shen, L1566 (HKAS 131615), living culture, KUNCC 23–13098; *ibid.*, on submerged decaying wood, 22 February 2023, H.W. Shen, L1572 (HKAS 131696), living culture, KUNCC 23–13104; *ibid.*, 23°41′49.2" N, 102°30'52.2″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L1870 (HKAS 131567), living culture, KUNCC 23–13441.

Notes: In phylogenetic analysis, the strains (KUNCC 23–13096, KUNCC 23–13098, and KUNCC 23–13441) are cluster together with *Apiospora marii* (CBS 497.90). Our collections are morphologically similar to *A. marii* in having ampulliform conidiogenous cell and globose to subglobose, lenticular conidia, and both their size of conidia (7–8 × 6–7 µm *vs.* 7.2–7.7 × 6.1–6.6 µm) are also similar. *A. marii* are found from atmosphere in Spin, but our strain is isolated from decaying wood in China. Therefore, based on the high similarity of morphology and molecular sequence data, these collections were identified as *A. marii*, which was reported for the first time in China.



Note a, b Colony on natural substrate. c Conidiophores and conidiogenous cells and conidia. d Conidia in face view. e Conidia in side view. f Germinated conidium. g Culture on PDA medium. Scale bars: c = 20 µm, d–f = 10 µm.

Figure 4.6 *Apiospora marii* (HKAS 131589, new habitat record)

Chaetosphaeriales

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

Notes: *Chaetosphaeriaceae* is one of the largest families within the *Sordariomycetes* and contains a highly diverse group of fungi. It was formally introduced by Réblová et al. (1999) to accommodate *Chaetosphaeria* and six closely related genera. Several studies in recent years have updated the accepted genera of *Chaetosphaeriaceae* with 49 genera (including three uncertain genera) accepted by Lin et al. (2019), 43 genera accepted by Hyde, Norphanphoun et al. (2020), 52 genera accepted in "Outline of Fungi and fungus-like taxa-2021" (Wijayawardene, Hyde et al., 2022), and 89 genera (including 22 new genera and 10 newly assigned genera) accepted by Wu and Diao (2022). Currently, more than 90 genera are accepted in *Chaetosphaeriaceae* (Wu & Diao, 2022; Fryar et al., 2023; Réblová & Nekvindová, 2023). Species of *Chaetosphaeriaceae* are highly diverse, cosmopolitan, and are known as the phialidic fungi (Lin et al., 2019; Wu & Diao 2022; Zhang et al., 2022; Réblová & Nekvindová, 2023). Species of *Chaetosphaeriaceae* are highly diverse, cosmopolitan, and are known as the phialides asexual morphs. Members of *Chaetosphaeriaceae* primarily as saprobes that occur on plant litter in terrestrial and freshwater habitats (Lin et al., 2019; Wu & Diao, 2022; Zhang et al., 2022; Réblová & Nekvindová, 2023).

Chaetosphaeria Tul. & C. Tul.

Notes: *Chaetosphaeria* Tul. & C.Tul. was introduced by Tulasne and Tulasne (1863) with *C. innumera* Berk. & Broome ex Tul. & C. Tul. as the type species. Until Réblová et al. (1999) formally established *Chaetosphaeriaceae*, the genus *Chaetosphaeria* had been placed in several families, such as *Sphaeriaceae* (Saccardo, 1883; Müller & von Arx, 1962), *Chaetosphaeriaceae* (Locquin, 1984) and *Losiosphaeriaceae* (Eriksson & Hawksworth, 1993). The sexual morph of *Chaetosphaeria* is characterized by non-stromatic, dark, papillate ascomata, persistent paraphyses, unitunicate asci with a shallow, refractive annulus and hyaline, ellipsoidal, fusiform to filiform, one to several-septate hyaline ascospores (Tulasne & Tulasne, 1863; Réblová et al., 1999; Réblová & Winka, 2000). The asexual morphs of *Chaetosphaeria* are diverse dematiaceous hyphomycetes characterized by phialidic conidiogenous cells (Réblová, 2000; Réblová & Winka, 2000; Wu & Diao, 2022; Réblová & Nekvindová, 2023). *Chaetosphaeria* has been shown to be a polyphyletic

group, with some species being transferred to other genera or elevated to new genus levels based on unique morphological and phylogenetic analyses (Wu & Diao, 2022; Réblová & Nekvindová, 2023).

Chaetosphaeria polygonalis J. Yang, Jian K. Liu & K.D. Hyde, Fungal Diversity 119: 114 (2023)

Fungal Names number: FN 559650, *Facesoffungi number*: FoF 12807; Figure 4.7

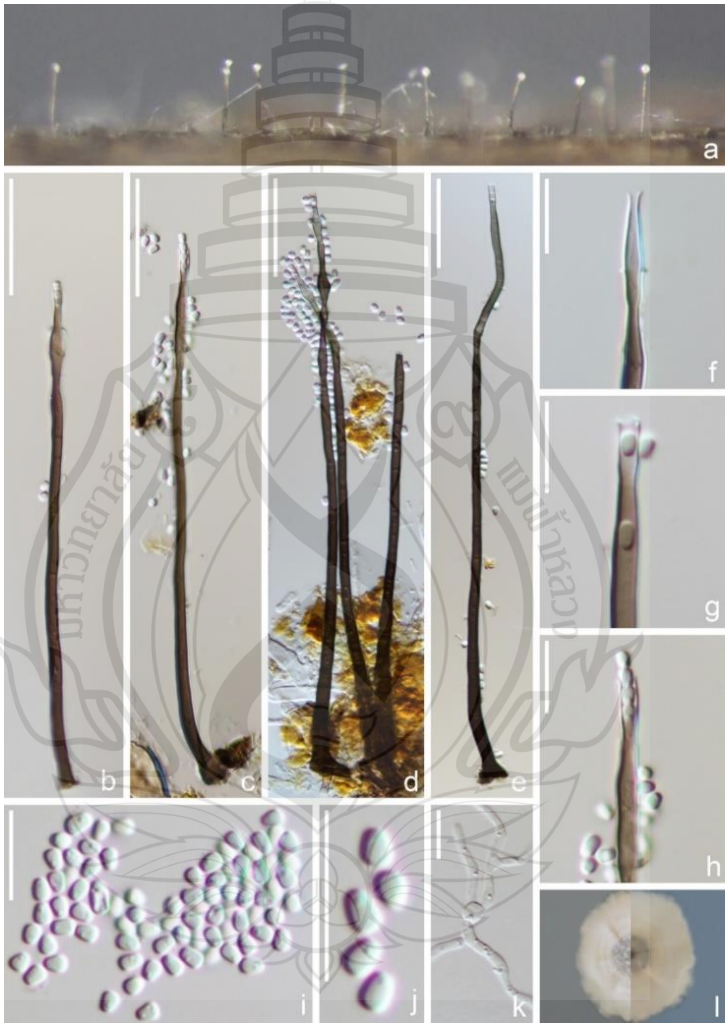
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered, pale brown to brown, with glistening masses of conidia at the apex. *Mycelium* partly superficial, partly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* (112–)124–181(–206) × 3–5 µm ($\bar{x}$ = 153 × 4 µm, n = 20), macronematous, mononematous, erect, solitary or in small groups, straight or slightly curved, cylindrical, septate, unbranched, smooth-walled, subhyaline to dark brown, subhyaline at the apical cell. *Conidiogenous cells* (16–)19–33(–41) × 3–4 µm ($\bar{x}$ = 26 × 3 µm, n = 20), monophialidic, integrated, terminal, determinate, subhyaline to pale brown, cylindrical to subcylindrical, paler towards the tip, slightly narrower below the collarette; collarettes 2–2.5 µm wide, 4.5–7 µm deep, cup-shaped, subhyaline, smooth-walled. *Conidia* 2.4–2.8 × 1.5–1.8 µm ($\bar{x}$ = 2.6 × 1.6 µm, n = 50), acrogenous, aggregated, cuneiform, hyaline, aseptate, smooth-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from around of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after two months at room temperature (around 25 °C) in dark, circular, dense, middle mastoid, pale to pale brown on the forward; pale gray, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujusnhu Lake, 24°32'15.6" N, 100°1′30.00″ E, on submerged decaying wood, 24 February 2023, Z.Q. Zhang, L2066 (HKAS 132048); *ibid.*, on submerged decaying wood, 24 February 2023, Z.Q. Zhang, L2077 (HKAS 132047), living culture, KUNCC 23–13789; *ibid.*, on submerged decaying wood, 24 February 2023, S. Luan, L2078 (HKAS 132040).

Notes: Phylogenetic analysis showed that our new isolates clustered with *Chaetosphaeria polygonalis* within a phylogenetic lineage with 99% ML and 1.00 PP support (Figure 4.8). Our isolates were morphologically similar to *C. polygonalis* in

having monophialidic, cylindrical to subcylindrical, collarette conidiogenous cells; and cuneiform, hyaline, aseptate conidia (Yang et al., 2023). Although our new collections show some differences in the size of conidia and conidiophores, there are no significant differences in the sequence data. The differences in size may be caused by habitat differences, therefore, based on morphological characteristics and the high similarity of sequence data, we identified these new collections as *C. polygonalis*.



Note a Colony on natural substrate. b–e Conidiophores. f–h Conidiogenous cells. i, j Conidia. k Germinated conidium. l Culture on PDA medium. Scale bars: b–e = 30 μm, f–k = 10 μm.

Figure 4.7 *Chaetosphaeria polygonalis* (HKAS 132047)

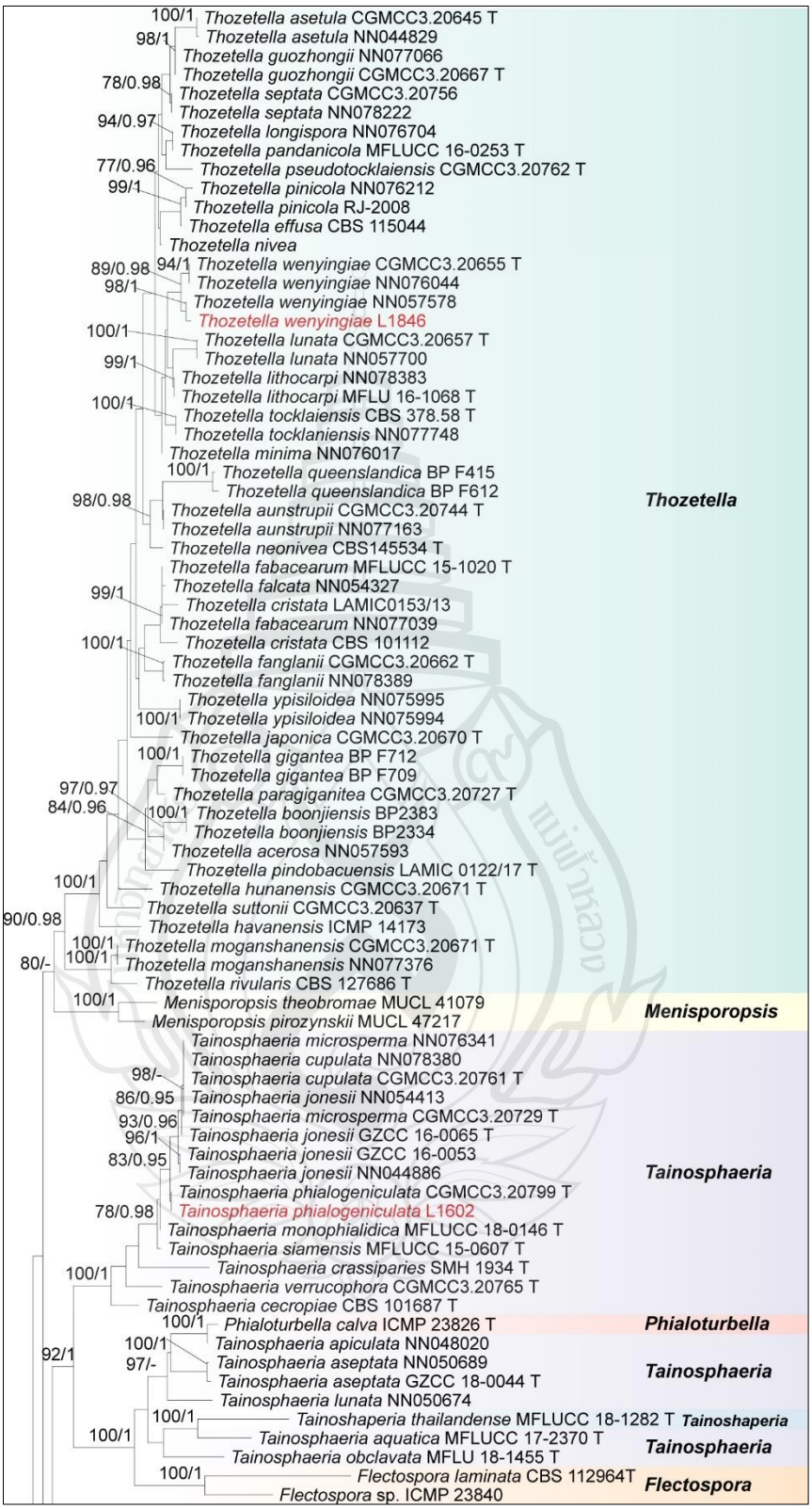


Figure 4.8 Phylogenetic tree of *Chaetosphaeriales*

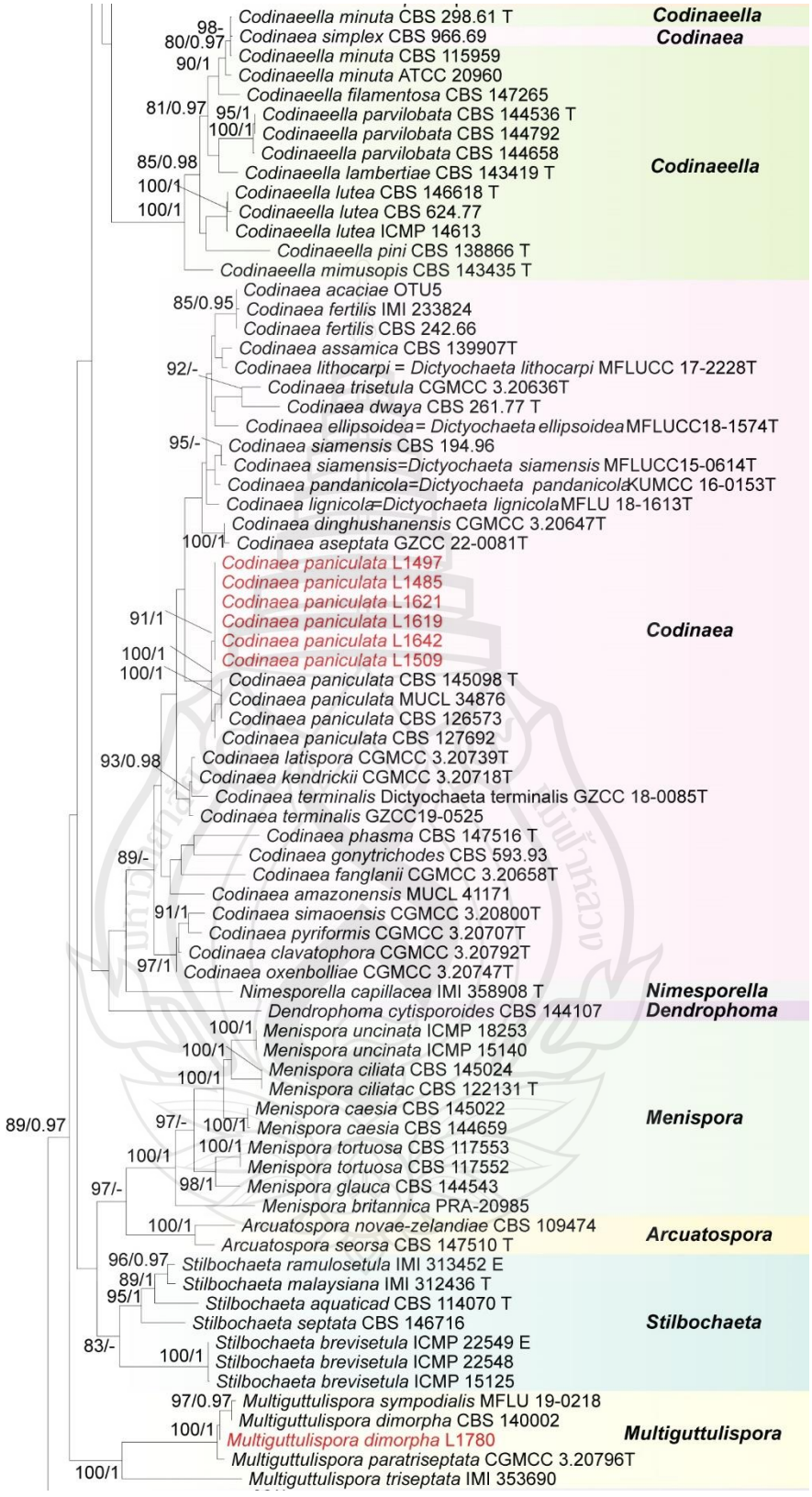


Figure 4.8 (continued)

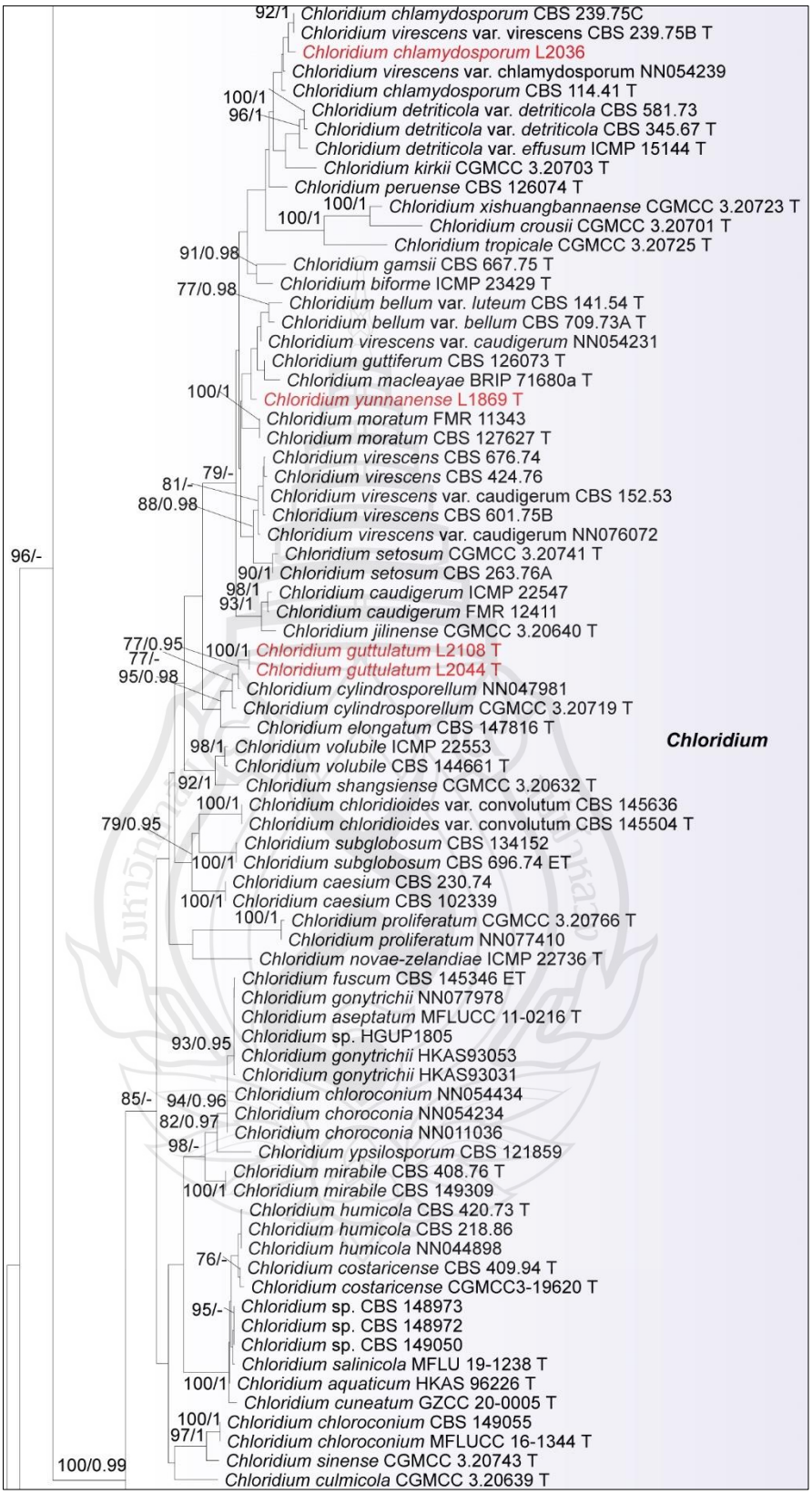
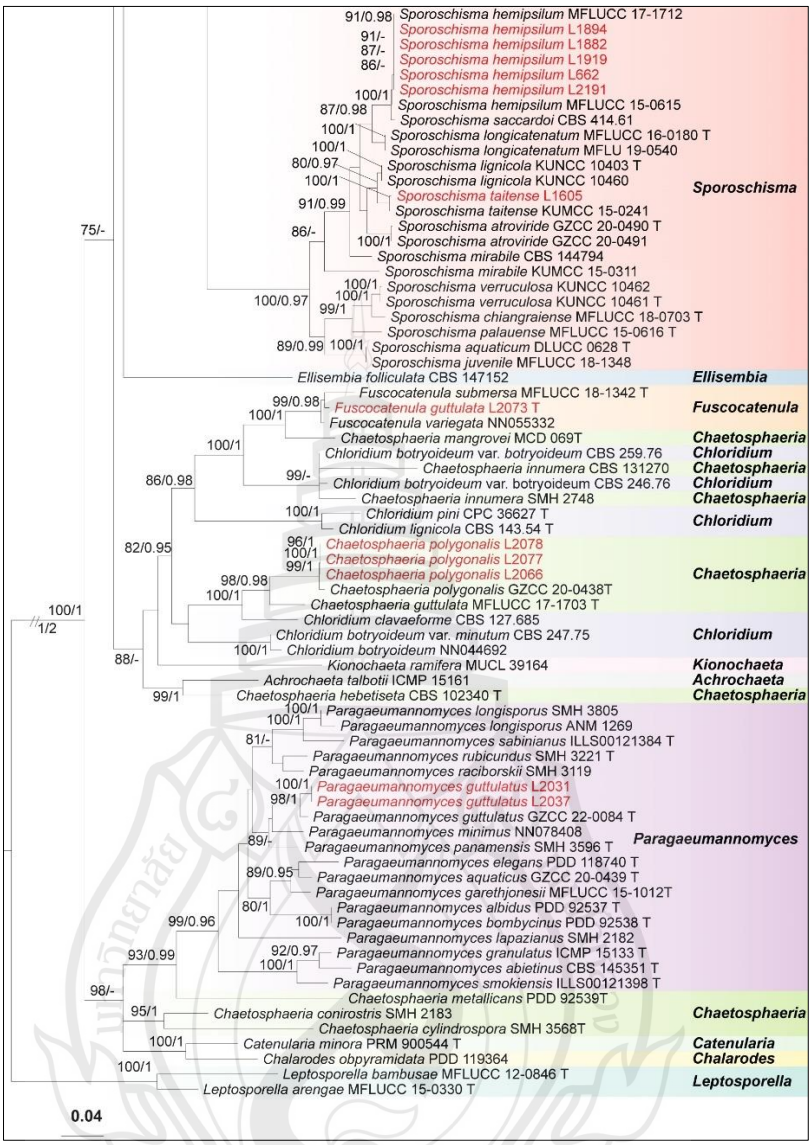


Figure 4.8 (continued)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS and *tef*1-α sequence dataset representing *Pleurotheciales*. 304 strains are included in the combined analyses which comprise 2181 characters including gaps (842 characters for LSU, 468 characters for ITS, 871 characters for *tef*1-α). *Leptosporella arengae* (MFLUCC 15-0330) and *Leptosporella bambusae* (MFLUCC 12-0846) were selected as the outgroup taxa. Bootstrap support values with a ML greater than 65%, and Bayesian posterior probabilities (PP) greater than 0.95 are given above the nodes, shown as "ML/PP". New species are indicated in red and type strains are indicated by a "T" after the strain number.

Figure 4.8 (continued)

Chloridium Link

Notes: *Chloridium* Link was introduced to accommodate a group of soil- and wood-inhabiting dematiaceous hyphomycetes, with phialidic conidiogenous cells on multiple loci (Réblová et al., 2022; Réblová & Nekvindová, 2023). Based on the consilience of molecular species delimitation methods, phylogenetic analyses, ancestral state reconstruction, morphological hypotheses, and global biogeographic analyses, Reblova et al. (2022) proposed a new generic concept for *Chloridium* and defined it as a monophyletic, polythetic genus divided into eight sections, and containing 37 species. *Chloridium* is delimited to phialidic dematiaceous hyphomycetes that produce conidia on multiple conidiogenous loci in sympodial manner on a central dome within the collarette; conidia are hyaline or pale brown, aseptate, ellipsoidal, subglobose, obclavate, occasionally deltoid, adhering in slimy heads or cirrhi (Réblová et al., 2022; Réblová & Nekvindová, 2023). Species of *Chloridium* mostly are saprobes on decaying plant litter in terrestrial and freshwater habitats (Luo et al., 2019; Réblová et al., 2022; Wu & Diao, 2022; Réblová & Nekvindová, 2023).

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

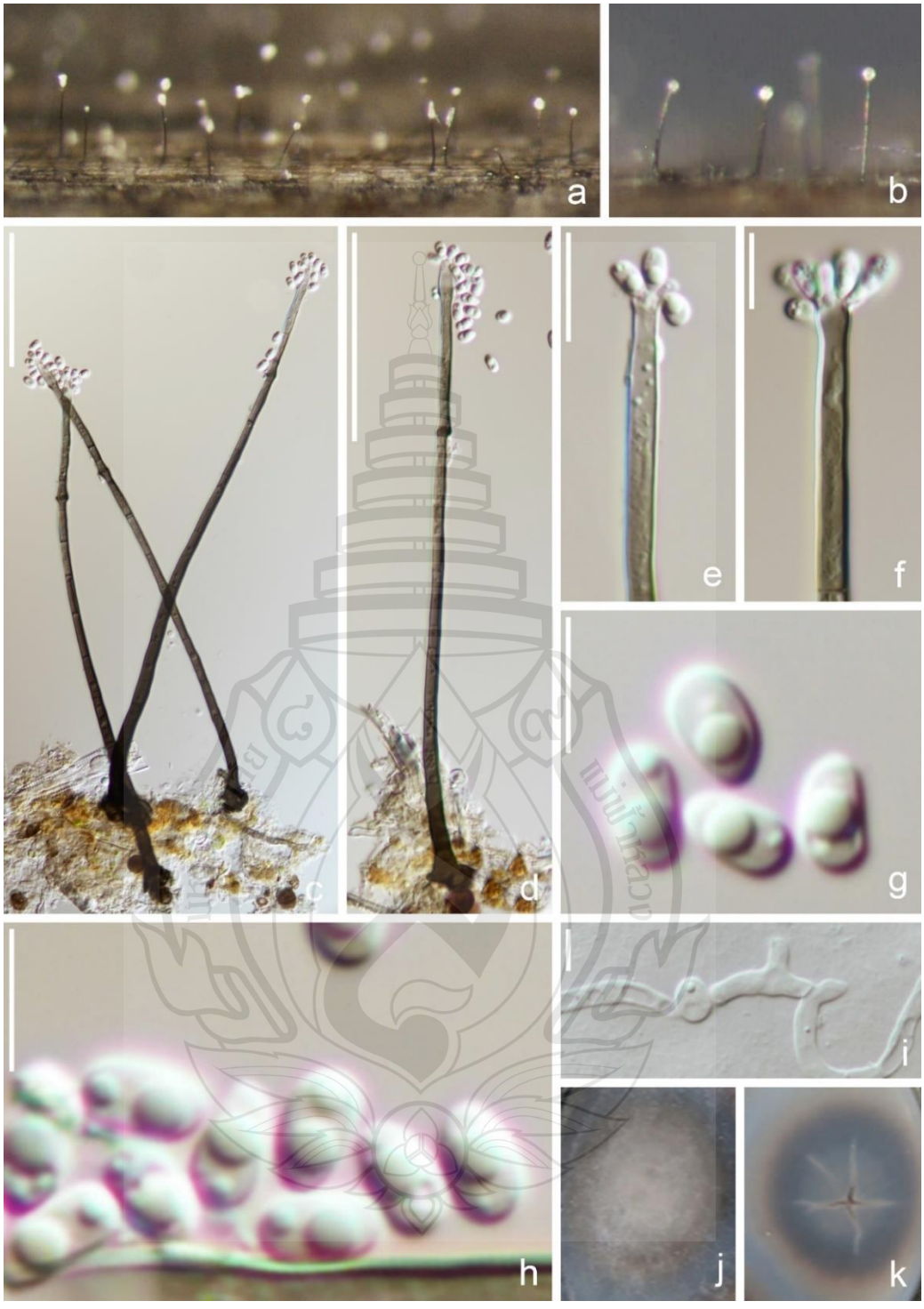
Fungal Names number: FN 344057, *Facesoffungi number*: FoF 12807; Figure 4.9

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered, pale brown to dark brown, with glistening masses of conidia at the apex. *Mycelium* mostly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* (130–)144–187(–215) × 3–5 µm ($\bar{x}$ = 165 × 4 µm, n = 35), macronematous, mononematous, erect, solitary, straight or slightly curved, cylindrical, septate, unbranched, smooth-walled, pale to dark brown, subhyaline at the apical cell. *Conidiogenous cells* (26–)30–41(–45) × 3–4 µm ($\bar{x}$ = 36 × 3 µm, n = 35), monophialidic, integrated, terminal, cylindrical to subcylindrical, subhyaline to pale brown with olivaceous tinge, paler towards the tip, slightly narrower below the collarette; collarettes flaring, funnel-shaped, subhyaline, smooth-walled. *Conidia* 4–5 × 2–3 µm ($\bar{x}$ = 4.5 × 2.6 µm, n = 50), acrogenous, aggregated, obovate to ellipsoidal-obovate, hyaline, aseptate, guttulate, smooth-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from around of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after two months at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, middle mastoid, pale brown to brown on the forward; brown to dark brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujusnhu Lake, 24°32′30.44" N, 101°1′39.51″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L2036 (HKAS 131834), living culture, KUNCC 23–13786.

Notes: Phylogenetic analysis showed that our isolates clustered within the *Chloridium chlamydosporum* species complex with low support (Figure 4.8). Morphologically, our isolate was similar to *C. chlamydosporum* in having cylindrical, septate, unbranched conidiophoresm subhyaline at the apical cell; monophialidic, cylindrical to subcylindrical, collarette conidiogenous cells; and obovate to ellipsoidal-obovate, hyaline, aseptate, guttulate conidia (Réblová et al., 2022). Therefore, based on highly similar morphological features and sequence data, we identified the new isolate as *C. chlamydosporum*, which was reported for the first time from a freshwater habitat.



Note a, b Colony on natural substrate. c, d Conidiophores. e, f Conidiogenous cells. g, h Conidia. i Germinated conidium. j, k Culture on PDA medium. Scale bars: c, d = 50 μm, e, f = 10 μm, g–i = 5 μm.

Figure 4.9 *Chloridium chlamydosporum* (HKAS 131834, new habitat record)

Chloridium guttulatum H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 571681; Figure 4.10

Etymology: "guttulatum" refers to the guttulate conidia.

Holotype: HKAS 132051.

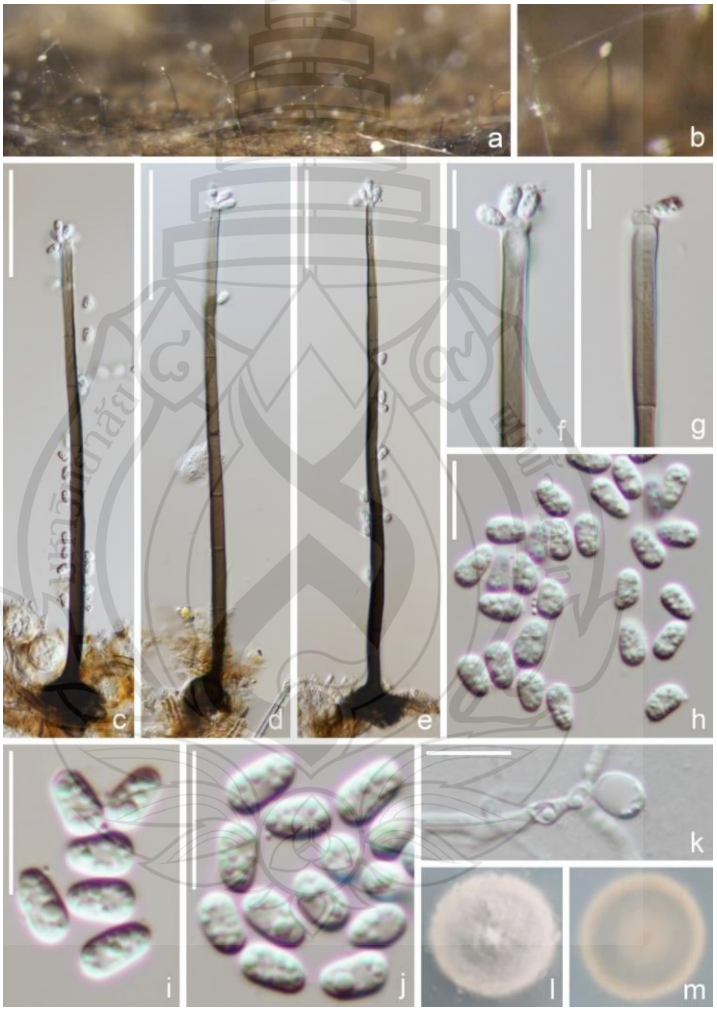
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered or gregarious, pale brown to dark brown, with white glistening masses of conidia at the apex. *Mycelium* partly superficial, partly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* (145–)152–188(–212) × 4.5–6 µm ($\bar{x}$ = 170 × 5 µm, n = 30), macronematous, mononematous, erect, solitary, straight or slightly curved, cylindrical, septate, unbranched, smooth-walled, pale brown to dark brown, subhyaline at the apical cell. *Conidiogenous cells* (28–)34–40 × 3.5–4.5 µm ($\bar{x}$ = 37 × 4 µm, n = 20), monophialidic, integrated, terminal, cylindrical to subcylindrical, subhyaline to pale brown, paler towards the tip, conidiogenous locus sometimes inflated, slightly narrower below the collarette; collarettes short, flaring, subhyaline, smooth-walled. *Conidia* 5–6 × 3–4 µm ($\bar{x}$ = 6 × 3 µm, n = 50), acrogenous, aggregated, obovate to ellipsoidal, cuneiform with rounded ends, hyaline, aseptate, guttulate, smooth-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from end of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after two months at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, middle mastoid, pale gray on the forward; pale gray to brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujusnhu Lake, 24°32'15.6" N, 100°1′30.00″ E, on submerged decaying wood, 24 February 2023, Z.Q. Zhang, L2108 (HKAS 132051, holotype), ex-holotype living culture, KUNCC 23–13787A = KUNCC 23–13787B.

Notes: Phylogenetic analysis showed that our two cultures (KUNCC 23–13787A and KUNCC 23–13787B) of *Chloridium guttulatum* clustered with *C. cylindrosporellum* and *C. elongatum* in a separate clade within *Chloridium* clade (Figure 4.8). *Chloridium guttulatum* is morphologically similar to *C. cylindrosporellum* and *C. elongatum* in having cylindrical, septate, unbranched conidiophores with subhyaline apical cell; monophialidic,

integrated, cylindrical to subcylindrical, subhyaline to pale brown conidiogenous cells, sometimes with inflated, slightly narrower, collarette conidiogenous locus; and obovate to ellipsoidal, hyaline, aseptate, guttulate, cuneiform conidia with rounded ends (Réblová et al., 2022; Wu & Diao, 2022). However, *C. guttulatum* can be distinguished from *C. cylindrosporellum* by its smaller conidiogenous cell [(28–)34–40 × 3.5–4.5 µm *vs.* 45–50 × 2.5–3.5 µm], and conidia (5–6 × 3–4 µm *vs.* 11–13 × 3–3.8 µm). Therefore, based on morphological and phylogenetic evidence, *C. guttulatum* was introduced as a new species.



Note a, b Colony on natural substrate. c–e Conidiophores. f, g Conidiogenous cells. h–j Conidia. k Germinated conidium. l, m Culture on PDA medium. Scale bars: c–e = 40 µm, f–k = 10 µm.

Figure 4.10 *Chloridium guttulatum* (HKAS 132051, holotype)

Chloridium yunnanense H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 571682; Figure 4.11

Etymology: "yunnanense" refers to the place where this species was collected, Yunnan Province.

Holotype: HKAS 131422.

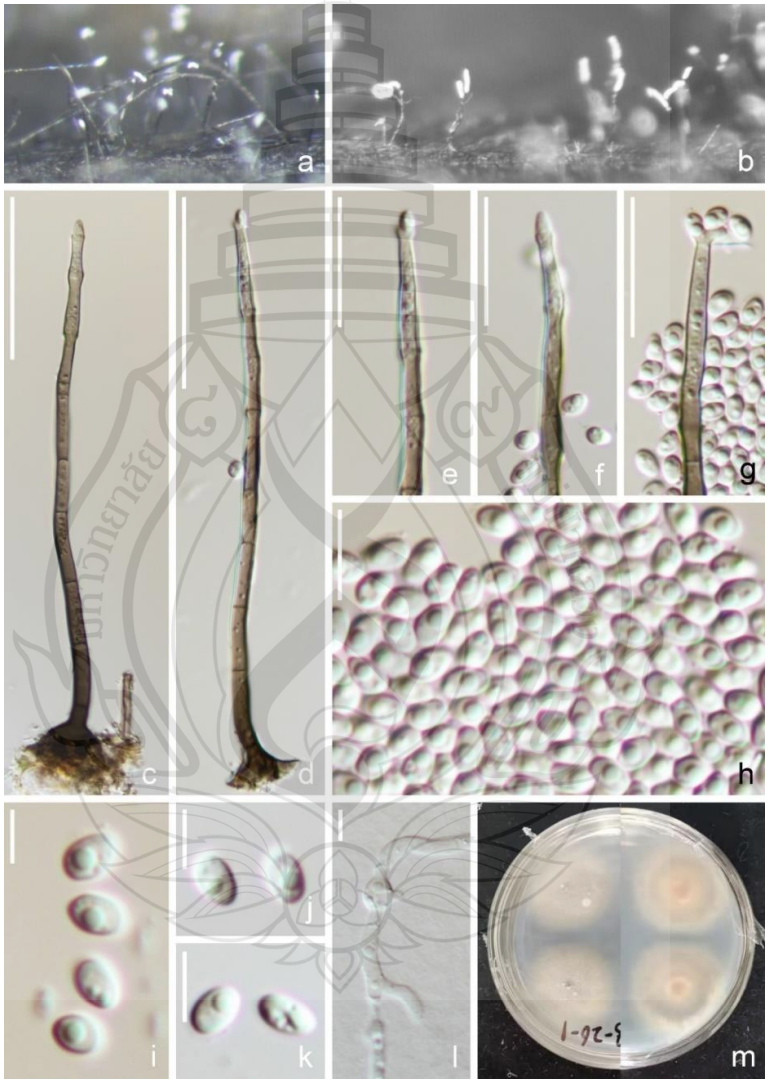
Saprobic on submerged decaying wood in freshwater lake. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered or gregarious, pale brown to dark brown, with white glistening masses of conidia at the apex. *Mycelium* partly superficial, partly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* (63–)110–167(–173) × 3–4 µm ($\bar{x}$ = 138 × 4 µm, n = 20), macronematous, mononematous, erect, solitary, straight or slightly curved, cylindrical, septate, unbranched, smooth-walled, pale to brown, subhyaline at the apical cell. *Conidiogenous cells* (21–)27–36 × 3–3.5 µm ($\bar{x}$ = 31 × 3 µm, n = 20), monophialidic, integrated, terminal, cylindrical to subcylindrical, subhyaline to pale brown, paler towards the tip, slightly narrower below the collarette; collarettes short, flaring, subhyaline, smooth-walled. *Conidia* 3–5 × 2–3 µm ($\bar{x}$ = 4 × 2.5 µm, n = 50), acrogenous, aggregated, obovate to ellipsoidal, hyaline, aseptate, guttulate, smooth-walled. **Sexual morph**: Undetermined.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from around of conidium within 12 h. Colonies on PDA medium reaching 3-3.5 cm diam. after three months at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, middle mastoid, pale brown to brown on the forward; brown to dark brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujusnhu Lake, 24°32′30.44" N, 101°1′39.51″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L1869 (HKAS 131422, holotype), ex-holotype living culture, KUNCC 23–13474.

Notes: *Chloridium yunnanense* (KUNCC 23–13474) was placed a distinct lineage within *Chloridium* clade with low support (Figure 4.8). *Chloridium yunnanense* differs from *C. moratum* in having longer conidiophores [(63–)110–167(–173) × 3–4 µm *vs.* 30–120 × 2.5–4 µm]. In a BLASTn search of NCBI GenBank, the closest matches of the ITS sequence of *C. yunnanense* (KUNCC 23–13474, ex-type) with 498/501 (99%)

similarity, was to *Chaetosphaeria* sp. (isolate E9430e, JN559404), the closest matches with the LSU sequence with 1240/1245 (99%) similarity, was to *C. virescens* (strain: M.R. 3803, OP455553), and the closest matches with the *tef*1-α sequences with 857/873 (98%) similarity, was to *C. guttiferum* (strain CBS 126073, OP464991). Based on morphological differences and phylogenetic evidence, we introduce *C. yunnanense* as a new species.



Note a, b Colony on natural substrate. c, d Conidiophores. e–g Conidiogenous cells. h–k Conidia. l Germinated conidium. m Culture on PDA medium. Scale bars: c, d = 40 μm, e–g = 20 μm, h = 10 μm. i–l = 5 μm.

Figure 4.11 *Chloridium yunnanense* (HKAS 131422, holotype)

Codinaea Maire

Notes: *Codinaea* Maire was introduced by Maire (1937) to accommodate species of phialidic dematiaceous hyphomycete, with *C. aristate* as type species. The type species of *Codinaea*, *C. aristate*, has detailed descriptions and illustrations, but unfortunately it lacks valuable molecular sequence data and the type material cannot be traced (Réblová, Kolařík et al., 2021). Réblová et al. (2021a) studied morphological, molecular, and biogeographic data of a large set of species, determined that *Codinaea* is polyphyletic, and proposed a new generic concept of *Codinaea*. Emended *Codinaea* is distinguished into four morphotypes based on the arrangement of setae and conidiophores and their branching pattern: type 1 (*Codinaea s. str.* morphotype): with dark brown, thick-walled central seta or setae arranged in a fascicle with shorter, paler, and thinner-walled conidiophores; type 2: with unbranched, dark brown, thick-walled conidiophores that closely resemble the setae and terminate into a monophialide; type 3: with conidiophores with a sterile setiform extension and integrated, terminal phialides borne in groups on short unilateral, branched stalks; and type 4: with branched conidiophores and discrete, lateral phialides borne on nodose hyphae or directly on conidiophores (Réblová, Kolařík et al., 2021). According to the emended generic concept, Réblová, Kolařík et al. (2021) accepted 14 species in *Codinaea*. Subsequently, Wu and Diao (2022) followed this treatment and accepted 35 species in *Codinaea* (including 11 newly described species). Species of *Codinaea* have been reported primarily as saprobes on plant litter in terrestrial and freshwater habitats (Lin et al., 2019; Luo et al., 2019; Réblová, Nekvindová et al., 2020; Réblová, Nekvindová, Miller et al., 2021; Wu & Diao, 2022).

Codinaea paniculata Réblová & J. Fourn., MycoKeys 74: 14 (2020)

Fungal Names number: FN 836526, *Facesoffungi number*: FoF 12807; Figure 4.12

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered or fasciculate, pale brown to dark brown, with white glistening masses of conidia at the apex. *Mycelium* mostly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Setae* (203–)232–301(–339) × 5–6 µm ($\bar{x}$ = 266 × 6 µm, n = 30), erect, straight or slightly flexuous, cylindrical, septate, unbranched, smooth-walled, dark brown, pale brown to subhyaline at the apex, tapering

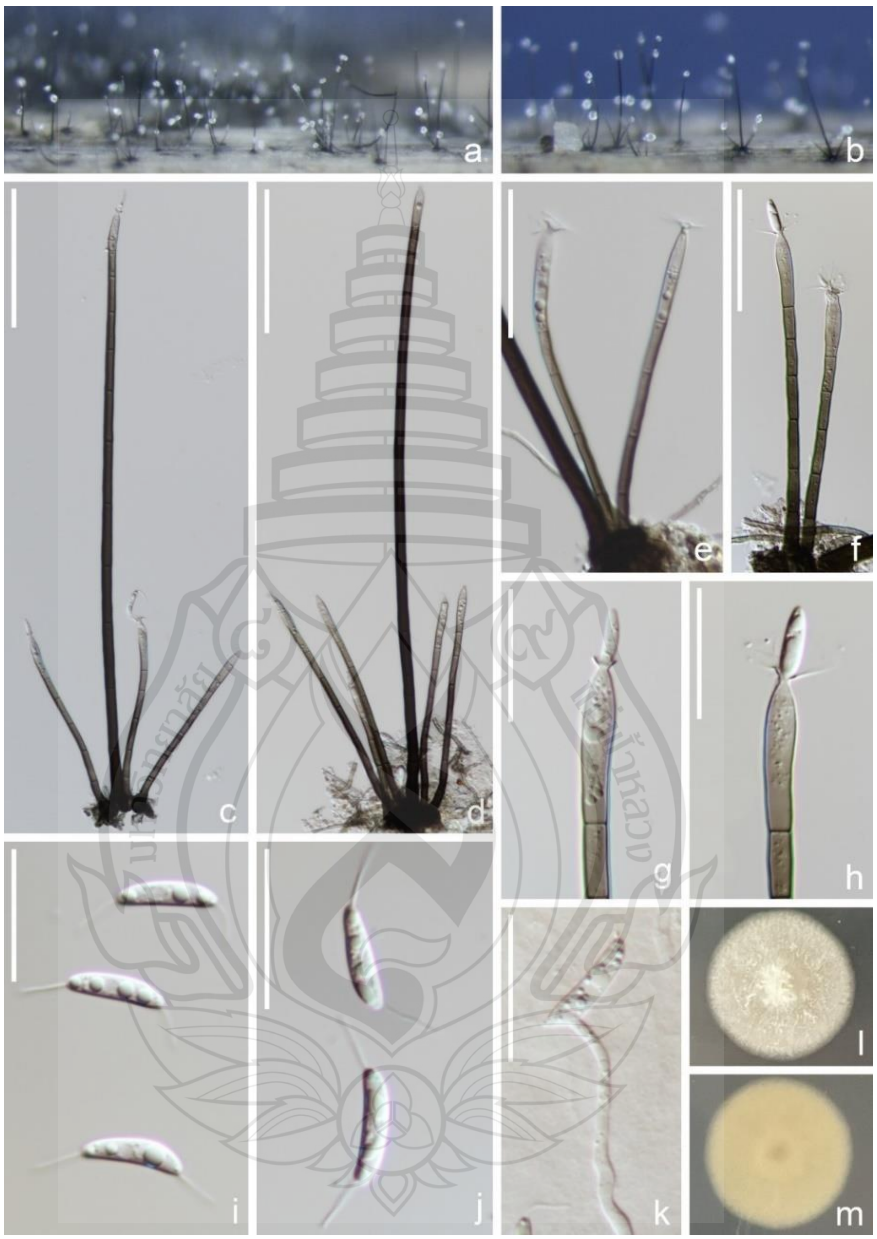
gradually towards the apex, fertile, developing into a monophialide at the apex. *Conidiophores* (84–)93–135(–172) × 3–4 µm ($\bar{x}$ = 114 × 4 µm, n = 50), macronematous, mononematous, erect, fasciculate, straight or slightly curved, cylindrical, septate, unbranched, smooth-walled, pale to dark brown, subhyaline at the apical cell. *Conidiogenous cells* 22–29(–34) × 3.7–4 µm ($\bar{x}$ = 26 × 4 µm, n = 50), monophialidic, integrated, terminal, cylindrical to cylindrical-lageniform, subhyaline to pale brown with olivaceous tinge, paler towards the tip, straight or slightly curved, narrower below the collarette; collarettes funnel-shaped, subhyaline, smooth-walled. *Conidia* 14–16 × 3–4 µm ($\bar{x}$ = 15 × 3 µm, n = 50), acrogenous, falcate, asymmetrical, hyaline, aseptate, guttulate, smooth-walled, with simple, straight or gently curved setulae at both ends.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from end of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after five weeks at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, middle mastoid, pale to pale creamy yellow on the forward; pale creamy yellow, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°52′49.72″ N, 102°39′36.82″ E, on submerged decaying wood, 18 February 2023, H.W. Shen, L1497 (HKAS 132029), living culture, KUNCC 23–13074; *ibid.*, on submerged decaying wood, 18 February 2023, H.W. Shen, L1509 (HKAS 132027), living culture, KUNCC 23–13076; *ibid.*, 24°50′23.95″ N, 102°39′50.72″ E, on submerged decaying wood, 18 February 2023, S. Luan, L1619 (HKAS 131485), living culture, KUNCC 23–13424; *ibid.*, on submerged decaying wood, 18 February 2023, S. Luan, L1621 (HKAS 131581), living culture, KUNCC 23–13425; *ibid.*, 24°45′25.39″ N, 102°36′25.06″ E, on submerged decaying wood, 18 February 2023, Y. Wang, L1485 (HKAS 131417), living culture, KUNCC 23–13073; *ibid.*, 24°49′14.15″ N, 102°45′57.58″ E, on submerged decaying wood, 18 February 2023, H.W. Shen, L1642 (HKAS 131490), living culture, KUNCC 23–13163.

Notes: In phylogenetic analysis, our six strains (L1497, L1485, L1621, L1619, L1642, L1509) are form a sister clade with *Codinaea paniculata* (CBS 145098) with 100% ML and 1.00 PP support (Figure 4.8). Compare the morphology our strains are similar with *C. paniculata*. However, our species are collected from decaying wood in Yunnan province, China. *C. paniculata* are collected from decaying wood of *Alnus*

glutinosa, *Fraxinus excelsior*, dead leave in a pool in France (Réblová, Nekvindová et al., 2020). Hence, we introduced our strain as new geographical record.



Note a, b Colony on natural substrate. c, d Setae and conidiophores. e, f Conidiophores. g, h Conidiogenous cells. i, j Conidia. k Germinated conidium. l, m Culture on PDA medium. Scale bars: c, d = 70 μm, e, f = 40 μm. g–k = 10 μm.

Figure 4.12 *Codinaea paniculata* (HKAS 131485, new geographical record)

Fuscocatenula Réblová & A.N. Mill.

Notes: *Fuscocatenula* was introduced by Réblová, Nekvindová, Miller et al. (2021) to accommodate catenularia-like fungi having cuneiform to obovoid, broadly rounded apically, aseptate, hyaline to pale brown conidia with protracted maturation and round outline, with *F. submersa* (Z.L. Luo, K.D. Hyde & H.Y. Su) Réblová & A.N. Mill. As type species (Réblová, Nekvindová, Miller et al., 2021; Wu & Diao, 2022). *Fuscocatenula* and *Catenularia* have similar morphological characteristics, but they can still be distinguished based on some subtle features (Réblová, Nekvindová, Miller et al., 2021; Wu & Diao, 2022). Conidia of *Fuscocatenula* are obovoid, truncated at base, with a round outline, hyaline when young and only later become pale brown, while the conidia of *Catenularia* are cuneiform, obclavate, rounded-obconic to broadly obovoid in side view, with an angular outline, hyaline when young but mature soon, and when released from the conidiogenous locus they are usually pigmented (Réblová, Nekvindová, Miller et al., 2021; Wu & Diao, 2022). Currently, the genus contains five species, *viz.*, *Fuscocatenula bambusicola*, *F. nabanhensis*, *F. chinensis*, *F. submersa* and *F. variegatea* (Réblová, Nekvindová, Miller et al., 2021; Wu & Diao, 2022; Liu, Hu et al., 2023). Among them, except for *F. submersa* and *F. variegata*, the other three species still lack valuable sequence data. Species of *Fuscocatenula* occur as saprobes on plant litter in terrestrial and freshwater habitats (Luo et al., 2019; Réblová, Nekvindová, Miller et al., 2021; Wu & Diao, 2022; Liu, Hu et al., 2023; Yang et al., 2023).

Fuscocatenula guttulata H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 571683; Figure 4.13

Etymology: "guttulata" refers to the guttulate conidia.

Holotype: HKAS 132055.

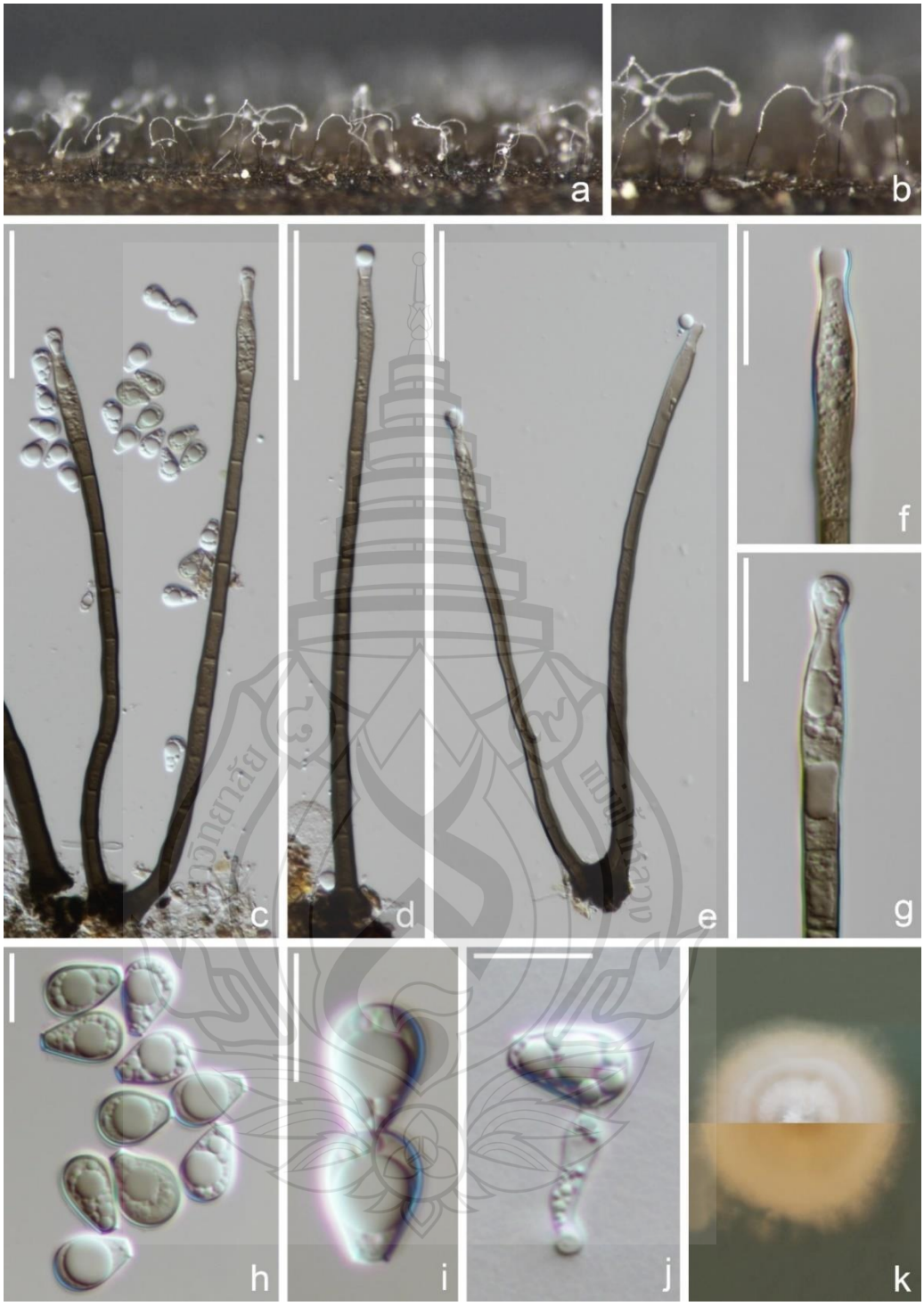
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered or gregarious, pale brown to dark brown, with white glistening chains of conidia at the apex. *Mycelium* partly superficial, partly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* (192–)200–259(–322) × 6–8 µm ($\bar{x}$ = 230 × 7 µm, n = 20), macronematous, mononematous, erect, solitary or in small group, straight or slightly curved, cylindrical,

septate, unbranched, swelled at the basal cell, pale brown to dark brown, smooth-walled, subhyaline at the apical cell. *Conidiogenous cells* 38–45(–50) × 6–8 µm ($\bar{x}$ = 42 × 7 µm, n = 20), monophialidic, integrated, terminal, cylindrical to slightly lageniform, subhyaline to pale brown, paler towards the tip, slightly narrower below the collarette; collarettes funnel- to vase-shaped, subhyaline, smooth-walled. *Conidia* 11–12 × 7–8 µm ($\bar{x}$ = 11 × 7.5 µm, n = 40), acrogenous, basocatenate, rounded-obconic to obovoid, hyaline to brown with pale olive-green tinge, aseptate, guttulate, truncate at the base, smooth-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from around of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after two months at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, middle mastoid, pale to pale creamy yellow on the forward; pale creamy yellow, dense on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujusnhu Lake, 24°32'15.6" N, 100°1′30.00″ E, on submerged decaying wood, 24 February 2023, S. Luan, L2073 (HKAS 132051, holotype), ex-type living culture, KUNCC 23–13791.

Notes: In phylogenetical analysis, *Fuscocatenula guttulata* (KUNCC 23–13791) form a sister clade with *F. variegate* (NN055332) with 99% ML and 0.98 PP support (Figure 4.8). Additionally, our species shares many characteristics with *F. variegata*, including cylindrical, septate conidiophores and obovoid conidia (Wu & Diao, 2022). However, *F. guttulata* differs from *F. variegate* by the bigger conidiophores [(192–)200–259(–322) × 6–8 µm *vs.* 150–270 × 4.5–8 µm], cylindrical to slightly lageniform conidiogenous cells and olive-green tinge conidia. Therefore, based on unique morphological and phylogenetic analyses, we introduced *F. guttulate* as a novel species.



Note a, b Colony on natural substrate. c–e Conidiophores. f, g Conidiogenous cells. h, i Conidia. j Germinated conidium. k Culture on PDA medium. Scale bars: c–e = 50 μm, f, g = 20 μm. h–j = 10 μm.

Figure 4.13 *Fuscocatenula guttulata* (HKAS 132055, holotype)

Multiguttulispora C.G. Lin & J.K. Liu

Notes: *Multiguttulispora* was proposed for dematiaceous hyphomycetes with macronematous conidiophores terminating in polyblastic, sympodial conidiogenous cells and septate, hyaline conidia with setulae, with *M. dimorpha* (Toyaz. & Udagawa) Réblová & Hern.-Restr. as type species (Lin et al., 2019; Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). *Multiguttulispora* is characterized by absence of setae, macronematous conidiophores terminated in a polyphialidic conidiogenous cells with sympodial extension, and ellipsoidal to oblong to ellipsoidal-fusiform, hyaline, 3-septate and multiguttulate conidia with a basal hilum and a gently curved setula at each end (Lin et al., 2019; Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). Based on morphological and phylogenetic analyses, *Codinaea dimorpha* and *C. triseptata* were transferred into *Multitiguttulispora*, and *M. sympodialis* was reduced to a synonym of *M. dimorpha* (Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). Four species are accepted in *Multiguttulispora*, which are reported as saprobes on plant litter (Lin et al., 2019; Réblová, Nekvindová, Hernandez-Restrepo et al., 2021; Wu & Diao, 2022) and also reported as leaf endophytes (Cannon & Simmons, 2002).

Multiguttulispora dimorpha (Toyaz. & Udagawa) Réblová & Hern.-Restr., Journal of Fungi 7(6, no. 438): 20 (2021)

Fungal Names number: FN 839480, *Facesoffungi number*: FoF 12807; Figure 4.14

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered or fasciculate, brown to dark brown, with white glistening masses of conidia at the apex. *Mycelium* mostly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* (90–)253–458(–556) × 7–8.5 µm ($\bar{x}$ = 356 × 7.5 µm, n = 50), macronematous, mononematous, erect, straight or slightly curved, cylindrical, septate, unbranched, smooth-walled, pale to dark brown, subhyaline at the apical cell. *Conidiogenous cells* polyphialidic, integrated, terminal, cylindrical to cylindrical-lageniform, extending sympodially over a short distance, subhyaline to pale brown with olivaceous tinge, straight or slightly curved, often with persistent remnants of the collarettes; collarettes funnel-shaped, subhyaline, smooth. *Conidia* 19–23 × 6–8 µm ($\bar{x}$ = 21 × 7 µm, n = 50), acropleurogenous, ellipsoidal to

oblong to ellipsoidal-fusiform, slightly curved, hyaline, 3-septate, guttulate, smooth-walled, with simple, straight or gently curved setulae at both ends.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from end of conidium within 12 h. Colonies on PDA medium reaching 1-1.5 cm diam. after two weeks at room temperature (around 25 °C) in dark, loose, flocculent, dense, middle mastoid, pale to pale creamy yellow to orange on the forward; pale creamy yellow, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Yangzonghai Lake, 24°54′43.70″ N, 103°1′3.64″E, on submerged decaying wood, 20 February 2023, S. Luan, L1780 (HKAS 131671), living culture, KUNCC 23–13563.

Notes: Phylogenetically, our new collection clustered with strains of *Multiguttulispora dimorpha* with low support (Figure 4.8). Morphologically, our isolate was similar to *M. dimorpha* in having straight to slightly curved, cylindrical, septate, unbranched conidiophores; polyphialidic, integrated, terminal, cylindrical to cylindrical-lageniform, collarettes conidiogenous cells; and ellipsoidal to oblong to ellipsoidal-fusiform, hyaline, guttulate, septate conidia (Lin et al., 2019; Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). Based on morphological and phylogenetic analysis, the new isolate was identified as *M. dimorpha*, which was first reported from China and in freshwater habitats.

Note a, b Colony on natural substrate. c, d Conidiophores. e–h Conidiogenous cells. i–l Conidia. m Germinated conidium. n, o Culture on PDA medium. Scale bars: c, d = 100 μm, e–h = 30 μm. i–m = 15 μm.

Figure 4.14 *Multiguttulispora dimorpha* (HKAS 131671, new geographical and habitat record)

Paragaeumannomyces Matsush.

Notes: *Paragaeumannomyces* was introduced by Matsushima (2003) to accommodate the type species, *P. sphaerocellularis*. Based on morphological and phylogenetic analysis, *Paragaeumannomyces* was emend to accommodate the morphologically and phylogenetically well-delimited group of chaetosphaeriaceous fungi with scolecospore ascospores and obeliospora-like anamorph (Réblová, Nekvindová et al., 2020). The sexual morphs of *Paragaeumannomyces* are characterized by perithecial, non-stromatic, superficial, subglobose to conical, solitary, white, yellow-white, light fawn-grey, ginger-brown, reddish-brown, russet to dark brown, papillate ascomata, with glabrous or setose, setae dark brown, acute, scattered over entire ascoma and/or clustered around the ostiole; outer layer, thin-walled, globose, subglobose to polyhedral cells; asci cylindrical-fusiform, stipitate, apex with a non-amyloid apical annulus; ascospores scolecosporous, multiseptate, asymmetrical, hyaline to light pink ascospores (Réblová, Nekvindová et al., 2020; Wu & Diao, 2022; Yang et al., 2023). The asexual morphs are craspedodidymum-like and chloridium-like (Réblová, Nekvindová et al., 2020). Based on morphological and phylogenetic data, Wu and Diao (2022) reduced *Obeliospora* to a synonym of *Paragaeumannomyces* and described two new asexual species. Subsequently, new sexual species, *P. aquaticus*, was introduced by Yang et al. (2023). Currently, 24 species are accommodated in *Paragaeumannomyces*, which occur as saprobes on plant litter in terrestrial and freshwater habitats (Réblová, Nekvindová et al., 2020; Wu & Diao, 2022; Zhang et al., 2022; Yang et al., 2023).

Paragaeumannomyces guttulatus J.Y. Zhang & Y.Z. Lu, Journal of Fungi 8(no. 643): 20 (2022)

Fungal Names number: FN 559700, *Facesoffungi number*: FoF 11041; Figure 4.15

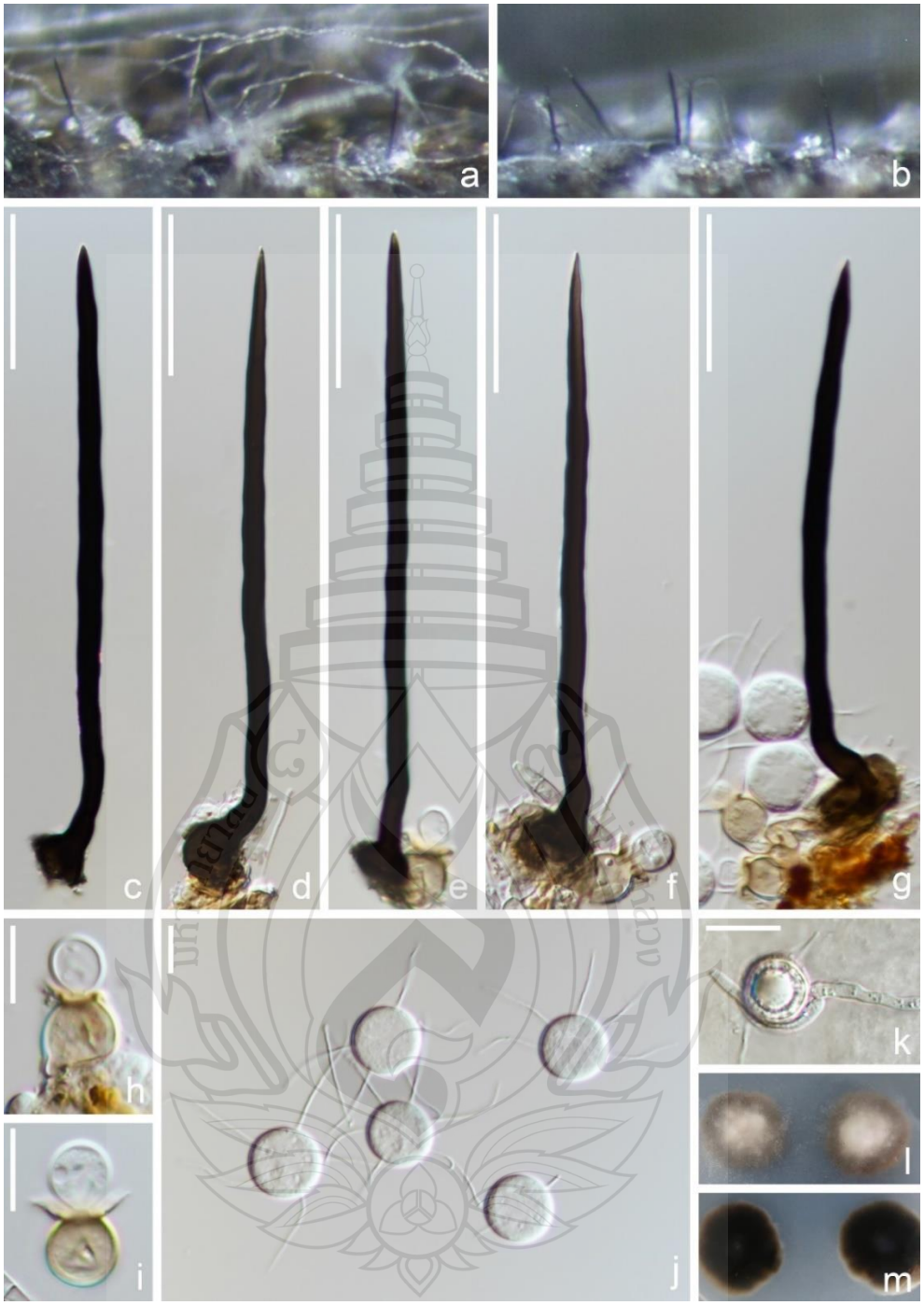
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered, brown to dark brown. *Mycelium* partly superficial, partly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Setae* (87–)102–124 × 4–5 µm ($\bar{x}$ = 113 × 4.5 µm, n = 15), erect, straight or slightly flexuous, cylindrical, septate, unbranched, smooth-walled, dark brown, basal cell expanded, tapering gradually towards the apex, acute at the apex, sterile.

Conidiophores semi-macronematous to micronematous, mononematous, sometimes reduced to conidiogenous cells, straight or slightly curved, septate, unbranched, smooth-walled, subhyaline to dark brown. *Conidiogenous cells* 9–15 × 8–9 µm ($\bar{x}$ = 12 × 8 µm, n = 15), monophialidic, integrated, terminal, globose to ellipsoidal, subhyaline to pale brown with a funnel-shaped, cup-shaped, subhyaline, smooth collarette; collarettes 8–12 µm wide, 3–4 µm deep. *Conidia* 13–15 µm diam. ($\bar{x}$ = 14 µm, n = 50), acrogenous, globose to subglobose, hyaline, aseptate, guttulate, smooth, thin-walled, with 4–7 thin, simple, hair-like, non-septate, hyaline setulae, 19–26 µm long.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from end of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after two months at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, pale to dark brown on the forward; brown to dark brown, smooth-edged, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L2031 (HKAS 131824), living culture, KUNCC 23–13784; *ibid.*, 24°32′30.44" N, 101°1′39.51″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L2037 (HKAS 132068), living culture, KUNCC 23–13785.

Notes: Obviously, *Paragaeumannomyces guttulatus* all the characters size are bigger than the closely species of *P. guttulatus* (GZCC 22–0084) (Zhang et al., 2022). Phylogenetical, *P. guttulatus* cluster with *P. guttulatus* with 98% ML and 1.00 PP support (Figure 4.8). Based on morphological and phylogenetic analyses, our two new collections were identified as *P. guttulatus*.



Note a, b Colony on natural substrate. c, d Setae. e–g Setae and conidiogenous cells with developing conidia. h, i Conidiogenous cells with developing conidia. j Conidia. k Germinated conidium. l, m Culture on PDA medium. Scale bars: c–g = 30 μm. h–k = 10 μm.

Figure 4.15 *Paragaeumannomyces guttulatus* (HKAS 131824)

Sporoschisma Berk. & Broome

Notes: *Sporoschisma* was introduced for *S. mirabile* Berk. & Broome. The asexual morphs of *Sporoschisma* characterized by reduced, unbranched, brown conidiophores; phialidic conidiogenous cells with deep, cylindrical collarettes; phragmosporous, brown conidia in basipetal chains; vesiculate, capitate setae with mucilaginous apices among the conidiophores and a stroma is sometimes present (Sivichai et al., 2000; Luo et al., 2016; Yang et al., 2016; Bao, Hyde et al., 2021). The sexual morphs have been linked to *Melanochaeta* (Sivichai et al., 2000). Species of *Sporoschismopsis* and *Sporoschisma* are morphologically remarkably similar with massive conidiophores, or stalked phialides, and brown, septate conidia that develop basipetally and successively, forming long fragile chains (Réblová, 2014). However, their sexual morph can be clearly distinguished by by different types of interthecial filaments (Réblová, 2014). Goh et al. (1997) emended the generic concepts of *Sporoschismopsis* and *Sporoschisma*, suggesting that the presence/absence of a swollen venter, would have greater taxonomic significance at the genus level. Réblová (2014) re-evaluated the delimitation of both genera considering the generic changes suggested by Goh et al. (1997) and proposed to follow their original concepts. Based on phylogenetic evidence, *Sporoschisopsis* was placed in the *Reticulascaceae* (*Glomerellales*), whereas *Sporoschisma* was placed in the *Chaetosphaeriaceae* (*Chaetosphaeriales*) (Réblová, 2014; Hyde, Norphanphoun et al., 2020). Currently 15 species are placed in *Sporoschisma*, which occur primarily as saprobes on woody debris in terrestrial and freshwater habitats (Goh et al., 1997; Sivichai et al., 2000; Luo et al., 2016; Yang et al., 2016; Bao, Hyde et al., 2021).

Sporoschisma hemipsilum (Berk. & Broome) Zelski, A.N. Mill. & Shearer, IMA Fungus 5(2): 433 (2014)

Fungal Names number: FN 816542, *Facesoffungi number*: FoF 02376; Figure 4.16

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered or gregarious, brown to dark brown, with brown to dark brown glistening chains of conidia at the apex. *Mycelium* partly superficial, partly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Setae* erect, solitary or scattered, capitate, usually with hyaline mucilage at the swollen apex,

straight or slightly flexuous, cylindrical, septate, unbranched, smooth-walled, pale brown to brown. *Conidiophores* (214–)241–289(–306) µm long ($\bar{x}$ = 265 µm, n = 30), macronematous, mononematous, erect, solitary or in small groups, straight or slightly curved, septate, unbranched, smooth-walled, dark brown, with bulbous base, a cylindrical, often curved stipe, 8–11 µm wide at base, and a swollen venter (15–19 µm at the widest) with a long cylindrical neck. *Conidiogenous cells* monophialidic, integrated, terminal, determinate, lageniform, subhyaline to dark brown. *Conidia* 44–51(–56) × 13–15 µm ($\bar{x}$ = 47 × 14 µm, n = 50), formed enteroblastically inside the tubular collarette of the conidiogenous cell and emerging in a chain, cylindrical, both ends rounded to sub-truncate, brown to dark brown, 3–5-septate, with conspicuously darkened septa, guttulate.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after two months at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, pale brown to pale brown on the forward; pale to brown, smooth-edged, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Lijiang City, Luguhu Lake, 27°45′01.83" N, 100°51′01.90" E, on submerged decaying wood, 3 March 2021, S. Luan, L662 (HKAS 131466); *ibid.*, Kunming City, Yangzonghai Lake, 24°56′41.76″ N, 103°1′11.61″ E, on submerged decaying wood, 20 February 2023, S. Luan, L1919 (HKAS 131726), living culture, KUNCC 23–13479; *ibid.*, 24°54′43.70″ N, 103°1′3.64″ E, on submerged decaying wood, 20 February 2023, H.W. Shen, L1882 (HKAS 131426), living culture, KUNCC 23–13480; *ibid.*, Honghe Prefecture, 23°39′18.69″ N, 102°35′49.15″ E, on submerged decaying wood, 22 February 2023, Y. Wang, L1894 (HKAS 132092), living culture, KUNCC 23–13481; *ibid.*, 23°40′56.4" N, 101°43'46.8″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L2191 (HKAS 132096), living culture, KUNCC 23–14294.

Notes: Phylogenetic analysis showed that our five freshwater fungal collections clustered with *Sporoschisma hemipsilum* (Figure 4.8). Morphologically, our new collections showed no significant differences from the description of *S. hemipsilum*. Therefore, based on morphological characteristics and phylogenetic analysis, our five strains were identified as *S. hemipsilum*.

Note a, b Colony on natural substrate. c–e Conidiophores. f Conidiogenous cells. g, h Conidia. i Germinated conidium. j Culture on PDA medium. Scale bars: c–e = 120 μm. f = 70 μm. g–i = 40 μm.

Figure 4.16 *Sporoschisma hemipsilum* (HKAS 132096)

Sporoschisma taitense (Mugambi & Huhndorf) A.N. Mill., IMA Fungus 7(1): 134 (2016)

Fungal Names number: FN 816829, *Facesoffungi number*: FoF 02375; Figure 4.17

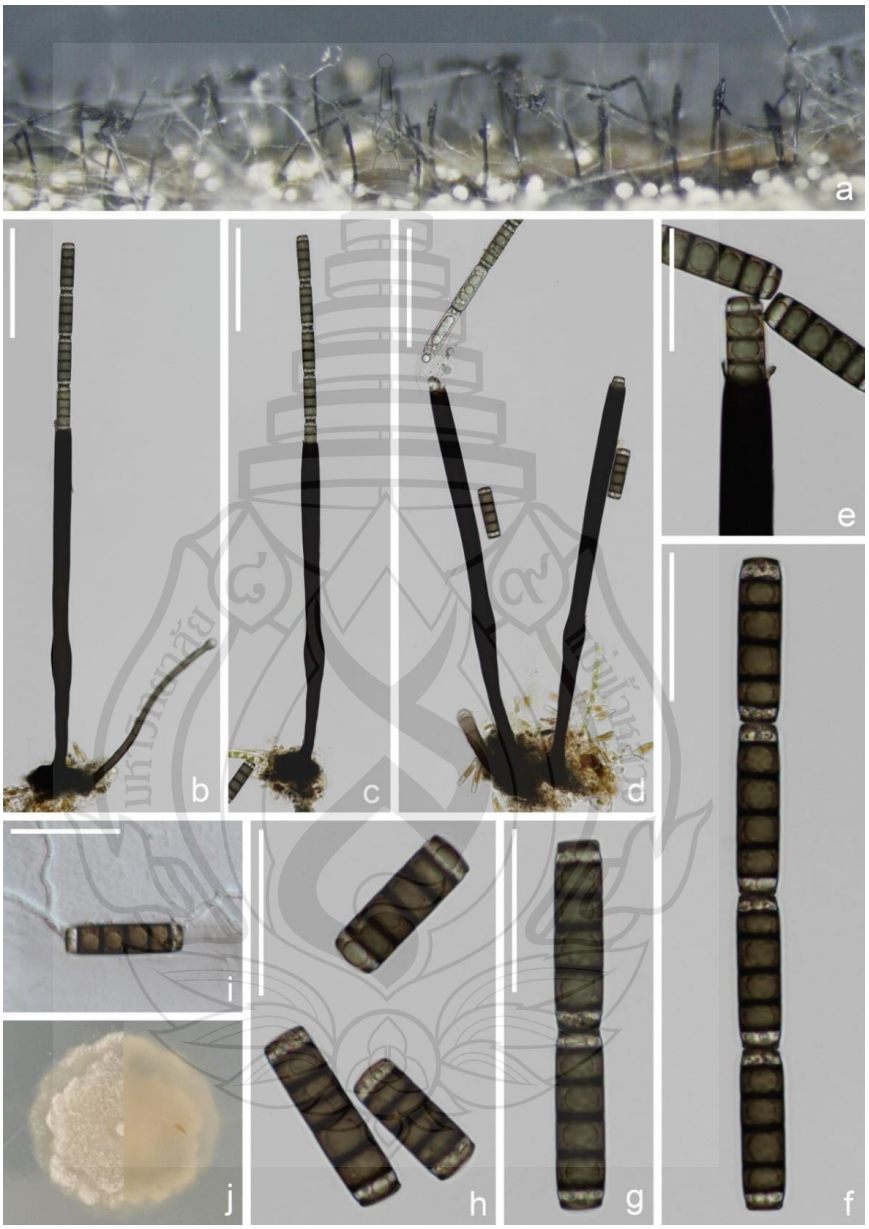
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered or gregarious, brown to dark brown, with brown to dark brown glistening chains of conidia at the apex. *Mycelium* partly superficial, partly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Setae* erect, solitary or scattered, capitate, usually with hyaline mucilage at the swollen apex, straight or slightly flexuous, cylindrical, septate, unbranched, smooth-walled, pale brown to brown. *Conidiophores* (279–)307–339(–350) × 15–19 µm ($\bar{x}$ = 323 × 17 µm, n = 20), macronematous, mononematous, erect, solitary or in small groups, straight or slightly curved, septate, unbranched, smooth-walled, dark brown, with bulbous base, a cylindrical, often curved stipe, and a swollen venter with a long cylindrical neck. *Conidiogenous cells* monophialidic, integrated, terminal, determinate, lageniform, subhyaline to dark brown. *Conidia* (29–)39–48(–54) × 12–13 µm ($\bar{x}$ = 44 × 12 µm, n = 50), formed enteroblastically inside the tubular collarette of the conidiogenous cell and emerging in a chain, cylindrical, both ends rounded to sub-truncate, pale brown to dark brown with olivaceous tinge, 3–6-septate, with conspicuously darkened septa, guttulate.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after five weeks at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, pale brown on the forward; pale to brown, smooth-edged, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L1605 (HKAS 131541), living culture, KUNCC 23–13385.

Notes: Phylogenetic analysis showed that our new isolate, KUNCC 23–13385, was closely related to *Sporoschisma taitense* with 100% ML and 1.00 PP support (Figure 4.8). Morphologically, our isolate was highly similar to *S. taitense* in having straight to slightly curved, unbranched, conidiophores with bulbous base, a cylindrical,

often curved stipe, and a swollen venter with a long cylindrical neck; the conidiogenous cells monophialidic, integrated, terminal, determinate, lageniform; and cylindrical, septate, guttulate conidia emerging in a chain.



Note a Colony on natural substrate. b–d Conidiophores. e Apex of conidiogenous cells. f–h Conidia. i Germinated conidium. j Culture on PDA medium. Scale bars: b–d = 100 μm. e–i = 40 μm.

Figure 4.17 *Sporoschisma taitense* (HKAS 131541)

Tainosphaeria F.A. Fernández & Huhndorf

Notes: *Tainosphaeria* was introduced by Fernández and Huhndorf (2005) to accommodate type species, *T. crassiparies*. The sexual morphs of *Tainosphaeria* are characterized by subglobose to ovoid ascomata, simple, septate, hyaline paraphyses, unitunicate, cylindrical, pedicellate asci, with an apical ring, and hyaline, septate ascospores (Fernández & Huhndorf, 2005; Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). The asexual morphs are codinaea-like, with mononematous, pigmented, simple conidiophores, mono- occasionally polyphialidic conidiogenous cells and falcate, hyaline, aseptate, conidia with setulae (Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). Recent phylogenetic analysis showed that the genus *Tainosphaeria* is polyphyletic (Lin et al., 2019; Luo et al., 2019; Li, Yu et al., 2021; Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). Réblová, Nekvindová, Hernandez-Restrepo et al. (2021) re-evaluated the generic concept of *Tainosphaeria* and showed correlation between molecular and morphological data, subsequently separating its species into three genera, *viz. Tainosphaeria*, *Phialogeniculata* and *Phialoturbella* (Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). Subsequently, based on morphological characteristics and molecular sequence data, the two new species introduced by Li, Yu et al. (2021) were placed in a new genus, *Tainosphaeriella* (Réblová, Nekvindová, Hernandez-Restrepo et al., 2021). Recently, five new species of *Tainosphaeria* from dead leaves, culm, wood, fruit and seed pod of plants were introduced by Wu and Diao (2022), and 13 species were accepted into *Tainosphaeria* (Wu & Diao, 2022). These species are saprobes on woody debris in terrestrial and freshwater habitats (Liu et al., 2016; Lu et al., 2016; Perera et al., 2016; Luo et al., 2019; Réblová, Nekvindová, Hernandez-Restrepo et al., 2021; Wu & Diao, 2022).

Tainosphaeria phialogeniculata W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 216 (2022)

Fungal Names number: FN 841592, *Facesoffungi number*: FoF 02375; Figure 4.18

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate, effuse, hairy, solitary, scattered or gregarious, pale brown to brown, with white glistening masses of conidia at the apex. *Mycelium* mostly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* 49–67(–84) × 3–4 µm

($\bar{x}$ = 58 × 3.5 µm, n = 35), macronematous, mononematous, erect, solitary or fasciculate, straight or slightly curved, septate, unbranched, smooth-walled, subhyaline to pale brown. *Conidiogenous cells* 29–38(–45) × 3–3.7 µm ($\bar{x}$ = 33 × 3.4 µm, n = 30), monophialidic, integrated, terminal, cylindrical to cylindrical-lageniform, subhyaline to pale brown with olivaceous tinge, paler towards the tip, straight or slightly curved, narrower below the collarette; collarettes funnel-shaped, subhyaline, smooth-walled. *Conidia* 15–17 × 2.6–3 µm ($\bar{x}$ = 16 × 3 µm, n = 50), acrogenous, lunate, falcate, asymmetrical, hyaline, aseptate, guttulate, smooth-walled, with simple, straight or gently curved setulae at both ends.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from end of conidium within 12 h. Colonies on PDA medium reaching 2.5-3 cm diam. after two months at room temperature (around 25 °C) in dark, circular, loose, flocculent, dense, pale brown to dark brown with grey-green tinge on the forward; pale to brown, smooth-edged, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L1602 (HKAS 131494), living culture, KUNCC 23–13396.

Notes: Phylogenetic analysis revealed that our newly isolate, KUNCC 23–13396, clustered closely with the type strain of *Tainosphaeria phialogeniculata* (CGMCC 3.20799) without significant phylogenetic distance (Figure 4.8). Morphologically, the conidia of our isolate were highly similar to *T. phialogeniculata*, in having subhyaline to pale brown with olivaceous tinge conidia (Wu & Diao, 2022), but slightly different from *T. phialogeniculata* in the size of conidiophores and conidiogenous cells. Based on the highly similar molecular sequence data and morphological characteristics, we identified the newly isolate, KUNCC 23–13396, as *T. phialogeniculata*. The type specimen of *T. phialogeniculata* was collected from terrestrial habitats, and our new collection was from a freshwater habitat, which is the first report of this species from freshwater habitat.

Note a Colony on natural substrate. b–e Conidiophores and conidiogenous cells. f–h Conidia. i Germinated conidium. j, k Culture on PDA medium. Scale bars: b–e = 20 μm. f–i = 10 μm.

Figure 4.18 *Tainosphaeria phialogeniculata* (HKAS 131494, new habitat record)

Thozetella Kuntze

Notes: Thozetella was introduced by Kuntze (1891), with *T. nivea* as type species. The genus is characterized by sporodochial or synnematous conidiomata, with terminated, phialidic conidiogenous cells and hyaline, naviculate to fusiform or ellipsoid, aseptate conidia, with unbranched setula at each end, and forming sterile microawns (Perera et al., 2016; (Wu & Diao, 2022). *Thozetella* is a monophyletic genus with species grouped in a single clade within the family *Chaetosphaeriaceae* (Wu & Diao, 2022). On the basis of morphology and phylogeny, and according to *Chaetosphaeria rivularis* (sexual species with thozetella-like asexual morph), Wu and Diao (2022) emend the concept of the genus *Thozetella*. Currently, 41 species are accepted into *Thozetella*, which occur primarily as saprobes on plant litter in terrestrial and freshwater habitats (Perera et al., 2016; Luo et al., 2019; Wu & Diao, 2022).

Thozetella wenyingiae W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 439 (2022)

Fungal Names number: FN 841655, *Facesoffungi number*: FoF 02375; Figure 4.19

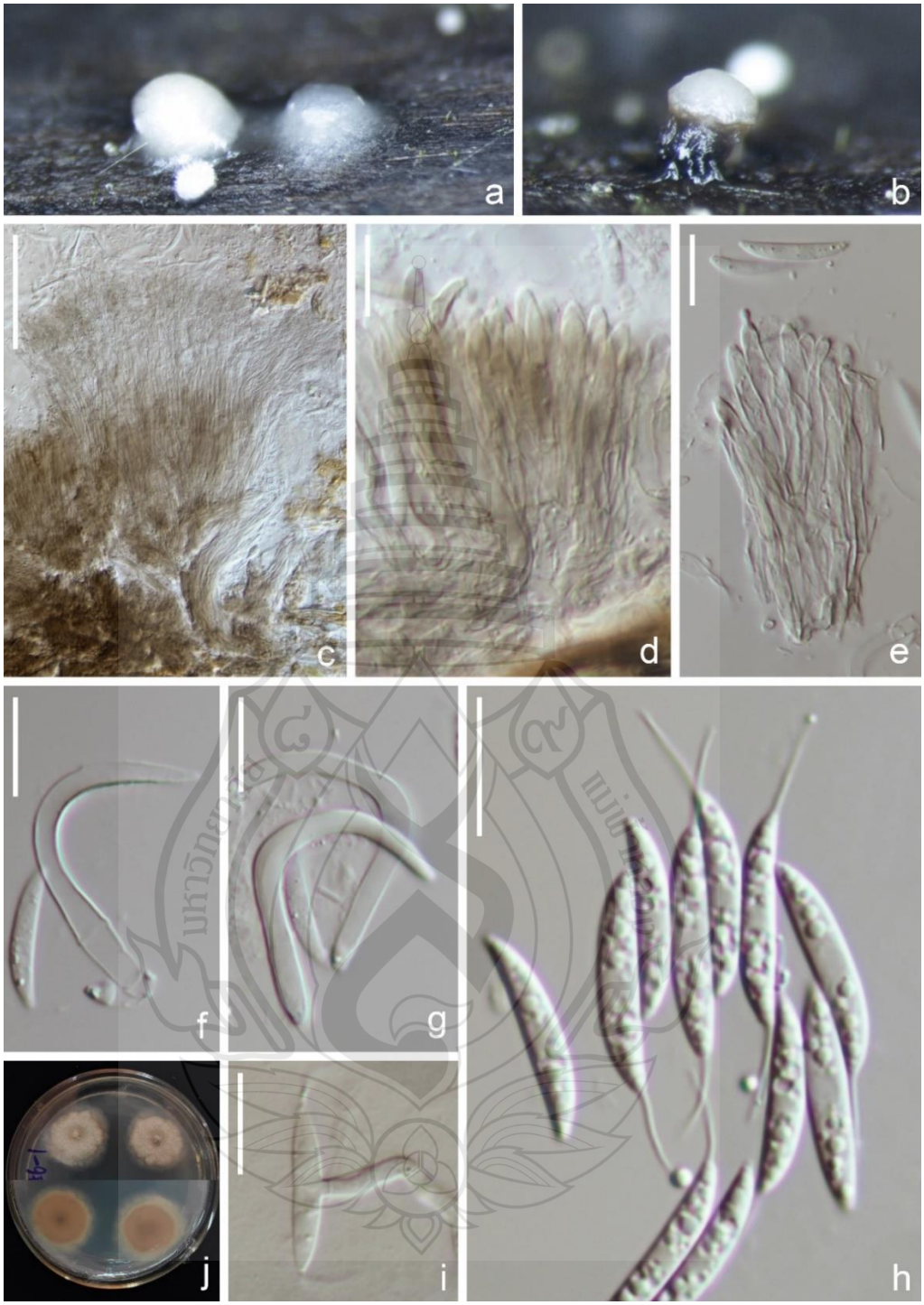
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* superficial, sporodochial, solitary, scattered, pale brown to brown, with white glistening masses of conidia at the apex. *Mycelium* mostly immersed, composed of septate, hyaline to pale brown, smooth, branched, septate, thin-walled hyphae. *Conidiophores* macronematous, mononematous, packed in a bundle, cylindrical, straight or slightly curved, septate, branched, smooth-walled, subhyaline to pale brown. *Conidiogenous cells* 18–26 × 2–3 µm ($\bar{x}$ = 22 × 2.4 µm, n = 25), monophialidic, integrated, terminal, cylindrical to cylindrical-lageniform, subhyaline to pale brown, paler towards the tip, straight or slightly curved, without collarettes or with inconspicuous collarettes, smooth, thin-walled. *Conidia* 15–16 × 2.3–2.7 µm ($\bar{x}$ = 15.5 × 2.5 µm, n = 50), acrogenous, fusiform to lunate, hyaline, aseptate, guttulate, smooth-walled, with simple, straight or gently curved setulae at both ends. *Microawns* 29–41 × 2.6–3.5 µm, vermiform-shaped, uncinate, variously shaped, hyaline, aseptate, rounded at the base, wide at the middle bend, gradually tapering toward the top, sharp or obtuse at the apex, smooth or verrucous.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from side of conidium within 12 h. Colonies on PDA medium reaching 3.5-4 cm diam. after five weeks at room temperature (around 25 °C) in dark, circular, loose,

flocculent, dense, middle mastoid, pale brown to brown on the forward; pale brown to reddish brown, smooth-edged, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L1846 (HKAS 131428), living culture, KUNCC 23–13383.

Notes: Phylogenetically, our strain cluster together with *Thozetella wenyingiae* with 98% ML and 1.00 PP support (Figure 4.8). Our strain the morphology also similar with *T. wenyingiae*, but our strain generates bigger conidiogenous cell (18–26 × 2–3 µm *vs.* 13–18 × 1.5–2 µm). based on morphological characteristics and phylogenetic analysis, we therefore, identified it as *T. wenyingiae*, reported for the first time in freshwater habitats.



Note a, b Colony on natural substrate. c Conidiophores. d, e Conidiogenous cells. f, g Microawns. h Conidia. i Germinated conidium. j Culture on PDA medium. Scale bars: c = 50 μm. d–i = 10 μm.

Figure 4.19 *Thozetella wenyingiae* (HKAS 131428, new habitat record)

Pleurotheciales Réblová & Seifert

Pleurotheciaceae Réblová & Seifert

Notes: *Pleurotheciaceae* was established by Réblová et al. (2016), with *Pleurothecium* as type genus. The sexual morphs of *Pleurotheciaceae* are characterized by dark, papillate, perithecial, astromatic, immersed to superficial ascomata, unitunicate asci with a distinct non-amyloid apical annulus, and fusiform to ellipsoidal, septate, hyaline ascospores (Reblova et al., 2016; Luo, Hyde, Bhat et al., 2018; Hyde, Dong et al., 2020). The asexual morphs of *Pleurotheciaceae* include species with diverse morphologies, comprising acrodictys-like (Hyde & Hyde, 2002; Sadowski et al., 2012), helicoön-like (Dayarathne et al., 2019; Réblová, Hernandez-Restrepo et al., 2020), monodictys-like (Hyde, Dong et al., 2020) and dactylaria-like taxa (Reblova et al., 2016; Luo, Hyde, Bhat et al., 2018). Species in *Pleurotheciaceae* are cosmopolitan with a worldwide distribution and have been reported from both aquatic and terrestrial habitats (Reblova et al., 2016; Luo, Hyde, Bhat et al., 2018; Hyde, Dong et al., 2020; Réblová, Hernandez-Restrepo et al., 2020).

Dematipyriforma L.Y. Sun, Hai-Yan Li, Xiang Sun & L.D. Guo

Notes: *Dematipyriforma* was established by Sun et al. (2017) to accommodate *D. aquilaria*, an endophytic fungus isolated from *Aquilaria crassna*, based on morphological and phylogenetic analyses. Initially, based on limited data, *Dematipyriforma* was placed within *Savoryellales*; however, subsequent studies reclassified it into *Pleurotheciaceae* (*Pleurotheciales*) based on morphological characteristics and phylogenetic evidence (Sun et al., 2017; Bao et al., 2022; Jayawardena et al., 2022). Currently, the genus comprises seven species that occur as endophytes and saprobes in both terrestrial and freshwater habitats, with five species reported from freshwater habitats (Sun et al., 2017; Bao et al., 2022; Jayawardena et al., 2022).

Dematipyriforma nilotica Abdel-Aziz & Abdel-Wahab, Fungal Diversity 117: 135 (2023)

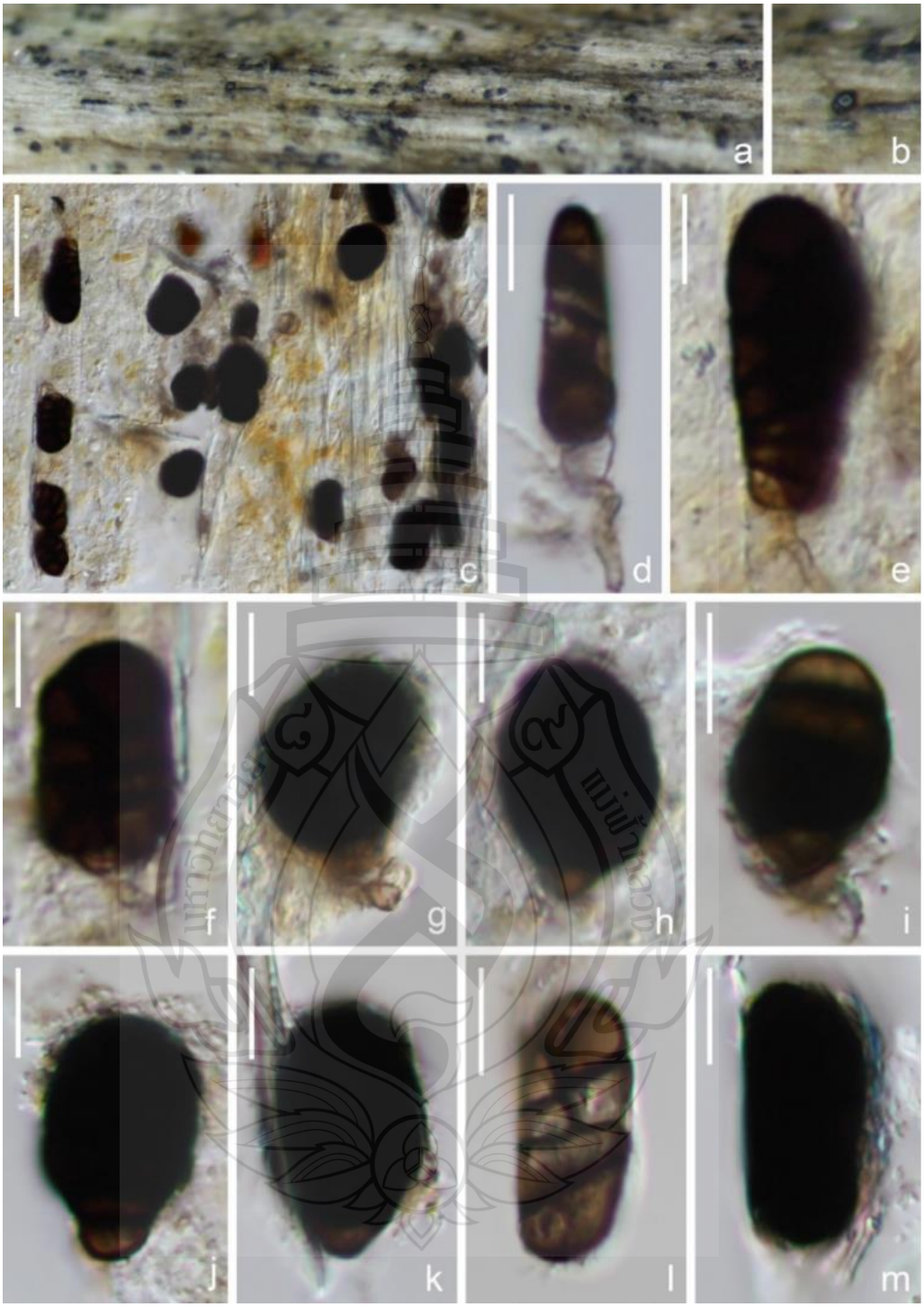
Fungal Names number: FN 900084; *Facesoffungi number*: FoF 13401; Figure 4.20

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, or semi-immersed in substrate, effuse, brown to dark brown, punctiform, scattered, glistening.

Mycelium immersed or superficial, composed of septate, pale to pale brown, smooth, thin-walled hyphae. *Conidiophores* absent or present, micronematous, mononematous, sub-hyaline to pale brown, flexuous, smooth-walled. *Conidiogenous cells*, monoblastic, integrated, terminal, ampulliform, clavate, subglobose, subhyaline to pale brown, smooth-walled. *Conidia* 22–31(–39) × (10–)13–19(–23) µm ($\bar{x}$ = 27 × 16 µm, n = 40), acrogenous, subcylindrical, pyriform, globose or subglobose, muriform, rounded at the apex, dark brown to black, guttulate, smooth -walled, with a brown to dark brown basal cell.

Material examined: CHINA, Yunnan Province, Kunming City, Yangzonghai Lake, 23°39′18.69″ N, 102°35′49.15″ E, on submerged decaying wood, 22 February 2023, Y. Wang, L2134 = L2177 (HKAS 132097), living culture, KUNCC 23–14334.

Notes: In the phylogenetic analysis, our new collections clustered with three *Dematipyriforma nilotica* strains (Figure 4.21). There is no significant difference in the morphology between our new collections and the type material of *D. nilotica* (Jayawardena et al., 2022). Therefore, we identified our collection as *D. nilotica*, representing a new geographical record from freshwater in China.



Note a, b Colony on natural substrate. d–g Conidiophores, conidiogenous cells and conidia. c, j–m Conidia. Scale bars: c = 50 μm, d–m = 10 μm.

Figure 4.20 *Dematipyriforma nilotica* (HKAS 132097, new geographical record)

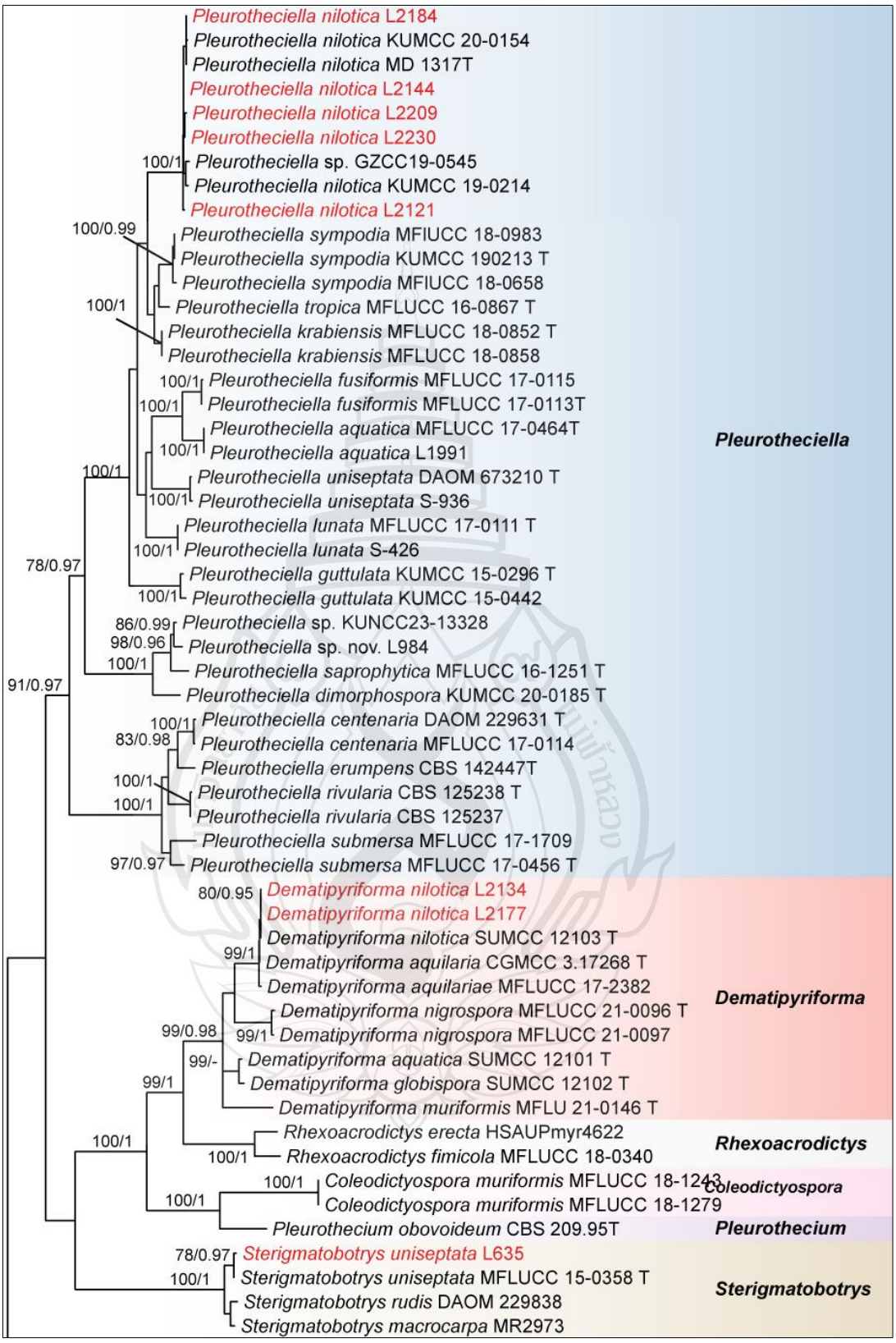
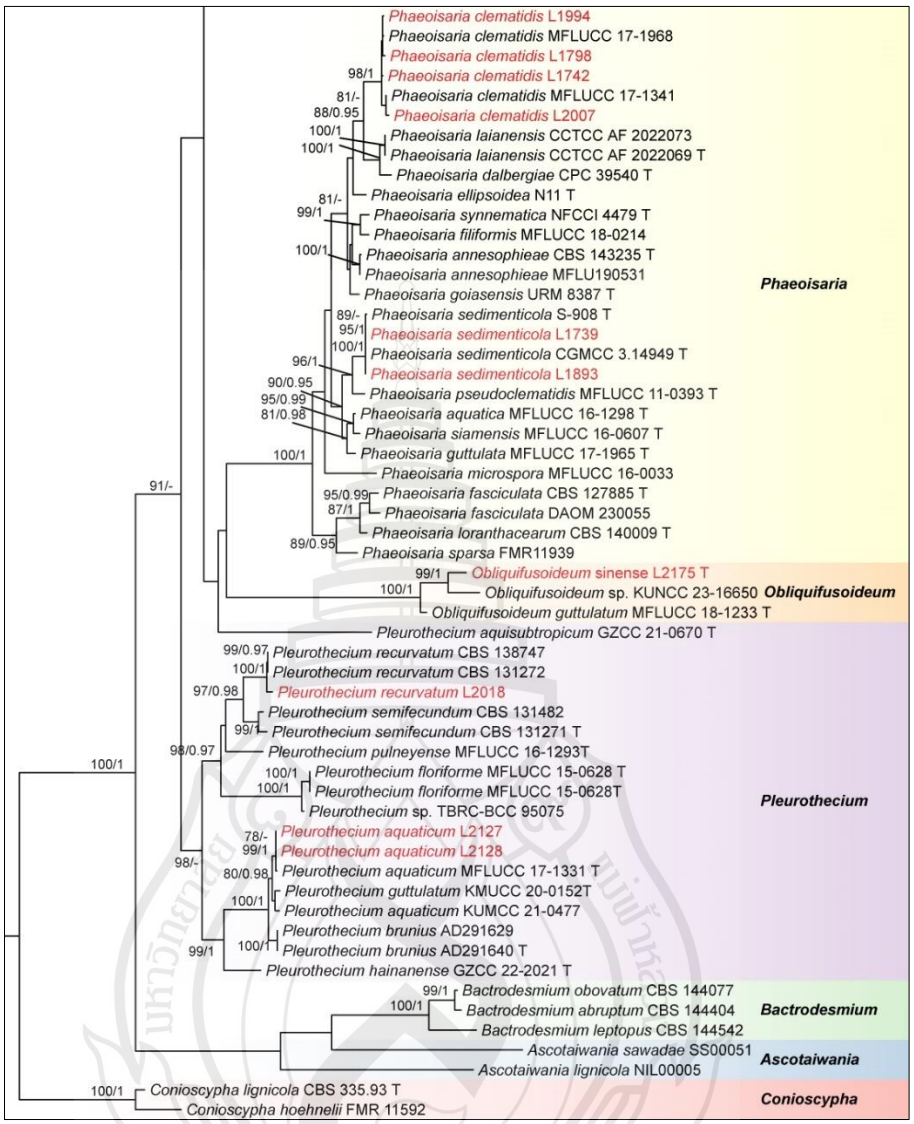


Figure 4.21 Phylogenetic tree of *Pleurotheciales*



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU and *rpb*2 sequence dataset representing *Pleurotheciales*. 111 strains are included in the combined analyses which comprise 3326 characters including gaps (826 characters for LSU, 482 characters for ITS, 977 characters for SSU, 1029 characters for *rpb*2). *Conioscypha lignicola* (CBS 335.93) and *C. hoehnelii* (FMR 11592) were selected as the outgroup taxa. Bootstrap support values with a ML greater than 65%, and Bayesian posterior probabilities (PP) greater than 0.95 are given above the nodes, shown as "ML/PP". New species are indicated in red and type strains are indicated by a "T" after the strain number.

Figure 4.21 (continued)

Obliquifusoideum W. Dong, Doilom and K.D. Hyde

Notes: The freshwater fungal genus *Obliquifusoideum* was introduced by Dong, Jeewon et al. (2021b) to accommodate a saprobic species, *O. guttulatum*, a lignicolous freshwater fungi from Thailand. Based on unstable phylogenetic results, *Obliquifusoideum* was placed in Savoryellomycetidae genera *incertae sedis*. However, Wang et al. (2024) later accepted *Obliquifusoideum* in *Pleurotheciaceae* based on morphological and phylogenetic analyses. Currently, *Obliquifusoideum* comprises two species *O. guttulatum* and *O. triseptatum*, both from freshwater habitats, and are known sexual morphs characterized by superficial, ellipsoidal, black, coriaceous, ostiolate ascomata with a lateral neck; hyaline to dark, subcylindrical necks oblique or horizontal to the host; unitunicate, cylindrical asci with a small, refractive, barrel- or jar-shaped, apical ring; uniseriate, fusoid to fusiform, septate, hyaline, guttulate ascospores without gelatinous sheath (Dong, Jeewon et al., 2021; Wang et al., 2024).

Obliquifusoideum sinense H.W. Shen, Z.L. Luo & K.D. Hyde, ***sp. nov.***

Fungal Names number: FN 571683; Figure 4.22

Etymology: "sinense" refers to China, where the type specimen of the species was collected.

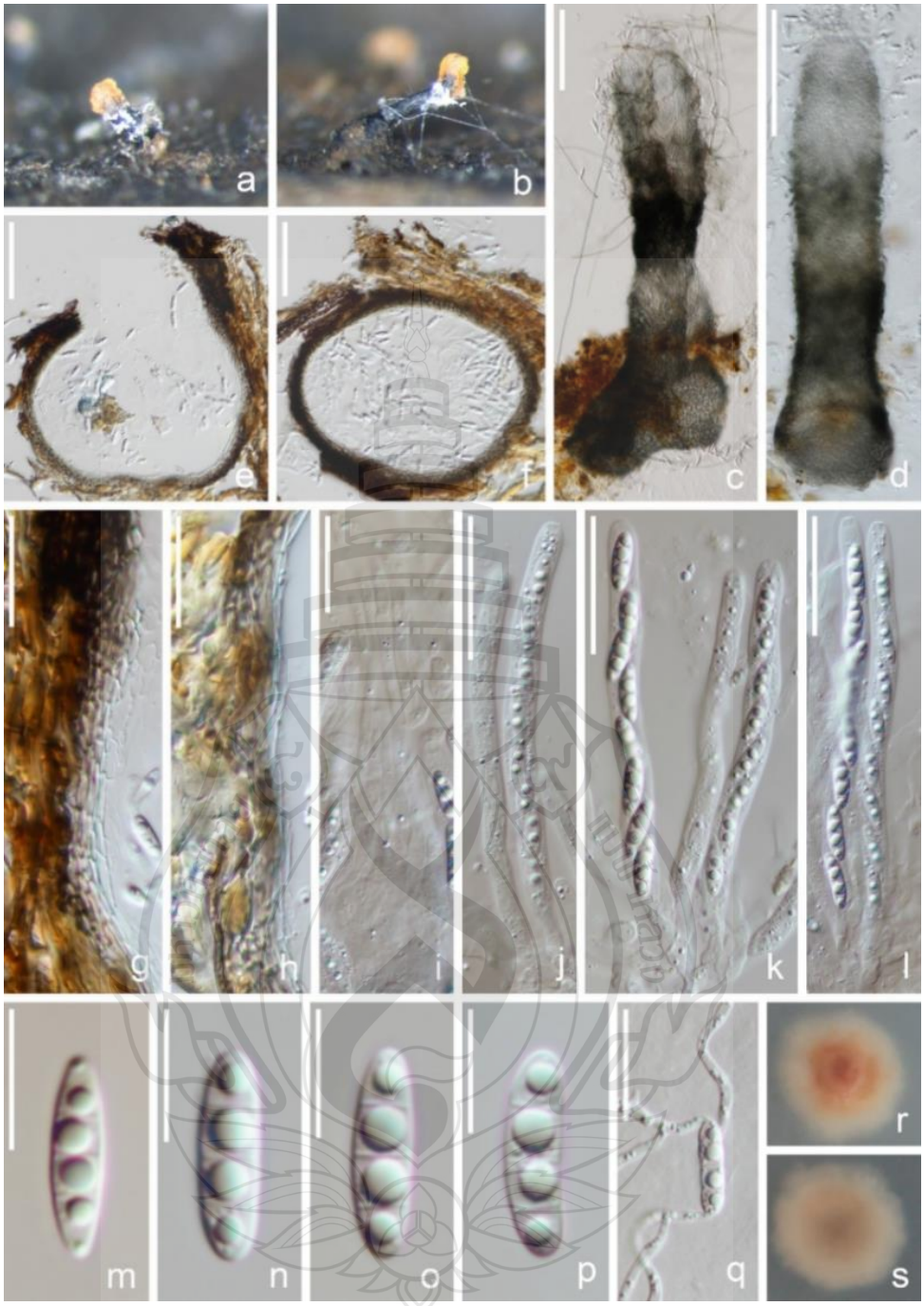
Holotype: HKAS 131502.

Saprobic on submerged decaying wood in freshwater lake. **Asexual morph**: Undetermined. **Sexual morph**: *Ascomata* 110–170 µm high, 145–175 µm wide, erumpent to immersed or semi-immersed, solitary or gregarious, perithecial, globose to subglobose, dark brown, ostiolate, bearing a long neck. *Neck* 190–400 µm tall, 55–70 µm wide, subcylindrical, hyaline to black, coriaceous. *Ostiole* central, periphysate. *Peridium* 9–17 µm wide, composed of several layers of thick, pale brown to brown, irregular cells of *textura angularis*. *Paraphyses* 2–4 µm wide, dense, hypha-like, septate, slightly constricted at the septate, unbranched, hyaline, smooth, thin-walled, embedded in a gelatinous matrix. *Asci* (81–)91–113(–121) × 6–8 µm ($\bar{x}$ = 102 × 7 µm, n = 20), 8-spored, unitunicate, cylindrical, straight or slightly curved, short pedicellate, slightly narrower and truncate at the apex, short pedicellate, with a small, distinct, refractive, barrel- or jar-shaped, apical ring, persistent. *Ascospores* 15–18(–20) × 4–5 µm ($\bar{x}$ = 16.5 × 4 µm, n = 40), overlapping uniseriate, fusiform to oval, straight or slightly curved, hyaline, 3-septate, guttulate, smooth-walled, thin-walled, without sheath.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after one month at room temperature (around 25 °C) in dark, circular, loose, smooth-edged, dense, pale brown to orange on the forward; circular, pale brown, dense on the reverse.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°41′49.2" N, 102°30'52.2″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L2175 (HKAS 131502, holotype), ex-holotype living culture, DLUCC 2175.

Notes: In the phylogenetic tree showed that our new isolate formed a separate clade within the *Obliquifusoideum* and form a sister clade to *Obliquifusoideum* sp. (KUNCC 23–16650) with 94% ML and 1.00 PP support (Figure 4.21). Morphologically, our new species fits well with the generic concept of *Obliquifusoideum*, and differs from the most similar species of *O. guttulatum* by its bigger ascospores (15–18 × 4–5 µm *vs.* 8–13 × 3–4 µm). Thus, we introduced this new isolate as *O. sinense* in the *Obliquifusoideum*.



Note a, b Appearance of ascomata on host substrate. c, d Neck. e, f Section of ascomata. g, h Peridium. i Paraphyses. j–l Asci. m–p Ascospore. q Germinated ascospore. l, m Colony on PDA. Scale bars: c, d = 100 µm. e, f = 50 µm. g–i, q = 20 µm. j–l = 30 µm. m–p = 10 µm.

Figure 4.22 *Obliquifusoideum sinense* (HKAS 131502, holotype)

Phaeoisaria Höhn.

Notes: *Phaeoisaria* was established by Höhnel (1909), with *P. bambusae* as the type species. *Phaeoisaria* species are primarily known from their asexual morphs, which are characterized by erect synnemata with parallelly adpressed conidiophores; polyblastic, sympodially conidiogenous cells with denticulate; ellipsoidal or obovoidal, aseptate or septate conidia (de Hoog & Papendorf, 1976; Reblova et al., 2016; Luo, Hyde, Bhat et al., 2018). The first sexual morph of *Phaeoisaria* was *P. filiformis*, which is characterized by immersed, globose-to-elongate ascomata with a long, cylindrical, black, ostiolar neck; filamentous, branched, septate paraphyses; unitunicate, cylindrical asci with a small refractive apical apparatus; and hyaline, filiform, multi-septate ascospores with tapering ends (Luo, Hyde, Bhat et al., 2018).

Phaeoisaria clematidis (Fuckel) S. Hughes, Can. J. Bot. 36: 794 (1958)

Fungal Names number: FN 302703; *Facesoffungi number*: FoF 03412; Figure 4.23

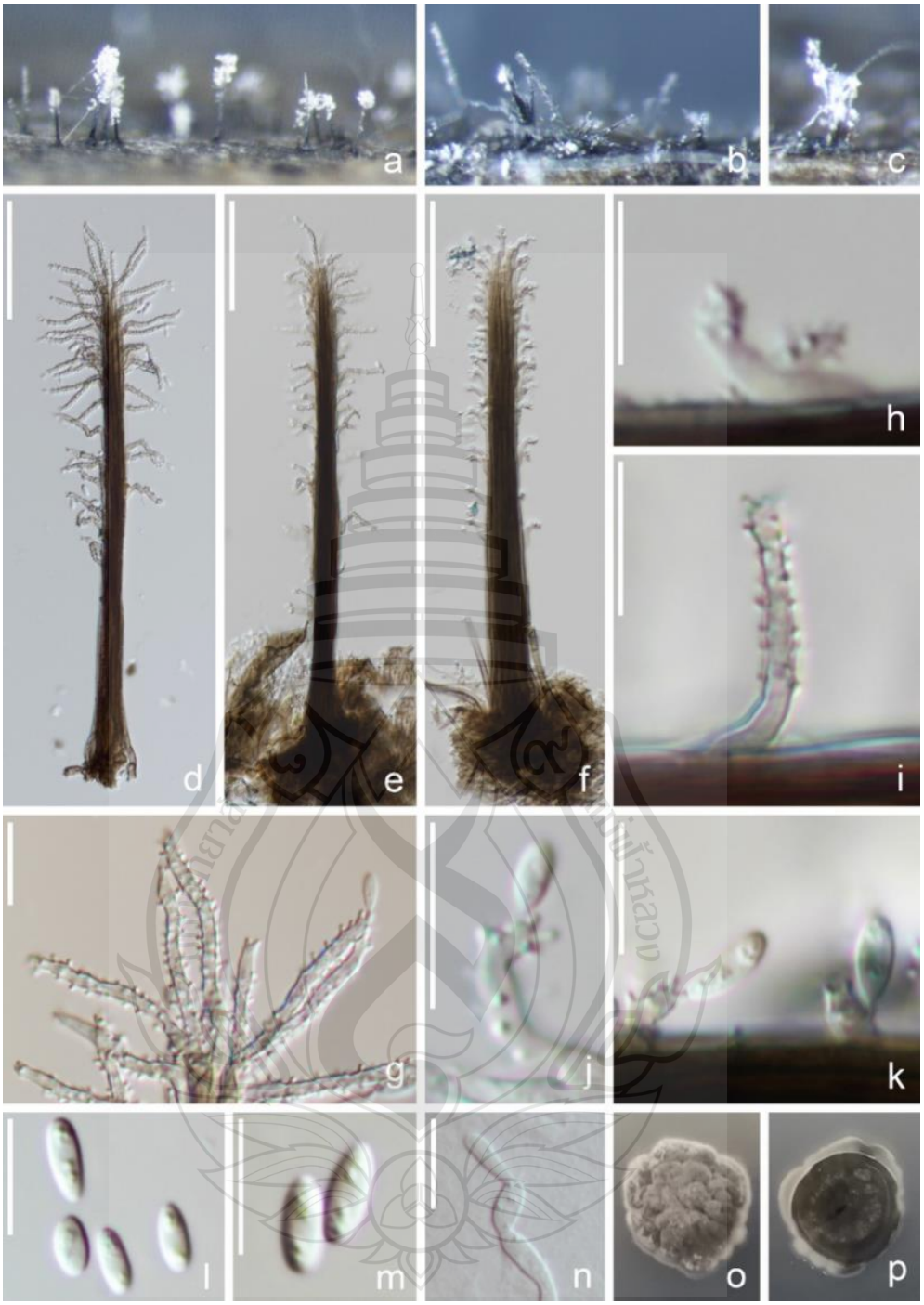
Saprobic on submerged decaying wood in freshwater lakes. **Sexual morph**: Undetermined. **Asexual morph**: *Synnemata* (167–)217–698(–918) × 11–20(–27) µm, on natural substrate superficial, effuse, hairy, scattered, brown to dark brown, composed of fasciculate, compact appressed conidiophores. *Conidiophores* macronematous, mononematous, fasciculate, erect, unbranched, cylindrical, septate, pale brown to brown, gradually to subhyaline towards the apex, smooth-walled. *Conidiogenous cells* polyblastic, integrated, terminal, subcylindrical to cylindrical, variable in length, 1.5–2 µm wide, subhyaline to pale brown, with conspicuous denticles, scattered or clustered in the apical region. *Conidia* (4–)5–6(–7) × 2.3–2.7 µm ($\bar{x}$ = 5.5 × 2.5 µm, n = 40), ellipsoidal to obovoid, straight, rounded at the apex, obtuse and tapering towards base, hyaline, aseptate, smooth-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after two months at room temperature (around 25 °C) in dark, circular, dense, smooth-edged, brown to dark brown on the forward; dark brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°39′18.69″ N, 102°35′49.15″ E, on submerged decaying wood, 22 February

2023, Y. Wang, L1798 (HKAS 132061), living culture, KUNCC 23–13520; *ibid.*, 23°40′56.4" N, 101°43'46.8″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L2007 (HKAS 132085), living culture, KUNCC 23–14267; *ibid.*, Kunming City, 24°53′50.48″ N, 102°45′44.51″ E, on submerged decaying wood, 19 February 2023, S. Luan, L1742 (HKAS 131442), living culture, KUNCC 23–14230; *ibid.*, on submerged decaying wood, 19 February 2023, S. Luan, L1994 (HKAS 131641), living culture, KUNCC 23–14246.

Notes: Phylogenetic analysis revealed that our four isolates grouped with two *Phaeoisaria clematidis* strains (Figure 4.21). In additionally, the morphology of our collections and *P. clematidis* are indistinguishable. Therefore, we identified our four new collections as new of *P. clematidis* based on identical morphology and phylogenetic analysis.



Note a–c Colony on natural substrate. d–e Conidiophores. g–k Conidiogenous cells with conidia. l, m Conidia. n Germinated conidium. o, p Culture on PDA medium. Scale bars: d–f = 50 μm, g–n = 10 μm.

Figure 4.23 *Phaeoisaria clematidis* (HKAS 132085)

Phaeoisaria sedimenticola X.L. Cheng & Wei Li ter, Mycotaxon 127: 20 (2014)

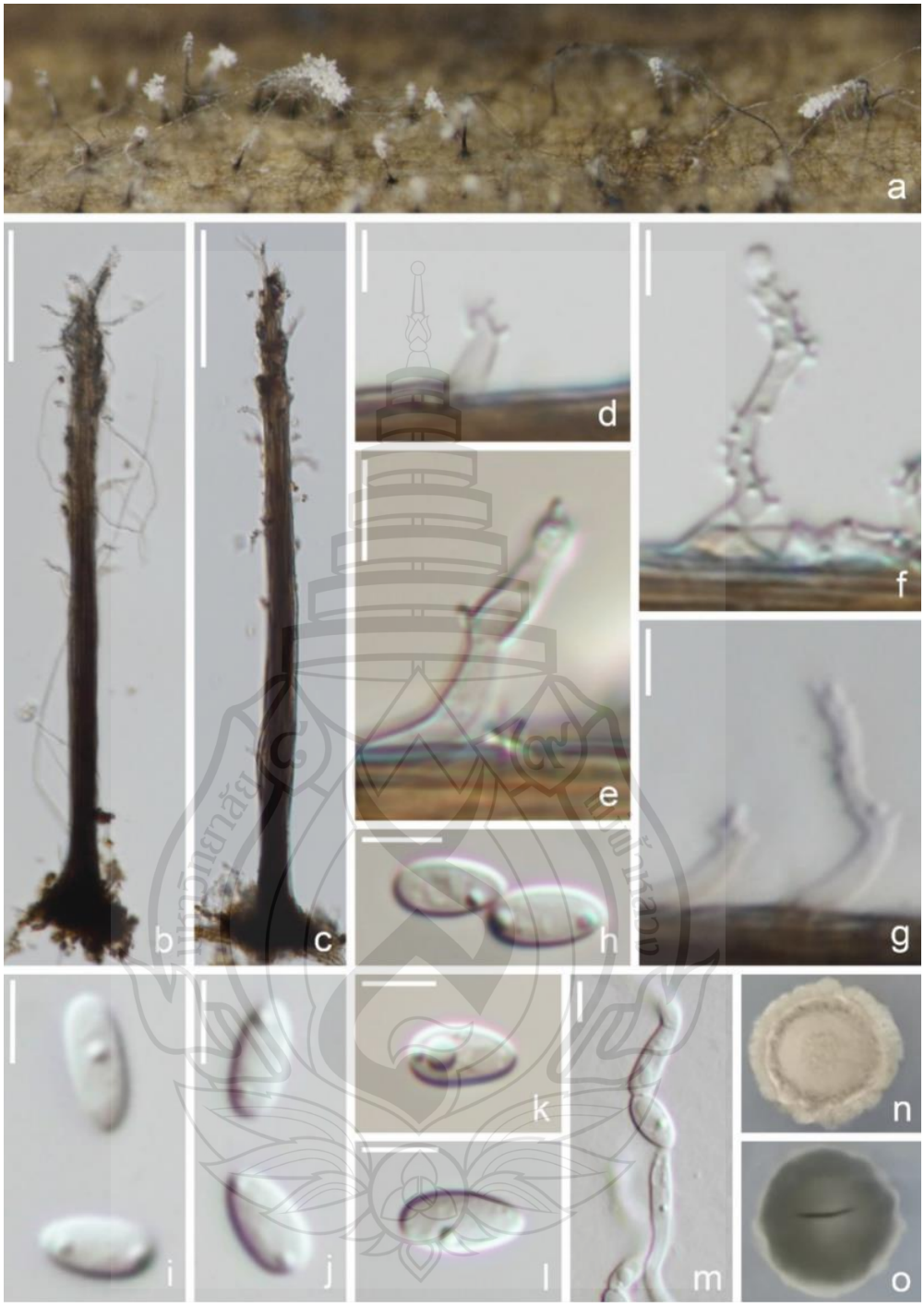
Fungal Names number: FN 563661; *Facesoffungi number*: FoF 03412; Figue 4.24

Saprobic on submerged decaying wood in freshwater lakes. **Sexual morph**: Undetermined. **Asexual morph**: *Synnemata* (135–)177–400(–530) × 8–12(–14) µm, on natural substrate superficial, effuse, hairy, scattered, brown to dark brown, composed of fasciculate, compact appressed conidiophores. *Conidiophores* macronematous, mononematous, fasciculate, erect, unbranched, cylindrical, septate, pale brown to dark brown, gradually to subhyaline towards the apex, smooth-walled. *Conidiogenous cells* polyblastic, integrated, terminal, subcylindrical to cylindrical, variable in length, hyaline, with conspicuous denticles, scattered or clustered in the apical region. *Conidia* 6–8(–9) × 3–4 µm ($\bar{x}$ = 7 × 3.5 µm, n = 40), ellipsoidal to obovoid, straight, rounded at the apex, obtuse and tapering towards base, hyaline, aseptate, guttulate, smooth-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after two months at room temperature (around 25 °C) in dark, circular, flocculent, dense, smooth-edged, pale brown to brown on the forward; dark brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°53′50.48″ N, 102°45′44.51″ E, on submerged decaying wood, 19 February 2023, S. Luan, L1739 (HKAS 131684), living culture, KUNCC 23–14229; *ibid.*, Honghe Prefecture, Yilonghu Lake, 23°41′49.2" N, 102°30'52.2″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L1893 (HKAS 131559).

Notes: Phylogenetically, our two isolates grouped with *Phaeoisaria sedimenticola* (Figure 4.21), which was described by Cheng et al. (2014) isolated from terrestrial habitat. Our collection matches with the type material of *P. sedimenticola* in the morphology except the conidia are longer. This may be due to different growing environments. We thus identified our collection as *P. sedimenticola*, representing a new habitat record from freshwater.



Note a Colony on natural substrate. b, c Conidiophores. d–g Conidiogenous cells. h–l Conidia. m Germinated conidium. n, o Culture on PDA medium. Scale bars: d, c = 50 μm, d–m = 5 μm.

Figure 4.24 *Phaeoisaria sedimenticola* (HKAS 131684)

Pleurotheciella Réblová

Notes: *Pleurotheciella* was established by Réblová et al. (2012) to accommodate two new species, *P. rivularia* and *P. centenaria*, both from freshwater habitats, with *P. rivularia* as the type species. Both sexual and asexual morphs of *Pleurotheciella* have been identified (Reblova et al., 2012; Wang et al., 2024). The sexual morph of *Pleurotheciella* is characterized by semi-immersed-to-superficial, glabrous ascomata; unitunicate, cylindric-clavate, eight-spored asci with an apical ring; and fusoid to fusiform, hyaline, septate ascospores. The asexual morph of *Pleurotheciella* characteristics by reduced or cylindrical, hyaline or brown, septate, unbranched conidiophores; terminal or integrated, subhyaline to hyaline, sympodially denticulate conidiogenous cells; and ellipsoidal to obovoidal or muriform, variedly shaped, unicellular or septate conidia (Reblova et al., 2012, 2016; Luo, Hyde, Bhat et al., 2018; Wang et al., 2024). *Pleurotheciella* represents a distinct group, with almost species reported from freshwater habitats (Luo et al., 2019; Wang et al., 2024).

Pleurotheciella nilotica Abdel-Aziz & Abdel-Wahab, Nova Hedwigia 110(1-2): 94 (2020)

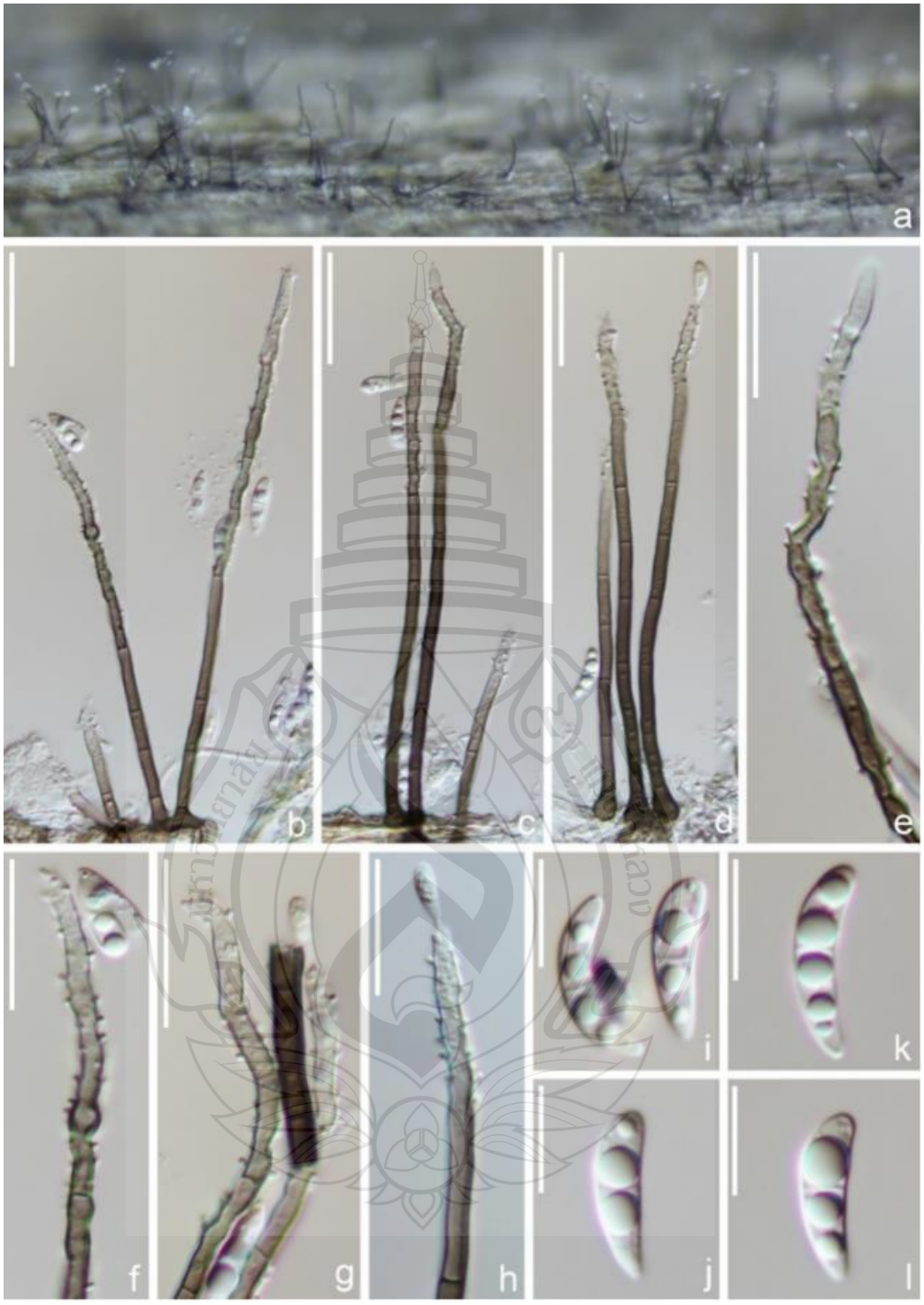
Fungal Names number: FN 833765; *Facesoffungi number*: FoF 03412; Figure 4.25

Saprobic on submerged decaying wood in freshwater lakes. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered or gregarious, with glistening conidial masses at apex. *Mycelium* mostly immersed, composed of septate, pale to pale brown, smooth, thin-walled hyphae. *Conidiophores* (68–)111–160(–172) × 3–4 µm ($\bar{x}$ = 135 × 3.3 µm, n = 25), macronematous, mononematous, solitary, erect, unbranched, cylindrical, straight or slightly curved, septate, subhyaline to dark brown, hyaline towards the apex, with an ampulliform to subglobose, enlarged cell, smooth-walled. *Conidiogenous cells* polyblastic, terminal, integrated, cylindrical to subcylindrical, pale brown to brown, smooth-walled, fertile part subhyaline to brown, (12–)24–59(–82) × 3–4 µm, conspicuous denticles. *Conidia* 13–16 × 3.5–4 µm ($\bar{x}$ = 15 × 4 µm, n = 40), clavate to lunate, rounded or acute at apex, acute at the base, 1-septate, hyaline, guttulate, smooth, thin-walled.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°56′33.79″ N, 102°38′31.93″ E, on submerged decaying wood, 18 February 2023,

Z.Q. Zhang, L2144 (HKAS 131513), living culture, KUNCC 23–14287; *ibid.*, Yangzonghai Lake, 24°54′43.70″ N, 103°1′3.64″ E, on submerged decaying wood, 20 February 2023, H.W. Shen, L2121 (HKAS 131501), living culture, KUNCC 23–14337; *ibid.*, 24°57′29.19″ N, 103°0′3.49″ E, on submerged decaying wood, 20 February 2023, Z.Q. Zhang, L2184 (HKAS 131506), living culture, KUNCC 23–14286; *ibid.*, 24°53′39.31″ N, 102°58′58.82″ E, on submerged decaying wood, 19 February 2023, H.W. Shen, L2209 (HKAS 131762); *ibid.*, on submerged decaying wood, 19 February 2023, S. Luan, L2230 (HKAS 131764).

Notes: Our collections match the morphology and dimensions of *Pleurotheciella nilotica*. Phylogenetically, our isolates grouped together with *P. nilotica* strains (Figure 4.21). In additionally, The LSU and ITS sequences of our specimens are identical to the type material of *P. nilotica*. Therefore, we recognize our collections as *P. nilotica*, extend its habitat to freshwater, and report a new geographical record in China.



Note a Colony on natural substrate. b–d Conidiophores. e–h Conidiogenous cells. i–l Conidia. Scale bars: b–d = 30 μm, e–h = 20 μm, i–l = 10 μm.

Figure 4.25 *Pleurotheciella nilotica* (HKAS 131764)

Pleurothecium Höhn.

Notes: *Pleurothecium* was introduced by Höhnel (1919) with *P. recurvatum* (Morgan) Höhn as type species. This genus is characterized by distinct brown conidiophores; polyblastic sympodially extended denticulate conidiogenous cells; and unicellular or septate, hyaline or pigmented conidia (Reblova et al., 2012; Luo, Hyde, Bhat et al., 2018). Species of *Pleurothecium* primarily occur as saprobes in terrestrial and freshwater habitats. Currently, eighteen species are accepted in the genus, seven of which are reported from freshwater habitats (Luo, Hyde, Bhat et al., 2018; Jayawardena et al., 2022; Liu et al., 2024).

Pleurothecium aquaticum Z.L. Luo, H.Y. Su & K.D. Hyde, Mycol. Progr. 17(5): 526 (2018)

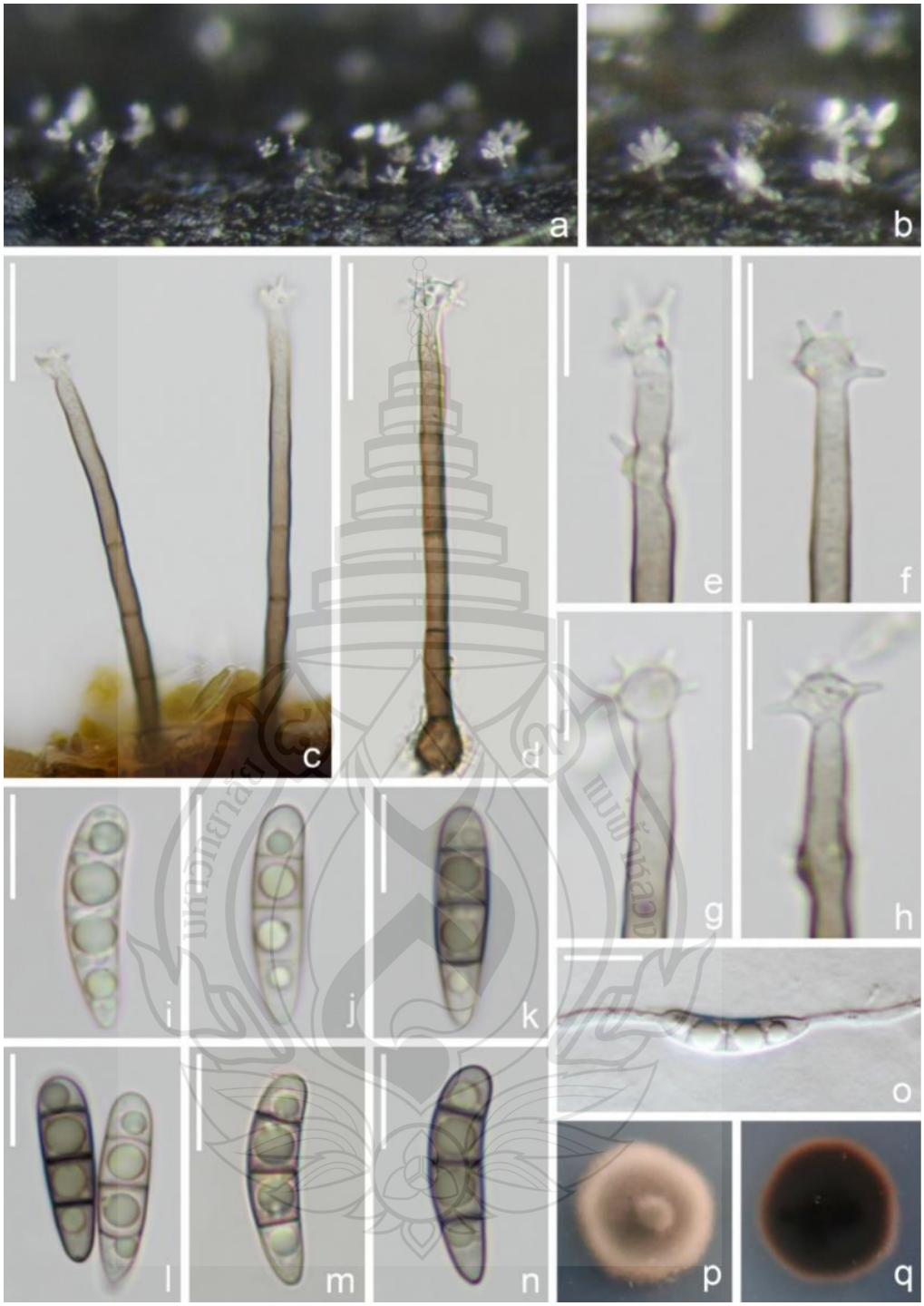
Fungal Names number: FN 821844; *Facesoffungi number*: FoF 03420; Figure 4.26

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, hyaline to pale brown, scattered or gregarious, with glistening conidial masses at apex. *Mycelium* mostly immersed, composed of septate, pale brown, smooth, thin-walled hyphae. Conidiophores (73–)77–105(–125) × 3–4 µm ($\bar{x}$ = 91 × 4 µm, n = 20), macronematous, mononematous, solitary, erect, unbranched, cylindrical, straight or slightly curved, septate, brown to dark brown, hyaline towards the apex, enlarged at the base, smooth-walled. *Conidiogenous cells* (24–)31–42 × 3–4 µm ($\bar{x}$ = 36× 3.5 µm, n = 20), polyblastic, terminal, integrated, cylindrical to subcylindrical, subhyaline to pale brown, smooth-walled, apical fertile part, globose to subglobose, denticulate; denticles cylindrical, flat-topped, hyaline, 2–3 µm long, smooth-walled. *Conidia* 22–24 × 5–6 µm ($\bar{x}$ = 23 × 6 µm, n = 20), fusiform, slightly curved, rounded at apex, truncate at the base, 3-septate, hyaline when young, pale brown, olive-green tinge when mature, guttulate, smooth, thin-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium growing slowly reaching 1-1.5 cm diam. after two months at room temperature (around 25 °C) in dark, circular, flocculent, dense, smooth-edged, pale brown to brown on the forward; brown to dark reddish brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu’er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L2127 (HKAS 131515), living culture, KUNCC 23–14332; *ibid.*, on submerged decaying wood, 24 February 2023, H.W. Shen, L2128 (HKAS 131711).

Notes: Following BLASTn searches of NCBI GenBank, the closest matches of the LSU and ITS sequences of our two new isolates are *Pleurothecium aquaticum* (strain MFLUCC 17–1331; LSU, 100% shared identity; ITS, 98. 9% shared identity). Our new collection fits well with the description of *P. aquaticum* in morphology. Phylogenetically, our isolates grouped together with *P. aquaticum* (MFLUCC 17–1331) with 99% ML/1.00 PP support (Figure 4.21). Thus, we identified this isolate as a new geographical record of *P. aquaticum* in China.



Note a, b Colony on natural substrate. c, d Conidiophores. e–h Conidiogenous cells. i–n Conidia. o Germinated conidium. p, q Culture on PDA medium. Scale bars: c, d = 20 μm, e–o = 10 μm.

Figure 4.26 *Pleurothecium aquaticum* (HKAS 131515)

Pleurothecium recurvatum (Morgan) Höhn., Centbl. Bakt. ParasitKde, Abt. II 60: 26 (1923)

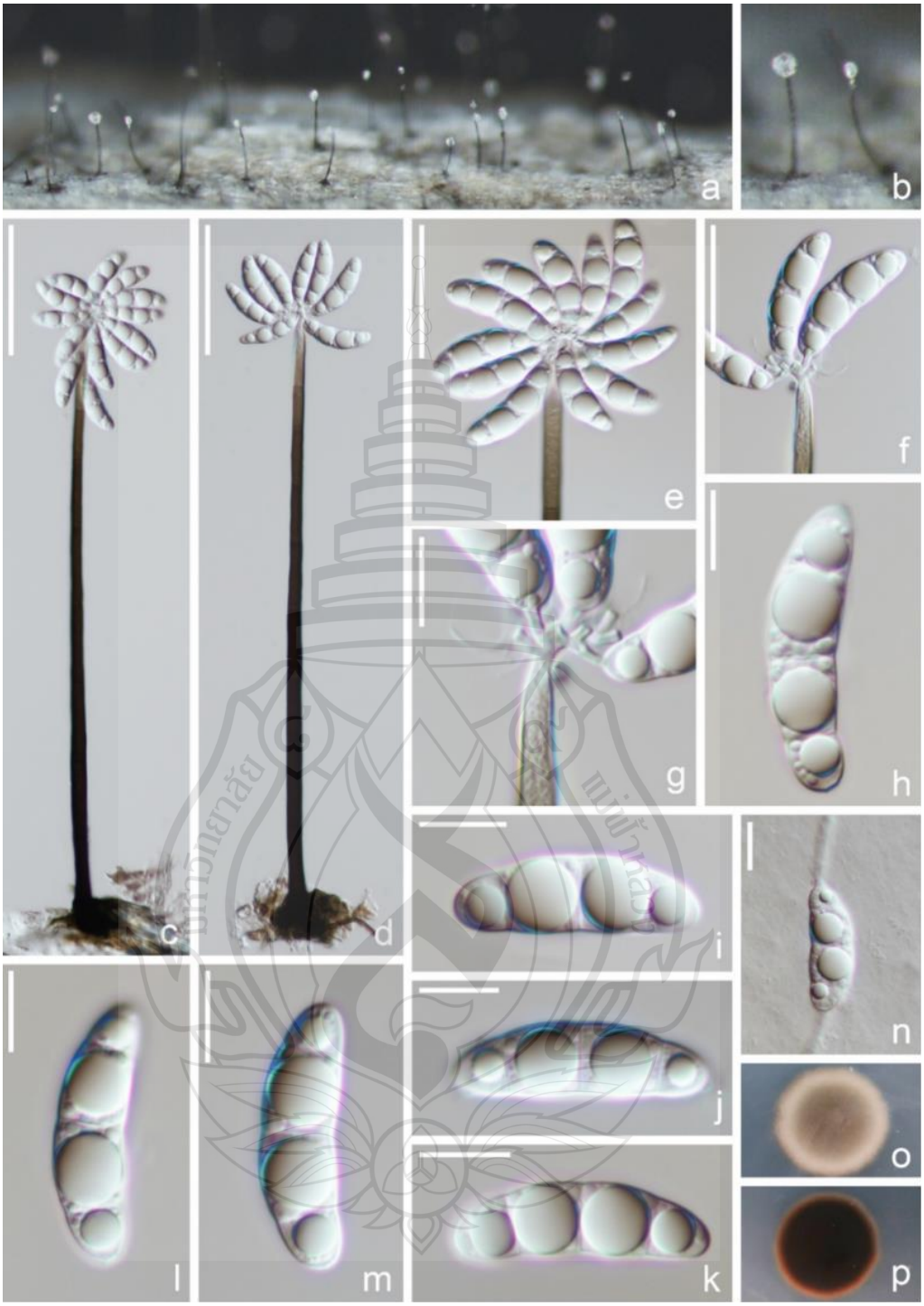
Fungal Names number: FN 276190; *Facesoffungi number*: FoF 05453; Figure 4.27

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, brown to dark brown, scattered or gregarious, with glistening conidial masses at apex. *Mycelium* mostly immersed, composed of septate, pale brown, smooth, thin-walled hyphae. *Conidiophores* (222–)254–295(–307) × (5–)6–7 µm ($\bar{x}$ = 274 × 7 µm, n = 25), macronematous, mononematous, solitary, erect, unbranched, cylindrical, straight or slightly curved, septate, brown to dark brown, hyaline towards the apex, enlarged at the base, smooth-walled. *Conidiogenous cells* 33–48 × 4–5 µm ($\bar{x}$ = 40× 5 µm, n = 15), polyblastic, terminal, integrated, cylindrical to subcylindrical-lageniform, subhyaline to pale brown, smooth-walled, fertile part terminal, hyaline, sympodial, denticulate, helicoid; denticles cylindrical, with a truncated tip, 3–4 × 1–2 µm, smooth-walled. *Conidia* (26–)28–33(–36) × (6–)8–9(–10) µm ($\bar{x}$ = 31 × 9 µm, n = 40), fusiform, slightly curved, rounded at apex, truncate at the base, 3-septate, hyaline, guttulate, smooth, thin-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after two months at room temperature (around 25 °C) in dark, circular, flocculent, dense, smooth-edged, pale brown to brown on the forward; brown to dark reddish brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°40′56.4" N, 101°43'46.8″ E, on submerged decaying wood, 23 February 2023, S. Luan, L2018 (HKAS 132082), living culture, KUNCC 23–14278.

Notes: Our collection matches the morphology and dimension of *Pleurothecium recurvatum* (Figure 4.21). The LSU and ITS sequence data of our isolate and the ex-type strain of *P. recurvatum* showed 99.88% (839/840 bp, one gap) and 99.63% (540/542 bp, one gap) sequence similarity, respectively. Thus, we identify our isolate as *P. recurvatum* based on their morphology and molecular evidence.



Note a, b Colony on natural substrate. c, d Conidiophores. e–g Conidiogenous cells. h–m Conidia. n Germinated conidium. o, p Culture on PDA medium. Scale bars: c, d = 60 μm, e = 40 μm, f = 30 μm, g–n = 10 μm.

Figure 4.27 *Pleurothecium recurvatum* (HKAS 132082)

Sterigmatobotrys Oudem.

Notes: *Sterigmatobotrys* was introduced by Oudemans (1886) for two species *S. elata* and *S. papyrogena*. *Sterigmatobotrys* is a conspicuous, cosmopolitan dematiaceous hyphomycete genus, and is characterized by macronematous, irregularly biverticillate to terverticillate conidiophores with stout, septate, darkly pigmented stipes and a penicillus consisting of appressed branches and/or whorls of metulae, terminating in polyblastic conidiogenous cells with minute, sympodially arranged denticles, and hyaline, septate conidia that turn brown at maturity and are aggregated in slime (Reblova & Seifert, 2011). Species of *Sterigmatobotrys* are distributed worldwide, occurring primarily as saprobes in terrestrial and freshwater habitats (Luo et al., 2019).

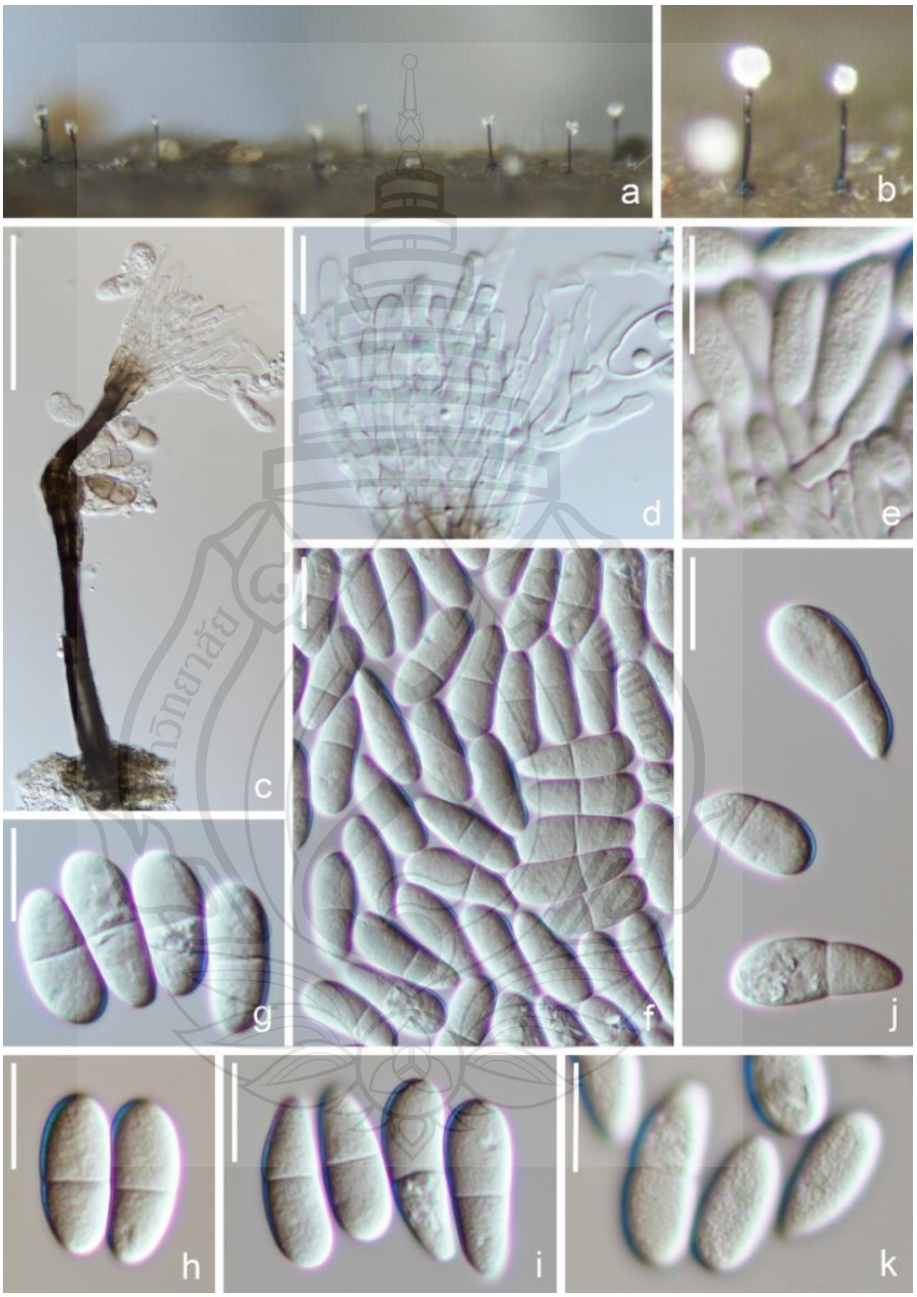
Sterigmatobotrys uniseptatus H.S. Chang [as 'uniseptata'], Mycol. Res. 95(9): 1142 (1991)

Fungal Names number: FN 626943; *Facesoffungi number*: FoF 03420; Figure 4.28

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, brown to dark brown, scattered or gregarious, with white glistening conidial masses at apex. *Mycelium* mostly immersed, composed of septate, pale brown, smooth, thin-walled hyphae. *Conidiophores* (101–)113–163(–183) × (5–)6–7 µm ($\bar{x}$ = 138 × 6 µm, n = 15), macronematous, mononematous, solitary, erect, cylindrical, straight or slightly curved, with a stout stipe and quaterverticillate head. *Stipe* mostly straight, brown to dark brown, septate, smooth-walled. *Penicillate head* terverticillate to quaterverticillate, subhyaline to pale brown. *Metula* subhyaline, with 1–3 hyaline conidiogenous cells. *Conidiogenous cells* polyblastic, terminal, integrated, sympodial, smooth, cylindrical, hyaline. *Conidia* ellipsoidal to clavate, (14–)16–18(–20) µm long, 6.7–7.5 µm wide at upper cell, 6.7–7.5 µm wide at basal cell, broad and rounded at the apex, gradually narrowing towards the base, slightly curved, 1-septate, constricted at the septum, hyaline, smooth or verrucose.

Material examined: CHINA, Yunnan Province, Lijiang City, Luguhu Lake, 27°45′01.83" N, 100°51′01.90" E, on submerged decaying wood, 3 March 2021, Z.Q. Zhang, L635 (HKAS 131469).

Notes: Morphological characters and molecular data (LSU and ITS sequences) both support the identification of this collection as *Sterigmatobotrys uniseptatus* (Figure 4.21). We therefore report a new habitat record of this species from freshwater.



Note a, b Colony on natural substrate. c Conidiophore. d, e Conidiogenous cells. f–k Conidia. Scale bars: c = 50 μm, d–k = 10 μm.

Figure 4.28 *Sterigmatobotrys uniseptatus* (HKAS 131469)

Pseudodactylariales Crous

Pseudodactylariaceae Crous

Notes: *Pseudodactylariaceae* was introduced by Crous et al. (2017) to accommodate newly genus *Pseudodactylaria*. Species of *Pseudodactylariaceae* are mainly reported as saprobes, and almost species are from terrestrial and freshwater habitats (Luo et al., 2019; Yang et al., 2023).

Pseudodactylaria Crous

Notes: *Pseudodactylaria* was established by Crous et al. (2017) for two dactylaria-like species, *P. hyalotunicata* (*Dactylaria hyalotunicata*) and *P. xanthorrhoeae* (type species). *Pseudodactylaria* is known as asexual morphs, which is characterized by single, unbranched, septate conidiophores, polyblastic, denticulate conidiogenous cells and solitary, fusoid-ellipsoid, hyaline conidia (Crous et al., 2017; Yang et al., 2023). Currently, ten species are accepted in the genus, which are reported as saprobes in terrestrial and freshwater habitats, of which, except for *P. brevis* and *P. xanthorrhoeae*, all other species are from freshwater habitats (Luo et al., 2019; Yang et al., 2023).

Pseudodactylaria guttulata H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572084; Figure 4.29

Etymology: "guttulata" refers to the place where this species was collected, Honghe City.

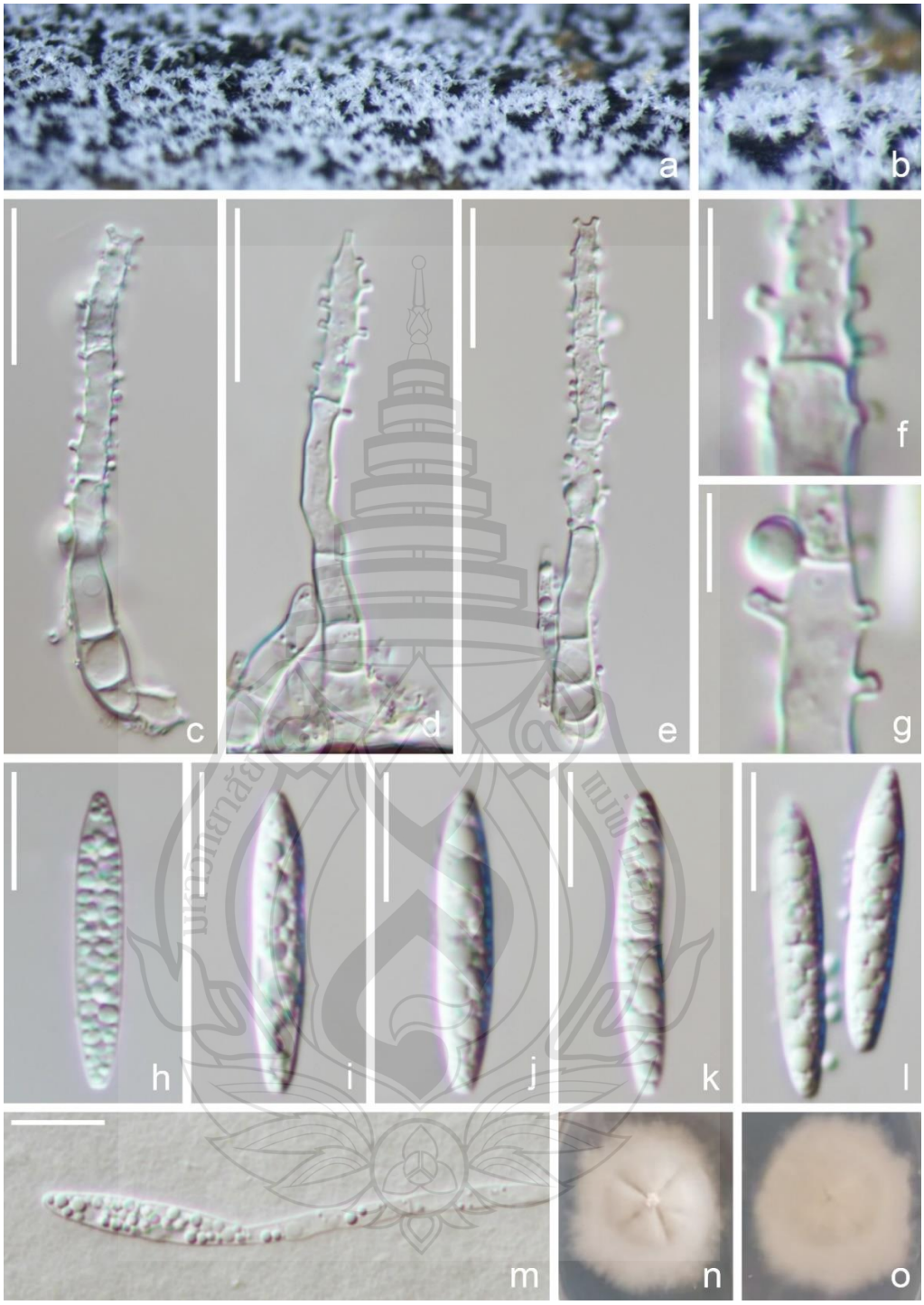
Holotype: HKAS 132058.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, scattered or aggregated, white, glistening. *Mycelium* mostly immersed, composed of septate, white to hyaline, smooth-walled hyphae. *Conidiophores* (39–)55–79(–93) × 5–6 µm ($\bar{x}$ = 67 × 6 µm, n = 30), macronematous, mononematous, solitary, erect, straight or slightly flexuous, unbranched, cylindrical, slightly enlarged at the base, tapering at the top, septate, hyaline, smooth-walled. *Conidiogenous cells* (15–)27–46(–53) × 4–5 µm ($\bar{x}$ = 37 × 4 µm, n = 35), polyblastic, integrated, sympodial, terminal, cylindrical, denticulate, denticles numerous, cylindrical, flat-topped, hyaline, smooth-walled. *Conidia* 23–25 × 4–5 µm ($\bar{x}$ = 24 × 4 µm, n = 40), acropleurogenous, solitary, fusiform, hyaline, guttulate, subtruncate at the base, subobtuse at apex, 1-transverse septum when mature, slightly constricted at the septum, smooth, thin-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from base of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after one month at room temperature (around 25 °C) in dark, circular, loose, smooth-edged, dense, pale on the forward, middle mastoid; pale, dense, irregular edged from reverse.

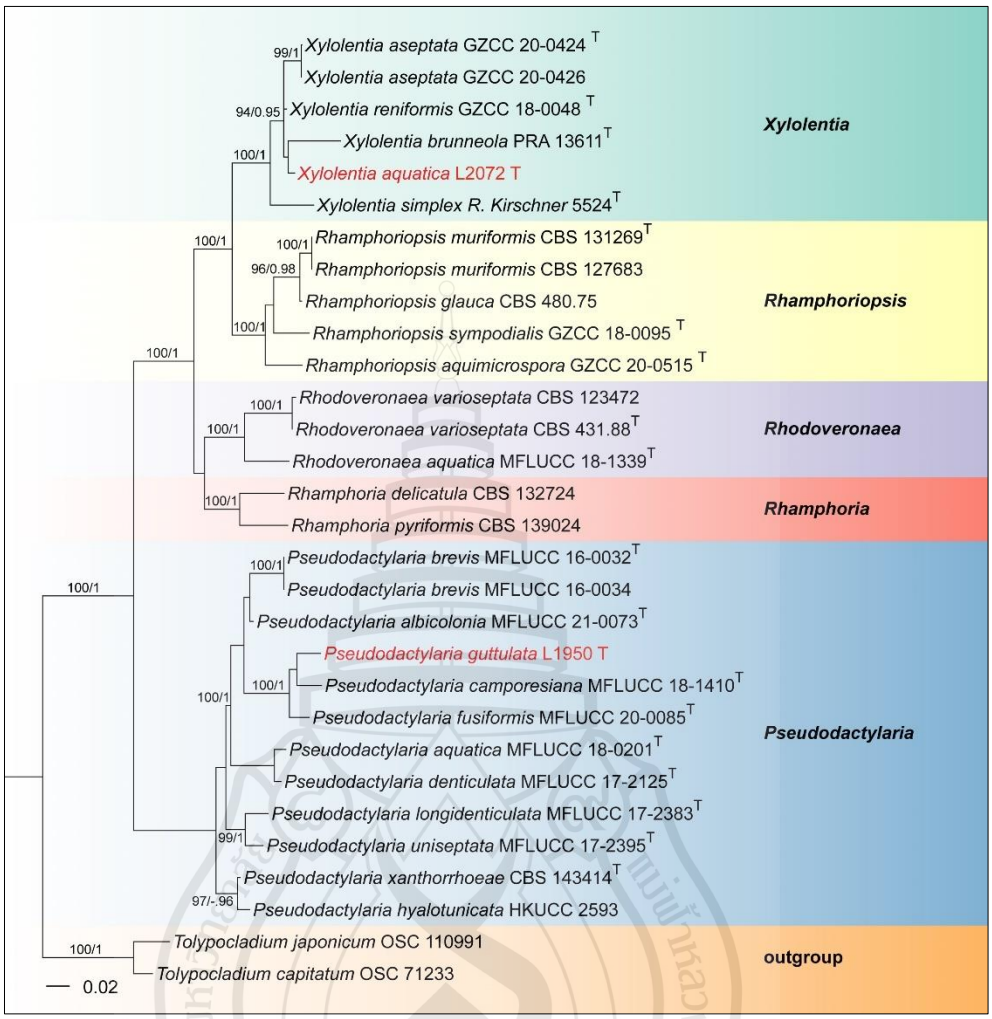
Material examined: CHINA, Yunnan Province, Honghe City, Yilonghu Lake, 23°40′56.4" N, 101°43'46.8″ E, on submerged decaying wood, 23 February 2023, S. Luan, L1959 (KUN-HKAS 132058, holotype), ex-holotype living culture, KUNCC 23–14329.

Notes: *Pseudodactylaria guttulata* resembles *P. albicolonia*; however, *P. guttulata* is characterized by its subobtuse apex and larger conidia (23–25 × 4–5 µm *vs.* 14–19.5 × 2.5–4 µm), whereas *P. albicolonia* has conidia that are rarely slightly constricted at the septum. In our phylogenetic analysis, *P. guttulata* is sister to *P. camporesiana* (MFLUCC 18–1410) and *P. fusiformis* (MFLUCC 20–0085) with low support (Figure 4.30). *Pseudodactylaria guttulata* is distinct from *P. camporesiana* by its hyaline and larger conidiophores [(39–)55–79(–93) × 5–6 µm *vs.* 35–45 × 3.5–5 µm], larger conidiogenous cells [(15–)27–46(–53) × 4–5 µm *vs.* 20–30 × 4–4.6 µm], and smaller conidia (23–25 × 4–5 µm *vs.* 18–22 × 3.5–4.5 µm), whereas *P. camporesiana* has brown conidiophores at the base. *Pseudodactylaria guttulata* is distinct from *P. fusiformis* by its larger conidiophores [(39–)55–79(–93) × 5–6 µm *vs.* 30–50 × 3.5–4.5 µm] and larger conidiogenous cells [(15–)27–46(–53) × 4–5 µm *vs.* 14–28 × 3.5–4.5 µm]. Excluding gaps, the nucleotide comparison between *P. guttulata* and *P. camporesiana* shows a difference of 6.5% (32/493 bp) across ITS, 1% (7/806 bp) across LSU, and no difference across SSU. Additionally, there are differences of 4% (19/472 bp) across ITS, 1% (7/807 bp) across LSU, 7.3% (69/950 bp) across *rpb*2, 5.4% (48/895 bp) across *tef*1-α, and no difference across SSU between *P. guttulata* and *P. fusiformis*. Based on these findings, we introduce *P. guttulata* as a novel species, following guidelines outlined by Jeewon and Hyde (2016) and Chethana et al. (2021).



Note a, b Colony on natural substrate. c–e Conidiophores. f, g Conidiogenous cells. h–l Conidia. m Germinated conidium. n, o Culture on PDA medium. Scale bars: c–e = 20 μm, f, g = 5 μm, h–m = 10 μm.

Figure 4.29 *Pseudodactylaria guttulata* (HKAS 132058, holotype)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS SSU, *rpb*2 and *tef*1-α sequence dataset representing *Pseudodactylariales* and *Rhamphoriales*. Thirty strains are included in the combined analyses which comprise 4107 characters including gaps (797 characters for LSU, 492 characters for ITS, 930 characters for SSU, 990 characters for *rpb*2, and 898 characters for *tef*1-α). *Tolypocladium capitatum* (OSC 71233) and *T. japonicum* (OSC 110991) were selected as the outgroup taxa. Bootstrap support values with a ML greater than 65%, and Bayesian posterior probabilities (PP) greater than 0.95 are given above the nodes, shown as "ML/PP". New species are indicated in red and type strains are indicated by a "T" after the strain number.

Figure 4.30 Phylogenetic tree of *Pseudodactylariales* and *Rhamphoriales*

Rhamphoriales K.D. Hyde & Hongsanan

Rhamphoriaceae Réblová

Notes: *Rhamphoriaceae* was established by Réblová and Štěpánek (2018) to accommodate four holomorphic genera, *Rhamphoria* (type), *Rhamphoriopsis*, *Rhodoveronaea*, and *Xylolentia*, and a dematiaceous hyphomycete *Linkosia multiseptum* based on strong phylogenetic support using a combined ITS, LSU, SSU, and *rpb*2 dataset (Reblova & Stepanek, 2018). Subsequently, *Rhamphoriaceae* was raised to a systematic ordinal rank as *Rhamphoriales* by Hyde et al. (2021) based on the phylogeny and divergence time estimation of *Rhamphoriaceae*. Members of this family are characterized by perithecial ascomata, a cylindrical or rostrate neck, leathery to fragile, two-layered peridium, cylindrical paraphyses, unitunicate asci with a distinct, non-amyloid apical annulus, and hyaline or brown ascospores, with dictyoseptate or transversely septate (Müller & Samuels, 1982; Reblova & Stepanek, 2018; Yuan et al., 2020; Yang et al., 2023). The Asexual morphs of *Rhamphoriaceae* are characterized by mononematous or loosely fasciculate, macronematous conidiophores, or conidiophores reduced to monoblastic or polyblastic conidiogenous cells, and conidia aseptate or septate, hyaline or brown (Reblova & Stepanek, 2018; Yuan et al., 2020; Yang et al., 2023). *Rhamphoriaceae* species as saprobes grow on decaying wood from terrestrial, freshwater habitats or on a fungal colony, mainly reported from Europe, and some from Argentina, Australia and China (Arzanlou et al., 2007; Reblova & Stepanek, 2018; Luo et al., 2019; Yuan et al., 2020; Yang et al., 2023).

Xylolentia Réblová

Notes: *Xylolentia* was introduced by Réblová and Štěpánek (2018) to accommodate a holomorphic species *X. brunneola* as type species, which collected from decaying wood of *Fagus sylvatica* in the Czech Republic. *Xylolentia* is distinct from other genera in *Rhamphoriaceae* by uni-septate brown ascospores (Reblova & Stepanek, 2018). In recent years, five additional species have been introduced into this genus, *viz. X. aseptata* on decaying wood submerged in a freshwater stream from China (Yang et al., 2023), *X. matsushimae* on dead material of plant from China and Japan, *X. palmicola* on dead leaves of palm from China (Wu & Diao, 2022), *X. reniformis* on decaying wood from China (Yuan et al., 2020), and *X. simplex* on dead petioles of the fern *Angiopteris lygodiifolia* from China (Kirschner & Hsieh, 2023). Therefore, species

of *Xylolentia*, are mainly reported as saprobes in China, some in Czech Republic and Japan.

Xylolentia aquatica H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572085; Figure 4.31

Etymology: "aquatica" refers to the freshwater lake in which this species was collected.

Holotype: HKAS 132053.

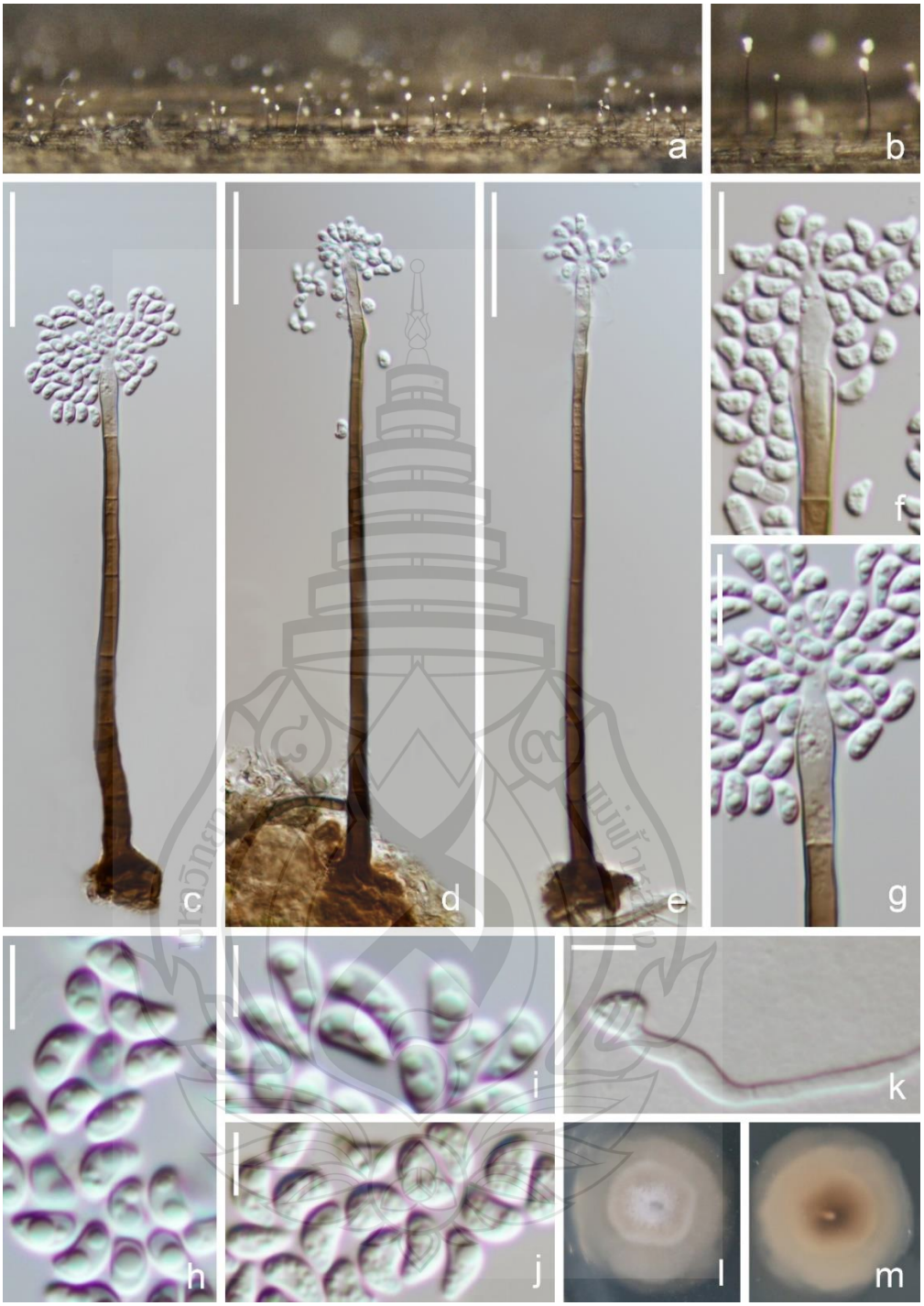
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered, with glistening conidial masses at apex. *Mycelium* mostly immersed, composed of septate, pale to pale brown, smooth, thin-walled hyphae. *Conidiophores* (116–)133–176(–194) × 4–6 µm ($\bar{x}$ = 154 × 5 µm, n = 20), macronematous, mononematous, solitary, erect, mostly straight, unbranched, cylindrical, enlarged at the base, tapering at the top, septate, brown to dark brown, gradually to subhyaline towards the apex. *Conidiogenous cells* 23–33(–36) × 3–4 µm ($\bar{x}$ = 28 × 4 µm, n = 20), polyblastic, integrated, terminal, determinate, subcylindrical, cylindrical-lageniform, pale brown to subhyaline, smooth-walled. *Conidia* 4–5 × 2–3 µm ($\bar{x}$ = 5 × 3 µm, n = 50), acrogenous, reniform, lunate, aseptate, hyaline, guttulate, smooth, thin-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from end cell of conidium within 12 h. Colonies on PDA medium reaching 2-3 cm diam. after one month at room temperature (around 25 °C) in dark, circular, loose, flocculent, smooth-edged, dense, white to pale brown, with white lines in the form of concentric circles on the forward, middle mastoid; white to pale brown, with white lines in the form of concentric circles, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32'15.6" N, 100°1′30.00″ E, on submerged decaying wood, 24 February 2023, S. Luan, L2072 (KUN-HKAS 132053, holotype), ex-holotype living culture, KUNCC 23–13819.

Notes: In our phylogenetic analysis, *Xylolentia aquatica* is sister to *X. brunneola* (PRA 13611) with low support (Figure 4.30). *Xylolentia aquatica* is distinct from *X. brunneola* by its asexual morph, whereas *X. brunneola* has both sexual and asexual

morphs. *Xylolentia aquatica* is further distinguished by its larger conidiophores [(116–)133–176(–194) × 4–6 µm *vs.* 5–120 × 4.5–5.5 µm], larger conidiogenous cells [(23–)33(–36) × 3–4 µm *vs.* 10–30 × 4–4.5 µm], and acrogenous, reniform, lunate, hyaline, guttulate conidia. In contrast, *Xylolentia brunneola* has ellipsoidal to subglobose to obovoid, straight, rounded at the apex, obtuse, and slightly tapering towards the base conidia. Excluding gaps, the nucleotide comparison between *Xylolentia aquatica* and *X. brunneola* shows differences of 1.2% (6/520 bp) across ITS, 0.3% (1171/1175 bp) across LSU, 5.4% (53/988 bp) across *rpb*2, and no difference across SSU. Based on these findings, we introduce *Xylolentia aquatica* as a novel species, following the guidelines outlined by Jeewon and Hyde (2016) and Chethana et al. (2021).



Note a, b Colony on natural substrate. c–e Conidiophores with conidia. f, g Conidiogenous cells with conidia. h–j Conidia. k Germinated conidium. l, m Culture on PDA medium. Scale bars: c–e = 30 μm, f, g = 10 μm, h–k = 5 μm.

Figure 4.31 *Xylolentia aquatica* (KUN-HKAS 132053, holotype)

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

Savoryellaceae Jaklitsch & Réblová

Notes: *Savoryellaceae* was established by Jaklitsch and Réblová (2016), is the only family in the monotypic order *Savoryellales*. Currently, there are six genera in *Savoryellaceae*, *viz. Ascotaiwania*, *Bactrodesmium*, *Canalisporium*, *Dematiosporium*, *Neoascotaiwania*, and *Savoryella* (type) (Réblová, Hernandez-Restrepo et al., 2020; Yang, Bao et al., 2022). Members of this family are characterized by immersed, semi-immersed or superficial, globose to pyriform, non-stromatic ascomata, paraphyses, unitunicate asci, 2–8-spored, clavate to cylindrical, with an inamyloid apical ring, and fusiform to ellipsoid ascospores, with or without a gelatinous sheath; while asexual morph is a dematiaceous hyphomycetous with globose to subglobose or obovate to oval conidia (Dayarathne et al., 2019; Hyde, Norphanphoun et al., 2020). *Savoryellaceae* mostly reported as saprobic fungi on bamboos, palms, *Machilus* sp., *Pandanus* sp., and *Pinus* sp., in terrestrial, freshwater, marine, brackish water, and water-cooling towers (Jones & Eaton, 1969; Manimohan et al., 2011; Tibpromma et al., 2018; Dayarathne et al., 2019; Zhang et al., 2019; Réblová, Hernandez-Restrepo et al., 2020; Yu et al., 2023).

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

Notes: *Dematiosporium* was established as a monotypic genus by Luo et al. (2019), typified by *D. aquaticum*, collected from decaying submerged wood. Recently, Yu et al. (2023)introduced another species, *D. bambusicola*, on dead bamboo in freshwater habitat. This genus is characterized by unbranched, aseptate, cylindrical conidiophores and globose to subglobose, dictyospores conidia with a pore in each cell (Luo et al., 2019; Yu et al., 2023). Species of *Dematiosporium* are often found as saprobes from aquatic environments, currently only reported in China and France (Luo et al., 2019; Réblová, Hernandez-Restrepo et al., 2020; Yu et al., 2023).

Dematiosporium hydei H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572086; Figure 4.32

Etymology: “hydei” refers to the renowned mycologist Professor K.D. Hyde, named in recognition of his contributions to mycology on the occasion of his 70th birthday.

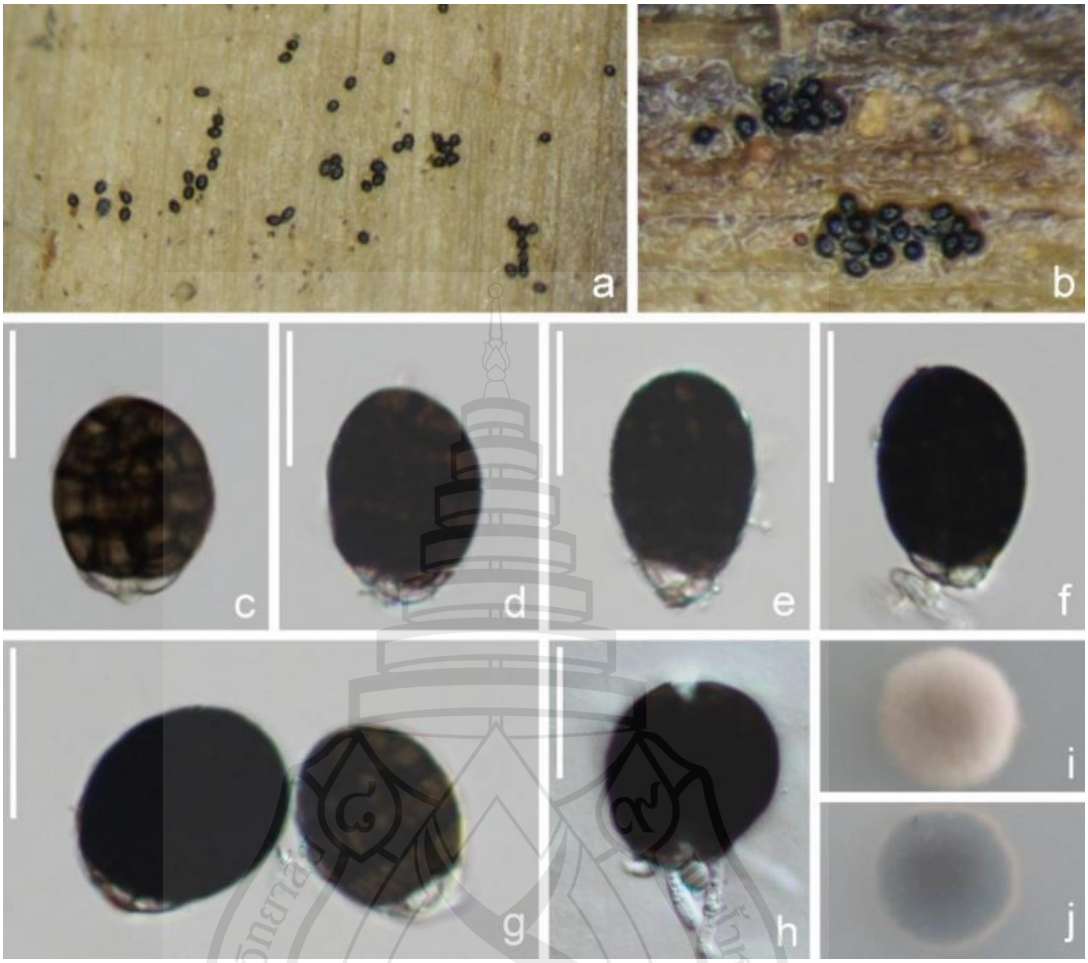
Holotype: HKAS 131511.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, brown to dark brown, punctiform, scattered or gregarious, glistening. *Mycelium* immersed or superficial, composed of septate, pale to pale brown, smooth, thin-walled hyphae. *Conidiophores* absent or present, micronematous, mononematous, sub-hyaline. *Conidiogenous cells* monoblastic, integrated, terminal, hyaline, smooth-walled. *Conidia* (24–)27–32 × 20–24 µm ($\bar{x}$ = 29 × 22 µm, n = 25), acrogenous, subglobose, ellipsoidal to pyriform, muriform, brown to dark brown, dictyospores, slightly constricted at the septa, guttulate, with subhyaline, distinct, smooth-walled, thin-walled, basal cells, 2–5 µm thick.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from basal cells of conidium within 12 h. Colonies on PDA medium growing slowly, reaching 1-1.5 cm diam. after two months at room temperature (around 25 °C) in dark, circular, flocculent, dense, smooth-edged, pale brown on the forward; dark dark brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°40′28.95″ N, 102°36′30.00″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L2199 (HKAS 131511, holotype), ex-holotype living culture, KUNCC 23–14306

Notes: Phylogenetic analysis showed that *Dematiosporium hydei* clustered with another new freshwater species of this study, *D. muriforme*, as a sister branch with low supported (Figure 4.33). Comparison of ITS, SSU, and *rpb*2 sequence between *D. hydei* (KUNCC 23–14306, ex-holotype) and *D. muriforme* (KUNCC 23–14263, ex-holotype) showed 23.8% (129/543 bp, including 59 gaps), 0.8% (6/782 bp, without gap), and 9.6% (101/1055 bp, including 1 gap) nucleotide base differences, respectively. Morphologically, *D. hydei* fits the generic concept of *Dematiosporium* with dark brown to black, globose to subglobose, smooth conidia Luo et al. (2019), and can be distinguished from *D. muriforme* by the subglobose conidia (this study). *Dematiosporium aquaticum* differs from *D. hydei* in having globose to subglobose, wider conidia (28 × 26 µm *vs.* 29 × 22 µm) Luo et al. (2019). Based on morphological characteristics and phylogenetic analysis, we introduce *D. hydei* as a new species.



Note a, b Colony on natural substrate. c–g Conidia. h Germinated conidium. i, j Culture on PDA medium. Scale bars: c–h = 20 μm.

Figure 4.32 *Dematiosporium hydei* (HKAS 131511, holotype)

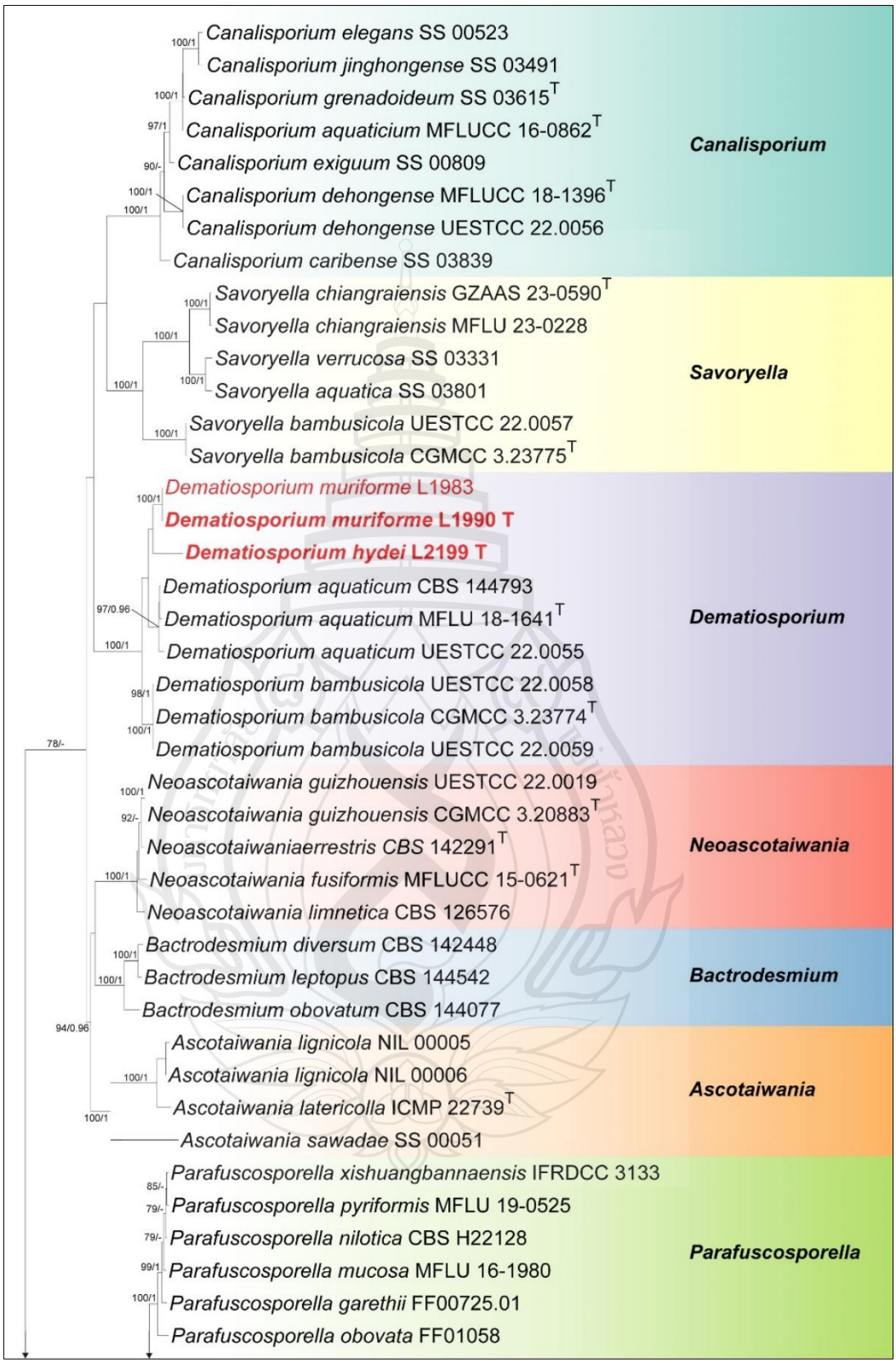
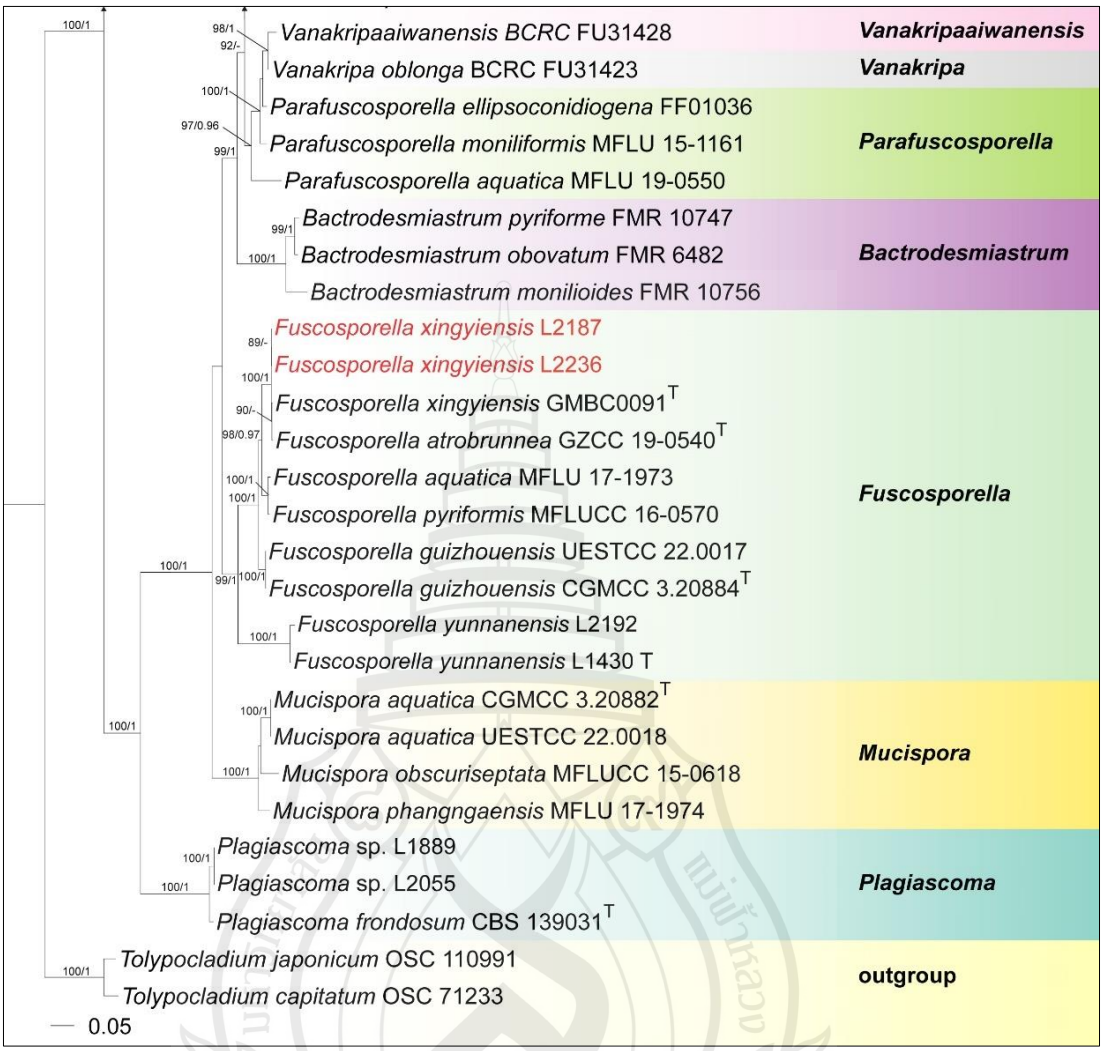


Figure 4.33 Phylogenetic tree of *Savoryellales*



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS SSU, *rpb*2and *tef*1-α sequence dataset representing *Savoryellales*. Sixty-eight strains are included in the combined analyses which comprise 4082 characters including gaps (872 characters for LSU, 487 characters for ITS, 993 characters for SSU, 862 characters for *rpb*2, and 869 characters for *tef*1-α). *Tolypocladium capitatum* (OSC 71233) and *T. japonicum* (OSC 110991) were selected as the outgroup taxa. Bootstrap support values with a ML greater than 65%, and Bayesian posterior probabilities (PP) greater than 0.95 are given above the nodes, shown as "ML/PP". New species are indicated in red and type strains are indicated by a "T" after the strain number.

Figure 4.33 (continued)

Dematiosporium muriforme H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572087; Figure 4.34

Etymology: "muriforme" refers to the muriform conidia of the species.

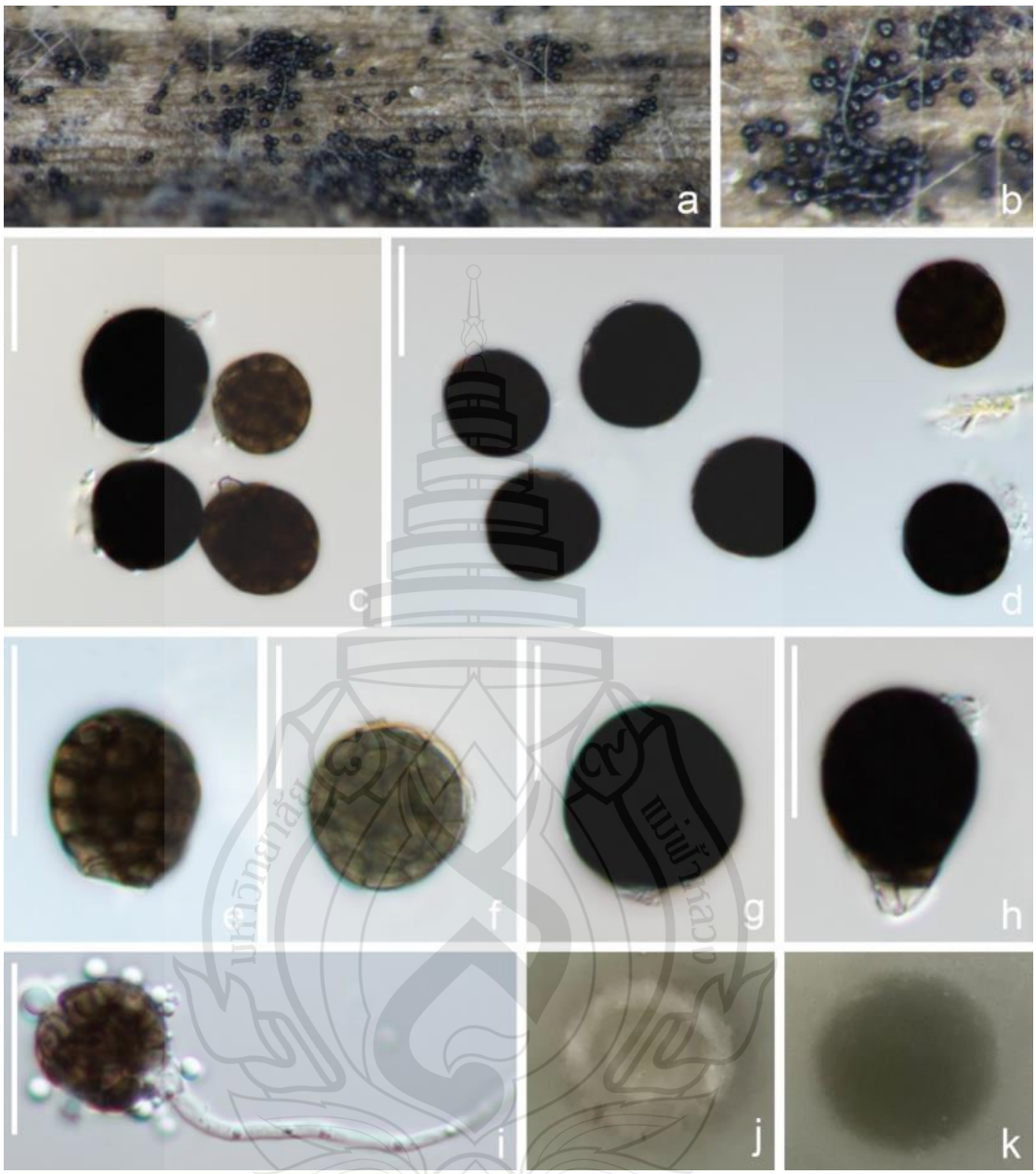
Holotype: HKAS 131712.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, brown to dark brown, punctiform, scattered or gregarious, glistening. *Mycelium* immersed or superficial, composed of septate, pale to pale brown, smooth, thin-walled hyphae. *Conidiophores* absent or present, micronematous, mononematous, sub-hyaline. *Conidiogenous cells*, monoblastic, integrated, terminal, hyaline, smooth-walled. *Conidia* 21–25(–28) µm diam. ($\bar{x}$ = 23 µm, SD = 2.0, n = 50), acrogenous, globose to subglobose, muriform, brown to dark brown, dictyospores, slightly constricted at the septa, guttulate, with distinct or indistinct, smooth-walled, thin-walled, subhyaline basal cells.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from basal cells of conidium within 12 h. Colonies on PDA medium growing slowly, reaching 1-1.5 cm diam. after two months at room temperature (around 25 °C) in dark, circular, flocculent, dense, smooth-edged, pale brown to brown on the forward; dark brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°53′50.48″ N, 102°45′44.51″ E, on submerged decaying wood, 19 February 2023, S. Luan, L1990 (HKAS 131712, holotype), ex-holotype living culture, KUNCC 23–14263; *ibid.*, on submerged decaying wood, 19 February 2023, S. Luan, L1983 (HKAS 131730, paratype), ex-paratype living culture, KUNCC 23–14260.

Notes: Phylogenetic analysis showed that *Dematiosporium muriforme* clustered with another new freshwater species of this study, *D. hydei*, as a sister branch with low supported (Figure 4.33). Significant base and morphological differences are compared in the notes of *D. hydei*. While *D. aquaticum* differs from *D. muriforme* in having globose to subglobose, bigger conidia (28 × 26 µm *vs.* 23 µm diam.) Luo et al. (2019). Based on morphological characteristics and phylogenetic analysis, we introduce *D. muriforme* as a new species.



Note a, b Colony on natural substrate. c–h Conidia. i Germinated conidium. j, k Culture on PDA medium. Scale bars: c–i = 20 μm.

Figure 4.34 *Dematiosporium muriforme* (HKAS 131712, holotype)

Sporidesmiales

Sporidesmiaceae Fr.

Notes: *Sporidesmiaceae* was established by Fries (1849) with rarely used in modern classification schemes, is the only family in *Sporidesmiales* (Su et al., 2016). *Sporidesmiaceae* comprises a single genus *Sporidesmium*, however, *Sporidesmium* has been shown to be polyphyletic (Yang, Maharachchikumbura et al., 2018; Liu et al., 2019; Bao, Hyde et al., 2021). Some sporidesmium-like taxa, which are phylogenetically distant from *Sporidesmiaceae* sensu stricto, have been placed in *Distoseptisporaceae* (Su et al., 2016), while others are uncertain. *Distoseptisporaceae* and *Sporidesmiaceae* are morphologically very similar, and DNA sequence data is the main evidence to delimit the two families.

Sporidesmium Link.

Notes: *Sporidesmium* was introduced by Link (1809), typified by *S. atrum*. The genus is heterogeneous, contains over 500 epithets are listed in Index Fungorum (2024). Shenoy et al. (2006) found that *Sporidesmium* was polyphyletic in *Ascomycota*. Subsequently, Su et al. (2016) restricted the genus to a monophyletic clade as *Sporidesmium* sensu stricto. *Sporidesmium* is characterized by mononematous, macronematous, cylindrical, brown, erect or somewhat repent, septate conidiophores, holoblastic, monoblastic, percurrent conidiogenous cells and euseptate or distoseptate, ovoid, obpyriform or rostrate conidia with or without an appendage or a mucilaginous sheath (Su et al., 2016; Yang, Maharachchikumbura et al., 2018; Liu et al., 2019; Bao, Hyde et al., 2021; Dong, Hyde et al., 2021; Hyde et al., 2021). species of *Sporidesmium* mostly reported as saprobes on plant material in terrestrial and aquatic habitats (Su et al., 2016).

Sporidesmium dianchiense H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572088; Figure 4.35

Etymology: “dianchiense” refers to Dianchi Lake, where the type specimen of the species was collected.

Holotype: HKAS 131544.

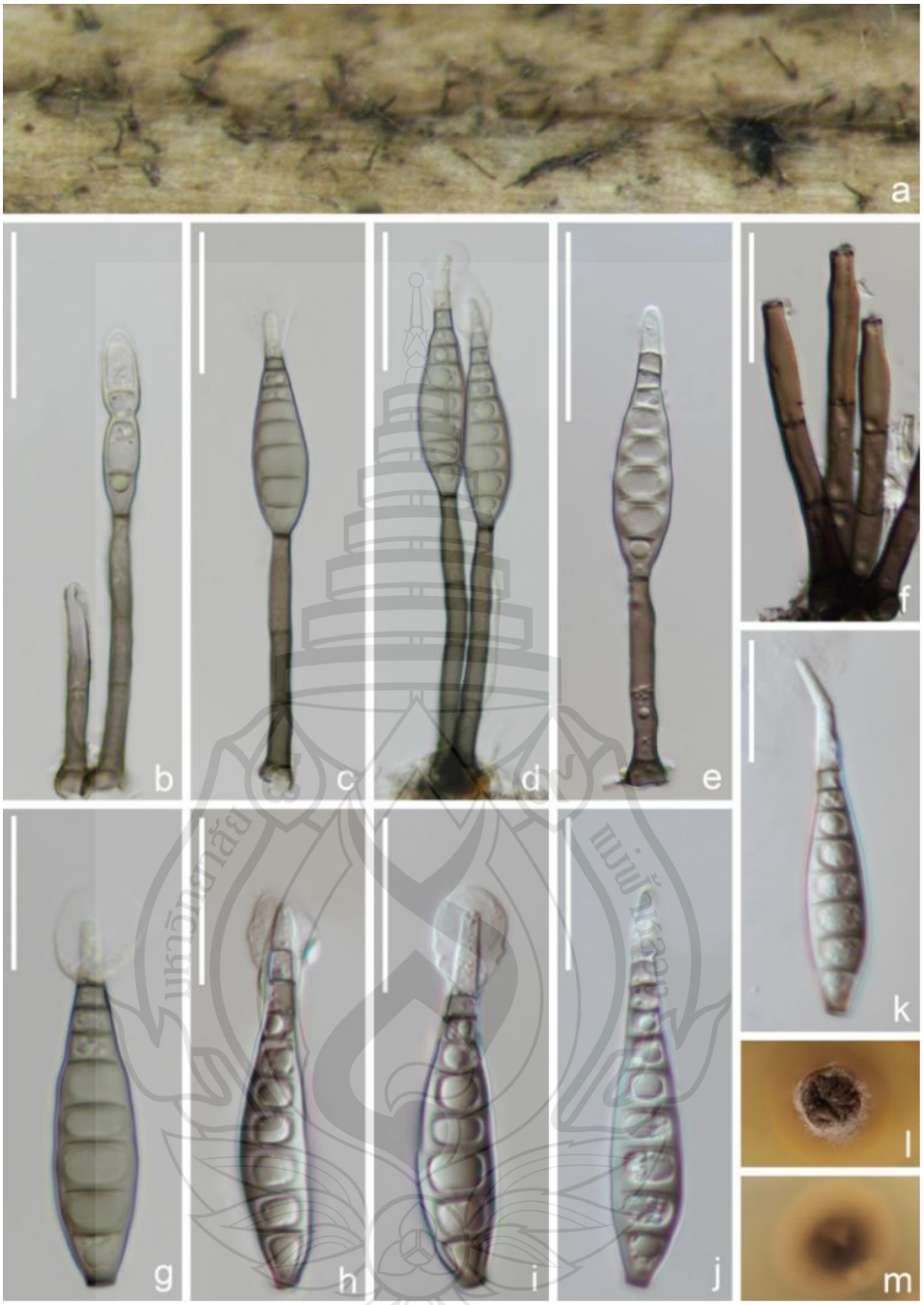
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered. *Mycelium* partly superficial and partly immersed, composed of

septate, pale brown to brown, smooth, thin-walled hyphae. *Conidiophores* (35–)47–60(–67) × 4–5 µm ($\bar{x}$ = 53 × 4 µm, n = 40), macronematous, mononematous, solitary or 2-4 in small groups, erect, mostly straight, unbranched, cylindrical, enlarged at the basal cell, lightly narrower at the apex, (1)2–3-septate, pale brown to brown with pale olive-green tinge. *Conidiogenous cells* (12–)17–21 × 4–5 µm ($\bar{x}$ = 19 × 4 µm, n = 40), monoblastic, terminal, determinate, cylindrical, narrower at the top, browm, smooth-walled. *Conidia* 46–55(–65) × 9–11 µm ($\bar{x}$ = 50 × 10 µm, n = 40), acrogenous, solitary, obpyriform, obclavate, rostrate, tapering towards the apex, straight or slightly curved, pale brown with pale olive-green tinge, subhyaline at the apical cells, guttulate, 7–9-septate, smooth-walled, sometimes the 1–2 cells at the tip of mature conidia are surrounded by a thin mucilaginous sheath, the sheaths 8–16 µm long, 8–12 µm wide. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from apex of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after two months at room temperature (around 25 °C) in dark, circular, flocculent, dense, smooth-edged, pale brown to dark brown on the forward; pale brown to brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°49′14.15″ N, 102°45′57.58″ E, on submerged decaying wood, 19 February 2023, H.W. Shen, L1960 (HKAS 131544, holotype), ex-holotype living culture, KUNCC 23–13509.

Notes: Phylogenetic analysis showed that *Sporidesmium dianchiense* clustered as an obvious, independent branch in *Sporidesmium* with 100 % ML and 1.00 PP (Figure 4.36) supported. Morphologically, *S. dianchiense* fits the generic concept of *Sporidesmium* with macronematous, unbranched conidiophores, terminal, monoblastic conidiogenous cells and brown, septate conidia with a mucilaginous sheath (Su et al., 2016; Liu et al., 2019; Yang et al., 2023). Based on morphological characteristics and phylogenetic analysis, we introduce *S. dianchiense* as a new species.



Note a Colony on natural substrate. b Conidiophores with developing conidium. c–e Conidiophores with conidia. f Conidiophores and conidiogenous cells. g–i Conidia surrounded with mucilaginous sheaths. j Conidium without sheath. k Germinated conidium. l, m Culture on PDA medium. Scale bars: b–e = 30 μm, f–k = 20 μm.

Figure 4.35 *Sporidesmium dianchiense* (HKAS 131544, holotype)

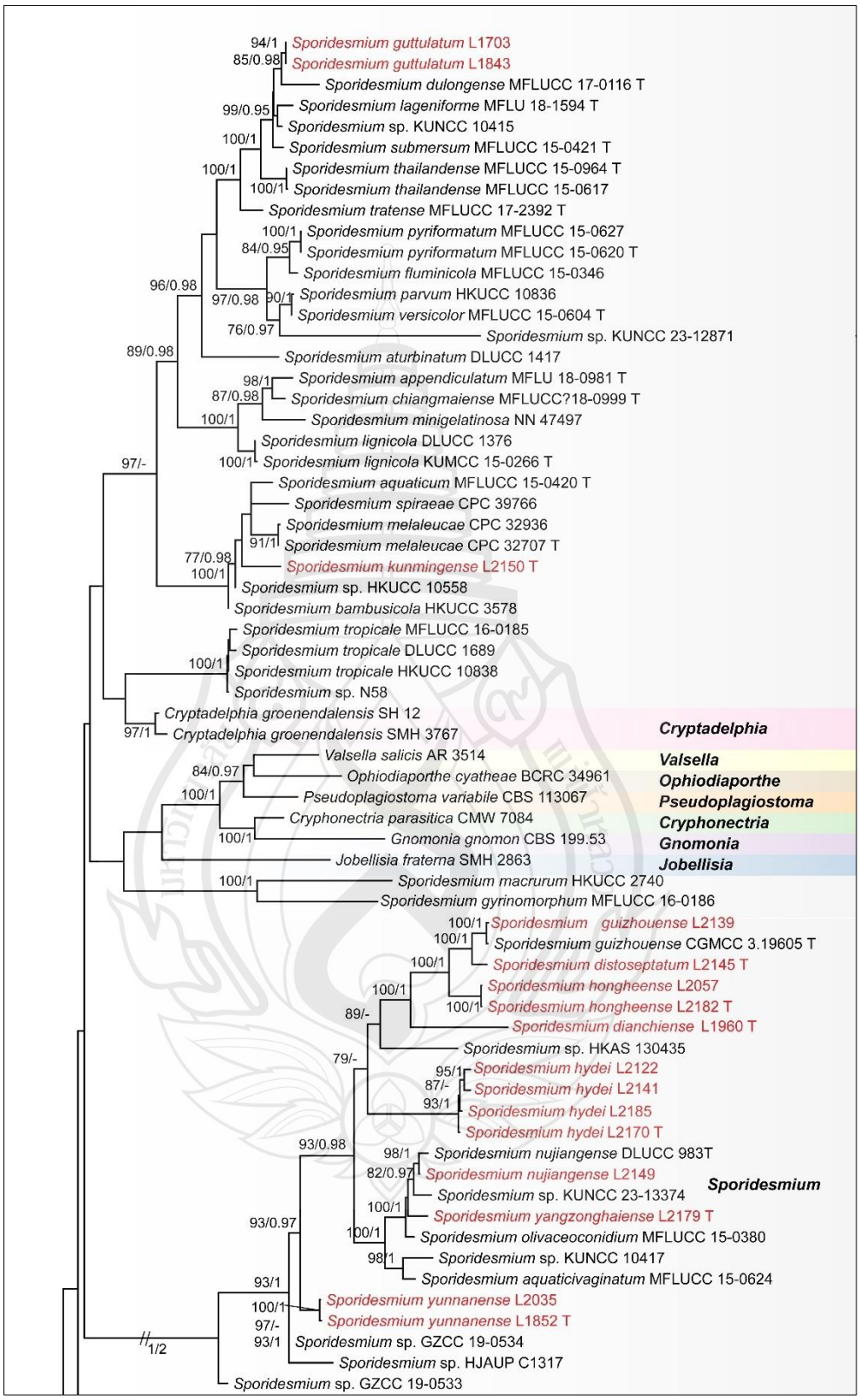
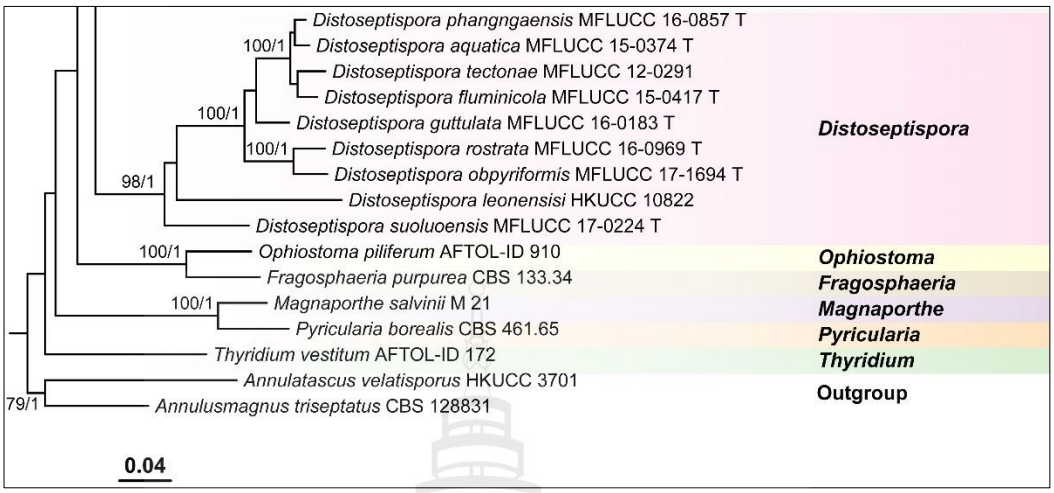


Figure 4.36 Phylogenetic tree of *Sporidesmiales*



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS SSU, *rpb*2and *tef*1-α sequence dataset representing *Sporidesmiales*. Eighty-one strains are included in the combined analyses which comprise 4079 characters including gaps (827 characters for LSU, 514 characters for ITS, 954 characters for SSU, 999 characters for *rpb*2, and 785 characters for *tef*1-α). *Annulatascus velatisporus* (HKUCC 3701) and *A. triseptatus* (CBS 128831) were selected as the outgroup taxa. Bootstrap support values with a ML greater than 65%, and Bayesian posterior probabilities (PP) greater than 0.95 are given above the nodes, shown as "ML/PP". New species are indicated in red and type strains are indicated by a "T" after the strain number.

Figure 4.36 (continued)

Sporidesmium distoseptatum H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572089; Figure 4.37

Etymology: "distoseptatum" refers to the "distoseptate" conidia of this species.

Holotype: HKAS 131709.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered, glistening. *Mycelium* mostly immersed, composed of septate, pale to pale brown, smooth, thin-walled hyphae. *Conidiophores* (43–)49–61(–67) × 4–5 µm ($\bar{x}$ = 55 × 5 µm, n = 35), macronematous, mononematous, solitary or in small groups,

erect, straight or slightly curved, unbranched, cylindrical, enlarged at the basal cell, lightly narrower at the apex, (1)2–3-septate, pale brown to brown with pale olive-green tinge. *Conidiogenous cells* 19–24 × 4–5 µm ($\bar{x}$ = 22 × 5 µm, n = 20), monoblastic, terminal, determinate, cylindrical, narrower at the top, browm, smooth-walled. *Conidia* 57–85(–97) × 9–12 µm ($\bar{x}$ = 71 × 11 µm, n = 40), acrogenous, solitary, obclavate, rostrate, tapering towards the apex, straight or slightly curved, subhyaline to pale brown with pale olive-green tinge, guttulate, 11–16-septate, smooth-walled, usually the 4-8 cells at the tip of mature conidia are surrounded by a thin mucilaginous sheath, the sheaths 28–46 µm long, 9–13 µm wide. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from apex of conidium within 12 h. Colonies on PDA medium reaching 2.5-3 cm diam. after three months at room temperature (around 25 °C) in dark, circular, flocculent, dense, smooth-edged, pale brown on the forward; pale brown to brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°50′23.95″ N, 102°39′50.72″ E, on submerged decaying wood, 18 February 2023, S. Luan, L2145 (HKAS 131709, holotype), ex-holotype living culture, KUNCC 23–14317.

Notes: Phylogenetic analysis showed that *Sporidesmium distoseptatum* clustered with the previous freshwater species, *S. guizhouense* strains (CGMCC 3.19605 and KUNCC 23–14315), as a sister branch with 100 % ML and 1.00 PP supported (Figure 4.36). Comparison of ITS, LSU, SSU, *tef*1-α and *rpb*2 sequence between *S. distoseptatum* (KUNCC 23–14317, ex-holotype) and *S. guizhouense* (CGMCC 3.19605, ex-type) showed 8.8% (42/479 bp, including 15 gaps), 1.6% (13/789 bp, without gap), 0.3% (3/971 bp, without gap), 1.7% (15/900 bp, without gap), and 3.5% (33/936 bp, without gap) nucleotide base differences, respectively. Morphologically, *S. distoseptatum* fits the generic concept of *Sporidesmium* with with macronematous, unbranched conidiophores, terminal, monoblastic conidiogenous cells and brown, septate conidia with a mucilaginous sheath (Su et al., 2016; Liu et al., 2019; Yang et al., 2023), and can be distinguished from *S. guizhouense* (HKAS 104644, holotype) by the longer and wider conidiophores and conidiogenous cells (conidiophores: 55 × 5 µm *vs.* 38 × 4 µm; conidiogenous cells: 22 × 5 µm *vs.* 18 × 3.7 µm)

(Liu et al., 2019). Therefore, based on morphological characteristics and phylogenetic analysis, we introduce *S. distoseptatum* as a new species.

Note a, b Colony on natural substrate. c–f Conidiophores with conidia. g Conidiophores and conidiogenous cells. h–k Conidia surrounded with mucilaginous sheaths. l Germinated conidium. m, n Culture on PDA medium. Scale bars: c–f = 30 μm, g–l = 20 μm.

Figure 4.37 *Sporidesmium distoseptatum* (HKAS 131709, holotype)

Sporidesmium guizhouense L.L. Liu & Z.Y. Liu, Phytotaxa 422(2): 149 (2019)

Fungal Names number: FN 830973; *Facesoffungi number*: FoF 06112; Figure 4.38

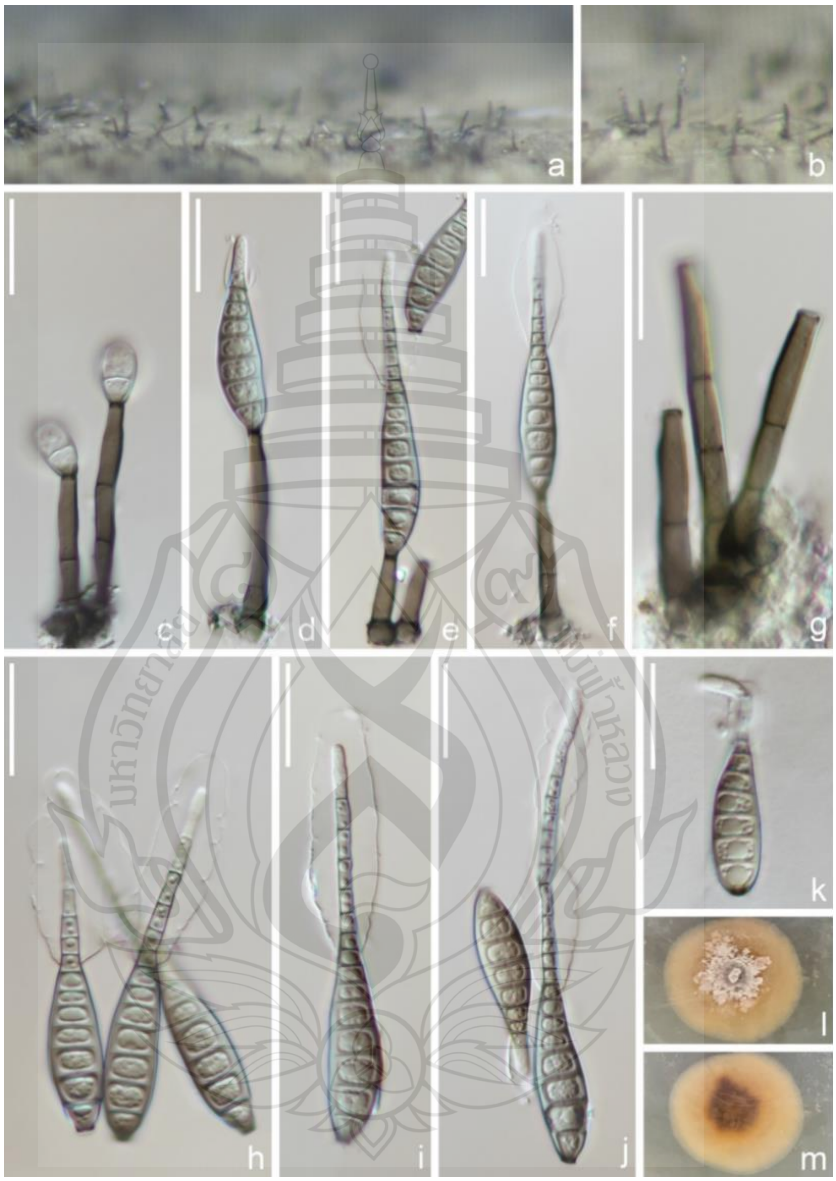
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered or gregarious, glistening. *Mycelium* mostly immersed, composed of septate, pale to pale brown, smooth, thin-walled hyphae. *Conidiophores* (20–)25–45(–55) × 4–5 µm ($\bar{x}$ = 35 × 4 µm, n = 30), macronematous, mononematous, solitary or 2–3 in small groups, erect, mostly straight, unbranched, cylindrical, enlarged at the base, lightly narrower at the apex, 1–3-septate, brown. *Conidiogenous cells* 14–20(–27) × 4 µm ($\bar{x}$ = 17 × 4 µm, n = 20), monoblastic, terminal, determinate, cylindrical, slightly narrower at the top, brown, smooth-walled. *Conidia* (42–)58–87(–119) × 9–10 µm ($\bar{x}$ = 72 × 10 µm, n = 40), acrogenous, solitary, obclavate to rostrate, tapering towards the apex, straight or slightly curved, subhyaline to pale brown with pale olive-green tinge, guttulate, 12–18(21)-septate, smooth-walled, usually the 5-7 cells at the tip of mature conidia are surrounded by a thin mucilaginous sheath, the sheaths 28–53 µm long, 8–14 µm wide. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from apex of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after one month at room temperature (around 25 °C) in dark, circular, loose, flocculent, smooth-edged, dense, white to pale brown on the forward; white to brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°52′49.72″ N, 102°39′36.82″ E, on submerged decaying wood, 18 February 2023, H.W. Shen, L2139 (HKAS 132033), living culture, KUNCC 23–14315.

Notes: Phylogenetic analysis showed that our collection (KUNCC 23–14315) clustered with *Sporidesmium guizhouense* (CGMCC 3.19605) with 100 % ML and 1.00 PP supported (Figure 4.36). Comparison of ITS, LSU, SSU, *tef*1-α and *rpb*2 sequence between our collection (KUNCC 23–14315) and *S. guizhouense* (CGMCC 3.19605) showed 1.9% (9/484 bp, including 1 gap), while there is no significant difference in the base comparison of other genes (≤ 0.6%). Morphologically, our collection and *S. guizhouense* (HKAS 104644, holotype) are similar in colors, shapes, and separations

of conidiophores, conidiogenous cells and conidia (Liu et al., 2019). Based on morphological characteristics and phylogenetic analysis, we introduce our collection as a new collection of *S. guizhouense* in this study.



Note a, b Colony on natural substrate. c Conidiophores with developing conidia. d–f Conidiophores with conidia. g Conidiophores and conidiogenous cells. h–j Conidia surrounded with mucilaginous sheaths. k Germinated conidium. l, m Culture on PDA medium. Scale bars: c–k = 20 μm.

Figure 4.38 *Sporidesmium guizhouense* (HKAS 132033)

Sporidesmium guttulatum H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572090; Figure 4.39

Etymology: "guttulatum" refers to the conidia characteristic of guttulate in this species.

Holotype: HKAS 131419.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, brown to dark brown, scattered or gregarious, glistening. *Mycelium* mostly immersed, composed of septate, pale brown to brown, smooth, thin-walled hyphae. *Conidiophores* (76–)112–171(–204) × 4–5 µm ($\bar{x}$ = 142 × 5 µm, n = 50), macronematous, mononematous, solitary or caespitose, erect, straight or slightly curved, unbranched, cylindrical, enlarged at the base, brown to dark brown, pale brown at the apex, septate, brown. *Conidiogenous cells* (11–)18–29 (–34) × 4–5 µm ($\bar{x}$ = 23 × 5 µm, n = 50), monoblastic, terminal, determinate or percurrent, cylindrical, pale brown to brown, smooth-walled, with brown to dark conidial detachment scars at the apex. *Conidia* 36–45(–52) × 14–16 µm ($\bar{x}$ = 41 × 15 µm, n = 50), acrogenous, solitary, ovoid to pyriform when young, usually rostrate when mature, tapering towards the apex, mostly straight, pale brown to dark brown, hyaline at the apex, 4–6-septate, slightly constricted at the septum, truncate at base, guttulate, smooth-walled, without sheath. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from end cell of conidium within 12 h. Colonies on PDA medium reaching 1-1.5 cm diam. after one month at room temperature (around 25 °C) in dark, circular, loose, flocculent, smooth-edged, dense, white on the forward; white to reddish brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L1843 (HKAS 131419, holotype), ex-holotype living culture, KUNCC 23–14564; *ibid.*, on submerged decaying wood, 24 February 2023, H.W. Shen, L1703 (HKAS 131441, paratype), ex-paratype living culture, KUNCC 23–14560.

Notes: Phylogenetic analysis showed that *Sporidesmium guttulatum* clustered with the previous freshwater species, *S. dulongense* strain (MFLUCC 17–0116), as a sister branch with 87 % ML and 0.98 PP supported (Figure 4.36). Comparison of ITS,

LSU, SSU, *tef*1-α and *rpb*2 sequence between *S. guttulatum* (KUNCC 23–14564, ex-holotype) and *S. dulongense* (MFLUCC 17–0116, ex-type) showed 12.3% (100/811 bp, including 3 gaps) in *tef*1-α while there is no significant difference in the base comparison of other genes (≤ 0.5%). Morphologically, *S. guttulatum* fits the generic concept of *Sporidesmium* with macronematous, unbranched conidiophores, terminal, monoblastic conidiogenous cells and brown, septate conidia without sheath (Su et al., 2016; Yang, Maharachchikumbura et al., 2018; Liu et al., 2019; Bao, Hyde et al., 2021; Dong, Hyde et al., 2021; Hyde et al., 2021), and can be distinguished from *S. dulongense* (HKAS 92659, holotype) by the longer conidiophores and narrower conidia (conidiophores: 142 × 5 µm *vs.* 106 × 6.5 µm; conidiogenous cells: 41 × 15 µm *vs.* 54 × 14 µm) (Bao, Hyde et al., 2021). Therefore, based on morphological characteristics and phylogenetic analysis, we introduce *S. guttulatum* as a new species.

Note a, b Colony on natural substrate. c, d Conidiophores. e Conidiophores with developing conidia. f, g Conidiogenous cells. h–l Conidia. m Germinated conidium. n, o Culture on PDA medium. Scale bars: c–e = 50 μm, f–m = 20 μm.

Figure 4.39 *Sporidesmium guttulatum* (HKAS 131419, holotype)

Sporidesmium hongheense H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572091; Figure 4.40

Etymology: "hongheense" refers to Honghe Prefecture, where the type specimen of the species was collected.

Holotype: HKAS 131699.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, brown to dark brown, scattered or gregarious, glistening. *Mycelium* mostly immersed, composed of septate, pale brown, smooth, thin-walled hyphae. *Conidiophores* 33–46 × 4–5 µm ($\bar{x}$ = 40 × 5 µm, n = 40), macronematous, mononematous, solitary or in small groups, erect, mostly straight, unbranched, cylindrical, enlarged at the basal cell, lightly narrower at the apex, 1–2(3)-septate, pale brown to brown. *Conidiogenous cells* 17–20 × 4–5 µm ($\bar{x}$ = 18 × 4 µm, n = 40), monoblastic, terminal, determinate, cylindrical, narrower at the top, browm, smooth-walled. *Conidia* (45–)52–65(–75) × 8–9 µm ($\bar{x}$ = 58 × 9 µm, n = 40), acrogenous, solitary, oblong-obclavate, rostrate, tapering towards the apex, straight or slightly curved, subhyaline to pale brown with pale olive-green tinge, guttulate, 9–10-septate, smooth-walled, mostly the 2-3 cells at the tip of mature conidia are surrounded by a thin mucilaginous sheath, the sheaths 12–30 µm long, 6–10 µm wide, sometimes conidia proliferate at the tip to form a second conidium. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from apex of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after six weeks at room temperature (around 25 °C) in dark, circular, flocculent, dense, smooth-edged, pale to brown on the forward, middle mastoid; white to pale brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°41′49.2" N, 102°30'52.2″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L2182 (HKAS 131699, holotype), ex-holotype living culture, KUNCC 23–14285; *ibid.*, Kunming City, Yangzonghai Lake, 24°54′43.70″ N, 103°1′3.64″ E, on submerged decaying wood, 20 February 2023, S. Luan, L2057 (HKAS 131836, paratype), ex-paratype living culture, KUNCC 23–13816.

Notes: Phylogenetic analysis showed that *Sporidesmium hongheense* clustered as an obvious, independent branch in *Sporidesmium* with 100 % ML and 1.00 PP supported (Figure 4.36). Morphologically, *S. hongheense* fits the generic concept of *Sporidesmium* with macronematous, mononematous, unbranched conidiophores, monoblastic, terminal conidiogenous cells and solitary, septate conidia with a mucilaginous sheath (Su et al., 2016; Dong, Hyde et al., 2021). Based on morphological characteristics and phylogenetic analysis, we introduce *S. hongheense* as a new species.

Note a, b Colony on natural substrate. c–e Conidiophores with conidia. f Conidiogenous cell. g–j Conidia surrounded with mucilaginous sheaths (j Conidium and proliferated conidium). k Germinated conidium. l, m Culture on PDA medium. Scale bars: c–e = 30 μm, f–k = 20 μm.

Figure 4.40 *Sporidesmium hongheense* (HKAS 131699, holotype)

Sporidesmium hydei H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572092; Figure 4.41

Etymology: "hydei" refers to the renowned mycologist Professor K.D. Hyde, named in recognition of his contributions to mycology on the occasion of his 70th birthday.

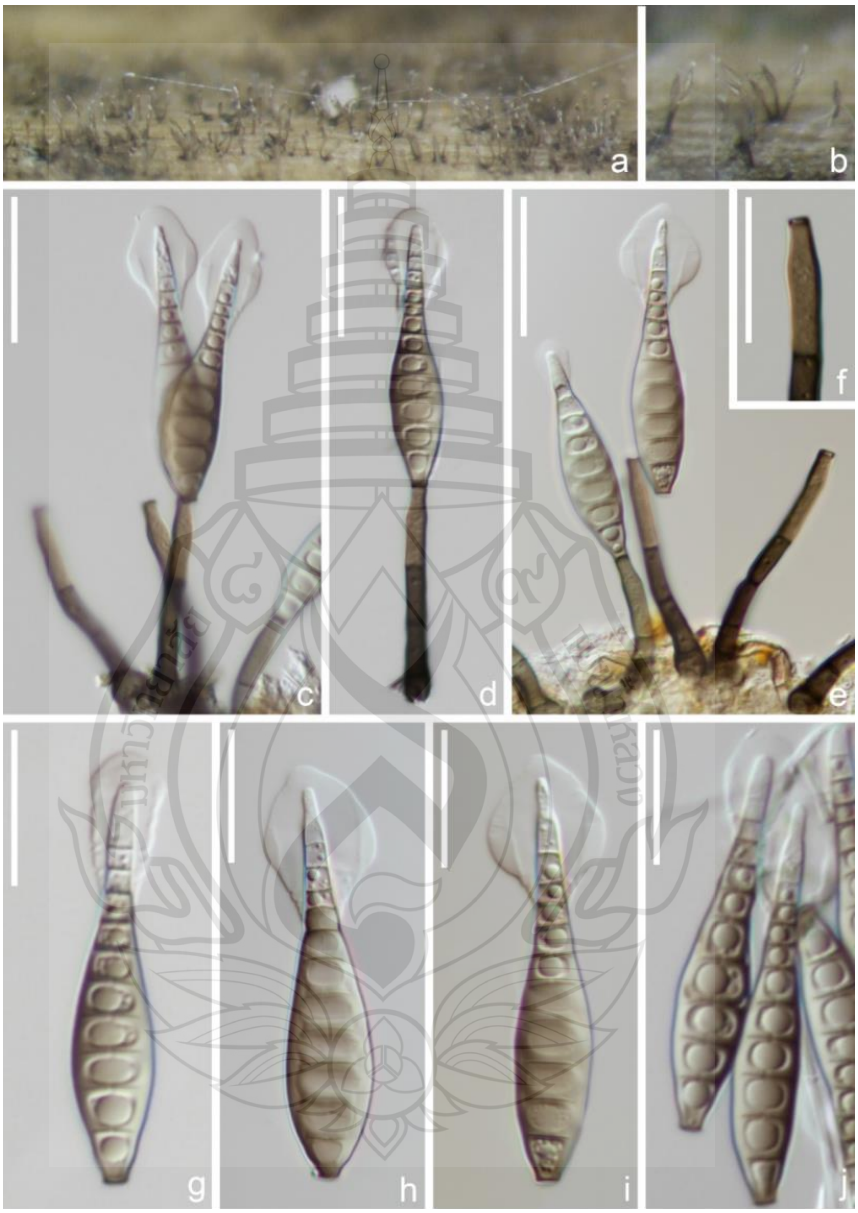
Holotype: HKAS 132094.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered, fascicular. *Mycelium* partly superficial and partly immersed, composed of septate, pale brown to brown, smooth, thin-walled hyphae. *Conidiophores* (31–)40–55(–64) × 4–5 µm ($\bar{x}$ = 48 × 4 µm, n = 50), macronematous, mononematous, solitary or in small groups, erect, straight or slightly curved, unbranched, cylindrical, enlarged at the basal cell, lightly narrower at the apex, 1–3-septate, apical cell (conidiogenous cell) sub-hyaline to pale brown, and other cells brown to dark brown. *Conidiogenous cells* 17–22 × 4 µm ($\bar{x}$ = 19 × 4 µm, n = 50), monoblastic, terminal, determinate, cylindrical, narrower at the top, pale browm, smooth-walled. *Conidia* (40–)49–59(–69) × 10–13 µm ($\bar{x}$ = 54 × 12 µm, n = 50), acrogenous, solitary, obpyriform, obclavate, rostrate, tapering towards the apex, straight or slightly curved, pale brown with pale olive-green tinge, subhyaline at the apical cells, guttulate, 9–11-distoseptate, smooth-walled, sometimes the 3-5 cells at the tip of mature conidia are surrounded by a thin mucilaginous sheath, the sheaths obovoid, thickened on both sides, 16–25 µm long, 10–17 µm wide. *Conidial secession* schizolytic.

Material examined: CHINA, Yunnan Province, Honghe Prefecture, Yilonghu Lake, 23°39′18.69″ N, 102°35′49.15″ E, on submerged decaying wood, 22 February 2023, Y. Wang, L2170 (HKAS 132094, holotype), ex-holotype living culture, KUNCC 23–14336; *ibid.*, 23°40′28.95″ N, 102°36′30.00″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L2185 (HKAS 131808, paratype); *ibid.*, on submerged decaying wood, 22 February 2023, H.W. Shen, L2122 (HKAS 131517)

Notes: Phylogenetic analysis showed that *Sporidesmium hydei* clustered as an obvious, independent branch in *Sporidesmium* with 79 % ML supported (Figure 4.36). Morphologically, *S. hydei* fits the generic concept of *Sporidesmium* with macronematous, mononematous, unbranched, cylindrical conidiophores, monoblastic, terminal

conidiogenous cells and solitary, septate conidia with a mucilaginous sheath (Su et al., 2016; Dong, Hyde et al., 2021). Based on morphological characteristics and phylogenetic analysis, we introduce *S. hydei* as a new species.



Note a, b Colony on natural substrate. c–e Conidiophores with conidia. f Conidiogenous cell. g–j Conidia surrounded with mucilaginous sheaths. Scale bars: c–e = 30 μm, f–j = 20 μm.

Figure 4.41 *Sporidesmium hydei* (HKAS 132094, holotype)

Sporidesmium kunmingense H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572093; Figure 4.42

Etymology: "kunmingense" refers to the place where this species was collected, Kunming City.

Holotype: HKAS 131503.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered or gregarious. *Mycelium* partly superficial and partly immersed, composed of septate, pale brown to brown, smooth, thin-walled hyphae. *Conidiophores* (17–)31–48(–53) × 4–5 µm ($\bar{x}$ = 39 × 5 µm, n = 20), macronematous, mononematous, solitary or in small groups, erect, straight or slightly curved, unbranched, subcylindrical, enlarged at the base, lightly narrower at the apex, 1–3-septate, dark brown, smooth-walled. *Conidiogenous cells* 14–18 × 4–5 µm ($\bar{x}$ = 16 × 4 µm, n = 20), monoblastic, terminal, determinate, subcylindrical, slightly narrower at the top, straight or slightly curved, browm, smooth-walled. *Conidia* (63–)82–115(–130) × 10–11 µm ($\bar{x}$ = 98 × 10 µm, n = 35), acrogenous, solitary, obclavate, rostrate, tapering towards the apex, straight or slightly curved, pale brown with pale olive-green tinge, subhyaline at the apex, 13–20-distoseptate, guttulate, smooth, thick-walled, without mucilaginous sheath. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from apex of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after two months at room temperature (around 25 ℃) in dark, circular, dense, wrinkled, smooth-edged, pale brown to pale yellowish brown on the forward, middle mastoid; pale brown to brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°52′49.72″ N, 102°39′36.82″ E, on submerged decaying wood, 18 February 2023, H.W. Shen, L2150 (HKAS 131503, holotype), ex-type living culture, KUNCC 23–14319.

Notes: Phylogenetic analysis showed that *Sporidesmium kunmingense* clustered as an obvious, independent branch in *Sporidesmium* with low supported (Figure 4.36). Morphologically, *S. kunmingense* fits the generic concept of *Sporidesmium* with macronematous, mononematous, unbranched, septate conidiophores, monoblastic,

terminal conidiogenous cells and solitary, tapering towards the apex, septate conidia without sheath (Su et al., 2016; Dong, Hyde et al., 2021). Based on morphological characteristics and phylogenetic analysis, we introduce *S. kunmingense* as a new species.

Note a, b Colony on natural substrate. c–f Conidiophores with conidia. g Conidiogenous cells. h–k Conidia. l Germinated conidium. m, n Culture on PDA medium. Scale bars: c–f = 30 μm, g = 10 μm, h–l = 20 μm.

Figure 4.42 *Sporidesmium kunmingense* (HKAS 131503, holotype)

Sporidesmium nujiangense D.F. Bao, H.Y. Su, K.D. Hyde and Z.L. Luo, 7(no. 669): 15 (2021)

Fungal Names number: FN 558594; *Facesoffungi number*: FoF 09916; Figure 4.43

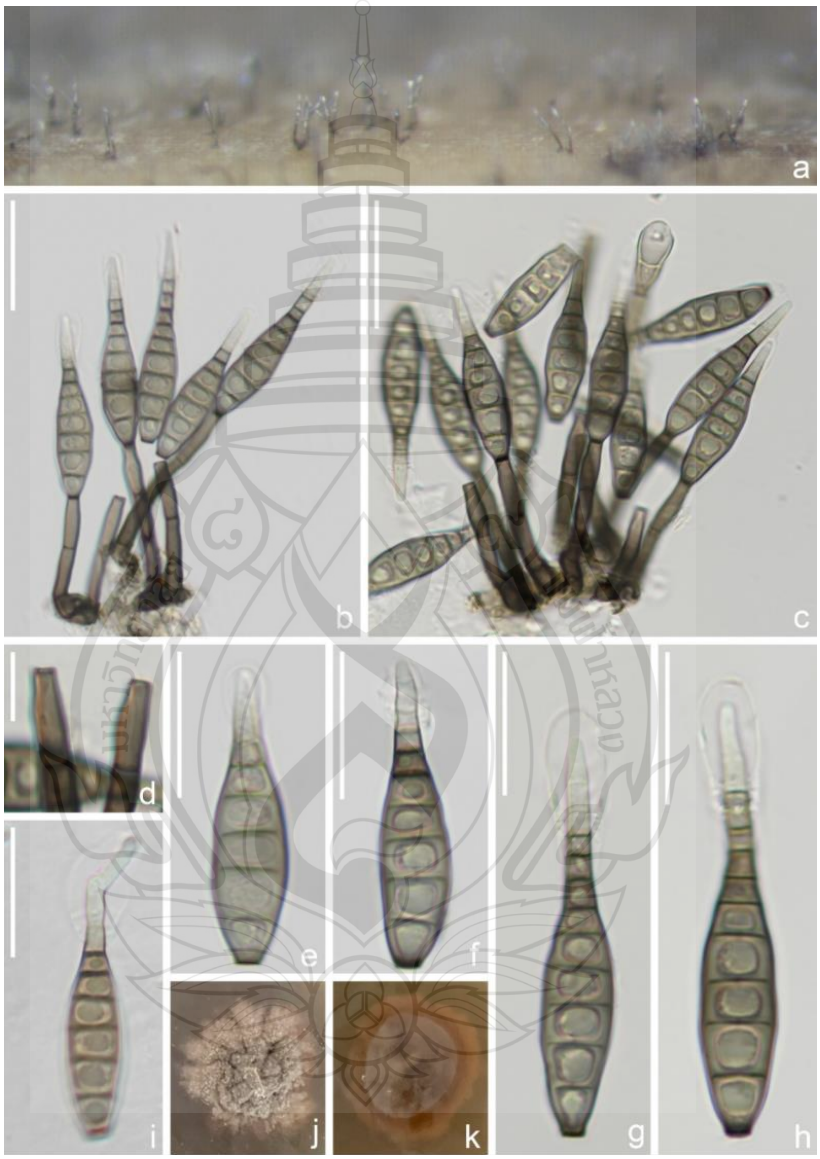
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered or gregarious, glistening. *Mycelium* mostly immersed, composed of septate, brown to dark brown, smooth, thin-walled hyphae. *Conidiophores* (25–)33–44(–50) × 3–4 µm ($\bar{x}$ = 38 × 4 µm, n = 40), macronematous, mononematous, solitary or in small groups, erect, mostly straight, unbranched, cylindrical, enlarged at the base, lightly narrower at the apex, 1–3-septate, brown. *Conidiogenous cells* 12–16 × 3–4 µm ($\bar{x}$ = 14 × 4 µm, n = 40), monoblastic, terminal, determinate, cylindrical, slightly narrower at the top, sometimes slightly swollen at the middle, browm, smooth-walled. *Conidia* 40–51(–61) × 9–10 µm ($\bar{x}$ = 46 × 10 µm, n = 40), acrogenous, solitary, obclavate, rostrate, tapering towards the apex, straight or slightly curved, pale brown with pale olive-green tinge, subhyaline at the apex, 6–9(11)-septate, guttulate, smooth-walled, usually the 3-5 cells at the tip of mature conidia are surrounded by a thin mucilaginous sheath. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from apex of conidium within 12 h. Colonies on PDA medium reaching 2-3 cm diam. after two months at room temperature (around 25 °C) in dark, circular, loose, flocculent, smooth-edged, dense, pale brown to brown on the forward, middle mastoid; pale brown to brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°52′49.72″ N, 102°39′36.82″ E, on submerged decaying wood, 18 February 2023, H.W. Shen, L2149 (HKAS 131701), living culture, KUNCC 23–14318.

Notes: Phylogenetic analysis showed that our collection (KUNCC 23–14318) clustered with *Sporidesmium nujiangense* (DLUCC 983) with 98 % ML and 1.00 PP supported (Figure 4.36). Comparison of LSU, SSU, *tef*1-α and *rpb*2 sequence between our collection (KUNCC 23–14318) and *S. nujiangense* (DLUCC 983) showed there is no significant difference in the base comparison of these genes (≤ 0.7%). Morphologically, our collection is similar to *S. nujiangense* (HKAS 115795, holotype) in having macronematous, mononematous, conidiophores, holoblastic, monoblastic,

cylindrical conidiogenous cells and solitary, obclavate, conidia with a mucilaginous sheath at the tip (Bao, Hyde et al., 2021). Based on morphological characteristics and phylogenetic analysis, we introduce our collection as a new collection of *S. nujiangense* in this study.



Note a Colony on natural substrate. b–c Conidiophores with conidia. d Conidiogenous cells. e–h Conidia surrounded with mucilaginous sheaths. i Germinated conidium. j, k Culture on PDA medium. Scale bars: b, c = 30 μm, d = 10 μm, e–i = 20 μm.

Figure 4.43 *Sporidesmium nujiangense* (HKAS 131701)

Sporidesmium yangzonghaiense H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572094; Figure 4.44

Etymology: "yangzonghaiense" refers to Yangzonghai Lake, where the type specimen of the species was collected.

Holotype: HKAS 131813.

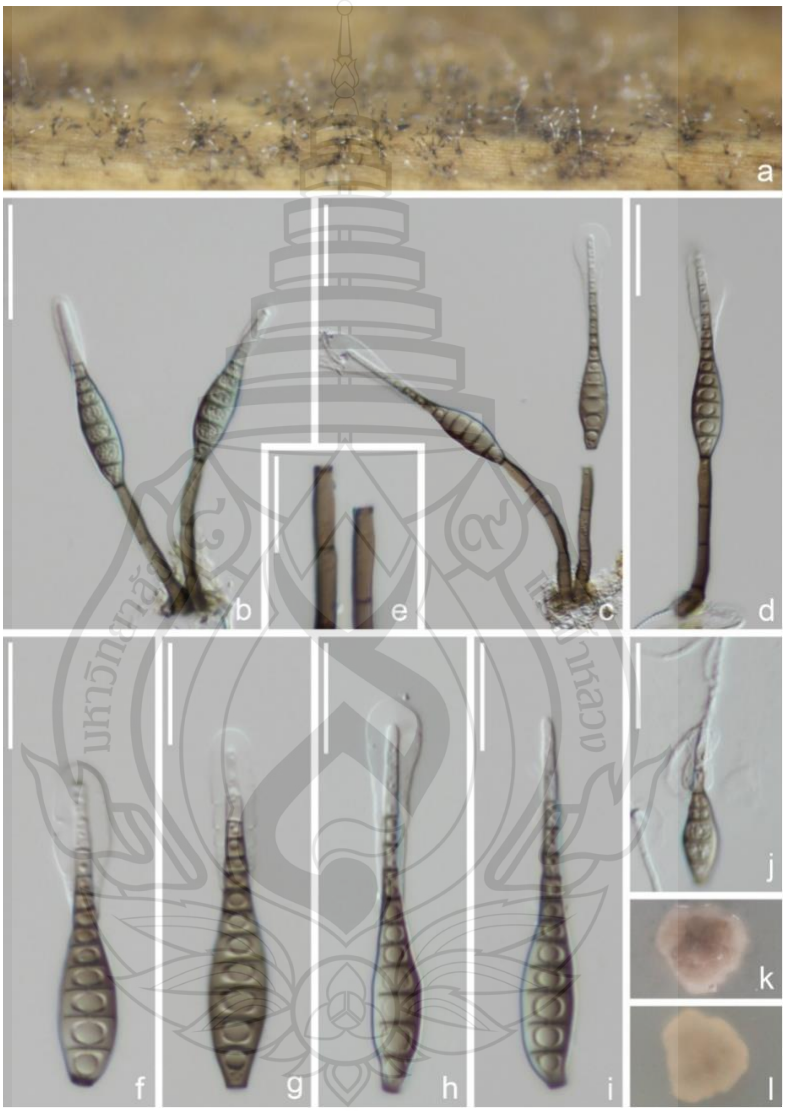
Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered or gregarious, fascicular. *Mycelium* mostly immersed, composed of septate, pale brown to brown, smooth, thin-walled hyphae. *Conidiophores* (35–)42–62(–74) × 4–5 µm ($\bar{x}$ = 52 × 4 µm, n = 40), macronematous, mononematous, solitary or in small groups, erect, straight or slightly curved, unbranched, cylindrical, enlarged at the basal cell, lightly narrower at the apex, 2–5-septate, pale brown to brown, smooth-walled. *Conidiogenous cells* 14–18 × 4–5 µm ($\bar{x}$ = 16 × 4 µm, n = 20), monoblastic, terminal, determinate, cylindrical, lightly narrower at the top, browm, smooth-walled. *Conidia* (44–)53–67(–76) × 9–11 µm ($\bar{x}$ = 60 × 10 µm, n = 35), acrogenous, solitary, obclavate, rostrate, tapering towards the apex, straight or slightly curved, pale brown with pale olive-green tinge, hyaline at the apical cells, guttulate, 10–12-distoseptate, smooth-walled, sometimes the 5-6 cells at the tip of mature conidia are surrounded by a thin mucilaginous sheath, the sheaths 23–36 µm long, 6–12 µm wide. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from apex of conidium within 12 h. Colonies on PDA medium reaching 2-2.5 cm diam. after two months at room temperature (around 25 °C) in dark, irregular, flocculent, dense, smooth-edged, white to pale brown on the forward; pale brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Yangzonghai Lake, 24°57′29.19″ N, 103°0′3.49″ E, on submerged decaying wood, 20 February 2023, S. Luan, L2179 (HKAS 131813, holotype), ex-type living culture, KUNCC 23–14290.

Notes: Phylogenetic analysis showed that *Sporidesmium yangzonghaiense* clustered as an obvious, independent branch in *Sporidesmium* with low supported (Figure 4.36). Morphologically, *S. yangzonghaiense* fits the generic concept of *Sporidesmium* with macronematous, mononematous, unbranched, cylindrical, septate

conidiophores, monoblastic, terminal conidiogenous cells and solitary, tapering towards the apex, septate conidia with a mucilaginous sheath (Su et al., 2016; Dong, Hyde et al., 2021). Based on morphological characteristics and phylogenetic analysis, we introduce *S. yangzonghaiense* as a new species.



Note a Colony on natural substrate. b–d Conidiophores with conidia. e Conidiogenous cells. f–h Conidia surrounded with mucilaginous sheaths. i Conidium without sheath. j Germinated conidium. k, l Culture on PDA medium. Scale bars: b–d = 30 μm, e–j = 20 μm.

Figure 4.44 *Sporidesmium yangzonghaiense* (HKAS 131813, holotype)

Sporidesmium yunnanense H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572095; Figure 4.45

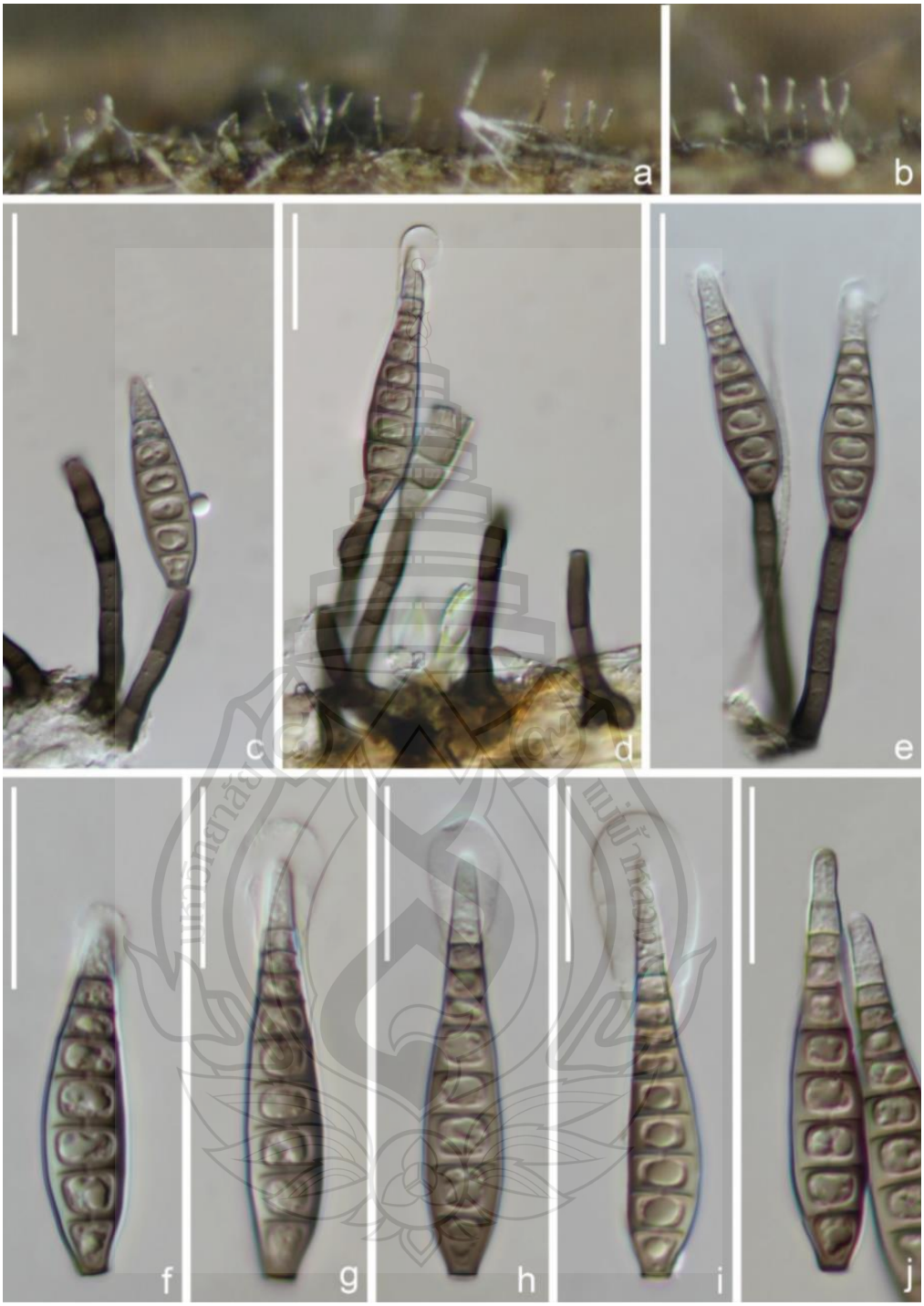
Etymology: "yunnanense" refers to Yunnan Province, where the type specimen of the species was collected.

Holotype: HKAS 131420.

Saprobic on submerged decaying wood in freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate effuse, hairy, pale brown to brown, scattered or gregarious. *Mycelium* mostly immersed, composed of septate, pale brown to brown, smooth, thin-walled hyphae. *Conidiophores* 27–39(–44) × 4–5 µm ($\bar{x}$ = 33 × 4 µm, n = 40), macronematous, mononematous, solitary or in small groups, erect, straight or slightly curved, unbranched, cylindrical, lightly enlarged at the basal cell, lightly narrower at the apex, 1–3(4)-septate, pale brown to brown, smooth-walled. *Conidiogenous cells* 11–13 × 3–4 µm ($\bar{x}$ = 12 × 4 µm, n = 20), monoblastic, terminal, determinate, cylindrical, lightly narrower at the top, brown, smooth-walled. *Conidia* 41–51(–58) × 8–10 µm ($\bar{x}$ = 46 × 9 µm, n = 40), acrogenous, solitary, obclavate, rostrate, tapering towards the apex, straight or slightly curved, pale brown with pale olive-green tinge, hyaline at the apical cells, guttulate, 7–9-distoseptate, smooth-walled, sometimes the 1-3(4) cells at the tip of mature conidia are surrounded by a thin mucilaginous sheath, the sheaths 12–17 µm long, 6–9 µm wide, . *Conidial secession* schizolytic.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H. W. Shen, L1852 (HKAS 131420, holotype); *ibid*., Honghe Prefecture, Yilonghu Lake, 23°40′56.4" N, 101°43'46.8″ E, on submerged decaying wood, 23 February 2023, S. Luan, L2035 (HKAS 132083, paratype).

Notes: Phylogenetic analysis showed that *Sporidesmium yunnanense* clustered as an obvious, independent branch in *Sporidesmium* with 93 % ML and 0.97 PP supported (Figure 4.36). Morphologically, *S. yunnanense* fits the generic concept of *Sporidesmium* with macronematous, mononematous, unbranched, cylindrical, septate conidiophores, monoblastic, terminal conidiogenous cells and solitary, tapering towards the apex, septate conidia with a mucilaginous sheath (Su et al., 2016; Dong, Hyde et al., 2021). Based on morphological characteristics and phylogenetic analysis, we introduce *S. yunnanense* as a new species.



Note a, b Colony on natural substrate. c–e Conidiophores with conidia. f–i Conidia surrounded with mucilaginous sheaths. j Conidium without sheath. Scale bars: c–j = 20 μm.

Figure 4.45 *Sporidesmium yunnanense* (HKAS 131420, holotype)

Diaporthomycetidae families *incertae sedis*

Junewangiaceae J.W. Xia & X.G. Zhang

Notes: *Junewangiaceae* was established by Xia et al. (2017) to accommodate a single genus *Junewangia*, based on phylogenetic analysis. Subsequently, two previous genera, *Dictyosporella* and *Sporidesmiella*, and the new genus, *Jennwenomyces*, were accepted into *Junewangiaceae*, based on multi-gene analyses (Luo et al., 2019; Goh & Kuo, 2020; Dong, Hyde et al., 2021). Currently, the family contains more than 50 species in four genera that occur primarily as saprophytes on a variety of plant debris in terrestrial and freshwater habitats (Xia et al., 2017; Luo et al., 2019; Goh & Kuo, 2020; Crous, Osieck et al., 2021; Dong, Hyde et al., 2021; Hyde et al., 2023).

Sporidesmiella P.M. Kirk

Notes: *Sporidesmiella* was introduced by Kirk (1982) to accommodate two new species, *S. claviformis* and *S. longissima* and several species transferred from *Sporidesmium* and *Endophragmia*, with *S. claviformis* as type species. *Sporidesmiella* is characterized by cuneate to obovoid conidia with fewer septa (Kirk, 1982). Currently, 44 species are included in Species Fungorum (2024), but many species lack molecular sequence data, so their relationships and phylogenetic placement are still unknown. Members of *Sporidesmiella* occur primarily as saprophytes on a variety of plant debris, most of which are reported from terrestrial habitats, and 10 species reported from freshwater habitats (Kirk, 1982; Kuthubutheen & Nawawi, 1993; Ma et al., 2012; Luo et al., 2019; Crous, Osieck et al., 2021; Dong, Hyde et al., 2021; Li, Liu et al., 2021; Xiong et al., 2024).

Sporidesmiella dujuanhuensis H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572096; Figure 4.46

Etymology: "dujuanhuensis" refers to the place where this species was collected, Dujuanhu Lake.

Holotype: HKAS 131790.

Saprobic on submerged decaying wood in the freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, pale brown to brown, hairy, solitary or gregarious, with pale brown glistening conidia at the apex. *Mycelium* mostly immersed, composed of septate, branch, subhyaline to pale brown, smooth-walled hyphae. *Conidiophores* (144–)159–207(–219) × 5–6 µm

($\bar{x}$ = 183 × 6 µm, n = 15), macronematous, mononematous, solitary, erect, flexuous, unbranched, cylindrical, swollen at the base, tapering at the top, 5–8-septate, pale brown to dark brown, smooth-walled. *Conidiogenous cells* (22–)33–46 × 4–5 µm ($\bar{x}$ = 40 × 5 µm, n = 15), polyblastic, integrated, terminal, subcylindrical, percurrent and sympodial proliferations, subhyaline to pale brown, smooth-walled. *Conidia* 24–28 × 10–11 µm ($\bar{x}$ = 26 × 11 µm, n = 40), acropleurogenous, solitary, dry, subcylindrical, clavate, obovoid, smooth-walled, guttulate, medium brown, (3–)4-distoseptate, rounded at the apex, truncate at base, smooth -walled.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from base of conidium within 12 h. Colonies on PDA medium reaching around 1.5 cm diam. after three months at room temperature (around 25 °C) in dark, irregular, dense, pale orange-brown on the forward; pale orange-brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L1854 (HKAS 131790, holotype), ex-type living culture, KUNCC 23–13445.

Notes: Phylogenetic analysis showed that *Sporidesmiella dujuanhuensis* clustered with the previous freshwater species, *S. aquatic*, with low support (Figure 4.47). Comparison of ITS, LSU, and *tef*1-α sequence between *S. dujuanhuensis* and *S. aquatic* showed 1.4% (12/492 bp, including 5 gaps), 6.5% (62/937 bp, including one gap), and 1.4% (12/864 bp) nucleotide base differences, respectively. And comparison of ITS, LSU, and *rpb*2 sequence between *S. dujuanhuensis* and *S. aquatic* showed 2.2% (17/501 bp, including 6 gaps), 0% (0/748 bp), and 1.0% (7/674 bp) nucleotide base differences, respectively. *S. dujuanhuensis* morphologically fits the generic concept of *Sporidesmiella* with medium brown, septate, obovoid conidia and can be distinguished from *S. aquatic* by the smaller conidia (24–28 × 10–11 µm *vs.* 51–59 × 18–22 µm). *S. juncicola* differs from *S. dujuanhuensis* in having short conidiophores (70–100 × 4–5 µm *vs.*159–207 × 5–6 µm), and less septa of conidiophore (2–3-septate *vs.* 5–8-septate). Based on morphological characteristics and phylogenetic analysis, we introduce *S. dujuanhuensis* as a new species. The morphology of *S. juncicola* was observed in culture, which may differ from fruiting bodies produced in the natural

environment. Therefore, *S. dujuanhuensis* and *Sporidesmiella juncicola* are distinguished by molecular data.

Note a, b Colony on natural substrate. c, d Conidiophores. e Conidiogenous cell with developing conidium. f Conidia. g Germinated conidium. h, i Culture on PDA medium. Scale bars: c, d = 60 μm. e = 20 μm. f, g = 10 μm.

Figure 4.46 *Sporidesmiella dujuanhuensis* (HKAS 131790, holotype)

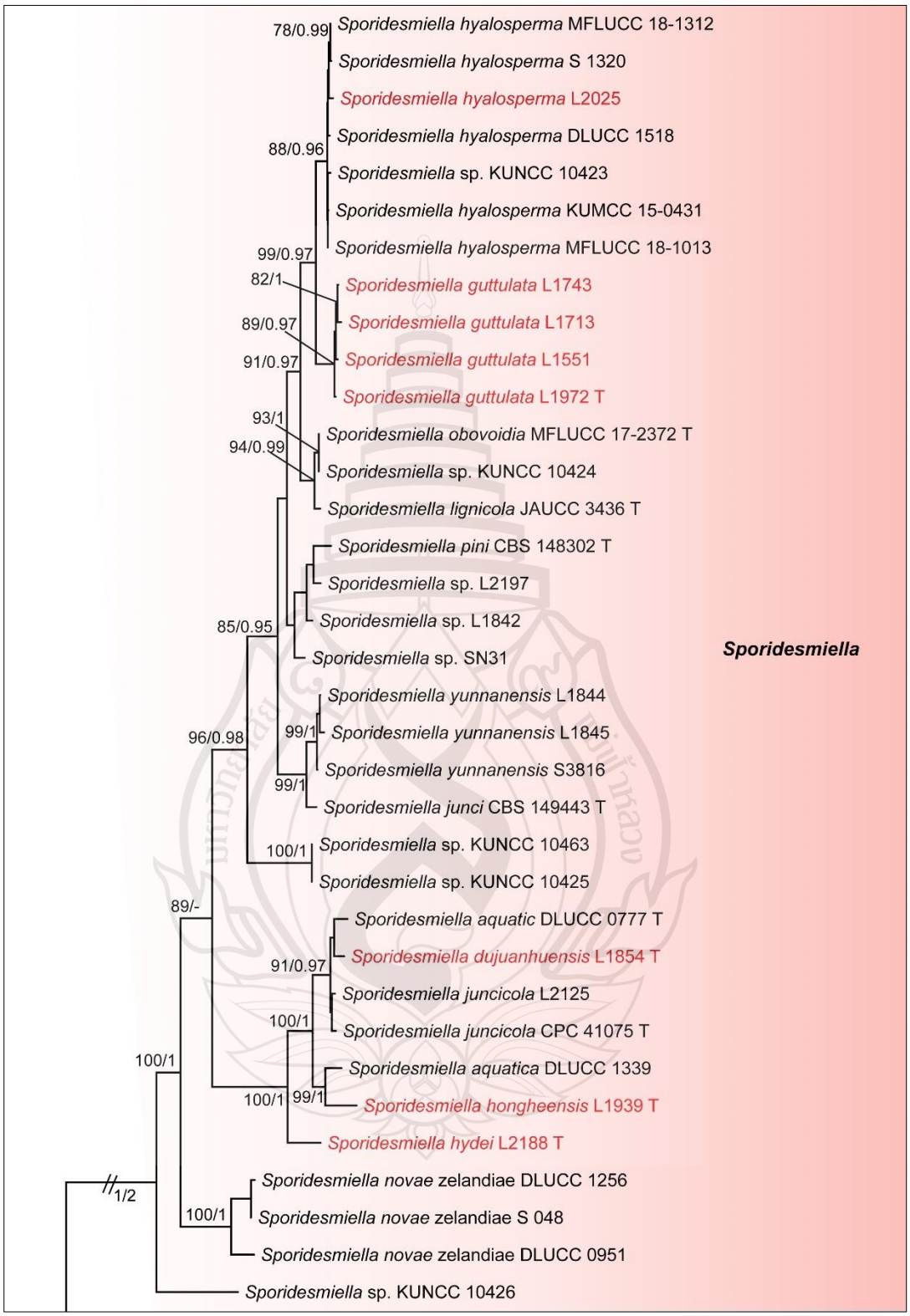
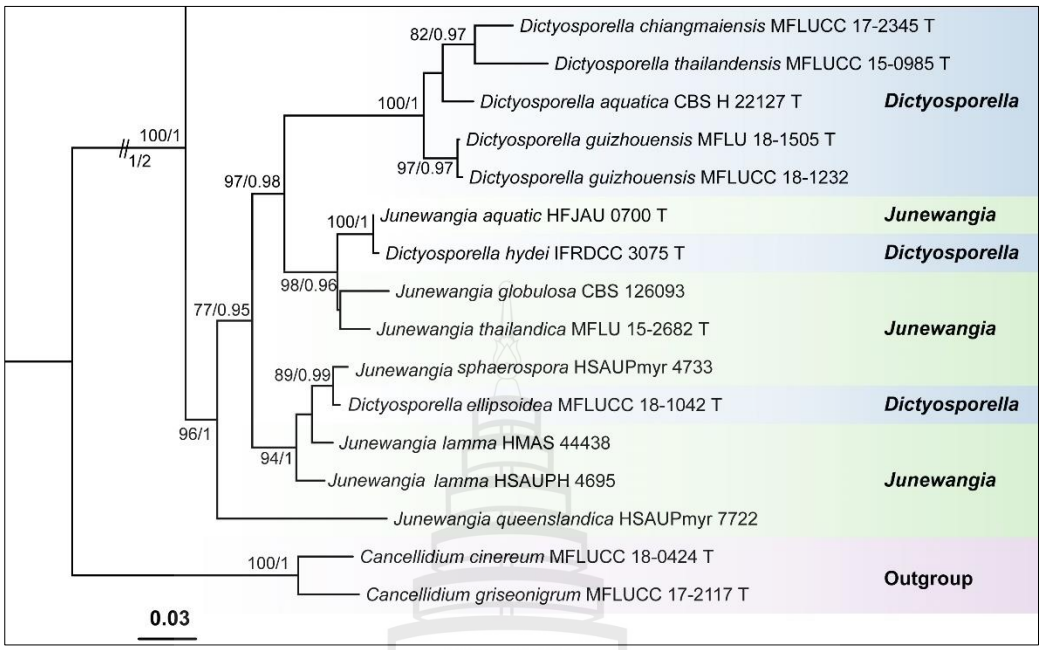


Figure 4.47 Phylogenetic tree of *Sporidesmiella*



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, *rpb*2and *tef*1-α sequence dataset representing *Junewangiaceae*. Fifty-one strains are included in the combined analyses which comprise 3130 characters including gaps (799 characters for LSU, 497 characters for ITS, 954 characters for SSU, 969 characters for *rpb*2, and 865 characters for *tef*1-α). *Cancellidium cinereum* (MFLUCC 18–0424) and *C. griseonigrum* (MFLUCC 17–2117) were selected as the outgroup taxa. Bootstrap support values with a ML greater than 65%, and Bayesian posterior probabilities (PP) greater than 0.95 are given above the nodes, shown as "ML/PP". New species are indicated in red and type strains are indicated by a "T" after the strain number.

Figure 4.47 (continued)

Sporidesmiella guttulata H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572097; Figure 4.48

Etymology: "gattulata" refers to the guttulate conidia of the species.

Holotype: HKAS 131543.

Saprobic on submerged decaying wood in the freshwater lakes. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, pale

brown to brown, hairy, solitary or gregarious, with glistening conidia at the apex. *Mycelium* mostly immersed, composed of septate, branch, subhyaline to pale brown, smooth-walled hyphae. *Conidiophores* (89–)106–134(–145) × 4–5 µm ($\bar{x}$ = 120 × 5 µm, n = 30), macronematous, mononematous, solitary, erect, straight or slightly flexuous, unbranched, cylindrical, swollen at the base, tapering at the top, 4–6-septate, pale brown to dark brown, smooth-walled. *Conidiogenous cells* (21–)30–47(–62) × 4–5 µm ($\bar{x}$ = 39 × 4 µm, n = 30), polyblastic, integrated, terminal, subcylindrical, sympodial, subhyaline to pale brown, smooth-walled. *Conidia* 24–28 × 11–13 µm ($\bar{x}$ = 26 × 12 µm, n = 40), acropleurogenous, solitary, dry, clavate, obovoid, smooth-walled, guttulate, medium brown, (3–)4-distoseptate, rounded at the apex, truncate at base, smooth - walled.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from base of conidium within 12 h. Colonies on PDA medium reaching 1-1.5 cm diam. after two months at room temperature (around 25 °C) in dark, irregular, loose, flocculent, dense, pale brown to brown on the forward; pale brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Dianchi Lake, 24°53′50.48″ N, 102°45′44.51″ E, on submerged decaying wood, 19 February 2023, S. Luan, L1972 (HKAS 131543, holotype), ex-holotype living culture, KUNCC 23–14257; *ibid.*, 24°49′14.15″ N, 102°45′57.58″ E, on submerged decaying wood, 19 February 2023, H.W. Shen, L1743 (HKAS 131676, paratype), ex-paratype living culture, KUNCC 23–14231; *ibid.*, 24°42′30.89″ N, 102°40′29.89″ E, on submerged decaying wood, 19 February 2023, C.C. Ao, L1713 (HKAS 131447), living culture, KUNCC 23–13416; *ibid.*, 24°52′49.72″ N, 102°39′36.82″ E, on submerged decaying wood, 18 February 2023, H.W. Shen, L1551 (HKAS 131592), *living* culture, KUNCC 23–13431.

Notes: Phylogenetic analysis showed that four collections of *Sporidesmiella guttulata* clustered cluster together and form an independent lineage within *Sporidesmiella*, and sisters to *S. hyalosperma* with 99% ML and 0.97 PP support (Figure 4.47). Morphologically, *S. guttulata* fits the concept of *Sporidesmiella* with medium brown, septate, obovoid conidia and resemble *S. hyalosperma* in having unbranched, septate, cylindrical, brown conidiophores, polyblastic, terminal,

sympodial conidiogenous cells, and clavate, obovoid, medium brown, septate conidia with rounded apex and truncated base (Luo et al., 2019). However, *S. guttulata* can be distinguished from *S. hyalosperma* by the larger conidia (24–28 × 11–13 µm *vs.* 17–21 × 8–10 µm). Comparison of ITS, LSU, *rpb*2 and *tef*1-α sequence between *S. guttulata* and *S. hyalosperma* showed 0.4% (4/511 bp, including 2 gaps), 0.3% (3/790 bp, including one gap), 3.3% (22/669 bp), and 1.7% (15/858 bp) nucleotide base differences, respectively. Therefore, based on morphological and phylogenetic evidence, we introduce *S. guttulata* as a new species.

Note a, b Colony on natural substrate. c–e Conidiophores. f, g Conidiogenous cells. h, i Conidia. j Germinated conidium. k, l Culture on PDA medium. Scale bars: c–e = 30 µm. f, g = 15 µm. h–j = 20 µm.

Figure 4.48 *Sporidesmiella gattulata* (HKAS 131543, holotype)

Sporidesmiella hongheensis H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572098; Figure 4.49

Etymology: "hongheensis" refers to the place where this species was collected, Honghe Prefcture.

Holotype: HKAS 132084.

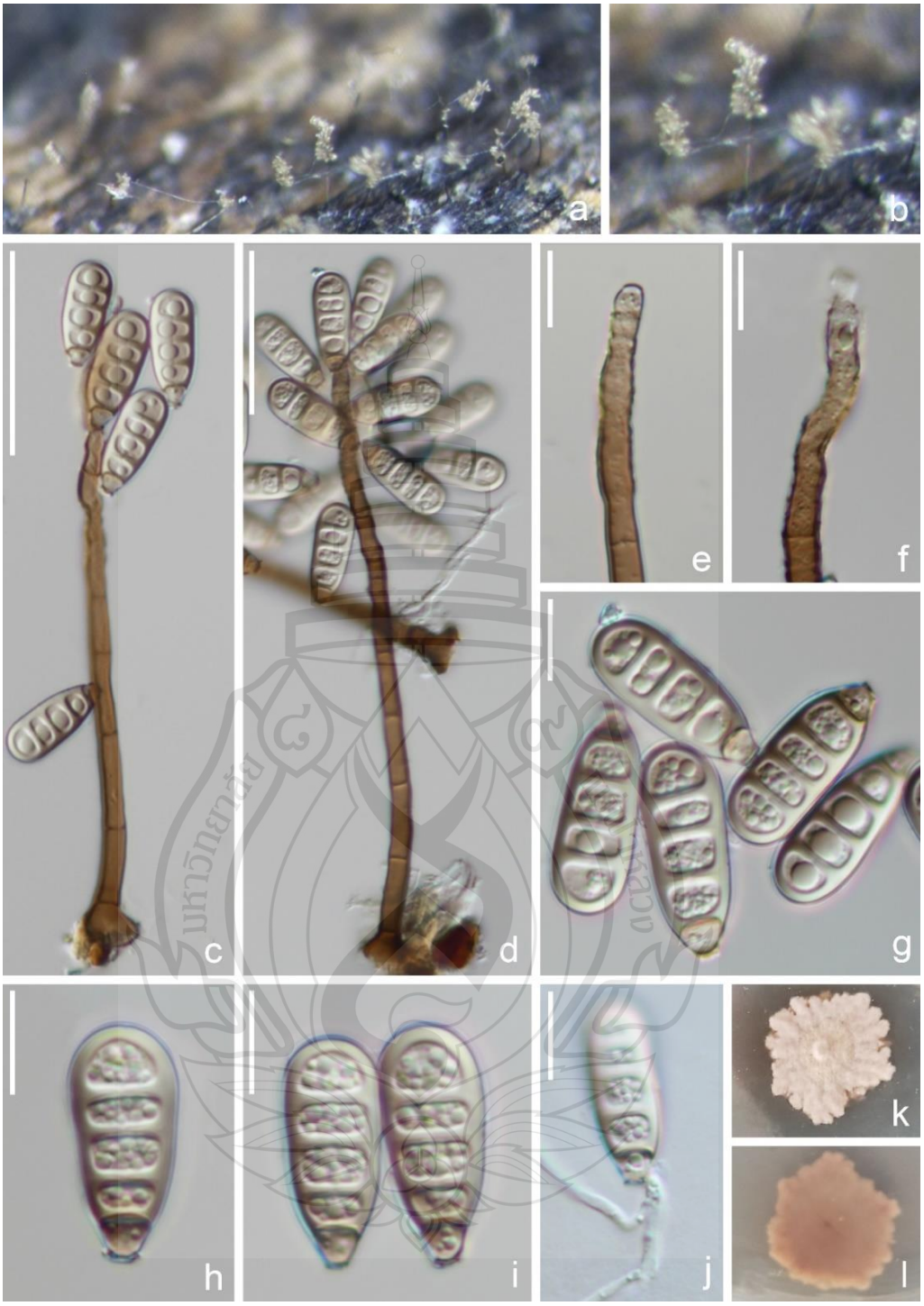
Saprobic on submerged decaying wood in the freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, pale brown to brown, hairy, solitary or gregarious, with pale brown glistening conidia at the apex. *Mycelium* mostly immersed, composed of septate, branch, subhyaline to pale brown, smooth-walled hyphae. *Conidiophores* 103–156(–165) × 4–5 µm ($\bar{x}$ = 129 × 5 µm, n = 20), macronematous, mononematous, solitary, erect, straight or slightly flexuous, unbranched, cylindrical, swollen at the base, tapering at the top, 4–9-septate, pale brown to dark brown, smooth-walled. *Conidiogenous cells* (22–)27–39(–45) × 4–5 µm ($\bar{x}$ = 33 × 4 µm, n = 20), polyblastic, integrated, terminal, subcylindrical, percurrent and sympodial proliferations, subhyaline to pale brown, smooth-walled. *Conidia* 22–26 × 10–11 µm ($\bar{x}$ = 29 × 11 µm, n = 40), acropleurogenous, solitary, dry, subcylindrical, clavate, obovoid, smooth-walled, guttulate, medium brown, 4-distoseptate, rounded at the apex, truncate at base, smooth -walled.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from base of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after two months at room temperature (around 25 °C) in dark, irregular, dense, pale on the forward; pale brown, dense, on the reverse.

Material examined: CHINA, Yunnan Province, Honghe Prefcture, Yilonghu Lake, 23°40′56.4" N, 101°43'46.8″ E, on submerged decaying wood, 23 February 2023, S. Luan, L1939 (HKAS 132084, holotype), ex-holotype living culture, KUNCC 23–13444.

Notes: Phylogenetic analysis showed that *Sporidesmiella hongheensis* clustered with a freshwater strain, DLUCC 1339 of previous species *S. aquatica*, with 99% ML and 1.00 PP support (Figure. 4.47). Strain DLUCC 1339 is a living culture of the paratype specimen MFLU 18–2331 of *S. aquatica*, but there is no valuable illustration or description of the specimen, so morphological comparison impossible. Compared the nucleotide base differences of LSU, *rpb*2 and *tef*1-α sequence data between

S. hongheensis (KUNCC 23–13444) and *S. aquatica* (DLUCC 1339) showed 0.4% (4/1000 bp), 2.4% (19/797 bp), and 3.2% (24/757 bp) differences, respectively. Compared the nucleotide base differences of ITS, LSU and *tef*1-α sequence data between *S. hongheensis* (KUNCC 23–13444) and *S. aquatica* (DLUCC 0777) showed 4.1% (26/492 bp, including 6 gaps), 0.3% (4/1224 bp), and 3.2% (28/867 bp) differences, respectively. Morphologically, *S. hongheensis* is easily distinguished from *S. aquatica* by its smaller conidia (22–26 × 10–11 µm *vs.* 51–59 × 18–22 µm). Therefore, based on the recommendation for establishing new fungi taxa by Jeewon and Hyde (2016) and the unique morphology, *S. hongheensis* was introduced as a new species.



Note a, b Colony on natural substrate. c, d Conidiophores. e, f Conidiogenous cells. g–i Conidia. j Germinated conidium. k, l Culture on PDA medium. Scale bars: c, d = 40 μm. e–j = 10 μm.

Figure 4.49 *Sporidesmiella hongheensis* (HKAS 132084, holotype)

Sporidesmiella hyalosperma (Corda) P.M. Kirk, Trans. Br. mycol. Soc. 79(3): 481 (1982)

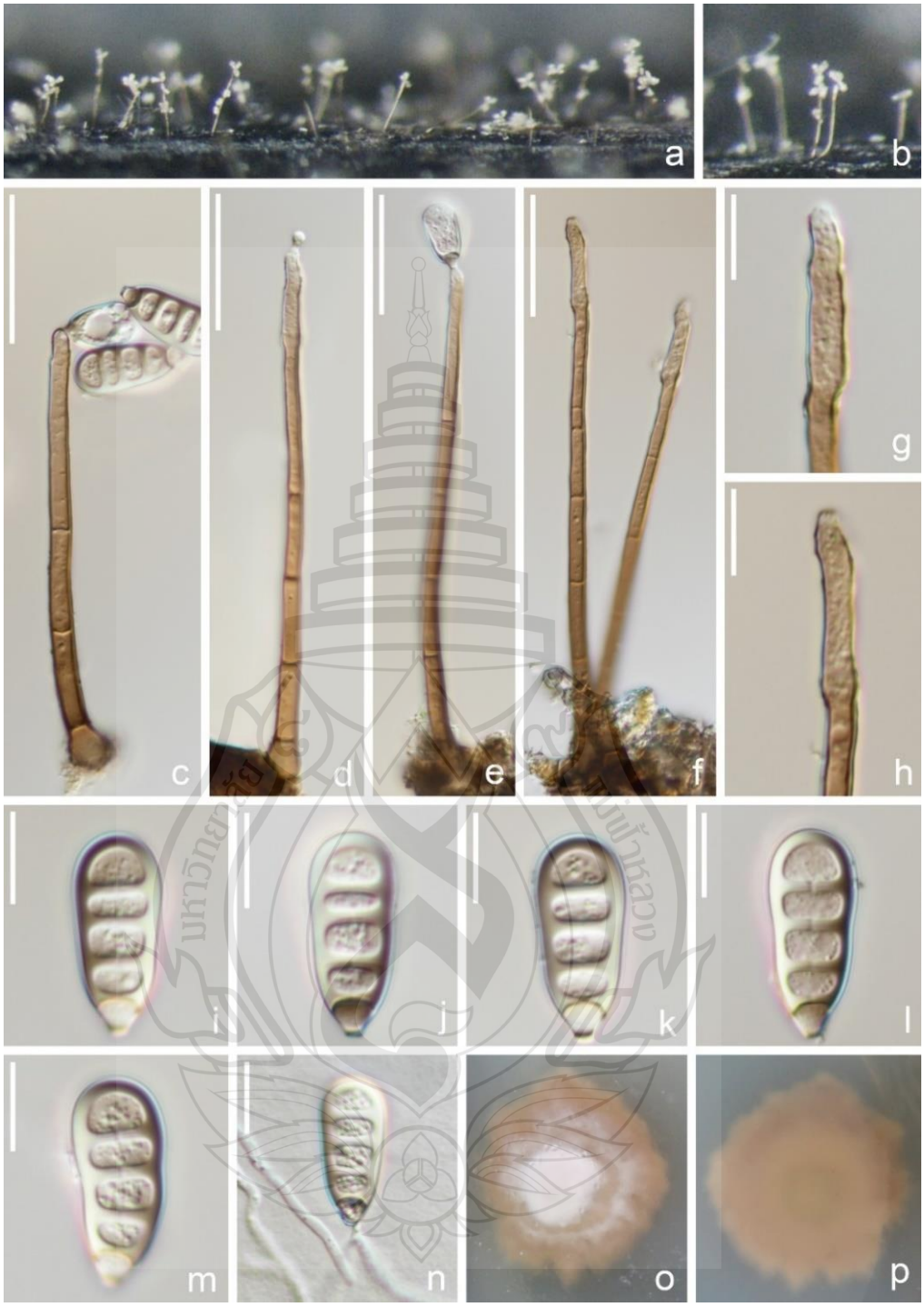
Fungal Names number: FN 110101; *Facesoffungi number*: FoF 05433; Figure 4.50

Saprobic on submerged decaying wood in the freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, pale brown to brown, hairy, solitary or gregarious, with glistening conidia at the apex. *Mycelium* mostly immersed, composed of septate, branch, subhyaline to pale brown, smooth-walled hyphae. *Conidiophores* (87–)101–131(–142) × 4–5 µm ($\bar{x}$ = 116 × 4 µm, n = 15), macronematous, mononematous, solitary, erect, straight or slightly flexuous, unbranched, cylindrical, swollen at the base, tapering at the top, 2–5-septate, pale brown to brown, smooth-walled. *Conidiogenous cells* 36–47(–54) × 3.5–4 µm ($\bar{x}$ = 41 × 4 µm, n = 15), polyblastic, integrated, terminal, subcylindrical, sympodial proliferation, subhyaline to pale brown, smooth-walled. *Conidia* 21–23 × 8.5–10 µm ($\bar{x}$ = 22 × 9 µm, n = 20), acropleurogenous, solitary, dry, clavate or obovoid, smooth-walled, guttulate, medium brown, (3–)4-distoseptate, apex obtuse, truncate at base, smooth, thick-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from basal cell of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after two months at room temperature (around 25 °C) in dark, loose, flocculent, smooth-edged, dense, white to pale brown on the forward; brown to dark pale brown, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′22.76 N, 101°1′6.85″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L2025 (HKAS 132100), living culture, KUNCC 23–13813.

Notes: Phylogenetic analysis showed that our strain KUNCC 23–13813 clustered with other strains of *Sporidesmiella hyalosperma* in a clade with general support (Figure 4.47). Our new collection is morphologically similar to *S. hyalosperma* with macronematous, mononematous, unbranched, cylindrical, septate, pale brown to brown conidiophores, polyblastic, integrated, terminal, sympodial, subhyaline to pale brown conidiogenous cells, and clavate or obovoid, distoseptate, medium brown conidia with obtuse apex and truncated base (Luo et al., 2019). Based on approximate morphological characters and phylogenetic analysis, we identified our new collection as *S. hyalosperma*.



Note a, b Colony on natural substrate. c–f Conidiophores. g, h Conidiogenous cells. i–m Conidia. n Germinated conidium. o, p Culture on PDA medium. Scale bars: c–f = 30 μm. g–n = 10 μm.

Figure 4.50 *Sporidesmiella hyalosperma* (HKAS 132100)

Sporidesmiella hydei H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572101; Figure 4.51

Etymology: "hydei" refers to the renowned mycologist Professor K.D. Hyde, named in recognition of his contributions to mycology on the occasion of his 70th birthday.

Holotype: DLU 2188.

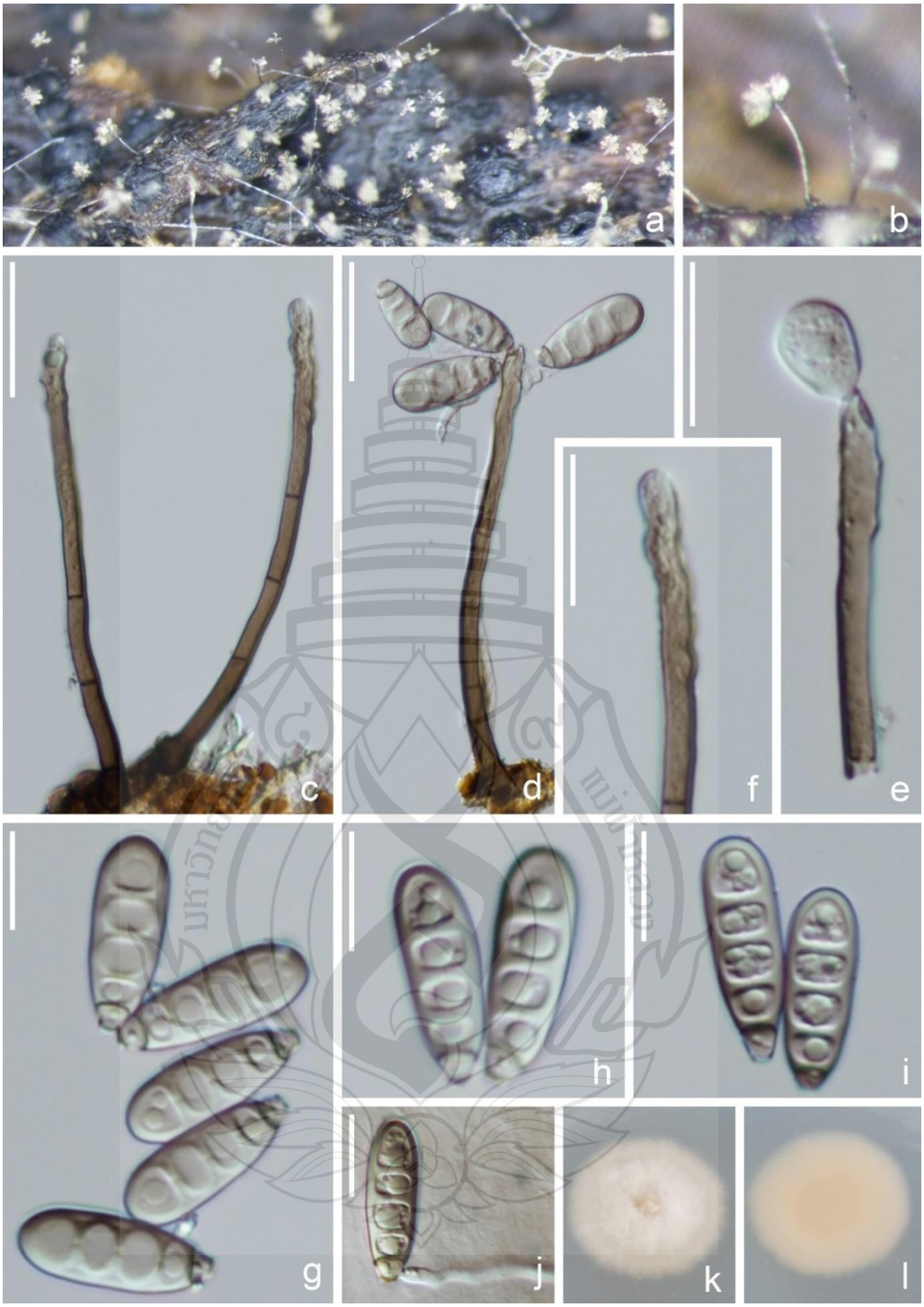
Saprobic on submerged decaying wood in the freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, pale brown to brown, hairy, solitary or gregarious, with pale brown glistening conidia at the apex. *Mycelium* mostly immersed, composed of septate, branch, subhyaline to pale brown, smooth-walled hyphae. *Conidiophores* 109–119 × 4–5 µm ($\bar{x}$ = 115 × 4.5 µm, n = 15), macronematous, mononematous, solitary, erect, straight or slightly flexuous, unbranched, cylindrical, swollen at the base, tapering at the top, 2–4-septate, pale brown to dark brown, smooth-walled. *Conidiogenous cells* (31–)39–50(–55) × 4–5.5 µm ($\bar{x}$ = 45 × 5 µm, n = 15), polyblastic, integrated, terminal, subcylindrical, sympodial proliferation, subhyaline to pale brown, smooth-walled. *Conidia* 28–31 × 10–12 µm ($\bar{x}$ = 29 × 11 µm, n = 40), acropleurogenous, solitary, dry, subcylindrical, clavate, obovoid, smooth-walled, guttulate, medium brown with grayish green tinge, (3–)4-distoseptate, rounded at the apex, truncate at base, smooth -walled.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from base of conidium within 12 h. Colonies on PDA medium reaching 1.5-2 cm diam. after two months at room temperature (around 25 °C) in dark, circular, flocculent, dense, white on the forward; pale creamy, circular, dense, smooth-edged on the reverse.

Material examined: CHINA, Yunnan Province, Yuxi City, Mofanghe Reservoir, 23°41'43.2" N, 101°43'19.8″ E, on submerged decaying wood, 23 February 2023, Z.Q. Zhang, L2188 (DLU 2188, holotype), ex-type living culture, KUNCC 23–14293.

Notes: In the phylogenetic analysis, *Sporidesmiella hydei* clusters with *S. aquatica*, *S. dujuanhuensis*, *S. hongheensis*, and *S. juncicola* in a lineage, and *S. hydei* is at the base of the lineage supported by 100% ML and 1.00 PP support (Figure 4.47). *S. hydei* is similar to other *Sporidesmiella* species, with fusiform conidia. clavate, obovoid to cuneiform conidia, with rounded or coronate apex and truncated base (Ma

et al., 2012; Luo et al., 2019; Dong, Hyde et al., 2021). Morphologically, *S. hydei* resemble *S. juncicola* with subcylindrical to obovoid, distoseptate, medium brown conidia, and approximate conidia size (28–31 × 10–12 µm *vs.* 28–32 ×9–10 µm) (Crous, Osieck et al., 2021), but they have significant molecular differences. Compared the nucleotide base differences of ITS, LSU, and *rpb*2 sequence data between *S. hydei* and *S. juncicola* showed 4.6% (34/517 bp, including 10 gaps), 1.6% (14/789 bp, including one gap), and 4.6% (31/674 bp) differences, respectively. *S. hydei* is also morphologically similar to *S. hongheensis* with subcylindrical to obovoid, distoseptate conidia, but the conidia of *S. hydei* are relatively larger (28–31 × 10–12 µm *vs.* 22–26 × 10–11 µm). In addition, the nucleotide base differences in the ITS, LSU, *tef*1-α and *rpb*2 sequences between them are 4.0% (36/501 bp, including 16 gaps), 1.1% (14/1241 bp, including one gap), 5.9% (59/1004 bp) and 3.3% (29/876 bp), respectively, the significant molecular differences prove that they are different species. Therefore, based on morphological and phylogenetic evidence, we introduce *S. hydei* as a new species.



Note a, b Colony on natural substrate. c, d Conidiophores. e, f Conidiogenous cells. g–i Conidia. j Germinated conidium. k, l Culture on PDA medium. Scale bars: c, d = 30 μm. e, f = 20 μm. g–j = 15 μm.

Figure 4.51 *Sporidesmiella hydei* (DLU 2188, holotype)

Papulosaceae Winka & O.E. Erikss.

Notes: *Papulosaceae* was proposed by Winka and Eriksson (2000) to accommodate *Papulosa amerospora* Kohlm. & Volkm.-Kohlm., based on molecular data and morphology. Currently, four genera, *viz*., *Brunneosporella*, *Fluminicola*, *Papulosa* and *Wongia*, are placed in *Papulosaceae* based on phylogenetic analysis and morphological characteristics (Ranghoo et al., 2001; Reblova 2013; Maharachchikumbura et al., 2015; Khemmuk et al., 2016; Zhang, Dong et al., 2017; Dong, Hyde et al., 2021). Fourteen species were accepted in *Papulosaceae*, almost of which were distributed in *Fluminicola* and *Wongia* (Zhang, Dong et al., 2017; Luo et al., 2019; Bao, Hyde et al., 2021; Dong, Hyde et al., 2021). These species occur mainly as saprophytes on decaying wood in freshwater, marine, and terrestrial habitats, and have also been reported as pathogens of plants (Eriksson & Winka, 1997; Khemmuk et al., 2016; Bao, Hyde et al., 2021; Yu et al., 2024). Members of this family have a restricted distribution and have been reported so far only in Australia (Khemmuk et al., 2016), China (Ranghoo et al., 2001; Luo et al., 2019; Zhang, Shen et al., 2023), Philippines (Wong et al., 1999), Thailand (Zhang, Dong et al., 2017; Bao, Hyde et al., 2021; Dong, Hyde et al., 2021), and USA (Winka & Eriksson, 2000).

Wongia Khemmuk, Geering & R.G. Shivas.

Notes: *Wongia* was established by Khemmuk et al. (2016) to accommodate two sexual plant root pathogenic fungi, *W. garrettii* (*Magnaporthe garrettii*) and *W. griffinii* (*M. griffinii*), with *W. garrettii* as type species. The sexual of *Wongia* is characterized by superficial and immersed ascomata with long or short neck, and asci without apical rings and 3-septate ascospores with dark brown middle cells and pale brown to subhyaline, shorter distal cells (Khemmuk et al., 2016). And the asexual morph is characterized by straight or flexuous, septate, dark brown, unbranched conidiophores, polyblastic, terminal, integrated, denticulate conidiogenous cells, and clavate to fusiform, septate conidia, with dark brown central cells and paler end cells (Luo et al., 2019; Bao, Hyde et al., 2021; Crous, Boers et al., 2022; Zhang, Shen et al., 2023; Yu et al., 2024). Currently, the genus contains seven species, all of which are asexual except for *W. garrettii* and *W. griffinii*. These species occur primarily as saprophytes on plant litter in terrestrial and freshwater habitats, and *W. garrettii* and *W. griffinii* have been reported as root-infecting fungi (Luo et al., 2019; Bao, Hyde et al., 2021; Crous, Boers

et al., 2022; Zhang, Shen et al., 2023; Yu et al., 2024). Three freshwater species, *W. aquatica*, *W. fusiformis* and *W. suae* were reported from lotic habitats in China and Thailand (Luo et al., 2019; Bao, Hyde et al., 2021; Zhang, Shen et al., 2023).

Wongia fusiformis D.F. Bao, H.Y. Su, K.D. Hyde & Z.L. Luo, Journal of Fungi 7(no. 669): 17 (2021)

Fungal Names number: FN 558595; *Facesoffungi number*: FoF 09917; Figure 4.52

Saprobic on submerged decaying wood in the freshwater lakes. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, pale brown, hairy, scattered or gregarious, plentiful. *Mycelium* superficial and immersed, composed of septate, branch, subhyaline to brown, smooth-walled hyphae. *Conidiophores* (69–)82–124(–136) × 3.5–4 µm ($\bar{x}$ = 103 × 3.8 µm, n = 15), macronematous, mononematous, solitary, erect, mostly flexuous, unbranched, cylindrical, swollen at the base, tapering at the top, septate, pale brown to dark brown, smooth-walled. *Conidiogenous cells* polyblastic, denticulate, integrated, terminal, sympodial proliferation, subhyaline to pale brown, smooth-walled. *Conidia* 16–18 × 4.5–5 µm ($\bar{x}$ = 17 × 5 µm, n = 40), acropleurogenous, solitary, dry, fusiform, clavate, 2–4(–5)-septate, with rounded apex and acute base, pale brown, guttulate, smooth-walled.

Culture characteristics: Conidia germinating on PDA medium and germ tubes produced from both ends of conidium within 12 h. Colonies on PDA medium reaching around 1.5-2 cm diam. after three weeks at room temperature (around 25 °C) in dark, circular, flocculent, dense, pale brown to brown on the forward; circular, pale brown to dark brown, dense on the reverse.

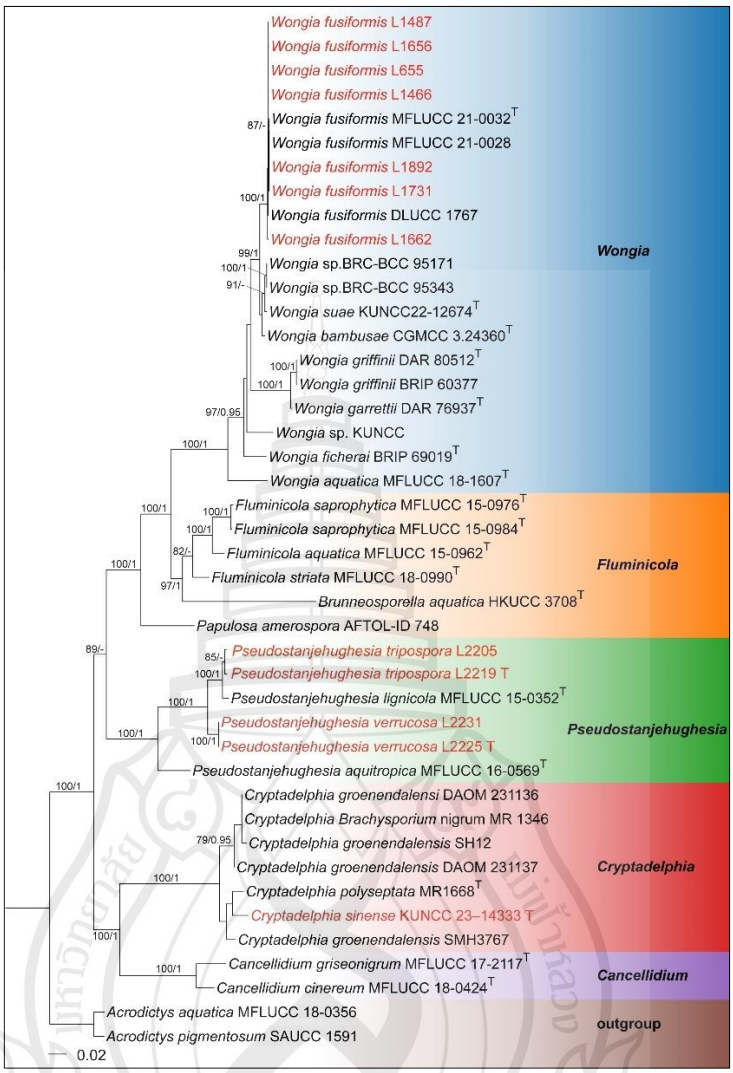
Material examined: CHINA, Yunnan Province, Yuxi City, Qiluhu Lake, 24°08′42" N, 102°43′11" E, on submerged decaying wood, 12 July 2021, Y.K. Jiang, L655 (HKAS 131467); *ibid.*, Kunming City, Dianchi Lake, 24°42′30.89″ N, 102°40′29.89″ E, on submerged decaying wood, 18 February 2023, C.C. Ao, L1487 (HKAS 132076), living culture, KUNCC 23–13071; *ibid.*, 24°53′50.48″ N, 102°45′44.51″ E, on submerged decaying wood, 19 February 2023, S. Luan, L1731 (HKAS 131821), living culture, KUNCC 23–14222; *ibid.*, 24°46′24.49″ N, 102°43′42.26″ E, on submerged decaying wood, 19 February 2023, Z.Q. Zhang, L1892

(HKAS 131791), living culture, KUNCC 23–13453; *ibid.*, Honghe Prefecture, Yilonghu Lake, 23°40′28.95″ N, 102°36′30.00″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L1466 (HKAS 131409), living culture, KUNCC 23–13040; *ibid.*, on submerged decaying wood, 22 February 2023, H.W. Shen, L1662 (HKAS 131487), living culture, KUNCC 23–13126; *ibid.*, 23°39′18.95″ N, 102°32′57.19″ E, on submerged decaying wood, 22 February 2023, H.W. Shen, L1656 (HKAS 131491), living culture, KUNCC 23–13125.

Notes: Based on an initial BLASTn search of the NCBI database, seven of our new collections exhibit high similarity to the existing species *Wongia fusiformis*. Morphologically, our collections match the characteristics of *W. fusiformis*, including the color, size, and shape of conidiophores, conidiogenous cells, and conidia. In phylogenetic analyses, seven of our collections (HKAS 131467, KUNCC 23–13071, KUNCC 23–14222, KUNCC 23–13453, KUNCC 23–13040, KUNCC 23–13126, KUNCC 23–13125) cluster with *W. fusiformis* (MFLUCC 21–0032, MFLUCC 21–0028, and DLUCC 1767) (Figure 4.53). Excluding gaps, no nucleotide differences were observed in the comparison of the ITS (536 bp) and LSU (775 bp) regions between our collection (KUNCC 23–13453) and *W. fusiformis* (MFLUCC 21–0032). Based on these results, we identify our isolate as *W. fusiformis*, following to the guidelines established by Chethana et al. (2021).

Note a Colony on natural substrate. b–d Conidiophores. e, f Conidiogenous cells. g–i Conidia. j Germinated conidium. k, l Culture on PDA medium. Scale bars: b–d = 30 μm. e, f = 20 μm. g–j = 10 μm.

Figure 4.52 *Wongia fusiformis* (HKAS 131487)



Note Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU, *tef*1-α and *rpb*2 sequence dataset representing Diaporthomycetidae families *incertae sedis*. Forty-three strains are included in the combined analyses which comprise 4029 characters including gaps (817 characters for LSU, 509 characters for ITS, 981 characters for SSU, 853 characters for *tef*1-α, and 869 characters for *rpb*2). *Acrodictys aquatica* (MFLUCC 18-0356) and *A. pigmentosum* (SAUCC 1591) were selected as the outgroup taxa. Bootstrap support values with a ML greater than 65%, and Bayesian posterior probabilities (PP) greater than 0.95 are given above the nodes, shown as "ML/PP". New species are indicated in red and type strains are indicated by a "T" after the strain number.

Figure 4.53 Phylogenetic tree of Diaporthomycetidae families *incertae sedis*

Pseudostanjehughesiaceae K.D. Hyde & Hongsanan

Pseudostanjehughesiaceae was established by Hyde et al. (2021) to accommodate the monophyletic genus *Pseudostanjehughesia*, based on both phylogeny and divergence time. Currently, *Pseudostanjehughesiaceae* accommodates two species, both of which are saprophytes occurring on woody substrates in freshwater habitats (Yang, Maharachchikumbura et al., 2018; Luo et al., 2019).

Pseudostanjehughesia J. Yang & K.D. Hyde

Notes: *Pseudostanjehughesia*, an aquatic genus introduced by Yang et al. (2018b) to accommodate a species, *P. aquitropica*, with fusiform or obclavate, septate, mid to dark brown conidia arising from terminal, integrated, monoblastic, cylindrical, brown from conidiogenous cells from freshwater stream in Thailand (Yang, Maharachchikumbura et al., 2018). Subsequently, a second freshwater species, *P. lignicola*, was introduced from a stream in Cangshan Mountain, Yunnan Province, China. *P. lignicola* has ovoid, multi-euseptate, verrucose, dark brown conidia, solitary or in group of 1–3. Currently, the genus includes two species, both of which are saprophytes, growing on decaying woody substrates in freshwater habitats in Asia (Yang, Maharachchikumbura et al., 2018; Luo et al., 2019). In the present study, two additional species were introduced from plateau lakes in Yunnan Province, China, based on morphological and phylogenetic analyses.

Pseudostanjehughesia tripospora H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572099; Figure 4.54

Etymology: "guttulata" refers to guttulate conidia of the species.

Holotype: HKAS 131767.

Saprobic on submerged decaying wood in the freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, dark brown, punctiform, scattered or gregarious, glistening. *Mycelium* superficial and immersed, composed of septate, branch, subhyaline to brown, smooth-walled hyphae. *Conidiophores* micronematous, subhyaline to brown, smooth-walled. *Conidiogenous cells* arise directly from mycelium, (4–)6–14(–17) × 3–4 µm ($\bar{x}$ = 10 × 4 µm, n = 15), monoblastic, integrated, terminal, subcylindrical, irregular, flexuous, subhyaline to pale brown, smooth-walled. *Conidia* (50–)55–68(–72) × 17–19 µm ($\bar{x}$ = 61 × 18 µm, n = 40), acrogenous, solitary, dry, obpyramidal, rigid, friable, 2–3 columns of cells arise from

the basal cell and grow in three different directions; basal cell globose to subglobose, verrucous, guttulate; columns of cells, ovoid to broad-obclavate, black, subhyaline at the apex, 8–10-septate, verrucose, constricted at the septa, easily fractured from the basal cell under the pressure of the coverslip, truncate, guttulate.

Culture characteristics: Conidia germinating on PDA medium and germ tube produced from base of conidium within 12 h. Colonies on PDA medium reaching around 2 cm diam. after two months at room temperature (around 25 °C) in dark, circular, flocculent, dense, brown to dark brown on the forward; circular, dark brown, dense on the reverse.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32'15.6" N, 100°1′30.00″ E, on submerged decaying wood, 24 February 2023, Z.Q. Zhang, L2219 (HKAS 131767, holotype), ex-holotype living culture, DLUCC 2219; *ibid.*, on submerged decaying wood, 24 February 2023, Z.Q. Zhang, L2205 (HKAS 131769, paratype).

Notes: *Pseudostanjehughesia guttulata* is morphologically similar to *P. lignicola*; however, *P. guttulata* is distinguished by its subobtuse apex and larger conidia [(50–)55–68(–72) × 17–19 µm *vs.* 51–62 × 16–22 µm]. It exhibits obpyramidal, rigid, friable columns of cells, arising from the basal cell in 2–3-columns and growing in three distinct directions, with globose to subglobose, verrucous, guttulate basal cells; the conidia are ovoid to broad-obclavate, 8–10-septate, and verrucose. In contrast, *P. lignicola* typically has solitary or grouped conidia (2–3) that are ovoid and slightly curved. Phylogenetic analysis positions *P. guttulata* as a sister species to *P. lignicola* (MFLUCC 15–0352) with 100%ML and 1.00 PP support (Figure 4.53). Nucleotide sequence comparisons, excluding gaps, reveal a 1.5% difference (7/476 bp) in ITS, 0.3% (2/787 bp) in LSU, 2% (14/783 bp) in *rpb*2, and 1.3% (11/857 bp) in *tef*1-α between *P. guttulata* and *P. lignicola*. Based on these morphological and genetic distinctions, we propose *P. guttulata* as a novel species, adhering to the criteria established by Jeewon and Hyde (2016) and Chethana et al. (2021).

Note a, b Colony on natural substrate. c Mycelium on the substrate surface. d–i Conidiogenous cells with developing conidia. j–l Conidia. m Column of conidia cells fractured from the basal cell. n Germinated conidium. o, p Culture on PDA medium. Scale bars: c–i = 10 μm. j–n = 30 μm.

Figure 4.54 *Pseudostanjehughesia tripospora* (HKAS 131767, holotype)

Pseudostanjehughesia verrucosa H.W. Shen, K.D. Hyde & Z.L. Luo, ***sp. nov.***

Fungal Names number: FN 572100; Figure 4.55

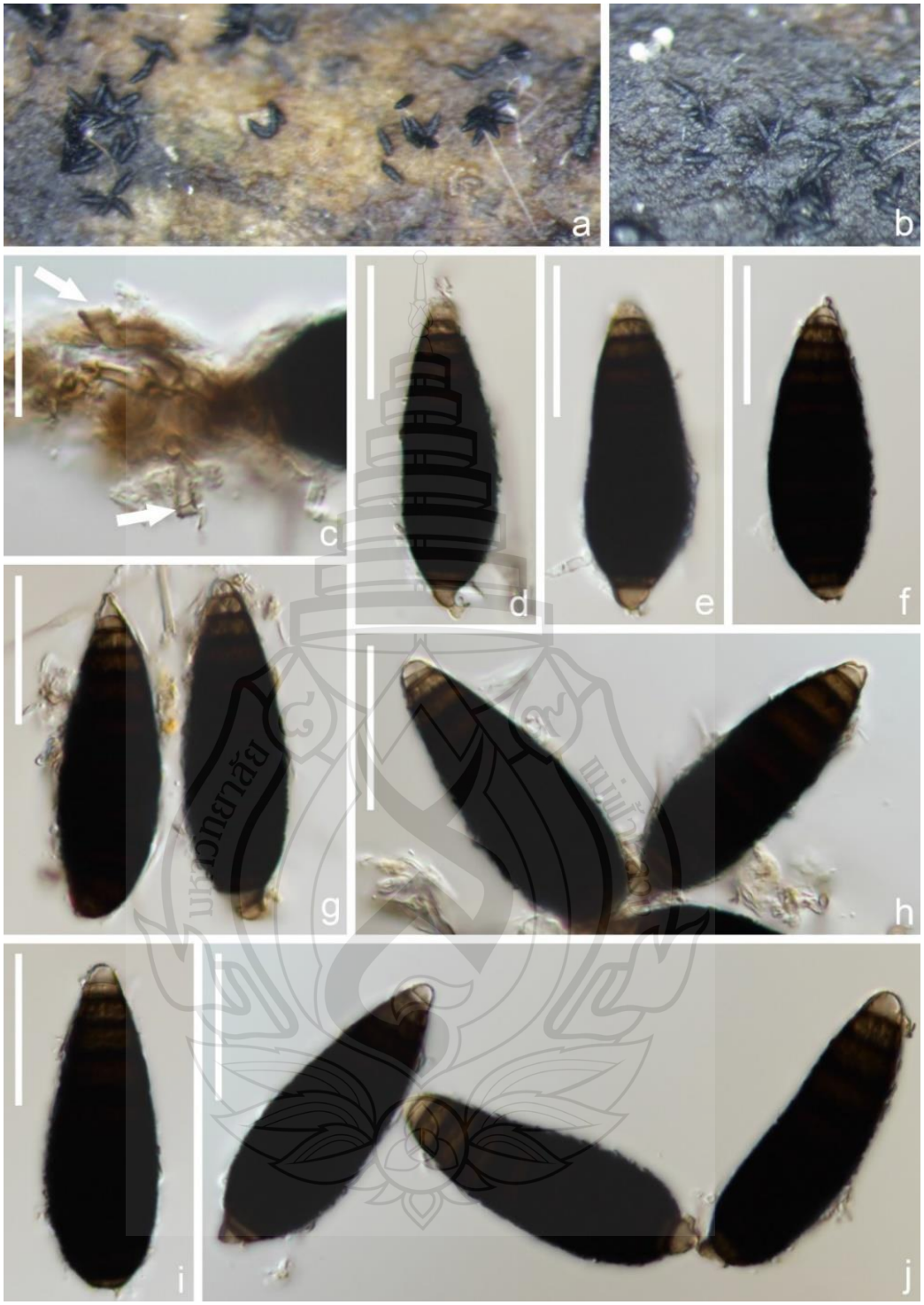
Etymology: "verrucosa" refers to verrucose conidia of the species.

Holotype: HKAS 132045.

Saprobic on submerged decaying wood in the freshwater lake. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* on natural substrate superficial, effuse, dark brown, punctiform, scattered or gregarious, glistening. *Mycelium* superficial and immersed, composed of septate, branch, subhyaline to brown, smooth-walled hyphae. *Conidiophores* micronematous, subhyaline to brown, smooth-walled. *Conidiogenous cells* arise directly from mycelium, monoblastic, terminal, cylindrical, unbranched, subhyaline to pale brown, smooth-walled. *Conidia* (56–)60–66 × 20–22 µm ($\bar{x}$ = 63 × 21 µm, n = 25), acrogenous, solitary, dry, ovoid to broad-obclavate, with a subhyaline to pale brown basal cell, rigid, bark brown to black, subhyaline at the apex, 8–9-septate, verrucous, guttulate, constricted at the septa, truncate at the base.

Material examined: CHINA, Yunnan Province, Pu'er City, Dujuanhu Lake, 24°32′30.44" N, 101°1′39.51″ E, on submerged decaying wood, 24 February 2023, H.W. Shen, L2231 (HKAS 132045, holotype), ex-holotype living culture, KUNCC 23–14310; *ibid.*, on submerged decaying wood, 24 February 2023, H.W. Shen, L2225 (HKAS 131774, paratype), ex-paratype living culture, KUNCC 23–14302.

Notes: *Pseudostanjehughesia verrucosa* is morphologically similar to *P. lignicola*; however, it is distinguished by its larger conidia [(56–)60–66 × 20–22 µm *vs.* 51–62 × 16–22 µm]. *Pseudostanjehughesia verrucosa* exhibits ovoid to broad-obclavate conidia with a subhyaline to pale brown basal cell, which are rigid, 8–9-septate, verrucous, and guttulate. In contrast, *P. lignicola* typically has solitary or grouped conidia (2–3) that are ovoid and slightly curved. Phylogenetic analysis positions *P. verrucosa* as a sister species to *P. lignicola* (MFLUCC 15–0352) with 100% ML and 1.00 PP support (Figure 4.53). Nucleotide sequence comparisons, excluding gaps, reveal a 5.5% difference (26/477 bp) in ITS, 2.8% (22/789 bp) in LSU, 4.3% (28/678 bp) in *rpb*2, and 1.9% (16/857 bp) across *tef*1-α between *P. verrucosa* and *P. lignicola*. Based on these morphological and genetic distinctions, we propose *P. verrucosa* as a novel species, adhering to the criteria established by Jeewon and Hyde (2016) and Chethana et al. (2021).



Note a, b Colony on natural substrate. c Conidiogenous cells (arrows indicate conidiogenous cells). d–j Conidia. Scale bars: c = 20 μm. d–j = 30 μm.

Figure 4.55 *Pseudostanjehughesia verrucosa* (HKAS 132045, holotype)

4.4 Discussion

Sordariomycetes is one of the most important groups of freshwater fungi, containing the largest number of freshwater fungal species (Calabon et al., 2022). A systematic study of freshwater *Sordariomycetes* was conducted Luo et al. (2019) compiled all known freshwater *Sordariomycetes* species and provided phylogenetic, taxonomic, and ecological information. Since then, the taxonomy and phylogenetics of *Sordariomycetes* have been continuously improved, with new taxa being continuously established (Hyde et al., 2021; Bao et al., 2023; Yang et al., 2023). In this study, we collected submerged wood specimens from several plateau lakes (including, Cibihu, Dianchi, Dujuanhu, Erhai, Fuxianhu, Luguhu, Qiluhu, Xihu, Xingyunhu, Yangzonghai and Yilonghu lakes) and studied the lignicolous freshwater fungi based on morphological and phylogenetic analyses. Phylogenetic and morphological analyses identified 47 species, including 24 new species, 6 new freshwater habitats records, 2 new records in China, and 15 known species. These species are distributed across 9 families and 23 genera within the orders *Amphisphaeriales*, *Chaetosphaeriales*, *Pleurotheciales*, *Pseudodactylariales*, *Rhamphoriales*, *Savoryellales*, *Sporidesmiales*, and *Diaporthomycetidae* families *incertae sedis*.

CHAPTER 5

SPECIES COMPOSITION OF LIGNICOLOUS FRESHWATER FUNGI IN DIANCHI, DUJUANHU, YANGZONGHAI, XINGYUNHU LAKES

This chapter provides an analysis and specieslist of species composition in Dianchi, Dujuanhu, Yangzonghai, Yilonghu lakes in Yunnan, China. Systematic sampling and investigations were conducted in these lakes, species and phylogenetic data of lignicolous freshwater fungi through morphological and phylogenetic analysis. Based on the existing data, a total of 56 species were found in Dianchi Lake, belonging to 35 genera, 29 families, 16 orders in *Dothideomycetes*, *Eurotiomycetes* and *Sordariomycetes*; 50 species were discovered in Ynagzonghai Lake, comprising 5 sexual species (ascomycetes) and 45 asexual species (38 hyphomycetes and 7 coelomycetes), they are belonging to 31 genera, 24 families, 16 orders under *Dothideomycetes*, *Eurotiomycetes*, *Orbiliomycetes* and *Sordariomycetes*; 46 species were discovered in Yilonghu Lake, comprising 4 sexual species (ascomycetes) and 42 asexual species (33 hyphomycetes and 9 coelomycetes), they are belonging to 29 genera, 20 families, 11 orders under *Dothideomycetes* and *Sordariomycetes*; and 66 species were discovered in Dujuanhu Lake, comprising 9 sexual species (ascomycetes) and 57 asexual species (hyphomycetes), they are belonging to 48 genera, 36 families, 23 orders under *Dothideomycetes*, *Eurotiomycetes*, *Leotiomycetes* and *Sordariomycetes*. The species composition of each lake was analyzed and compared with related studies, and the problems and challenges of current research were discussed.

5.1 Sampling Site

Submerged decaying woods were collected from four plateau lakes (Dianchi lake, Dujuanhu lake, Yangzonghai lake and Yilonghu lake) on February 18-24, 2023 (Figure 5.1).

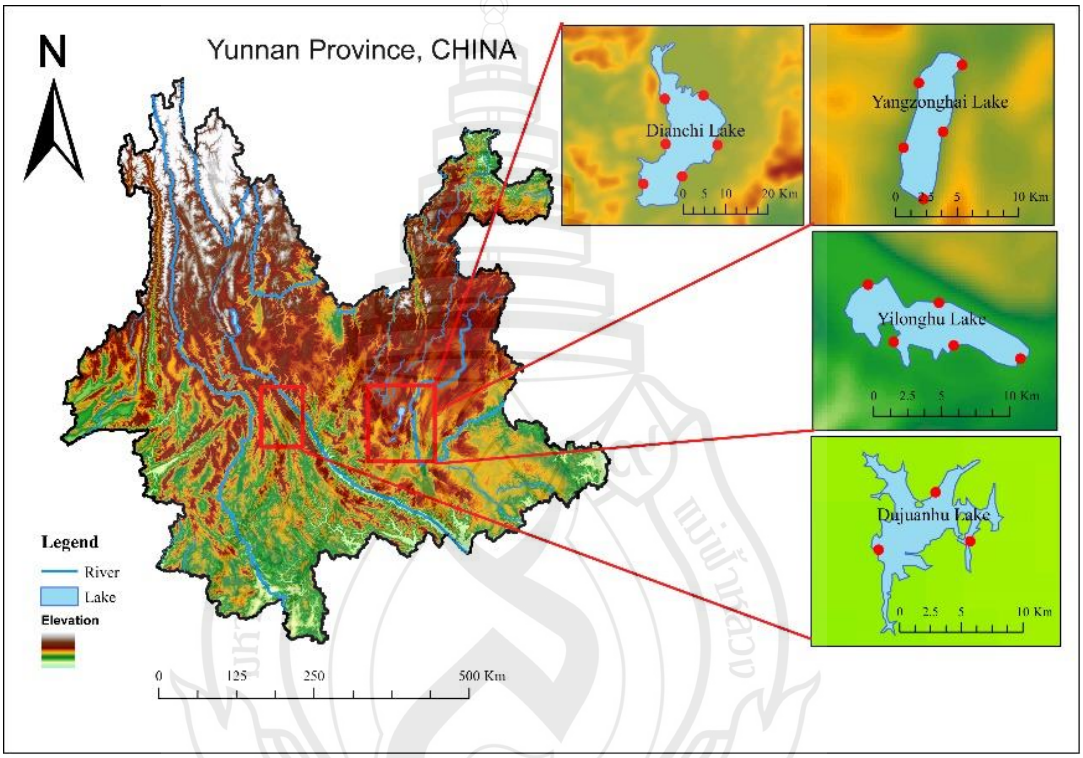


Figure 5.1 Sampling points

5.2 Materials and Methods

Sample collection, processing and cultivation; morphological studies and isolation; DNA extraction, PCR amplification and sequencing; phylogenetic analyses are carried out according to the steps in chapter 2.

5.3 Data Analysis

The ITS and LSU sequences of all strains were obtained and analyzed using maximum likelihood analysis to determine their taxonomic placement. Detailed information on the strains was statistically processed using Microsoft Excel software. Species correlation analysis was conducted on the online platform SRplot: https://www.bioinformatics.com.cn/srplot (Tang et al., 2023).

5.4 Taxonomic Composition of Lignicolous Freshwater Fungi in Dianchi Lake

170 submerged wood specimens were collected from Dianchi Lake on February 18-19, 2023. After two weeks of incubation, the lignicolous freshwater fungi colonies were observed using an Optec SZ 760 compound stereomicroscope. Following morphological examination, 186 lignicolous freshwater fungi strains were obtained. Phylogenetic analysis combined with morphological characteristics showed that they were classified into 57 species, comprising 7 sexual species (ascomycetes) and 50 asexual species (41 hyphomycetes and 9 coelomycetes), they are belonging to 35 genera, 29 families, 16 orders under *Dothideomycetes*, *Eurotiomycetes* and *Sordariomycetes* (Table 5.1). 43.7% of the species were distributed in *Lentitheciaceae* (10.5%), *Neopyrenochaetaceae* (10.5%), *Myrmecridiaceae* (8.7%), *Pleurotheciaceae* (7%) and *Sporidesmiaceae* (7%). Common asexual genera are *Apiospora*, *Halobyssothecium*, *Myrmecridium*, *Neopyrenochaeta*, *Periconia*, *Sporidesmium*. Dominant species included *Periconia thysanolaenae* (13.4%), *Myrmecridium schulzeri* (11.2%), *Codinaea paniculata* (9.6%) and *Wongia fusiformis* (9.6%).

Table 5.1 The occurrence of lignicolous freshwater fungi in Dianchi Lake

Taxa	Frequency	Stage of lifecycle	Remark
Dothideomycetes			
Pleosporales			
Dictyosporiaceae			
Dictyocheirospora rotunda	4	H	Known
Digitodesmium aquaticum	4	H	Known
Lentitheciaceae			
Halobyssothecium caohaiense	2	C	Known
Halobyssothecium kunmingense	1	C	Known
Halobyssothecium phragmitis	1	C	Known
Setoseptoria arundelensis	2	A	Known
Tingoldiago graminicola	3	A	Known
Towyspora aestuari	3	C	Known
Leptosphaeriaceae			
Alternaria sp.	2	H	Undet.
Lindgomycetaceae			
Aquimassariosphaeria aquatica	3	H	New
Aquimassariosphaeria typhicola	1	A	Known
Neopyrenochaetaceae			
Neopyrenochaeta acicola	1	C	Known
Neopyrenochaeta annellidica	2	C	Known
Neopyrenochaeta maesuayensis	2	C	Known
Neopyrenochaeta sp.	1	C	Undet.
Paradictyoarthriniaceae			
Paradictyoarthrinium hydei	1	H	Known
Periconiaceae			
Periconia cookei	2	H	Known
Periconia thysanolaenae	25	H	Known
Periconia yunnanensis sp.nov.	4	H	New
Paraphoma ledniceana	1	C	Known

Table 5.1 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Teichosporaceae			
Floricola aquatica	1	A	New
Torulaceae			
Dendryphion europaeum	3	H	Known
Torula sp.2	1	H	Undet.
Dothideomycetes* genera *incertae sedis			
Diplocladiella scalaroides	1	H	Known
Eurotiomycetes			
Chaetothyriales			
Herpotrichiellaceae			
Thysanorea lotorum	1	H	Known
Amphisphaeriales			
Apiosporaceae			
Apiospora arundinis	5	H	Known
Apiospora guangdongensis	2	H	Known
Apiospora marii	7	H	Known
Chaetosphaeriales			
Chaetosphaeriaceae			
Codinaea paniculata	18	H	Known
Conioscyphales			
Conioscyphaceae			
Conioscypha yunnanensis	2	H	Known
Distoseptisporales			
Distoseptisporaceae			
Distoseptispora euseptata	1	H	Known
Glomerellales			
Reticulascaceae			
Cylindrotrichum clavatum	1	H	Known

Table 5.1 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Hypocreales			
Stachybotryaceae			
Stachybotrys chartarum	2	H	Known
Magnaporthales			
Ophioceraceae			
Ophioceras sp.	1	A	Undet.
Magnaporthales			
Pseudohalonectriaceae			
Pseudohalonectria lignicola	6	A	Known
Microascales			
Halosphaeriaceae			
Aniptodera margarition	1	A	Known
Myrmecridiales			
Myrmecridiaceae			
Myrmecridium sambuci	2	H	Known
Myrmecridium schulzeri	21	H	Known
Myrmecridium sp.1	2	H	Undet.
Myrmecridium sp.2	1	H	Undet.
Neomyrmecridium aquaticum	1	H	Known
Pleurotheciales			
Pleurotheciaceae			
Phaeoisaria clematidis	3	H	Known
Phaeoisaria sedimenticola	1	H	Known
Pleurotheciella aquatica	1	H	Known
Pleurotheciella nilotica	1	H	Known
Savoryellales			
Savoryellaceae			
Dematiosporium muriforme	2	H	New
Dematiosporium sp.	1	H	Undet.
Savoryella claviformis	2	H	Known

Table 5.1 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Sporidesmiales			
Sporidesmiaceae			
Sporidesmium dianchiense	1	H	New
Sporidesmium distoseptatum	1	H	New
Sporidesmium guizhouense	1	H	Known
Sporidesmium hydei	1	H	New
Sporidesmium kunmingense	1	H	New
Sporidesmium nujiangense	1	H	Known
Xylariales			
Xylariales* genera *incertae sedis			
Circinotrichum sp.	1	H	Undet.
Diaporthomycetidae* families *incertae sedis			
Papulosaceae			
Wongia fusiformis	18	H	Known
Junewangiaceae			
Sporidesmiella guttulata	4	H	New

Note In the "Stage of lifecycle" column, "A" indicates ascomycetes, the sexual stage; "C" indicates coelomycetes, the asexual stage; "H" indicates hyphomycetes, the asexual stage. In the Remarks column, "New" indicates a new species, "Known" indicates a known species, and "Undet." indicates that the species has not been identified to the species level.

5.5 Taxonomic Composition of Lignicolous Freshwater Fungi in Yangzonghai Lake

160 submerged wood specimens were collected from Yangzonghai Lake on February 19-20, 2023. After two weeks of incubation, the lignicolous freshwater fungi colonies were observed using an Optec SZ 760 compound stereomicroscope. Following

morphological examination, 152 lignicolous freshwater fungi strains were obtained. Phylogenetic analysis combined with morphological characteristics showed that they were classified into 50 species, comprising 5 sexual species (ascomycetes) and 45 asexual species (38 hyphomycetes and 7 coelomycetes), they are belonging to 31 genera, 24 families, 16 orders under *Dothideomycetes*, *Eurotiomycetes*, *Orbiliomycetes* and *Sordariomycetes* (Table 5.2). 48% of the species were distributed in *Dictyosporiaceae* (14%), *Lentitheciaceae* (14%), *Nectriaceae* (8%), *Herpotrichiellaceae* (6%) and *Periconiaceae* (6%). Common genera are *Dictyocheirospora*, *Halobyssothecium*, *Thysanorea*. Dominant species included *Pseudohalonectria lignicola* (15.1%) and *Dictyocheirospora rotunda* (7.8%).

Table 5.2 The occurrence of lignicolous freshwater fungi in Yangzonghai Lake

Taxa	Frequency	Stage of lifecycle	Remark
Dothideomycetes			
Botryosphaeriales			
Botryosphaeriaceae			
Dothiorella acericola	1	H	Known
Pleosporales			
Dictyosporiaceae			
Dictyocheirospora heptaspora	8	H	Known
Dictyocheirospora multiappendiculata	3	H	Known
Dictyocheirospora pseudomusae	1	H	Known
Dictyocheirospora rotunda	12	H	Known
Dictyocheirospora sp.	1	H	Undet.
Dictyocheirospora yunnanensis	1	H	New
Digitodesmium aquaticum	3	H	Known
Lentitheciaceae			
Halobyssothecium cangshanense	1	A	Known
Halobyssothecium caohaiense	1	C	Known
Halobyssothecium phragmitis	6	C	Known
Halobyssothecium sp.1	1	C	Undet.

Table 5.2 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Halobyssothecium sp.2	1	C	Undet.
Setoseptoria phragmitis	3	C	Known
Towyspora aestuari	1	C	Known
Lindgomycetaceae			
Hongkongmyces sinensis	1	A	New
Neopyrenochaetaceae			
Neopyrenochaeta annellidica	5	C	Known
Parabambusicolaceae			
Paratrimmatostroma	1	H	New
Periconiaceae			
Periconia cookei	1	H	Known
Periconia thysanolaenae	5	H	Known
Periconia yunnanensis sp.nov.	1	H	New
Tetraplosphaeriaceae			
Tetraploa yunnanensis	1	H	Known
Torulaceae			
Torula sp.1	2	H	Undet.
Torula sp.2	1	H	Undet.
Eurotiomycetes			
Chaetothyriales			
Herpotrichiellaceae			
Thysanorea lacustris	2	H	New
Thysanorea lotorum	2	H	Known
Thysanorea yunnanensi	3	H	Known
Leotiomycetes			
Helotiales			
Helotiales* genera *incertae sedis			
Dactylaria fusiformis	1	H	Known
Orbiliomycetes			
Orbiliomycetes sp.	1	H	Undet.

Table 5.2 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Sordariomycetes			
Amphisphaeriales			
Apiosporaceae			
Apiospora guangdongensis	1	H	Known
Apiospora marii	2	H	Known
Nectriaceae			
Chaetopsina fulva	2	H	Known
Chaetopsina submersa	4	H	New
Chaetosphaeriales			
Chaetosphaeriaceae			
Multiguttulispora dimorpha	1	H	Known
Sporoschisma hemipsilum	7	H	Known
Fuscosporellales			
Fuscosporellaceae			
Plagiascoma guttulatum	1	A	Known
Glomerellales			
Reticulascaceae			
Cylindrotrichum clavatum	5	H	Known
Hypocreales			
Nectriaceae			
Fusarium sp.	1	H	Undet.
Mariannaea catenulata	1	H	Known
Stachybotrys chartarum	1	H	Known
Magnaporthales			
Pseudohalonectriaceae			
Pseudohalonectria lignicola	23	A	Known
Microascales			
Halosphaeriaceae			
Cucurbitinus constrictus	2	H	Known
Myrmecridiales			

Table 5.2 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Myrmecridiaceae			
Myrmecridium sambuci	1	H	Known
Myrmecridium schulzeri	4	H	Known
Pleurotheciales			
Pleurotheciaceae			
Pleurotheciella nilotica	7	H	Known
Savoryellales			
Savoryellaceae			
Savoryella claviformis	4	H	Known
Savoryella sp.	7	A	Undet.
Sporidesmiales			
Sporidesmiaceae			
Sporidesmium hongheense	1	H	New
Sporidesmium yangzonghaiense	2	H	New
Diaporthomycetidae* families *incertae sedis			
Papulosaceae			
Wongia fusiformis	1	H	Known

Note In the "Stage of lifecycle" column, "A" indicates ascomycetes, the sexual stage; "C" indicates coelomycetes, the asexual stage; "H" indicates hyphomycetes, the asexual stage. In the Remarks column, "New" indicates a new species, "Known" indicates a known species, and "Undet." indicates that the species has not been identified to the species level.

5.6 Taxonomic Composition of Lignicolous Freshwater Fungi in Yilonghu Lake

120 submerged wood specimens were collected from Yilonghu Lake on February 22, 2023. After two weeks of incubation, the lignicolous freshwater fungi colonies were observed using an Optec SZ 760 compound stereomicroscope. Following morphological examination, 126 lignicolous freshwater fungi strains were obtained. Phylogenetic analysis combined with morphological characteristics showed that they were classified into 46 species, comprising 4 sexual species (ascomycetes) and 42 asexual species (33 hyphomycetes and 9 coelomycetes), they are belonging to 29 genera, 20 families, 11 orders under *Dothideomycetes* and *Sordariomycetes* (Table 5.3). 56.2% of the species were distributed in *Lentitheciaceae* (13%), *Apiosporaceae* (8.6%), *Pleurotheciaceae* (8.6%), *Lindgomycetaceae* (6.5%), *Myrmecridiaceae* (6.5%), *Nectriaceae* (6.5%) and *Periconiaceae* (6.5%). Common asexual genera are *Apiospora*, *Halobyssothecium*, *Myrmecridium* and *Periconia*. Dominant species are *Wongia fusiformis* (11.9%) and *Myrmecridium schulzeri* (8.7%).

Table 5.3 The occurrence of lignicolous freshwater fungi in Yilonghu Lake

Taxa	Frequency	Stage of lifecycle	Remark
Dothideomycetes			
Pleosporales			
Dictyosporiaceae			
Dictyocheirospora pseudomusae	1	H	Known
Dictyosporium digitatum	5	H	Known
Lentitheciaceae			
Halobyssothecium caohaiense	1	C	Known
Halobyssothecium guttulatum	7	C	New
Halobyssothecium phragmitis	1	C	Known
Halobyssothecium sp.1	3	C	Undet.
Setoseptoria phragmitis	1	C	Known

Table 5.3 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Setoseptoria suae	4	C	Known
Leptosphaeriaceae			
Alternaria sp.	2	H	Undet.
Lindgomycetaceae			
Aquimassariosphaeria aquatica	4	H	New
Hongkongmyces hongheensis	6	C	New
Hongkongmyces sp.	1	C	Undet.
Neopyrenochaetaceae			
Neopyrenochaeta annellidica	2	C	Known
Occultibambusaceae			
Occultibambusa jonesi	1	A	Known
Periconiaceae			
Periconia cookei	1	H	Known
Periconia hongheensis	4	H	New
Periconia thysanolaenae	7	H	Known
Tetraplosphaeriaceae			
Tetraploa submersa	1	H	Known
Tetraploa verrucosa	1	H	New
Torulaceae			
Dendryphion europaeum	1	H	Known
Torula sp.2	1	H	Undet.
Sordariomycetes			
Amphisphaeriales			
Apiosporaceae			
Apiospora guangdongensis	1	H	Known
Apiospora guizhouensis	2	H	Known
Apiospora hongheensis	2	H	New
Apiospora marii	6	H	Known
Chaetopsina septata	2	H	New

Table 5.3 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Chaetosphaeriales			
Chaetosphaeriaceae			
Sporoschisma hemipsilum	2	H	Known
Hypocreales			
Nectriaceae			
Mariannaea sp.	1	H	Undet.
Mariannaea yunnanensis	1	H	Known
Stachybotrys chartarum	3	H	Known
Microascales			
Halosphaeriaceae			
Neomoromyces lacustris	1	H	New
Pseudocirrenalia aquialpina	1	H	Known
Myrmecridiales			
Myrmecridiaceae			
Myrmecridium sambuci	2	H	Known
Myrmecridium schulzeri	11	H	Known
Myrmecridium sp.1	1	H	Undet.
Pleurotheciales			
Pleurotheciaceae			
Dematipyriforma nilotica	1	H	Known
Obliquifusoideum sinense	1	A	New
Phaeoisaria clematidis	1	H	Known
Phaeoisaria sedimenticola	2	H	Known
Savoryellales			
Savoryellaceae			
Dematiosporium hydei	1	H	New
Savoryella claviformis	6	H	Known

Table 5.3 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Sordariales			
Lasiosphaeriaceae			
Zopfiella pilifera	2	A	Known
Zopfiella sp.	1	A	Undet.
Sporidesmiales			
Sporidesmiaceae			
Sporidesmium hongheense	2	H	New
Sporidesmium hydei	4	H	New
Diaporthomycetidae* families *incertae sedis			
Papulosaceae			
Wongia fusiformis	15	H	Known

Note In the "Stage of lifecycle" column, "A" indicates ascomycetes, the sexual stage; "C" indicates coelomycetes, the asexual stage; "H" indicates hyphomycetes, the asexual stage. In the Remarks column, "New" indicates a new species, "Known" indicates a known species, and "Undet." indicates that the species has not been identified to the species level.

5.7 Taxonomic Composition of Lignicolous Freshwater Fungi in Dujuanhu Lake

115 submerged wood specimens were collected from Dujuanhu Lake on February 24, 2023. After two weeks of incubation, the lignicolous freshwater fungi colonies were observed using an Optec SZ 760 compound stereomicroscope. Following morphological examination, 107 lignicolous freshwater fungi strains were obtained. Phylogenetic analysis combined with morphological characteristics showed that they were classified into 66 species, comprising 9 sexual species (ascomycetes) and 57 asexual species (hyphomycetes), they are belonging to 48 genera, 36 families, 23 orders under *Dothideomycetes*, *Eurotiomycetes*, *Leotiomycetes* and *Sordariomycetes*

(Table 5.4). 36.1% of the species were distributed in *Chaetosphaeriaceae* (13.6%), *Junewangiaceae* (9%), *Distoseptisporaceae* (6%), *Sporidesmiaceae* (4.5%) and *Xenospadicoidaceae* (4.5%). Common genera are *Chloridium*, *Distoseptispora*, *Sporidesmiella*, *Sporidesmium*. Dominant species included *Distoseptispora proliferans* (9.3%) and *D. aquatica* (7.4%).

Table 5.4 The occurrence of lignicolous freshwater fungi in Dujuanhu Lake

Taxa	Frequency	Stage of lifecycle	Remark
Dothideomycetes			
Kirschsteiniotheliales			
Kirschsteiniotheliaceae			
Kirschsteiniothelia dujuanhuensis	1	H	New
Microthyriales			
Microthyriaceae			
Paramirandina guttulata	1	H	New
Minutisphaerales			
Acrogenosporaceae			
Acrogenospora sp.	1	H	Undet.
Pleosporales			
Dictyosporiaceae			
Pseudodictyosporium yunnanense	1	H	New
Lindgomycetaceae			
Lindgomyces yunnanensis	2	A	New
Lophiotremataceae			
Lophiotrema neoarundinaria	1	A	Known
Massarinaceae			
Helminthosporium velutinum	2	H	Known
Parabambusicolaceae			
Paramonodictys dispersa	1	H	Known
Periconiaceae			
Periconia dujuanhuensis	2	H	New

Table 5.4 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Pleomassariaceae			
Beverwykella grandispora	2	H	New
Roussoellaceae			
Roussoella dujuanhuensis	1	A	New
Tetraplosphaeriaceae			
Pseudotetraploa aquatica	1	A	New
Tetraplosphaeriaceae			
Triplosphaeria yunnanensis	1	H	New
Tubeufiales			
Tubeufiaceae			
Muripulchra aquatica	1	H	Known
Eurotiomycetes			
Chaetothyriales			
Herpotrichiellaceae			
Veronaea polyconidia	1	H	Known
Sclerococcales			
Dactylosporaceae			
Gamsomyces aquaticus	1	H	Known
Leotiomycetes			
Helotiales			
Pezizellaceae			
Cylindrocephalum aureum	1	H	Known
Leotiomycetes sp.1	3	H	Undet.
Leotiomycetes sp.2	1	H	Undet.
Sordariomycetes			
Amphisphaeriales			
Apiosporaceae			
Apiospora qinlingensis	1	A	Known
Nectriaceae			
Chaetosphaeria polygonalis	3	H	Known

Table 5.4 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Atractosporales			
Atractosporaceae			
Atractospora yunnanensis	1	A	New
Conlariaceae			
Conlarium multiseptatum	1	H	New
Conlarium yunnanense	2	H	New
Cancellidiales			
Cancellidiaceae			
Cancellidium applanatum	1	H	Known
Cancellidium cinereum	1	H	Known
Chaetosphaeriales			
Chaetosphaeriaceae			
Catenularia minor	1	H	Known
Chloridium chlamydosporum	1	H	Known
Chloridium guttulatum	1	H	New
Chloridium yunnanense	2	H	New
Fuscocatenula guttulata	1	H	New
Paragaeumannomyces guttulatus	2	H	Known
Sporoschisma taitense	1	H	Known
Tainosphaeria phialogeniculata	1	H	Known
Thozetella wenyingiae	1	H	Known
Conioscyphales			
Conioscyphaceae			
Conioscypha aquatica	1	H	Known
Conioscypha yunnanensis	1	H	Known
Distoseptisporales			
Distoseptisporaceae			
Distoseptispora aquatica	8	H	Known
Distoseptispora dujuanhuensis	1	H	New
Distoseptispora jingdongensis	2	H	New

Table 5.4 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Distoseptispora proliferans	10	H	New
Fuscosporellales			
Fuscosporellaceae			
Fuscosporella yunnanensis	1	H	New
Hypocreales			
Nectriaceae			
Mariannaea yunnanensis	1	H	Known
Magnaporthales			
Ophioceraceae			
Ophioceras sp.	2	A	Undet.
Pisorisporiales			
Pisorisporiales sp.	1	A	Undet.
Pleurotheciales			
Pleurotheciaceae			
Pleurotheciella nilotica	2	H	Known
Pleurothecium aquaticum	2	H	Known
Savoryellales			
Savoryellaceae			
Dematiosporium muriforme	1	H	New
Dematiosporium sp.	3	H	Undet.
Sporidesmiales			
Sporidesmiaceae			
Sporidesmium guttulatum	2	H	New
Sporidesmium sp.	2	H	Undet.
Sporidesmium yunnanense	1	H	New
Xenospadicoidales			
Xenospadicoidaceae			
Neospadicoides lignicola	2	H	Known
Neospadicoides sp.	2	H	Undet.
Xenospadicoidales			

Table 5.4 (continued)

Taxa	Frequency	Stage of lifecycle	Remark
Xenospadicoidaceae			
Spadicoides klotzschii	1	H	Known
Xylariales			
Clypeosphaeriaceae			
Digitodochium sp.	1	A	Undet.
Diaporthomycetidae families incertae sedis			
Rhamphoriaceae			
Xylolentia aquatica	1	H	New
Junewangiaceae			
Sporidesmiella dujuanhuensis	2	H	New
Sporidesmiella hyalosperma	1	H	Known
Sporidesmiella juncicola	1	H	Known
Sporidesmiella pini	1	H	Known
Sporidesmiella yunnanensis	2	H	New
Pseudostanjehughesiaceae			
Pseudostanjehughesia tripospora	3	H	New
Pseudostanjehughesia verrucosa	2	H	New
Sordariomycetes* families *incertae sedis			
Trichosphaeriaceae			
Brachysporium sinense	1	H	New
Diaporthomycetidae* genera *incertae sedis			
Stanjehughesia polypora	1	H	Known

Note In the "Stage of lifecycle" column, "A" indicates ascomycetes, the sexual stage; "C" indicates coelomycetes, the asexual stage; "H" indicates hyphomycetes, the asexual stage. In the Remarks column, "New" indicates a new species, "Known" indicates a known species, and "Undet." indicates that the species has not been identified to the species level.

5.8 Comparison with Previous Studies

The study of lignicolous freshwater fungi in Yunnan plateau lakes was first reported over 20 years ago. Several studies have documented a large number of lignicolous freshwater fungi species in Dianchi lake and Fuxian lake, analyzing species composition and diversity. Factors that may affect the community, distribution, and diversity of lignicolous freshwater fungi in lakes have been speculated (Cai et al., 2002; Luo et al., 2004). The fungal communities in Dianchi lake, Fuxianhu lake, Yangzonghai lake, Yilonghu lake and Dujuanhu lake are compared in Table 5.5.

Table 5.5 Comparison of fungal communities in similar studies

Location	Dianchi Lake (Luo et al., 2004)	Fuxianhu Lake (Cai et al., 2002)	Dianchi Lake (this study)	Dujuabhu Lake	Yangzonghai Lake	Yilonghu Lake
Elevation	1886 m	1721 m	1886 m	2500 m	1770 m	1407 m
Species richness	97	64	57	66	50	46
Dothideomycetes	35	31	24	14	24	21
Sordariomycetes	51	25	32	47	21	25
Sexual species	56	35	7	9	5	4
Asexual species	41	29	50	57	45	42
Three families with the most species	*Halosphaeriaceae* (12%) *Lasiosphaeriaceae* (7.2%) *Lophiostomataceae* (6.2%)	*Halosphaeriaceae* (11%) *Aliquandostipitaceae* (7.8%) *Massarinaceae* (7.8%)	*Lentitheciaceae* (10.5%) *Neopyrenochaetaceae* (10.5%) *Myrmecridiaceae* (8.7%)	*Chaetosphaeriaceae* (13.6%) *Junewangiaceae* (9%) *Distoseptisporaceae* (6%)	*Dictyosporiaceae* (14%) *Lentitheciaceae* (14%) *Nectriaceae* (8%)	*Lentitheciaceae* (13%) *Apiosporaceae* (8.6%) *Pleurotheciaceae* (8.6%)
Three most common species	*Pseudohalonectria lignicola* (25%) *Savoryella lignicola* (21%) *Aniptodera lignicola* (11%)	*Dictyosporium heptasporum* (15%) *Aniptodera chesapeakensis* (10%) *Savoryella lignicola* (9%)	*Periconia thysanolaenae* (13.4%) *Myrmecridium schulzeri* (11.2%) *Wongia fusiformis* (9.6%)	*Distoseptispora proliferans* (9.3%) *Distoseptispora aquatica* (7.4%) *Chaetosphaeria polygonalis* (2.8%)	*Pseudohalonectria lignicola* (15.1%) *Dictyocheirospora rotunda* (7.8%) *Dictyocheirospora heptaspora* (5.2%)	*Wongia fusiformis* (11.9%) *Myrmecridium schulzeri* (8.7%) *Halobyssothecium guttulatum* (5.5%)
New species	-	-	9	28	8	12
Knwon species	-	-	40	29	34	27

In previous studies, 97 species were reported in Dianchi Lake, including 56 sexual and 41 asexual species, mainly belonging to *Dothideomycetes* (35 species) and *Sordariomycetes* (51 species) (Luo et al., 2004). *Halosphaeriaceae* (12%), *Lasiosphaeriaceae* (7.2%), and *Lophiostomataceae* (6.2%) were the three most prominent families of lignicolous freshwater fungi, mainly including sexual species. However, our study found 57 species in Dianchi Lake, with only seven are sexual morphs and 50 species are asexual morphs, mainly belonging to *Dothideomycetes* (24 species) and *Sordariomycetes* (32 species). *Lentitheciaceae* (10.5%), *Neopyrenochaetaceae* (10.5%), and *Myrmecridiaceae* (8.7%) were the important families, mainly including asexual species. Additionally, the dominant species shifted from *Pseudohalonectria lignicola* (25%), *Savoryella lignicola* (21%), and *Aniptodera lignicola* (11%) to *Periconia thysanolaenae* (13.4%), *Myrmecridium schulzeri* (11.2%), and *Wongia fusiformis* (9.6%).

The two studies revealed significant differences in the composition of sexual and asexual lignicolous freshwater fungi. Our study reported only seven sexual species, far fewer than the previous 56 species, but found 50 asexual species, compared to the earlier 41 species (Luo et al., 2004). Although the seven sexual species identified here seem unrelated to those previously reported, many taxa were reclassified through molecular phylogenetic analysis, such as *Setoseptoria magniarundinacea* and *Lentithecium clioninum*, previously linked to *Massarina* (Tanaka et al., 2015). Some species, previously identified based only on morphologically, have been reassigned, such as, several *Dictyosporium* species reclassified to *Dictyocheirospora* (Yang, Liu et al., 2018; Boonmee et al., 2021). The significant difference in the number of sexual species between the two studies is incredible. While various factors, including specimen type, seasons, identification methods, vegetation, water pollution, and climate change may explain this discrepancy. In addition to the above factors, we speculate that the time of sample incubation may be the main factor affecting the number of sexual and asexual morphs of lignicolous freshwater fungi. These results and challenges encourage

us to develop a detailed research plan to conduct deeper and comprehensive study in the future.

Compared with another study on lignicolous freshwater fungi in Fuxian Lake (Cai et al., 2002), our survey of the four lakes showed a similar situation, with only a few sexual species found: Dianchi Lake (7 species), Dujuanhu Lake (9 species), Yangzonghai Lake (5 species), and Yilonghu Lake (4 species). However, we identified more asexual species than in previous studies: Dianchi Lake (50 species), Dujuanhu Lake (57 species), Yangzonghai Lake (45 species), and Yilonghu Lake (42 species), compared to the previous findings in Dianchi Lake and Fuxianhu Lake of 41 and 29 species, respectively (Cai et al., 2002; Luo et al., 2004). In Fuxian Lake, the dominant species are *Dictyosporium heptasporum* (15%), *Aniptodera chesapeakensis* (10%), and *Savoryella lignicola* (9%), similar to the earlier study of Dianchi Lake. In our survey, the dominant species in Yangzonghai Lake mirrored those in Fuxian Lake, with *Dictyosporium heptasporum* occupying an important ecological role in both lakes. Additionally, *Pseudohalonectria lignicol*a was a dominant species in previous study of Dianchi Lake and our current study in Yangzonghai Lake, playing an important role in both lakes.

The results of our survey of lignicolous freshwater fungi in the four lakes indicated that except for Dujuanhu Lake, species of *Lentitheciaceae* play an important role in Dianchi Lake, Yangzonghai Lake, and Yilonghu Lake, representing 10.5%, 14%, and 13% of the species, respectively. This distribution appears related to the vegetation types of the lakeshore zones. Previous studies have shown that species of *Lentitheciaceae* have a close relationship with species of *Poaceae* (Calabon, Jones, Hyde et al., 2021; Shen et al., 2023).

Species correlation analysis showed that Dianchi Lake overlapped with Dujuanhu Lake, Yangzonghai Lake, and Yilonghu Lake by 5 species, 21 species, and 19 species, respectively (Figure 5.2). Dujuanhu Lake overlapped with Yangzonghai Lake and Yilong Lake by one species each, while Yangzonghai Lake overlapped with

Yilonghu Lake by 16 species. Dianchi lake, Yangzonghai Lake, and Yilonghu Lake shared 12 species in common. Compared to other lakes, Dianchi Lake and Yangzonghai Lake had more similar lignicolous freshwater fungal communities, with 21 overlapping species, likely due to their similar geographical location and climate. Fungal communities in regions with similar geography or climate tend to be more similar than those in unrelated locations or different climates (Luo et al., 2004). Compared with Dujuanhu Lake, Dianchi Lake, Yangzonghai Lake, and Yilonghu Lake have more overlapping species. Combined with altitude data and vegetation type analysis, the species composition and diversity of lignicolous freshwater fungi in lakes may be influenced by the vegetation type and altitude of the study area (Luo et al., 2004; Hyde, Fryar et al., 2016).

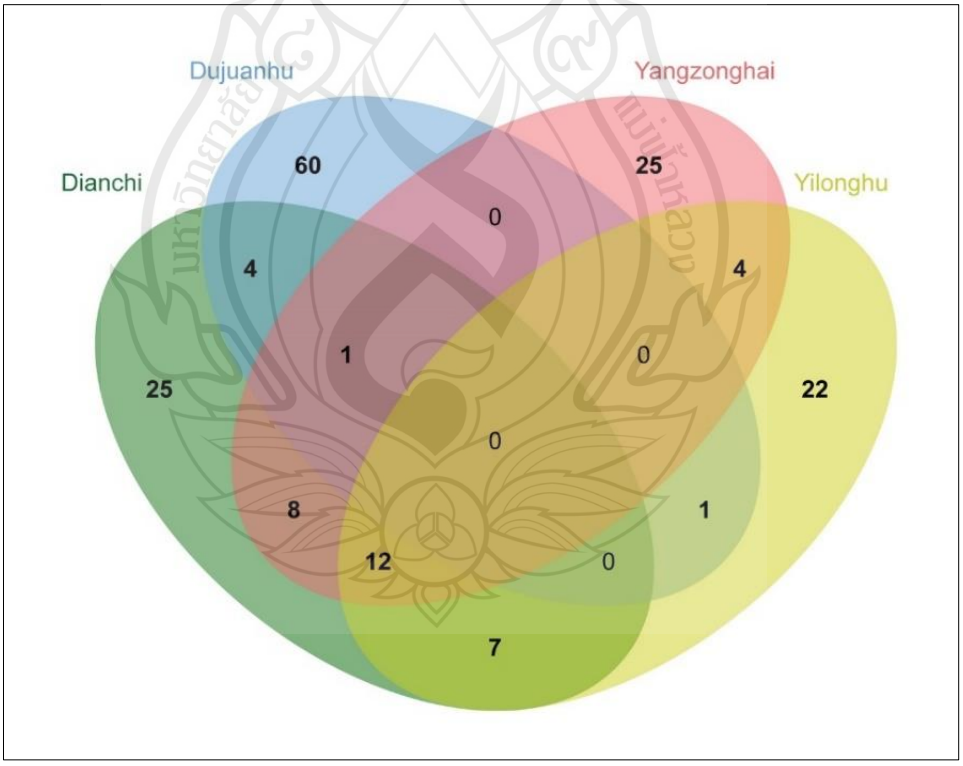


Figure 5.2 Venn diagram of relationships among lignicolous freshwater fungal species in four lakes

Dujuanhu Lake, located in the Ailao Mountains at an altitude of 2,500 meters and surrounded by dense vegetation, has never been studied for lignicolous freshwater fungi woody freshwater fungi before. This preliminary study revealed that the lignicolous freshwater fungi in Dujuanhu Lake significantly different from those in other lakes (Table 5.5). We identified 66 species, including 9 sexual (ascomycetes) and 57 asexual (hyphomycetes), across 48 genera, 36 families, and 23 orders within *Dothideomycetes*, *Eurotiomycetes*, *Leotiomycetes*, and *Sordariomycetes*. Notably, 14 species belong to *Dothideomycetes* and 47 to *Sordariomycetes*, with *Chaetosphaeriaceae*, *Junewangiaceae*, and *Distoseptisporaceae* are important components. Species correlation analysis of Dianchi Lake, Dujuanhu Lake, Yangzonghai Lake, and Yilonghu Lake showed that the lignicolous freshwater fungi of Dujuanhu Lake were unique among the four lakes, with 60 endemic species, 5 overlapping species with Dianchi Lake, 1 species overlapping with Yangzonghai Lake, and 1 species overlapping with Yilonghu Lake (Figure. 5.2). Dujuanhu Lake differs from other lakes in having a higher altitude and high vegetation coverage, which may be the main factors that make the lignicolous freshwater fungi in this lake unique from those in other lakes. However, due to the lack of data on vegetation and coverage, further research is needed to determine whether altitude and vegetation are the primary factors affecting the abundance and species diversity of lignicolous freshwater fungi in lakes.

5.9 Discussion

Previous studies have documented comparable numbers of sexual and asexual lignicolous freshwater fungi species in two plateau lakes of Yunnan Province, China (Cai et al., 2002; Luo et al., 2004). However, in this study, we found few sexual species (fewer than ten), but a larger number of asexual species in four plateau lakes of Yunnan Province. Although research suggests that factors such as specimen type, seasons, identification methods, vegetation, water pollution, and climate change can influence

the community composition and species diversity of lignicolous freshwater fungi (Luo et al., 2004; Hyde, Fryar et al., 2016), we believe that the difference in the number of sexual and asexual species may be due to the duration of sample incubation. In our study, samples were incubated for two weeks before examination. Once fungal colonies were isolated, we air-dried the specimens in a short time. In contrast, Cai et al. (2002) and Luo et al. (2004) regularly checked the sample for a certain period of time. Since the development of sexual morphs of ascomycetes takes longer time than asexual morphs, the sample incubation time may affect fungal growth, reproduction, and their interaction with environmental factors.

The study of lignicolous freshwater fungi in Dianchi Lake shows significant differences in species composition and abundance compared to previous studies (Luo et al., 2004). Without considering community succession and evolution, these differences may be related to advances in taxonomy. In previous surveys of lignicolous freshwater fungi in Dianchi Lake, species identification relied on morphological characteristics, and many different species may be considered to be the same species. However, current taxonomic methods, which combine morphological characteristics with phylogenetic analysis, different strains of the same species may be assigned to different groups. For example, the strain CBS 123126 of *Massariosphaeria typhicola* was placed in *Amniculicolaceae* (Zhang, Schoch et al., 2009), while KT 667, KT 797, and CBS 609.86 were assigned to *Lindgomycetaceae* (Dong et al., 2020). Additionally, some species previously classified under *Dictyosporium* have been reclassified into other genera, such as *Dictyocheirospora* (Yang, Liu et al., 2018; Boonmee et al., 2021).

In this study, except for Dujuanhu Lake, *Lentitheciaceae* occupies an important position in Dianchi Lake, Yangzonghai Lake, and Yilonghu Lake, accounting for 10.5%, 14%, and 13% of the total species in each lake, respectively. Similarity analysis of lignicolous freshwater fungi communities in different lakes showed that the fungi similarity between Dianchi Lake and Yangzonghai Lake had the highest similarity, followed by Dianchi Lake and Yilonghu Lake, and finally between Yangzonghai and

Yilonghu Lake. The altitudes of Dianchi Lake, Yangzonghai Lake, and Yilonghu Lake are 1886m, 1770m, and 1407m, respectively, with vegetation dominated by gramineous plants. Dujuanhu Lake, situated in the hinterland of Ailao Mountain at an altitude of 2500m, features rich vegetation species and high coverage. The results of this study indicate that the lignicolous freshwater fungi in Dujuanhu Lake are unique, with fewer than five overlapping species with other lakes. Studies have shown that some lignicolous freshwater fungal species are related to their host types (Calabon, Jones, Hyde et al., 2021; Shen et al., 2023). Based on the incomplete data on vegetation types and coverage, we speculate that altitude and vegetation type may affect the species composition and diversity of freshwater fungi in lakes. Further research is needed to determine the relationship between vegetation type, altitude and lignicolous freshwater fungi.

Lakes with high vegetation coverage appear to harbor a large number of novel freshwater fungal species. The rich diversity of vegetation types and coverage seems to provide more survival options for lignicolous freshwater fungi. This preliminary study found that the lignicolous freshwater fungi in Dujuan Lake are significantly different from those in other lakes. A total of 107 collections were obtained from 115 submerged specimens, identified as 66 species, 28 of which had never been reported before. In addition, the results showed that each lake has endemic species: 25 species in Dianchi Lake, 25 species in Yangzonghai Lake, 22 species in Yilonghu Lake, and 60 species in Dujuanhu Lake. These endemic species may be highly adaptable to specific habitats and can serve as indicators for assessing ecosystem health and water quality. They can also be used to analyze whether lignicolous freshwater fungi species have endemic evolutionary paths due to geographical or ecological isolation.

CHAPTER 6

CONCLUSIONS

6.1 Overall Conclusion

This study collected submerged wood specimens from several plateau lakes in Yunnan. Based on molecular techniques and morphological studies, 50 new species were identified, and 32 known species were taxonomically classified. The species diversity, community composition, and possible influencing factors of lignicolous freshwater fungi in Yunnan plateau lakes were explored. The lignicolous freshwater fungi recorded in this study were primarily distributed in *Dothideomycetes* and *Sordariomycetes*, with several species reported in *Eurotiomycetes* and *Leotiomycetes*. Eighty-two lignicolous freshwater fungal species in *Dothideomycetes* and *Sordariomycetes* were described and illustrated in detail, belonging to 12 genera, 10 families, and 9 orders. These included 1 new genus, 32 new species, 9 new habitats records, 5 new records in China, and 18 new collections. The composition analysis of the lignicolous freshwater fungi community in Dianchi Lake, Yangzonghai Lake, Xingyunhu Lake, and Dujuanhu Lake showed that each lake contains unique species, which may have strong adaptability to specific environments and can be used as indicators for assessing ecosystem health and water quality. Additionally, our study found that the number of asexual species is much higher than that of sexual species, almost 7-8 times greater, indicating that asexual species dominate in freshwater lakes and that the asexual stage may be more suitable for the growth, reproduction, and spread of lignicolous freshwater fungi. sporidesmium-like taxa, dictyosporium-like taxa, ramichloridium-like taxa and chaetosphaeriaceous taxa are the most common groups of lignicolous freshwater fungi in Yunnan plateau lakes, and they occupy an important position among the asexual

species of freshwater fungi. Their special conidia and structures may determine their better adaptation to lotic freshwater habitats. For example, species in the dictyosporium-like taxa have cheiroid, flat conidia with appendages; sporidesmium-like taxa have cylindrical to rostrate conidia usually with a gelatinous sheath; chaetosphaeriaceous taxa usually have filiform conidial appendages, while ramichloridium-like taxa have extremely small but large numbers conidia, sometimes with a gelatinous sheath. These special structures facilitate the spread and dissemination of lignicolous freshwater asexual species. Compared with the study of lignicolous freshwater fungi in Dianchi Lake 20 years ago, the number of sexual species has decreased sharply. Considering environmental and human factors, we believe that the main reason for the significant difference in the number of sexual species between the two studies may be the sample cultivation time. The analysis of the number of species found in the four lakes shows that the Yunnan plateau lakes contain a large number species of lignicolou freshwater fungal, including many novel species that have not been discovered. Especially in lakes with rich vegetation species and high coverage, more than half of the species are new. In summary, there is a lack of knowledge about lignicolous freshwater fungi in the plateau lakes of the Yunnan Province. The knowledge about the community structure, species composition, diversity, and distribution characteristics of lignicolous freshwater fungi in this region is limited. The study of lignicolous freshwater fungi in plateau lakes is of great significance for understanding the formation and evolution of lignicolous freshwater fungi species, biodiversity, ecological functions, and scientific research

6.2 Research Advantages

6.2.1 Detailed descriptions and illustrations of 82 species of *Dothideomycetes* and *Sordariomycetes* were provided, including 50 new species, 9 new records in China, 5 new records in freshwater habitats, and 18 known species.

6.2.2 This study conducted a survey of lignicolous freshwater fungi in Yunnan plateau lakes, including a systematic survey of Dianchi Lake, Yangzonghai Lake, Yilong Lake and Dujuan Lake, and provided a species list for the four lakes.

6.2.3 The species composition, species similarity, uniqueness, and dominant groups of lignicolous freshwater fungi in Dianchi Lake, Yangzonghai Lake, Yilonghu Lake, and Dujuan Lake were analyzed.

6.2.4 This study preserves a large number of lignicolous freshwater fungi germplasm resources in plateau lakes, which can provide possible support for the formation and evolution, biology, ecological functions, and scientific research of freshwat

6.3 Future Work

6.3.1 Identifying species and clarifying species boundaries are important foundations for fungal taxonomy research. Currently, many new species are introduced based on only one holotype specimen, with limited morphological and molecular data. This may lead to the establishment of unnecessary species. Multiple specimens can better exclude morphological differences caused by interspecific variation and environmental factors. When possible, new species should be established based on multiple methods and multiple data.

6.3.2 Increase research on lignicolous freshwater fungi in lentic freshwater habitats. Previous research on lignicolous freshwater fungi has mainly focused on lotic habitats, such as rivers and streams. The research on lignicolous freshwater fungi in lentic habitats needs to be further deepened.

6.3.3 Conduct research on the ecological functions and application value of lignicolous freshwater fungi. Currently, research on lignicolous freshwater fungi mainly focuses on phylogeny and taxonomy, while its ecological value and application are relatively underexplored.

6.4 List of Publications

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APPENDICES

APPENDIX A

MEDIA

1. Malt Extract Agar (MEA) used for fungal cultivation

Agar 15 g

Peptone 0.78 g

Glycerol 2.35 g

Dextrin 2.75 g

Maltose, Technical 12.75 g

Suspend 33.6 g of malt extract agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the power and bring volume to 1000 ml. Autoclave at 121^{o}C for 20 minutes.

2. Potato dextrose agar (PDA) used for fungal cultivation

Potato starch (from the infusion) 4 g

Dextrose 20 g

Agar 15 g

Suspend 39 g of Potato dextrose agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the powder and bring volume to 1000 ml. Autoclave at 121^{o}C for 20 minutes.

APPENDIX B

ABSTRACT OF PUBLICATIONS

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Sclerococcum pseudobactrodesmium sp. nov. from a terrestrial habitat in China

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Abstract

In this study, four terrestrial collections of bactrodesmium-like hyphomycetous fungi were isolated from rotten wood in Guizhou Province, China. Phylogenetic analyses based on the combined LSU, ITS, mtSSU, and SSU sequence matrix indicate that these four isolates represent one species belonging to the *Sclerococcum* within the Dactylosporaceae, and present a distinct lineage. Therefore, *Sclerococcum pseudobactrodesmium sp. nov*. was introduced with corresponding morphological descriptions. *Sclerococcum pseudobactrodesmium* represents the first lignicolous asexual species from a terrestrial habitat.

Key words: 1 new species, asexual morph, phylogeny, Sclerococcales, taxonomy

Introduction

The family Dactylosporaceae (Sclerococcales) comprises six genera, namely *Cylindroconidiis*, *Fusichalara*, *Gamsomyces*, *Pseudosclerococcum*, *Rhopalophora*, *Sclerococcum*, and three beetle-associated strains. These genera have been studied and cited in various sources (Réblová *et al*. 2017; Yu *et al*. 2018; Olariaga *et al*. 2019; Dong *et al*. 2020; Thiyagaraja *et al*. 2022). They encompass a range of habitats, hosts, and morphological characteristics, as illustrated in Table 1 (Réblová *et al*. 2017; Diederich *et al*. 2018; Yu *et al*. 2018; Olariaga *et al*. 2019; Dong *et al*. 2020; Thiyagaraja *et al*. 2022; Paz-Bermúdez *et al*. 2023). For example, most Dactylosporaceae species are found in both freshwater and terrestrial habitats (Dong *et al*. 2020; Thiyagaraja *et al*. 2022; Paz-Bermúdez *et al*. 2023). However, three *Sclerococcum* species, namely *S. haliotrephum*, *S. mangrovei*, and *S. vrijmoediae*, have been discovered in marine regions (Jones *et al*. 1999; Pang *et al*. 2014; Diederich *et al*. 2018; Thiyagaraja *et al*. 2022). From the perspective of the host, Dactylosporaceae species were mainly collected from decaying wood (Réblová *et al*. 2017; Yu *et al*. 2018; Olariaga *et al*. 2019; Dong *et al*. 2020; Thiyagaraja *et al*. 2022). Among them, most *Sclerococcum* species are reported as lichenicolous fungi, and three strains have even been isolated from beetles' intestinal flora (Vargas-Asensio *et al*. 2014).

Morphologically, Dactylosporaceae is highly diverse (Réblová *et al*. 2017; Diederich *et al*. 2018; Yu *et al*. 2018; Olariaga *et al*. 2019; Dong *et al*. 2020; Thiyagaraja *et al*. 2022). For instance, *Cylindroconidiis* is characterized by solitary conidiophores, polyblastic nodose conidiogenous cells, and ellipsoidal to cylindrical conidia (Yu *et al*. 2018).

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Morphological and Multi-Gene Phylogenetic Analyses Reveal *Pseudotubeufia* gen. nov. and Two New Species in Tubeufiaceae from China

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Abstract: Three helicosporous hyphomycete collections representing two species were obtained from rotting wood found in freshwater and terrestrial habitats in the Guizhou and Guangxi Provinces, China. A new genus *Pseudotubeufia* (Tubeufiaceae, Tubeufiales), comprising *Ps. hyalospora* sp. nov. and *Ps. laxispora* sp. nov., was introduced with morphological characteristic and molecular data. In addition, the molecular evidence showed that *Helicomyces* sp. (G.M. 2020-09-19.1), *H. roseus* (CBS: 102.76), and the new genus *Pseudotubeufia* clustered together with high support based on a multi-gene (LSU, ITS, *tef1α*, and *rpb2*) phylogenetic analysis. Detailed descriptions, illustrations, and notes of the three new collections are provided.

Keywords: three new taxa; asexual morph; taxonomy; Tubeufiales

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1. Introduction

Tubeufia was first introduced by Penzig and Saccardo [1], which included the type species *T. javanica* and two other species (*T. anceps* and *T. coronata*). Based on *Tubeufia*, the family Tubeufiaceae and order Tubeufiales were subsequently established [2,3]. The latest comprehensive study on Tubeufiaceae was carried out by Lu et al. [4]. Currently, there are 46 accepted genera in the family Tubeufiaceae, including *Acanthohelicospora*, *Acanthophiobolus*, *Acanthostigma*, *Acanthostigmina*, *Acanthotubeufia*, *Aquaphila*, *Artocarpomyces*, *Berkleasmium*, *Bifrontia*, *Boerlagiomyces*, *Chaetosphaerulina*, *Chlamydotubeufia*, *Dematiohelicoma*, *Dematiohelicomyces*, *Dematiohelicosporum*, *Dematiotubeufia*, *Dictyospora*, *Helicangiospora*, *Helicoarctatus*, *Helicodochium*, *Helicohyalinum*, *Helicoma*, *Helicomyces*, *Helicosporium*, *Helicotruncatum*, *Helicotubeufia*, *Kamalomyces*, *Kevinhydea*, *Manoharachariella*, *Muripulchra*, *Neoacanthostigma*, *Neochlamydotubeufia*, *Neohelicoma*, *Neohelicomyces*, *Neohelicosporium*, *Neomanoharachariella*, *Neotubeufia*, *Parahelicomyces*, *Pleurohelicosporium*, *Podonectria*, *Pseudohelicoon*, *Tamhinispora*, *Thaxteriella*, *Thaxteriellopsis*, *Tubeufia*, and *Zaanenomyces* [2–16]. Among them, five genera, *viz. Acanthophiobolus*, *Bifrontia*, *Boerlagiomyces*, *Podonectria*, and *Thaxteriella*, only have morphological data available, and their systematic evolutionary relationships have not been confirmed by molecular data.

Helicosporous hyphomycetes are asexual fungi that produce various forms of coiled two- or three-dimensional hollow conidia, which is the most common asexual morph in the family Tubeufiaceae [4,17–21]. The classification of helicosporous hyphomycetes has been studied for more than 200 years [22–24]. These fungi are widely distributed in tropical and subtropical regions, mostly acting as saprobes on plant litter, rotten wood, and decaying twigs in freshwater and terrestrial habitats [4,20,21]. However, there have been rare reports of endophytic fungi with coiled conidia [25,26].

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Article

Multi-Gene Phylogenetic Analyses Revealed Five New Species and Two New Records of *Distoseptisporales* from China

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Abstract: Eight hyphomycetes were collected as part of an investigation into the diversity of hyphomycetous fungi in China. Based on morphology and multi-loci (LSU, ITS, *tef1α*, and *rpb2*) phylogenetic analyses, five new taxa, including a new *Aquapteridospora* species *A. hyalina* and four novel *Distoseptispora* species, *viz D. aquisubtropica*, *D. septata*, *D. tropica*, and *D. wuzhishanensis* were introduced in *Distoseptisporales* (*Sordariomycetes*). Two new habitat records, *viz Distoseptispora pachyconidia* and *D. xishuangbannaensis* were firstly reported. Also provided in this study are detailed descriptions of eight new collections and a revised phylogenetic tree for the *Distoseptisporales*.

Keywords: new taxa; *Aquapteridospora*; *Distoseptispora*; hyphomycete; submerged wood; taxonomy

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1. Introduction

The two genera, *Distoseptispora* (*Distoseptisporaceae*) and *Aquapteridospora* (*Aquapteridosporaceae*) were recently introduced to *Distoseptisporales* (*Diaporthomycetidae*) [1–3]. Yang et al. [4] established *Aquapteridospora* (*Diaporthomycetidae*) as a monotypic genus, with *A. lignicola* as the type species. In later research, Hyde et al. [1] introduced *Aquapteridosporaceae* to accommodate *Aquapteridospora* and placed this family in the order *Distoseptisporales* based on divergence estimates, morphological characteristics, and phylogenetic analysis. This was followed in the "Outline of Fungi and fungus-like taxa" by Wijayawardene et al. [5]. Currently, *Aquapteridospora* consists of five species, most of which were collected from freshwater habitats. Only, *A. bambusinum* was discovered on dead bamboo culms [6]. The genus is distinguished by its macronematous, mononematous, solitary, unbranched, cylindrical conidiophores; its polyblastic, pale brown conidiogenous cells; and its fusiform, euseptate, guttulate conidia [1,4]. According to phylogenetic analyses, *Aquapteridospora* formed a distinct sister clade to all *Distoseptispora* species [4,7]. Morphologically, *Aquapteridospora* has macronematous, mononematous and unbranched conidiophores, monoblastic conidiogenous cells, and solitary conidia, similar to *Distoseptispora*. However, *Aquapteridospora* differs from *Distoseptispora* in its terminal conidiogenous cells, longer conidiophores, and fusiform euseptate conidia [2–4,8].

The type species of *Distoseptispora* was designated as *D. fluminicola* by Su et al. [9]. In recent years, a number of *Distoseptispora* (*Distoseptisporaceae*, *Distoseptisporales*) species have been accepted. Currently, 55 species including 41 freshwater species and 14 terrestrial species have been accepted in *Distoseptispora* [2,10–16]. Most *Distoseptispora* species are located in Asia, primarily in China and Thailand, with 26 species in the former and

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Research Article

Morphological and phylogenetic analyses reveal three new species and one new record of *Tubeufia* (Tubeufiales, Tubeufiaceae) from southern China

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Abstract

During an investigation of helicosporous fungi in China, a total of seven helicosporous hyphomycetes were obtained from decaying wood in the southern region of the country. Based on phylogenetic analyses using a combined LSU, ITS, *tef1α*, and *rpb2* sequence matrix, in conjunction with morphological comparisons, these taxa were classified within *Tubeufia* (Tubeufiaceae, Tubeufiales) and were recognized as three new species, *viz*. *Tubeufia guttulata*, *T. hainanensis*, and *T. muriformis*, as well as one new distribution record, *viz*. *T. cocois*. Evidence for these new taxa and the new record, descriptions, illustrations, notes, and phylogenetic evidence are provided for the newly collected helicosporous species.

Key words: asexual morph, new taxa, phylogeny, taxonomy

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Introduction

Tubeufia was introduced by Penzig and Saccardo (1897) with the type species *T. javanica* and two other species (*T. anceps* and *T. coronata*). *Tubeufia* species are widely distributed in tropical and temperate regions, including freshwater and terrestrial habitats, occurring primarily on well-rotted wood (Barr 1979; Rossman 1987; Ho et al. 2002; Tsui and Berbee 2006; Tsui et al. 2007; Zhao et al. 2007; Boonmee et al. 2011, 2014; Chaiwan et al. 2017; Dai et al. 2017; Doilom et al. 2017; Lu et al. 2017, 2018a, 2018b, 2022, 2023; Tian et al. 2022). There are currently 56 accepted species in *Tubeufia*, as listed in Table 1. These species exhibit a wide range of morphological characteristics in both their sexual and asexual morphs. For example, although *Tubeufia bambusicola*, *T. javanica*, and *T. latispora* shared a close phylogenetic affinity, they possess distinct morphological features. *Tubeufia bambusicola* and *T. latispora* possess black ascomata that are densely covered with long, flexuous setae. These ascomata contain sessile asci, each containing eight fusiform ascospores. In contrast, *T. javanica* has white ascomata without seta and short pedicellate asci with eight filiform ascospores (Boonmee

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Research Article

Three new species of *Neohelicomyces* (Tubeufiales, Tubeufiaceae) from freshwater and terrestrial habitats in China

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Abstract

Neohelicomyces species are a group of helicosporous hyphomycetes with the potential to produce secondary metabolites. During our investigation of helicosporous fungi, six collections were isolated from both terrestrial and freshwater habitats in Guizhou Province, China. Based on multigene phylogenetic analysis (ITS, LSU, *tef1α* and *rpb2*), coupled with morphological data, three new *Neohelicomyces* species, viz. *N. guizhouensis*, *N. helicosporus* and *N. hydei* were established. A list of accepted *Neohelicomyces* species with molecular data was provided. The strain of *Neohelicomyces pallidus* (UAMH 10535) was synonymised under *N. denticulatus* based on molecular data.

Key words: Asexual morphs, Dothideomycetes, new taxa, phylogeny, taxonomy

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Introduction

Genus *Neohelicomyces* Z.L. Luo, Bhat & K.D. Hyde (Tubeufiaceae) is a group of helicosporous hyphomycetes which are characterised by coiled and helical conidia (Luo et al. 2017; Lu et al. 2018b; Tibpromma et al. 2018; Crous et al. 2019a, 2019b; Dong et al. 2020; Hsieh et al. 2021; Lu et al. 2022; Yang et al. 2023). That genus, typified by *N. aquaticus*, was established by Luo et al. (2017), based on morphological characterisation and phylogenetic analysis of the combined ITS, LSU and *tef1α* sequence data. In their study, three new species (including the type species), *N. aquaticus*, *N. grandisporus* and *N. submersus*, were collected from submerged decaying wood substrata in Yunnan Province, China. Thereafter, Tibpromma et al. (2018) reported the fourth *Neohelicomyces* species, *N. pandanicola* from *Pandanus* sp. in the same province, China. Moreover, Lu et al. (2018b) re-assessed Tubeufiales, based on multi-locus phylogeny and mor-

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