

MICROFUNGI ON MEDICINAL PLANTS IN SOUTHERN CHINA AND NORTHERN THAILAND

YARU SUN

DOCTOR OF PHILOSOPHY
IN
BIOLOGICAL SCIENCE

SCHOOL OF SCIENCE
MAE FAH LUANG UNIVERSITY
2024
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ABSTRACT

Medicinal plants have been integral to human culture and medicine since prehistoric times, with over 70% of the global population relying on them. The international trade of medicinal plants is projected to reach USD 5 trillion by 2050. Fungi, a diverse group of organisms, are significantly associated with medicinal plants, forming important ecological relationships. Fungi can pose threats to medicinal plants, causing severe diseases and economic losses. But they play crucial roles in drug development, green pesticides, disease prevention and control and nutrient recycling.

Despite the critical role fungi play, research gaps persist in our understanding of their relationships with medicinal plants. Many fungi associated with medicinal plants lack detailed morphological or molecular data, hindering our ability to fully exploit their potential benefits. Therefore, fungi associated with medicinal plants need further discovery and research. In this study, 158 specimens were collected from around 60 different medicinal plants in southern China and northern Thailand. Based on morphological characteristics and phylogenetic analyses, 135 species are identified and distributed across three classes (Dothideomycetes, Leotiomycetes and Sordariomycetes), 17 orders, 39 families and 81 genera. We introduce one new order, Oncopodiellales, four new families,

Catenuliconidiaceae, Diplocladiellaceae, Oncopodiellaceae and Vamsapriyaceae, two new genera, *Biascospora* and *Pleocatenata*, and 72 new species: *Achroiostachys brunnea*, *A. catenate*, *A. fusiformispora*, *Acrocalymma xishuiense*, *Amphisphaeria hibiscicola*, *Apiculospora thailandensis*, *Apiospora tropica*, *Arecophila maolanensis*, *A. yunanensis*, *Bambusicola nanensis*, *Barriopsis caryotae*, *Biascospora chishuiensis*, *Brunneofusispora mahoniae*, *Conioscypha synnemata*, *Diaporthe ervatamiae*, *D. kunmingensis*, *D. litseae*, *D. tuchungicola*, *D. xishuiensis*, *Diplocladiella. hainanensis*, *Distoseptispora bambusae*, *D. gelatinosa*, *D. olivaceoviridis*, *Gregatothecium diflugossae*, *Helicosporium multiseptatum*, *Helminthosporium thailandicum*, *Kalmusia tetrastigmae*, *Keissleriella yunnanensis*, *Kirschsteiniothelia thailandica*, *Lasiodiplodia houttuyniae*, *L. poacearum*, *Leptospora houttuyniae*, *Lophiotrema asexuale*, *L. guizhouense*, *Melanopsamma tongrenensis*, *Memnoniella chiangmaiensis*, *Montagnula aquatica*, *M. guiyangensis*, *Murichromolaenicola dendrobii*, *Neoheleiosa brunnea*, *Neohelicascus guizhouensis*, *Neohelicomyces sexualis*, *Neohendersonia tongrenensis*, *Neomassaria fibraureae*, *Neooccultibambusa fusispora*, *Neopestalotiopsis amomi*, *N. hyperici*, *N. photiniae*, *N. suphanburiensis*, *Neoscytalidium dendrobii*, *Parabahusutrabeeja hyalina*, *Paramyrothecium xishuiense*, *Pestalotiopsis chiangmaiensis*, *P. loeiana*, *P. smilacicola*, *Phaeosphaeria boehmeriae*, *P. guiyangensis*, *Phaeosphaeriopsis oblongispora*, *Pleocatenata chiangraiensis*, *Porodiplodia guizhouensis*, *Psiloglonium bambusicola*, *P. brunneum*, *P. guizhouense*, *Roussoella panzhouensis*, *R. wudangensis*, *Seriascoma guizhouense*, *Sphaeropsis guiyangensis*, *Striaticonidium olivaceobrunneum*, *Tamhinispora obpyriformis*, *Vamsapriya chiangmaiensis*, *V. chiangraiensis* and *Virgatospora thailandica*, with illustrations, discussions of their taxonomic placement, and comparisons with morphologically similar taxa. Eleven new combinations are introduced: *Conioscypha obovoidea* (≡*Vanakripa obovoidea*), *C. chiangmaiense* (≡*Vanakripa chiangmaiense)* and *C. minutiellipsoidea* (≡*Vanakripa minutiellipsoidea*), *Keissleriella acacia* (≡*Pleurophoma acaciae*), *K. italicum* (≡*Pleurophoma italica*), *K. ossicula* (≡*Pleurophoma ossicola*), *K. pleurospora* (≡*Phoma pleurospora*), *Phaeosphaeria*

brachylaenae (≡*Didymocyrtis brachylaenae*), *P. pini* (≡*Didymocyrtis pini*), *P. septata* (≡*Didymocyrtis septata*) and *Torula sundara* (≡*Dwayabeeja sundara* = *Pseudotorula sundara*). Additionally, we report 40 new host records from medicinal plants and ten new geographical records for China and Thailand. We also resolved inter-generic synonymy for three species. Reference specimen is provided for *Diplocladiella taurina*.

The study reveals a rich diversity of microfungi associated with medicinal plants in southern China and northern Thailand, which not only enhances our understanding of microbial diversity in these regions but also provides new insights into the conservation and utilization of these medicinal plants. Future research will continue to explore the impact of these fungi on medicinal plants and their potential chemical functions, aiming to provide scientific evidence for the sustainable development and utilization of medicinal plant resources and the pharmaceutical industry.

Keywords: 72 new species, 4 new families, 1 new order, 158 new collections, 11 new combinations, Catenuliconidiaceae, Diplocladiellaceae, Oncopodiellales, Oncopodiellaceae, Phylogeny, Taxonomy, Vamsapriyaceae

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ABBREVIATIONS AND SYMBOLS

com.	combination
diam.	diameter
e.g.	for example
et al.	and others
h	hours
gen.	genus/genera
ibid.	ibidem
min	minute
ml	maximum likelihood support
mm	millimetre
nov.	novum (Latin for new thing)
pp	posterior probabilities
sp.	species
spp.	species (plural)
viz.	that is
vs.	versus
$\bar{x}$	average
°C	degree centigrade
µm	micrometer
µl	microliter
%	percent

CHAPTER 1

INTRODUCTION

1.1 Background and Rationale

1.1.1 Overview of Medicinal Plants in Southern China and Northern Thailand

Southern China and northern Thailand are recognized as biodiversity hotspots, particularly noted for their rich variety of medicinal plants (Chi et al., 2017; Hyde et al., 2018; Wijayawardene et al., 2021). These regions are home to numerous plants used in traditional medicine, such as *Dendrobium catenatum*, *Eucommia ulmoides*, and *Pinellia ternate* (Schippmann et al., 2002; Petrovska, 2012). These plants have been utilized for centuries in traditional Chinese and Thai medicine for their therapeutic properties, ranging from nourishing the stomach and producing body fluid, nourishing yin and clearing away heat, relieving cough and resolving phlegm, lowering blood pressure and boosting the immune system. The diverse climatic and ecological conditions of these regions support a wide array of plant species (Rasool-Hassan, 2012; Sofowora et al., 2013; Phumthum et al., 2019; Zahra et al., 2020). The importance of these plants extends beyond their medicinal use; they also play a vital role in local cultures and economies (Mofokeng et al., 2022). Despite their significance, the ecological interactions between these medicinal plants and their associated microfungi remain largely unexplored, however, research specifically focusing on microfungi associated with medicinal plants is still very limited.

1.1.2 Importance of Microfungi in Plant Health and Ecosystem Functioning

Microfungi are integral components of plant ecosystems, significantly influencing plant health, growth, and resilience. Microfungi contribute to soil health by decomposing organic matter, cycling nutrients, and promoting plant biodiversity (Hyde & Lee 1995; Hyde et al., 2019). Their interactions with plants can lead to increased resistance to environmental stresses, such as drought and disease. Additionally, these fungi form symbiotic relationships with plants, such as mycorrhizal associations, which enhance nutrient uptake, improve water absorption, and protect against pathogens. In medicinal plants, microfungi can also play a crucial role in the biosynthesis of bioactive compounds, thereby potentially enhancing the medicinal properties of the host plants (Köberl et al., 2013; Mohamad et al., 2019; Silva Santos et al., 2022).

1.1.3 Current Knowledge Gaps in the Taxonomy and Ecological Roles of Microfungi

Despite the recognized importance of microfungi in plant health and ecosystem functioning, there has been limited research in recent years on microfungi associated with medicinal plants in northern Thailand and southern China (Hyde & Lee 1995; Mohamad et al., 2019; Silva Santos et al., 2022). These regions are renowned for their rich biodiversity and the extensive use of medicinal plants in traditional medicine (Numpulsuksant et al., 2021; Feng et al., 2023). However, the microfungi inhabiting these plants have largely been overlooked, and the specific interactions between these fungi and medicinal plants, including their potential benefits and roles in enhancing their medicinal properties, remain poorly understood (Jia et al., 2016; Sun et al., 2023). Accurately identifying and classifying these fungi can greatly expand our understanding of fungal biodiversity in these regions, potentially leading to the discovery of new species and genera, critical for effective biodiversity conservation and ecosystem management. Additionally, studying these fungi contributes to a broader

understanding of plant-microbe interactions, offering insights that can inform strategies for sustainable agriculture and conservation.

1.2 Significance of the Study

Medicinal plants hold significant importance in various aspects. They serve as natural sources of drugs for healthcare and are crucial in the discovery of new pharmaceutical ingredients (Sun, 2009; Rasool Hassan, 2012). These plants drive the development of the pharmaceutical industry and contribute to international trade (Marinelli, 2004; Wiart, 2006; Rasool et al., 2020). Additionally, they play a vital role in protecting biodiversity and ensuring the sustainable use of natural resources. Medicinal plants also preserve traditional medical knowledge and foster cultural exchanges. As such, they are key pillars for human health, economic development, ecological conservation, and cultural heritage (Petrovska, 2012; Dar et al., 2017).

The study of microfungi on medicinal plants may play a crucial role in promoting the growth of medicinal plants, enhancing their disease resistance, and boosting the concentration of their medicinal compounds (Kaul et al., 2012; Chowdhary & Kaushik, 2015; Li et al., 2015; Huang et al., 2021; Madasi et al., 2021). By investigating these fungi, we can deepen our understanding of the complex interactions between plants and microorganisms, providing scientific evidence for the sustainable development and use of medicinal plants. Furthermore, this research could lead to the discovery of new fungal species and bioactive compounds with medicinal potential, which is vital for the conservation of medicinal plant resources and the development of new drugs (Yang et al., 2017, 2023; Liang et al., 2018; Matić et al., 2019; Manganyi et al., 2020; Wang et al., 2023). Additionally, studying these fungi contributes to biodiversity conservation, supports ecosystem management, and aids in the preservation and innovation of traditional medicine (Mohamad et al., 2019; Monkai et al., 2023).

1.3 Objectives

1.3.1 To document any new taxa on different medicinal plants from southern China and northern Thailand.

1.3.2 To study the biodiversity of microfungi associated with medicinal plants from southern China and northern Thailand based on morphology and multi-locus phylogeny.

1.3.3 To provide reference specimens for some poorly studied species.

1.3.4 To provide a worldwide checklist of some plant pathogens on medicinal plants.

1.4 Expected Outcomes

1.4.1 This study will record the host, lifestyle, and perform the taxonomy and phylogeny of microfungi on medicinal plants.

1.4.2 This study will provide the reference specimen and new sequences for some poorly studied species.

1.4.3 This work will document any new taxa associated with medicinal plants in southern China and northern Thailand.

1.5 Research Contents

This study focuses on the taxonomy and phylogeny of microfungi associated with medicinal plants in southern China and northern Thailand, comprising five chapters.

Chapter 1 is a general introduction, introduces the background and rationale for the study, discussing the importance of medicinal plants and their associated microfungi in these biodiverse regions. It outlines the significance of the study, clearly stating the research objectives, expected outcomes and the outline of the thesis.

In Chapter 2, an in-depth overview of the medicinal plants, along with a detailed review of microfungi, and the relationships between them, is provide.

Chapter 3 details the methodologies used for collecting, examining, and isolating microfungi from medicinal plants. It describes the DNA extraction, PCR amplification, and sequencing processes, followed by the methods employed for phylogenetic analyses to accurately classify and identify the fungi.

Chapter 4 deals with the taxonomic and phylogenetic study of microfungi related to medicinal plants in southern China and northern Thailand. The description and illustrations for each taxon are provided. Brief notes for each species and genus are given. The phylogenetic analyses for each group are separately carried out based on the datasets of multi-gene sequences. In addition, we synonymized 14 species and provide 11 new combinations.

Chapter 5 provides an overall conclusion, the research advantages, and future work.

CHAPTER 2

LITERATURE REVIEW

2.1 Overview of Medicinal Plants

2.1.1 Introduction of Medicinal Plants

Medicinal plants can be defined as plants that possess preventive, therapeutic properties, or healthcare effects on the human or animal body (Namdeo, 2018). All or part of the plant is used for medicinal purposes or as raw material for the pharmaceutical industry (Sun, 2009; Rasool Hassan, 2012). Early humans were driven by instinct, taste, and experience to treat diseases and relieve pain with plants. Therefore, the history of medicinal plants is as long as that of humans (Petrovska, 2012). The oldest written evidence of medicinal plant usage for the preparation of medicines was found on a Sumerian clay slab from Nagpur, approximately 5,000 years old (Kelly, 2009). The Chinese Shennong Ben Cao Jing, written between 200 and 250 CE, lists 365 drugs, including 252 medicinal plants, and has been recognized as the most valuable and the world's first organized body of medicinal knowledge (Bottcher, 1965; Wiart, 2006; Petrovska, 2012). Medicinal plants are distributed all over the world, and traditional medicine practices are widespread in China, India, Japan, Pakistan, Sri Lanka, and Thailand (Dar et al., 2017; Rasool et al., 2020). According to the International Union for Conservation of Nature and the World Wildlife Fund, about 50,000–80,000 plants are used because of their medicinal values (Marinelli, 2004). The Fourth National Survey of Traditional Chinese Medicine Resources indicated 383 families and more than 13,000 medicinal plants in China (https://www.nature.com/articles/d42473-020-00001-6, 20 June 2024). Phumthum et al. (2019) reported that there are 2,187 plant species used for medicinal purposes in Thailand.

2.1.2 The Value of Medicinal Plants

Medicinal plants play a significant role in the treatment and prevention of human diseases, healthcare, and economic improvement (Farnsworth et al., 1985; Rasool Hassan 2012; Rasool et al., 2020; Awuchi et al., 2023). Some medicinal plants can be used directly without processing. For example, safflower is a medicine for promoting blood circulation and removing blood stasis, which can be used orally or externally to treat local injuries (https://www.iplant.cn/info/Carthamus?t=foc, 20 June 2024). The World Health Organization estimates that 80% of the world's inhabitants continue to rely mainly on herbal medicine for the treatment of diseases, mostly in Africa and other developing nations (Farnsworth et al., 1985). Plant natural products have also played an important role in human lives as a source of medicine. Different plants produce different compounds, which are the main components of many medicines (Saboon et al., 2019). For example, berberine isolated from *Coptis chinensis* can be anti-cancer and is the main component of many anti-cancer drugs (Zhu et al., 2017). Some plants are also called medicinal and edible homologous plants, which can be used as tonics and condiments, such as *Panax ginseng* and *Amomum villosum* (Sun, 2009). In addition, some medicinal plants not only have medicinal value but also high ornamental value, such as *Ginkgo biloba* and *Lycoris radiata* (Ding et al., 1970). Due to their characteristic benefits and important value, the demand for medicinal plants has increased worldwide (Zahra et al., 2020). The international trade of medicinal plants and their products was estimated to be USD 60 billion in 2010. The cultivation of medicinal plants has become a popular method to alleviate poverty in some poor and developing countries (Sher et al., 2014; Rasool et al., 2020).

2.2 Overview of Microfungi

2.2.1 Microfungi

Fungi are eukaryotic organisms that digest food and absorb nutrients directly through their cell walls (Kirk et al., 2008). They are a hyper-diverse and heterogeneous group of organisms that represent a large and diverse component of microbial diversity (Hawksworth, 2001; Blackwell, 2011; Hernandez-Restrepo et al., 2017). Microfungi

are defined as fungi with microscopic spore-producing structures (Hawksworth et al., 1995). They are a paraphyletic group, distinguished from macrofungi only by the absence of a large, multicellular fruiting body. Microfungi are ubiquitous in all terrestrial, freshwater, and marine environments. They are distributed worldwide and exhibit various morphologies (Cannon & Sutton, 2004).

2.2.2 Sexual and Asexual Morphs of Microfungi

Many microfungi have been found on medicinal plants. They are not only distributed in Dothideomycetes and Sordariomycetes, but also in Eurotiomycetes (Bhagat et al., 2012; Niu et al., 2016; Long et al., 2019; Ma et al., 2019). The sexual stage refers to the production of meiospores (ascospores) in spore sacs (asci) (Eriksson et al., 2009). The sexual morph of ascomata has different types, such as apothecia (open cup-shaped), perithecia (flask-shaped), cleistothecia (closed fruiting bodies), and pseudothecia (Pöggeler et al., 2006; Money et al., 2016). The position of ascomata in the host is mainly divided into three types: superficial, semi-immersed, and immersed. They also have a variety of colors and shapes, and some of them have paraphyses. The ascomatal wall is also diverse; it can be *textura angularis*, *textura oblita*, or *textura porrecta*. The color can be dark, brown, yellow. The asci are mainly divided into three types: prototunicate, unitunicate, and bitunicate. They have different shapes, such as ovoid, obovoid, clavate, and obclavate. Some of them have special characteristics, such as an apical ring and an ocular chamber. Ascospores have various shapes and colors, with some having a sheath or appendage. Ascospore characteristics are important in the identification of ascomycetes to genus, particularly to species level.

The asexual morph of Ascomycota mainly consists of hyphomycetes and coelomycetes (Eriksson et al., 2009). Hyphomycetes are characterized by solitary, synnematal, or sporodochial conidiomata and the formation of conidia on conidiophores that are not contained in a fruiting body. The conidiophores can be macro- to micronematous, mononematous or synnematous, branched or unbranched, straight or

flexuous, septate or aseptate, hyaline or pigmented, and standard or reduced to conidiogenous cells. The conidiogenous cells can be arthric or thallic, blastic, phialidic, annelledic, tretic, basauxic, and gangliar. Conidia are varied in color and shape among hyphomycetes. The conidia can be solitary or catenate, acropleurogenous, acrogenous or pleurogenous, dry or wet, smooth or verruculose, thin- or thick-walled, smooth- or rough-walled, aseptate or septate with constricted or unconstructed septa, and with or without appendages (Kirk et al., 2008; Bhat 2010; Seifert et al., 2011; Lin et al., 2024; Liu et al., 2024).

Coelomycete is a general term used for asexual fungi that produce conidia in fruiting bodies. Conidiomata are diverse and can be acervular, cupulate, pycnidial, sporodochial, synnematous, and pycnothyrial (Sutton, 1980; Nag Raj, 1993; Li et al., 2020). The conidiomatal wall can be *textura angularis*, *textura epidermoidea*, or *textura intricata* (Sutton, 1980; Nag Raj, 1993; Li et al., 2020). The conidiophores are mainly hyaline, branched or unbranched, and arise from inner layer cells of the cavity. The conidiogenous cells are mainly divided into three types: holoblastic, enteroblastic, and thallic. Conidia of coelomycetes are varied in color and shape (Sutton, 1980; Nag Raj, 1993; Li et al., 2020). The difference between coelomycetes and hyphomycetes is that coelomycetes produce conidia in conidiomata and have various paraphyses and conidiomatal walls (Sutton, 1980; Nag Raj, 1993; Li et al., 2020).

2.3 Studies of Microfungi Associated with Medicinal Plants

2.3.1 Endophytes Associated with Medicinal Plants

The study of endophytic fungi in medicinal plants is of great significance for elucidating the distribution, growth and development characteristics, resource regeneration, and accumulation of medicinal substances in these plants. There is a high diversity of endophytic fungi associated with medicinal plants (Sun et al., 2008; Guo, 2016). These fungi are very important for the pharmaceutical industry and medicine

due to their production of bioactive metabolites such as alkaloids, ergochromes, peptides, and polyketides isolated from fungal endophytes of medicinal plants. For example, *Taxomyces andreanae*, an endophyte isolated from *Taxus brevifolia*, can produce paclitaxel, which is used to treat various cancers (Stierle et al., 1993). Another endophyte, *Diaporthe* sp., isolated from the medicinal plant *Erythrina crista-galli*, can produce an anti-inflammatory metabolite (phomol) (Weber et al., 2004). Astins, originating from the endophyte *Cyanodermella asteris* living within the medicinal plant *Aster tataricus*, have antitumor effects (Schafhauser et al., 2019). Endophytic fungi related to medicinal plants are also used for biological control. Castillo et al. (2002) isolated an endophytic fungus from the medicinal plant *Kennedia nigriscans*, which produced antibiotics with a wide spectrum of activity against many plant pathogens. In addition, endophytes associated with medicinal plants can be used for plant cultivation and planting (Jia et al., 2016). White and Cole (1985) reported that endophytes can confer some disease resistance to their host. Sieber and Hugentobler (1987) and Guo (2016) studied the endophytes associated with *Panax quinquefolium* and confirmed this report. Endophytic fungi can increase the yield and quality of medicinal plants. For example, *Glomus manihottis* promoted the growth of *Cinnamomum cassia*, and *Glomus caledonium* increased the medicinal content of *Aloe barbadensis* by 2.2–7.2 times (Gong et al., 2002; Luo et al., 2004).

2.3.2 Microfungi Associated with Medicinal Plants Disease

Microfungi can be harmful, causing diseases in medicinal plants and impacting their value. With the increasing demand for medicinal plants, many countries have begun to grow them on a large scale (Dar et al., 2017). Diseases can reduce the production of medicinal plants, leading to economic losses. In Hungary, privet (*Ligustrum vulgare*) and its cultivars are widely planted. A canker disease caused by *Colletotrichum gloeosporioides* was observed in the southeastern part of Hungary, causing severe losses of *Ligustrum vulgare* in 1999. The frequency of disease

occurrence ranged between 30 and 40%. Affected bark on the cankers split, exposing the wood. Plants died when twigs or stems were girdled (Vajna & Bagyinka, 2002). Alves et al. (2016) reported that approximately 50% of *Carthamus tinctorius* showed brown spots on leaves caused by *Alternaria carthami* in Brazil, which greatly affected the quality of *Carthamus tinctorius*. Abtahi and Nourani (2017) listed some of the most important fungal diseases of several medicinal plants. They reported that *Bunium persicum*, widely used in traditional Iranian medicine, was infected by *Alternaria alternata* and *Fusarium solani*, causing up to a 38% reduction in yield. *Lasia spinosa* has high medicinal value and is mainly distributed in Thailand, Malaysia, northeastern India, Myanmar, and southwest China. Currently, there is no artificial cultivation of this plant. Zhang et al. (2020) reported the leaf blight of *Lasia spinosa* caused by *Xepicula yifeii*. The disease likely causes the death of plants and may lead to the extinction of *Lasia spinosa* due to the lack of experience in artificial cultivation.

2.3.3 Saprobes Associated with Medicinal Plants

Some saprobic fungi, as decomposers, can release elements such as nitrogen and phosphorus from decaying matter, making them available to other living organisms. They can convert dead organic material into fungal biomass, carbon dioxide (CO_2), and small molecules such as organic acids. Fungi generally decompose complex substrates such as cellulose and lignin, which accelerates the degradation of roots and stems of some medicinal plants. They also help maintain a sustainable ecosystem for the plants that share the same habitat. Manandhar et al. (1987) and Wen and Chen (2001) studied the interaction between pathogenic and saprobic fungi and reported that saprobic fungi have an inhibitory effect on the growth of pathogenic fungi. Some saprobic fungi, such as *Aspergillus* and *Fusarium*, can produce mycotoxins which can contaminate agricultural commodities (Ciegler, 1978; Castañares et al., 2019). It is reported that 20–25% of crops worldwide contain mycotoxin contamination (Eskola et al., 2020). Different plants comprise different chemical contents which may influence the fungi

on a particular host (Tang et al., 2005; Paulus et al., 2006; Hyde et al., 2007). So far, there is no comprehensive study on saprobic fungi related to medicinal plants, but there are many studies focused on saprobic fungi with specific host species. For instance, *Camellia japonica* (Japan, Koide et al., 2005), *Anacardium occidentale* (India, Shanthi & Vittal 2010), *Alnus alnobetula* (Switzerland, Senn-Irlet et al., 2012), *Antidesma madagascariense* (Mauritius, Jeewon et al., 2013), and *Clematis* sp. (Belgium, China, Italy, Thailand, and the UK, Phukhamsakda et al., 2020).

CHAPTER 3

RESEARCH METHODOLOGY

3.1 Collection, Examination, Isolation, and Deposition of Specimens

Fresh healthy leaves and twigs, diseased leaves and twigs, and decaying leaves, twigs and branches of different medicinal plants were collected from Guangxi, Guizhou, Hainan, Sichuan, Yunnan and Zhejiang Provinces in southern China and Chiang Mai, Chiang Rai, Loei and Nan Provinces in northern Thailand from 2019 to 2023. Samples were brought to the laboratory in Ziploc plastic bags or paper envelopes for examination. The fruiting bodies on natural substrates were observed and photographed using a stereomicroscope (SteREO Discovery, V12, Carl Zeiss Microscopy GmBH, Germany; VHX-7000, Keyence, Japan). Morphological characteristics were observed using a Nikon Eclipse Ni compound microscope (Nikon, Japan) and photographed with a Nikon DS-Ri2 digital camera (Nikon, Japan) or using a Carl Zeiss compound microscope (Carl Zeiss AG, Germany) and an Axiocam 208 color digital camera (Carl Zeiss AG, Germany). For ascomycetes and coelomycetes, free hand sections of the fruiting body structures were mounted in water on slides for microscopic studies and photomicrography. For hyphomycetes, fungal structures were picked and added to water drop on slide using a needle. Indian ink was used to reveal the presence of a gelatinous sheath around the ascospores or conidia. Melzer's iodine reagent was used to identify amyloid apical apparatus in characterized Sordariomycetous taxa. Measurements were made with the Tarosoft (R) Image Frame Work program and photo-plates were processed with Adobe Photoshop CS6 software (Adobe Systems, San Jose, CA, USA).

For endophytes, materials were washed under running tap water, immersed in 70% ethanol for 2 min, followed by soaking in 4% NaOCl for 1 min, rinsed three times in sterile distilled water and then dried on a sterile filter paper. For control, the final sterile water rinse was plated and observed post-incubation period. Absence of fungal growth indicated the leaf surface was sterile (Kjer et al., 2010). The sterilized materials were cut into 2-5 mm2 segments and placed on potato dextrose agar (PDA) containing 50 μg/ml penicillin and 50 μg/ml streptomycin (Sun et al., 2023). The plates were observed every day and mycelia on the edge of fungal colonies be transferred to pure PDA dishes to obtain pure cultures. For other samples, single-spore isolation be carried out as described by Senanayake et al. (2020). Fruiting bodies' contents were transferred to a drop of sterile water on a sterilized spot plate. The spore suspension be spread over petri dishes containing potato dextrose agar (PDA) or water agar (WA) or malt extract agar (MEA) and incubated at 25 °C for 12 hours or longer. Germinated spores were transferred onto fresh PDA or MEA media plates. Culture plates were incubated at 25 °C in incubators and inspected every week. The pure cultures were deposited in Mae Fah Luang University Culture Collection (MFLUCC), Chiang Rai, Thailand, the Culture Collection of Kunming Institute of Botany, the Chinese Academy of Sciences (KUNCC), Kunming, China, and the Culture Collection of the Department of Plant Pathology, Agriculture College, Guizhou University (GUCC), Guiyang, China. Specimens were deposited in the herbarium of Mae Fah Luang University (MFLU) Chiang Rai, Thailand, and the Herbarium of Cryptogams, Kunming Institute of Botany, Academia Sinica (HKAS), Kunming, China,. Facesoffungi (FoF) numbers were acquired as described by Jayasiri et al. (2015). Taxonomic descriptions and nomenclature were deposited at Fungal Names (https://nmdc.cn/fungalnames/registe, 20 June 2024) following the description in Wang, Wang et al. (2022) and Index Fungorum (2024).

3.2 DNA Extraction, PCR Amplification, and Sequencing

Fungal mycelia were scraped off and transferred to a 1.5 mL microcentrifuge tube using a sterilized lancet for genomic DNA extraction. Biospin Fungus Genomic DNA Extraction Kits (GD2416 BIOMIGA, San Diego, CA, USA) were used to extract DNA following the manufacturer's instructions. PrepManTM Ultra Sample Preparation Reagent (Thermo Fisher Scientific, Yokohama, Japan) was used to extract DNA directly from fruiting bodies. Polymerase chain reactions (PCR) were carried out using a BIO-RAD T100 Thermal Cycler in a 20 μL reaction volume which contained 10 μL 2x PCR Master Mix, 7 μL ddH2O, 1 μL of each primer, and 1 μL template DNA. The PCR thermal cycle program and primers are given (Table 3.1). The PCR products will be sent for sequencing to SinoGenoMax, Shanghai, China.

3.3 Phylogenetic Analyses

The closest taxa to our strains were determined with standard nucleotide blast searches in NCBI (http://www.ncbi.nlm.nih.gov/). The published sequences used in the analyses were obtained from GenBank and extracted from relevant literatures. The download available sequences from GenBank were aligned using MAFFT version 7 (http//mafft.cbrc.jp/alignment/server/index.html) or AliView (Larsson, 2014). The alignments were checked visually and improved manually where necessary in BioEdit (Hall, 1999) or AliView (Larsson, 2014). TrimAl v1.4 software was used for automated removal of spurious or poorly aligned regions in each single gene alignment with gap threshold was 0.6 (Capella-Gutiérrez et al., 2009).

Phylogenetic analyses of both individual and combined datasets were carried out based on maximum-likelihood (ML) and Bayesian posterior probability (BYPP). Maximum likelihood analyses were performed using raxmlGUI 2.0 (Edler et al., 2021), or at the CIPRES SCIENCE GATEWAY (Miller et al., 2010) using the online tool RAxML-HPC v.8 on XSEDE or using IQ-TREE (Nguyen et al., 2015; Trifinopoulos

et al., 2016) on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at, 10 June 2024) under partitioned models. The tree search included 1,000 non-parametric bootstrap replicates and the best scoring tree was selected from suboptimal trees under the estimated substitution model.

The BYPP analyses were performed in MrBayes 3.2.6 (Ronquist et al., 2012). The best nucleotide substitution model for each data partition were evaluated by MrModeltest 2.2 (Nylander, 2004). The Markov Chain Monte Carlo (MCMC) sampling approach was used to calculate posterior probabilities (PP) (Rannala & Yang, 1996). Six simultaneous Markov chains were run for 10 million generations and trees were sampled every 1,000th generation; The first 20% of trees, representing the burn-in phase of the analyses, were discarded and the remaining trees were used for PP value in the majority rule consensus tree.

Phylograms were visualized with FigTree v1.4.4 program (Rambaut, 2018) and reorganized followed the methods described in Xie et al. (2023) (https://www.chiplot.online/) and Adobe Illustrator CS6 software (Adobe Systems, USA).

Table 3.1 Partial gene regions, primers and PCR amplification conditions used in this study

Locus	Primers		PCR procedures	Reference
	Name	Sequence (5'-3')		
Large subunit (LSU)	LR0R	ACCCGCTGAACTTAAGC	94℃ – 3 min; 94℃ – 30 s; 52℃ – 30 s; 72℃ – 1 min; Repeat 2–4 for 35 cycles; 72℃ – 8 min; 4℃ on hold	Vilgalys and Hester (1990), Rehner and Samuels (1994)
	LR5	TCCTGAGGGAAACTTCG		
Small subunit (SSU)	NS1	GTAGTCATATGCTTGTCTC		White et al. (1990)
	NS4	CTTCCGTCAATTCCTTTAAG		
Internal transcribed spacer (ITS)	ITS5	GGAAGTAAAAGTCGTAACAAGG		
	ITS4	TCCTCCGCTTATTGATATGC		
Elongation factor-1 alpha (EF1-α)	EF1-983F	GCYCCYGGHCAYCGTGAYTTYAT	94℃ – 2 min; 66℃ – 56℃ (touchdown 9 cycles); 94℃ – 30 sec; 56℃ – 1 min; 72℃ – 1 min; Repeat 3–5 for 36 cycles; 72℃ – 10 min; 4℃ on hold	Rehner and Buckley (2005)
	EF1-2218R	ATGACACCRACRGCRACRGTYTG		
	EF-728F	CATCGAGAAGTTCGAGAAGG	94℃ – 5 min; 94℃ – 30 s; 55℃ – 50 s; 72℃ – 1 min; Repeat 2–4 for 34 cycles; 72℃ – 5 min; 4℃ on hold	Carbone and Kohn (1999)
	EF-986R	TACTTGAAGGAACCCTTACC		
	EF2	GGA RGT ACC AGT SAT CAT GTT		
RNA polymerase II subunit (RBP2)	fRPB2-5F	GAYGAYMGWGATCAYTTYGG	94℃ – 3 min; 94℃ – 20 sec; 55℃ – 30 sec; 72℃ – 1 min; Repeat 2–4 for 40 cycles; 72℃ – 10 min; 4℃ on hold	Liu et al. (1999)
	fRPB2-7cR	CCCATRGCTTGYTTRCCCAT		
	H3-1b	GCGGGCGAGCTGGATGTCCTT		

Table 3.1 (continued)

Locus	Primers		PCR procedures	Reference
	Name	Sequence (5'-3')		
Beta (β) tubulin (TUB)	Bt2a	GGTAACCAAATCGGTGCTGCTTTC	94°C – 3 min; 94°C – 30 sec; 55°C – 50 sec; 72°C – 1 min; Repeat 2–4 for 35 cycles; 72°C – 10 min; 4°C on hold	Glass and Donaldson (1995) O'Donnell and Cigelnik (1997)
	Bt2b	ACCCTCAGTGTAGTGACCCTTGGC		
	T1	AACATGCGTGAGATTGTAAGT		
Calmodulin (CAL)	CAL228F	GAGTTCAAGGAGGCCTTCTCCC	95°C – 5 min; 95°C – 30 sec; 55°C – 50 sec; 72°C – 1 min; Repeat 2–4 for 40 cycles; 72°C – 10 min; 4°C on hold	Carbone and Kohn (1999)
	CAL737R	CAT CTT TCT GGC CAT CAT GG		
Histone H3(his3)	CYLH3F	AGG TCC ACT GGT GGC AAG	98°C – 3 min; 98°C – 10 sec; 58°C – 10 sec; 72°C – 10 sec; Repeat 2–4 for 39 cycles; 72°C – 5 min; 4°C on hold	Glass and Donaldson (1995)

CHAPTER 4

MORPHOLOGY AND MOLECULAR PHYLOGENY OF MICROFUNGI ON MEDICINAL PLANTS IN SOUTHERN CHINA AND NORTHERN THAILAND

4.1 Introduction

Medicinal plants, as vital natural resources used for treating diseases, alleviating symptoms, preventing illnesses, or in drug development, play a crucial role in the history, economy, medicine, and agricultural development of human society (Farnsworth et al., 1985; Lim, 2012; Rasool-Hassan, 2012; Sofowora et al., 2013; Phumthum et al., 2019). They not only have a long history of use across various traditional medical systems, such as Traditional Chinese Medicine (Xu et al., 2019), Ayurveda in India (Kumar et al., 2017), and African traditional medicine (Sofowora, 1996) but also hold a significant position in the global economy (Sher et al., 2014; Dar et al., 2017; Zahra et al., 2020). For many developing countries, medicinal plants and their derivatives represent an essential source of economic revenue (Namdeo, 2018; Mofokeng et al., 2022). In the medical field, these plants are a treasure trove for modern drug discovery, with many contemporary medicines being derived from or inspired by them (Rasool et al., 2020). Additionally, medicinal plants contribute to agriculture by enhancing ecosystem biodiversity and promoting the sustainability of agricultural production (Schippmann et al., 2002; Köberl et al., 2013). As understanding of the value of medicinal plants deepens, their role in drug development and ecological balance becomes increasingly prominent, suggesting that research and application in this natural resource will bring more hope and possibilities for future medical advances and human health (Rasool et al., 2020).

The ecological significance of micro-fungi in relation to medicinal plants is profound, impacting agriculture, ecological balance, and new medical research (Köberl et al., 2013). In agricultural contexts, fungi are both benefactors and adversaries to crops, including medicinal plants (Zeilinger et al., 2015). For instance, mycorrhizal fungi enhance plant nutrient uptake and stress resistance, thereby increasing the yield and quality of medicinal plant crops (Abd_Allah et al., 2015; Sun, Zhang et al., 2021). Conversely, pathogenic fungi can cause diseases that diminish plant health and cause economic losses (Obregón et al., 2018; Wang et al., 2019). For example, in Hungary, privet and its cultivars suffered severe losses from a canker disease caused by *Colletotrichum gloeosporioides*, affecting 30–40% of plants (Vajna & Bagyinka, 2002). Similarly, diseases such as brown spots caused by *Alternaria carthami* in *Carthamus tinctorius* in Brazil and various fungal infections in *Bunium persicum* in Iran have led to substantial yield reductions and quality degradation (Alves et al., 2016).

Saprobic fungi contribute positively to ecosystems by decomposing dead organic matter and releasing essential nutrients, facilitating a sustainable environment for cohabiting plants. Their role extends to inhibiting pathogenic fungi growth, albeit some saprobic fungi can produce harmful mycotoxins, contaminating 20–25% of global crops with mycotoxins (Eskola et al., 2020). Despite the complexity of interactions, studies on specific host species, such as *Camellia japonica* and *Anacardium occidentale*, reveal the intricate balance between plant chemistry and fungal influence (Koide et al., 2005; Shanthi & Vittal, 2010).

The significance of endophytic fungi in medicinal plants is profound, offering a source of bioactive metabolites with therapeutic potentials (Weber et al., 2004; Chowdhary & Kaushik, 2015; Jia et al., 2016; Rana et al., 2020). For example, paclitaxel from *Taxomyces andreanae*, associated with *Taxus brevifolia*, can be used for cancer treatment (Strobel et al., 1993). These fungi not only enhance plant resistance to diseases but also improve growth and medicinal quality, for examples, *Glomus manihottis* promoted the

growth of *Ginnamornum cassia*, *Glomus caledonium* can increase the medicine content of *Aloe barbadensis* by 2.2–7.2 times (Gong et al., 2002; Luo et al., 2004).

Despite fungi playing a key role in medicinal plants, research gaps remain: (1) Studies are often limited to specific regions or a small number of medicinal plant species, which limits our understanding of fungal diversity patterns in different environments (Zhang, Wijayawardene et al., 2020; Monkai et al., 2023; Wu et al., 2024). (2) The identification of species presents challenges, especially for those that are rare or undescribed. (3) The taxonomic status of some species remains unclear, with some studies focusing on introducing the diversity and ecology of fungi related to medicinal plants, neglecting morphological descriptions and systematic analysis, leading to certain species lacking a clear taxonomic placement (Rai et al., 2012; Köberl et al., 2013; Chowdhary & Kaushik, 2015). In this study, I provide detailed taxonomic and phylogenetic information for 135 species associated with medicinal plants in southern China and northern Thailand.

4.2 Results

The taxa identified in this study were organized and assigned following the latest outline of fungi (Wijayawardene et al., 2022). The new species were established in accordance with the guidelines provided by Jeewon and Hyde (2016), Chethana et al. (2021), Jayawardena, Hyde et al. (2021), and Maharachchikumbura et al. (2021). Taxa illustrated below are in alphabetical order. They represent 135 species, 81 genera in 39 families, 17 orders and three classes in Ascomycota. There species name with their host, lifestyle, and location are provided in the Table 4.1.

Table 4.1 Species isolated and identified in this study

Class	Order	Family	Species	Life mode	Country	Host
Dothideomycetes	Botryosphaeriales	Botryosphaeriaceae	*Barriopsis caryotae*	S	Thailand	*Caryota* sp. (Arecaceae)
	Botryosphaeriales	Botryosphaeriaceae	*Botryosphaeria agaves*	P	Thailand	*Agave sisalana* (Asparagaceae)
	Botryosphaeriales	Botryosphaeriaceae	*Lasiodiplodia houttuyniae*	S	China	*Houttuynia cordata* (Saururaceae)
	Botryosphaeriales	Botryosphaeriaceae	*Lasiodiplodia poacearum*	P	Thailand	*Dracaena* sp. (Liliaceae)
	Botryosphaeriales	Botryosphaeriaceae	*Neoscytalidium dendrobii*	P	Thailand	*Dendrobium* sp. (Orchidaceae)
	Botryosphaeriales	Botryosphaeriaceae	*Sphaeropsis guiyangensis*	P/S	China	*Mahonia fortune* (Berberidaceae)
	Hysteriales	Hysteriaceae	*Psiloglonium bambusicola*	S	China	Poaceae sp.
	Hysteriales	Hysteriaceae	*Psiloglonium brunneum*	S	China	Poaceae sp.
	Hysteriales	Hysteriaceae	*Psiloglonium guizhouense*	S	China	Poaceae sp.
	Hysteriales	Hysteriaceae	*Rhytidhysteron hongheense*	S	China	*Ulmus parvifolia* (Ulmacea)
	Hysteriales	Hysteriaceae	*Rhytidhysteron rufulum*	S	China	*Ligustrum* sp. (Oleaceae)
	Kirschsteiniotheliales	Kirschsteiniotheliaceae	*Kirschsteiniothelia thailandica*	S	Thailand	Poaceae sp.
	Monoblastiales	Monoblastiaceae	*Neoheleiosa brunnea*	S	China	*Osmanthus fragrans* (Oleaceae)
	Oncopodiellales	Diplocladiellaceae	*Diplocladiella hannanensis*	S	China	Unidentified plant
	Oncopodiellales	Diplocladiellaceae	*Diplocladiella taurina*	S	China	Unidentified plant
	Patellariales	Incertae sedis	*Yuccamyces citri*	S	Thailand	Trachycarpus sp. (Arecaceae)

Table 4.1 (continued)

Class	Order	Family	Species	Life mode	Country	Host
	Pleosporales	Acrocalymmaceae	*Acrocalymma xishuienses*	S	China	*Castanopsis fargesii* (Fagaceae)
	Pleosporales	Bambusicolaceae	*Bambusicola nanensis*	S	Thailand	Poaceae sp.
	Pleosporales	Dictyosporiaceae	*Aquadictyospora clematidis*	S	China	*Buxus sinica* (Buxaceae)
	Pleosporales	Dictyosporiaceae	*Dendryphiella vinosa*	S	China	*Dendrobium officinale* (Orchidaceae)
	Pleosporales	Dictyosporiaceae	*Dictyocheirospora xishuiensis*	S	China	*Camphora* sp. (Lauraceae)
	Pleosporales	Dictyosporiaceae	*Dictyosporium zhejiangense*	S	China	Unidentified plant
	Pleosporales	Didymosphaeriaceae	*Montagnula aquatica*	S	Thailand	Poaceae sp.
	Pleosporales	Didymosphaeriaceae	*Montagnula guiyangensis*	S	China	*Helwingia himalaica* (Helwingiaceae)
	Pleosporales	Didymosphaeriaceae	*Montagnula donacina*	S	China	Unidentified plant
	Pleosporales	Didymosphaeriaceae	*Kalmusia tetrastigmae*	p	China	*Tetrastigma planicaule* (Vitaceae)
	Pleosporales	Didymosphaeriaceae	*Paraphaeosphaeria neglecta*	p	China	*Rosa roxburghii* (Rosaceae)
	Pleosporales	Lentitheciaceae	*Keissleriella yunnanensis*	S	China	Poaceae sp.
	Pleosporales	Lophiotremataceae	*Lophiotrema asexuale*	S	China	Unidentified plant
	Pleosporales	Lophiotremataceae	*Lophiotrema guizhouense*	S	China	Unidentified plant
	Pleosporales	Lophiostomataceae	*Oleaginea sichuanensis*	p	China	Mahonia fortune (Berberidaceae)

Table 4.1 (continued)

Class	Order	Family	Species	Life mode	Country	Host
	Pleosporales	Massariaceae	*Massarioramusculicola chiangraiensis*	S	Thailand	*Gardenia jasminoides* (Rubiaceae)
	Pleosporales	Massarinaceae	*Helminthosporium thailandicum*	P	Thailand	*Elaeis* sp. (Arecaceae)
	Pleosporales	Massarinaceae	*Helminthosporium sinense*	S	Thailand	Unidentified plant
	Pleosporales	Melanommataceae	*Camposporium valdivianum*	S	China	*Debregeasia orientalis* (Urticaceae)
	Pleosporales	Morosphaeriaceae	*Neohelicascus guizhouensis*	S	China	Unidentified plant
	Pleosporales	Neohendersoniaceae	*Neohendersonia tongrenensis*	S	China	*Lithocarpus corneus* (Fagaceae)
	Pleosporales	Neomassariaceae	*Neomassaria fibraureae*	S	China	*Fibraurea recisa* (Menispermaceae)
	Pleosporales	Nigrograna ceae	*Nigrograna hydei*	S	China	*Mahonia fortune* (Berberidaceae)
	Pleosporales	Nigrograna ceae	*Nigrograna oleae*	S	China	*Mahonia* sp. (Berberidaceae)
	Pleosporales	Nigrograna ceae	*Nigrograna schinifolii*	S	China	*Rhododendron delavayi* (Ericaceae)
	Pleosporales	Occultibambusaceae	Brunneofusispora mahoniae	S	China	Mahonia sp. (Berberidaceae)
	Pleosporales	Occultibambusaceae	Neooccultibambusa fusispora	S	Thailand	Poaceae sp.
	Pleosporales	Occultibambusaceae	Seriascoma guizhouense	S	China	Poaceae sp.
	Pleosporales	Occultibambusaceae	Occultibambusa aquatica	S	China	Poaceae sp.
	Pleosporales	Occultibambusaceae	Occultibambusa sichuanensis	S	China	Poaceae sp.

Table 4.1 (continued)

Class	Order	Family	Species	Life mode	Country	Host
	Pleosporales	Paradictyoarthriniaceae	*Paradictyoarthrinium diffractum*	S	Thailand	*Cassia fistula* (Fabaceae)
	Pleosporales	Phaeoseptaceae	*Phaeoseptum manglicola*	S	China	*Mahonia* sp. (Berberidaceae)
	Pleosporales	Phaeoseptaceae	*Pleopunctum ellipsoideum*	S	Thailand	*Dendrobium nobile* (Orchidaceae)
	Pleosporales	Phaeosphaeriaceae	*Phaeosphaeria boehmeriae*	S	China	*Boehmeria* sp. (Caryophyllaceae)
	Pleosporales	Phaeosphaeriaceae	*Phaeosphaeria guiyangensis*	S	China	Poaceae sp.
	Pleosporales	Phaeosphaeriaceae	*Leptospora houttuyniae*	S	China	*Houttuynia cordata* (Saururaceae)
	Pleosporales	Phaeosphaeriaceae	*Leptospora hydei*	S	China	*Mentha canadensis* (Lamiaceae)
	Pleosporales	Phaeosphaeriaceae	*Murichromolaenicola dendrobii*	p	Thailand	*Dendrobium nobile* (Orchidaceae)
	Pleosporales	Phaeosphaeriaceae	*Phaeosphaeriopsis oblongispora*	P	China	*Spineless yucca* (Asparagaceae)
	Pleosporales	Parabambusicolaceae	*Parabambusicola yunnanensis*	S	China	*Poaceae sp.*
	Pleosporales	Roussoellaceae	*Roussoella panzhouensis*	S	China	*Poaceae sp.*
	Pleosporales	Roussoellaceae	*Roussoella siamensis*	S	Thailand	*Poaceae sp.*
	Pleosporales	Roussoellaceae	*Roussoella wudangensis*	S	China	*Poaceae sp.*
	Pleosporales	Torulaceae	*Torula sundara*	S	Thailand	*Poaceae sp.*
	Pleosporales	Incertae sedis	*Biascospora chishuiensis*	S	China	*Unidentified plant*

Table 4.1 (continued)

Class	Order	Family	Species	Life mode	Country	Host
	Pleosporales	Incertae sedis	*Pleocatenata chiangraiensis*	S	Thailand	*Clerodendrum quadriloculare* (Lamiaceae)
	Tubeufiales	Tubeufiaceae	*Helicosporium multiseptatum*	S	China	Poaceae sp.
	Tubeufiales	Tubeufiaceae	*Neohelicomyces sexualis*	S	China	Unidentified plant
	Tubeufiales	Tubeufiaceae	*Tamhinispora obpyriformis*	S	Thailand	Poaceae sp.
Leotiomycetes	Rhytismatales	Pezizellaceae	*Apiculospora thailandensis*	S	Thailand	Poaceae sp.
	Rhytismatales	Pezizellaceae	*Porodiplodia guizhouensis*	S	China	Unidentified plant
Sordariomycetes	Amphisphaeriales	Amphisphaeriaceae	*Amphisphaeria hibiscicola*	S	China	*Hibiscus mutabilis* (Malvaceae)
	Amphisphaeriales	Apiosporaceae	*Apiospora tropica*	S	Thailand	Poaceae sp.
	Amphisphaeriales	Apiosporaceae	*Nigrospora sphaerica*	P	Thailand	Dracaena sp. (Liliaceae)
	Amphisphaeriales	Sporocadaceae	*Bartalinia pini*	P	Thailand	Smilax sp. (Liliaceae)
	Amphisphaeriales	Sporocadaceae	*Neopestalotiopsis amomi*	P	China	Amomum villosum (Zingiberaceae)
	Amphisphaeriales	Sporocadaceae	*Neopestalotiopsis hyperici*	P	China	Hypericum monogynum (Hypericeae)
	Amphisphaeriales	Sporocadaceae	*Neopestalotiopsis photiniae*	P	China	Photinia serratifolia (Rosaceae)
	Amphisphaeriales	Sporocadaceae	*Neopestalotiopsis suphanburiensis*	S	Thailand	Unidentified plant

Table 4.1 (continued)

Class	Order	Family	Species	Life mode	Country	Host
	Amphisphaeriales	Sporocadaceae	*Neopestalotiopsis* sp. 1	P	China	*Lithocarpus* sp. (Fagaceae)/ *Smilax china* (Liliaceae)/ *Dryopteris crassirhizoma* (Dryopteridaceae)
	Amphisphaeriales	Sporocadaceae	*Neopestalotiopsis* sp. 2.	S/E	Thailand	*Ceiba pentandra* (Rhizophoraceae)/ *Pinellia ternata* (Araceae)
	Amphisphaeriales	Sporocadaceae	*Neopestalotiopsis rhapidis*	P	China	*Podocarpus macrophyllus* (Podocarpaceae)
	Amphisphaeriales	Sporocadaceae	*Neopestalotiopsis rhododendri*	P	Thailand	*Dracaena fragrans* (Liliaceae)
	Amphisphaeriales	Sporocadaceae	*Pestalotiopsis chamaeropis*	E/S	China	*Peristrophe japonica* (Acanthaceae)
	Amphisphaeriales	Sporocadaceae	*Pestalotiopsis chiangmaiensis*	P	China	*Phyllostachys edulis (Poaceae)*
	Amphisphaeriales	Sporocadaceae	*Pestalotiopsis dracontomelon*	S	Thailand	*Podocarpus sp. (Podocarpaceae)*
	Amphisphaeriales	Sporocadaceae	*Pestalotiopsis hispanica*	E	China	*Peristrophe japonica (Acanthaceae)*
	Amphisphaeriales	Sporocadaceae	*Pestalotiopsis hydei*	S	China	*Unidentified plant*
	Amphisphaeriales	Sporocadaceae	*Pestalotiopsis loeiana*	S	Thailand	*Unidentified plant*
	Amphisphaeriales	Sporocadaceae	*Pestalotiopsis smilacicola*	P	Thailand	*Smilax sp. (Liliaceae)*
	Amphisphaeriales	Sporocadaceae	*Pseudopestalotiopsis theae*	S	Thailand	*Ceriops tagal (Rhizophoraceae)*
	Amphisphaeriales	Sporocadaceae	*Seiridium vernicola*	P	China	*Camellia japonica (Theaceae)*

Table 4.1 (continued)

Class	Order	Family	Species	Life mode	Country	Host
	Chaetosphaeriales	Chaetosphaeriaceae	*Parabahusutrabeeja hyalina*	S	China	*Rubus* sp. (Rosaceae)
	Chaetosphaeriales	Chaetosphaeriaceae	*Pseudolachnella minima*	S	China	Unidentified plant
	Conioscyphales	Conioscyphaceae	*Conioscypha synnemata*	S	China	Unidentified plant
	Conioscyphales	Conioscyphaceae	*Vanakripa obovoidea*	S	Thailand	*Jatropha integerrima*（Euphorbiaceae)
	Diaporthales	Diaporthaceae	*Diaporthe arecae*	P	China	*Magnolia officinalis* (Magnoliaceae)
	Diaporthales	Diaporthaceae	*Diaporthe ervatamiae*	P	China	*Ervatamia kwangsiensis* (Apocynaceae)
	Diaporthales	Diaporthaceae	*Diaporthe goulteri*	S	Thailand	*Bidens alba (Asteraceae)*
	Diaporthales	Diaporthaceae	*Diaporthe kunmingensis*	S	China	*Unidentified plant*
	Diaporthales	Diaporthaceae	*Diaporthe litseae*	E	China	*Litsea kobuskiana (Lauraceae)*
	Diaporthales	Diaporthaceae	*Diaporthe psoraleae-pinnatae*	S	China	*Rhododendron sp. (Ericaceae)*
	Diaporthales	Diaporthaceae	*Diaporthe pseudobiguttulata*	S	China	*Sarcococca sp. (Buxaceae)*
	Diaporthales	Diaporthaceae	*Diaporthe sojae*	E	China	*Phellodendron sp. (Rutaceae)*, *Eucommia ulmoides (Eucommiaceae)*
	Diaporthales	Diaporthaceae	*Diaporthe siamensis*	P	Thailand	*Hymenocallis littoralis (Amaryllidaceae)*
	Diaporthales	Diaporthaceae	*Diaporthe subclavate*	S	Thailand	*Unidentified plant*
	Diaporthales	Diaporthaceae	*Diaporthe tuchungicola*	E	China	*Eucommia ulmoides (Eucommiaceae)*

Table 4.1 (continued)

Class	Order	Family	Species	Life mode	Country	Host
	Diaporthales	Diaporthaceae	*Diaporthe tulliensis*	P	Thailand	*Pandanus odoratissimus* (Pandanaceae)
	Distoseptisporales	Distoseptisporaceae	*Distoseptispora bambusae*	S	China/Thailand	Poaceae sp.
	Distoseptisporales	Distoseptisporaceae	*Distoseptispora effuse*	S	China	Poaceae sp.
	Distoseptisporales	Distoseptisporaceae	*Distoseptispora gelatinosa*	S	Thailand	Poaceae sp.
	Distoseptisporales	Distoseptisporaceae	*Distoseptispora olivaceoviridis*	S	Thailand	*Clerodendrum quadriloculare* (Lamiaceae)
	Distoseptisporales	Distoseptisporaceae	*Distoseptispora tectonae*	S	Thailand	Poaceae sp.
	Distoseptisporales	Distoseptisporaceae	*Distoseptispora tectonigena*	S	Thailand	Poaceae sp.
	Distoseptisporales	Distoseptisporaceae	*Distoseptispora yongxiuensis*	S	China	Poaceae sp.
	Glomerellale	Plectosphaerellaceae	*Acrostalagmus annulatus*	P/S	Thailand	*Agastache rugosa* (Lamiaceae)
	Glomerellales	Malaysiascaceae	*Malaysiasca phaii*	P	Thailand	*Dracaena fragrans* (Asparagaceae)
	Hypocreales	Stachybotryaceae	*Achroiostachys brunnea*	S	Thailand	Poaceae sp.
	Hypocreales	Stachybotryaceae	*Gregatothecium diflugossae*	S	China	*Diflugossa divaricata* (Acanthaceae)
	Hypocreales	Stachybotryaceae	*Melanopsamma tongrenensis*	S	China	*Osmanthus fragrans* (Oleaceae)
	Hypocreales	Stachybotryaceae	*Memnoniella alishanensis*	S	China	*Dendrobium nobile* (Orchidaceae)
	Hypocreales	Stachybotryaceae	*Striatibotrys rhabdosporus*	P	China	*Macleaya cordata* (Papaveraceae)
	Hypocreales	Stachybotryaceae	*Striaticonidium olivaceobrunneum*	S	Thailand	Poaceae sp.

Table 4.1 (continued)

Class	Order	Family	Species	Life mode	Country	Host
	Hypocreales	Stachybotryaceae	*Virgatospora thailandica*	S	Thailand	Poaceae sp.
	Hypocreales	Stachybotryaceae	*Paramyrothecium acadiense*	S	China	Unidentified plant
	Hypocreales	Stachybotryaceae	*Paramyrothecium xishuiense*	S	China	Unidentified plant
	Hypocreales	Stachybotryaceae	*Achroiostachys catenata*	S	Thailand	Poaceae sp.
	Hypocreales	Stachybotryaceae	*Achroiostachys fusiformispora*	S	Thailand	*Carica papaya* (Caricaceae)
	Hypocreales	Stachybotryaceae	*Memnoniella ellipsoidea*	S	Thailand	*Ricinus communis* (Euphorbiaceae)
	Hypocreales	Stachybotryaceae	*Memnoniella chiangmaiensis*	S	Thailand	*Bidens alba* (Asteraceae)
	Hypocreales	Stachybotryaceae	*Memnoniella levispora*	S	Thailand	Unidentified plant
	Hypocreales	Stachybotryaceae	*Myxospora poaceicola*	S	China	Poaceae sp.
	Xylariales	Cainiaceae	*Arecophila maolanensis*	S	China	Unidentified plant
	Xylariales	Cainiaceae	*Arecophila yunanensis*	S	China	Poaceae sp.
	Xylariales	Xylariaceae	*Catenuliconidia uniseptata*	S	China	Poaceae sp.
	Xylariales	Xylariaceae	*Occultitheca rosae*	S	China	*Rubus* sp. (Rosaceae)
	Xylariales	Vamsapriyaceae	*Vamsapriya chiangmaiensis*	S	Thailand	Poaceae sp.
	Xylariales	Vamsapriyaceae	*Vamsapriya chiangraiensis*	S	Thailand	Poaceae sp.
	Xylariales	Vamsapriyaceae	*Vamsapriya indica*	S	Thailand	Poaceae sp.

Note The life mode is given as endophyte (E), pathogen (P), and saprobe (S)

4.2.1 Dothideomycetes

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98(6): 1050 (2007)

Botryosphaeriaceae Theiss. & P. Syd., Annales Mycologici 16 (1–2): 16 (1918)

Barriopsis A.J.L. Phillips, A. Alves & Crous Persoonia 21: 39 (2008)

Notes: The holomorphic genus, *Barriopsis* was established when Phillips et al. (2008) transferred *Physalospora fusca* to *Barriopsis fusca* based on different morphology and phylogeny. The sexual morph of *Barriopsis* has bitunicate asci, aseptate, brown ascospores, and lack terminal apiculi (Phillips et al., 2008). The coelomycetous asexual morph is defined as having holoblastic, hyaline conidiogenous cells, containing conidia that are hyaline, aseptate when young, brown and septate with irregular longitudinal striations when mature (Phillips et al., 2008; Doilom et al., 2014). So far, only six species have been found as saprobes and endophytes from China, Cuba, Iran and Thailand (Dissanayake et al., 2016; Rathnayaka et al., 2021).

Barriopsis caryotae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16404; Figure 4.1

Etymology: The specific epithet refers to the host genus.

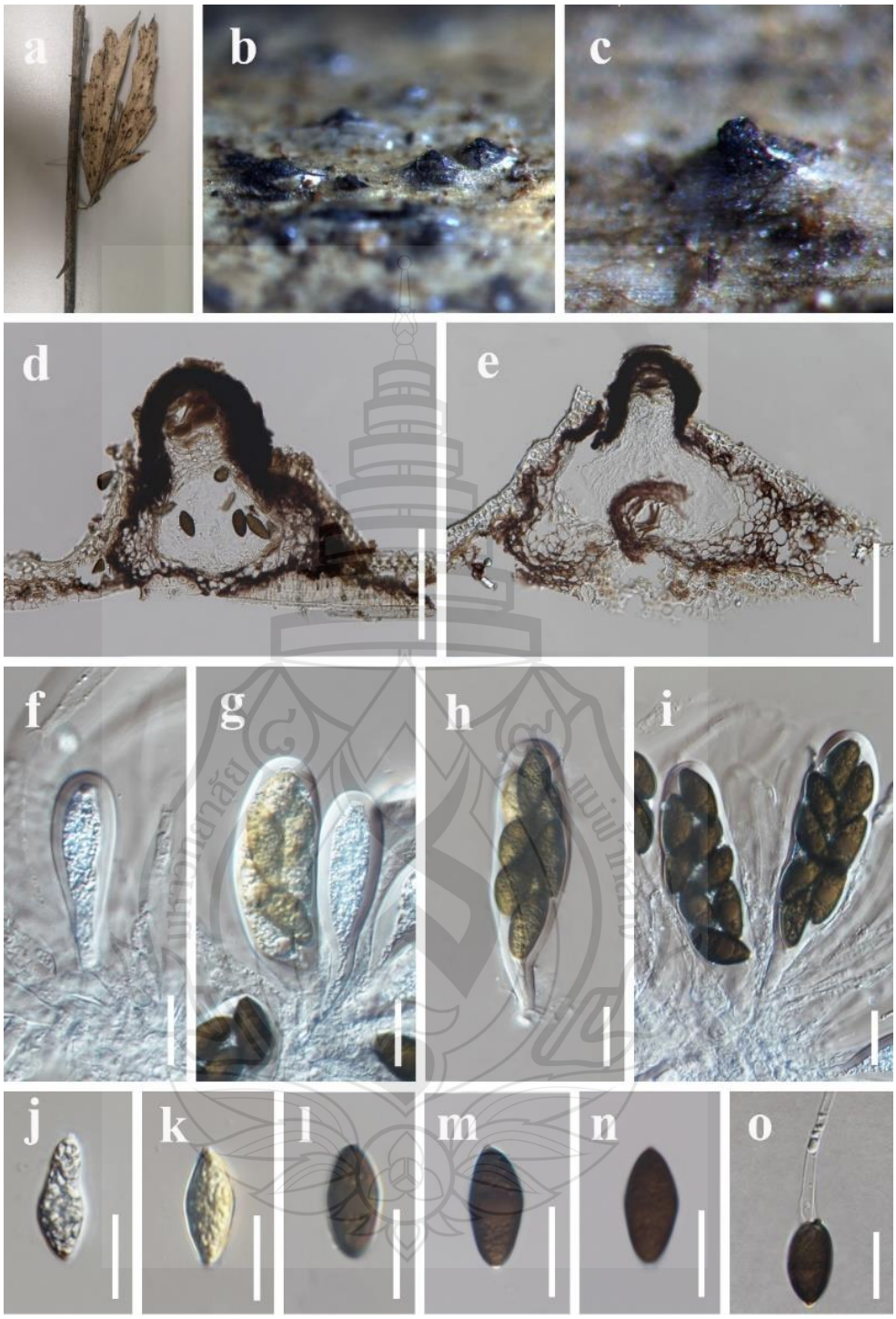
Holotype: HGUP 24-0028.

Saprobic on dead branch of *Caryota* sp. **Sexual morph**: *Ascostromata* 185–255 µm high, 220–335 µm diam ($\bar{x}$ = 220 × 285 µm, n = 10), solitary to aggregated, semi-immersed, erumpent at maturity, uniloculate, subglobose, minutely papillate. *Ostiole* raised, centric. *Peridium* 16–38 µm wide, fused with host tissues, comprising two layers of cells of *textura angularis*. Outer layers dark brown to black, thick-walled, and inner layers hyaline and thin-walled. *Hamathecium* comprising hyaline, around 3 µm wide, septate, cellular pseudoparaphyses. *Asci* cylindrical-clavate, 8-spored, bitunicate, short-pedicellate, 80–130 × 22–30 µm ($\bar{x}$ = 98 × 27 µm, n = 10). *Ascospores* 2-seriate, ellipsoid to ovoid, aseptate, hyaline when young, becoming dark brown when mature, with a large central guttule, some with terminal apiculi at both ends, smooth-walled, 19–28 × 9–13 µm ($\bar{x}$ = 24 × 12 µm, n = 25). **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 12 hours and germ tubes produced from one end of the ascospores. Colonies on PDA reached 8–9 cm diam. after 7 days at 25°C, mycelium white, flossy, circular, with the entire edge, white at the edge, and grey in the middle. After 21 days of incubation, colonies become grey both above and below.

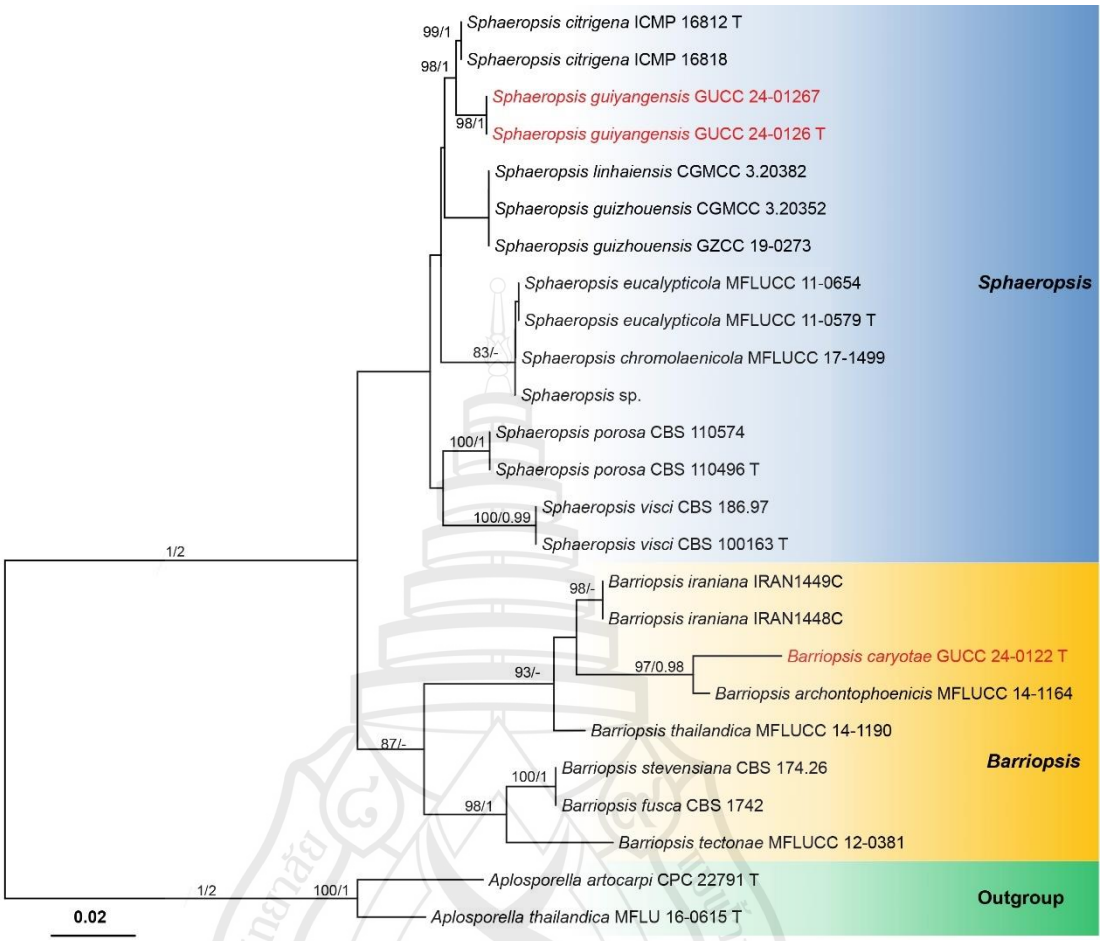
Material examined: THAILAND, Suphan Buri Province, on stem of *Caryota* sp. (Arecaceae), 5 September 2020, S Wang, TN02 (HGUP 24-0028, **holotype**); ex-type culture GUCC 24-0122.

Notes: Phylogenetically, our collection formed a well-supported (97% ML and 1.00 BYPP) sister clade to *B. archontophoenicis* which was also isolated from Arecaceae plant (Figure 4.2). Morphologically, *B. caryotae* differs from *B. archontophoenicis* by its thick peridium (16–38 μm *vs.* 5–14 μm). In addition, *B. archontophoenicis* produces ascospores that are broad at the middle and exhibit a distinct mucilaginous sheath, whereas *B. caryotae* lacks these characteristics (Konta et al., 2016). Thus, we introduced our collection as a novel *Barriopsis* species based on morphology and phylogeny. It is worth noting that the *TEF1-α* gene (KX235305) of *B. archontophoenicis* does not match the length of other *Barriopsis* sequences, rendering it unsuitable for gene comparison. Therefore, it is urgent to amplify a suitable *TEF1-α* sequence for *B. archontophoenicis*.



Note a Host. c, d Appearance of ascomata on host substrate. d Section of stromata. e Peridium. f Paraphyses and immature ascus. g–i. Asci. j–n Ascospores. o Germinated ascospores. Scale bars: d, e = 100 µm, f–o = 20 µm

Figure 4.1 *Barriopsis caryotae* (HGUP 24-0028, holotype)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Aplosporella artocarpi* (CPC 22791) and *A. thailandica* (MFLU 16-0615). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.2 Phylogenetic tree of *Barriopsis* and *Sphaeropsis*

Botryosphaeria Ces. & De Not., Comm. Soc. crittog. Ital., 1(fasc. 4): 211 (1863)

Notes: *Botryosphaeria* was introduced by Cesati and De Notaris (1863). It has a variety of hosts and worldwide distributes (Liu et al., 2012; Hattori et al., 2021; Jayawardena et al., 2022). *Botryosphaeria* species are important plant pathogens and commonly associated

with canker diseases (Kurbetli & Demirci, 2014; Zheng et al., 2020; Dong et al., 2021; Kovač et al., 2021). Some are found in medicinal plants as endophytic fungi that produce valuable metabolites (Rai et al., 2012; Ntemafack et al., 2021). The sexual morphs are characterized by brown to black, globose ascostromata, with a central ostiole, papillate or not, septate pseudoparaphyses, bitunicate, clavate asci, with a short pedicellate and a small ocular chamber, and hyaline, aseptate, fusoid to ovoid ascospores (Liu et al., 2012). The asexual morphs have uni- to multilocular pycnidial, frequently embedded in stromatic tissue, holoblastic, hyaline, subcylindrical conidiogenous cells, with 1–2 percurrent proliferation, and hyaline, aseptate, narrowly fusiform, or irregularly fusiform conidia (Slippers et al., 2004; Crous et al., 2006).

Botryosphaeria agaves (Henn.) E.J. Butler, Ann. Mycol.9: 415 (1911)

≡ ***Physalospora agaves*** Henn., Bot. Jb. 34: 51 (1905)

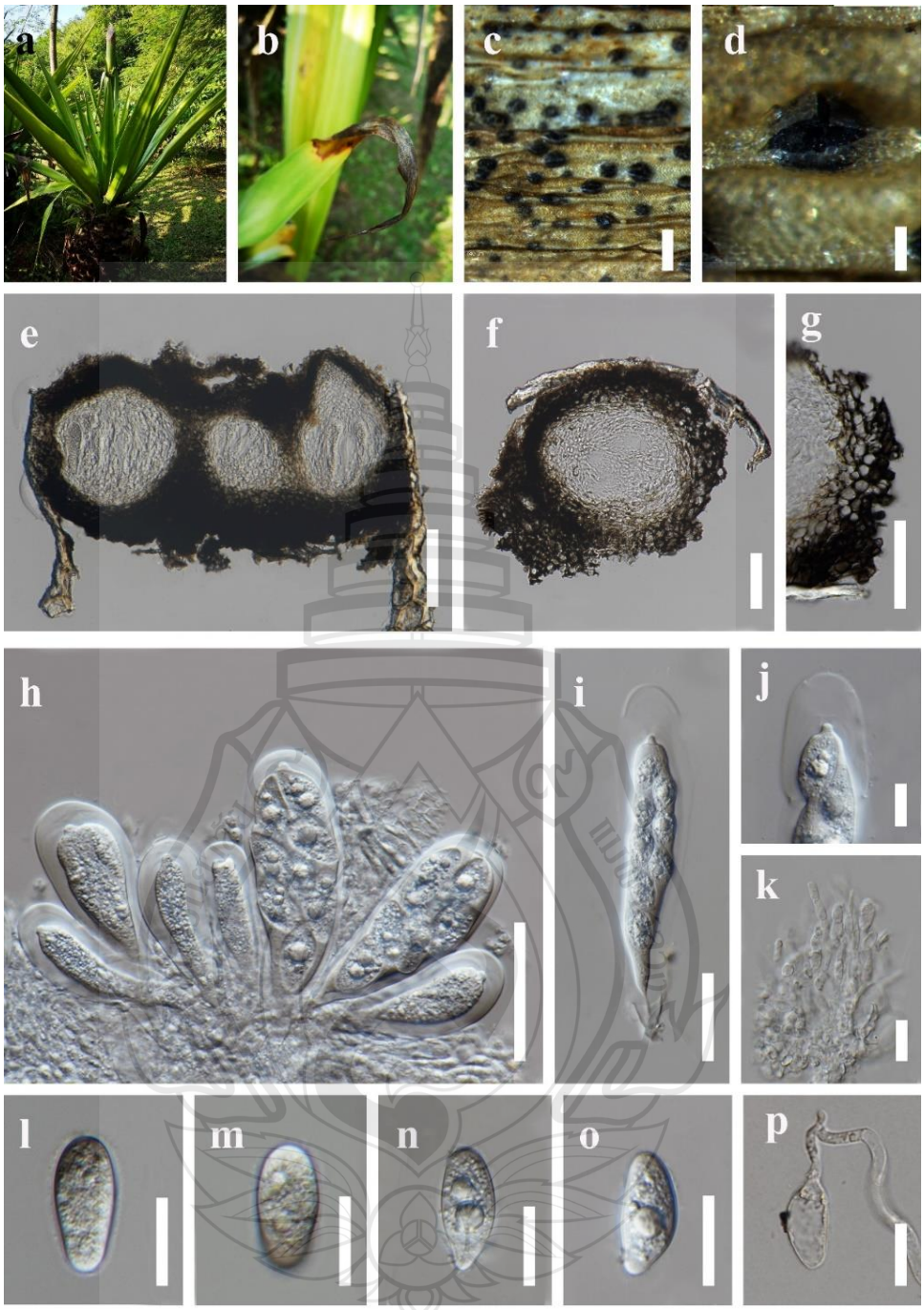
Index Fungorum number: IF 119799; Facesofungi number: FoF 02410; Figure 4.3

Associated with leaf blight of *Agave sisalana*. **Sexual morph**: *Ascomata* 150–300 µm wide, 225–300 µm high, semi-immersed, solitary or scattered, erumpent through host epidermis, black shiny dots are visible on the host surface, globose to subglobose, uniloculate to multiloculate, black, thick-walled, with a central ostiole. *Ostioles* central., *Peridium* 40–65 µm wide, comprising several layers of pale to dark brown walled cells of textura angularis. *Pseudoparaphyses* 2–4.5 µm wide, septate, numerous. *Asci* 90–180 × 25–39 µm, 8–spored, bitunicate, fissitunicate, clavate to cylindroclavate, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 26–37 × 13–18 µm ($\bar{x}$ = 31 × 16 µm, n = 30), 2–seriate at the ascus apex, 1–seriate at the base, hyaline, aseptate, ellipsoidal, fusiform, or inequilateral, guttulate, some membrane swells in water and surrounds the ascospore. **Asexual morph**: Not observed.

Culture characteristics: Conidia germinated on PDA within 12 h at 26 °C. Colonies on PDA reached 10 cm diam. after 3 weeks at 26 °C; mycelium brown, flossy, dark brown from above, black from reverse.

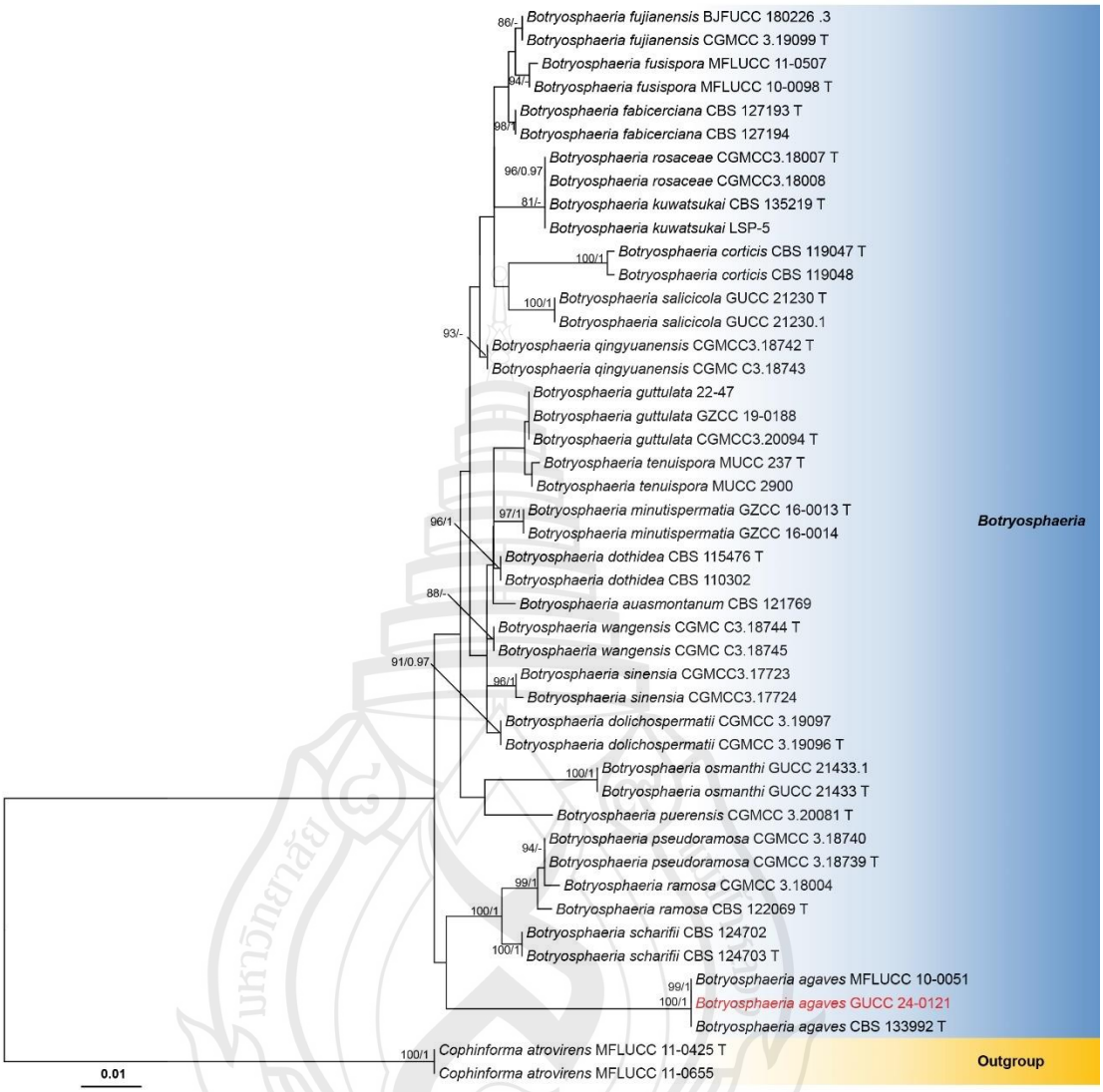
Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on leaves of *Agave sisalana*, 3 May 2020, Y.R. Sun, B23 (HGUP 24-0027), living culture GUCC 24-0121.

Notes: Our collection clustered together with *B. agaves* (MFLUCC 10-0051 and CBS133992) which were also isolated from *Agave* sp. in the phylogenetic tree (Figure 4.4). They also exhibit very similar morphological characteristics, including colour and size of ascomata, asci and ascospores (Liu et al., 2012; Phillips et al., 2013). Therefore, MFLU B23 was identified as *B. agaves*, representing a new collection. Liu et al. (2012) proposed a specimen from *Agave* sp. collected in Thailand (MFLU 11–0161) as the epitype for *B. agaves*. However, Phillips et al. (2013) deemed this proposal was invalid since Liu et al. (2012) neither cited nor examined the holotype, and subsequently designated the specimen from Thailand as the neotype. Liu et al. (2012) described the spores of *B. agaves* as surrounded by a mucilaginous sheath but Phillips et al. (2019) disagreed, and believed that it was the membrane rather than the true sheath. We share the same viewpoint as Phillips et al. (2019) through careful observation of the slides.



Note a, b Host. c, d Appearance of ascomata on host substrate. e, f Section of stromata. g Peridium. h–i Asci. j Apical inner layer of an ascus with small ocular chamber. k Paraphyses. l–o Ascospores. p Germinated ascospores. Scale bars: c = 1000 µm, d = 200 µm, e = 100 µm, f–i = 50 µm, j–p = 20 µm

Figure 4.3 *Botryosphaeria agaves* (HGUP 24-0027)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Cophinforma atrovirens* (MFLUCC 11-0425 and MFLUCC 11-0655). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.4 Phylogenetic tree of *Botryosphaeria*

Lasiodiplodia Ellis & Everh.

Notes: *Lasiodiplodia* was established by Clendenin (1896) and typified by *L. tubericola*. It has both asexual and sexual morphs (Wu et al., 2021). *Lasiodiplodia* species are known to be plant pathogens, causing diseases in a wide world. These fungi can infect various crops, including fruits, vegetables, and medicinal plants, leading to economic losses in agriculture (Abdollahzadeh et al., 2010; Netto et al., 2014; Dong et al., 2019; Meng et al., 2021). So far, there are 82 validly published *Lasiodiplodia* species in Species Fungorum (accessed on 21 June 2024). In this study, we introduce two new *Lasiodiplodia* species from medicinal plants.

Lasiodiplodia houttuyniae Y.R. Sun, Yong Wang bis & K.D. Hyde, sp. nov.

Facesoffungi number: FoF 16405; Figure 4.5

Etymology: Referring to the host genus.

Holotype: HGUP 24-0029.

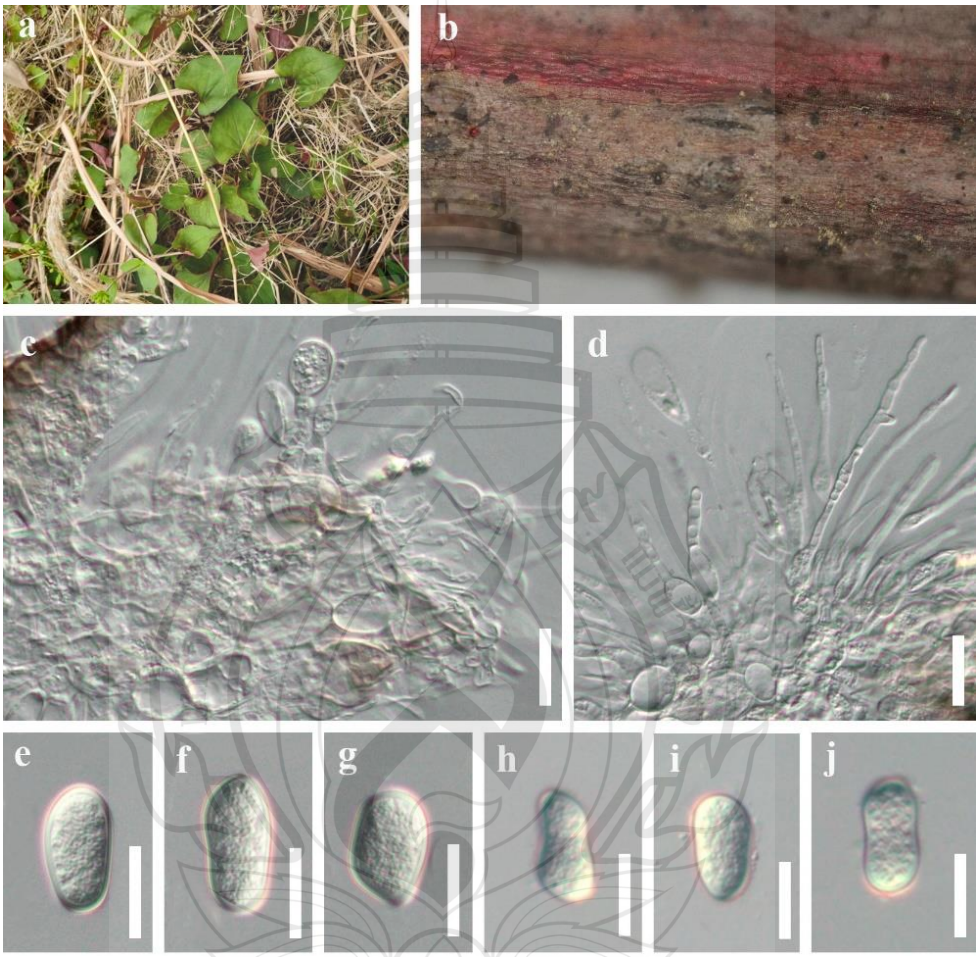
Saprobic on *Houttuynia cordata*, forming conspicuous, black spots on the host surface. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* semi-immersed in the substrate, solitary, gregarious or confluent, globose to subglobose, dark brown. *Paraphyses* 2.5–6 μm wide, hyaline, cylindrical, aseptate, not branched, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.5–5 μm wide, hyaline, cylindrical., *Conidia* 24–31 × 12–17 μm ($\bar{x}$ = 28 × 14 μm, n = 25), subglobose to oval, hyaline, aseptate, guttulate, thick-walled.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies reaching 10 cm diam. after 3 weeks at 26 °C, circular, white during the first few days, sparse, aerial, surface smooth with crenate edge, filamentous, after 2 weeks becoming black.

Material examined: CHINA, Guizhou Province, Tongren City, Jiangkou District, Yamugou Parkland, on twigs of *Houttuynia cordata*, 20 May 2022, Y.R Sun, JK29 (HGUP 24-0029, **holotype**), ex-type culture GUCC 24-0123.

Notes: *Lasiodiplodia houttuyniae* is phylogenetically sister to *Lasiodiplodia fici* which was isolated from diseased leaves of *Ficus altissima* in China (Xia et al., 2022) (Figure 4.7). The former differs in producing thinner conidiogenous cells (2.5–5 μm in *L. houttuyniae*

vs. 10–15 µm in *L. fici*) and wider conidia (11–17 µm in *L. houttuyniae vs.* 10–12 µm in *L. fici)*. In addition, there are 7 bp different (without gap, 296 bp) between GUCC 24-0123 and ZHKUCC 21-0125 in the *TEF1-α* gene. We thus introduced *L. houttuyniae* herein, representing a new species isolated from the medicinal plant, *Houttuynia cordata* in China.



Note a Host. b Conidiomata on host surface. c, d Conidia developing on conidiogenous cells and Paraphyses. e–j Conidia. Scale bars: c–j = 20 µm

Figure 4.5 *Lasiodiplodia houttuyniae* (HGUP 24-0029, holotype)

Lasiodiplodia liliacearum Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16406; Figure 4.6

Etymology: The specific epithet refers to the host family.

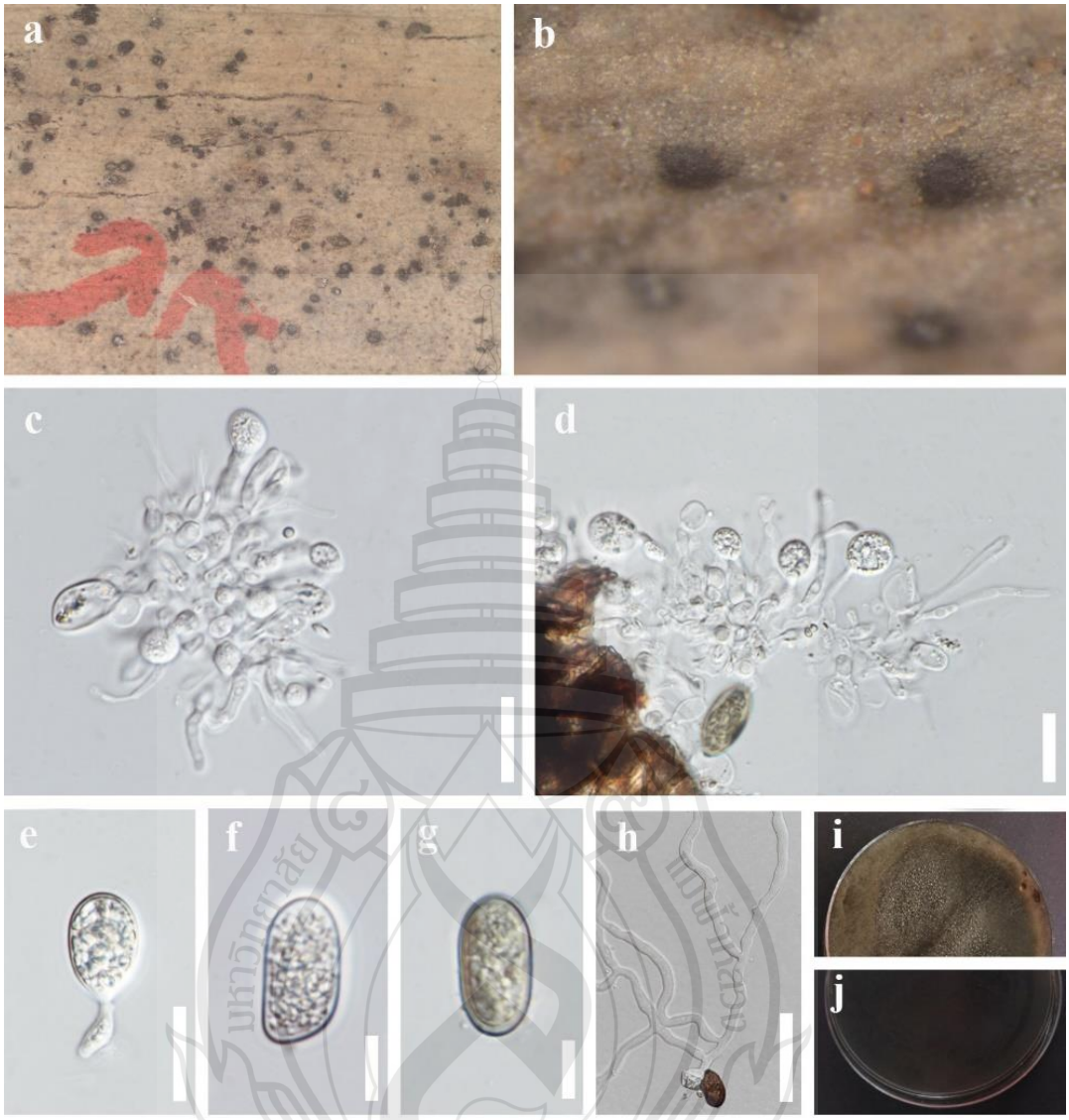
Holotype: HGUP 24-0030.

Associated with diseased leaves of *Dracaena* sp., forming conspicuous, black spots on the host surface. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* around 170 μm diam., semi-immersed in the substrate, solitary, gregarious or confluent, globose to subglobose, short neck, dark brown. *Paraphyses* 1.5–4 μm wide, hyaline, cylindrical, aseptate, not branched, rounded at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–4 μm wide, hyaline, cylindrical., *Conidia* 17–24 × 9–15 μm ($\bar{x}$ = 21 × 11 μm, n = 20), subglobose to oval, rounded at the apex, hyaline when young, brown when mature, aseptate or 1-septate, guttulate, thick-walled.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies reaching 10 cm diam. after 2 weeks at 26 °C, circular, white during the first few days, sparse, aerial, surface smooth with crenate edge, filamentous, after 2 weeks becoming black.

Material examined: THAILAND, Chiang Rai Province, Ban Du, on leaves pf *Dracaena* sp. (Liliaceae), 17 Jan 2021, Y.R Sun, CR19 (HGUP 24-0030, **holotype**), ex-type culture GUCC 24-0124.

Notes: *Lasiodiplodia liliacearum* is phylogenetically sister to *L. chonburiensis* (MFLUCC 16-0376) (Figure 4.7). In morphology, *L. liliacearum* differs from *L. chonburiensis* in having 1-septate, brown mature conidia and hyaline, unbranched, cylindrical paraphyses. In addition, there are 6 bp different (2.2%, without gap) in the *TEF1-α* region. We thus introduce *L. liliacearum* as a new species.



Note a, b Conidiomata on host surface. c, d Conidia developing on conidiogenous cells. e–g Conidia. h Germinating conidium. i, j Colonies after 7 days on PDA (i from above, j from below). Scale bars: c–e = 20 µm, f, g = 10 µm, h = 50 µm

Figure 4.6 *Lasiodiplodia liliacearum* (HGUP 24-0030, holotype)

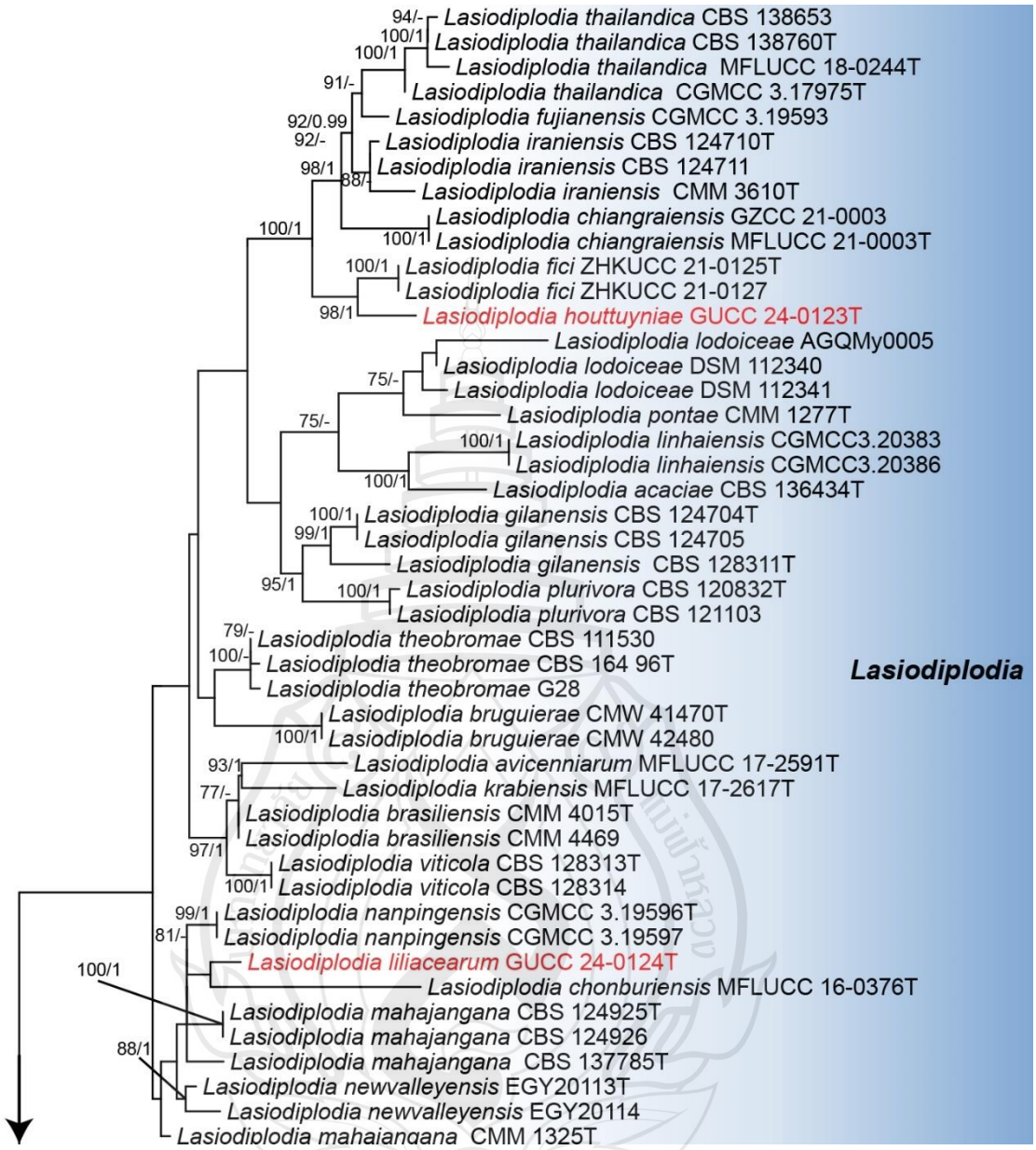
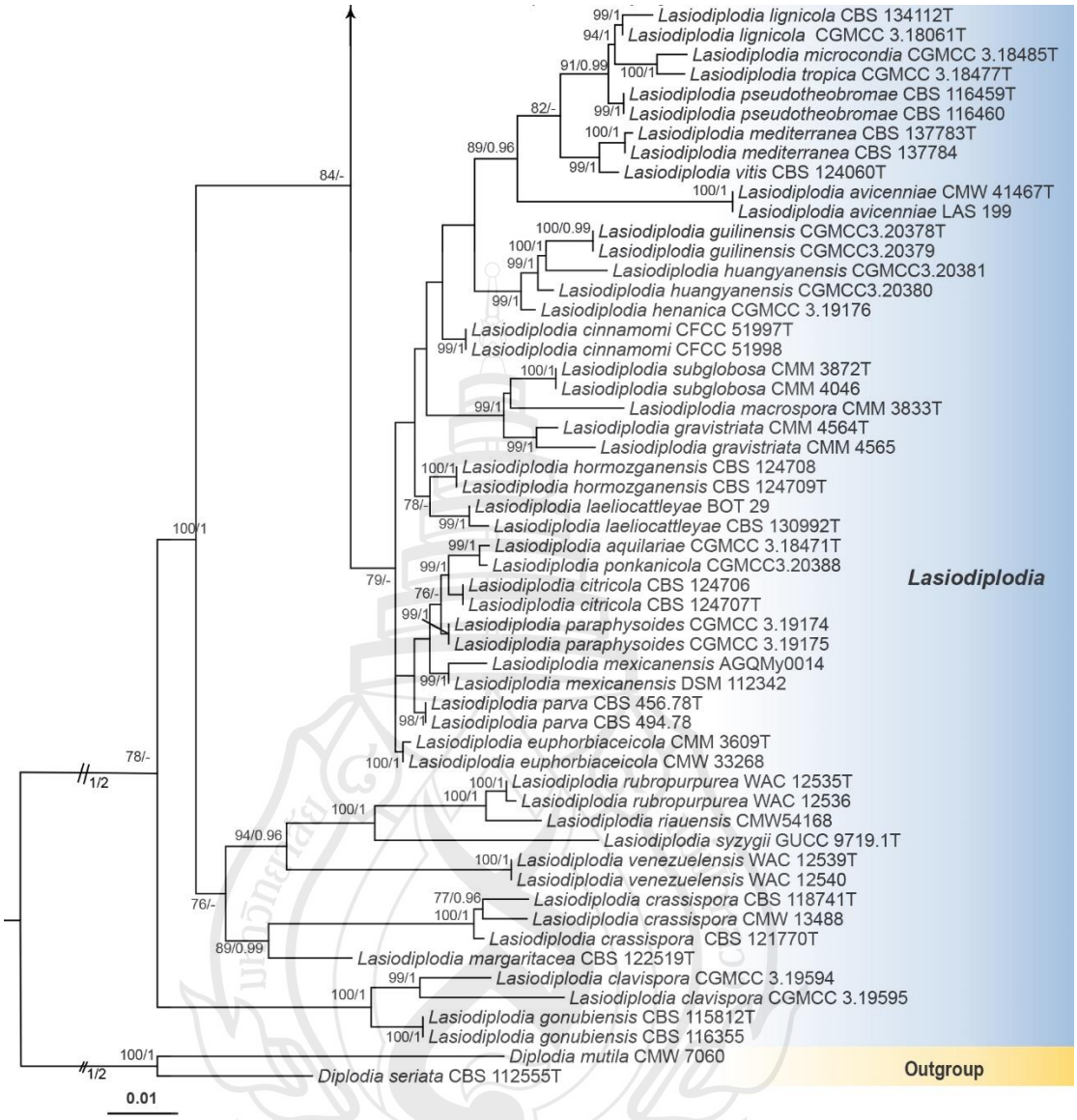


Figure 4.7 Phylogenetic tree of *Lasiodiplodia*



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Diplodia mutila* (CMW7060) and *D. seriata* (CBS 112555). The new collections are indicated in red and ex-type strains are indicated with T after the strain number.

Figure 4.7 (continued)

Neoscytalidium Crous & Slippers, Stud. Mycol. 55: 244 (2006)

Notes: Crous et al. (2006) introduced this genus and typified by *Neoscytalidium dimidiatum*. *Neoscytalidium* has been reported from America, Australia, Niger, Oman and Thailand as a plant pathogen, human pathogen and saprobe (Huang et al., 2016; Calvillo-Medina et al., 2019; Wonglom et al., 2023). Only five species are listed under this genus and the sexual morph has not been reported for any species (Wonglom et al., 2023; Species Fungorum 2024). The coelomycetous asexual morphs are characterized by stromatic, erumpent, unilocular to multilocular, glabrous, brown to black, globose to subglobose, papillate or not conidiomata, blastic, phialidic, cylindrical to subcylindrical, hyaline conidiogenous cells and ellipsoidal to oval, hyaline conidia (Huang et al., 2016; Nouri et al., 2018). The hyphomycetous syn-asexual morph has catenate, cylindrical to oblong, or doliiform, dark brown, 0–2-septate arthroconidia (Crous et al., 2006).

Neoscytalidium dendrobii Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16407; Figure 4.8

Etymology: Referring to the host genus which the fungus was collected.

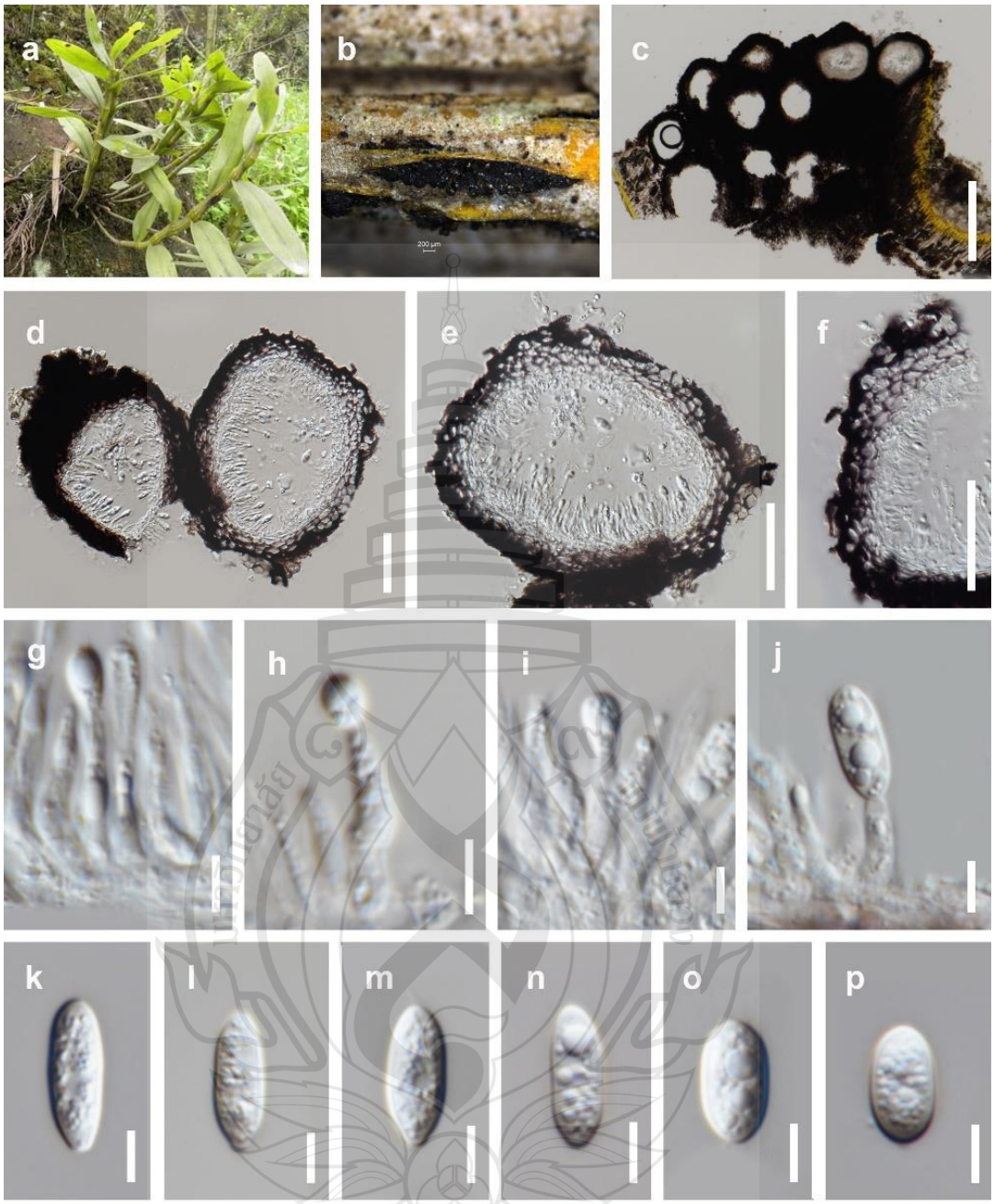
Holotype: HGUP 24-0031.

Associated with diseased twigs of *Dendrobium* sp. **Asexual morph**: *Conidiomata* stromatic, erumpent, grouped, subglobose or flask-shaped, unilocular to multilocular (2~10-loculate), black, without ostiole. *Peridium* 16–28 μm wide, thick-walled, dark brown, composed of dark brown, or brown to hyaline cells of textura angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–2 μm wide, enteroblastic, phialidic, cylindrical to subcylindrical, hyaline, smooth-walled. *Conidia* ellipsoidal to oval, hyaline, smooth, guttulate, aseptate, 10–14 × 4–6 μm ($\bar{x}$ = 12 × 5, n = 30). **Sexual morph**: Not observed.

Culture characteristics: Conidia germinated on PDA within 12 h at 26 °C. Colonies on PDA reached 10 cm diam. after 3 weeks at 25 °C; mycelium white, flossy, gray or pale brown from above, brown from reverse.

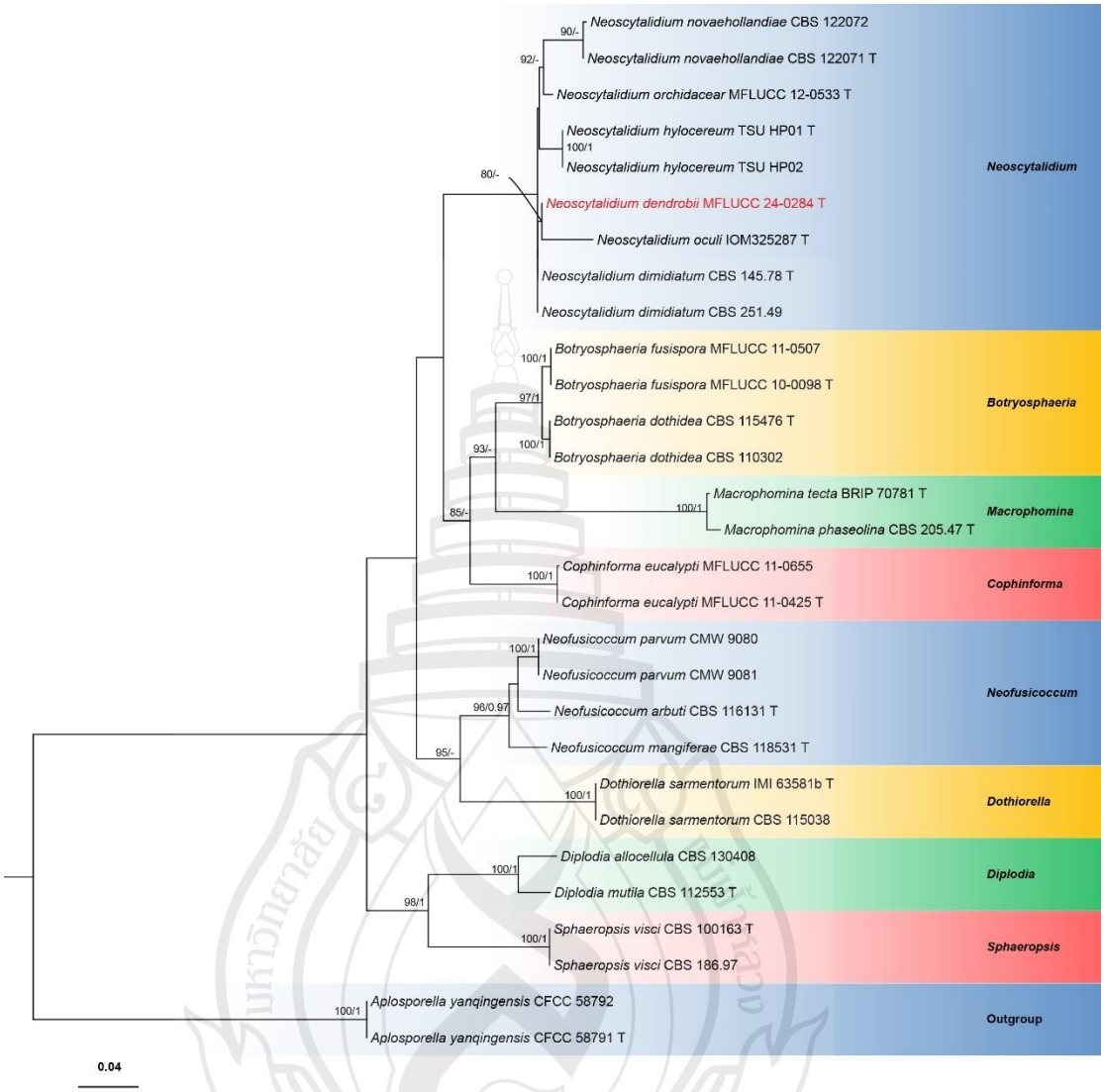
Material examined: THAILAND, Chiang Rai Province, Bandu District, saprobic on twigs of *Dendrobium* sp. plants, 6 March 2021, Y.R. Sun, 38 (HGUP 24-0031, **holotype**); ex-type culture MFLUCC 24-0284.

Notes: *Neoscytalidium dendrobii* is related to *N. oculi* and *N. dimidiatum* in the phylogenetic tree (Figure 4.9). In morphology, *N. dendrobii* can be distinct from other *Neoscytalidium* species by its multilocular conidiomata. Therefore, we propose the introduction of *N. dendrobii* sp. nov., isolated from the medicinal plant *Dendrobium* sp. in Thailand.



Note a Host. b Conidiomata on host surface. c–e Section through conidiomata. f Peridium. g–j Conidia developing on conidiogenous cells. k–p Conidia. Scale bars: c = 100 µm, d–f = 50 µm, g–p = 5 µm

Figure 4.8 *Neoscytalidium dendrobii* (HGUP 24-0031, holotype)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Aplosporella yanqingensis* (CFCC 58792) and (CFCC 58791). The new collections are indicated in red and ex-type strains are indicated with T after the strain number.

Figure 4.9 Phylogenetic tree of *Neoscytalidium*

Sphaeropsis Sacc., Michelia 2 (no. 6): 105 (1880)

Notes: *Sphaeropsis* was introduced to accommodate *Diplodia* species with brown, aseptate conidia (Saccardo, 1880). This genus was linked with *Phaeobotryosphaeria* by Phillips et al. (2008) based on the sexual and asexual morphs of *S. visci*. The sexual morph of *Sphaeropsis* is charactered by bitunicate, 8-spored, well-developed apical chamber asci, and brown, aseptate ascospores with small apiculus at either end (Phillips et al., 2008). The asexual morph has hyaline, discrete conidiogenous cells, oval, oblong or clavate, aseptate, moderately thick-walled conidia (Phillips et al., 2008; Phillips et al., 2013). There are 139 *Sphaeropsis* species were accepted in the Species Fungorum (2024) but only low proportion with DNA sequences. In this study, we introduced one new species and synonymized *Sphaeropsis guizhouensis* under *Sphaeropsis linhaiensis*.

Sphaeropsis guiyangensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16408; Figure 4.10

Etymology: The specific epithet refers to the location, where the fungus was collected.

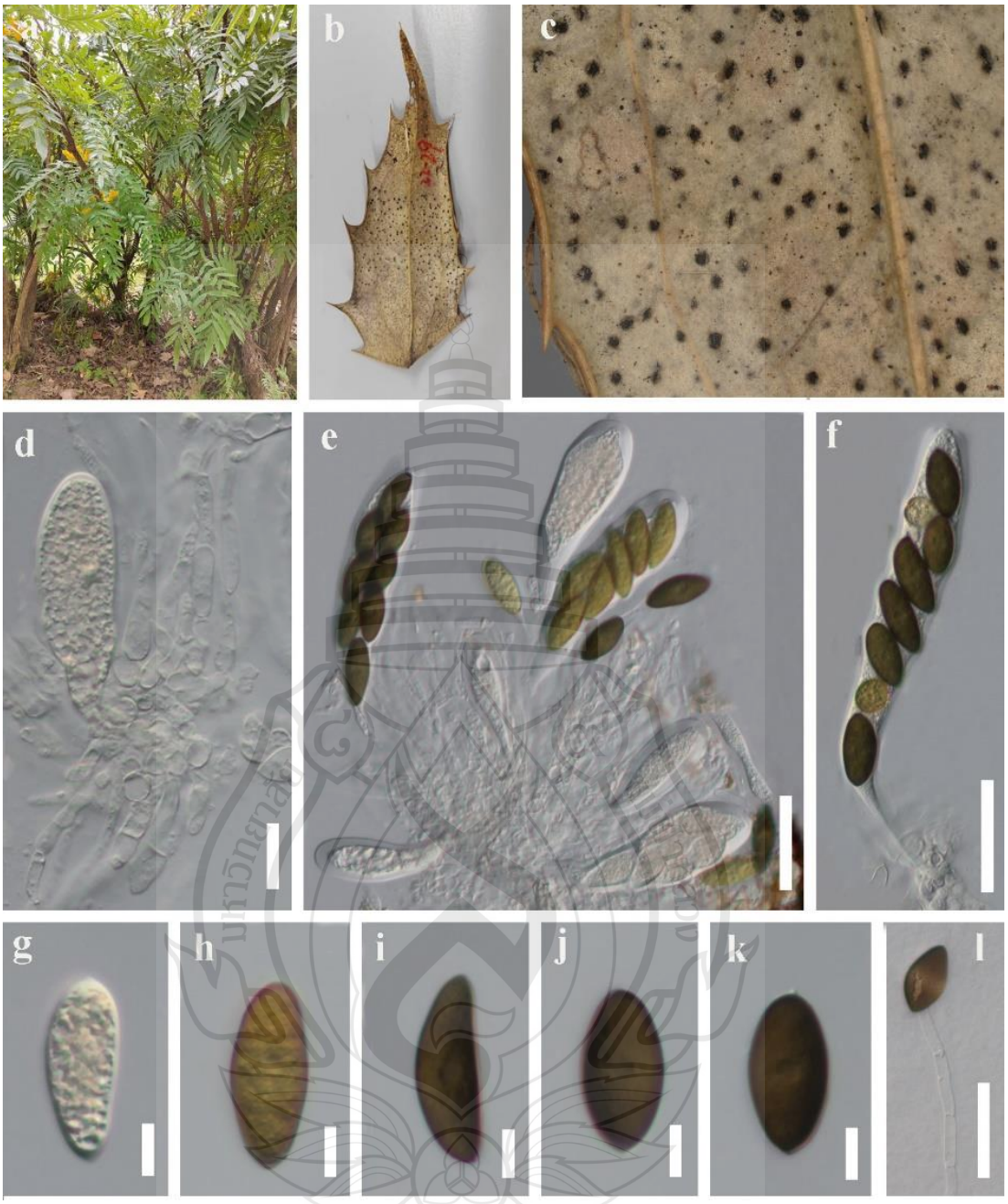
Holotype: HGUP 24-0032.

Associated with diseased leaves of *Mahonia fortune*. **Sexual morph**: *Ascostromata* black, convex on host tissue, semi-immersed, solitary or gregarious, globose to sub-globose. *Ostiole* raised, centric. *Hamathecium* comprising 3–7 μm wide, hyaline, numerous, septate pseudoparaphyses. *Asci* 130−205 × 25–30μm ($\bar{x}$ = 155 × 28 μm, n = 15), 8-spored, bitunicate, straight or slightly curved, cylindro-clavate or clavate, apically rounded with an ocular chamber. *Ascospores* 24–40 × 12–16 μm ($\bar{x}$ = 33 × 14 μm, n = 25), overlapping biseriate, aseptate, smooth, ellipsoid to ovoid or fusiform, hyaline when young, gradually changes from brown to dark brown, ends rounded. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 12 h. Germ tubes produced from germ pore of ascospores. Colonies on PDA reaching 5 cm after 7 days at 25 °C, flat or effuse, undulate, initially white, brownish grey in the center, white at the edge.

Material examined: CHINA, Guizhou Province, Guiyang City, Guizhou Province, on diseased leaves of *Mahonia fortune*, 12 Dec 2022, Y.R Sun, 22-29 (HGUP 24-0032, **holotype**); ex-type culture GUCC 24-0126; ibid., on decaying twigs, 12 Dec 2022, Y.R Sun, 22-2 (HGUP 24-0033); living culture GUCC 24-0127.

Notes: *Sphaeropsis guiyangensis* was isolated from the diseased leaves of *Mahonia fortune* and dead twigs of unknown plant in Guiyang City, China. Two collections HGUP 24-0032 and HGUP 24-0033 clustered together with good support (ML-BS = 98%, BYPP = 1) and formed a sister clade to *S. citrigena* (ICMP 16812 and ICMP 16818) (Figure 4.2). *Sphaeropsis guiyangensis* differs from *S. citrigena* in having brown to dark brown, narrower ascospores (12–16 μm in *S. guiyangensis vs.* 15.5–18μm in *S. citrigena*), and narrower asci (25–30 μm in *S. guiyangensis vs.* 35–43 μm in *S. citrigena*) (Phillips et al., 2013).



Note a Host. b, c Appearance of ascomata on host substrate. d Paraphyses and immature ascus. e–f Asci. g–k Ascospores. i. Germinated ascospores. Scale bars: d = 20 µm, e, f, l = 50 µm, g–k = 10 µm

Figure 4.10 *Sphaeropsis guiyangensis* (HGUP 24-0032, holotype)

Sphaeropsis linhaiensis X.E. Xiao, Crous & H.Y. Li, Persoonia 47: 131 (2021)

= *Sphaeropsis guizhouensis* Ya Ya Chen, Dissan. & Jian K. Liu, Journal of Fungi 7 (no. 893): 31 (2021)

Notes: *Sphaeropsis linhaiensis* was formally introduced as a new species with an asexual morph by Xiao et al. (2021), while *Sphaeropsis guizhouensis* presented with a sexual morph, was introduced by Dissanayake et al. (2021). Due to their close publication dates, their phylogenetic results did not incorporate with each other. Notably, these two collections clustered together in our phylogenetic tree (Figure 4.2) and no base pair differences were observed in the ITS and *TEF1-α* gene regions. Consequently, we propose the synonymization of *S. guizhouensis* under *S. linhaiensis* based on their published data.

Hysteriales Lindau. Nat. Pflanzenfam., Teil. I (Leipzig) 1: 265 (1896)

Hysteriaceae Chevall. 1826, Flore Générale des Environs de Paris 1: 432 (1826).

Psiloglonium Höhn., Annls mycol. 16(1/2): 149 (1918)

Notes: *Psiloglonium* was initially proposed by von Höhnel (1918), Petrak (1923) designated *P. lineare* as the type species. Zogg (1962) synonymized *Psiloglonium* under *Glonium*, a decision supported by von Arx and Müller (1975). Boehm et al. (2009) re-established *Psiloglonium* in Hysteriaceae, to accommodate nonsubiculate species with apically obtuse, hyaline didymospores. Li et al. (2016) introduced *Psiloglonium macrosporum* with brown ascospores. Two *Psiloglonium* species with brown ascospores were also introduced in this study. Therefore, we considered the color of spores not suitable as a basis for intergeneric classification and have updated the description. The sexual morphs have hysterothecial, dark, superficial ascomata, 4–8-spored, bitunicate, fissitunicate, clavate asci and fusiform, hyaline or brown, septated ascospore with or without sheath. The asexual morph is sporidesmium-like (Rossman et al., 2016). The genus has a broad geographical distribution and is primarily isolated as saprobes from Caprifoliaceae, Ephedraceae, Loganiaceae, and Poaceae (Boehm et al., 2009; Liu et al., 2015; Li et al., 2016). There are 16 species are accepted in Species Fungorum (2024) but only seven with molecular data.

Psiloglonium bambusicola Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902588; Facesoffungi number: FoF 16409; Figure 4.11

Etymology: Bambusicola, referring to the host.

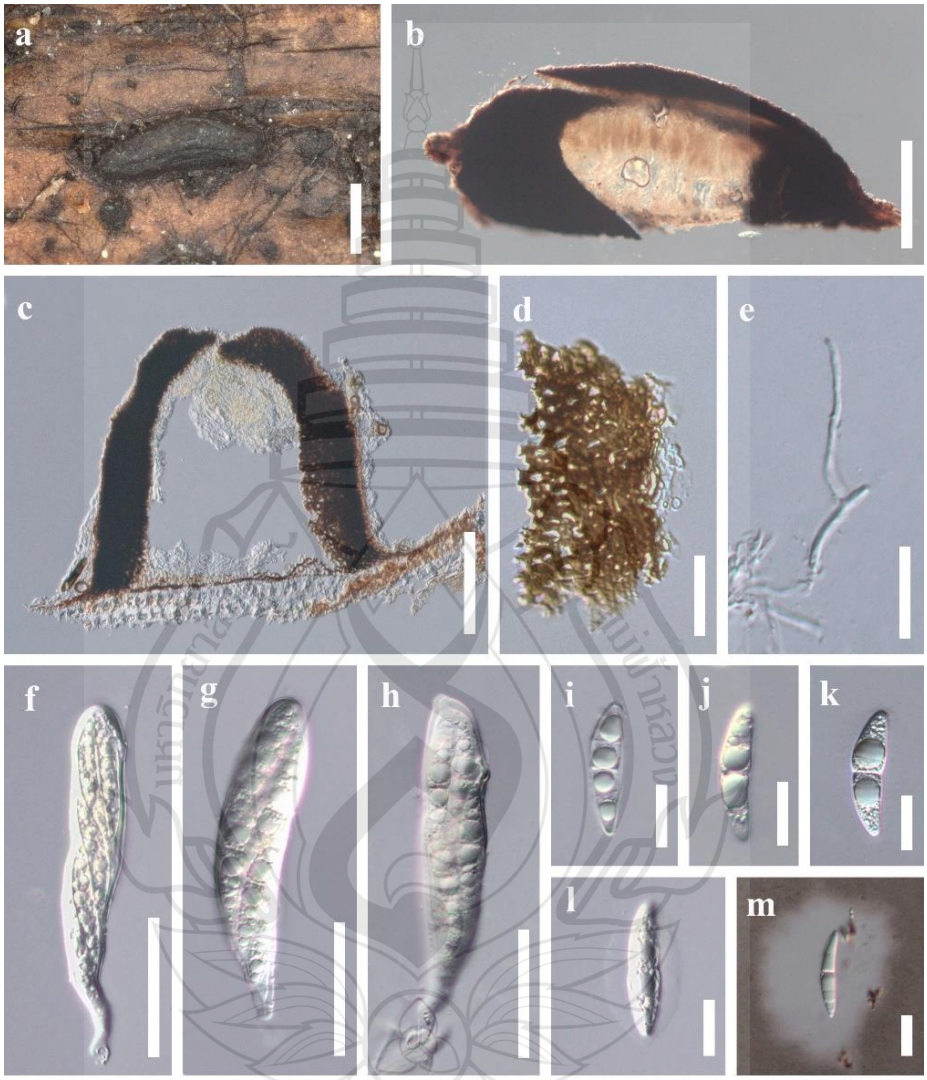
Holotype: HKAS 136907.

Saprobic on dead branch of bamboo. **Sexual morph**: *Ascomata* hysterothecial, gregarious, superficial, solitary, dark, elongate, shieldshaped, or irregular, joined at ridges, slightly straight, with central slit-like opening, 270–320 μm high, 230–260 μm wide, 800–1087 μm long. *Peridium* 56–75 μm wide, carbonaceous, thick-walled, brown, composed of several cell layers of small, brown, dull cells arranged in *textura angularis* to *textura globulosa*. *Hamathecium* composed of 1–2 μm wide, dense, trabeculate, anastomosing, pseudoparaphyses. *Asci* 121–137 × 17–25 μm ($\bar{x}$ = 129 × 22 μm, n = 10), 8-spored, bitunicate, fissitunicate, clavate, slightly curved, short pedicellate with obtuse ends, apically rounded. *Ascospores* 40–52 × 6–12 μm ($\bar{x}$ = 46×10 μm, n = 20), overlapping 1–3-seriate, fusiform, hyaline, 1–2-septate, constricted at the septa, slightly curved, smooth-walled, guttulate, surrounded by mucilaginous sheath. **Asexual morph**: Not observed.

Material examined: CHINA, Yunnan Province, Yuxi City, Xinping Yi and Dai Autonomous County, Gasa Town, the Ailao Mountain Nature Reserve, Dujuan Lake, on branches of bamboo, 22 February 2022, H.W. Shen, YN06 (HKAS136907, **holotype**); ex-type culture GUCC 24-0065.

Notes: *Psiloglonium bambusicola* was isolated from bamboo in a terrestrial habitat in China. It formed a distinct clade and related to *P. guizhouense, P. sasicola* and *P. simulans* in the phylogenetic tree (Figure 4.16). The distinguishing feature between *P. bambusicola* and *P. sasicola* lies in the larger ascospores of the former, measuring 40–52 × 6–12 μm as opposed to 25–32 × 5–8 μm in the latter (Boehm et al., 2009). *Psiloglonium bambusicola* can be differentiated from *P. simulans* by its larger ascospores with a sheath (40–52 × 6–12 μm *vs.* 14–16 × 5–6 μm) (Boehm et al., 2009). Furthermore, *Psiloglonium bambusicola* has larger asci than *P. guizhouense* (121–137 × 17–25 μm *vs.* 108–126 μm long, 15–17 μm wide) (This study). The ascospore size of *P. bambusicola* is similar to that of *P. hysterinum* (without

molecular data); however, the ascospores in *P. hysterinum* exhibit acuminate spore apices, and there is no sheath (Boehm et al., 2009). We thus introduced *P. bambusicola* as a novel species herein.



Note a Appearance of ascomata on substrate. b, c Section through ascoma. d Peridium. e Pseudoparaphyses. f–h asci. i–l Ascospores. m Ascospores with gelatinous sheath in Indian ink. Scale bars: a, b = 500 µm, c, = 100 µm, d, f–h, o = 50 µm, e, i–n = 20 µm

Figure 4.11 *Psiloglonium bambusicola* (HKAS136907, holotype)

Psiloglonium brunneum Y.R. Sun, Yong Wang bis & K.D. Hyde, sp. nov.

Index Fungorum number: IF902582; Facesoffungi number: FoF 16410; Figure 4.12

Etymology: The specific epithet brownii refers to the brown ascospores.

Holotype: HKAS 136873.

Saprobic on dead branch of Poaceae plant. **Sexual morph**: *Ascomata* hysterothecial, gregarious, superficial, dark, elongate, shieldshaped, or irregular, joined at ridges, with central, slit-like opening, 280–387 μm high, 227–297 μm wide, 677–845 μm long. *Peridium* 16–44 μm wide, carbonaceous, thick-walled, opaque dark and glossy, composed of several cell layers of small, opaque, dark, dull cells arranged in textura angularis to textura globulosa. *Hamathecium* composed of 1–3 μm wide, dense, trabeculate, anastomosing, pseudoparaphyses, slightly swollen at the apex. *Asci* 62–70 × 8–11 μm, 8-spored, bitunicate, fissitunicate, clavate, short pedicellate with obtuse ends, apically rounded. *Ascospores* 18–21 × 5–7 μm ($\bar{x}$ = 19 × 6 μm, n = 20), overlapping 1–2-seriate, fusiform with acute ends, some with unobvious polar appendages, hyaline when young and becoming brown at maturity, 1-septate, constricted at the septa, slightly curved, smooth-walled. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 12 h. Colonies reaching 3 cm diam. on PDA after 21 days at 25 °C, circular, effuse, dense, smooth surface with entire to slightly undulate edge, gray from the above, dark brown to black from below.

Material examined: CHINA, Guizhou Province, Guiyang City, Huaxi District, Gaopo Gaopo Township, Shuitang Village, on branches of Poaceae plant, 18 November 2022, Y.R. Sun, H3 (HKAS 136873, **holotype**); ex-type culture GUCC 24-0061.

Notes: Our collection was placed in *Psiloglonium* and grouped with *P. araucanum*, *P. colihuae* and *P. multiseptatum* in the phylogenetic tree (Figure 4.16). In morphology, our collection differs from them in having brown ascospores. In addition, *P. brunneum* has smaller spores than *P. araucanum* (18–21 × 5–7 μm *vs.* 22–28 × 8–10 μm; L/W: 3.2 *vs*. 2.7) (Boehm et al., 2009). *Psiloglonium brunneum* differs from *P. colihuae* in having smaller asci (62–70 × 8–11μm *vs.* 80–95×17–18 μm) and shorter spores (18–21 × 5–7 μm *vs.* 30–35 × 4–

6 µm) (Boehm et al., 2009). *Psiloglonium brunneum* is different from *P. multiseptatum* by 1-septate ascospores without sheath (Liu et al., 2015). Therefore, we introduced *P. brunneum* sp. nov., isolated from Poaceae plant in China.



Note a Host. b, c Appearance of ascomata on host substrate. d, e Section of stromata. f Pseudoparaphyses. g–i Asci. j–m Ascospores. n Germinated ascospores. Scale bars: d–f = 50 µm, g–i, n = 20 µm, j–m = 10 µm

Figure 4.12 *Psiloglonium brunneum* (HKAS 136873, holotype)

Psiloglonium guizhouense Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902589; Facesoffungi number: FoF 16411; Figure 4.13

Etymology: guizhouense, referring to the location where the fungus was collected.

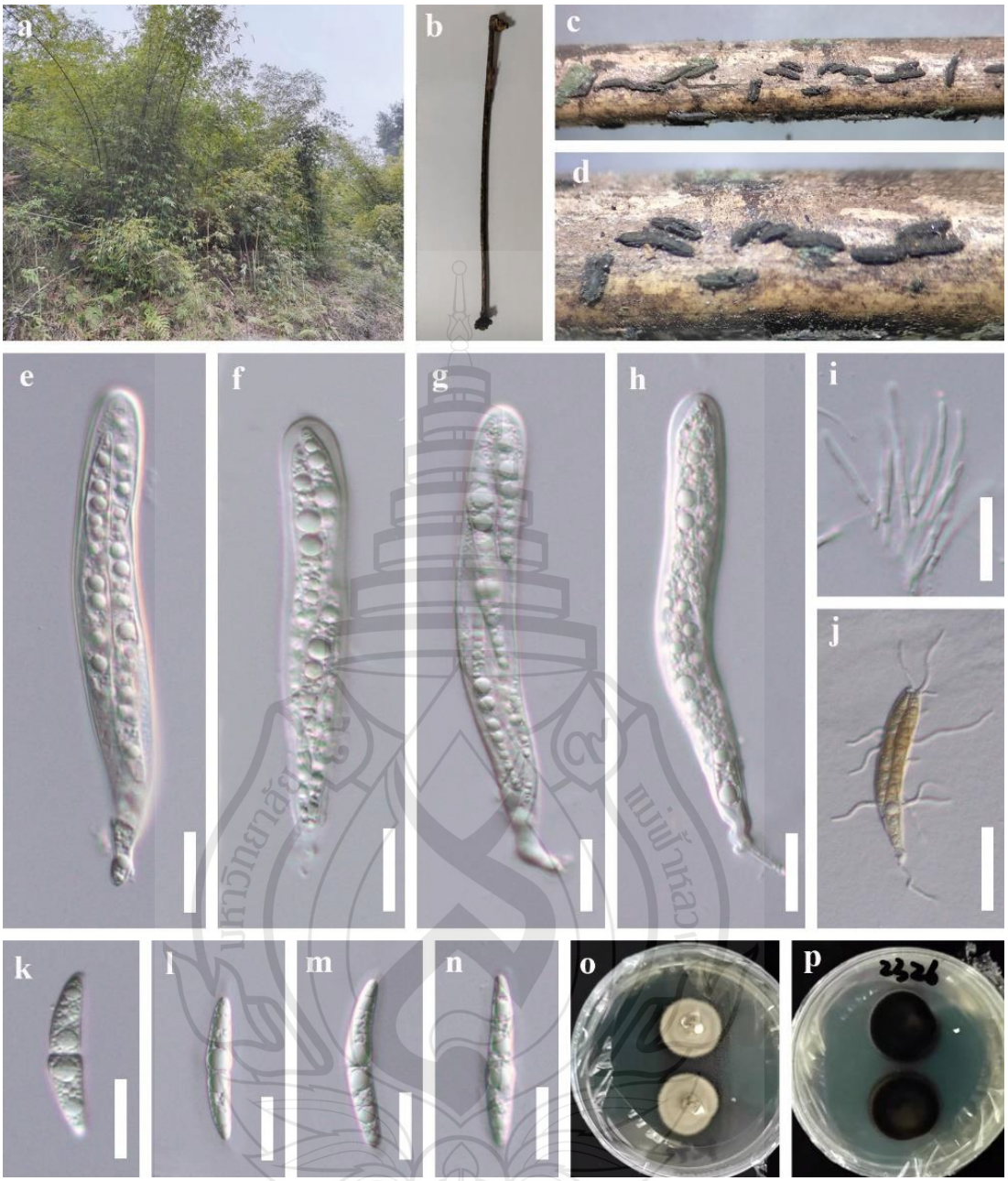
Holotype: HKAS 136880.

Saprobic on dead branchs of bamboo. **Sexual morph**: *Ascomata* hysterothecial, gregarious, superficial, solitary, dark, elongate, shieldshaped, or irregular, joined at ridges, with central slit-like opening. *Peridium* carbonaceous, thick-walled, dark brown, composed of several cell layers of small, brown, dull cells arranged in *textura angularis* to *textura globulosa*. *Hamathecium* composed of 1–2 μm wide, dense, trabeculate, anastomosing, pseudoparaphyses. *Asci* 108–126 μm long, 15–17 μm wide, 8-spored, bitunicate, fissitunicate, clavate, slightly curved, short pedicellate with obtuse ends, apically rounded. *Ascospores* 41–50 × 6–10 μm ($\bar{x}$ = 45 × 8 μm, n = 20), overlapping 1–3-seriate, fusiform, hyaline or brown, 1-septate, constricted at the septa, slightly curved, smooth-walled, with small and large guttulate, surrounded by mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 12 h. Colonies reaching 30 mm diam. on PDA after 21 days at 26 °C, circular, effuse, dense, smooth surface, with the entire edge, gray from the above, black from below.

Material examined: CHINA, Guizhou Province, Guiyang City, Wudang District, Xiangzhigou Village, on branches of bamboo, 13 February 2023, Y.R. Sun, 2326 (HKAS 136880, **holotype**); ex-type culture GUCC 24-0066.

Notes: *Psiloglonium guizhouense* formed a distinct branch, sistering to *P. sasicola* in the phylogenetic tree (Figure 4.16). This species and *P. sasicola* differ in that the former possesses larger spores (41–50 × 6–10 μm *vs*. 25–32 × 5–8 μm), lacking a sheath (Boehm et al., 2009). The preceding arguments substantiate the proposal to classify *P. guizhouense* as a noval species.



Note a, b Host. c, d Appearance of ascomata on host substrate. e–h Asci. i Pseudoparaphyses. j Germinated ascus. k–n Ascospores. o, p Colony on PDA medium. Scale bars: j = 50 µm, e–i, k–n = 20 µm.

Figure 4.13 *Psiloglonium guizhouense* (HKAS 136880, holotype)

Rhytidhysteron Speg. [as '*Rhytidhysterion*'], Anal., Soc. cient. argent. 12(4): 188 (1881).

Notes: *Rhytidhysteron* was introduced by Spegazzini (1881), and Clements and Shear (1931) subsequently designated *R. brasiliense* as the type species. Most *Rhytidhysteron* species have been recognized as saprobes in both terrestrial and marine habitats, with a subset reported as endophytes or weak pathogens (Thambugala et al., 2016; Soto-Medina & Lücking, 2017; Hyde, de Silva et al., 2020; Wanasinghe et al., 2021; Ren et al., 2022; Du et al., 2023). There are 33 species listed in this genus (Species Fungorum, 2024).

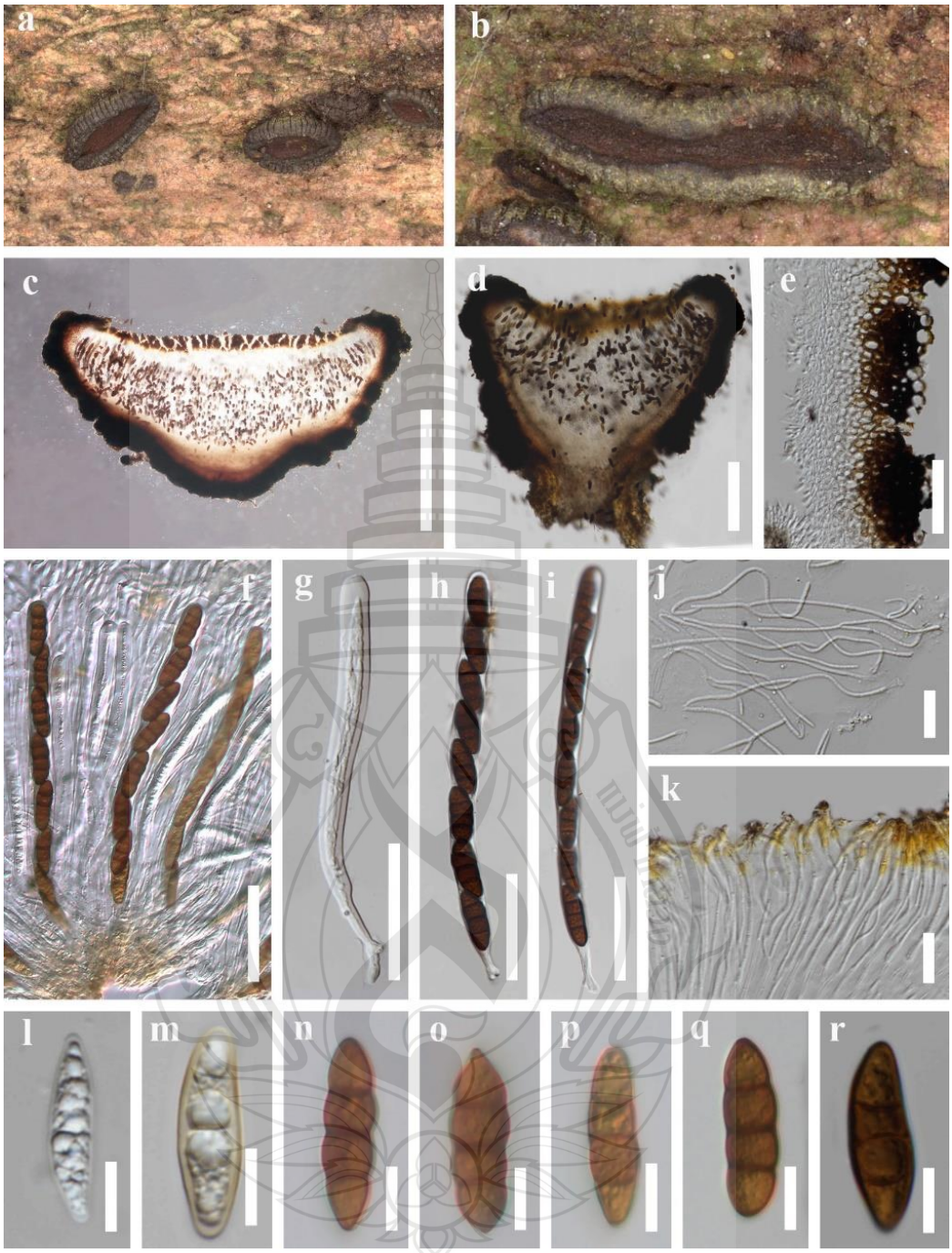
Rhytidhysteron rufulum (Spreng.) Speg., Anal., Soc. cient. argent. 90(1-6): 177 (1921) [1920]

Index Fungorum number: IF121714; Facesoffungi number: FoF 01839; Figure 4.14

Saprobic on decaying twigs of *Ligustrum* sp. **Sexual morph**: *Hysterothecia* 1046–2278 μm long, 357–983 μm high, 795–1063 μm wide, black, solitary, superficial, coriaceous, elliptical or irregular in shape, elongated with a longitudinal slit. *Exciple* 68–100 μm wide, composed of dark brown, thick-walled cells of *textura angularis*, outer layer brown to dark brown, inner layer hyaline to pale brown. *Hamathecium* 1–2.5 μm wide, dense, hyaline, septate, numerous, branched, cellular pseudoparaphyses, forming a yellow epithecium above asci when mounted in water. *Asci* 153–220 × 8–14 μm ($\bar{x}$ = 190 × 12 μm, n = 15), 8-spored, bitunicate, cylindrical, with a short furcate pedicel, apically rounded, surround by pseudoparaphyses. *Ascospores* 26–32 × 7–12 μm ($\bar{x}$ = 29 × 10 μm, n = 40), uni-seriate, hyaline to pale brown when young, brown when mature, 1–3-septate, oval to fusiform, slightly rounded or pointed at both ends, with granular appearance. **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, on twigs of *Ligustrum* sp., 31 August 2019, Y.R. Sun, MX9 (HGUP 24-0070); ibid, China, Guizhou Province, Chishui City, Chishui Danxia Tourist Area, on dead wood, 12 April 2023, Y.R. Sun, 23101 (HKAS 136869).

Notes: Our two collections clustered together and related to *Rhytidhysteron esperanzae*, *R. mexicanum* and *R. rufulum* in the phylogenetic tree (Figure 4.16). Our collections can be distinct from *R. esperanzae* and *R. mexicanum* by smaller ascospore (26–32 × 7–12 µm in our collection *vs.* 45–47 × 17–19 µm in *R. esperanzae vs.*34–40 × 10–12 µm in *R. mexicanum*) (Cobos-Villagrán, Raymundo et al., 2021; Cobos-Villagrán, Valenzuela et al., 2021). They did not cluster together with *R. rufulum* but showed similar morphological characteristics and size to *R. rufulum* (Thambugala et al., 2016). In addition, few differences exist among their ITS (7/530, without gaps) and LSU (3/645, without gaps), respectively. We thus report our collection as a new host record of *R. rufulum* isolated from *Ligustrum* sp. in China.



Note a, b Appearance of hysterothecia on the host. c, d Vertical section through hysterothecium. e Exciple. f–i Asci. j Pseudoparaphyses. k Epithecium mounted in water. l–r Ascospores. Scale bars: c = 500 µm, d = 200 µm, e–i = 50 µm, j, k = 20 µm, l–r = 10 µm

Figure 4.14 *Rhytidhysteron rufulum* (HKAS 136869)

Rhytidhysteron hongheense Wanas. J. Fungi 7, 180 (2021)

Index Fungorum number: IF 837992; Figure 4.15

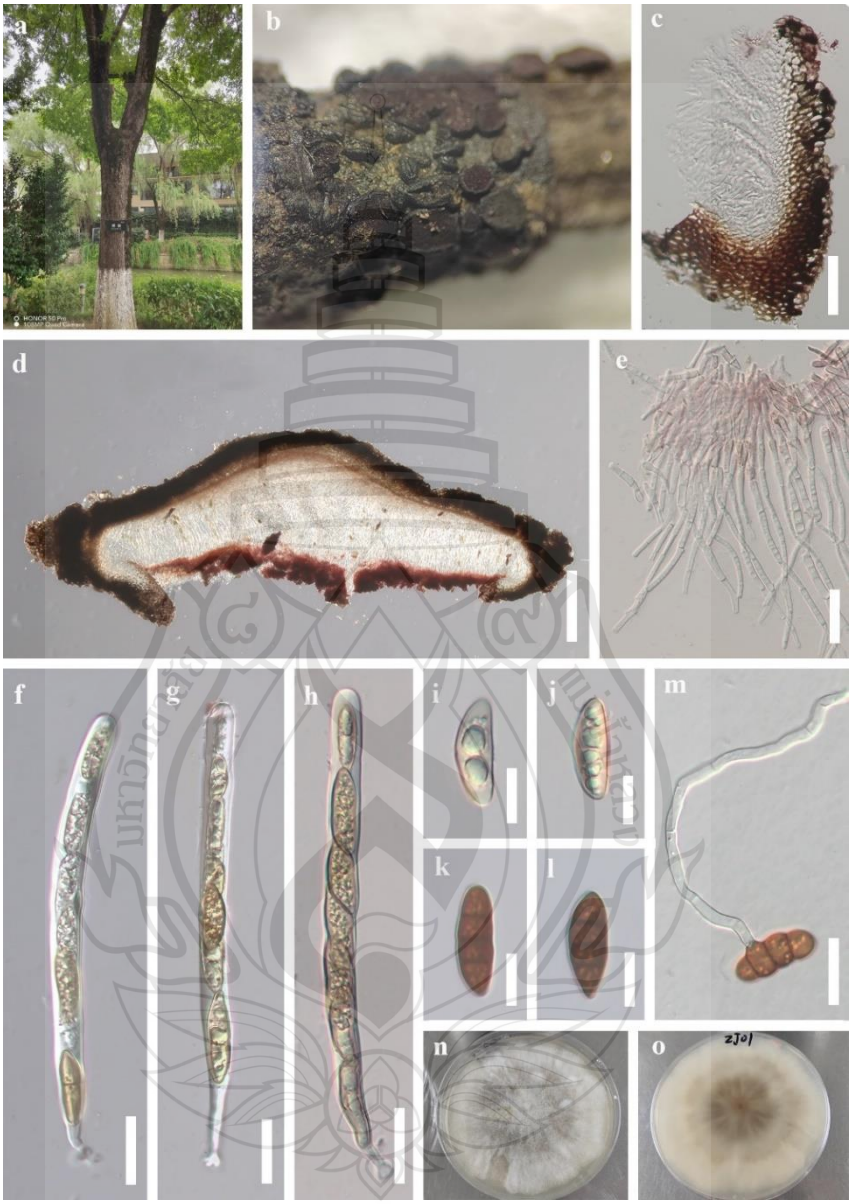
Saprobic on dead twigs of *Ulmus parvifolia* (Ulmaceae). **Sexual morph**: *Hysterothecia* 1100–2000 µm long, 330–500 high, 620–1000 µm wide, black, superficial, arising singly or in small groups, coriaceous, elliptical or irregular in shape, elongated with a longitudinal slit. Receptacle cupulate, black, flat or slightly concave, with a slightly dentate margin. *Exciple* 60–90 µm wide, composed of dark brown, thick-walled cells of *textura angularis*, outer layer brown, inner layer hyaline to pale brown. *Hamathecium* 2–4 µm wide, dense, hyaline, septate, numerous, branched and pink pigmented. The branched apices form a layer on hymenium to develop pseudo-epithecium. *Asci* 120–180 × 12–16 µm ($\bar{x}$ = 160 × 14 µm, n = 20), 8-spored, bitunicate, long cylindrical, with a short furcate pedicel, apically rounded, surround by pseudoparaphyses. *Ascospores* 19–30 × 9–13 µm ($\bar{x}$ = 25 × 11 µm, n = 30), uni-seriate, hyaline to pale brown when young, brown when mature, 1–3-septate, ellipsoidal to fusoid, with granular appearance. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated on PDA within 12 h and germ tubes produced from the meddle of spores. Colonies on PDA reached 10 cm diameter after three weeks at 26 °C. The colony is flossy, velvety, circular, slightly raised, white to gray from above and below.

Material examined: CHINA, Zhejiang Province, Tongxiang City, Zhenxing East Road, Tongxiang Botanical Garden, on twigs of *Ulmus parvifolia*, 15 August 2023, Y.R. Sun, ZJ01 (HKAS 136908); living culture GUCC 24-0068.

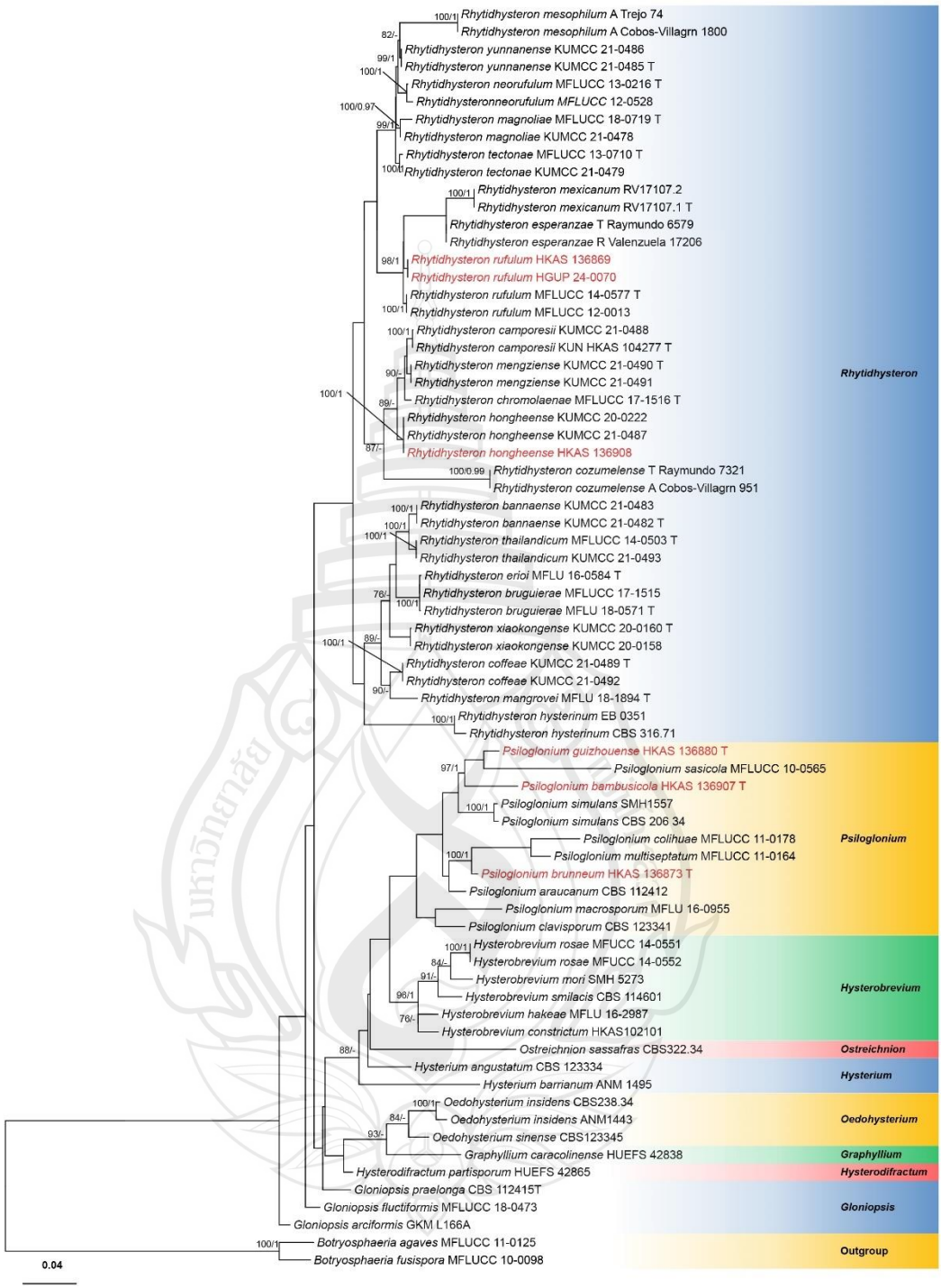
Notes: Wanasinghe et al. (2021) firstly discovered *R. hongheense* in China, which was isolated from *Dodonaea* sp. Du et al. (2023) identified the presence of this species in *Phyllanthus emblica*. Our collection grouped together with *R. hongheense* (KUMCC 20-0222, KUMCC 21-0487) in the phylogenetic tree (Figure 4.16). In addition, our collection shows similar morphological characteristics with *R. hongheense* in having solitary to aggregated, slightly striated hysterothecia, 8-spored, cylindrical, short pedicellate asci, and uni-seriate ellipsoidal to fusoid ascospores, brown when mature (Wanasinghe et al., 2021).

Therefore, our collection was reported as a new host record of *R. hongheense* from *Ulmus parvifolia* in Zhejiang Province in China.



Note a Host. b Appearance of hysterothecia on the host. c Exciple. d Vertical section through hysterothecium. e Pseudoparaphyses. f–h Asci. i–l Ascospores. m Germinated ascospore. Scale bars: c = 50 µm; d = 200 µm; e–h, m = 20 µm, i–l = 10 µm

Figure 4.15 *Rhytidhysteron hongheense* (HKAS 136908, new host record)



Note The tree is rooted with *Botryosphaeria agaves* (MFLUCC 11-0125) and *B. fusispora* (MFLUCC 10-0098). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.16 Phylogenetic tree of Hysteriaceae

Kirschsteiniotheliales Hern.-Restr., R.F. Castañeda, Gené & Crous, Stud. Mycol. 86: 72 (2017)

Kirschsteiniotheliaceae Boonmee & K.D. Hyde, Mycologia 104(3): 705 (2012)

Kirschsteiniothelia D. Hawksw., Bot. J. Linn. Soc. 91: 182 (1985)

Notes: *Kirschsteiniothelia* was introduced by Hawksworth (1985) based on the type species *Kirschsleiniothelia aethiops*. It has both asexual and sexual morphs. The sexual morph of *Kirschsleiniothelia* has brown or black, hemisphaerical or subglobose ascomata, cylindrical-clavate, bitunicate, 8-spored asci and ellipsoidal, brown to dark brown, smoothwalled, 1–2-septate ascospores (Hawksworth, 1985; Boonmee et al., 2012; Hyde et al., 2013; Mehrabi et al., 2017). There are two types of asexual morphs in *Kirschsteiniothelia*, *viz. dendryphiopsis*-like and *sporidesmium*-like. *Dendryphiopsis* was linked with *Kirschsteiniothelia*, which was confirmed by Hawksworth (1985) and Boonmee et al. (2012). Subsequently, Su et al. (2016) reported a *sporidesmium*-like asexual morph (*Kirchsteiniothelia submerse*) in *Kirschsteiniothelia*. Wijayawardene et al. (2014) recommended using *Kirschsteiniothelia* over *Dendryphiopsis* considering fewer name changes.

Kirschsteiniothelia thailandica Y.R. Sun, Yong. Wang bis & K.D. Hyde ***sp. nov.***

Index Fungorum number: IF557949; Facesoffungi number: FoF 09289; Figure 4.17

Etymology: Referring the fungus collected from Thailand

Holotype: MFLU 20-0263.

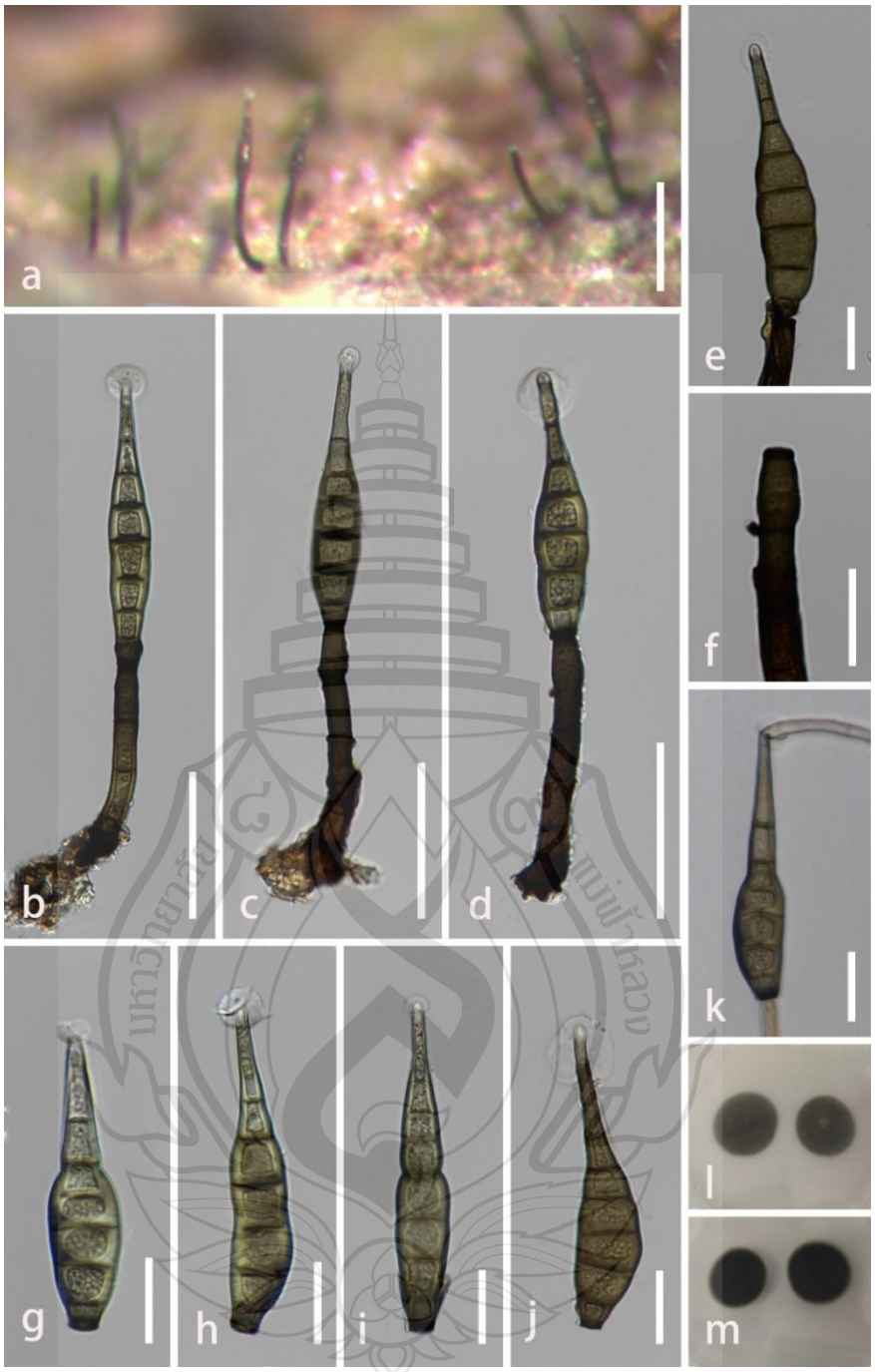
Saprobic on dead wood. **Sexual morph:** Unknown. **Asexual morph**: Hyphomycetous. *Colonies* effuse, scattered, brown to dark-brown, hairy. *Mycelium* mostly immersed, composed of pale to dark brown, septate, branched, smooth, hyaline to subhyaline hyphae. *Conidiophores* macronematous, mononematous, solitary, erect, cylindrical, straight or slightly flexuous, unbranched, septate, brown to dark brown 55–93 × 7–10 μm ($\bar{x}$ = 75.5 × 9 μm, n = 15). *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, cylindrical, brown to dark brown. *Conidia* acrogenous, solitary, straight, obclavate, smooth-walled, 6–8 distoseptate, shiny, olivaceous or brown, hyaline towards apex, truncate at base,

tapering towards apex, with a conspicuous, gelatinous, hyaline sheath around tip, 74–110 μm long ($\bar{x}$ = 91 μm, n = 20), 13–20 μm at the widest ($\bar{x}$ = 17 μm, n = 20).

Culture characteristics: Conidia germinated on PDA within 12 hours and germ tubes produced from both ends. Colony reached 25 mm in 4 weeks at 26 °C on PDA media, circular, flat, surface rough, dark-olivaceous from above and below.

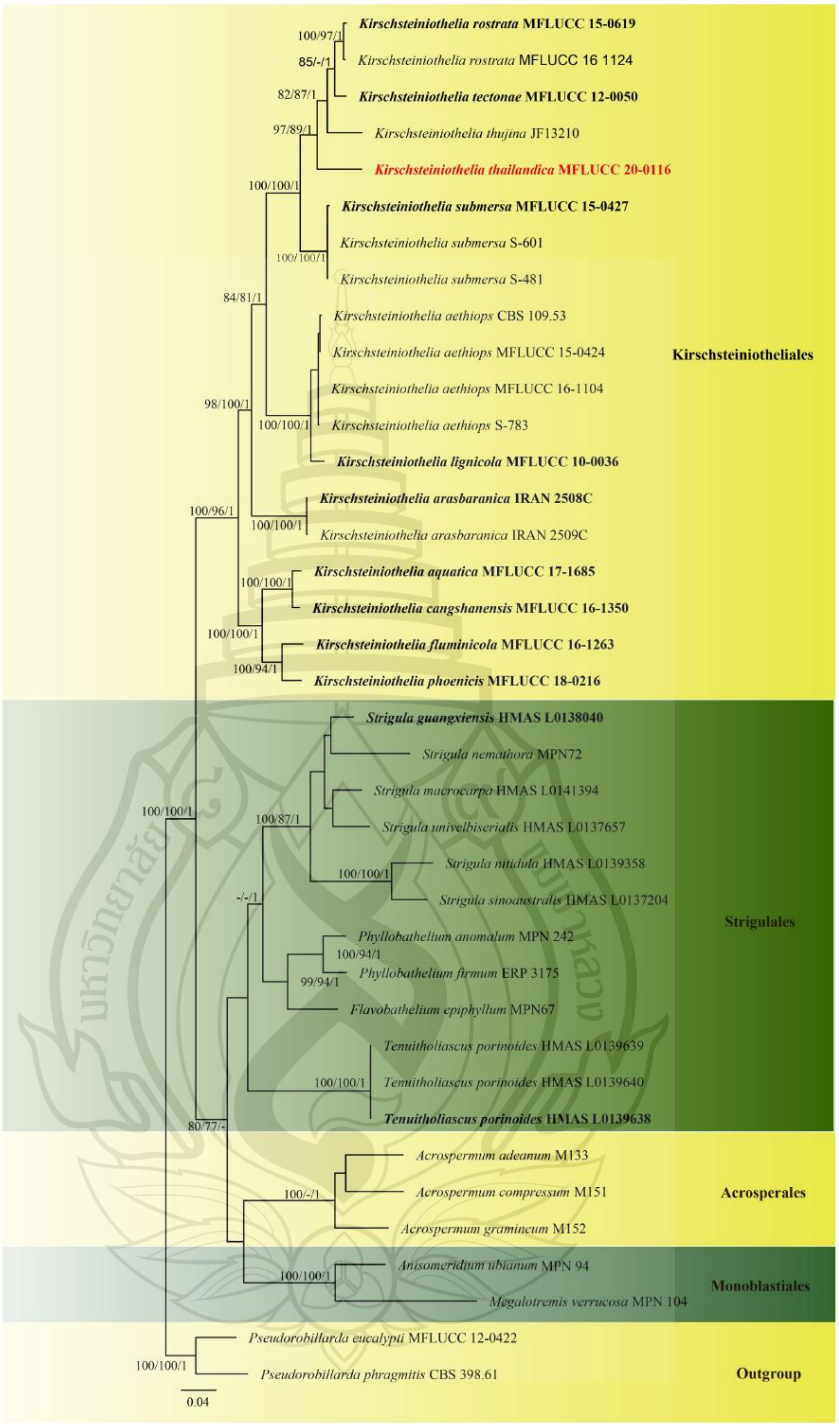
Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on twigs of *Ficus microcarpa*, 11 November 2019, Y.R. Sun, B4 (MFLU 20-0263, **holotype)**; ex-type living culture MFLUCC 20-0116.

Notes: Phylogenetic analysis showed that *K. thailandica* clustered with *K. rostrata*, *K. tectonae* and *K. thujina*, and they formed a sister clade with *K. submersa*. *Kirschsteiniothelia thujina* is known only its sexual morph (Hawksworth, 1985). *Kirschsteiniothelia thailandica* resembles to *K. rostrate* and *K. tectonae* in having unbranched, cylindrical conidiophores, integrated, terminal conidiogenous cells and obclavate, rostrate conidia with mucilaginous sheaths. However, *K. thailandica* has shorter conidiophores than *K. rostrata* (55–93 μm *vs*. 190–450 μm). *Kirschsteiniothelia thailandica* differs from *K. tectonae* in having shorter conidia (74–110 μm *vs*. 135–150 μm) and shorter conidiophores (55–93 μm *vs*. up to 200 μm). In addition, polymorphic nucleotides from the ITS sequence data showed the more than one fifth of bases were different.



Note a Colonies on natural substrate. b–d Conidiophores with conidia. e Conidiogenous cell with conidium. f Conidiogenous cell. g–j Conidia. k Bipolar-germinated conidium. l, m Colony on PDA. Scale bars: a = 100 μm, b–d = 50 μm, e–k = 20 μm.

Figure 4.17 *Kirschsteiniothelia thailandica* (MFLU 20-0263, holotype)



Note The tree is rooted with *Pseudorobillarda eucalypti* (MFLUCC 12-0422) and *P. phragmitis* (CBS 398.61). The ex-type strains are indicated in bold and the new isolates are in red and bold.

Figure 4.18 Phylogenetic tree of Kirschsteiniotheliales

Monoblastiales Lücking, M.P. Nelsen & K.D. Hyde, Fungal Diversity 63: 8 (2013)

Monoblastiaceae Walt. Watson, New Phytol. 28: 106 (1929)

Neoheleiosa Mortimer, Frontiers in Microbiology: 6 (2021)

Notes: *Neoheleiosa* was introduced by Mortimer et al. (2021) with *N. lincangensis* as the type species. Only three species are reported in this genus with their sexual morph (Species Fungorum, 2024). The sexual morphs are characterized by globose to subglobose, dark brown to black ascomata, 8-spored, bitunicate, cylindrical asci and uniseriate, narrowly ovoid to clavate, or oblong, 1-septate, pale to dark brown ascospores without sheath (Mortimer et al., 2021; Zhang, Liu et al., 2023).

Neoheleiosa brunnea Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902586; Facesoffungi number: FoF 16412; Figure 4.19

Etymology: brownii, referring to the brown ascospores.

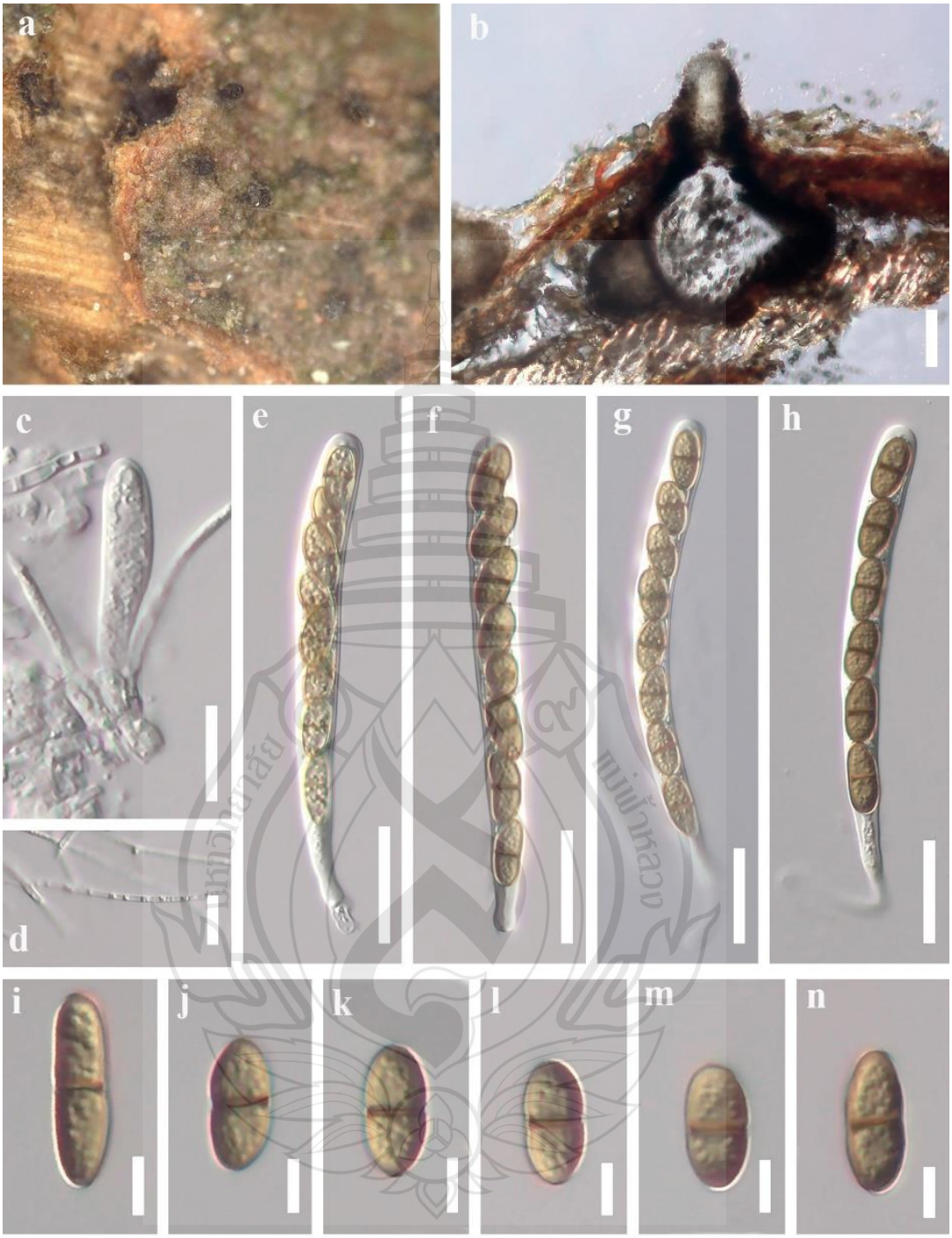
Holotype: HKAS 136883.

Saprobic on decaying twigs in terrestrial habitat. **Sexual morph**: *Ascomata* 173–261 µm high, 188–247 µm wide, immersed to erumpent, solitary, scattered, globose to subglobose, dark brown to black, ostiolate. *Ostiole* around 100 µm long, 55 µm wide, centric, papillate, black. *Peridium* 16–27 µm wide, comprising two layers of pale brown to brown cells of *textura globulosa*. *Hamathecium* 1–1.5 µm wide, comprising numerous, filamentous, branched, septate, pseudoparaphyses. *Asci* 89–103 µm long, 8–9.5 µm wide, 8-spored, bitunicate, fissitunicate, cylindrical, rounded and thick-walled at the apex, with an ocular chamber. *Ascospores* 10–15(17) × 5–6.5 µm ($\bar{x}$ = 12.5 × 5.5 µm, n = 30), overlapping uniseriate, narrowly ovoid or oblong, 1-septate, slightly constricted at the septum, brown, with conically rounded ends, verrucose, thick-walled. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated on PDA within 12 h at 26 °C. Germ tube produced from one end of the spore. Colonies on PDA reached 10 mm diam. after 3 weeks at 26 °C; mycelium black, tight, circular, with the entire edge; black with a white circular from above, black from below.

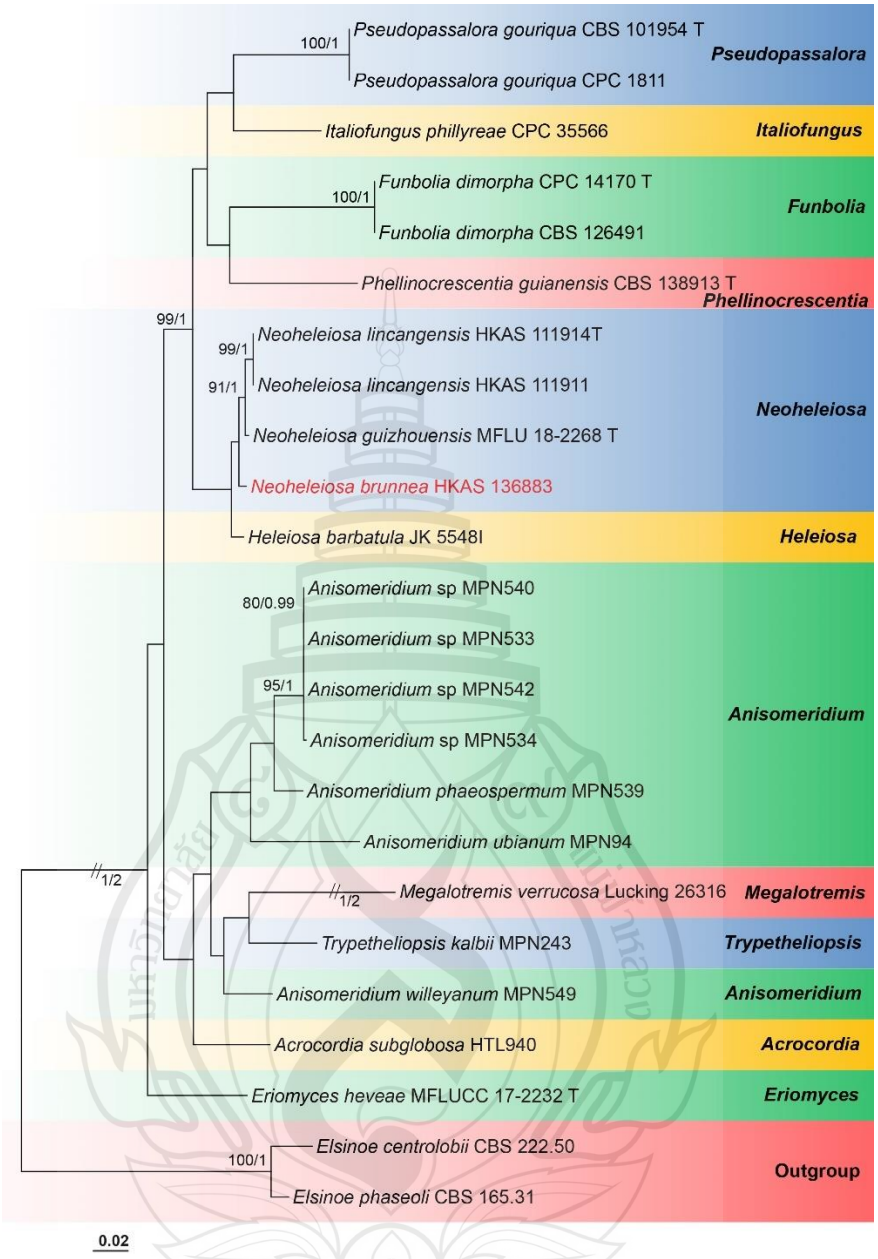
Material examined: CHINA, Guizhou Province, Zunyi City, Xishui District, Xishui National Nature Reserve, on decaying twigs, 14 April 2023, Y.R. Sun, 2357 (HKAS 136883, **holotype**); ex-type culture GUCC 24-0062.

Notes: Our collection shows a close relationship with *Neoheleiosa* species in the phylogenetic tree (Figure 4.20). *Neoheleiosa brunnea* differs from *N. lincangensis* by smaller asci (89–103 × 8–9.5 µm *vs.* 115–135 × 10–12 µm) and ascospores (10–15 × 5–6.5 µm *vs.* 16.5–17.5 × 7–9 µm) (Mortimer et al., 2021). *Neoheleiosa brunnea* is different from *N. guizhouensis* in having brown ascospore and shorter asci (89–103 µm long, 8–9.5 µm wide *vs.* 79–85(–88) × 8–9.5 µm) (Zhang, Liu et al., 2023). Therefore, we introduced it as a novel species.



Note a Appearance of ascomata on the substrate. b Section through ascoma. d Pseudoparaphyses. c, e–h Asci. i–n Ascospores. Scale bars: b = 50 µm, c, d = 10 µm, e–h = 20 µm, i–n = 5 µm.

Figure 4.19 *Neoheleiosa brunnea* (HKAS 136883, holotype)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Elsinoe centrolobii* (CBS 222.50) and *E. phaseoli* (CBS 165.31). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.20 Phylogenetic tree of *Neoheleiosa*

Oncopodiellales Y.R. Sun, Yong Wang bis & K.D. Hyde, ***ord. nov.***

Facesoffungi number: FoF 16413.

Etymology: Name reflects the type family

Type family: Oncopodiellaceae

Sexual morph: Not observed. **Asexual morph**: Hyphomycetous. *Conidiophores* macronematous or micronematous, mononematous, unbranched, cylindrical, hyaline to pale brown. *Conidiogenous cells* mono- or polyblastic, sympodial, subhyaline to pale brown. Conidia solitary, dematiaceous, muriform, various shaped trigonous, turbinate, subglobose, ellipsoidal, obovoid, pyriform and fusiform or Y-shaped, with horned protruding cells or filiform appendages

Notes: In the phylogenetic analyses (Figure 4.23), Oncopodiellales formed a distinct clade and was found to be related to Asterinales and Jahnulales. This topology echoes recent study (Yang, Liu et al., 2023). Species of Asterinales predominantly parasitize plant leaves, forming distinctive black, star-shaped spots (Hongsanan et al., 2014; Hongsanan et al., 2020b). Jahnulales typically inhabit aquatic environments as saprophytic fungi, primarily in their sexual form, with chain-like conidia in their asexual stage (Hongsanan et al., 2020b). This order includes two genera, *Diplocladiella* and *Oncopodiella*, which were proposed simultaneously, but deemed invalid due to the absence of a Latin diagnosis (Arnaud, 1954). Rifai (1965) validated *Oncopodiella*, while Ellis (1976) confirmed *Diplocladiella*. We introduced two new families, Diplocladiellaceae fam. nov. and Oncopodiellaceae fam. nov to accommodate these two genera, respectively, and designated Oncopodiellaceae as type family based on the chronological priority.

Diplocladiellaceae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***fam. nov.***

Facesoffungi number: FoF 16414.

Etymology: Name reflects the type genus

Type genus: Diplocladiella

Saprobic on dead wood in terrestrial or freshwater habitat. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, subhyaline to pale brown, velvety,

glistening. *Conidiophores* macronematous, mononematous, septate, erect, flexuous, unbranched, cylindrical, hyaline to pale brown, thick-walled. *Conidiogenous cells* mono- or polyblastic, integrated, terminal, determinate, subhyaline to pale brown, with sympodial proliferations. *Conidia* acropleurogenous, solitary, Y-shaped, with two horned arms, septate, pale brown to brown, with or without hyaline to pale brown appendage. **Sexual morph**: Not observed.

Notes: We establish a new family Diplocladiellaceae to accommodate the hyphomycetous genus *Diplocladiella*, which was previously treated in Dothideomycetes, *genera incertae sedis*. In the phylogenetic analyses (Figure 4.23), Diplocladiellaceae forms an independent branch and sisters to Oncopodiellaceae. Diplocladiellaceae can be distinguished from Oncopodiellaceae by their Y-shaped conidia with two horned arms, while the latter has muriform conidia in various shapes and with horned, protruding cells (Rifai, 1965; Revay, 1995).

Diplocladiella G. Arnaud ex M.B. Ellis, More Dematiaceous Hyphomycetes (Kew): 229 (1976)

Notes: For the description and notes see Yang, Liu et al. (2023). In this study, we introduce a new *Diplocladiella* species, namely, *Diplocladiella hannanensis* and provide sequences and a reference specimen for *Diplocladiella taurina.*

Diplocladiella hainanensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902587, Facesoffungi number: FoF 16415; Figure 4.21

Holotype: HKAS 128915.

Etymology: Referring to the location in which the fungus was collected.

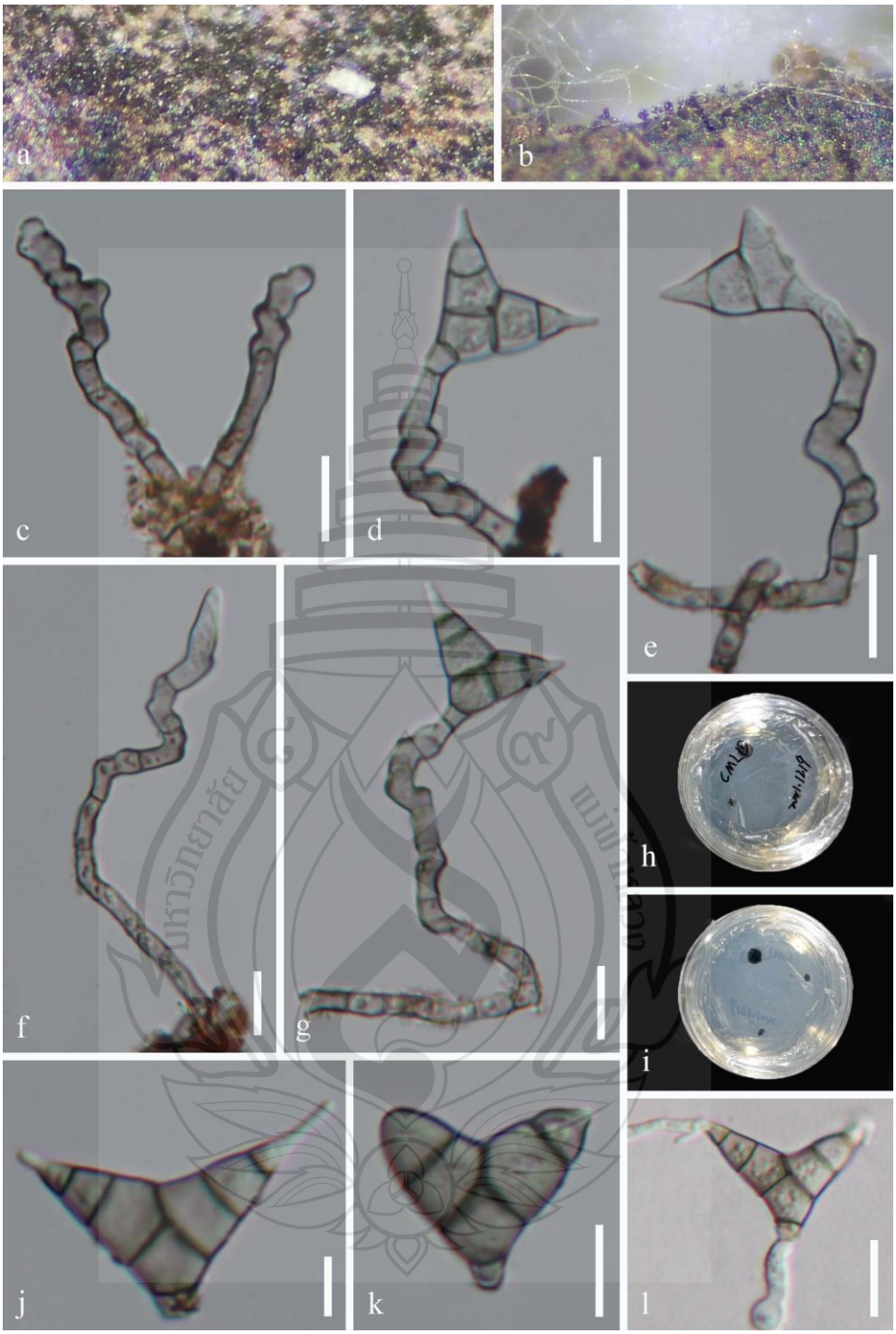
Saprobic on decaying submerged wood in freshwater habitats. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, subhyaline to pale brown, velvety, glistening. *Mycelium* mostly immersed, consisting of branched, septate, smooth-walled, subhyaline to pale brown hyphae. *Conidiophores* 25–82 × 3–5 μm, macronematous, mononematous, septate, erect, flexuous, unbranched, cylindrical, pale brown. *Conidiogenous cells* 10–25 × 3–5 μm, mono- or polyblastic, integrated, terminal, subhyaline to pale brown,

with sympodial proliferations. *Conidia* acropleurogenous, solitary, Y-shaped, with two horned arms, a middle pentagonal cell and trapezoidal basal cell from front view, septate, smooth-walled, hyaline when young, brown when mature, axis 2-celled, 10–12 μm long, (measured from the truncate base to the curvature of the arms), pentagonal cells 5.5–8 μm wide, the arms (excluding the appendages) 7–10 μm long, 5.5–8 um wide at the base, narrowing to 2–3 μm at the lighter coloured apical cell, ending in a long, thin, hyaline, non-septate appendage, 2.5–17 μm long, around 2.5 μm at the base, the tip is filamentous, 17–43.5 μm wide between two horn tips. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 18 h. Colonies on PDA are circular, with flat surface, edge undulate, brown to black brown from above and below, reaching 0.8 cm diam. after 4 weeks of incubation at 25 °C.

Material examined: CHINA, Hainan Province, Dongfang City, on rotting wood in a freshwater stream, 11 December 2021, Jian Ma, CMLYUAN1 (HKAS 128915, **holotype**, GZAAS 22-2123, **isotype**), ex-type culture, GZCC 22-2123.

Notes: *Diplocladiella hainanensis* is phylogenetically close to *Diplocladiella scalaroides* (GZCC 19-0563) and *Diplocladiella taurina.* However, *D. hainanensis* morpholohically differs from *D. scalaroides* by having longer conidiophores (25–82 × 3–5 μm *vs*. 19–48 × 2.5–4 μm) and brown conidia (Yang, Liu et al., 2023). And *D. hainanensis* differs *D. taurina* by shorter appendage (2.5–17 μm long *vs*. 14–23 μm long) (Cazau et al., 1993). We also conducted a morphological comparison between *D. hainanensis* and other unsequenced species within *Diplocladiella*, discovering that *D. hainanensis* resembles *Diplocladiella alta*. However, *D. hainanensis* has shorter conidiophores (25–82 × 3–5 μm *vs.* 116–329 × 4–7.5 μm) and smaller conidia (Kirschner & Chen, 2004). Therefore, *D. hannanensis* sp. nov is introduced herein.



Note a, b Colonies on natural substrates. c–g Conidiophores and conidia. j, k Conidia. l Germinating conidium. h, i Colonies on PDA (h from above, i from below). Scale bars: c–g, l= 10 μm, j, k = 5 μm.

Figure 4.21 *Diplocladiella hainanensis* (HKAS 12891, holotype)

Diplocladiella taurina Cazau, Aramb. & Cabello, Mycotaxon 46: 237 (1993)

Index Fungorum number: IF 359306, Facesoffungi number: FoF 16416; Figure 4.22

Saprobic on decaying submerged wood in freshwater habitats. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, subhyaline to pale brown, glistening. *Mycelium* mostly immersed, consisting of branched, septate, smooth-walled, subhyaline to pale brown hyphae. *Conidiophores* 31–33 × 3.5–4.5 μm, macronematous, mononematous, septate, erect, slightly flexuous, unbranched, cylindrical, hyaline to pale brown. *Conidiogenous cells* 13–19 × 3–4.5 μm, mono- or polyblastic, integrated, terminal, determinate, subhyaline to pale brown, with sympodial proliferations. *Conidia* acropleurogenous, solitary, Y-shaped, 8-celled, with two horned arms, a middle pentagonal cell and trapezoidal basal cell from front view, septate, smooth-walled, hyaline when young, becoming pale brown, axis 2-celled, 9–11 μm long, (measured from the truncate base to the curvature of the arms), pentagonal cells 4–6 μm wide, the arms (excluding the appendages) 7.5–10 μm long, 4.5–6.5 um wide at the base, narrowing to 2 μm at the lighter coloured apical cell, ending in a long, thin, hyaline, non-septate appendage, 14–23 μm long, around 2 μm at the base and tapers toward the tip, 34–47 μm wide between two horn tips. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA are circular, with flat surface, edge undulate, brown to black brown from above and below, reaching 0.8 cm diam. after 4 weeks of incubation at 25 °C.

Material examined: CHINA, Hainan Province, Qiongzhong Li and Miao Autonomous County, Baihualing Rainforest cultural tourism area, 18°98′ N, 109°82′ E, on rotting wood in a freshwater stream, 29 December 2021, Jian Ma, BH8 (GZAAS 22-2108), living culture GZCC 22-2107.

Notes: *Diplocladiella taurina* was introduced by Cazau et al. (1993) in Argentina. The conidiophores and conidial dimensions of our collection are comparable to that in Cazau et al. (1993), including the conidial axis, arms, and appendage. We designate our collection as a reference specimen for *D. taurina.* Additionally, LSU, ITS, *TEF1-α* and RPB2 sequences

were generated for *D. taurina*. In the phylogenetic analysis (Figure 4.23), *D. taurina* grouped with *D. hainanensis* and *D. scalaroides* with strong support (ML-bs = 90%).



Note a, b Colonies on natural substrates. c, d Conidiophores and conidia. e, f Conidiogenous cells. g, i Conidia. h Germinating conidium. j, k Colonies on PDA (j from above, k from below). Scale bars: c = 10 μm, d–i = 5 μm.

Figure 4.22 *Diplocladiella taurina* (GZAAS 22-2108, reference specimen)

Oncopodiellaceae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***fam. nov.***

Facesoffungi number: FoF 16417.

Etymology: Name reflects the type genus.

Type genus: Oncopodiella

Saprobic on dead wood in terrestrial or freshwater habitats. **Asexual morph**: Hyphomycetous. *Colonies* dark brown, punctiform or granular. *Conidiophores* macronematous or micronematous, mononematous, smooth-walled, subhyaline to pale brown. *Conidiogenous cells* mono- or poly-blastic. *Conidia* solitary, smooth-walled, brown, corniculate, hyaline to brown, various shapes (trigonous, turbinate, subglobose, ellipsoidal, obovoid, pyriform and fusiform), with hornlike protruding cells. **Sexual morph**: Not observed. (Adapted from Yang et al., 2023)

Notes: Oncopodiellaceae is introduced within Oncopodiellaceaeles to accommodate *Oncopodiella* which was previously treated in Dothideomycetes *genera incertae sedis*. The morphological differences between Oncopodiellaceae and its related family see the notes in Diplocladiellaceae (this study). So far, fourteen *Oncopodiella* species are accepted (Species Fungorum, 2024) but only *Oncopodiella trigonella* has molecular data.

Oncopodiella G. Arnaud ex Rifai, Persoonia 3(4): 409 (1965)

Notes: The descriptions and notes see Yang, Liu et al. (2023).

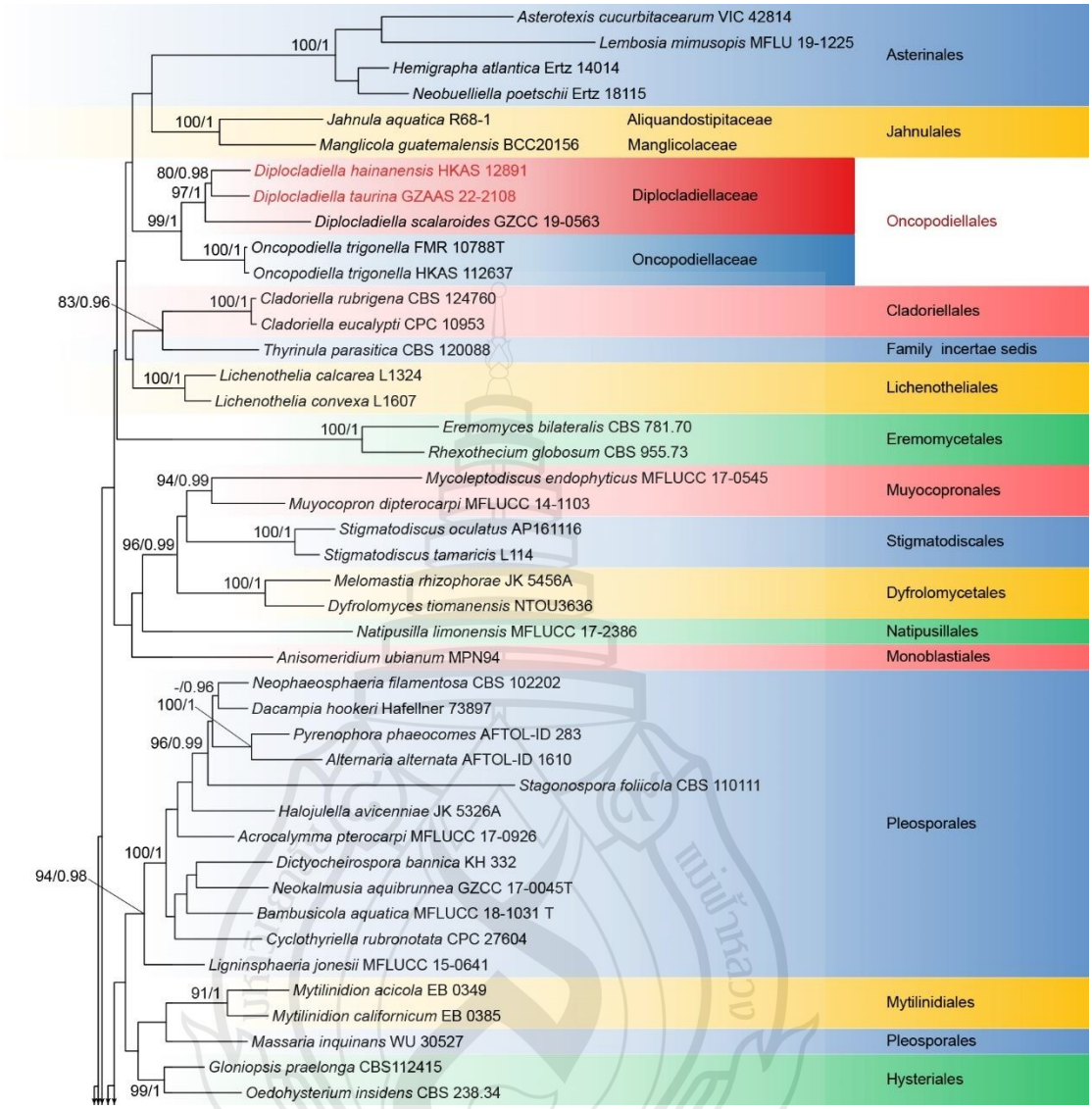
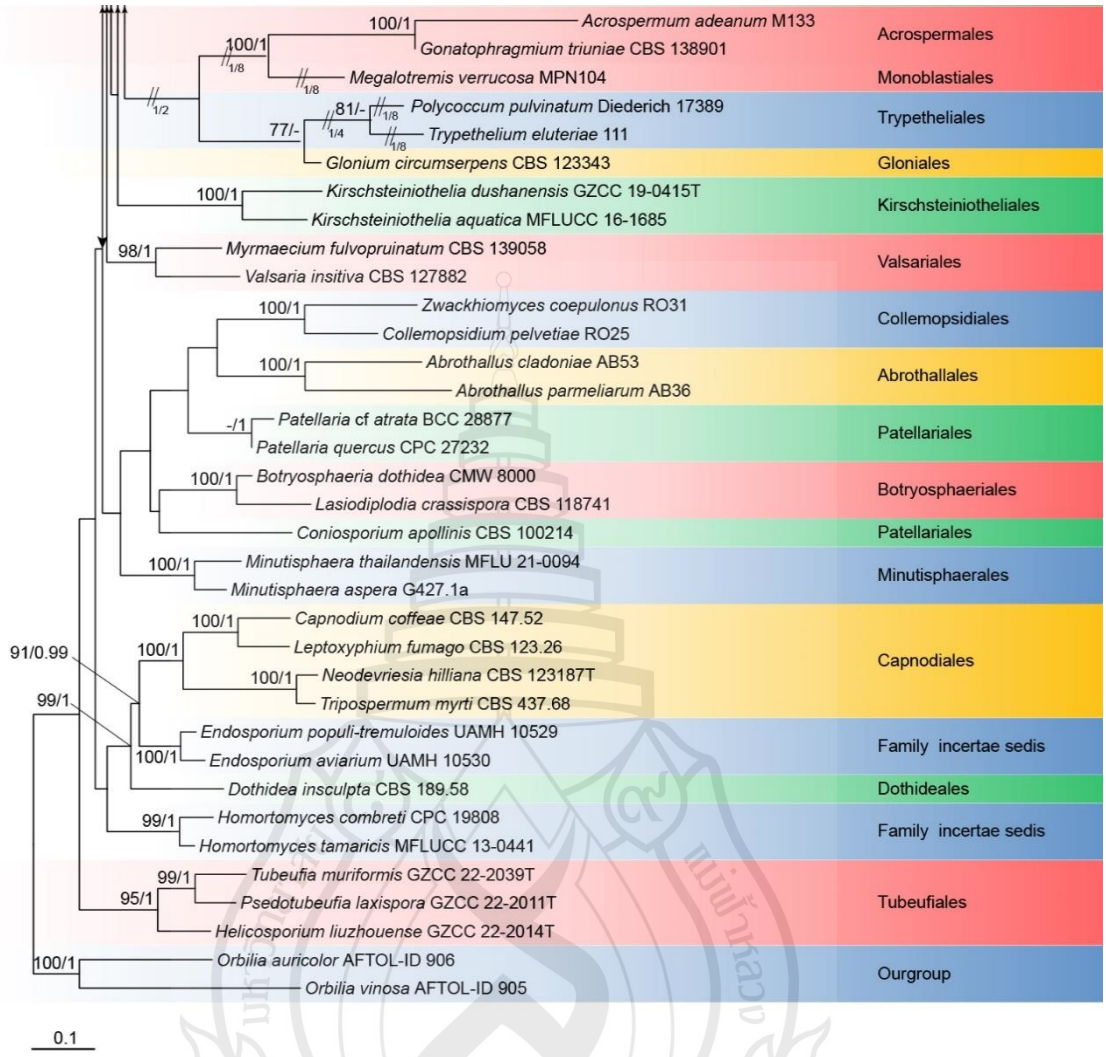


Figure 4.23 Phylogenetic tree of Dothideomycetes



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Orbilia auricolor* (AFTOL-ID 906) and *O. vinosa* (AFTOL-ID 905). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.23 (continued)

Patellariales D. Hawksw. & O.E. Erikss, Syst. Ascom. 5(1): 181 (1986)

Patellariales genera incertae sedis

Yuccamyces Gour, Dyko & B. Sutton, Trans. Br. mycol. Soc. 72(3): 413 (1979)

Notes: *Yuccamyces* was introduced by Dyko and Sutton (1979) with *Y. purpureus* as the type species. The genus has sporodochial, pink colonies, blastic, terminal conidiogenous cells and catenate, cylindrical, septate, hyaline conidia (Dyko & Sutton, 1979). Recently, Crous et al. (2017) introduced *Yuccamyces citri* with description and molecular data. So far, six species are accepted in this genus and only *Y. citri* and *Y. pilosus* with sequences (Species Fungorum, 2024).

Yuccamyces citri Crous, in Crous et al., Persoonia 39: 383 (2017)

Index Fungorum number: IF 823390; Facesoffungi number: FoF 16418; Figure 4.24

Saprobic on dead leaves of palm in terrestrial habitat. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, sporodochial, pink, glistening. *Mycelium* mostly immersed, composed of hyaline, branched hyphae. *Conidiophores* micronematous or semi-macronematous, mononematous, erect, short, cylindrical, hyaline, simple. *Conidiogenous cells* monoblastic, integrated, terminal, hyaline. *Conidia* 23–66 × 1.5–3 µm ($\bar{x}$ = 48.5 × 2, n = 25), catenate, formed in acropetal, branched chains, septate or aseptate, long cylindrical to vermiform, hyaline, smooth-walled.

Culture characteristics: Conidia germinated on PDA media within 24 h, and germ tubes produced from both ends of the conidia. Colonies on PDA media circular, flat, with undulate edge, white from above, green at the center, white at the outer ring from reverse.

Material examined: THAILAND, Chiang Rai Province, Bandu, on dead leaves of palm, 4 May 2020, Y.R. Sun, CR200504 (HGUP 24-0034), living cultures MFLUCC 24-0285.

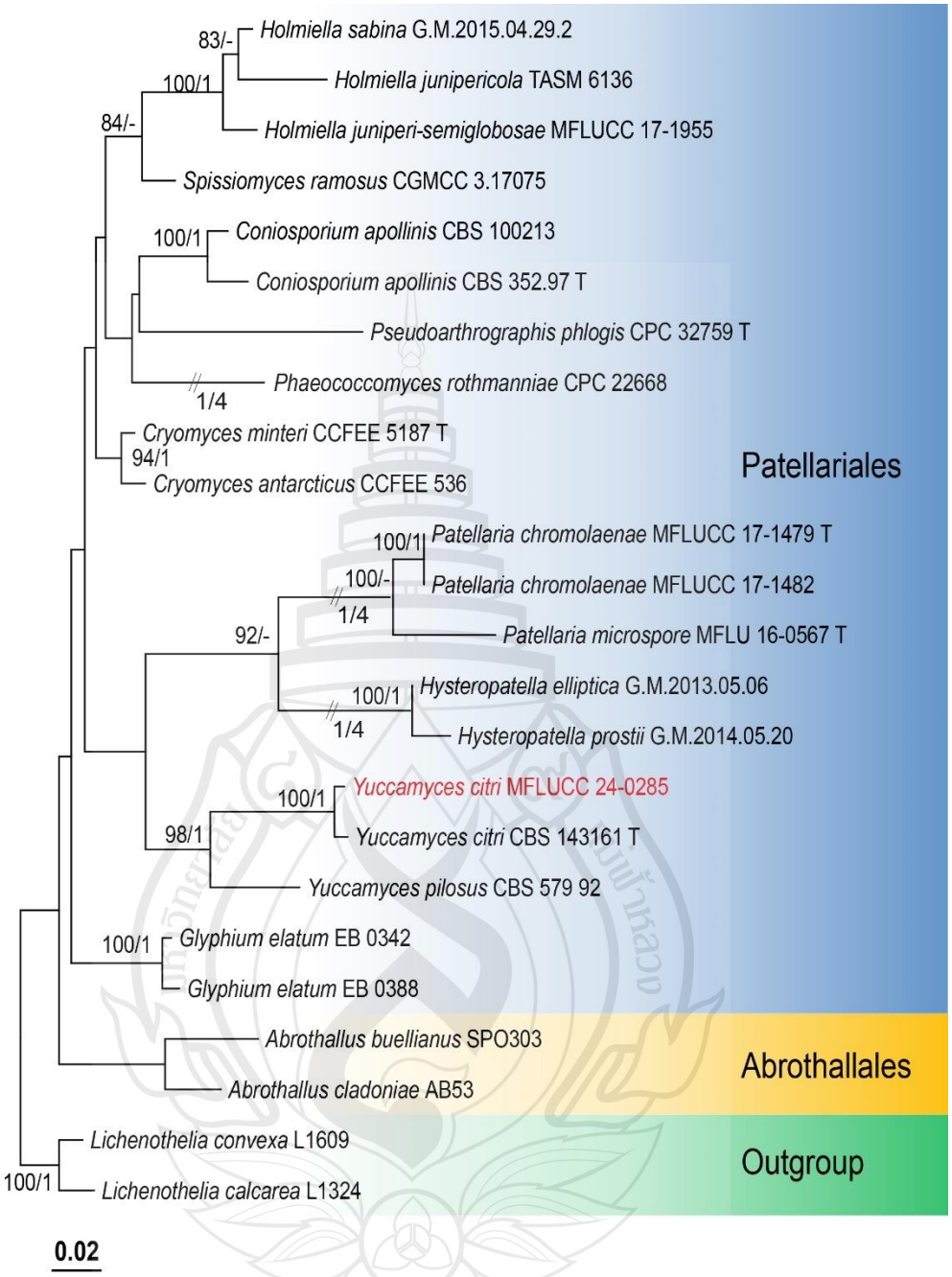
Notes: Our strain phylogenetically clustered together with *Y. citri* (CBS 143161), which was isolated from the leaf litter of *Citrus limon* in Italy (Crous et al., 2017) (Figure 4.25). Morphologically, our collection resembles *Y. citri* by having terminal, hyaline conidiogenous cells and hyaline catenate, septate, cylindrical conidia (Crous et al., 2017).

The comparisons of ITS and LSU sequences between our isolates and the ex-type CBS 143161 show there are only 4 bp differences (486 bp, without gap) in the ITS and 6 bp differences (821 bp, without gap) in the *TEF1-α*, respectively. Therefore, we identify our strain as *Y. citri*, representing a new host (palm) and geographical (Thailand) record.



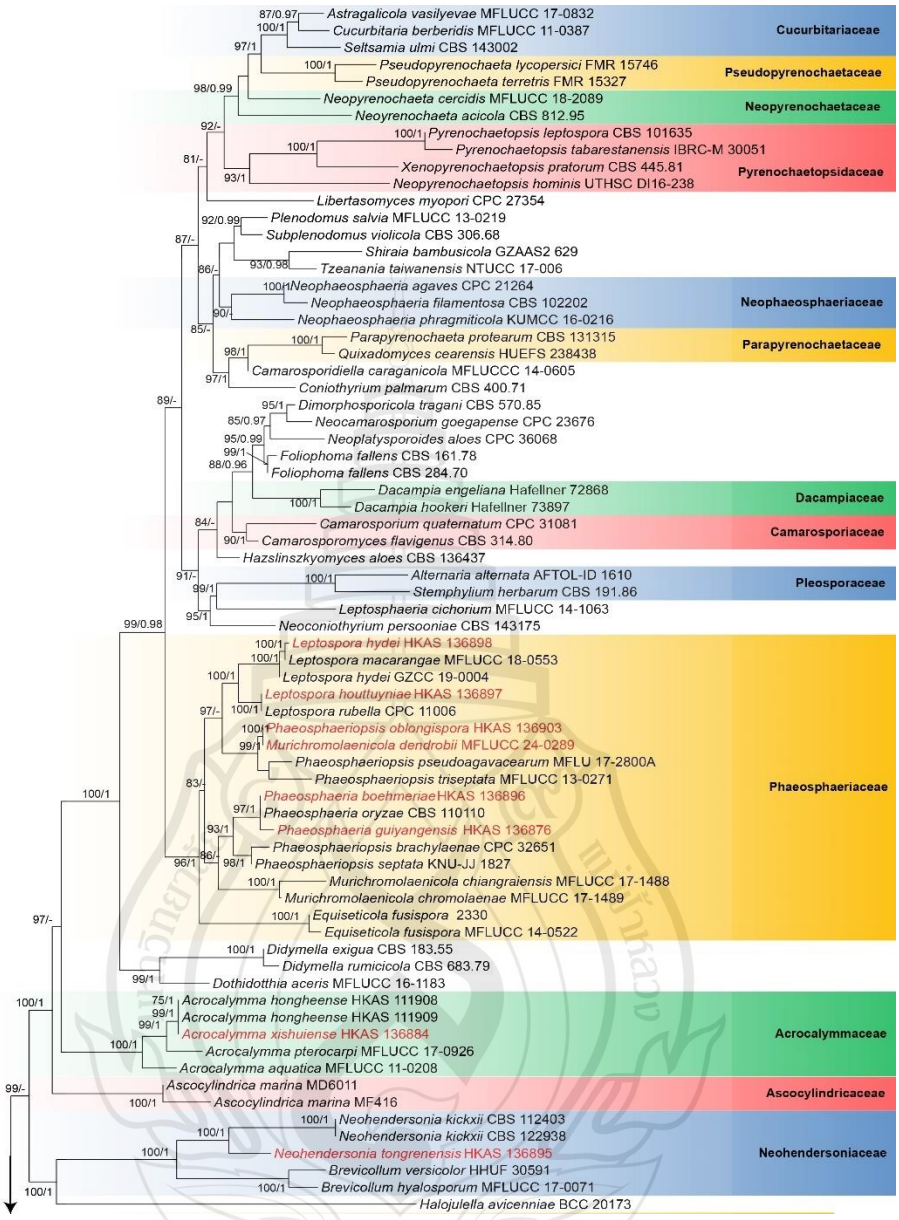
Note a, b Colonies on the host. c, d Fruiting bodies in the water. e–h Conidia. i, j Colonies on PDA from below and above. Scale bars: c, d = 50 μm, e–h = 20 μm

Figure 4.24 *Yuccamyces citri* (HGUP 24-0034, new record)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Lichenothelia calcarea* (L1324) and *L. convexa* (L1609). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.25 Phylogenetic tree of Patellariales



Note Bootstrap support values for maximum likelihood (ML) greater than 75% and bayesian posterior probabilities greater than 0.95 are indicated above branches as ML-BS/PP. The tree is rooted with *Hysterium angustatum* (CBS 123334) and *H. smilacis* (CBS 114601). The new collections are in red.

Figure 4.26 Phylogenetic tree of Pleosporales species

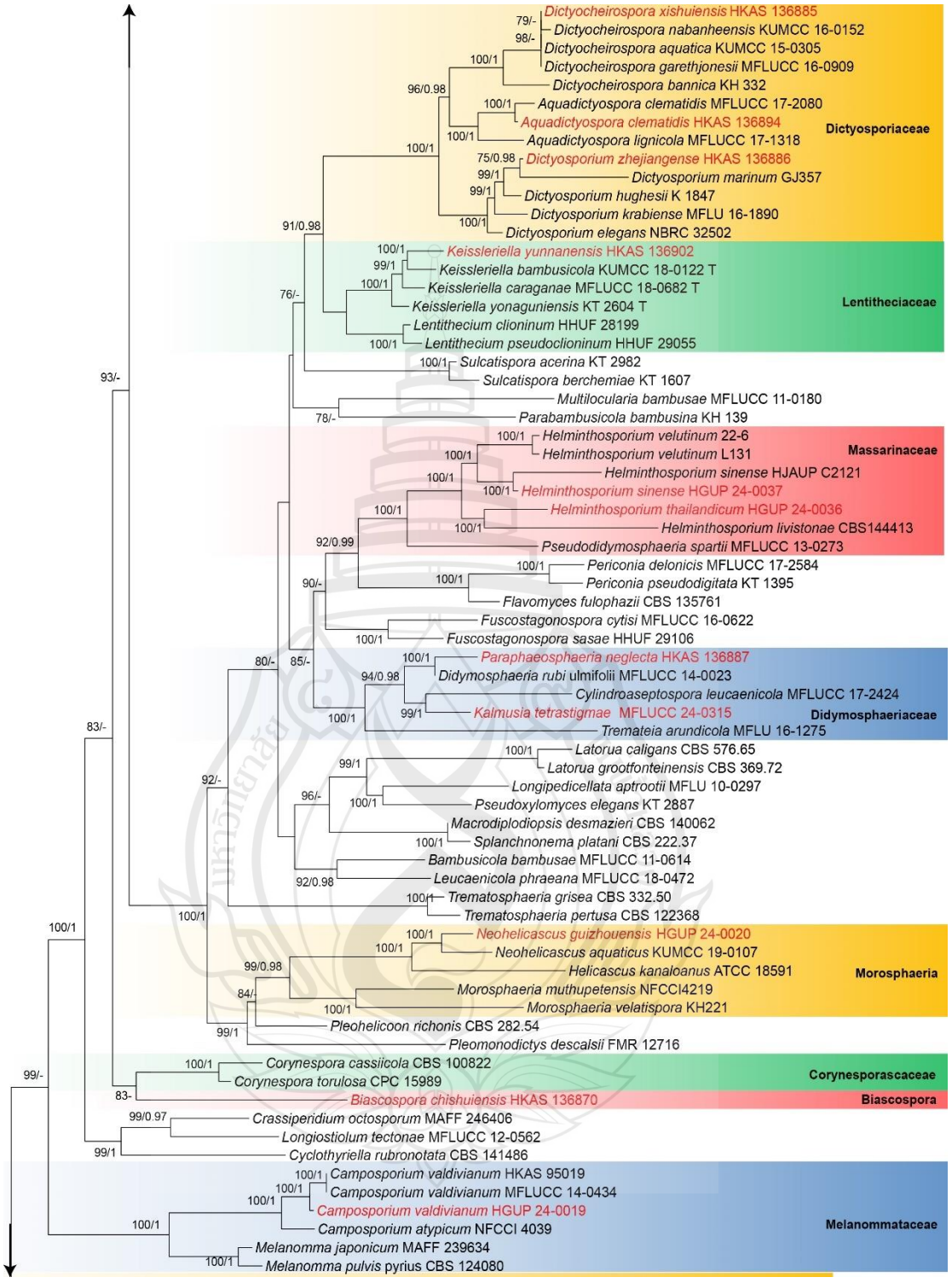


Figure 4.26 (continued)

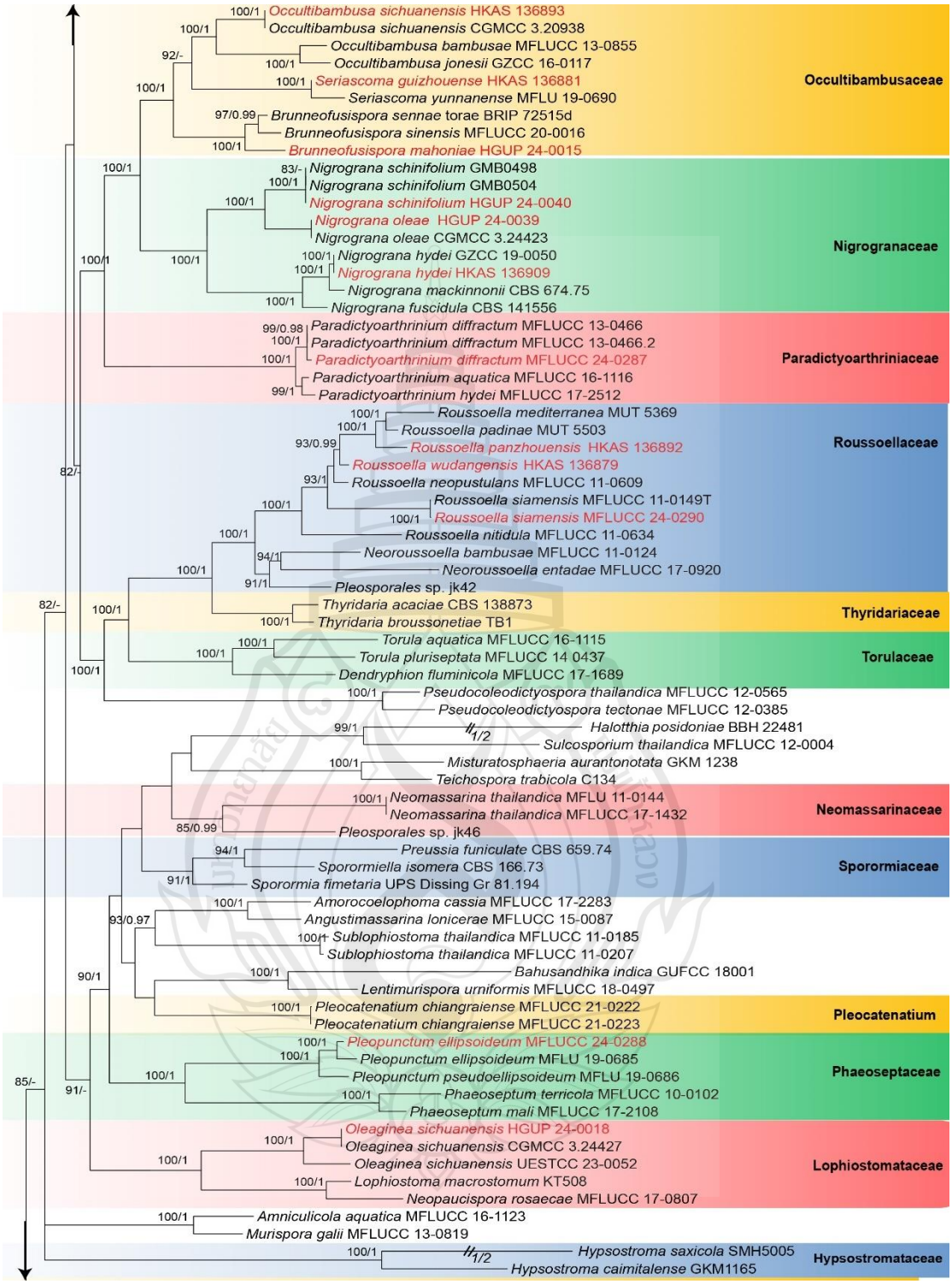


Figure 4.26 (continued)

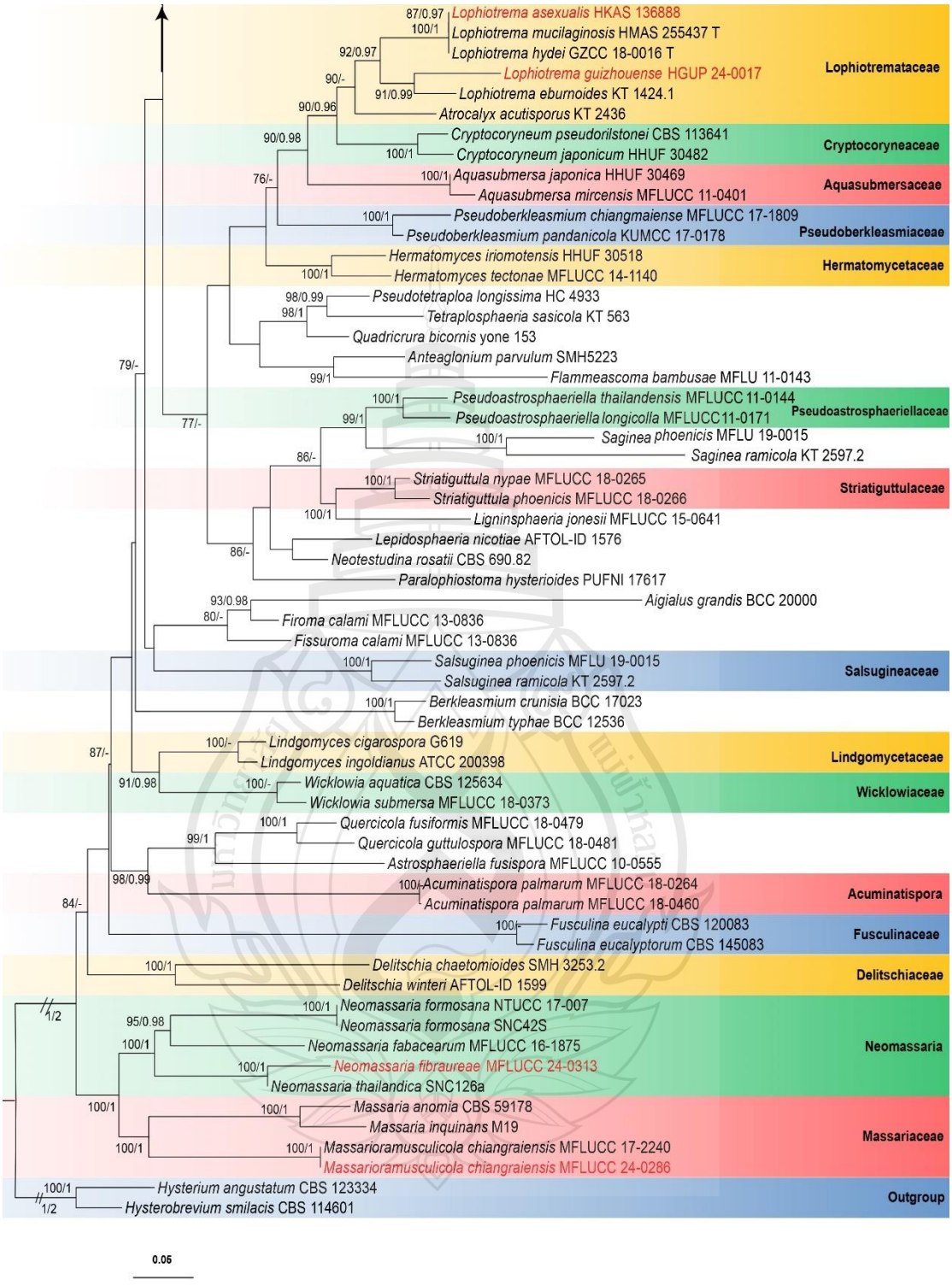


Figure 4.26 (continued)

Pleosporales Luttr. ex M.E. Barr.

Acrocalymmaceae Crous & Trakun., IMA Fungus 5(2): 404 (2014).

Acrocalymma Alcorn & J.A.G. Irwin, Trans. Br. Mycol. Soc. 88(2): 163 (1987).

Alcorn and Irwin (1987) introduced *Acrocalymma* and designated *A. medicaginis* as the type species. Currently, 17 species are acknowledged within this genus (Species Fungorum, 2024). These species have been documented as plant pathogens, endophytes, and saprobes, occurring in both plant and human superficial tissues within terrestrial and freshwater habitats (Jayasiri et al., 2019; Dong et al., 2020; Tennakoon et al., 2021; Liu & Zeng, 2022; Zhang, Liu et al., 2023). Certain species, such as *A. cycadis*, *A. magnoliae*, and *A. pterocarpi*, are isolated from medicinal plants (Crous et al., 2014; Jayasiri et al., 2019; de Silva et al., 2022).

Acrocalymma xishuiense Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902590; Facesoffungi number: FoF 16419; Figure 4.27

Etymology: Referring to the location where the fungus was collected

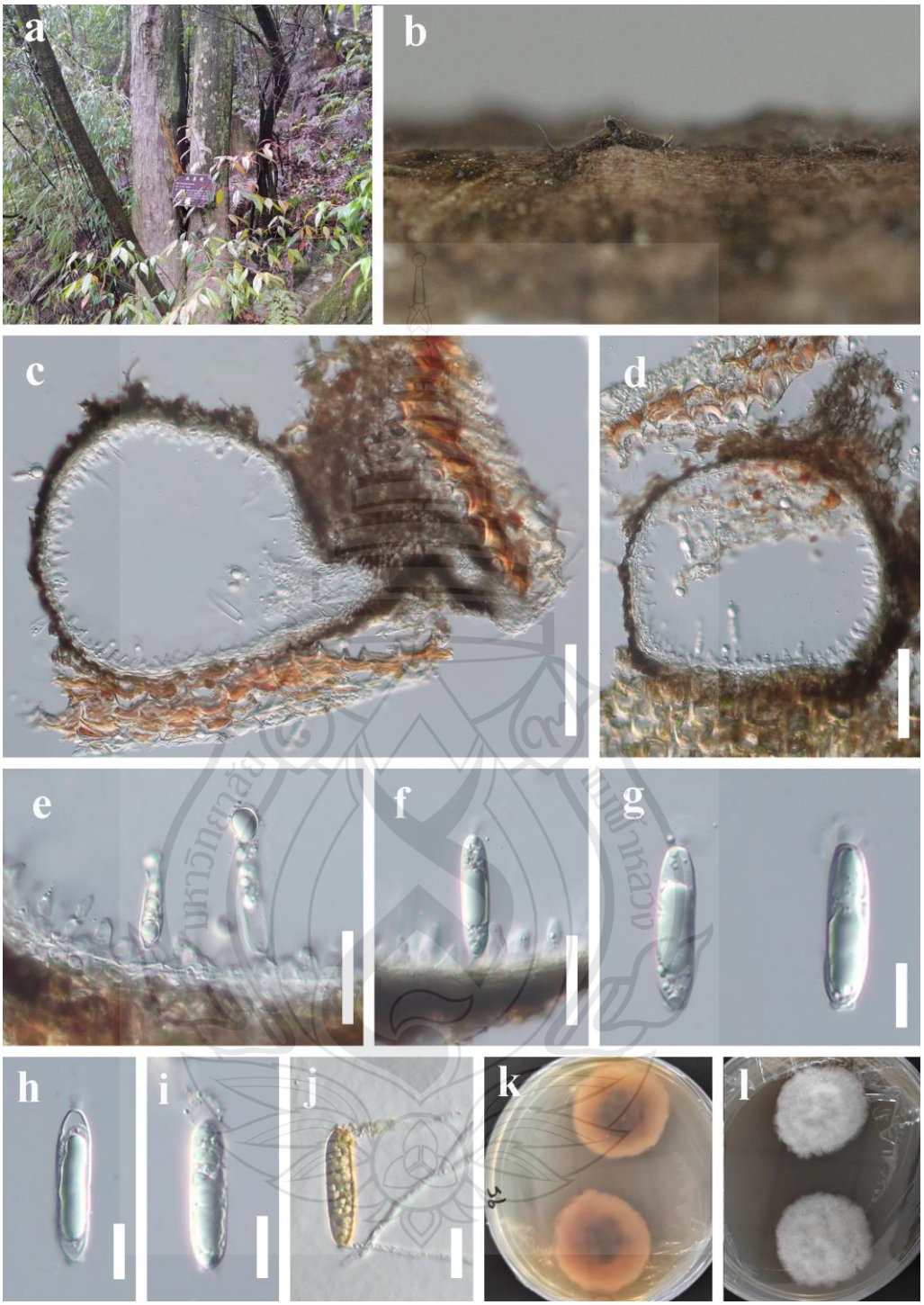
Holotype: HKAS 136884.

Saprobic on *Castanopsis fargesii* in terrestrial habitat. **Sexual morph**: Not observed. **Asexual morph**: coelomycetous. *Conidiomata* 120–155 µm high, 160–280 µm wide, pycnidial, unilocular, dark brown, immersed to semi-erumpent, globose, papillate, ostiolate. *Ostiole* single. *Peridium* 6–25 µm, composed of thick-walled, dark brown cells of *textura angularis* in the outer layers, and hyaline cells of textura angularis in the inner layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–8 × 2–4 µm, formed from the inner cells of the pycnidial wall, blastic, subcylindrical or ampulliform, hyaline, smooth. *Conidia* 22–30 × 5–6.5 µm ($\bar{x}$ = 27 × 6 µm, n = 20), solitary, subcylindrical, straight, hyaline or yellow brown, aseptate, smooth, guttulate, with flaring mucoid apical appendage.

Culture characteristics: Conidia germinated on PDA media within 12 h. Germ tubes produced from both ends. Colonies on PDA media circular, flossy, cotton, pale to brown from below, white from above.

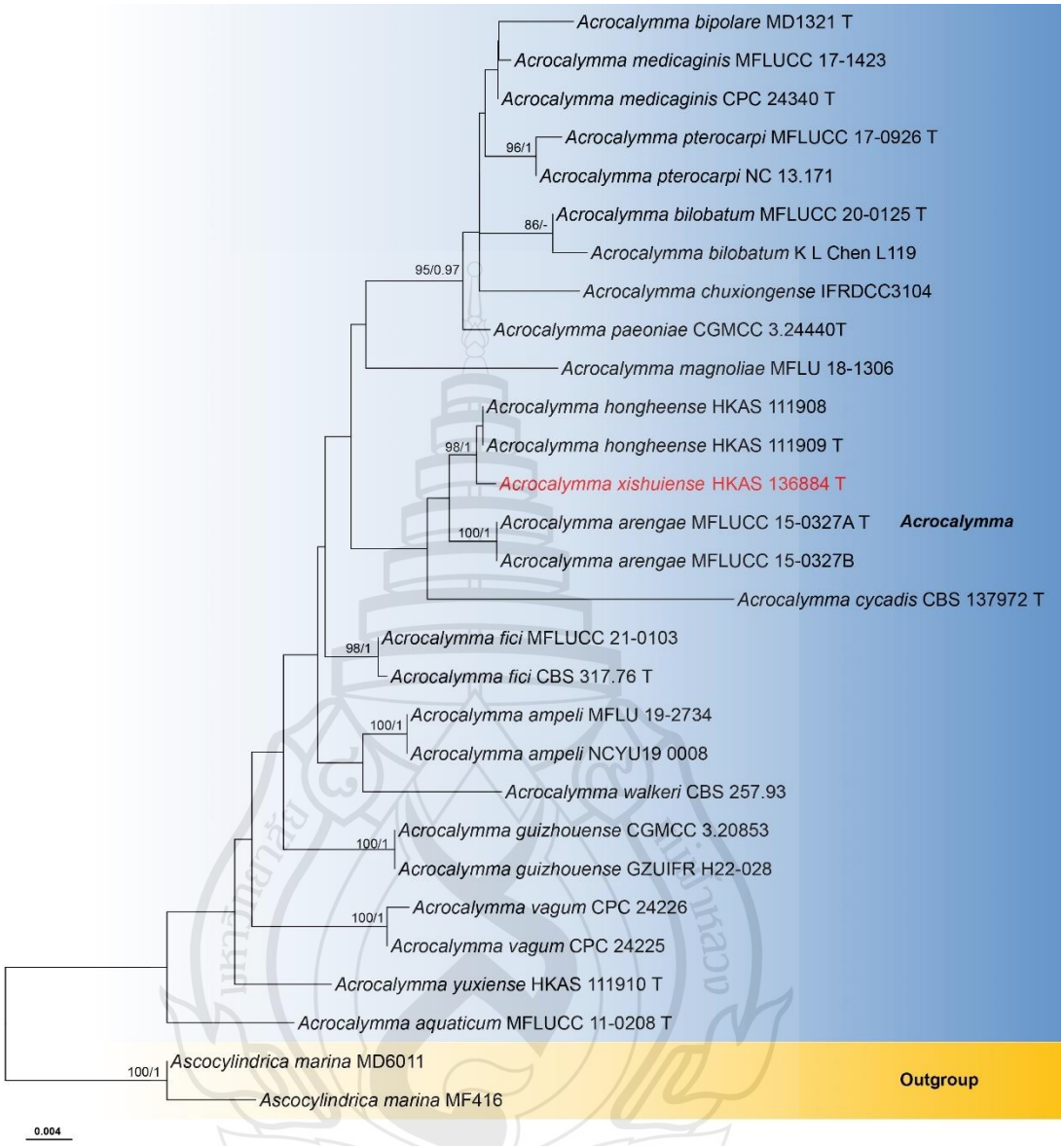
Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on twigs of *Castanopsis fargesii*, 14 April 2023, Y.R. Sun, 2395 (HKAS 136884, **holotype**); ex-type culture GUCC 24-0067.

Notes: *Acrocalymma xishuiense* is phylogenetically closes to *A. hongheense* (Figure 4.28). In morphology, *A. xishuiense* can be distinct from *A. hongheense* by shorter conidiomata (120–155 µm high *vs.* 150–200 µm high), smaller conidiogenous cells (2–8 × 2–4 µm *vs.* 8–17 × 3.5–7 µm) and yellowish brown, thinner conidia (22–30 × 5–6.5 µm *vs.* 20–35 × 7–9 µm) (Mortimer et al., 2021). Therefore, based on morphological differences and phylogenetic analyses, we introduced *A. xishuiense* as a novel species.



Note a Host. b Conidiomata observed on host substrate. c, d Vertical sections of conidiomata. e, f Conidiogenous cells. g–i Conidia. j Germinated conidium. k, l Colonies on PDA. Scale bars: c, d = 50 µm, e, f = 20 µm, g–j = 10 µm.

Figure 4.27 *Acrocalymma xishuiense* (HKAS 136884, holotype)



Note RAxML bootstrap values equal or greater than 75% are indicated near the nodes. New sequences generated in this study are given in red. The tree is rooted with *Ascocylindrica marina* (MD6011) and (MF416).

Figure 4.28 Phylogenetic tree of *Acrocalymma*

Bambusicolaceae D.Q. Dai & K.D. Hyde, in Hyde et al., Fungal Diversity 63: 49 (2013)

Bambusicola D.Q. Dai & K.D. Hyde, Cryptog. Mycol. 33(3): 367 (2012)

Bambusicola was introduced by Dai et al. (2012) with *B. massarinia* as the type species. It belongs to Bambusicolaceae, Pleosporales, Dothideomycetes (Hyde et al., 2013; Dai et al., 2017; Hongsanan et al., 2020). *Bambusicola* appears as black dots on the surfaces of its host plants and is only known to occur on Bambusoideae species (Jayasiri et al., 2019). Most taxa within the genus have been isolated from bamboo, either as pathogens or saprobes, and are capable of decomposing bamboo and woody materials (Cai et al., 2006). Initially, *Bambusicola* included four species identified from bamboo in tropical regions (Dai et al., 2012). Currently, there are 18 species listed under *Bambusicola* in Species Fungorum (2024).

Bambusicola nanensis Y.R Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558825; Facesoffungi number: FoF 09934, Figure 4.29

Etymology: In reference to the location, Nan Province, where the holotype was collected.

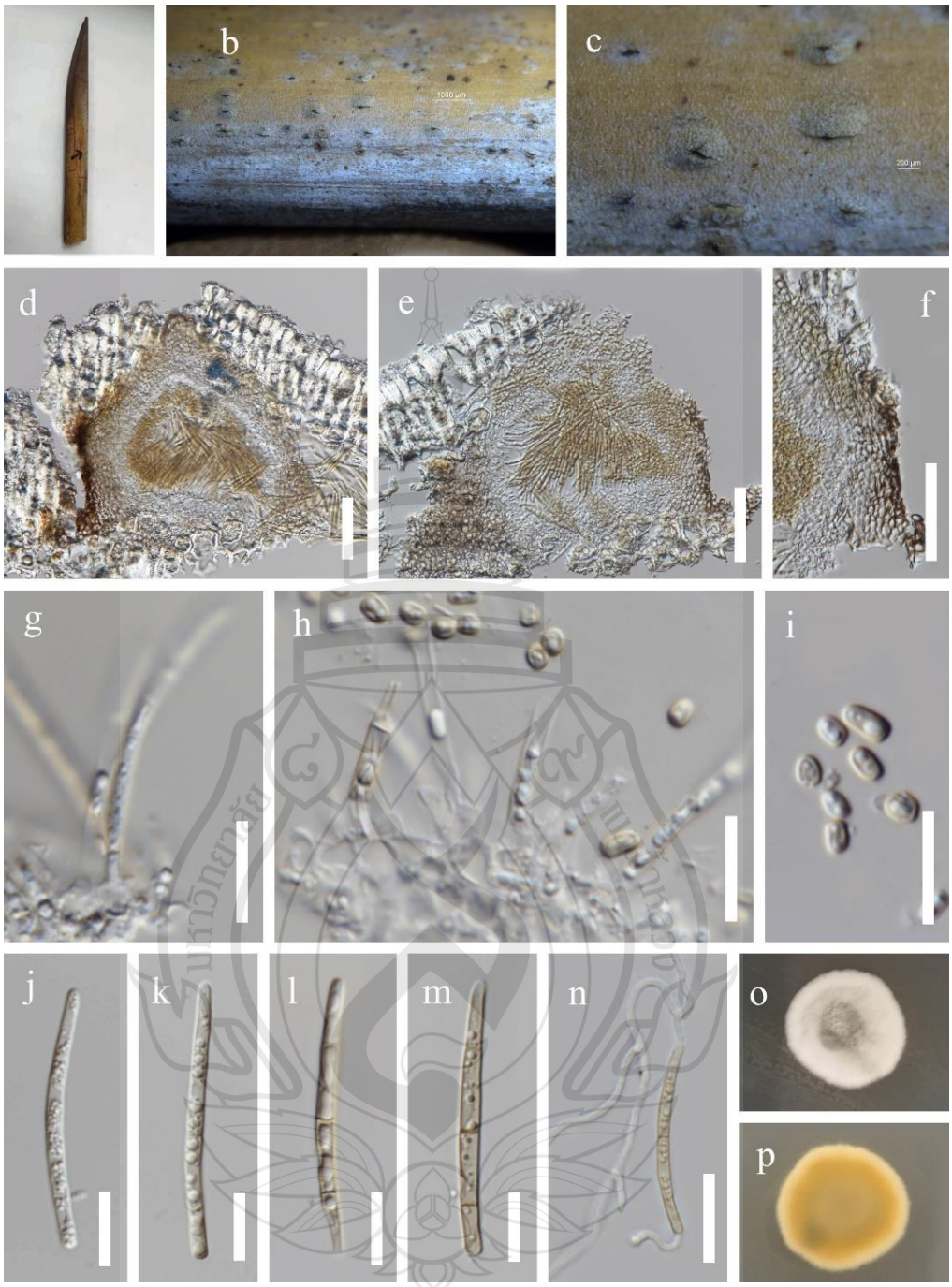
Holotype: MFLU 21-0090.

Saprobic on dead bamboo culms. **Asexual morph**: Coelomycetous. *Conidiomata* 140–190 × 200–250 μm, solitary to gregarious, pycnidial, mostly immersed under host tissues, partly erumpent, subglobose, brown. *Conidiomatal wall* 20–55 μm wide, composed of pale brown to brown cells of textura angularis, outer layer somewhat partial carbonaceous, inner layer composed of subhyaline gelatinous cells bearing conidiogenous layer. *Conidiogenous cells* holoblastic, phialidic, cylindrical, smooth, hyaline. *Conidia* has two types, macro- and microconidia. *Macroconidia* 32–42 × 1.8–3 μm ($\bar{x}$ = 38 × 2.5 μm, n = 20), vermiform to cylindrical, elongate, rounded at the ends, slightly curved, 2–3-septate, hyaline when young, pale brown to brown when mature, smooth-walled, guttulate. *Microconidia* 2.5–4.5 × 1.2–2.5 μm ($\bar{x}$ = 3 × 2 μm, n = 20), globose or oblong to ellipsoidal, rounded at the ends, aseptate, hyaline to pale brown, guttulates. **Sexual morph**: Not observed.

Culture characteristics: Macroconidia germinated within 12 h on PDA from single spores. Both ends produced germ tubes. Colony diameter reached 15–20 mm after 4 weeks at 26 °C on PDA, circular, with entire margin, flat, cottony, white from above, yellow from below.

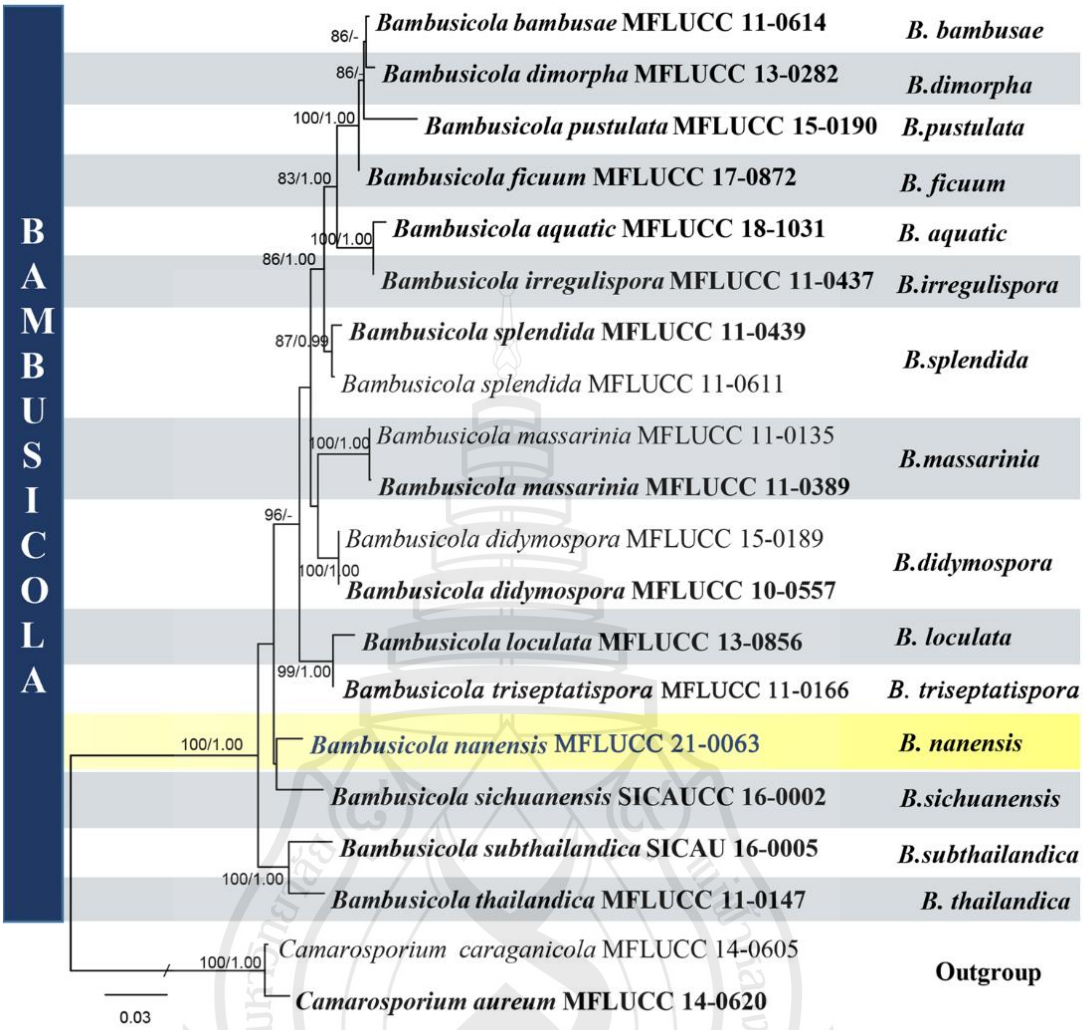
Material examined: Thailand, Nan Province, on dead bamboo culms, 15 January 2020, Y.R Sun, NFB5 (MFLU 21-0090, **holotype**); ex-type living culture MFLUCC 21-0063.

Notes: *Bambusicola nanensis* was collected from dead bamboo culms in Thailand. In the multigene analyses, the new taxon formed a sister clade to *Bambusicola sichuanensis* (SICAUCC 16–0002) (Figure 4.30), which was reported from branches of *Phyllostachys heteroclada* in China (Yang et al., 2019). However, *B. nanensis* has smaller conidiomata (140–190 × 200–250 μm *vs*. 422–750 × 420–700 μm) and longer macroconidia (32–42 × 1.8–3 μm *vs*. 16.5–19 × 4 μm) than *B. sichuanensis*. In addition, analysis of nucleotide polymorphism in the ITS region revealed 7.2% (37/515) base differences (without gaps) between these two strains. Therefore, we introduce *B. nanensis* as a novel taxon.



Note a Host. b, c Fruiting body on bamboo host. d, e Section of pycnothyrium. f Peridium. g, h Conidiogenous cells and developing conidia. i Micro- conidia. j–m Macroconidia. n Geminating macroconidia. o, p Colonies on PDA after 4 weeks. Scale bars: d–f = 50 µm, g–m = 10 µm, n = 20 µm

Figure 4.29 *Bambusicola nanensis* (MFLU 21-0090, holotype)



Note Maximum likelihood bootstrap support values equal to or greater than 75% and BPP equal to or greater than 0.95 are given above the nodes. *Camarosporium aureum* (MFLUCC 14–0620) and *C. caraganicola* (MFLUCC 14–0605) were used as outgroup taxa. The newly generated sequence is indicated in blue and the type-derived sequences are given in bold.

Figure 4.30 Phylogenetic tree of *Bambusicola*

Dictyosporiaceae Boonmee & K.D. Hyde, Fungal Diversity [7] (2016)

Aquadictyospora Z.L. Luo, K.D. Hyde & H.Y. Su, Mycosphere 8(10): 1590 (2017)

Notes: *Aquadictyospora* was established to accommodate a freshwater dictyosporous taxon, with *A. lignicola* designated as the type species (Li, Luo et al., 2017). Phukhamsakda et al. (2020) introduced the second *Aquadictyospora* species isolated from *Clematis sikkimensis* in terrestrial habitat. So far, only these two species are accepted in this genus, and no sexual morph has been reported (Li, Luo et al., 2017; Phukhamsakda et al., 2020).

Aquadictyospora clematidis Phukhams., D.J. Bhat & K.D. Hyde, Fungal Diversity 102: 17 (2020)

Index Fungorum number: IF557125; Facesoffungi number: FoF 07250; Figure 4.31

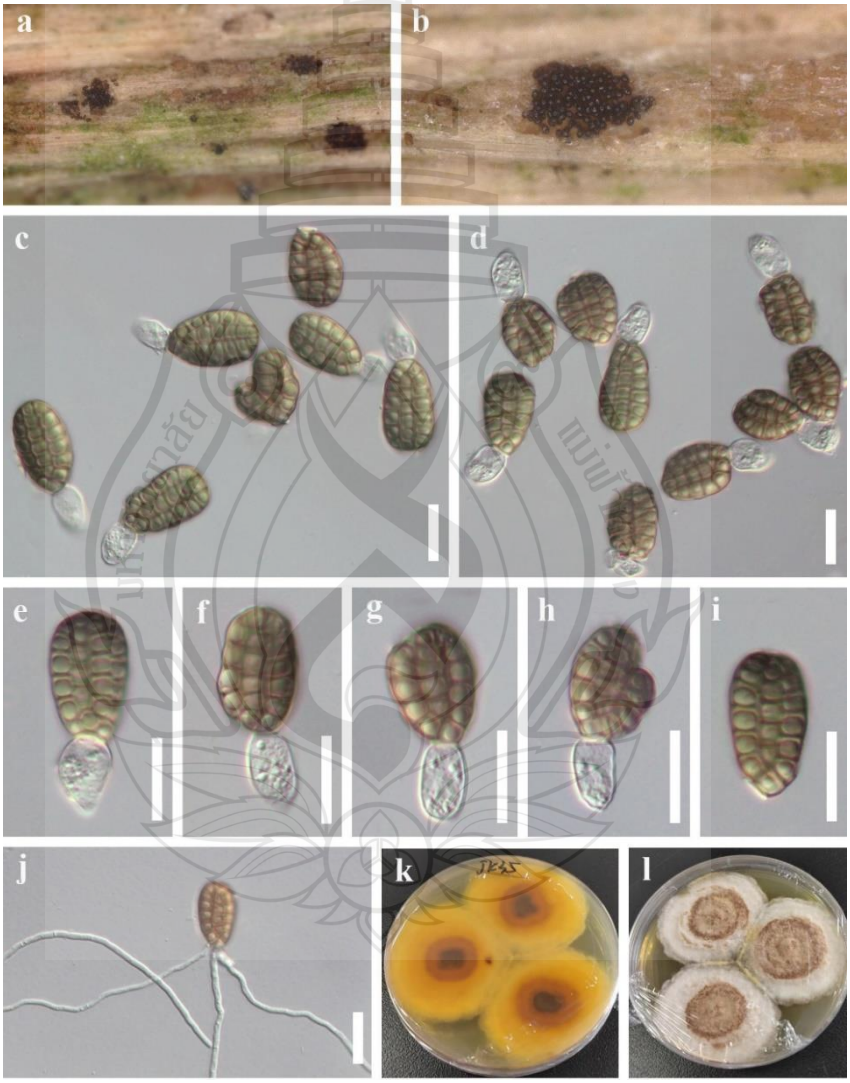
Saprobic on dead twigs of *Buxus sinica* in terrestrial habitat. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown to black, glistening, punctiform. *Mycelium* mostly immersed, composed of branched septate hyphae. *Conidiophores* micronematous, hyaline. *Conidiogenous cells* monoblastic, integrated, terminal, hyaline. *Conidia* 22–34 × 15–23 μm ($\bar{x}$ = 29 × 20 μm, n = 50), solitary, pyriform, cheiroid, non-complanate, consisting of 3–4 closely compact arms arising from a basal cell, multi-septate in each arm, guttulate, golden brown, smooth-walled, often with an ellipsoidal, hyaline basal cell, 13–20 × 8–13 μm.

Culture characteristics: Conidia germinating on PDA media within 12 h and germ tubes produced from the basal cell. Colonies on PDA media circular, dense, flat, with entire edge, brown at the center and white at the outer ring from above; dark brown at the center, brownish yellow at the middle ring, and yellow at the outer ring from reverse.

Material examined: CHINA. Guizhou Province, Tongren City, Jiangkou District, Yamugou Parkland, on dead twigs of *Buxus sinica*, 20 May 2022, Y.R Sun, JK35 (HKAS 136894), living culture GUCC 24-0069.

Notes: *Aquadictyospora clematidis* was primarily described by Phukhamsakda et al. (2020) in Thailand. Our collection is phylogenetically clustered together with *A. clematidis* (MFLUCC 17-0280) (Figure 4.36). There are no base pair differences in LSU, ITS and SSU

genes between HKAS 136894 and MFLUCC 17-0280, and only 11bp (11/913) differences exist in *TEF1-α* gene. Besides, they share similar morphological characteristics, except that our collection produces larger basal cells (13–20 × 8–13 µm *vs.* 5–11 × 4–11 µm) (Phukhamsakda et al., 2020). We regard these differences are insufficient to establish a new taxon. Therefore, we identify our collection as *A. clematidis*, representing a new record from China.



Note a, b Colonies on the substratum. c–i Conidia. j Germinating conidium. k, l Culture colonies on PDA. Scale bars: c–j = 20 µm.

Figure 4.31 *Aquadictyospora clematidis* (HKAS 136894, new geographical record)

Dendryphiella Bubák & Ranoj., Annales Mycologici 12, 417 (1914)

Notes: *Dendryphiella* is an asexual genus placed in the Dictyosporiaceae and was established by Ranojevic (1914). There are 16 species so far described in the genus and only five have sequence data (Liu et al., 2017b; Hyde et al., 2018; Iturrieta-González et al., 2018; Index Fungorum, 2020). A new record of *Dendryphiella vinosa* is reported from *Dendrobium officinale* in Guangxi, China.

Dendryphiella vinosa (Berk. & M.A. Curtis) Reisinger, Bulletin de la Société Mycologique de France 84, 27 (1968)

Index Fungorum number: IF329796; Facesoffungi number: FoF08673, Figure 4.32

Saprobic on the stem of *Dendrobium officinale*. **Sexual morph**: Not observed. **Asexual morph**: *Colonies* on natural substrate clustered, superficial, effuse, brown to dark brown. *Conidiophores* 70–106 µm ($\bar{x}$ = 86 µm), n = 25) macronematous, mononematous, erect, straight or slightly flexuous, unbranched, dark brown at base, slightly paler towards the apex, smooth or delicately rough-walled, septate, wider at septa. *Conidiogenous cells* polytretic, terminal and intercalary, integrated, proliferating asymmetrically, brown, enlarged at vertex. *Conidia* 17–29 × 5– 8 µm ($\bar{x}$ = 21.74 × 6.73 µm, n = 30), oblong with obtuse ends, rounded at apex, truncate at the base, forming simple or branched chains, pale brown when young, brown or dark brown, 3(4)-septate when mature, slightly constricted at septa, smooth or occasionally verruculose.

Culture characteristics: Conidia germinated on PDA within 12 h and germ tubes produced from both ends. Colonies reached about 5 cm diameter after 2 weeks on PDA at 26 °C. Mycelia are superficial, with entire edge, floccose at the center, white to light brown from above and light brown from below.

Material examined: China, Guangxi Province, Nanning City, on the stem of *Dendrobium officinale* (Orchidaceae), 14 September 2019, Yaru Sun G19 (MFLU 20-0444).

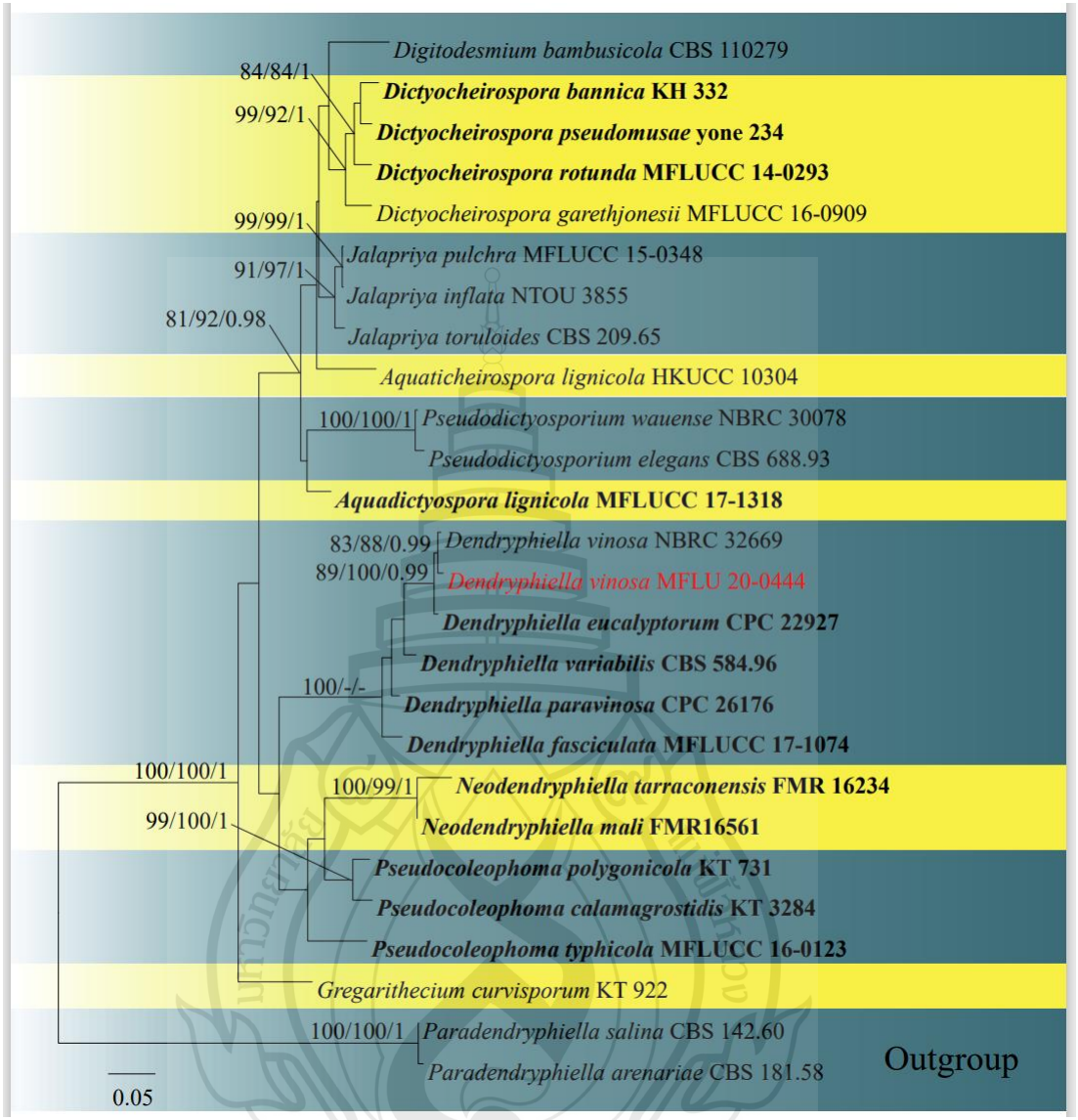
Notes: Our collection only differs from the holotype of *Dendryphiella vinosa* in having shorter conidiophores (70−106 µm *vs*. up to 400 µm). Detailed morphological study and molecular analysis of combined LSU and ITS sequence data indicated that our isolate

clustered together with another strain of *D. vinosa*. Based on the morphology and phylogeny, we identified it as *D. vinosa*. This is the first report of *D. vinosa* on *Dendrobium officinale* in China.



Note a Host. b Colonies on natural substrate. c, d Conidiophore with conidia. e Conidiogenous cell. f–l Conidia. Scale bars: c–d = 20 μm, e–l = 10 μm.

Figure 4.32 *Dendryphiella vinosa* (MFLU 20-0444, new geographical and host record)



Note Bootstrap support values for ML and MP greater than 80% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with P. salina (CBS 142.60) and P. arenariae (CBS 181.58). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Figure 4.33 Phylogenetic tree of *Dendryphiella*

Dictyocheirospora D'souza, Boonmee & K.D. Hyde, Fungal Diversity: [10] (2016)

Notes: Boonmee et al. (2016) introduced *Dictyocheirospora*, with *D. rotunda* as its type species. *Dictyocheirospora* species are commonly encountered as saprobes in freshwater ecosystems and terrestrial habitats (Boonmee et al., 2016; Wang et al., 2016; Yang, Liu et al., 2018; Shen et al., 2022). Some also are related to medicinal plants (Prasher & Verma, 2015). The sexual morph has not been described for this genus and the hyphomycetous asexual morphs are charactered by sporodochial colonies, holoblastic, cylindrical conidiogenous cells and solitary, cheiroid, not complanate, ellipsoid to cylindrical, brown to dark brown conidia (Boonmee et al., 2016; Phukhamsakda et al., 2020). There are 25 species listed in this genus (Species Fungorum, 2024).

Dictyocheirospora xishuiensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902591; Facesoffungi number: FoF 16420; Figure 4.34

Etymology: Referring to the location in which the fungus was collected

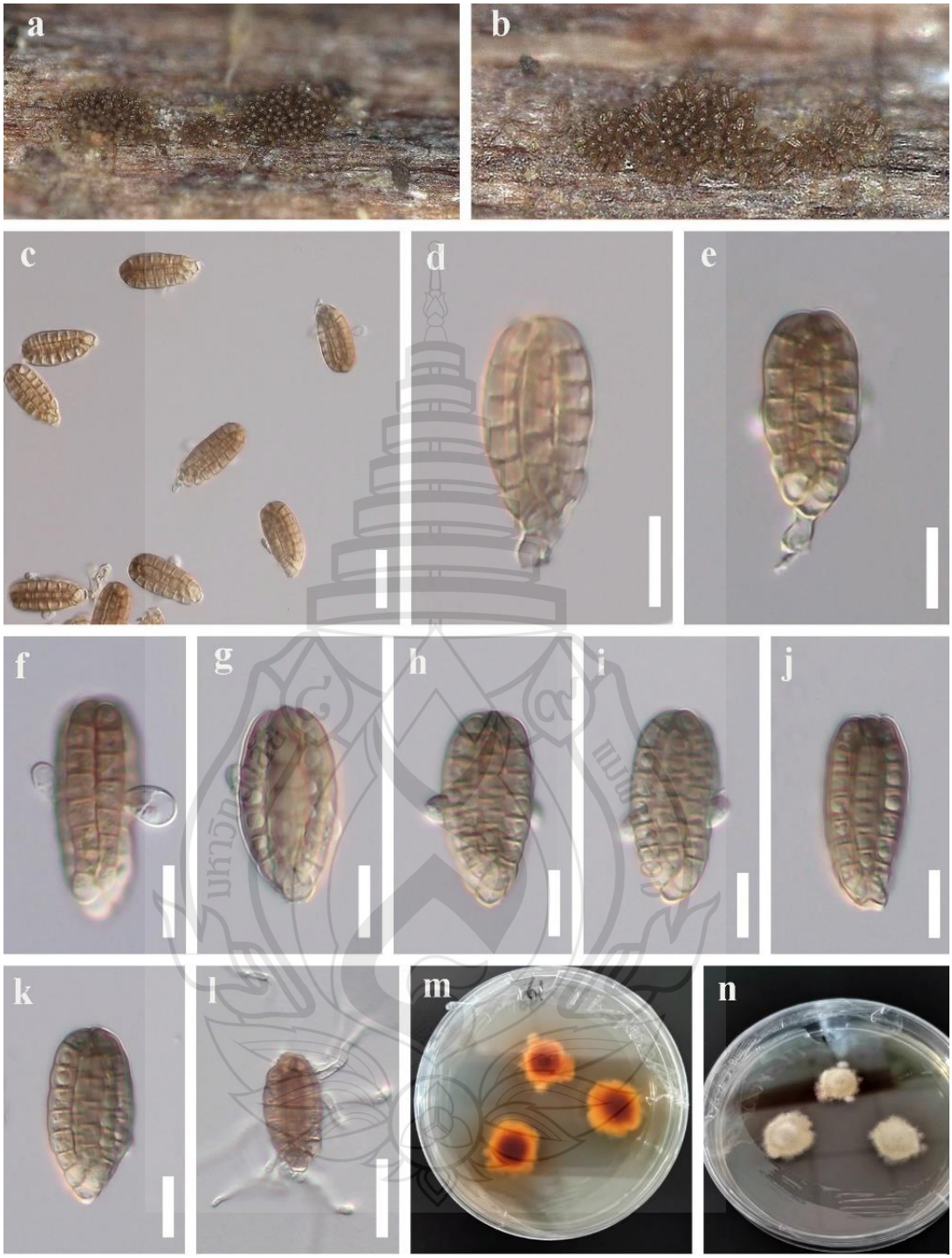
Holotype: HKAS 136885.

Saprobic on dead twigs of *Camphora* sp. in terrestrial habitat. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* punctiform, sporodochial, scattered and brown. Mycelium partly superficial, composed of hyaline to pale brown, septate, branched hyphae. *Conidiophores* micronematous, mononematous, cylindrical, pale brown, smooth. *Conidiogenous cells* holoblastic, cylindrical, hyaline to pale brown, smooth. *Conidia* 23–31 × 10–13 µm ($\bar{x}$ = 27 × 12 µm, n = 30), solitary, cheiroid, ellipsoid, not complanate, brown, composed of several compact rows of cells tightly clustered at the apex, euseptate, each row with 7–9 cells, sometimes with globose to subglobose, hyaline appendages attached at the central cells of the outer cell-row.

Culture characteristics: Ascospores germinated on PDA within 12 h at 26 °C. Colonies on PDA reached 15 mm diam. after 3 weeks at 26 °C; mycelium hyaline, tight, circular, white from above, red brown with a white circular from below.

Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on dead twigs of Camphora sp., 14 April 2023, Y.R. Sun, 2361 (HKAS 136885, **holotype**); ex-type culture GUCC 24-0070.

Notes: *Dictyocheirospora xishuiensis* is phylogenetically related to *D. aquatica*, *D. garethjonesii* and *D. nabanheensis* (Figure 4.36). In morphology, *D. xishuiensis* differs from *D. aquatica* and *D. garethjonesii* by possessing conidia with appendages (Wang et al., 2016). *Dictyocheirospora xishuiensis* produces conidia of smaller dimensions compared to *D. nabanheensis*, measuring 23–31 × 10–13 µm *vs*. 35–40 × 18–21 µm, respectively (Tibpromma, Hyde, McKenzie et al., 2018). Based on these distinctions, we propose *D. xishuiensis* as a new species.



Note a, b Colonies on the substratum. c–e Conidiogenous cells and conidia. f–k Conidia with or without appendages. l Germinating conidium. m, n Culture colonies on PDA. Scale bars: c, l = 20 µm, d–k = 10 µm.

Figure 4.34 *Dictyocheirospora xishuiensis* (HKAS 136885, holotype)

Dictyosporium Corda, Weitenweber's Beitr. Nat. 1: 87 (1837)

Notes: *Dictyosporium* was formally established by Witenweber (1838) and defined *D. elegans* as its type species. *Dictyosporium* species are prevalent globally in both aquatic and terrestrial environments, where they serve as saprobes, commonly inhabiting decaying wood, plant litter, and soil. (Van Emden 1975; Boonmee et al., 2016; Yang, Liu et al., 2018; Zhang, Liu et al., 2023). Some *Dictyosporium* species isolated from medicinal plants (Goh et al., 1999; Silva et al., 2015). So far, there are 64 species listed in this genus (Species Fungorum, 2024).

Dictyosporium zhejiangense Wongs., H.K. Wang, K.D. Hyde & F.C. Lin, Cryptog. Mycol. 30(4): 358 (2009)

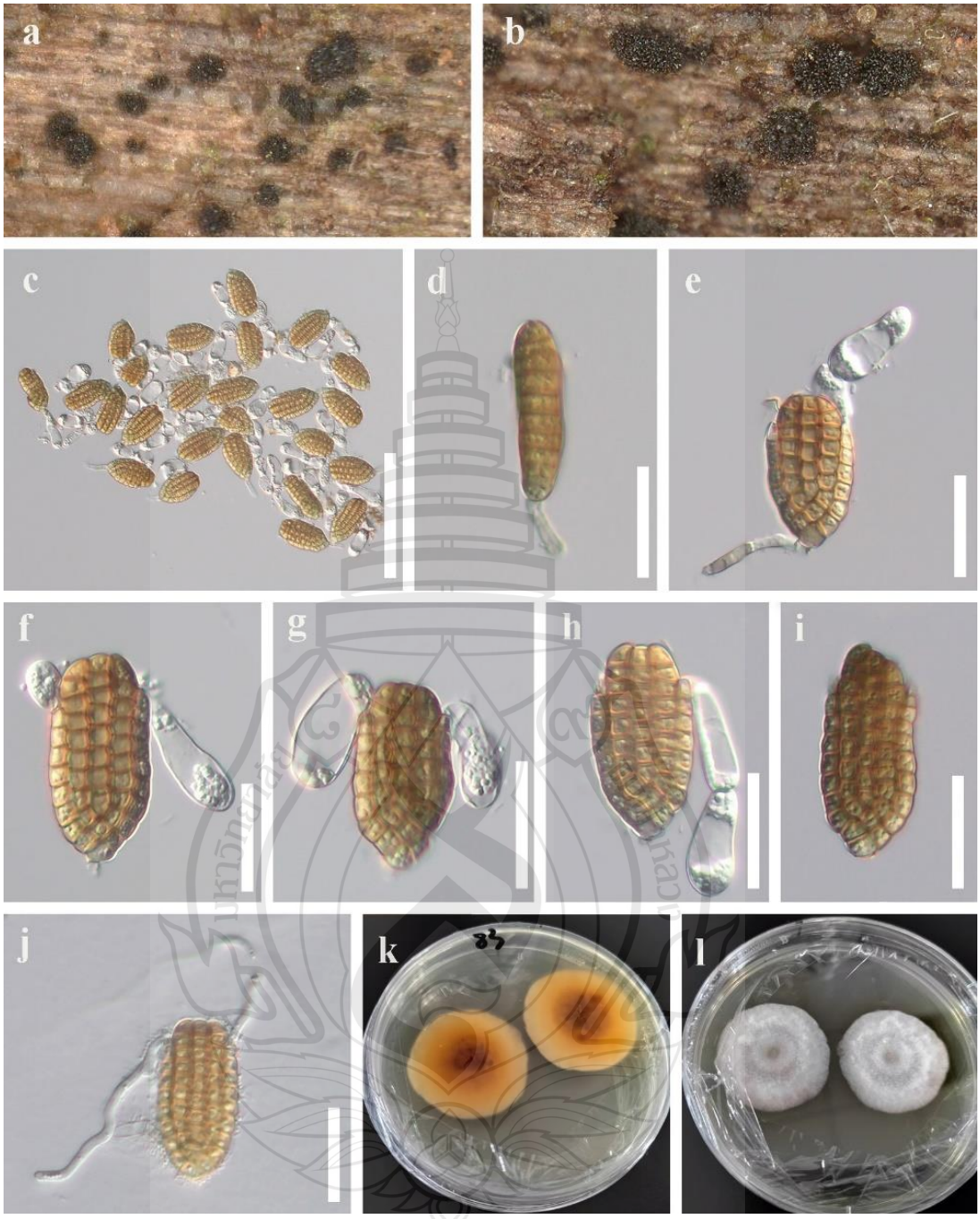
Index Fungorum number: IF51525; Facesoffungi number: FoF 16421; Figure 4.35

Saprobic on dead twigs in terrestrial habitat. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* punctiform, sporodochial, scattered and black. Mycelium partly immersed, partly superficial, composed of hyaline to pale brown, septate hyphae. *Conidiophores* micronematous, mononematous, septate, cylindrical, pale brown, smooth and thin-walled. *Conidiogenous cells* 1.5–4 µm wide, monoblastic, cylindrical, terminal, determinate, hyaline to pale brown, smooth, thin-walled. *Conidia* 24–36 × 12–19 µm ($\bar{x}$ = 30 × 16 µm, n = 50), acrogenous, solitary, yellowish-brown, complanate, cylindrical when young, cheiroid when mature, composed of 3–5 rows of cells (mostly 5), 7–10 euseptate in each row. The two outer rows are usually shorter, the apical cells of each outer row are provided with 1–2 appendages which are thin-walled, hyaline, smooth, 25–38 × 5.5–9.5 µm, rounded to cylindrical., The appendages were frequently detached from conidia under slightly pressure.

Culture characteristics: Ascospores germinated on PDA within 12 h at 26 ℃. Colonies on PDA reached 15 mm diam. after 3 weeks at 26 ℃; mycelium hyaline, tight, circular, white from above, red brown in the center, yellow on the outside from below.

Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on dead twigs, 14 April 2023, Y.R. Sun, 2383 (HKAS 136886); living culture GUCC 24-0071.

Notes: *Dictyosporium zhejiangense* was introduced by Wongsawas et al. (2009) from freshwater habitat in China. Our collection clustered together with *D. zhejiangense* MW2009a in the phylogenetic tree (Figure 4.36), and the ITS of these two strains exhibit a difference of only 4 base pairs. These two collections exhibit similar morphological characteristics, except the conidia of our strain are slightly narrower (L/W: 1.9 *vs*. 1.5). Besides, the shapes of the appendages are not as diverse as those reported in Wongsawas et al. (2009). The slight difference observed could be caused by different habitats. We thus identify our collection as *D. zhejiangense*, which represents a new record from terrestrial habitat.



Note a, b Colonies on the substratum. c–e Conidiogenous cells and conidia. f–i Conidia with or without appendages. j Germinating conidium. k, l Culture colonies on PDA. Scale bars: c = 50 µm, d–j = 20 µm.

Figure 4.35 *Dictyosporium zhejiangense* (HKAS 136886, new habitat record)

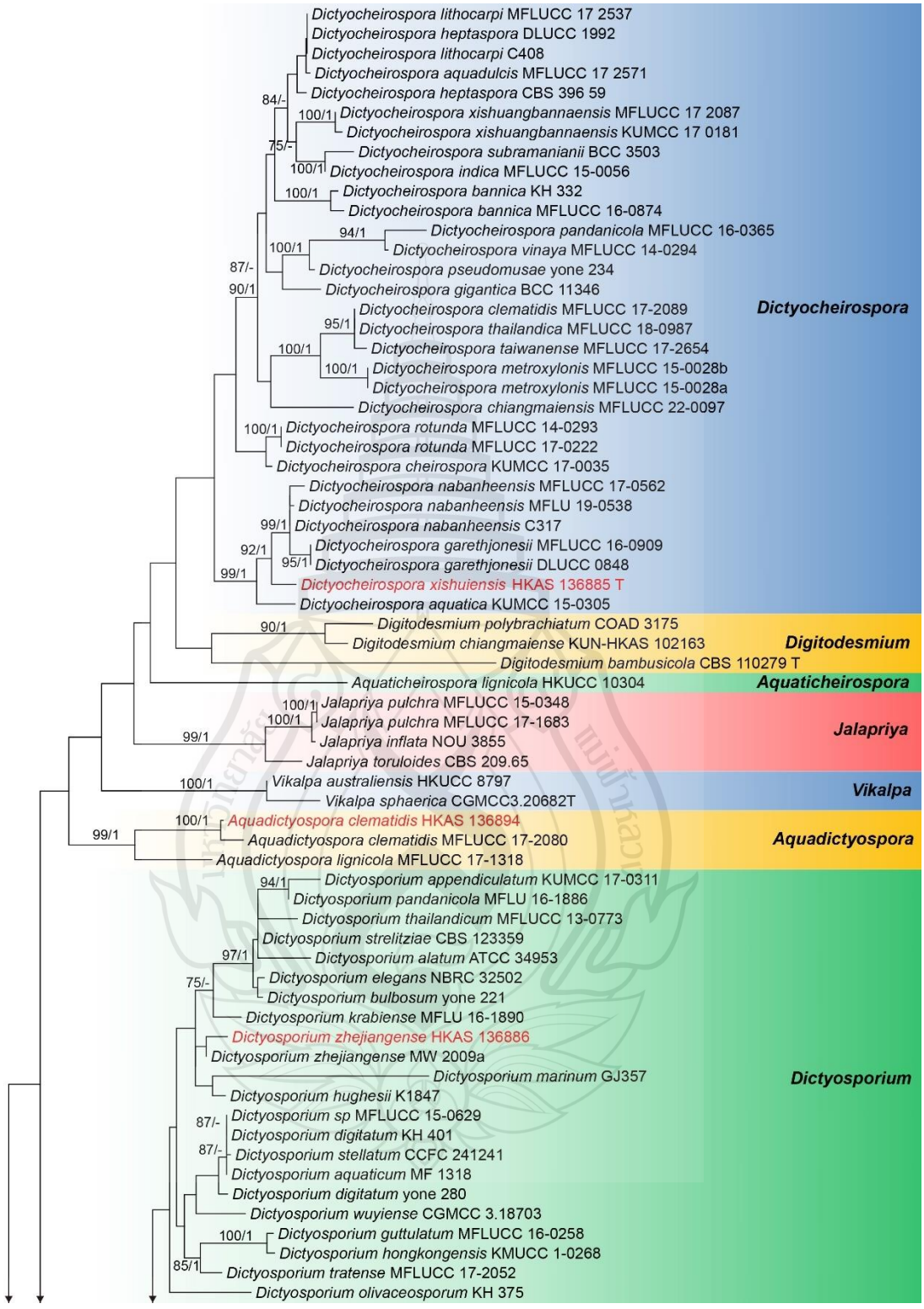
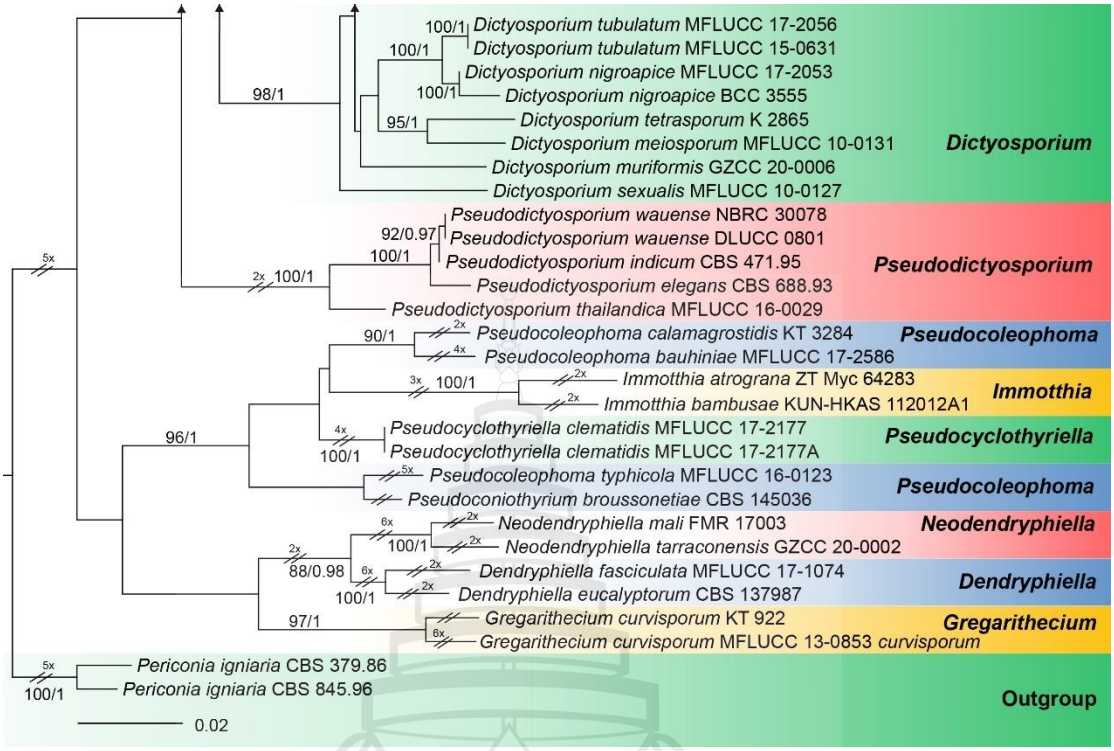


Figure 4.36 Phylogenetic tree of Dictyosporiaceae



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Periconia igniaria* (CBS 379.86) and (CBS 845.96). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.36 (continued)

Didymosphaeriaceae Munk, Dansk bot. Ark. 15(no. 2): 128 (1953).

Montagnula Berl., Icon. fung. (Abellini) 2(2-3): 68 (1896)

Notes: *Montagnula* was introduced by Berlese (1896) and typified by *M. infernalis.* About a century later, *Montagnula* species was once again discovered by taxonomists (Crivelli, 1983). Leuchtmann (1984) included phragmosporous and didymosporous species in this genus, making species identification heterogeneous. Aptroot (1995) established *Munkovalsaria* to accommodate *Mu. donacina* based on valsoid ascomata, bitunicate, fissitunicate asci and 1-septate ascospores. Wanasinghe et al. (2016)

synonymized *Munkovalsaria* under *Montagnula* based on analyses of combined LSU, SSU and ITS sequence data.

Most *Montagnula* species exist in dead leaves and twigs by their sexual morph, and they have a wide geographic and host distribution (Berlese, 1896; Crous et al., 2012; Liu et al., 2015; Tibpromma, Hyde, Bhat et al., 2018; Mapook et al., 2020; Du et al., 2021). The sexual morph is characterized by globose or sphaerical, immersed to erumpent, brown to dark ascomata with or without ostiole. The peridium is *textura angularis*. Asci are cylindric-clavate to clavate, bitunicate, 4 or 8 spored and ascospores are pale to dark brown, phragmosporous, didymosporous or dictyosporous (Berlese, 1896; Tennakoon et al., 2016; Hyde et al., 2020; Mapook et al., 2020; Boonmee et al., 2021). Only one species, *M. cylindrospora* was reported as an asexual morph. The coelomycetous asexual morph has solitary, superficial, brown to dark brown, globose to subglobose conidiomata, phialidic, ampulliform to dolioform, hyaline conidiogenous cells and aseptate, hyaline, cylindrical conidia (Crous et al., 2020). There are 41 validly published *Montagnula* species in Species Fungorum (accessed on 30 June 2024) and among them only 18 species have molecular data.

Montagnula aquatica Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900129; Facesoffungi number: FoF 12922; Figure 4.37

Holotype: MFLU 22-0171.

Etymology: Referring to the aquatic habitat of the fungus.

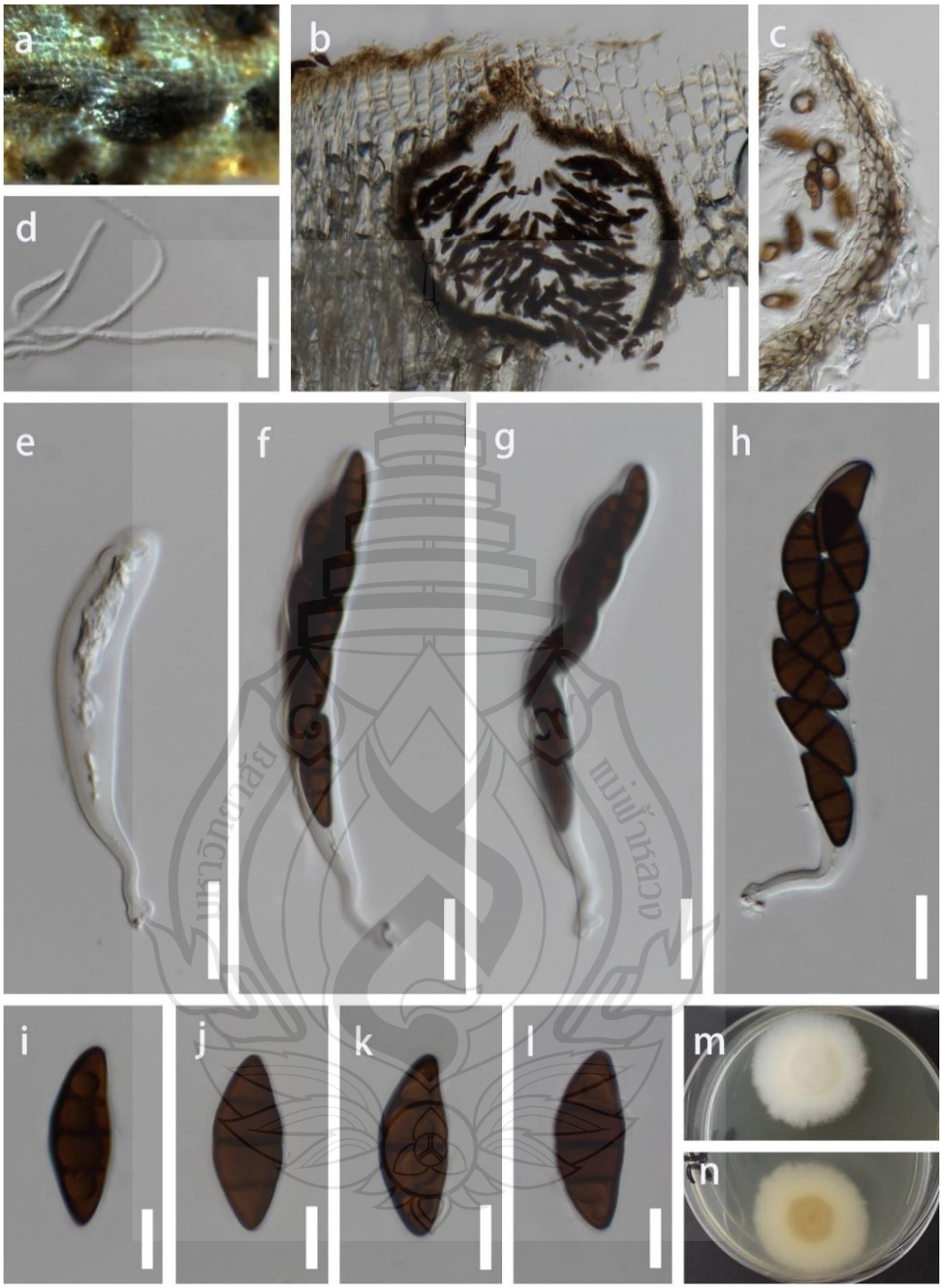
Saprobic on submerged decaying wood in freshwater habitat. **Sexual morph:** *Ascomata* 250–430 μm long, 250–340 μm high, semi-immersed, solitary or scattered, globose, uniloculate, black, smooth-walled, with a central ostiole. *Ostiole* papillate, central., *Peridium* 10–22 μm wide, fused with host tissues, comprising of 2 layers of pale brown to brown cells of *textura angularis*. *Hamathecium* comprising 1.3–2.0 μm wide, numerous filamentous, branched, hyaline, septate, guttulate, pseudoparaphyses. *Asci* 110–130 × 13–19 μm ($\bar{x}$ = 122 × 15.5 μm, n = 10), bitunicate, 8-spored, cylindric-clavate, slightly curved.

Ascospores 24–35 × 7.5–14 µm ($\bar{x}$ = 30.5 × 10.5 µm, n = 30), hyaline to yellow-brown when immature, dark brown when mature, 2- seriate, fusiform to broadly fusiform, 3-septate, widest at the centre, tapering towards ends, conical both end, guttulate, without appendages and mucilaginous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 12 h at 25 ˚C, germ tubes produced from both ends. Colonies on PDA reaching 5 cm diam after 3 weeks at 25 ˚C, mycelium white, flossy, circular, slightly flattened, undulate, with the entire edge; white to yellow in reverse.

Material examined: THAILAND, Chiang Rai Province, Bandu District, on decaying wood, 6 March 2021, Y.R. Sun, 26 (MFLU 22–0171, **holotype**).

Notes: *Montagnula aquatica* phylogenetically formed as a distinct clade. Morphologically, *M. aquatica* can be distinguished by larger ascospores from its related species in Clade 1 (Figure 4.40) (24–35 × 7.5–14 µm in *M. aquatica vs*. 18–25 × 5–88 µm in *M. camporesii vs*. 18–23.5 × 6.5–9.5 µm in *M. cirsii vs*. 20–23 × 7–9 µm in *M. scabiosae*) (Hongsanan et al., 2015; Hyde et al., 2016; Hyde et al., 2020; Du et al., 2021). In addition, *M. aquatica* has thinner peridium than *M. cirsii* (10–22 µm *vs*. 41–58.5 µm), *M. aquatica* has larger asci than *M. camporesii* (110–130 × 13–19 µm *vs*. 80–120 × 10–15 µm) (Hyde et al., 2016, 2020). Thus, *M. aquatica* sp. nov is introduced and it is the first *Montagnula* species reported from freshwater habitats.



Note a Appearance of ascomata on the substrate. b Section through ascomata. c Peridium. d Trabeculate pseudoparaphyses e–h Immature and mature asci. i–l Ascospores. m, n Colony on PDA medium. Scale bars: b = 100 µm, c–h = 20 µm, i–l = 10 µm.

Figure 4.37 *Montagnula aquatica* (MFLU 22-0171, holotype)

Montagnula guiyangensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF900130; Facesoffungi number: FoF 12923; Figure 4.38

Holotype: HKAS 124556.

Etymology: Referring to the location in which the fungus was collected.

Saprobic on twigs of *Helwingia himalaica* in terrestrial habitat. **Sexual morph:** *Ascomata* 300–400 × 350–400 µm, semi-immersed, solitary or scattered, globose, uniloculate, black, with a central ostiole. *Ostiole* papillate, central., *Peridium* 20–40 µm wide, fused with host tissues, comprising of 2 layers of pale brown to brown cells of *textura angularis*. *Hamathecium* comprises 1.5–3.0 µm wide, branched, hyaline, septate, pseudoparaphyses. *Asci* 84–135 × 10–15 µm ($\bar{x}$ = 104 × 12 µm, n = 15), bitunicate, 8-spored, clavate, with a short, bulbous long pedicel, slightly curved. *Ascospores* 10–20 × 3.5–6 µm ($\bar{x}$ = 15.5 ×5 µm, n = 35), hyaline to olivaceous when immature, brown when mature, overlapping uniseriate or 2-seriate, fusiform, 1-septate, constricted at the septum, slightly widest at the upper cell and tapering towards ends, guttulate, sheath drawn out to form polar appendages, from both ends of the ascospores, straight or slightly curved. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA within 12 h at 25 ˚C, germ tubes produced from both ends. Colonies on PDA reaching 7 cm diam after 4 weeks at 25 ˚C, mycelium white to gray, flossy, circular, slightly flattened, undulate, yellow in reverse.

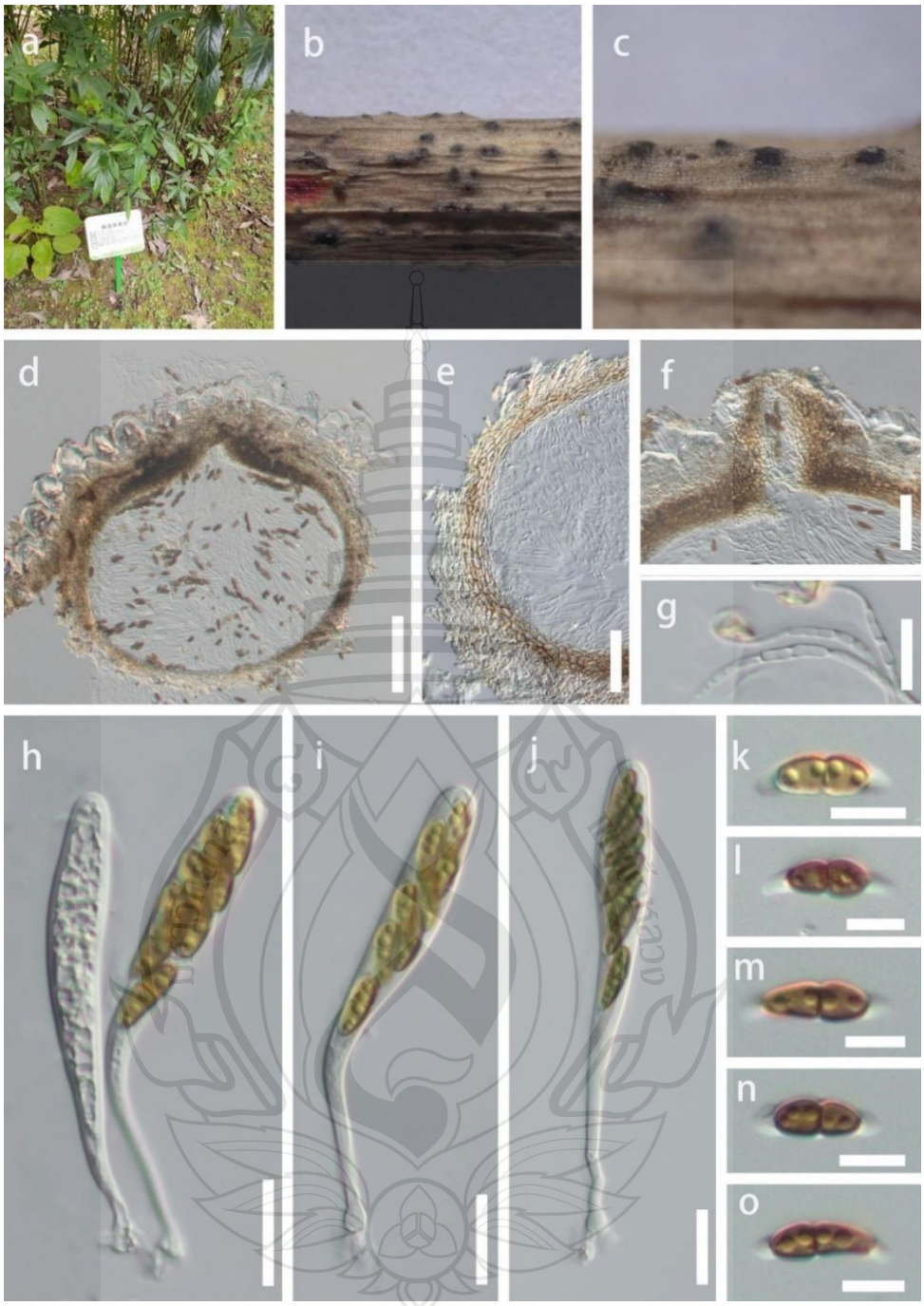
Material examined: China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, on twigs of *Helwingia himalaica*, 22 December 2021, Y.R. Sun, 22-41 (HKAS 124556, **holotype**; ex-type living culture GUCC 22-0816); ibid, on twigs of *Helwingia himalaica*, 22 December 2021, Y.R. Sun, 41-2 (HGUP 800, paratype; living culture GUCC 22-0817).

Notes: *Montagnula guiyangensis* was isolated from *Helwingia himalaica,* an important medicinal plant. Multi-gene analyses showed that *M. guiyangensis* is a phylogenetically distinct species in Clade 2 (Figure 4.40). Morphologically, *M. guiyangensis* resembles *M. appendiculata, M. chiangraiensis* and *M. chromolaenae* in having fusiform,

1-septate ascospores with appendages. However, *M. guiyangensis* differs by larger ascomata from *M. chromolaenae* and *M. appendiculata* (300–400 × 350–400 µm in *M. guiyangensis vs*. 170–190 × 170–190 µm in *M. chromolaenae vs*. 100–200 µm in *M. appendiculata*) (Mapook et al., 2020). *Montagnula guiyangensis* has larger asci than *M. chiangraiensis* (84–135 × 10–15 µm *vs*. 60– 75 × 8–11). *Montagnula guiyangensis* can be distinguished from *M. aloes* by 1-septate, fusiform ascospores with appendages, while the latter has 3-euseptate, ovoid to ellipsoid ascospores (Crous et al., 2012). In addition, comparisons of ITS, LSU and SSU sequences between *M. guiyangensis* and phylogenetically related species are provided (Table 4.2).

Table 4.2 Number of polymorphic nucleotide differences between *M. guiyangensis* HKAS 124556 with *M. aloes*, *M. appendiculata*, *M. chiangraiensis* and *M. chromolaena* (without gap)

Species	Strain	ITS	LSU	SSU
M. aloes	CBS 132531	20 (497bp)	10 (815bp)	not available
M. appendiculata	CBS 10927	18 (497bp)	16 (813bp)	not available
M. chiangraiensis	MFLUCC 17-1420	13 (497bp)	18 (813bp)	27 (987bp)
M. chromolaena	MFLUCC 17-1435	14 (497bp)	18 (813bp)	32 (987bp)



Note a. Host. b, c Appearance of ascomata on the substrate. d Section through ascomata. e Peridium. g Trabeculate pseudoparaphyses. h–j Asci. k–o Ascospores. Scale bars: d = 100 µm, e, f = 50 µm, g–j = 20 µm, k–o = 10 µm.

Figure 4.38 *Montagnula guiyangensis* (HKAS 124556, holotype)

Montagnula donacina (Niessl) Wanas., E.B.G. Jones and K.D. Hyde, Fungal Biology 120 (11): 1365 (2016)

= *Montagnula chromolaenicola* Mapook and K.D. Hyde.

= *Montagnula puerensis* Tibpromma and Du.

= *Montagnula saikhuensis* Wanas., E.B.G. Jones and K.D. Hyde.

= *Montagnula thailandica* Mapook and K.D. Hyde.

Index Fungorum number: IF557299; Facesoffungi number: FoF 07792; Figure 4.39

Saprobic on decaying wood in terrestrial habitat. **Sexual morph**: *Ascomata* 405–470 µm high, 280–380 µm wide, semi-immersed, solitary or scattered, globose, uniloculate, black, with a central ostiole. *Ostiole* papillate, central., Peridium 15–30 µm wide, fused with host tissues, comprising of two layers of pale to brown cells of textura angularis. *Hamathecium* comprising 1–2.5 µmwide, branched, hyaline, septate, pseudoparaphyses. *Asci* 80–125 × 9–12 µm, bitunicate, 8-spored, clavate, with a bulbous long pedicel, slightly curved. *Ascospores* 10–15 × 4–7 µm (x = 13.5 × 5.5 µm, n = 30), brown, overlapping uniseriate or 2-seriate, fusiform, 1-septate, constricted at the septum, slightly widest at the upper cell and tapering towards ends, guttulate, straight or slightly curved. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated on PDA within 12 h at 25 ◦C. Germ tubes produced from one side of the middle of ascospore. Colonies on PDA reached 5 cm diam after four weeks at 25 ◦C, mycelium white to gray, flossy, circular, undulate, gray in reverse.

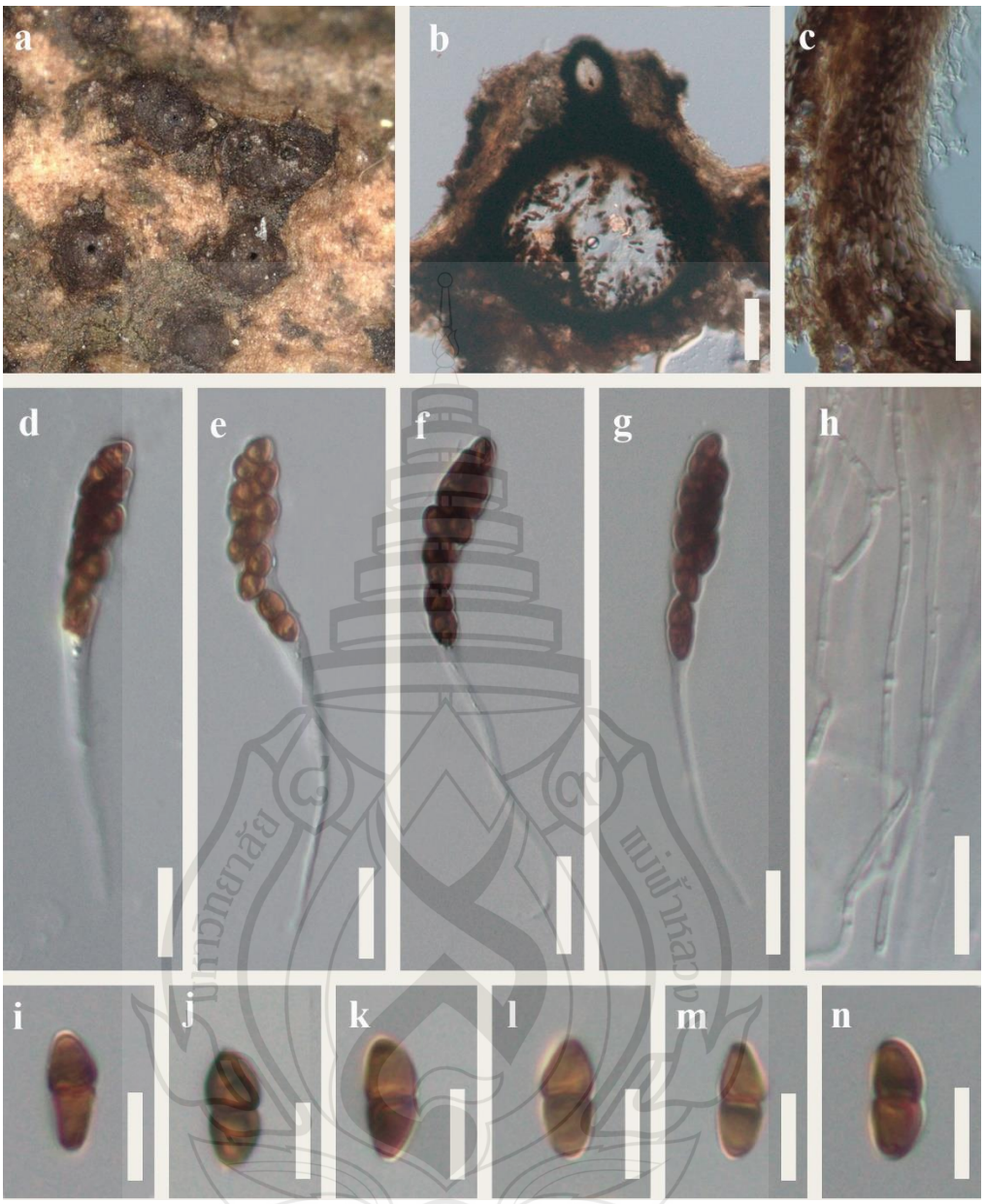
Material examined: China, Guizhou Province, Qianxinan Bouyei and Miao Autonomous Prefecture, Anlong County, on dead wood, 16 March 2022, J.Y. Zhang, Y312 (HKAS 124552; living culture GUCC 22-0818).

Notes: *Montagnula chromolaenicola*, *M. donacina*, *M. puerensis*, *M. saikhuensisi*, and *M. thailandica* clustered together without obvious branches in the phylogenetic tree (Figure 4.40). Morphologically, they have similar ascomata, asci, and ascospores, including measurement size. It is worth noting that Wanasinghe et al. (2016) took multi-loculate

ascomata as the difference between *M. donacina* and *M. saikhuensis*. Du et al. (2021) distinguished *M. donacina* and *M. puerensis* by *M. donacina* having carbonaceous ascostromata. However, the previous literature did not mention that *M. donacina* has multi-loculate, carbonaceous ascostromata (Aptroot, 1995; Pitt, 2014). Comparisons of ITS, LSU, SSU, and tef1-α sequences between *M. donacina* and phylogenetically related species are provided in Table 4.3. Few differences exist among their ITS, LSU, and SSU sequences, respectively, and there is a maximum difference of 10 bp in tef1-α gene. We conclude that the evidence for these five species as independent species is insufficient. The slight difference of multi-genes may represent the intraspecific variation. Therefore, we synonymize *M. chromolaenicola*, *M. puerensis*, *M. saikhuensisi*, and *M. thailandica* under *M. donacina* based on the nomenclatural priority. Our new collection HKAS 124552 has overlapping characteristics with these *M. donacina* isolates.

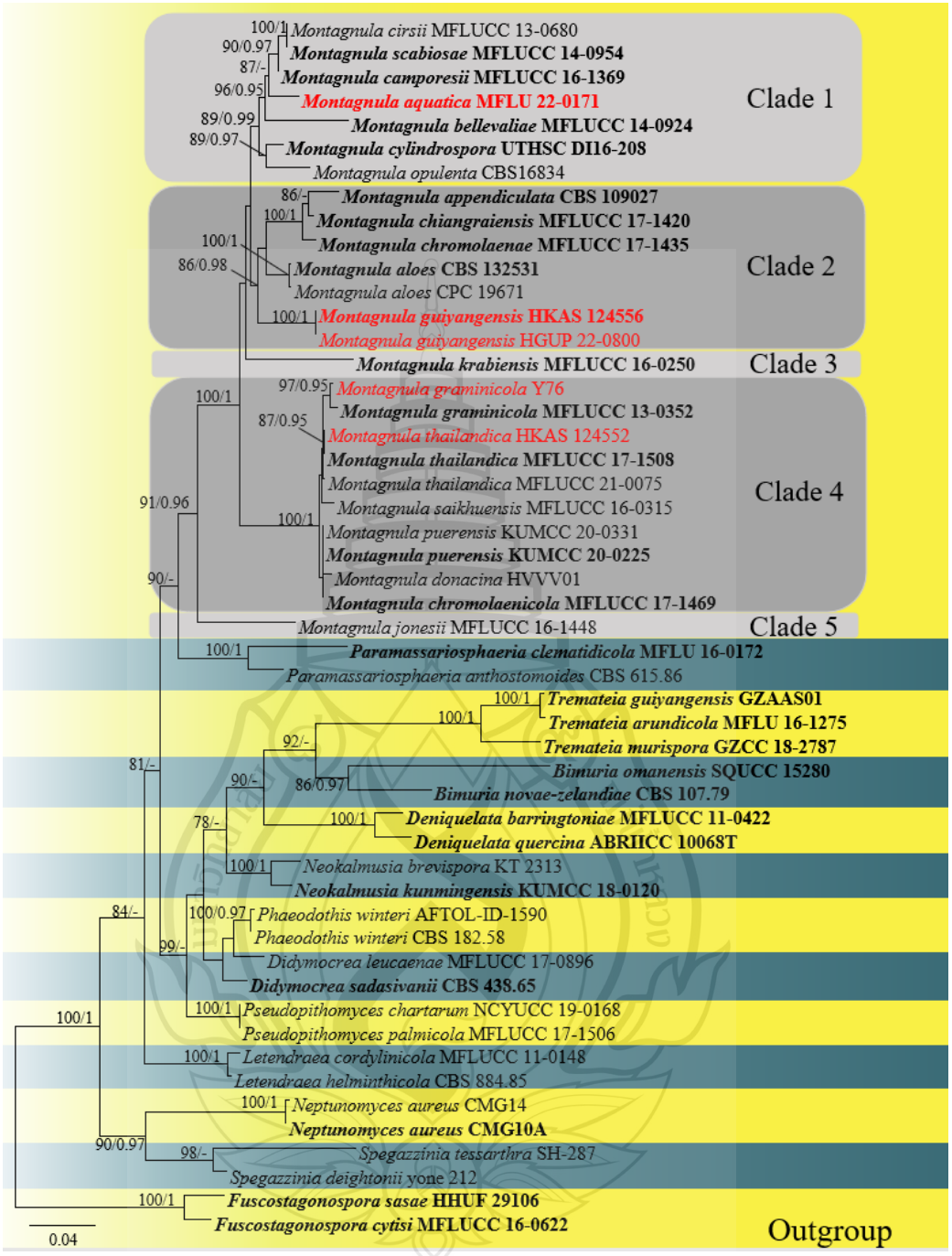
Table 4.3 Comparison of nucleotide differences between *M. donacina* (KUMCC 21–0653) and *M. chromolaenicola*, *M. puerensis*, *M. saikhuensis*, and *M. thailandica*

Species	Strain	ITS (504 bp)	LSU (842 bp)	SSU (971 bp)	tef1-α (840 bp)
M. chromolaenicola	MFLUCC 17-1469	0	3	1	10
M. puerensis	KUMCC 20-0225	0	0	1	8
M. saikhuensis	MFLUCC 16-0315	4	2	3	not available
M. thailandica	MFLUCC 17-1508	3	2	3	2



Note a Appearance of ascomata on the substrate. b Section through ascomata. c Peridium. h Paraphyses. d–j Asci. i–n Ascospores. Scale bars: b = 100 µm, c–h = 20 µm, i–n = 10 µm.

Figure 4.39 *Montagnula donacina* (HKAS 124552)



Note The tree is rooted with *Fuscostagonospora sasae* (HHUF 29106) and *F. cytisi* (MFLUCC 16-0622). Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. Ex-type strains are in bold, the new isolates are in red.

Figure 4.40 Phylogenetic tree of *Montagnula*

Kalmusia Niessl, Verh. nat. Ver. Brünn 10: 204 (1872).

Notes: *Kalmusia* was introduced by Niessl (1872) with *K. ebuli* as the type species. There are 29 species listed in this genus, and only five have been described by their asexual morph (Manawasinghe et al., 2022; Species Fungorum, 2024). The sexual morphs are characterized by brown to black, immersed to erumpent ascomata, filiform, delicate, septate pseudoparaphyses, bitunicate, clavate asci and pale brown, narrowly ovoid to clavate, 3-septate ascospores; the asexual morphs have pycnidia, semi-immersed, papillate, brown conidiomata, cylindrical to globose, hyaline, holoblastic conidiogenous cells and oblong to oval, aseptate, hyaline conidia (Liu et al., 2015; Hongsanan et al., 2020a; Manawasinghe et al., 2022). We introduce the sixth asexual morph *Kalmusia* species here, representing a new species isolated from the medicinal plant, *Tetrastigma planicaule*.

Kalmusia tetrastigma*e** Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.

Facesoffungi number: FoF 16422; Figure 4.41

Etymology: The specific epithet refers to the host genus.

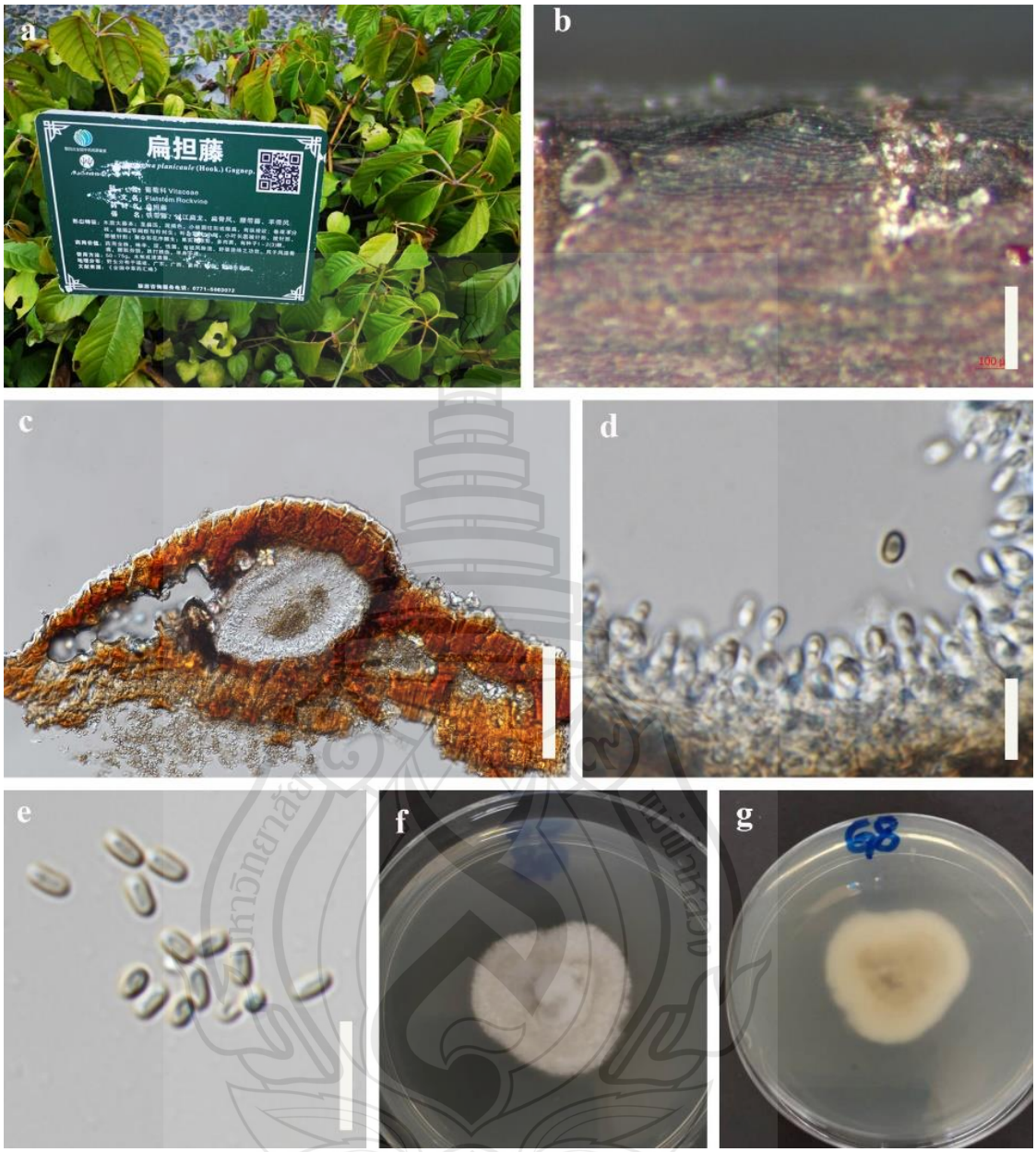
Holotype: HGUP 24-0026.

Associated with diseased twigs of *Tetrastigma planicaule*. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* 140–170 μm wide, around 100 μm high, pycnidia, solitary, semi-immersed, globose to subglobose, apapillate, black, coriaceous. *Pycnidial wall* around 10 μm wide, comprising several layers of brown, thick-walled, cells of *textura angularis*. *Conidiophores* reduce to conidiogenous cells. *Conidiogenous cells* 1–2 μm wide, holoblastic, cylindrical to globose, hyaline, smooth. *Conidia* 2.5–4 × 1–2 μm ($\bar{x}$ = 3×1.5 μm, n = 40), oblong, aseptate, hyaline when young, pale brown when mature, smooth-walled.

Culture characteristics: Conidia germinated on PDA within 12 h at 26 °C. Colonies on PDA reached 2 cm diam. after 3 weeks at 26 °C; mycelium white, flossy, cotton, white from above, white to pale brown from reverse.

Material examined: CHINA, Guangxi Province, Nanning City, on twigs of *Tetrastigma planicaule*, 14 September 2019, Y.R. Sun, G8 (H HGUP 24-0026, **holotype**); ex-type culture GUCC 24-0072.

Notes: *Kalmusia tetrastigma*e was isolated from the medicinal plant, *Tetrastigma planicaule*, in China. It is phylogenetically sister to *K. cordylines,* which was isolated from medicinal plant, *Cordyline fruticose* (Figure 4.43). Morphologically, *K. tetrastigma*e differs from *K. cordylines* by its thinner conidiogenous cells (1–2 µm *vs.* 5–10 × 5–6 µm) and smaller conidia (2.5–4 × 1–2 µm *vs.* 3–5 × 5–10 µm) (Manawasinghe et al., 2022). In addition, there are 13 bp differences (without gap, 544 bp) in the ITS region. We thus introduce *K. tetrastigma*e as a new species.



Note a Host. b Conidiomata observed on host substrate. c Vertical section of conidioma. d Conidiogenous cells. e Conidia. f, g Colonies on PDA. Scale bars: b = 200 μm, c = 100 μm, d, e = 10 μm.

Figure 4.41 *Kalmusia tetrastigmae* (HGUP 24-0026, holotype)

Paraphaeosphaeria O.E. Erikss., Ark. Bot., Ser. 2 6: 405 (1967).

Notes: Eriksson (1967) established the genus *Paraphaeosphaeria* to accommodate four species characterized by oblong-cylindrical ascospores. Ariyawansa et al. (2014) placed it in Didymosphaeriaceae (= Montagnulaceae) based on multi-locus phylogeny, which was confirmed by recent studies (Hongsanan et al., 2020a; Tennakoon et al., 2022; Wijayawardene et al., 2022). Currently, there are 37 species listed in this genus (Species Fungorum, 2024).

Paraphaeosphaeria neglecta Verkley, Riccioni & Stielow, Persoonia 32: 44 (2014)

Index Fungorum number: IF800767; Facesoffungi number: FoF16423; Figure 4.42

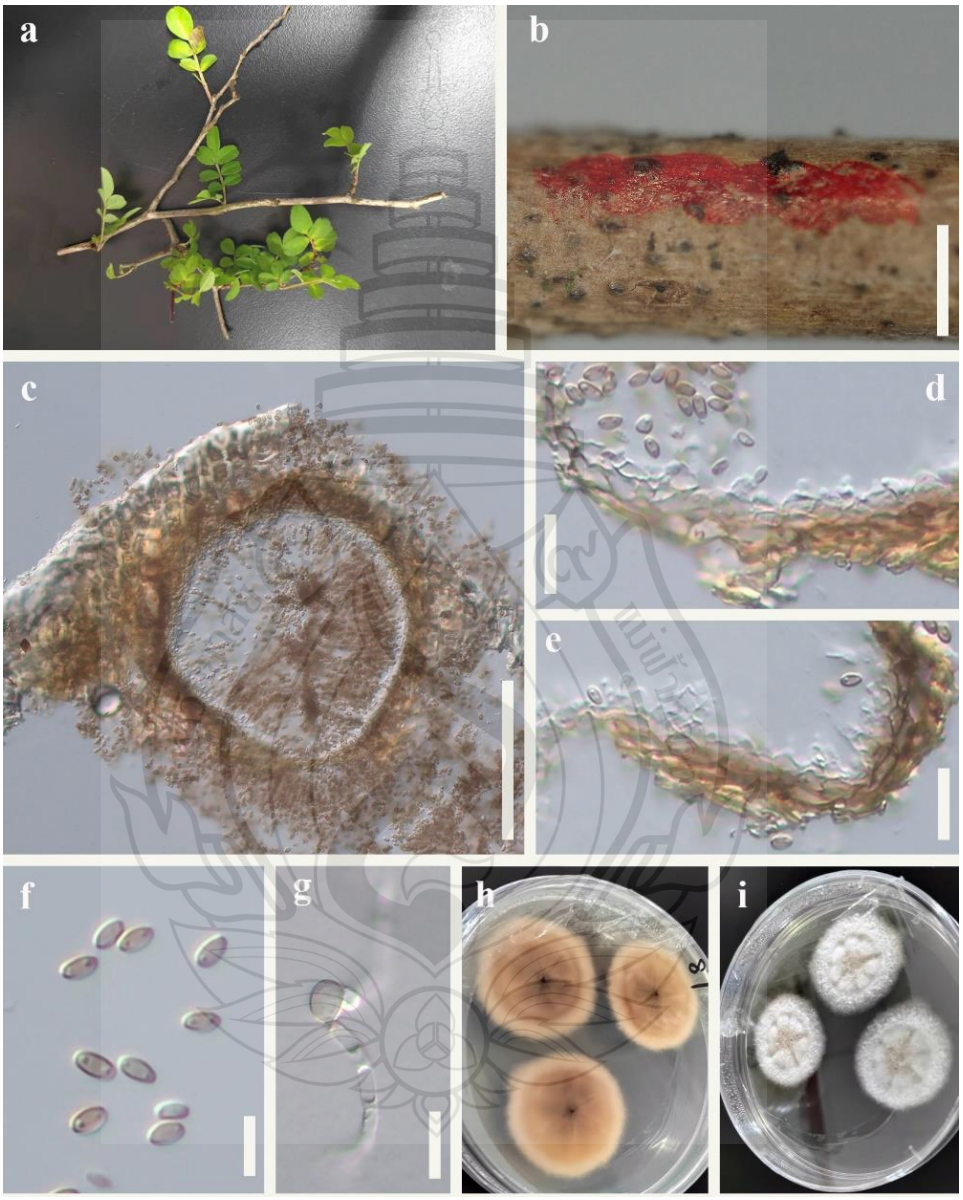
Associated with diseased twigs of *Rosa roxburghii*. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* around 250 μm diam, pycnidia, solitary, semi-immersed, globose to subglobose, apapillate, black, coriaceous. *Pycnidial wall* around 5–10 μm wide, fused with host tissues, comprising two layers of *textura angularis*, outer layer brown, thick-walled, inner layer hyaline. *Conidiophores* reduce to conidiogenous cells. *Conidiogenous cells* 1–2 μm wide, holoblastic, doliiform to ampulliform, hyaline, smooth. *Conidia* 3–4 × 1.5–3 μm ($\bar{x}$ = 3.5 × 2 μm, n = 30), subglobose, ellipsoid to obovoid-pyriform, aseptate, pale brown, smooth-walled.

Culture characteristics: Conidia germinated on PDA within 12 h at 26 °C. Colonies on PDA reached 3 cm diam. after 3 weeks at 26 °C; circular, flat, mycelium white, flossy, cotton, white from above, pale to brown from reverse.

Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, on twigs of *Rosa roxburghii*, 13 April 2023, Y.R. Sun, 2387 (HKAS 136887); living culture GUCC 24-0073.

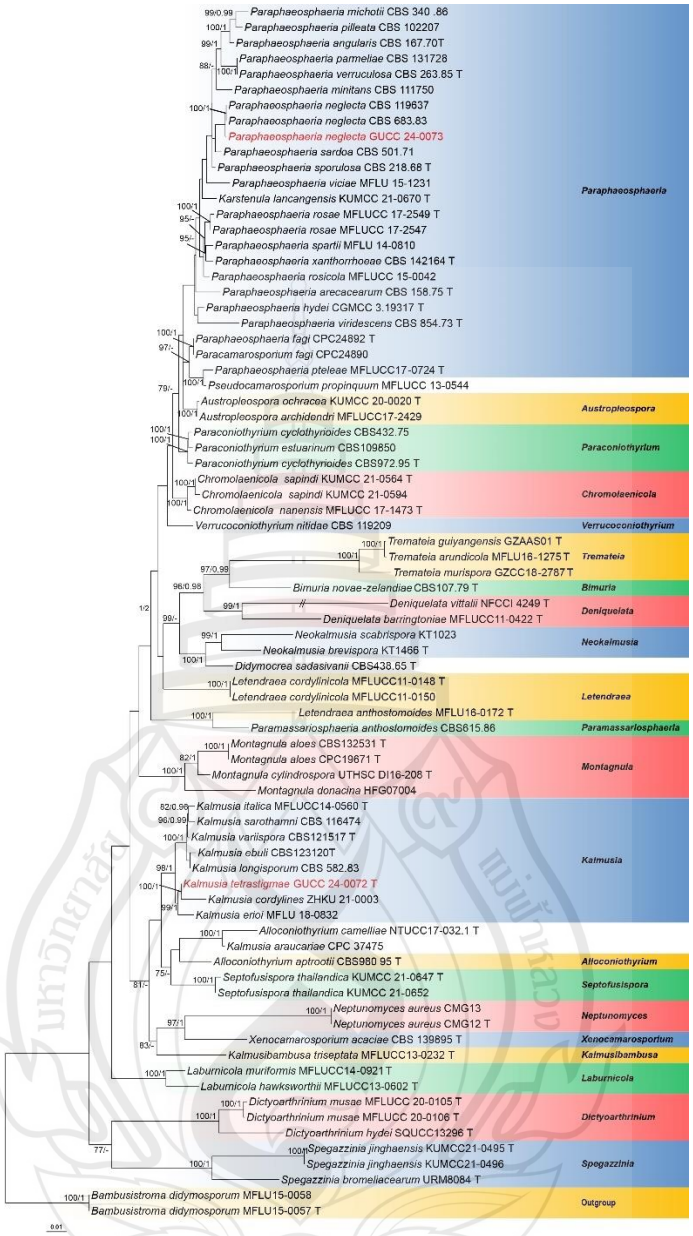
Notes: *Paraphaeosphaeria neglecta* was introduced by Verkley et al. (2014). It was isolated from plant tissue and soil in Europe (Verkley et al., 2014). In the phylogenetic analyses, new strain from our collection clustered with *Paraphaeosphaeria neglecta* (Figure 4.43). In the conidial characteristics, both species share very similar characteristics, including color and size (Verkley et al., 2014). In addition, there is no base pair difference

in the LSU gene region and only two base pair differences in the ITS gene region. Therefore, we identified our collection as *Paraphaeosphaeria neglecta*, representing a new host record from *Rosa roxburghii* in China.



Note a Host. b Conidiomata observed on host substrate. c Vertical section through conidioma. d Conidiogenous cells. e Peridium. f Conidia. g Germinating conidium. h, i Colonies on PDA. Scale bars: b = 1000 µm, c = 100 µm, d, e, g = 10 µm, f = 5 µm.

Figure 4.42 *Paraphaeosphaeria neglecta* (HKAS 136887, new host record)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Bambusistroma didymosporum* (MFLU 15-0057) and (MFLU 15-0058). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.43 Phylogenetic tree of *Didymosphaeriaceae*

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

Keissleriella Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 128(7-8): 582 (1919)

= *Pleurophoma* Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 123: 117 (1914)

Notes: *Keissleriella* was introduced by Höhnel (1919) and typified by *Keissleriella aesculi*. The genus is characterized by immersed to erumpent, globose to subglobose, ascomata with a papillate ostioles covered by short dark setae, mostly 8-spored, cylindric-clavate, bitunicate, fissitunicate asci, and hyaline or pale brown, ellipsoidal or fusiform, septate ascospores with or without a mucilaginous sheath (Liu et al., 2015; Thambugala et al., 2017; Jiang, Phookamsak et al., 2019; Hyde, Dong et al., 2020). Hyde, Dong et al. (2020) introduced the asexual morph species, *Keissleriella camporesii*, supported by molecular data. However, this asexual morph was similar to *Pleurophoma*. *Pleurophoma* is known in asexual morphs (de Gruyter et al., 2010) and based on *P. pleurospora* (Höhnel, 1914). Crous, Wingfield, Guarro et al. (2015) described *P. ossicula* with both sexual and asexual morphs, suggesting a potential link with *Keissleriella*. Tibpromma et al. (2017) introduced the second sexual morph *Pleurophoma* species, also resembling to *Keissleriella*. Li et al. (2020) proposed a potential relationship between *Keissleriella* and *Pleurophoma* based on morphology and phylogeny.

In our phylogenetic analyses (Figure 4.45), *Pleurophoma* clustered together with *K. genistae* and *K. rosacearum* within *Keissleriella*. We suggest *Pleurophoma* represents the asexual morph of *Keissleriella*. Index Fungorum (2024) listed fifty epithets for *Keissleriella*, while *Pleurophoma* had only nine. Choosing for *Pleurophoma* might necessitate more nomenclature changes than *Keissleriella*. Therefore, we proposed to use *Keissleriella* over *Pleurophoma*, and the former also was better established in the literature than *Pleurophoma*. In addition, we introduced one new species and four combinations based on morphology and phylogeny.

Keissleriella yunnanensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902592; Facesoffungi number: FoF 16424; Figure 4.44

Etymology: Named after the fungus collected location.

Holotype: HKAS 136902.

Saprobic on *Yucca* sp. **Sexual morph**: *Ascomata* 150–230 μm high, 105–160 μm diam., visible as raised, black dots on host surface, scattered, solitary or in groups, semi-immersed, subglobose, ostiolate at centre, with minute papilla, filled with short, dark brown, aseptate periphyses. *Peridium* 10–16 μm wide, outer layer composed of brown to dark brown, thick-walled cells of *textura angularis*; inner layer composed of hyaline to pale brown cells of *textura prismatica*. *Hamathecium* 1–2 μm wide, composed of dense, filamentous, septate, branched pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 64–80 × 6–8 μm ($\bar{x}$ = 73 × 7 μm, n = 15), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded. *Ascospores* 16–20 × 2.5–4.5 μm ($\bar{x}$ = 17 × 3.5 μm, n = 20), overlapping 1–2-seriate, hyaline when young, pale brown when mature, fusiform, with rounded ends, (–4) 5-septate, slightly curved, slightly constricted at the septate, smooth-walled, with small guttules, surrounded by a distinct mucilaginous sheath. **Asexual morph**: Not observed.

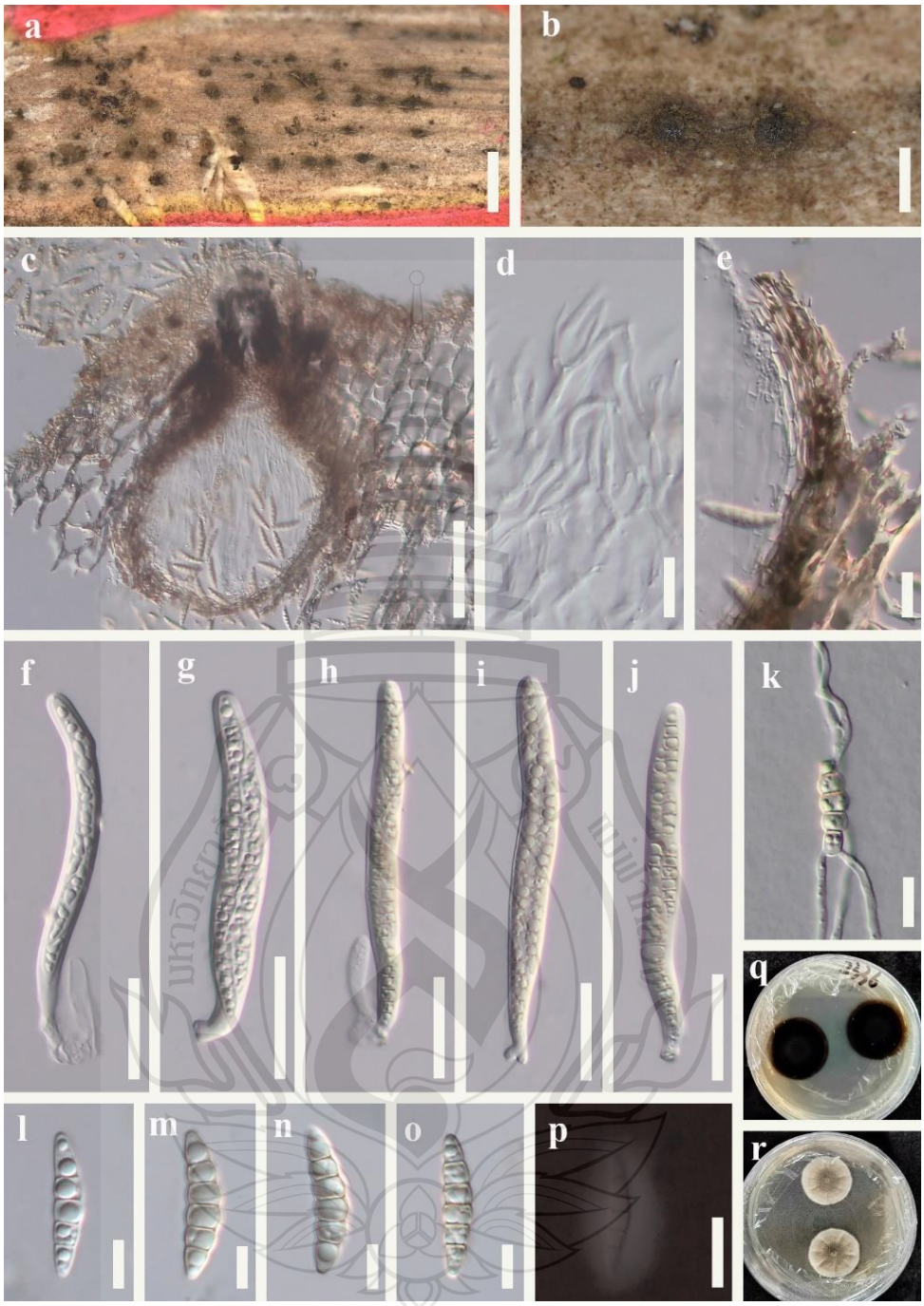
Culture characteristics: Ascospores germinating on PDA within 12 h at 26 °C. Colony reaching 3.5 cm diam. after 30 days, circular, with flat surface, edge entire, cotton, gray from above, dark from below.

Material examined: CHINA, Yannan Province, Kunming City, Yiliang District, Yangzonghai Garden, on leaves of *Yucca* sp., 20 February 2023, H.W. Shen, 2336 (HKAS 136902, **holotype**); ex-type culture GUCC 24-0074.

Notes: *Keissleriella yunnanensis* is closely related to *K. bambusicola*, *K. caraganae* and *K. yonaguniensis* in the phylogenetic tree (Figure 4.45). Morphologically, it differs from *K. bambusicola* in having smaller asci (64–80 × 6–8 μm *vs.* 100–125 × 10–14 μm) and spores (16–20 × 2.5–4.5 μm *vs.* 20–25 × 5–6 μm) (Jiang, Phookamsak et al., 2019).

Keissleriella yunnanensis can be distinguished from *K. caraganae* by its thinner asci (64–80 × 6–8 μm *vs*. 39–75 × 10–12 μm) and (4)5-septate ascospores (Phookamsak et al., 2019). The distinction between *K. yunnanensis* and *K. yonaguniensis* lies in the former having fusiform spores, whereas the latter possesses cylindrical spores (Tanaka et al., 2015). Therefore, we introduced *K. yunnanensis* sp. nov. in this study.

In our study, *Keissleriella* species did not cluster together and was divided into two groups in the phylogenetic tree (Figure 4.45). The same result also appeared in previous literatures (Tibpromma et al., 2017; Hyde, Dong et al., 2020; Shen et al., 2023). It is noteworthy that all the species in clade 2 had pale brown spores, while in clade 1, only two species produced yellow spores, with the rest being hyaline-spored species. Species in clade 2 were exclusively represented by their sexual morphs, making it impossible to compare differences in their asexual morphs between these two clades. Future research might consider the possibility of dividing *Keissleriella* into two genera based on either spore color or differences in the asexual morph.



Note a, b Ascomata on the host substrate. c Section of an ascoma. d Paraphyses. e Section of peridium. f–j Asci. k Germinated ascospore. l–o Ascospores. p Ascospore in the Indian ink. q, r Culture (r from above, q from below). Scale bars: a = 1000 µm, b = 200 µm, c = 50 µm, d, e, k, p = 10 µm, f–j = 20 µm, l–o = 5 µm.

Figure 4.44 *Keissleriella yunnanensis* (HKAS 136902, holotype)

Keissleriella* acaciae** (Crous) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov.

≡ *Pleurophoma acaciae* Crous, Persoonia 37: 357 (2016)

Facesoffungi number: FoF 06721.

Notes: *Pleurophoma acaciae* was introduced by Crous, Wingfield, Burgess et al. (2016) from leaves of *Acacia glaucoptera* in Australia. It produces globose, erumpent, uni- to multilocular conidiomata, hyaline, smooth, subcylindrical to ampulliform conidiogenous cells and subcylindrical, aseptate, hyaline conidia (Crous, Wingfield, Burgess et al., 2016). In their phylogenetic analyses, *Pleurophoma acaciae* grouped with *K. cladophila*, *K. sparticola*, *P. ossicula* and *P. pleurospora*. However, due to lack of sufficient data to prove the relationship between *Keissleriella* and *Pleurophoma*, they introduced *P. acaciae* within *Pleurophoma.*

In our phylogenetic analyses based on combined LSU, ITS, SSU and *TEF1-α* sequence data (Figure 4.45), *Pleurophoma acaciae* grouped with other *Keissleriella* species and formed a distinct clade within *Keissleriella*. Thus, we proposed to transfer *P. acaciae* under the new combination *Keissleriella acaciae* based on the morphological and phylogenetic analyses.

Keissleriella italicum (Tibpromma, Camporesi & K.D. Hyde) Y.R. Sun & K.D. Hyde, ***comb. nov.***

≡ *Pleurophoma italica* Tibpromma, Camporesi & K.D. Hyde, Fungal Diversity 83: 62 (2017)

Facesoffungi number: FoF 16425.

Notes: *Pleurophoma italica* was introduced as a new species with both sexual and asexual morphs (Tibpromma et al., 2017). They mentioned that *P. italica* shares similar asexual morphology with the type species, *Pleurophoma pleurospora,* but constitutes a separate branch in the phylogenetic tree. Tibpromma et al. (2017) suggested synonymizing *Keissleriella sparticola*, *K. cladophila* and *K. genistae* under *Pleurophoma* if their asexual morphs are discovered, as these three taxa clustered with *Pleurophoma* species.

In our phylogenetic analyses based on combined LSU, ITS, SSU and *TEF1-α* sequence data (Figure 4.45), *Pleurophoma italica* was sister to *Keissleriella rosacearum* and *P. ossicola* and placed an inner clade in *Keissleriella*. We also compared the morphology of *P. italica* and

Keissleriella species and concluded that *P. italica* conforms to the morphological characteristics of *Keissleriella*. Since *Keissleriella italica* already exists within the genus *Keissleriella*, we recommended moving *Pleurophoma italica* under the new combination *Keissleriella italicum* based on the morphological and phylogenetic analyses.

Keissleriella ossicula (Crous, Krawczynski & H.-G. Wagner) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov.***

≡ *Pleurophoma ossicola* Crous, Krawczynski & H.-G. Wagner, Persoonia 34: 203 (2015)

Facesoffungi number: FoF 16426.

Notes: *Pleurophoma ossicula* was introduced by Crous, Wingfield, Guarro et al. (2015) from old bone of presumed cattle in Germany. *Pleurophoma ossicula* was close to *Keissleriella genistae* and *P. pleurospora* in their phylogenetic analysis but can be distinct by characteristics (Crous, Wingfield, Guarro et al., 2015). *Pleurophoma ossicula* is the first report of the sexual morph for *Pleurophoma*. Crous, Wingfield, Guarro et al. (2015) suggested that *Pleurophoma* might be related to *Keissleriella.*

In our phylogenetic analyses based on combined LSU, ITS, SSU and *TEF1-α* sequence data, *P. ossicula* sister to *Keissleriella rosacearum* (Figure 4.45). However, it can be distinct by its hyaline, obovoid ascospore without sheath (Crous, Wingfield, Guarro et al., 2015; Wanasinghe et al., 2018). Thus, we synonymized *P. ossicula* under *Keissleriella ossicula* based on the morphological and phylogenetic analyses.

Keissleriella pleurospora (Sacc.) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov.***

≡ *Phoma pleurospora* Sacc., Michelia 2(no. 6): 97 (1880)

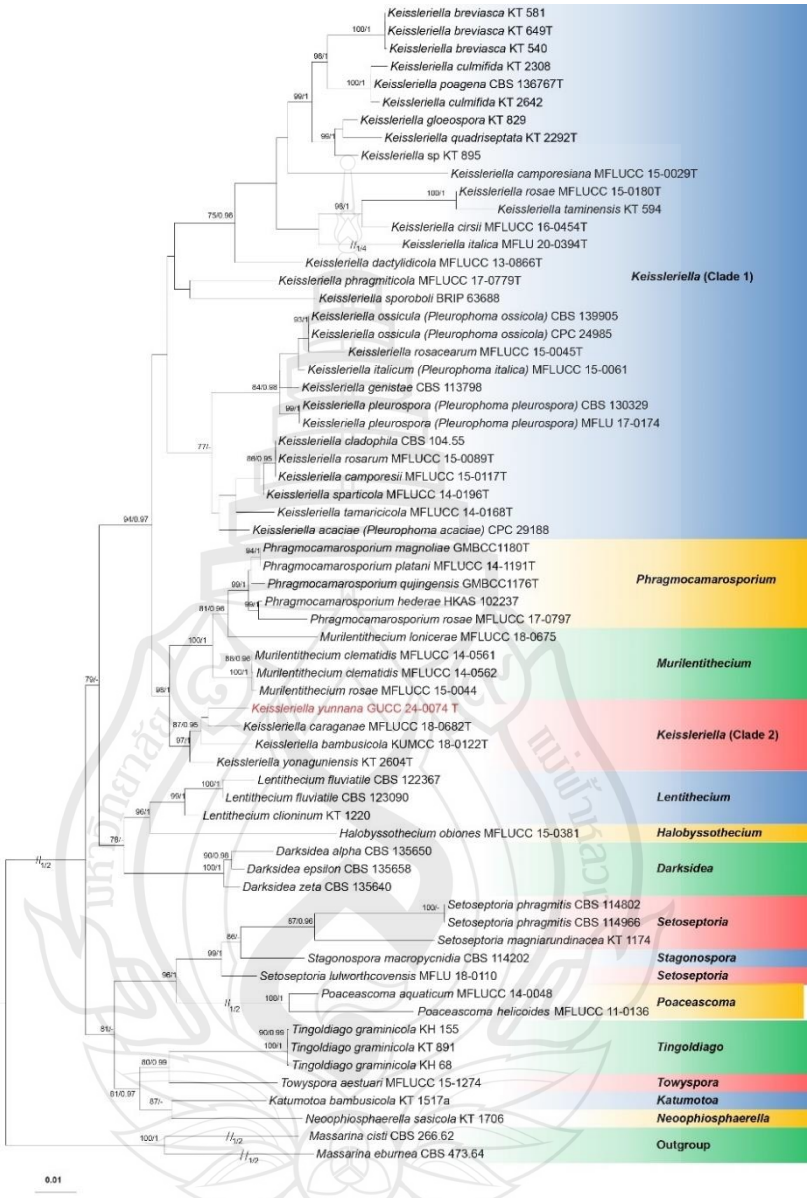
= *Pleurophoma pleurospora* (Sacc.) Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 123: 117 (1914)

= *Dinemasporium pleurospora* (Sacc.) Shkarupa [as 'pleuropsora'], Nov. sist. Niz. Rast. 17: 108 (1980)

Facesoffungi number: FoF 06763.

Notes: *Phoma pleurospora* was initially reported by Saccardo (1880). Subsequently, it underwent two synonymizations. In our phylogenetic analyses, it was placed within *Keissleriella.*

Therefore, we proposed using *Keissleriella pleurospora* over *Dinemasporium pleurospora.*



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Massarina cisti* (CBS 266.62) and M. *eburnea* (CBS 473.64). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.45 Phylogenetic tree of *Keissleriella*

Lophiotremataceae K. Hiray. & Kaz. Tanaka, Mycoscience 52: 405 (2011)

Lophiotrema Sacc., Michelia 1 (no. 3): 338. (1878)

Notes: *Lophiotrema* was introduced by Saccardo (1883) to accommodate species that have immersed ascomata with a crestlike ostiolar neck, cylindrical asci and hyaline ascospores. These taxa were initially accommodated in Lophiostomataceae but later, being reassigned to Lophiotremataceae by Hirayama and Tanaka (2011). Tanaka and Harada (2003) proposed that *Lophiotrema* has a pleurophomopsis-like asexual morph, but no asexual species have been reported in the past two decades (Zhang et al., 2009; Hirayama & Tanaka, 2011; Mathiassen et al., 2017a; Mathiassen et al., 2017b; Zhang et al., 2018; Phookamsak et al., 2019; Zhang, Liu et al., 2023). In this study, we reported a coelomycetous species and emendated the asexual morph of this genus. The coelomycetous asexual morphs are characterized by pycnidial, semi-immersed globose to subglobose conidiomata with a long neck, blastic, phialidic, cylindrical to lageniform, hyaline conidiogenous cells and oblong, hyaline, aseptate or 1-septate conidia.

Lophiotrema guizhouense Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902585; Facesoffungi number: FoF 16427; Figure 4.46

Etymology: Referring to the province where the fungus was collected

Holotype: HGUP 24-0017.

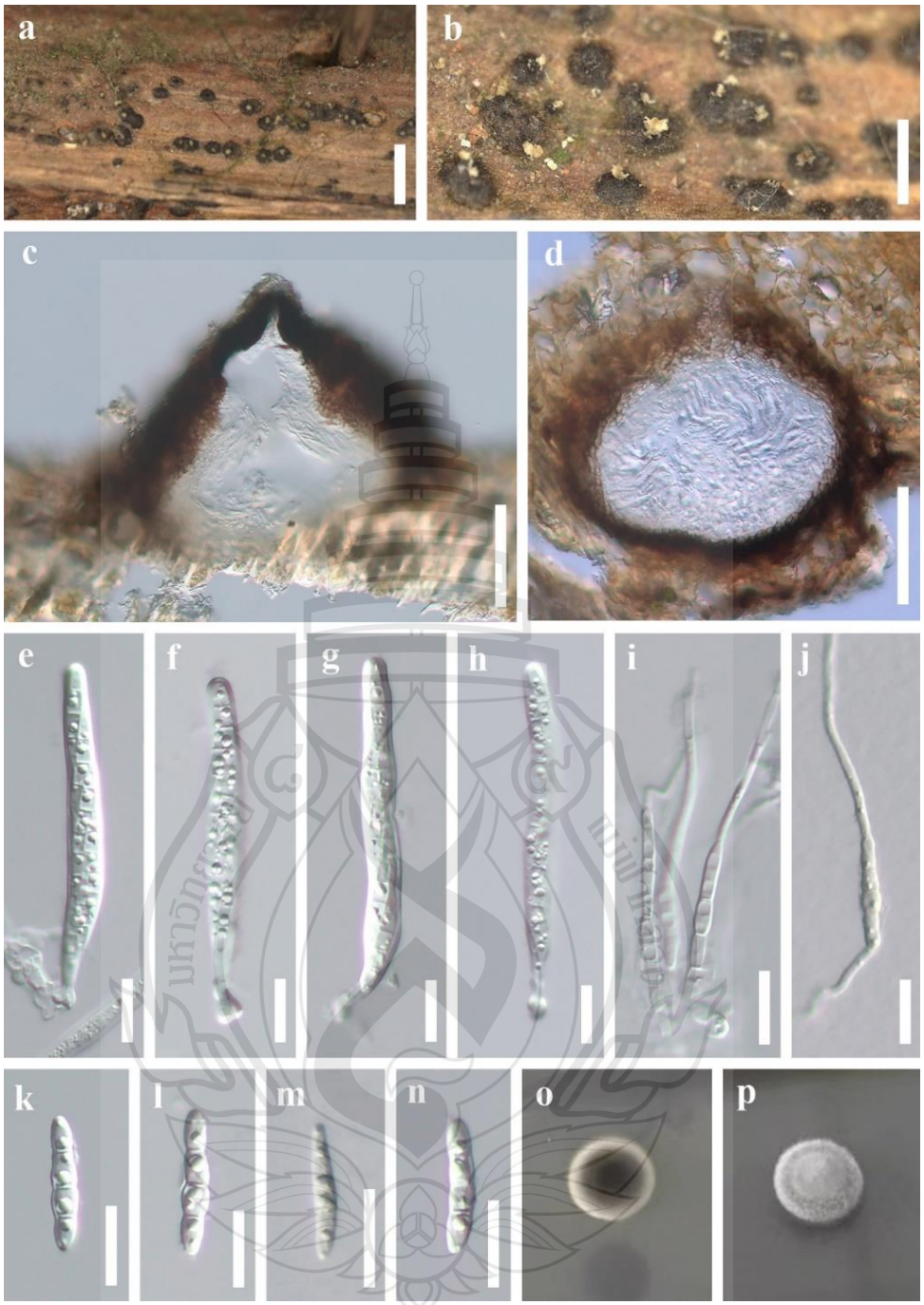
Saprobic on dead twigs. **Sexual morph**: *Ascomata* 115–182 µm high, 133–280 µm wide, solitary or gregarious, semi-immersed, subglobose to ellipsoidal, dark brown to black, uni-loculate, glabrous, coriaceous, ostiolate. *Ostiole* central, carbonaceous, papillate. *Peridium* 12–32 µm wide, composed of several layers of angular, thick-walled pseudoparenchymatous cells arranged in *textura angularis*, outer layer dark brown, inner layer pale brown to brown. *Hamathecium* comprised of 1–3 µm wide, numerous, filamentous, hyaline, simple, distoseptate pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded, 54–62 µm long, 54–62 µm wide. *Ascospores* 11–19 × 1.5–4 µm ($\bar{x}$ = 15× 3 µm, n = 30), overlapping bi-seriate,

subcylindrical, narrower towards both ends, straight or slightly curved, hyaline, one-celled when young and become 3-euseptate at maturation, slightly constricted at septa, guttulate, smooth-walled. **Asexual morph**: Not observed.

Culture characters: Ascospores germinating on PDA within 24 h and germ tubes produced from both ends. Colonies on PDA circular, with raised center and entire edge, white to greyish white from above, dark brown to black in the center, olivaceous brown in the middle ring, pale brown in the outer ring from below.

Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on dead twigs, 14 April 2023, Y.R. Sun, 2356 (HGUP 24-0017, **holotype**); ex-type culture GUCC 24-0064.

Notes: The BLASTn searches of the LSU sequence of *Lophiotrema guizhouense* resulted in 98.05% and 97.94% matches with*L. neoarundinaria* (KUMCC 21-0514) and *L. vagabundum* (KT330). The ITS gene BLASTn results showed 89.25% and 89.01% matches with *L. mucilaginosis* (HKAS 122873) and *L. neoarundinaria* (KUMCC 21-0514). The multi-gene phylogeny (Figure 4.48) showed that *L. guizhouense* forms a distinct clade within *Lophiotrema.* In morphology, our isolate can be distinguished from *L. mucilaginosis* and *L. vagabundum* by its 3-septate ascospores without a sheath while the latter possess 1-septate ascospore surrounding by a sheath (Tanaka & Harada, 2003; Phookamsak et al., 2019). *Lophiotrema guizhouense* resembles *L. neoarundinaria* but the former has smaller ascospore (11–19 × 1.5–4 µm vs. 17–25 × 3–5 µm) (Tanaka & Harada, 2003). Hence, we hereby propose the introduction of *Lophiotrema guizhouense* sp. nov.



Note a, b Ascomata on the host. b, c Vertical section of ascoma. c–h Asci. i Pseudoparaphyses. j Germinating ascospores. k–n Ascospores. o, p Culture characteristics on PDA (o = from below, p = from above). Scale bars: a = 1000 µm, b = 500 µm, c, d =50 µm, e–n =10 µm.

Figure 4.46 *Lophiotrema guizhouense* (HGUP 24-0017, holotype)

Lophiotrema asexuale Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902584; Facesoffungi Number: FoF 16428; Figure 4.47

Etymology: The species epithet 'asexualis' refers to the asexual morph.

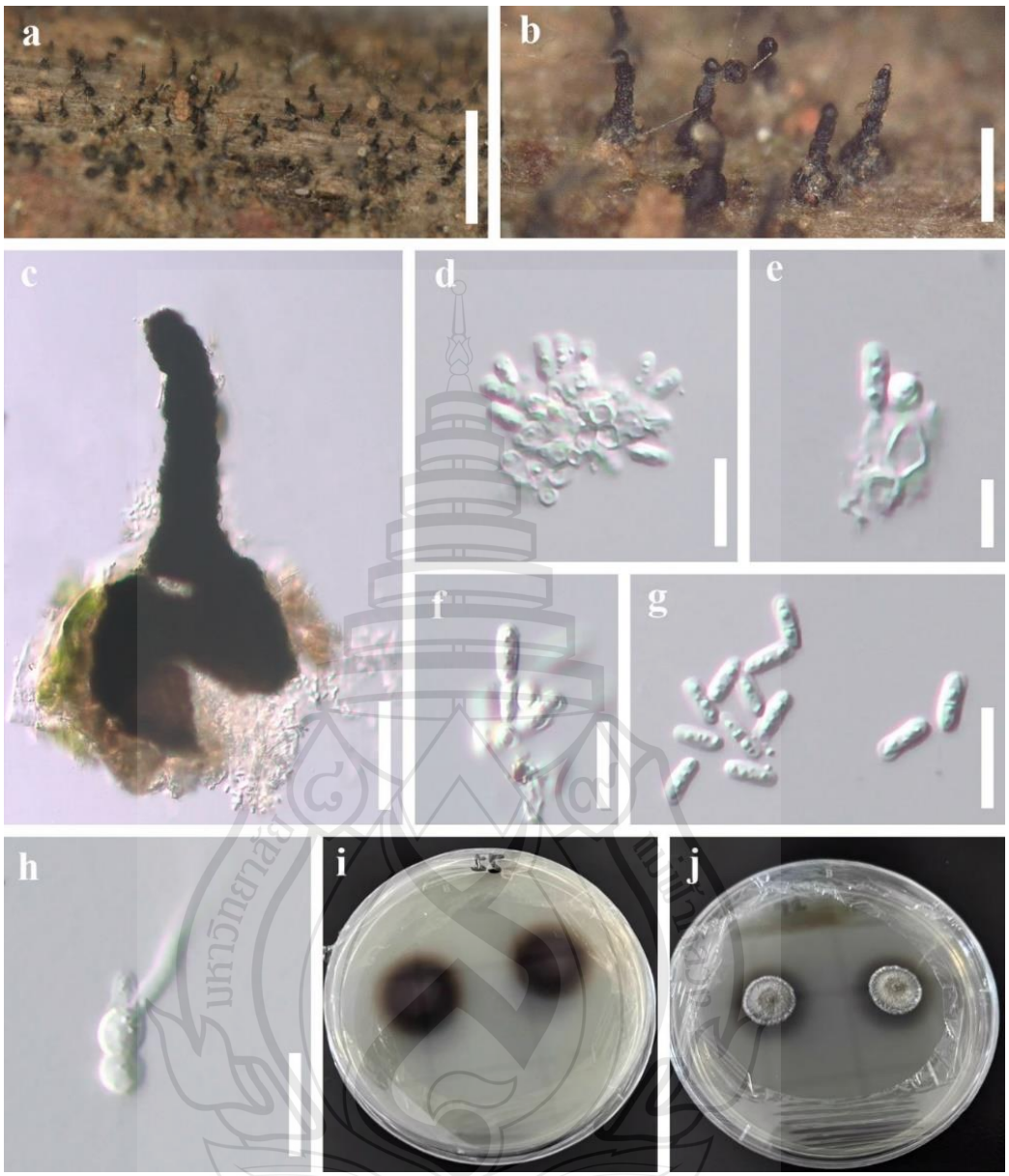
Holotype: HKAS 136888.

Saprobic on dead twigs. **Asexual morph**: *Conidiomata* pycnidial, semi-immersed, gregarious, globose to subglobose with a long neck, dark brown to black, unilocular, ostiolate. *Ostiole* single, long cylindrical, straight or curved. *Conidiomatal wall* thin. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–2.5 µm wide, enteroblastic, phialidic, cylindrical to lageniform, hyaline, smooth. *Conidia* 5–8 × 1.5–3 µm ($\bar{x}$ = 6 × 2.5 µm, n = 40), solitary, oblong with rounded ends, hyaline, aseptate or 1-septate, guttulate, smooth-walled. **Sexual morph**: Not observed.

Culture characters: Conidia germinating on PDA within 24 h and germ tubes produced from one or both ends. Colonies on PDA circular, with raised center and entire edge, greyish white, with an obvious white middle ring and sparse dark brown mycelia in the outer ring from above, dark brown in the center, brown in the outer ring from below.

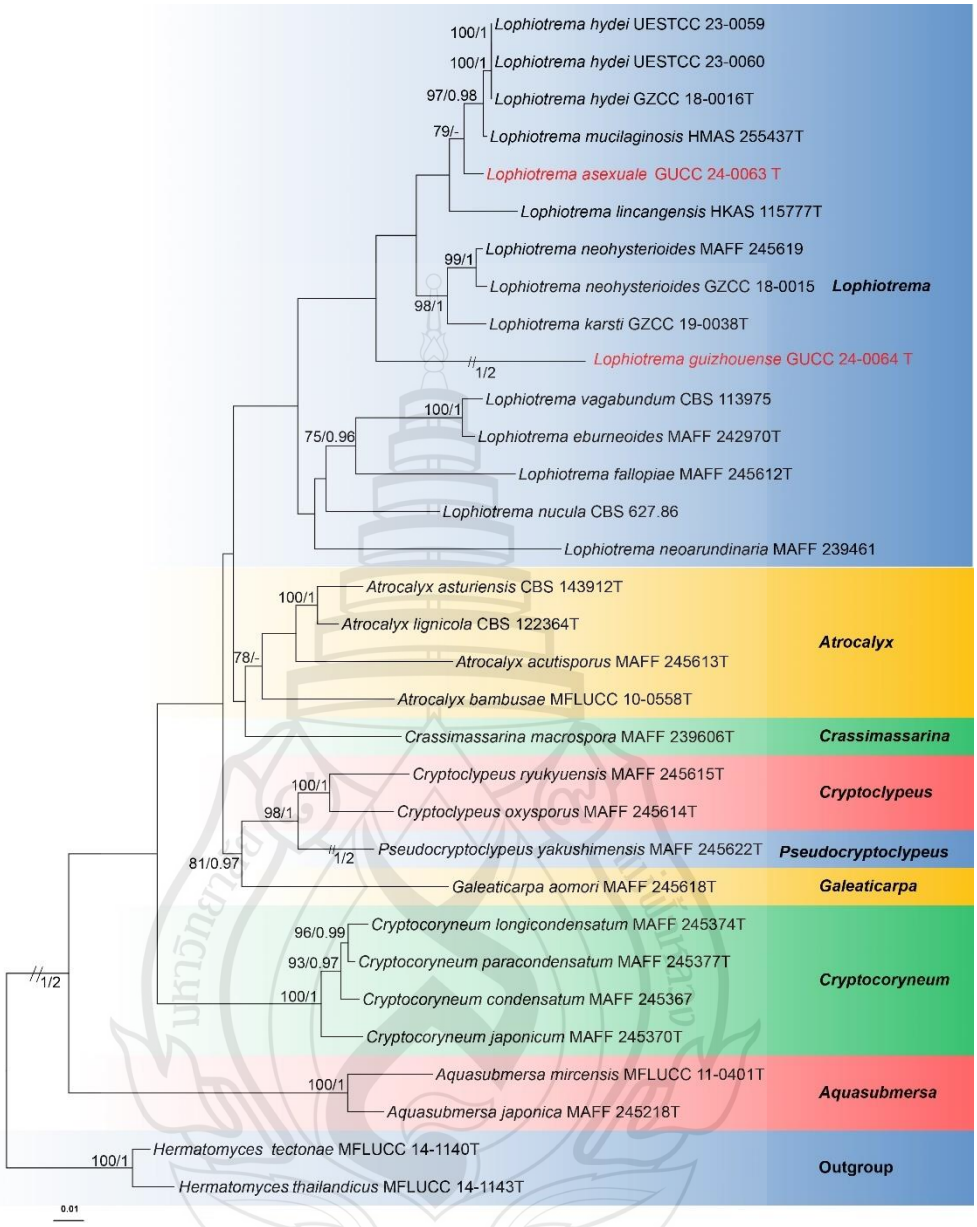
Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on dead twigs, 14 April 2023, Y.R. Sun, 2355 (HKAS 136888, **holotype**); ex-type culture GUCC 24-0063.

Notes: In the phylogenetic analysis of combined gene regions of LSU, ITS, SSU, RPB2 and *TEF1-α*, our new strain grouped with *Lophiotrema hydei*, *L. lincangensis* and *L. mucilaginosis* (Figure 4.48). However, the other four species are sexually-typified thus, morphologically, cannot be compared with new collection as our new collection is represented only by its asexual morph. By comparing the ITS genes, we found that our strain has 2.1% (11/510, without gap), 1.9% (10/518, without gap), and 2.2% (14/642, without gap) base pair differences with *L. hydei*, *L. lincangensis* and *L. mucilaginosis* respectively. Hence, we introduced *Lophiotrema asexuale* as the novel species belonging to *Lophiotrema* s. str., following the guidelines for species delineation proposed by Jeewon and Hyde (2016).



Note a, b Conidiomata appear on host substrate. c Conidioma on the slide. d–f Conidiogenous cells attached to conidia. g Conidia. h Germinating conidium. i Reverse view of colony on PDA. j Surface view of colony on PDA. Scale bars: a = 1000 μm, b = 200 μm, c = 50 μm, d, f–h = 10 μm, e = 5 μm.

Figure 4.47 *Lophiotrema asexuale* (HKAS 136888, holotype)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Hermatomyces tectonae* (MFLUCC 14-1140) and *H. thailandicus* (MFLUCC 14-1143). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.48 Phylogenetic tree of *Lophiotrema*

Lophiostomataceae Sacc., Syll. fung. (Abellini) 2: 672 (1883).

Oleaginea W.L. Li & Jian K. Liu, Mycosphere 14(1): 1484 (2023)

Notes: *Oleaginea* was introduced based on *Oleaginea sichuanensis*, which isolated from branches of *Olea europaea* in China (Li et al., 2023). The genus was placed in Lophiostomataceae and Li et al. (2023) mentioned that *Oleaginea* can be distinguished from other Lophiostomataceae genera by its broadly fusiform or ellipsoid, hyaline, 1-septate, ascospores, lacking a mucilaginous sheath and terminal appendages. However, in this study, we discovered an *Oleaginea* species from *Mahonia fortune* that has brown ascospores. Consequently, we do not consider spore color to be a reliable characteristic for distinguishing genera.

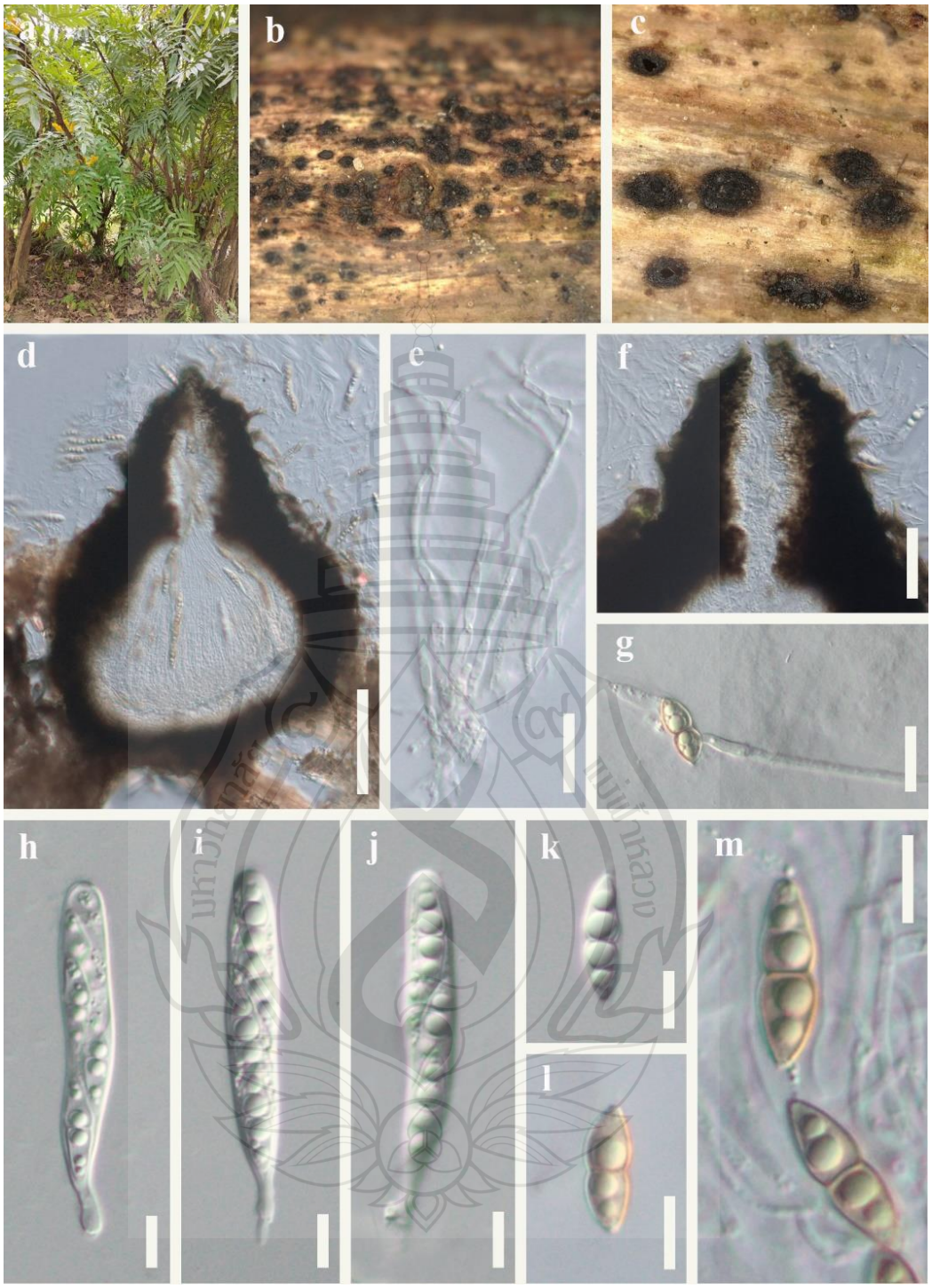
Oleaginea sichuanensis W.L. Li & Jian K. Liu, Mycosphere 14(1): 1485 (2023)

Index Fungorum number: 849151; Facesoffungi number: FoF 14412; Figure 4.49

Associated with diseased twigs of *Mahonia fortune*. **Sexual morph**: *Ascomata* 240–300 μm wide, 287–390 μm high, solitary or scattered, semi-immersed, globose to subglobose, uniloculate, coriaceous, dark brown to black, thick-walled, papillate, ostiolate. *Ostiole* central, dark brown, filled with short periphyses. *Peridium* 25– 33 μm wide, comprising two layers of pale brown to brown cells of textura prismatica. *Hamathecium* 1–2.5 μm wide, numerous, filiform, unbranched, septate, hyaline, pseudoparaphyses. *Asci* 100–125 × 12–18 μm ($\bar{x}$ = 115 × 16 μm, n = 15), 8-spored, bitunicate, fissitunicate, clavate, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 2-seriate, broadly fusiform, hyaline with an inconspicuous terminal appendage when young, brown without a terminal appendage at mature, 1-septate, constricted at the septum, containing four refractive globules, smooth, 19–26 × 6–7.5 μm ($\bar{x}$ = 24 × 6.5 μm, n = 20). **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Baiyun District, heishitou Village, on twigs of *Mahonia fortune*, 22 October 2022, Y.R. Sun, JF3 (HGUP 24-0018); living culture GUCC 24-0075.

Notes: *Oleaginea sichuanensis* was firstly isolated from the dead branches of *Olea europaea* in Sichuan Province, China (Li et al., 2023). Our isolate is associated with the medicinal plant, *Mahonia fortune.* In phylogenetic analyses (Figure 4.26), our strain grouped with *O. sichuanensis* and they formed a distinct clade in Lophiostomataceae. In morphology, our collection shares the similar characters and size with *O. sichuanensis.* However, our collection processes the brown spores when mature while Li et al. (2023) not mentioned. We speculate that Li et al. (2023) may not have observed mature ascospores. We identified HGUP 24-0018 as *Oleaginea sichuanensis*, representing a host record from *Mahonia fortune*.



Note a Host. b, c Appearance of ascomata on host surface. d Vertical section through ascoma. e Hamathecium. f Peridium. g Germinating ascospore. h–j Asci. k–m Ascospores. Scale bars: d = 100 µm, e, g = 20 µm, f = 50 µm, h–m = 10 µm.

Figure 4.49 *Oleaginea sichuanensis* (HGUP 24-0018, new host record)

Massariaceae Nitschke, Verh. Naturh. Ver. preusss. Rheinl. 26: 73 (1869).

Massarioramusculicola Huanral, Thambug. & K.D. Hyde, Phytotaxa 371(1): 20 (2018)

Notes: The monospecific genus *Massarioramusculicol* was recently established based on *Massarioramusculicola chiangraiensis,* a species from dead twig in Thailand (Huanraluek et al., 2018). The genus, which is phylogenetically close to *Massaria* and *Neomassaria*, but can be distinguished by its two strata peridium, hyaline ascospores with 3-septate (Huanraluek et al., 2018). In this study, we reported a new *Massarioramusculicola* collection from *Gardenia jasminoides.*

Massarioramusculicola chiangraiensis Huanraluek., Thambugala & K.D. Hyde Phytotaxa 371(1): 20 (2018)

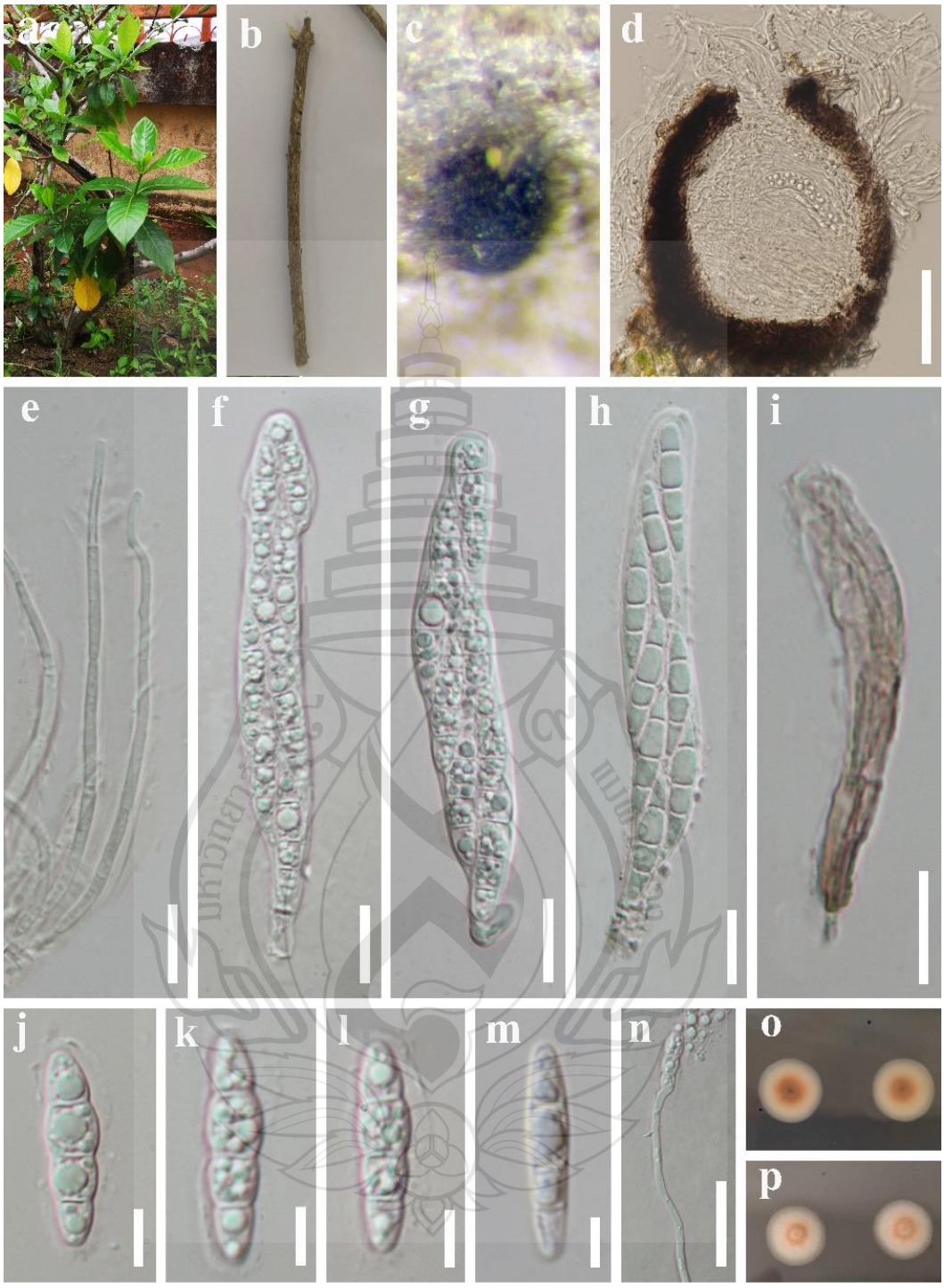
Index Fungorum number: IF554426; Facesoffungi number: FoF 04479; Figure 4.50

Saprobic on fresh twigs of *Gardenia jasminoides*. **Sexual morph**: *Ascomata* 150–250 μm high × 130–250 μm diam., semi-immersed, solitary or scattered, coriaceous, subglobose, black, uniloculate, ostiolate. *Peridium* 20–30 μm wide, comprising of 3–5 cell layers, outermost layer composed dark brown cells of *textura globulosa*, inner layer composed pale brown to hyaline cells of *textura angularis*. *Hamathecium* comprising 1–2 μm wide, massed, filiform, branched and septate pseudoparaphyses. *Asci* 67–85 × 8–11 μm ($\bar{x}$ = 72 × 9 μm, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, with a distinct ocular chamber. *Ascospores* 16–24 × 4–7 μm ($\bar{x}$ = 21 × 5 μm, n = 20), overlapping 1–2-seriate, hyaline, fusiform, 3-septate, slightly constricted at the septa, guttulate, surrounded by a mucilaginous sheath, smooth-walled. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated on PDA within 12 h at 25 ◦C. Germ tubes produced from one end of ascospore. Colonies on PDA reached 1.5 cm diam. after 3 weeks at 25 ◦C; circular, flat to slightly raised, flossy, dry, with the entire edge; the center is orange, surrounded by a cream outer ring.

Specimen examined: THAILAND, Chiang Rai Province, Thasud District, Fahthai 4, on fresh twig of *Gardenia jasminoides*, 28 March 2019, Y.R. Sun, S22 (HGUP 24-0035); living culture GUCC 24-0129.

Notes: *Massarioramusculicola chiangraiensis* was isolated from dead twigs in Chiang Rai, Thailand (Huanraluek et al., 2018). Isolate S22 was recovered from fresh twigs of *Gardenia jasminoides* in Chiang Rai, Thailand. The new isolate clusters with the ex-type strains *M. chiangraiensis* (MFLUCC 17-2240) by strong bootstrap support (ML-bs = 100%, BYPP = 1) (Figure 4.26). The morphology of our strain shares similar shapes of ascomata, asci, and ascospores with MFLUCC 17-2240, as well as sharing similar sizes of asci (67–85 × 8–11 μm *vs*. 70–86 × 8–11 μm) and ascospores (16–24 × 4–7 μm *vs*. 20–24(–26) × (3.5–)4–5.8 μm) (Huanraluek et al., 2018). Therefore, we introduced our strain as *M. chiangraiensis,* representing a new host record from *Gardenia jasminoides*.



Note a, b Host. c Appearance of ascomata on host tissue. d Vertical sections through ascomata. e Hamathecium. f–i Asci. j–m Ascospores. n Germinating ascospore. Scale bars: d = 50 µm, e–i = 10 µm, j–m = 5 µm, n = 20 µm.

Figure 4.50 *Massarioramusculicola chiangraiensis* (HGUP 24-0035, new host record)

Massarinaceae Munk, Friesia 5: 305 (1956).

Helminthosporium Link, Mag. Gesell. naturf. Freunde, Berlin 3 (1-2): 10 (1809).

The species-rich genus, *Helminthosporium* was established by Link (1809a) with *H. velutinum* as the type species. *Helminthosporium* have been reported as saprobes and plant pathogens on various hosts with a worldwide distribution (Zhu et al., 2016; Voglmayr & Jaklitsch, 2017; Boonmee et al., 2021; Konta et al., 2021; Liu et al., 2022; Hu, Liu, Xu et al., 2023). Recent molecular data revealed that *Helminthosporium* is polyphyletic, as certain members are intertwined with other genera such as *Byssothecium*, *Helminthosporiella*, *Pseudosplanchnonema*, *and Synhelminthosporium* (Konta et al., 2021; Chen et al., 2022). There are more than 700 species listed in this genus but most lack sequence (Species Fungorum, 2024). In this study, we introduce one new species and one new record of *Helminthosporium.*

Helminthosporium thailandicum Y.R. Sun & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16429; Figure 4.51

Etymology: Named after the fungus collected country.

Holotype*:* HGUP 24-0036.

Saprobic on dead leaves of *Elaeis* sp. in terrestrial habitat. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown, velvety. *Mycelium* mostly immersed, composed of hyaline to pale brown hyphae. *Conidiophores* 85–153 µm long, 6–7 µm wide, macronematous, mononematous, erect, straight or broadly curved, cylindrical, brown, slightly paler at the apex, unbranched, septate, thick-walled. *Conidiogenous cells* monotretic, integrated, terminal, cylindrical, pale to brown, with non-cicatrized, indistinct pores. *Conidia* 53–123 × 5.5–8.5 µm ($\bar{x}$ = 92 ×7 µm, n = 30), catenate, formed in short, acropetal chains, straight or curved, cylindrical, rounded at ends, greyish brown, with thickened and darkened base, mostly 7-distosepate, verrucose.

Culture characteristics: Conidia germinated on PDA media within 24 h. Germ tubes produced from conidial base. Colonies on PDA media circular, dense, flat, with entire edge, pale brown at center, brown at middle ring, dark brown at outer ring from above; brown at center and outer ring, dark brown at middle ring from reverse.

Material examined: THAILAND, Chiang Rai Province, Chiang Rai City, Mae Chan District, Pa Tueng, on leaves of *Elaeis* sp., 16 January 2021, Y.R. Sun, CR12 (HGUP 24-0036, **holotype**); ex-type culture GUCC 24-0130.

Notes: *Helminthosporium thailandicum* formed a sister to *H. chlorophorae* in the phylogenetic tree (Figure 4.53). In morphology, *H. thailandicum* can be distinguished by its shorter conidiophores (85–153 *vs.* 120–270 μm) (Ellis, 1961). The base pair differences in ITS gene (14/494 bp, 2.8%) also support its introduction as a new species (Jeewon & Hyde, 2016).



Note a, b Colonies on natural substrate. c Conidiophores and conidia. d Conidiogenous cells and conidia. e–h Conidia. i Germinated conidium. j, m Colonies on the PDA. Scare bars: a = 200 µm. b = 100 µm, c, d, f, i = 50 µm, g = 20 µm, e, g, h = 20 µm.

Figure 4.51 *Helminthosporium thailandicum* (HGUP 24-0036, holotype)

Helminthosporium sinense Jing W. Liu & Jian Ma [as 'sinensis'], MycoKeys 94: 81 (2022)

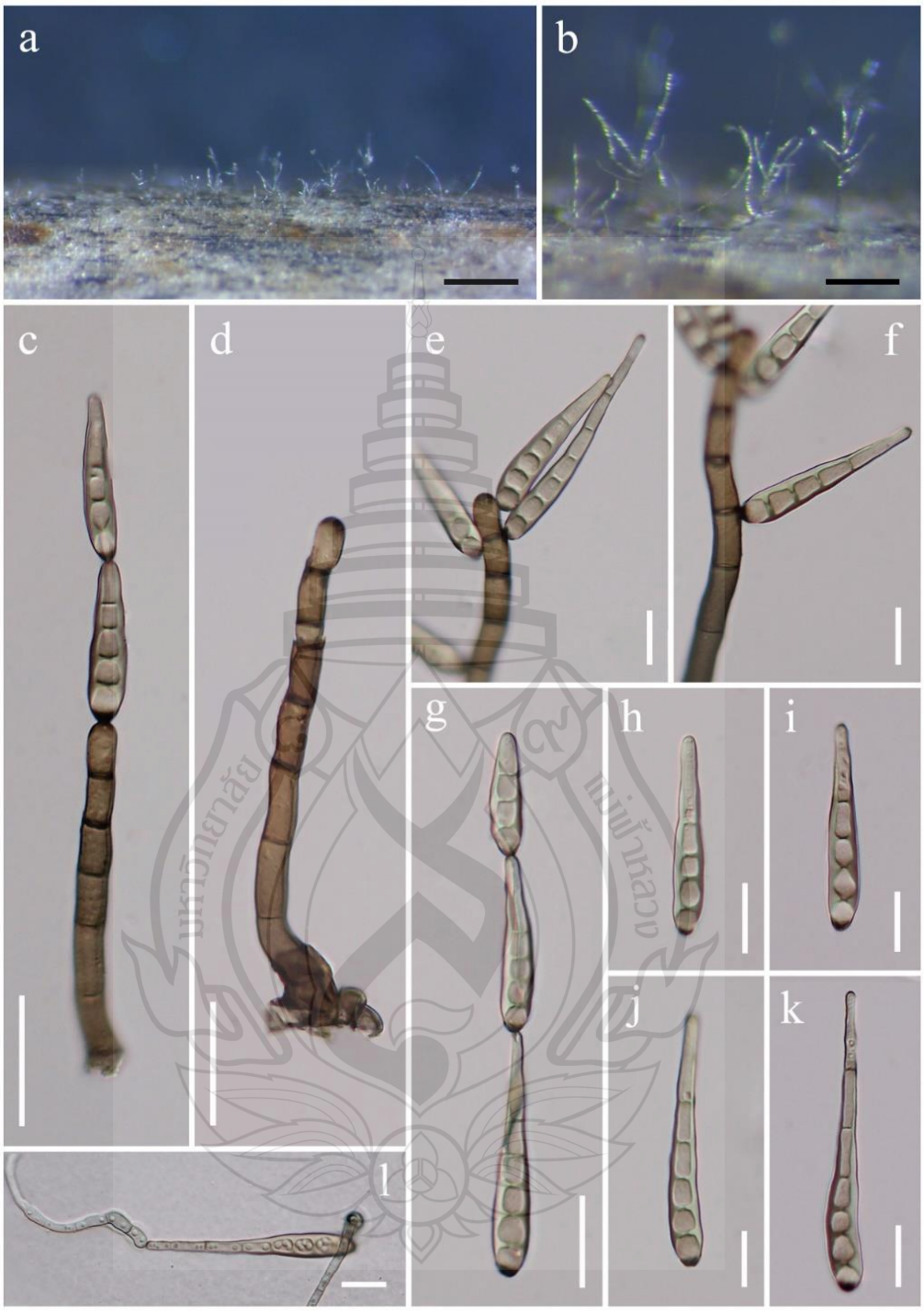
Index Fungorum number: IF 559981; Facesoffungi number: FoF 16430; Figure 4.52

Saprobic on dead twigs in terrestrial habitat. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, greyish brown, hairy, velvety. *Mycelium* mostly immersed, composed of septate, guttulate, brown hyphae. *Conidiophores* mononematous, smooth, unbranched, straight or slightly flexuous, median brown, septate, thick-walled. *Conidiogenous cells* 11–15 × 5–7 μm, polytretic, integrated, terminal and intercalary in the upper part of the conidiophores, thick-walled, brown, cylindrical., *Conidia* 37–69 × 6.5–9 μm ($\bar{x}$ = 49 ×7.5 μm, n = 20), solitary or catenate, when catenate in acropetal chain, dry, obclavate, cylindrical, 3–6-pseudoseptate, smooth, golden brown. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on water agar within 24 h. Germ tubes produced from both ends of the conidia. Mycelia superficial, dense, irregular, with undulate or lobate edge, pale green in the middle, white at the edge from above, dark green in the middle, paler towards the edge from below.

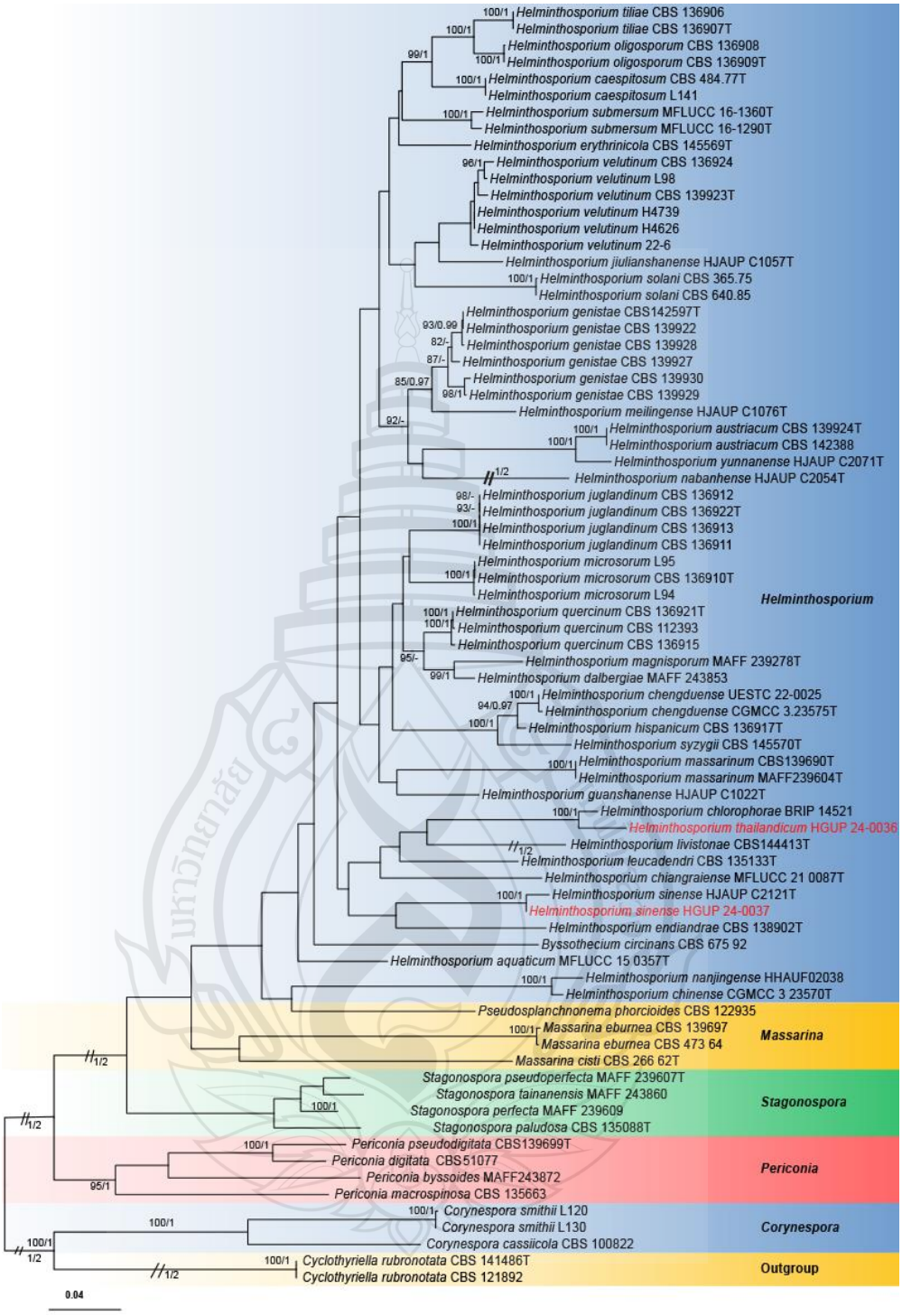
Material examined: THAILAND, Phrae Province, Rong Kwang, on decaying wood, 10 January 2018, N.G. Liu, N005 (HGUP 24-0037); living culture GUCC 24-0131.

Notes: *Helminthosporium sinense*, introduced by Liu et al. (2022), was collected from Yunnan, China. Based on phylogenetic analysis of combined LSU, ITS, RPB2, SSU and *TEF1-α* sequence data, our isolate GUCC 24-0131 clustered with *H. sinense* by 100% ML-BS and 1.00 BYPP bootstrap support (Figure 4.53). Our isolate morphologically resembles *H. sinense,* including the measurement size of the conidiophores, conidiogenous cells and conidia. Moreover, there are only two base pair differences in the ITS and LSU gene regions. Therefore, we identify our collection as *H. sinense*, and this is a new record from Thailand.



Note a, b Colonies on natural substrate. c, d Conidiophores and conidia. e, f Conidiogenous cells and conidia. g–k Conidia. l Germinated conidium. Scare bars: a = 500 µm. b = 150 µm, c, d = 30 µm, g = 20 µm, e–f, h–l = 15 µm.

Figure 4.52 *Helminthosporium sinense* (HGUP 24-0037, new record)



Note The tree is rooted with *Cyclothyriella rubronotata* (CBS 121892) and (CBS 141486). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.53 Phylogenetic tree of *Helminthosporium*

Melanommataceae G. Winter [as 'Melanommeae'], Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.2: 220 (1885).

Camposporium Harkn., Bull. Calif. Acad. Sci. 1(no. 1): 37 (1884).

Notes: *Camposporium* was introduced by Harkness (1884) with *Camposporium antennatum* as the type species. This genus has procumbent, dematiaceous, simple conidiophores, terminal, integrated, denticulate conidiogenous cells, and cylindrical and elongate, multi-septate conidia with or without apical appendages. Li, Jeewon et al. (2017) introduced a Hyphomycetous genus *Fusiconidium*, which has erect, straight, cylindrical conidiophores and ellipsoidal to fusiform conidia. However, the authors did not involve *Camposporium* in their phylogenetic analyses, and several subsequent studies indicated *Camposporium* and *Fusiconidium* were mixed together (Dong et al., 2020; Hyde, Dong et al., 2020). Koukol and Delgado (2021) synonymized *Fusiconidium* under *Camposporium*.

Camposporium valdivianum (Speg.) G. Delgado & Koukol, IMA Fungus 12(no. 26): 5 (2021)

Index Fungorum number: IF838825; Facesoffungi number: FoF 02484; Figure 4.54

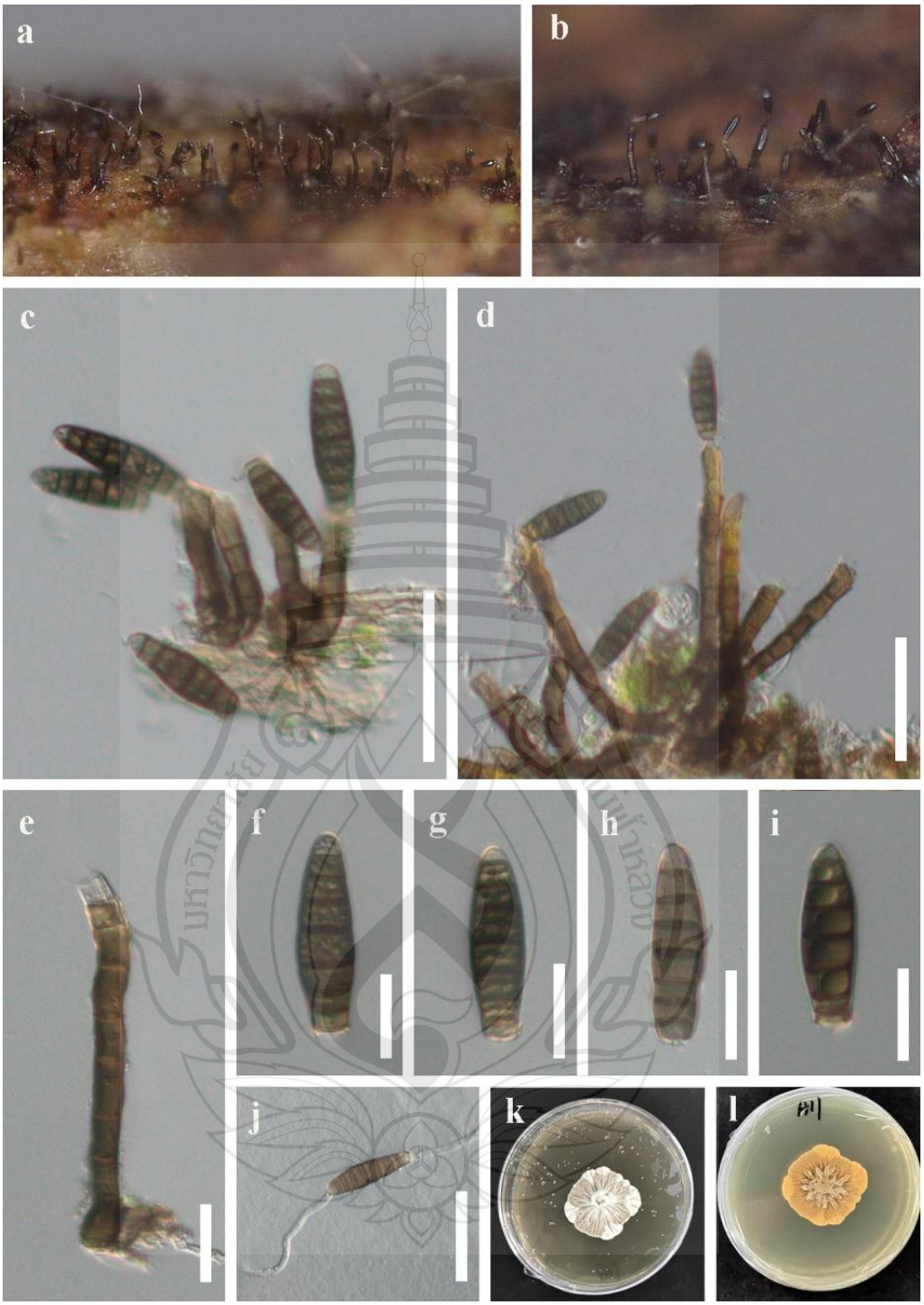
Saprobic on twigs of *Debregeasia orientalis* in terrestrial habitat. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrates effuse, dark brown to black, velvety. *Mycelium* mostly immersed. *Conidiophores* macronematous, mononematous, erect, straight or flexuous, cylindrical, brown, paler towards the apex, unbranched, septate, thick-walled, 40–115 × 5.5–8.5 μm ($\bar{x}$ = 76 × 7 μm, n = 20). *Conidiogenous cells* 5.5–7.5 μm wide, monoblastic, integrated, terminal, pale brown to brown, percurrently proliferating. *Conidia* 24–47 × 9–13 μm ($\bar{x}$ = 40 × 11 μm, n = 30), acrogenous, solitary, ellipsoidal to fusiform with round apex and truncate base, olivaceous brown, paler at the apical cell, 7-septate, verrucose.

Culture characteristics: Conidia germinated on PDA media within 12 h and germ tubes produced from polar cells of the conidia. Colonies on PDA media subcircular, wrinkled, with raised center and entire edge, white to greyish white from above, yellowish

brown from below.

Material examined: CHINA, Guizhou Province, Guiyang City, Huaxi District, Gaopo Township, Shuitang Village, on twigs of *Debregeasia orientalis*, 19 November 2022, Y.R. Sun, H11 (HGUP 24-0019); living culture, GUCC 24-0076.

Notes: Koukol and Delgado (2021) transferred *Fusiconidium mackenziei* to *Camposporium valdivianum* based on morphology. Liu, Hyde et al. (2024) descripted *C. valdivianum* from decaying wood in China. Our collection resembles *C. valdivianum* in having mononematous, erect, cylindrical and unbranched conidiophores, monoblastic, terminal conidiogenous cells and fusiform to ellipsoidal, brown and 7-septate conidia (Spegazzini, 1910; Li, Jeewon et al., 2017; Koukol & Delgado, 2021; Liu, Hyde et al., 2024). The subtle difference between our collection and the previously described *C. valdivianum* is that our collection has narrower conidia (24–47 × 9–13 μm *vs*. 38–40 × 12–15 μm) (Li, Jeewon et al., 2017; Liu, Hyde et al., 2024). Our collection cluster together with *C. valdivianum* in the phylogenetic tree (Figure 4.26). The comparison results between our strain and holotype (MFLU 16-2139) showed no difference in LSU, only 1 bp in SSU (946 bp), and 7 bp in ITS gene regions (839 bp). Therefore, based on morphology and molecular evidence, we identify our collection as *C. valdivianum,* representing a new host record of *Debregeasia orientalis*.



Note a, b Colonies on the host. c, d Conidiophores with conidia. e Conidiogenous cell. f–i conidia. j Germinating conidium. k, l Colony on PDA. Scale bars: c, d, j = 50 µm, e–i = 20 µm.

Figure 4.54 *Camposporium valdivianum* (HGUP 24-0019, new host record)

Morosphaeriaceae Suetrong, Sakayaroj, E.B.G. Jones & C.L. Schoch, Stud. Mycol. 64:161 (2009).

Neohelicascus W. Dong, H. Zhang, K.D. Hyde & Doilom, Fungal Diversity: [146] (2020)

Notes: Dong et al. (2020) refined Morosphaeriaceae and introduced the new genus, *Neohelicascus,* with *Neohelicascus aquaticus* designated as the type species. They also transferred seven species from *Helicascus* to *Neohelicascus.* Currently, ten species are accepted in this genus based on morphology and molecular data (Species Fungorum, 2024), this study). All of them are isolated from freshwater habitats and in this study, we reported the first *Neohelicascus* species from terrestrial habitats (Zhang et al., 2014; Luo et al., 2016; Dong et al., 2020; Yang, Liu et al., 2023).

Neohelicascus guizhouensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902593; Facesoffungi number: FoF 16430; Figure 4.55

Etymology: refers to the location where the fungus was encountered.

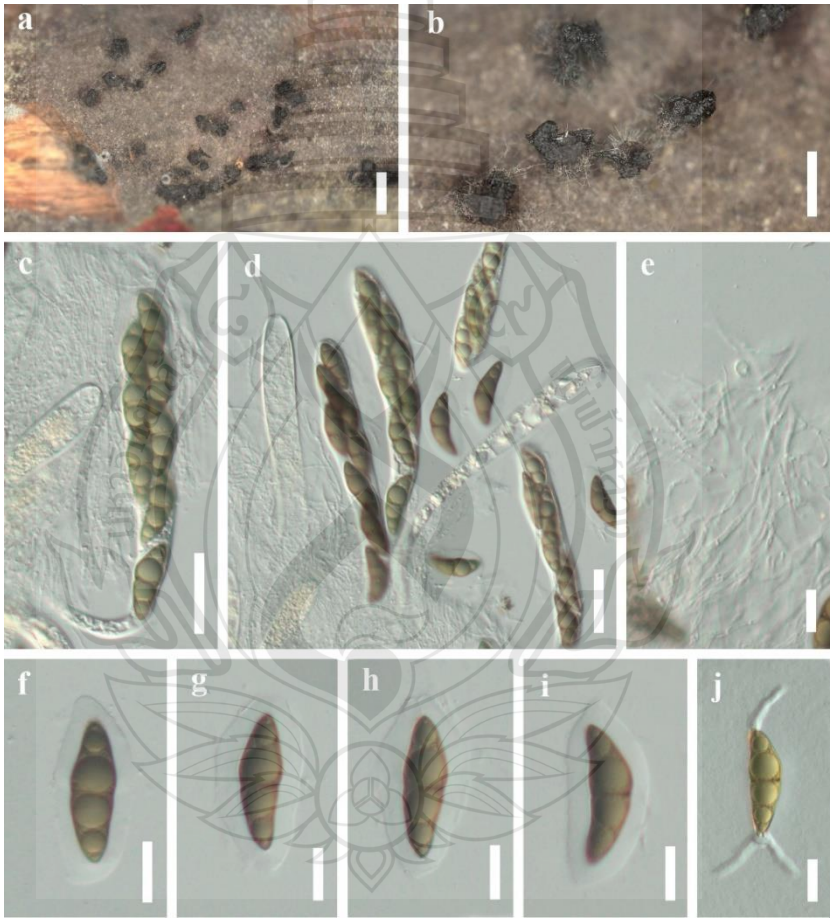
Holotype: HGUP 24-0020.

Saprobic on dead wood. S**exual morph**: *Ascomata* semi-immersed, solitary, scattered, subglobose to globose, black. *Ostioles* central, periphysate. *Hamathecium* 1–2 µm wide, comprising septate pseudoparaphyses. *Asci* 220–290 µm long, 29–32 µm wide, 8-spored, bitunicate, fissitunicate, clavate, rounded at the apex, with an ocular chamber, pedicellate, with a long tail-like extension. *Ascospores* 39–54 × 11–17 µm ($\bar{x}$ = 48 × 15 µm, n = 40), 2-seriate, fusiform, 1-septate, guttulate, brown, smooth and thick-walled, surrounding by a sheath. **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Qiannan Bouyei and Miao Autonomous Prefecture, Libo District, on unidentified wood, 12 March 2022, Y.R. Sun, ML14, (HGUP 24-0020, **holotype**), ex-type GUCC 24-0077.

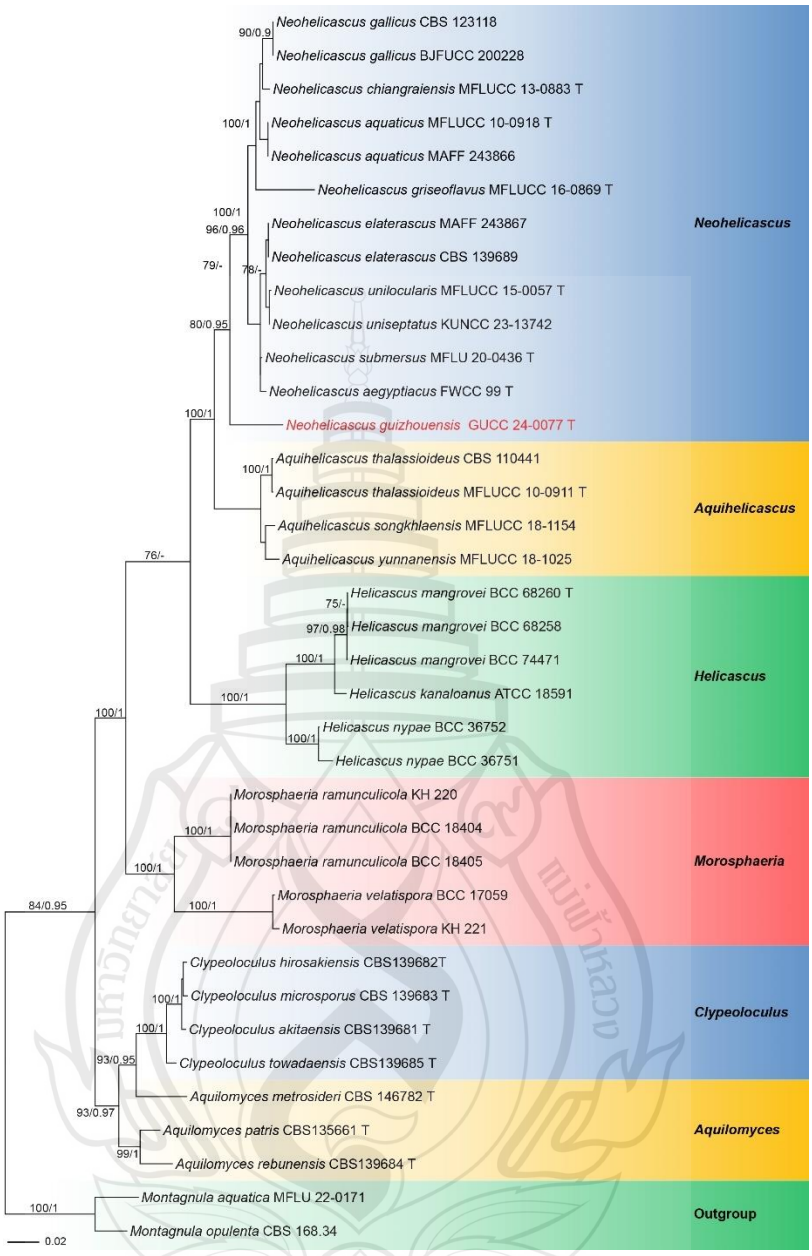
Notes: In phylogenetic analyses, our isolate formed a distinct clade and placed within *Neohelicascus* (Figure 4.56). The BLASTn searches of the LSU sequence of *N. guizhouensis*

resulted in 98.83% matches with *N. gallicus* (GZCC 20-0367) and *N. chiangraiensis* (MFLU 19-2103). The ITS, SSU and *TEF1-α* gene BLASTn results also showed high similarity with these species. In morphology, *N. guizhouensis* is differ from *N. chiangraiensis* and *N. gallicus* by its larger asci (220–290 × 29–32 µm in *N. guizhouensis vs.* 77–146 × 16–19 µm in *N. chiangraiensis vs.* 112–128 × 18–22 µm in *N. gallicus*) and larger ascospores (39–54 × 11–17 µm *vs*. 24.5–27.5 × 8.5–10.5 µm *vs*. 25.1–31.3 × 9.3–12.1) (Zhang et al., 2014; Luo et al., 2016). We thus introduced *N. guizhouensis* sp. nov herein.



Note a, b Appearance of ascomata on the substrate. c, d Asci. e Pseudoparaphyses. f–i Ascospores. j Germinated ascospore. Scale bars: a = 1000 µm, b = 500 µm, c, d = 50 µm, e–i = 20 µm.

Figure 4.55 *Neohelicascus guizhouensis* (HGUP 24-0020, holotype)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Montagnula aquatica* (MFLU 22-0171) and *M. opulenta* (CBS 168.34). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.56 Phylogenetic tree of *Neohelicascus*

Neohendersoniaceae A. Giraldo & Crous, Mycol. Progr. 16: 343 (2017).

Neohendersonia Petr., Annls mycol. 19(3–4): 190 (1921)

Notes*:* Petrak (1921) introduced *Neohendersonia* with *N. pyriformis* designated as the type species. Giraldo et al. (2017) suggested *N. pyriformis* to be synonymous with *N. kickxii*, a proposition later supported by subsequent literature (Wijayawardene et al., 2016; Hongsanan et al., 2020a). Tanaka et al. (2017) assigned this genus to Noehendersoniaceae, a classification affirmed by Hongsanan et al. (2020). Presently, three species are acknowledged within this genus, and only one with sequence. We contribute the illustration and molecular of the fourth species, *Neohendersonia tongrenensis*, in this study.

Neohendersonia tongrenensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902594; Facesoffungi number: FoF 16431; Figure 4.57

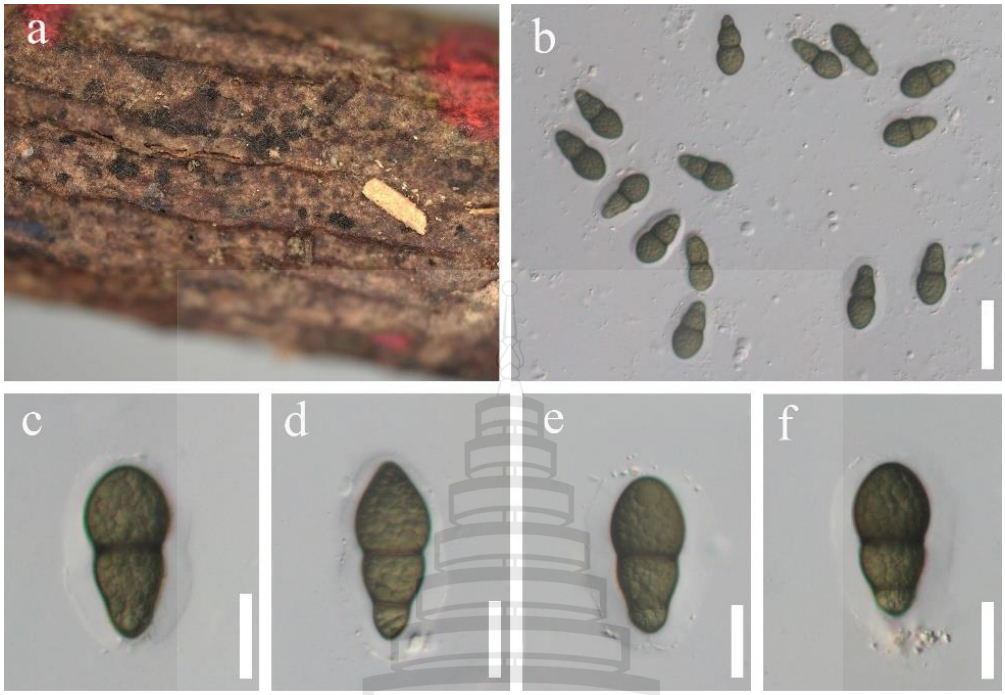
Etymology: Referring to the location in which the fungus was collected.

Holotype: HKAS 136895.

Saprobic on dead wood. **Sexual morph**: Not observed. **Asexual morph**: Coelomycetous. *Conidiomata* solitary, immersed, dark brown to black, erumpent at maturity, subglobose, unilocular. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, determinate, hyaline, smooth-walled. *Conidia* 35– 50 µm long, 16–22 µm wide at the widest, obovoid, obtuse apex, base truncate, 1–2-euseptate, slightly constricted at septa, brown, verrucous, with a gelatinous sheath.

Material examined: CHINA, Guizhou Province, Tongren City, Jiangkou District, Taiping town, on dead wood, 20 May 2022, Y.R. Sun, JK18 (HKAS 136895, **holotype**).

Notes: Wijayawardene et al. (2016) provided a key to species of *Neohendersonia*. Our strain formed a distinct clade and sister to *N. kickxii* in the phylogenetic tree (Figure 4.26). In morphology, it can be distinguished from other *Neohendersonia* species by its obovoid, 1–2-euseptate conidia surrounding by a sheath (Wijayawardene et al., 2016). Therefore, we introduced *N. tongrenensis* as a novel species.



Note a Colonies on natural substrate. b–f Conidia. Scale bars: b = 50 μm, c–f = 20 μm.

Figure 4.57 *Neohendersonia tongrenensis* (HKAS 136895, holotype)

Neomassariaceae H.A. Ariyaw., Jaklitsch & Voglmayr, Cryptog. Mycol. 39(3): 367 (2018)

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

Notes: *Neomassaria* was introduced by Hyde et al. (2016) with *N. fabacearum* as the type species. So far, six species are accepted in this genus. Among them, *N. khayae* is associated with medicinal plant (Yang, Liao et al., 2023). Sexual morph of *Neomassaria* has coriaceous, globose to subglobose, brown to dark brown ascomata, oblong to cylindrical, short pedicellate, 8-spored asci and hyaline, ellipsoid to broadly fusiform, 1-septate ascospores (Hyde et al., 2016; de Silva et al., 2022; Yang et al., 2022). In this study, we introduced a hyphomycetous *Neomassaria* species.

Neomassaria fibraureae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16432; Figure 4.58

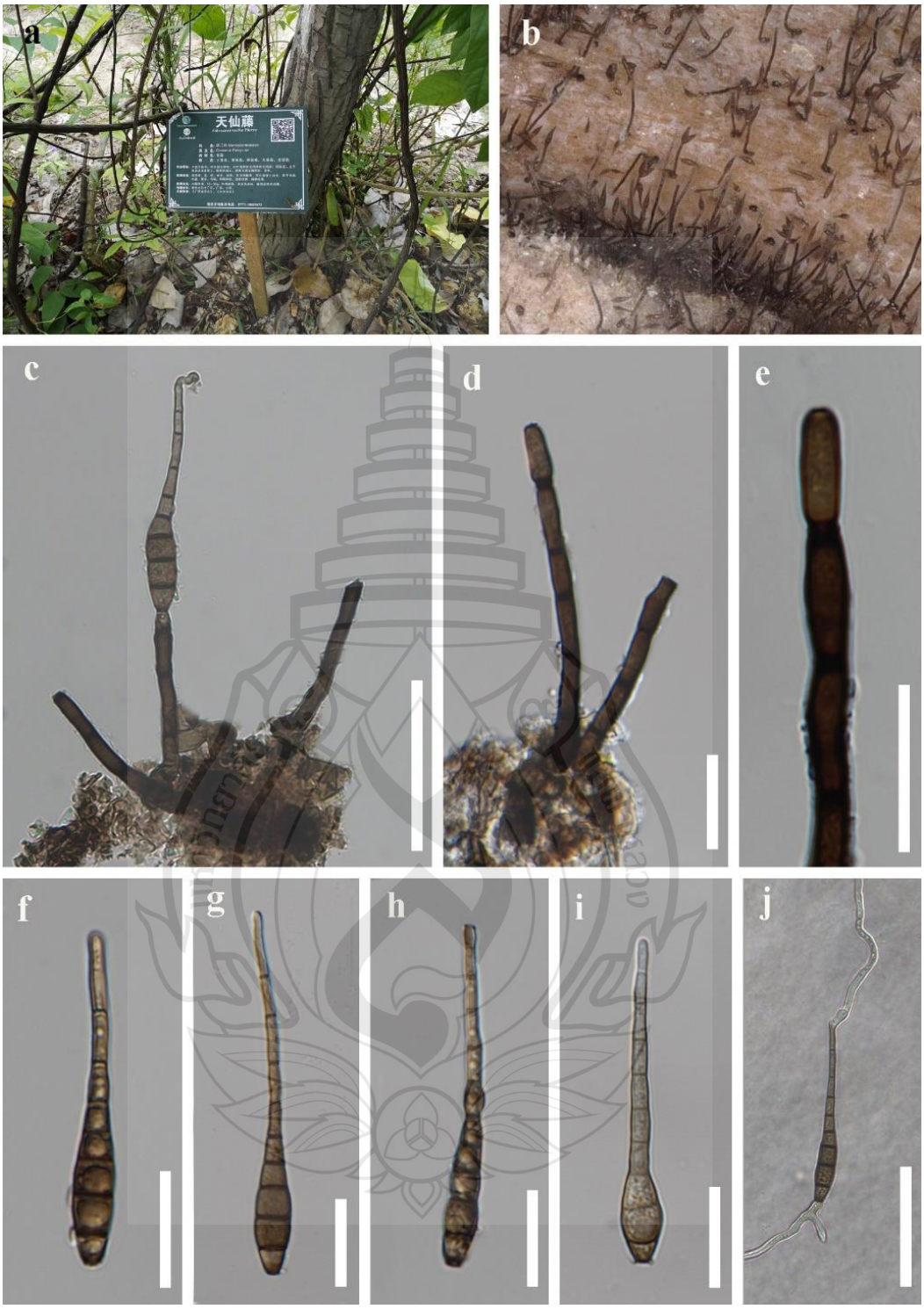
Holotype: HGUP 24-0038.

Etymology: Referring to the host genus.

Saprobic on twigs of *Fibraurea recisa* in terrestrial habitats. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown, velvety. *Mycelium* immersed, composed of septate, branched, hyaline to subhyaline hyphae. *Conidiophores* macronematous, mononematous, erect, straight or slightly curved, cylindrical, unbranched, 3–6-septate, brown or dark brown, thick-walled, 64–92 μm long, 4–7 μm wide. *Conidiogenous cells* monoblastic, integrated, terminal, determinate, cylindrical, dark brown. *Conidia* 41–96 μm long, 5.5–12 μm at the widest, acrogenous, solitary, straight, obclavate, brown, 7–10-euseptate, slightly constricted at septa, rounded at the apex, truncate at the base, tapering towards apex.

Material examined: CHINA, Guangxi Province, Nanning City, Xingning District, 22°19’ N, 108°19’ E, on twigs of *Fibraurea recisa* Pierre, 14 September 2019, Y.R. Sun, G16 (HGUP 24-0038, **holotype**); ex-type culture MFLUCC 24-0313.

Notes: Our strain, isolated from the medicinal plant *Fibraurea recisa* in China, is phylogenetically related to *Neomassaria thailandica* and clusters with *Neomassaria* species (Figure 4.26). BLASTn searches of LSU and ITS are similar to *N. thailandica* (SNC126a), with 98.9% similarity (PP621061) and 91.2% similarity (PP592437), respectively. Therefore, we introduced *Neomassaria fibraureae* as a novel species, marking the first hyphomycetous species in *Neomassaria*.



Note a Host. b Colonies on natural substrate. c, d Conidiophores with or without conidia. e Conidiogenous cell. f–i Conidia. j Germinated conidium. Scale bars: c–j = 20 μm.

Figure 4.58 *Neomassaria fibraureae* (HGUP 24-0038, holotype)

Nigrogranaceae Jaklitsch & Voglmayr, Stud. Mycol. 85: 54 (2016).

Nigrograna Gruyter, Verkley & Crous, Stud. Mycol. 75: 31 (2012).

Notes*: Nigrograna* was introduced by De Gruyter et al. (2013) with *Nigrograna mackinnonii* as its type species. They have worldwide distributions and various host and, can be found in both terrestrial and aquatic environments (De Gruyter et al., 2013; Jaklitsch & Voglmayr, 2016; Kolařík, 2018; Dayarathne et al., 2020; Zhang, Liu et al., 2020; Li et al., 2023). Since 2020, 18 additional species have been incorporated into this genus (Dong et al., 2020; Mapook et al., 2020; Lu, Karunarathna et al., 2022; Hu, He et al., 2023; Senanayake et al., 2023). As of now, *Nigrograna* comprises a total of 30 species, with some of them being isolated from medicinal plants, including *N. acericola*, *N. impatientis*, and *N. obliqua* (Jaklitsch & Voglmayr, 2016; Zhang, Liu et al., 2020; Li et al., 2023; Species Fungorum, 2024). We provided three *Nigrograna* taxa from medicinal plants, *Mahonia fortune* and *Rhododendron delavayi* in China herein. There are two *Biatriospora* species placed within *Nigrograna* in the phylogenetic analyses (Figure 4.68). We agree with Hongsanan et al. (2020a) and maintain these two species in *Biatriospora* (Biatriosporaceae) due to the significant differences in morphology.

Nigrograna hydei J.F. Zhang, Jian K. Liu & Z.Y. Liu Mycol Progress 19:1369 (2020)

Index Fungorum number: IF556749; Facesoffungi number: FoF 06294; Figure 4.59

Saprobic on twigs of *Mahonia fortune*. **Sexual morph**: *Ascomata* 160–260 μm wide, ×200–290 μm high, scattered, solitary, uniloculate, immersed, globose or subglobose, with long necks. *Ostiole* around 65 μm wide, central, filled with hyaline periphyses. *Peridium* 15–31 μm, thick wall, fused with host tissues, comprising two layers of pale to brown cells of *textura angularis*. *Hamathecium* 1–2.5 μm wide, comprising numerous, filiform, hyaline pseudoparaphyses. *Asci* 41–59 × 5.5–7 μm ($\bar{x}$ = 41 × 6.5 μm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, pedicellate with an obtuse to furcate base, apically rounded. *Ascospores* 8–11 × 2.5–4 μm ($\bar{x}$ = 10 × 3 μm, n = 20), 1–2 seriate, partially overlapping, fusoid to clavate, yellowish brown or olive brown, mostly 3-septate,

constricted at the middle septum. **Asexual morph**: Not observed.

Material examined: CHINA, Zhejiang Province, Tongxiang City, Zhenxing East Road, Tongxiang Botanical Garden, on a branch of *Mahonia fortune*, 15 Aug 2023, Y.R. Sun, ZJ10 (HKAS 136909); living culture GUCC 24-0079.

Notes: *Nigrograna hydei* was initially described by Zhang, Liu et al. (2020) from unidentified hosts in Thailand. Li et al. (2023) reported it from *Paeonia suffruticola* in China. Our collection showed similar morphology to *N. hydei*. In the phylogenetic analyses (Figure 4.68), our new collection clustered together with the ex-type strain of *N. hydei* (GZCC 19-0050) with high support (98% ML/1.00 BYPP). We thus identified our collection as *N. hydei*, representing a new host record from medicinal plant, *Mahonia fortune*.



Note a, b Ascomata on the substrate. c, d Cross sections of ascomata. e Section of the peridium. f–h Asci. i Pseudoaraphyses. j–m Ascospores. Scale bars: c, d = 50 μm, e–i = 10 μm, j–m = 5 μm.

Figure 4.59 *Nigrograna hydei* (HKAS 136909, new host record)

Nigrograna oleae W.L. Li & Jian K. Liu, in Li, Liang, Dissanayake & Liu, Mycosphere 14(1): 1503 (2023)

≡ *Nigrograna trachycarpi* H.M. Hu & Q.R. Li, MycoKeys: 141 (2023)

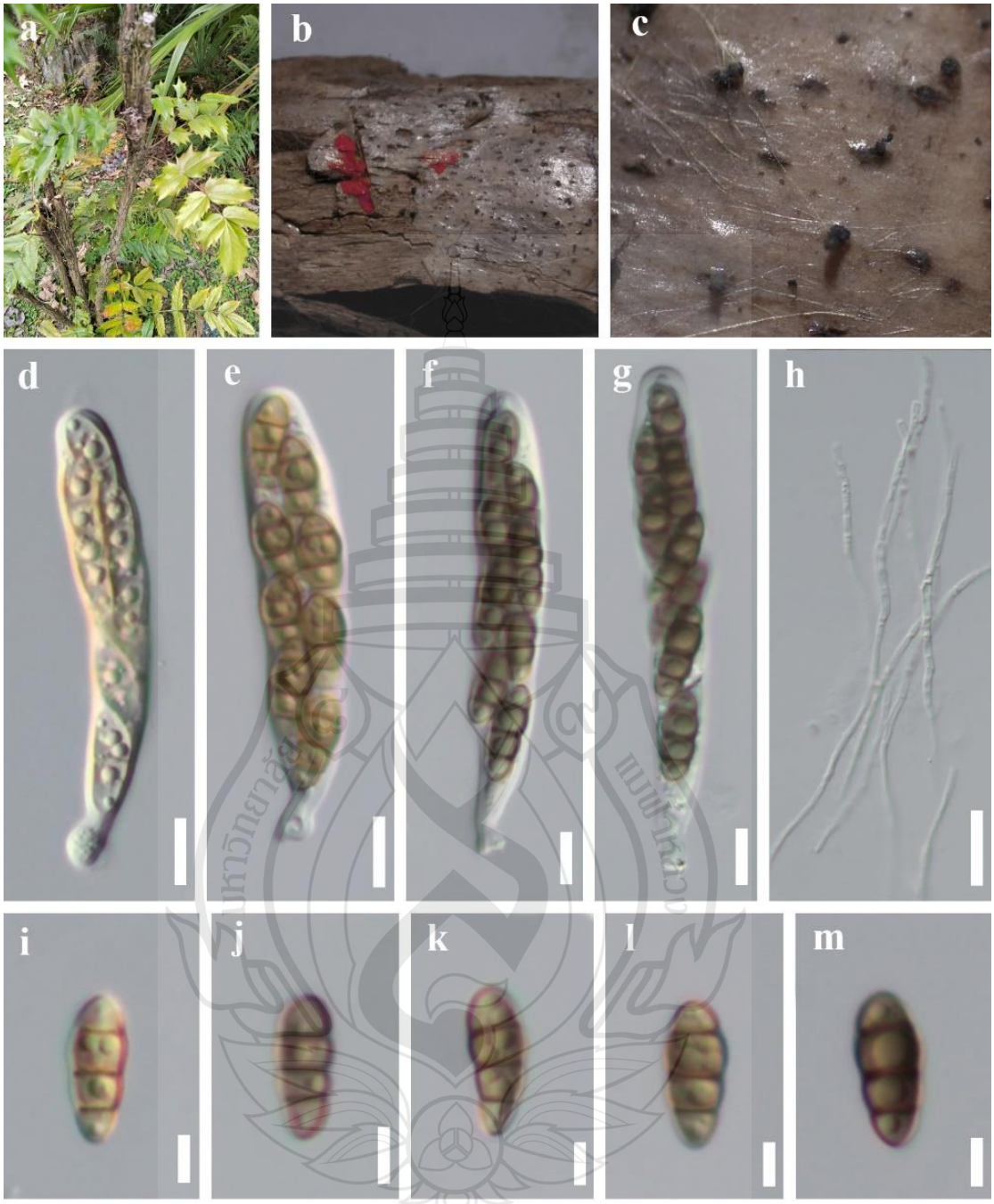
Index Fungorum number: IF 849157; Facesoffungi number: FoF 14406; Figure 4.60

Saprobic on branches of *Mahonia* sp. **Sexual morph**: *Ascomata* immersed, solitary, scattered, with a cylindrical ostiolar neck, coriaceous, obpyriform, brown to dark brown. *Ostiole* central or eccentric, periphysate. *Peridium* consisting of several layers of brown-walled cells of *textura angularis*. *Hamathecium* 1.5–3 μm wide, composed of filiform, septate, branched pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with a short pedicel, apically rounded with a smaller ocular chamber, 64–88 × 10–14 μm. *Ascospores* 14–18.5 × 5–7 μm ($\bar{x}$ = 16 × 6 μm, n = 35), 1–2-seriate, overlapping, fusoid to clavate, apical cell mostly obtuse, straight, 1-septate, hyaline to pale brown when young, becoming 3-septate, brown at maturation, constricted at the septa, guttulate. **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Nanming District, Guiyang medicinal botanical garden, on branches of *Mahonia* sp., 22 December 2021, Y.R. Sun, 22-10 (HGUP 24-0039), living culture (GUCC 24-0056).

Notes: *Nigrograna oleae* was introduced by Li et al. (2023) from *Olea europaea* and *Acer truncatum* in Sichuan Province, China. Hu, He et al. (2023) introduced *Nigrograna trachycarpi* from *Trachycarpus* sp. in Guizhou Province, China. However, due to their close publication dates, Hu et al. (2023) did not compare *N. trachycarpi* with *N. oleae.* Upon analyzing the two species, we observed that their morphologies are remarkably similar (Hu et al., 2013; Li et al., 2023), and there are no base pair differences in the accessible genes (ITS and *tef*1) to both. Thus, we regard they are conspecific and transfer *N. trachycarpi* under *N. oleae* based on the chronological priority of the species names.

Our collection, encountered from *Mahonia* sp. in China, is morphologically similar to the holotype (HKAS 127172) of *Nigrograna oleae*. Both share characteristics such as 8-spored, bitunicate, fissitunicate, cylindrical to clavate asci with a short pedicel, and brown, fusiform ascospores (Li et al., 2023). Their asci and spores also have similar sizes (asci: 14–18.5 × 5–7 μm in HGUP 24-0039 *vs*. 63.5–76 × 11–13.5 μm in HKAS 127172; ascospores: 14–18.5 × 5–7 μm in HGUP 24-0039 *vs*. 15–16.5 × 5.5–7 μm in HKAS 127172). In the phylogenetic tree (Figure 4.68), our isolate (HGUP 24-0039) cluster together with *N. oleae* (HKAS 127172, GMB0505 and GMB0499) with good support (87% ML, 1.00 BYPP). Moreover, these two strains have no base pair differences in the LSU, ITS and *tef*1 gene regions. Therefore, we identify our collection as *N. oleae,* representing a new host record from *Mahonia* sp.



Note a Host. b, c Ascomata on the substrate. d–g Asci. h Pseudoaraphyses. i–m Ascospores. Scale bars: d–g = 10 µm, h = 20 µm, i–m = 5 µm.

Figure 4.60 *Nigrograna oleae* (HGUP 24-0039, new host record)

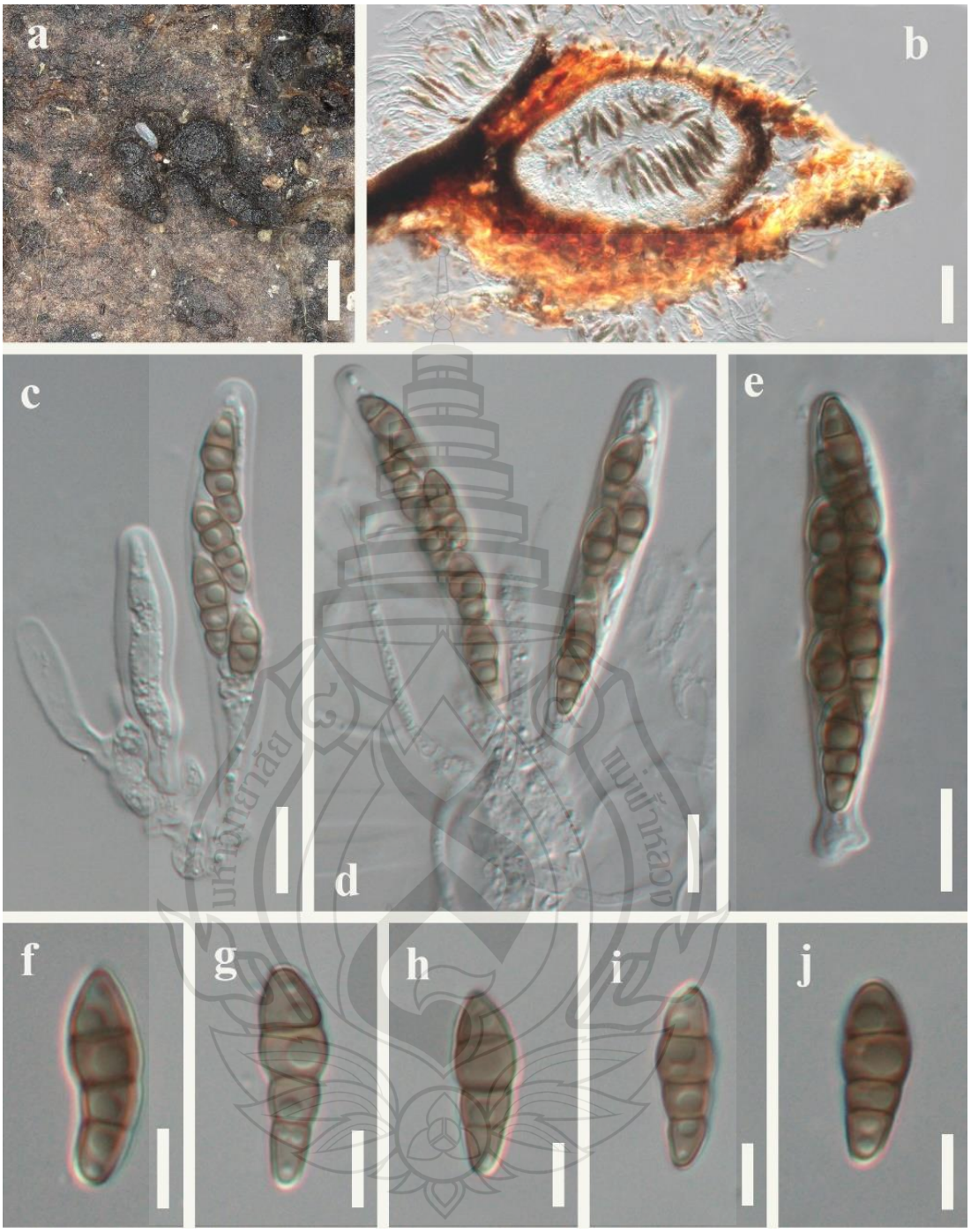
Nigrograna schinifolii H.M. Hu & Q.R. Li, MycoKeys: 137 (2023)

Index Fungorum number: IF851363; Facesoffungi number: FoF 16433; Figure 4.61

Saprobic on dead branches of *Rhododendron delavayi.* **Sexual morph**: *Ascomata* around 250 μm wide, 160 μm high, solitary or aggregated, black, semi-immersed, with a cylindrical ostiolar neck. *Ostioles* black, central or eccentric, periphysate. *Peridium* thick, fused with host tissues, comprising two layers of pale brown to brown cells of *textura angularis*. *Hamathecium* comprising 1–2 μm wide, cylindrical to filiform, septate, branched, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 44–64 × 7–10 μm ($\bar{x}$ = 53 × 8 μm, n = 15), 8-spored, bitunicate, fissitunicate, cylindrical to broadly filiform, with a short pedicel, apically rounded with an ocular chamber. *Ascospores* 10–16 × 2.5–4.5 μm ($\bar{x}$ = 13 × 3.5 μm, n = 20), broadly fusiform to inequilaterally ellipsoid, with the second cell slightly enlarged, straight or slightly curved, with obtuse to rounded ends, brown, 3-septate, slightly constricted at the septum. **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Yunyan District, Luchongguan Road, Guizhou Botanical Garden, on branches of *Rhododendron delavayi*, 14 February 2022, Y.R. Sun, 22-66 (HGUP 24-0040); living culture GUCC 24-0080.

Notes: *Nigrograna schinifolii* was described by Hu et al. (2023) from an edible medicinal plant, *Zanthoxylum schinifolium* in China. Our collection shared a similar morphology to *N. schinifolii.* In phylogenetic analyses, our collection clustered together with two strains of *N. schinifolii.* Therefore, we identified our collection as *N. schinifolii*, which is reported from the medicinal plant, *Rhododendron delavayi* for the first time.



Note a Ascomata on the substrate. b Cross sections of ascoma. c–e Asci and pseudoaraphyses. f–j Ascospores. Scale bars: a = 200 µm, b = 50 µm, c–e = 10 µm, f–j = 5 µm.

Figure 4.61 *Nigrograna schinifolii* (HGUP 24-0040, new host record)

Occultibambusaceae D.Q. Dai & K.D. Hyde, Fungal Divers. 82(1): 25 (2017).

Brunneofusispora S.K. Huang & K.D. Hyde, Fungal Diversity 95: 36 (2019)

Notes*:* *Brunneofusispora* was introduced by Phookamsak et al. (2019) with *B. sinensis* as its type species. This genus has been documented in Australia, China, and Thailand, encompassing a total of five species. Most *Brunneofusispora* species are discovered as saprobes, but *Brunneofusispora sennae-torae* is associated with leaf spots of *Senna tora* (Tan et al., 2021). There are two *Brunneofusispora* species associated with medicinal plants, *viz*. *B. clematidis* on *Clematis subumbellata* and *B. sennae-torae* on *Senna tora* (Phukhamsakda et al., 2020; Tan et al., 2021). We introduce the sixth species namely, *Brunneofusispora mahoniae*, isolated from medicinal plant herein.

Brunneofusispora mahoniae Y.R. Sun and K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902574; Facesoffungi number: FoF 16398; Figure 4.62

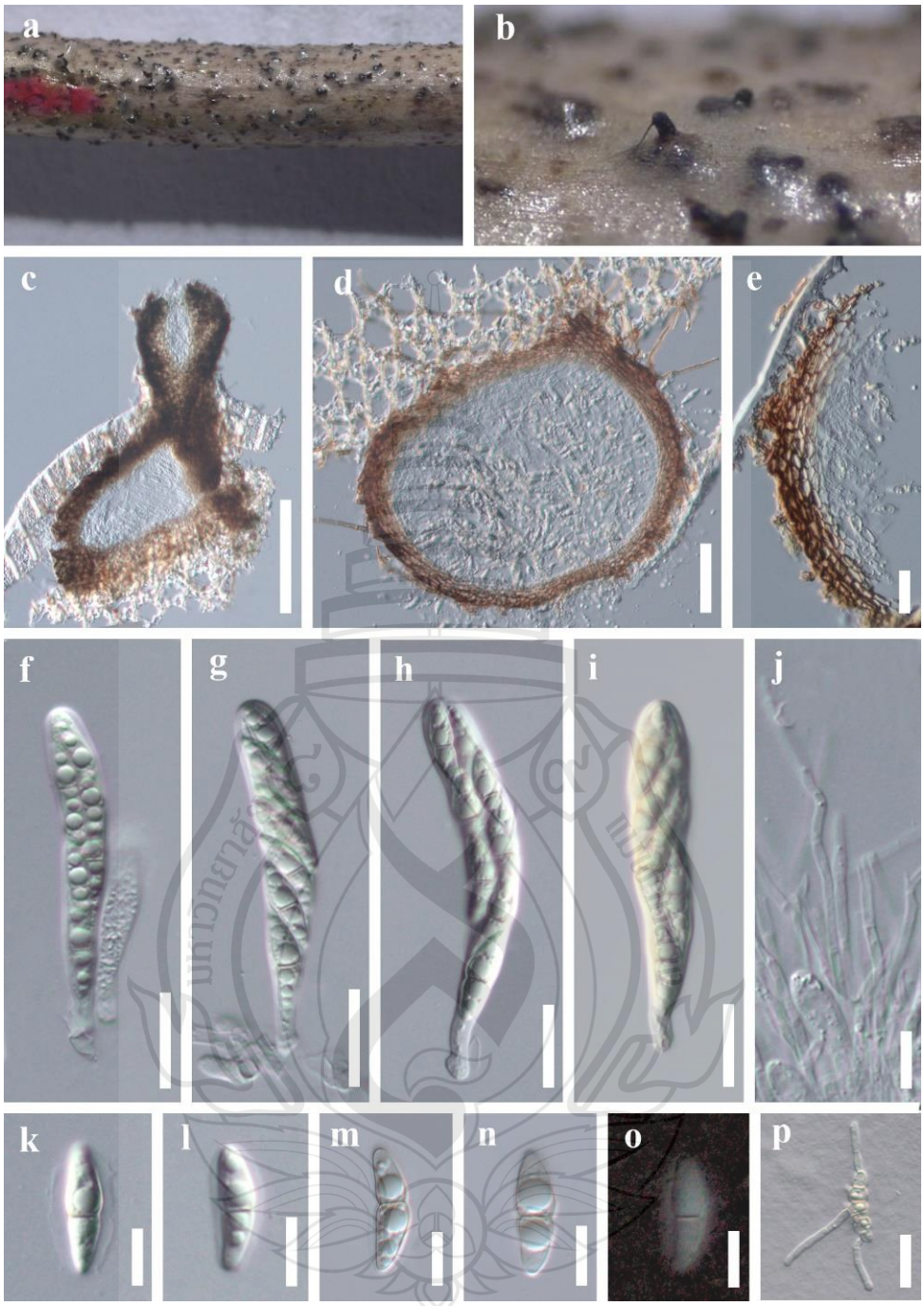
Etymology: Name refers to the host genus.

Holotype: HGUP 24-0015.

Saprobic on twigs of *Mahonia* sp. **Sexual morph**: *Ascomata* 165–250 µm high, 177–235 µm wide, solitary to gregarious, semi-immersed, visible as black domes on the substrate, subglobose to ampulliform, uni-loculate, papillate with long beak. *Ostioles* central, lined with periphyses. *Peridium* 19–35 µm wide, composed of several layers of hyaline to brown, thick-walled cells of *textura angularis*. *Hamathecium* 1–2.5 µm wide, composed of numerous, filamentous, cellular, septate pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 66–88 long, 10–14 µm wide, 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, straight or slightly curved, shortly pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 2-seriate, overlapping, fusiform, hyaline to pale brown, 1-septate, constricted at the septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath, 16–24 × 4–7 µm ($\bar{x}$ = 19 × 5 µm, n = 20). **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Nanming District, Guiyang Botanical Garden of Medical Plants, on twigs of *Mahonia* sp., 22 December 2021, Y.R. Sun, 22-40 (HGUP 24-0015, **holotype**), ex-type culture (GUCC 24-0060).

Notes: *Brunneofusispora mahoniae* phylogenetically formed an inner clade and is closely related to *B. sennae-torae* and *B. sinensis* within the genus *Brunneofusispora* (Figure 4.68). Morphologically, *B. mahoniae* can be distinguished from *B. sinensis* by its smaller ascomata (165–250 μm high, 177–235 μm wide *vs*. 325–370 μm in diameter) and brown peridium (Phookamsak et al., 2019). We are unable to compare the morphological differences between *B. mahoniae* and *B. sennae-torae* because *B. sennae-torae* lacks a morphological description (Tan et al., 2021). Comparison of 496 nucleotides across the ITS region reveals 15 bp (3%) differences between GUCC 24-0060 and *B. sennae-torae* (BRIP 72575d). Therefore, we introduce *B. mahoniae* as a new species following the guidelines for species delineation proposed by Jeewon and Hyde (2016).



Note a, b Ascomata on the substrate. c, d Cross sections of ascomata. e Section of the peridium. f–i Asci. j Pseudoaraphyses. k–n Ascospores. o Ascospore with sheath surrounded in Indian ink. p Germinated ascospore. Scale bars: c, d = 50 μm, e–i, p = 20 μm, j–o = 20 μm

Figure 4.62 *Brunneofusispora mahoniae* (HGUP 24-0015, holotype)

Neooccultibambusa Doilom & K.D. Hyde, Fungal Diversity 82, 126 (2016)

Index Fungorum number: IF551981, Facesoffungi number: FoF01852

Notes*: Neooccultibambusa* was introduced by Doilom et al. (2017) and typified with *N. chiangraiensis*. This genus occurs as saprobes on several plants in China, Italy and Thailand (Jayasiri et al., 2016; Doilom et al., 2017; Tibpromma, Hyde, Bhat et al., 2018; Yu et al., 2021). The sexual morphs of *Neooccultibambusa* species are characterized by solitary to gregarious, scattered, immersed to semi-immersed, uniloculate, globose to sub-globose ascomata, 8-spored, bitunicate, cylindrical to subcylindrical asci, overlapping biseriate, hyaline to pale brown, fusoid ascospores with 1–3 transverse septa (Doilom et al., 2017). The asexual morphs have macronematous, septate, straight or slightly flexuous, dark brown conidiophores, holoblastic, integrated, terminal, brown, cylindrical conidiogenous cells and acrogenous, solitary, obclavate, pale to dark brown conidia (Jayasiri et al., 2016; Hyde et al., 2018). There are six species accepted in *Neooccultibambusa* with descriptions and molecular data (Wijayawardene et al., 2022; Index Fungorum, 2024).

Neooccultibambusa fusispora Y.R. Sun, Yong Wang bis & K.D. Hyde, sp. nov., Figure 4.63

Facesoffungi number: FOF14842

Etymology: The epithet "fusispora" refers to the fusiform ascospores.

Holotype: HGUP 24-0041.

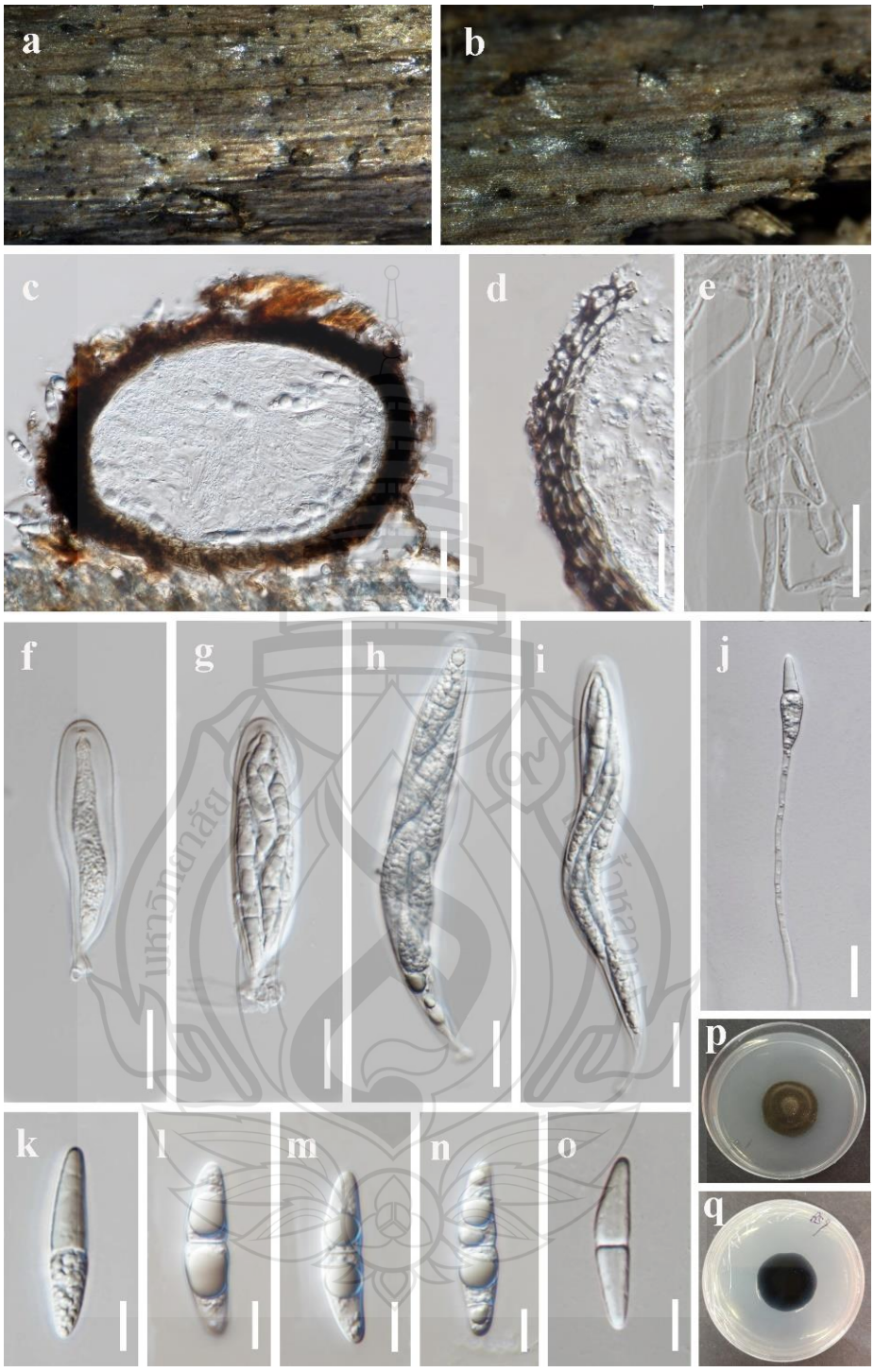
Saprobic on dead twigs. **Sexual morph**: *Ascomata* solitary or scattered, globose, uniloculate, immersed, visible as black dots on host surface, in vertical section 190–240 μm high, 250–290 μm wide. *Ostiole* central, periphysate. *Peridium* 17–25 μm wide, comprising two layers of pale brown to brown cells of textura angularis. *Hamathecium* 1.5–3 μm wide, cellular pseudoparaphyses, anastomosing above asci, embedded in a gelatinous matrix. *Asci* 80–149 × 16–22 μm ($\bar{x}$ = 106 × 18 μm, n = 15), 8-spored, cylindrical to clavate, bitunicate, with short furcate pedicel, apically rounded, with an ocular chamber. *Ascospores* 31–37 × 5–7.5 μm ($\bar{x}$ = 34 × 6.5 μm, n = 25), overlapping biseriate, hyaline, fusiform, 1–3-septate, constricted at the center septum, guttulate when young, smooth,

surrounded by a gelatinous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated on PDA within 12 h at 25 °C. Germ tube produced from one end of ascospore. Colonies on PDA reached 2.5 cm diam. after 4 weeks; mycelium pale brown to brown, flossy, circular, with the entire edge; surface rough, olivaceous to brown from above, dark from below.

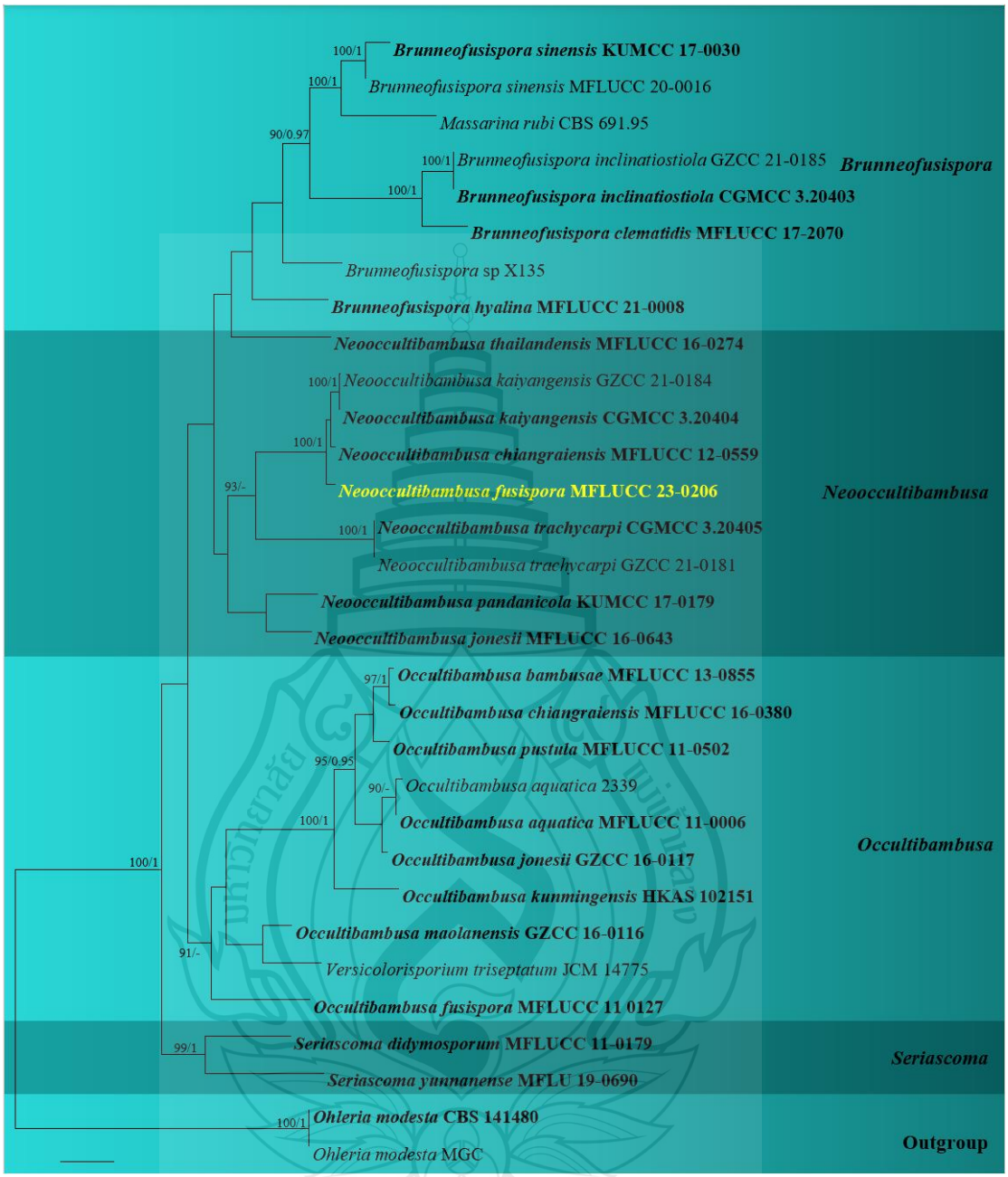
Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on dead twigs, 23 October 2020, Y.R. Sun, B59 (HGUP 24-0041, **holotype**); ex-type living culture MFLUCC 23–0206.

Notes: The multi-loci phylogenetic analyses of the combined LSU, SSU, ITS, RPB2 and *TEF1*-α sequences confirmed our strain belongs to *Neooccultibambusa*, where it is sister to *N. chiangraiensis* and *N. kaiyangensis* with maximum bootstrap support (100% ML/1.00 BYPP). Morphologically, *Neooccultibambusa fusispora* differs from *N. chiangraiensis* in having smaller ascomata (250–290×190–240 µm *vs*. 345–355 × 245–295 µm) and thinner ascospores (31–37 × 5–7.5 µm *vs*. 36–37 × 8–13 µm) (Doilom et al., 2017). *Neooccultibambusa fusispora* is also distinguished from *N. kaiyangensis* by its larger asci (80–149 × 16–22 µm *vs*. 70–108 × 7.5–11 µm) and larger ascospores (31–37 × 5–7.5 µm *vs*. 16–23.5 × 3–5.5 µm) (Yu et al., 2021). Thus, *N. fusispora* sp. nov is introduced here.



Note a, b Ascomata on host surface. c Section through ascomata. d Peridium. e Pseudoparaphyses. f–i Asci. j Germinated ascospore. k–o Ascospores. p, q Colonies on PDA (upper view and lower view). Scale bars: c = 50 µm, d–j = 20 µm, k–o = 10 µm.

Figure 4.63 *Neooccultibambusa fusispora* (HGUP 24-0041, holotype)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The tree is rooted with *Ohleria* modesta (CBS 141480) and *O. modesta* (MGC). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Figure 4.64 Phylogenetic tree of *Neoocculitibambusa*

Occultibambusa D.Q. Dai & K.D. Hyde, Fungal Diversity 82, 25 (2016)

Notes*: Occultibambusa* was recently established to accommodate two bambusicolous species (Dai et al., 2016). The sexual morph is characterized by solitary or gregarious, immersed, subglobose to conical, dark brown, ascostromata with black, papillate ostioles, bitunicate, 8-spored, broadly cylindrical to clavate asci, and fusiform, pale brown to brown, 1–(3)-septate ascospores (Dai et al., 2016; Hyde et al., 2016; Yu et al., 2022). The asexual morph has immersed, solitary to gregarious, globose to subglobose, black conidiomata with long papillate necks, blastic, cylindrical to ampulliform, hyaline, aseptate conidiogenous cells and oblong to cylindrical, hyaline, aseptate, conidia (Dai et al., 2016). There are ten *Occultibambusa* species isolated from bamboo in China and Thailand (Dai et al., 2016; Hyde et al., 2016; Zhang et al., 2017; Jiang et al., 2021; Yu et al., 2022). In this study, we introduced a new record of *Occultibambusa aquatica* isolated from bamboo in China.

Occultibambusa aquatica Huang Zhang & K.D. Hyde, Fungal Diversity 80: 81 (2016)

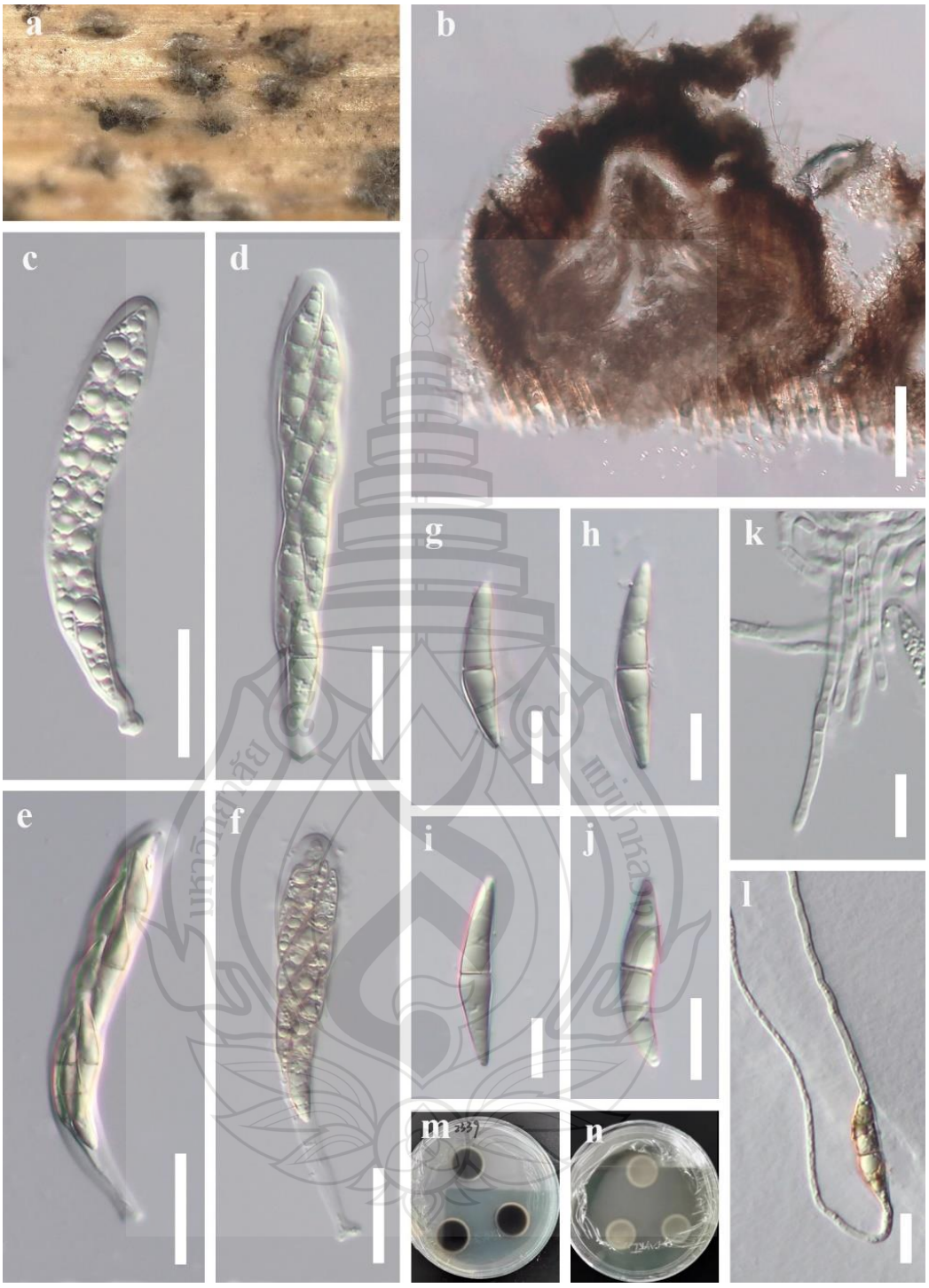
Index Fungorum number: IF552366; Facesoffungi number: FoF02439; Figure 4.65

Saprobic on dead bamboo culms. **Sexual morph**: *Ascomata* solitary or scattered, globose, uniloculate, immersed, visible as black dots on host surface, 250–280 µm high, 230–270 µm wide. *Ostiole* central, periphysate. *Peridium* 25–30 µm wide, comprising two layers of pale brown to brown cells of *textura angularis*. *Hamathecium* 1–3 µm wide, cellular pseudoparaphyses, anastomosing above asci, embedded in a gelatinous matrix. *Asci* 53–88 × 9–13 µm ($\bar{x}$ = 74 × 11 µm, n = 15), 8-spored, cylindrical to clavate, bitunicate, with short furcate pedicel, apically rounded, with a small ocular chamber. *Ascospores* 21–29 × 3–6 µm ($\bar{x}$ = 25 × 4.5 µm, n = 20), mostly 2-seriate, pale brown to brown, fusiform, straight to curved, 1-septate, septum mostly median, slightly swollen near the septum, with one large guttule in each cell, smooth, surrounded by a gelatinous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated on PDA within 12 h at 25 ºC. Germ tube produced from both ends of ascospore. Colonies on PDA reached 2.5 cm diam. after 4 weeks; dense, flossy, circular, with the entire edge; surface rough, olivaceous to brown in below, dark from below.

Material examined: China, Yunnan Province, Kunming City, Yiliang District, Yangzonghai Garden, on dead bamboo culms, 20 February 2023, H.W. Shen, 2339 (HGUP 23-2339); living culture GUCC 2339.

Notes: Our strain (GUCC 2339) clustered together with *Occultibambusa aquatica* (MFLUCC 11-0006) by high support in the phylogenetic tree. Morphologically, they have similar ascomata, asci, and ascospores, including measurement size. *Occultibambusa aquatica* was reported from submerged wood in a freshwater stream in Thailand (Hyde et al., 2016). In this study, we introduced our isolate as the new record of *O. aquatica* from terrestrial habitat in China.



Note a Ascomata on the host surface. b Section through ascomata. c–f Asci. g–j Ascospores. k Pseudoparaphyses. l Germinated ascospore. m, n Colonies on PDA. Scale bars: b = 100 µm, c–f = 20 µm, g–l = 10 µm.

Figure 4.65 *Occultibambusa aquatica* (HGUP 23-2339, new habitat record)

Occultibambusa sichuanensis X.D. Yu, S.N. Zhang & Jian K. Liu, Journal of Fungi 8 (7, no. 720): 14 (2022)

Index Fungorum number: IF843720; Facesoffungi number: FoF 16434; Figure 4.66

Saprobic on dead branches of Bamboo in freshwater habitat. **Sexual morph**: *Ascomata* solitary to gregarious, semi-immersed, visible as black domes on the substrate, in vertical section 130–180 µm high, 340–440 µm diam., subglobose, coriaceous, uniloculate. *Peridium* 25–90 µm wide, composed of several layers of brown, thick-walled cells of textura angularis. *Hamathecium* 1–2 µm wide, hyphae-like, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 83–117 × 17–24 µm ($\bar{x}$ = 103 × 19 µm, n = 15), 8-spored, bitunicate, fissitunicate, obovoid to pyriform, straight or slightly curved, shortly pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 2–3-seriate, overlapping, fusiform, straight to somewhat curved, brown, 1-septate, constricted at the middle septum, guttulate, smooth-walled, surrounded by a mucilaginous sheath, 28–38 × 6–11 µm ($\bar{x}$ = 33 × 8 µm, n = 20). **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Libo County, Guizhou Maolan National Nature Reserve, on branches of bamboo in a stream, 12 March 2022, Y.R. Sun, ML20 (HKAS 136893); living culture GUCC 24-0082.

Notes: *Occultibambusa sichuanensis* was introduced by Yu et al. (2022) from bamboo in a terrestrial environment. Our collection shared a similar morphology with it. In phylogenetic analyses (Figure 4.68), these two taxa clustered together with high support (100% ML, 1.00 BYPP). Additionally, there are no base pair differences in the ITS and *TEF1-α* genes and only 3 base pair differences in the LSU gene regions. Thus, we confirmed our collection as a new habitat record of *O. sichuanensis.*



Note a, b Ascomata on the substrate. c Cross sections of ascoma. d Section of the peridium. e Pseudoaraphyses. f–j Asci. k–o Ascospores. p Ascospore with sheath surrounded in Indian ink. q Germinated ascospore. Scale bars: c = 100 µm, d, e = 50 µm, f–q = 20 µm.

Figure 4.66 *Occultibambusa sichuanensis* (HKAS 136893, new habitat record)

Seriascoma Phookamsak, D.Q. Dai & K.D. Hyde, Fungal Divers. 82(1): 30 (2017).

Notes: Dai et al. (2016) introduced *Seriascoma* with *S. didymospora* as the type species. The most obvious morphological difference between *Seriascoma* and other genera in Occultibambusaceae is that the position of its ascostromata under a clypeus (Dai et al., 2016; Hongsanan et al., 2020a). Five bambusicolous species are accepted in this genus and three of which are reported in China (Dai et al., 2016; Rathnayaka et al., 2019; Jiang et al., 2021; Senanayake et al., 2023); this study). In this study, we introduced a new species and synonymized a *Seriascoma* species, based on morphology and molecular data.

Seriascoma guizhouense Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902595; Facesoffungi number: FoF 16435; Figure 4.67

Etymology: based on the province where fungus was collected.

Holotype: HKAS 136881.

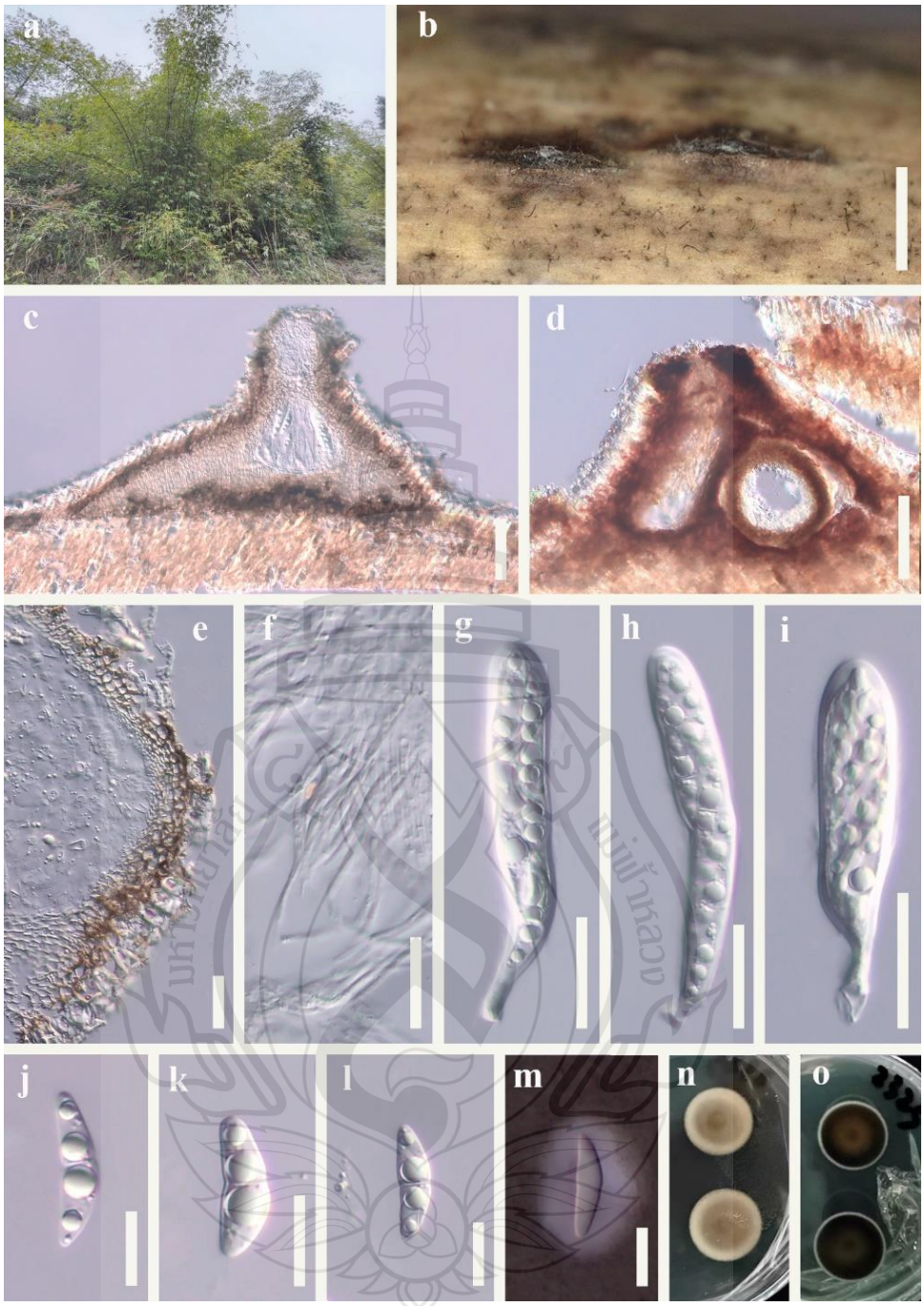
Saprobic on bamboo culms in terrestrial habitat. **Sexual morph**: *Ascostromata* 127–304 µm wide, 134–171 µm high, solitary to gregarious, immersed beneath clypeus, coriaceous, raised, erumpent in linear rows, with slit-like opening, uni- or multiloculate, subglobose to ampulliform, with ostiolate. *Ostioles* brown, central., *Peridium* 14–37 µm wide, thick-walled, composed of brown cells of *textura angularis* out layer and hyaline to pale brown inner layer. *Hamathecium* 1–3 µm wide, composed of hyaline, filamentous, distinctly, septate, cellular, pseudoparaphyses. *Asci* 49–87 × 9–13 µm ($\bar{x}$ = 69× 11 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate or cylindrical, short pedicellate, apically rounded, with well-developed, ocular chamber. *Ascospores* 14–21 × 4–7 µm ($\bar{x}$ = 18.5× 5 µm, n = 20), 2-seriate, overlapping, fusiform, with rounded ends, hyaline, 1-septate, slightly constricted at the septum, straight to curved, smooth-walled, with guttules. **Asexual morph**: Not observed.

Culture characters: Ascospores germinated on PDA within 12 h at 26 °C. Colonies on PDA reaching 20 mm diam. after 4 weeks at 26 °C, colonies circular, dense, flat, smooth with entire edge, velvety to floccose, gray to pale brown from above, dark brown with a

white outer ring from below.

Material examined: CHINA, Guizhou Province, Guiyang City, Wudang District, Xiangzhigou, on culms of bamboo, 13 February 2023, Y.R. Sun, 2323 (HKAS 136881, **holotype**), ex-type culture GUCC 24-0081.

Notes: *Seriascoma guizhouense* formed a sister clade to *S. yunnanense* (MFLU 19-0690) with high support (100% ML, 1.00 BYPP) in the phylogenetic tree (Figure 4.68). In the morphology, *S. guizhouense* has smaller ascospores (14–21 × 4–7 μm *vs*. 22–30 × 5–7.2 μm) than *S. yunnanense* (Rathnayaka et al., 2019). In addition, there are 13 base pair differences in the *TEF1-α* gene region (414 bp). We thus introduced *S. guizhouense* sp. nov. herein with description and illustration.



Note a, b Ascomata on the substrate. c, d Cross sections of ascomata. e Section of the peridium. f Pseudoaraphyses. g–i Asci. j–l Ascospores. m Ascospore with sheath surrounded in Indian ink. n, o Colonies on the PDA (n from above, o from below). Scale bars: b = 500 μm, c, d = 50 μm, e–i = 20 μm, j–m = 10 μm.

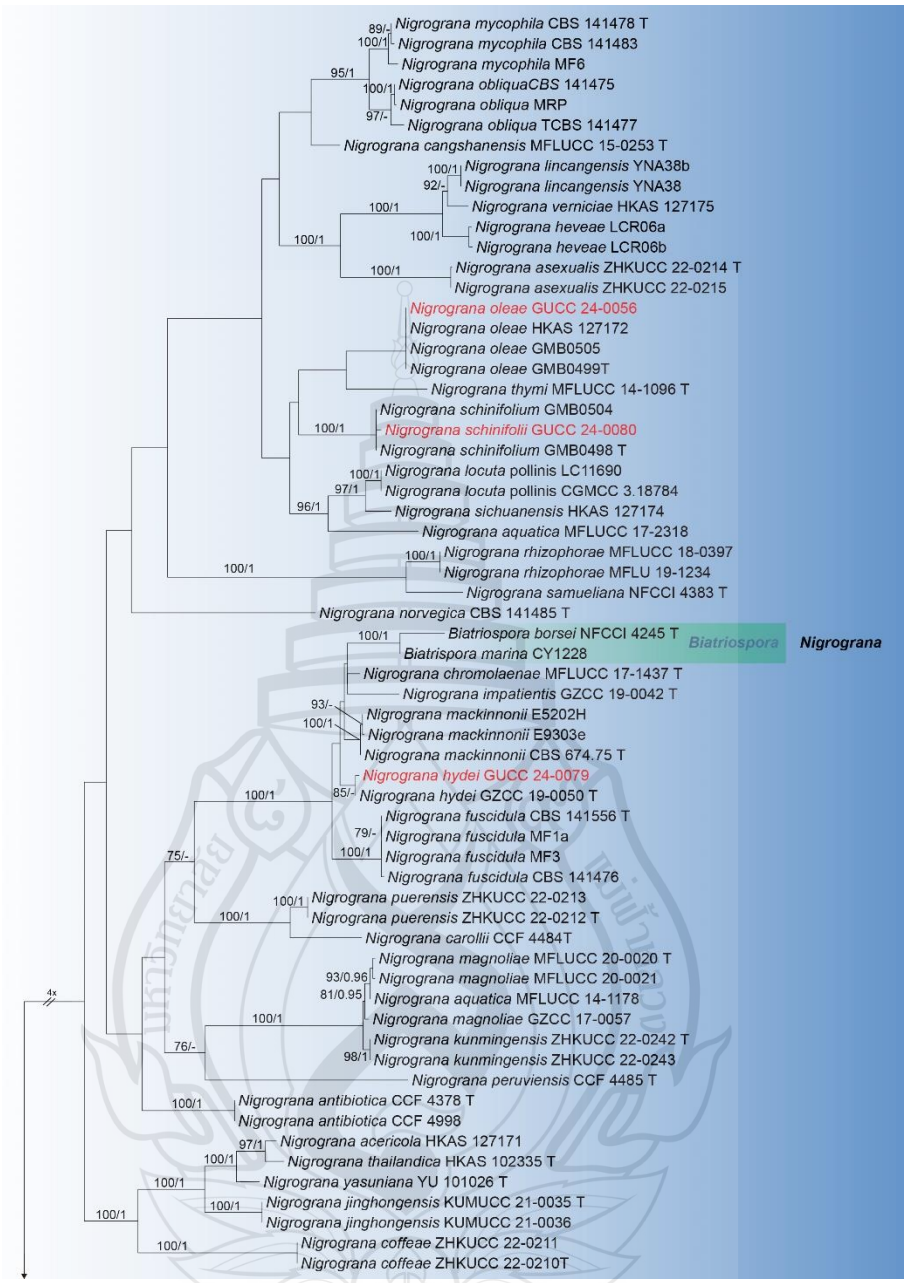
Figure 4.67 *Seriascoma guizhouense* (HKAS 136881, holotype)

Seriascoma bambusae H.B. Jiang, K.D. Hyde & Phookamsak, Life 11(no. 932): 10 (2021)

= *Seriascoma honghense* H.B. Jiang, Phookamsak & K.D. Hyde, Fungal Diversity 111: 86 (2021)

Index Fungorum number: IF558430; Facesoffungi number: FoF 09885

Notes: *Seriascoma bambusae* was introduced by Jiang et al. (2021) in September while *Seriascoma honghense* was described by Boonmee et al. (2021) in December. It is worth noting that these two strains were collected by the same person from bamboo in the same location on the same date. Their morphology exhibits almost no difference. In addition, there are no base pair differences in LSU, SSU, ITS, RPB2 and *TEF1-α* genes. Therefore, we proposed that they are conspecific and recommend using *S. bambusae* over *S. honghense.*



Note Bootstrap support for maximum likelihood (ML) greater than 50% and clade credibility values greater than 0.90 from Bayesian inference analysis are gave. The new isolate is indicated in red. The tree is rooted with *Paradictyoarthrinium diffractum* (MFLUCC 13-0466) and *P. tectonicola* (MFLUCC 13-0465).

Figure 4.68 Phylogenetic tree of Nigrograna and Occultibambusaceae

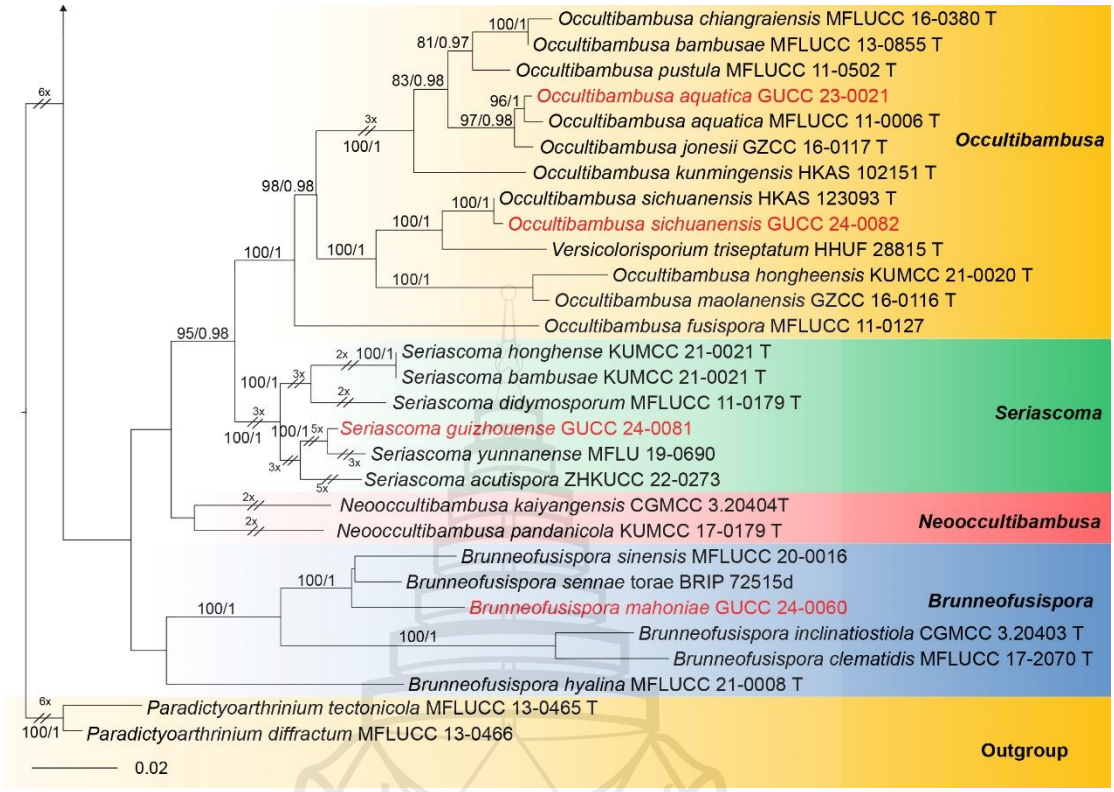


Figure 4.68 (continued)

Paradictyoarthriniaceae Doilom, Jian K. Liu & K.D. Hyde, Fungal Divers., 72: 133 (2015)

Paradictyoarthrinium Matsush., Matsush. Mycol. Mem. 9: 18 (1996)

Notes: The hyphomycetous genus, *Paradictyoarthrinium* was introduced by Matsushima (1996) with *P. diffractum* as the type species. They have a wide geographical distribution and are commonly found as saprophytic fungi in terrestrial and freshwater environments (Liu et al., 2018; Htet, Prematunga et al., 2023). Currently, five species are accepted in this genus with molecular data (Liu et al., 2015; Liu et al., 2018; Htet, Prematunga et al., 2023; Species Fungorum, 2024).

Paradictyoarthrinium diffractum Matsush., Matsush. Mycol. Mem. 9: 18 (1996)

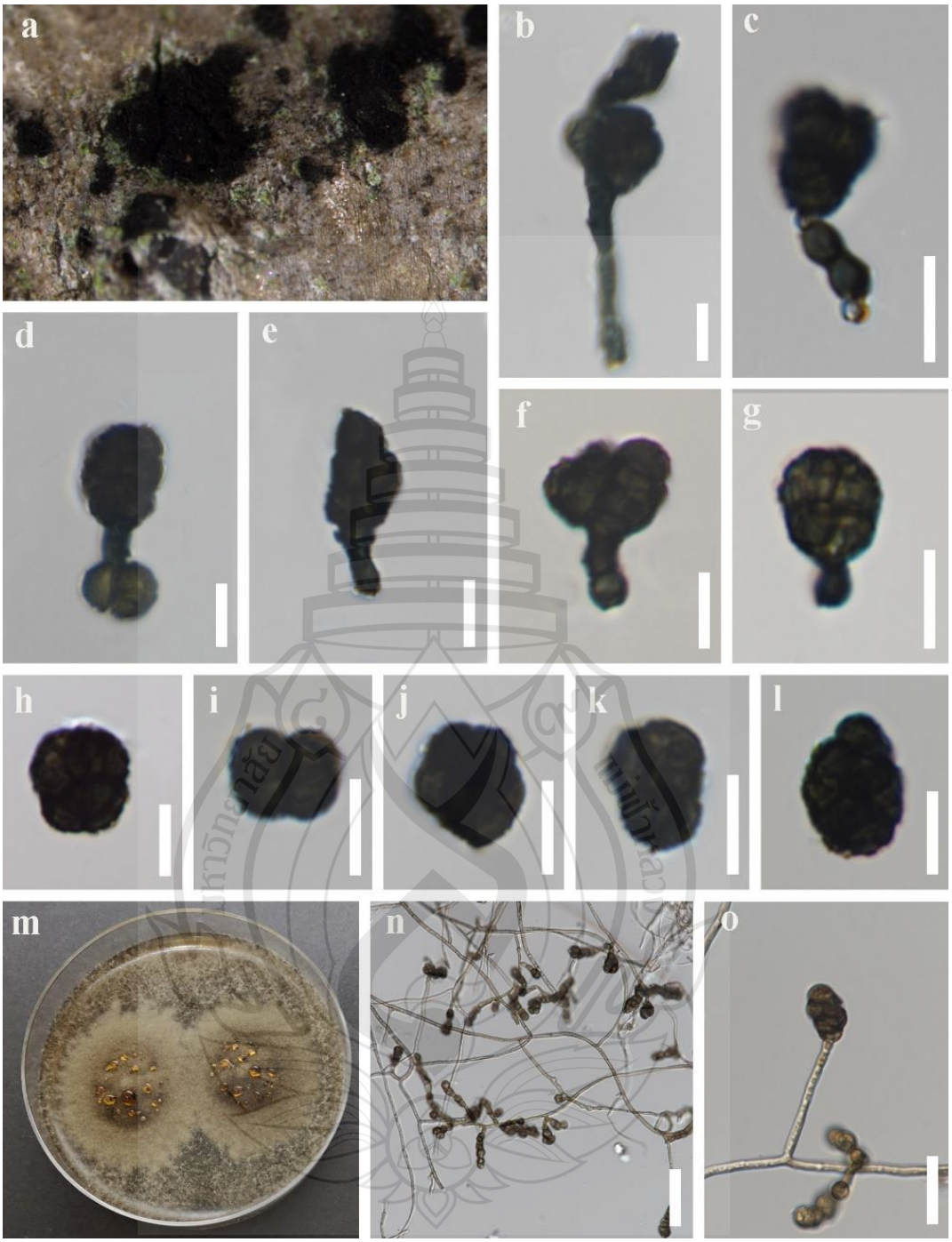
Index Fungorum number: IF 41584; Facesoffungi number: FoF 01854; Figure 4.69

Saprobic on *Cassia fistula* in terrestrial habitat. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, black, punctiform or powdery. *Mycelium* mostly immersed, composed of pale to brown hyphae. *Conidiophores* 2–4 μm diam., macronematous, mononematous, erect, short, flexuous, subcylindrical, green to dark green, unbranched or branched, septate, constricted at the septa, thick-walled. *Conidiogenous cells* monoblastic, integrated, terminal, green to dark green. *Conidia* 9–20 × 7–15 μm ($\bar{x}$ = 13 × 11 μm, n = 30), solitary or catenate, subglobose, ellipsoidal to irregular, green to dark green, muriform, deeply constricted at the septa, verrucose.

Culture characteristics: Conidia germinated on PAD media within 12 h. Colonies on PDA media circular, with raised center and undulate edge, brown at center, pale brown at outer ring from above. Hyphomycetous asexual morph in culture, *conidiophores* micronematous. *Conidiogenous cells* monoblastic, integrated, terminal, pale to brown. *Conidia* irregular, brown, phragmoseptate or muriform, constricted at the septate, verrucose, 13–31 × 5–16 μm ($\bar{x}$ = 20 × 10 μm, n = 20).

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on twigs of *Cassia fistula*, 7 January 2010, Y.R. Sun, B86 (HGUP 24-0042); living culture MFLUCC 24-0287.

Notes: *Paradictyoarthrinium diffractum*, was initially described from a rivulet in South Africa and later collected from India (Matsushima, 1996; Prabhugaonkar & Bhat, 2011). Liu et al. (2015) provided isolates MFLUCC 12-0557 and MFLUCC 13-0466 as *P. diffractum* without morphology. Yang, Tibpromma et al. (2022) reported this species from *Mangifera indica* in China. Our collection cluster together with other *P. diffractum* strains by strong support (ML-bs = 100%, BYPP = 1) (Figure 4.26). Thus, we identify our strain as *P. diffractum,* representing a new host and geographical record.



Note a Colonies on wood. b–g Conidia with conidiophores. h–l conidia. m Colonies on PDA. n, o Conidia with conidiophores produced from culture. Scale bars: b–l = 10 µm, n = 50 µm, o = 20 µm.

Figure 4.69 *Paradictyoarthrinium diffractum* (HGUP 24-0042, new geographical record)

Phaeoseptaceae Boonmee, Thambugala & K.D. Hyde, Mycosphere 9(2): 323 (2018)

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

Notes*: Phaeoseptum* was described and placed within Halotthiaceae by Zhang et al. (2013). Hyde et al. (2018) transferred *Phaeoseptum* to a new family Phaeoseptaceae. *Phaeoseptum* contains saprobes from terrestrial and freshwater environments and are characterized by semi-immersed to immersed ascomata, narrowly cellular, anastomosed pseudoparaphyses, cylindrical to clavate, pedicellate asci and fusiform to ellipsoidal or vermiform, asymmetrical and brown muriform ascospores (Zhang et al., 2013; Hyde et al., 2018; Dayarathne et al., 2020; Jayawardena et al., 2022). Currently, seven species are accepted in this genus (Species Fungorum, 2024).

Phaeoseptum manglicola Devadatha, V.V. Sarma & E.B.G. Jones, Mycosphere 11(1): 56 (2020)

Index Fungorum number: IF555722; Facesoffungi Number: FoF 06167; Figure 4.70

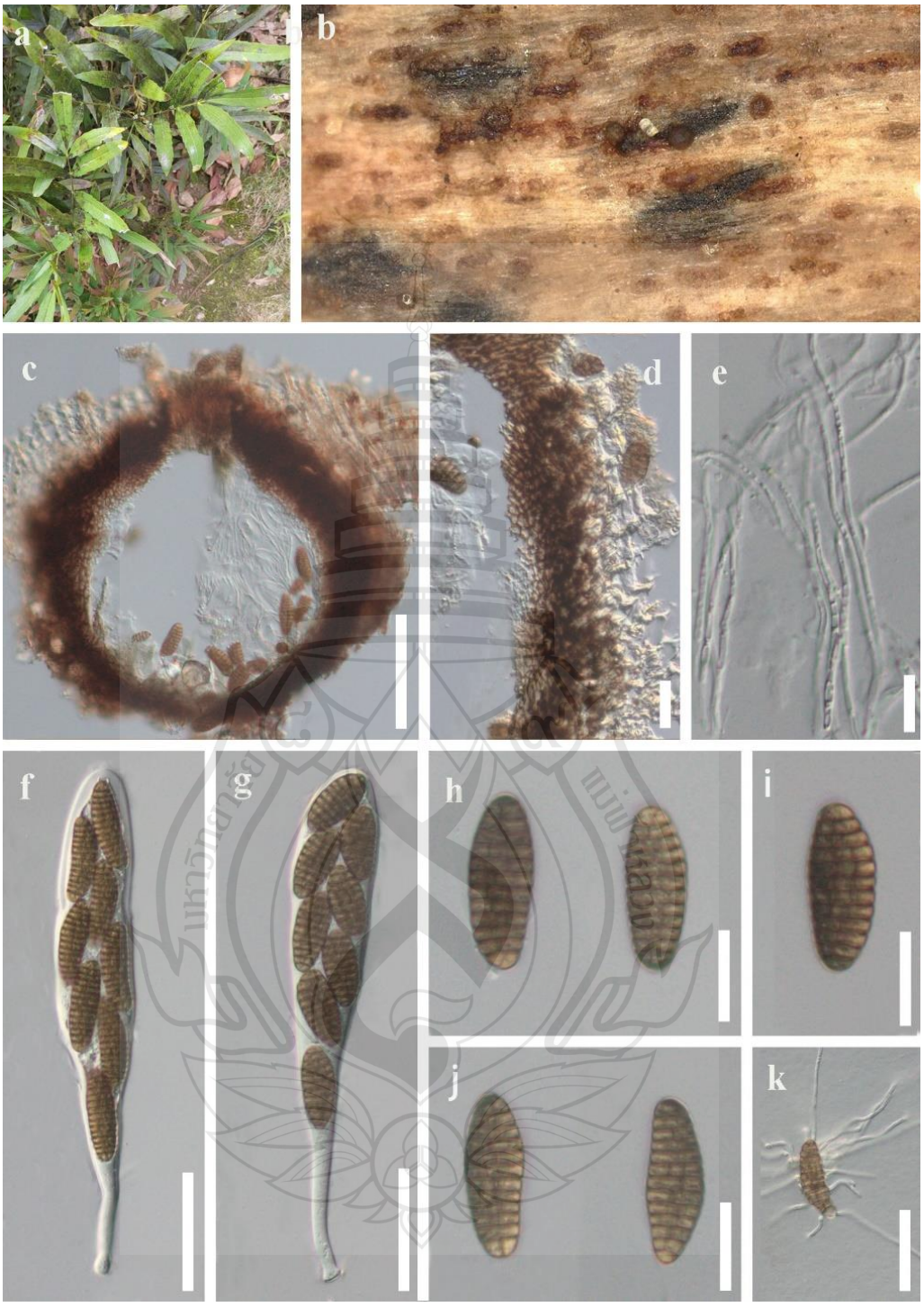
Saprobic on branches of *Mahonia fortunei*. **Sexual morph**: *Ascomata* solitary or aggregate, semi-immersed, erumpent through the host tissue, ostiolate, globose to subglobose, raised as dark brown to black spots on the surface of the host, 250–450 µm high, 200–355 µm wide. *Ostiole* central, short, pale to brown. *Peridium* 15–60 µm ($\overline{x}$ = 37 µm, n=20) wide, the outer layer thick-walled and brown cells of *textura angularis*, the inner layer hyaline to pale brown cells of *textura angularis*, fusing at the outside with the host tissues. *Hamathecium* composed of 1–2.5 µm wide, filamentous, branched, cellular, septate, hyaline, narrow pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 150–225 × 25–35 µm, 8-spored, bitunicate, fissitunicate, cylindrical to clavate, apically rounded. *Ascospores* 32–45× 11–16 µm ($\overline{x}$ = 38 × 13 µm, n=40), 1–2-seriate, overlapping, broadly fusiform, with rounded ends, brown, smooth-walled, flattened, lacking a mucilaginous sheath, straight or slightly curved, 9–15 transverse septa, 1–2 longitudinal septa in each row. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PDA producing germ tubes from both ends of the ascospores within 12 hours. Colonies reaching 10 mm in diam. after

incubation for three weeks, cottony, undulate, umbonate, and irregular, pearl grey to dawn grey from above, warm blackish brown from below.

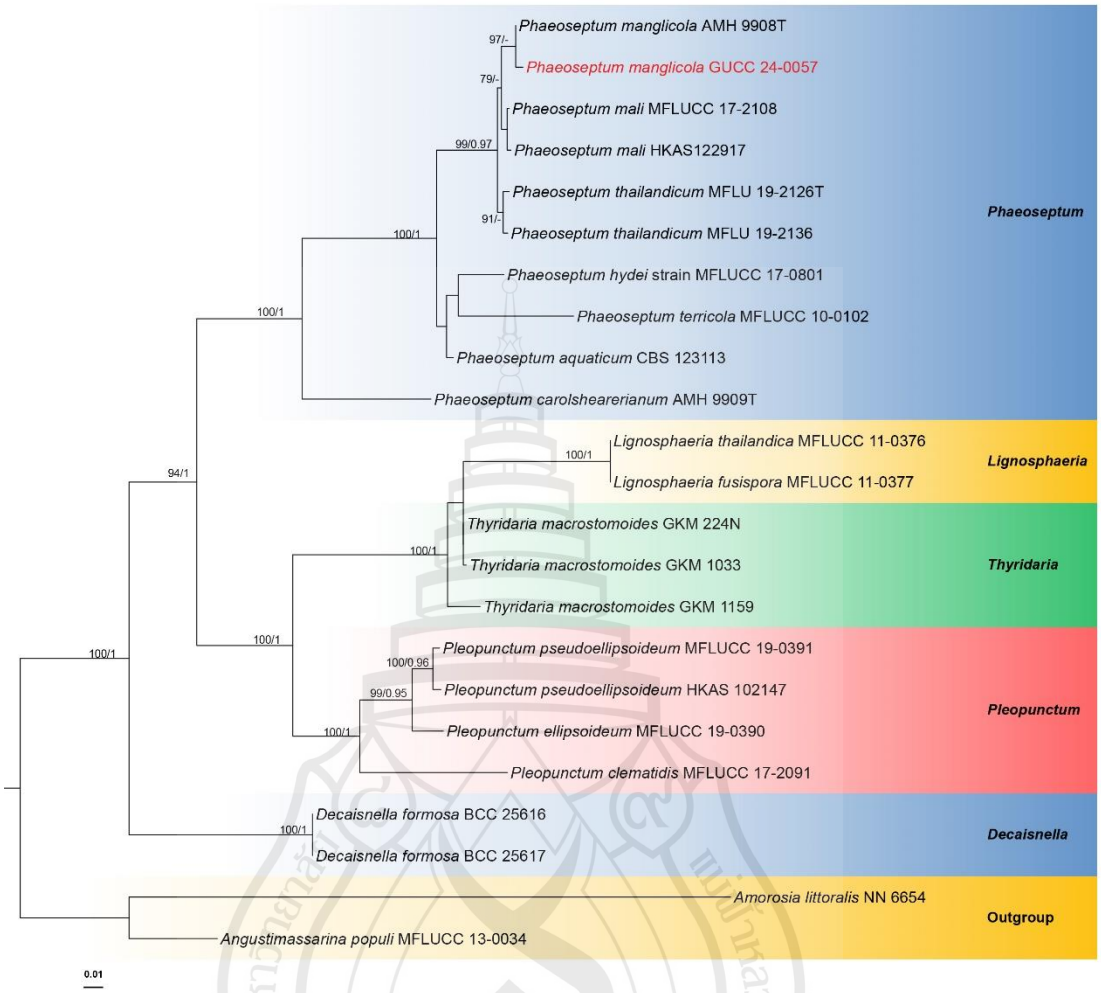
Material examined: CHINA, Guizhou Province, Guiyang City, Baiyun District, Junfacheng, on branches of *Mahonia fortunei*, 22 October 2022, Y.R. Sun, JF2 (HGUP 24-0016), living culture GUCC 24-0057.

Notes: Our strain, collected from the medicinal plant *Mahonia fortunei* in China, is phylogenetically clustered with *Phaeoseptum manglicola* (AMH 9908), which was isolated from the dead decaying wood of *Avicennia marina* in India (Dayarathne et al., 2020). Comparing the base pair differences of the genes possessed by the two strains revealed only one base pair difference in the ITS gene region. Morphologically, our collection shares similar characteristics with *P. manglicola*, having 8-spored, bitunicate, cylindrical to clavate asci, and broadly fusiform, brown ascospores with 9–15 transverse septa and 1–2 longitudinal septa. Thus, we identify our strain as *P. manglicola*, representing a new host and geographical record.



Note a Host. b Ascomata on the substrate. c Cross sections of ascomata. d Section of the peridium. e Pseudoaraphyses. f–g Asci. h–j Ascospores. k Germinated ascospore. Scale bars: c = 100 µm, d, e, h–j = 20 µm, f, g, k = 50 µm.

Figure 4.70 *Phaeoseptum manglicola* (HGUP 24-0016, new host record)



Note The best scoring RAxML tree with a final likelihood value of − 7867.54129 is presented. Bootstrap support for ML equal to or greater than 75% and clade credibility values greater than 0.95 from Bayesian inference analysis are labelled at each node. The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number. The tree is rooted with *Amorosia littoralis* (NN 6654) and *Angustimassarina populi* (MFLUCC 13-0034).

Figure 4.71 Phylogenetic tree of *Phaeoseptum*

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

Notes: Liu, Hyde et al. (2019) introduced *Pleopunctum* to accommodate two dematiaceous hyphomycetous species from terrestrial habitat. Subsequently, Xu et al. (2023) and Zhang, Chen et al. (2023) reported *Pleopunctum* species from freshwater habitats. Although the morphology of *Pleopunctum* is similar to that of *Berkleasmium*, their phylogenetic status is different. Koukol and Delgado (2021) transferred a *Hermatomyces* species into *Pleopunctum.* Currently, 10 species are accepted in this genus with their morphology and molecular data. In this study, we report *Pleopunctum ellipsoideum* from the medicinal plant, *Dendrobium nobile* in Thailand.

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

Index Fungorum: IF556523; Facesoffungi number: FoF 06114; Figure 4.72

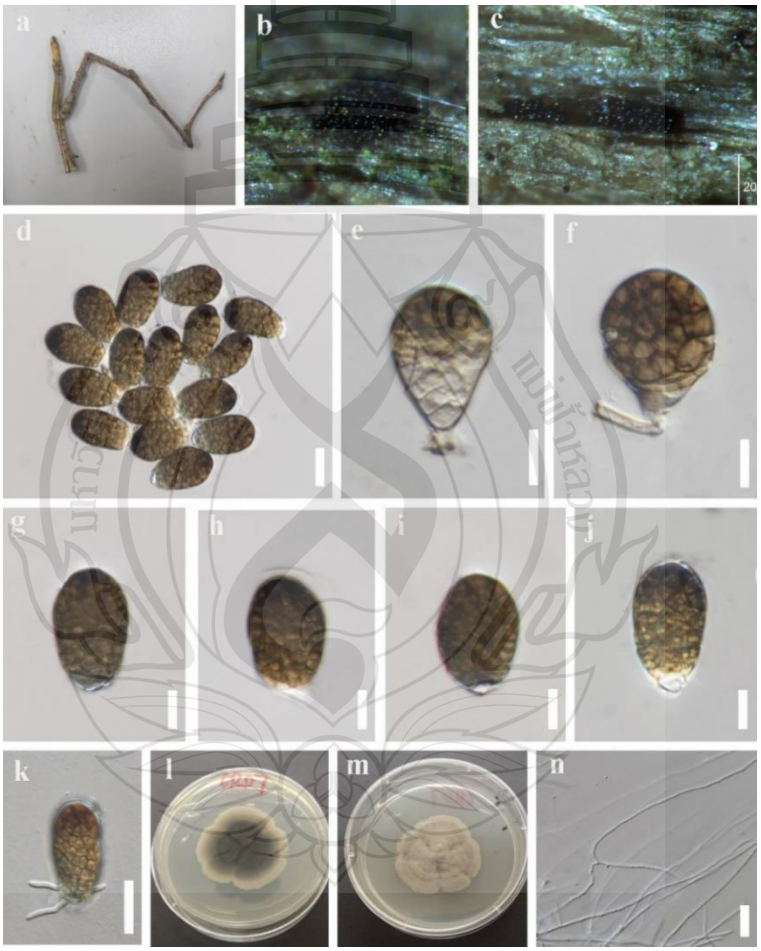
Saprobic on twigs of *Dendrobium nobile*. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate sporodochial, superficial, black, gregarious, punctiform, glistening. *Mycelium* immersed in the substratum, composed of septate, branched, subhyaline to hyaline hyphae. *Conidiophores* micronematous to semi-macronematous, mononematous, cylindrical., *Conidiogenous cells* monoblastic, terminal, integrated, pale brown. *Conidia* acrogenous, solitary, oval to ellipsoidal, broadly obtuse at apex, truncate at base, muriform, constricted at septa, brown to dark brown, 25–35 × 15–27 μm, the basal cell not observed.

Culture characteristics: Conidium germinated on PDA within 12 h at 25°C. Germ tubes produced from basal cell. Mycelia superficial, irregular, dry, rough, wrinkled, flat, grey from above. Dark brown in the central cycle and gray the outer circle from below.

Material examined: THAILAND, Chiang Rai City, Mae Chan District, Pa Tueng, on twigs of *Dendrobium nobile*, 16 January 2021, Y.R. Sun, CR07 (HGUP 24-0043); living culture MFLUCC 24-0288.

Notes: *Pleopunctum ellipsoideum* was descripted by Liu, Hyde et al. (2019) from the decaying wood in China. Subsequently, Jayawardena et al. (2022) reported it from

bamboo in Thailand and Xu et al. (2023) documented it from freshwater habitat in China. Our collection phylogenetically clustered together with the ex-type strain (MFLUCC 19-0390) of *P. ellipsoideum* (Figure 4.26). Our collection GUCC 24-0133 has smaller conidia (25–35 × 15–27 µm *vs*. 39–51 × 17–24 µm) than those of the holotype (MFLU 19-0685), and those 32–40 × 17–23 µm in Xu et al. (2023). ITS comparison shows there are only 2 bp differences between GUCC 24-0133 and MFLUCC 19-0390. Thus, we identify our strain as *P. ellipsoideum*, representing a new host record of *Dendrobium nobile.*



Note a Host. b, c Colonies on natural substrates. d, g–j Conidia. e, f Conidia with conidiogenous cells. k Germinated conidium. l, m Colonies on PDA media. n Mycelium. Scale bars: d, k, n = 20 µm, e–j = 10 µm

Figure 4.72 *Pleopunctum ellipsoideum* (HGUP 24-0043, new host record)

Phaeosphaeriaceae M.E. Barr, Mycologia 71(5): 948 (1979)

Leptospora Rabenh., Hedwigia 1: 116 (1857).

Notes: *Leptospora* was documented by Rabenhorst (1857) with *L. rubella* as the type species. Hyde et al. (2016) provided a reference specimen for *L. rubella*. Species of this genus have been frequently reported in recent years, mostly from terrestrial habitats (Zhang et al., 2019; Mapook et al., 2020; Phukhamsakda et al., 2020; Tennakoon et al., 2021). Currently, 16 species are accepted in this genus (Species Fungorum, 2024). In this study, we introduce a new species and a new host record from the medicinal plant, *Houttuynia cordata* and *Mentha canadensis*.

Leptospora houttuyniae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902598; Facesoffungi number: FoF 16436; Figure 4.73

Etymology: Referring to the host genus.

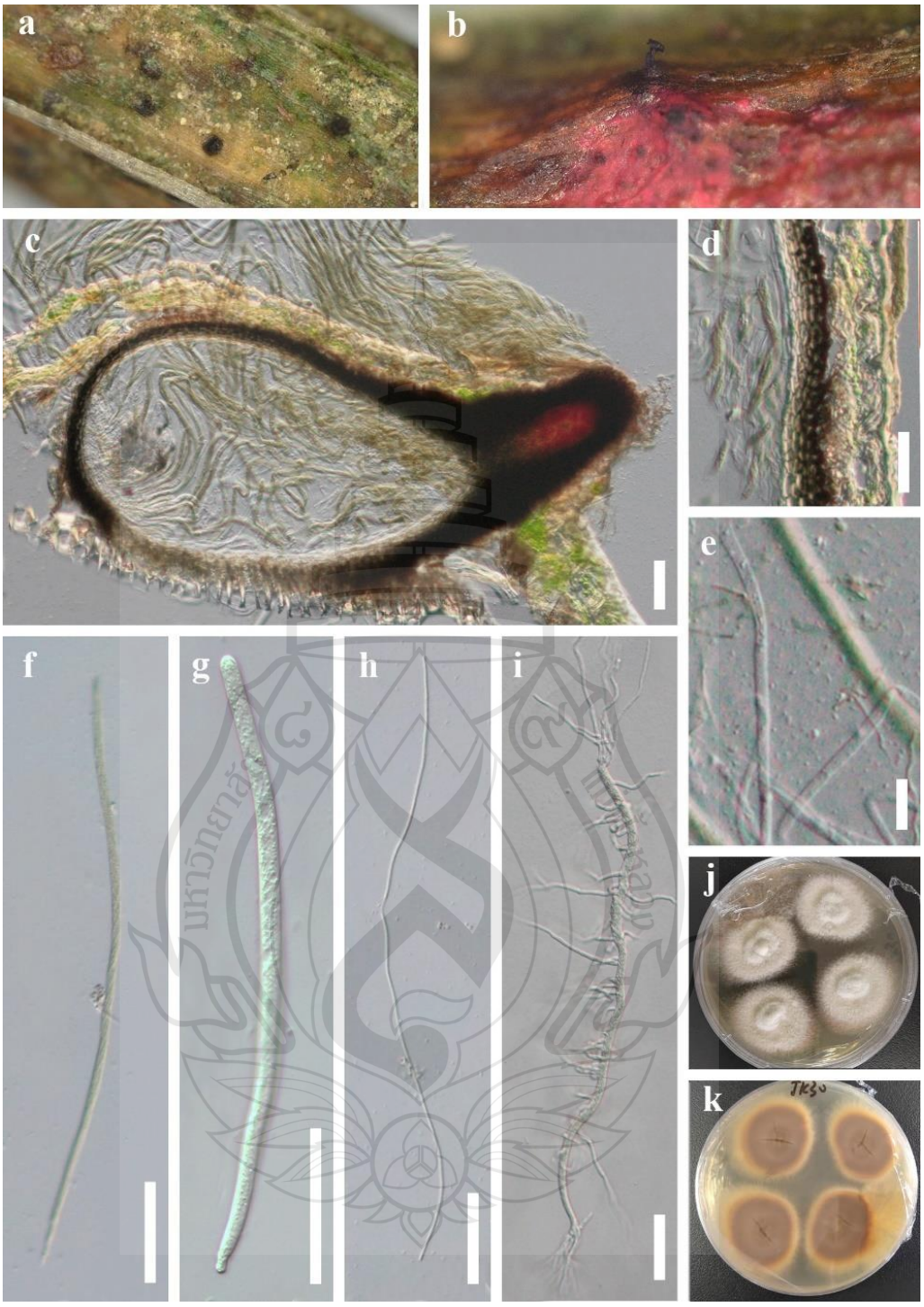
Holotype: HKAS 136897.

Saprobic on twig of *Houttuynia cordata*. **Sexual morph**: *Ascomata* solitary, immersed to semi-immersed, erumpent, subglobose, apapillate, ostiolate, around 500 µm high, 220 µm wide, visible as raised, black spots on host surface. *Ostiole* central, papillate, brown to dark brown, heavily pigmented at outer layer, smooth, red around pore. *Peridium* 15–30 µm wide, comprising sereval layers of pale brown to brown, inwardly lighter, thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, branched, cellular, hyaline, pseudoparaphyses. *Asci* 8-spored, bitunicate, long-cylindrical, short pedicellate, apex rounded, 180–350 × 5–7 µm. *Ascospores* 250–345 µm long, around 2 µm wide, arranged spirally in the ascus, filiform, straight or curved, initially hyaline becoming pale brown at maturity, ascospores are sometimes longer than asci. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated within 12h in PDA at 25 °C. Colonies on PDA reaching 40 mm diam. after 4 weeks at 25 °C, circular, dry, cotton, umbonate, white to cream from above, pale brown to brown from below.

Material examined: CHINA, Guizhou Province, Tongren City, Jiangkou district, on twigs of *Houttuynia cordata*, 20 May 2022, Y.R. Sun, JK30 (HKAS 136897, **holotype**); ex-type culture GUCC 24-0085.

N*o*tes: The morphological characters of *Leptospora houttuyniae* fit into the generic concept of *Leptospora* in having immersed to semi-immersed, subglobose ascomata, central papillae with red tips, long-cylindrical asci and filiform, hyaline to pale brown ascospore. The combined LSU, ITS, SSU and *TEF1-α* phylogenetic analyses show that our strain (JK30) sister to *L. rubella* (ML-bs = 92%, BYPP = 1; Figure 4.79). In morphology, our collection differs from *L. rubella* by its longer asci (180–350 µm *vs*. 100–150 µm) and longer ascospores (250–345 µm *vs*. 90–125µm) (Hyde et al., 2016). The base pair difference results of ITS showed that the two strains have 19 base pair differences (total 545 bp, without gap). Based on clear morphological differences and molecular data, here we introduce *Leptospora houttuyniae* as a noval species.



Note a, b Appearance of ascomata on host surface. c Vertical section through ascomata. d Peridium. e Pseudoparaphyses. f, g Asci. h Ascospore. i Germinated ascus. j Colony from above. k Colony from below. Scale bars: c, e = 20 μm, d, f–i = 50 μm.

Figure 4.73 *Leptospora houttuyniae* (HKAS 136897, holotype)

Leptospora hydei J.F. Zhang, J.K. Liu & Z.Y. Liu, Mycosphere 8(1): 213 (2019)

Index Fungorum number: IF 556264; Facesoffungi Number: FoF 05840; Figure 4.74

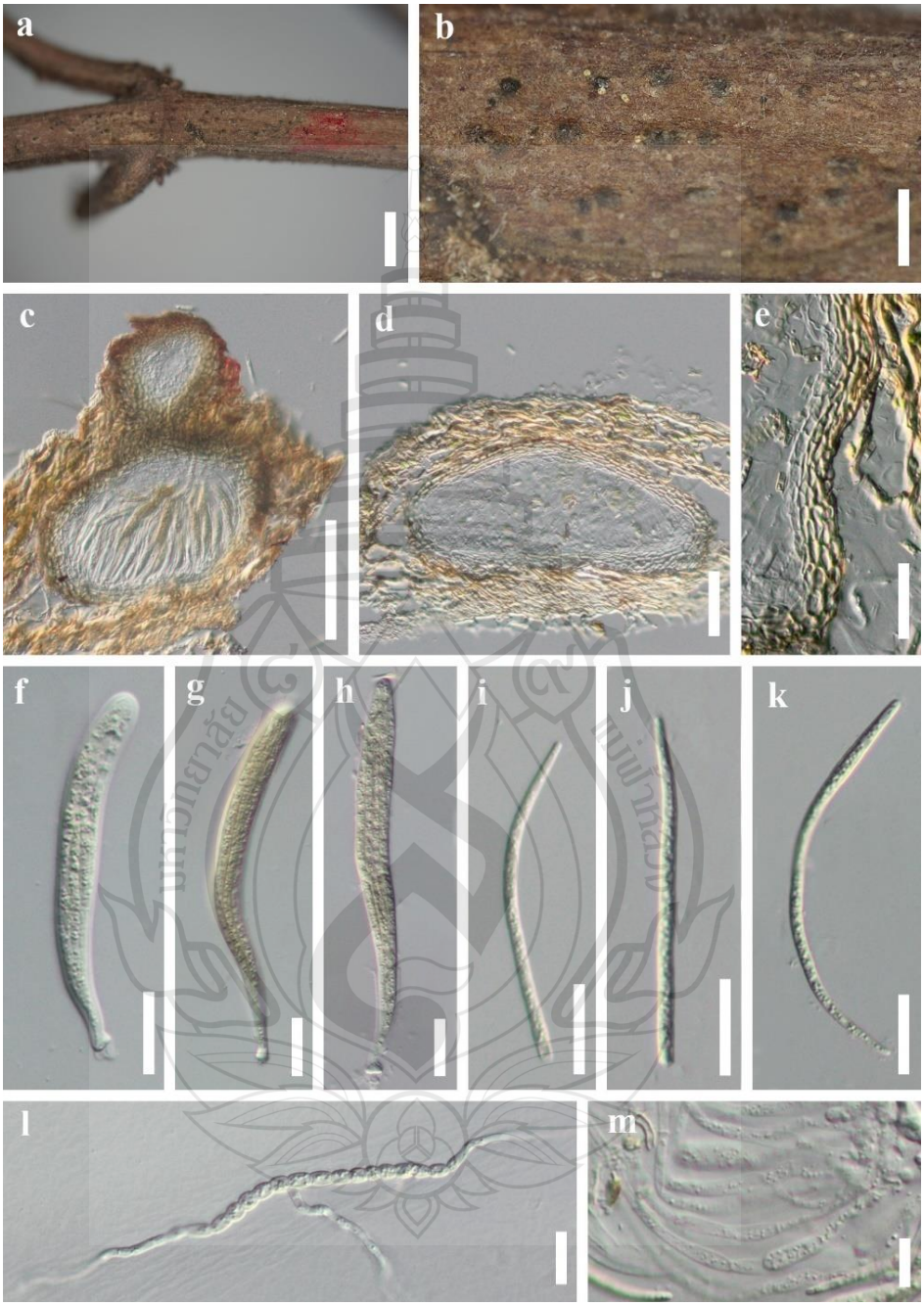
Saprobic on twigs of *Mentha canadensis*. **Sexual morph**: *Ascomata* 110–240 µm high, 180–270 µm diam, sime-immersed, solitary, scattered, globose to subglobose, black spots appear on the host surface, ostiolate. *Ostiole* central, papillate, cylindrical, truncate at the apex, brown. *Peridium* 10–25 µm wide, coriaceous, composed of several layers of thick-walled, hyaline to brown, pseudoparenchymatous cells, arrange in a *textura angularis* to *prismatica*, often surrounded by plant tissue. *Hamathecium* comprising 1.5–4 µm wide, numerous, filamentous, hyaline, trabeculate pseudoparaphyses anastomosing above and between the asci. *Asci* 100–154 × 9–12 µm ($\bar{x}$ = 125 × 10 µm, n = 15), 8-spored, bitunicate, cylindrical to cylindrical-clavate, with short pedicel, slightly curved, apically rounded to truncate with a minute ocular chamber. *Ascospores* 77–156 × 3–4 µm ($\bar{x}$ = 97 × 3.5 µm, n = 20), fasciculate, multiseriate, scolecosporous, filiform, tapering towards the ends, minute guttules in each cell, hyaline when young, and become pale brown at maturation, with inconspicuous glial sheath at the end. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated within 12h in PDA at 25 °C. Germ tubes produced from both ends. Colonies on PDA reaching 40 mm diam. after 4 weeks, medium dense, irregular, having a knobby protuberance, greyish-green from above, pale brown to olive from below.

Material examined: CHINA, Guizhou Province, Tongren City, Jiangkou district, on twigs of *Mentha canadensis*, 20 May 2022, Y.R. Sun, JK41 (HKAS 136898), living culture GUCC 24-0086.

Notes: *Leptospora hydei* was isolated from decaying branch in Guiyang City, China (Zhang et al., 2019). Our collection HKAS 136898 was recovered from twigs of *Mentha canadensis* in Tongren City, China. The new isolate clusters with the ex-type strain *L. hydei* (GZCC 19-0004) with strong bootstrap support (100% ML/1.00 BYPP) (Figure 4.79). The ITS and LSU base pair difference between the new isolate and GZCC 19-0004 are 1 (516 bp, without gap) and 0 (822 bp), respectively. Therefore, we introduced our strain as *L. hydei,*

representing a new host record from *Mentha canadensis*.



Note a, b Appearance of ascomata on host surface. c, d Vertical section through ascomata. e Peridium. f–h Asci. i–k Ascospores. l Germinated ascospore. m Pseudoparaphyses. Scale bars: a = 2000 µm, b = 500 µm, c = 100 µm, d, e = 50 µm, f–l = 20 µm, m = 10 µm.

Figure 4.74 *Leptospora hydei* (HKAS 136898, new host record)

Murichromolaenicola Mapook & K.D. Hyde, in Mapook et al., Fungal Diversity 101: 71 (2020).

Notes: *Murichromolaenicola* was proposed by Mapook et al. (2020) to accommodate two *Murichromolaenicola* species from Thailand. Htet , Tibpromma et al. (2023) subsequently documented the third *Murichromolaenicola* species, discovered on *Chromolaena odorata* in Thailand. Presently, all three recognized *Murichromolaenicola* species have been found in *Chromolaena odorata* in Thailand. In this study, we present a new collection obtained from the medicinal plant *Dendrobium* sp.

Murichromolaenicola dendrobii Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16437; Figure 4.75

Etymology: Referring to the host genus.

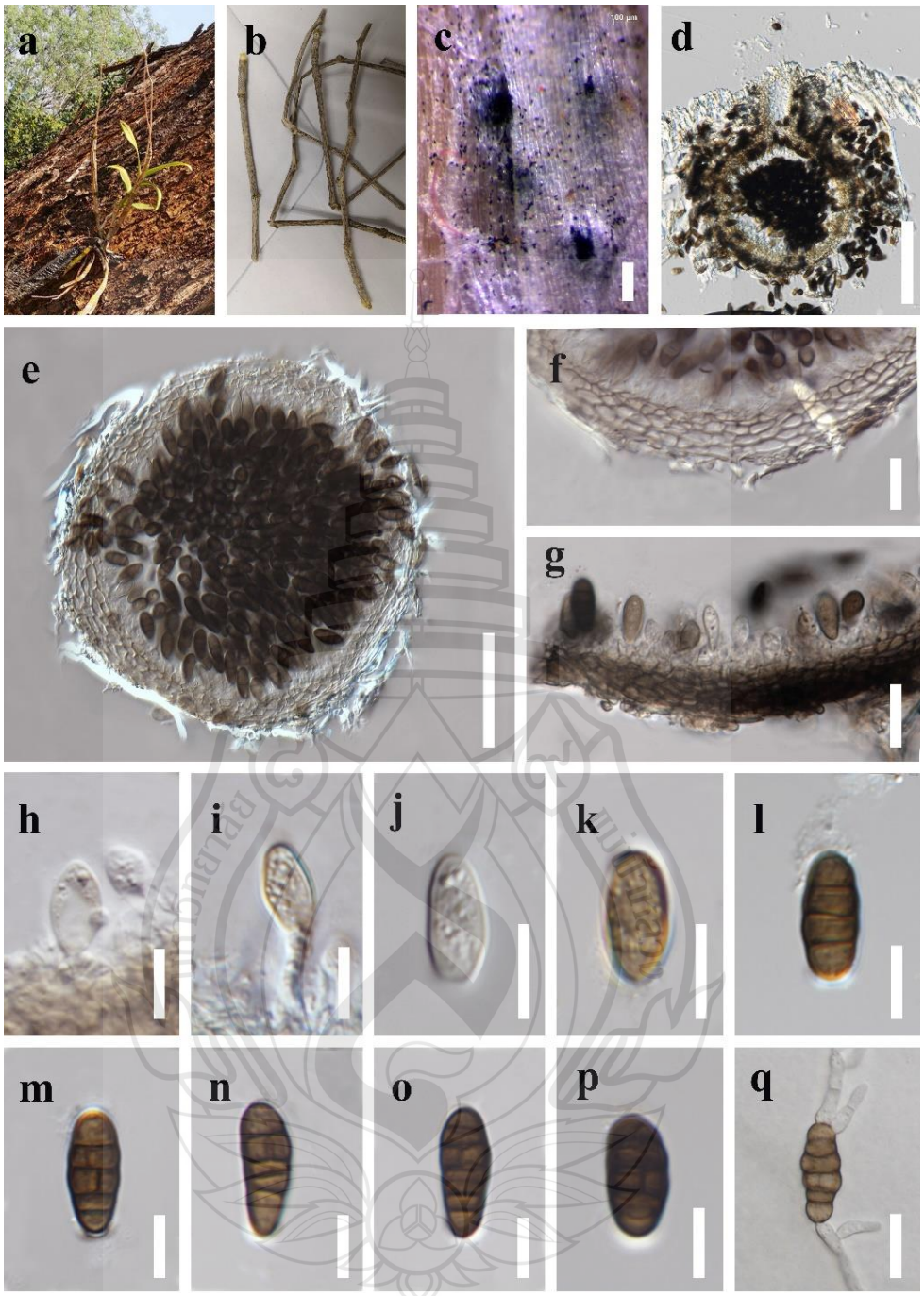
Holotype: HGUP 24-0044.

Associated with diseased twigs of *Dendrobium* sp. **Asexual morph**: *Conidiomata* 193–252 high, 172–241 µm wide, pycnidial, solitary, semi-immersed, unilocular, globose to subglobose, brown to black, with small papillate. *Ostiole* central., *Peridium* 13–23 µm wide, comprised of two layers cells arranged in textura angularis, the outer lay pale brown, the inner lay hyaline to pale brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–4 µm wide, enteroblastic, phialidic, hyaline, globose to subglobose. *Conidia* 16–22 × 6–9 µm ($\bar{x}$ = 19 × 8, n = 25), hyaline to brown when young, dark brown at maturity, oval or obovoid, round at both ends, 3–5 transverse with one longitudinal septum, some slightly constricted at the septa, with gelatinous appendages. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinating on PDA, colonies circular, entire, concentric, flat, opaque, white from above, pale yellow at the reverse.

Material examined: THAILAND, Nan Province, Song Khwae district, on twigs of *Dendrobium* sp., 14 January 2020, Y.R. Sun, NFshihu (HGUP 24-0044, **holotype**); ex-type culture MFLUCC 24-0289.

Notes: In the phylogenetic tree, our new collection from *Dendrobium* sp. forms a distinct clade in *Murichromolaenicola s. str* (Figure 4.79). Morphologically, it resembles *M. chromolaenae* and *M. thailandensis* but can be distinct from *M. chromolaenae* by its oval or obovoid, dark brown conidia with 3–5 transverse septa. *Murichromolaenicola dendrobii* differs from *M. thailandensis* in that it produces larger conidiomata (193–252 × 172–241 μm *vs*. 130–150 × 140–160 μm) (Htet, Tibpromma et al., 2023). Therefore, we introduce our new collection as a novel taxon of *Murichromolaenicola*, i.e. *M. dendrobii*.



Note a, b. Host. c, d. Conidiomata on the substrate. e. Vertical section through conidioma. f. Section through pycnidial wall. g–i. Conidiogenous cells with conidia. j–p. Conidia. q. Germinated conidium. Scale bars: c = 200 µm, d = 100 µm, e = 50 µm, f, g, q = 20 µm, h–p = 10 µm.

Figure 4.75 *Murichromolaenicola dendrobii* (HGUP 24-0044, holotype)

Phaeosphaeria I. Miyake, Bot. Mag., Tokyo 23: 93 (1909).

Notes: *Phaeosphaeria oryzae* is the type species of *Phaeosphaeria*, whose members are distributed across various terrestrial and aquatic environments worldwide, inhabiting a range of hosts (Quaedvlieg et al., 2013; Marin-Felix et al., 2019; Phookamsak et al., 2019; Hyde, Dong et al., 2020; Magaña-Dueñas et al., 2021; Wanasinghe & Maharachchikumbura, 2023). Some *Phaeosphaeria* species play critical roles as saprobes, contributing to essential processes like decomposition and nutrient cycling (Liu et al., 2015; Hyde, Norphanphoun et al., 2017). Some members are recognized as plant pathogens, capable of causing diseases in multiple hosts, leading to economic losses (Stukenbrock et al., 2006; Crous et al., 2021).

Recent phylogenetic analyses have revealed that *Phaeosphaeria* is polyphyletic, leading to the reassigned of many species into different genera within Phaeosphaeriaceae, such as *Amarenomyces*, *Loratospora*, *Neosetophoma*, *Paraloratospora*, *Pseudophaeosphaeria*, and *Septoriella* (Quaedvlieg et al., 2013; Phookamsak et al., 2014; Hongsanan et al., 2020a; Wanasinghe & Maharachchikumbura, 2023). In this study, we observed that two newly isolated strains showed high similarity to *Phaeosphaeria* strains based on BLAST similarity indices from GenBank. These findings provide data to better understand the relationships within *Phaeosphaeria*. Based on morphological and molecular data, we provide detailed descriptions of these two new species. Additionally, we have transferred *Didymocyrtis brachylaenae*, *D. pini* and *D. septate* to *Phaeosphaeria* and regarded them as novel combinations.

Phaeosphaeria boehmeriae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902596; Facesoffungi number: FoF 16438; Figure 4.76

Etymology: Referring to the host genus.

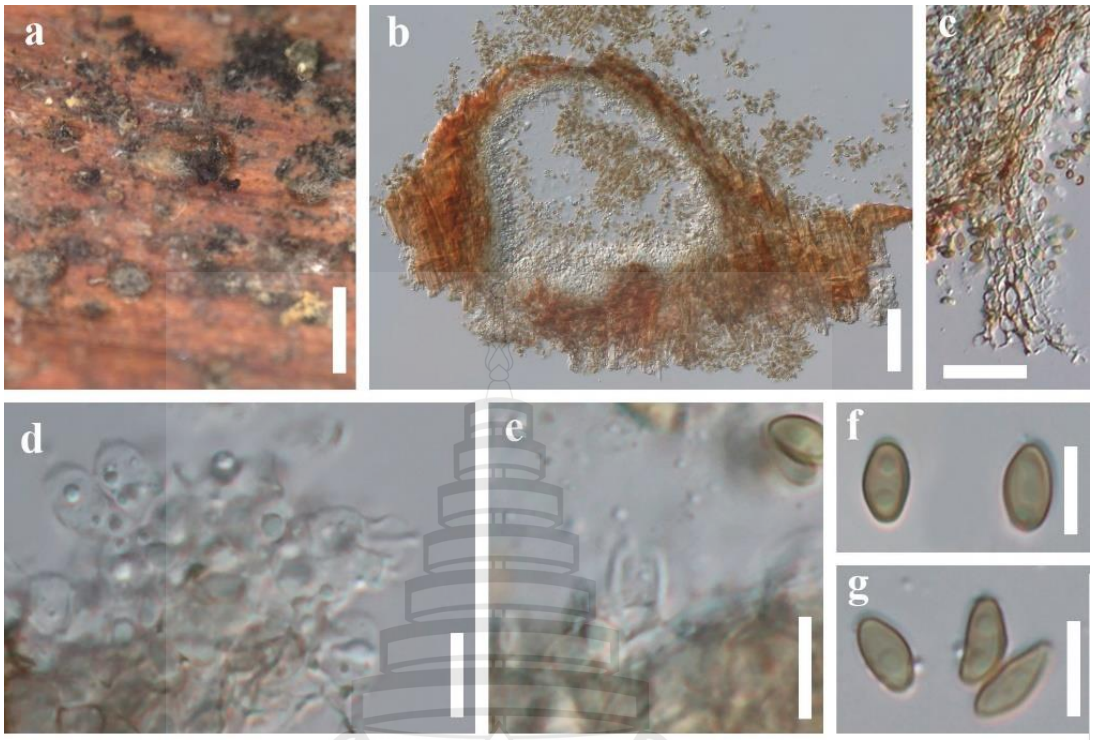
Holotype: HKAS 136896.

Saprobic on twigs of *Boehmeria* sp. **Asexual morph**: *Conidiomata* 110–185 × 110–190 μm diam, scattered, semi-immersed to immersed, globose or ellipsoidal, black, with central ostiole. *Conidiomata wall* 10–40 μm thick, composing two layers of irregular cells arranged in a textura angularis, the outer layer with brown flattened cells, the inner layer comprising hyaline cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* producing from the

inner layer, cylindrical, hyaline, 2–3 µm wide. *Conidia* 3.5–5 × 1.5–2.5 µm, ($\bar{x}$ = 4.5 × 2 µm, n = 30), fusoid or ellipsoidal, straight or slightly curved, brown, aseptate, apex subobtuse, smooth walled, guttulate. **Sexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Tongren City, Jiangkou district, on twigs of *Boehmeria* sp., 20 May 2022, Y.R. Sun, JK36 (HKAS 136896, **holotype**); ex-type culture GUCC 24-0083.

Notes: Our two isolates *Phaeosphaeria boehmeriae* and *P. guiyangensis* grouped with *P. brachylaenae* (CPC 32651), and they formed a top clade in *Phaeosphaeria* (Figure 4.79.). In morphology, *P. boehmeriae* differs from *P. brachylaenae* and *P. guiyangensis* by its aseptate and smaller conidia (3.5–5 × 1.5–2.5 µm *vs*. 9–10 × (2–)3 µm *vs*. 5–10 × 2.5–4 µm) (Crous et al., 2018). In addition, the base pair difference results of the ITS gene region showed 30 bp (550 bp, without gap) differences between *P. boehmeriae* and *P. brachylaenae*, and 23 bp (542 bp, without gap) differences between *P. guiyangensis*. Therefore, we introduced *P. boehmeriae* sp. nov. herein.



Note a Appearance of conidiomata on the host surface. b Section through conidiomata. c Pycnidial wall. d, e Conidiogenous cells. f, g Conidia. Scale bars: a = 500 μm, b, c = 20 μm, d–g = 5 μm.

Figure 4.76 *Phaeosphaeria boehmeriae* (HKAS 136896, holotype)

Phaeosphaeria brachylaenae (Crous) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov.***

Facesoffungi number: FoF 16439.

≡ *Didymocyrtis brachylaenae* Crous Persoonia 40: 381 (2018); Index Fungorum number: IF 825436; Holotype CBS H-23565

Notes: Crous et al. (2018) introduced *Didymocyrtis brachylaenae.* They mentioned that the sequences of *D. brachylaenae* have high similar with species of both *Didymocyrtis* and *Phaeosphaeria*. However, in their phylogenetic analysis, they did not include all species of *Didymocyrtis* and *Phaeosphaeria* for analysis, but rather only those species with high sequence homology from the NCBI database. Additionally, some sequences in the

NCBI database are not linked to their type specimens, which raises doubts about certain sequences. For instance, Crous et al. (2018) selected the sequence of *D. cladoniicola* (UTHSC DI16-330) for their phylogenetic analysis, but this sequence was provided without any description and illustration (Valenzuela-Lopez et al., 2017). Moreover, this strain did not cluster with other strains of *D. cladoniicola*. We believe that the sequence of this strain is unreliable and needs further verification. These issues have led to the misidentification of *D. brachylaenae* and later newly discovered species. Our phylogenetic analysis includes all genera of Phaeosphaeriaceae and most species of *Didymocyrtis* and *Phaeosphaeria*. In our analysis (Figure 4.79), three *Didymocyrtis* species, *viz., D. brachylaenae*, *D. pini* and *D. septata* clustered together with *Phaeosphaeria*, and their morphology also match the morphological characteristics of *Phaeosphaeria.* Based on these findings, it was determined that a reclassification of these three species within the genus *Phaeosphaeria* was warranted. Therefore, we propose new combinations *P. brachylaenae* comb. nov., *P. pini* comb. nov. and *P. septata* comb. nov. for *D. brachylaenae, D. pini* and *D. septata,* respectively.

Phaeosphaeria guiyangensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902597; Facesoffungi number: FoF 16440; Figure 4.77

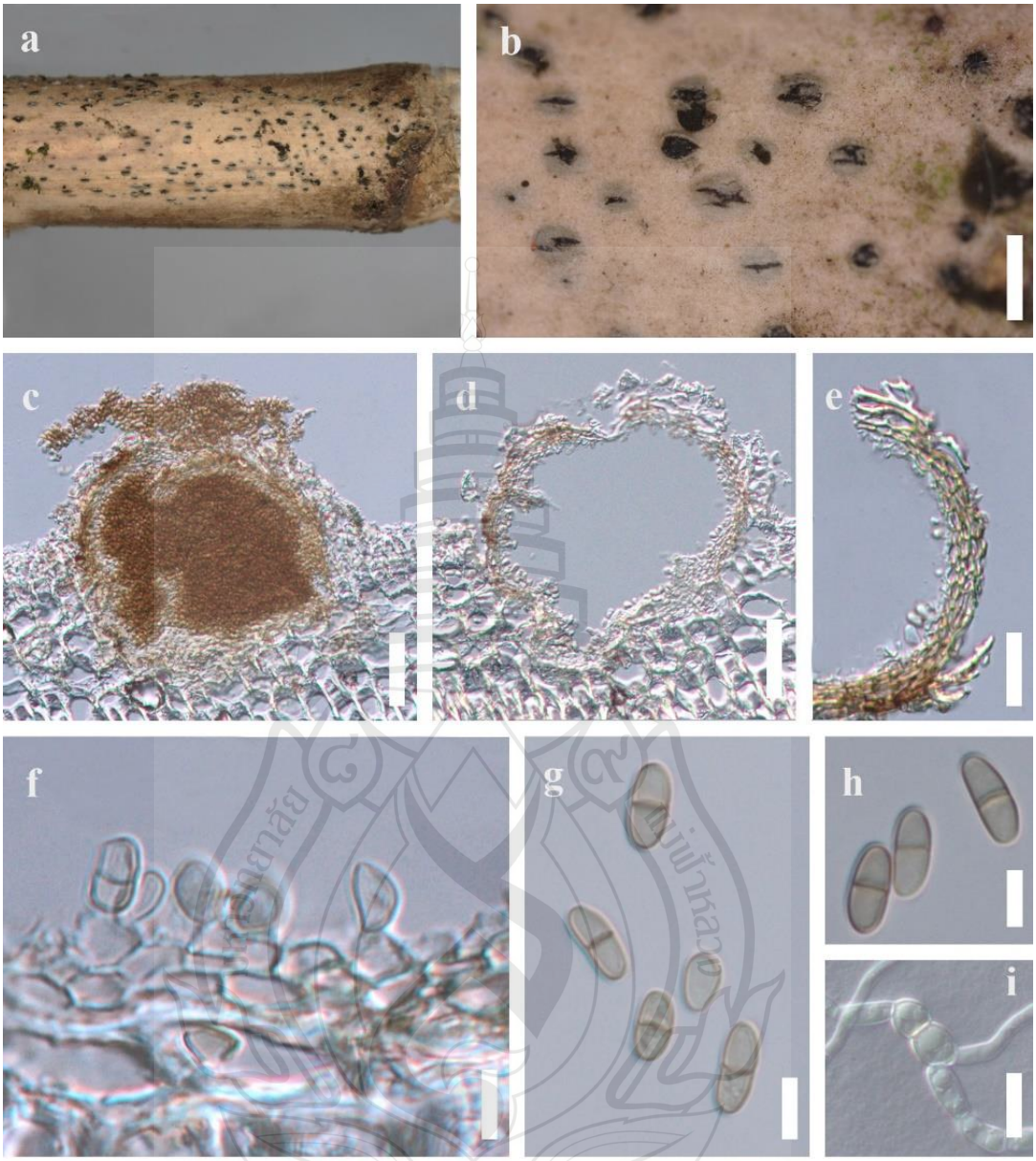
Etymology: Referring to the Guiyang City where the specimen was collected.

Holotype: HKAS 136876

Saprobic on dry bamboo culms. **Asexual morph**: *Conidiomata* 156–190 × 147–170 μm diam, scattered, semi-immersed, globose or ellipsoidal, black, with central ostiole. *Peridium* 8–15 μm thick, composing two layers of irregular cells arranged in a textura angularis, the outer layer with light brown to brown flattened cells, the inner layer comprising hyaline cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* producing from the inner layer, ampulliform to doliiform, hyaline, around 2 μm wide. *Conidia* ellipsoidal, 1-septate, apex and base subobtuse, pale to medium brown, smooth, 5–10 × 2.5–4 μm, ($\bar{x}$ = 7 × 3 μm, n = 40). **Sexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Huaxi district, on bamboo culms, 26 January 2022, Y.R. Sun, 22-59 (HKAS 136876, **holotype**), ex-type culture GUCC 24-0084.

Notes: *Phaeosphaeria guiyangensis* and *P. boehmeriae* were separated by *P. brachylaenae* in the phylogenetic tree (Figure 4.79). See the notes of *Phaeosphaeria boehmeriae* to differentiate *P. guiyangensis* and *Phaeosphaeria boehmeriae* (this study). *Phaeosphaeria guiyangensis* is morphologically differs from *P. brachylaenae* by its smaller conidiomata (156–190 × 147–170 μm *vs*. 200–350 μm) (Crous et al., 2018). Besides, *P. guiyangensis* has ellipsoidal, 1-septate, apex and base subobtuse conidia while *P. brachylaenae* process fusoid-ellipsoid to subcylindrical, 1(–3)-septate, apex subobtuse, base truncate conidia. The base pair difference results of these two strains showed that there are 11 bp (555 bp, without gap) differences in the ITS gene and 16 bp (360 bp, without gap) differences in the TUB gene. Based on morphology and molecular analyses, we introduced *Phaeosphaeria guiyangensis* as a novel species.



Note a, b Appearance of conidiomata on the host surface. c, d Vertical sections through conidiomata. e Pycnidial wall. f Conidiogenous cells and young conidia attached to the cells. g, h Conidia. i Germinating conidium. Scale bars: b = 500 μm, c, d = 50 μm, e = 20 μm, f–i = 5 μm.

Figure 4.77 *Phaeosphaeria guiyangensis* (HKAS 136876, holotype)

Phaeosphaeria pini (P. Monteiro & M. Gonçalves) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov.***; Facesoffungi number: FoF 16441.

≡ *Didymocyrtis pini* P. Monteiro & M. Gonçalves, Eur. J. Pl. Path.12 (2021); Index Fungorum number: IF 840198

Notes: Monteiro et al. (2021) introduced *Didymocyrtis pini* based on its morphology and phylogenetic analysis. The species is associated with diseased *Pinus radiata* needles and is characterized by brown to black, globose conidiomata, ampulliform, hyaline conidiogenous cells and fusiform, 1-septate, olivaceous conidia (Monteiro et al., 2021). In our phylogenetic analysis, *D. pini* accommodated in *Phaeosphaeria s. str.* Hence, we transfer *D. pini* to *Phaeosphaeria* as *P. pini*.

Phaeosphaeria septata (K. Das, S.Y. Lee & H.Y. Jung) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov***., Facesoffungi number: FoF 16442.

≡ *Didymocyrtis septata* K. Das, S.Y. Lee & H.Y. Jung, Mycobiology 49(1): 16 (2020); Index Fungorum number: IF 835967

Notes: *Didymocyrtis septata* was introduced by Das et al. (2021), which was isolated from the soil in Korea. It has dark brown to black, pycnidial conidiomata, globose to subglobose, or ampulliform to doliiform, hyaline conidiogenous cells and clavate to subcylindrical, 1-septate, greenish to light yellowish conidia (Das et al., 2021). In our phylogenetic analysis, *D. septata* is sister to *Phaeosphaeria sichuanensis* (KUNCC 23-13569) with high support (ML-bs = 92%, BYPP = 1). In morphology, *D. septata* process clavate to subcylindrical, 1-septate, greenish to light yellowish conidia while *P. sichuanensis* has ovoid to ellipsoid, pale brown to brown and 1-2 septate conidia. Therefore, we propose the transfer of *D. septata* to the genus *Phaeosphaeria*, and subsequently it should be recognized as *P. septata*, comb. nov.

Phaeosphaeriopsis M.P.S. Câmara, M.E. Palm & A.W. Ramaley, Mycol. Res. 107(5): 519 (2003)

Notes: *Phaeosphaeriopsis* was introduced by Câmara et al. (2003) with *P. glaucopunctata* as its type species. *Phaeosphaeriopsis* species are ubiquitously distributed, acting as both pathogens and saprobes within the plant families Amaryllidaceae, Asparagaceae, and Proteaceae worldwide (Câmara et al., 2003; Crous, Wingfield, Burgess et al., 2016; Crous, Wingfield, Richardson et al., 2016, Crous et al., 2021; Tibpromma et al., 2017). It is worth noting that a total of 17 species are accepted in *Phaeosphaeriopsis*, 15 of which are related to Asparagaceae plants (Tibpromma et al., 2017; Marin-Felix et al., 2019; Hyde, Dong et al., 2020; Species Fungorum, 2024). The strong association with Asparagaceae plants suggests a high degree of host specificity within *Phaeosphaeriopsis*. Understanding the reasons behind this specificity could provide insights into the ecological and evolutionary relationships between the *Phaeosphaeriopsis* species and their host plants.

Phaeosphaeriopsis oblongispora Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902611; Facesoffungi number: FoF 16443; Figure 4.78

Etymology: Referring to the oblong ascospores.

Holotype: HKAS 136903.

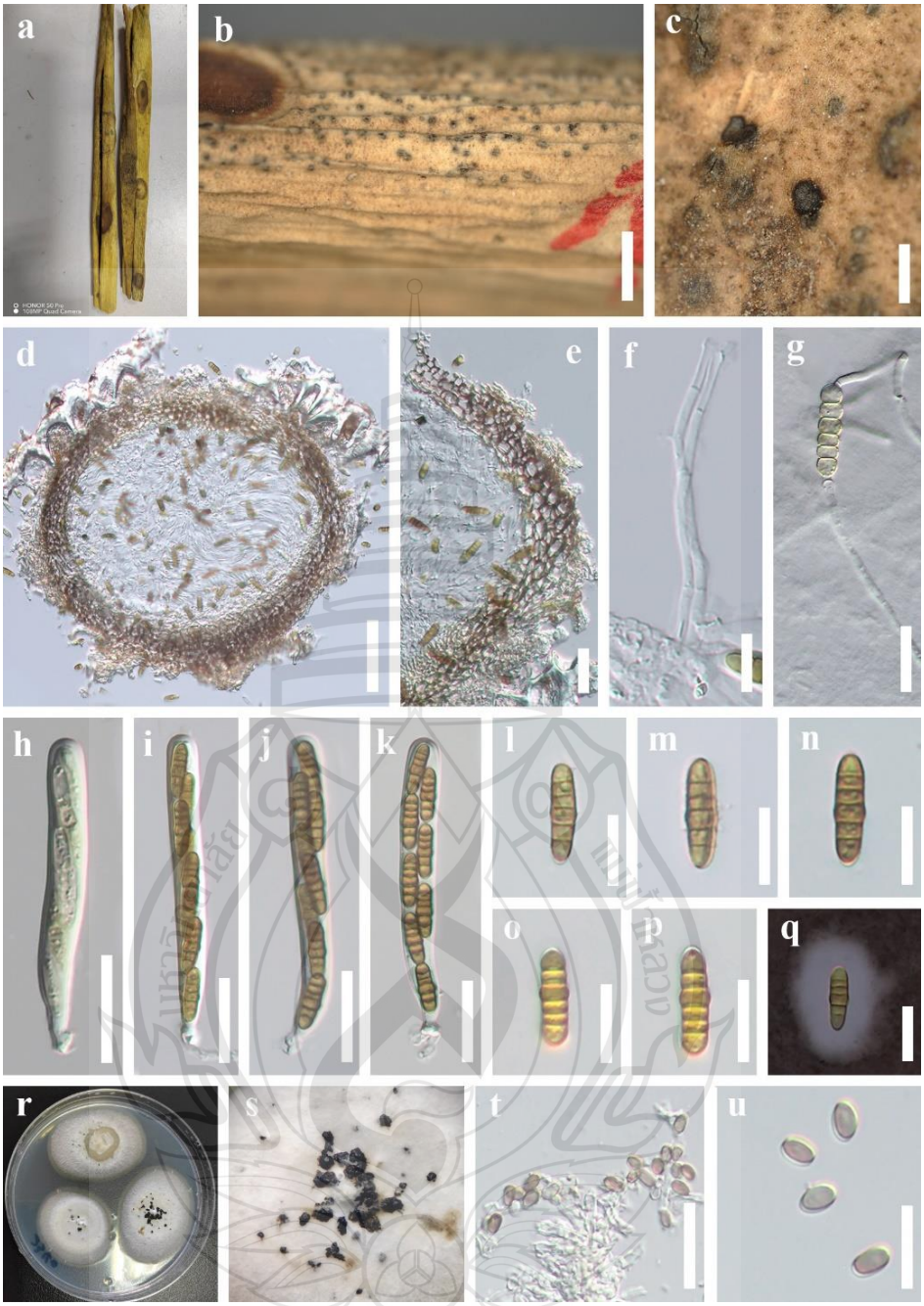
Associated with leaf spot of *Spineless yucca* (Asparagaceae). **Sexual morph:** *Ascomata* 190–210 μm high, 215–250 μm wide, scattered to clustered, gregarious, slightly raised to erumpent, visible as black dots on the host surface, immersed, globose to subglobose, uni-loculate, glabrous, ostiole central, with minute papilla. *Peridium* 16–40 μm wide, fused with host tissues, comprising two layers of pale to brown cells of *textura angularis*. *Hamathecium* 1–2 μm wide, composed of numerous, septate, filamentous, anastomosed pseudoparaphyses, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to subcylindric-clavate, subsessile to short pedicellate, blunt to rounded apex, 70–90 ×7–10 μm ($\bar{x}$ = 90 × 10 μm, n = 10). *Ascospores* 10–15 × 2.5–4 μm ($\bar{x}$ = 14 × 3.5 μm, n = 35), overlapping 1–2-seriate, oblong to subcylindrical, golden brown, 5-septate, enlarged at the 4th cell from above, verruculose, surrounded by a distinct mucilaginous sheath. **Asexual morph**: Coelomycetous morph from the culture.

Conidiomata solitary, globose, black. *Conidiophores* reduced to conidiogenous cells. *Conidia* 3.5–6 × 2–3.5 µm ($\bar{x}$ = 5 × 3 µm, n = 25), solitary, hyaline to pale brown when young, brown at maturity, aseptate, ellipsoidal to oblong, apex obtuse, base bluntly rounded.

Culture characteristics: Ascospores germinated on PDA within 12 h at 25 °C. Germ tubes produced from both ends. Colonies on PDA reached 4 cm diam. after 3 weeks at 25 °C; mycelium white, flat, circular, with the entire edge; white to pale brown in reverse.

Material examined: CHINA, Yunnan Province, Kunming City, Yiliang District, Yangzonghai Garden, on leaves of *Yucca gigantea* (Asparagaceae), 20 February 2023, H.W. Shen, 2340 (HKAS 136903, **holotype**); ex-type culture GUCC 24-0087.

Notes: Our strain formed a sister clade to *Phaeosphaeriopsis pseudoagavacearum* in the phylogenetic analyses (Figure 4.79). *Phaeosphaeriopsis pseudoagavacearum* was initially characterized based on its asexual morph, isolated from agaves in France (Marin-Felix et al., 2019). Hyde, Dong et al. (2020) later reported its sexual morph through a new collection obtained from *Yucca gloriosa* in Italy. Our collection can be distinguished by its smaller asci (70–90 ×7–10 µm vs. (85–)90–110(–119) × (9–)10–12(–14) µm) and smaller spores (10–15 × 2.5–4 µm *vs*. (18–)20–23(–2 5) × (4.5–)5–6.5 µm) (Marin-Felix et al., 2019). Furthermore, the former produced ellipsoidal to oblong, aseptate, conidia, measuring 3.5–6 × 2–3.5 µm while the latter produced subcylindrical, 1-septate conidia measuring (6–) 8–9(–10) × 4(–4.5) µm. Consequently, we identified our strain as a new species isolated from *Spineless yucca* in China.



Note a Host. b, c Appearance of ascomata on host surface. d Vertical section through ascoma. e Peridium. f Pseudoparaphyses. g Germinated ascospore. h–k Asci. l–q Ascospores (q Ascospore in the Indian Ink). r Colonies on PDA. s Close-up view of conidiomata. t Conidia and conidiogenous cells. u Conidia. Scale bars: b = 2000 µm, c = 500 µm, c = 100 µm, d = 50 µm, e, g–k, t = 20 µm, f, l–q, u = 10 µm.

Figure 4.78 *Phaeosphaeriopsis oblongispora* (HKAS 136903, holotype)

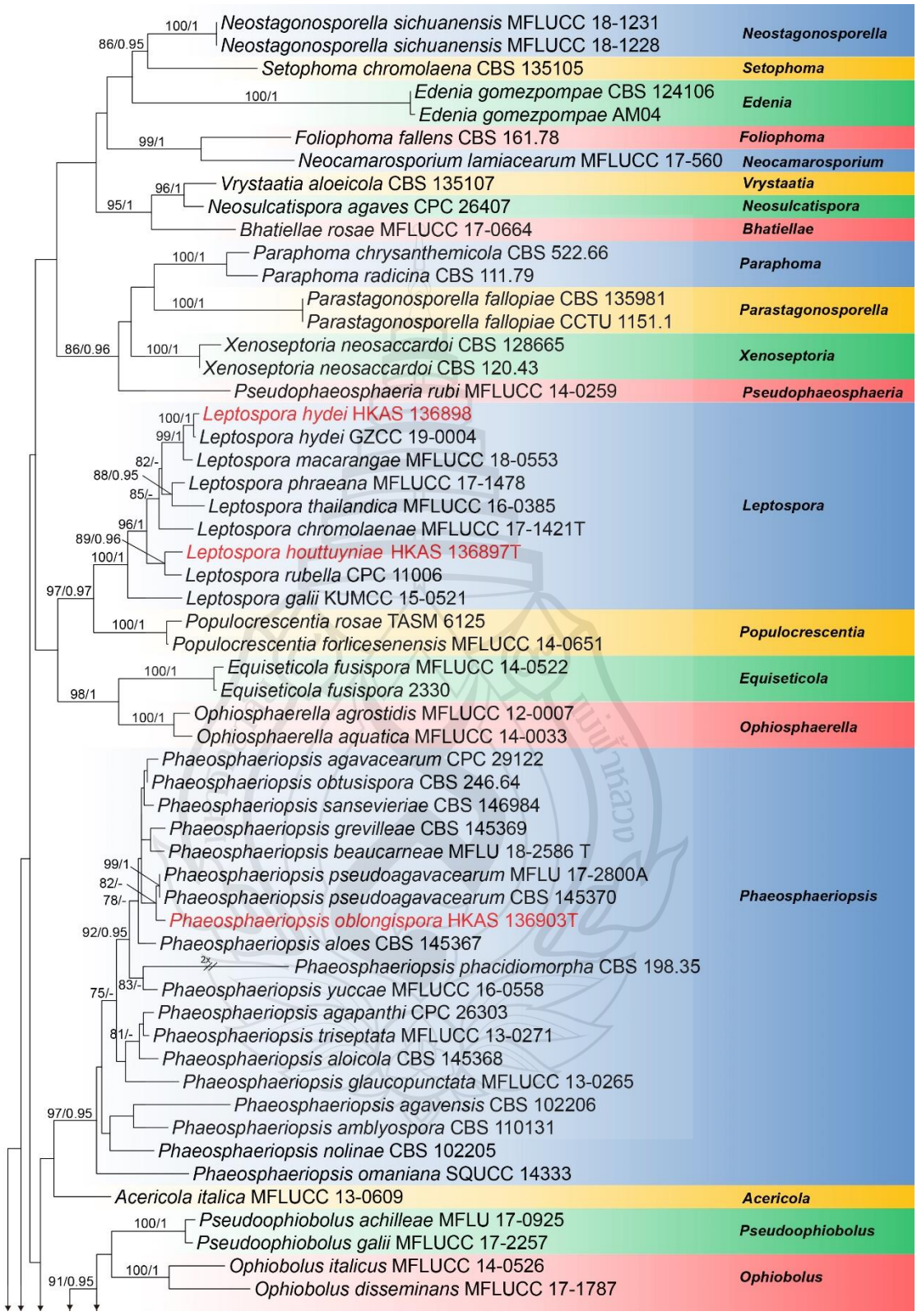
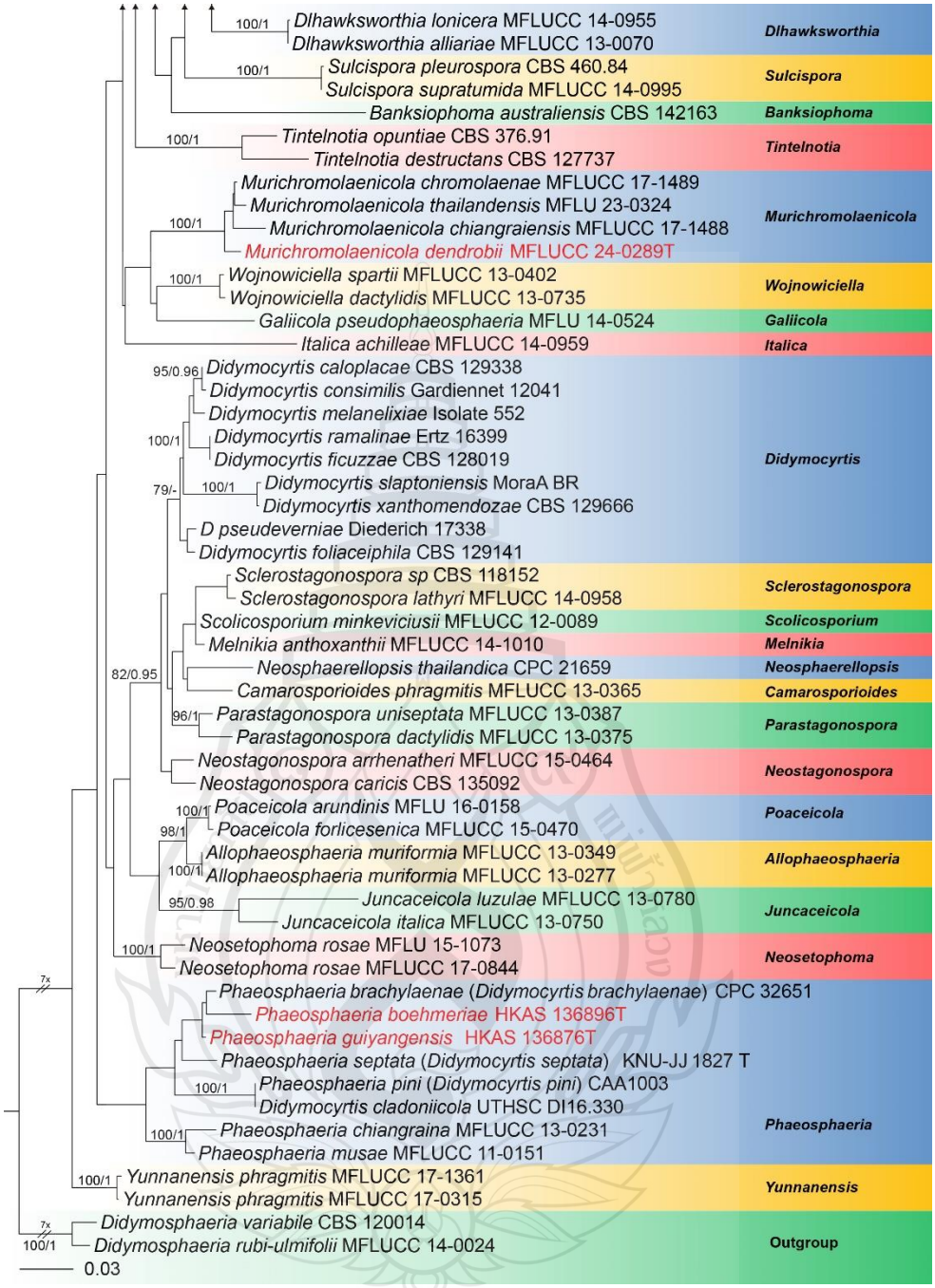


Figure 4.79 Phylogenetic tree of Phaeosphaeriaceae



Note The tree is rooted with *Didmosphaeria rubi-ulmifolii* (MFLUCC 14-0024) and *D. variable* (CBS 120014). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.79 (continued)

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

Parabambusicola Kaz. Tanaka & K. Hiray

Parabambusicola, as introduced by Tanaka et al. (2015), was based on morphological and molecular analyses. This genus comprises only four species: three isolated from Poaceae plants in terrestrial habitats and one from decaying wood in freshwater (Tanaka et al., 2015; Phookamsak et al., 2019; Dong et al., 2020; Xie et al., 2022b).

Parabambusicola yunnanensis L.S. Han & D.Q. Dai, Phytotaxa 589(3): 250 (2023)

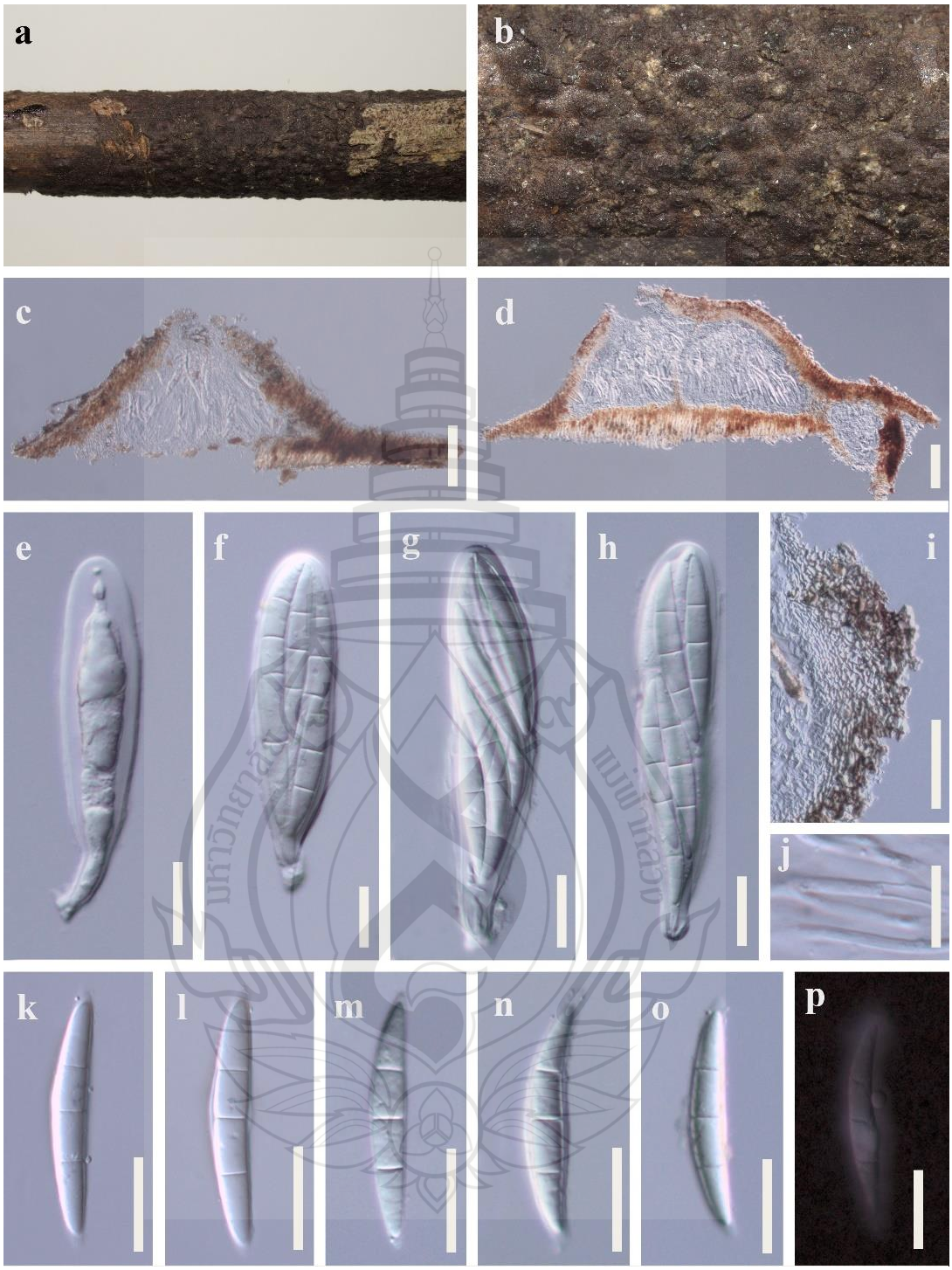
Index Fungorum number: IF559989; Facesoffungi number: FoF 12952, Figure 4.80

Saprobic on submerged decayed stems of bamboo in freshwater habitats, appearing as raised, dome-shaped areas on the host surface. **Sexual morph**: *Ascomata* 175–260 µm high, 375–675 µm wide, immersed, subglobose, mostly clustered together, sometimes solitary. Peridium 25–60 µm wide, thick, 2-layered; outer layer consisting of thickwalled, multi-rows of brown, polyhedral cells of *textura angularis*, inner layer comprising multi-rows of pale brown to hyaline, elongated cells of *textura angularis* or *taxtura prismatica*. *Hamathecium* composed of numerous, filamentous, 1–2.5 µm wide, septate pseudoparaphyses. *Asci* 85–130 × 18–24 µm ($\bar{x}$ = 108 × 21 µm, n = 25), broadly cylindrical to cylindric-clavate, 8-spored, hyaline, bitunicate, subsessile, rounded at the apex, with clearly visible inconspicuous ocular chamber when young. *Ascospores* 45.5–57 × 6–8.5 µm ($\bar{x}$ = 51 × 7.5 µm, n = 25), overlapping 2–3-seriate, hyaline, fusiform to vermiform, slightly curved, narrower towards the lower cell, 3–(4)-septate, primary septum mostly median, smooth-walled, with sheath. **Asexual morph**: Not observed.

Culture characteristics: *Colonies* on PDA reaching 35 mm diam. after 4 weeks at 25 °C. Colony dense, circular, flattened, surface smooth, with entire edge, velvety to floccose; from above greenish grey to dark green, paler at the edge; from below, black; produced dark brown pigmentation around colony on agar medium.

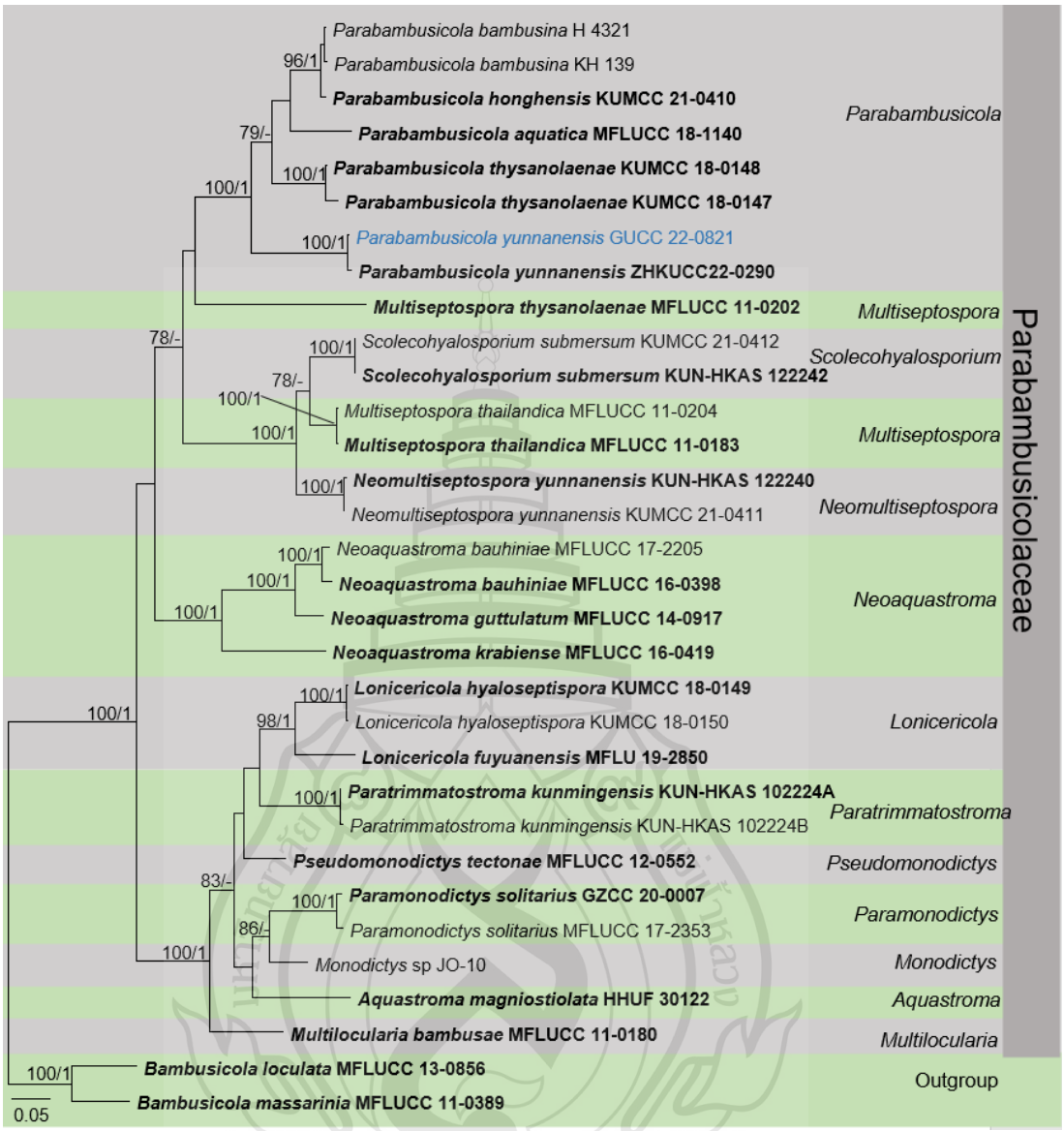
Material examined: China, Guizhou Province, Guiyang City, Changpoling Forest Park, on submerged decayed stems of bamboo in fresh water stream, 20 August 2021, Y.R. Sun, CL19 (HGUP 22-0810), living culture GUCC 22-0821.

Notes*: Parabambusicola yunnanensis* was introduced by Han et al. (2023) from dead culm of bamboo in terrestrial habitats. Phylogenetically, our isolate GUCC 22-0821 clusters together with *P. yunnanensis* ZHKUCC22-0290 by high support (100% ML and 1.00 BYPP; Figure 4.81). Morphologically, GUCC 22-0821 shares similar ascomatal and sporous characters with ZHKUCC22-0290 but shorter asci (85–130 µm *vs*. 130–180 µm). This may be caused by the different habitats. In addition, the nucleotide pairwise comparison of LSU and SSU sequences showed no base pair difference and the ITS sequence showed only 6 base pair differences. Thus, we introduced our isolate as a new habitat record of *P. yunnanensis.*



Note a, b Appearance of ascomata on host substrate. c, d Section through ascoma. e–h Asci. i Peridium. j Pseudoparaphyses. k–o Ascospores. p Ascospores stained in Indian ink. Scale bars: c, d = 100 µm, e–h, k–p = 20 µm, i = 50 µm, j = 10 µm.

Figure 4.80 *Parabambusicola yunnanensis* (HGUP 22-0810, new habitat record)



Note Bootstrap support values for ML equal to or greater than 75% and BYPP equal to or greater than 0.95 are given above the nodes. *Bambusicola loculate* (MFLUCC 13-0856) and *B.* massarinia (MFLUCC 11-0389) were used as the outgroup taxa. The newly generated sequence is indicated in blue. The ex-type strains are indicated in bold.

Figure 4.81 Phylogenetic analyses for *Parabambusicola*

Pleosporales genera incertae sedis

Biascospora Y.R. Sun, Yong Wang bis & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF902601; Facesoffungi number: FoF 16444

Etymology: The generic epithet "*Biascospora*" refers to two ascospore in one ascus.

Saprobic on dead wood. **Sexual morph**: *Ascomata* superficial, solitary, scattered, subglobose to globose, dark brown to black, without a central ostiole. *Peridium* thin-walled, composed of hyaline inner layer and dark brown outer layer. *Hamathecium* comprising numerous, filiform, hyaline, septate, branched pseudoparaphyses. *Asci* 2-spored, bitunicate, cylindrical, sessile, apically rounded. Ascospores overlapping uniseriate, fusiform, tapering towards rounded ends, slightly curved, hyaline, 6–8-septate, constricted at the middle septa, smooth-walled. **Asexual morph**: Not observed.

Type species: *Biascospora chishuiensis* Y.R. Sun, Yong Wang bis & K.D. Hyde, Figure 4.63

Notes: A phylogenetic analysis based on a combined dataset of LSU, ITS, SSU, RPB2 and *TEF1-α* sequence data showed that *Biascospora* formed a distinct clade and closely related to *Corynespora* (Corynesporascaceae) in Pleosporales (Figure 4.26). The morphology of *Biascospora* is distinguished from members of other families in Pleosporales by its 2-spored asci and hyaline ascospores. To avoid establishing a new family for a single species, *Biascospora* was introduced as a new genus and assigned to Pleosporales, genera incertae sedis. *Biascospora* was a monotypic genus reported from terrestrial habitats, lacking a known asexual morph. Further discoveries of additional species within *Biascospora* or in phylogenetically related genera with supported monophyly will determine the familial classification of *Biascospora*.

Biascospora chishuiensis Y.R. Sun, Yong Wang bis & K.D. Hyde, s***p. nov.***

Index Fungorum number: IF902602; Facesoffungi number: FoF 16445; Figure 4.82

Etymology: Referring to the location where the fungus was collected.

Holotype: HKAS 136870.

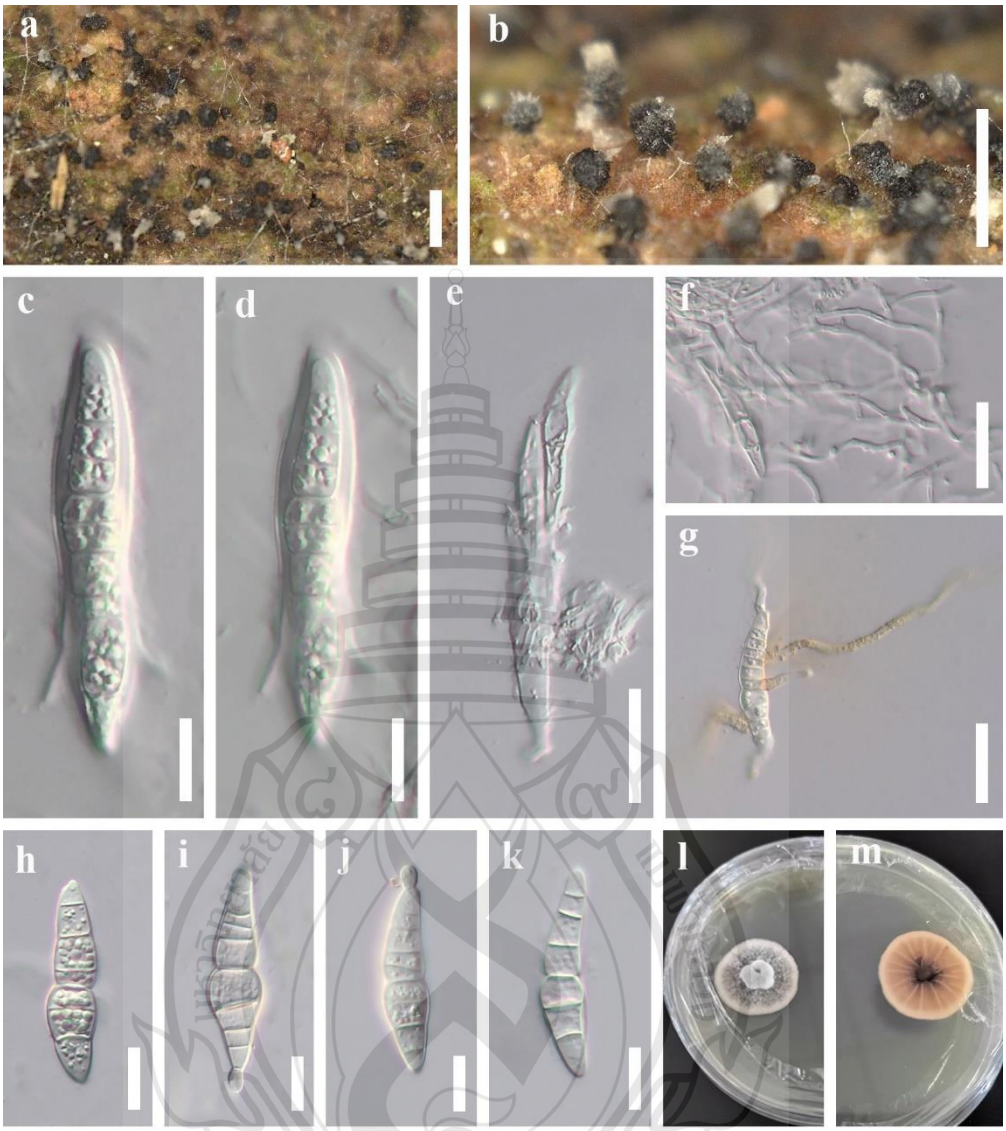
Saprobic on dead twigs of unidentified arbor in forest. **Sexual morph**: *Ascomata*

superficial, solitary, scattered, subglobose to globose, dark brown to black, without a central ostiole. *Peridium* thin-walled, composed of hyaline inner layer and dark brown outer layer. *Hamathecium* 1–2.5 μm wide, comprising numerous, filiform, hyaline, septate, branched pseudoparaphyses. *Asci* 40–53 × 9–11 μm, 2-spored, bitunicate, cylindrical, sessile, apically rounded, without an ocular chamber. *Ascospores* 27–47 μm long, 5–11 μm at the widest, overlapping uniseriate, fusiform, tapering towards rounded ends, slightly curved, hyaline, 6–8-septate, constricted at the middle septa, lower cell slightly wider than upper cell, smooth-walled. **Asexual morph**: Not observed.

Culture characteristics: Ascospore germinated on PDA within 12 h at 25 °C and produced germ tubes. Mycelia superficial, circular, dry, wrinkled, flat, cotton, grey from above. Dark brown in the central cycle and orange the outer circle from below.

Material examined: CHINA, Guizhou Province, Chishui City, Chishui Danxia Tourist Area, on dead wood, 12 April 2023, Y.R. Sun, 23102 (HKAS 136870, **holotype**); ex-type culture GUCC 24-0089.

Notes: Our isolate formed a distinct clade and closed to *Corynespora cassiicola* and *C. torulosa* in Pleosporales (Figure 4.26). In morphology, our isolate differs from the latter by its 2-spored asci and hyaline, 6–8-septate ascospore while the latter have 8-spored asci and brown, 1-septate ascospore (Sivanesan, 1996). Therefore, we introduced our isolate as a novel species.



Note a, b Ascomata on host surface. c–e Asci. f Pseudoparaphyses. g Gemmating ascospores. h–k Ascospores. l, m Colonies on PDA. Scale bars: a, b = 500 μm, c–e, h–k = 10 μm, f, g = 20 μm.

Figure 4.82 *Biascospora chishuiensis* (HKAS 136870, holotype)

Pleocatenata Y.R. Sun, Yong Wang bis & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF559457 Facesoffungi number: FoF 10630

Etymology. "Pleo-" an abbreviation of Pleosporales, the order in which this fungus is classified; "-catenata" refers to the catenate conidia of this fungus.

Description: *Saprobic* on decaying twigs in terrestrial habitats. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, dark, velvety. Conidiophores macronematous, mononematous, straight or slightly curved, cylindrical, unbranched, septate, brown or dark brown. *Conidiogenous cells* monotretic, integrated, terminal, cylindrical, brown to dark brown. *Conidia* catenate, formed in acropetal chains, straight or bent, obclavate, olivaceous to dark brown, multi-euseptate, slightly constricted at septa, distal conidia rounded at apex, truncate at base, intercalary conidia truncate at both ends, with thickened and darkened scars at base or both ends. **Sexual morph**: Not observed.

Type species: *Pleocatenata chiangraiensis* Y.R. Sun, Yong Wang bis & K.D. Hyde

Notes: The morphology of *Pleocatenata* is distinguished from members in other families in Pleosporales by its tretic conidiogenous cells and catenate, euseptate conidia, and phylogenic analyses indicated it does not belong to any existing families. To avoid establishing a new family with only one species, *Pleocatenata* is introduced as a new genus and assigned to Pleosporales, genera incertae sedis. *Pleocatenata* is a monotypic genus reported from terrestrial habitats but without a known sexual morph. Further discovery of other species in *Pleocatenata* or phylogenetic related genera with supported monophyly will determine the familial level of *Pleocatenata*.

Pleocatenata chiangraiensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF559458 Facesoffungi number: FoF 10631 Figure 4.83

Etymology. The epithet referring to the location in which the fungus was collected.

Holotype. MFLU 22-0002.

Saprobic on twigs of *Clerodendrum quadriloculare* and *Tarenna stellulata*. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, dark, velvety. *Mycelium* immersed, composed of septate, branched, hyaline to subhyaline hyphae.

Conidiophores macronematous, mononematous, erect, straight or slightly curved, cylindrical, unbranched, robust, 4–6-septate, brown or dark brown, rough, 35–100 μm long, 5.5–8.5 μm wide. *Conidiogenous cells* monotretic, integrated, terminal, determinate, cylindrical, dark brown. *Conidia* catenate, formed in acropetal chains of 2–3, straight or curved, obclavate, olivaceous to brown when young, blackish brown when mature, 5–8-euseptate, slightly constricted at septa, distal conidia rounded at apex, truncate at base, intercalary conidia truncate at both ends, with thickened and darkened scars at base or both ends, 34–70 μm long, 6.5–12 μm at the widest. **Sexual morph**: Unknown.

Culture characteristics: Conidia germinated on PDA within 12 hours at 26 °C. Germ tubes were produced from both ends. Colony reached 20–25 mm diameter after 4 weeks at room temperature on PDA media. Mycelia superficial, irregularly circular, entire edge, dark brown from above, black from below, pigment produced which turns the media reddish brown.

Material examined: Thailand, Chiang Rai Province, Mae Fah Luang University, on twigs of Tarenna stellulata, 3 July 2020, Y.R. Sun, MFU5 (MFLU 22-0002, **holotype**), ex-type living culture MFLUCC 21-0222. Thailand, Chiang Rai Province, Medicinal Plants Garden, on twigs of Clerodendrum quadriloculare, 7 June 2020, Y.R. Sun, B45 (MFLU 22-0001), living culture MFLUCC 21-0223.

Notes: Two isolates collected from different hosts share similar morphology and clustered together in the phylogenic tree. There are no base pair differences in LSU and tef1-α genes between these two isolates. One base pair and two base pair differences (without gaps) are observed in ITS and rpb2, respectively. Therefore, the two isolates MFLUCC 21-0222 and MFLUCC 21-0223 are identified as conspecific.



Note a Host (*Tarenna stellulata*). b, c Colonies on natural substrate. d, e Conidiophores with conidia f Conidiogenous cells g–k Conidia. l Germinated conidium. m, n Colonies on PDA (upper view and lower view). Scale bars: b = 1 mm, c = 100 µm, d–l = 20 µm.

Figure 4.83 *Pleocatenata chiangraiensis* (MFLU 22-0002, holotype)

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

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

Notes: *Roussoella* was introduced by Saccardo and Paoletti (1885) with *R. nitidula* as the type species. The genus is characterized by immersed, loculate ascostromata, cylindrical and bitunicate asci, brown, fusiform to ellipsoidal, ornamented, and two-celled ascospores; immersed conidiomata blastic, phialidic, cylindrical to ampulliform conidiogenous cells and oblong to ellipsoidal, hyaline to brown, aseptate conidia (Liu et al., 2014; Dai et al., 2016; Phookamsak et al., 2019; Hyde, de Silva et al., 2020; Dai et al., 2022; Hyde et al., 2023). *Roussoella* species mainly occurs on bamboo and palms in terrestrial habitats around the world (Hyde, de Silva et al., 2020; Dai et al., 2022). In this study, we report two new species, *R. panzhouensis* and *R. wudangensis*, and one new collection of *R. siamensis* with illustrate and molecular.

Roussoella panzhouensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902599; Facesoffungi number: FoF 16446; Figure 4.84

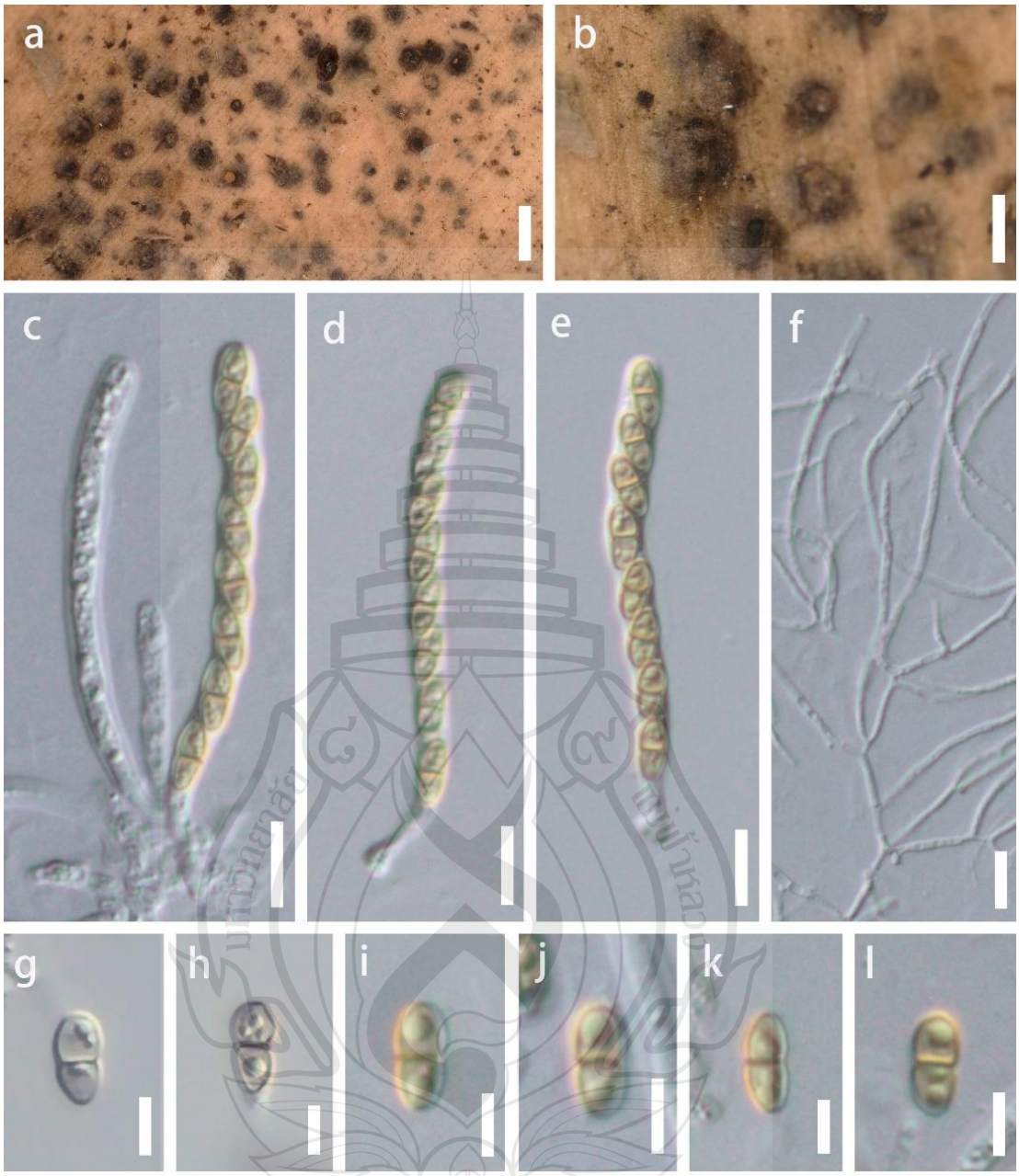
Etymology: refers to the location where the fungus was collected.

Holotype: HKAS 136892.

Saprobic on dead bamboo culms. **Sexual morph**: *Ascostromata* gregarious, immersed to erumpent through host surface by papilla, globose to subglobose, uni-loculate, with a central ostiole. *Peridium* unequal thickness, slightly thinner at the base, brown to dark brown. *Hamathecium* composed of dense, 1–2.5 μm wide, distinctly septate, hyaline, branched cellular pseudoparaphyses. *Asci* 61–79 × 4.5–6 μm, 8-spored, bitunicate, cylindrical, slightly bent, short pedicellate, with furcate or knob-like pedicel. *Ascospores* 7.5–10 × 3–4 μm ($\bar{x}$ = 8 × 3.5 μm, n = 35), overlapping, uni-seriate, ellipsoidal, brown, 2-celled, slightly constricted at the septum, smooth-walled, with guttules. **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Liupanshui City, Panzhou City, Zhuhai Town, on branches of bamboo, 4 Augest 2023, Y.R. Sun, ZH20 (HKAS 136892, **holotype**).

Notes: Our isolate closed to *Roussoella padinae* in the phylogenetic tree (Figure 4.87). *Roussoella padinae* was introduced by Poli et al. (2020) based on molecular data analyses and morphology of colonies and vegetative structures. Dai et al. (2022) provided the asexual morphs for this species. No sexual form has been reported for this species yet, and we cannot compare the morphology of these two strains because our strain does not produce asexual amorphs. The comparisons of ITS and *TEF1-α* sequences between our isolates and the ex-type MUT 5503 show there are 5 bp differences (510 bp, without gap) in the ITS and 16 bp differences (857 bp, without gap) in the *TEF1-α*. Similar ITS base pair differences between species *R. japanensis* and *R. hysterioides* also appeared. Therefore, we identified our isolate as a novel species.



Note a, b Ascostromata on bamboo culm. c–e Asci. f Pseudoparaphyses. g–l Ascospores. Scale bars: a = 1000 μm, b = 500 μm, c–f =10 μm, j–l = 5 μm.

Figure 4.84 *Roussoella panzhouensis* (HKAS 136892, holotype)

Roussoella siamensis Phook., Jian K. Liu & K.D. Hyde, Phytotaxa 181(1): 18 (2014)

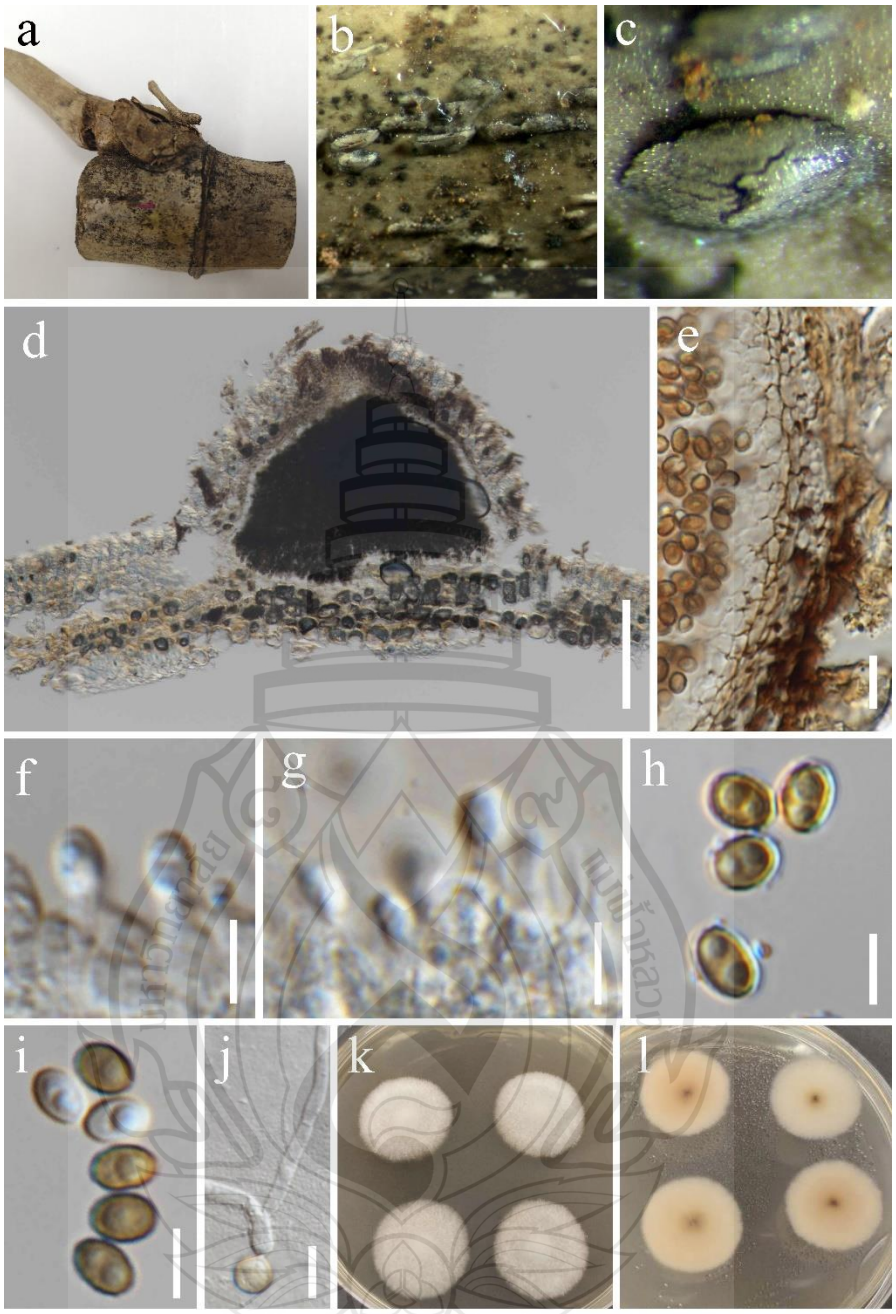
Index Fungorum number: IF550665; Facesoffungi number: FoF01984; Figure 4.85

Saprobic on bamboo culms. **Asexual morph**: Coelomycetous. *Conidiomata* 130–150 μm high, 150–220 μm wide, pycnidial, immersed in host epidermis, raised, hemisphaerical to subconical, scattered or clustered, solitary or gregarious, uniloculate, ostiolate. *Pycnidial wall* 10–23 μm wide, composed of several layers of pale brown to dark brown pseudoparenchymatous cells of *textura angularis*, outer layer fused with the host tissue. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* arising from the inner layer of conidiomata, around 2 μm wide, blastic, phialidic, cylindrical to ampulliform, unbranched, hyaline, aseptate, smooth-walled. *Conidia* 4–6 × 3–4 μm ($\bar{x}$ = 5 × 3.5 μm, n = 30), ellipsoidal, hyaline when young, brown at mature, aseptate with two guttules, smooth-walled. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinated on PDA within 12h at 25 ºC, with germ tubes produced from a one end. Colonies on PDA circular, flat, and velvety, colony originally white to cream, becoming dark green to dark brown.

Specimen examined: THAILAND, Chiang Rai Province, Muang District, Mae Fah Luang University campus grounds, on dead branch of Bamboo, 13 May 2019, N. Wu, S35.1 (HGUP 24-0045); living culture GUCC 24-0135.

Notes: *Roussoella siamensis* was first reported in Thailand by Liu et al. (2014) in its sexual morph. Hyde, de Silva et al. (2020) provided its asexual from *Phragmites australis* in China. In morphology, our strain shares similar characters with *R. siamensis* in having cylindrical to ampulliform, unbranched, hyaline conidiogenous cells and ellipsoidal, aseptate conidia (Hyde, de Silva et al., 2020). However, our strain has larger conidia (4–6 × 3–4 μm *vs.* 3–4 × 1.5–2.5 μm). A comparison of ITS sequences between our isolates and MFLUCC 11-0149 shows only 1bp differences (537 bp, without gap). In addition, our collection cluster together with the ex-type MFLUCC 11-0149 by strong support (ML-bs= 100%, BYPP = 1) in the phylogenetic tree (Figure 4.87). Therefore, we identified our strain as *Roussoella siamensis*.



Note a Host. b, c Conidiomata on host substrate. d Vertical section of conidioma. e Pycnidium wall. f, g Conidiogenous cells and developing conidia. h, i Conidia. j Germinated conidium. k, l Colonies on the PDA (k from above, l from below). Scale bars: d = 50 µm, e, j = 10 µm, f–i = 5 µm.

Figure 4.85 *Roussoella siamensis* (HGUP 24-0045)

Roussoella wudangensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902600; Facesoffungi number: FoF 16447; Figure 4. 86

Etymology: wudangensis, refers to the location, Wudang District, where the fungus was collected.

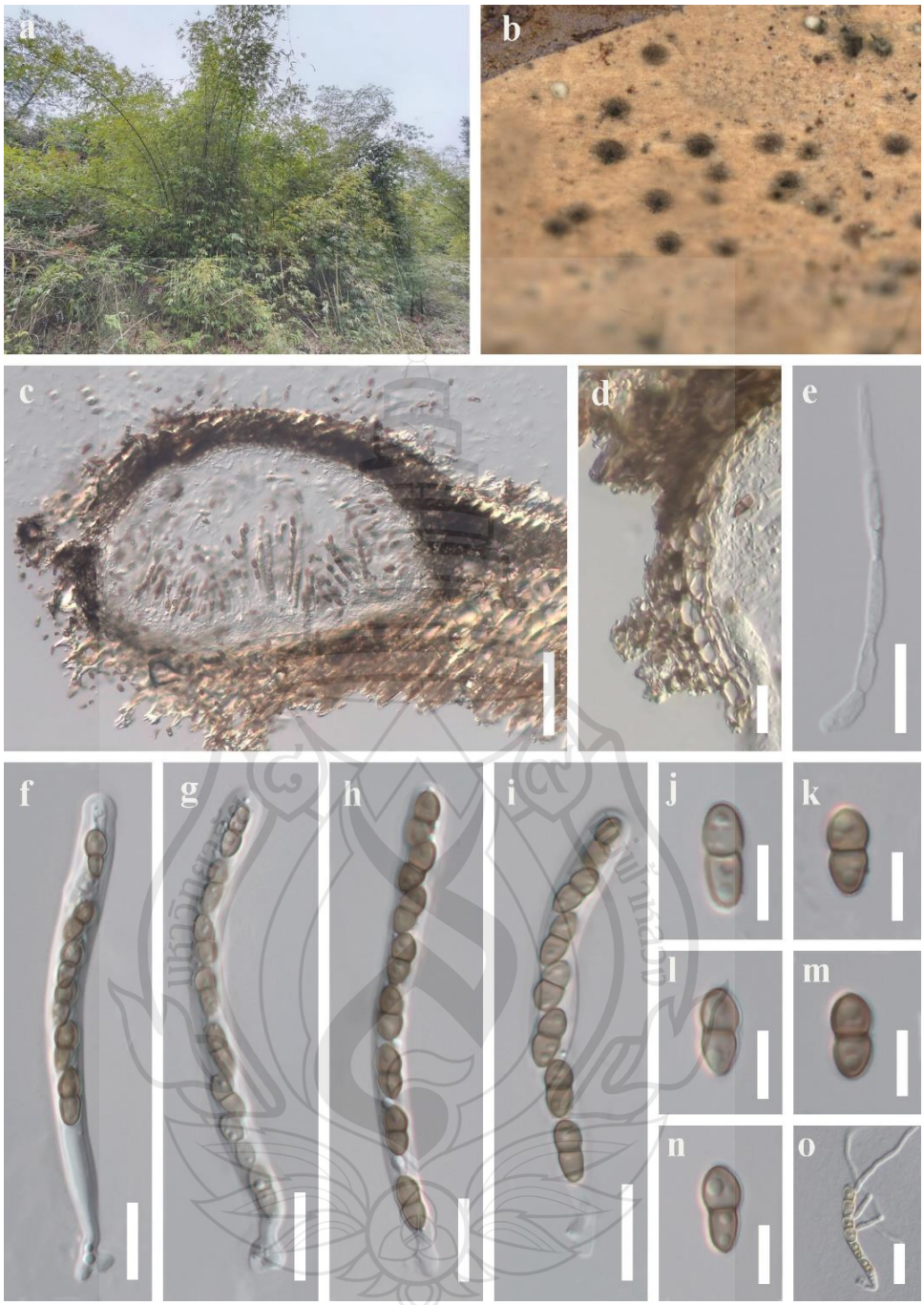
Holotype: HKAS 136879.

Saprobic on dead bamboo culms. **Sexual morph**: Ascostromata 150–250 μm high, 170–280 μm wide, gregarious, immersed to erumpent through host surface by papilla, globose to subglobose, uni-loculate, with a central ostiole. Peridium 13–30 μm wide, of unequal thickness, slightly thinner at the base, composed of several layers of flattened, brown to dark brown, textura prismatica or *textura angularis* pseudoparenchymatous cells. Hamathecium composed of dense, 1–2.5 μm wide, hyaline, cellular pseudoparaphyses, distinctly septate, constricted at the septum. Asci 48–64 × 3.5–5.5 μm, 8-spored, bitunicate, cylindrical, short pedicellate, with furcate or knob-like pedicel, apically rounded with indistinct ocular chamber. Ascospores 4.5–8 × 2–3.5 μm ($\bar{x}$ = 6.5 × 2.5 μm, n = 50), overlapping, uni-seriate, ellipsoidal to fusiform, with rounded to acute ends, brown, 2-celled, slightly constricted at the septum, upper cells bigger, smooth-walled. **Asexual morph**: Not observed.

Culture characteristics: Ascospore germinated on PDA within 12h at 25 ºC, with germ tubes produced from a one end. Colonies on PDA reached 8–9 cm diam. after 21 days at 25 °C, mycelium white, flossy, irregularly circular, with the entire edge, wrinkled, white from above, brown from below.

Material examined: CHINA, Guizhou Province, Guiyang City, Wudang District, Panlong mountain, on branches of bamboo, 13 February 2023, Y.R. Sun, 2303 (HKAS 136879, **holotype**), ex-type culture GUCC 24-0088.

Notes: *Roussoella wudangensis* is introduced as a novel here. It is phylogenetically close to *R. neopustulans* which was isolated from bamboo in Thailand (Liu et al., 2014) (Figure 4.87). In morphology, *R. wudangensis* can be distinct from *R. neopustulans* by having smaller asci (48–64 × 3.5–5.5 μm *vs.* 80−95 × 5.5−6.5 μm) and ascospores (4.5–8 × 2–3.5 μm *vs.* (8−)11−12.5(−14) × (7−)3.5−4.5 μm).



Note a Host. b Ascostromata on bamboo culm. c Section of ascostroma. d Peridium. e Pseudoparaphyses. f–i Asci. j–n Ascospores. o Geminating ascospore. Scale bars: c = 50 µm, d–i =10 µm, j–n = 5 µm, o = 20 µm.

Figure 4.86 *Roussoella wudangensis* (HKAS 136879, holotype)

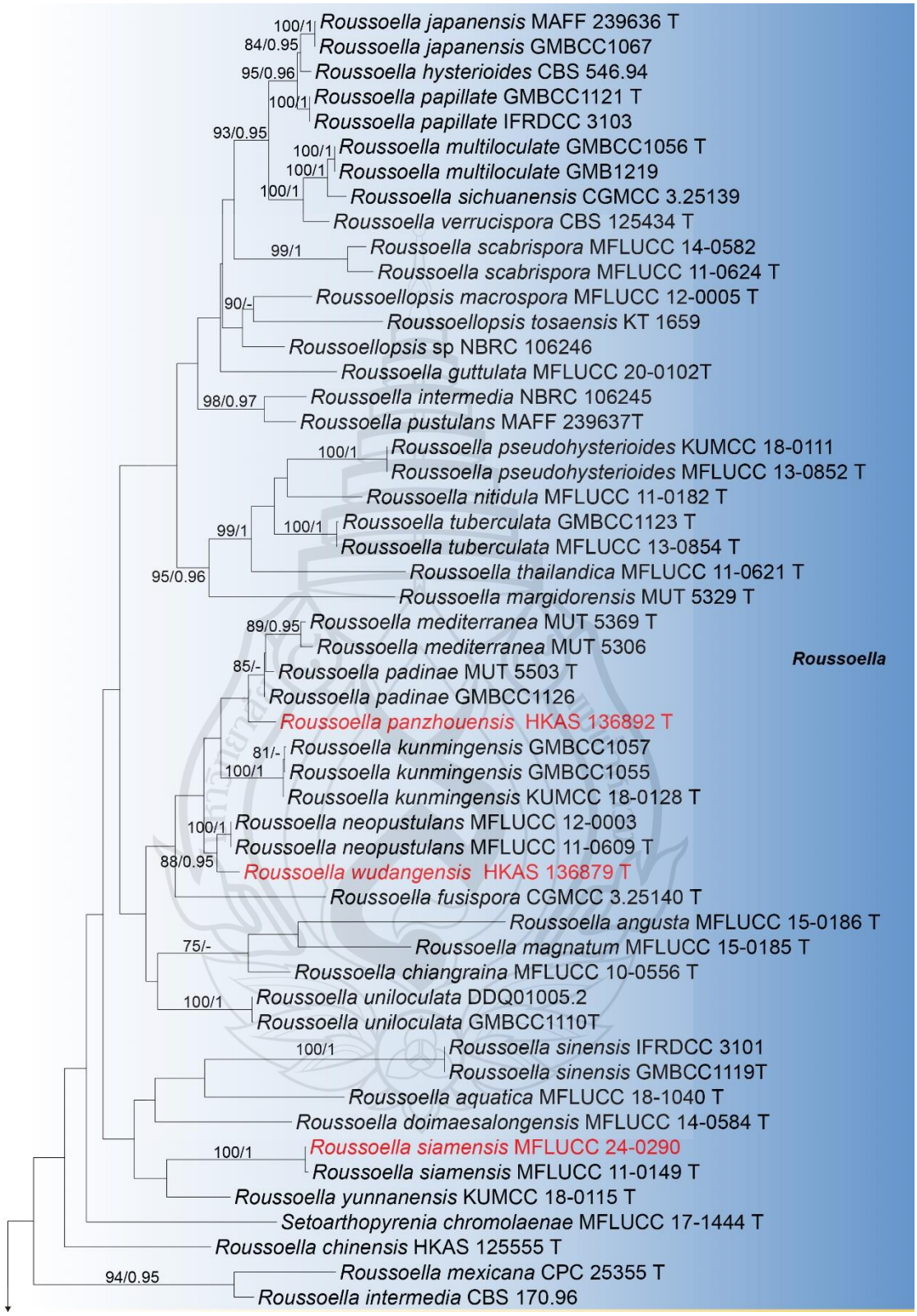
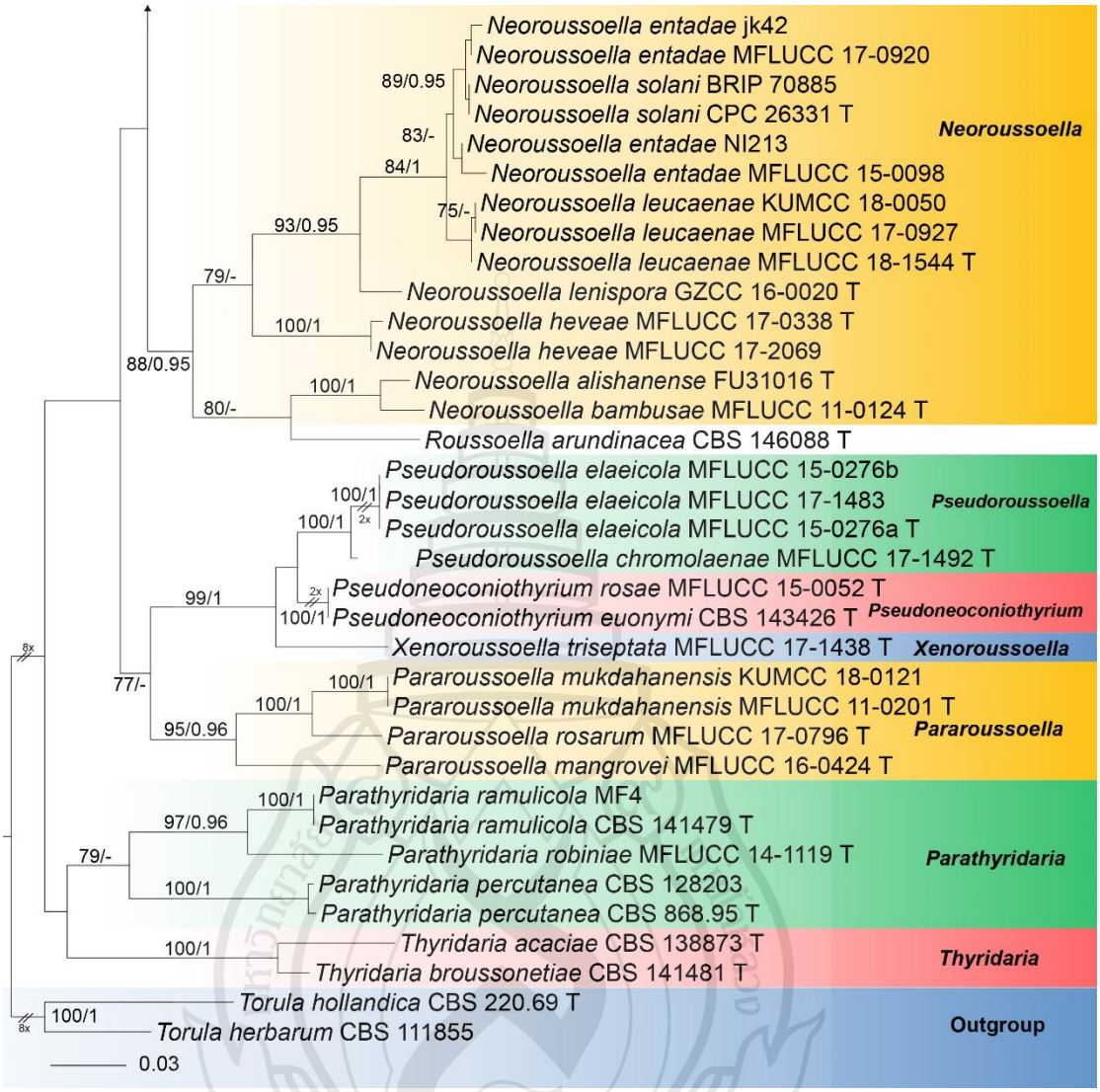


Figure 4.87 Phylogenetic tree of *Roussoella*



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Torula herbarum* (CBS 111855) and *T. hollandica* (CBS 220.69). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.87 (continued)

Torulaceae Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.) 2: 71 (1829)

Torula sundara (Subram.) Y.R. Sun, Yong Wang bis & K.D, Hyde, ***comb. nov.***

≡*Dwayabeeja sundara* Subram., J. Indian Bot. Soc.37: 56 (1958).

≡*Pseudotorula sundara* (Subram.) J.L. Crane & A. Mill

Index Fungorum number: IF559464; Facesoffungi number: FoF09933; Figure 4.88

Saprobic on decaying bamboo culms in terrestrial habitat. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate superficial, powdery, dark brown to black. *Mycelium* immersed, composed of branched, septate, pale brown to brown hyphae. *Conidiophores* 2.5–4 μm wide, micronematous to semi-macronematous, mononematous, solitary, erect, sample, straight or slightly flexuous, unbranched, paler brown to brown, thin-walled, septate, with ampulliform cells, arising from prostrate hypha. *Conidiogenous cells* polyblastic, terminal, with the apex thin-walled and freuently collapsing and becoming coronate, dark brown to black, ellipsoid to coronal., *Conidia* two types, short conidia and long conidia. Short conidia 41–60 × 9–15 μm ($\bar{x}$ = 53 × 12 μm, n = 30), acrogenous, phragmosporous, single or in chains, broadly fusiform, yellow brown to dark brown, 5–10-septate, slightly constricted at some septa, verruculose. Long conidia acrogenous, phragmosporous, single, straight or flexuous, cylindrical, up to 50-septate, constricted at the septa, brown to dark brown, up to 200 μm long. **Sexual morph**: Not observed.

Culture characteristics: Conidium germinated on PDA within 12 hours. Colonies on PDA reaching 20 mm in two weeks at 26°C. Mycelia superficial, circular, entire, flat, white from above, pale brown from below.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, MRC, on bamboo culms, 10 September 2020, H.W. Shen, M55 (MFLU 21-0089); living culture, MFLUCC 21-0067).

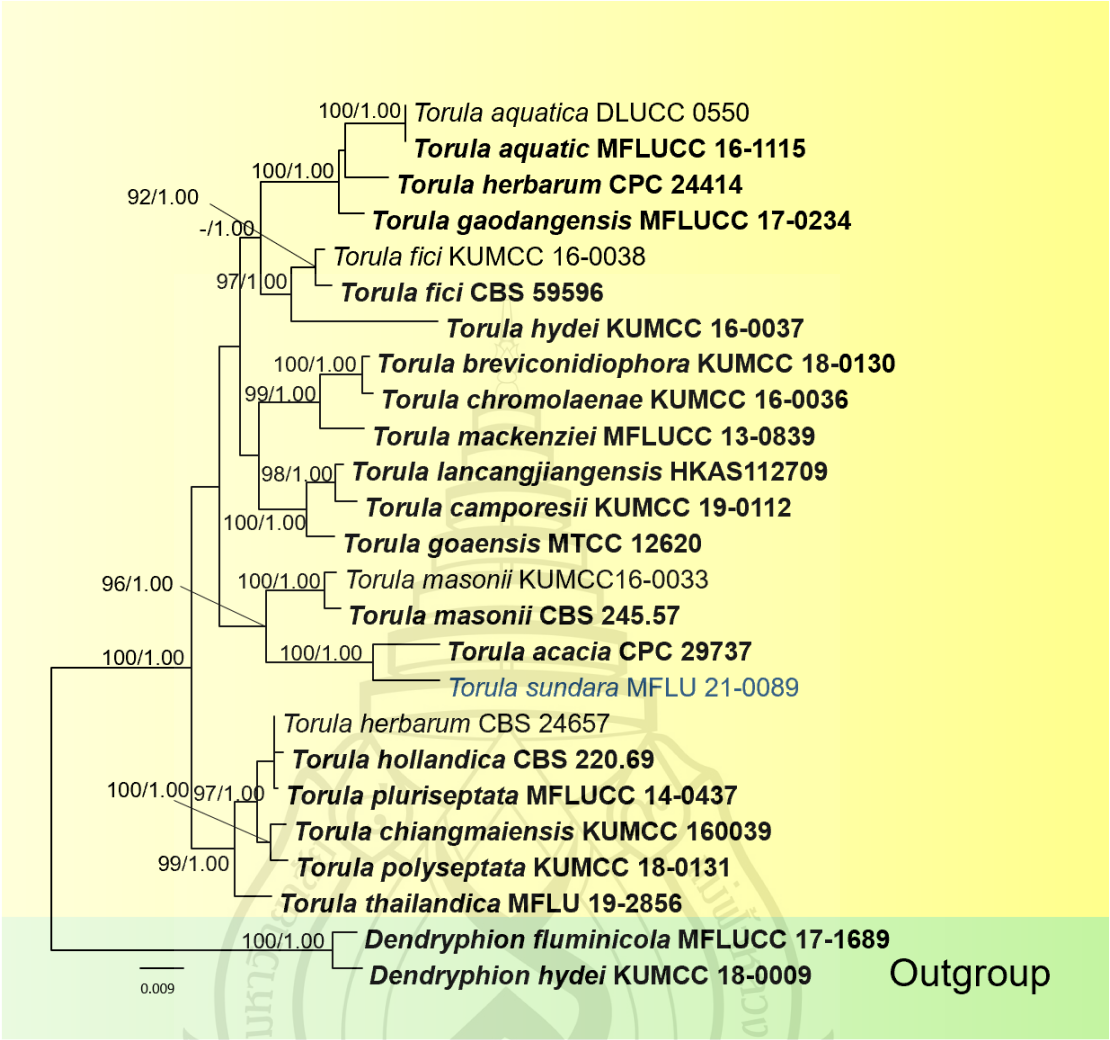
Notes: *Dwayabeeja sundara* as the type species in *Dwayabeeja* was introduced by Subramanian (1958). It has dark blackish brown colonies and two type conidia. Crane and Miller (2016) transfered *D. sundara* to *Pseudotorula* based on in chains phragmoconidia. It was recollected and isolated from bamboo culms in Chiang Mai Province, Thailand and is

provided sequences here. Phylogenetic analyses show it is a distinct clade in *Torula* and sister to *T. acaciae* with high support (MLBS/BYPP 100/1.00) (Figure 4.89). According to the similarities morphology along with phylogenetic analyses, we propose *P. sundara* as a synonym of *T. sundara*.



Note a, b Colonies on the host. c–e Conidiophores and conidia. f–l Conidia. m Germinated conidium. Scale bars: c = 10 µm, d–m = 20 µm.

Figure 4.88 *Torula sundara* (MFLU 21-0089, new combination)



Note The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Dendryphion fluminicola* (MFLUCC 17-1689) and *D. hydei* (KUMCC 18-0009). Ex-type strains are in bold and newly generated sequences are in blue. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given above the nodes.

Figure 4.89 Phylogenetic tree of *Torula*

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

Tubeufiaceae M.E. Barr, Mycologia 71(5): 948 (1979)

Helicosporium Nees, Syst. Pilze (Würzburg): 68 (1816) [1816-17]

Notes: *Helicosporium* was introduced by Nees (1817) based on the type species *H. vegetum*. Lu et al. (2018) reviewed the status of all known *Helicosporium* species and redefined the generic concept including species with superficial, pale yellow to yellow-green colonies, discrete, determinate, denticulate, conidiogenous cells, and hyaline to yellow-green conidia whose filaments do not exceed 25 µm diam. They accepted 13 species in this genus based on morphology and phylogeny. Recently, more *Helicosporium* species have been reported from aquatic habitats in China and Thailand (Dong et al., 2020; Boonmee et al., 2021; Lu, Ma et al., 2022). Three sexual *Helicosporium* species are accepted in this genus (Brahmanage et al., 2017; Xiao, Ma et al., 2023), and we introduced the fourth sexual *Helicosporium* species from a terrestrial habitat in China herein.

Helicosporium multiseptatum Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902603; Facesoffungi number: FoF 15817; Figure 4.90

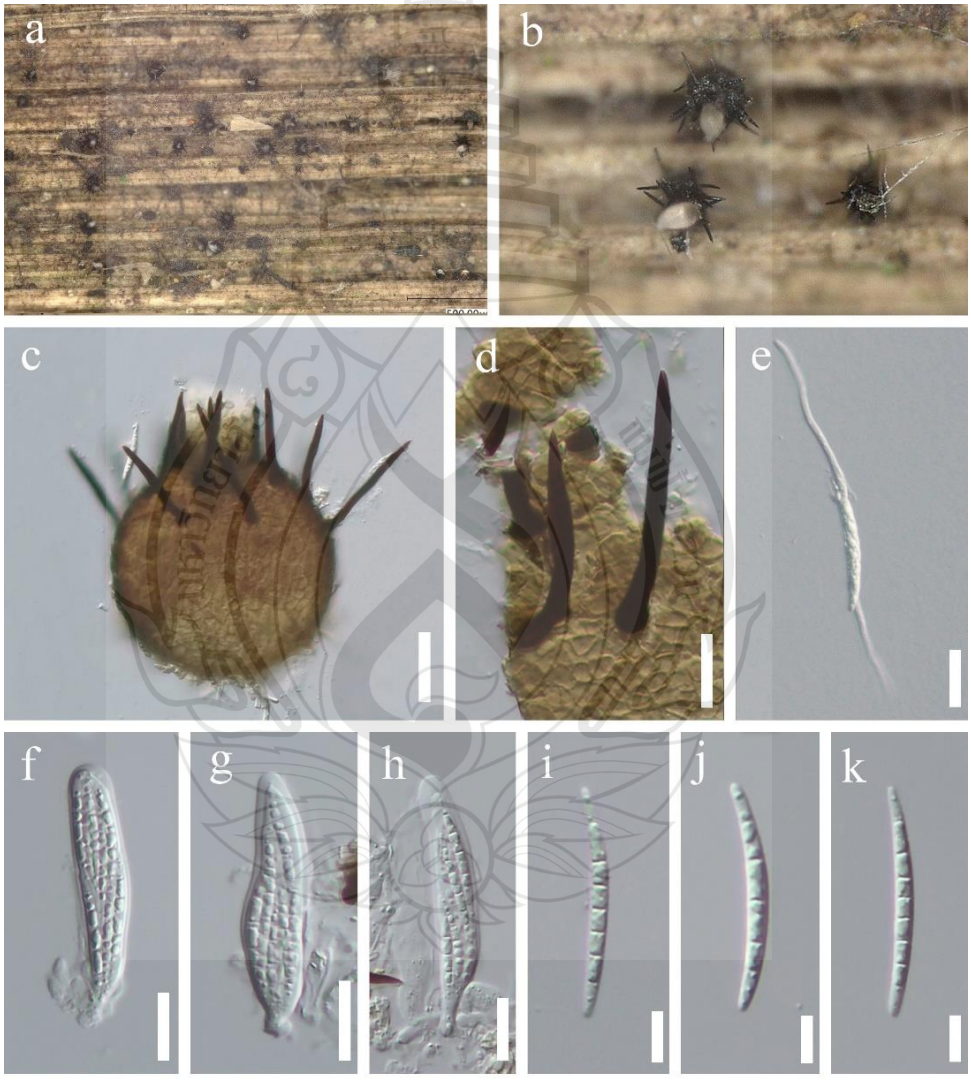
Holotype: HKAS 136882.

Etymology: Referring to the multi-septate ascospores of this fugus.

Saprobic on bamboo culms. **Sexual morph**: *Ascomata* 190–225 × 130–200 µm, superficial, solitary, scattered, globose to subglobose, brown to dark brown, with sparsely setae. *Setae* 45–70 × 4–5.5 µm, stiff, subcylindrical, tapering to an acute tip, dark brown, smooth-walled. *Peridium* yellowish brown, lacking pseudoparaphyses. *Asci* 57–88 × 10–12 µm, 8-spored, bitunicate, cylindric-clavate, rounded at apex, sessile or short pedicelate. *Ascospores* 35–54 × 3–4.5 µm, multi-seriate, fasciculate, narrowly fusiform to vermiform, subacute ends, straight to slightly curved, hyaline, 4–8-septate, not constricted at septa, smooth-walled. **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Wudang District, Xiangzhigou, on dead bamboo culms in a terrestrial habitat, 13 February 2023, Y.R Sun, 2324 (HKAS 136882, **holotype**); ex-type living culture GUCC 24-0090.

Notes: *Helicosporium multiseptatum* resembles the sexual morphs of *Helicosporium* in having superficial, globose to subglobose, pale brown to dark brown ascomata with setae, 8-spored, bitunicate, cylindric-clavate asci and multi-seriate, narrowly fusiform, hyaline ascospores. It is phylogenetically basal to *Helicosporium*. with 97% ML-BS, 1.00 BYPP support (Figure 4.93); the result shows that it is a distinct species. Therefore, we introduced *H. multiseptatum* as a novel species here.



Note a, b Superficial ascomata on substrate. c Ascoma in the slide. d Seta. e Germinating ascospore. f–h Asci. i–k Ascospores. Scale bars: c = 50 µm, d–h =20 µm, i–k =10 µm.

Figure 4.90 *Helicosporium multiseptatum* (HKAS 136882, holotype)

Neohelicomyces Z.L. Luo, Bhat & K.D. Hyde, Cryptog. Mycol. 38(1): 39 (2017)

Notes: *Neohelicomyces* was established by Luo, Bhat et al. (2017) to accommodate three fresh water species. Species of this genus are usually found from freshwater or terrestrial habitats in Asia (Luo, Bhat et al., 2017; Lu et al., 2018; Dong et al., 2020; Yang, Liu et al., 2023). Currently, 16 species are accepted in this genus with their morphology and molecular, and all of them are present by their asexual morphs. In this study, we provided a sexual *Neohelicomyces* species with description and phylogeny.

Neohelicomyces sexualis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16448; Figure 4.91

Etymology: '*sexualis*' referring to sexual morph.

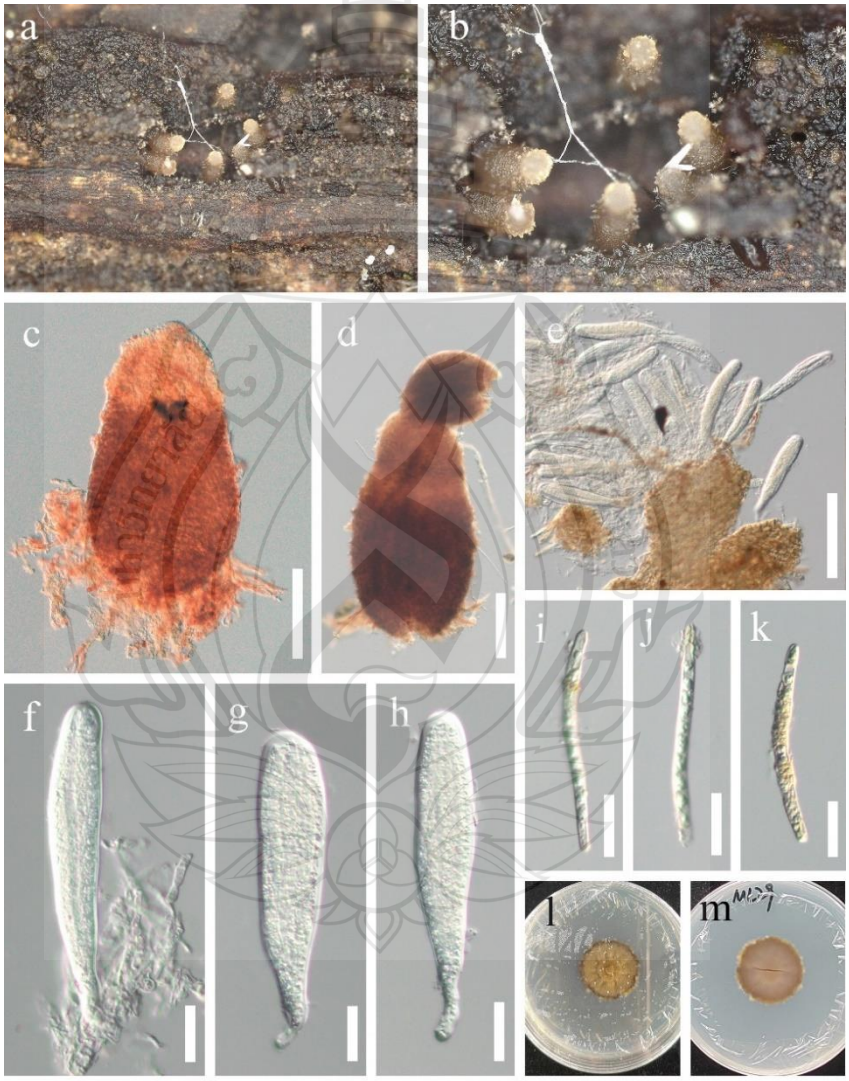
Holotype: HGUP 24-0021.

Saprobic on bamboo culms. **Sexual morph**: *Ascomata*150–200 μm wide, 310–460 μm high, superficial, solitary, scattered, subglobose, light brown on natural substrate, reddish brown to brown on the slide, without setae. *Peridium* yellowish brown, thin-walled. *Hamathecium* comprising 1.5–3.5 μm wide, filiform, septate, hyaline pseudoparaphyses. *Asci* 112–120 × 16–26 μm, 8-spored, bitunicate, cylindric-clavate, rounded at apex, short pedicelate. *Ascospores* multi-seriate, narrowly cylindrical, straight to slightly curved, hyaline to pale brown, septate, not constricted at septa, rough, 70–75 μm long, 4–6 μm wide. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on PAD within 12 h. Colonies reaching to 2 cm diam. After 21 days at 25°C, circular with an entire edge, flat, dry, wrinkled, and brown from above and below.

Material examined: CHINA, Guizhou Province, Qiannan Buyei and Miao Autonomous Prefecture, Libo County, Maolan National Nature Reserve, on dead wood in a terrestrial habitat, 12 March 2022, Y.R Sun, ML29 (HGUP 24-0021, **holotype**); ex-type culture GUCC 24-0110.

Notes: In an NCBI BLASTn search based on ITS sequences, the closest match of *Neohelicomyces* sexualis was *N. deschampsiae* (GenBank no: NR_163367) with only 91.47% similarity. In the phylogenetic analyses, *N. sexualis* formed a distinct inner clade in *Neohelicomyces*, indicating it is a distinct species (Figure 4.93). Besides, *N. sexualis* differed from other *Neohelicomyces* species by the capacity to form its sexual morphs. Therefore, we introduced *N. sexualis* as a new species, and it is the first sexual *Neohelicomyces* species.



Note a, b Superficial ascomata on substrate. c, d Ascomata in the slide. e–h Asci. i, k Ascospores. l, m Colony in on the PDA. Scale bars: c–e = 100 µm, f–k =20 µm.

Figure 4.91 *Neohelicomyces sexualis* (HGUP 24-0021, holotype)

Tamhinispora Rajeshk. & Rah. Sharma, Mycosphere 4(2): 166 (2013)

Notes*:* The hyphomycetous genus *Tamhinispora* was introduced by Rajeshkumar and Sharma (2013) with *T. indica* as the type species. The genus has effused, blackish brown to black colonies, almost sessile conidiogenous cells and solitary, ovoid, obpyriform, Y-shaped or irregular, dictyoseptate conidia (Rajeshkumar & Sharma, 2013; Rajeshkumar et al., 2018; Sommai et al., 2019). So far, only three species have been accepted in *Tamhinispora*, and all of them reported in Asia (Sommai et al., 2019; Species Fungorum 2024). In this study, we introduce the fourth species in this genus.

Tamhinispora obpyriformis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16449; Figure 4.92

Holotype: HGUP 24-0047.

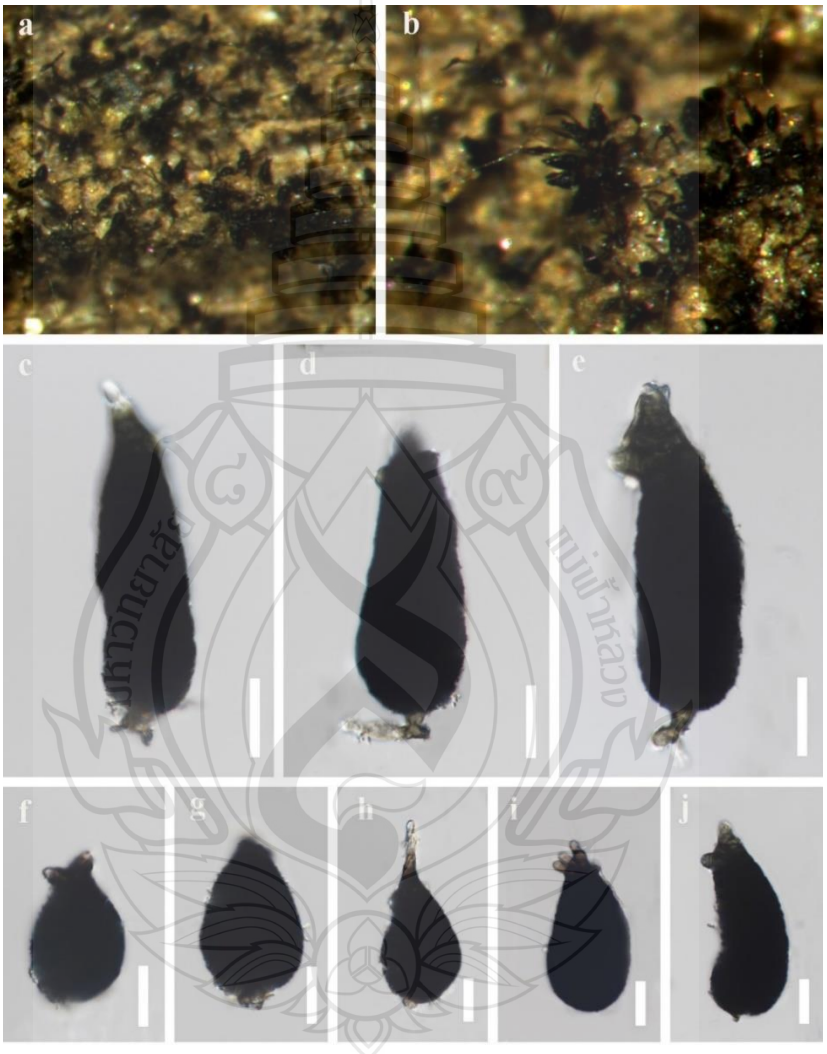
Etymology: referring to the obpyriform conidia of this fungus.

Saprobic on dead twigs. **Sexual morph**: Not observed. **Asexual morph**: Colonies superficial, black, scattered, solitary or gregarious, effuse, shiny. Mycelium immersed in the substratum, composed of septate, branched hyphae. Conidiophores macronematous, mononematous, cylindrical, brown. Conidiogenous cells 2.5–5 µm wide, monoblastic, terminal, integrated, brown, almost sessile. Conidia solitary, dry, simple, ovoid or obpyriform, brown to blackish, dictyoseptate, with rhexolytic secession, paler towards tip when young, 42–92 µm long, 21–39 µm at the widest, smooth, with rudimentary or well-developed appendages 0–6, simple, pale to dark brown, septate, 4.5–12 µm long.

Material examined: THAILAND, Chiang Rai Province, on dead twigs in a terrestrial habitat, 16 January 2021, Y.R Sun, CR05 (HGUP 24-0047, **holotype**), ex-type culture MFLUCC 24-0291.

Notes: *Tamhinispora obpyriformis* phylogenetically group with *T. indica* (NFCCI 2924) and *T. srinivasanii* (NFCCI 4231) and sister to *T. saraburiensis* (TBRC 10035 and TBRC 10036) (Figure 4.93). It could not be differentiated from *T. indica* and *T. srinivasanii* in the phylogenetic tree due to the lack of ITS sequence in our strain. In morphology, *T. obpyriformis* can be distinguished from *T. indica* by having fewer and shorter apical

appendages (0–6, 4.5–12 µm long *vs.* 0–9, 13.5–95 × 3.8–6.3 µm) (Rajeshkumar & Sharma, 2013). *Tamhinispora obpyriformis* differs from *T. srinivasanii* by having ovoid or obpyriform conidia while the latter has branched and Y-shaped conidia (Rajeshkumar et al., 2018). Therefore, we introduce *T. obpyriformis sp. nov*. herein.



Note a, b Colonies on natural substratum. c–e Conidiogenous cells with conidia. f–j Conidia with or without apical appendages. Scale bars: c–j = 20 µm.

Figure 4.92 *Tamhinispora obpyriformis* (HGUP 24-0047, holotype)

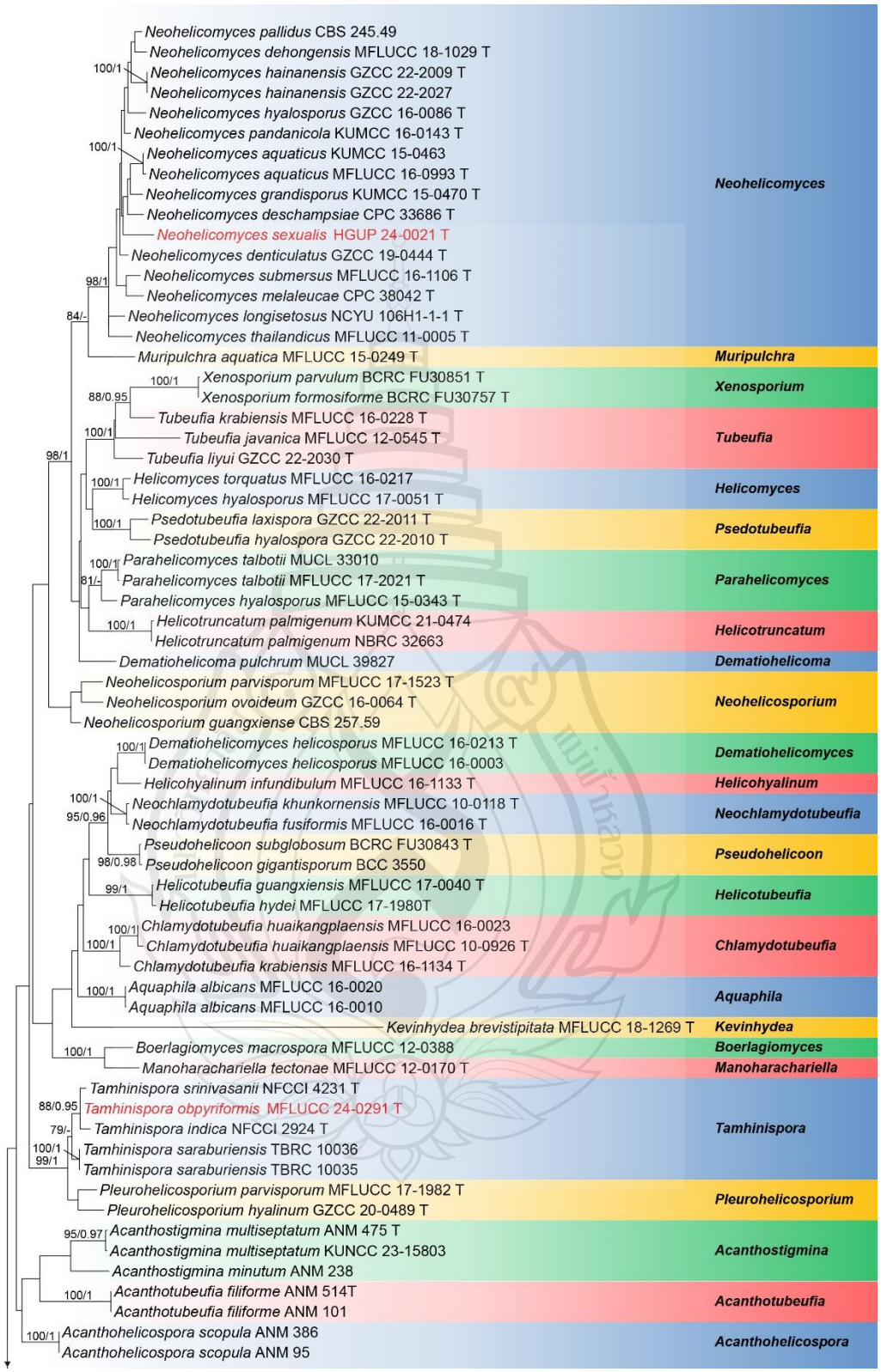
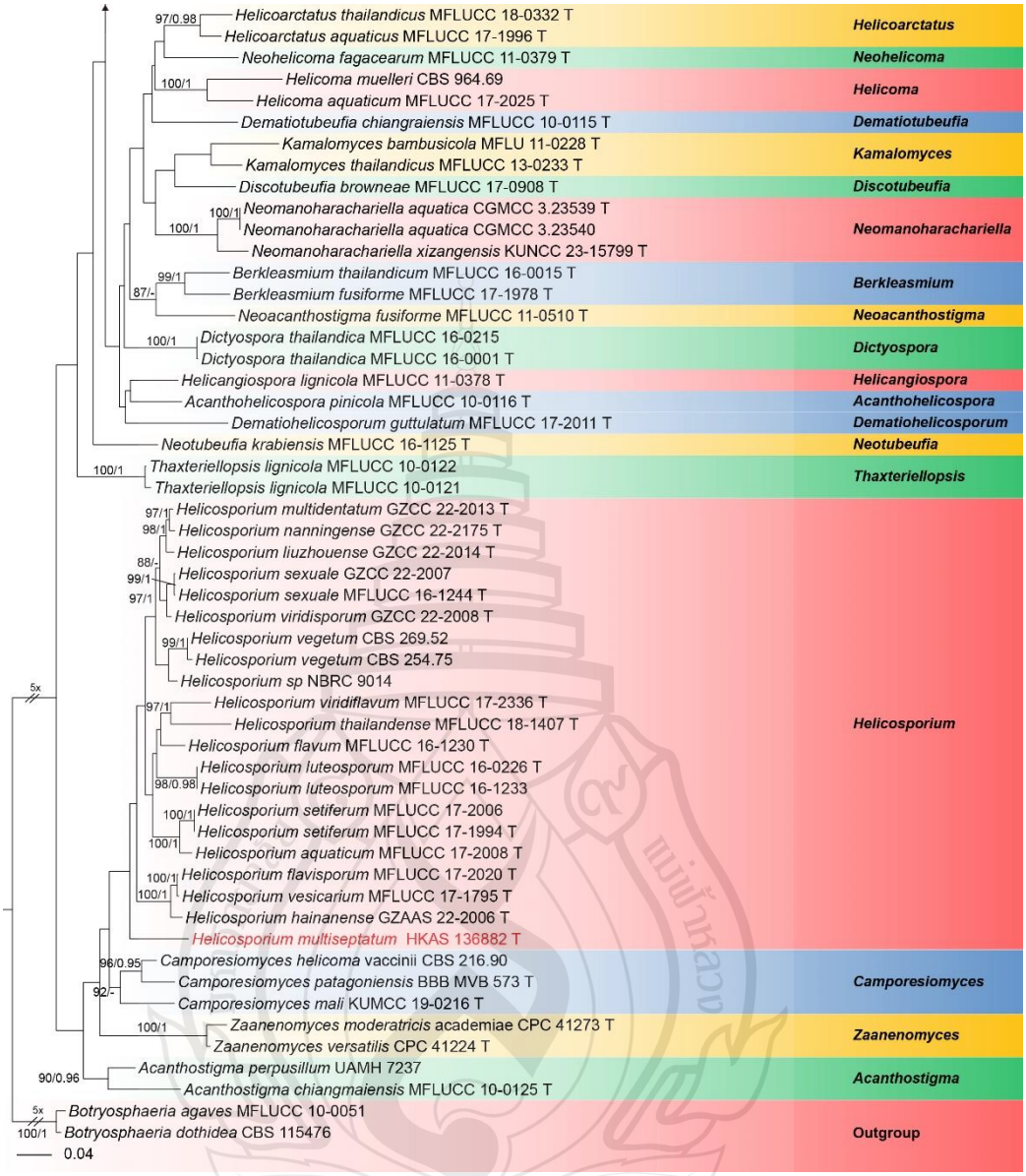


Figure 4.93 Phylogenetic tree of Tubeufiaceae



Note The best scoring RAxML tree with a final likelihood value of −19,614.282564 is presented. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Botryosphaeria agaves* (MFLUCC 10-0051) and *B. dothidea* (CBS 115476). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.93 (continued)

4.2.2 Leotiomycetes

Rhytismatales M.E. Barr ex Minter, Syst. Ascom. 5(1): 182 (1986)

Pezizellaceae Velen., Monogr. Discom. Bohem. (Prague): 154 (1934)

Apiculospora Wijayaw., Camporesi, A.J.L. Phillips & K.D. Hyde, Fungal Diversity [42] (2016)

Notes: Wijayawardene et al. (2016) introduced *Apiculospora* with *A. spartii* as the type species, and accommodated in *Helotiales* genera *incertae sedis*. Later, however, transferred to *Rhytismatales* genera *incertae sedis* by Hyde, de Silva et al. (2020) based on multi-gene phylogenetic analyses. Nevertheless, Karunarathna et al. (2021) regarded it in *Pezizellaceae* based on molecular data analyses. The sexual morph of *Apiculospora* is undetermined and the coelomycetous asexual morphs are characterized by solitary to gregarious, globose to subglobose, unilocular conidiomata, hyaline, holoblastic, cylindrical conidiogenous cells and dark brown, fusiform, 1-septate conidia (Wijayawardene et al., 2016; Karunarathna et al., 2021). Currently, only two species are accepted in this genus with their illustration and molecular data (Wijayawardene et al., 2016; Karunarathna et al., 2021). In this study, we introduce the third *Apiculospora* species which encounter form Thailand.

Apiculospora thailandensis Y.R. Sun & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16450; Figure 4.94

Etymology: Referring to the country, Thailand, where the fungus was collected.

Holotype: HGUP 24-0048.

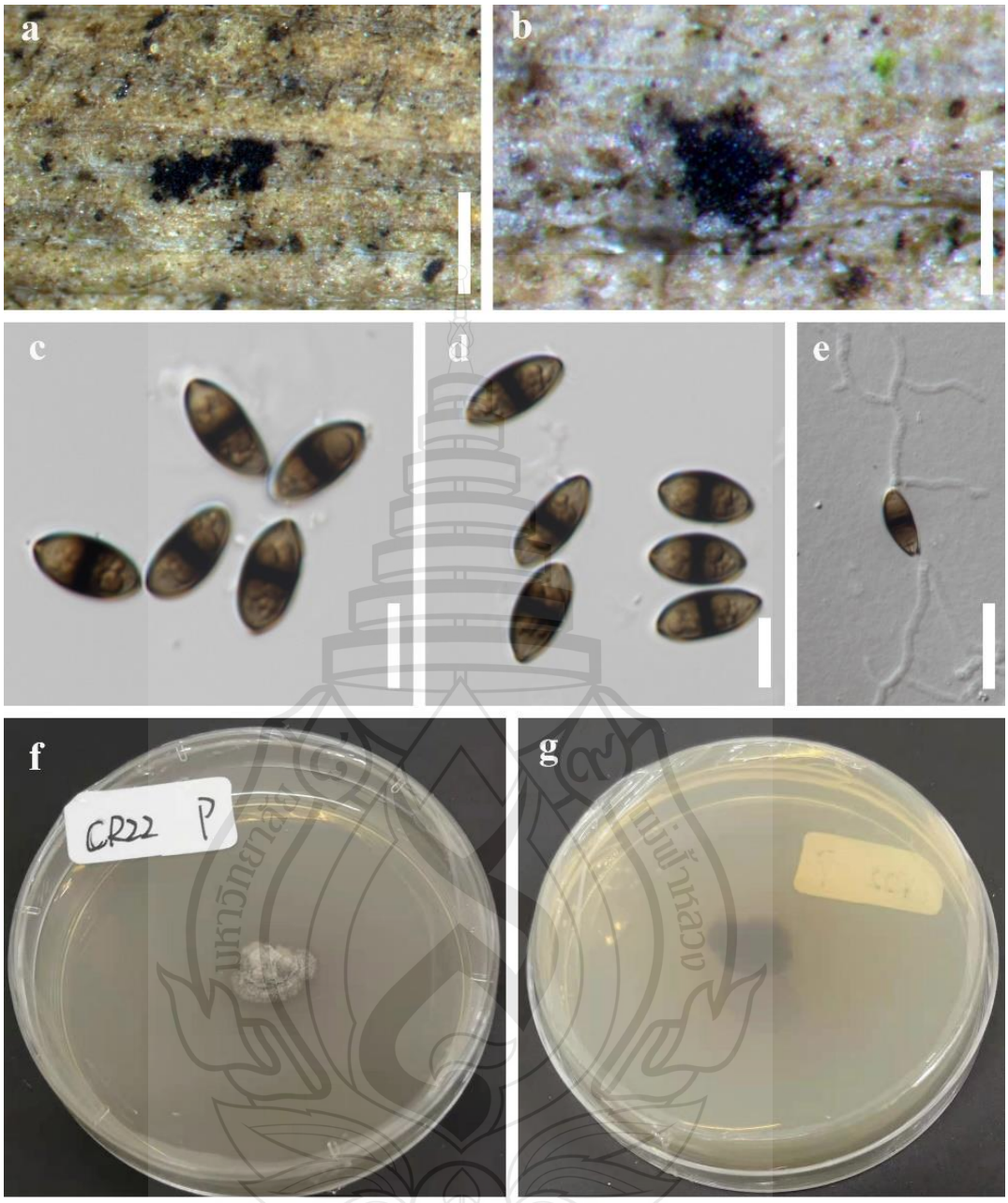
Saprobic on dried *Poaceae* plant leaves. **Asexual morph**: *Colonies* on natural substrate effuse, solitary, black. *Conidiophores* and *Conidiogenous cells* not observed. *Conidia* 12–16.5 × 5–8 µm ($\bar{x}$ = 15 × 7 µm, n = 40), ellipsoid, 1-septate, brown and notable dark brown region at the septum, both apices without clear apiculi, guttulate, smooth-walled. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinated on PDA within 12 hours at 26°C. Germ tubes were produced from the both end of the conidium. Colony reached 10 mm diameter after 4 weeks at room temperature on PDA media. Mycelia superficial, circular, entire edge, dry,

umbonate, white from above, brown from below.

Material examined: THAILAND, Chiang Rai Province, Chiang Rai City, Bandu District, on dead leaves of *Poaceae* plant, 16 Jan 2021, Y.R. Sun, CR22 (HGUP 24-0048, **holotype**); ex-type culture MFLUCC 24-0292.

Notes: *Apiculospora thailandensis* forms a sister clade with *A. penniseti* (NCYUCC 19-0363), which was isolated from decaying stems of *Pennisetum purpureum* (Poaceae) in Taiwan Province, China. In morphology, *A. thailandensis* differs from *A. penniseti* by having smaller conidia (12–16.5 × 5–8 μm *vs.* 15–20 × 5–8 μm), which are ellipsoid and brown without clear apiculi, whereas the latter has ellipsoid to subcylindrical conidia that are pale brown to dark brown, with clear apiculi at both apices (Karunarathna et al., 2021). Additionally, the ITS comparison between our strain and NCYUCC 19-0363 revealed 15 bp differences (3%, without gaps) out of a total of 504 bp. These distinctions provide sufficient support for the introduction of *A. thailandensis* as a novel species.



Note a, b Conidiomata on the host. c, d Conidia. e Germinating conidium. f, g Colony on PDA from above and below. Scale bars: a = 500 µm, b = 200 µm, c, d = 10 µm, e = 20 µm.

Figure 4.94 *Apiculospora thailandensis* (HGUP 24-0048, holotype)

Porodiplodia Crous, Persoonia 40: 363 (2018)

Notes: *Porodiplodia* was introduced by Crous et al. (2018) with *P. livistonae* as the type species. The genus was initially placed in *Porodiplodiaceae*, *Helotiales* by Crous et al. (2018). Later, Ekanayaka et al. (2019) analyzed the classification of *Leotiomycetes* and placed *Porodiplodia* in *Pezizellaceae*, *Rhytismatales*. The characteristics of this genus are eustromatic conidiomata, and pale to brown, 1-septate, catenate conidia with a central pore (Crous et al., 2018; Crous et al., 2019). Currently, *Porodiplodia* consists of two species, from Malaysia and the USA respectively (Crous et al., 2018; Crous et al., 2019). In this study, we report the third *Porodiplodia* species, which was found in China.

Porodiplodia guizhouensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902604; Facesoffungi number: FoF 16451; Figure 4.95

Etymology: Referring to the location in which the fungus was collected.

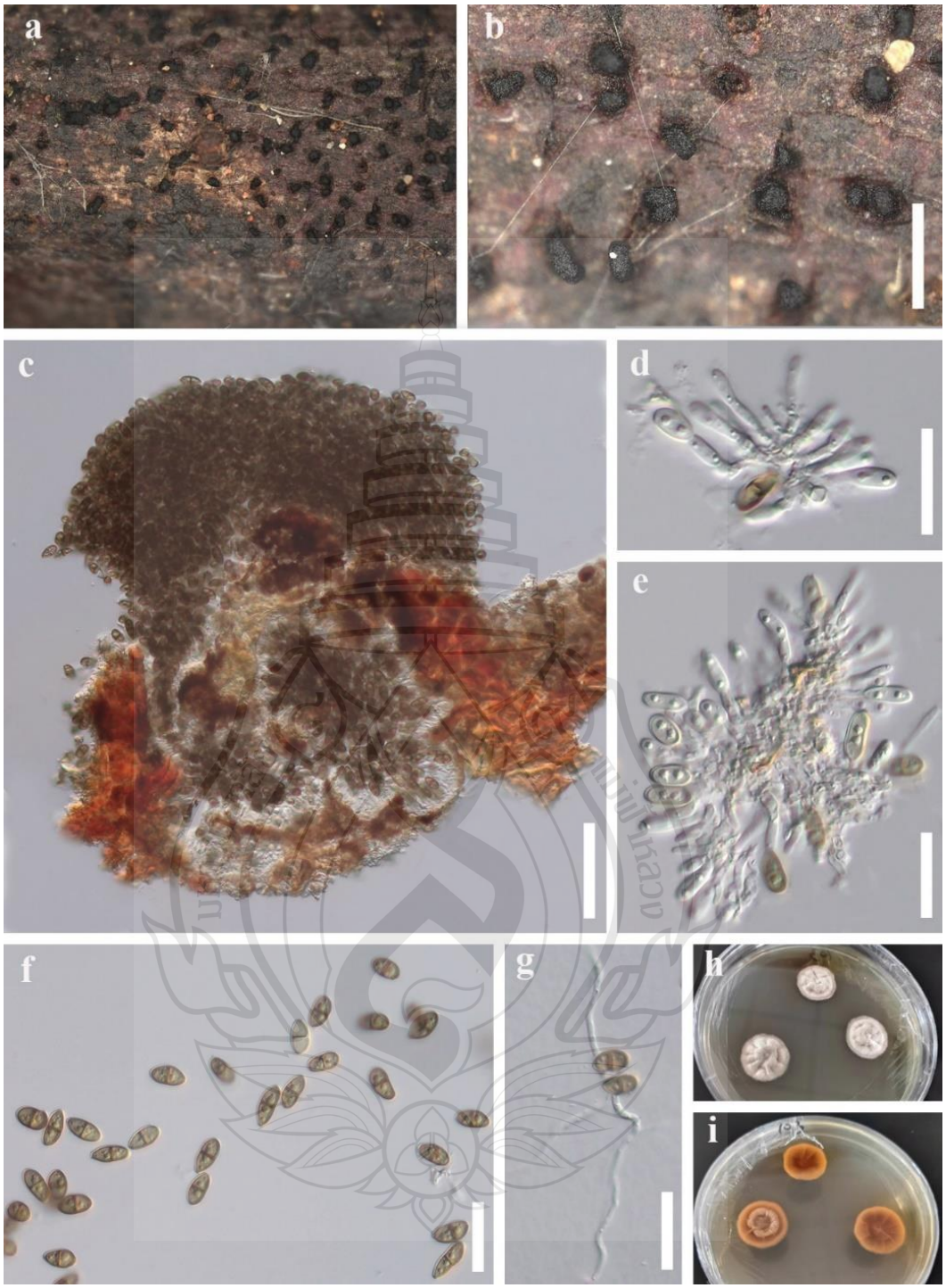
Holotype: HKAS 136871.

Saprobic on dead twigs. **Sexual morph**: Not observed. **Asexual morph**: Conidiomata eustromatic, semi-immersed, dark brown to black, globose to subglobose in section view, unilocular, 150–250 µm wide, 125–215 µm high. Conidiophores lining inner cavity, unbranched, 1–2-septate, reduced to conidiogenous cells. Conidiogenous cells 1–2.5 µm wide, around 5 µm long, subcylindrical, blastic, phialidic with percurrent proliferation, hyaline, smooth-walled. Conidia catenate, formed in acropetal short chains, fusoid-ellipsoid to subcylindrical, hyaline to pale brown when young, brown when mature, finely verruculose, guttulate, thick-walled, 1-septate, apex obtuse, base truncate with central pore, 7.5–13 × 3.5–5.5 µm ($\bar{x}$ = 10 × 4.5 µm, n = 40).

Culture characteristics: Conidia germinated on PDA within 12 hours at 26°C. Germ tubes were produced from the middle of the conidium. Colony reached 20–25 mm diameter after 4 weeks at room temperature on PDA media. Mycelia superficial, circular, entire edge, white from above, orange-brown from below.

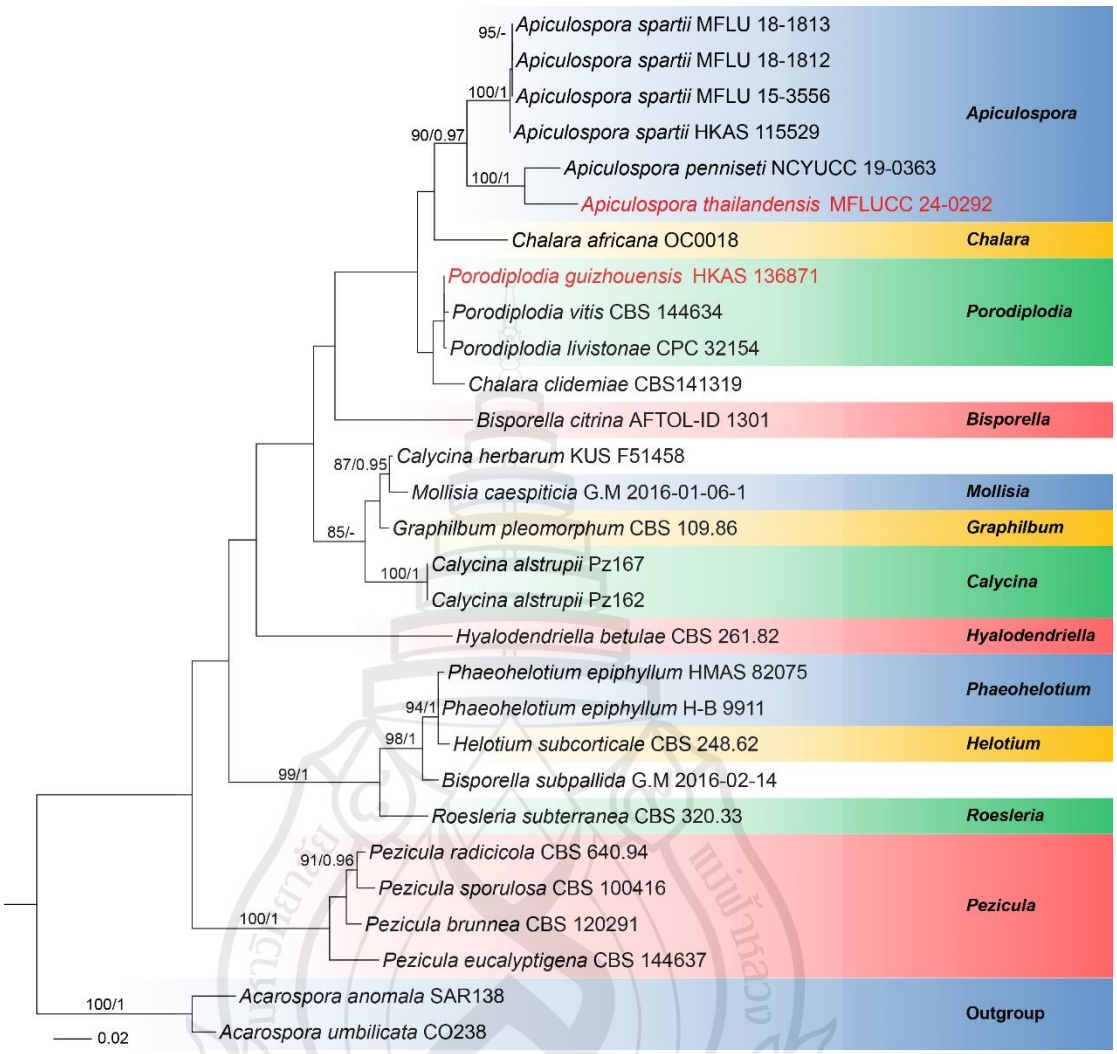
Material examined: CHINA, Guizhou Province, Chishui City, Lianghekou Town, Yanziyan National Forest Park, on dead twigs, 12 April 2023, Y.R. Sun, 23103 (HKAS 136871, **holotype**); ex-type culture GUCC 24-0091.

Notes: Our isolate (HKAS 136871) group with other two *Porodiplodia* species, *viz. P. livistonae* (CPC 32154) and *P. vitis* (CBS144634) in the multi-loci phylogenetic tree (Figure 4.96). However, the resolution of species separation in *Porodiplodia* s. str. clade is not distinct in the phylogenetic tree, but unique morphologies are adequate for species differentiation. Crous et al. (2019) introduced *Porodiplodia vitis* as a separate species, distinguished by its shorter and wider conidia. Consequently, based on our isolate's conidia dimensions (7.5–13 × 3.5–5.5 μm in *Porodiplodia guizhouensis vs.* 15–17 × 5(–6) μm in *Porodiplodia livistonae vs.* 14–16 × (5–)6(–8) μm in *Porodiplodia vitis*), we propose it as a novel species.



Note a, b Conidiomata on the host. c Vertical section through ascoma. d, e Conidia attach to conidiogenous cells. f Conidia. g Germinating conidium. h, i Colony on PDA from above and below. Scale bars: b = 500 µm, c = 50 µm, d–g = 20 µm.

Figure 4.95 *Porodiplodia guizhouensis* (HKAS 136871, holotype)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Acarospora anomala* (SAR138) and *A. umbilicata* (CO238). The new collections are indicated in red.

Figure 4.96 Phylogenetic tree of Rhytismatales

4.2.3 Sordariomycetes

Amphisphaeriales D. Hawksw. & O.E. Erikss., Syst. Ascom. 5(1): 177 (1986)

Amphisphaeriaceae G. Winter [as 'Amphisphaerieae'], Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.2: 259 (1885)

Amphisphaeria Ces. & De Not., Comm. Soc. crittog. Ital., 1(fasc. 4): 223 (1863)

Notes: *Amphisphaeria* was introduced by Cesati and De Notaris (1863). Samarakoon et al. (2020) examined the morphology and phylogeny of *Amphisphaeria* and *Lepteutypa*, and ultimately merging *Lepteutypa* into *Amphisphaeria*. The genus has both sexual and asexual morphs and the descriptions see (Samarakoon et al., 2020; Samarakoon et al., 2022). Recently, Wang et al. (2023) reported an endophytic *Amphisphaeria* species isolated from the medicinal plant *Orixa japonica*, with its hyphomycetous asexual morph. This marks the first instance of a hyphomycetous asexual morph being documented within this genus. Although the introduction of *Amphisphaeria* species has gradually increased in recent years, no species are from eastern China (Dissanayake, Samarakoon et al., 2020; Samarakoon et al., 2020; Samarakoon et al., 2022; Samarakoon 2023; Wang et al., 2023; Zhang, Liu et al., 2023; Li, Liang et al., 2024; Liu, Wang et al., 2024). Here, we introduce a new *Amphisphaeria* species isolated from the medicinal plant in Zhejiang, China.

Amphisphaeria hibiscicola Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902605, Facesoffungi number: FoF 16452; Figure 4.97

Etymology: The specific epithet "*hibiscicola*" refers to the host genus.

Holotype: HKAS 136910.

Saprobic on branch of *Hibiscus mutabilis*. **Sexual morph**: Ascomata 212–450 μm high, 456–570 μm diam., immersed, solitary, scattered, globose to sub-globose, visible as black spots on the host surfaces, brown to dark brown, 1–2-loculate, papillate. Ostiole central., Peridium 12–20 μm, with brown to dark brown, textura angularis cell layers. Paraphyses 2.5–4 μm wide, hyaline, branched, cellular, septate, guttulate, embedded in a gelatinous matrix. Asci 122–152 × 6–8 μm ($\bar{x}$ = 131 × 7 μm, n = 10), 8-spored, unitunicate, cylindrical, with short pedicel, apically rounded. Ascospores 8–14 × 3.5–5 μm ($\bar{x}$ = 11 × 4 μm, n = 35),

overlapping uniseriate, fusiform, obtuse ends, guttulate, hyaline when young, becoming brown at maturity, uniseptate, smooth-walled, surrounded by a gelatinous sheath. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinated on PDA within 12 h at 26°C. Germ tubes produced from one end of ascospore. Colonies on PDA reached 10 mm diam. after 3 weeks at 26 °C; mycelium white, flossy, circular, dense, with the entire edge; pale to brown in reverse, pigment produced which turns the media brown.

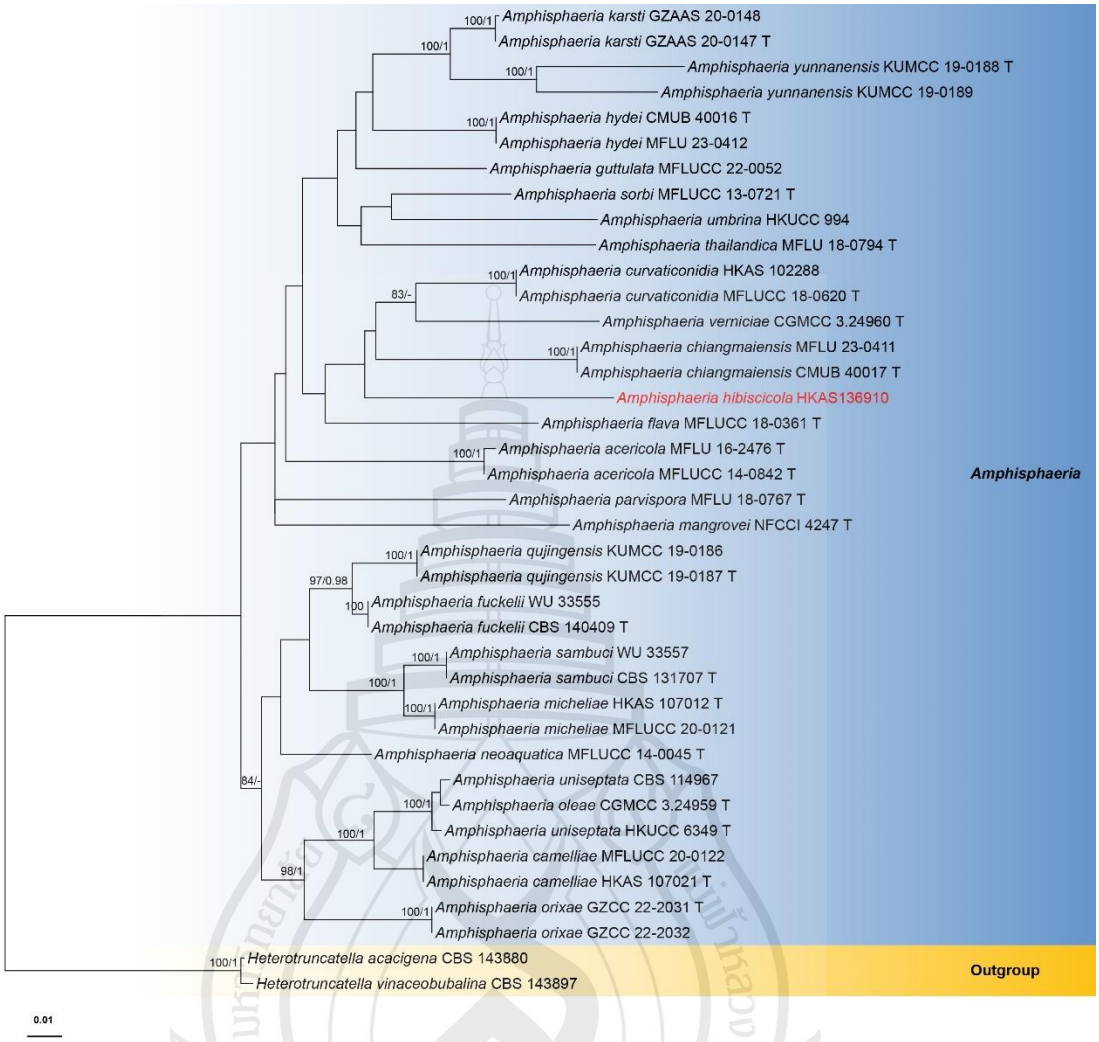
Material examined: CHINA, Zhejiang Province, Tongxiang City, Zhenxing East Road, Tongxiang Botanical Garden, on diseased leaves of *Hibiscus mutabilis*, 15 August 2023, Y.R. Sun, ZJ09 (HKAS 136910, **holotype**); ex-type culture GUCC 24-0092.

Notes: The BLASTn searches of the LSU sequence of *Amphisphaeria hibiscicola* (GUCC 24-0092) resulted in 97.46% and 97.45% matches with *A. oleae* (UESTCC 23.0120) and *A. uniseptata* (CBS 114967). The ITS BLASTn results showed 90.14% and 89.04% matches with *A. umbrina* (PRA-JV24328) and *A. curvaticonidia* (MFLUCC 18-0620). The phylogenetic analyses (Figure 4.98) showed that *A. hibiscicola* is close to *A. chiangmaiensis*, *A. curvaticonidia* and *A. verniciae*. Regarding morphology, *A. hibiscicola* can be distinguished from *A. chiangmaiensis* by its brown spores, whereas the latter exhibits hyaline spores (Samarakoon, 2023). Additionally, *A. hibiscicola* possesses spores with sheaths, a characteristic absent in *A. oleae*, *A. umbrina*, *A. uniseptate*, and *A. verniciae* (Tsui et al., 2001; Senanayake et al., 2015; Li, Liang et al., 2024). Furthermore, *A. hibiscicola* differs from *A. curvaticonidia* in the number of septa present in its spores, with the former displaying 1-septate spores and the latter featuring 3-septate spores (Samarakoon et al., 2020). Thus, *A. hibiscicola* is hereby introduced as a novel species from *Hibiscus mutabilis* in China.



Note a Host. b, c Appearance of ascomata on the substrate. d, e Section of ascomata. f–j Asci. k Paraphyses. l Germinating ascospore. m–p Ascospores (p in Indian Ink). q, r Colonies on PDA. Scale bars: d, e = 200 µm, f–l = 20 µm, m–p = 10 µm.

Figure 4.97 *Amphisphaeria hibiscicola* (HKAS 136910, holotype)



Note The best scoring RAxML tree with a final likelihood value of −19,614.282564 is presented. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Heterotruncatella acacigena* (CBS 143880) and *H. vinaceobubalina* (CBS 143897). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.98 Phylogenetic tree of *Amphisphaeria*

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr, Sydowia 50(1): 23 (1998)

Apiospora Sacc. Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 4 4: 85 (1875)

Notes: *Apiospora* was introduced by Saccardo (1875) and belongs to *Apiosporaceae* (Hyde, de Silva et al., 2020; Wijayawardene et al., 2020; Pintos & Alvarado, 2021). *Apiosporaceae* was established by Hyde et al. (1998) and is typified by *Apiospora* (Ellis, 1971; Senanayake et al., 2015; Feng et al., 2021). The asexual morph *Arthrinium* has been linked to the sexual morph of *Apiospora* (Ellis, 1971; Seifert et al., 2011). Crous and Groenewald (2013) synonymized *Apiospora* under *Arthrinium* based on the one fungus-one name principle, but the genera are regarded as distinct based on molecular data (Pintos & Alvarado, 2021). Six genera are recognized in *Apiosporaceae*, *viz. Appendicospora*, *Arthrinium*, *Apiospora*, *Dictyoarthrinium*, *Endocalyx* and *Nigrospora* (Hyde, de Silva et al., 2020; Wijayawardene et al., 2020; Pintos & Alvarado, 2021). The sexual morph of *Apiospora* is similar to *Khuskia* and *Nigrospora* (Pintos & Alvarado, 2021). The asexual morphs of *Apiospora* and *Arthrinium* sensu stricto are also similar in having basauxic conidiogenesis cells (Hughes, 1953; Pintos & Alvarado, 2021). *Apiospora* is a distinct lineage in the phylogenetic analyses and is morphologically distinct from the other genera in *Apiosporaceae*.

Apiospora tropica Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558826; Facesoffungi number: FoF 09901, Figure 4.99

Etymology: epithet "*tropica*" means humid tropical.,

Holotype: MFLU 21-0084

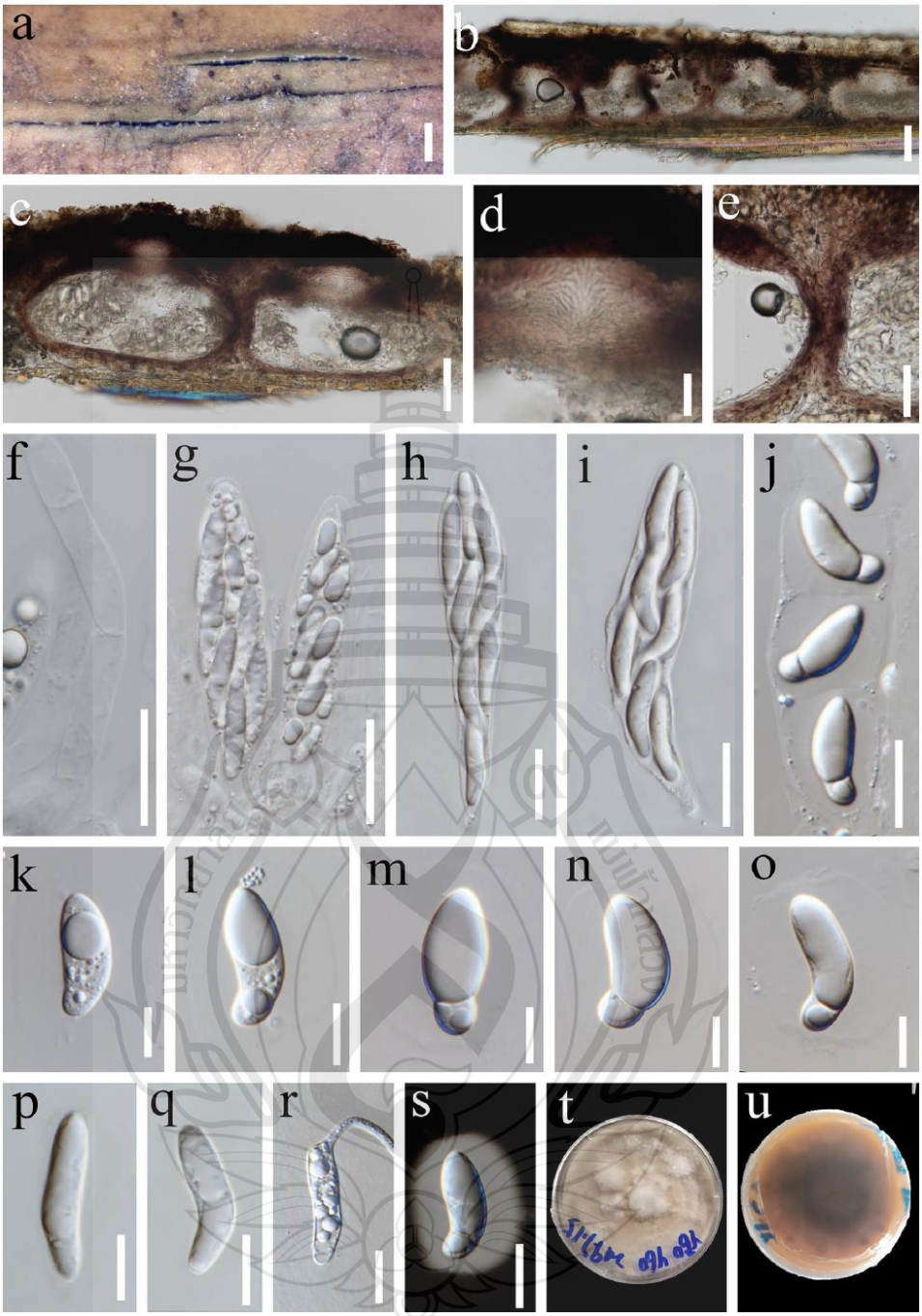
Saprobic on dead bamboo culms. **Sexual morph**: *Ascostromata* raised, immersed to erumpent, raised areas on the host surface, with ascostromata breaking through raised cracks at the black centre, multi-loculate, forming groups in stromata, gregarious, fusiform. *Locules* 136–188 µm diam., 87–103 µm high, immersed in stromata, perithecial, arranged in a row, ampulliform to subglobose, brown to reddish-brown, ostioles with periphyses. *Peridium* comprising 3–5 layers, thick-walled, composed of dark brown cells of textura angularis. *Hamathecium* composed of long, 5–6.5 µm wide, septate, unbranched paraphyses, not

anastomosing. *Asci* 83–98 × 15–18 µm ($\bar{x}$ = 88.5 × 16.5 µm, n = 15), 8-spored, unitunicate, clavate, apically rounded, sessile to subsessile. *Ascospores* 21–26 × 5.5–10 µm ($\bar{x}$ = 24 × 7 µm, n = 20), biseriate, partly overlapping, reniform, rarely straight, hyaline, septate, slightly constricted at the septum, sometimes with an indistinct septum when mature, usually 2-celled, with a large upper cell and a smaller lower cell, mostly curved at the lower cell, smooth-walled, surrounded by a large entire sheath, becoming shallow when dry. **Asexual morph**: Not observed.

Culture characteristics: Ascospores germinating on WA within 12 h at 25 °C. The hyaline germ tube germinates from a point of one cell of the ascospores. Colonies slow-growing on PDA at room temperature, circular, with an irregular edge, cottony, dense at the center, white from above, dark brown to brown in the center from below.

Material examined: Thailand, Kanchanaburi Province, Thong Pha Phum District, Pilok Subdistrict, dead bamboo culms, 28 June 2019, Guang-Cong Ren, Y60 (MFLU 21-0084, **holotype**); ex-type living culture MFLUCC 21-0056.

Notes: The multi-gene phylogenetic analysis of combined LSU, ITS, *TEF1-α*, and *TUB2* sequence data revealed that *Apiospora tropica* forms a sister clade to *A. neosubglobosa* and *A. subglobosum* with strong bootstrap support (MLBS/BPP 100/1.00) (Figure 4.100). In a BLASTn search in GenBank, the closest match of the ITS sequence of *Apiospora tropica* (MFLUCC 21-0056) was 86.33% similar across 100% of the query sequence, which translates into 86.33% similarity to *A. pterosperma* (CBS 134000). The closest match of the LSU and *TUB2* sequences of *A. tropica* were 97.51% and 85% similar across 94% and 70% of the query sequence, which translates into 91.66% and 59.5% similarity to *A. neosubglobosa* (GZAAS 20-0099), respectively. *Apiospora tropica* is morphologically similar to *A. gelatinosa* in the shape of ascostromata, asci and ascospores (Feng et al., 2021). However, the locules, asci and ascospores of *A. tropica* are smaller than *A. gelatinosa* (locules 87–103 × 136–188 µm *vs.* 144–199 × 184–214 µm, asci 83–98 × 15–18 µm *vs.* 85–121 × 15–24 µm and ascospores 21–26 × 5.5–10 µm *vs.* 28–31 × 6–8 µm). Therefore, we introduce *A. tropica* as a novel species based on both phylogenetic evidence and morphology.



Note a Stromata on bamboo host. b, c Section of an ascostroma. d Ostiole with periphyses. e Peridium. f Paraphyses. g–j Asci. k–q, s Ascospores. r Germinated ascospore (s Ascospore stained in Indian ink). t–u Culture on PDA. Scale bars: a = 300 μm, b–c = 50 μm, d–j = 20 μm, k–s =10 μm.

Figure 4.99 *Apiospora tropica* (MFLU 21-0084, holotype)

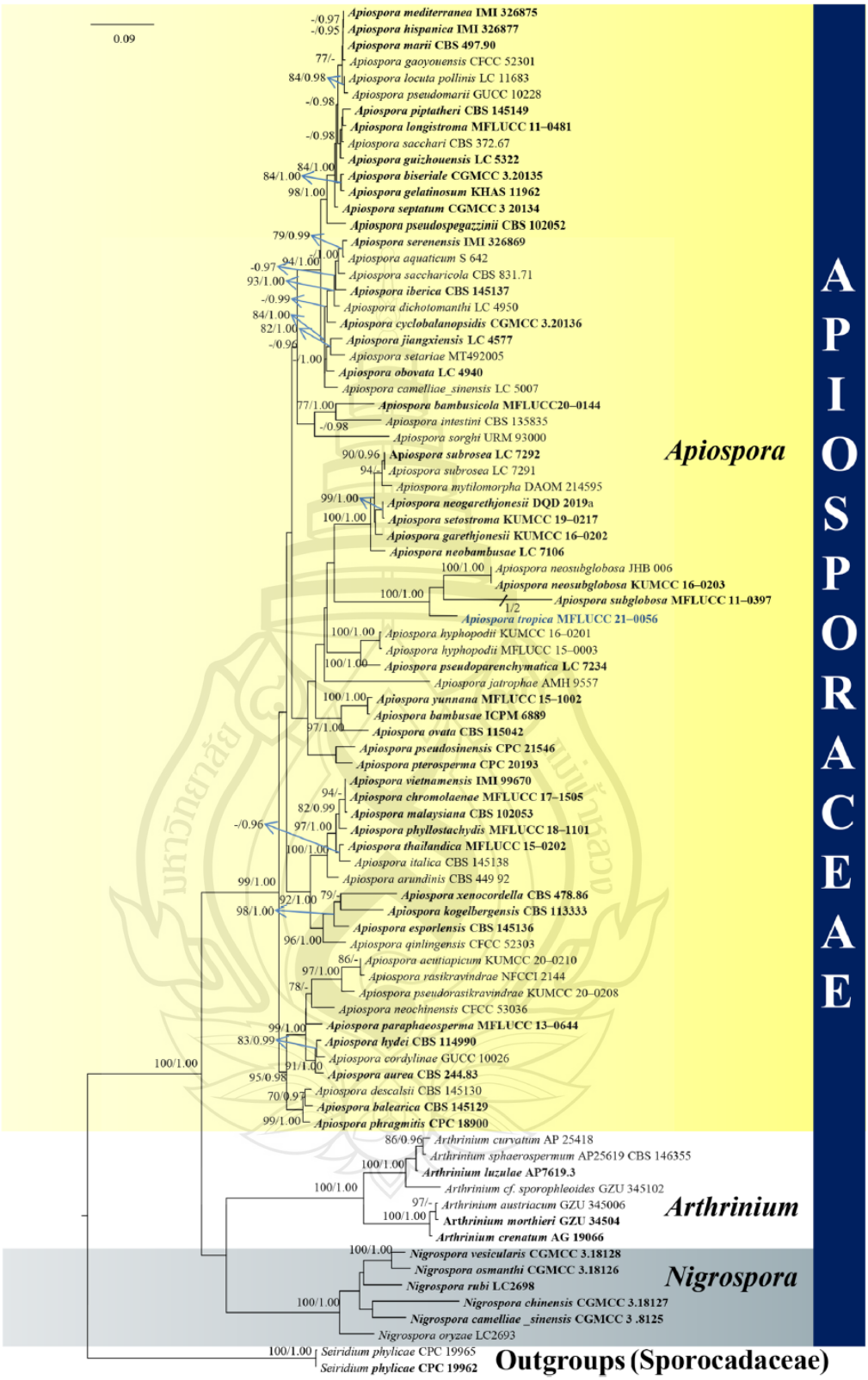


Figure 4.100 Phylogenetic tree of Apiosporaceae

Nigrospora Zimm., Centbl. Bakt. ParasitKde, Abt. I 8: 220 (1902)

Notes: *Nigrospora* was introduced by Zimmerman (1902) with *N. panici* as the type species. The genus is characterized by spherical to subspherical conidiogenous cells and dark brown to black, aseptate and globose to subglobose conidia (Zimmerman, 1902; Zhang et al., 2024). These species thriving across diverse substrates such as myriad plants, soil, and air, encompasses species acknowledged as significant plant pathogens (Abass & Mohammed, 2014; Hao et al., 2020; Hyde, de Silva et al., 2020). Some fungal strains isolated from medicinal plants process rich secondary metabolites, which are treasures for the development of industry and medicine (Zhao et al., 2012; Luo, Zhou et al., 2017). In this study, we report *Nigrospora sphaerica*, from the *Dracaena* sp. in Thailand.

Nigrospora sphaerica (Sacc.) E.W. Mason, Trans. Brit. Mycol. Soc. 12: 158. (1927)

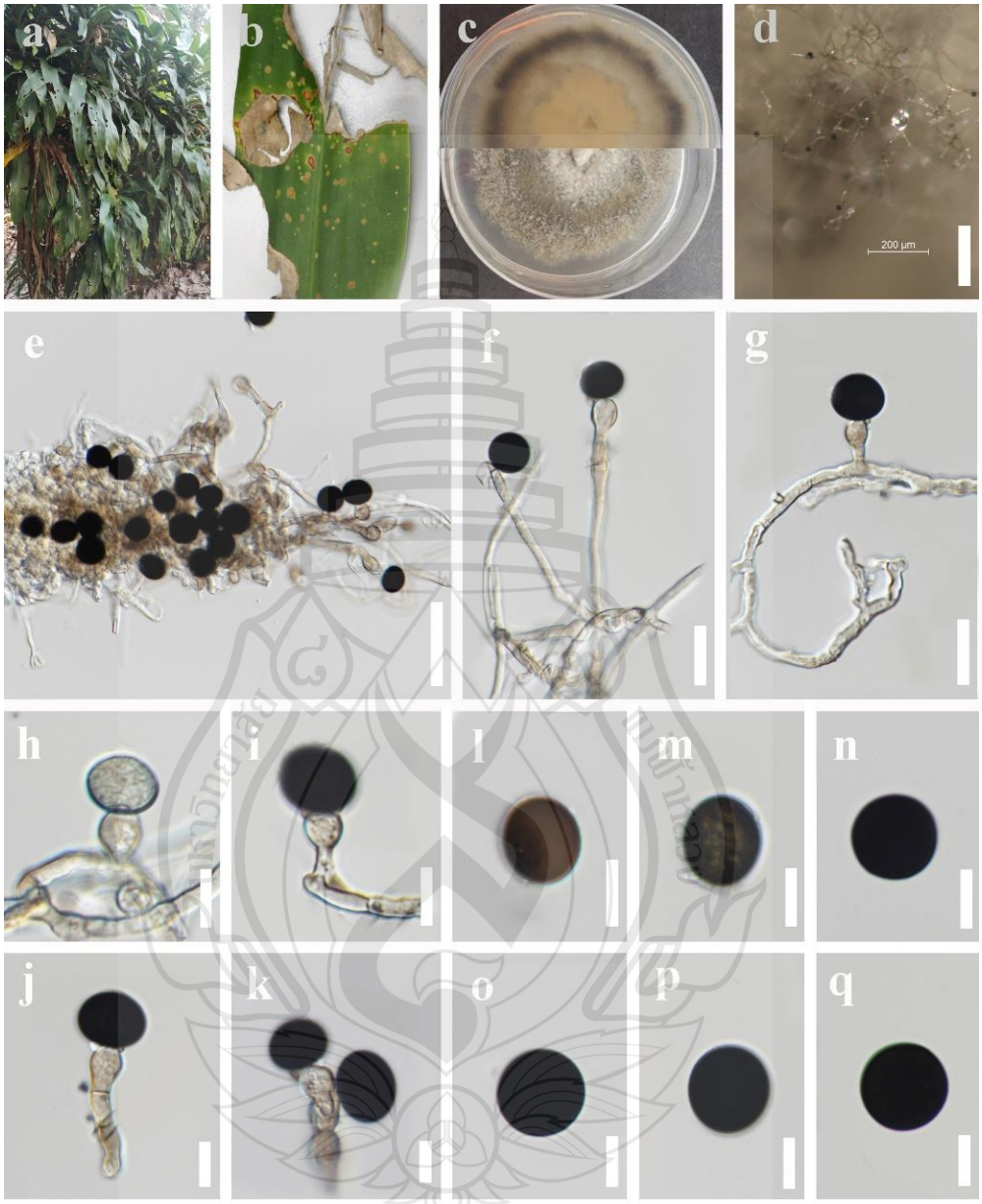
Index Fungorum number: IF254776; Facesoffungi number: FoF06599; Figure 4.101

Pathogenic on diseased leaves of *Dracaena* sp. Mycelium fluffy, pale brown, septate, branched. **Sexual morph**: Not observed. **Asexual morph**: *Conidiophores* 2–4 μm wide, micronematous or macronematous, flexuous or straight, branched, septate, hyaline to pale brown, smooth, *Conidiogenous cells* holoblastic, monoblastic, determinate, pale brown, subglobose, ellipsoidal to doliform, 6–11 μm diam. *Conidia* 12–20 μm ($\bar{x}$ = 15 μm, n=30) diam., solitary, globose or subglobose, brown to black, shining, smooth, aseptate,

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, leaf spots of *Dracaena* sp. (*Liliaceae*), 15 September 2020, S Wang, LD2, living culture GUCC 24-0139.

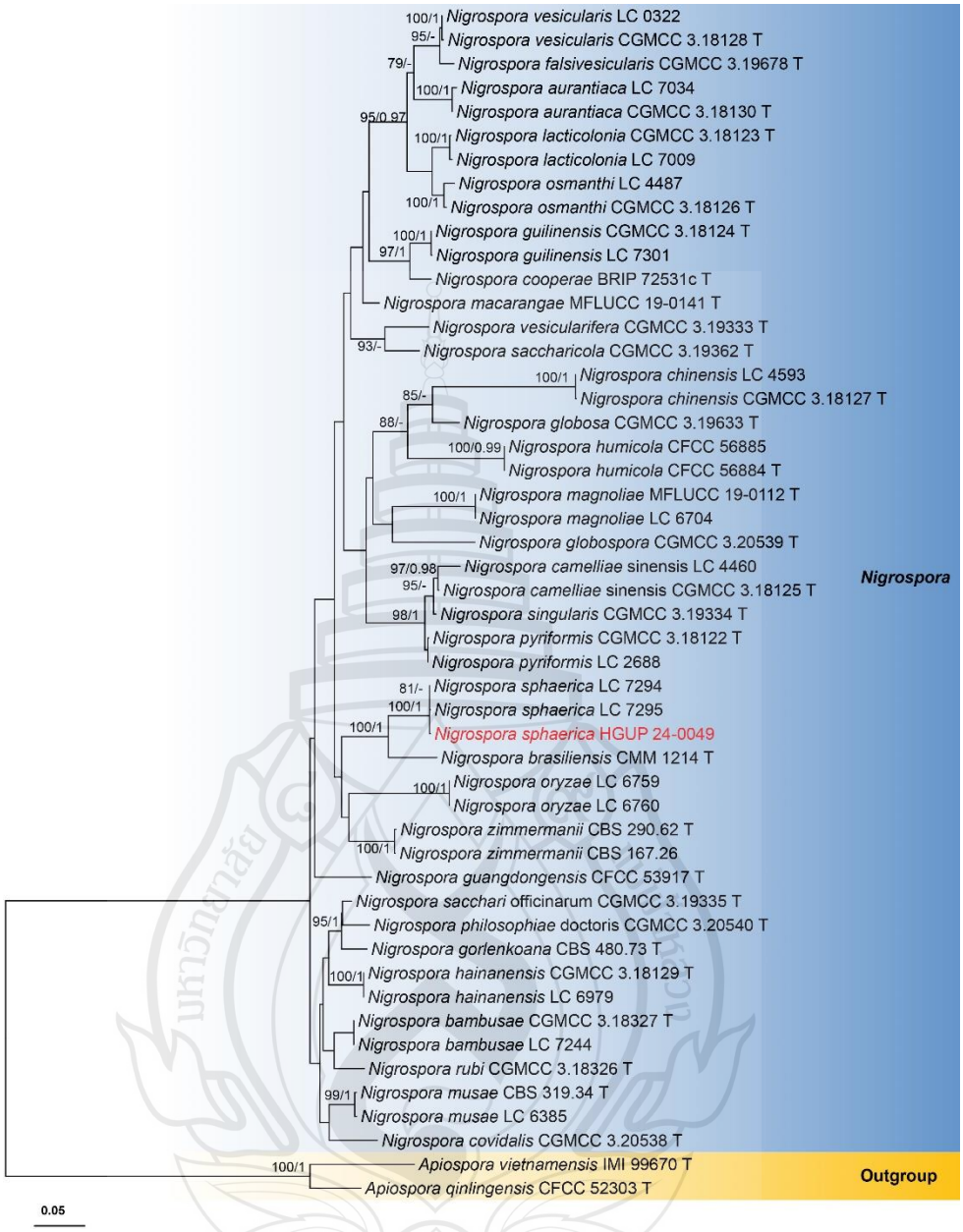
Notes: *Nigrospora sphaerica* was introduced by Mason (1927). Subsequently, it was reported as saprobes, pathogens, and endophytic fungi from different countries (Abass et al., 2013; Abass & Mohammed, 2014; Dutta et al., 2015; Cui et al., 2018; Hyde, de Silva et al., 2020). *Nigrospora sphaerica* most commonly reported as a pathogen capable of causing leaf spot disease in a variety of plants (Abass et al., 2013; Dutta et al., 2015; Cui et al., 2018). Hyde et al. (2020) summarized the hosts of *N. sphaerica*, including *Actinidia* sp., *Camellia* sp., *Citrus* sp., *Deutzia* sp., *Harpullia longipetala*. In this study, a new host, *Dracaena* sp. is

reported for *N. sphaerica* in Thailand.



Note a Host. b Diseased host leaf. c Upper surface and reverse overview of culture on PDA. d Colonies on PDA. e–k Conidiophores and conidiogenous cells and conidia. l–q Conidia. Scale bars: d = 200 µm, e = 50 µm, f, g = 20 µm, h–q = 10 µm.

Figure 4.101 *Nigrospora sphaerica* (GUCC 24-0139, new host record)



Note The best scoring RAxML tree with a final likelihood value of −19,614.282564 is presented. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Apiospora qinlingensis* (CFCC 52303) and *A. vietnamensis* (IMI 99670). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.102 Phylogenetic tree of *Nigrospora*

Sporocadaceae Corda, Icon. Fungorum (Prague) 5: 34 (1842)

Bartalinia Tassi, Bulletin Labor. Orto Bot. de R. Univ. Siena 3: 4 (1900)

Notes: Tassi (1900) introduced *Bartalinia*, designating *B. robillardoides* as its type species. *Bartalinia* species have been documented worldwide and various hosts (Phookamsak et al., 2019; Jayawardena et al., 2022; Konta et al., 2023). These fungi exhibit a global presence, thriving as saprobes on various host trees (Wanasinghe et al., 2018; Jayawardena et al., 2022), including some found in freshwater habitats (Nguyen et al., 2019), while frequently being associated with leaf spots (Liu, Bonthond et al., 2019; Tibpromma et al., 2020). Currently, 25 species are accepted in this genus (Species Fungorum, 2024).

Bartalinia pini F. Liu, L. Cai & Crous, Stud. Mycol. 92: 309 (2018) [2019]

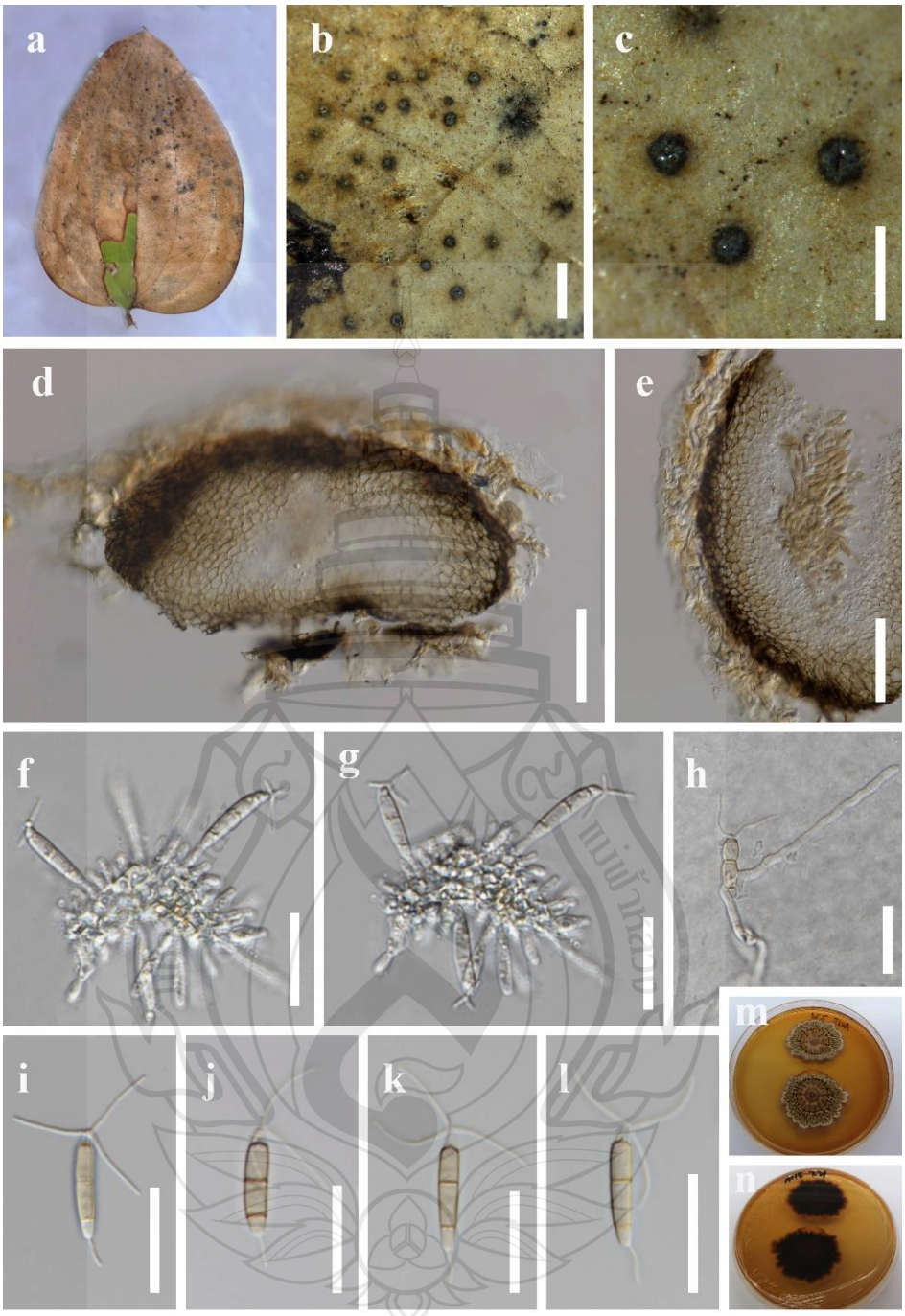
Index Fungorum number: IF828321; Facesoffungi number: FoF X; Figure 4.103

Pathogenic on diseased leaves of *Smilax* sp. **Asexual morph**: *Conidiomata* 220–260 µm wide, 110–150 µm high, black, solitary to gregarious or confluent, sub-immersed, globose, unilocular, thick-walled, glabrous. *Conidiomata wall* 30–40 µm wide, composed of thick-walled, brown cells, gradually merging with hyaline cells of textura angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* annellidic, discrete, lageniform or ampulliform, hyaline, smooth. *Conidia* cylindrical with acute or obtuse ends, straight or slightly curved, 3-septate, smooth, 16–22 × 2.5–4.5 µm; basal cell obconic with a truncate base, thin-walled, hyaline, 3–4 µm long; 2-median cells, cylindrical, pale brown, fairly thick-walled, the second cell from base 6.5–8.5 µm long; third cell 5–7 µm long; apical cell conic with an acute apex, thin-walled, hyaline, 3–4 µm long; apical appendage with three branches, attenuated, tubular, filiform, flexuous, divergent, 12–17 µm long; basal appendage single 3.5–8 µm long. **Sexual morph**: unknown.

Culture characteristics: colonies on PDA reached 4 cm in diameter after 4 weeks at 25 °C, colonies filamentous to circular, medium dense, aerial mycelium on surface flat or raised, with filiform margin, brown in the middle surrounded by white circles viewed from above, dark brown from reverse, pigment produced which turns the media brown.

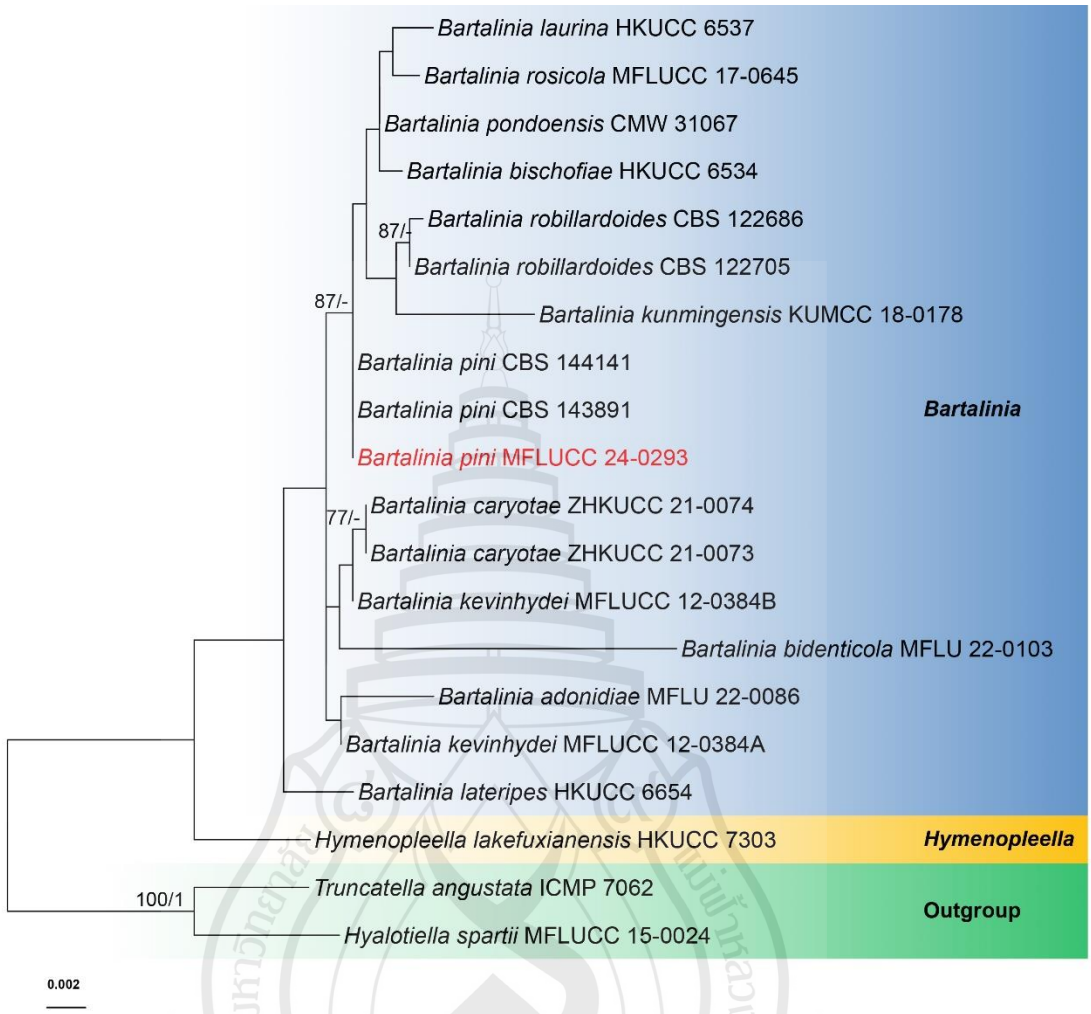
Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, leaf spots of *Smilax* sp. (*Liliaceae*), 16 July 2020, Y.R. Sun, M15 (HGUP 24-0050); living culture MFLUCC 24-0293.

Notes: *Bartalinia pini* was first introduced by Liu, Bonthond et al. (2019), which was isolated from needles of *Pinus patula* needles (in Uganda) and leaves of *Acacia koa* (in USA). Dehghani et al. (2022) reported it is associated with the leaf spot of mango trees in Iran. Our strain is phylogenetically close to *B. pini* in the analyses (Figure 4.104). The analysis of nucleotide polymorphism in the ITS and LSU region also revealed no base differences between our strain and *Bartalinia pini* (CBS 143891). In morphology, our collection is similar to *Bartalinia pini* in having annellidic, discrete, lageniform or ampulliform conidiogenous cells and cylindrical with acute or obtuse ends, 3-septate, pale brown to brown conidia (16–22 × 2.5–4.5 μm *vs.* 13.5–20.5 × 1.5–3.5 μm) (Liu, Bonthond et al., 2019). The slight difference in conidial size may be due to the fact that our conidia were observed directly from native substrates, whereas the latter were cultured on culture media. In addition, we first provided the characteristics and dimensions of conidiomata and conidiomatal walls. We identified our strain as *Bartalinia pini* herein, representing a new record from *Smilax* sp. in Thailand.



Note a Host. b, c Close up view of conidiomata. d Section through conidioma. e Section through pycnidial wall. f–h Immature conidia attached to conidiogenous cells. i–l Conidia. m Germinated conidium. Scale bars: b = 1000 µm, c = 500 µm, d, e = 50 µm, f–l = 20 µm.

Figure 4.103 *Bartalinia pini* (HGUP 24-0050, new host record)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Hyalotiella spartii* (MFLUCC 15-0024) and *Truncatella angustata* (ICMP 7062). The new collections are indicated in red.

Figure 4.104 Phylogenetic tree of *Bartalinia*

Neopestalotiopsis Maharachch., K.D. Hyde & Crous, Stud. Mycol. 79: 135 (2014)

Notes: *Neopestalotiopsis* is a genus of fungi known for its diverse ecological roles, including acting as pathogens and endophytes (Maharachchikumbura et al., 2014; Liu et al., 2017; Ariyawansa & Hyde, 2018; Sun et al., 2023). They have been implicated in various plant diseases, such as leaf spots and fruit rots, affecting a wide range of host plants (Prasannath et al., 2021; Fiorenza et al., 2022). Molecular phylogenetic studies have been instrumental in delineating the species and understanding the evolutionary relationships within *Neopestalotiopsis*. However, the genus faces challenges in accurate species identification and classification due to its morphological similarities with closely related genera, necessitating ongoing taxonomic revisions and advanced molecular analyses (Li et al., 2022; Sun et al., 2023).

Neopestalotiopsis amomi Y.R. Sun & Yong Wang bis, ***sp. nov.***

Index Fungorum number: IF571230; Facesoffungi number: FoF12912; Figurre 4.105

Etymology: Refers to the name of the host plant from which the fungus was isolated.

Holotype: HKAS 124563

Associated with leaf blight of *Amomum villosum*. Symptoms irregular shape, pale to brown, slightly sunken spots appear on the leaves of *Amomum villosum*, which later expand outwards. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, subglobose to globose, unilocular, brown, semi-immersed on leaves. *Conidiophores* 3–5 µm long, often reduced to conidiogenous cells. *Conidiogenous cells* 1–2 µm wide, subcylindrical, ampulliform, hyaline. *Conidia* 18–30 × 4–7 µm, ($\bar{x}$ = 25 × 6 µm, n = 40), L/W ratio = 4.2, fusiform, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline, smooth-walled, 3–7 µm long; three median cells 12–19 µm long ($\bar{x}$ = 16 µm, n = 40), pale brown to brown, concolourous, wall rugose, septa darker than the rest of the cell; second cell from base pale brown to brown, 3–8 µm long; third cell pale brown to brown, 3–7 µm long; fourth cell pale brown to brown, 3–7 µm long; apical cell 2–5 µm long, hyaline, conic to acute; with 2–3 tubular appendages on apical cell, inserted

at different loci in a crest at the apex of the apical cell, unbranched, 7–17 μm long; single basal appendage, unbranched, tubular, centric, 2–5 μm long.

Culture characteristics: Conidia germinated on PDA within 12 hours from single-spore isolation. Colony diameter reached 8 cm after two weeks at 25°C on PDA media, circular, surface rough, flat, white from above and below.

Material examined: China, Guizhou Province, Qiannan Bouyei and Miao Autonomous Prefecture, Luodian District, leaf blight of *Amomum villosum* Lour. (*Zingiberaceae*), 3 September 2021, Y.R. Sun, L8 (HKAS 124563, **holotype**); ibid., on leaf blight of *Amomum villosum*, 3 September 2021, Y.R. Sun, L8-1 (HKAS 124564).

Notes: *Neopestalotiopsis amomi* was isolated from the diseased leaves of *Amomum villosum* in China. Two collections HKAS 124563 and HKAS 124564 clustered together with good support (ML-BS = 100%, BYPP = 1) and formed a sister clade to *N. zingiberis* (GUCC 21001) which was also isolated from a *Zingiberaceae* plant (He et al., 2022). The former differs in producing thinner conidia (4–7 μm in *N. amomi vs.* 6–9.5 μm in *N. zingiberis*) and shorter conidiophores (3–5 μm in *N. amomi vs.* 12–25 μm in *N. zingiberis*). In addition, there are 4 base pairs differences between HKAS 124563 and GUCC 21001 in the ITS gene and 10 base pairs differences in the *TEF1-α* gene. *Neopestalotiopsis amomi* also differs by smaller conidia (18–30 × 4–7 μm *vs.* 42–46 × 9.5–12 μm) from *N. magna*. Thus, we introduce *N. amomi* as a new species.



Note a Host. b Leaf blight on *Acrostichum aureum*. c Close up view of conidiomata. d conidiogenous cells. e Immature conidia attached to conidiogenous cells. f–i Conidia. j Germinated conidium. Scale bars: d, e = 10 µm, f–j = 20 µm.

Figure 4.105 *Neopestalotiopsis amomi* (HKAS 124563, holotype)

Neopestalotiopsis hyperici Y.R. Sun & Yong Wang bis, ***sp. nov.***

Index Fungorum number: IF 571228; Facesoffungi number: FoF12913; Figure 4.106

Etymology: The specific epithet is referring to Hypericum, the host plant which the fungus was isolated.

Holotype: HKAS 124561.

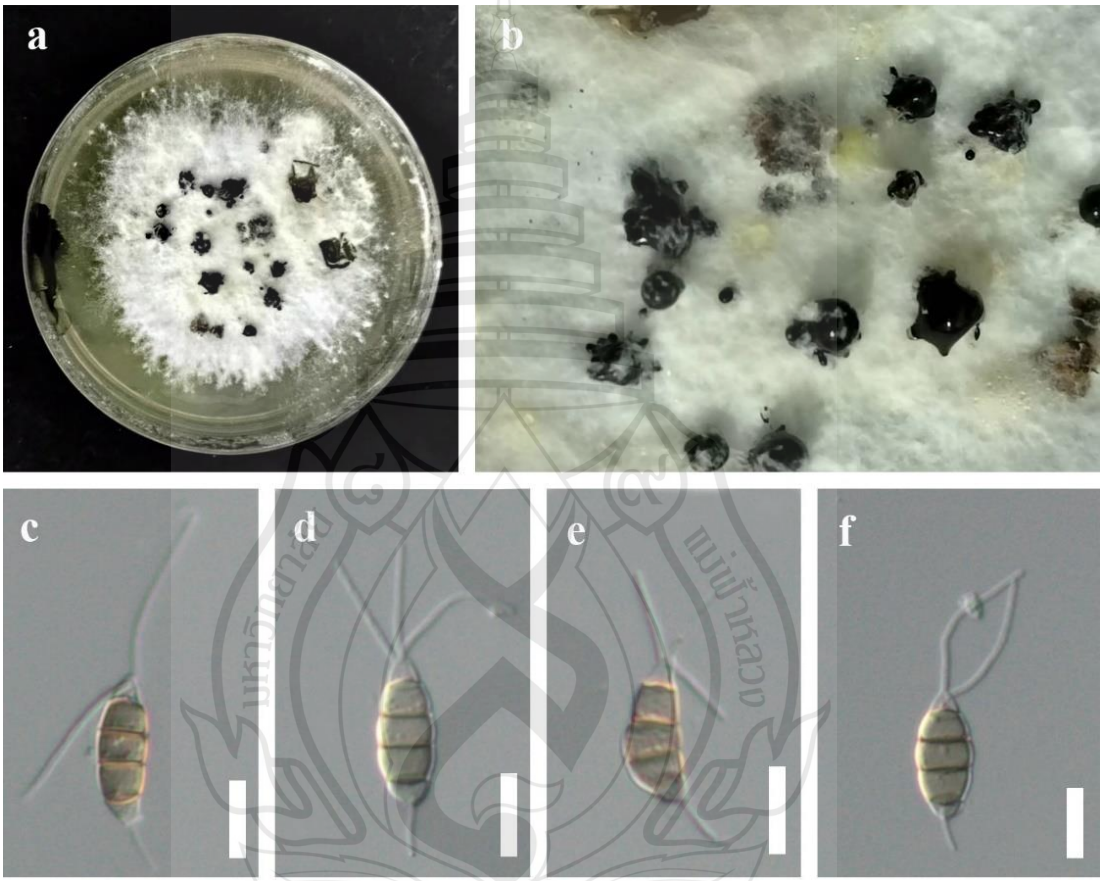
Associated with leaf spots of *Hypericum monogynum*. Symptoms irregular shape, pale to brown, slightly sunken spots appear on the leaves of *Hypericum* sp., which later expand outwards. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, unilocular, dark. *Conidiophores* often reduced to conidiogenous cells. *Conidiogenous cells* indistinct. *Conidia* 17–22(–24) × 5–8 μm, ($\bar{x}$ = 19 × 7 μm, n = 30), L/W ratio = 2.8, fusoid, sub-cylindrical, straight to slightly curved, 4-septate; basal cell conic to obconic with a truncate base, hyaline to sub-hyaline, 2–4 μm long; three median cells 10–14(–17) μm long ($\bar{x}$ = 12 μm, n = 30), wall rugose, concolorous; second cell from base pale brown to brown, 3–5 μm long; third cell pale brown to brown, 3–6 μm long; fourth cell pale brown to brown, 2–6 μm long; apical cell 1–4 μm long, hyaline, rugose and thin-walled; with 2–3 tubular apical appendages, arising from the apical crest, unbranched, filiform, 11–23 μm long; single basal appendage 4–7 μm long, unbranched, tubular, centric.

Culture characteristics: Colonies on PDA reaching up to 10 cm after 2 weeks, dense mycelium on the surface, white from above and below. Fruiting bodies were observed after 14 days.

Material examined: China, Guizhou Province, Guiyang City, Baiyun District, Changpoling National Forest Park, leaf spot of *Hypericum monogynum* L. (*Clusiaceae*), 20 August 2021, Y.R. Sun, CL5-1 (HKAS 124561, **holotype**); ex-type culture, KUNCC 22-12597 = GUCC 21-0812; ibid., on leaf spots of *Hypericum monogynum*, 20 August 2021, Y.R. Sun, CL5-1-1, living culture KUNCC 22-12598 = GUCC 21-0811.

Notes: *Neopestalotiopsis hyperici* is related to *N. rhododendri* and *N. protearum* in the phylogenetic analysis (Figure 4.113), but they can be distinct from concolourous conidia and the size of their median cells (10–14 μm in *N. hyperici vs.* 14–20 μm in *N. rhododendri vs.*

16–17 µm in *N. protearum* (Maharachchikumbura et al., 2014; Yang et al., 2021). In addition, there are 13 base pairs differences between *N. hyperici* and *N. rhododendri*, and 10 base pairs differences between *N. hyperici* and *N. protearum* in the *TEF1-α* region. Thus, we introduce *N. hyperici* as a new species.



Note a Culture. b Close up view of conidiomata. c–f Conidia. Scale bars: c–f = 10 µm.

Figure 4.106 *Neopestalotiopsis hyperici* (HKAS 124561, holotype)

Neopestalotiopsis photiniae Y.R. Sun & Yong Wang bis, ***sp. nov.***

Index Fungorum number: IF571231; Facesoffungi number: FoF12914; Figure 4.107

Etymology: Referring to the host plant from which the fungus was isolated.

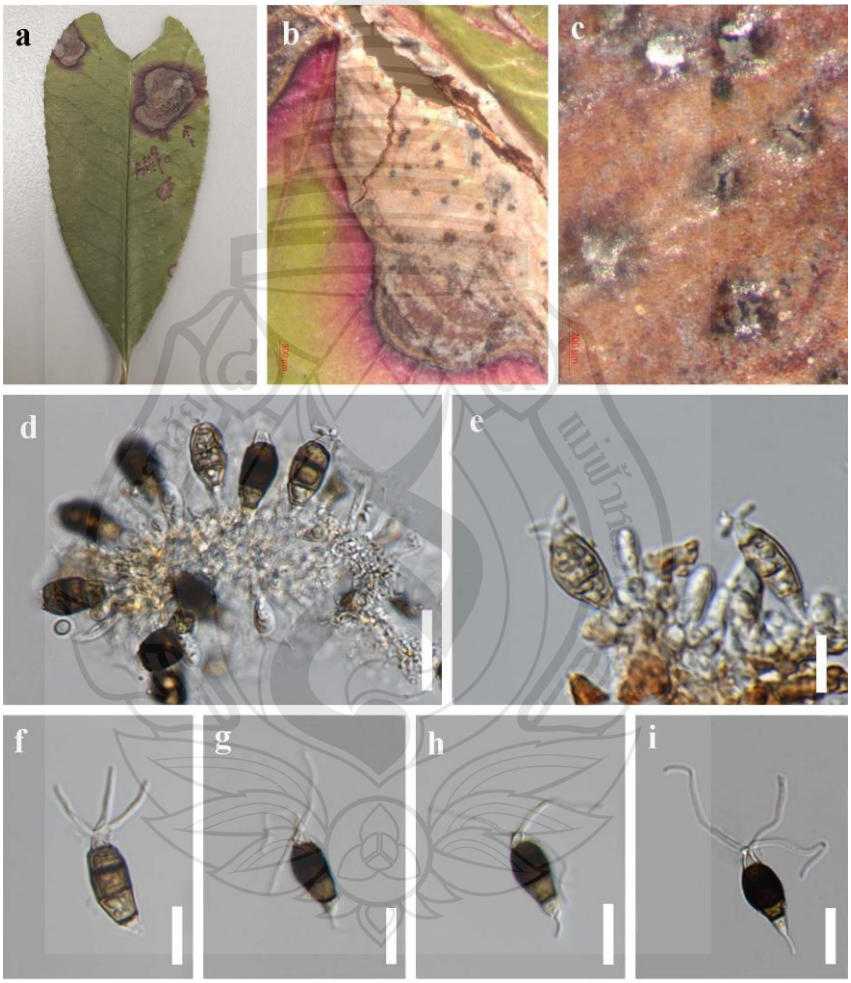
Holotype: HKAS 125895.

Associated with leaf spots of *Photinia serrulat*. Symptoms irregular shape, pale to brown, slightly sunken spots appear on the leaves of *Photinia serrulata*, which later expand outwards. Small spots gradually enlarged, changing to brown circular ring spots with a dark brown border. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, subglobose to globose, unilocular, dark brown, semi-immersed on leaves. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* 1–3 × 2–4 µm, sub-cylindrical, ampulliform, hyaline. *Conidia* 20–29 × 5–12 µm, ($\bar{x}$ = 23 × 9 µm, n = 40), L/W ratio = 2.6, broadly fusiform, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline to pale brown, 1–5 µm long; three median cells 13–19 µm long ($\bar{x}$ = 16 µm, n = 40), brown to dark, wall rugose, versicolourous; second cell from base pale brown to brown, 4–6 µm long; the third and fourth cells dark brown to black, are not easily distinguished, septate indistinct, 10–13 µm long; apical cell 2–4 µm long, hyaline, conic to acute; with 2–3 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 17–33 µm long; single basal appendage, unbranched, tubular, centric, 1–6 µm long.

Culture characteristics: Conidia germinated on PDA within 12 hours at 25 °C from single-spore isolation. Apical cells produced germ tubes. Colony diameter reached 80 mm after three weeks at 25 °C on PDA media, circular, surface rough, flat, white from above and below.

Material examined: China, Guizhou Province, Guiyang City, Nanming District, xiaochehe road, Guiyang Ahahu National Wetland Park, on leaf spots of *Photinia serrulata* Lindl. (Rosaceae), 21 September 2019, Y.R. Sun, AH9 (HKAS 125895, **holotype**); ex-type culture, MFLUCC 22-0129; ibid., on leaf spots of *Photinia* sp. (*Rosaceae*), 21 September 2019, Y.R. Sun, AH9-1, living culture, GUCC 21-0820.

Notes: *Neopestalotiopsis photiniae* is phylogenetically sister to *N. sichuanensis* and *N. vheenae* (Figure 4.113). *Neopestalotiopsis photiniae* differs by its thinner conidia (L/W ratio = 2.6 *vs.* L/W ratio = 4.1) from *N. sichuanensis* (Jiang et al., 2021). *Neopestalotiopsis photiniae* is morphologically distinguishable from *N. vheenae* in shorter conidiogenous cells (1–3 × 2–4 µm *vs.* 5–10 × 3–5 µm) (Prasannath et al., 2021). Therefore, *N. photiniae* is introduced as a new species.



Note a Host. b Leaf spot on *Photinia serrulata*. c Close up view of conidiomata. d, e conidia attached to conidiogenous cells. f–i Conidia. Scale bars: d = 1000 µm, c = 200 µm, d = 20 µm, f–i = 10 µm.

Figure 4.107 *Neopestalotiopsis photiniae* (HKAS 125895, holotype)

Neopestalotiopsis suphanburiensis Y.R. Sun & Yong Wang bis, ***sp. nov.***

Index Fungorum number: IF571232; Facesoffungi number: FoF12916; Figure 4.108

Etymology: Refers to the province where the fungus was collected, Suphan Buri Province.

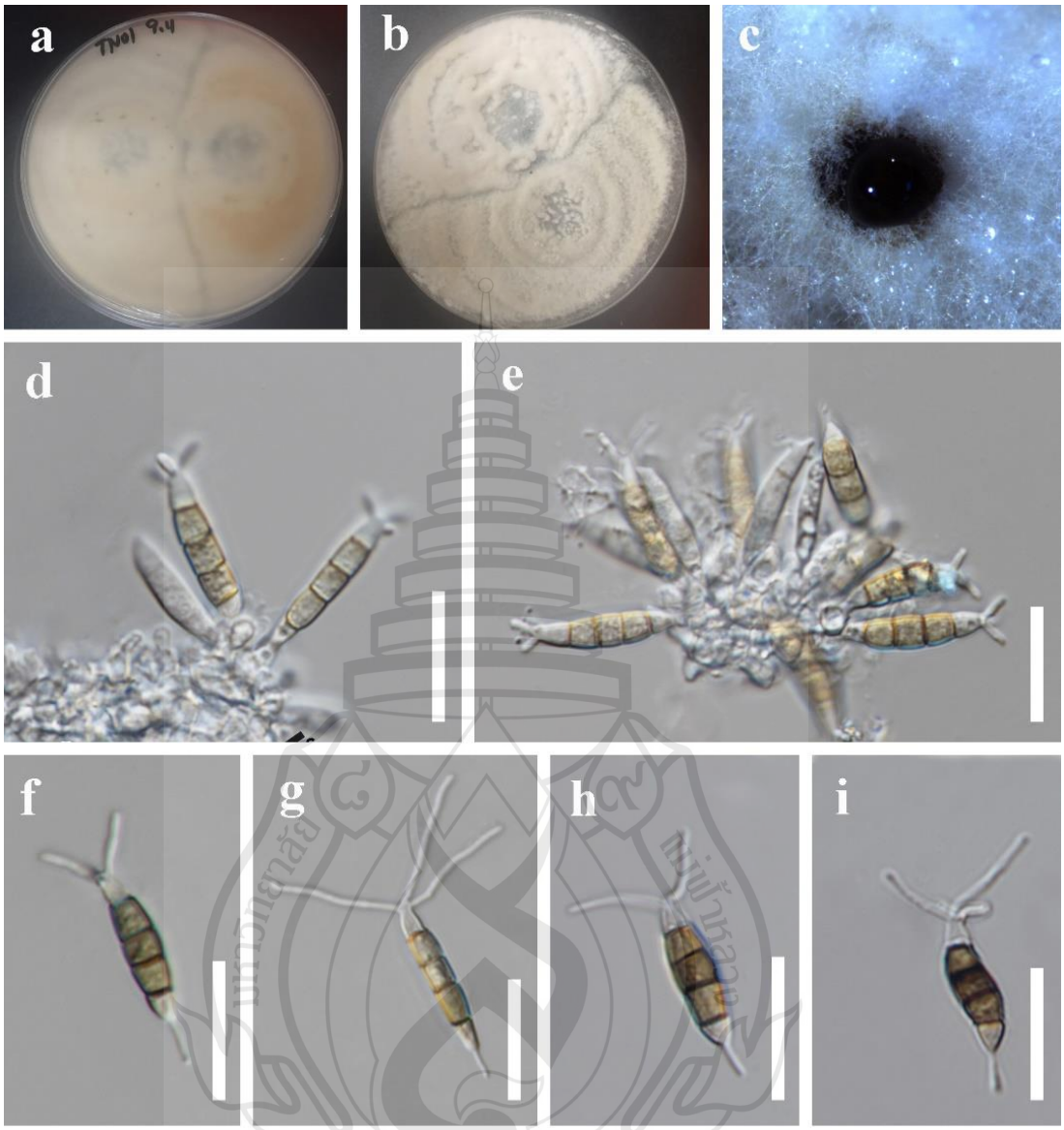
Holotype: MFLU 22-0168.

Saprobic on stems of an unidentified plant. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, subglobose to globose, unilocular, brown to dark, immersed on stems. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* sub-cylindrical, ampulliform, hyaline. *Conidia* 19–29 × 4–7 µm, ($\bar{x}$ = 25 × 5 µm, n = 40), L/W ratio = 4.9, fusiform, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline, smooth-walled, 3–7 µm long; three median cells 12–19 µm long ($\bar{x}$ = 16 µm, n = 40), pale brown to brown, wall rugose, concolor, septa darker than the rest of the cell, versicolourous; second cell from base pale brown to brown, 3–7 µm long; third cell pale brown to brown, 3–6 µm long; fourth cell pale brown to brown, 4–6 µm long; apical cell 3–6 µm long, hyaline, conic to acute; with 2–3 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 9–21 µm long; single basal appendage, unbranched, tubular, centric, 2–11 µm long.

Culture characteristics: Colony diameter reached 8 cm after two weeks at 25 °C on PDA media, circular, surface rough, flat, white from above, white to pale gray from below.

Material examined: Thailand, Suphan Buri Province, dead stem of an unidentified plant, 5 September 2020, S Wang, TN01 (MFLU 22-0168, **holotype**); ex-type culture, MFLUCC 22-0126.

Notes: *Neopestalotiopsis suphanburiensis* is phylogenetically sister to *N. eucalyptorum* which was isolated from leaves and stems of *Eucalyptus globulus* (Figure 4.113). In morphology, *N. suphanburiensis* differs from *N. eucalyptorum* in having thinner conidia (4–7 µm *vs.* 7.6–8.1 µm). In addition, there are 10 base pair differences (without gap, 445 bp) in the *TEF1-α* region. We thus introduce *N. suphanburiensis* as a new species.



Note a, b Cultures. c Colony on culture. d, e Conidia attached to conidiogenous cells. f–i Conidia. Scale bars: d–i = 10 µm.

Figure 4.108 *Neopestalotiopsis suphanburiensis* (MFLU 22-0168, holotype)

***Neopestalotiopsis* sp.1**

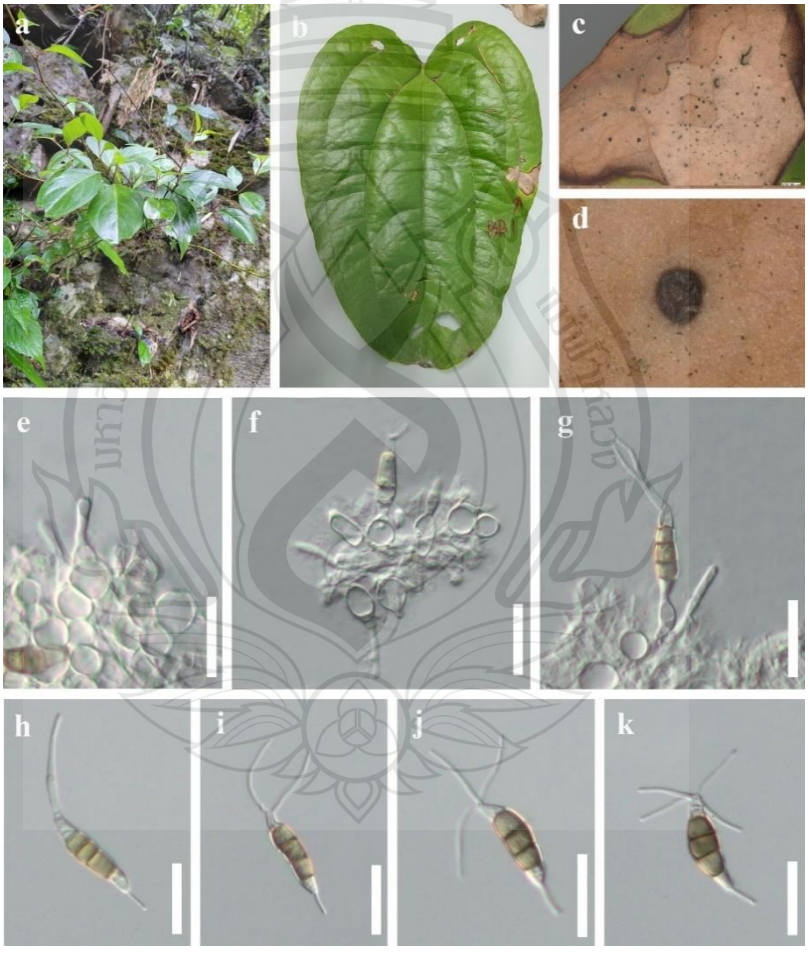
Figure 4.109

Associated with leaf spot of *Cyrtomium fortune*, *Lithocarpus* sp. and *Smilax scobinicaulis*. Symptoms irregular shape, pale brown, small spots gradually enlarged, changing to brown circular ring spots with a dark brown border. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, subglobose to globose, unilocular, dark brown, semi-immersed on leaves. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* subcylindrical or ampulliform, hyaline. *Conidia* 21–31 × 4–7 µm, ($\bar{x}$ = 26 × 6 µm, n = 30), L/W ratio = 4.4, fusiform, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline, 3–7 µm long; three median cells doliiform to cylindrical, 11–18 µm long ($\bar{x}$ = 15 µm, n = 30), yellow to brown, concolourous, septa darker than the rest of the cell; second cell from base yellow to brown, 3–6 µm long; third cell yellow to brown, 3–7 µm long; fourth cell yellow to brown, 4–7 µm long; apical cell 2–6 µm long, hyaline, conic to acute; with 1–4 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 13–26 µm long; single basal appendage, unbranched, tubular, centric, 2–7 µm long.

Culture characteristics: Conidia germinated on PDA within 12 hours at 25 °C from single-spore isolation. Apical cells produced germ tubes. Colony diameter reached 80 mm after two weeks at 25 °C on PDA media, circular, surface rough, flat, white from above, yellow from below.

Material examined: China, Guizhou Province, Tongren City, Jiangkou District, Yamugou Parkland, leaf spot of *Lithocarpus* sp.(*Fagaceae*), 20 May 2022, Y.R. Sun, JK15-2 (HKAS 124565); living culture, KUNCC 22-12592 = GUCC 21-0808; China, Guizhou Province, Qiannan Bouyei and Miao Autonomous Prefecture, Libo District, leaf spot of *Smilax china* L.(*Liliaceae*), 12 March 2022, Y.R. Sun, bb1 (HKAS 124560); China, Guizhou Province, Guiyang City, Baiyun District, Changpoling National Forest Park, leaf spot of *Dryopteris crassirhizoma* Nakai (*Dryopteridaceae*), 20 August 2021, Y.R. Sun, CL1-2, living culture, GUCC 21-0813.

Notes: Three strains (KUNCC 22-12592, HKAS 124560 and GUCC 21-0813) have identical ITS, *TEF1-α*, and *TUB2* sequences to isolates CFCC-54337 and ZX12-1, which were previously provided by Jiang et al. (2021). However, they did not introduce it as a new species due to lack of distinguished characters from close clades. In this study, these five strains clustered together and formed a distinct clade in the tree. We keep these five strains as *Neopestalotiopsis* sp.1 for the same reasons as before. We speculate *Neopestalotiopsis* sp.1 could be a common phytopathogen as it has been found in leaf spots on different plants.



Note a Host. b Leaf spot on *Smilax scobinicaulis*. c, d Close up view of conidiomata. e–g Conidia attached to conidiogenous cells. h–k Conidia. Scale bars: e–k = 20 µm.

Figure 4.109 *Neopestalotiopsis* sp.1 (HKAS 124560)

***Neopestalotiopsis* sp.2**

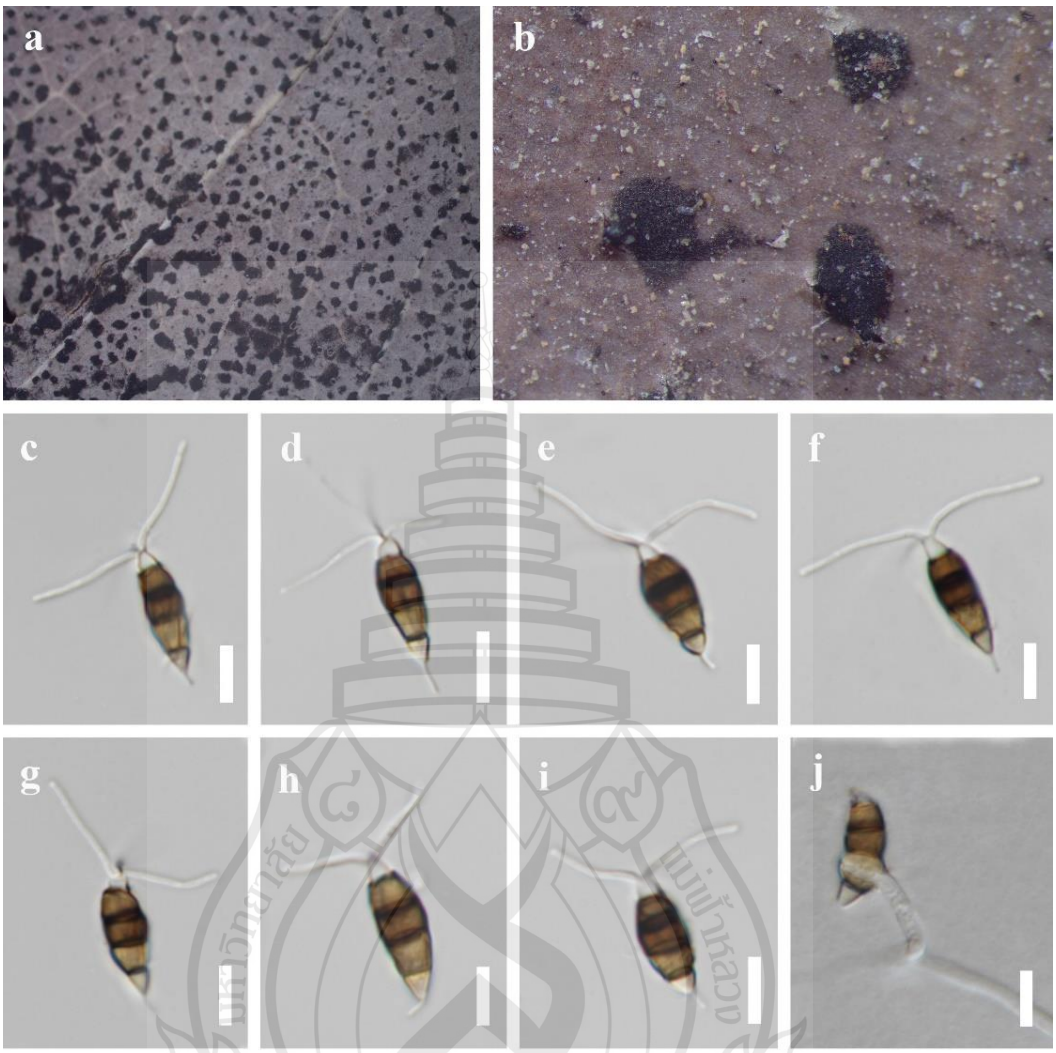
Figure 4.110

Saprobic on *Ceiba pentandra* leaves and endophytic from *Pinellia ternata*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, unilocular, dark, immersed on stems. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* indistinct. Conidia 19–25 ×6–8 μm ($\bar{x}$ = 22 × 7 μm, n = 30), L/W ratio = 3.1, fusoid, ellipsoid to subcylindrical, straight to slightly curved, 4-septate; basal cell conic to obconic with a truncate base, hyaline to subhyaline, 3–6 μm long; three median cells 13–15 μm long ($\bar{x}$ = 14 μm, n = 30), wall rugose, versicolourous, septa darker than the rest of the cell; second cell from base pale brown to brown, 3–5 μm long; third cell brown, 3–6 μm long; fourth cell brown, 3–6 μm long; apical cell 2–4 μm long, hyaline, rugose and thin-walled; with 2 (seldom 3) tubular apical appendages, arising from the apical crest, unbranched, filiform, 11–20 μm long; single basal appendage 2–5 μm long, unbranched, tubular, centric.

Culture characteristics: Colonies on PDA reaching up to 8 cm in two weeks, dense aerial mycelium on the surface with undulate edge, white. Fruiting bodies were observed after 14 days.

Material examined: Thailand, Chiang Rai Province, dead leaves of *Ceiba pentandra* (L.) Gaertn. (*Bombacaceae*), 16 Jan 2021, Y.R. Sun, CR20 (MFLU 22-0170); living culture, MFLUCC 22-0131; China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, on healthy leaves of *Pinellia ternata* (Thunb.) Breit. (*Araceae*), 1 May 2022, Y.R. Sun, E2, living culture KUNCC 22-12596 = GUCC 21-0805.

Notes: Our isolates KUNCC 22-12596 and MFLUCC 22-0170 clustered together with *Neopestalotiopsis* sp.2 (CFCC 54340 and ZX22B) and these four isolates formed a distinct clade in the phylogenetic tree (Figure 4.113). Four isolates have similar characteristics. We keep these four strains as *Neopestalotiopsis* sp.2 as explained above. Interestingly, KUNCC 22-12596, MFLUCC 22-0170, ZX22B and CFCC 54340 have different habitats. KUNCC 22-12596 was endophytic in healthy leaves of *Pinellia ternata*, MFLUCC 22-0170 was saprobic on decaying leaves of *Ceiba pentandra*, and CFCC 54340, ZX22B were isolated from leaf spots of *Castanea mollissima*.



Note a, b Conidiomata on the host. c–i Conidia. j Germinated conidium. Scale bars: c–j = 10 µm.

Figure 4.110 *Neopestalotiopsis* sp.2 (MFLU 22-0170)

Neopestalotiopsis rhapidis Qi Yang & Yong Wang bis, Biodiversity Data Journal 9 (no. e70446): 9 (2021)

Index Fungorum number: IF 840065; Facesoffungi number: FoF12917; Figure 4.111

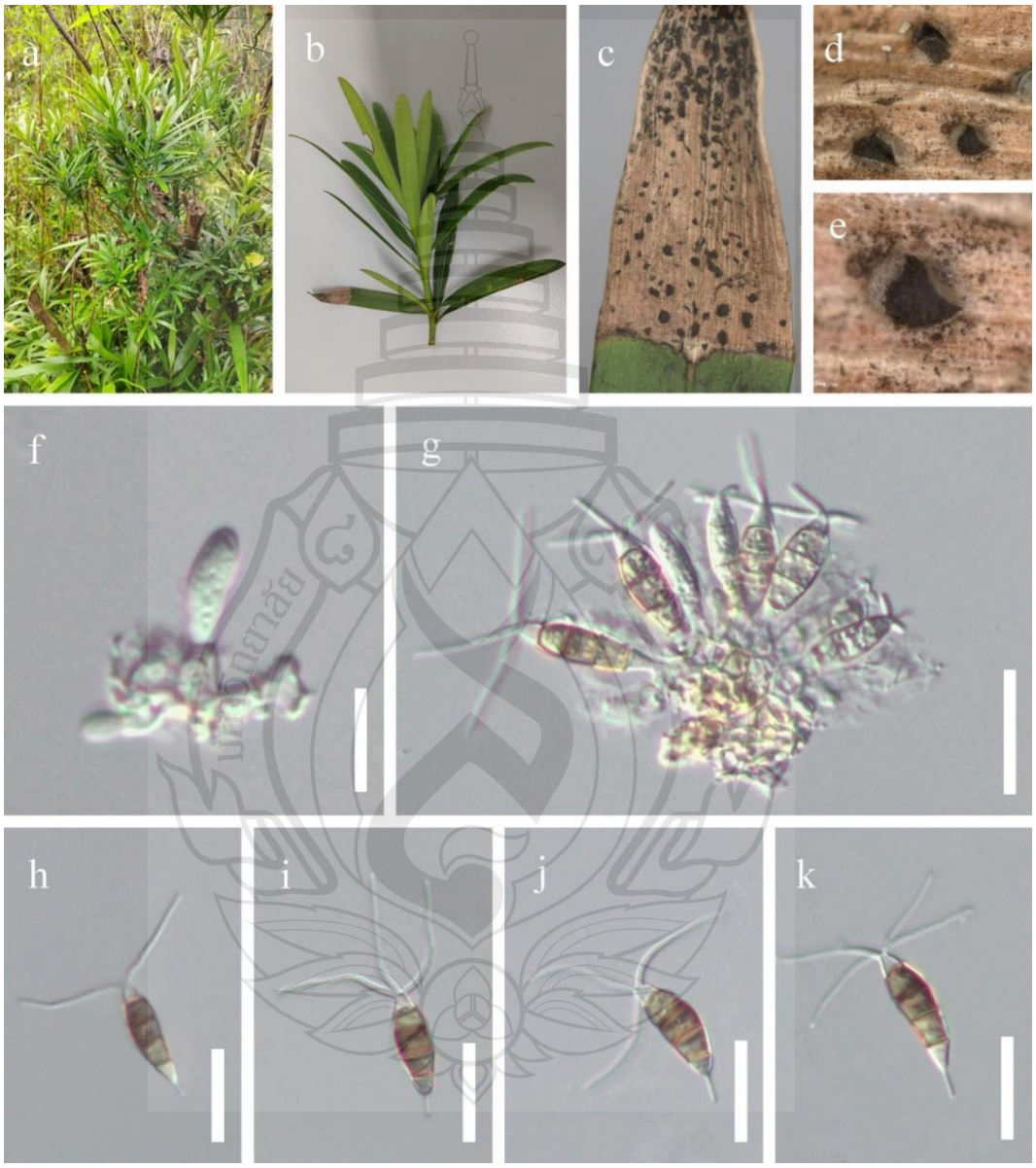
Associated with leaf spot on leaves tip of *Podocarpus macrophyllus*. Symptoms irregular shape, brown, dry, slightly sunken on leaves tip. **Sexual morph**: Unknown. **Asexual morph**: *Conidiomata* solitary, subglobose to globose, unilocular, dark brown to dark, semi-immersed on leaves. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* subcylindrical or ampulliform, short, hyaline. *Conidia* 17.5–25 × 5–8 μm, $\bar{x}$ ± SD = 22 ± 1.4 × 6.5 ± 0.7 μm (n = 40), L/W ratio = 3.4, fusiform, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline, 3–6 μm long ($\bar{x}$ ± SD = 4.3 ± 0.65 μm); three median cells doliiform to cylindrical, 11.5–17 μm long ($\bar{x}$ ± SD = 14.5 ± 1 μm), pale to brown, versicolourous, septa darker than the rest of the cell; second cell from base pale to brown, 3–6 μm long ($\bar{x}$ ± SD = 4.5 ± 0.65 μm); third cell pale to brown, 3–6.5 μm long ($\bar{x}$ ± SD = 5 ± 0.6 μm); fourth cell pale to brown, 2.5–5.5 μm long ($\bar{x}$ ± SD = 4.2 ± 0.7 μm); apical cell 2–5 μm long ($\bar{x}$ ± SD = 3 ± 0.6 μm), hyaline, conic to acute; with 2–4 (mostly 3) tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 12–28 μm long ($\bar{x}$ ± SD = 20.5 ± 3.4 μm); single basal appendage, unbranched, tubular, centric, 2.5–7 μm long ($\bar{x}$ ± SD = 4.8 ± 1.2 μm).

Culture characteristics: Conidia germinated on PDA within 12 hours at 25°C from single-spore isolation. Apical cells produced germ tubes. Colony diameter reached 80 mm after 7 days at 25°C on PDA media, circular, surface rough, flat, white from above, yellow from below.

Material examined: China, Guizhou Province, Qiannan Buyi and Miao Autonomous Prefecture, Libo District, leaf spots of *Podocarpus macrophyllus*, 12 March 2022, Y.R. Sun, ML3 (HKAS 124559); living cultures KUNCC 22-12590.

Notes: *Neopestalotiopsis rhapidis* was introduced by Yang et al., (2021) from leaf spot of *Rhapis excelsa* (Arecaceae) in China. Our isolate KUNCC 22-12590 clustered together with *N. rhapidis* (GUCC 21501) in the phylogenetic tree. These two species have overlapping conidial measurements (17.5–25 × 5–8 μm for KUNCC 22-12590 *vs.* (22–)25.5 × 4(–6) μm

for GUCC 21501) (Yang et al., 2021). Both isolates were associated with leaf spots in China. Therefore, we identify KUNCC 22-12590 and GUCC 21501 to be conspecific species, and KUNCC 22-12590 represents a new host record.



Note a, b Host. c Leaf blight on Podocarpus macrophyllus. d, e Close up view of conidiomata. f, g Conidia attached to conidiogenous cells. h–k Conidia. Scale bars: f = 10 µm, g–k = 20 µm.

Figure 4.111 *Neopestalotiopsis rhapidis* (HKAS 124559, new host record)

Neopestalotiopsis rhododendri Qi Yang & Yong Wang bis, Biodiversity Data Journal 9(no. e70446): 9 (2021)

Index Fungorum number: IF840066; Facesoffungi number: FoF12918; Figure 4.112

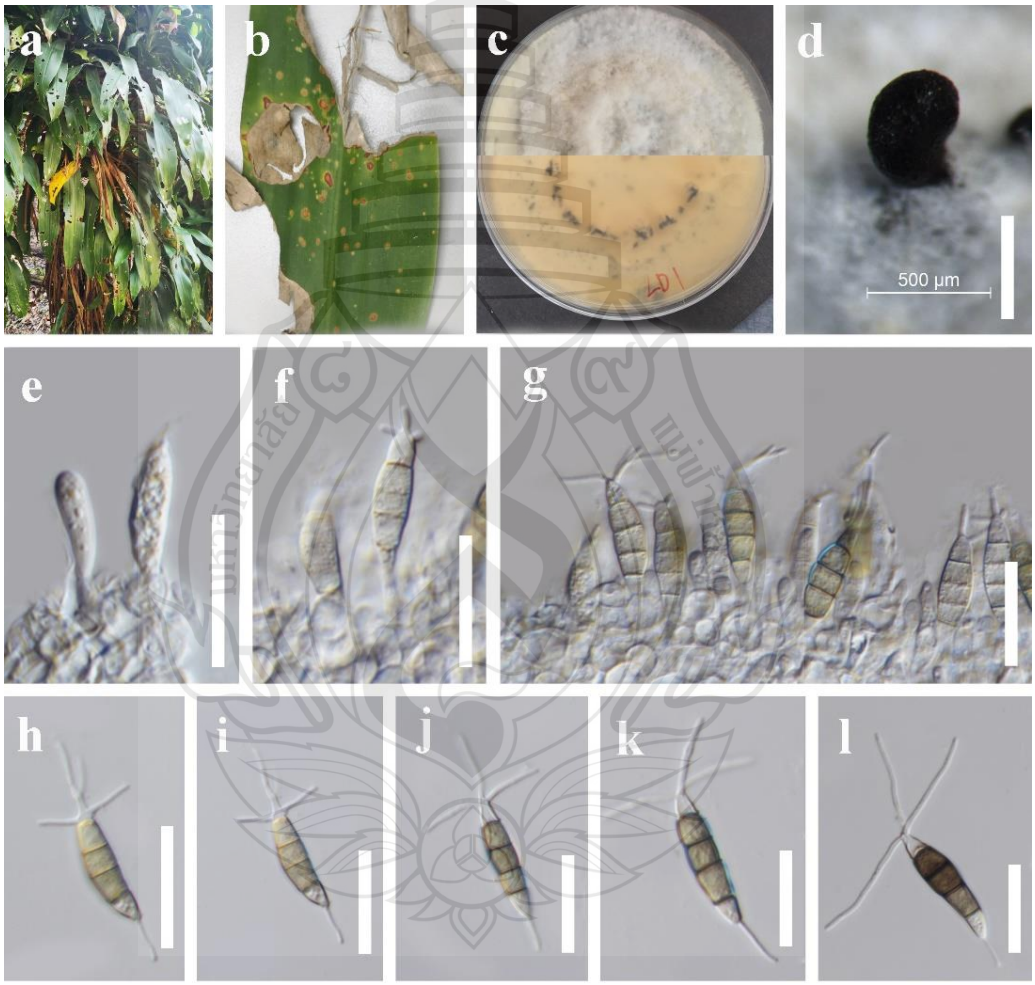
Associated with leaf spots of *Dracaena fragrans*. Symptoms subcircular to circular, yellow to brown, slightly sunken spots appear on the leaves of *Dracaena* sp, which later expand outwards. Small auburn spots appeared initially and then gradually enlarged. **Sexual morph**: Unknown. **Asexual morph**: *Conidiomata* on PDA pycnidial, subglobose to cylindrical, solitary or aggregated, dark, semi-immersed or partly erumpent; exuding black conidial masses. *Conidiophores* indistinct. *Conidiogenous cells* cylindrical to sub-cylindrical or ampulliform to lageniform, hyaline. *Conidia* pale brown to dark brown, fusiform, straight to slightly curved, 4-septate, 19–28 × 5–7 µm, $\bar{x}$ ± SD = 24 ± 2 × 6 ± 0.5 µm (n = 40), L/W ratio = 4; basal cell obconic with a truncate base, hyaline or pale brown, 3–6 µm long ($\bar{x}$ ± SD = 4.3 ± 0.6 µm, n = 40); three median cells 12–18(–18.5) µm long ($\bar{x}$ ± SD = 12.8 ± 1.5 µm, n = 40), pale brown to dark brown, wall rugose, septa darker than the rest of the cell, somewhat constricted at the septa, versicolourous; second cell from base pale brown, 3.5–6.5 µm long ($\bar{x}$ ± SD = 4.8 ± 0.7 µm, n = 40); third cell brown, 3–6 µm long ($\bar{x}$ ± SD = 4.5 ± 0.7 µm, n = 40); fourth cell brown, 3.5–6 µm long ($\bar{x}$ ± SD = 4.5 ± 0.66 µm, n = 40); apical cell 2–5.5 µm long ($\bar{x}$ ± SD = 3.8 ± 0.7 µm, n = 40), hyaline, conic to acute; with 3–5 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 10–26 µm long ($\bar{x}$ ± SD =15.5 ± 4.8 µm); 1–3 basal appendage, unbranched, tubular, centric, 3.5–12 µm long ($\bar{x}$ ± SD = 7.5 ± 2.6 µm).

Culture characteristics: Colony diameter reached 8 cm after two weeks at 25 °C on PDA medium, circular, surface rough, flat, white from above, yellow from below.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, leaf spots of *Dracaena fragrans*, 15 September 2020, S Wang, LD1, living cultures MFLUCC 22-0130.

Notes: *Neopestalotiopsis rhododendri* was introduced by Yang et al. (2021) from the diseased leaf of *Rhododendron simsii* (*Ericaceae*) in China. Based on our phylogenetic analysis

of combined *TEF1-α*, *TUB2* and ITS sequence data, our isolate MFLUCC 22-0130 clustered with the type species, *N. rhododendri* (GUCC 21504) with maximum support (ML-BS = 100%, MP-BS = 100%, BYPP = 1.0). Our collection also shares similar morphological features with the holotype of *N. rhododendri* (GUCC 21504). Both isolates were associated with leaf spots. Therefore, we identify our collection as *N. rhododendri*, which represents a new host and geographical record.



Note a Host. b Leaf spot of *Dracaena fragrans*. c Cultures. d Colonies on PDA. e–g Conidiogenous cells and developing conidia. h–l Conidia. Scale bars: d = 500 µm, e–l = 20 µm.

Figure 4.112 *Neopestalotiopsis rhododendri* (MFLUCC 22-0130, new record)

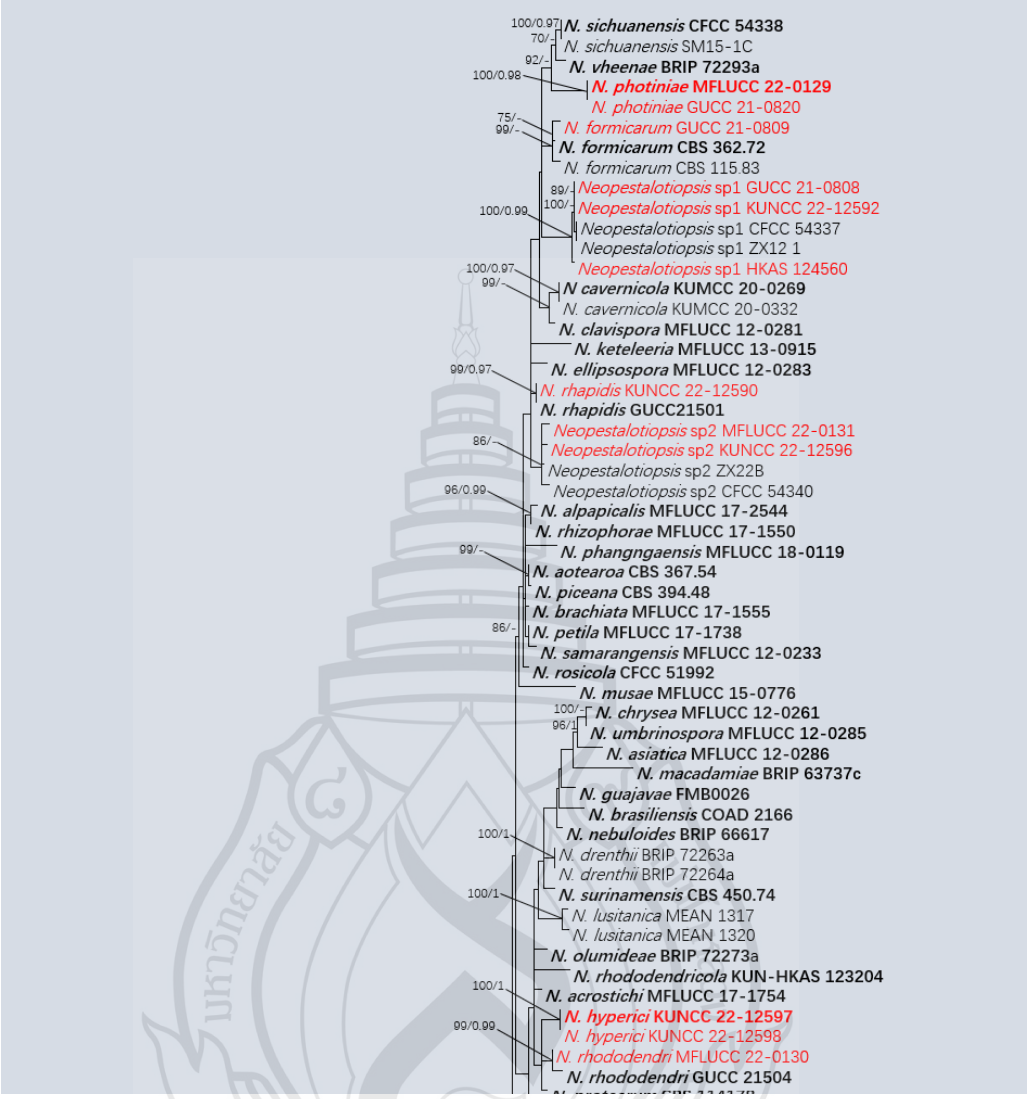
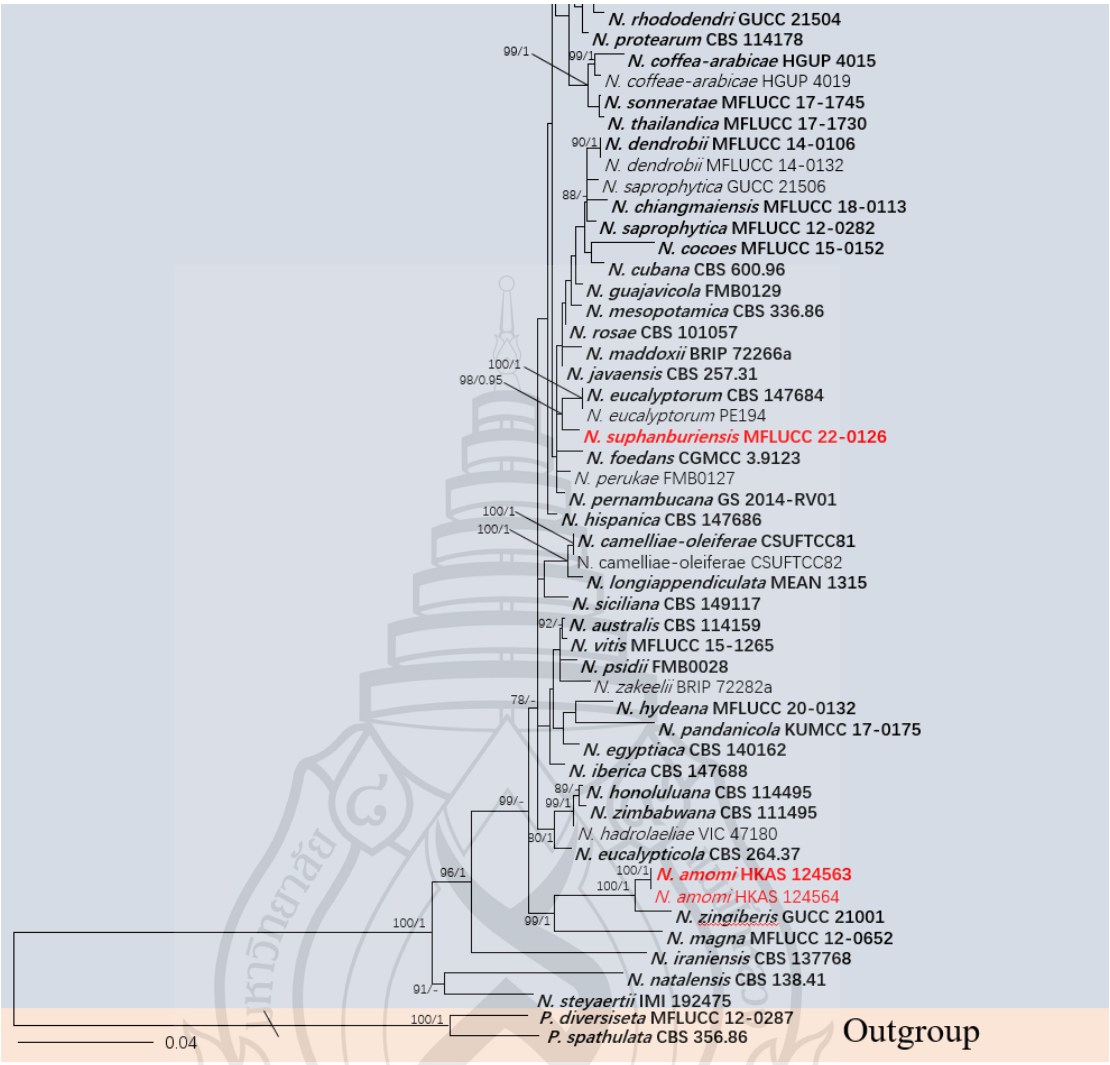


Figure 4.113 Phylogenetic tree for *Neopestalotiopsis*



Note The tree is rooted with *Pestalotiopsis diversiseta* (MFLUCC 12-0287) and *P. spathulata* (CBS 356.86). Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The new isolates are in red and ex-type strains are in bold.

Figure 4.113 (continued)

Pestalotiopsis Steyaert, Bull. Jard. bot. État Brux. 19: 300 (1949).

Notes: *Pestalotiopsis* was split from *Pestalotia* by Steyaert (1949). *Pestalotiopsis* species are known to be widespread and can be found in various habitats worldwide, including soil, plant debris, and living plant tissues (Maharachchikumbura et al., 2014; Liu et al., 2017; Ariyawansa & Hyde, 2018; Sun et al., 2023). These fungi are capable of causing diseases in a wide range of plants, including trees, shrubs, and crops (Song et al., 2014; Moslemi & Taylor, 2015; Hlaiem et al., 2018). Some may also produce beneficial metabolites, and some have the potential for bioremediation and plastic waste management (Russell et al., 2011; Xu et al., 2014; Xu et al., 2016).

Pestalotiopsis chiangmaiensis Y.R. Sun & Yong Wang bis, ***sp. nov.***

Index Fungorum number: IF571225; Facesoffungi number: FoF04525; Figure 4.114

Etymology: Refers to the location where the fungus was encountered.

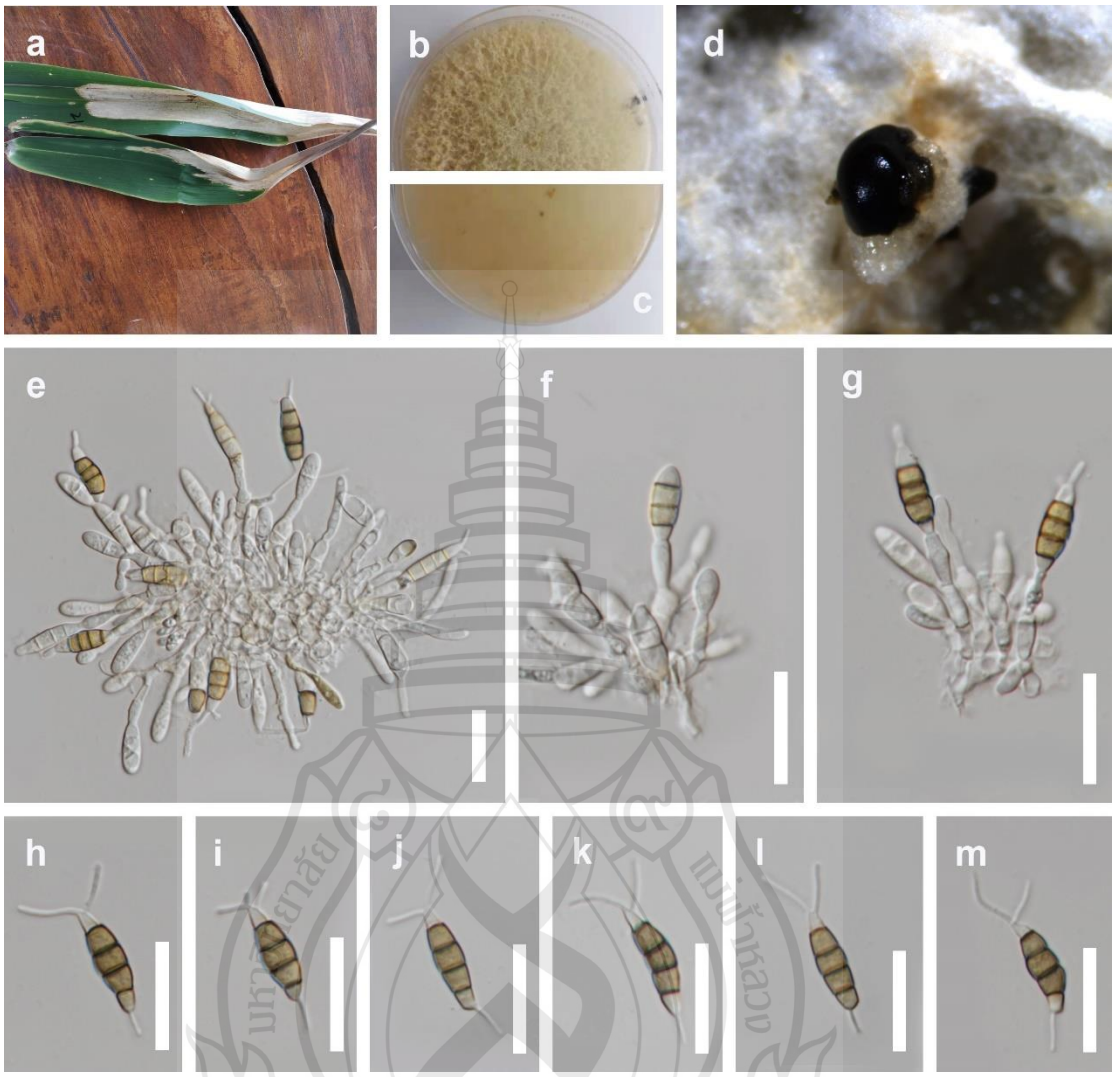
Holotype: MFLU 22-0164.

Associated with leaf strips of *Phyllostachys edulis*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* on PDA pycnidial, subglobose to globose, solitary or aggregated, dark, semi-immersed or partly erumpent; exuding black conidial masses. Conidiophores hyaline, smooth, simple, reduced to conidiogenous cells. *Conidiogenous cells* 5–11 × 1–3 µm, cylindrical to sub-cylindrical or ampulliform to lageniform, hyaline, smooth. *Conidia* pale brown, fusiform, straight to slightly curved, (3)4-septate, 16–26 × 4–7 µm, ($\bar{x}$ = 21 × 5 µm, n = 40), L/W ratio = 4.2; basal cell obconic with a truncate base, hyaline or sometimes pale brown, smooth-walled, 2–6 µm long; three median cells 10–16 µm long ($\bar{x}$ = 14 µm, n = 40), pale brown, concolourous, wall rugose, septa darker than the rest of the cell, somewhat constricted at the septa; second cell from base pale brown, 3–6 µm long; third cell brown, 3–6 µm long; fourth cell brown, 3–6 µm long; apical cell 2–5 µm long, hyaline, conic to acute; with 2(–3) tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 8–13 µm long; single basal appendage 2–7 µm, unbranched, tubular, centric.

Culture characteristics: Colonies on PDA reaching 5–6 cm diam. after 7 days at 25 °C, colonies filamentous to circular, medium dense, aerial mycelium on surface flat or raised, with filiform (curle) margin, fluffy, white from above and below; fruiting bodies black.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, leaf strip of *Phyllostachys edulis* (Carriere) J. Houzeau (*Poaceae*), 15 July 2020, Y.R. Sun, M18 (MFLU 22-0164, **holotype**); ex-type culture, MFLUCC 22-0127.

Notes: *Pestalotiopsis chiangmaiensis* formed a distinct lineage and was sister to *P. smilacicola* and *P. dracontomelon* in the phylogenetic tree (Figure 4.121). It differs by longer conidiogenous cells (5–11 μm *vs.*1–4 μm) from *P. smilacicola* and shorter apical appendages (8–13 μm *vs.*10–22 μm) from *P. dracontomelon*. In addition, there are 14 base pair differences (without gap, 474 bp) in the *TEF1-α* region between *P. chiangmaiensis* (MFLUCC 22-0127) and *P. smilacicola* (MFLUCC 22-0125), and 15 base pair differences (without gap, 464 bp) between *P. chiangmaiensis* (MFLUCC 22-0127) and *P. dracontomelon* (MFLUCC 10-0149). Therefore, we introduce *P. chiangmaiensis* as a new species.



Note a Host. b, c Cultures. d Colonies on PDA. e–g Conidiogenous cells and developing conidia. h–m Conidia. Scale bars: e–m = 20 µm.

Figure 4.114 *Pestalotiopsis chiangmaiensis* (MFLU 22-0164, holotype)

Pestalotiopsis loeiana Y.R. Sun & Yong Wang bis, ***sp. nov.***

Index Fungorum number: IF571226; Facesoffungi number: FoF12919; Figure 4.115

Etymology: Refers to the collected site, Loei province.

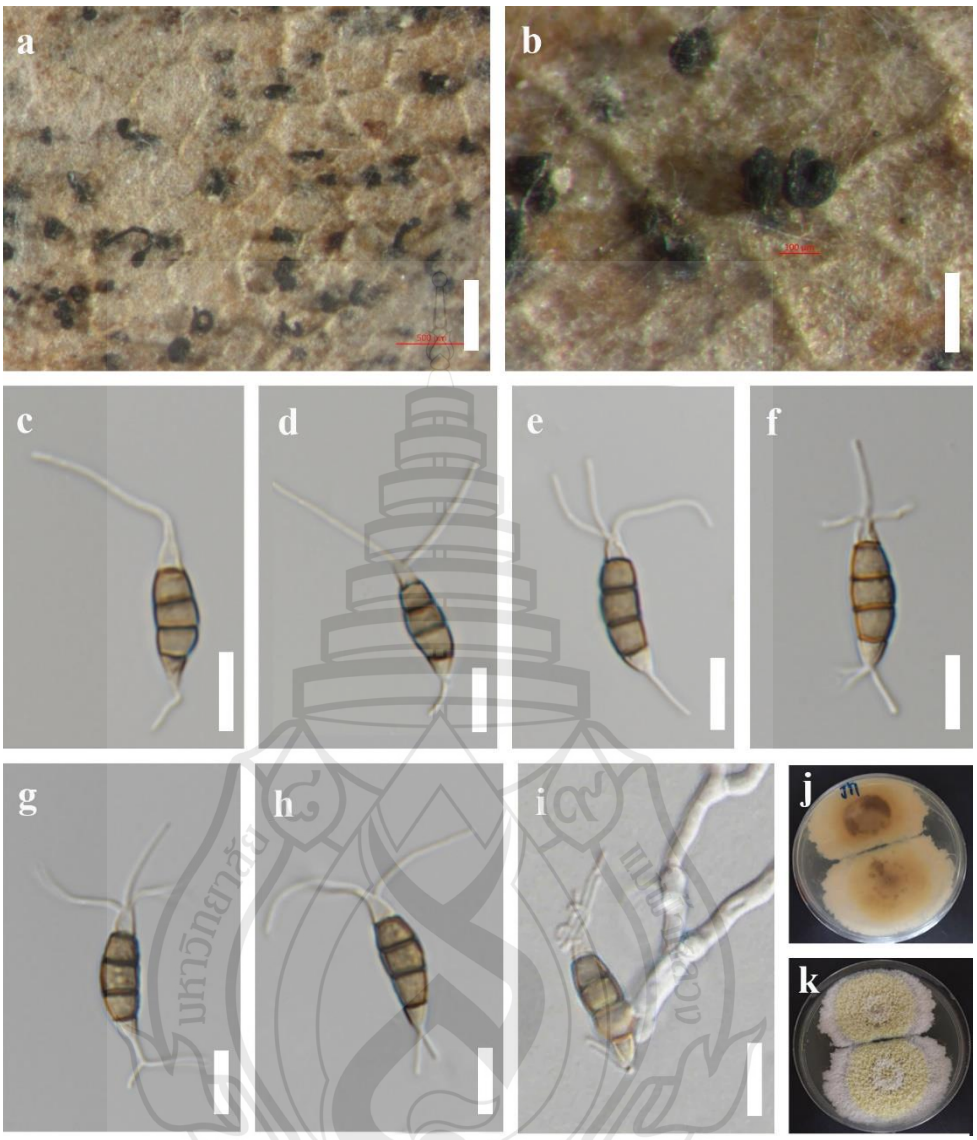
Holotype: MFLU 22-0167.

Saprobic on dead leaves. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, black, semi-immersed on leaves. *Conidiophores* indistinct and conidiogenous cells indistinct. *Conidia* 17–22 × 4–6 µm, ($\bar{x}$ = 19 × 5 µm, n = 40), L/W ratio = 3.7, fusiform, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, rugose walled, 3–6 µm long, with 1-3 basal appendages, unbranched, tubular, centric, 3–13 µm long ($\bar{x}$ = 9 µm); three median cells 10–14 µm, ($\bar{x}$ = 12, n = 40), doliiform to cylindrical, brown, concolourous, wall rugose, septa darker than the rest of the cell, somewhat constricted at the septa; second cell from base brown, 3–6 µm long; third cell brown, 3–5 µm long; fourth cell brown, 2–5 µm long; apical cell 3–5 µm long, hyaline, conic to acute; with 1–3 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 13–24 µm long.

Culture characteristics: Colonies on PDA reaching 8 cm diam. after two weeks at 25°C, colonies filamentous to circular, medium dense, mycelium on surface flat or raised, with filiform margin, fluffy, yellow circle in the middle surrounded by white mycelium from above, light yellow to pale brown from the reverse.

Material examined: Thailand, Loei Province, dead leaves of an identified plant, 27 February 2020, J.Y. Zhang, JY1 (MFLU 22-0167, **holotype**); ex-type culture, MFLUCC 22-0123.

Notes: *Pestalotiopsis loeiana* (MFLUCC 22-0123) is phylogenetically sister to *P. rhizophorae* and *P. thailandica*, which were isolated from leaf spots of *mangroves* (Figure 4.121). Morphologically, *P. loeiana* is distinguishable by its more than one basal appendage and smaller conidia (17–22 × 4–6 µm in *P. loeiana vs.* 21–27 × 6. 5–7. 5 µm in *P. rhizophorae vs.* 21–25 × 6–7 µm in *P. thailandica*). Therefore, we introduce *P. loeiana* as a new species.



Note a, b Conidiomata on the host. c–h Conidia. i Germinated conidium. j, k Colonies on PDA. Scale bars: a = 500 µm, b = 200 µm, c–i = 10 µm.

Figure 4.115 *Pestalotiopsis loeiana* (MFLU 22-0167, holotype)

Pestalotiopsis smilacicola Y.R. Sun & Yong Wang bis, ***sp. nov.***

Index Fungorum number: IF571227; Facesoffungi number: FoF12921; Figure 4.116

Etymology: Refers to the host plant from which the fungus was isolated.

Holotype: MFLU 22-0165.

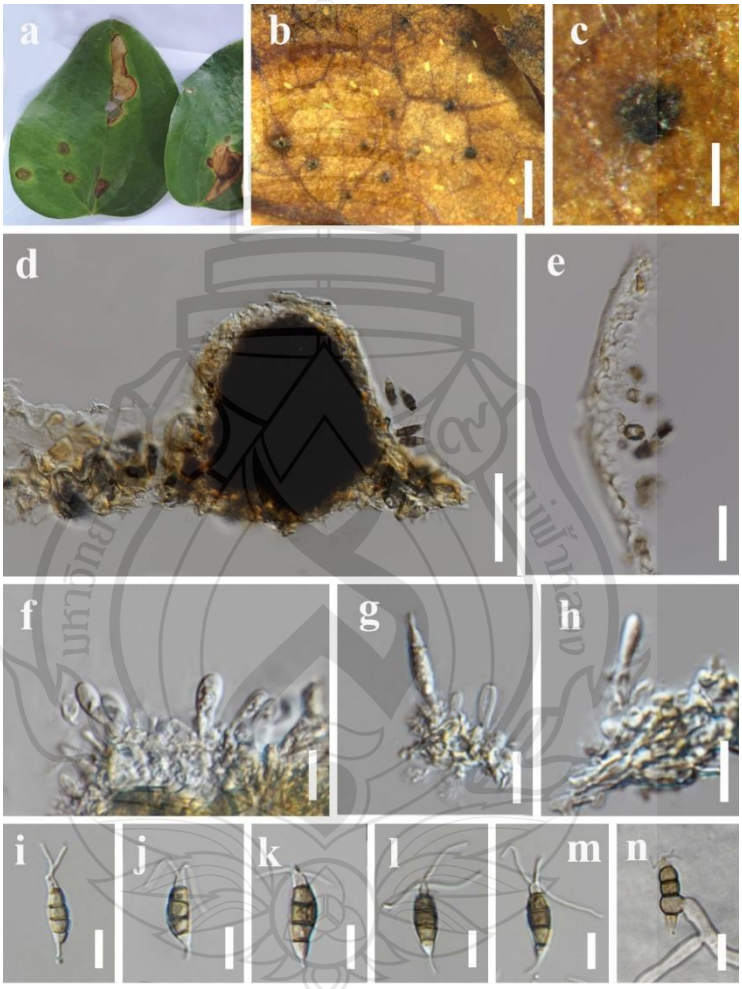
Associated with leaf spots of *Smilax* sp. Symptoms subcircular to irregular shape, brown, slightly sunken spots appear on the leaves of *Smilax china*, which later expand outwards. Small auburn spots appeared initially and then gradually enlarged. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, subglobose, unilocular, black, semi-immersed on leaves. *Conidiomatal wall* 7–10 μm wide, thin walled, pale brown. Conidiophores indistinct. *Conidiogenous cells* 1–4 × 1–3 μm, subcylindrical to ampulliform, hyaline, smooth. *Conidia* 18–22 × 4–7 μm, ($\bar{x}$ = 20 × 5 μm, n = 40), L/W ratio = 3.8, fusiform, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, smooth walled, 3–5 μm long; three median cells 9–15 μm long ($\bar{x}$ = 12 μm, n = 40), pale brown to brown, concolourous, wall rugose, septa darker than the rest of the cell, somewhat constricted at the septa; second cell from base pale brown to brown, 3–5 μm long; third cell brown, 2–5 μm long; fourth cell brown, 3–5 μm long; apical cell 2–5 μm long, hyaline, conic to acute; with 2–3 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 6–14 μm long; single basal appendage, unbranched, tubular, centric, 2–6 μm long.

Culture characteristics: Colonies on PDA reaching 10 cm diam. after two weeks at 25°C, colonies filamentous to circular, medium dense, aerial mycelium on surface flat or raised, with filiform margin, fluffy, white from above and reverse.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, leaf spots of *Smilax* sp. (*Liliaceae*), 16 July 2020, Y.R. Sun, M26 (MFLU 22-0165, **holotype**), ex-type culture, MFLUCC 22-0125. ibid., leaf spots of *Smilax china* L. (*Liliaceae*), 15 July 2020, Y.R. Sun, M13 living culture, MFLUCC 22-0124.

Notes: Two isolates MFLUCC 22-0125 and MFLUCC 22-0124 share similar morphology. These two isolates clustered together and formed a sister clade to *P. dracontomelon*

(MFLUCC 10-0149) in the phylogenetic tree. There are only 1 base pair difference in *TEF1-α* and *TUB2* genes and 3 base pair differences in the ITS gene between these two isolates. For the differences between *P. smilacicola* and its related species see the notes of *P. chiangmaiensis* (this study). Therefore, these two isolates are identified as conspecific, representing a new species.



Note a Host. b, c Close up view of conidiomata. d Section through conidioma. e Section through pycnidial wall. f–h Immature conidia attached to conidiogenous cells. i–m Conidia. n Germinated conidium. Scale bars: b = 1000 µm, c = 200 µm, d = 50 µm, e = 20 µm, f–n = 10 µm.

Figure 4.116 *Pestalotiopsis smilacicola* (MFLU 22-0165, holotype)

Pestalotiopsis chamaeropis Maharachch., K.D. Hyde & Crous

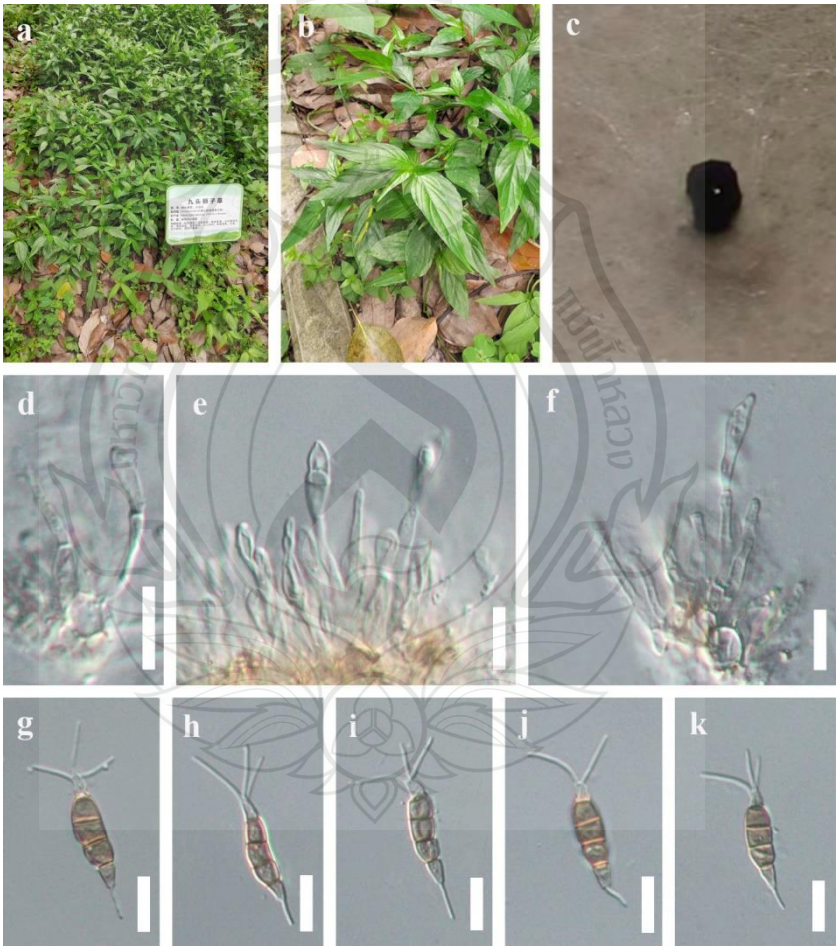
Index Fungorum number: IF809735; Facesoffungi number: FoF11691; Figure 4.117

Endophytic from *Peristrophe japonica*. Colonies on PDA white with grey mycelia in the center, felty, black conidiomata, lobed edge. **Sexual morph**: Unknown. **Asexual morph**: *Conidiomata* on PDA pycnidial, solitary or aggregated, subglobose to globose, dark, semi-immersed or erumpent; exuding black conidial masses. Conidiophores hyaline, smooth, simple, reduced to conidiogenous cells. *Conidiogenous cells* 1–2 µm wide, cylindrical to sub-cylindrical, hyaline, smooth. *Conidia* brown, fusiform, straight to slightly curved, 4-septate, 20–27.5 × 3.5–6 µm, $\bar{x}$ ± SD = 24.5 ± 1.3 × 5± 0.4 µm (n = 40), L/W ratio = 4.9; basal cell obconic with a truncate base, hyaline to pale brown, smooth walled, 3–6 µm long ($\bar{x}$ ± SD = 4.8 ± 0.5 µm); three median cells 12.5–17.5 µm long ($\bar{x}$ ± SD = 14.5 ± 0.9 µm), brown, septa darker than the rest of the cell, somewhat constricted at the septa; second cell from base brown, 4–6 µm long ($\bar{x}$ ± SD = 5 ± 0.4 µm); third cell brown, 3.5–6 µm long ($\bar{x}$ ± SD = 4.7 ± 0.4 µm); fourth cell brown, 4–6 µm long ($\bar{x}$ ± SD = 4.7 ± 0.4 µm); apical cell 3–5 µm long ($\bar{x}$ ± SD = 4.1 ± 0.5 µm), hyaline, conic to acute; with 2–3 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 8.5–18 µm long ($\bar{x}$ ± SD =13.8 ± 2.1 µm); single basal appendage, unbranched, tubular, centric, 4–9.5 µm long ($\bar{x}$ ± SD = 5.6 ± 0.7 µm).

Material examined: China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, on healthy leaves of *Peristrophe japonica* (Thunb.) Bremek. (*Acanthaceae*), 1 May 2022, Y.R. Sun, E33, living culture KUNCC 22-12591 = GUCC 21-0800; ibid, China, Yannan Province, Kunming City, Yiliang District, Yangzonghai Garden, on leaves of *Spineless yucca*, 20 February 2023, H.W. Shen, 2347 (HGUP 23-0006); living culture GUCC 23-0020.

Notes: *Pestalotiopsis chamaeropis* was originally reported on leaves of *Chamaerops humilis* in Italy by Maharachchikumbura et al. (2014). Subsequently, many studies have proven that *P. chamaeropis* is a serious phytopathogen, which can cause diseases of *Camellia sinensis*, *Camellia oleifera* and *Eurya nitida* (in China), *Erica arborea* (in Tunisia), J*apanese andromeda*

(in Japan) and *Prostanthera rotundifolia* (in Australia) (Moslemi & Taylor, 2015; Jiang et al., 2017; Ariyawansa & Hyde, 2018; Hlaiem et al., 2018; Nozawa et al., 2019; Wang et al., 2019; Chen et al., 2021; Qiu et al., 2022; Santos et al., 2022). Park et al. (2017) reported *P. chamaeropis* as an endophyte, from the leaves of woody plants in Korea. In this study, our strain KUNCC 22-12591 is phylogenetically clustered with *P. chamaeropis* CBS 186.71 with good support (ML-BS = 100%, BYPP = 0.95), and it has overlapping characteristics with *P. chamaeropis* (CBS 186.71). Thus, we identify KUNCC 22-12591 as *P. chamaeropis*, representing a new host record.



Note a, b Host. c Close up view of conidiomata. d–f Conidia attached to conidiogenous cells. g–k Conidia. Scale bars: d–k = 10 µm.

Figure 4.117 *Pestalotiopsis chamaeropis* (KUNCC 22-12591, new record)

Pestalotiopsis dracontomelon Maharachch & K.D. Hyde

Index Fungorum number: IF550943; Facesoffungi number: FoF00457; Figure 4.118

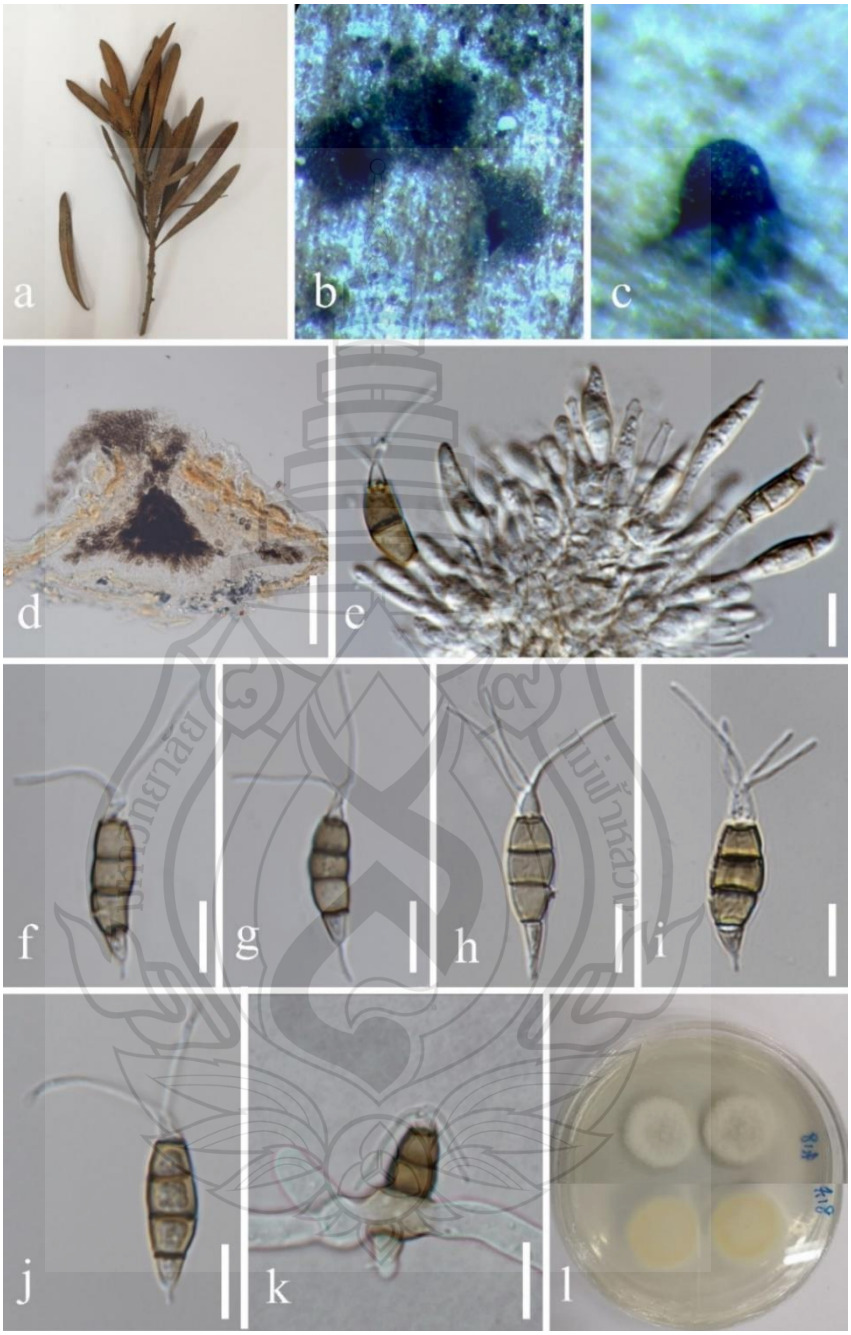
Associated with dead leaves of *Podocarpus* sp. **Sexual morph**: Unknown. **Asexual morph**: *Conidiomata* solitary, subglobose, unilocular, black, semi-immersed on leaves. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* sub-cylindrical to cylindrical, hyaline, rugose walled, 1.5–3 µm wide. *Conidia* 19–26 × 5.5–8 µm, $\bar{x}$ ± SD = 23 ± 1.7 × 7 ± 0.6 µm (n = 30), L/W ratio = 3.3, fusiform, ellipsoid, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, rugose walled, 3–5 µm long ($\bar{x}$ ± SD = 4 ± 0.5 µm); three median cells 11–16.5 µm long ($\bar{x}$ ± SD = 14.5 ± 1.6 µm), doliiform to cylindrical, pale brown to brown, concolourous, wall rugose, septa darker than the rest of the cell, somewhat constricted at the septa; second cell from base pale brown to brown, 4–6 µm long ($\bar{x}$ ± SD = 5 ± 0.6 µm); third cell pale brown to brown, 3–5.5 µm long ($\bar{x}$ ± SD = 4.5 ± 0.6 µm); fourth cell pale brown to brown, 3.5–5.5 µm long ($\bar{x}$ ± SD = 4.5 ± 0.5 µm); apical cell 3–5.5 µm long ($\bar{x}$ ± SD = 4.3 ± 0.6 µm), hyaline, conic to acute; with 2–4 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 10–22 µm long ($\bar{x}$ ± SD =13.5 ± 4 µm); single basal appendage, unbranched, tubular, centric, 2–6 µm long ($\bar{x}$ ± SD = 3.8 ± 1.3 µm).

Culture characteristics: Colonies on PDA reaching 2.5 cm diam after 7 days at 25 °C, colonies filamentous to circular, medium dense, aerial mycelium on the surface flat or raised, fluffy, white from above and below.

Material examined: Thailand, Chiang Rai Province, Mae Fah Luang University, leaf spots of *Podocarpus* sp. (*Podocarpaceae*), 15 January 2019, Y.R. Sun, S18 (MFLU 22-0166); living culture, MFLUCC 22-0122.

Notes: *Pestalotiopsis dracontomelon* was isolated from diseased leaves of *Dracontomelon mangifera* (*Anacardiaceae*) in Thailand (Liu et al., 2015). Our isolate MFLUCC 22-0122 was grouped with *P. dracontomelon* (MFLUCC 10-0149) in the phylogenetic tree. Morphologically, they have overlapping conidial measurements (19–26 × 5.5–8 µm for MFLUCC 22-0122 *vs.* 18–23×5.5–7.5 µm for MFLUCC 10-0149). Therefore,

we identify MFLUCC 22-0122 as the new host record of *P. dracontomelon*.



Note a Host. b, c Close up view of conidiomata. d Section through conidioma. e Conidia attached to conidiogenous cells. f–j Conidia. k Germinated conidium. l Colony. Scale bars: b = 1000 µm, d = 50 µm, e, k = 20 µm, f–j = 10 µm.

Figure 4.118 *Pestalotiopsis dracontomelon* (MFLU 22-0166, new host record)

Pestalotiopsis hispanica F. Liu, L. Cai & Crous

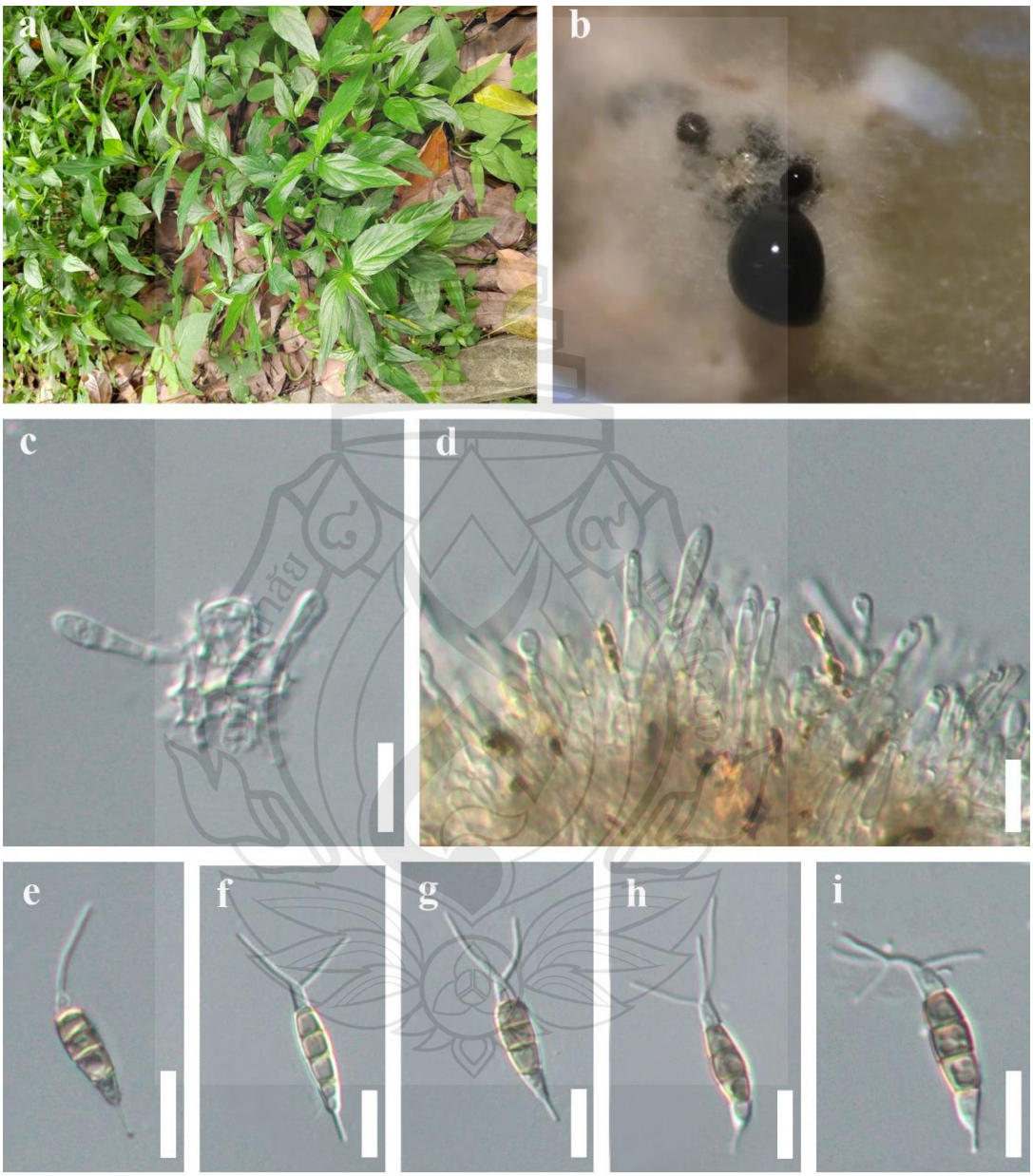
Index Fungorum number: IF828379; Facesoffungi number: FoFXX; Figure 4.119

Endophytic from *Peristrophe japonica*. Colonies on PDA white with grey mycelia in the center, felty, black conidiomata, lobed edge; reverse white with pale to brown concentric circles. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* on PDA pycnidial, solitary or aggregated, subglobose to globose, dark, semi-immersed or erumpent; exuding black conidial masses. *Conidiophores* hyaline, smooth, simple, reduced to conidiogenous cells. *Conidiogenous cells* 1–3 µm wide, cylindrical to sub-cylindrical or ampulliform to lageniform, hyaline, smooth. *Conidia* pale to brown, fusiform, straight to slightly curved, 4-septate, 20–29 × 4.5–6 µm, $\bar{x}$ ± SD = 24.5 ± 2 × 5.2 ± 0.4 µm (n = 40), L/W ratio = 4.7; basal cell obconic with a truncate base, hyaline, smooth walled, 4.5–7 µm long ($\bar{x}$ ± SD = 5.5 ± 0.6 µm); three median cells 12–17 µm long ($\bar{x}$ ± SD = 14 ± 1.1 µm), pale to brown, wall rugose, septa darker than the rest of the cell, somewhat constricted at the septa; second cell from base pale to brown, 3.5–6 µm long ($\bar{x}$ ± SD = 5 ± 0.4 µm); third cell pale to brown, 3.5–6 µm long ($\bar{x}$ ± SD = 4.5 ± 0.4 µm); fourth cell pale to brown, 3.5–6 µm long ($\bar{x}$ ± SD = 4.5 ± 0.5 µm); apical cell 2.5–6 µm long ($\bar{x}$ ± SD = 4 ± 0.6 µm), hyaline, conic to acute; with 1–4 (mostly 2) tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 7.5–17.5 µm long ($\bar{x}$ ± SD =12.2 ± 2.5 µm); single basal appendage, unbranched, tubular, centric, 2.5–5 µm long ($\bar{x}$ ± SD = 3.8 ± 0.5 µm).

Material examined: China, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Botanical Garden, on healthy leaves of *Peristrophe japonica* (Acanthaceae), 1 May 2022, Y.R. Sun, E53, living culture KUNCC 22-12595 = GUCC 21-0803; ibid., on healthy leaves of *Peristrophe japonica*, 1 May 2022, Y.R. Sun, E55, living culture KUNCC 22-12593 = GUCC 21-0802; ibid., on healthy leaves of *Peristrophe japonica*, 1 May 2022, Y.R. Sun, E52, living culture KUNCC 22-12594 = GUCC 21-0804.

Notes: *Pestalotiopsis hispanica* was originally reported on *Proteaceae* plants in Spain by Liu et al. (2019). In this study, three strains were obtained from healthy leaves of *Peristrophe japonica* in China. These three strains grouped with *P. hispanica* (CBS 115391) with maximum

support (ML-BS = 100%, BYPP = 1), and it has overlapping characteristics with *P. hispanica* (CBS 115391). Thus, we identify KUNCC 22-12594, KUNCC 22-12595 and KUNCC 22-12593 as *P. hispanica*, representing a new record.



Note a Host. b Close up view of conidiomata. c, d Conidia attached to conidiogenous cells. e–i Conidia. Scale bars: c–i = 10 μm.

Figure 4.119 *Pestalotiopsis hispanica* (KUNCC 22-12595, new host record)

Pestalotiopsis hydei Huanraluek & Jayaward

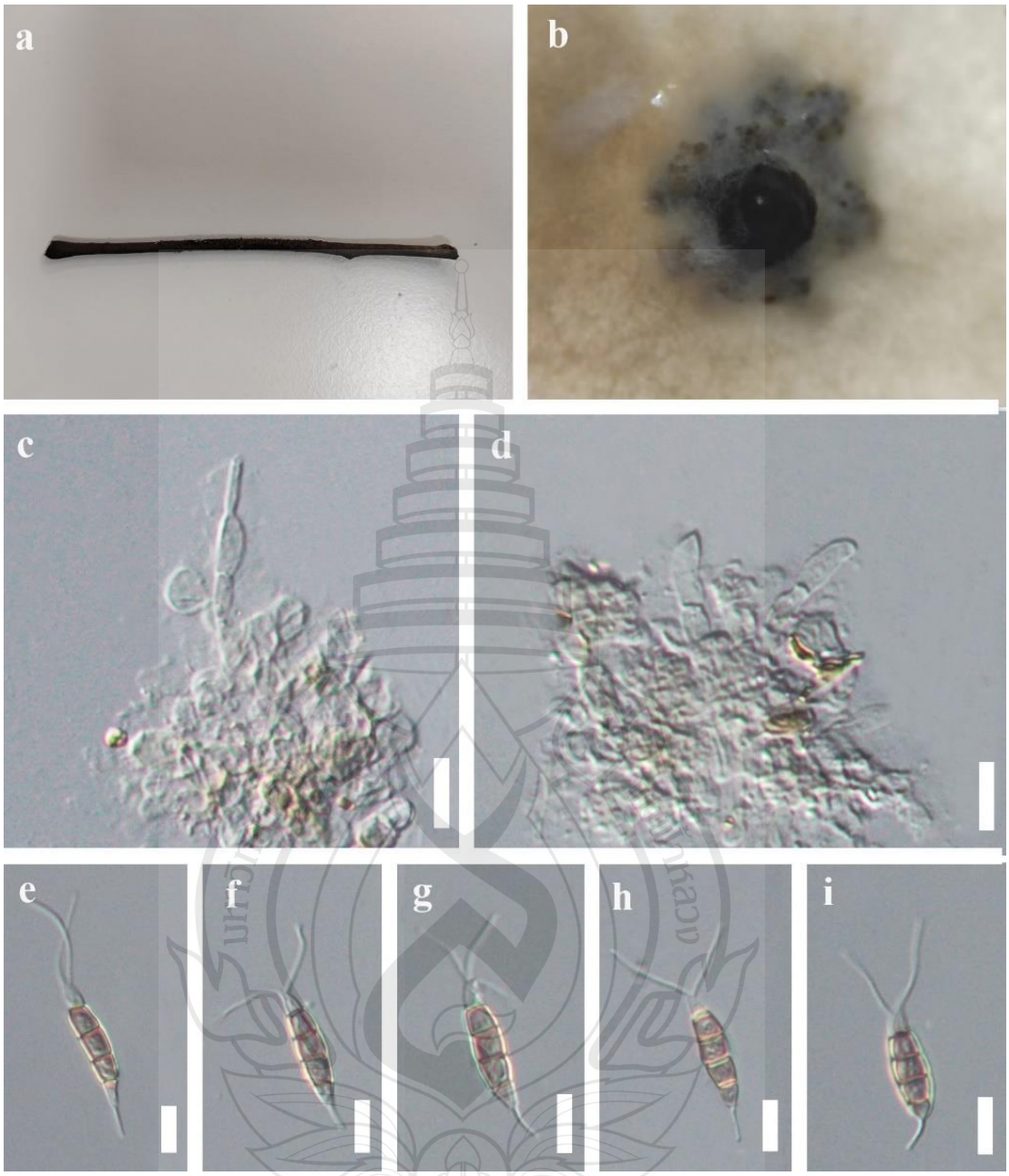
Index Fungorum number: IF558100; Facesoffungi number: FoF09460; Figure 4.120

Saprobic on dead twigs. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* solitary, unilocular, dark, immersed on stems. *Conidiophores* hyaline, smooth, simple, reduced to conidiogenous cells. *Conidiogenous cells* cylindrical to subcylindrical, hyaline, 2–2.5 µm wide. *Conidia* 19.5–26 ×4.5–6 µm ($\bar{x}$ ± SD = 22.5 ± 1.1 × 5 ± 0.3 µm (n = 40), L/W ratio = 4.5, fusiform, straight to slightly curved, 4-septate; basal cell conic to obconic with a truncate base, hyaline to subhyaline, 3–6 µm long; three median cells 11.5–16 µm long ($\bar{x}$ ± SD = 13.5 ± 0.7 µm), wall rugose, pale to brown, concolourous, septa darker than the rest of the cell; second cell from base pale to brown, 3–5.5 µm long; third cell pale to brown, 3–5 µm long; fourth cell pale to brown, 4–5.5 µm long; apical cell 3–5 µm long, hyaline, rugose and thin-walled; with 1–3 tubular apical appendages, arising from the apical crest, unbranched, filiform, 7–17.5 µm long; single basal appendage 3–8.5 µm long, unbranched, tubular, centric.

Culture characteristics: Colonies on PDA reaching 8 cm diam after 2 weeks at 25 °C, colonies filamentous to circular, medium dense, aerial mycelium on the surface flat or raised, fluffy, white from above and reverse.

Material examined: China, Guizhou Province, Qiannan Bouyei and Miao Autonomous Prefecture, Libo District, on dead twigs, 12 March 2022, J.E. Sun, L19-1, living culture, GUCC 21-0819.

Notes: *Pestalotiopsis hydei* was isolated from the leaf spots of *Litsea petiolate* in Thailand (Huanaluek et al., 2021). Our isolate GUCC 21-0819 clustered together with *P. hydei* (MFLUCC 20-0135) in the phylogenetic tree. GUCC 21-0819 also has a similar conidial measurement to MFLUCC 20-0135 (19.5–26 ×4.5–6 µm in GUCC 21-0819, 18–35 × 3–6 µm in MFLUCC 20-0135). Besides, there are only 3 base pair differences in the ITS and *TEF1-α* gene. Therefore, we identify GUCC 21-0819 as a new geographical record of *P. hydei*.



Note a Host. b Close up view of conidiomata. c, d Conidiogenous cells. e–i Conidia. Scale bars: c–i = 10 μm.

Figure 4.120 *Pestalotiopsis hydei* (GUCC 21-0819, new geographical record)

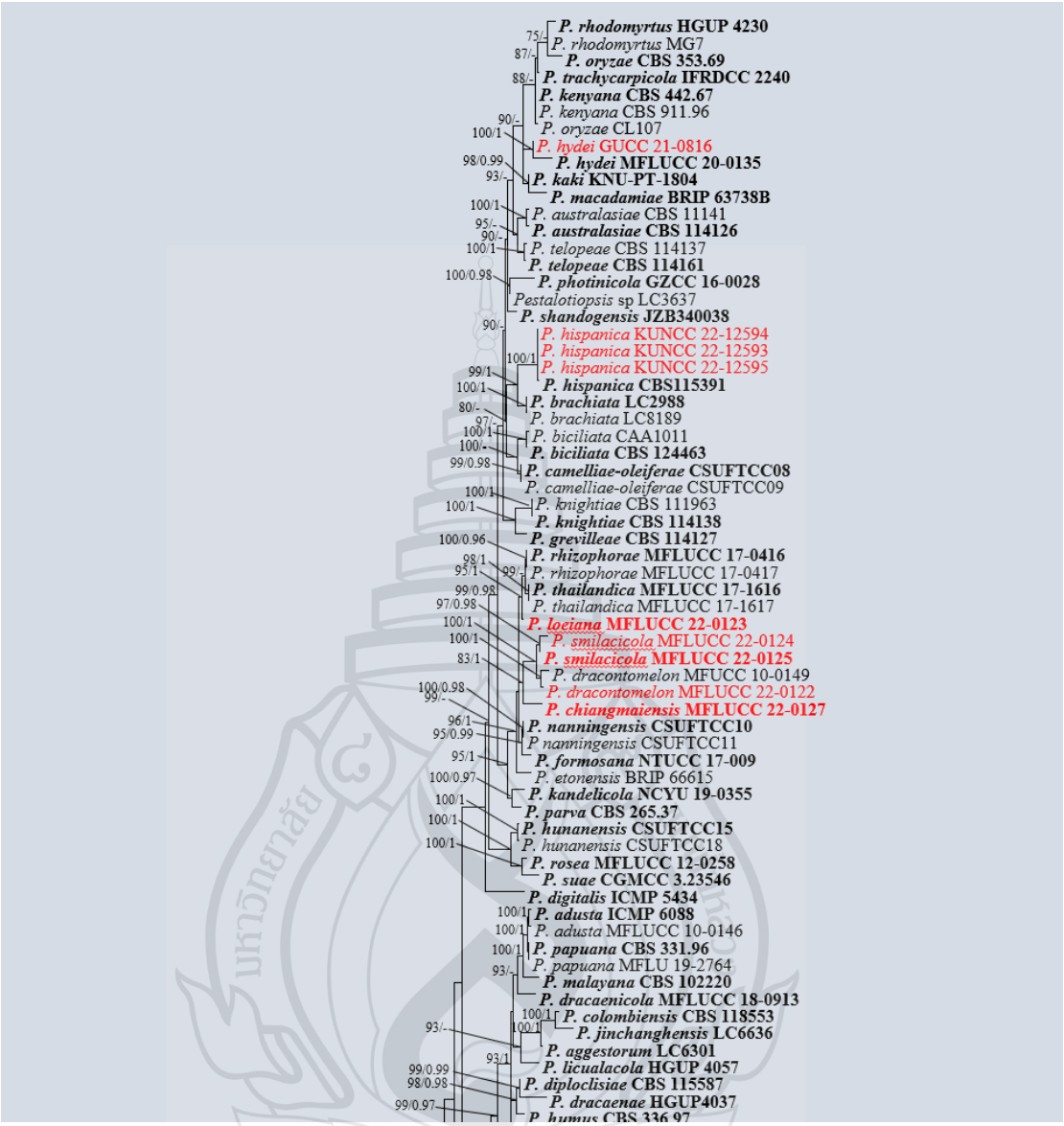
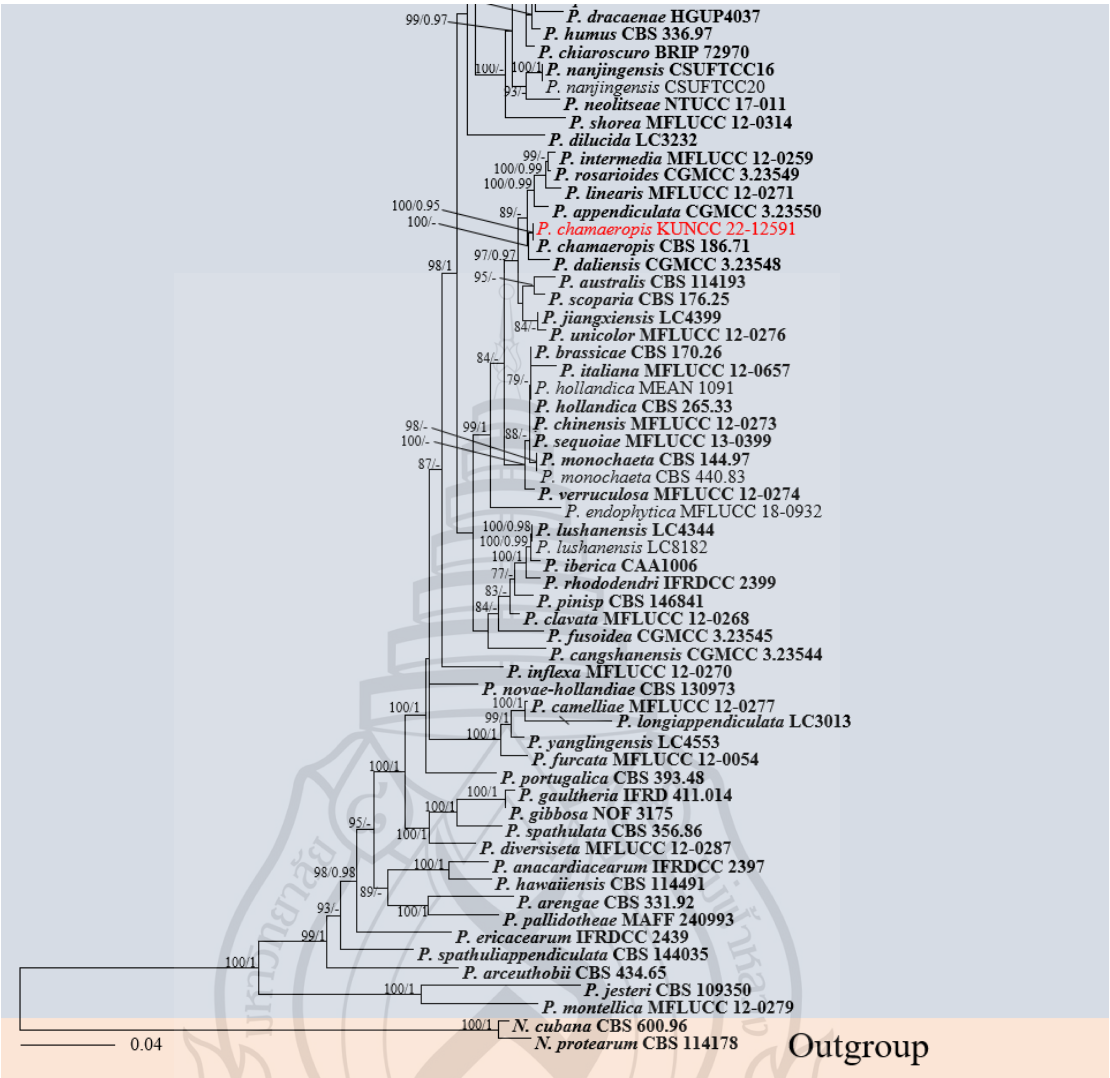


Figure 4.121 Phylogenetic tree of *Pestalotiopsis*



Note The tree is rooted with *Neopestalotiopsis protearum* (CBS 114178) and *N. cubana* (CBS 600.96). Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The new isolates are in red and the ex-type strains are in bold.

Figure 4.121 (continued)

Pseudopestalotiopsis Maharachch., K.D. Hyde & Crous, Stud. Mycol. 79: 180 (2014)

Notes: *Pseudopestalotiopsis* is a genus of fungi known for its plant pathogenic and endophytic species (Maharachchikumbura et al., 2014; Liu et al., 2017; Ariyawansa & Hyde, 2018; Sun et al., 2023). It is characterized by its distinct conidial morphology, which includes multi-septate, fusiform conidia with apical appendages (Maharachchikumbura et al., 2014). Species within this genus have been isolated from a wide range of host plants, causing diseases such as leaf spots and fruit rots (Maharachchikumbura et al., 2016; Gualberto et al., 2021). Recent studies utilizing molecular phylogenetic analyses have helped to clarify the taxonomy and evolutionary relationships within *Pseudopestalotiopsis*.

Pseudopestalotiopsis theae (Sawada) Maharachch., K.D. Hyde & Crous

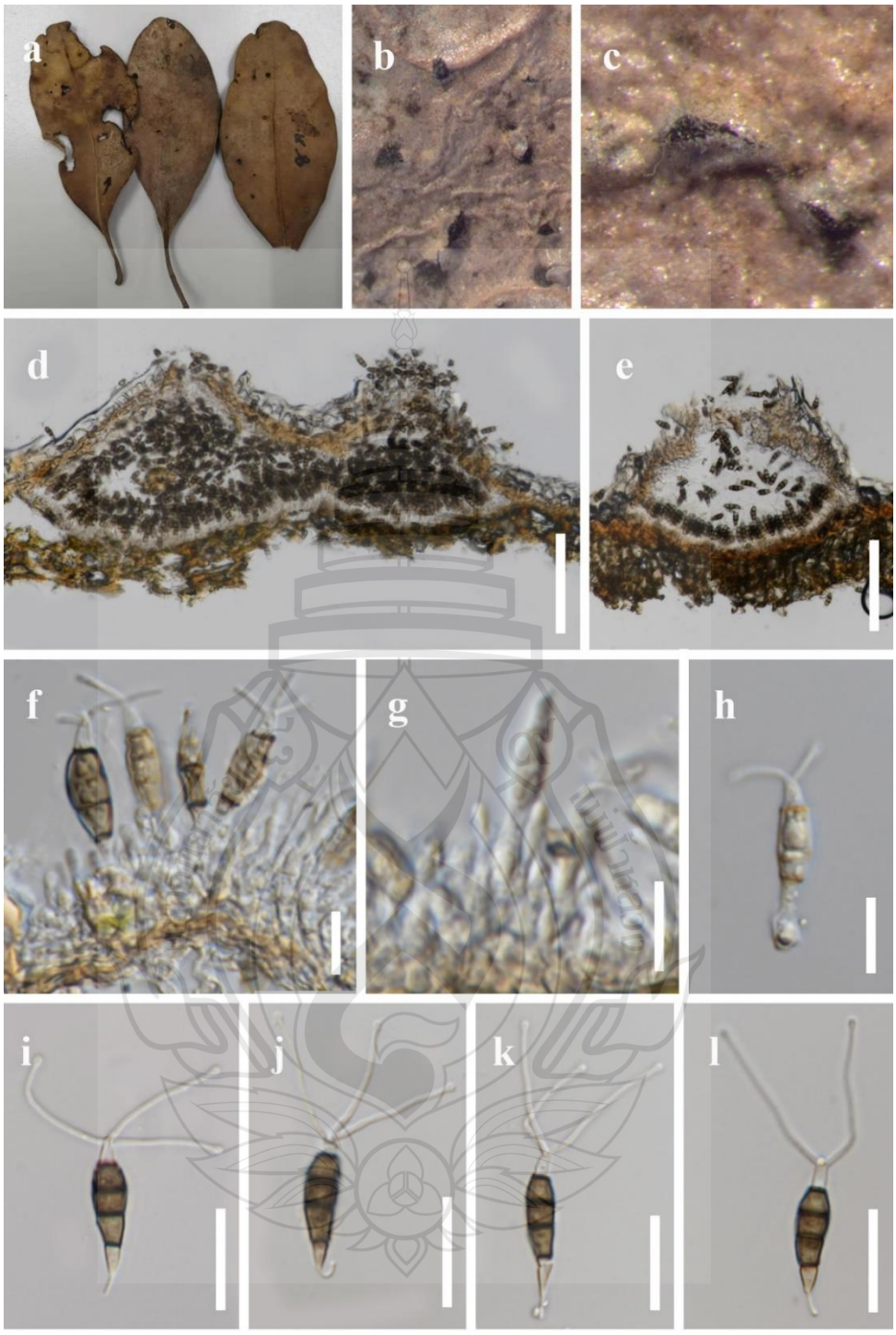
Index Fungorum number: IF809756; Facesoffungi number: FoF07204; Figure 4.122

Associated with dead leaves of *Ceriops tagal.,* **Sexual morph**: Unknown. **Asexual morph**: *Conidiomata* solitary, subglobose, unilocular or bilocular, brown, semi-immersed on leaves. *Conidiophores* indistinct, often reduced to conidiogenous cells. *Conidiogenous cells* sub-cylindrical to cylindrical, hyaline, rugose walled. *Conidia* 22–31 × 5–7 µm, $\bar{x}$ ± SD = 26 ±1.9 × 6 ± 0.5 µm (n = 40), L/W ratio = 4.3, fusiform, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, rugose walled, 3–7 µm long ($\bar{x}$ ± SD = 5.2 ± 0.7 µm); three median cells 14–20 µm long ($\bar{x}$ ± SD = 15.8 ± 1.3 µm), doliiform to cylindrical, pale brown to brown, concolourous, wall rugose, septa darker than the rest of the cell; second cell from base pale brown to brown, 4–7.5 µm long ($\bar{x}$ ± SD = 5.5 ± 0.7 µm); third cell pale brown to brown, 3.5–6.5 µm long ($\bar{x}$ ± SD = 5.0 ± 0.7 µm); fourth cell pale brown to brown, 2.5–7 µm long ($\bar{x}$ ± SD = 5 ± 0.9 µm); apical cell 2.5–5.5 µm long ($\bar{x}$ ± SD = 4 ± 0.7 µm), hyaline, conic to acute; with 2–3 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, unbranched, 18–29 µm long ($\bar{x}$ ± SD =24.5 ± 2.7 µm); single basal appendage, unbranched, tubular, centric, 3–6 µm long ($\bar{x}$ ± SD = 4.5 ± 0.6 µm).

Culture characteristics: Colonies on PDA reaching 10 cm diam after two weeks at 25 °C, colonies filamentous to circular, medium dense, aerial mycelium on the surface flat or raised, fluffy, white from above and below.

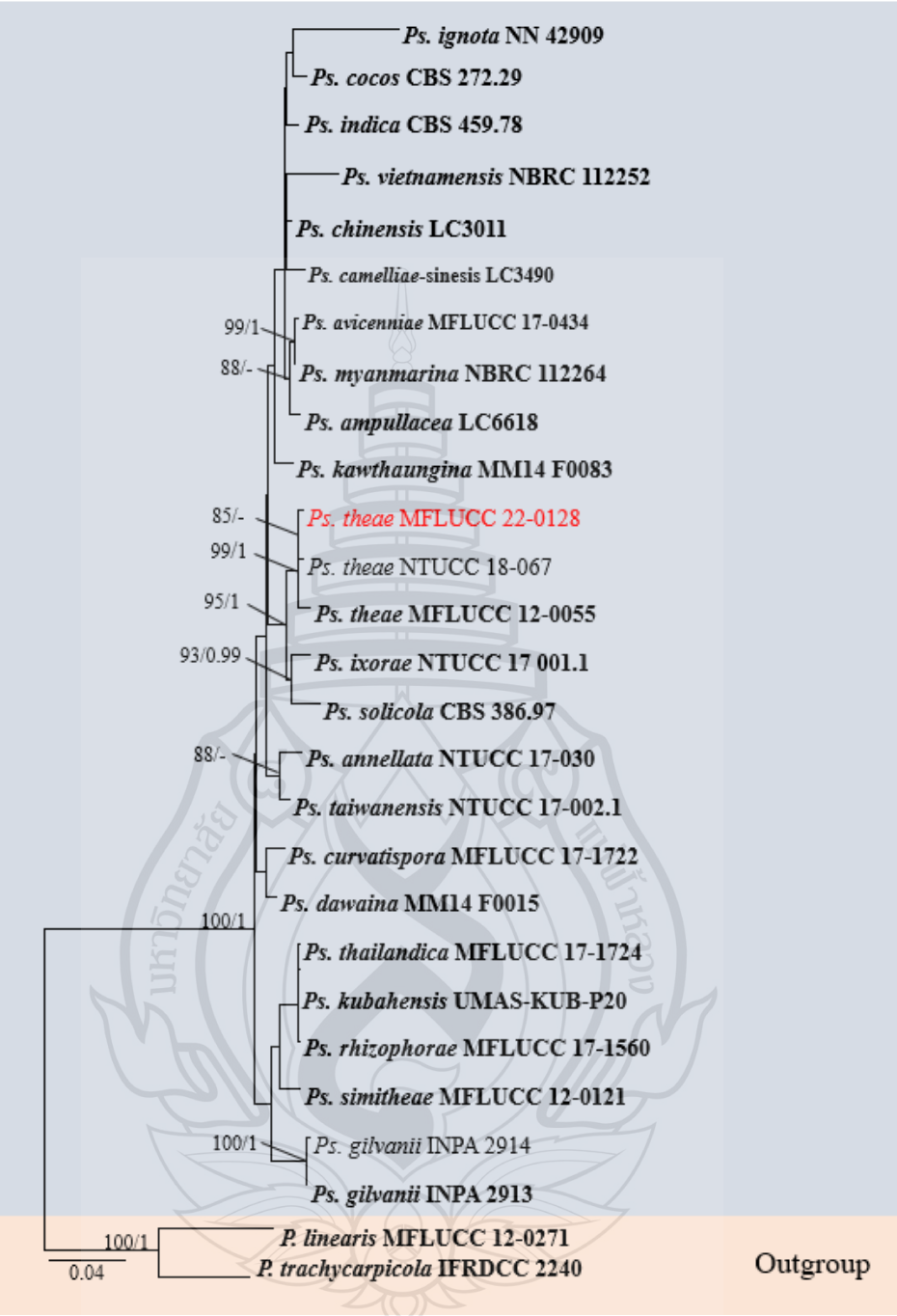
Material examined: Thailand, Suphan Buri Province, dead leaf of *Ceriops tagal* (perr.) C. B. Rob. (*Rhizophoraceae*), 5 September 2020, S Wang, TN07 (MFLU 22-0169); living culture, MFLUCC 22-0128.

Notes: Our isolate MFLUCC 22-0128 is phylogenetically grouped with the type species of *Pseudopestalotiopsis*, *Ps. Theae* (Figure 4.123). Morphologically, our new collection MFLU 22-0169 resembles *Ps. theae* (MFLUCC 12-0055) in color and size of the conidiogenous cells, conidia and appendages. Therefore, we report this isolate as a new host record of *Ps. theae* from the *Ceriops tagal.,*



Note a Host. b, c Close up view of conidiomata. d, e Section through conidioma. e Section through pycnidial wall. f, h Conidia attached to conidiogenous cells. h–l Conidia. Scale bars: d, e = 100 µm, f–h = 10 µm, i–l = 20 µm.

Figure 4.122 *Pseudopestalotiopsis theae* (MFLU 22-0169, new host record)



Note The tree is rooted with *P. trachycarpicola* (IFRDCC 2240) and *P. linearis* (MFLUCC 12-0271). Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The new isolates are in red and the ex-type strains are in bold.

Figure 4.123 Phylogenetic tree of *Pseudopestalotiopsis*

Seiridium Nees, Syst. Pilze (Würzburg): 22 (1816)

Notes: *Seiridium* was established by Nees (1816) and reported as a holomorphic genus. The sexual morphs have immersed or semi-immersed, globose to pyriform, scattered or confluent ascomata with or without papillate, unitunicate, cylindrical, 8-spored asci with amyloid rings and cylindrical or oblong, 3–5-septate, yellow to dark brown spores. The coelomycetous asexual morphs are characterized by immersed to erumpent, scattered or confluent, dark grey to black conidiomata, hyaline, cylindrical, branched conidiophores, discrete, hyaline, cylindrical conidiogenous cells and fusiform or lunate to falcate, 5-septate conidia with a single apical appendage (Marin-Felix et al., 2019; Li, Dissanayake et al., 2022). Seiridium species are widely distributed in terrestrial habitats (some have been reported in freshwater) and have worldwide distribution (Bonthond et al., 2018; Luo et al., 2019). Some species are plant pathogenic species, causing significant economic damage globally (Jiang, Liang et al., 2019; Marin-Felix et al., 2019; Li, Dissanayake et al., 2022). Some also associated with medicinal plants, such as *S. embeliae*, *S. italicum* (Dubey & Pandey, 2009; Samarakoon et al., 2022). Currently, 49 species are accepted in this genus (Species Fungorum, 2024).

Seiridium vernicola W.L. Li & Jian K. Liu, Journal of Fungi 8(11, no. 1175): 24 (2022)

Index Fungorum number: IF845411; Facesoffungi number: FoF12751; Figure 4.124

Pathogenic on diseased leaves of *Camellia japonica*. **Asexual morph**: Conidiomata solitary, immersed to erumpent from tissue, unilocular, subglobose, appear as black spots on leaves. Conidiophores cylindrical, branched, septate, hyaline to pale brown. Conidiogenous cells 3–10 × 2–3 µm, discrete, hyaline, cylindrical, smooth- and thin-walled. Conidia 20–28 × 5–8 µm, lunate to falcate, slightly curved, 5-septate, with a single apical appendage, around 2–5 µm long; the basal cell and apical cell conical, hyaline, smooth-walled; four median cells smooth, cylindrical to doliiform, brown to dark brown, with septa darker than the rest of the cells. **Sexual morph**: not observed.

Material examined: CHINA, Zhejiang Province, Tongxiang City, Zhenxing East Road, Tongxiang Botanical Garden, on diseased leaves of *Camellia japonica*, 15 August

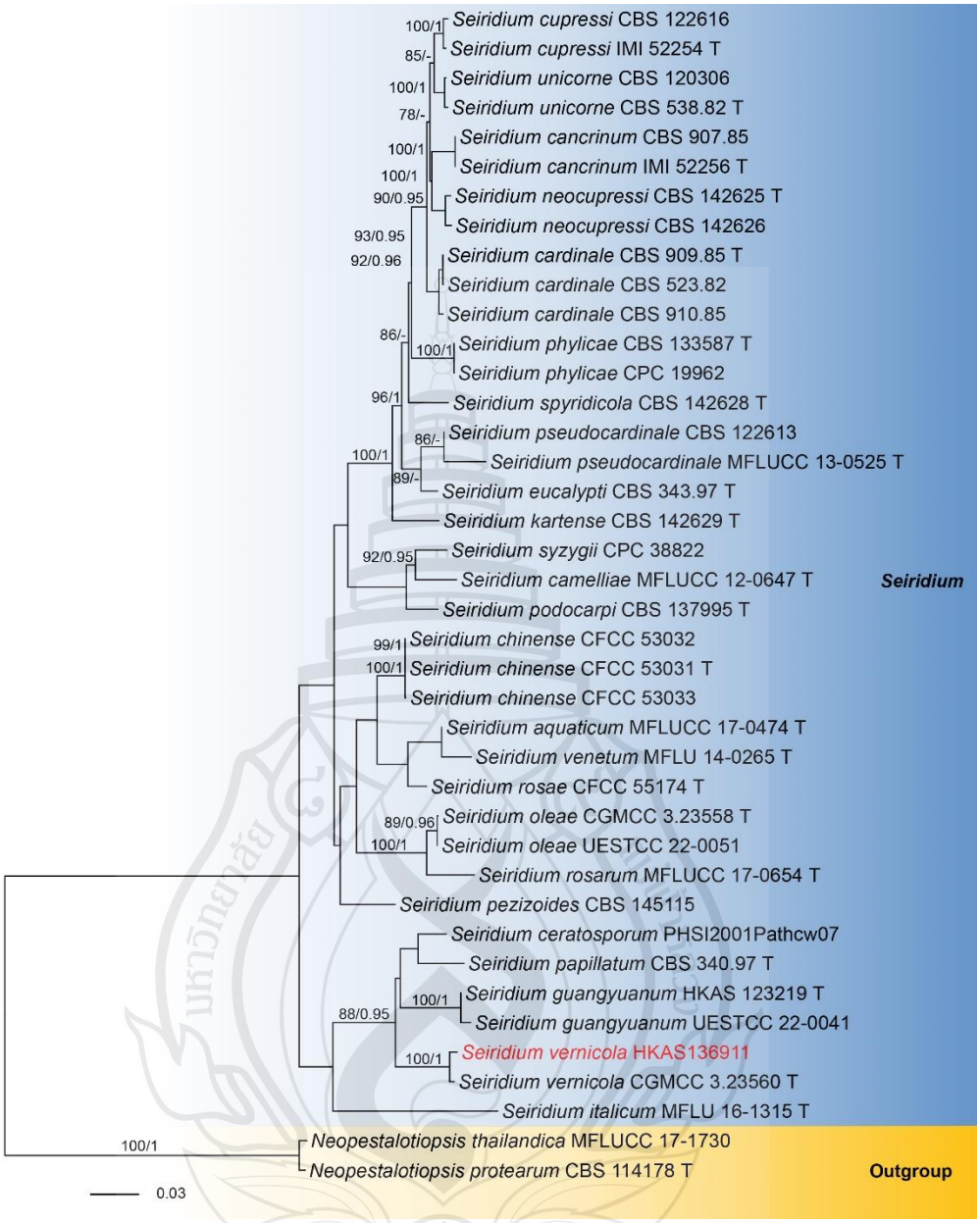
2023, Y.R. Sun, ZJ03 (HKAS 136911); living culture GUCC 24-0093.

Notes: *Seiridium vernicola* was introduced by Li, Dissanayake et al. (2022), which was isolated from diseased branches of *Vernicia fordii* in Sichuan Province, China. Our strain clustered together with the ex-type of *S. vernicola* (CGMCC3.23560) with high statistical support in the phylogenetic tree (ML-bs = 100%, BYPP = 1) (Figure 4.125). In morphology, our collection resembles *S. vernicola* in cylindrical, branched, septate conidiophores, discrete, hyaline, cylindrical conidiogenous cells and lunate to falcate, slightly curved, 5-septate conidia (Li, Dissanayake et al., 2022). However, the conidia of our collection are smaller (20–28 × 5–8 μm *vs.* 25–32 × 8–10 μm). This disparity may arise because our conidia were cultivated on culture media, whereas the latter were observed directly from natural substrates. Therefore, we identified our isolate as *Seiridium vernicola*, representing a new host record from *Camellia japonica*.



Note a Host. b Diseased leaves. c Colonies on PDA. d, e Conidiogenous cells and conidia. f–k Conidia. Scale bars: d–k = 10 μm.

Figure 4.124 *Seiridium vernicola* (HKAS136911, new host record)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Neopestalotiopsis protearum* (CBS 114178) and *N. thailandica* (MFLUCC 17-1730). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.125 Phylogenetic tree of *Seiridium*

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández, Mycologia 96(2): 378 (2004)

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels, Sydowia 51(1): 56 (1999)

Parabahusutrabeeja W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 190 (2022)

Notes*:* *Parabahusutrabeeja* was introduced by Wu and Diao (2022) to accommodate a single species, *P. minima*. *Parabahusutrabeeja* is a saprobic genus on dead material of plants reported from Guangdong and Guangxi Provinces in China (Wu & Diao, 2022). Asexual morph of *Parabahusutrabeeja* is characterized by macronematous, mononematous, dark brown conidiophores, monophialidic conidiogenous cells with indistinct collarette, and globose to subglobose, hyaline conidia with an apical setula (Wu & Diao, 2022). Sexual morph has not been observed. In this study, we introduce a second species *Parabahusutrabeeja hyalina* in this genus.

Parabahusutrabeeja hyalina Y.R. Sun, K.D. Hyde & Yong Wang bis, ***sp. nov.***

Index Fungorum number: IF902606, Facesoffungi number: FoF 16454; Figure 4.126

Etymology: name refers its hyaline conidia.

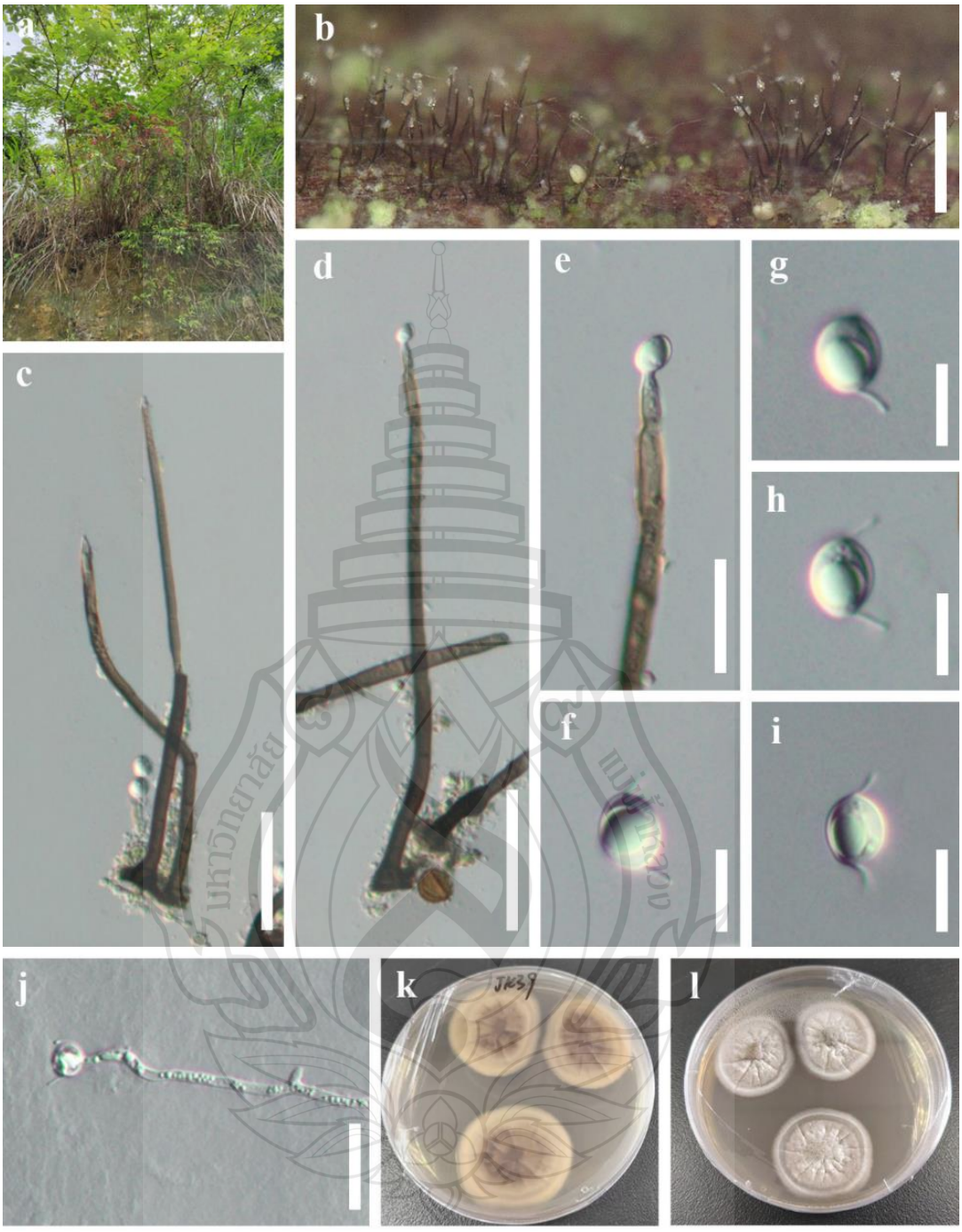
Holotype: HKAS 136901.

Saprobic on *Rubus* sp. **Sexual morph**: Unknown. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, brown to dark brown with apical hyaline conidial mass, velvety, glistening. *Mycelium* partly immersed, partly superficial, composed of hyaline, branched, septate, smooth hyphae. *Conidiophores* macronematous, mononematous, solitary, straight or flexuous, cylindrical, dark brown at base, paler towards apex, unbranched, 2–5-septate, thick-walled, 100–207 µm long, 4–6 µm wide. *Conidiogenous cells* 2–3.5 µm wide, monophialidic, integrated, terminal, pale brown, with an inconspicuous apical collarette. *Conidia* 9–11 × 6–9 µm, aggregated to slimy, hyaline, glistening heads, subglobose to broadly ellipsoidal, aseptate, smooth-walled, with a large central guttule and a single, unbranched setula at each end.

Culture characters: Conidia germinating on PDA media within 24 h. Germ tubes produced form conidial periphery. Colonies on PDA circular, wrinkled, with raised center and entire edge, white from above, yellowish brown at center and pale yellow at outer ring from below.

Material examined: CHINA, Guizhou Province, Tongren City, Jiangkou district, on dead twigs of *Rubus* sp., 20 May 2022, Y.R. Sun, JK39 (HKAS 136901, **holotype**); ex-type culture GUCC 24-0094.

Notes: Our collection is morphologically similar with *Parabahusutrabeeja minima*. However, our collection has subglobose to broadly ellipsoidal and larger (9–11 × 6–9 μm) conidia with two setulae, while the latter has globose to subglobose and smaller (7–8 μm diam.) conidia with one setula (Wu & Diao, 2022). In the phylogenetic analyses (Figure 4.128), our collection (HKAS 136901) clustered with three isolates (NN055337, NN055327 and NN043967) of *P. minima* with maximum support (MLBS = 100%). ITS comparison between HKAS 136901 and the ex-type strain (NN55337) of *P. minima* shows there are 52 bp (16 gaps, totally 472 bp) differences. Therefore, we introduce our collection as a new species based on both morphology and phylogeny.



Note a Host. b Colonies on natural substrate. c, d Conidiophores. e Conidiogenous cell with immature conidium. f–i Conidia. j Germinated conidium. k, l Colony on PDA (k from below, l from above). Scale bars: b = 200 µm, c, d = 50 µm, e–i = 10 µm, j =20.

Figure 4.126 *Parabahusutrabeeja hyalina* (HKAS 136901, holotype)

Pseudolachnella Teng, Sinensia 7: 775 (1936)

Notes: *Pseudolachnella* was introduced by Teng (1936) who segregated it from *Pseudolachnea*. Most *Pseudolachnella* species were reported from China and Japan (Nag Raj, 1993; Zhao et al., 2004; Hashimoto et al., 2015; Wu & Diao, 2022). It is characterized by its coelomycetous asexual morph, which has stromatic, cupulate conidiomata with abundant setae, phialidic, hyaline conidiogenous cells and navilicate to fusiform, cylindrical, vermiform, hyaline, aseptate or multi-septate conidia with setulae (Hashimoto et al., 2015; Wu & Diao, 2022) Sexual morph has not been observed. Currently, 20 species are listed in Species Fungorum (June 2024).

Pseudolachnella minima W.P. Wu & Y.Z. Diao, Fungal Diversity 116: 499 (2022)

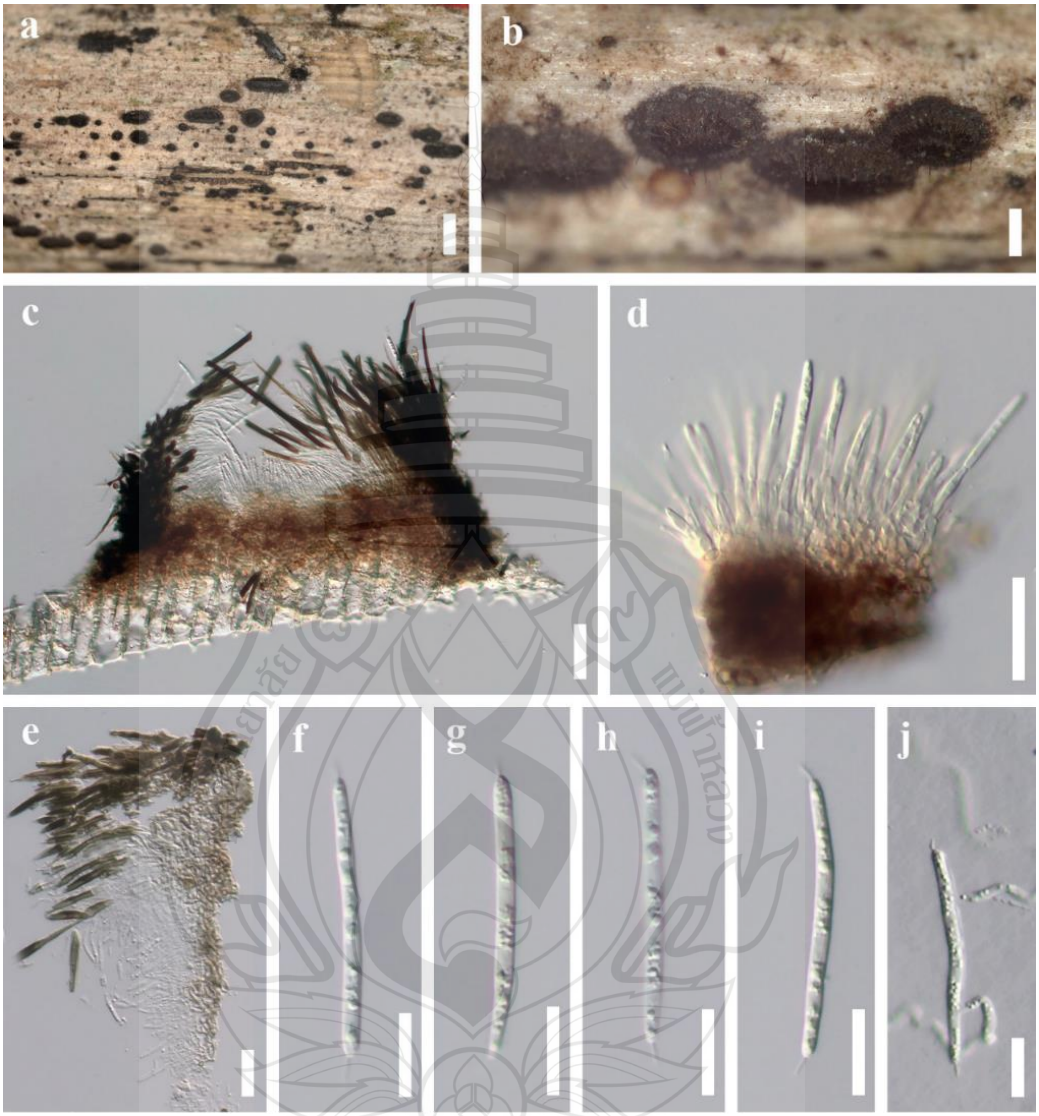
Index Fungorum number: IF 841673; Facesoffungi number: FoF 16455; Figure 4.127

Saprobic on dead twigs. **Sexual morph**: Unknown. **Asexual morph**: Coelomycetous. *Colonies* on natural substrate effuse, dark brown to black, pulvinate. *Conidiomata* stromatic, initially closed, later opening out to become cupulate, basal stroma of *textura angularis*. *Setae* abundant, acuminate, brown to dark brown, simple, septate, originating from basal stroma or the periphery. *Conidiophores* formed from the basal walls, cylindrical, hyaline, simple or sparingly branched, thin-walled. *Conidiogenous cells* 1–2 μm wide, enteroblastic, phialidic with periclinal thickening, integrated, subcylindrical to lageniform. *Conidia* 30–38 μm long, 1.5–2.5 μm wide, solitary, long cylindrical, ends subobtusely rounded, straight or broadly curved, hyaline, aseptate, guttulate, with a single, hyaline, unbranched setula at each end.

Material examined: CHINA, Yunnan Province, Kunming City, on dead twigs, 19 February 2023, H.W. Shen, 2337 (HKAS136904); living culture GUCC 24-0095.

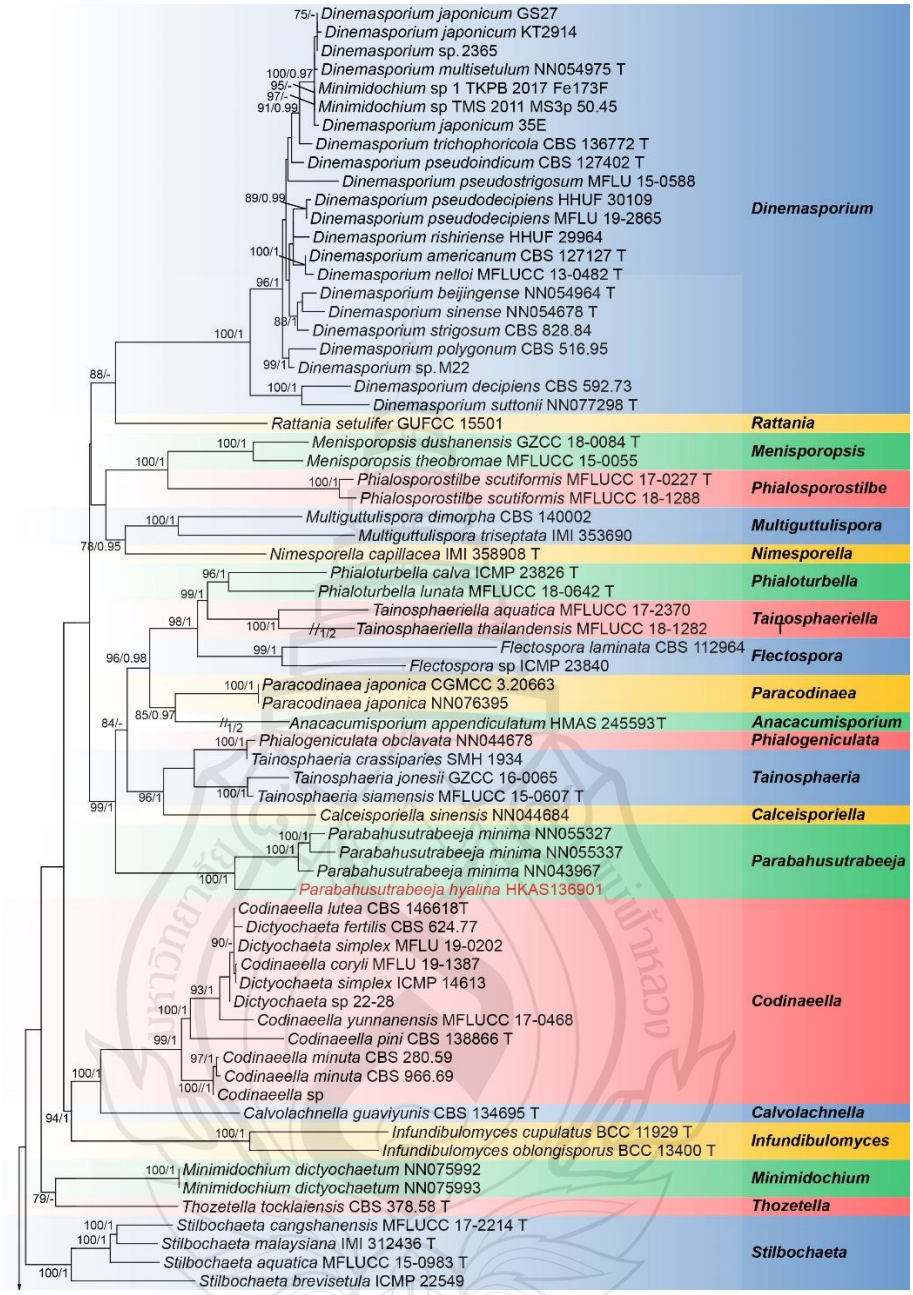
Notes: *Pseudolachnella minima* was introduced by Wu and Diao (2022) on bamboo and *Miscanthus* from different provinces of China. Only ITS sequence (OL627799) of the ex-type of *P. minima* was deposit in GenBank, and comparison shows there is only 1 gap with our strain (2337) (totally 429 bp). Morphologically, our collection has longer (30–38 μm) conidia than those of the holotype (19–25 μm), however, this could be intraspecific variations (Wu & Diao, 2022). Thus, we temporarily identity our collection as *Pseudolachnella minima*.

Other sequences, such as *TEF1-α* gene, are needed to verify the phylogenetic relationship of these two isolates.



Note a, b Conidiomata on the host. c Vertical section through a pycnidia d Conidiophores and conidiogenous cells. e Conidiomata wall. f–i Conidia. j Germinated conidium. Scale bars: a = 1000 μm, b = 200 μm, c–e = 20 μm, f–i = 10 μm.

Figure 4.127 *Pseudolachnella minima* (HKAS136904)



Note The tree is rooted with *Leptosporella arengae* (MFLUCC 15-0330) and *L. bambusae* (MFLUCC 12-0846). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.128 Phylogenetic tree of Chaetosphaeriaceae

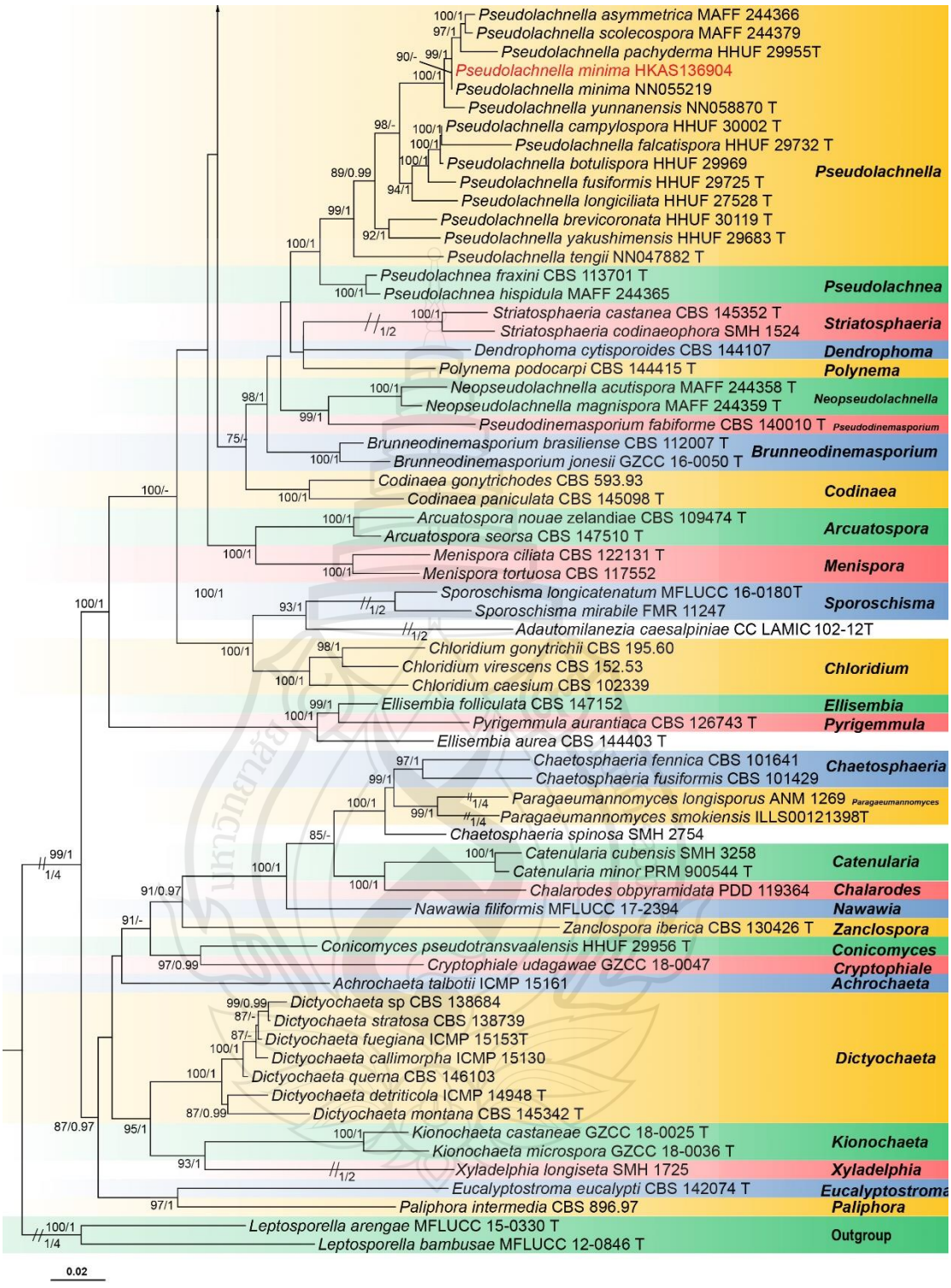


Figure 4.128 (continued)

Conioscyphales Réblová & Seifert, Persoonia 37: 63 (2015)

Conioscyphaceae Réblová & Seifert, Persoonia 37: 63 (2015)

Notes: Réblová et al. (2016) established Conioscyphaceae and Conioscyphales to accommodate *Conioscypha* within Hypocreomycetidae. Hongsanan et al. (2017) introduced a new subclass, Savoryellomycetidae qualified by MCC tree (Hyde, Maharachchikumbura et al., 2017), and transferred Conioscyphales from Hypocreomycetidae to Savoryellomycetidae based on multi-gene phylogeny. Most Conioscyphaceae species have been found as saprobes from submerged substrates or decaying wood in terrestrial and aquatic environments (Zelski et al., 2015; Liu, Bhat et al., 2019; Luo et al., 2019; Hyde, Dong et al., 2020; Li, Du et al., 2024; Xu, Thiyagaraja et al., 2024). Interestingly, two isolates of *Vanakripa minutiellipsoidea* phylogenetically resided within *Conioscypha* (Yang et al., 2020), and this phenomenon was further proven in subsequent studies (Phukhamsakda et al., 2022; Yang, Liu et al., 2023; Liu, Hyde et al., 2024). Recently, Goh et al. (2023) synonymized *Parafuscosporella* under *Vanakripa*, and placed *Vanakripa* in Fuscosporellaceae (Fuscosporellales). However, several species, e.g., *Vanakripa minutiellipsoidea* and *Vanakripa chiangmaiense*, which phylogenetically close to *Conioscypha* and distant from *Parafuscosporella*, were excluded from *Vanakripa*, and treated as *Vanakripa s.l.*

Conioscypha Höhn, Annls mycol. 2(1): 58 (1904)

Notes: Höhnel (1904) introduced *Conioscypha* with *C. lignicola* as the type species. The sexual morphic characteristics of *Conioscypha* have perithecial, astromatic, subhyaline to pale orange or pale brown ascomata with neck, filiform, septate, unbranched paraphyses, 8-spored, unitunicate, cylindrical to clavate asci with J- apical ring and 2–4-seriate, hyaline to subhyaline, ellipsoid to fusiform, septate ascospores (Réblová & Seifert, 2004; Hyde, Norphanphoun et al., 2020). The asexual morph concept of *Conioscypha* is emended in the present study, as we describe a new *Conioscypha* species with synnemata and treat some previous *Vanakripa* species as a synasexual morph in *Conioscypha*. The asexual morphs are trimorphic: (1) conidiomata are sporodochial; conidiophores are micronematous;

conidiogenous cells are phialidic with cup-shaped collarette; conidia are globose to irregular shaped. (2) conidiomata are synnematal; conidiophores are macronematous; conidiogenous cells are phialidic with cup-shaped collarette; conidia are globose to obovoid. (3) conidiomata are sporodochial; conidiophores are micronematous; conidiogenous cells are blastic; conidia are ellipsoidal to obovoid. (Réblová & Seifert, 2004; Zelski et al., 2015; Liu, Bhat et al., 2019; this study). Currently, 23 species are accepted in this genus (Species Fungorum, 2024).

Conioscypha synnemata Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902607; Facesoffungi number: FoF 16456; Figure 4.129

Etymology: The name refers to the synnematous conidiophores.

Holotype: HKAS 136889.

Saprobic on dead twigs in terrestrial habitat. **Sexual morph**: Unknown. **Asexual morph**: Hyphomycetous. *Colonies* on natural substates effuse, dark brown to black, velvety. *Mycelium* immersed, composed hyaline, branched, septate hyphae. *Synnemata* erect, rigid, brown to dark brown, slightly paler towards apex, composed of compact parallel conidiophores. *Conidiophores* 117–360 μm long, 21–48 μm wide at the base, 9–15 μm wide at the middle, macronematous, synnematous, erect, cylindrical, brown to dark brown, septate, think-walled. *Conidiogenous cells* monophialidic, integrated, cyathiform, pale to brown, with a hyaline cup-shaped collarette. *Conidia* 6–12 × 5–11 μm ($\bar{x}$ = 9.5 × 8 μm, n = 30), solitary, globose to obovoid, olivaceous brown to brown, aseptate, smooth-walled, often with a large guttule.

Culture characters: Conidia germinated on WA with 24 h and germ tubes produced around the conidia. Colonies on PDA media circular, dense, flat, with entire edge, slow growth, white from above, yellow from reverse.

Material examined: China, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on dead twigs, 14 April 2023, Y.R. Sun, 2397 (HKAS 136889, **holotype**); ex-type culture GUCC 24-0096.

Notes: *Conioscypha synnemata* is introduced as a new species here. It is placed within *Conioscypha* and formed a sister clade with *Conioscypha bambusicola* (JCM 7245) in the

phylogenetic tree (Figure 4.131). In morphology, *Conioscypha synnemata* resembles other *Conioscypha* species in phialidic conidiogenous cells with a hyaline cup-shaped collarette (Réblová et al., 2016; Liu, Bhat et al., 2019). However, its unique synnematal conidiomata distinctly differ it from other existing *Conioscypha* species, which has sporodochial conidiomata. This is the first species found in *Conioscypha* with synnematous conidiophores.



Note a, b Colonies on natural substrate. c, d Conidiophores and conidia. e, f Conidiogenous cells and conidia. g Germinated conidium. h–k Conidia. l, m Colonies on PDA. Scale bars: c, d = 50 µm, e–g = 20 µm, h–k = 10 µm.

Figure 4.129 *Conioscypha synnemata* (HKAS 136889, holotype)

Conioscypha obovoidea **(**N.G. Liu, Jian K. Liu & K.D. Hyde) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov.***

≡ ***Vanakripa obovoidea*** N.G. Liu, Jian K. Liu & K.D. Hyde, Fungal Diversity: online

Facesoffungi number: FoF 15706; Figure 4.130

Saprobic on *Jatropha integerrima* in terrestrial habitat. **Sexual morph**: Unknown. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, black, punctiform, glistening. *Mycelium* mostly immersed, composed of hyaline hyphae. *Conidiophores* micronematous, hyaline, smooth. *Conidiogenous cells* monoblastic, integrated, terminal, hyaline. *Separating cells* long subcylindrical to vermiform, with dense cytoplasm, hyaline, smooth-walled, 3–5 μm wide. *Conidia* 15–20 × 9–13 μm ($\bar{x}$ = 18 × 11 μm, n = 30), solitary, ellipsoidal to obovoid, rounded at the apex, truncate at the base, hyaline when young, brown to dark brown when mature, aseptate, verrucose. Conidial secession rhexolytic.

Culture characteristics: Conidia germinating on PDA media within 12 h and germ tubes produced from the base of the conidia. Colonies on PDA media subcircular to irregular, dense, wrinkled, with raised center and undulate edge, yellow to yellowish brown from above, pale yellow from reverse.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on twigs of *Jatropha integerrima*, 7 January 2010, Y.R. Sun, B83 (HGUP 24-0051); living culture GUCC 24-0141.

Notes: Phylogenetically, our strain GUCC 24-0141 grouped together with *Vanakripa obovoidea* (MFLUCC 24-0084) with maximum support (Figure 4.131). Morphological and base pair comparisons of ITS sequences indicate they are conspecific.

Goh et al. (2023) narrowed generic concept of *Vanakripa* with conidia having a septum near the base. Conidia of our collection are unicellular which are not fitting with *Vanakripa*, and it is phylogenetically mixed within *Conioscypha* group. In order to avoid taxonomic confusions, we temporarily treat *V. chiangmaiense*, *V. minutiellipsoidea* and *V. obovoidea* as the synasexual morph of *Conioscypha*, until further solution or more

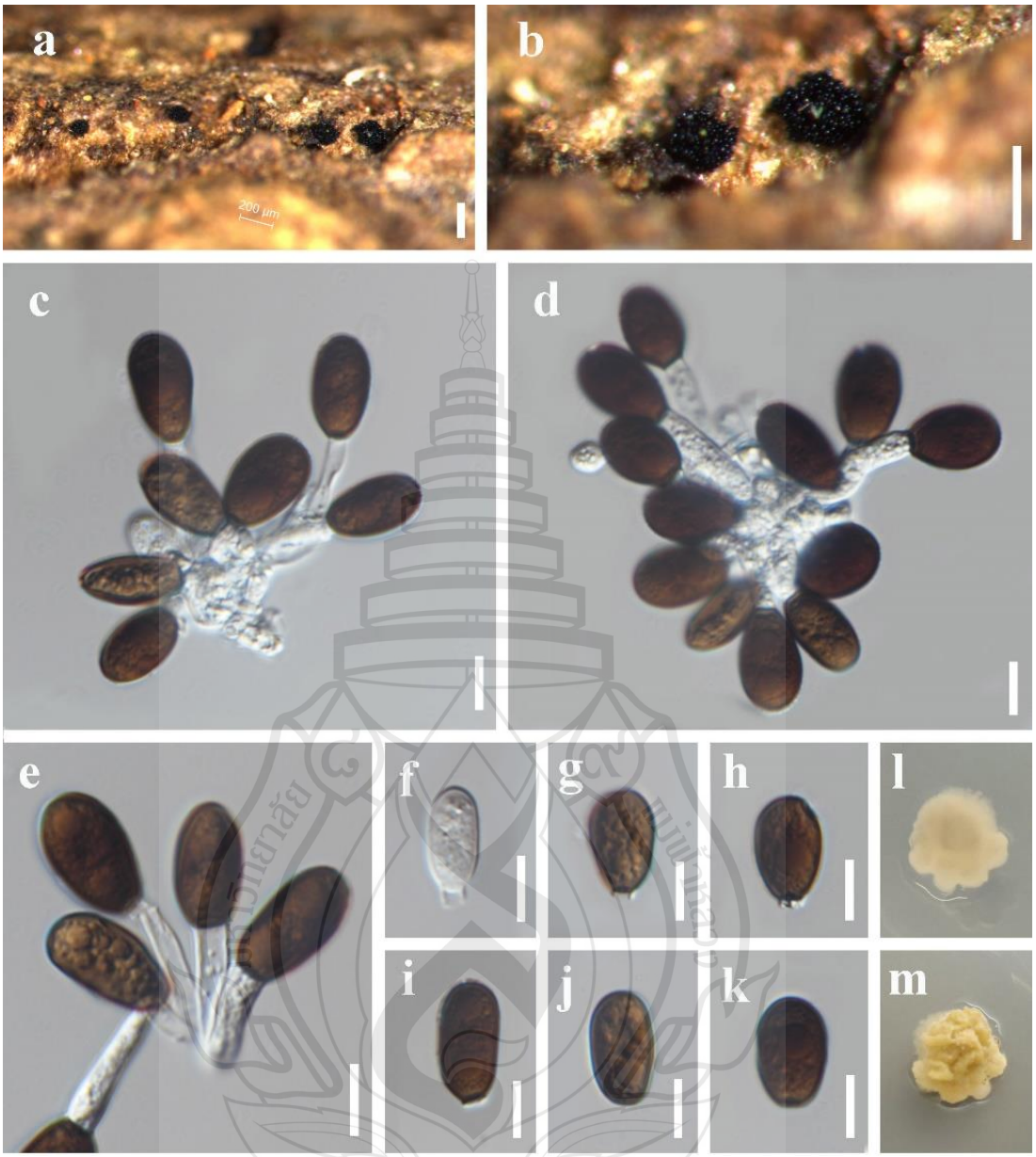
informative molecular markers applied for this group (Goh et al., 2023). Other "*Vanakripa*" species without sequence data, e.g., *V. chinensis*, are waiting more evidence to confirm their phylogenetic placements. Consequently, another two new combinations are proposed.

Conioscypha chiangmaiense (X.G. Tian & Karun.) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov.***, Facesoffungi number: FoF 16457.

≡ *Vanakripa chiangmaiense* X.G. Tian & Karun., Fungal Diversity: 10.1007/s13225-022-00502-3, [25] (2022)

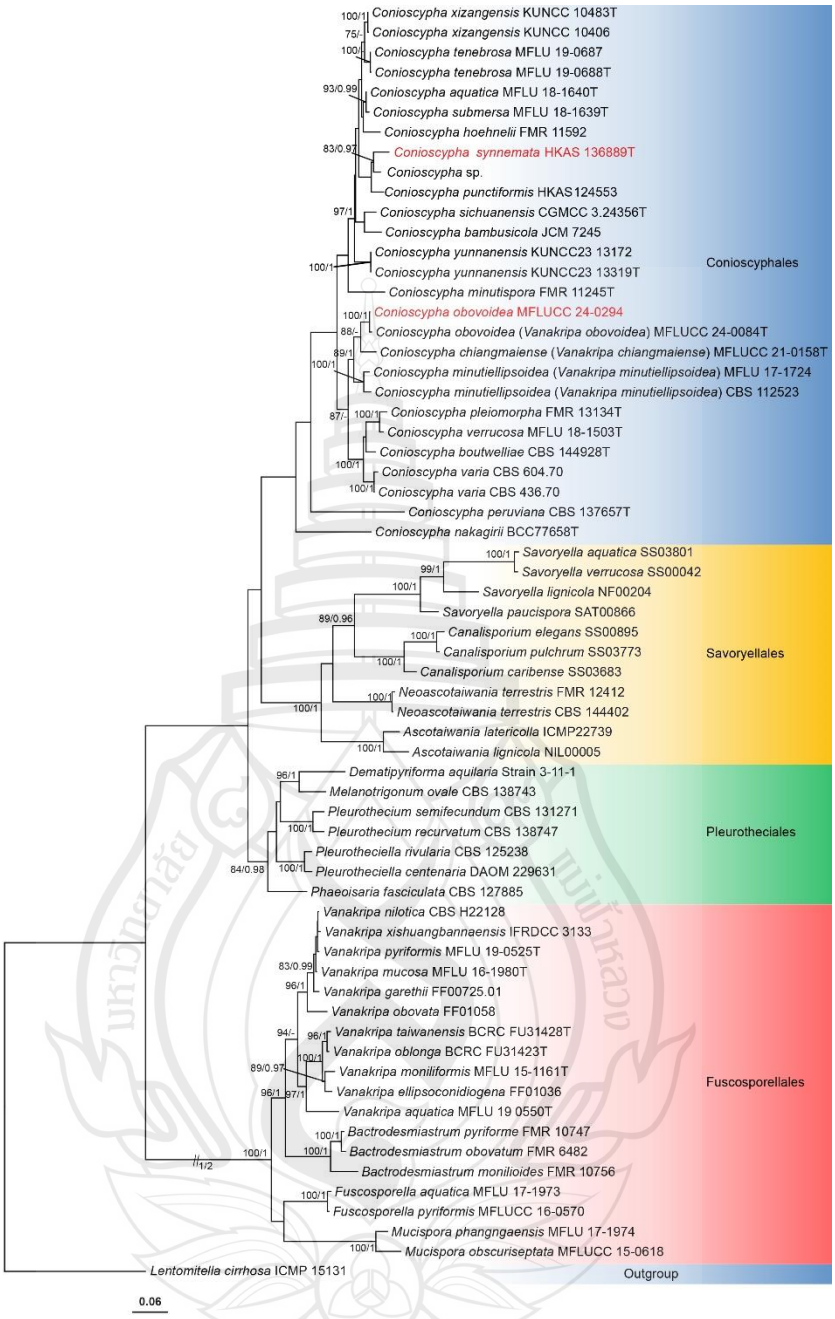
Conioscypha minutiellipsoidea (Pinnoi) Y.R. Sun, Yong Wang bis & K.D. Hyde, ***comb. nov.***, Facesoffungi number: FoF 16458.

≡ *Vanakripa minutiellipsoidea* Pinnoi, Nova Hedwigia 77 (1-2): 217 (2003)



Note a, b Colonies on the host. c–e Conidiophore with conidia. f–k Conidia. l, m Culture on PDA after two weeks of incubation on PDA. Scale bars: a, b = 200 µm, c–k = 10 µm

Figure 4.130 *Conioscypha obovoidea* (HGUP 24-0051, new combination)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Lentomitella cirrhosa* (ICMP 15131). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.131 Phylogenetic tree of Conioscyphales

Diaporthales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 53 (1932)

Diaporthaceae Höhn., Am. J. Bot. 13: 638 (1926)

Diaporthe Nitschke, Pyrenomyc. Germ. 2: 240 (1870)

Notes: *Diaporthe* (also known as *Phomopsis*) has significant historical and biological diversity, including numerous species that act both as important pathogens and endophytes in ecosystems (Udayanga et al., 2012; Hyde et al., 2014; Huang et al., 2015; Hyde, Norphanphoun et al., 2017; Yang, Maharachchikumbura et al., 2018; Norphanphoun et al., 2022). As pathogens, *Diaporthe* species significantly impact many crops and economically important plants, such as *Diaporthe citri* causing citrus canker (Huang et al., 2013; Chaisiri et al., 2022), *Diaporthe phaseolorum* leading to soybean stem canker (Udayanga et al., 2015), and *Diaporthe helianthi* affecting sunflowers (Yang et al., 1984; Gao et al., 2017). As endophytes, these species can live within host plants without causing obvious symptoms and can enhance the host's disease resistance and stress tolerance (Huang et al., 2015).

Diaporthe species have garnered attention for their applications and potential in medicinal plants. Studies have found that secondary metabolites from *Diaporthe* species possess various pharmacological activities and pathogen inhibitions. For example, *Diaporthe* sp. LG23, isolated from the medicinal plant *Mahonia fortunei*, is capable of producing a potent tetracyclic triterpenoid with antibacterial properties (Li et al., 2015). *Diaporthe endophytica* and *D. terebinthifolii*, isolated from medicinal plants, have demonstrated significant inhibitory effects against *Phyllosticta citricarpa* which caused citrus black spot (Dos Santos et al., 2016). These discoveries broaden our understanding of *Diaporthe* fungi and provide new avenues for developing antibacterial, anti-inflammatory drugs and green pesticides. Recently, Dissanayake et al. (2024) refined the genus and divided the genus into seven sections and provided the boundaries for 13 species and 15 species-complexes. In this study, we adopted the new classification system proposed by Dissanayake et al. (2024) and introduced 11 *Diaporthe* species.

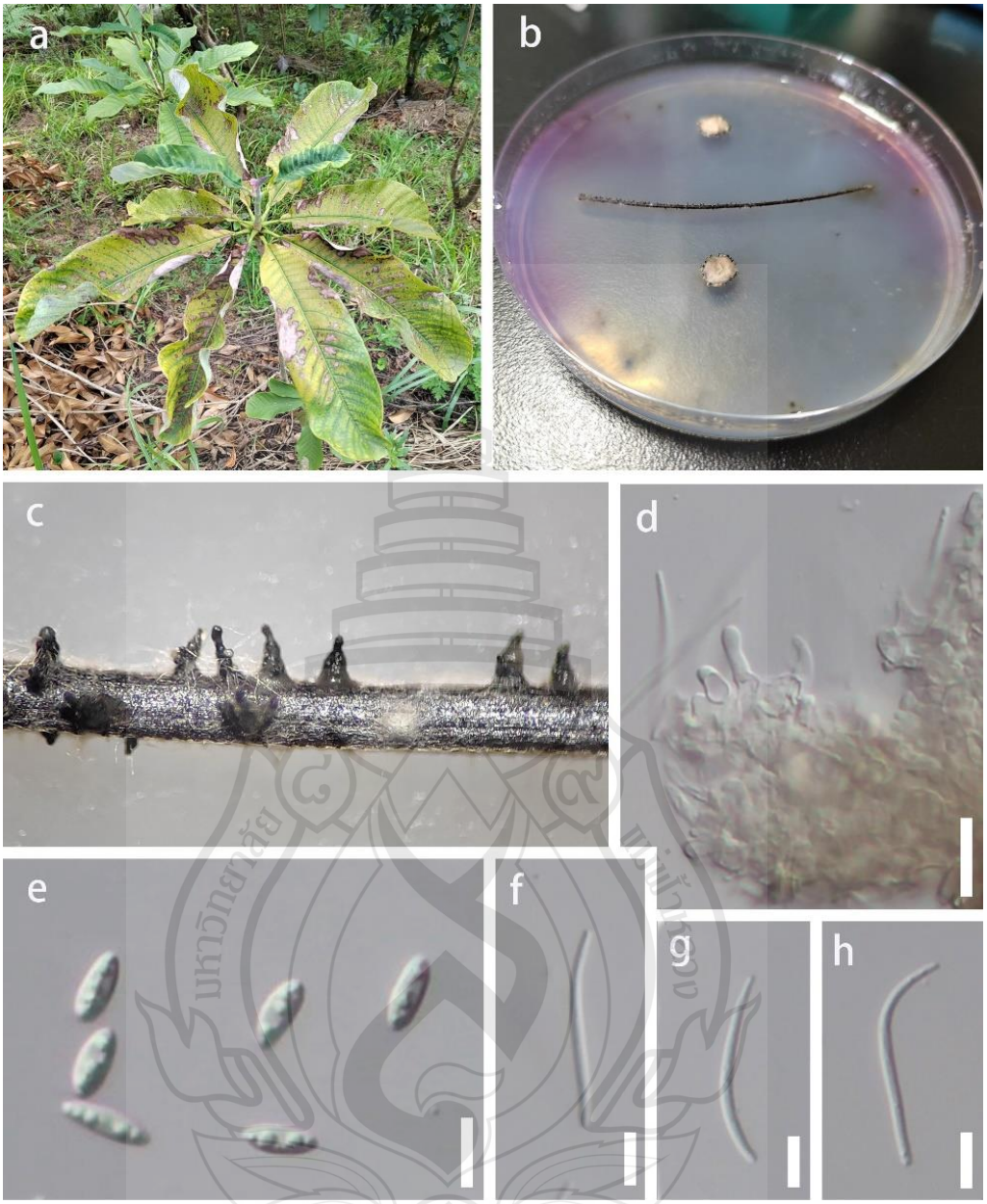
Diaporthe arecae (H.C. Srivast., Zakia & Govindar.) R.R. Gomes, Glienke & Crous, Persoonia 31: 16 (2013)

Index Fungorum number*:* IF 802924; *Facesoffungi number:* FoF 08405; Figure 4.132

Associated with leaf disease of *Magnolia officinalis* in China. Symptoms subcircular to irregular, pale brown, with brown at margin. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* superficial, solitary, scattered, dark brown to black, subglobose to globose, with a long neck in culture. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, ampulliform or cylindrical, hyaline, unbranched, aseptate, straight, slightly tapering towards the apex. Alpha conidia 4.5–7 × 1.5–2.5 µm ($\bar{x}$ = 6 × 2 µm, n = 30), fusiform, hyaline, aseptate, 3–4-guttulate, smooth. *Beta conidia* 18–25 µm long, around 1 µm wide, filiform, hyaline, aseptate, straight to sinuous at one end. *Gamma conidia* not observed.

Material examined: CHINA, Guizhou Province, Anshun City, Xixiu District, Yaowang Valley Tourism Resort, on dead leaves of *Magnolia officinalis*, 3 August 2022, Y.R. Sun, HP4 (HKAS 136866); living culture GUCC 24-0097.

Notes: Norphanphoun et al. (2022) accepted 13 species complexes in *Diaporthe* and included 45 species in *Diaporthe arecae* species complex. Dissanayake et al. (2024) used phylogenetic analysis, GCPSR, and coalescence-based models to determine that *D. arecae* is a single species. They also included *D. caricae-papayae*, *D. euginiae*, *D. persiae*, and *D. phoenicicola* within this species clade. Our new strain isolated from the diseased leaves of *Magnolia officinalis,* an important medicinal plant in Guizhou Province, China. In the phylogenetic analyses (Figure 4.144), our isolate placed within *D. arecae* clade. *Diaporthe arecae* has been documented form many plants, viz. *Areca*, *Citrus*, *Musa* and Olea, but none have been reported from *Magnolia* (Based on molecular data) (Pereira et al., 2023). Therefore, we identified our isolate as a new host record of *Diaporthe arecae.*



Note a Host. b Front view of culture. c Conidiomata on pine needles in culture medium. d Conidiophores and conidiogenous cells. e Alpha conidia. f–h Beta conidia. Scale bars: d = 10 µm, e–h = 5 µm.

Figure 4.132 *Diaporthe arecae* (HKAS 136866, new host record)

***Diaporthe leucospermi* species complex**

Diaporthe kunmingensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902608; Facesoffungi number: FoF 16459; Figure 4.133

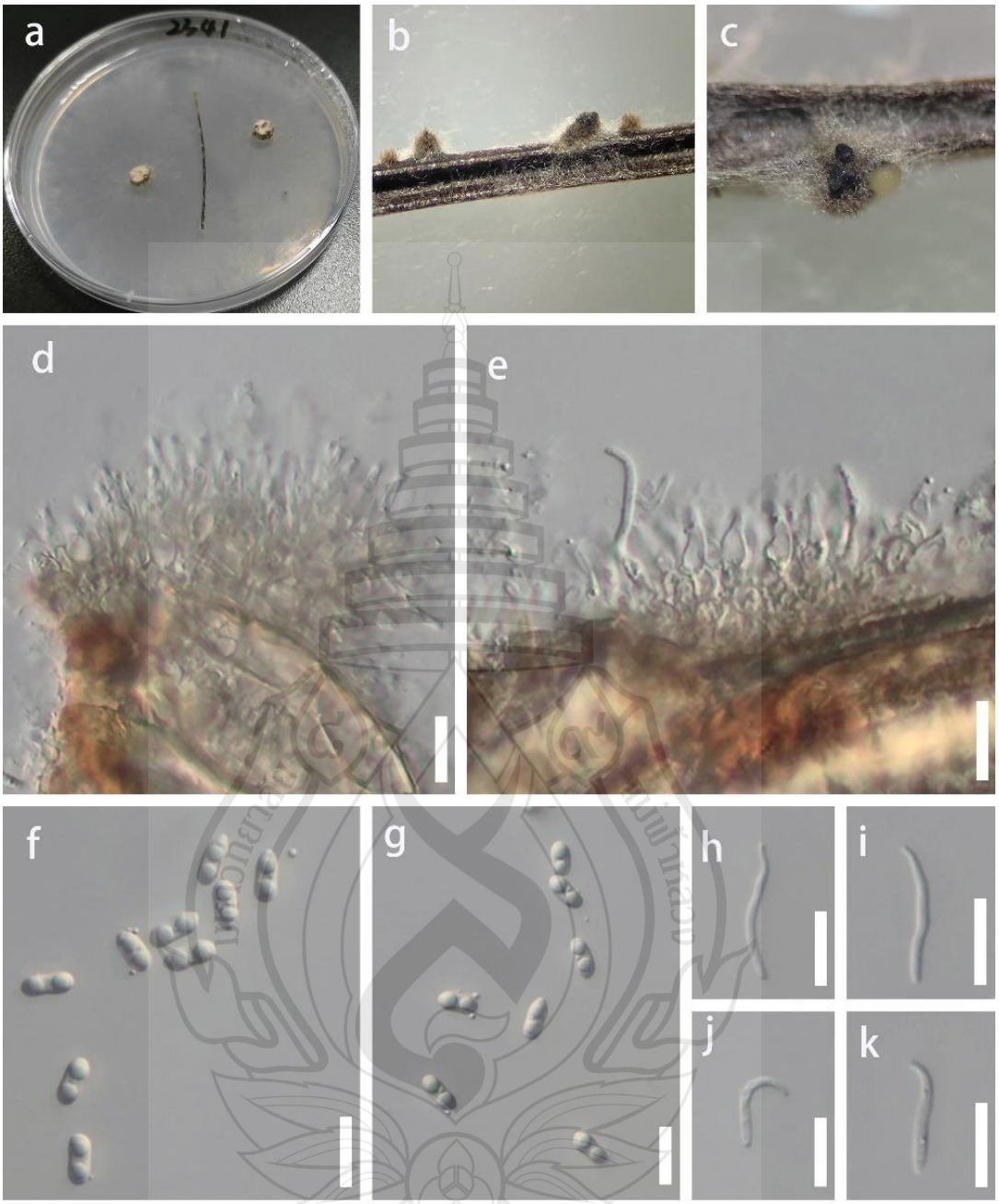
Etymology: referring to the Kunming City where the fungus was collected.

Holotype: HKAS 136905.

Saprobic on dead twigs. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* superficial, solitary, scattered, dark brown to black, globose. *Conidiophores* 2–3 µm wide, aseptate, cylindrical, straight or sinuous, short, terminal., *Conidiogenous cells* 5–9.5 × 1.5–3 µm, phialidic, ampulliform, hyaline, tapered towards the apex. *Alpha conidia* 5.5–8 × 2–3.5 µm ($\bar{x}$ = 7 × 3 µm, n = 30), oblong to oval, hyaline, aseptate, biguttulate, smooth, round at both ends. *Beta conidia* filiform, hyaline, aseptate, curved, 11–17 µm long, around 1–1.5 µm wide. *Gamma conidia* not observed.

Material examined: CHINA, Yannan Province, Kunming City, Yiliang District, Yangzonghai Garden, on dead twigs, 20 February 2023, H.W. Shen, 2341 (HKAS 136905, **holotype**); ex-type culture GUCC 24-0098.

Notes: Our new isolate collected from the dead twigs in Yunnan Province. The multi-gene analyses showed our isolate formed a distinct clade and sister to *D. myracrodruonis* in *D. leucospermi* species complex. However, our isolate can be distinguished from *D. myracrodruonis* in ITS loci (52 bp differences/518 bp, without gap). Therefore, we introduced *Diaporthe kunmingensis* sp. nov. here.



Note a Front view of culture. b, c Conidiomata on pine needles in culture medium. d, e Conidiophores and conidiogenous cells. f, g Alpha conidia. h–k Beta conidia. Scale bars: d–k = 10 μm.

Figure 4.133 *Diaporthe kunmingensis* (HKAS 136905, holotype)

Diaporthe litseae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902549; Facesoffungi number: FoF 16399; Figure 4.134

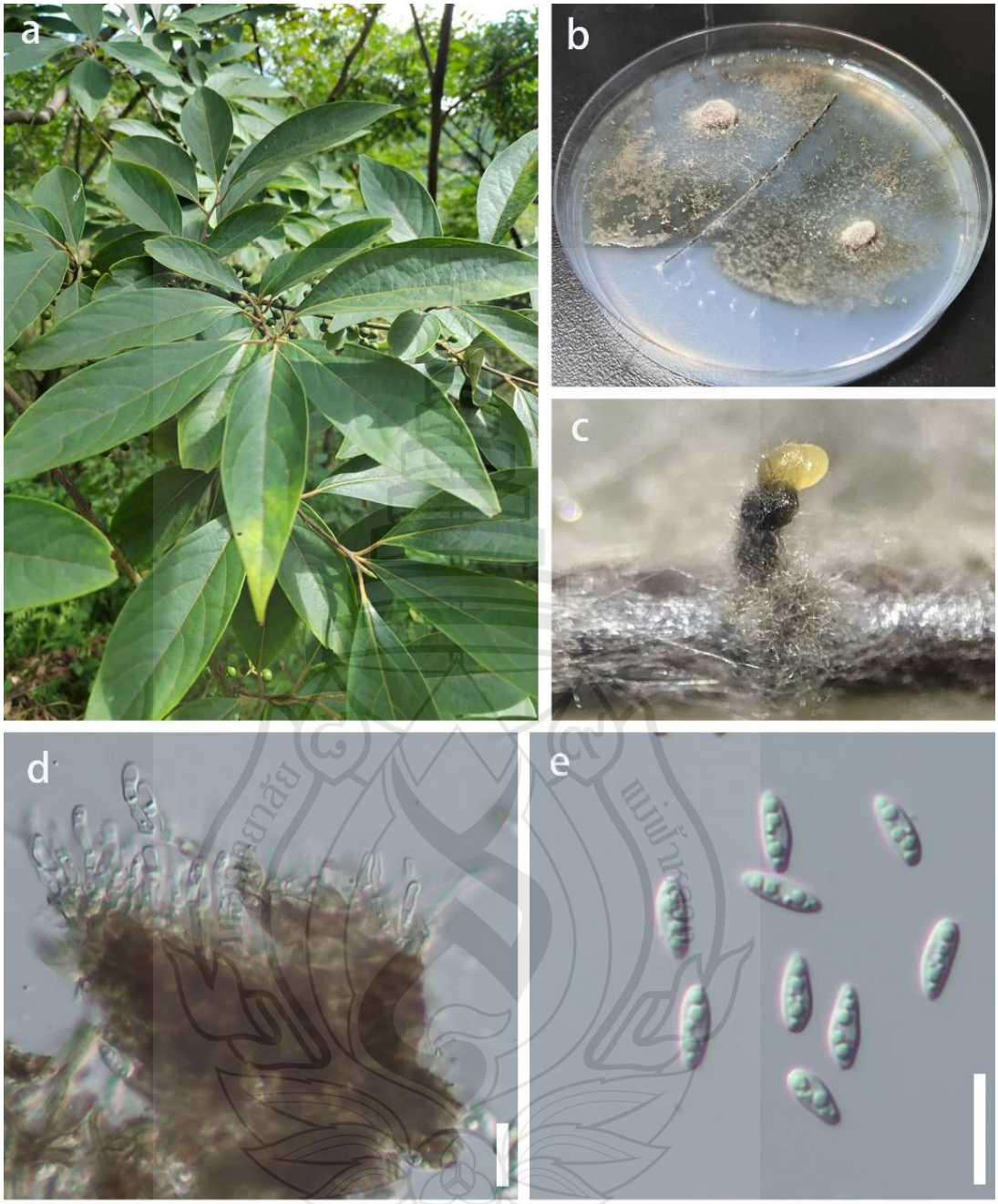
Etymology: referring to the host genus.

Holotype: HGUP 24-0011.

Endophytic from healthy leaves of *Litsea kobuskiana*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* superficial, solitary, scattered on the pine needle in the WA, dark brown to black, globose. *Conidiophores* 1–2 µm wide, aseptate, cylindrical, straight or sinuous, densely aggregated, terminal., *Conidiogenous cells* phialidic, cylindrical., *Alpha conidia* 5–9 × 2–3.5 µm ($\bar{x}$ = 7 × 2.5 µm, n = 40), fusiform, hyaline, aseptate, 4–5-guttulate, both ends obtuse. *Beta conidia* not observed.

Material examined*:* China, Guizhou Province, Anshun City, Xixiu District, Yaowang Valley Tourism Resort, on heathy leaves of *Litsea kobuskiana*, 3 August 2022, Y.R. Sun, MJZY1-1 (HGUP 24-0011, **holotype**); ex-type living culture GUCC 23-0022; ibid, on heathy leaves of *Litsea kobuskiana*, 3 August 2022, Y.R. Sun, MJZY1 (HGUP 23-0008, living culture GUCC 24-0055).

Notes*:* BLASTn searches of the ITS sequence of *Diaporthe litseae* resulted in 97.6% similarity with *D. citrichinensis* (Synonym: *D. ukurunduensis*) (W2). The BLASTn results of *cal* and *tef1-α* are 92.26% and 88.85% similar to *D. citri* (SICAUCC 22-0129) and *D. citri* (ZGPF1) respectively. The multi-gene analyses showed *D. litseae* close to *D. citri* and form a sister clade to *D. citrichinensis* species complex (Figure 4.144). In morphology, *Diaporthe litseae* differs from *D. citri* by its fusiform, 4–5-guttulate, smaller and thinner alpha conidia (7 × 2.5 µm *vs*. 8.5 × 3.7 µm, L/W: 2.8 *vs*. 2.3) while the latter has ovate to ellipsoidal, 1–2-guttules alpha conidia (Udayanga et al., 2014b; Hongsanan et al., 2023). Therefore, we introduced *D. litseae* as a novel species and not belonging to any species complex following the recent literatures (Jeewon & Hyde, 2016; Jayawardena, Bhunjun et al., 2021; Dissanayake et al., 2024).



Note a Host. b Front view of culture. c Conidiomata on pine needles in culture medium. d Conidiophores and conidiogenous cells. e Alpha conidia. Scale bars: d, e = 10 μm.

Figure 4.134 *Diaporthe litseae* (HGUP 24-0011, holotype)

***Diaporthe longicolla* species complex**

Diaporthe ervatamiae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16460; Figure 4.135

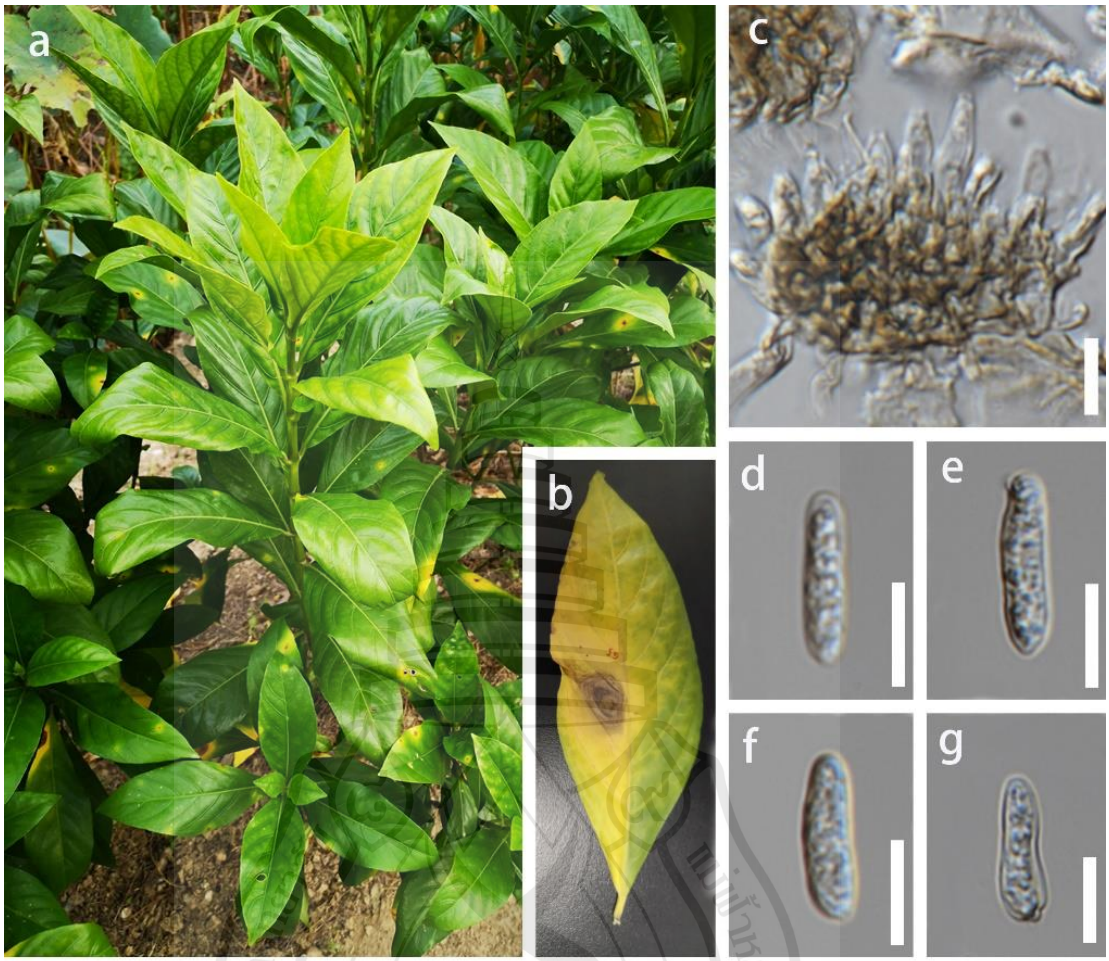
Etymology: referring to the host's genus.

Holotype: HGUP 24-0052.

Associated with leaf spot of *Ervatamia kwangsiensis* in China. Symptoms subcircular pale brown to brown. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* superficial, solitary, scattered, dark brown to black, subglobose to globose. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, cylindrical, hyaline, unbranched, aseptate, straight, slightly tapering towards the apex. *Alpha conidia* 4.5–7 × 1.5–2.5 μm ($\bar{x}$ = 6 × 2 μm, n = 30), elongated to cylindrical, hyaline, aseptate, rounded at both ends, rough. *Beta* and *gamma conidia* not observed.

Material examined: CHINA, Guangxi Province, Nanning City, Xingning District, Guangxi Medical Botanical Garden, on diseased leaves of *Ervatamia kwangsiensis*, 14 September 2019, Y.R. Sun, G5 (HGUP 24-0052, **holotype**); ex-type culture GUCC 24-0099.

Notes: *Diaporthe ervatamiae* was isolated from the diseased leaves of the medicinal plant, *Ervatamia kwangsiensis,* in China. It is phylogenetically placed in *D. longicolla* species complex and formed a distinct clade, indicating it is a new species (Figure 4.144).



Note a Host. b Diseased leaf. c Conidiophores and conidiogenous cells. d–g Alpha conidia. Scale bars: c–g = 10 μm.

Figure 4.135 *Diaporthe ervatamiae* (HGUP 24-0052, holotype)

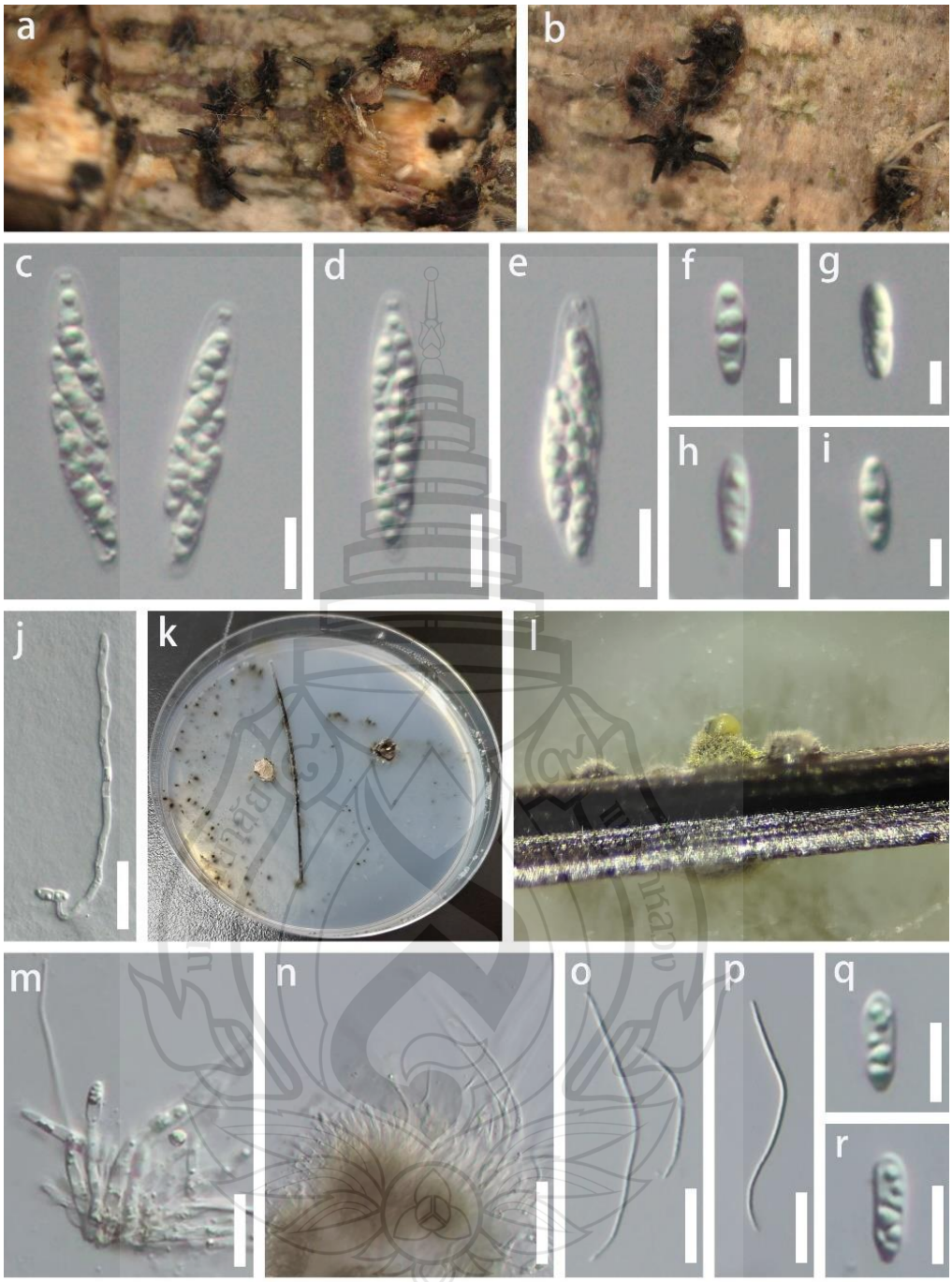
Diaporthe psoraleae-pinnatae Crous & M.J. Wingf., Persoonia 31: 205 (2013)

Index Fungorum number: IF805823; Facesoffungi number: FoF 16461; Figure 4.136

Saprobic on stems of *Rhododendron* sp. **Sexual morph**: *Ascomata* black, globose to irregular, scattered on dead twigs, semi-immersed in host tissue, protruding through substrata, with a long neck. *Asci* 31–45 × 5.5–8 µm ($\bar{x}$ = 37.5 × 7, n = 20), 8-spored, unitunicate, sessile, elongate to clavate. *Ascospores* 7.5–13 × 2.5–4 µm ($\bar{x}$ = 10 × 3, n = 20), hyaline, elongated, two-celled, slightly constricted in the middle, often 4-guttulate, with larger guttules at center and smaller ones at ends. **Asexual morph**: *Conidiomata* superficial, solitary, scattered on the pine needle in the WA, dark brown to black, globose. *Conidiophores* 1–2 µm wide, aseptate, cylindrical, straight or sinuous, densely aggregated, terminal., *Conidiogenous cells* phialidic, cylindrical., *Alpha conidia*, hyaline, smooth, elongated, aseptate, guttulate, apex subobtuse, base subtruncate, 4.5–6.5 × 1.5–2.5 µm ($\bar{x}$ = 5.5 × 2 µm, n = 30). *Beta conidia* hyaline, aseptate, filiform, curved, 24–36 µm long, around 0.7 µm wide. *Gamma conidia* not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Huaxi District, Gaopo, on dead twigs of *Rhododendron* sp., 18 November 2022, Y.R. Sun, H7 (HKAS 136874); living culture GUCC 24-0100.

Notes: Our isolate is phylogenetically related to *Diaporthe ellipsospora, D. jinxiu* and *D. zaobaisu,* forming an inner clade within *Diaporthe* (Figure 4.144). However, Dissanayake et al. (2024) synonymized eight species under *Diaporthe psoraleae-pinnatae* including these three species. The result was supported by morphology, phylogeny, GCPSR principle and coalescent methods of PTP and mPTP. Therefore, we identified our isolate as *D. psoraleae-pinnatae,* representing a new host record isolated from *Rhododendron* sp.



Note a, b Ascomata on the host surface. c–e Asci. f–i Ascospores. j Germinating ascospore. k 14 days old culture on PDA from above. l Conidiomata on pine needle. m, n Conidiophores. o, p Beta conidia. q, r Alpha conidia. Scale bars: c–e, m, o, p = 10 µm, f–i, q, r = 5 µm, j = 20 µm.

Figure 4.136 *Diaporthe psoraleae-pinnatae* (HKAS 136874, new host record)

***Diaporthe siamensis* species complex**

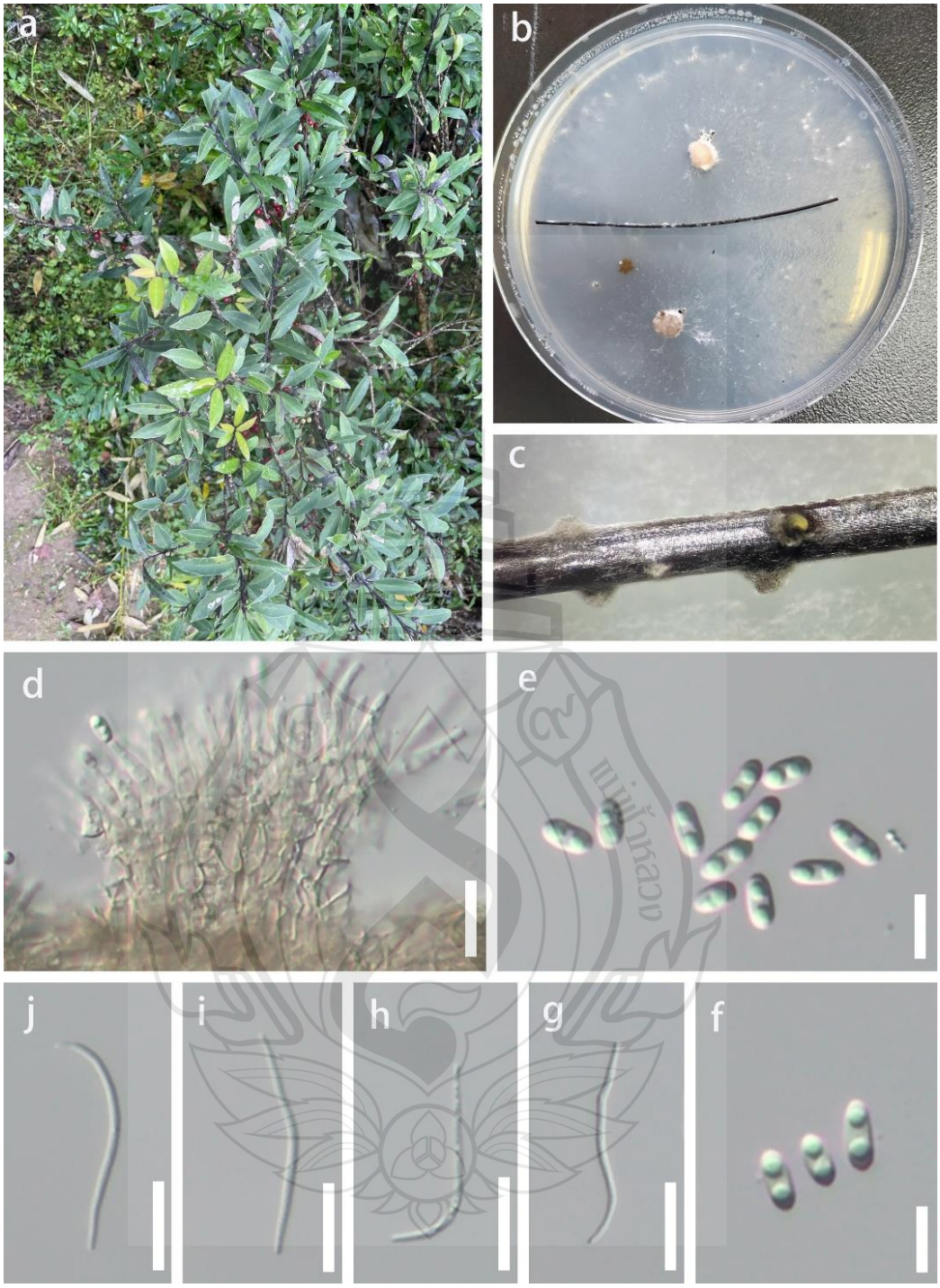
Diaporthe pseudobiguttulata I. Senanayake & S. Hongsanan, Mycosphere 14(1): 1086 (2023)

Index Fungorum number: IF 827907; Facesoffungi Number: FoF 14509; Figure 4.137

Saprobic on dead twigs of *Sarcococca* sp. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* superficial, solitary, scattered on the pine needle in the WA culture, dark brown to black, globose. *Conidiophores* cylindrical, straight or sinuous, terminal, reduced to conidiogenous cells. *Conidiogenous cells* phialidic, ampulliform, hyaline, tapered towards the apex. *Alpha conidia* 3.5–5 × 1.5–2.5 μm ($\bar{x}$ = 4 × 2 μm, n = 30), ellipsoidal to oval, hyaline, aseptate, biguttulate, smooth, round at both ends. *Beta conidia* filiform, hyaline, aseptate, curved, 17–26 μm long, around 1 μm wide. *Gamma conidia* not observed.

Material examined: CHINA, Guizhou Province, Guiyang City, Huaxi District, Gaopo, on dead twigs of *Sarcococca* sp., 18 November 2022, Y.R. Sun, H13 (HKAS 136875); living culture GUCC 24-0101.

Notes: *Diaporthe biguttulata* reported by Huang et al. (2015) is illegitimate because Gao et al. (2015) published the same name earlier in 2014. Strains in Huang et al. (2015) belong to the *D. sojae* species complex, while the strains in Gao et al. (2015) belong to the *D. eres* species complex in the phylogenetic analyses. Thus, Hongsanan et al. (2023) proposed the new name *Diaporthe pseudobiguttulata* for the strains described by Huang et al. (2015). The species was reported from diseased branches of *Juglans regia* and healthy branches of *Citrus limon* in China (Huang et al., 2015; Yang, Maharachchikumbura et al., 2018). In this study, our isolate grouped with *D. pseudobiguttulata* and placed in *D. siamensis* species complex section which is similar to the result in Dissanayake et al. (2024) (Figure 4.144). It's morphological characters also fit *D. pseudobiguttulata* (Huang et al., 2015). Therefore, we identified our isolate as a new host record of *D. pseudobiguttulata.*



Note a Host. b Front view of culture. c Conidioma on pine needle in culture medium. d Conidiophores and conidiogenous cells. e, f Alpha conidia. g–j Beta conidia. Scale bars: d, g–j = 10 µm, e, f = 5 µm.

Figure 4.137 *Diaporthe pseudobiguttulata* (HKAS 136875)

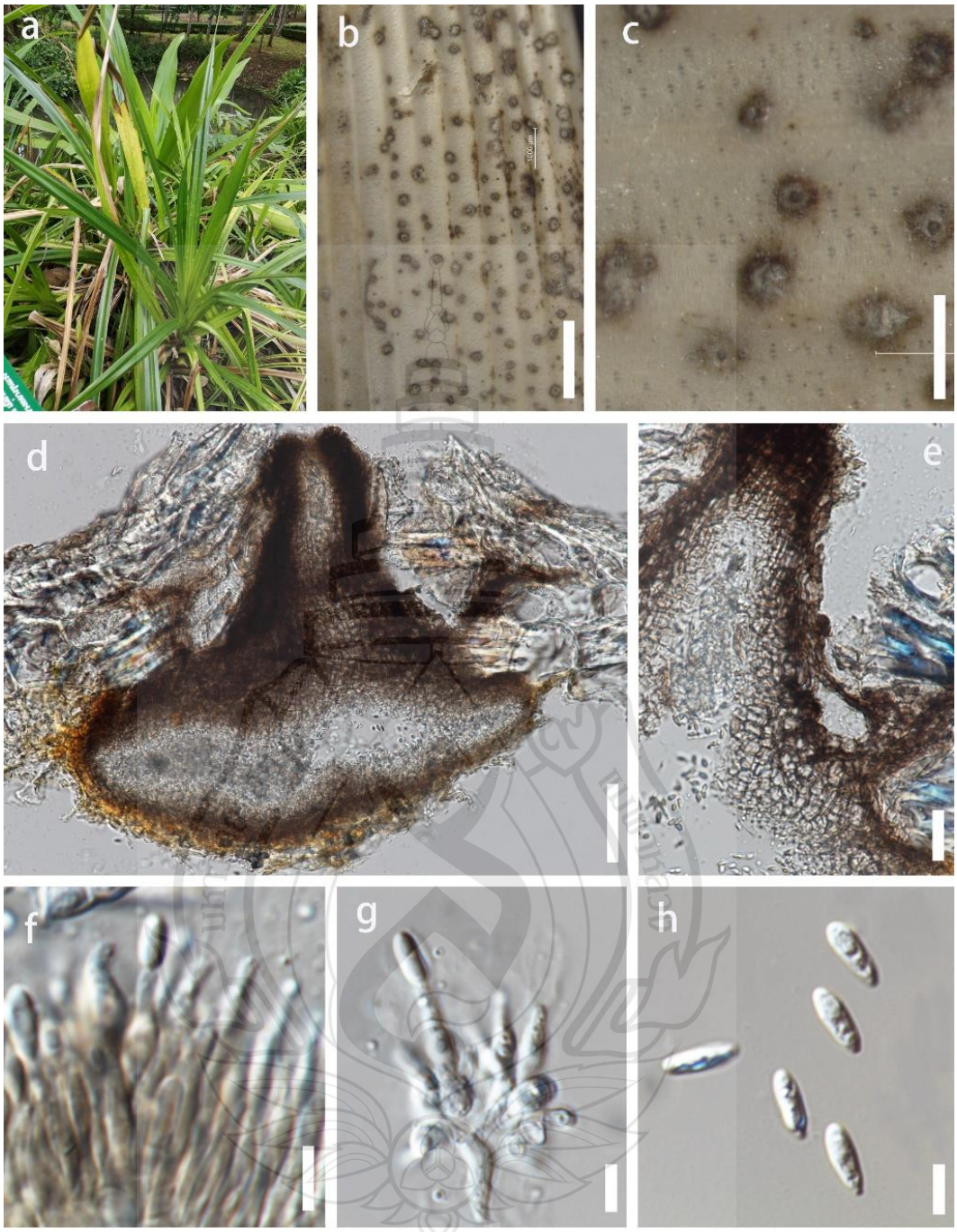
Diaporthe siamensis Udayanga, Xing Z. Liu & K.D. Hyde, Cryptog. Mycol. 33(3): 298 (2012)

Index Fungorum number: IF 800826; Facesoffungi number: FoF 02398; Figure 4.138

Associated with leaf blight of *Hymenocallis littoralis* in Thailand. Symptoms subcircular pale brown to brown. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* semi-immersed, solitary, scattered, subglobose, brown to dark brown, 150–300 µm wide, 140–270 µm high. *Conidiomata wall* 2-layered; outer layer composed of dark brown thick-walled cells of *textura angularis*, inner layer comprising thin-walled, hyaline to light brown cells of *textura angularis*. *Conidiophores* formed from the inner layer of the locular wall, reduced to conidiogenous cells. *Conidiogenous cells* 1–2 µm wide, phialidic, cylindrical, hyaline, unbranched, aseptate, straight, slightly tapering towards the apex. *Alpha conidia* 5–8 × 2–3 µm ($\bar{x}$ = 6 × 2.5 µm, n = 30), fusiform, hyaline, aseptate, rounded at both ends, rough. *Beta* and *gamma conidia* not observed.

Material examined: Thailand, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on diseased leaves of *Hymenocallis littoralis* (Amaryllidaceae), 10 June 2019, Y.R. Sun, B38 (HGUP 24-0054, living culture MFLUCC 24-0296); ibid, on dead leaves of *Hymenocallis littoralis* (Amaryllidaceae), 10 June 2019, Y.R. Sun, B38-1 (HGUP 24-0055, living culture GUCC 24-0144).

Notes: *Diaporthe siamensis* was initially reported on diseased leaves of *Dasymaschalon* sp. (Annonaceae) in Thailand and later found as an endophytic fungus in *Pandanus* sp. (Pandanaceae) in Thailand (Udayanga et al., 2012; Tibpromma, Hyde, Bhat et al., 2018). Additionally, Cui et al. (2021) reported it on diseased fruit of *Citrus sinensis* (Rutaceae) in China and provided a pathogenicity test. Our collection isolated from the diseased leaves of *Hymenocallis littoralis* (Amaryllidaceae) and it phylogenetically grouped with *D. siamensis.* In morphology, our isolate resembles the characters of *D. siamensis,* including the phialidic, cylindrical, hyaline 1–2 µm wide conidiogenous cells and hyaline, aseptate, 5–8 × 2–3 µm alpha conidia (Udayanga et al., 2012; Cui et al., 2021). Therefore, we identified our isolate as *D. siamensis,* representing a new host record from *Hymenocallis littoralis.*



Note a Host. b, c Conidiomata on the host. d Vertical section through a pycnidia e Conidiomatal wall. f, g Conidiophores and conidiogenous cells. h Alpha conidia. Scale bars: b = 2000 µm, c = 500 µm, d = 50 µm, e = 20 µm, f–h = 5 µm.

Figure 4.138 *Diaporthe siamensis* (HGUP 24-0054, new host record)

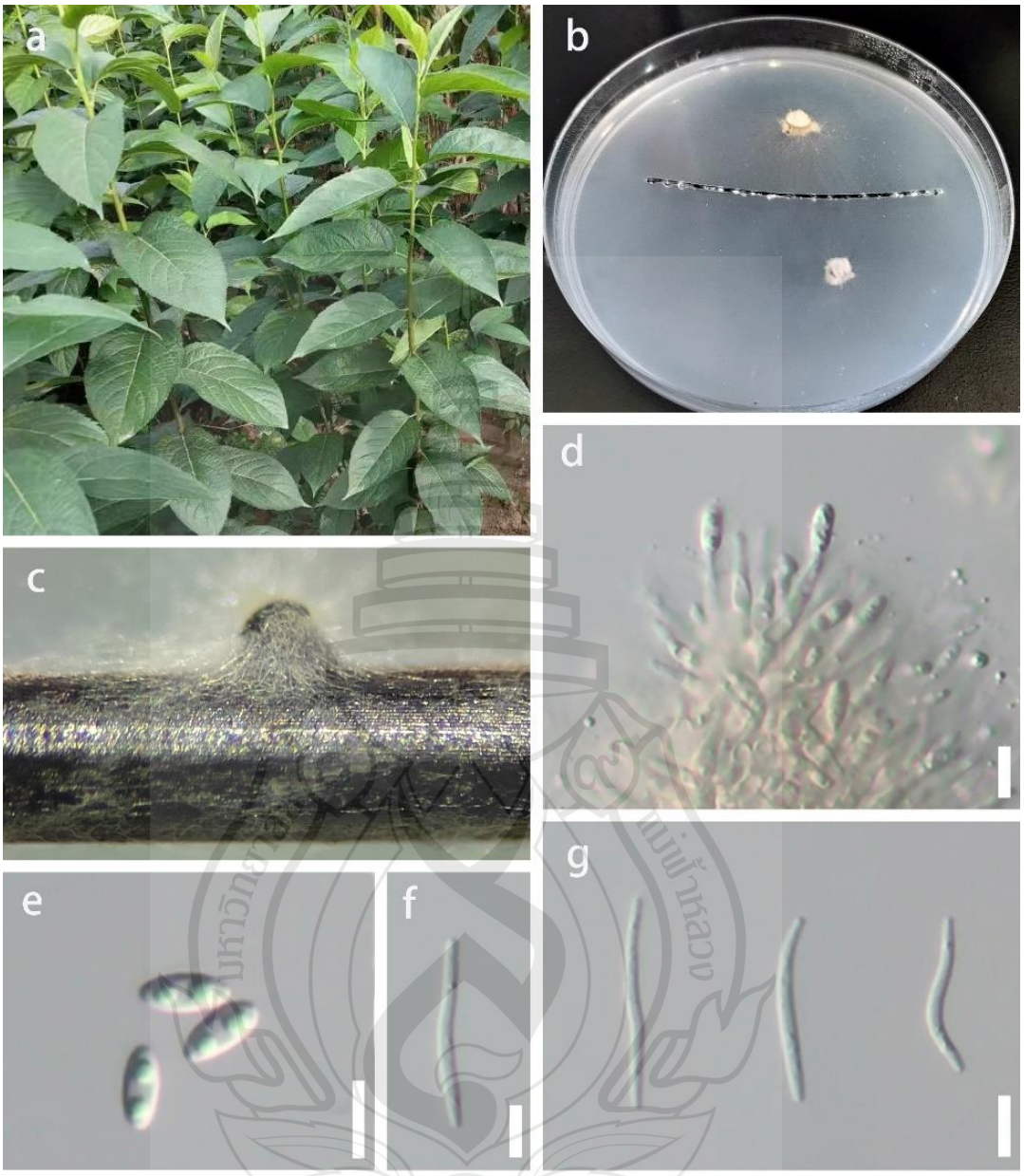
Diaporthe sojae Lehman, Ann. Mo. bot. Gdn 10: 128 (1923)

Index Fungorum number: IF 278338, Facesoffungi number: FoF 06582; Figure 4.139

Endophytic from heathy twigs of Tu-chung (*Eucommia ulmoides*). **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* superficial, solitary, subglobose, dark brown, surround by hyaline hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, cylindrical, hyaline, unbranched, straight, slightly tapering towards the apex. *Alpha conidia* 4.5–6.5 × 1.5–2.5 µm ($\bar{x}$ = 5.5 × 2 µm, n = 30), fusiform to ovate to ellipsoidal, hyaline, aseptate, biguttulate, rounded at both ends. *Beta conidia* filiform, hyaline, aseptate, straight to slightly curved, 14–19 µm long, around 1–1.5 µm wide. *Gamma conidia* not observed.

Material examined: CHINA, Guizhou Province, Anshun City, Xixiu District, Yaowang Valley Tourism Resort, on heathy twigs of *Eucommia ulmoides*, 3 August 2022, Y.R. Sun, DZJ2 (HKAS 136867); living culture GUCC 24-0103; ibid, on heathy leaves of *Phellodendron* sp., 3 August 2022, Y.R. Sun, AS2-2 living culture GUCC 24-0102.

Notes: *Diaporthe sojae* is a highly destructive pathogen that causes diseases in soybeans and other field crops globally (Udayanga et al., 2015). It also affects cucurbits plants and causes storage diseases in navel oranges, leading to severe economic losses (Udayanga et al., 2015; Zhao et al., 2022; Xiao, Zou et al., 2023). In this study, we obtained two *Diaporthe* isolates from heathy twigs and leaves of *Eucommia ulmoides* and *Phellodendron* sp. in China. These two isolates grouped with *D. sojae* in the phylogenetic tree (Figure 4.144). In morphology, they resemble to *Diaporthe sojae* in having ovate to ellipsoidal, hyaline, aseptate, biguttulate, 4.5–6.5 × 1.5–2.5 µm alpha conidia. Therefore, we identified our isolates as *D. sojae,* this is the first time isolated from the *Eucommia ulmoides* and *Phellodendron* sp.



Note a Host. b Front view of culture. c Conidioma on pine needle in culture medium. d Conidiophores and conidiogenous cells. e Alpha conidia. f, g Beta conidia. Scale bars: d–g = 5 μm.

Figure 4.139 *Diaporthe sojae* (HKAS 136867, new host record)

***Diaporthe subclavata* species complex**

Diaporthe goulteri R.G. Shivas, S.M. Thomps. & Y.P. Tan, Persoonia 35: 43 (2015)

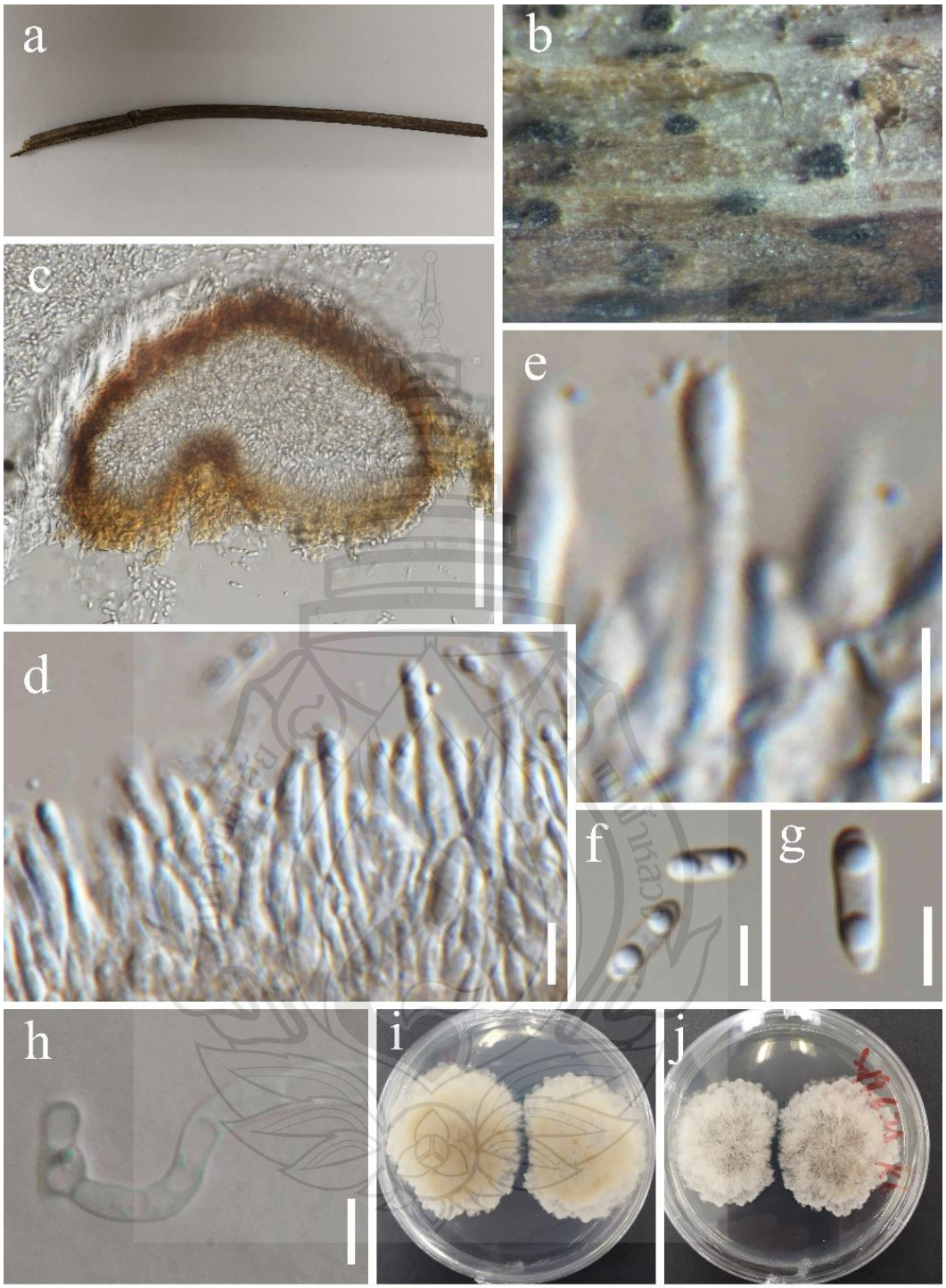
Index Fungorum number: IF 808669; Facesoffungi number: FoF 09714; Figure 4.140

Saprobic on twigs of *Bidens alba*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* semi-immersed, solitary, scattered, subglobose, visible black dots appear on the surface of the host. *Conidiomata wall* 2-layered; outer layer composed of brown to dark brown thick-walled cells of *textura angularis*, inner layer comprising thin-walled, hyaline to light brown cells of *textura angularis*. *Conidiophores* formed from the inner layer of the locular wall, reduced to conidiogenous cells. *Conidiogenous cells* around 2 μm wide, phialidic, cylindrical, hyaline, tapered towards the apex. *Alpha conidia* 6–8.5 × 2–3 μm ($\bar{x}$ = 7 × 2.5 μm, n = 30), elongated to fusiform, hyaline, aseptate, biguttulate, rounded at the apex, smooth. Beta and gamma conidia not observed.

Material examined: THAILAND, Chiang Rai Province, Thoeng District, Ngio village, on dead twigs of *Bidens alba*, 10 June 2019, Y.R. Sun, R6 (HGUP 24-0053); living culture MFLUCC 24-0295.

Culture characteristics: Conidia germinated on PDA within 12 hours at 25°C. Germ tube was produced from one end of conidium. Colonies on PDA, reaching 4 cm diam. after 2 weeks, flat, irregular, dry, undulate, white to cream from above, pale brown from below.

Notes: *Diaporthe goulteri* was firstly documented by its asexual morph from *Helianthus annuus* in Australia (Thompson et al., 2015). Bundhun et al. (2021) provided its sexual morph from dead branch in Thailand based on phylogenetic analyses. Our isolate grouped with *D. goulteri* by high support in the phylogenetic tree (Figure 4.144). The insignificant differences in base pairs in the CAL, *his*-3 and TUB sequence data for the two strains (<1.5%) support them as a single species (Jeewon & Hyde, 2016). In morphology, our collection resembles *D. goulteri* in having hyaline, aseptate, cylindrical conidiophores and fusiform, hyaline, biguttulate, 6–9 × 2–3 μm alpha conidia (Thompson et al., 2015). Therefore, we identified our isolate as *D. goulteri,* representing a new host record from *Bidens alba*.



Note a Host branch. b Conidiomata on the host. c Vertical section through a pycnidia d, e Conidiophores and conidiogenous cells. f, g Alpha conidia. h Germinated conidium. i, j Colony on the PDA. Scale bars: c = 50 μm, d–h = 5 μm.

Figure 4.140 *Diaporthe goulteri* (HGUP 24-0053, new host record)

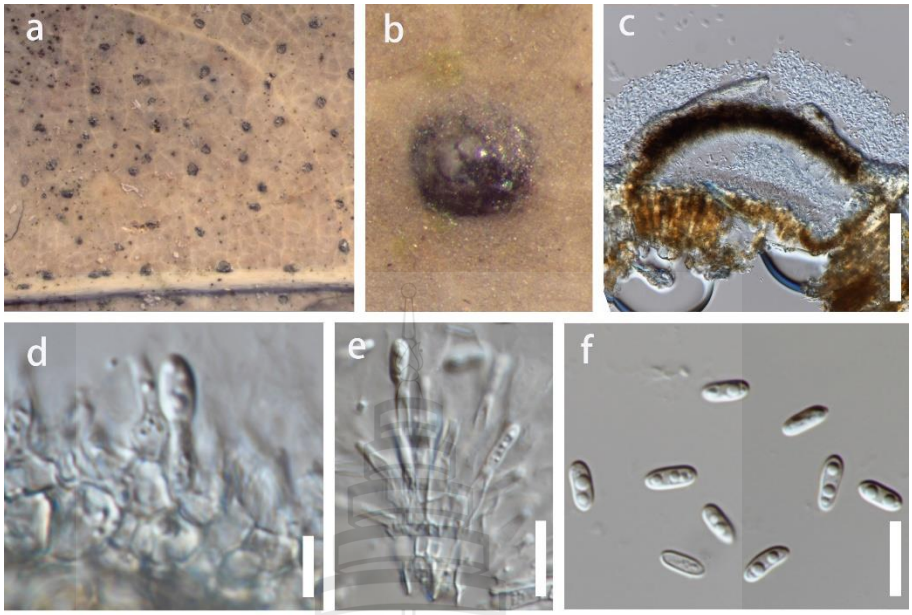
Diaporthe subclavata F. Huang, K.D. Hyde & Hong Y. Li, Fungal Biology 119: 343 (2015).

Index Fungorum number: IF 810583; Facesoffungi number: FoF 03257; Figure 4.141

Saprobic on dry leaves. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* semi-immersed, solitary, scattered, globose, visible black dots appear on the surface of the host. *Conidiophores* septate, cylindrical, straight or sinuous. *Conidiogenous cells* 1–2 μm wide, phialidic, cylindrical, hyaline, tapered towards the apex. *Alpha conidia* 5–7 × 2–3 μm ($\bar{x}$ = 6 × 2.5 μm, n = 30), elongated to fusiform, some oval, hyaline, aseptate, 2–3-guttulate, smooth. Beta and gamma conidia not observed.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, on dead and dry leaves, 15 July 2020, Y.R. Sun, M58 (HGUP 24-0056); living culture MFLUCC 24-0297.

Notes: Dissanayake et al. (2024) synonymized *Diaporthe heliconiae under D. subclavata* based on morphology and molecular analyses. *Diaporthe subclavate* has been reported from the diseased leaves of *Citrus unshiu* (Huang et al., 2015), the symptomatic petiole of *Heliconia metallica* (Sun, Zhang et al., 2021), and the healthy stem of *Morinda officinalis* (Luo et al., 2022) in China. Our isolate grouped with *D. subclavate* by high support in the phylogenetic tree (Figure 4.144). In morphology, our collection resembles *D. subclavate* in having hyaline, aseptate, cylindrical conidiophores and hyaline, aseptate, 2–4 guttulate, 5–7 × 2–3 μm alpha conidia (Sun, Zhang et al., 2021). Therefore, we identified our isolate as *D. subclavate,* representing a new geographical record in Thailand.



Note a, b Conidiomata on the host. c Vertical Section through a pycnidia d, e Conidiophores and conidiogenous cells. f Alpha conidia. Scale bars: c = 100 μm, d = 5 μm, e, f = 10 μm.

Figure 4.141 *Diaporthe subclavate* (HGUP 24-0056, new geographical record)

Diaporthe tuchungicola Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902610; Facesoffungi number: FoF 16462; Figure 4.142

Etymology: referring to the host's English name, "Tu-chung".

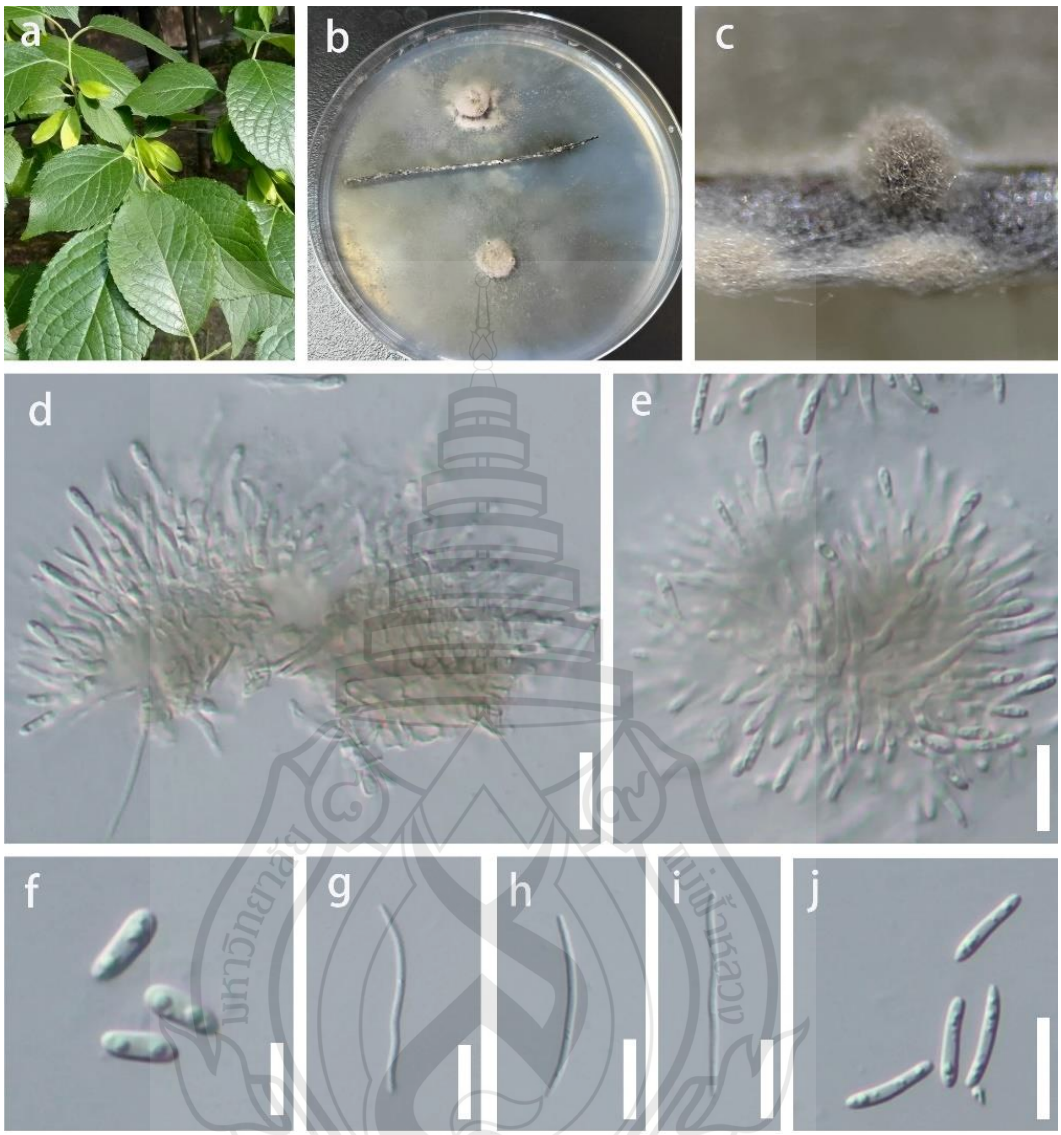
Holotype: HKAS 136868.

Endophytic from heathy twigs of Tu-chung (*Eucommia ulmoides*). **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* superficial, solitary, globose, dark brown, scattered on the pine needle in the WA. *Conidiophores* aseptate, cylindrical, straight or sinuous, reduced to conidiogenous cells. *Conidiogenous cells* phialidic, cylindrical, hyaline, unbranched, straight, slightly tapering towards the apex. *Alpha conidia* 4.5–7 × 1.5–2.5 μm ($\bar{x}$ = 5 × 2 μm, n = 30), elongated to fusiform, hyaline, aseptate, biguttulate. *Beta conidia* filiform, hyaline, aseptate, straight to slightly curved, 17–28 μm long, around 1 μm wide. *Gamma conidia* 6–11 × 1–2 μm, cylindrical, hyaline, aseptate, straight to slightly curved,

guttulate.

Material examined: CHINA, Guizhou Province, Anshun City, Xixiu District, Yaowang Valley Tourism Resort, on heathy twigs of *Eucommia ulmoides*, 3 August 2022, Y.R. Sun, DJ1 (HKAS 136868, **holotype**); ex-type culture GUCC 24-0104.

Notes: *Eucommia ulmoides* is a traditional medicinal plant that has been used for centuries, particularly in Traditional Chinese Medicine, it is renowned for its various therapeutic properties and health benefits (Hu, 1979). *Diaporthe* species related to *Eucommia ulmoides* have also been reported previously (Gao et al., 2017; Wang et al., 2022). In this study, we obtained an endophytic *Diaporthe* isolate from the heathy twigs of *Eucommia ulmoides.* Our isolate is phylogenetically sister to *D. minima* by high support (ML-bs = 100%, BYPP = 1) (Figure 4.144). In morphology, our strain can be distinguished by having elongated to fusiform, smaller alpha conidia (5 × 2 μm *vs*. 7 × 2 μm) (Dissanayake, Chen et al., 2020). In addition, the ITS base pair difference results showed that there are 18 base pairs that are different (488 bp, without gap). Therefore, we identified our isolate as a new species and introduced *D. tuchungicola* herein.



Note a Host. b Front view of culture. c Conidiomata on pine needles in culture medium. d, e Conidiophores and conidiogenous cells. f Alpha conidia. g–i Beta conidia. j Gamma conidia. Scale bars: d, e = 10 µm.

Figure 4.142 *Diaporthe tuchungicola* (HKAS 136868, holotype)

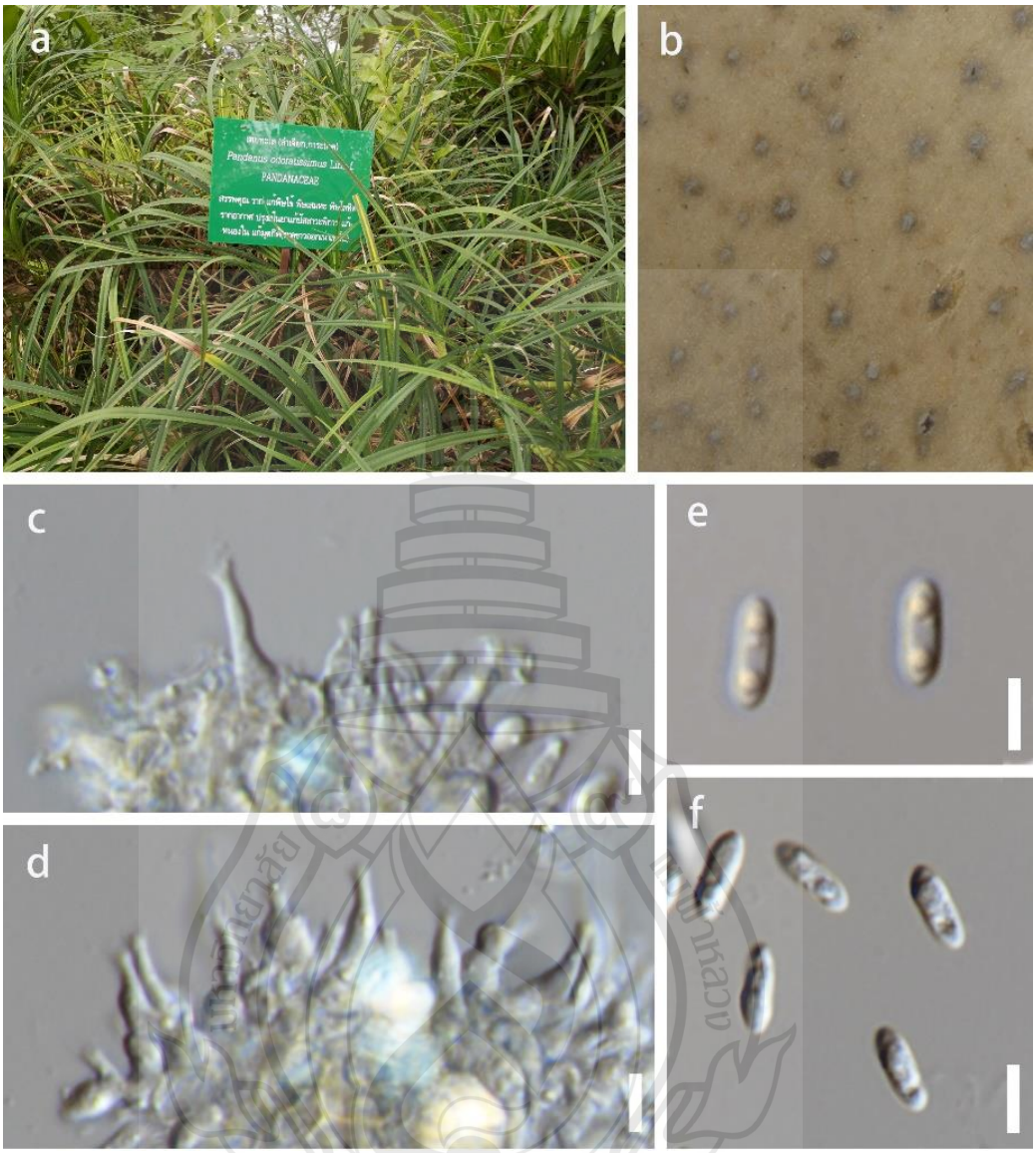
Diaporthe tulliensis R.G. Shivas, Vawdrey & Y.P. Tan, Persoonia 35: 301 (2015)

Index Fungorum number: IF812896; Facesoffungi Number: FoF 16300; Figure 4.143

Associated with leaf blight of *Pandanus odoratissimus* in Thailand. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* semi-immersed, solitary, scattered, subglobose, brown to dark brown. *Conidiophores* formed from the inner layer of the locular wall, reduced to conidiogenous cells. *Conidiogenous cells* 1–2 μm wide, phialidic, cylindrical, hyaline, unbranched, aseptate, straight, slightly tapering towards the apex. *Alpha conidia* 5.5–7.5 × 3–5.5 μm ($\bar{x}$ = 6.5 × 4 μm, n = 30), ellipsoidal to oblong, hyaline, biguttulate, blunt at both ends. *Beta* and *gamma conidia* not observed.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on diseased leaves of *Pandanus odoratissimus*, 10 June 2019, Y.R. Sun, B36 (HGUP 24-0057); living culture MFLUCC 24-0298.

Notes: Our collection was isolated from the diseased leaves of *Pandanus odoratissimus* and it phylogenetically grouped with *Diaporthe tulliensis. Diaporthe tulliensis* was introduced from *Theobroma cacao* in Australia (Crous, Wingfield, Roux et al., 2015). Later six *D. tulliensis*-related species were reported (Gao et al., 2017; Manawasinghe et al., 2019; Luo et al., 2022) but were synonymized by Dissanayake et al. (2024). They also provided all hosts and locations for *D. tulliensis* but none has been reported from *Pandanus odoratissimus*. Therefore, we identified our isolate as *D. tulliensis,* representing a new record from *Pandanus odoratissimus*.



Note a Host. b Conidiomata on the host. c, d Conidiophores and conidiogenous cells. e, f Alpha conidia. Scale bars: c–f = 5 μm.

Figure 4.143 *Diaporthe tulliensis* (HGUP 24-0057, new host record)

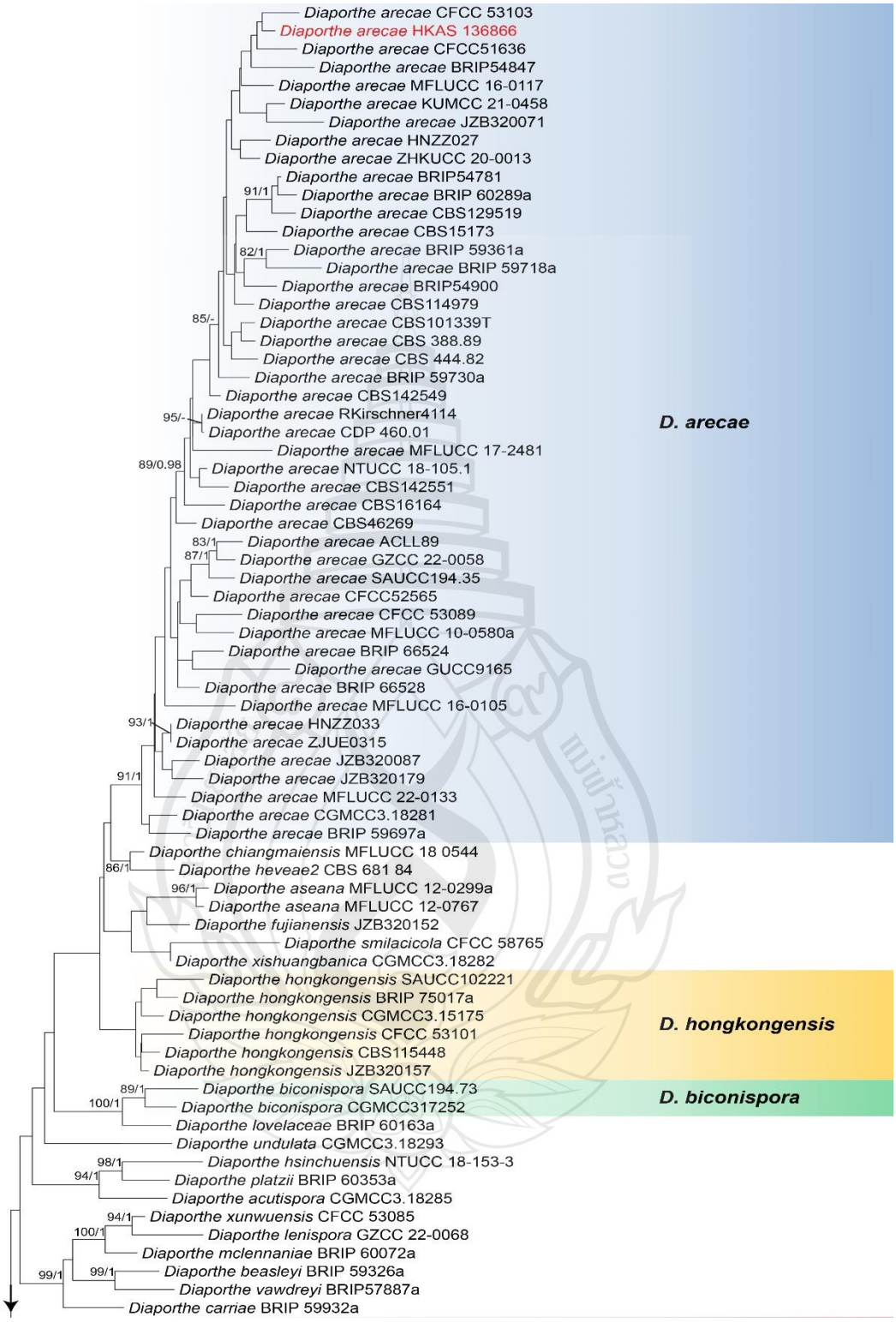


Figure 4.144 Phylogenetic tree of *Diaporthe*

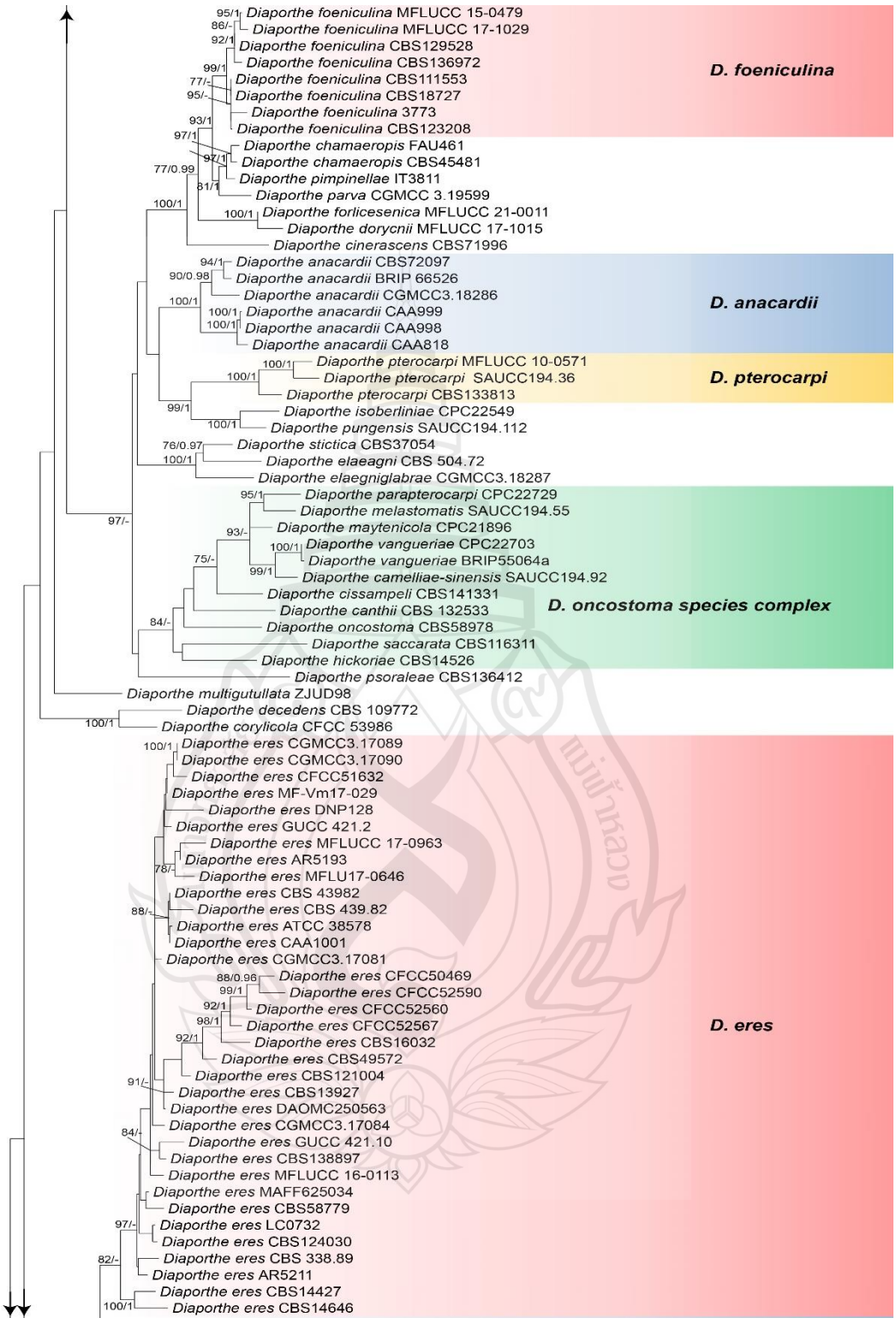


Figure 4.144 (continued)

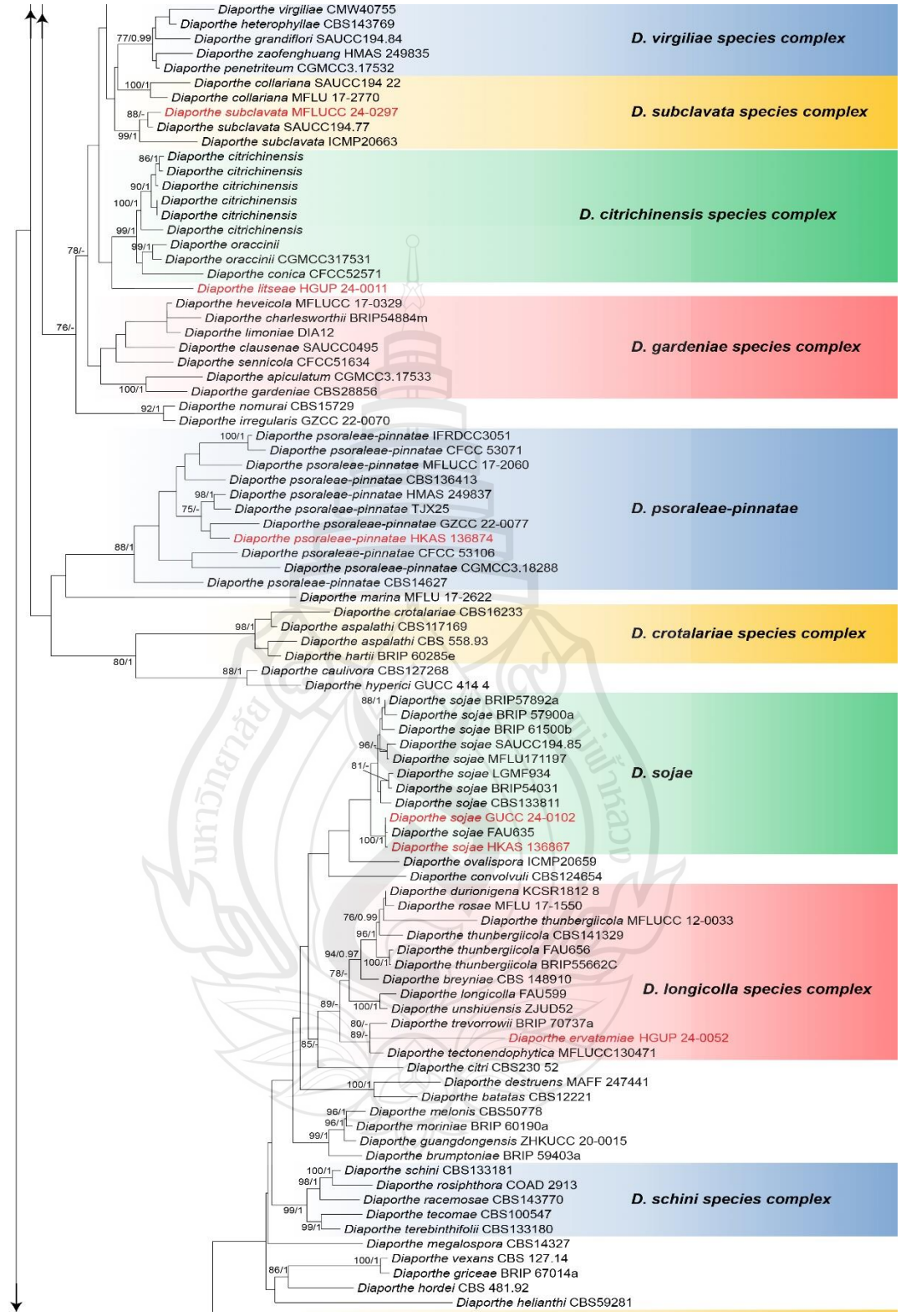


Figure 4.144 (continued)

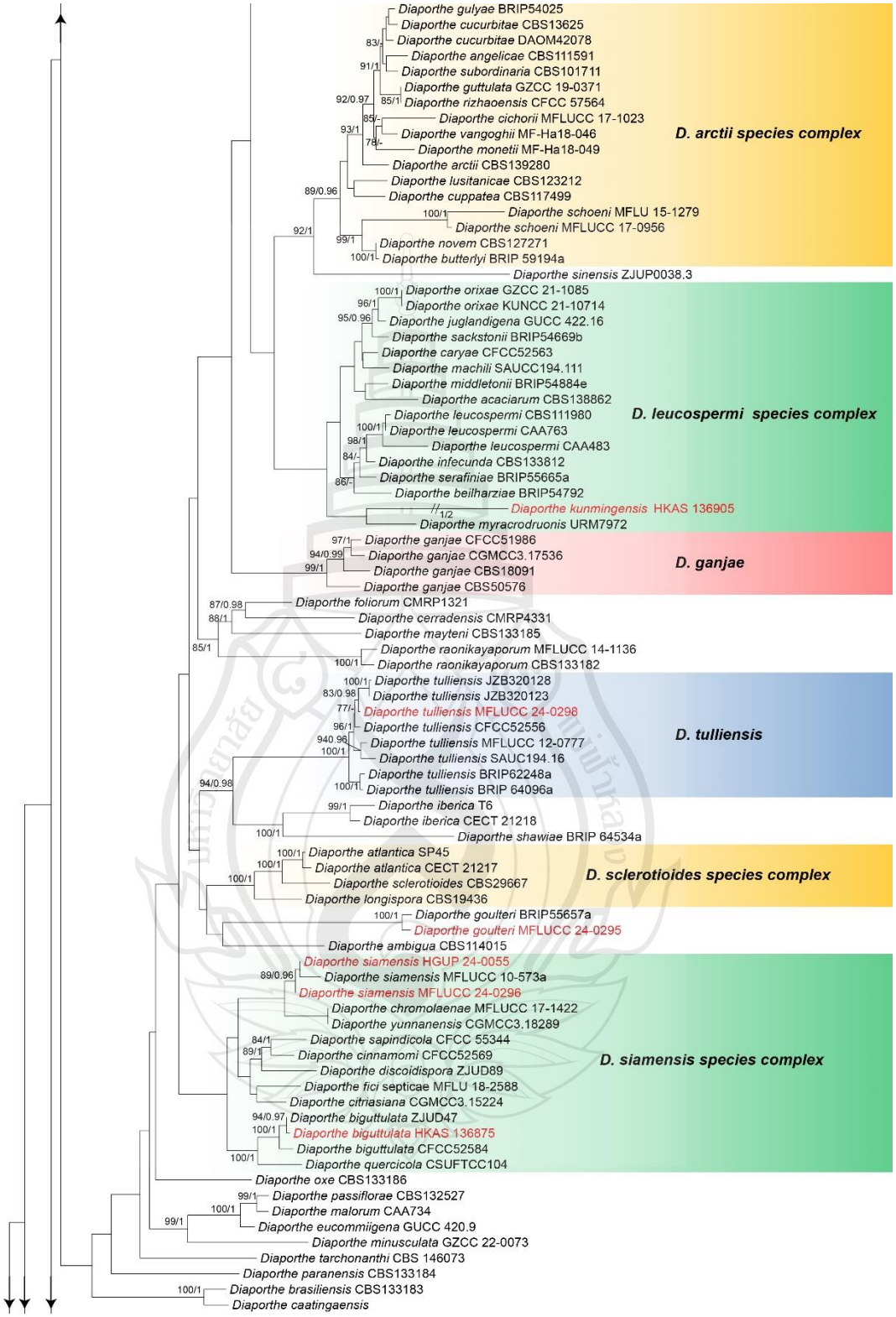
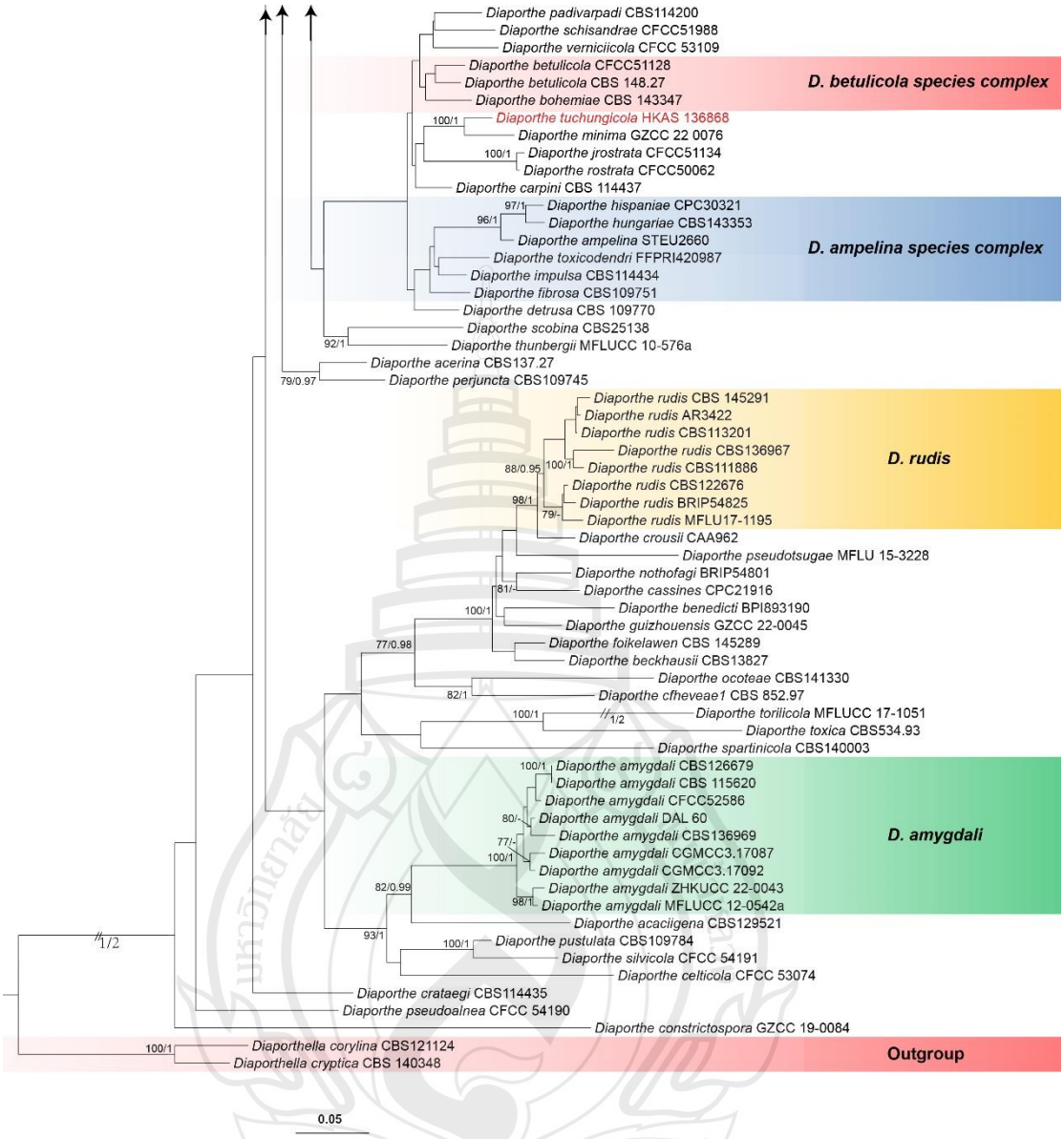


Figure 4.144 (continued)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Diaporthella corylina* (CBS121124) and *D. cryptica* (CBS 140348). The new collections are indicated in red.

Figure 4.144 (continued)

Distoseptisporales Z.L. Luo, K.D. Hyde & H.Y. Su, Fungal Diversity: [32] (2019)

Distoseptisporaceae K.D. Hyde & McKenzie, in Su et al., Fungal Diversity 80: 402 (2016)

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

Notes: *Distoseptispora* was introduced by Su et al. (2016) with *Distoseptispora fluminicola* as the type species. Species of *Distoseptispora* are distributed across several countries, including China, Thailand, Malaysia, and other parts of Asia (Tibpromma, Hyde, McKenzie et al., 2018; Hyde et al., 2021; Liu et al., 2023). Their primary habitats are moist forest environments and freshwater habitats, where they commonly inhabit decaying plant materials such as twigs, leaves, and bark (Luo et al., 2018; Zhai et al., 2022; Shen et al., 2024). *Distoseptispora* plays a significant role in the decomposition process within these ecosystems, contributing to nutrient cycling and the breakdown of organic matter. The unique ecological niche and morphological characteristics of the genus make it a focus of mycological and ecological research, especially in the past five years, with more than 50 species reported, making this genus a research hotspot (Luo et al., 2019; Phukhamsakda et al., 2020; Yang et al., 2021; Hu, Liu, Luo et al., 2023; Hyde et al., 2023; Shen et al., 2024). Currently, 79 species are listed in this genus (Index Fungorum, 2024).

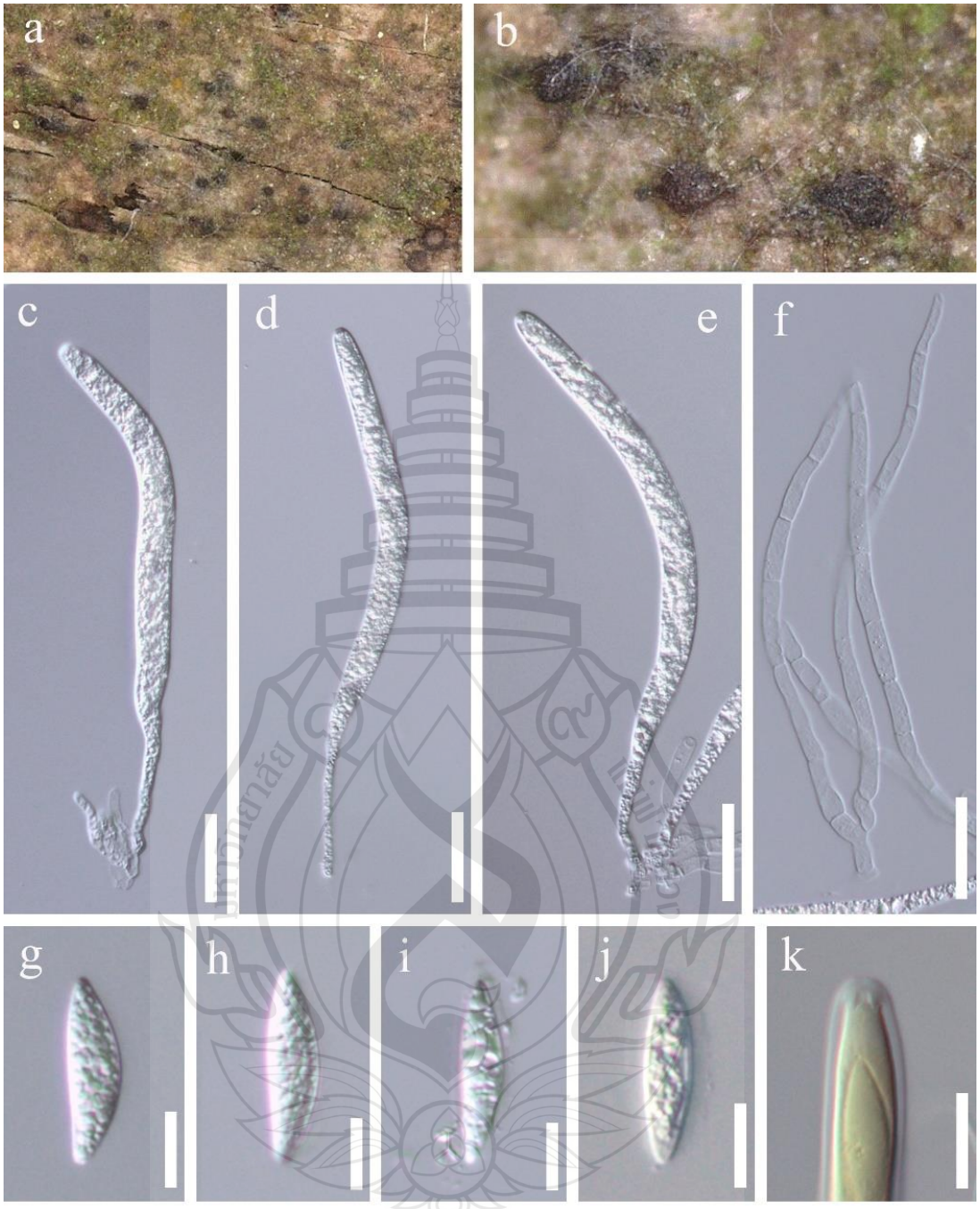
Distoseptispora bambusae Y.R. Sun, I.D. Goonasekara, Yong. Wang bis & K.D. Hyde, ***sp. nov***

Index Fungorum number: IF 557452; Figure 4.145, 4.146

Saprobic on bamboo culms in terrestrial habitat. **Sexual morph**: *Ascomata* solitary, immersed to semi-immersed, perithecial, subglobose, dark brown. *Ostiole* and *ascomatal wall* not observed. *Paraphyses* branched, septate, hyaline, constricted at the septa, 3–8 µm wide. *Asci* 92–171 × 8–12 µm, cylindrical, with a short pedicel, obtuse at the apex, 8-spored, apex with a non-amyloid apical annulus. *Ascospores* 20–28 × 5.5–8 µm, overlapping, uniseriate, fusiform, hyaline, aseptate, smooth-walled, guttulate, thin-walled, surrounded by a mucilaginous sheath. **Asexual morph**: Not observed.

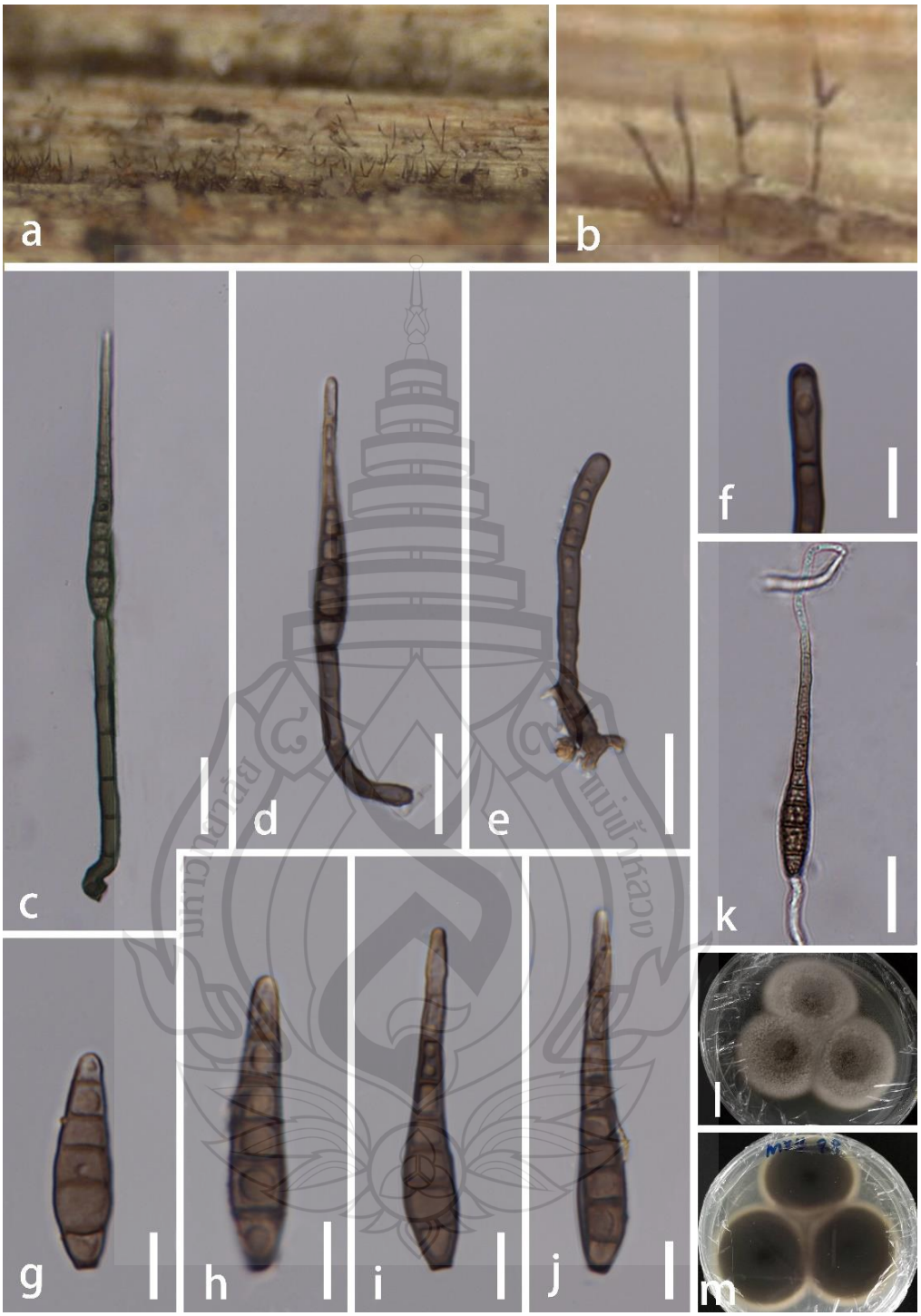
Material examined: CHINA, Guizhou Province, Guiyang City, Nanming District, Guiyang Medicinal Plant Garden, on on dead bamboo culms, 30 Augest 2019, Y.R. Sun, MX4 (MFLU 20-0261, **holotype**); ibid, Qiannan Bouyei and Miao Autonomous Prefecture, Libo District, on dead bamboo culms, 12 March 2022, Y.R. Sun, ML4 (HGUP 24-0058); living culture GUCC 24-0147.

Notes: Our isolate fits within the sexual morphs of *Distoseptispora*, characterized by hyaline, branched paraphyses, 8-spored cylindrical asci, and fusiform hyaline ascospores (Yang et al., 2021). Phylogenetic analyses (Figure 4.153) show it clusters together with *D. bambusae*, introduced by Sun et al. (2020) in its asexual morph. Additionally, the ITS base pair differences revealed only four variations between these two strains. Therefore, we identified our isolate as the sexual morph of *D. bambusae*.



Note a, b Ascomata on woody substrate. c–e Asci. f Paraphyses. g–j Ascospores. k Apical ring. Scale bars: c–f = 30 µm, g–k = 10 µm.

Figure 4.145 *Distoseptispora bambusae* (HGUP 24-0058, sexual morph)



Note a, b. Colonies on natural substrate; c, d. Conidiophore with Conidia; e. Conidiophore; f. Conidiogenous cell; g–j. Conidia; k. Germinating conidium; l, m. Colony on PDA. Scale bars: c–e, k = 20 μm, f–j = 10 μm.

Figure 4.146 *Distoseptispora bambusae* (MFLU 20-0261, holotype, asexual morph)

Distoseptispora effusa L.L. Liu & Z.Y. Liu, Frontiers in Microbiology 7(no. 945): 12 (2021)

= *Distoseptispora phragmiticola* Qian Zhang, Yong Wang bis & K.D. Hyde, Mycosphere 14(1): 688 (2023)

Index Fungorum number: IF 558406; Facesoffungi number: FoF09863; Figure 4.147

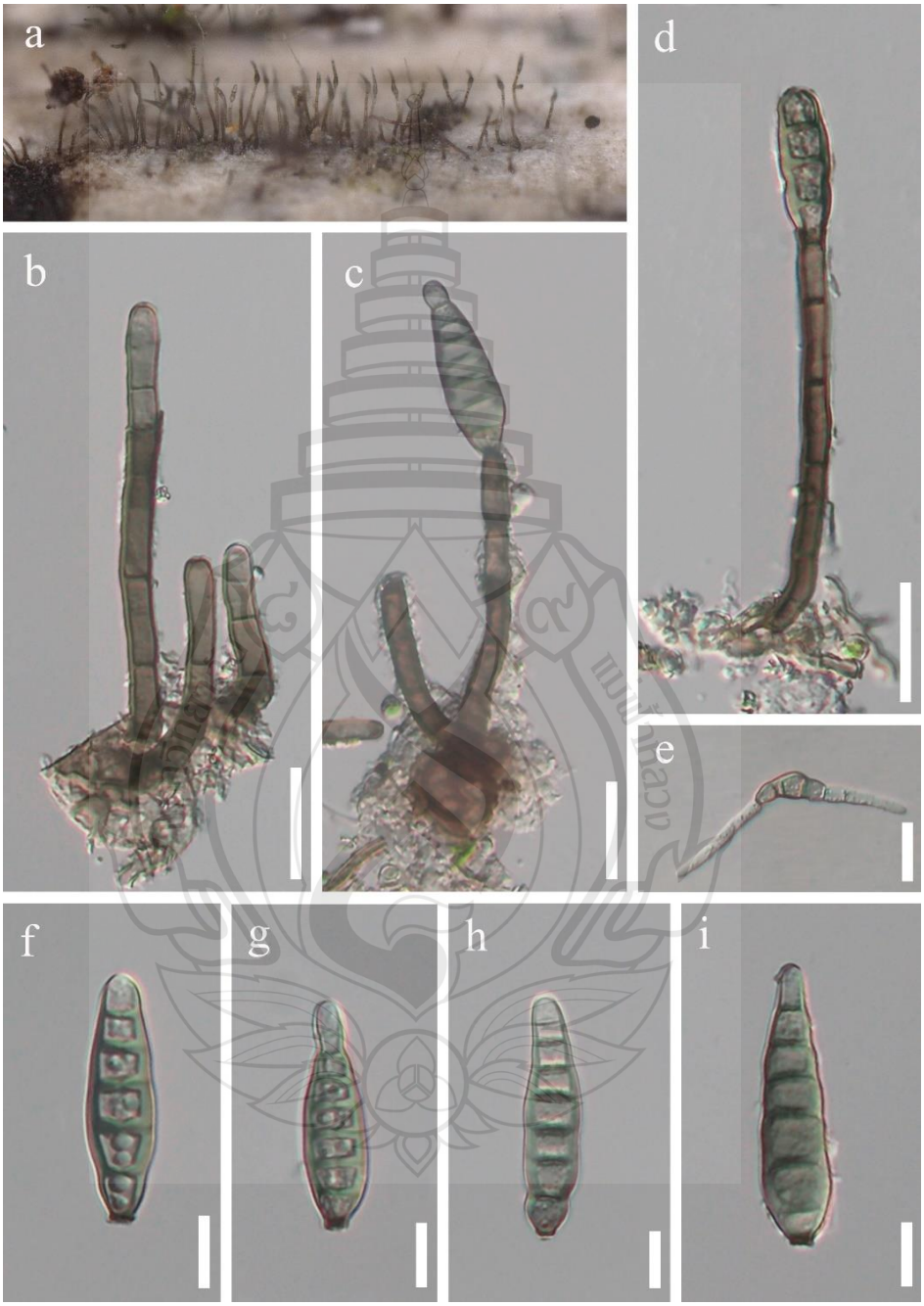
Saprobic on culms of bamboo. **Sexual morph**: Not observed. **Asexual morph**: *Colonies* on natural substrate, effuse, single or in groups, numerous, erect, dark brown, hairy. *Conidiophores* 49–94 × 4–6 μm, macronematous, mononematous, erect, cylindrical, straight to slightly curved, unbranched, septate, olivaceous or pale brown when young, brown to dark brown at mature, thick-walled. *Conidiogenous cells* monoblastic, integrated, terminal, cylindrical, brown, smooth. *Conidia* 46–115 × 8–12 μm, ($\bar{x}$ = 80 × 9 μm, n = 15), solitary, obclavate, rounded at apex, straight or slightly curved, olivaceous, slightly paler towards the apex, 12–16-septate, verruculose.

Material examined: CHINA, Guizhou Province, Guiyang City, Baiyun District, on bamboo culms, 30 August 2021, Y.R. Sun, CL13 (HKAS 124562); living culture GUCC 24-0148.

Notes: *Distoseptispora effusa* was firstly described by Yang et al. (2021) from decaying wood in freshwater stream in China. Hyde et al. (2023) proposed *D. phragmiticola*, and mentioned it different from *D. effusa* by its larger number of septa (4–25 *vs.* 4–9) and larger conidia (34–155 × 10.5–17.5 μm *vs*. 35.5–113 × 7–12.5 μm). However, we observed that conidia in this genus vary in length and color at different growth stages. In addition, there are only t3 bp differences (559 bp, without gap) in the ITS genes and no base pair differences in the LSU gene between the ex-type (GZCC 19-0532) of *D. effusa* and ex-type (GUCC 220201) of *D. phragmiticola*. Thus, we regard they are conspecific and transferred *D. phragmiticola* under *D. effusa* based on the chronological priority of the species names.

Our collection was encountered on bamboo in Guizhou Province, China. There is little morphological difference between our species and *D. effuse* and there are no base pair differences

in the ITS and LSU genes between our isolate and the ex-type strain GZCC 19-0532. Therefore, we identify our collection as *D. effusa,* representing a new host record from bamboo.



Note a Colonies on the host. b Conidiophores. c, d Conidiophores attached to conidia. e Germinated conidium. f–i Conidia. Scale bars: b–e = 20 μm, f–i = 10 μm.

Figure 4.147 *Distoseptispora effusa* (HKAS 124562, new host record)

Distoseptispora gelatinosa Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16463; Figure 4.148

Etymology: The epithet refers to the conidia surrounded by gelatinous sheath.

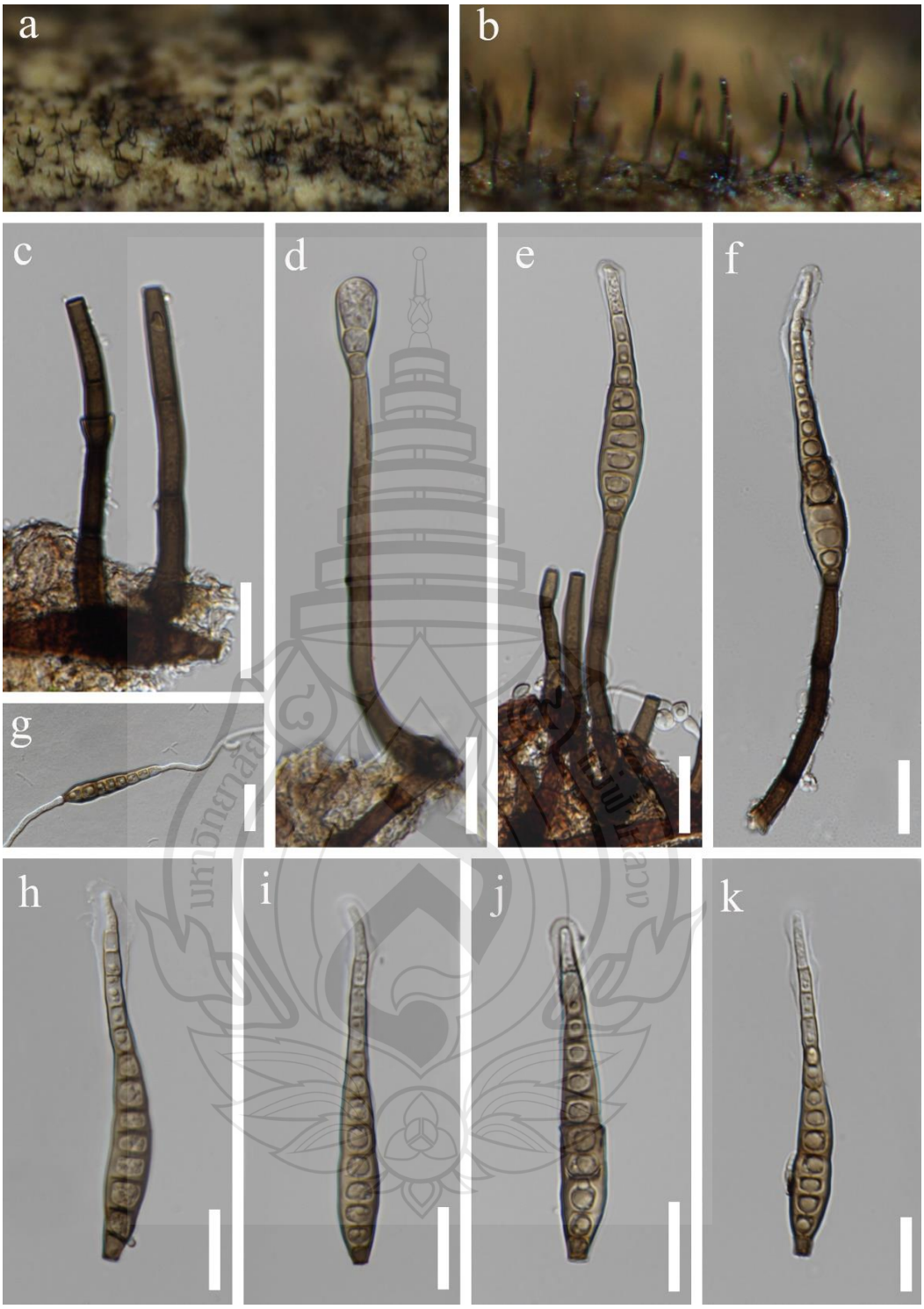
Holotype: HGUP 24-0059.

Saprobic on bamboo culms in terrestrial habitats. **Asexual morph**: Hyphomycetous. *Colonies* effuse, scattered, hairy, brown to dark-brown. *Mycelium* mostly immersed, composed of branched, septate, brown hyphae. *Conidiophores* 48–122 μm long, 4–6 μm wide ($\bar{x}$ = 85 × 5 μm, n = 20), macronematous, mononematous, solitary or in groups, erect, straight or slightly flexuous, septate, unbranched, cylindrical, brown to dark brown, smooth. *Conidiogenous cells* 2.5–4 μm wide, monoblastic, integrated, terminal, brown, cylindrical., *Conidia* 50–100 μm long, 8–13 μm wide ($\bar{x}$ = 76 × 11 μm, n = 25), acrogenous, solitary, pale brown or olivaceous when young, brown at mature, obclavate, truncate at base, tapering towards the apex, straight or slightly curved, 9–13-septate, guttulate, smooth, the conidia tip surrounded by a gelatinous sheath. **Sexual morph**: Not observed.

Cultural characteristics: conidia germinating on PDA within 12 h and germ tube produced from both ends. Colonies on PDA reaching about 40 mm diam. after 4 weeks at 25 °C, circular, entire, wrinkled, with dense, velvety, whitish brown mycelium on the surface, dark brown from below.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on culms of bamboo, 11 November 2019, Y.R. Sun, B26 (HGUP 24-0059, **holotype**); ex-type culture GUCC 24-0149.

Notes: Our isolate is phylogenetically close to *Distoseptispora lignicola,* which was reported from aquatic habitat in China and Thailand (Luo et al., 2019; Yang et al., 2021) (Figure 4.153). In morphology, our strain differs from *D. lignicola* by processing 9–13-septate conidia surrounding by an apical gelatinous sheath while the latter has 5–9-euseptate conidia without a sheath. In addition, there are 10 bp differences in the ITS gene region (526 bp, without gap). We thus introduced *D. gelatinosa* as a novel species herein.



Note a, b Colonies on the host. c Conidiophores. d, e Conidiophores attached to conidia. f Conidiogenous cell and conidium. h–k Conidia. Scale bars: c–k = 20 μm.

Figure 4.148 *Distoseptispora gelatinosa* (HGUP 24-0059, holotype)

Distoseptispora tectonae Doilom & K.D. Hyde Fungal Diversity 81: 222 (2016)

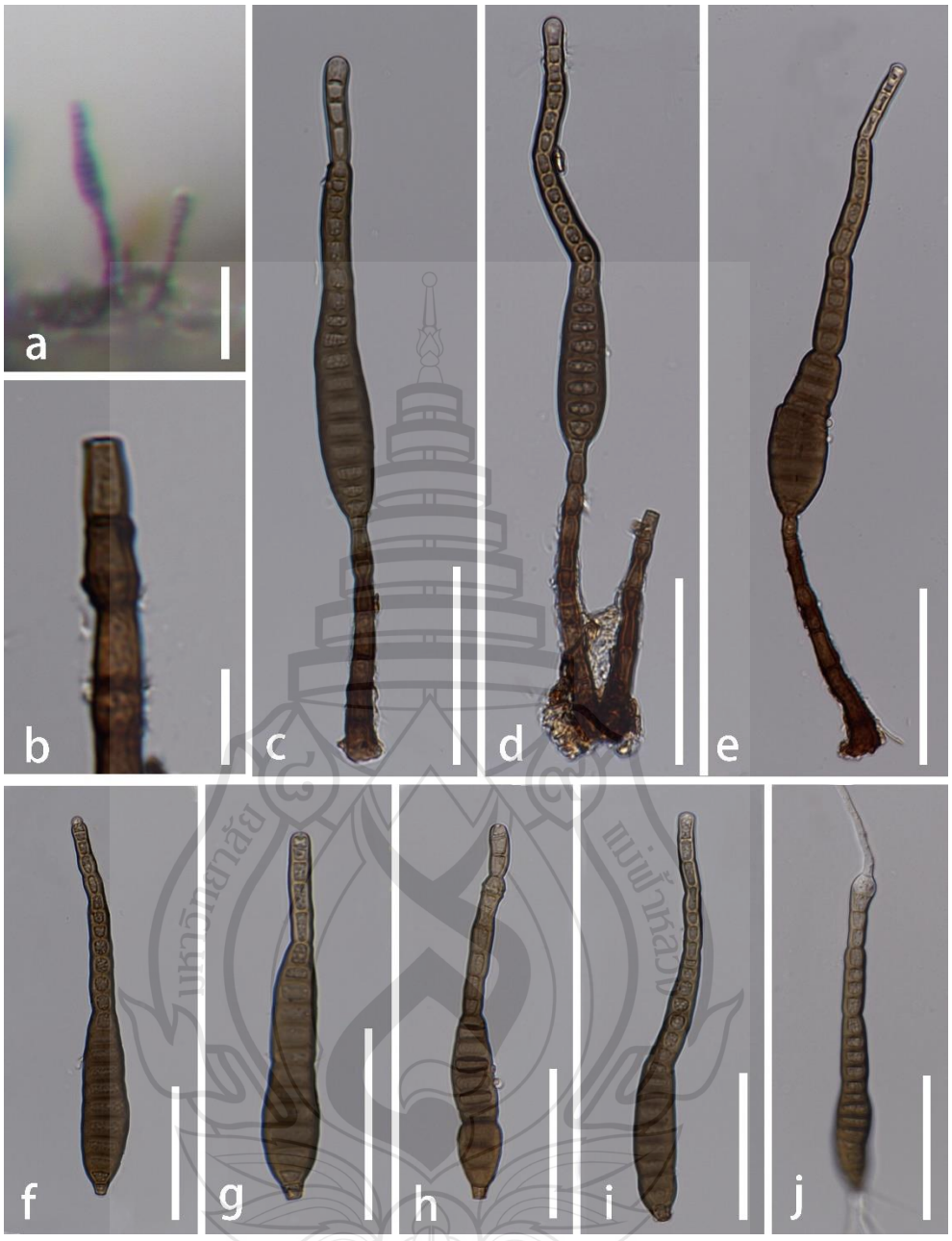
Index Fungorum number: IF552223; Facesoffungi number: FoF01877; Figure 4.149

Saprobic on stems of dead wood. Sexual morph: Unknown. Asexual morph: Hyphomycetous (Figure 4.153). Colonies effuse, brown to dark brown, hairy. Mycelium mostly immersed, composed of brown, septate, branched hyphae. Conidiophores macronematous, mononematous, septate, single or in groups of two, straight or slightly flexuous, cylindrical, dark brown, 34–95 × 5–8 μm ($\bar{x}$ = 61.5 × 6 μm, n = 15). Conidiogenous cells integrated, terminal, monoblastic, cylindrical, brown. Conidia acrogenous, solitary, straight or slightly flexuous, rostrate, 11–23-distoseptate, differently constricted at the septa, thick-walled, truncate at the base, tapering towards apex, brown at the base, pale brown at the apex, 89–176 μm long ($\bar{x}$ = 121 μm, n = 25), 12–19 μm at the widest ($\bar{x}$ = 15 μm, n = 25).

Culture characteristics: Conidia germinated on PDA within 12 hours and germ tubes were produced from both ends. On PDA, colony circular, reaching 40 mm diam after 4 weeks at 26°C, brown from above, dark brown from below, surface flat and slightly rough, edge entire.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on dead twigs, 11 November 2019, Y.R. Sun, B5 (MFLU 20–0262; living culture MFLUCC 20–0117.

Notes: *Distoseptispora tectonae* was introduced by Hyde et al. (2016), from a terrestrial habitat in Thailand. *Distoseptispora tectonae* has macronematous, cylindrical, septate conidiophores, monoblastic, integrated, terminal, cylindrical conidiogenous cells and obclavate, straight or slightly curved, septate, smooth conidia. Our collection was also from Thailand. The morphological characters of our collection are the same as in the holotype, except that our isolate has longer and wider conidiophores (34–95 × 5–8 μm *vs*. up to 40 × 4–6 μm) and less septa (11–23 *vs*. 20– 28), compared to those of *D. tectonae* MFLUCC 12–0291. In this study, we also provide new sequences for *D. tectonae.*



Note a. Colonies on natural substrate; b. Conidiogenous cell; c–e. Conidiophores and conidia; f–i. Conidia; j. Germinating conidium. Scale bars: b = 10 μm, a, c–j = 50 μm.

Figure 4.149 *Distoseptispora tectonae* (MFLU 20-0262)

Distoseptispora tectonigena Doilom & K.D. Hyde, Fungal Diversity 80: 222 (2016)

Index Fungorum number: IF552224; Facesoffungi number: FoF01878; Figure 4.150

Saprobic on bamboo culms in a stream. **Sexual morph**: Not observed. Asexual morph: Hyphomycetous. *Colonies* on natural substrate, effuse, single or in groups, numerous, dark brown, hairy. *Conidiophores* up to 30–80 µm long, 6–10 µm wide, macronematous, mononematous, erect, cylindrical, straight to slightly curved, unbranched, septate, brown to dark brown. *Conidiogenous cells* 3–4 µm wide, monoblastic, integrated, terminal, lageniform or cylindrical, brown, smooth. *Conidia* 120–260 µm long, 10–17 µm wide, cylindrical or obclavate, rounded at apex, straight or slightly curved, olivaceous or brown, slightly paler towards the apex, multi-septate, verruculose, smooth.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies reaching 15 mm diam. after 3 weeks at 25 °C, edge entire, veined, raised, velvety, grey from above, dark brown from below.

Material examined: THAILAND, Chiang Rai Province, Mueang Chiang Rai District, Ban Du, Pong Phra Bat Water Fall, on bamboo culms, 6 March 2021, Y.R. Sun, 21 (HGUP 24-0062); living cultures MFLUCC 24-0300.

Notes: Our collection MFLUCC 24-00x matches well with the holotype of *Distoseptispora tectonigena* (MFLU 15-3418), including conidial size (Hyde et al., 2016). Comparison of LSU and ITS sequences between our strain and the ex-type strain (MFLU 15-3418) showed 100% similarity, respectively. We therefore identify our collection as *D. tectonigena*, and this is a new host and habitat record.



Note a, b Colonies on the host. c–f Conidiophores attached to conidia. g–i Conidia. j, k Colonies on PDA medium. Scale bars: c–i = 30 µm.

Figure 4.150 *Distoseptispora tectonigena* (HGUP 24-0062, new host and habitat record)

Distoseptispora olivaceoviridis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16464; Figure 4.151

Etymology: The epithet refers to the green or olive-green conidia.

Holotype: HGUP 24-0060.

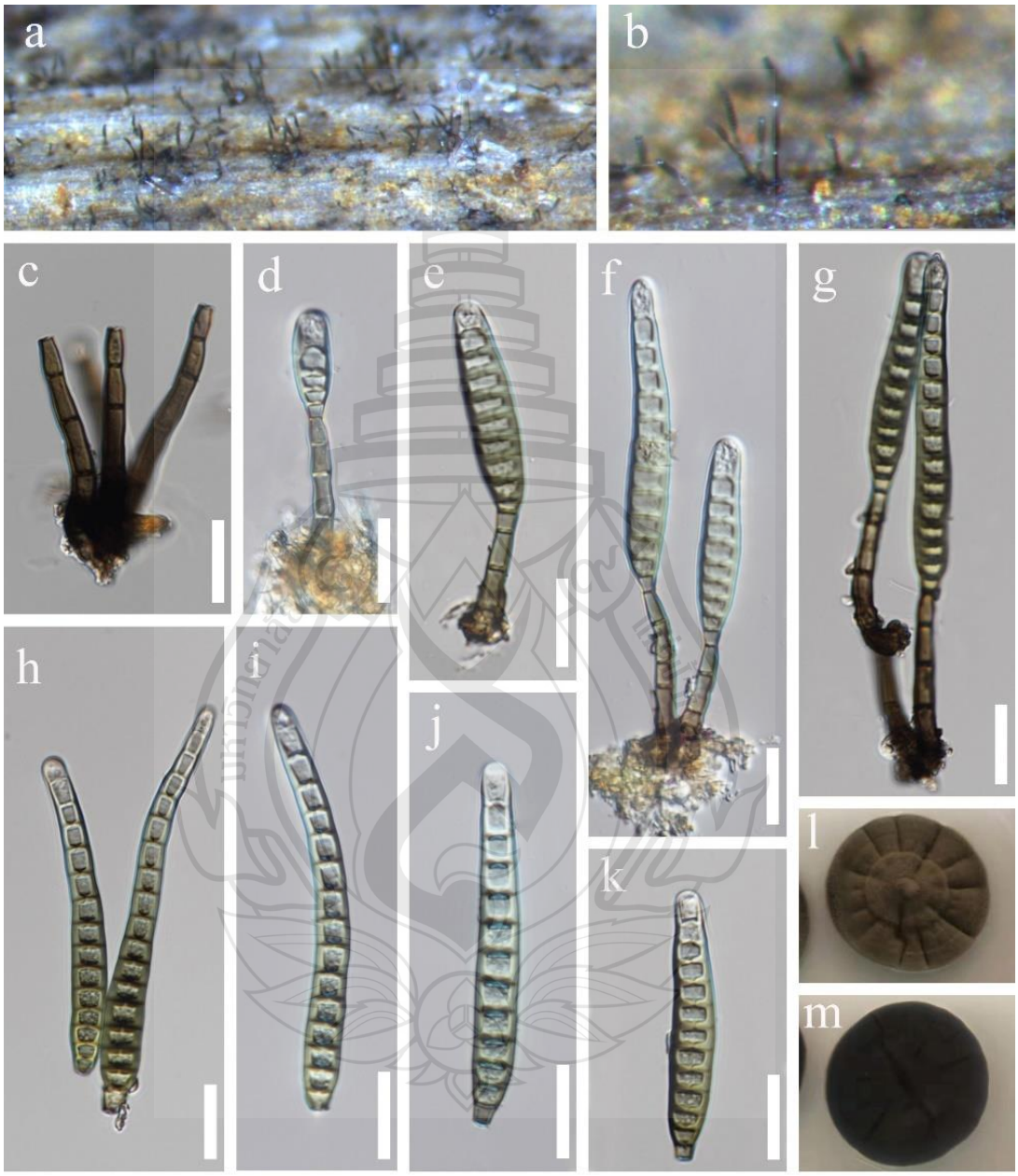
Saprobic on twigs of *Clerodendrum quadriloculare*. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, single or in groups, numerous, hairy, dark brown. *Conidiophores* 34–78 × 5–7 μm, macronematous, mononematous, erect, cylindrical, straight to slightly curved, unbranched, septate, olivaceous or pale brown when young, brown to dark brown at mature. *Conidiogenous cells* 6–11 μm long, 3–6 μm wide, monoblastic, integrated, terminal, cylindrical, brown, smooth. *Conidia* 46–115 × 8–12 μm, ($\bar{x}$ = 80 × 9 μm, n = 15), solitary, obclavate, rounded at apex, straight or slightly curved, green or olivaceous, slightly paler towards the apex, 12–16-septate, verruculose, thick-walled, smooth.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies reaching 25 mm diam. after 3 weeks at 25 °C, edge entire, veined, flat or slightly raised, velvety, brown from above, dark brown from below.

Material examined: THAILAND, Chiang Rai Province, Mueang Chiang Rai District, Mae Fah Luang University, on twigs of *Clerodendrum quadriloculare*, 6 March 2020, Y.R. Sun, B46 (HGUP 24-0060, **holotype**); ex-type cultures MFLUCC 24-0299.

Notes: *Distoseptispora olivaceoviridis* is phylogenetically close to *D. sinensis*, *D. tectonae* and *D. yichunensis* and they form a distinct inner clade within *Distoseptispora* (Figure 4.153). In morphology, *D. olivaceoviridis* can be distinguished from *D. tectonae* and *D. yichunensis* by its smaller conidia (46–115 × 8–12 μm *vs*. 130–140 × 13–14 μm vs. 113.7–272.7 × 12.2–16.9 μm) (Hyde et al., 2016; Hu, Liu, Luo et al., 2023); *D. olivaceoviridis* differs from *D. sinensis* in having green or olivaceous, 12–16-septate while the latter has 10–25-septate, brown to dark brown conidia (Liu et al., 2023). Additionally, the comparison of ITS and *TEF1-α* genes between *D. olivaceoviridis* and *D. sinensis*, *D. tectonae* and *D. yichunensis* showed that there are 13, 8 and 11 differences (a total 542 bp, without gap) in the ITS gene, respectively,

and 22, 18 and 20 differences (a total 910 bp, without gap) in the *TEF1-α* gene, respectively. Therefore, we introduce *Distoseptispora olivaceoviridis* as a new species herein.



Note a, b Colonies on the host. c Conidiophores. d–g Conidiophores attached to conidia. h–k Conidia. l, m Colonies on PDA medium. Scale bars: c–k = 20 μm.

Figure 4.151 *Distoseptispora olivaceoviridis* (HGUP 24-0060, holotype)

Distoseptispora yongxiuensis Z.J. Zhai & D.M. Hu, MycoKeys 88: 42 (2022)

Index Fungorum number: IF 842066; Facesoffungi number: FoF 16465; Figure 4.152

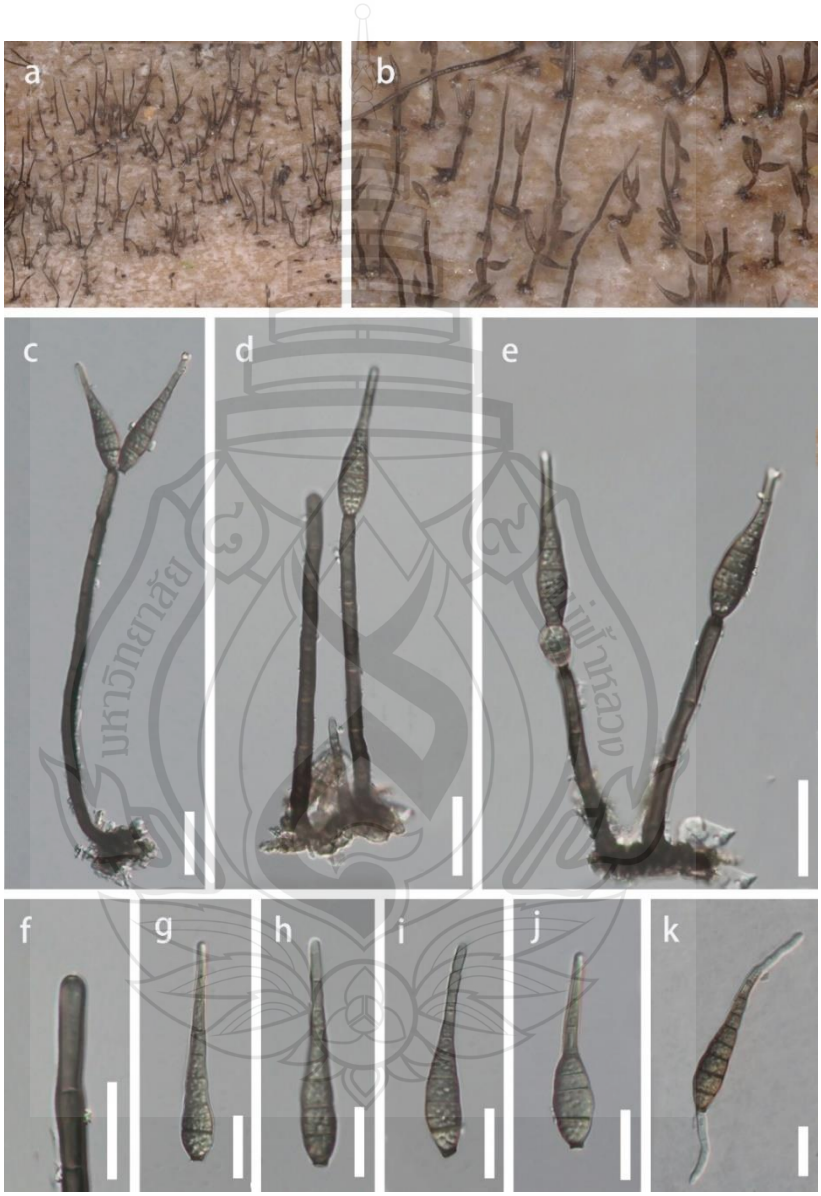
Saprobic on decaying bamboo culms. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate, effuse, scattered, single or in groups, numerous, erect, dark brown, hairy. *Mycelium* mostly immersed in the substratum, composed of hyaline to pale brown, septate, branched hyphae. *Conidiophores* 35–193 μm long, 4–7 μm wide, macronematous, mononematous, solitary or aggregated at the base, cylindrical, straight or slightly flexuous, brown to dark brown, unbranched, septate, thick-walled, sharply curving near the base. *Conidiogenous cells* 18–27 μm long, 3–6 μm wide, mono- or polyblastic, integrated, terminal, cylindrical, olivaceous to brown. *Conidia* 40–83 × 6–13 μm (x = 59 × 10 μm, n = 20), acrogenous, solitary, rostrate, obclavate, base truncate, straight or flexuous, 5–10-septate, olivaceous to brown, becoming paler or hyaline towards the apex, verrucose.

Cultural characteristics: Conidia germinating on PDA within 12 h and germ tubes produced from both ends. Colonies on PDA reaching 30 mm diam. after two weeks at 25 °C, circular, with dense, light olivaceous mycelium on the surface with entire margin, veined, raised, wrinkled; brown from above, dark brown to black form below.

Material examined: CHINA, Guizhou Province, Guiyang City, Huaxi District, Huaxi Park, on dead culms of bamboo, 26 January 2022, Y.R. Sun, 22-54 (HKAS 124555); ibid., 26 January 2022, Y.R. Sun, 22-56 (HKAS 124557); ibid., Sichuan Province, Chengdu City, Pidu District, on dead culms of bamboo, 6 August 2021, N.G. Liu, cd11 (HGUP 24-0046).

Notes: Our three isolates were collected from culms of bamboo from the terrestrial habitats in Guizhou and Sichuan Province in China. In the phylogenetic tree (Figure 4.153), they grouped with the ex-type strain of *Distoseptispora yongxiuensis* which was introduced by Zhai et al. (2022) and originally found in a freshwater environment. There is little morphological difference between our species and *D. yongxiuensis*. Additionally, there are

no base pair differences in the LSU gene and only two base pair differences in the ITS gene between our isolate and the ex-type strain JAUCC 4725. We therefore identify our collection as *D. yongxiuensis,* and this is the first report of *D. yongxiuensis* from terrestrial habitat.



Note a, b Colonies on the host. c–e Conidiophores attached to conidia. f Conidiogenous cell. g–j Conidia. k Germinating conidium. Scale bars: c–e = 30 μm, f–k = 20 μm.

Figure 4.152 *Distoseptispora yongxiuensis* (HKAS 124555, new habitat record)

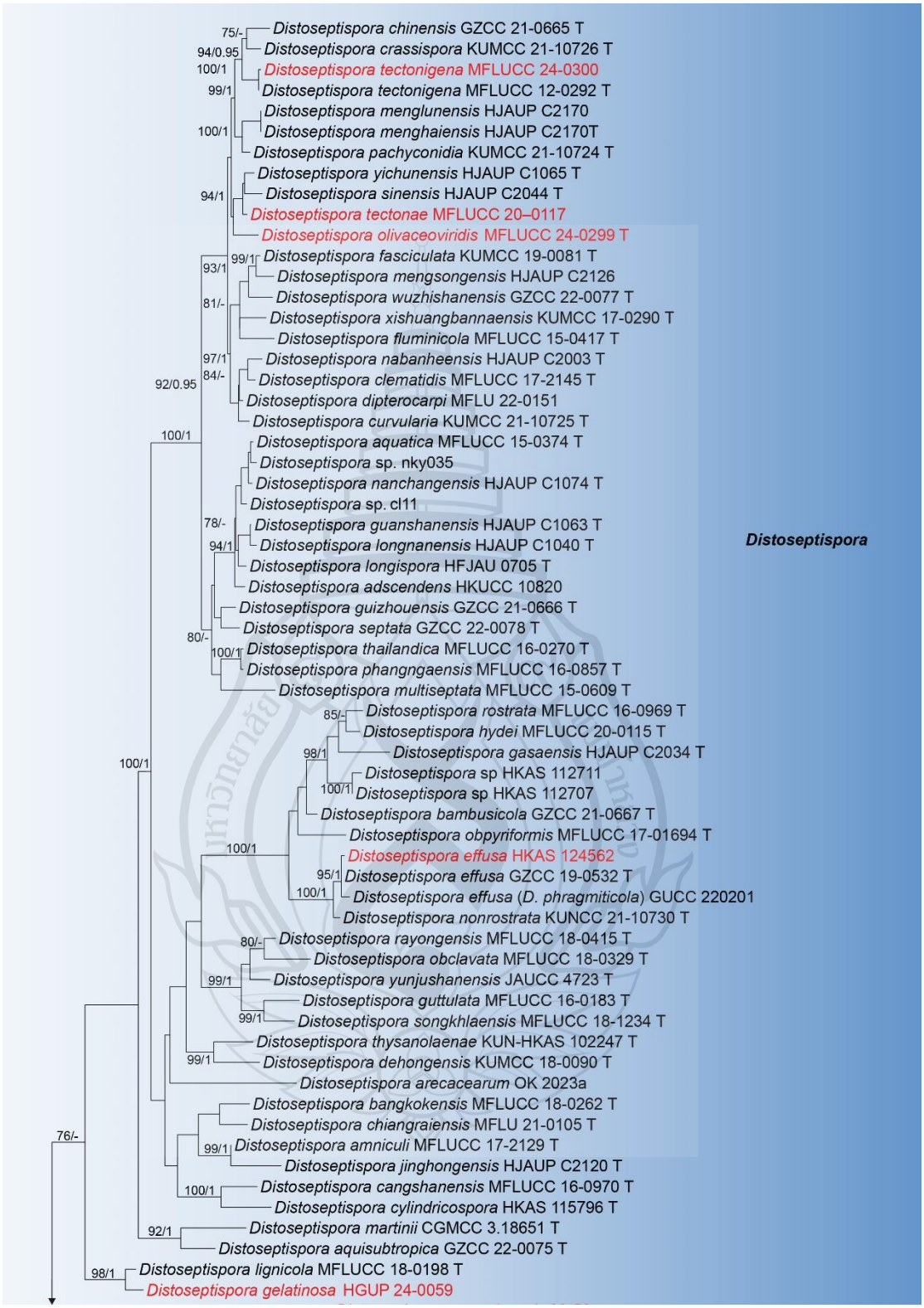
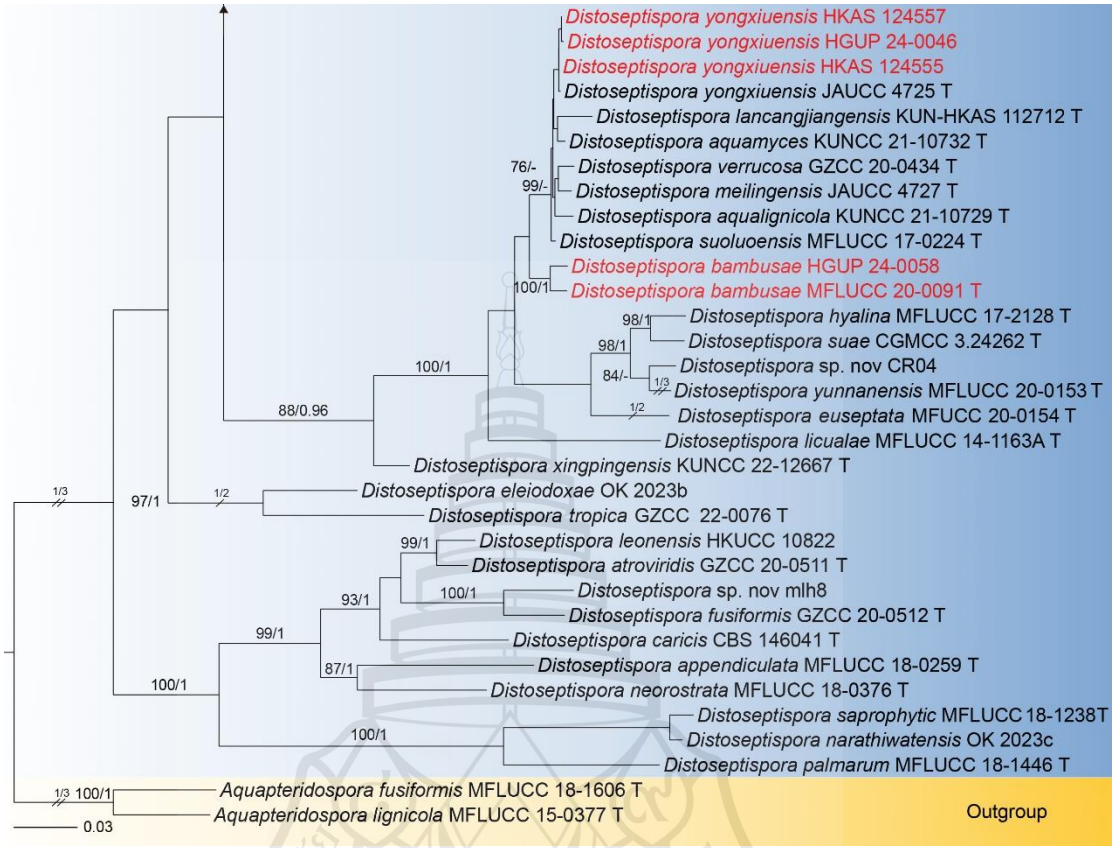


Figure 4.153 Phylogenetic tree of *Distoseptispora*



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Aquapteridospora fusiformis* (MFLUCC 18-1606) and *A. lignicola* (MFLUCC 15-0377). The new collections are indicated in red and ex-type strains are indicated with "T" after the strain number.

Figure 4.153 (continued)

Glomerellales Chadef., Stud. Mycol. 68: 170 (2011)

Malaysiascaceae Tibpromma & K.D. Hyde, Fungal Divers. 93: 88 (2018)

Malaysiasca Crous & M.J. Wingf., Persoonia 36: 373 (2016)

Notes: The holomorphic genus, *Malaysiasca* was introduced by Crous, Wingfield, Richardson et al. (2016) with *Malaysiasca phaii* as the type species. The sexual morph has obpyriform, papillate, dark brown ascomata, hyaline, branched, septate paraphyses, cylindrical-clavate, 8-spored asci and ellipsoid to oblong, 1-septate, pale brown ascospores; the asexual morph has cylindrical, unbranched, macronematous, erect conidiophores, terminal, phialidic, subcylindrical conidiogenous cells and cylindric-ellipsoid, aseptate, hyaline conidia (Crous, Wingfield, Richardson et al., 2016; Tibpromma, Hyde, McKenzie et al., 2018). So far, only one species is listed in this genus (Species Fungorum, 2024).

Malaysiasca phaii Crous & M.J. Wingf., Persoonia 36: 373 (2016)

Index Fungorum number: IF817045; Facesoffungi number: FoF04538; Figure 4.154

Associated with diseased leaves of *dracaena fragrans*. **Sexual morph**: Unknown. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown to black, gregarious. *Mycelium* mostly immersed, composed hyaline, branched hyphae. *Conidiophores* 143–260 × 5–8 µm, macronematous, mononematous, erect, loosely fasciculate, straight or flexuous, cylindrical, dark brown at base, paler towards the apex, unbranched, septate, thick-walled. *Conidiogenous cells* 33–74 µm long, 4–7 µm wide, monophialidic, integrated, terminal, cylindrical, subhyaline to pale brown, with an inconspicuous apical collarette. *Conidia* 13–23 × 7–11 µm ($\bar{x}$ =14 × 8 µm, n = 30), acrogenous, solitary, ellipsoidal to oval, hyaline, aseptate, verrucose or sometimes guttulate, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA, irregular, edge undulate, flat, light orange at the center and yellow at the outer ring from above, orange-red at the center and yellow at the outer ring from below, Mycelium superficial, flossy.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, the Medicinal Plant Garden, on diseased leaves of *dracaena fragrans*, 7 June 2020, Y.R. Sun, B35 (HGUP 24-0065); living culture GUCC 24-0155.

Notes: *Malaysiasca phaii* was firstly documented from leaves of *Phaius reflexipetalus* in Malaysia (Crous, Wingfield, Richardson et al., 2016). Tibpromma, Hyde, McKenzie et al. (2018) isolated it from dead leaves of *Freycinetia javanica* in Thailand. In this study, our strain clustered together with *M. phaii* (CPC 27548 and MFLUCC 16–0256) by high support in the phylogenetic tree (Figure 4.156). In morphology, our strain also shares the similar characters with *Malaysiasca phaii,* in having cylindrical, unbranched conidiophores, phialidic, subcylindrical conidiogenous cells and aseptate, hyaline conidia (Tibpromma, Hyde, McKenzie et al., 2018). In addition, they have similar size. Therefore, we identified our strain as *M. phaii,* representing a new host record from *dracaena fragrans*.



Note a Host. b, c Colonies on natural substrate. d, e Conidiophore with Conidia. f g Conidiogenous cells with conidia. h–m Conidia. n Germinated conidium. o, p Colony on PDA from above and below. Scale bars: b = 1000 µm, c = 500 µm, d–e = 50 µm, f–g, n = 20 µm, h–m = 10 µm.

Figure 4.154 *Malaysiasca phaii* (HGUP 24-0065, new host record)

Plectosphaerellaceae W. Gams, Summerb. & Zare, Nova Hedwigia 85(3–4): 476 (2007)

Acrostalagmus Corda, Icon. fung. (Prague) 2: 15 (1838)

Notes: *Acrostalagmus* was introduced by Corda (1838) with *A. cinnabarinus* as the type species. However, *A. cinnabarinus* has been found to be identical to *Verticillium luteoalbum* (≡ *Sporotrichum luteoalbum*), as introduced by Link (1809b). Zare et al. (2004) proposed *Acrostalagmus luteoalbus* as the type species. The genus is characterized by mononematous or synnematous conidiophores, cylindrical, phialidic conidiogenous cells, and hyaline or bright orange to reddish, oval, ellipsoidal to cylindrical conidia (Corda, 1838; Hyde et al., 2019). Currently, 13 species are listed in (Species Fungorum, 2024).

Acrostalagmus annulatus (Berk. & M.A. Curtis) Seifert, in Réblová, Gams & Seifert, Stud. Mycol. 68: 186 (2011)

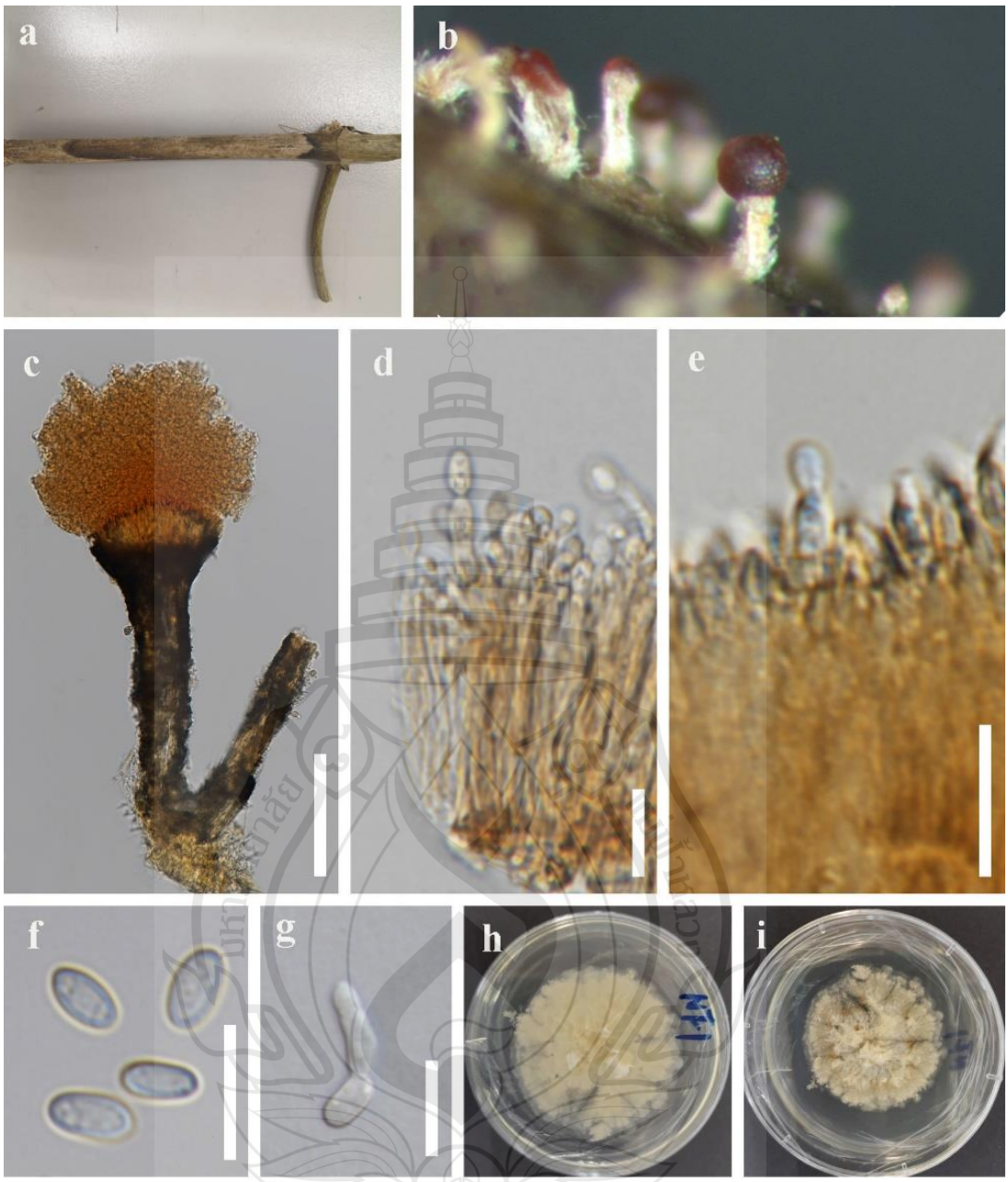
Index Fungorum number: IF518663; Facesoffungi number: FoF05253; Figure 4.155

Associated with diseased twig of *Agastache rugosa*. **Sexual morph**: Unknown. **Asexual morph**: Hyphomycetous. *Colonies* effuse, solitary, reddish. *Mycelium* mostly immersed, composed of septate, branched, hyaline hyphae. *Synnemata* solitary, erect, pale brown to reddish, 300–360 µm tall with a cylindrical stipe from 20 to 85 µm wide, pale to dark brown, terminated into a slimy head of conidia, slimy head 100–140 µm high, 180–210 µm wide. *Conidiophores* synnematous, solitary, often reduced to conidiogenous cells. *Conidiogenous cells* terminal, hyaline, smooth-walled, cylindrical, 1.5–2.5 µm wide. *Conidia*, sub-globose to cylindrical, aseptate, hyaline, smooth-walled, 5–7 × 2–4 µm ($\bar{x}$ = 6 × 3 µm, n = 30).

Culture characteristics: Conidia germinated on PDA within 12 hours from single-spore isolation. Germ tube produced at one end. Colonies diameter reached 30–50 mm after 4 weeks at 26 °C on PDA media, circular, wrinkled, umbonate, light yellow from above and below.

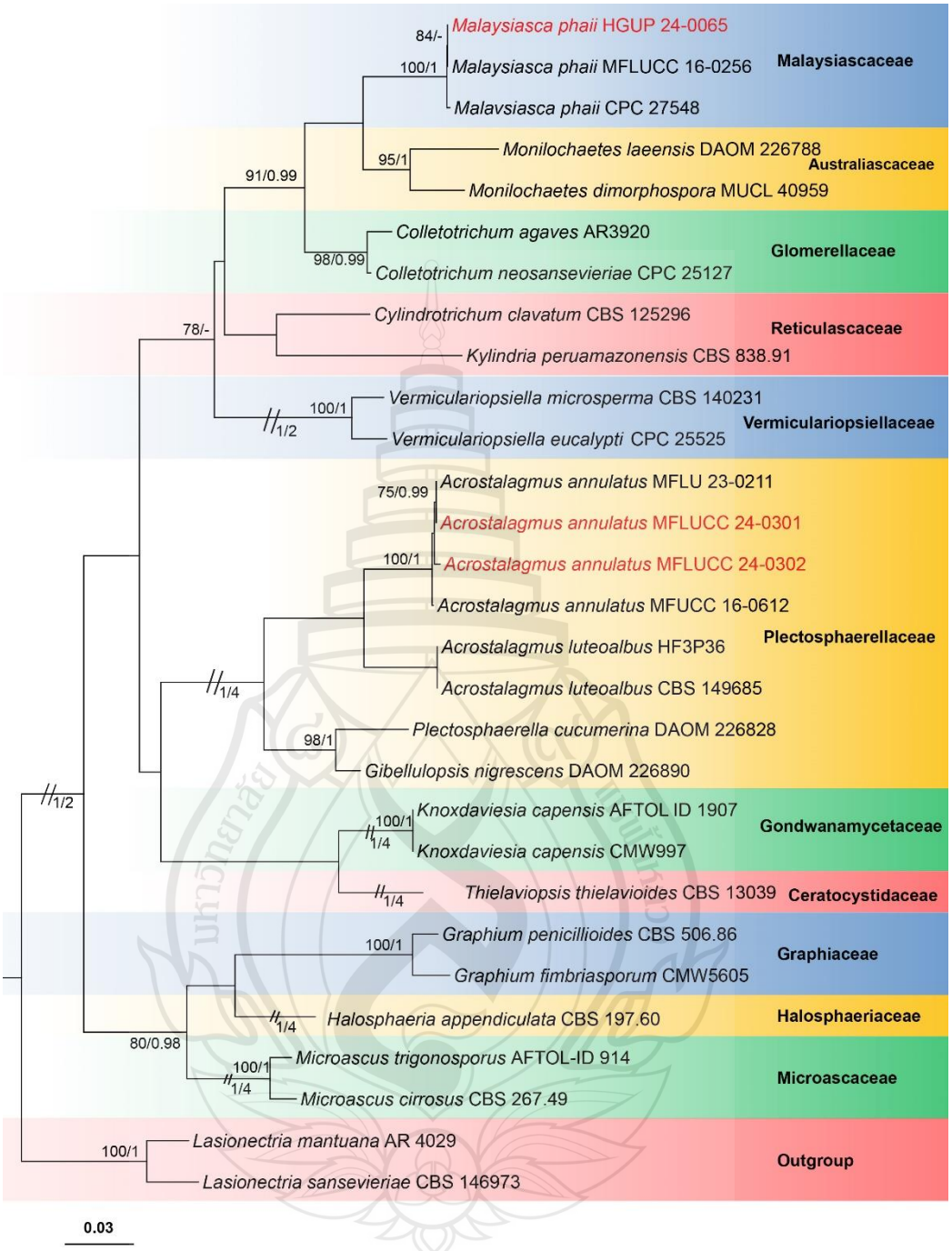
Material examined: THAILAND, Nan province, on *twig of Agastache rugosa*, 15 January 2020, Y.R Sun, NF1 (HGUP 24-0063); living culture MFLUCC 24-0301, ibid; Chiang Rai Province, Mae Fah Luang University, on dead twigs, 11 November 2019, Y.R Sun, S68 (HGUP 24-0064); living culture MFLUCC 24-0302.

Notes: Our two collections clustered together with *Acrostalagmus annulatus* (MFLUCC 16-0612 and MFLU 23-0211) in the phylogenetic tree (Figure 4.156). In morphology, our strain shares similar characters with *A. annulatus* (Réblová et al., 2011; Hyde et al., 2019). *Acrostalagmus annulatus* has a world wild distributions and various hosts but none are found on *Agastache rugosa* (Hyde et al., 2019; Tian et al., 2024). Therefore, we described our strains as *A. annulatus*, representing a new host from the medicinal plant, *Agastache rugosa*.



Note a Host. b Colonies on natural substrate. c Synnemata with conidia mass. d, e Conidiogenous cells with conidia. f Conidia. g Germinated conidium. h, i Colony on PDA from below and above. Scale bars: c = 100 μm, d–g = 10 μm.

Figure 4.155 *Acrostalagmus annulatus* (HGUP 24-0063, new host record)



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Lasionectria mantuana* (AR 4029) and *L. sansevieriae* (CBS 146973). The new collections are indicated in red.

Figure 4.156 Phylogenetic tree of Glomerellales

Hypocreales Lindau, Nat. Pflanzenfam., Teil. I (Leipzig) 1(1): 343 (1897)

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

Achroiostachys L. Lombard & Crous, Persoonia 36: 172 (2016)

Notes: *Achroiostachys* was introduced by Lombard et al. (2016) to accommodate a group of fungi that are similar to stachybotrys, characterized by their hyaline, thin-walled conidiophores and hyaline, ellipsoidal to limoniform conidia. The genus has a worldwide distribution, and most species are isolated from terrestrial plant debris and soil (Lombard et al., 2016; Dubey, 2021). Currently, the genus lists seven species, six of which are supported by molecular data (Lombard et al., 2016; Dubey, 2021; Species Fungorum, 2024). In this study, we described three new species based on both morphological and phylogenetic analyses.

Achroiostachys brunnea Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16466; Figure 4.157

Etymology: refers to its brown conidiophores.

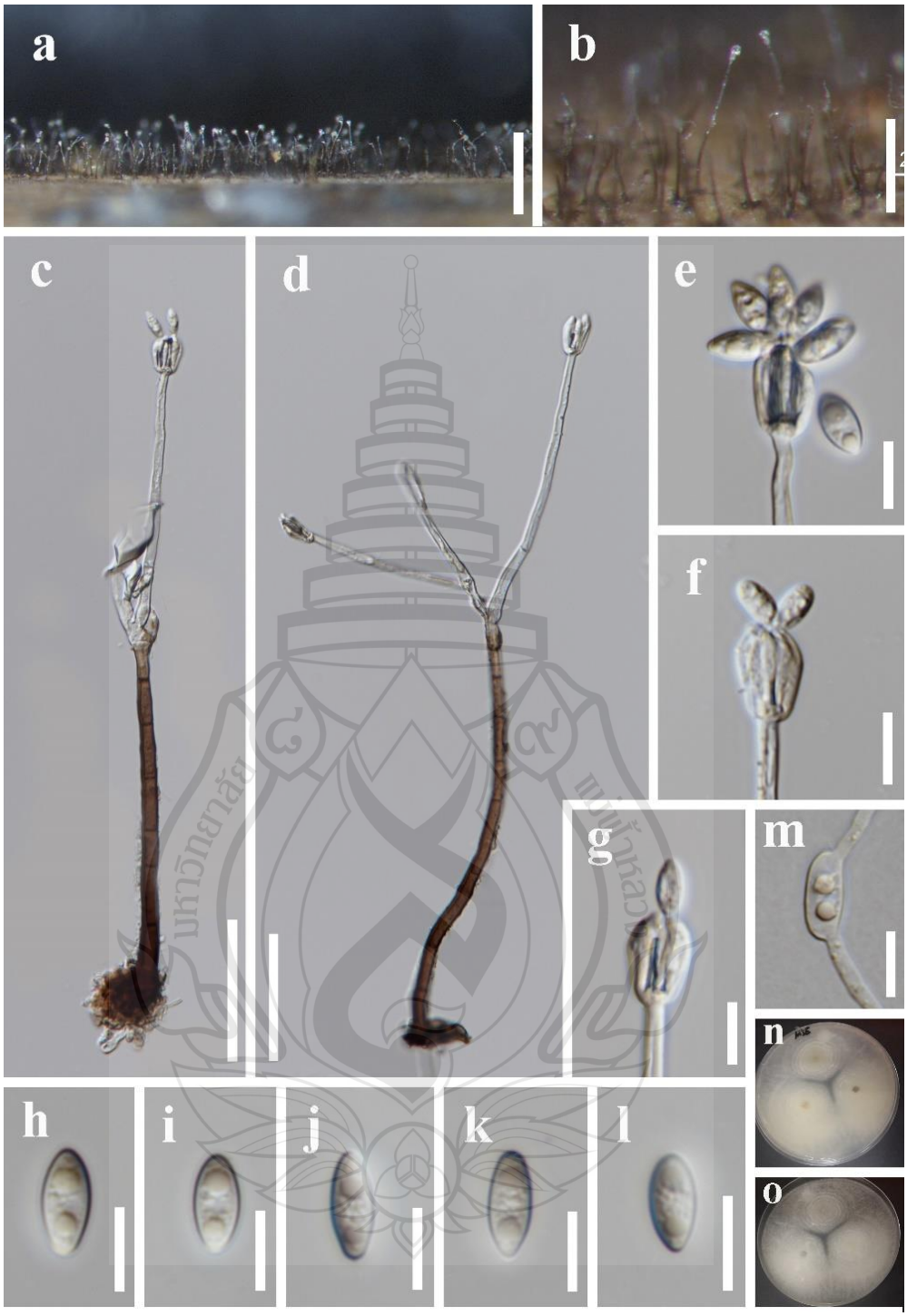
Holotype: HGUP 24-0067.

Saprobic on Poaceae plant in terrestrial habitat. **Sexual morph**: Unknown. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, dark brown with white conidial mass at the apex, velvety. *Mycelium* mostly immersed, composed of hyaline to pale brown hyphae. *Conidiophores* 170–315 µm long, 3.5–7 µm wide at the brown part, 2–3.5 µm wide at the hyaline part, macronematous, mononematous, erect, straight or flexuous, apically branched or unbranched, brown to dark brown at main stem, hyaline at the branches, septate, thick-walled, with apical cluster of conidiogenous cells. *Conidiogenous cells* monophialidic, discrete, elongate ampulliform to ventricose, hyaline, 9–15 µm long. *Conidia* 8–13 × 3.5–6 µm ($\bar{x}$ = 11 ×5 µm, n = 40), solitary, fusiform, containing 2 large guttules, hyaline to subhyaline, aseptate, verrucose.

Cultural characters: Conidia germinated on PDA within 12 h, germ tubes produced from both ends. Colonies reached 5 cm diam. within four weeks at 26 °C, cottony, flat, circular, edge entire, white from above and below.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Pa Pae, Mushroom Research Center, on bamboo culms, 10 September 2020, H.W. Shen, M56 (HGUP 24-0067, **holotype**); ex-type culture MFLUCC 24-0304; ibid; on Poaceae plant, 10 September 2020, H.W. Shen, M53 (HGUP 24-0066); living culture MFLUCC 24-0303.

Notes: In this study, our two strains clustered together and grouped with *Achroiostachys catenate* and *A. phyllophila* in the phylogenetic tree (Figure 4.172). Morphologically, our collections exhibit characteristics of *Achroiostachys* but can be distinguished from other *Achroiostachys* species by their brown, branched conidiophores. Moreover, our collections can be differentiated from *A. catenate* by their solitary, smaller conidia (8–13 × 3.5–6 µm *vs*. 11–17 ×5–7 µm) and longer conidiophores (170–315 µm *vs*. 80–105 µm) (This study). Our collections are distinct from *A. phyllophila* by having longer conidiophores (170–315 µm *vs*. 40–70 × 3–5 µm) and larger conidia (8–13 × 3.5–6 µm *vs*. 8.5– 9.5× 3–4 µm) (Lombard et al., 2016). Thus, we introduced a new species here, namely, *Achroiostachys brunnea.*



Note a, b Colonies on the host. c, d Conidiophores with conidia. e–g Conidiogenous cells and conidia. h–l Conidia. m Germinating conidium. n, o Colonies on PDA. Scale bars: a = 500 µm, b = 200 µm, c, d = 50 µm, e–m = 10 µm.

Figure 4.157 *Achroiostachys brunnea* (HGUP 24-0067, holotype)

Achroiostachys catenata Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16467; Figure 4.158

Etymology: refers to the catenate conidia of this fungus.

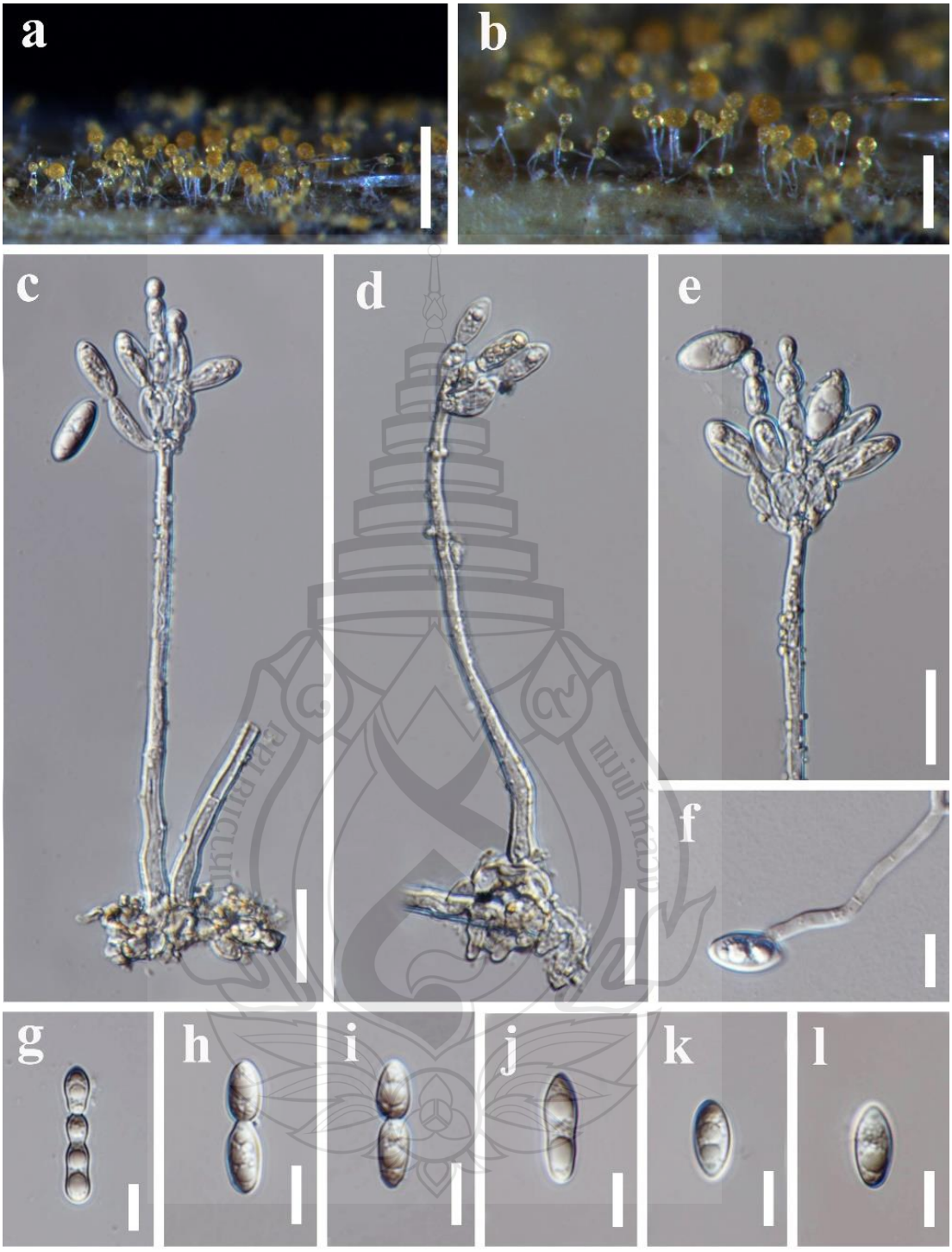
Holotype: MFLU 23-0496.

Saprobic on decaying wood. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, velvety, orange. *Conidiophores* single or in groups, mononematous, macronematous, erect, straight to slightly flexuous, unbranched, hyaline, septate, bearing at its apex a whorl of 4–6 conidiogenous cells, 80–105 µm long, 2.5–5 µm wide. *Conidiogenous cells* monophialidic, terminal, integrated, determinate, hyaline, smooth, clustered at the apex of conidiophores, elongate doliiform to subcylindrical, reniform, 12–14.5 µm long. *Conidia* developing in basipetal chains, acrogenous, fusiform, hyaline, with two globules, 11–17 × 5–7 µm ($\bar{x}$ = 14.5 × 6 µm, n = 30).

Cultural characters: Conidia germinated on PDA within 12 h. Colonies reached 2.5 cm diam. within four weeks at 26 °C, cottony, flat, irregular, lobate edge, white from above, brown from below.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Pa Pae, Mushroom Research Center, on dead twigs, 15 July 2020, Y.R Sun, M19 (MFLU 23-0496, **holotype**); ex-type culture MFLUCC 24-0307.

Notes: *Achroiostachys catenata* forms a sister clade with *A. brunnea* in the phylogenetic tree (Figure 4.172). For a comparison of morphological differences with *A. brunnea*, see this paper. *Achroiostachys catenata* also phylogenetically close to *A. phyllophila* but can be distinguished by its longer conidiophores (80–105 µm vs. 40–70 × 3–5 µm) and catenate conidia (Lombard et al., 2016). Therefore, we introduced *A. catenata* as a novel species.



Note a, b Conidioma on the material surface. c, d Conidiophores with conidia. e Conidiogenous cells and conidia. f Germinated conidium. g–l Conidia. Scale bars: a = 500 µm, b = 200 µm, c–e = 20 µm, f–l = 10 µm.

Figure 4.158 *Achroiostachys catenate* (MFLU 23-0496, holotype)

Achroiostachys fusiformispora Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16468; Figure 4.159

Etymology: refers to its fusiform conidia.

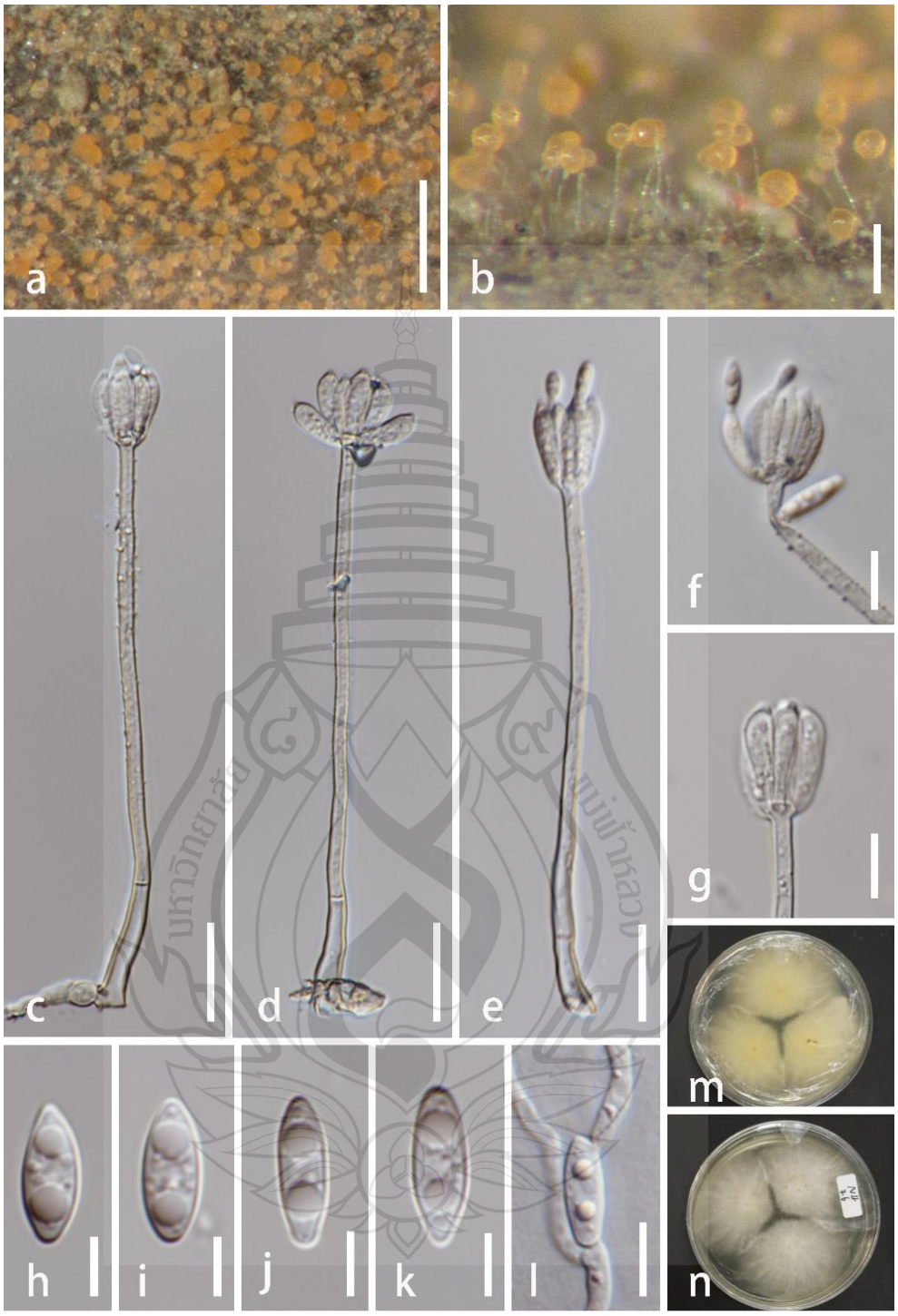
Holotype: MFLU 23-0497.

Saprobic on decaying twigs of *Carica papaya*. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, velvety, orange. *Conidiophores* single or in groups, mononematous, macronematous, erect, straight to slightly flexuous, unbranched, hyaline, 1-2-septate, bearing at its apex a whorl of 6–8 conidiogenous cells, 100–125 μm long, 2–4.5 μm wide. *Conidiogenous cells* monophialidic, terminal, integrated, determinate, hyaline, smooth, clustered at the apex of conidiophores, elongate doliiform to subcylindrical, reniform, 13–15.5 μm long. Conidial mass slimy, orange. *Conidia* acrogenous, fusiform, hyaline, aseptate, with two globules, smooth-walled, 11–14 × 3.5–5 μm ($\bar{x}$ = 12 × 4 μm, n = 30).

Culture characters: Conidia germinated on PDA within 12 hours. Colonies reached about 4.5 cm diameter after 3 weeks on PDA at 26 °C. Mycelia are superficial, medium sparse, flat, white from above, light yellow from below.

Material examined: THAILAND, Chiang Rai Province, Wiang Chiang Rung District, Thuang Ko, on dead twigs of *Carica papaya*, 7 Jan 2020, N.G. Liu, N4 (MFLU 23-0497, **holotype**); ex-type culture MFLUCC 24-0308.

Notes: *Achroiostachys fusiformispora* forms a sister clade with *A. aurantispora* in the phylogenetic tree (Figure 4.172). Morphologically, *A. fusiformispora* is distinguished from the latter by having longer conidiophores (100–125 μm long *vs*. 70–100 × 2.5–3.5 μm), longer conidiogenous cells (13–15.5 μm *vs*. 10–13 × 3.5–4.5 μm) and fusiform, larger conidia (11–14 × 3.5–5 μm *vs*. 7.5–8.5 × 4–5 μm) (Lombard et al., 2016). Therefore, we introduced *A. fusiformispora* as a novel species.



Note a, b Conidioma on the material surface. c–e Conidiophores. f, g Conidiogenous cells and Conidia. h–k. Conidia. l Germinated conidium. m, n Colony on PDA. Scale bars: a = 200 μm, b = 100 μm, c–e = 20 μm, f, g, l = 10 μm, h–k = 5 μm.

Figure 4.159 *Achroiostachys fusiformispora* (MFLU 23-0497, holotype)

Gregatothecium L. Lombard & Crous, Persoonia 36: 191 (2016)

Notes: Lombard et al. (2016) introduced *Gregatothecium,* designating *Gregatothecium humicola* as the type species. The characteristics of this genus are sporodochial, stromatic, superficial, cupulate, scattered or gregarious conidiomata, phialidic, hyaline, aseptate conidiogenous cells and aseptate, hyaline to subhyaline, cylindrical to subcylindrical conidia (Lombard et al., 2016). Currently, the genus consists of one species, isolated from soil (Species Fungorum, 2024). In this study, we introduce one new species, i.e. *G. diflugossae,* isolated from medicinal plant *Diflugossa divaricata* in China.

Gregatothecium diflugossae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16469; Figure 4.160

Etymology: refers to the host genus, *Diflugossa*.

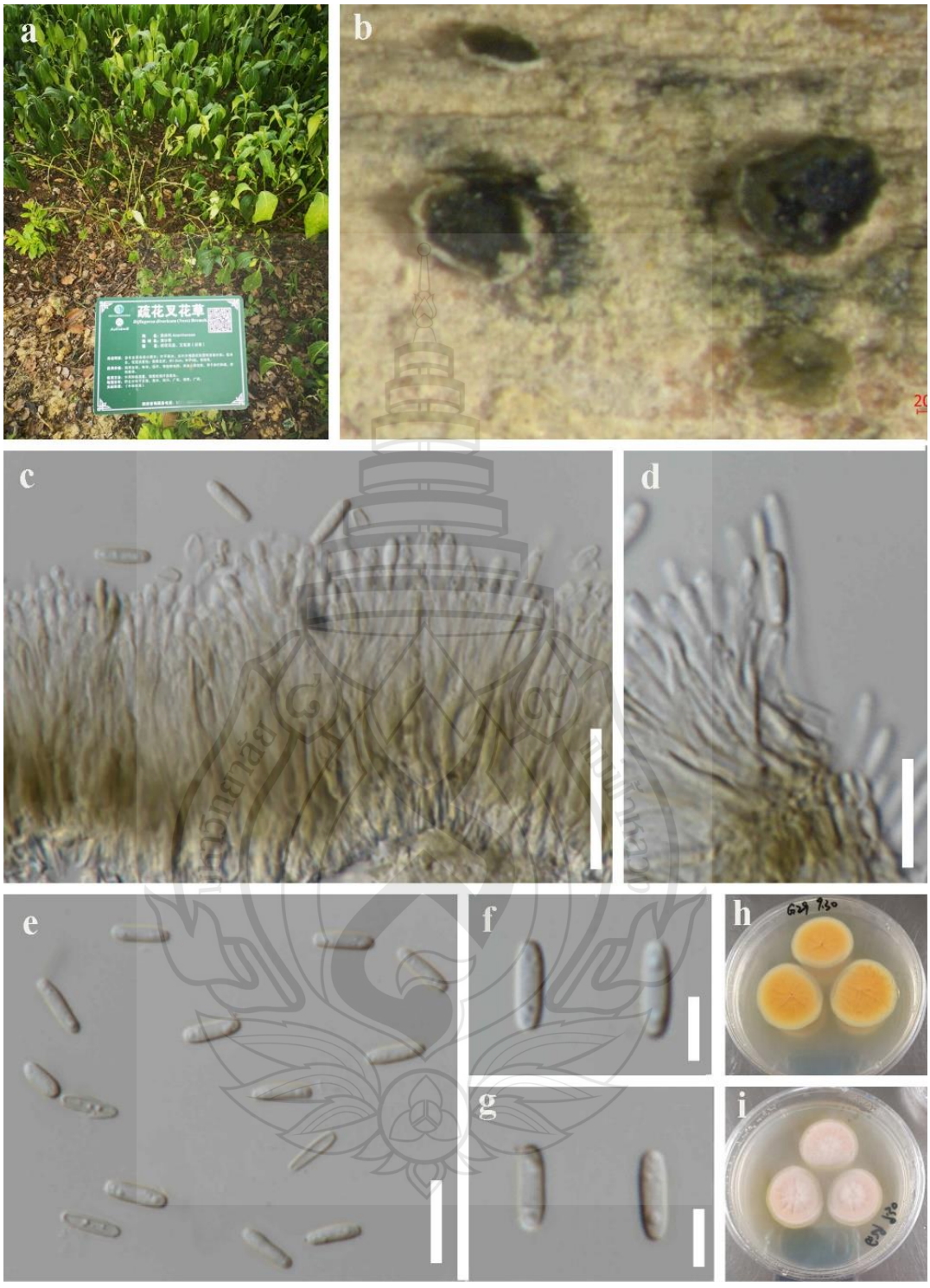
Holotype: HGUP 24-0068.

Saprobic on twigs of *Diflugossa divaricata*. **Sexual morph**: Not observed. **Asexual morph**: *Conidiomata* sporodochial, stromatic, superficial, cupulate, scattered or gregarious, oval or irregular in outline, with or without a pale brown setose fringe surrounding an olivaceous green to dark green slimy mass of conidia. *Stroma* poorly developed, subhyaline to pale brown, smooth, of *textura globulosa* and *textura angularis*. *Conidiophores* arising from the basal stroma, unbranched, pale to brown, smooth, produced conidiogenous cells. *Conidiogenous cells* phialidic, cylindrical to subcylindrical, hyaline, aseptate, smooth, straight to slightly curved, 1–2 µm wide, with conspicuous collarettes and periclinal thickenings. *Conidia* aseptate, hyaline to subhyaline, cylindrical to subcylindrical, with two granular protrusions, 6–8 × 1.5–2.5 µm ($\bar{x}$ = 7 × 2 µm, n = 30), rounded at both ends.

Cultural characters: Conidia germinated on PDA within 12 h. Colonies reached 3.5 cm diam. within four weeks at 26 °C, cottony, flat, dry, circular, entire, veined, white to light pink from above, orange from below.

Material examined: CHINA, Guangxi Province, Nanning City, on steam of *Diflugossa divaricata*, 14 Septamber 2019, Y.R. Sun, G29 (HGUP 24-0068, **holotype**), ex-type culture MFLUCC 24-0314.

Notes: Our new collection from *Diflugossa divaricata* phylogenetically close to *Gregatothecium humicola* in Stachybotriaceae (Figure 4.172). It differs from the latter by having larger conidia (6–8 × 1.5–2.5 µm *vs*. 5–6 × 1–2 µm) (Lombard et al., 2016). *Gregatothecium diflugossae*'s conidiophores produce single conidiogenous cells, in contrast to *G. humicola*, which produces 3–6 conidiogenous cells. Setae were not observed in *G. diflugossae* while were produced in *G. humicola.* Therefore, we introduced *G. diflugossae* as a novel species.



Note a Host. b Colonies on the host. c, d Conidiogenous cells and conidia. e–g Conidia. h, i Colonies on PDA. Scale bars: c = 20 μm, d, e = 10 μm, f, g = 5 μm.

Figure 4.160 *Gregatothecium diflugossae* (HGUP 24-0068, holotype)

Melanopsamma Niessl, Verh. nat. Ver. Brünn 14: 200 (1876)

Notes: *Melanopsamma* species have a long evolutionary history, characterized by their ability to produce both sexual and asexual morphs (Lombard et al., 2016). The sexual morph features superficial, solitary or in groups, ostilate, papillate ascomata, unitunicate, 8-spored, cylindrical to clavate asci, numerous, hyaline paraphyses and ellipsoidal, 1-septate, hyaline ascospores. The asexual morph is characterized by macronematous, mononematous, erect, solitary or in groups, unbranched conidiophores, phialidic, subcylindrical to clavate to elongate doliiform, smooth, hyaline conidiogenous cells and aseptate, hyaline to dark brown, limoniform to obovoid to globose to ellipsoidal conidia (Lombard et al., 2016). Wang et al. (2015) synonymised this genus under Stachybotrys whereas Lombard et al. (2016) resurrected it based on phylogenetic analyses also designating CBS 101322 as the ex-type for the genus's type species, *Melanopsamma pomiformis*. Although the genus boasts a wide variety of species, the majority of those identified in the last century are missing molecular data (Species Fungorum, 2024). In this study, we introduced a new *Melanopsamma* species with a description, illustration and molecular data.

Melanopsamma tongrenensis Y.R. Sun, Yong Wang bis and K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16470; Figure 4.161

Etymology: Name reflects the location where this fungus was collected.

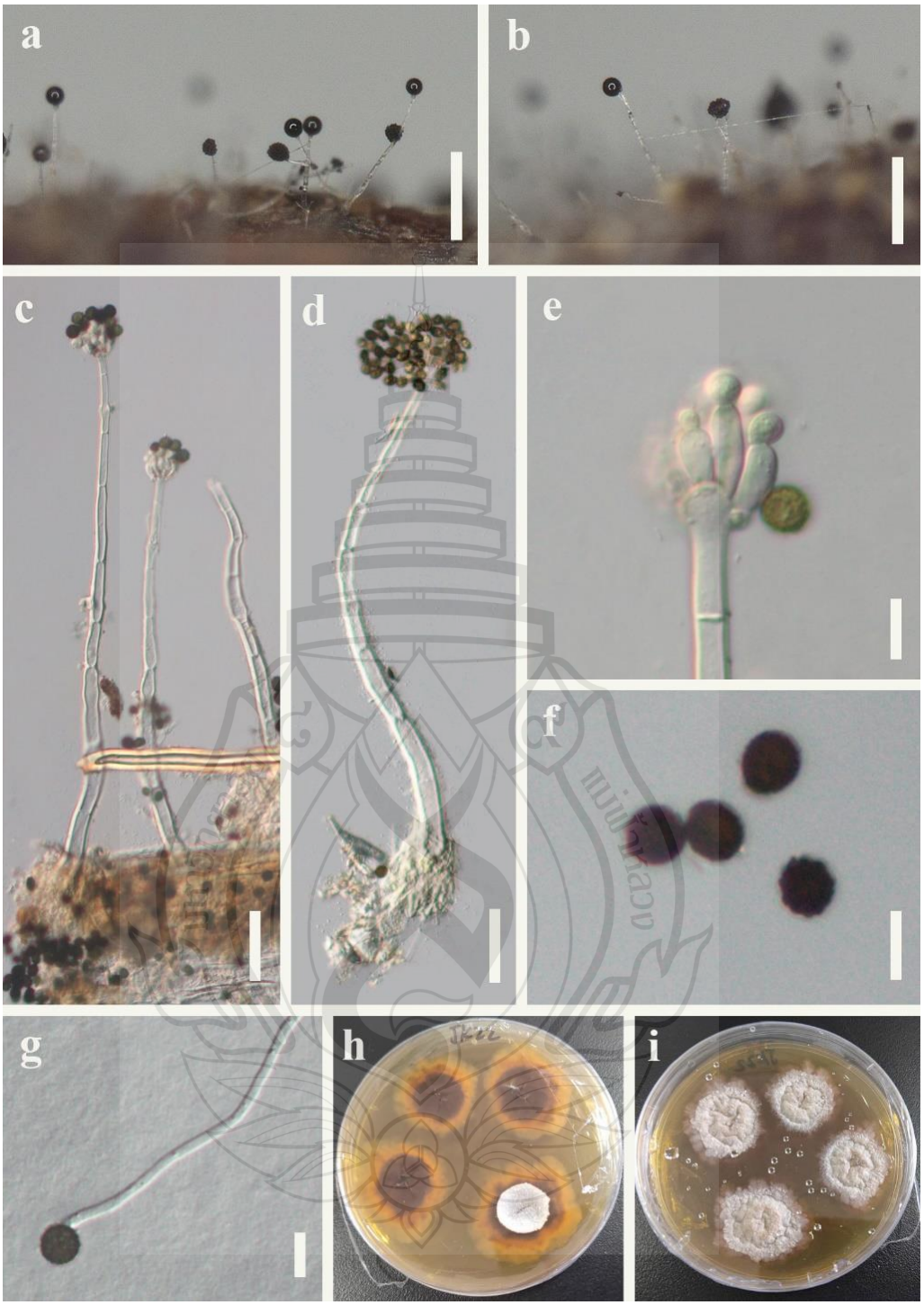
Holotype: HKAS 136899.

Saprobic on dead twigs of *Osmanthus fragrans*. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, velvety, black. *Conidiophores* simple, macronematous, mononematous, single or in groups, unbranched, erect, straight to slightly flexuous, hyaline, 5–9-septate, smooth, 180–395 × 8–12 µm, with a bulbous apice, bearing a whorl of 4–10 conidiogenous cells. *Conidiogenous cells* 9–13 µm long, phialidic, elongate doliiform to subcylindrical, hyaline, smooth. *Conidia* acrogenous, aseptate, globose to subglobose, hyaline at young, brown at mature, verrucose, 7–11.5 × 6.5–10.5 µm ($\bar{x}$ = 9.5 × 8 µm, n = 25).

Cultural characters: Conidia germinated on PDA within 12 h. Colonies reaching 2–2.5 cm diam. within three weeks at 26 °C, cottony, raised, dry, circular, undulate, veined, white from above, orange to brown from below.

Material examined: CHINA. Guizhou Province, Tongren City, Jiangkou District, Yamugou Parkland, on dead twigs of *Osmanthus fragrans*, 20 May 2022, Y.R Sun, JK22 (HKAS 136899, **holotype**); ex-type culture GUCC 24-0111.

Notes: *Melanopsamma tongrenensis* grouped with *M. pomiformis* and *M. xylophila* and placed within Stachybotriaceae by high support (ML-bs = 100%, BYPP = 1) (Figure 4.172). Morphologically, our collection differs from *M. pomiformis* by 5–9-septate, longer conidiophores (180–395 × 8–12 μm *vs*. 30–60 × 5–7 μm) and larger conidia (7–11.5 × 6.5–10.5 μm *vs*. 6.5–7.5(–9) × (3–)3.5–4.5(–5) μm) (Lombard et al., 2016). *Melanopsamma tongrenensis* can be distinguished from *M. xylophila* by its longer conidiophores (180–395 × 8–12 μm *vs*. 105–200 × 8–15 μm) and globose to subglobose, brown conidia (Lombard et al., 2016). Therefore, we introduced *M. tongrenensis* as a novel species.



Note a, b Colonies on the host. c, d Conidiophores with conidia. e Conidiogenous cells. f Conidia. g Germinated conidium. h, i Colonies on PDA. Scale bars: a, b = 200 μm, c, d = 50 μm, e–g = 10 μm.

Figure 4.161 *Melanopsamma tongrenensis* (HKAS 136899, holotype)

Memnoniella Höhn., Zentralbl. Bakt. ParasitKde, Abt. II, 60: 16. 1923

Notes: *Memnoniella* species, which exhibit morphological characteristics similar to those of Stachybotrys, are extensively studied for their ability to produce spores that thrive in humid indoor environments (Wang et al., 2015; Lin et al., 2016; Lombard et al., 2016; Tennakoon et al., 2021). They boast a worldwide distribution, occupy a variety of hosts, and are predominantly identified as saprophytic fungi (Lombard et al., 2016; Zheng et al., 2019; Tennakoon et al., 2021; Yeh et al., 2023). Currently, sixteen species are listed in Species Fungorum (2024), with some, including *M. alishanensis*, *M. celtidis* and *M. mori* being associated with medicinal plants (Tennakoon et al., 2021). In this study, we reported one new species, two new records and two new collections in this genus.

Memnoniella alishanensis Tennakoon, C.H. Kuo & K.D. Hyde, Fungal Diversity: [168] (2021)

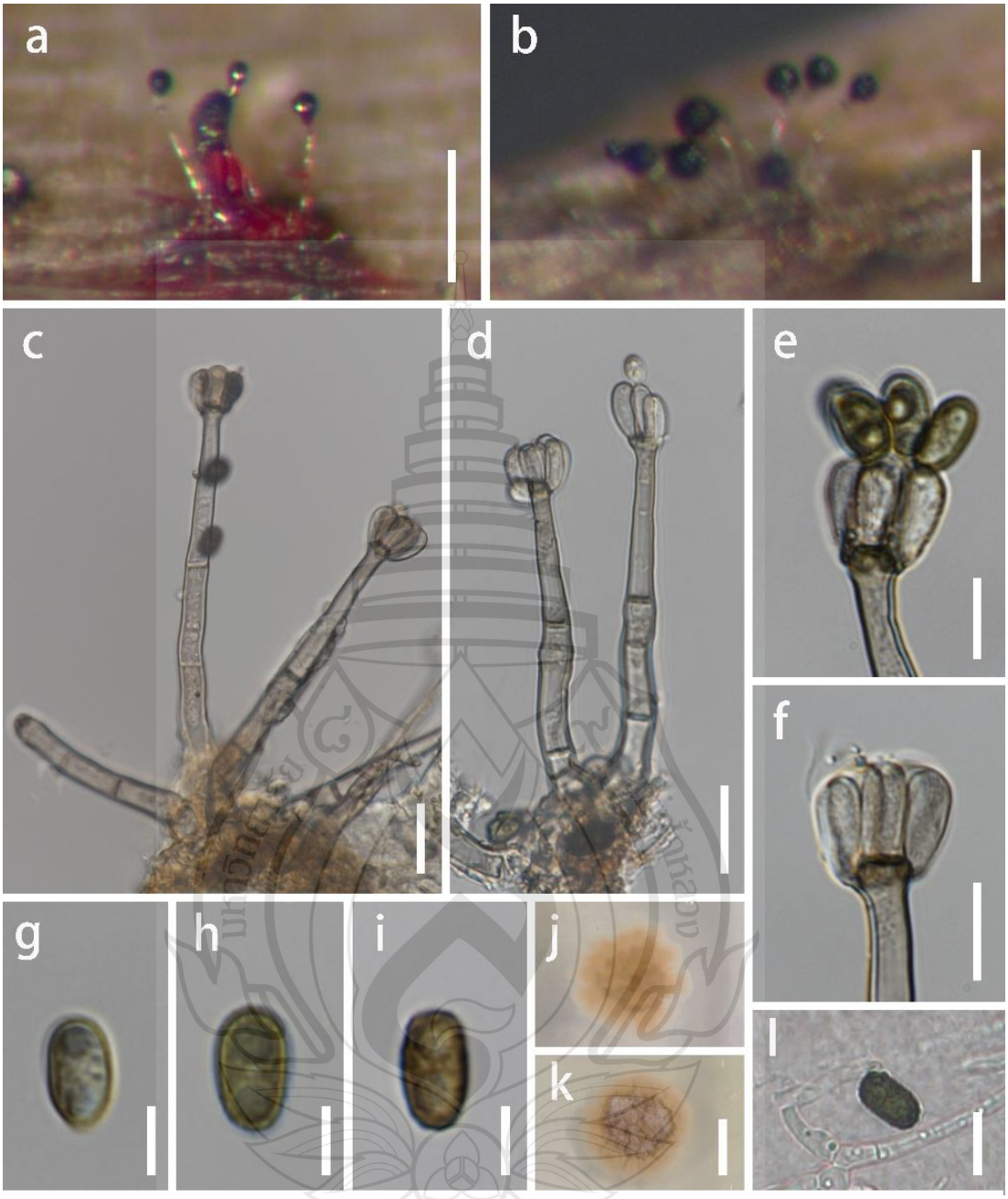
Index Fungorum number: IF555612; Facesoffungi number: FoF 09365; Figure 4.162

Saprobic on steam of *Dendrobium nobile*. **Sexual morph** Not observed. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate effuse, velvety, dark. *Conidiophores* single or in groups, mononematous, macronematous, erect, straight to slightly flexuous, unbranched, hyaline, 2-3-septate, bearing at its apex a whorl of 4–6 conidiogenous cells, 100–125 µm long, 2–4.5 µm wide. *Conidiogenous cells* monophialidic, terminal, integrated, determinate, hyaline, smooth, clustered at the apex of conidiophores, elongate doliiform to subcylindrical, reniform, 8–15 µm long. *Conidia* acrogenous, reniform, hyaline or olivaceous when young, brown or dark brown when mature, aseptate, with two globules, 11–13 × 4–6 µm ($\bar{x}$ = 12 × 5 µm, n = 30).

Culture characters: Conidia germinated on PDA within 12 hours. Colonies reached about 4 cm diameter after 3 weeks on PDA at 26°C. Mycelia are superficial, center is brown, outer ring is orange from above, orange from below.

Material examined: CHINA, Guangxi Province, Nanning City, on twigs of *Dendrobium nobile*, 14 September 2019, Y.R. Sun, G18 (HGUP 24-0069); living culture MFLUCC 24-0316.

Notes: *Memnoniella alishanensis* was reported on dead leaves of *Macaranga tanarius* in Taiwan Province, China (Tennakoon et al., 2021). Our collection clustered together with *M. alishanensis* by high support (ML-bs = 100%, BYPP = 1) in the phylogenetic tree (Figure 4.172). In morphology, these two collections share similar morphology in having macronematous, mononematous, erect conidiophores, elongate doliiform to clavate, hyaline to subhyaline conidiogenous cells and aseptate, reniform, verrucose, olivaceous to dark brown conidia (Tennakoon et al., 2021). They also share overlapped size range of conidiophores (100–125 µm long, 2–4.5 µm wide *vs*. 100–150 × 3–5 µm), conidiogenous cells (8–15 µm long *vs*. 7–10 × 3.5–5 µm) and conidia (11–13 × 4–6 µm *vs*. 10–12 × 5–6 µm) (Tennakoon et al., 2021). Therefore, we identified our collection as *M. alishanensis,* representing a new host record from the medicinal plant, *Dendrobium nobile.*



Note a, b Conidioma on the material surface. c, d Conidiophores attached conidia. e, f Conidiogenous cells and Conidia. g–i Conidia. j, k Colony on the PDA. l Germinated conidium. Scale bars: a, b = 100 μm, c, d = 20 μm, e, f, l = 10 μm, g–i = 5 μm.

Figure 4.162 *Memnoniella alishanensis* (HGUP 24-0069, new host record)

Memnoniella chiangmaiensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16471; Figure 4.163

Etymology: Name reflects the location, Chiang Mai Province, where this fungus was collected.

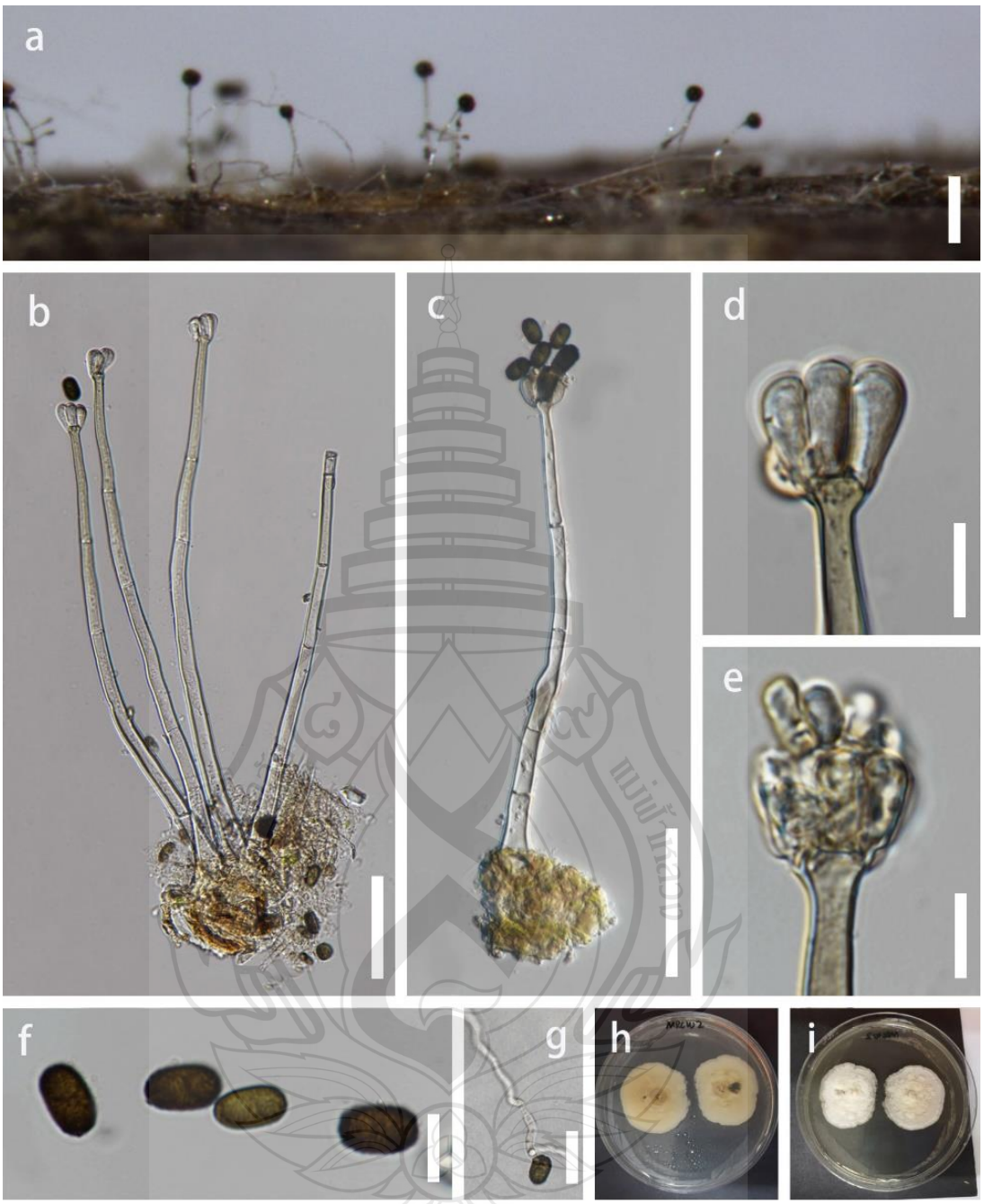
Holotype: MFLU 23-0499.

Saprobic on dead twigs of *Bidens alba*. **Sexual morph** Not observed. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate effuse, velvety, dark. *Conidiophores* single or in groups, mononematous, macronematous, erect, straight to slightly flexuous, unbranched, hyaline at lower half, hyaline to pale brown at the upper part, 2-5-septate, smooth, bearing at its apex a whorl of 4–6 conidiogenous cells, 75–274 × 5–8.5 µm ($\bar{x}$ = 189 × 7 µm, n = 10). *Conidiogenous cells* monophialidic, terminal, integrated, determinate, hyaline, smooth, clustered at the apex of conidiophores, elongate doliiform to subcylindrical, 10–14 µm long. *Conidia* acrogenous, aseptate, reniform to oval, hyaline when young, brown to dark brown when mature, verruculose, with two globules, 9–11.5 × 4.5–7 µm ($\bar{x}$ = 10 × 5.5 µm, n = 30).

Culture characters: Conidia germinated on PDA within 12 hours. Colonies reached about 4.5 cm diameter after 3 weeks on PDA at 26°C. Mycelia are superficial, flat, cotton, white from above, pale yellow from below.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Pa Pae, Mushroom Research Center, on dead twigs of *Bidens alba*, 10 September 2020, S. Wang, MRCW2 (MFLU 23-0499, **holotype**); ex-type culture MFLUCC 24-0310.

Notes: *Memnoniella chiangmaiensis* is phylogenetically related to *M. brunneoconidiophora* which was isolated from decayed leaf in Venezuela (Lombard et al., 2016) (Figure 4.172). This species can be distinguished from the latter by its hyaline to pale brown, 2-5-septate, longer conidiophores (75–274 ×5–8.5 µm *vs*. 30–45 × 3–5 µm), longer conidiogenous cells (10–14 µm *vs*. 7–11 × 3–5 µm) and larger conidia (9–11.5 × 4.5–7 µm *vs*. (6–)7.5–8.5(–9) × (3–)3.5–4.5(–5) µm) (Lombard et al., 2016). Thus, we introduced *M. chiangmaiensis* as a novel species.



Note a Conidioma on the material surface. b, c Conidiophores attached conidia. d, e Conidiogenous cells and Conidia. f Conidia. g Germinated conidium. h, i Colony on the PDA. Scale bars: a = 200 µm, b, c = 50 µm, d–f = 10 µm, g = 20 µm.

Figure 4.163 *Memnoniella chiangmaiensis* (MFLU 23-0499, holotype)

Memnoniella ellipsoidea L. Lombard & Crous, Persoonia 36: 197 (2016)

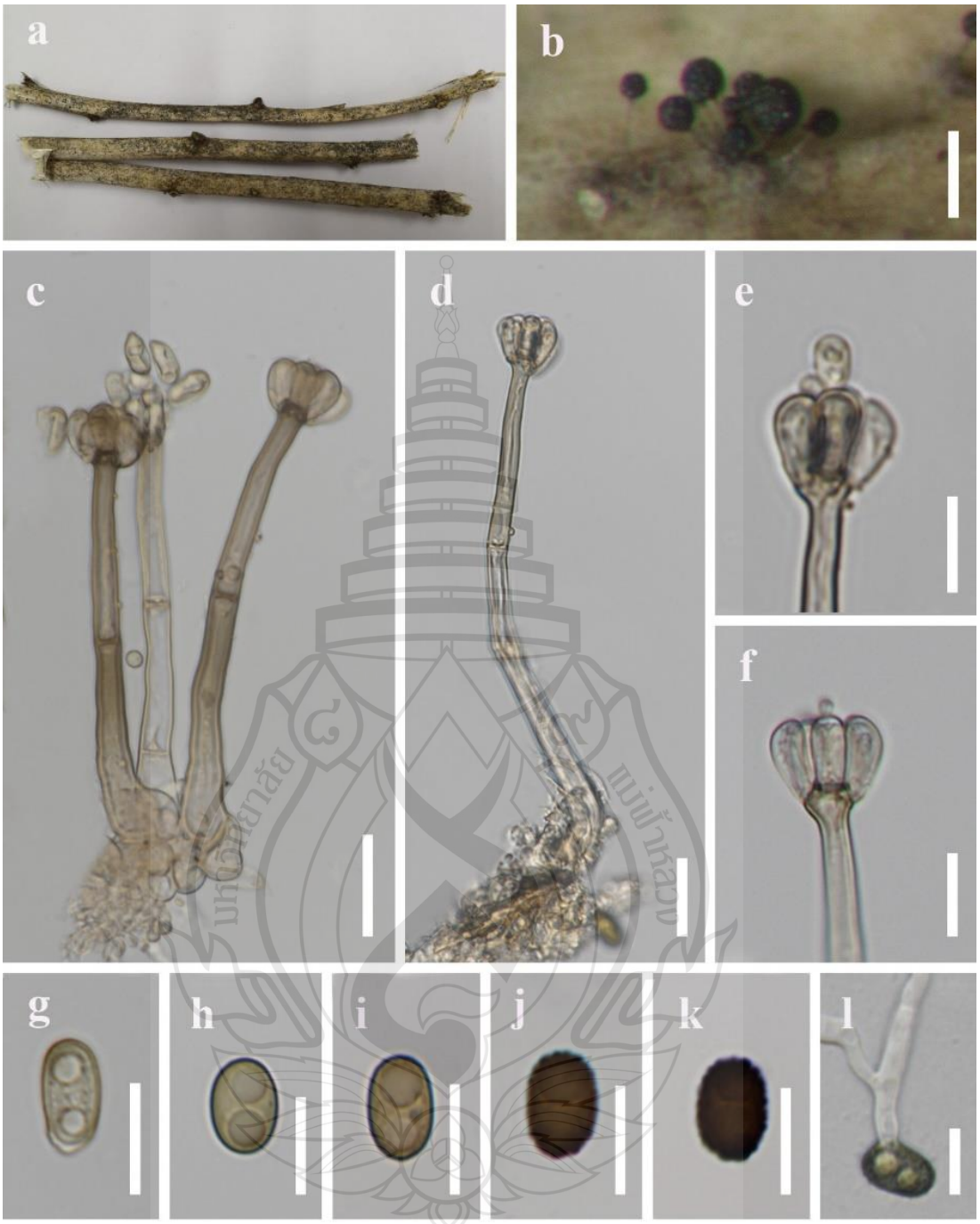
Index Fungorum number: IF 816005; Facesoffungi number: FoF xx; Figure 4.164

Saprobic on steam of *Ricinus communis*. **Sexual morph** Not observed. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate effuse, velvety, dark. *Conidiophores* single or in groups, mononematous, macronematous, erect, straight to slightly flexuous, unbranched, hyaline to pale brown, 1-2-septate, smooth, bearing at its apex a whorl of 4–6 conidiogenous cells, 45–160 ×4.5–7 µm ($\bar{x}$ = 89 × 5.5 µm, n = 20). *Conidiogenous cells* monophialidic, terminal, integrated, determinate, hyaline, smooth, clustered at the apex of conidiophores, elongate doliiform to subcylindrical, 8–13.5 µm long. *Conidia* acrogenous, aseptate, ellipsoidal, hyaline or olivaceous when young, brown to dark brown when mature, smooth when young, verruculose when mature, with two globules, 8.5–10 × 4–6 µm ($\bar{x}$ = 9 × 5 µm, n = 40).

Culture characters: Conidia germinated on PDA within 12 hours. Colonies reached about 4.5 cm diameter after 3 weeks on PDA at 26°C. Mycelia are superficial, center is white, outer ring is orange from above, yellow to orange from below.

Material examined: THAILAND, Nan City, on steam of *Ricinus communis*, 14 January 2020, Y.R. Sun, NFB6 (MFLU 23-0498); living culture MFLUCC 24-0309.

Notes: *Memnoniella ellipsoidea* was reported from *Bromelia* sp. in Brazil (Lombard et al., 2016). Our collection shares similar morphology with *M. ellipsoidea* in having hyaline to pale brown, 1–2-septate, unbranched conidiophores, monophialidic, terminal, hyaline, subcylindrical conidiogenous cells and acrogenous aseptate, ellipsoidal conidia (Lombard et al., 2016). These two strains also share an overlapping size range of conidiophores (45–160 × 4.5–7 µm *vs*. 55–140 × 4–8 µm), conidiogenous cells (8–13.5 µm long *vs*. 8–12 × 4–6 µm) and conidia (8.5–10 × 4–6 µm *vs*. 8.5–9.5 × 4.5–5.5 µm) (Lombard et al., 2016). In phylogenetic analyses (Figure 4.172), these two strains clustered together with high support (ML-bs = 99%, BYPP = 1). Therefore, we identified our collection as *M. ellipsoidea,* representing a new record isolated from *Ricinus communis* in Thailand.



Note a Host. b Conidioma on the material surface. c, d Conidiophores. e, f Conidiogenous cells and Conidia. g–k Conidia. l Germinated conidium. Scale bars: b = 100 μm, c, d = 20 μm, e–j = 10 μm.

Figure 4.164 *Memnoniella ellipsoidea* (MFLU 23-0498, new host record)

Memnoniella levispora Subram., J. Indian bot. Soc. 33: 40 (1954)

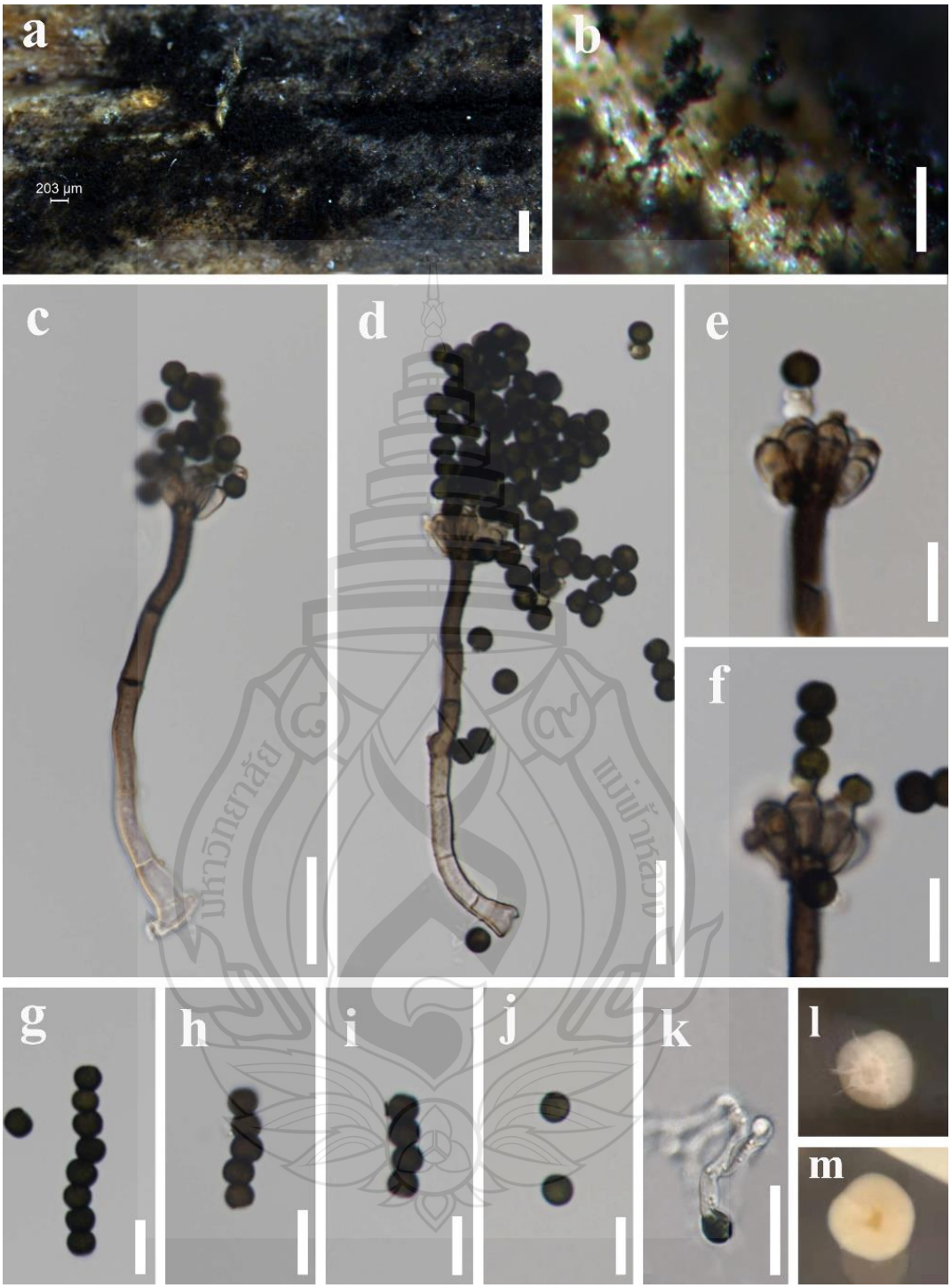
Index Fungorum number: IF555612; Facesoffungi number: FoF01874; Figure 4.165

Saprobic on dead twigs. **Sexual morph**: Not observed. **Asexual morph**: colonies on the substrate surface, gregarious, scattered, superficial, black, powdery and bouquet-like. *Conidiophores* macronematous, straight or flexuous, unbranched, bearing a crown of phialides at the apex, pale brown at lower half, brown to dark brown at the upper part, thick-walled, 3–6-septate, 41–90 × 4–6.5 µm ($\bar{x}$ = 67 × 4 µm, n = 15). *Conidiogenous cells* monophialidic, terminal, integrated, determinate, pale to brown, smooth, clustered at the apex of conidiophores, doliiform or reniform, 6–11.5 × 3.5–4.5 µm ($\bar{x}$ = 8 × 4 µm, n = 20). *Conidia* 4.5–6 × 4–5.5 µm ($\bar{x}$ = 5.5 × 5 µm, n= 25), in unbranched chains, simple, spherical to subspherical, dark brown to black, smooth.

Culture characteristics: Conidia germinated on PDA after 12 h. Colonies reaching 20 mm diameter after 3 weeks at 25 °C, circular, flat or effuse, fluffy, medium sparse, aerial, white from above, pale yellowish from below.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Pa Pae, Mushroom Research Center, on dead twigs, 15 July 2020, Y.R Sun, M30 (HGUP 24-0022); living culture MFLUCC 24-0312.

Notes: *Memnoniella levispora* was initially described by Subramanian (1954). Wang et al. (2015) synonymised *Memnoniella* under *Stachybotrys* and treated *M. levispora* as *Stachybotrys levisporus.* However, Lombard et al. (2016) resurrected *Memnoniella* and accepted *M. levispora* based on multigene phylogenetic analysis. *Memnoniella levispora* has been reported in China, Cuba, India, Pakistan and Thailand from different plants (Barrios & Pérez, 2005; Doilom et al., 2017; Samarakoon et al., 2021). In this study, our isolate clustered together with *M. levispora* by high support in the phylogenetic tree (Figure 4.172). They also share similar morphological characteristics, including shape and size (Doilom et al., 2017). Thus, we identified our collection as *M. levispora.*



Note a, b Conidioma on the material surface. c, d Conidiophores attached conidia. e, f Conidiogenous cells and Conidia. g–j Conidia. k Germinated conidium. l, m Colony on the PDA. Scale bars: a = 500 µm, b = 100 µm, c, d, k = 20 µm, e–j = 10 µm.

Figure 4.165 *Memnoniella levispora* (HGUP 24-0022)

Myxospora L. Lombard & Crous, Persoonia 36: 202 (2016)

Notes: Lombard et al. (2016) introduced *Myxospora* based on morphology and phylogenetic analyses, designating *M. masonii* as the type species. The genus is characterized by cylindrical to pyriform, unbranched synnemata with an olive-brown to brown head, macronematous, verticillately or penicillately or straight, branched, hyaline to pale brown conidiophores, phialidic, hyaline, cylindrical to subcylindrical conidiogenous cells and aseptate, fusiform, hyaline to pale brown conidia. Thick-walled, septate, flexuous, subhyaline Setae can observed in the culture (Lombard et al., 2016; Vieto et al., 2022). Currently, seven species are accepted in this genus (Species Fungorum, 2024).

Myxospora poaceicola Y.P. Chen, Z.H. Lu & Maharachch., Phytotaxa 625(3): 283 (2023)

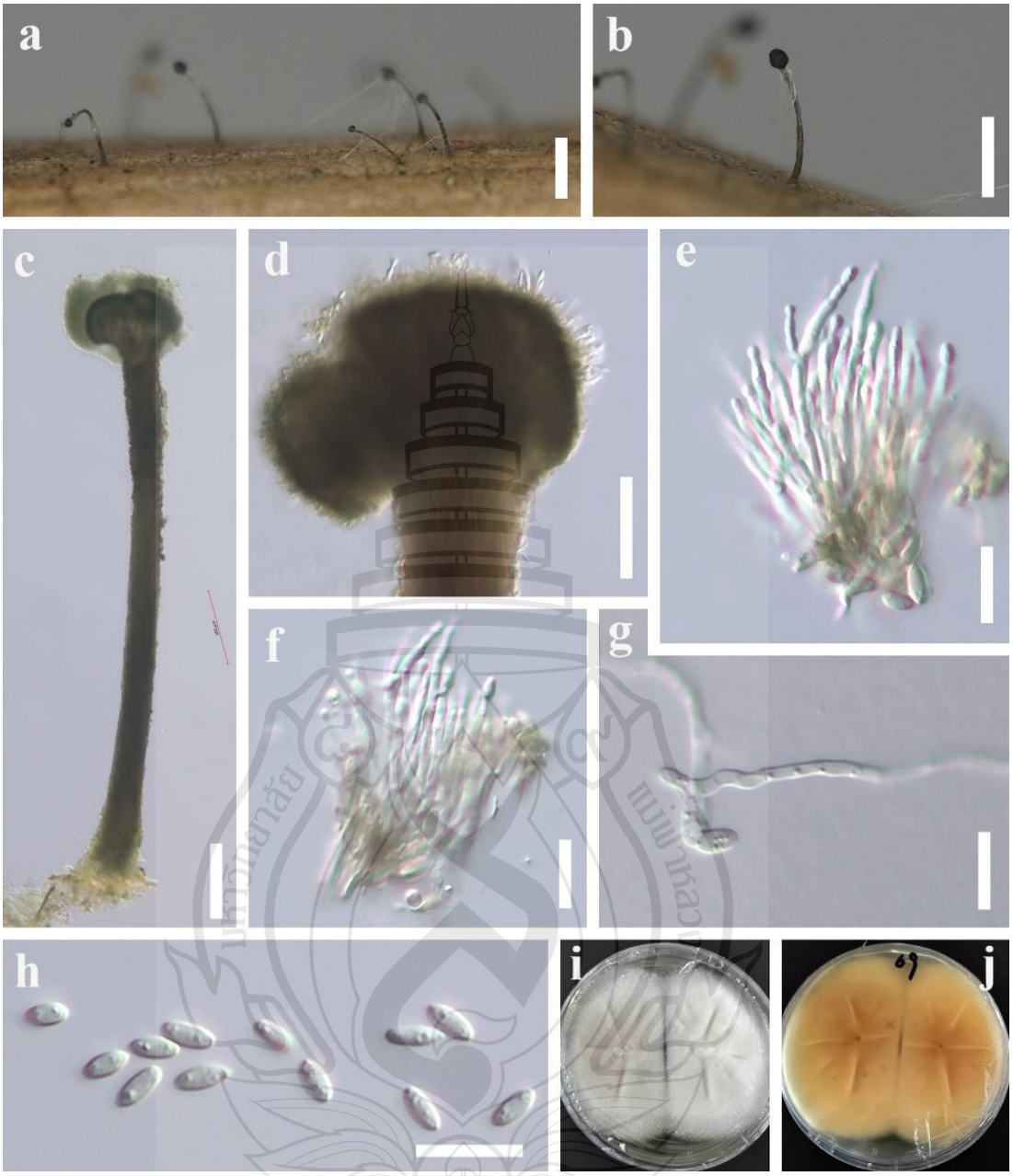
Index Fungorum number: IF555612; Facesoffungi number: FoF01874; Figure 4.166

Saprobic on stems and leaves of Poaceae. **Asexual morph**: *Conidiamata* synnematous, solitary, straight to slightly flexuous, unbranched, consisting of bundles of parallel, longitudinal, closely compacted hyphae, terminating with an olive brown head composed of conidiogenous cells and conidia, 714–1,000 μm long, 34–50 μm wide. *Conidiophores* subcylindrical, hyaline, septate, bunched forming synnemata. *Conidiogenous cells* around 1 μm wide, phialidic, cylindrical, hyaline, with conspicuous collarettes, smooth. *Conidia* 4–6 μm long, around 2 μm wide, fusiform, hyaline to pale brown, aseptate, with two granular protrusions. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinated on PDA within 12 h. Colonies reaching 8 cm diameter after 3 weeks at 25 °C, circular, flat, edge entire, white to gray from above, light brown from below.

Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on decaying culm of Poaceae, 14 April 2023, Y.R. Sun, 2369 (HGUP 24-0023); living culture GUCC 24-0115.

Notes: *Myxospora poaceicola* was introduced by Chen et al. (2023), which was isolated from Poaceae plant in Sichuan Province, China. Similarly, our collection was also isolated from a Poaceae plant in China. In phylogenetic analyses (Figure 4.172), these two collections clustered together with high support (ML-bs = 100%, BYPP = 1). Our collection shares similar morphological characters to *M. poaceicola,* having synnematous, solitary, straight to slightly flexuous, unbranched conidiamata, phialidic, cylindrical, hyaline conidiogenous cells and aseptate, hyaline conidia (Chen et al., 2023). However, our collection exhibits fusiform conidia measuring 4–6 μm in length, whereas the latter has short cylindrical conidia measuring 6–8 × 2–4 μm. These subtle differences in conidia may reflect geographical variations. All in all, we identified our collection as *M. poaceicola.*



Note a, b Conidioma on the material surface. c Conidiophores attached conidia. d–f Conidiogenous cells and Conidia. g Germinated conidium. h Conidia. i, j Colony on the PDA. Scale bars: a, b = 500 μm, c = 100 μm, d = 50 μm, e–h = 10 μm.

Figure 4.166 *Myxospora poaceicola* (HGUP 24-0023)

Paramyrothecium L. Lombard & Crous, Persoonia 36: 206 (2016)

Notes: *Paramyrothecium* was introduced by Lombard et al. (2016) with *P. roridum* as the type species. *Paramyrothecium* species have a wide range of habitats, distributed in Brazil, China, India, Namibia, Netherlands, Philippines and Thailand (Lombard et al., 2016; Matić et al., 2019; Aumentado & Balendres, 2022; Pinruan et al., 2022; Armand et al., 2023). They generally comprise common soil-inhabiting and saprophytic fungi (Lombard et al., 2016). Some species cause plant leaf diseases and caused economic losses, such as *P. amorphophalli*, *P. eichhorniae* and *P. foliicola* (Matić et al., 2019; Aumentado & Balendres, 2022; Pinruan et al., 2022). *Paramyrothecium roridum*, an endophytic fungus isolated from the medicinal plant, *Morinda officinalis*, which can produce secondary metabolites with anti-tumor activity (Liu et al., 2020). Currently, 22 species are accepted in this genus (Species Fungorum, 2024). In this study, we collected *Paramyrothecium acadiense* from twigs of an unknown plant.

Paramyrothecium acadiense (Seifert & G. Sampson) L. Lombard & Crous, Persoonia 36: 206 (2016)

≡ *Myrothecium acadiense* Seifert & G. Sampson, Mycotaxon 87: 320. 2003.

Index Fungorum number: IF 815945; *Facesoffungi number:* FoF 16472; Figure 4.167

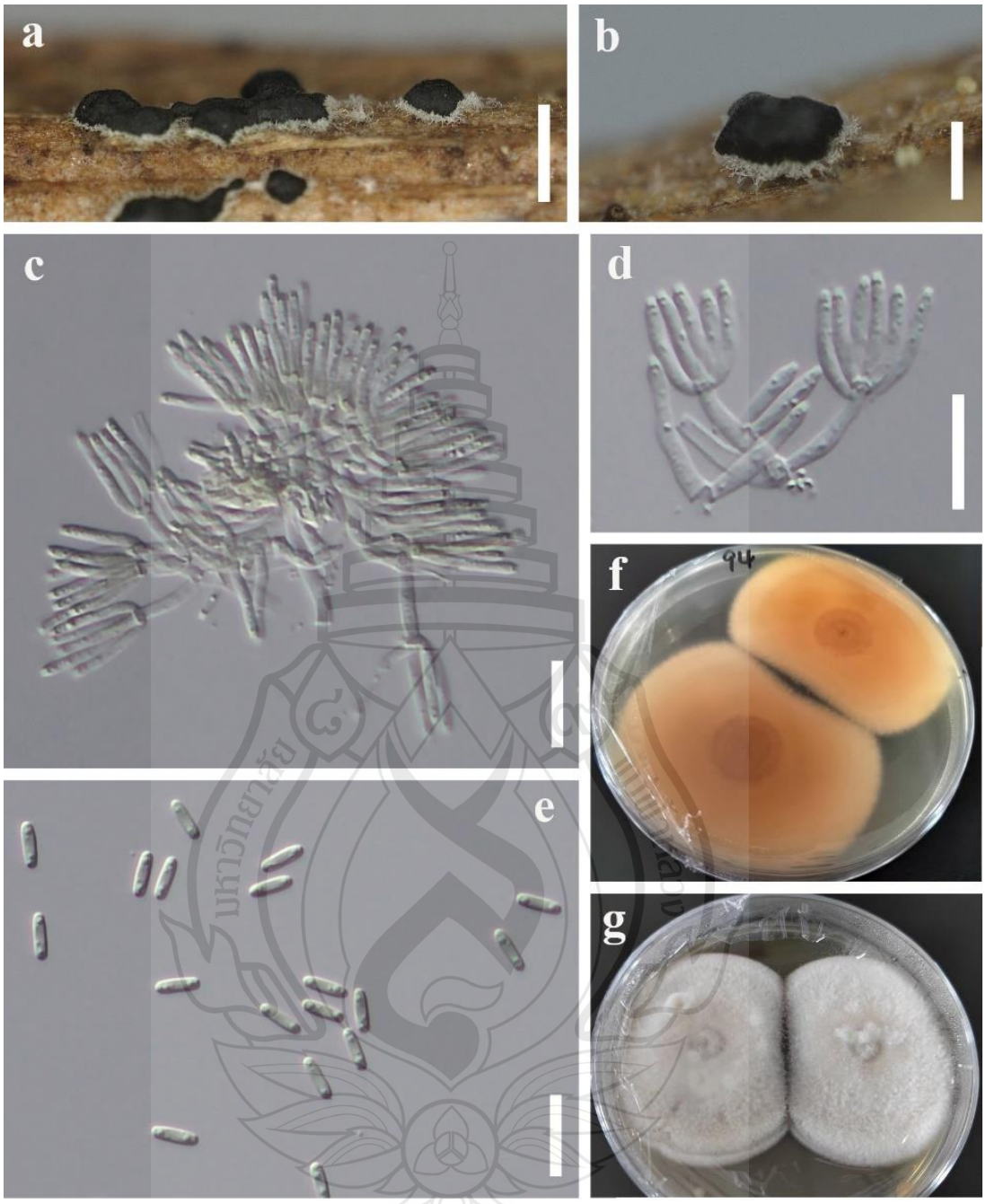
Saprobic on dead twigs. **Sexual morph**: Unknown. **Asexual morph**: *Colonies* on natural substrate effuse, black, scattered or gregarious. *Mycelium* partly immersed, partly superficial, composed of hyaline, branched, septate, smooth hyphae. *Conidiomata* stromatic, pulvinate, with a shiny white margin generally visible around the conidial mass. *Conidiophores* arising from the basal stroma, composed of a stipe and a penicillately branched conidiogenous apparatus; stipe cylindrical, hyaline, aseptate, thin-walled; conidiogenous apparatus composed of 4–6 conidiogenous cells. *Conidiogenous cells* 8–14 × 1–2 µm ($\bar{x}$ = 10.5 × 1.5 µm, n = 30), phialidic, discrete, cylindrical, hyaline, tinily guttulate, with inconspicuous collarettes and periclinal thickenings. *Conidia* 5–6 × 1–2 µm ($\bar{x}$ = 5.5 × 1.5 µm, n = 50), aggregated to black conidial mass above the conidiomata, solitary, oblong

with obtuse ends, hyaline to subhyaline, aseptate, with two small, polar guttules, smooth.

Culture characteristics: Conidia germinated on PDA within 12 hours at 25 °C. Colony reached 8 cm diameter after 4 weeks on PDA media. Mycelia superficial, irregularly circular, entire edge, cotton, flat, white to cream from above, orange to pale brown from below.

Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on dead twigs, 14 April 2023, Y.R. Sun, 2394 (HKAS 136890); living culture GUCC 24-0113.

Notes: Seifert et al. (2003) introduced *Myrothecium acadiense* from lesions of *Tussilago farfara* in Canada. Lombard et al. (2016) regarded that this species is phylogenetically distinct from *Myrothecium s. str.* thus, introduced a new genus, *Paramyrothecium*, and transferred *M. acadiense* to the new genus as *Paramyrothecium acadiense*. Our new collection clustered with *P. acadiense* with high statistical support (ML-bs = 97%, BYPP = 1) in the phylogenetic tree (Figure 4.172). In morphology, both species share similar characteristics. We identified our strain as *P. acadiense,* representing a new geographical record in China.



Note a, b Conidioma on the material surface. c, d Conidiogenous cells. e Conidia. f, g Colony on the PDA. Scale bars: a = 500 μm, b = 200 μm, c–e = 10 μm.

Figure 4.167 *Paramyrothecium acadiense* (HKAS 136890, new record)

Paramyrothecium xishuiense Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16473; Figure 4.168

Holotype: HKAS 136891.

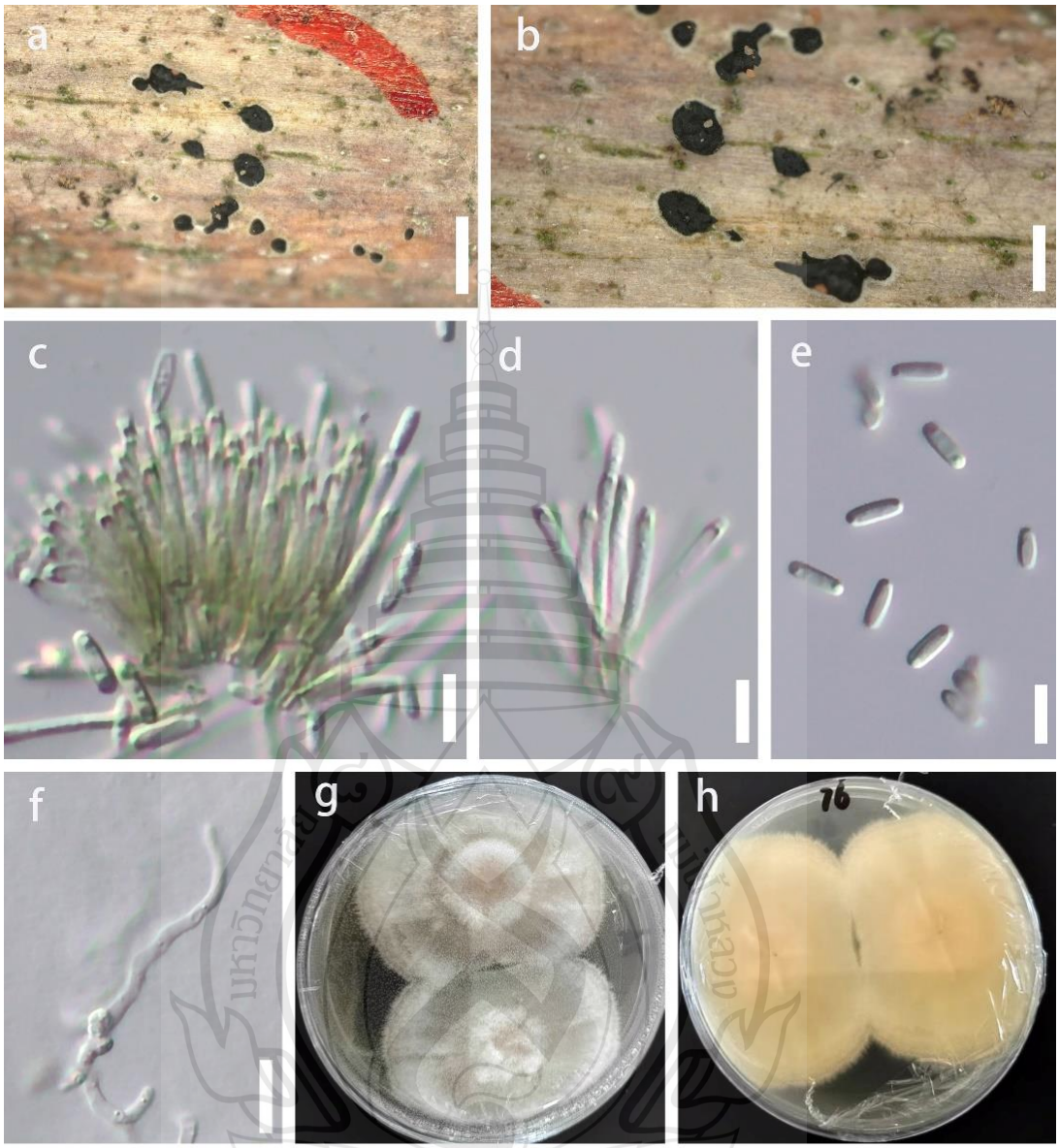
Etymology: Name reflects the location where the fungus was collected.

Saprobic on dead twigs. **Sexual morph**: Unknown. **Asexual morph**: *Colonies* on natural substrate effuse, dark green, scattered or gregarious. *Conidiomata* stromatic, pulvinate, with a shiny white margin generally visible around the conidial mass. *Conidiophores* arising from the basal stroma, hyaline to olive green, composed of a stipe and a penicillately branched conidiogenous apparatus; stipe cylindrical, aseptate, thin-walled; conidiogenous apparatus composed of 4–6 conidiogenous cells. *Conidiogenous cells* 10–17 × 1–2 μm ($\bar{x}$ = 10.5 × 1.5 μm, n = 30), phialidic, discrete, cylindrical, hyaline, tinily guttulate, with inconspicuous collarettes and periclinal thickenings. *Conidia* aggregated to dark green conidial mass above the conidiomata, solitary, oblong with obtuse ends, hyaline, aseptate, with two small, polar guttules, smooth, 3.5–5 × 1–2 μm ($\bar{x}$ = 4.5 × 1.5 μm, n = 40).

Culture characteristics: Conidia germinated on PDA within 12 hours at 25 °C. Colony reached 9 cm diameter after 4 weeks on PDA media. Mycelia superficial, circular, entire edge, cotton, raised, white from above, light yellow from below.

Material examined: CHINA, Guizhou Province, Zunyi City, Xishui County, Xishui National Nature Reserve, on decaying twigs, 14 April 2023, Y.R. Sun, 2376 (HKAS 136891, **holotype**); ex-type culture GUCC 24-0114.

Notes: *Paramyrothecium xishuiense* formed a sister clade with *P. acadiense* by high support (ML-bs = 97%, BYPP = 1) in the phylogenetic tree (Figure 4.172). The two species differ morphologically in that *P. xishuiense* produces smaller conidia (3.5–5 × 1–2 μm *vs*. 5–16.5 × 1–2.5 μm) (Seifert et al., 2003). In addition, polymorphic nucleotides from the TUB sequence data showed eight base pairs (340 bp, without gap) differences. Therefore, we identified our isolate as a new species.



Note a, b Conidioma on the material surface. c, d Conidiophores, conidiogenous cells attached conidia. e Conidia. f Germinated conidium. g, h Colony on the PDA. Scale bars: a = 1000 μm, b = 500 μm, c–e = 5 μm, f = 10 μm.

Figure 4.168 *Paramyrothecium xishuiense* (HKAS 136891, holotype)

Striatibotrys L. Lombard & Crous, Persoonia 36: 224 (2016)

Notes: Lombard et al. (2016) described *Striatibotrys* based on morphology and phylogenetic analyses, designating *S. eucylindrospora* as the type species. *Striatibotrys* species have not only sexual morphs but also asexual morphs. The sexual morphs are characterized by perithecial, scattered, subglobose to obpyriform ascomata, erect, hyaline, cylindrical setae, clavate, 8-spored asci and ellipsoidal to fusiform, hyaline to orange ascospores (Lombard et al., 2016; Lechat et al., 2021). The asexual morphs have mononematous, erect, unbranched or branched conidiophores with an apical cluster of 3–6 conidiogenous cells, phialidic, clavate to subclavate conidiogenous cells and aseptate, longitudinally striate, ellipsoidal to subcylindrical to fusiform conidia (Lombard et al., 2016). So far, nine species are listed in this genus with molecular data and most isolated from soil (Lombard et al., 2016; Lechat et al., 2021; Species Fungorum, 2024).

Striatibotrys rhabdosporus L. Lombard & Crous [as 'rhabdospora'], Persoonia 36: 226 (2016)

Index Fungorum number: IF 821468; Facesoffungi number: FoF 16474; Figure 4.169

Associated with diseased branches of *Macleaya cordata*. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, velvety, black. *Conidiophores* single or in groups, mononematous, macronematous, erect, straight to slightly flexuous, unbranched, plae brown to brown, 1–3-septate, bearing at its apex a whorl of 4–6 conidiogenous cells, 60–100 µm long, 3–5 µm wide. *Conidiogenous cells* 9–13.5 × 3.5–6 µm monophialidic, terminal, integrated, determinate, pale brown, smooth, clustered at the apex of conidiophores, elongate doliiform to subcylindrical, reniform. *Conidia* developing in basipetal chains, acrogenous, fusiform, brown, aseptate, longitudinally striate, with two globules, 9–13 ×3–4.5 µm ($\bar{x}$ = 11.5 × 4 µm, n = 30).

Culture characteristics: Conidia germinated on PDA within 12 hours. Colonies reached about 2.5 cm diameter after 3 weeks on PDA at 26°C, superficial, circular, flat, brown from above and below.

Material examined: CHINA, Guizhou, Guiyang, Nanming district, Guiyang medicinal botanical garden, on diseased branched of Macleaya cordata, 22 December 2021, Y.R. Sun, 22-22 (HKAS 136877); living culture GUCC 24-0112.

Notes: Our strain clustered together with *Striatibotrys rhabdospora* in the phylogenetic tree (Figure 4.172). In morphology, our strain shares similar morphology with *S. rhabdospora* in having macronematous, mononematous, erect, 1–3-septate conidiophores, phialidic, clavate conidiogenous cells and aseptate, fusiform, brown, longitudinally striate conidia (Lombard et al., 2016). They also share overlapped size range of conidiophores (60–100 µm long, 3–5 µm wide *vs*. 50–70 × 4–6 µm), conidiogenous cells (9–13.5 × 3.5–6 µm *vs*. 8–10 × 4–6 µm) and conidia (9–13 × 3–4.5 µm *vs*. 9.5–10.5 × 3–4) (Lombard et al., 2016). *Striatibotrys rhabdospora* was reported from soil and Caltha palustris in Belgium, Spain and USA (Lombard et al., 2016). Therefore, we identified our strain as *S. rhabdospora*, representing a new record from the medicinal plant, *Macleaya cordata*, in China.



Note a Host. b Conidioma on the material surface. c, d Conidiophores with conidiogenous cells. e, f Conidiogenous cells. g–j Conidia. k Germinated conidium. l, m Colony on the PDA. Scale bars: c, d = 20 µm, e, f, k = 10 µm, g–j = 5 µm.

Figure 4.169 *Striatibotrys rhabdospora* (HKAS 136877, new host and geographical record)

Striaticonidium L. Lombard & Crous, Persoonia 36: 227 (2016)

Notes: Lombard et al. (2016) established *Striaticonidium* to accommodate myrothecium-like species which have phialidic, hyaline, cylindrical to subcylindrical conidiogenous cells, and aseptate, fusiform to ellipsoidal, olivaceous green to brown, longitudinally striate conidia with an apical hilum. Currently, five species are accepted in this genus with their asexual morph. Among them, *S. brachysporum*, *S. cinctum* are associated with medicinal plants (Lombard et al., 2016; Crous et al., 2017; Species Fungorum, 2024). In this study, we described one new species, *S. olivaceobrunneum,* in Thailand.

Striaticonidium olivaceobrunneum Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16475; Figure 4.170

Etymology: Name reflects the olive brown conidia.

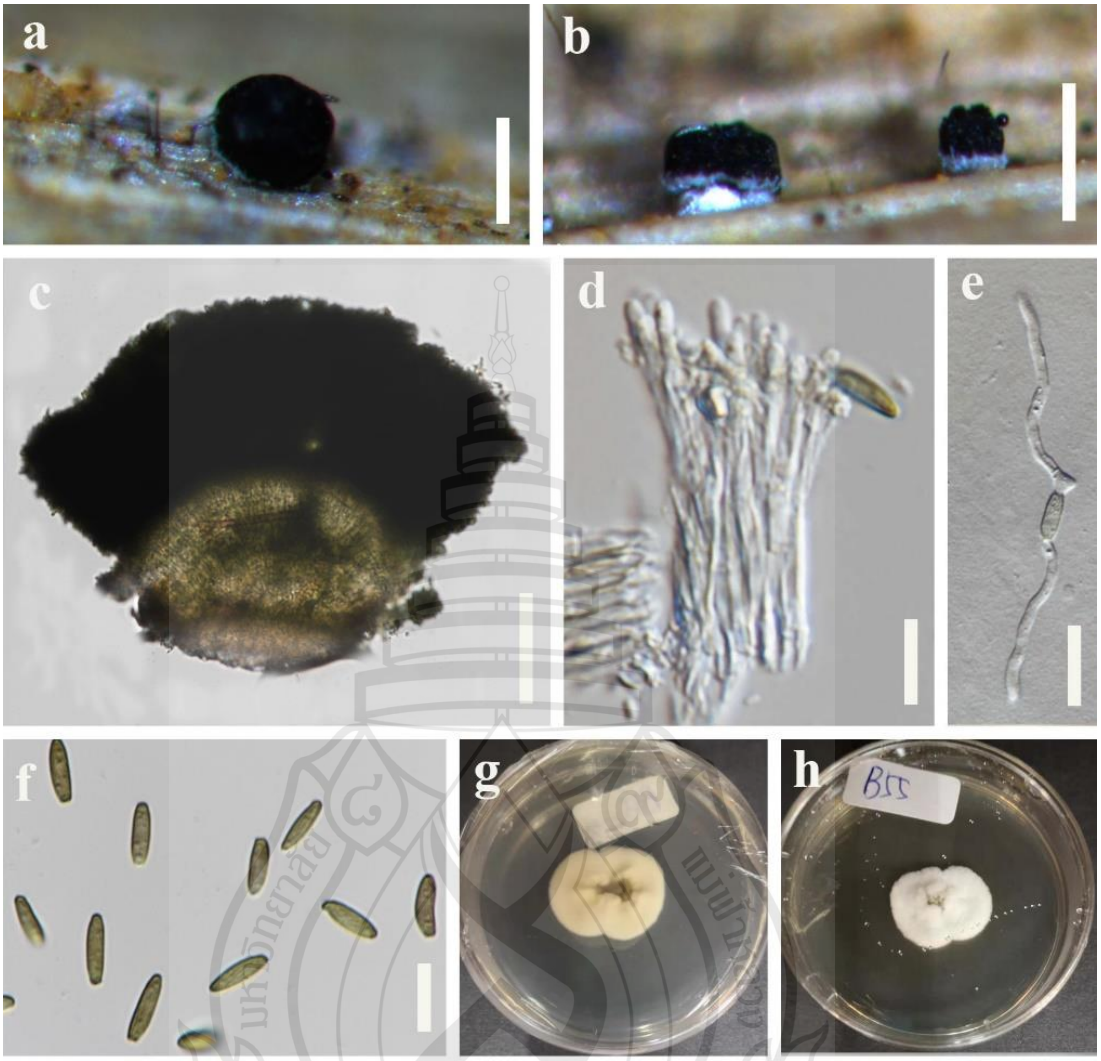
Holotype: MFLU 23-0494.

Saprobic on leaves of grass. **Asexual morph**: Hyphomycetes. *Conidiomata* synnematous, solitary, 100–150 μm high, 96–229 μm wide, cylindrical, unbranched, consisting of bundles of parallel, longitudinal, closely compacted hyphae, enclosed by marginal hyphae arising from the stroma and covered by a dark green slimy mass of conidia. Marginal hyphae 2–3 μm wide, sinuous, unbranched to rarely branched, hyaline to olivaceous green, verrucose. Stroma well developed, hyaline, of textura globulosa and textura angularis. *Conidiogenous cells* monophialidic, cylindrical to subcylindrical, hyaline, smooth, 1–2.5 μm wide, with periclinal thickenings. *Conidia* aseptate, fusiform, hyaline to light green when young, olive-brown when mature, longitudinally striate, granular on the surface, 8–12 × 2–3.5 μm ($\bar{x}$ = 9.5 × 3 μm, n = 40), with an apical hilum. **Sexual morph**: Not observed.

Culture characteristics: Conidia germinated on PDA within 12 h. Germ tubes were produced from both ends. Colonies reaching 20 mm diameter after 3 weeks at 25 °C, circular, flat, entire, white from above, light yellow from below.

Material examined: THAILAND, Chiang Rai Province, Mae Fah Luang University, Garden of Medicinal Plants, on leaves of grass (Poaceae), 11 November 2019, Y.R. Sun, B55 (MFLU 23-0494, **holotype**); ex-type culture MFLUCC 24-0305.

Notes: Our new collection forms a sister clade to *Striaticonidium synnematum* (which was isolated from the leaf of a palm in Japan) in the phylogenetic tree (Figure 4.172) (Lombard et al., 2016). The two species differ morphologically in that our strain produces the larger conidiomata (100–150 μm high, 96–229 μm wide *vs*. 50–85 μm high, 35–70 μm wide at the base, 45–85 μm at the apex) and larger conidia (8–12 × 2–3.5 μm *vs*. 7–8 × 2–3 μm) (Lombard et al., 2016). In addition, polymorphic nucleotides from the TUB and CAL sequence data showed eleven (345 bp, without gap) and 39 (480 bp, without gap) base pair differences respectively. Based on distinct morphology and phylogeny, *Striaticonidium olivaceobrunneum* is introduced as a novel taxon.



Note a, b Conidiomata on the host surface. c Conidioma in the slide. d Conidia attached to conidiogenous cells. e Germinated conidium. f Conidia. g, h Colony on the PDA (g from below, h from above). Scale bars: a, b = 200 µm, c = 100 µm, d, f = 10 µm, e = 20 µm.

Figure 4.170 *Striaticonidium olivaceobrunneum* (MFLU 23-0494, holotype)

Virgatospora Finley, Mycologia 59(3): 538 (1967)

Notes: Finley (1967) introduced *Virgatospora*, designating *V. echinofibrosa* as the type species. The characteristics of this genus have effuse, erect colonies, synnematous, scattered, erect, straight or slightly flexuous conidiomata, monophialidic, terminal, integrated, cylindrical, hyaline conidiogenous cells and aseptate or septate, simple, oval to fusiform conidia (Finley, 1967; D'Souza et al., 2002). Currently, only two species are accepted in this genus (Species Fungorum, 2024). In this study, we described one new species, namely, *Virgatospora thailandica*, isolated from branches of Poaceae plant in China.

Virgatospora thailandica Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16476; Figure 4.171

Etymology: Name reflects the location, Thailand, where this fungus was collected.

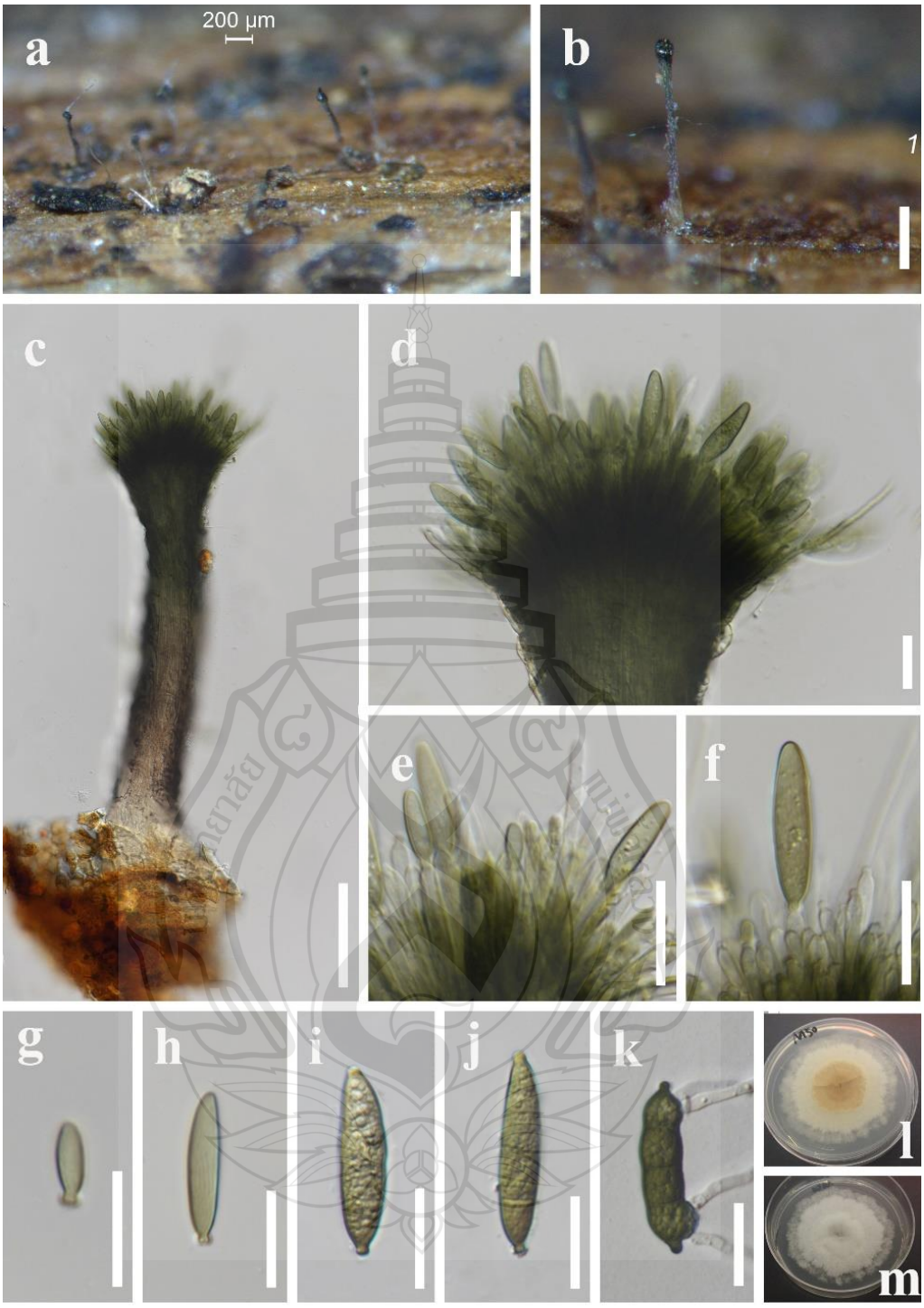
Holotype: MFLU 23-0495.

Saprobic on branches of Poaceae plant. **Asexual morph**: Hyphomycetes. *Colonies* effuse, olivaceous black, composed of a number of irregularly scattered erect, gray, synnematal conidiomata with dark green slimy heads. *Mycelium* immersed, composed of smooth, septate, branched, hyaline hyphae. *Conidiomata* synnematous, scattered, erect, straight or slightly flexuous, dark green, slight swollen at the base and apex, up to 460 μm long, around 60 μm wide. *Conidiophores* macronematous, septate, unbranched or branched, straight or flexuous, smooth, thin-walled, green to dark green. *Conidiogenous cells* monophialidic, terminal, integrated, smooth, cylindrical, hyaline to pale green, 1–3 μm wide. *Conidia* aggregated in large, dark green masses, acrogenous, simple, fusiform, thin-walled, pale green, aseptate at young, dark green, 1–3 septate at mature, slightly contracted at the septate, 24–44 × 4.5–10 μm ($\bar{x}$ = 35 × 7.5 μm, n = 20). **Sexual morph**: Not observed.

Culture characteristics: Conidia germinated on PDA within 12 h. Colonies reaching 5 cm diameter after 3 weeks at 25 °C, circular to irregular, raised, undulate, white from above, pale orange in the center and white around the outer edge from below.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Pa Pae, Mushroom Research Center, on dead branches of Poaceae plant, 15 July 2020, Y.R Sun, M50 (MFLU 23-0495, **holotype**); ex-type culture MFLUCC 24-0306.

Notes: *Virgatospora thailandica* phylogenetically grouped with *V. echinofibrosa* by high support (ML-bs = 100%, BYPP = 1) (Figure 4.172). Morphologically, *V. thailandica* exhibits conidiomata up to 460 μm in length, with smooth conidiophores and smaller conidia lacking vertical stripes, whereas *V. echinofibrosa* features conidiomata reaching up to 1.5 mm, echinulatae conidiophores, and conidia with distinct vertical stripes (Finley, 1967). *Virgatospora thailandica* distinguishes from *V. natarajanensis* (another species in *Virgatospora,* without sequence data) by its fusiform, 1–3 septate, 24–44 × 4.5–10 μm conidia without vertical stripes whereas the latter presents elliptical or fusiform, aseptate, 10–13.5 × 3.5–4.5 μm conidia with distinct longitudinal (D'Souza et al., 2002). Consequently, we propose the introduction of *V. thailandica* as a novel species.



Note a, b Conidioma on the material surface. c Conidiophores with conidiogenous cells. d–f Conidiogenous cells attached conidia. g–j Conidia. k Germinated conidium. l, m Colony on the PDA. Scale bars: a = 500 µm, b = 200 µm, c = 100 µm, d–k = 20 µm.

Figure 4.171 *Virgatospora thailandica* (MFLU 23-0495, holotype)

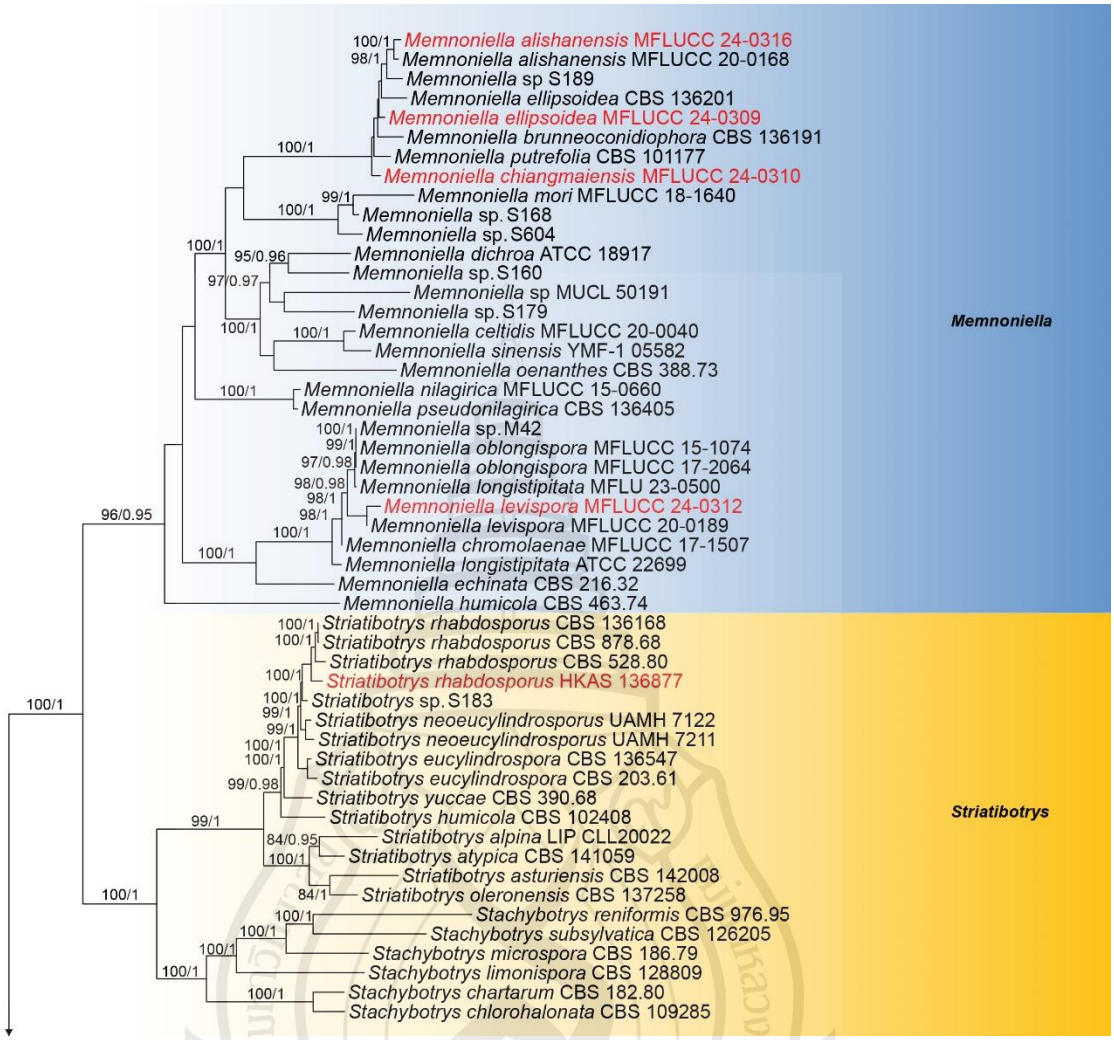
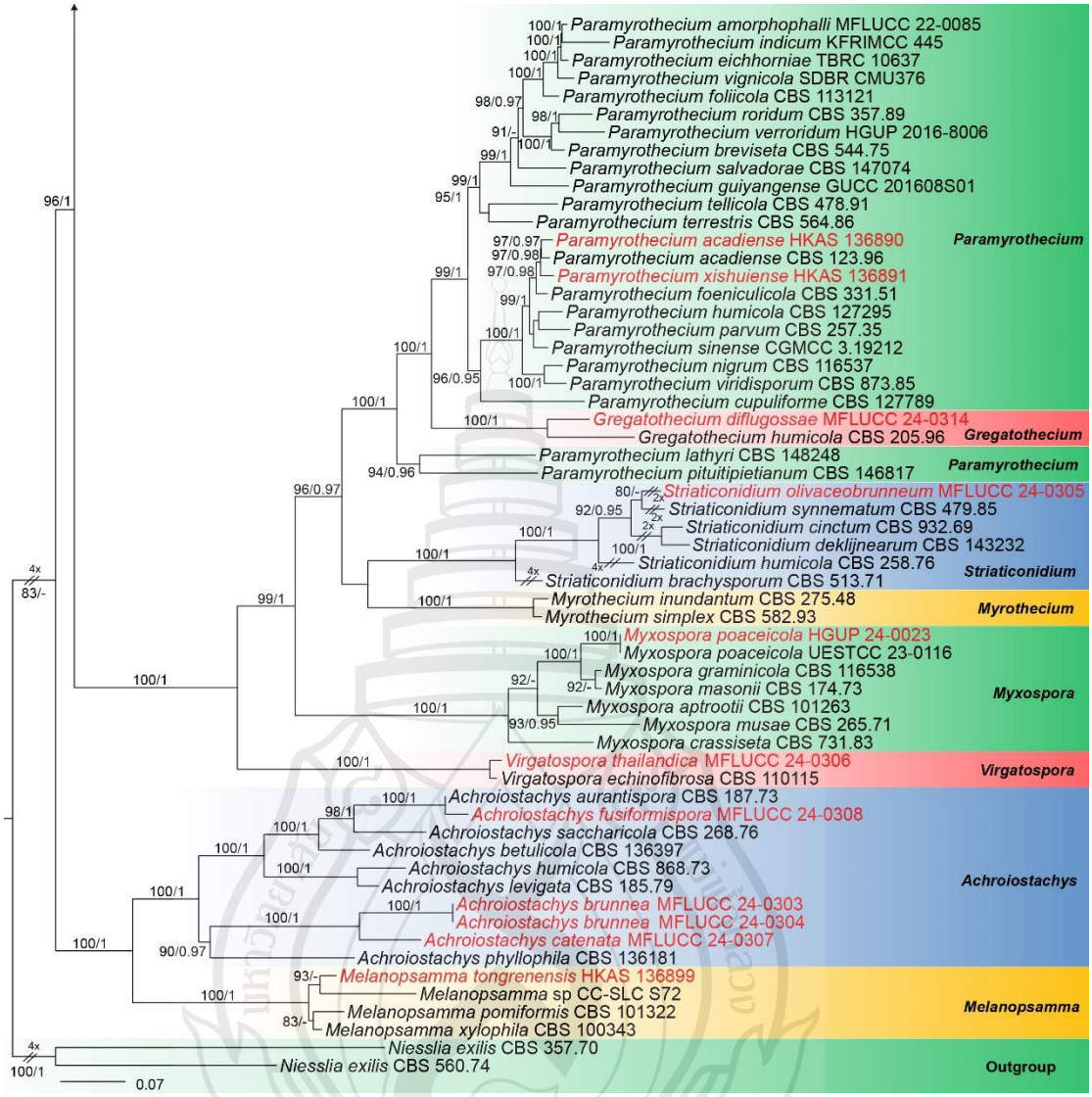


Figure 4.172 Phylogenetic tree of Stachybotryaceae



Note Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near the nodes, respectively. The tree is rooted with *Niesslia exilis* (CBS 357.70) and *N. exilis* (CBS 560.74). The new collections are indicated in red.

Figure 4.172 (continued)

Xylariales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 66 (1932)

Cainiaceae J.C. Krug Sydowia 30(1-6): 123 (1978) [1977]

Arecophila K.D. Hyde, Nova Hedwigia 63(1-2): 82 (1996)

Notes: Hyde (1996) introduced *Arecophila* in Amphisphaeriaceae based on morphology, and *A. gulubiicola* was designated as the type species. Kang et al. (1999) reviewed the genus and placed *Arecophila* in Cainiaceae. This classification opinion has been verified based on molecular analysis (Jeewon et al., 2003; Smith et al., 2003; Senanayake et al., 2015; Hyde, Norphanphoun et al., 2020; Li, Zhang et al., 2022). Currently, eighteen species are accepted in *Arecophila* but most of them lack molecular data (Li, Zhang et al., 2022; Species Fungorum, 2024). The phylogenetic analyses (Figure 4.180) showed two clades in *Arecophila*, and this phenomenon has also been reported by Li, Zhang et al. (2022). More collections and molecular data are needed to resolve this problem.

Arecophila yunanensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF902612; Facesoffungi number: FoF 14910; Figure 4.173

Etymology: Name reflects the collected site, Yunnan Province.

Holotype: HKAS 136906.

Saprobic on a bamboo culm. **Sexual morph**: *Ascomata* immersed, solitary, scattered or gregarious, subglobose to globose, with a central, erumpent, cone-shaped papilla. *Ostioles* papillate black, central., *Peridium* comprising several layers, outer layer brown, thick-walled, inner layer hyaline. *Paraphyses* 1.5–5.5 µm ($\bar{x}$ = 3 µm, n =15) wide, hyaline, unbranched, septate, verruculose. *Asci* 130–160 long, 9.5–11 µm wide, 8-spored, unitunicate, cylindrical, short-pedicellate, apically rounded, with a square-shaped, J+, apical ring. *Ascospores* 15–23 × 5–7 µm ($\bar{x}$ = 19.5 × 5.5 µm, n = 25), overlapping uniseriate, oblong with obtuse ends to oval, yellow-green to olive green when young, brown when mature, 1-septate, septum darkened, slightly constricted at the septum, with inconspicuous longitudinal wall striations, surrounded by a thick mucilaginous sheath. **Asexual morph**: Not observed.

Material examined: CHINA, Yannan Province, Kunming City, Yiliang District, Yangzonghai Garden, on bamboo culms, 20 February 2023, H.W. Shen, 2346 (HKAS 136906,

holotype); ex-type culture GUCC 24-0117.

Notes: *Arecophila yunanensis* formed a distinct branch in Clade 2 and closed to *A. bambusae* in the phylogenetic tree (Figure 4.180). In morphology, it differs from *A. bambusae* by its larger asci (130–160 µm long, 9.5–11 µm wide *vs*. 132.5–140 × 7.5–8 µm) and inconspicuous longitudinal wall striations conidia (Umali et al., 1999). Therefore, we introduced *A. yunanensis* as a novel species here.



Note a Ascomata on the surface of host b Longitudinal section of ascoma. c–e Asci. f paraphyses. g ascus apex with a J+, apical ring (stained in Melzer's reagent). h–k Ascospores. l Germinated ascospore. Scale bars: c–g, l = 20 µm, h–k = 10 µm.

Figure 4.173 *Arecophila yunanensis* (HKAS 136906, holotype)

Arecophila maolanensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16477; Figure 4.174

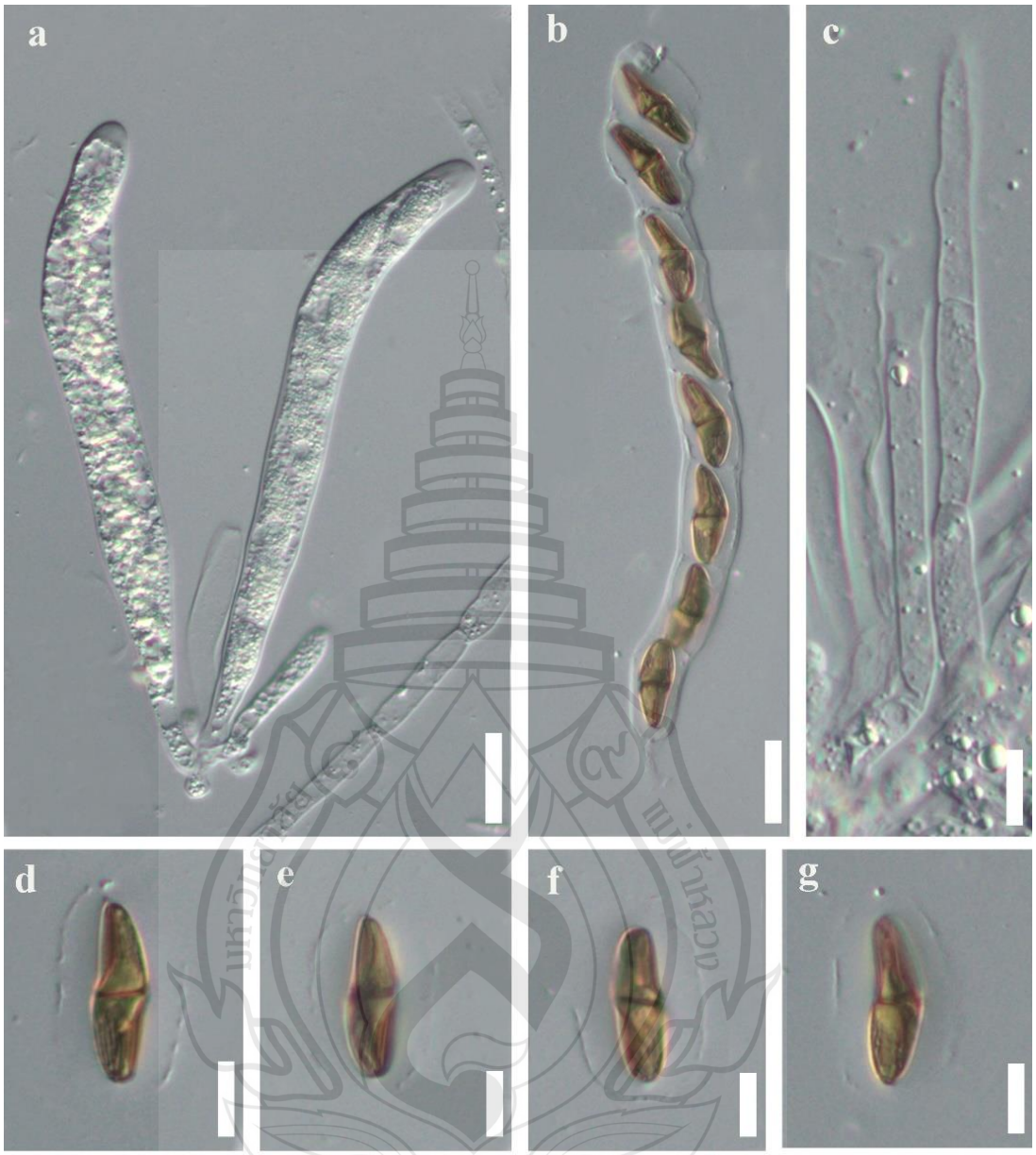
Etymology: Name reflects the collected site, Yunnan Province.

Holotype: HGUP 24-0024.

Saprobic bamboo culms. **Sexual morph**: *Ascomata* immersed, solitary, slightly raised, scattered or gregarious, subglobose to globose, with papilla. *Ostioles* papillate on the centre, black. *Peridium* comprising several layers, outer layer brown to dark brown, thick-walled angular cells, inner layer hyaline to pale brown. *Paraphyses* 2.5–4.5 µm wide, hyaline, unbranched, septate, verruculose. *Asci* 8-spored, unitunicate, cylindrical, short-pedicellate, apically rounded, with apical ring, 147–170 × 11–16 µm. *Ascospores* 20–25 × 6.5–8 µm ($\bar{x}$ = 23 × 7 µm, n = 20), overlapping uniseriate, ellipsoidal, hyaline when young, brown when mature, 1-septate, constricted at the septum, with longitudinal wall striations, surrounded by a mucilaginous sheath, lacking germ slits and appendages. **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Qiannan Buyi and Miao Autonomous Prefecture, Libo district, on bamboo culms, 12 March 2022, Y.R. Sun, ML9 (HGUP 24-0024, **holotype**); ex-type cultures GUCC 24-0116.

Notes: The combined gene analysis of LSU, ITS, RPB2 and TUB sequences (Figure 4.180) showed that our isolate (GUCC 24-0116) formed a distinct clade in *Arecophila*. Morphologically, our collection differs from *A. australis* and *A. clypeata* by smaller asci (147–170 × 11–16 µm *vs*. 140–230 × 15.5–24 µm *vs*. 180–245 × 10.5–14.5 µm). Our collection also has smaller ascospores than *A. australis* (20– 25 × 6.5–8 µm *vs*. 22.5–29 × 8–11 µm). Thus, we introduced *Arecophila maolanensis* sp. nov. here.



Note a, b Asci. c paraphyses. d–g Ascospores. Scale bars: a, b = 20 μm, c–g = 10 μm.

Figure 4.174 *Arecophila maolanensis* (HGUP 24-0024, holotype)

Catenuliconidiaceae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***fam. nov.***

Facesoffungi number: FoF 16478

Etymology: Name reflects the type genus

Type genus: *Catenuliconidia* N.G. Liu & K.D. Hyde

Saprobic on dead plant tissue. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* on natural substrate effuse, clustered, black, velvety. *Mycelium* immersed, composed of branched, hyaline, septate hyphae. *Conidiophores* macronematous, mononematous, in clusters, brown to dark brown, erect, cylindrical, straight and some curved, unbranched, septate, smooth, thick-walled. *Conidiogenous cells* blastic, terminal, integrated, cylindrical, brown to dark brown, produced conidia. *Conidia* catenate, developing in acropetal chains, ellipsoid to cylindrical, brown to dark brown, 1-septate, septum darkened, slightly constricted at the septum, truncate at both ends.

Notes: Yuan et al. (2020) proposed the genus *Catenuliconidia* and placed it as Xylariales genus *incertae sedis*. In our phylogenetic analyses, three *Catenuliconidia* strains formed a distinct clade and was close to Barrmaeliaceae and Graphostromataceae. Morphologically, *Catenuliconidia* is distinguished from Barrmaeliaceae and Graphostromataceae by its macronematous, fasciculate, brown to dark brown, cylindrical conidiophores, blastic conidiogenous cells and catenate, ellipsoid to cylindrical, brown to dark brown conidia, while Barrmaeliaceae has a libertella-like coelomycetous asexual morph, and Graphostromataceae has *nodulisporium*-like, *periconiella*-like or *xylocladium*-like asexual morphs. Therefore, based on its distinctness in morphology and phylogenetic placement, we establish a new family, Catenuliconidiaceae to accommodate *Catenuliconidia* (Wendt et al., 2018; Yuan et al., 2020).

Catenuliconidia N.G. Liu & K.D. Hyde, Fungal Diversity: [97] (2020)

Notes: *Catenuliconidia* was introduced by Yuan et al. (2020), designating *C. uniseptata* as the type species. The genus comprises a single species with a Hyphomycetous asexual morph. It is distinguished by macronematous, clustered, erect, brown unbranched conidiophores, blastic, terminal, integrated, cylindrical, brown

conidiogenous cells and catenate, ellipsoid to cylindrical, septate, brown conidia (Yuan et al., 2020).

Catenuliconidia uniseptata N.G. Liu & K.D. Hyde, Fungal Diversity, [97] (2020)

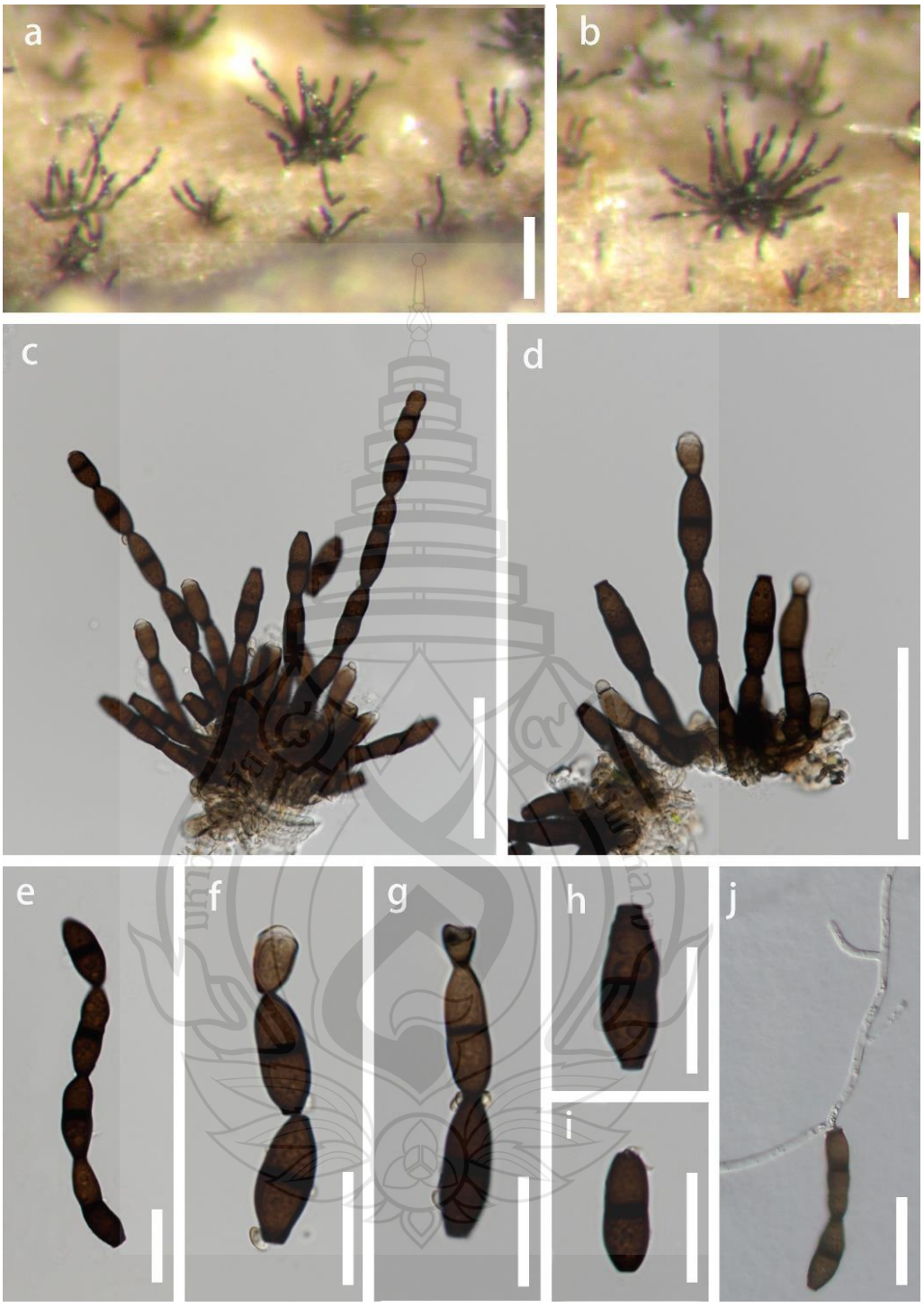
Index Fungorum number: IF556465; Facesoffungi number: FoF 06117; Figure 4.178

Saprobic on dead bamboo culms in terrestrial habitat. *Colonies* on natural substrate effuse, clustered, black, velvety. *Mycelium* immersed, composed of branched, hyaline, septate hyphae. *Conidiophores* macronematous, mononematous, in clusters, brown to dark brown, erect, cylindrical, straight and some curved, unbranched, septate, smooth, thick-walled. *Conidiogenous cells* 3–5 μm wide, blastic, terminal, integrated, cylindrical, brown to dark brown, produced conidia. *Conidia* catenate, developing in acropetal chains, ellipsoid to cylindrical, brown to dark brown, 1-septate, septum darkened, slightly constricted at the septum, truncate at both ends, 17–30 × 6–11 μm ($\bar{x}$ = 25 × 8 μm, n = 30).

Culture characteristics: Conidia germinating on PDA within 24 h and producing germ tubes from one or both ends. Colonies growing slowly on PDA medium, surface velvety, with entire edge, white, center fairly dense and protuberant, middle ring flat, outer ring sparse from above; center yellow, color decreasing from the center to periphery from below.

Material examined: CHINA, Guizhou Province, Guiyang City, Nanming District, Xiaochehe Road, Guiyang Ahahu National Wetland Park, on dead bamboo culms, 22 March 2023, Y.R. Sun, 2354 (HKAS 136878); living culture GUCC 24-0118; ibid; Baiyun District, Changpoling National Forest Park, decaying wood, 30 August 2019, Y.R. Sun, cpx9 (HGUP 24-0025), living culture GUCC 24-0119.

Notes: Yuan et al. (2020) initially described *Catenuliconidia uniseptate*, a fungal species found in decaying wood in China. Our strains formed a distinct cluster alongside *C. uniseptate* (MFLU 19-0689) with strong statistical support in the phylogenetic tree (Figure 4.180). Additionally, our strains exhibited comparable morphological features in terms of shape and size to those of *C. uniseptate*. Thus, we identified our strains as *C. uniseptate,* with GUCC 24-0118 representing a new host record.



Note a, b Colonies on natural substrate. c Sporodochium. d Conidiophores, Conidiogenous cells and conidia. e–g Conidial chains. h, i Conidia. j Germinating conidium. Scale bars: a, b = 100 µm, c, d = 50 µm, e–j = 20 µm.

Figure 4.175 *Catenuliconidia uniseptata* (HKAS 136878, new host record)

Vamsapriyaceae Y.R. Sun, Yong Wang bis & K.D. Hyde, ***fam.nov.***

Index Fungorum number: IF558620; Facesoffungi number: FoF09926

Etymology: Name reflects the type genus

Type genus: *Vamsapriya* Gawas & Bhat

Saprobic on dead wood. **Sexual morph**: *Ascomata* solitary, scattered, immersed, subglobose, brown with ostiolate. *Peridium* thin-walled, brown. Paraphyses hyaline, septate. *Asci* unitunicate, cylindrical, short pedicellate, 8-spored, with J+ apical ring. *Ascospores* apiosporous, fusiform to broad fusiform, hyaline. **Asexual morph**: Hypho-mycetous. *Colonies* on natural substrate effuse, black, velvety. Mycelium immersed, septate, branched. *Synnemata* present or absent, when present (*Didymobotryum*, *Podo-sporium*, *Tretophragmia*, *Vamsapriya*), synnemata erect, rigid, dark brown, composed of compact parallel conidiophores. *Conidiophores* erect, straight or curved, cylindrical, dark brown, septate. *Conidiogenous cells* mono- or polytretic, integrated, terminal, cla-vate to cylindrical, brown. *Conidia* catenate or solitary, acrogenous, simple, pigmented, multi-shaped, septate; when absent (*Diabolocovidia*, adapted from Crous et al., 2020), *conidiophores* mi-cronematous, flexuous, mostly reduced to a terminal conidiogenous cell. *Conidiogenous cells* monoblastic, subcylindrical to clavate, pale brown, smooth. *Conidia* catenate, acrogenous, brown, ellipsoid to obovoid, thin-walled, aseptate.

Notes: A new family, Vamsapriyaceae is introduced to accommodate *Diabolocovidia*, *Didymobotryum*, *Podosporium*, *Tretophragmia* and *Vamsapriya*. Their phylogenetic posi-tion, which is distinct from other families, supports the establishment of the new family within Xylariales. The sexual morph of *Vamsapriya* is different from those of Xylariaceae in having hyaline, apiosporous ascospores (Castañeda-Ruiz et al., 2017; Dai et al., 2017). Clypeosphaeriaceae and Indura-tiaceae are the sister clade of Vamsapriyaceae but they are distinct in morphology. It was noteworthy that the sexual morph of *Vamsapriya* is similar to Induratiaceae with 8-spored, asci with J+ apical ring asci and hyaline, apiosporous ascospores, but *Induratia* (Induratiaceae) has geniculosporium asexual morphs. *Apioclypea* is mor-phologically similar to the sexual morph of *Vamsapriya* in

8-spored, pedunculate, cy-lindrical asci, biseriate, fusiform, hyaline, ascospores with a mucilaginous sheath, but its asexual morph is unknown (Hyde et al., 2020). Although, the phylogeny of *Podosporium* and *Tretophragmia* is unable to infer due to the absence of molecular data, their morpho-logical characters resemble *Didymobotryum* and *Vamsapriya* in having brown to dark, simple, straight synnemata, monotretic conidiogenous cells and solitary, obclavate, multi-septate, dark brown conidia (Zhuang, 2001; Wang et al., 2017). We thus temporarily accept *Podosporium* and *Tretophragmia* in Vamsapriyaceae based on morphology. Sequence data are urgently needed to resolve their phylogenetic affinities.

Vamsapriya Gawas & Bhat, Mycotaxon 94: 150 (2006) [2005]

Notes: *Vamsapriya* was introduced by Gawas and Bhat (2005), with *Vamsapriya indica* designated as the type species. *Vamsapriya* was initially placed in Xylariaceae. Sun, Huang et al. (2021) refined the Xylariales and transferred it to Vamsapriyaceae based on morphology and molecular analyses. *Vamsapriya* species are known to inhabit both aquatic and terrestrial environments, with the majority of species reported in China and Thailand (Dai et al., 2014; Hyde, Norphanphoun et al., 2017; Jiang et al., 2018; Sun, Huang et al., 2021; Samarakoon et al., 2022). So far, twelve species are accepted in this genus (Species Fungorum, 2024).

Vamsapriya chiangmaiensis Y.R. Sun, Yong Wang bis & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558618; Faces of fungi number: FoF09927; Figure. 4.175

Etymology: Name reflects the collected site.

Holotype: MFLU 21–0087

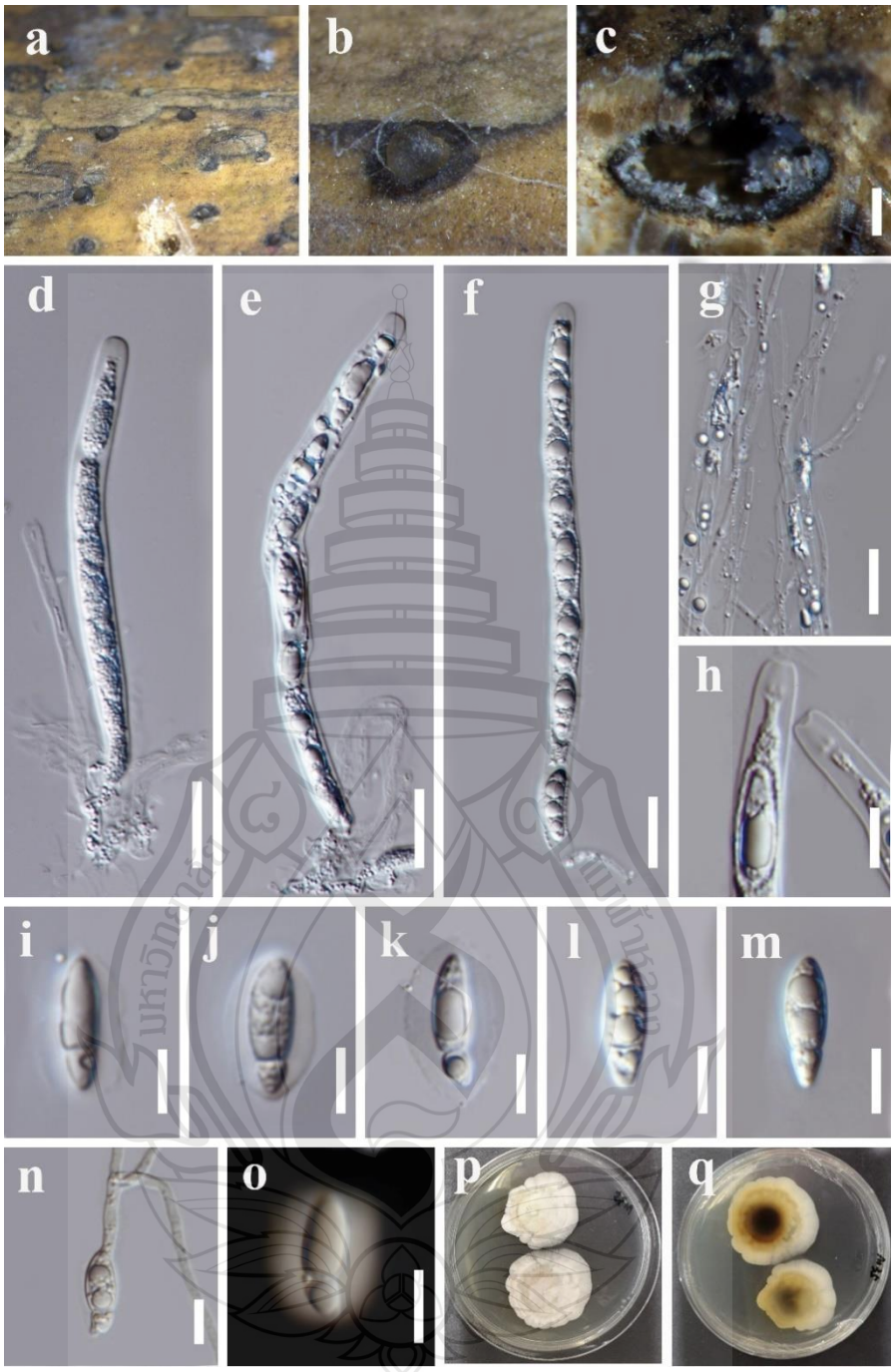
Saprobic on dead bamboo culms, immersed, spots on the host surface, visible as black, circular, transparent, gelatinous. **Sexual morph**: *Ascomata* 650–850 µm high, 650–1000 µm wide, solitary scattered, immersed within the host cortex, in cross section globose to subglobose. *Ostiole* raised, centric, periphysate ostiolar canal., *Peridium* composed of hyaline inner layer and dark brown to dark outer layer. *Paraphyses* long, 1.5–4 µm wide ($\bar{x}$ = 2 µm, n=15), hyaline, unbranched, septate. *Asci* 140–190 × 6.5–12 µm ($\bar{x}$ = 160×9 µm,

n=15), 8-spored, unitunicate, straight or slightly curved, cylindrical, short pedicellate, with apical ring. *Ascospores* 17–26×5.5–8 µm ($\bar{x}$ = 20.5×6.5 µm, n=30), uniseriate, fusiform, apiosporous, constricted apiosporous with a large cell 12.5–22 µm length, guttulate; basal cell 3.5–6.5 length, hyaline, smooth wall, surround a gelatinous muci-laginous sheath. **Asexual morph**: Not observed.

Culture characters: Ascospores germinated on PDA within 12 hours and germ tubes produced from one end. Colonies reached 45 mm diam within four weeks at 26 °C, flat, circular, cottony. White from above; brown to dark brown in the center, white to pale brown around, from the below.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Center, on bamboo culms, 15 July 2020, Y.R. Sun, M35 (MFLU 21-0087, holotype); ex–type living culture, MFLUCC 21-0065.

Notes: *Vamsapriya chiangmaiensis* is the second species that has a sexual morph in Vamsapriya. It is similar to *V. bambusicola* in having solitary, subglobose ascomata, 8-spored, unitunicate, cylindrical asci and fusiform hyaline ascospores. But it can be distinguished by the longer asci (140–190 µm *vs.* 115–140 µm). In addition, polymor-phic nucleotides from the ITS region showed 37 base differences. Therefore, we identified *V. chiangmaiensis* as a new species.



Note a, b Appearance of ascomata on host substrate. c Vertical section of ascomata. d–f Asci. g Paraphyses. h Apical ring of asci. i–m Ascospores. n Germinated ascospores. o Ascospore stained in Indian ink. p, q Colonies on PDA. Scale bars: c = 200 µm, d–g = 20 µm, f, h–o = 10 µm.

Figure 4.176 *Vamsapriya chiangmaiensis* (MFLU 21-0087, holotype)

Vamsapriya chiangraiensis Y.R. Sun & K.D. Hyde, ***sp. nov.***

Facesoffungi number: FoF 16479; Figure 4.176

Etymology: Name reflects the collected site.

Holotype: MFLU 23-0500.

Saprobic on dead bamboo culms. *Colonies* on natural substrate effuse, black, velvety. **Asexual morph**: Hyphomycetous. *Mycelium* immersed, composed of septate, branched, hyaline to brown hyphae. *Conidiophores* synnematous, macronematous, erect, straight or curved, dark brown to black, cylindrical., *Synnemata* up to 900 μm long, 25–50 μm wide in the middle, erect, rigid, dark brown to black, composed of compact parallel conidiophores. *Conidiogenous cells* 5–8 × 3–6 μm ($\bar{x}$ = 6.5 × 5 μm, n = 15), monotretic, integrated, terminal, clavate, pale to brown. *Conidia* 14–46 × 7–10 μm ($\bar{x}$ = 28.5 × 8 μm, n = 40), solitary, oval or oblong when young, obclavate when mature, obtuse at base, rostrate at tip, olivaceous to brown, 1–6-septate, slightly constricted at the septa, some with globule.

Cultural characters: Conidia germinated on PDA within 12 h and germ tubes produced from both ends. Colonies reached 20 mm within four weeks at 26 °C, flat, circular, cottony, gray to pale brown from above, from below pale brown in the center, black around.

Material examined: THAILAND, Chiang Rai City, Mae Lah Luang University, Garden of Medicinal Plants, on bamboo culms, 15 November 2020, Y.R. Sun, B91 (MFLU 23-0500, **holotype**); ex-type culture MFLUCC 24-0311.

Notes: *Vamsapriya chiangraiensis* formed an inner clade within *Vamsapriya* and closed related to *V. indica* and *V.* uniseptate in the phylogenetic tree (Figure 4.180). In morphology, it produced solitary, obclavate, 1–6-septate conidia while *V. indica* produced catenate, acrogenous, cylindrical conidia and *V. uniseptate* has catenate, oblong, 1-septate conidia (Gawas & Bhat, 2005; Sun, Huang et al., 2021). We thus introduced *V. chiangraiensis* as a novel species.



Note a Colonies on natural substrate. b, c Conidiophores and conidia. d, e Conidiogenous cells and developing conidia. f–l Conidia. m Germinated conidium. n, o Colonies on PDA. Scale bars: b, c = 100 μm, d, m = 50 μm, e = 20 μm, f–l = 10 μm.

Figure 4.177 *Vamsapriya chiangraiensis* (MFLU 23-0500, holotype)

Vamsapriya indica Gawas & Bhat, Mycotaxon 94: 150 (2006) [2005]

Index Fungorum number: IF550801; Faces of fungi number: FoF00374; Figure 4.177

Saprobic on dead bamboo culms. **Sexual morph**: Not observed. **Asexual morph**: Hyphomycetous. *Colonies* effuse, dark brown, hairy. *Conidiophores* macronematous, synnematous, single, erect, cylindrical, straight or slightly flexuous, dark brown, smooth-walled. *Synnemata* erect, straight or slightly flexuous, dark brown, rigid, with cylindrical to clavate apical fertile part, composed of compactly arranged conidio-phores, 1300–1900 um long, 80–150 μm wide at the base, 30–40 μm wide in the middle, 60–140 μm wide at the apical fertile region, with basal portion immersed. *Conidiogenous cells* 4.5–8.5 × 3–4.5 μm ($\bar{x}$ = 6.5 × 4 μm, n = 30), monotretic, integrated, terminal, brown, cylindrical to clavate, apically rounded, smooth-walled. *Conidia* catenate, acrogenous, cylindrical, rounded at the apex, taper and subtruncate at the base, olivaceous brown to brown, 2–8-septate, slightly constricted at the septa, smooth, 20–48 × 4.5–6.5 μm ($\bar{x}$= 32 × 5.5 μm, n = 20).

Cultural characters: Conidia germinated on PDA within 12 hours and germ tubes were produced from both ends. Colonies reached 20 mm diam within four weeks at 26 °C, cottony, flat, circular, edge entire, white from above, white to yellow from the below.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, Pa Pae, Mushroom Research Center, on bamboo culms, 10 September 2020, H.W. Shen, M38 (MFLU 21-0088); living culture MFLUCC 21-0066.

Notes: *Vamsapriya indica* is the type species of *Vamsapriya* introduced by Gawas and Bhat (2005). Dai et al. (2014) recollected *V. indica* from Thailand and provided the culture characters and sequences data. Bao et al. (2021) reported it from a bamboo plant in a freshwater habitat in China. Including our collection, all of these four strains are rec-orded from bamboo.



Note a, b Colonies on natural substrate. c Conidiophore and conidia. d–f Conidiogenous cells and developing conidia. g–k Conidia. l Germinated co-nidium. Scale bars: a = 2000 µm, b = 1000 µm, c = 200 µm, d–l = 20 µm.

Figure 4.178 *Vamsapriya indica* (MFLU 21-0088)

Occultitheca J.D. Rogers & Y.M. Ju, Sydowia 55(2): 359 (2003)

Notes: Rogers and Ju (2003) established *Occultitheca* and designated *O. costaricensis* as the type species. Samarakoon et al. (2022) reported the second *Occultitheca* species which isolated from *Rosa* sp. in China. The genus has semi-immersed or immersed ascomata, cylindrical, short pedicellate asci with J +, apical ring, and brown ascospores with hyaline dwarf cells (Rogers & Ju, 2003; Samarakoon et al., 2022). This study described a new host record species in this genus.

Occultitheca rosae Samarak., Jian K. Liu & K.D. Hyde, Fungal Diversity 112: 72 (2022)

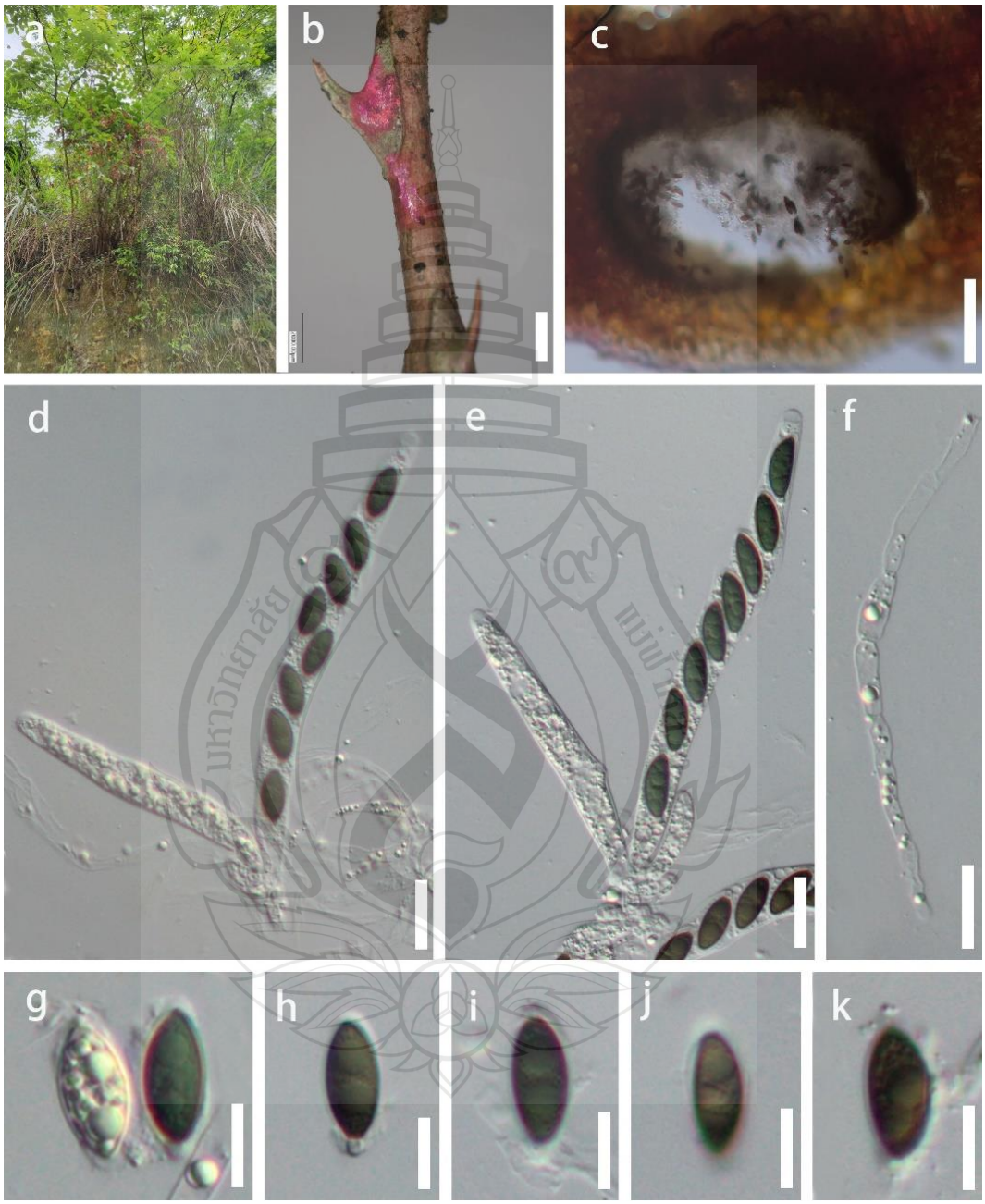
Index Fungorum number: IF558741; Facesoffungi number: FoF 10222; Figure 4.179

Saprobic on a dead branch of *Rubus sp*. **Sexual morph**: Ascomata semi-immersed, solitary or aggregated, appear as black spots on the host surface, in cross-section globose to subglobose. *Ostioles* centric. *Peridium* 15–25 μm wide, fused with host tissues, comprising two layers, outer layer thick, comprising brown to dark brown, thick-walled cells of *textura angularis*, inner layer thin, composed of hyaline, thin-walled cells of *textura angularis*. *Paraphyses* filamentous, septate, constricted at the septa, guttulate, 2–6.5 μm wide. *Asci* 90–155 × 11–13 μm, 8-spored, unitunicate, cylindrical, short pedicellate, apically rounded, with rectangular to slightly obconic, apical ring. *Ascospores* 14–21 × 5.5–8 μm ($\bar{x}$ = 18 × 7 μm, n = 30), uniseriate, hyaline to olivaceous when young, brown at mature, ellipsoidal or fusiform, aseptate, guttulate, with small hyaline cell on one end, surrounding by a thin mucilaginous sheath. **Asexual morph**: Not observed.

Material examined: CHINA, Guizhou Province, Tongren City, Jiangkou District, on a dead branch of *Rubus* sp. (Rosaceae), 20 May 2022, Y.R. Sun, JK47 (HKAS 136900); living culture GUCC 24-0120.

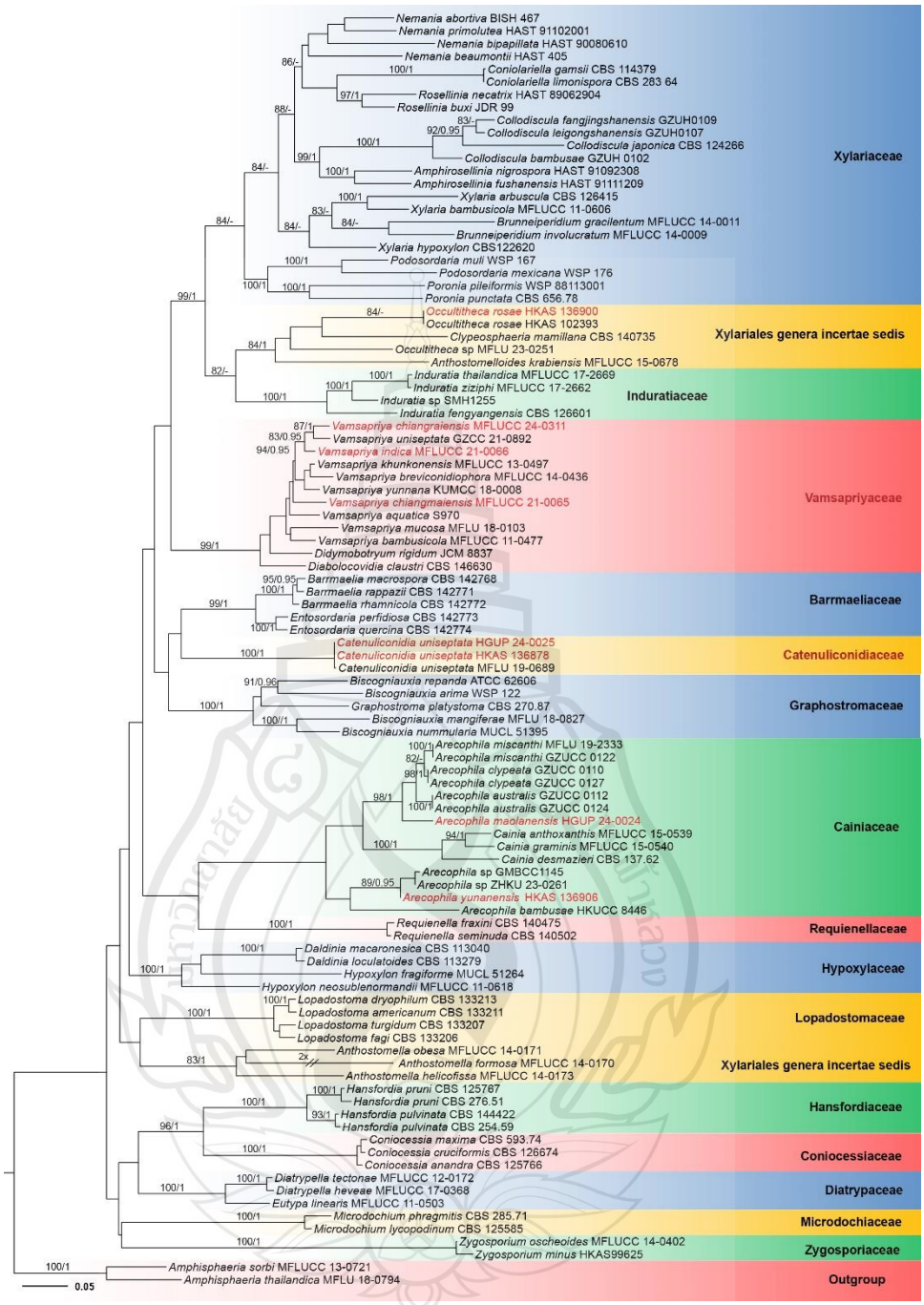
Notes: Samarakoon et al. (2022) reported *Occultitheca rosae*, a fungal species isolated from *Rosa* sp. (Rosaceae) in China. In our study, our strain clustered together with *Occultitheca rosae* (HKAS 102393) by well statistical support (Figure 4.180). Additionally, our strains share similar morphological features in terms of shape and size to *Occultitheca rosae*. Thus, we

identified our strains as *Occultitheca rosae,* representing a new host record from the medicinal plant, *Rubus* sp.



Note a Host. b Ascoma on the host c section of ascoma. d, e Asci. f paraphyses. g–k Ascospores. Scale bars: b = 2000 µm, c = 50 µm, d–f = 20 µm, g–k = 10 µm.

Figure 4.179 *Occultitheca rosae* (HKAS 136900, new host record)



Note The tree is rooted with *Amphisphaeria sorbi* (MFLUCC 13-0721) and *A. thailandica* (MFLU 18-0794). Bootstrap support values for ML greater than 50% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The new collections are indicated in red.

Figure 4.180 Phylogenetic tree of Xylariales

4.3 Discussion

4.3.1 Diversity and Distribution

We collected samples from the rainforests, mountains, and plains of Hainan, Guizhou, Guangxi, Yunnan, and Zhejiang provinces in southern China, as well as from Chiang Mai, Chiang Rai, and Nan provinces in northern Thailand. From these specimens, we isolated 158 fungal strains, representing 135 species distributed across 3 classes, 17 orders, 39 families, and 81 genera. The results reveal that there is a rich and diverse fungal community within medicinal plant ecosystems in these regions, with these fungi exhibiting a broad range of distribution and ecological interactions. From tropical to subtropical regions, and from high-altitude mountains to low-altitude plains, the distribution of these fungi reflects their high adaptability to different ecological environments. This diversity and wide distribution provide us with valuable opportunities to gain deeper insights into the interactions between fungi and medicinal plant ecosystems.

4.3.2 Host Specificity

In this study, we did not identify any fungal groups with pronounced host specificity among the endophytes and pathogens associated with medicinal plants. However, within the saprophytic fungi, we observed that *Phaeosphaeriopsis* and *Nigrograna* exhibited a certain degree of host preference. *Phaeosphaeriopsis* species are globally distributed, functioning both as pathogens and saprobes (Câmara et al., 2003; Crous, Wingfield, Burgess et al., 2016; Crous, Wingfield, Richardson et al., 2016; Crous et al., 2021; Tibpromma et al., 2017). Notably, there are 17 recognized species within *Phaeosphaeriopsis*, with 15 of these species specifically linked to plants in the Asparagaceae (Tibpromma et al., 2017; Marin-Felix et al., 2019; Hyde, Dong et al., 2020; Species Fungorum, 2024). This strong association with Asparagaceae plants indicates a significant degree of host specificity within Phaeosphaeriopsis, underscoring their specialized ecological relationships.

Most species of *Nigrograna* are reported as saprobes in terrestrial habitats (Mapook et al., 2020; Lu, Karunarathna et al., 2022; Li et al., 2023; Liu, Wang et al., 2024; Xu, Karunarathna et al., 2024), with a few found in aquatic environments (Tibpromma et al., 2017; Dong et al., 2020). Our analysis of reported species revealed that 70% of *Nigrograna* species have woody plants as their hosts, including coffee, oil wood plants, and yulan magnolia. These hosts share the distinctive characteristic of having smooth surfaces with a conspicuous waxy layer on their leaves or stems (Jaklitsch & Voglmayr, 2016; Wanasinghe et al., 2020; Lu, Karunarathna et al., 2022; Li et al., 2023; Shu et al., 2023). This finding provides valuable insights into the interactions and adaptations between *Nigrograna* fungi and their hosts, highlighting the ecological and evolutionary dynamics at play.

4.3.3 Pestalotioid Species on Medicinal Plants

This study identified a total of 33 fungal strains associated with medicinal plant diseases, with 13 strains belonging to Pestalotioid species. Through comprehensive global research, we found that these fungal species are widely distributed among dicotyledonous plants (Table 4.4). The frequent discovery of these fungi suggests they may significantly impact the occurrence and development of various medicinal plant diseases. This pervasive presence indicates a potential threat to medicinal plant health and productivity.

Future research should focus on understanding how these fungi affect medicinal plant growth and the synthesis of medicinal compounds through their pathogenic activities. Investigating the mechanisms of fungal infection and its influence on plant biochemistry will be crucial., Additionally, developing effective disease control strategies is essential to mitigate the adverse effects of these fungi on medicinal plants. This could include exploring resistant plant varieties, biocontrol agents, and sustainable agricultural practices to ensure the health and efficacy of medicinal plants.

Table 4.4 Checklist of pestalotioid species associated with medicinal plants

Species	Life mode	Disease (if any)	Host	Location
Neopestalotiopsis acrostichi	P	Leaf spot	*Acrostichum aureum* (F)	Thailand
Neopestalotiopsis alpapicalis	E		*Rhyzophora mucronate* (D)	Thailand
Neopestalotiopsis amomi	P	Leaf spot	*Amomum villosum* (M)	China
Neopestalotiopsis brachiata	P	Leaf spot	*Rhizophora apiculate* (D)	Thailand
Neopestalotiopsis clavispora	P	Leaf spot, branch blight	*Dendrobium officinale*, *Taxus×media* (M/G)	China
Neopestalotiopsis cubana	P	Leaf blight	*Ixora chinensis* (D)	Malaysia
Neopestalotiopsis dendrobii	E		*Dendrobium cariniferum* (M)	Thailand
Neopestalotiopsis ellipsospor	Unknown		*Ardisia crenata* (D)	Hong Kong, China
Neopestalotiopsis eucalypticola	Unknown		*Eucalyptus globulus* (D)	Unknown
Neopestalotiopsis eucalyptorum	P	Leaf necrosis, stem basal cankers	*Eucalyptus globulus* (D)	Fundão/Guarda/Portugal
Neopestalotiopsis formicarum	P	Leaf spot	*Photinia serrulata*	China
Neopestalotiopsis haikouensis	P	Leaf spot	*Ilex chinensis* (D)	China
Neopestalotiopsis hispanica	P	Leaves and stem necrosis	*Eucalyptus globulus* (D)	Fundão/Guarda/Spain
Neopestalotiopsis hydeana	P	Leaf spot	*Alpinia malaccensis* (M)	Thailand
Neopestalotiopsis hyperici	P	Leaf spot	*Hypericum monogynum* (D)	China
Neopestalotiopsis iberica	P	Leaves and stem necrosis	*Eucalyptus globulus* (D)	Pegões/Portugal/Spain
Neopestalotiopsis longiappendiculata	P	Leaves and stem necrosis	*Eucalyptus globulus*/ *E. nitens (D)*	Furadouro/Portugal
Neopestalotiopsis lusitanica	P	Leaves and stem necrosis	*Eucalyptus globulus* (D)	Pegões/Portugal
Neopestalotiopsis pernambucana	Unknown		*Vismia guianensis* (D)	Brazil
Neopestalotiopsis petila	P	Leaf spot	*Rhizophora mucronate* (D)	Thailand
Neopestalotiopsis photiniae	P	Leaf spot	*Photinia serrulate* (D)	China
Neopestalotiopsis rhapidis	P	Leaf spot	*Podocarpus macrophyllus* (G)	China
Neopestalotiopsis rhizophorae	P	Leaf spot	*Rhizophora mucronate* (D)	Thailand

Table 4.4 (continued)

Species	Life mode	Disease (if any)	Host	Location
Neopestalotiopsis rhododendri	P	Leaf spot	*Dracaena fragrans* (M)	Thailand
Neopestalotiopsis rosae	Unknown		*Paeonia suffruticosa* (D)	U.S.A.
Neopestalotiopsis rosicola	P*	Stem canker	*Rosa chinensis* (D)	China
Neopestalotiopsis saprophytica	S		*Litsea rotundifolia* (D)	Hong Kong, China
Neopestalotiopsis surinamensis	E		*Scurrula atropurpurea* (D)	Indonesia
Neopestalotiopsis thailandica	P	Leaf spot	*Rhizophora mucronate* (D)	Thailand
Pestalotiopsis adusta	E, P*	Leaf spot	*Clerodendrum canescens/Sinopodophyllum hexandrum/Rubus idaeus* (D)	China
Pestalotiopsis affinis	P	Leaf spot	*Taxus chinensis* (G)	China
Pestalotiopsis alpiniae	P	Leaf spot	*Alpinia galanga* (M)	China
Pestalotiopsis antiaris	P	Leaf spot	*Antiaris toxicaria* (M)	China
Pestalotiopsis bicilia	S		*Viburnum opulus* (D)	Canada
Pestalotiopsis biciliata	P*	Stem canker	*Pistacia lentiscus* (D)	Tunisia
Pestalotiopsis bicolor	S		*Smilax* sp. (M)	U.S.A.
Pestalotiopsis bruguierae	Unknown		*Bruguiera gymnorhiza* (D)	India
Pestalotiopsis bulbophylli	S		*Bulbophyllum thouars (M)*	China
Pestalotiopsis chamaeropis	E, P*	Leaf spot	*Eurya nitida, Peristrophe japonica* (D)	China
Pestalotiopsis chiangmaiensis	P	Leaf strip	Bamboo (M)	Thailand
Pestalotiopsis cruenta	Unknown		*Polygonum lasianthum* (D)	Japan
Pestalotiopsis digitalis	p	Leaf spot	*Digitalis purpurea* (D)	New Zealand
Pestalotiopsis dilleniae	p	Leaf spot	*Dillenia turbinate* (M)	China
Pestalotiopsis diploclisiae	Unknown		*Diploclisia glaucescens* (D)	Hong Kong, China
Pestalotiopsis dracaenae	S		*Dracaena fragrans* (M)	China
Pestalotiopsis ellipsospora	p*	Stem canker	*Acanthopanax divaricatus* (D)	Korea
Pestalotiopsis gibbosa	S		*Gaultheria shallon* (D)	U.S.A.
Pestalotiopsis heucherae	Unknown		*Heuchera parviflora*	U.S.A.
Pestalotiopsis hispanica	E		*Peristrophe japonica*	China
Pestalotiopsis hughesii	Unknown		*Cyperus articulates* (M)	Ghana
Pestalotiopsis japonica	Unknown		*Cedrela sinensis* (D)	Japan
Pestalotiopsis jinchanghensis	E		*Vaccinium dunalianum* (D)	China

Table 4.4 (continued)

Species	Life mode	Disease (if any)	Host	Location
Pestalotiopsis kenyana	P*	Leaf spot	*Zanthoxylum schinifolium* (D)	China
Pestalotiopsis kunmingensis	E		*Podocarpus macrophyllus* (G)	China
Pestalotiopsis kwangsiensis	P	Leaf spot	*Sinopimelodendron kuwangsiensis* (D)	China
Pestalotiopsis lespedezae	Unknown		*Lespedeza bicolor* (D)	Japan
Pestalotiopsis linearis	E		*Trachelospermum* sp. (D)	China
Pestalotiopsis lushanensis	P*	Brown leaf spot, leaf bilght	*Sarcandra glabra, Podocarpus macrophyllus* (G)	China
Pestalotiopsis microspora	S		*Hedera helix* (D)	Argentina
Pestalotiopsis moluccensis	Unknown		*Xylocarpus moluccensis* (D)	India
Pestalotiopsis neolitseae	P*	Leaf spot	*Neolitsea villosa* (D)	Taiwan, China
Pestalotiopsis oenotherae	Unknown		*Oenothera laciniata* (D)	U.S.A.
Pestalotiopsis pandani	Unknown		*Pandanus odoratissimus* (M)	Taiwan, China
Pestalotiopsis paraguariensis	Unknown		*Ilex paraguariensis* (D)	Brazil
Pestalotiopsis pestalozzioides	Unknown		*Clematis ligusticifolia* (D)	New Mexico
Pestalotiopsis pipericola	Unknown		*Piper nigrum* (D)	India
Pestalotiopsis quadriciliata	Unknown		*Vitis vulpine* (D)	Canada
Pestalotiopsis rhodomyrtus	Unknown		*Rhodomyrtus tomentosa* (D)	China
Pestalotiopsis smilacicola	P	Leaf spot	*Smilax china, Dioscorea* sp. (M)	Thailand
Pestalotiopsis sinensis	Unknown		*Ginkgo biloba* (G)	China
Pestalotiopsis tecomicola	Unknown		*Tecoma radicans* (D)	U.S.A.
Pestalotiopsis thailandica	P	Leaf spot	*Rhizophora apiculate* (D)	Thailand
Pseudopestalotiopsisis ampullace	E		*Magnolia candolli* (D)	China
Pseudopestalotiopsis curvatispora	P	Leaf spot	*Rhizophora mucronate* (D)	Thailand
Pseudopestalotiopsis gilvanii	P*	Leaf spot	*Paullinia cupana* (D)	Brazil
Pseudopestalotiopsis indica	Unknown		*Hibiscus rosa-sinensis* (D)	India
Pseudopestalotiopsis simitheae	S, E		*Pandanus odoratissimus/ Magnolia candolli* (M/D)	Thailand/China
Pseudopestalotiopsis thailandica	P	Leaf spot	*Rhizophora mucronate* (D)	Thailand
Pseudoestalotiopsis theae	S		*Ceriops tagal* (D)	Thailand

Note [a]The mode of life is given as endophyte (E), pathogen (P), and saprobe (S). For the species, those with confirmed pathogenicity data are marked with an asterisk (*). [c]The taxonomic status of the host is given as dicotyledons (D), ferns (F), gymnosperms (G), and monocotyledons (M).

CHAPTER 5

CONCLUSIONS

5.1 Overall Conclusion

The study of microfungi on medicinal plants in southern China and northern Thailand has provided valuable insights into the rich and complex fungal world on medicinal plants in these regions. Through extensive research and analysis, significant progress has been made in identifying and classifying fungal species, particularly the phylum of ascomycota. We obtained a total of 158 fungal isolates, representing 135 species, mainly distributed in Dothideomycetes and Sordariomycetes, and a few distributed in Leotiomycetes (see Figure 5.1), including one new order, four new families, two new genera, 72 new species and 40 new records. These species encompassed a broad range of taxa distributed across 81 genera, 39 families and 17 orders, among them, the dominant species in Dothideomycetes primarily include Pleosporales and Botryosphaeriales, while in Sordariomycetes, the dominant strains are mainly from Amphisphaeriales and Hypocreales. In addition, we connected *Keissleriella* (the sexual genus) and *Pleurophoma* (the asexual genus) based on morphological and molecular evidence and provided three new combinations. Reference sequences are provided to elucidate the phylogenetic placement of *Diplocladiella taurine* and *Torula sundara*, which was previously described. Detailed descriptions, DNA sequence data, photo plates, and notes of comparisons with similar species were provided for each species.

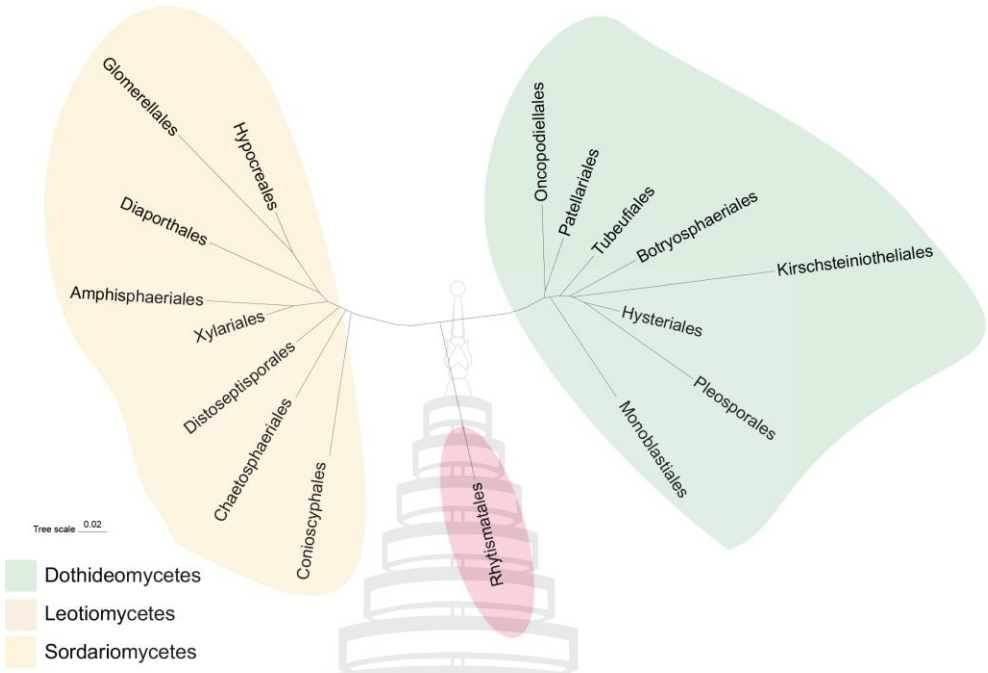


Figure 5.1 Distribution of micro-fungi on medicinal plants in southern China and northern Thailand obtained in this study

By analyzing the 159 fungal isolates we obtained, we found that these strains mainly come from Sordariomycetes, followed by Dothideomycetes (Figure 5.2). The newly discovered species are primarily from Dothideomycetes, followed by Sordariomycetes. Analysis of their lifestyles reveals that the strains obtained in this study are mainly saprobic fungi, followed by fungi related to medicinal plant diseases, and then endophytic fungi. The distribution of saprobic fungi in Dothideomycetes and Sordariomycetes shows no significant difference. Potential pathogens are mainly from Sordariomycetes, with a few from Dothideomycetes. All endophytic fungi are from Sordariomycetes, possibly because these fungi have a stronger symbiotic ability. The number of Leotiomycetes strains is the least, however, new species were still discovered, indicating their unique importance in specific ecological niches.

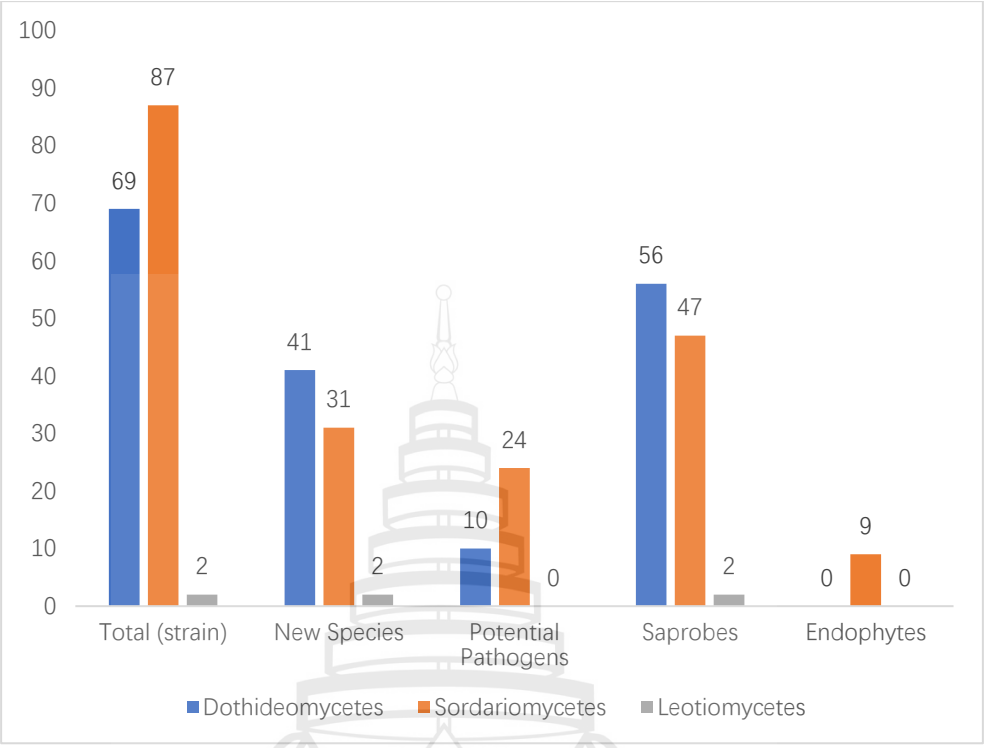


Figure 5.2 The proportion of new species and strains with three different lifestyles in the three different classes Dothideomycetes, Sordariomycetes, and Leotiomycetes

We also analyzed the national habitats of fungi from different orders and found that Pleosporales and Amphisphaeriales are the most common fungal orders in both China and Thailand, with a particularly higher number in China. Hysteriales were found only in China, while Glomerellale and Patellariales were found exclusively in Thailand, reflecting the ecological differences between the two countries. (see Figure 5.3)

Order	China	Thailand
Pleosporales	35	13
Amphisphaeriales	20	11
Hypocreales	7	9
Diaporthales	10	5
Distoseptisporales	6	5
Xylariales	5	3
Botryosphaeriales	3	4
Hysteriales	6	0
Tubeufiales	2	1
Glomerellale	0	3
Oncopodiellales	2	0
Rhytismatales	1	1
Chaetosphaeriales	2	0
Conioscyphales	1	1
Kirschsteiniotheliales	0	1
Monoblastiales	1	0
Patellariales	0	1

Figure 5.3 Distribution of fungi of different orders in China and Thailand

In our study, we collected more than 150 samples from various medicinal plants, across 41 plant families and 28 orders (see Figure 5.4). The result showed that plants in Poales are the most common hosts, with a total of 48 strains. This is followed by Asparagales and Lamiales, with 14 and 12 strains, respectively. Ranunculales and Rosales each have 8 strains, Malpighiales has seven strains, and Arecales, Piperales, Ericaceae, Laurales, and Liliales each have four strains. Other orders, such as Buxales, Aquifoliales, and Fagales, have between one to three strains, indicating lower host diversity.

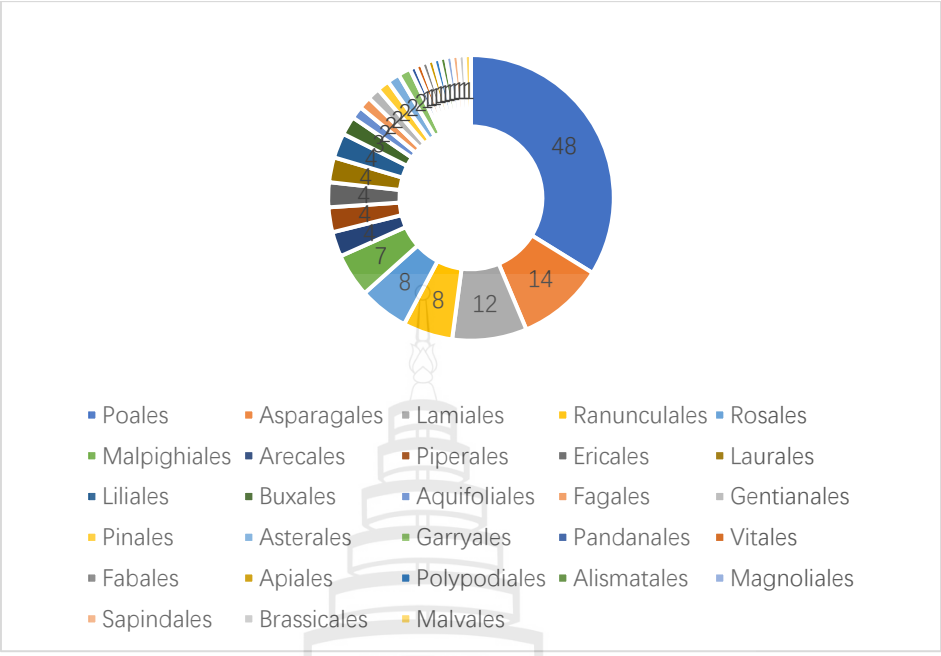


Figure 5.4 Distribution of different host obtain in this study

By analyzing the fungi isolated from different hosts, we found significant differences in host preferences between Dothideomycetes and Sordariomycetes on medicinal plants (excluding the order with less than four hosts) (see Figure 5.5). Both groups have the highest number of species in Poales, with 18 Dothideomycetes and 22 Sordariomycetes, indicating a strong host effect. They also have similar numbers in Asparagales (nine Dothideomycetes and seven Sordariomycetes) and Lamiales (six Dothideomycetes and eight Sordariomycetes). However, Dothideomycetes exhibit a stronger preference for Ranunculales (sixth species) and Piperales (five species), while Sordariomycetes have fewer or no species in these orders. In contrast, Sordariomycetes show a higher preference for Malpighiales (sixth species) and Liliales (four species), where Dothideomycetes have fewer or no species. Additionally, Sordariomycetes have more species in Ericales (three species), compared to Dothideomycetes with only one species.

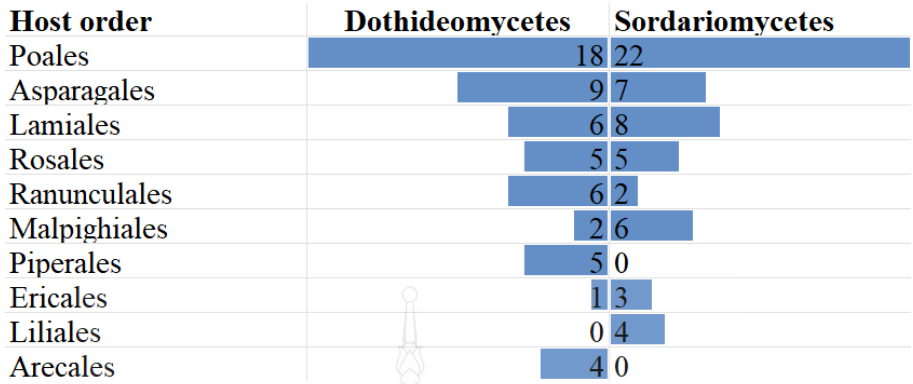


Figure 5.5 Distribution of fungi obtained from different hosts in Dothideomycetes and Sordariomycetes

5.2 Research Advantages

5.2.1 Biodiversity Insight

This study significantly contributes to our understanding of biodiversity in southern China and northern Thailand. By introducing one new order, four new families, two new genera, 72 new species, and 40 new records, our research adds substantial new data to the fungal diversity of these areas. This not only enriches the overall species richness but also provides critical insights into fungal taxonomy and ecology, particularly in regions that have historically been overlooked. The findings underscore the vast potential for discovering and cataloging species in these biodiversity hotspots, which is essential for the comprehensive understanding and conservation of China's immense biological diversity.

5.2.2 Medicinal Potential

The well-preserved herbarium specimens and axenic cultures obtained in this study, especially the endophytic fungi associated with medicinal plants, form a valuable resource for future research. These collections provide a solid foundation for the exploration of bioactive compounds with medicinal potential, paving the way for the discovery of new drugs and therapeutic agents. The study, therefore, not only

contributes to biodiversity knowledge but also has the potential to drive advancements in pharmacology and medicine.

5.2.3 Conservation Efforts

By documenting and describing fungal species in these regions, this research plays a vital role in conservation efforts. It highlights the importance of preserving both fungal and plant diversity, which is crucial for maintaining healthy ecosystems. The data generated can inform the development of strategies to protect these ecosystems from threats such as habitat loss, climate change, and the over-exploitation of medicinal plants. This work thereby contributes to the broader goals of ecological conservation and sustainability.

5.2.4 Enhancement of Molecular Databases

The research contributes to the enrichment of molecular databases by providing DNA sequences of 100 fungal species associated with medicinal plants. This expanded molecular data repository aids in more accurate species identification, evolutionary studies, and the discovery of novel genes with potential biotechnological and pharmaceutical applications. In addition, it also resolves some synonymy issues and the classification of poorly studied fungi.

5.3 Future Work

5.3.1 Ecological and Functional Studies

Further investigations are needed to explore the ecological roles and functional interactions between these fungi and their host plants. This includes studying the mutualistic, parasitic, or saprophytic nature of these relationships and their impact on plant health and productivity. Understanding these interactions can inform sustainable agricultural practices and the development of biocontrol strategies using beneficial fungi to promote plant growth and disease resistance.

5.3.2 Development of an Online Database

A dedicated website should be developed to host a comprehensive database of fungal species identified on medicinal plants. This online resource would provide

detailed information on the taxonomy, genetic sequences, and bioactive compounds of these fungi. The website would serve as a valuable tool for researchers worldwide, facilitating data sharing, collaboration, and further studies on these fungal species.

5.3.3 Pathogen Testing

This study reported 34 fungi associated with medicinal plant diseases, but no pathogen testing experiments were conducted. Future experiments should focus on verifying the pathogenicity of the isolated fungal species to medicinal plants and understanding the pathogenic mechanisms. Understanding the mechanisms of pathogenicity and host-pathogen interactions will help in developing effective control measures. These measures are crucial for protecting valuable medicinal plants from fungal infections, ensuring their sustainability and availability for medicinal use.

5.3.4 In-Depth Studies of Specific Medicinal Plants:

Given the vast diversity of medicinal plants, the current study may not have explored each plant species in sufficient depth. Future research should select specific medicinal plants that were not thoroughly investigated and conduct detailed studies on their fungal associations. This includes understanding the ecological roles of fungi on these plants, the production of bioactive compounds, and their potential benefits or threats to plant health. By focusing on particular medicinal plants, researchers can uncover unique fungal interactions and their implications for both plant and human health. Such targeted studies will provide deeper insights into the medicinal value of these plants and contribute to their conservation and sustainable use.

5.4 Publications

List of publications

5.4.1 First Author

Sun, Y. R., Goonasekara, I., Thambugala, K. M., Jayawardena, R. S., Wang, Y., & Hyde, K. D. (2020). *Distoseptispora bambusae* sp. nov. (Distoseptisporaceae) on bamboo from China and Thailand. *Biodiversity Data Journal, 8*, e53678. https://doi.org/10.3897/BDJ.8.e53678

Sun, Y. R., Jayawardena, R. S., Hyde, K. D., & Wang, Y. (2021). *Kirschsteiniothelia thailandica* sp. nov. (Kirschsteiniotheliaceae) from Thailand. *Phytotaxa*, *490*, 172–182. https://doi.org/10.11646/PHYTOTAXA.490.2.3

Sun, Y. R., Liu, N. G., Samarakoon, M. C., Jayawardena, R. S., Hyde, K. D., & Wang, Y. (2021). Morphology and phylogeny reveal Vamsapriyaceae fam. nov. (Xylariales, Sordariomycetes) with two novel *Vamsapriya* species. *Journal of Fungi*, *7*, 891. https://doi.org/10.3390/jof7110891

Sun, Y. R., Liu, N. G., Hyde, K. D., Jayawardena, R. S., & Wang, Y. (2022). *Pleocatenata chiangraiensis* gen. et. sp. nov. (Pleosporales, Dothideomycetes) from medicinal plants in northern Thailand. *MycoKeys*, *87*, 77–98. https://doi.org/10.3897/mycokeys.87.79433

Sun, Y. R., Zhang, J. Y., Hyde, K. D., Wang, Y., & Jayawardena, R. S. (2023). Morphology and phylogeny reveal three *Montagnula* species from China and Thailand. *Plants*, *12*(4), 738. https://doi.org/10.3390/plants12040738

Sun, Y. R., Jayawardena, R. S., Sun, J. E., & Wang, Y. (2023). Pestalotioid species associated with medicinal plants in Southwest China and Thailand. *Microbiology Spectrum*, *11*(1), e03987-03922. https://doi.org/10.1128/spectrum.03987-22

Sun, Y. R., Hyde, K. D., Liu, N. G., Al-Otibi, F., Wang, Y., & Jayawardena, R. S. (2024). Four fungal species associated with *Mahonia* in Guizhou Province, China [Menuscript preparation]. *Mycological Progress*.

Sun, Y. R., Liu, N. G., Al-Otibi, F., Wang, Y., Hyde, K. D., & Jayawardena, R. S. (2024). A new endophytic species, *Diaporthe litseae*, from medicinal plants in Guizhou Province, China [Menuscript preparation]. *Phytotaxa*.

Sun, Y. R., Hyde, K. D., Liu, N. G., Al-Otibi, F., Wijayawardene, N. N., Jayawardena, R. S., . . . Wang, Y. (2024). Microfungi on medicinal plants in southern China and northern Thailand [Menuscript preparation]. *Fungal Diversity*.

5.4.2 Co-author

Chethana, K. W. T., Niranjan, M., Dong, W., Samarakoon, M. C., Bao, D. F., Calabon, M. S., . . . Hyde, K. D. (2021). AJOM new records and collections of fungi: 101–150. *Asian Journal of Mycology, 4*, 113-260. https://doi.org/10.5943/ajom/4/1/8

He, Y. K., Yang, Q., Sun, Y. R., Zeng, X. Y., Jayawardena, R., Hyde, K., . . . Wang, Y. (2022). Additions to *Neopestalotiopsis* (Amphisphaeriales, Sporocadaceae) fungi: Two new species and one new host record from China. *Biodiversity Data Journal, 10*, e90709. https://doi.org/10.3897/BDJ.10.e90709

Jayawardena, R. S., Hyde, K. D., de Farias, A. R. G., Bhunjun, C. S., Ferdinandez, H. S., Manamgoda, D. S., . . . Thines, M. (2021). What is a species in fungal plant pathogens? *Fungal Diversity, 109*, 239-266. https://doi.org/10.1007/s13225-021-00484-8

Jayawardena, R. S., Hyde, K. D., Wang, S., Sun, Y. R., Suwannarach, N., Sysouphanthong, P., . . . Wang, Y. (2022). Fungal diversity notes 1512–1610: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 117*, 1–272. https://doi.org/10.1007/s13225-022-00513-0

Liu, N. G., Hyde, K. D., Sun, Y. R., Bhat, D. J., Jones, E. B. G., Jumpathong, J., . . . Liu, J. K. (2024). Notes, outline, taxonomy and phylogeny of brown-spored hyphomycetes [Manuscript preparation]. *Fungal Diversity*.

Liu, N. G., Liu, J. K., & Sun, Y. R. (2023). Phylogenetic placement of *Tretospeira cheirospora* in Phaeosphaeriaceae. *Phytotaxa, 579*(3), 175–186. https://doi.org/10.11646/PHYTOTAXA.579.3.3

Lu, Q. T., Zhang, J. Y., Sun, Y. R., Tang, X., Lu, Y. Z., & Zhang, Z. (2022). *Diaporthe orixae* sp. nov., an endophytic species isolated from Orixa japonica in southern China. *Phytotaxa, 544*, 37–51. https://doi.org/10.11646/PHYTOTAXA.544.1.3

Phukhamsakda, C., Nilsson, R. H., Bhunjun, C. S., de Farias, A. R. G., Sun, Y. R., Wijesinghe, S. N., . . . Hyde, K. D. (2022). The numbers of fungi: Contributions from traditional taxonomic studies and challenges of metabarcoding. *Fungal Diversity, 114*, 327–386. https://doi.org/10.1007/s13225-022-00502-3

Senanayake, I. C., Rossi, W., Leonardi, M., Weir, A., McHugh, M., Rajeshkumar, K. C., . . . Song, J. (2023). Fungal diversity notes 1610–1726: Taxonomic and phylogenetic contributions on fungal genera and species emphasis in south China. *Fungal Diversity, 122*, 161–403. https://doi.org/10.1007/s13225-023-00523-6

Xun, W. Z., Wu, C. W., Wu, X., Bai, Q. R., Sun, Y. R., Shi, J. Y., . . . Jin, L. H. (2023). First report of Bayberry leaf blight caused by *Pestalotiopsis kenyana* in Zhejiang Province, China. *Plant Disease, 107*, 2860. https://doi.org/10.1094/PDIS-03-23-0450-PDN

REFERENCES

REFERENCES

Abass, M. H., Hameed, M. A., & Ahmed, A. N. (2013). First report of *Nigrospora sphaerica* (Sacc.) Mason as a potential pathogen on date palm (*Phoenix dactylifera* L.). *Canadian Journal of Plant Pathology, 35*(1), 75-80. https://doi.org/10.1080/07060661.2012.732612

Abass, M. H., & Mohammed, N. H. (2014). Morphological, molecular and pathological study on *Nigrospora oryzae* and *Nigrospora sphaerica*, the leaf spot fungi of date palm. *Basra Journal for Date Palm Researches, 13*, 26-38.

Abd_Allah, E. F., Hashem, A., Alqarawi, A. A., Bahkali, A. H., & Alwhibi, M. S. (2015). Enhancing growth performance and systemic acquired resistance of medicinal plant *Sesbania sesban* (L.) Merr using arbuscular mycorrhizal fungi under salt stress. *Saudi Journal of Biological Sciences, 22*(3), 274-283. https://doi.org/10.1016/j.sjbs.2015.03.004

Abdollahzadeh, J., Javadi, A., Goltapeh, E. M., Zare, R., & Phillips, A. J. L. (2010). Phylogeny and morphology of four new species of *Lasiodiplodia* from Iran. *Persoonia, 25*(1), 1-10. https://doi.org/10.3767/003158510X524150

AbuQamar, S. F., Abd El-Fattah, H. I., Nader, M. M., Zaghloul, R. A., Abd El-Mageed, T. A., Selim, S., . . . El-Tarabily, K. A. (2023). Exploiting fungi in bioremediation for cleaning-up emerging pollutants in aquatic ecosystems. *Marine Environmental Research, 190*, 106068. https://doi.org/10.1016/j.marenvres.2023.106068

Alves, J. L., Saraiva, R. M., Mizubuti, E. S. G., Carneiro, S. M. P. T. G., Borsato, L. C., Woudenberg, J. H. C., . . . Lourenço, V., Jr. (2016). First report of *Alternaria carthami* causing leaf spots on *Carthamus tinctorius* in Brazil. *New Disease Reports, 33*, 3. https://doi.org/10.5197/j.2044-0588.2016.033.003

Aptroot, A. (1995). Redisposition of some species excluded from *Didymosphaeria* (Ascomycotina). *Nova Hedwigia, 60*, 325-380.

Ariyawansa, H. A., Tanaka, K., Thambugala, K. M., Phookamsak, R., Tian, Q., Camporesi, E., . . . Hyde, K. D. (2014). A molecular phylogenetic reappraisal of the *Didymosphaeriaceae* (= *Montagnulaceae*). *Fungal Diversity, 68*, 69-104. https://doi.org/10.1007/s13225-014-0305-6

Armand, A., Bundhun, D., Bhunjun, C. S., Punyaboon, W., & Jayawardena, R. S. (2023). *Paramyrothecium amorphophalli* sp. nov., a causal agent of leaf blight on elephant foot yam in northern Thailand. *Current Research in Environmental & Applied Mycology, 13*(1), 57-67. https://doi.org/10.5943/cream/13/1/4

Arnaud, G. (1954). Mycologie concrète: Genera II. *Bulletin Trimestriel de la Société Mycologique de France, 69*, 265-306.

Aumentado, H. D., & Balendres, M. A. (2022). Identification of *Paramyrothecium foliicola* causing crater rot in eggplant and its potential hosts under controlled conditions. *Journal of Phytopathology, 170*(3), 148-157. https://doi.org/10.1111/jph.13062

Bao, D. F., Hyde, K. D., McKenzie, E. H., Jeewon, R., Su, H. Y., Nalumpang, S., . . . Luo, Z. L. (2021). Biodiversity of lignicolous freshwater hyphomycetes from China and Thailand and description of sixteen species. *Journal of Fungi, 7*, 669. https://doi.org/10.3390/jof7080669

Barrios, L. M., & Pérez, I. O. (2005). Nuevos registros de hongos en semillas de *Oryza sativa* en Cuba. *Manejo Integrado de Plagas y Agroecología, 75*, 64-67.

Bhunjun, C. S., Phukhamsakda, C., Jayawardena, R. S., Jeewon, R., Promputtha, I., & Hyde, K. D. (2021). Investigating species boundaries in *Colletotrichum*. *Fungal Diversity, 107*, 107-127. https://doi.org/10.1007/s13225-021-00471-z

Bills, G. F., & Gloer, J. B. (2017). Biologically active secondary metabolites from the fungi. *The Fungal Kingdom*, 1087-1119. https://doi.org/10.1128/9781555819583.ch54

Boehm, E. W. A., Mugambi, G. K., Miller, A. N., Huhndorf, S. M., Marincowitz, S., Spatafora, J. W., . . . Schoch, C. L. (2009). A molecular phylogenetic reappraisal of the *Hysteriaceae, Mytilinidiaceae* and *Gloniaceae* (Pleosporomycetidae, Dothideomycetes) with keys to world species. *Studies in Mycology, 64*(1), 49-83. https://doi.org/10.3114/sim.2009.64.03

Bonthond, G., Sandoval-Denis, M., Groenewald, J. Z., & Crous, P. W. (2018). *Seiridium* (Sporocadaceae): An important genus of plant pathogenic fungi. *Persoonia, 40*(1), 96-118. https://doi.org/10.3767/persoonia.2018.40.04

Boonmee, S., D'souza, M. J., Luo, Z. L., Pinruan, U., Tanaka, K., Su, H. Y., . . . Hyde, K. D. (2016). *Dictyosporiaceae* fam. nov. *Fungal Diversity, 80*, 457-482. https://doi.org/10.1007/s13225-016-0363-z

Boonmee, S., Wanasinghe, D. N., Calabon, M. S., Huanraluek, N., Chandrasiri, S. K. U., Jones, G. E. B., . . . Hyde, K. D. (2021). Fungal diversity notes 1387–1511: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 111*, 1-335. https://doi.org/10.1007/s13225-021-00489-3

Boonmee, S., Ko, T. W. K., Chukeatirote, E., Hyde, K. D., Chen, H., Cai, L., . . . Hassan, B. A. (2012). Two new *Kirschsteiniothelia* species with *Dendryphiopsis* anamorphs cluster in *Kirschsteiniotheliaceae* fam. nov. *Mycologia, 104*, 698-714. https://doi.org/10.3852/11-089

Brahmanage, R. S., Lu, Y. Z., Bhat, D. J., Wanasinghe, D. N., Yan, J. Y., Hyde, K. D., . . . Boonmee, S. (2017). Phylogenetic investigations on freshwater fungi in *Tubeufiaceae* (*Tubeufiales*) reveals the new genus *Dictyospora* and new species *Chlamydotubeufia aquatica* and *Helicosporium flavum*. *Mycosphere, 8*(7), 917-933. https://doi.org/10.5943/mycosphere/8/7/8

Bundhun, D., Senanayake, I. C., Jayawardena, R. S., Camporesi, E., Huang, Y. H., Dong, Z. Y., . . . Cheewangkoon, R. (2021). First reports of the sexual morphs of *Diaporthe forlicesenica* nom. nov. and *Diaporthe goulteri* (*Diaporthaceae*, *Diaporthales*) revealed by molecular phylogenetics. *Phytotaxa*, *516*(1), 1-27. https://doi.org/10.11646/phytotaxa.516.1.1

Calabon, M. S., Hyde, K. D., Jones, E. B. G., Chandrasiri, S., Dong, W., Fryar, S. C., . . . Bao, D. F. (2020). www.freshwaterfungi.org, an online platform for the taxonomic classification of freshwater fungi. *Asian Journal of Mycology, 3*(1), 419-445. https://doi.org/10.5943/ajom/3/1/14

Calvillo-Medina, R. P., Martínez-Neria, M., Mena-Portales, J., Barba-Escoto, L., Raymundo, T., Campos-Guillén, J., . . . Bautista-de Lucio, V. M. (2019). Identification and biofilm development by a new fungal keratitis aetiologic agent. *Mycoses, 62*(1), 62-72. https://doi.org/10.1111/myc.12849

Câmara, M. P. S., Ramaley, A. W., & Castlebury, L. A. (2003). *Neophaeosphaeria* and *Phaeosphaeriopsis*, segregates of *Paraphaeosphaeria*. *Mycological Research, 107*(5), 516-522. https://doi.org/10.1017/S0953756203007731

Capella-Gutiérrez, S., Silla-Martínez, J. M., & Gabaldón, T. (2009). trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. *Bioinformatics, 25*(15), 1972-1973. https://doi.org/10.1093/bioinformatics/btp348

Cazau, M. C., Arambarri, A. M., & Cabello, M. N. (1993). New hyphomycetes from Santiago river. VI. (Buenos Aires province, Argentina). *Mycotaxon, 46*, 235-240.

Cesati, V., & De Notaris, G. (1863). Schema di classificazione degli sferiacei italici aschigeri: più o meno appartenenti al genere *Sphaeria* nell'antico significato attribuitogli dal Persoon. *Commentario della Società Crittogamica Italiana, 1*, 177-240.

Chaisiri, C. C., Liu, X. Y., Lin, Y., & Luo, C. X. (2022). *Diaporthe citri*: A fungal pathogen causing melanose disease. *Plants, 11*(12). https://doi.org/10.3390/plants11121600

Chaiwan, N., Gomdola, D., Wang, S., Monkai, J., Tibpromma, S., Doilom, M., . . . Hyde, K. D. (2021). An online database providing updated information of microfungi in the Greater Mekong Subregion. *Mycosphere, 12*(1), 1513-1526.

Chen, Y., Tian, W., Guo, Y., Madrid, H., & Maharachchikumbura, S. S. N. (2022). *Synhelminthosporium* gen. et sp. nov. and two new species of *Helminthosporium* (Massarinaceae, Pleosporales) from Sichuan Province, China. *Journal of Fungi, 8*(7). https://doi.org/10.3390/jof8070712

Chen, Y. P., Lu, Z. H., Faraj, T. K., & Maharachchikumbura, S. S. N. (2023). *Myxospora poaceicola* sp. nov. (Stachybotryaceae, Hypocreales), a novel *myrothecium*-like fungus from *Digitaria sanguinalis* (Poaceae). *Phytotaxa, 625*(3), 280-288. https://doi.org/10.11646/phytotaxa.625.3.4

Chethana, K. W. T., Manawasinghe, I. S., Hurdeal, V. G., Bhunjun, C. S., Appadoo, M. A., Gentekaki, E., . . . Hyde, K. D. (2021). What are fungal species and how to delineate them. *Fungal Diversity, 109*, 1-25. https://doi.org/10.1007/s13225-021-00483-9

Chowdhary, K., & Kaushik, N. (2015). Fungal endophyte diversity and bioactivity in the Indian medicinal plant *Ocimum sanctum* Linn. *PLOS ONE, 10*(11), e0141444. https://doi.org/10.1371/journal.pone.0141444

Cobos-Villagrán, A., Raymundo, T., Calvillo-Medina, R. P., & Valenzuela, R. (2021). *Rhytidhysteron mexicanum* sp. nov. (*Dothideomycetes*, *Ascomycota*) from the Sierra of Guadalupe, Trans Mexican Volcanic Belt. *Phytotaxa, 479*(3), 275-286. https://doi.org/10.11646/phytotaxa.479.3.4

Cobos-Villagrán, A., Valenzuela, R., Hernández-Rodríguez, C., Calvillo-Medina, R. P., Villa-Tanaca, L., Mateo-Cid, L. E., . . . Raymundo, T. (2021). Three new species of *Rhytidhysteron* (*Dothideomycetes*, *Ascomycota*) from Mexico. *MycoKeys, 83*, 123-144. https://doi.org/10.3897/mycokeys.83.68582

Corda, A. C. J. (1838). *Icones fungorum hucusque cognitorum 2*. Apud J. G. Calve.

Crane, J. L., & Miller, A. N. (2016). Studies in genera similar to *Torula*: *Bahusaganda*, *Bahusandhika*, *Pseudotorula*, and *Simmonsiella* gen. nov. *IMA Fungus, 7*, 29-45. https://doi.org/10.5598/imafungus.2016.07.01.03

Crous, P. W., Cowan, D. A., Maggs-Kölling, G., Yilmaz, N., Thangavel, R., Wingfield, M. J., . . . Groenewald, J. Z. (2021). Fungal Planet description sheets: 1182–1283. *Persoonia, 46*, 313-528. https://doi.org/10.3767/persoonia.2021.46.11

Crous, P. W., Schumacher, R. K., Akulov, A., Thangavel, R., Hernández-Restrepo, M., Carnegie, A. J., . . . Groenewald, J. Z. (2019). New and interesting fungi. 2. *Persoonia, 3*, 57-134. https://doi.org/10.3114/fuse.2019.03.06

Crous, P. W., Shivas, R. G., Quaedvlieg, W., Van der Bank, M., Zhang, Y., Summerell, B. A., . . . Groenewald, J. Z. (2014). Fungal Planet description sheets: 214–280. *Persoonia, 32*, 184-306. https://doi.org/10.3767/003158514X682395

Crous, P. W., Slippers, B., Wingfield, M. J., Rheeder, J., Marasas, W. F., Philips, A. J., . . . Groenewald, J. Z. (2006). Phylogenetic lineages in the *Botryosphaeriaceae*. *Studies in Mycology, 55*(1), 235−253. https://doi.org/10.3114/sim.55.1.235

Crous, P. W., Summerell, B. A., Shivas, R. G., Burgess, T. I., Decock, C. A., Dreyer, L. L., . . . Groenewald, J. Z. (2012). Fungal Planet description sheets: 107–127. *Persoonia, 28*, 138-182. https://doi.org/10.3767/003158512X652633

Crous, P. W., Wingfield, M. J., Burgess, T. I., Carnegie, A. J., Hardy, G. E. S. J., Smith, D., . . . Groenewald, J. Z. (2017). Fungal Planet description sheets: 625–715. *Persoonia, 39*, 270.

Crous, P. W., Wingfield, M. J., Burgess, T. I., Hardy, G. E. S. J., Gené, J., Guarro, J., . . . Groenewald, J. Z. (2018). Fungal Planet description sheets: 716–784. *Persoonia, 40*, 240-393. https://doi.org/10.3767/persoonia.2018.40.10

Crous, P. W., Wingfield, M. J., Burgess, T. I., Hardy, G. E., Crane, C., Barrett, S., . . . Groenewald, J. Z. (2016). Fungal Planet description sheets: 469–557. *Persoonia, 37*, 218-403. https://doi.org/10.3767/003158516X694499

Crous, P. W., Wingfield, M. J., Chooi, Y. H., Gilchrist, C. L. M., Lacey, E., Pitt, J. I., . . . Groenewald, J. Z. (2020). Fungal Planet description sheets: 1042–1111. *Persoonia, 44*, 301.

Crous, P. W., Wingfield, M. J., Guarro, J., Hernández-Restrepo, M., Sutton, D. A., Acharya, K., . . . Groenewald, J. Z. (2015). Fungal Planet description sheets: 320–370. *Persoonia, 34*, 167–266. https://doi.org/10.3767/003158515X688433

Crous, P. W., Wingfield, M. J., Richardson, D. M., Le Roux, J. J., Strasberg, D., Edwards, J., . . . Groenewald, J. Z. (2016). Fungal Planet description sheets: 400–468. *Persoonia, 36*(1), 316-458.

Crous, P. W., Wingfield, M. J., Roux, J. J. Le, Richardson, D. M., Strasberg, D., Shivas, R. G., . . . Groenewald, J. Z. (2015). Fungal Planet description sheets: 371–399. *Persoonia, 35*(1), 264–327.

Cui, M. J., Wei, X., Xia, P. L., Yi, J. P., Yu, Z. H., Deng, J. X., . . . Li, Q. L. (2021). *Diaporthe taoicola* and *D. siamensis*, two new records on *Citrus sinensis* in China. *Mycobiology, 49*(3), 267–274. https://doi.org/10.1080/12298093.2021.1912254

Cui, Y. P., Wu, B., Peng, A. T., Li, Z. L., Lin, J. F., & Song, X. B. (2018). First report of *Nigrospora* leaf blight on sugarcane caused by *Nigrospora sphaerica* in China. *Plant Disease, 102*(4), 824–824. https://doi.org/10.1094/PDIS-07-17-1060-PDN

D'Souza, M., Singh, S. K., & Bhat, D. (2002). *New conidial fungi from Andaman Islands, India*. Department of Botany, Goa University.

Dai, D. Q., Bahkali, A. H., Li, Q. R., Bhat, D. J., Wijayawardene, N. N., Li, W. J., . . . Hyde, K. D. (2014). *Vamsapriya* (*Xylariaceae*) re-described, with two new species and molecular sequence data. *Cryptogamie, Mycologie*, *35*(4), 339–357. https://doi.org/10.7872/crym.v35.iss4.2014.339

Dai, D. Q., Phookamsak, R., Wijayawardene, N. N., Li, W. J., Bhat, D. J., Xu, J. C., . . . Chukeatirote, E. (2016). Bambusicolous fungi. *Fungal Diversity*, *82*, 1–105. https://doi.org/10.1007/s13225-016-0367-8

Dai, D. Q., Wijayawardene, N. N., Dayarathne, M. C., Kumla, J., Han, L. S., Zhang, G. Q., . . . Chen, H. H. (2022). Taxonomic and phylogenetic characterizations reveal four new species, two new asexual morph reports, and six new country records of bambusicolous *Roussoella* from China. *Journal of Fungi*, *8*(5). https://doi.org/10.3390/jof8050532

Dar, R. A., Shahnawaz, M., & Qazi, P. H. (2017). General overview of medicinal plants: A review. *The Journal of Phytopharmacology*, *6*(6), 349-351. https://doi.org/10.31254/phyto.2017.6608

Das, K., Lee, S. Y., & Jung, H. Y. (2021). Morphology and phylogeny of two novel species within the class *Dothideomycetes* collected from soil in Korea. *Mycobiology*, *49*(1), 15–23. https://doi.org/10.1080/12298093.2020.1838114

Dayarathne, M. C., Jones, E. B. G., Maharachchikumbura, S. S. N., Devadatha, B., Sarma, V. V., Khongphinitbunjong, K., . . . Hyde, K. D. (2020). Morpho-molecular characterization of microfungi associated with marine based habitats. *Mycosphere*, *11*(1), 1–188. https://doi.org/10.5943/mycosphere/11/1/1

de Gruyter, J., Woudenberg, J. H. C., Aveskamp, M. M., Verkley, G. J., Groenewald, J. Z., & Crous, P. W. (2010). Systematic reappraisal of species in *Phoma* section *Paraphoma*, *Pyrenochaeta* and *Pleurophoma*. *Mycologia*, *102*(5), 1066–1081. https://doi.org/10.3852/09-240

de Gruyter, J., Woudenberg, J. H. C., Aveskamp, M. M., Verkley, G. J. M., Groenewald, J. Z., & Crous, P. W. (2013). Redisposition of *Phoma*-like anamorphs in *Pleosporales*. *Studies in Mycology*, *75*(1), 1–36. https://doi.org/10.3114/sim0004

de Silva, N., Hyde, K. D., Lumyong, S., Phillips, A. J. L., Bhat, D. J., Maharachchikumbura, S. S. N., . . . Karunarathna, S. C. (2022). Morphology, phylogeny, host association and geography of fungi associated with plants of Annonaceae, Apocynaceae and Magnoliaceae. *Mycosphere*, *13*(1), 955–1076. https://doi.org/10.5943/mycosphere/13/1/12

Dehghani, K., Amirmijani, A. R., & Pordel, A. (2022). Fungal species associated with leaf spot on mango trees in Iran. *Mycologia Iranica*, *9*(1), 75–83.

Dissanayake, A. J., Chen, Y. Y., Cheewangkoon, R., & Liu, J. K. (2021). Occurrence and morpho-molecular identification of *Botryosphaeriales* species from Guizhou Province, China. *Journal of Fungi*, *7*(11), 893. https://doi.org/10.3390/jof7110893

Dissanayake, A. J., Chen, Y. Y., & Liu, J. J. K. (2020). Unravelling *Diaporthe* species associated with woody hosts from Karst formations (Guizhou) in China. *Journal of Fungi*, *6*(4), 251. https://doi.org/10.3390/jof6040251

Dissanayake, A. J., Phillips, A. J. L., Li, X. H., & Hyde, K. D. (2016). *Botryosphaeriaceae*: Current status of genera and species. *Mycosphere*, *7*, 1001–1073. https://doi.org/10.5943/mycosphere/si/1b/13

Dissanayake, A. J., Zhu, J. T., Chen, Y. Y., Maharachchikumbura, S. S. N., Hyde, K. D., & Liu, J. K. (2024). A re-evaluation of *Diaporthe*: Refining the boundaries of species and species complexes. *Fungal Diversity*, *126*, 1-125. https://doi.org/10.1007/s13225-024-00538-7

Dissanayake, L. S., Samarakoon, M. C., Mortimer, P. E., Lu, Y. Z., Li, Q. R., Hyde, K. D., . . . Kang, J. C. (2020). Morpho-molecular characterization of two novel amphisphaeriaceous species from Yunnan, China. *Phytotaxa*, *446*(3), 144–158. https://doi.org/10.11646/phytotaxa.446.3.1

Doilom, M., Dissanayake, A. J., Wanasinghe, D. N., Boonmee, S., Liu, J. K., Bhat, D. J., . . . Hyde, K. D. (2017). Microfungi on *Tectona grandis* (teak) in Northern Thailand. *Fungal Diversity*, *82*, 107–182. https://doi.org/10.1007/s13225-016-0368-7

Doilom, M., Shuttleworth, L. A., Roux, J., Chukeatirote, E., & Hyde, K. D. (2014). *Barriopsis tectonae* sp. nov. a new species of *Botryosphaeriaceae* from *Tectona grandis* (teak) in Thailand. *Phytotaxa*, *176*, 81–91. https://doi.org/10.11646/phytotaxa.176.1.10

Dong, W., Wang, B., Hyde, K. D., McKenzie, E. H. C., Raja, H. A., Tanaka, K., . . . Zhang, H. (2020). Freshwater *Dothideomycetes*. *Fungal Diversity*, *105*, 319-575. https://doi.org/10.1007/s13225-020-00463-5

Dong, X. L., Cheng, Z. Z., Leng, W. F., Li, B. H., Xu, X. M., Lian, S., . . . Wang, C. X. (2021). Progression of symptoms caused by *Botryosphaeria dothidea* on apple branches. *Phytopathology*, *111*(9), 1551–1559. https://doi.org/10.1094/PHYTO-12-20-0551-R

Dong, Z. Y., Shu, Y. X., Luo, M., Zhang, W. L., Chen, X. Y., & Xiao, Y. X. (2019). First report of black root rot disease on *Morinda officinalis* caused by *Lasiodiplodia pseudotheobromae* in China. *Plant Disease, 103*(10), 2693. https://doi.org/10.1094/PDIS-04-19-0857-PDN

Dos Santos, P. J. C., Savi, D. C., Gomes, R. R., Goulin, E. H., Senkiv, C. D. C., Tanaka, F. A. O., . . . Glienke, C. (2016). *Diaporthe endophytica* and *D. terebinthifolii* from medicinal plants for biological control of *Phyllosticta citricarpa*. *Microbiological Research, 186*, 153–160. https://doi.org/10.1016/j.micres.2016.04.002

Du, T. Y., Hyde, K. D., Mapook, A., Mortimer, P. E., Xu, J. C., & Karunarathna, S. C. (2021). Morphology and phylogenetic analyses reveal *Montagnula puerensis* sp. nov. (Didymosphaeriaceae, Pleosporales) from southwest China. *Phytotaxa, 514*, 1–25. https://doi.org/10.11646/phytotaxa.514.1.1

Du, T. Y., Dai, D. Q., Mapook, A., Lu, L., Stephenson, S. L., Suwannarach, N., . . . Tibpromma, S. (2023). Additions to *Rhytidhysteron* (Hysteriales, Dothideomycetes) in China. *Journal of Fungi, 9*(2). https://doi.org/10.3390/jof9020148

Dubey, R. (2021). *Achroiostachys bambusicola* (Stachybotryaceae, Hypocreales) – A novel species of achrois fungus reported from Tansa Wild Life Sanctuary (Western Ghats), Maharashtra, India. *Species, 22*(70), 318–322.

Dubey, R., & Pandey, A. K. (2009). New species of *Seiridium* and *Sporotrichum* from India. *Journal of Mycology and Plant Pathology*, *39*(2), 297–299.

Dutta, J., Gupta, S., Thakur, D., & Handique, P. J. (2015). First report of *Nigrospora* leaf blight on tea caused by *Nigrospora sphaerica* in India. *Plant Disease, 99*(3), 417–417. https://doi.org/10.1094/PDIS-05-14-0545-PDN

Dyko, B. J., & Sutton, B. C. (1979). Two new and unusual deuteromycetes. *Transactions of the British Mycological Society, 72*(3), 411–417. https://doi.org/10.1016/S0007-1536(79)80147-3

Edler, D., Klein, J., Antonelli, A., & Silvestro, D. (2021). raxmlGUI 2.0: A graphical interface and toolkit for phylogenetic analyses using RAxML. *Methods in Ecology and Evolution, 12*(2), 373–377. https://doi.org/10.1111/2041-210X.13512

Ekanayaka, A. H., Hyde, K. D., Gentekaki, E., McKenzie, E. H. C., Zhao, Q., Bulgakov, T. S., & Camporesi, E. (2019). Preliminary classification of *Leotiomycetes*. *Mycosphere, 10*, 310–489. https://doi.org/10.5943/mycosphere/10/1/7

Ellis, M. B. (1961). Dematiaceous hyphomycetes. III. *Mycological Papers, 82*, 1–55.

Ellis, M. B. (1976). *More dematiaceous hyphomycetes*. Commonwealth Mycological Institute.

Eriksson, O. (1967). On graminicolous pyrenomycetes from Fennoscandia. I, II, III. *Arkiv för Botanik Serie, 26*, 339–446.

Eskola, M., Kos, G., Elliott, C. T., Hajšlová, J., Mayar, S., & Krska, R. (2020). Worldwide contamination of food-crops with mycotoxins: Validity of the widely cited 'FAO estimate' of 25%. *Critical Reviews in Food Science and Nutrition, 60*(16), 2773-2789. https://doi.org/10.1080/10408398.2019.1658570

Farnsworth, N. R., Akerele, O., Bingel, A. S., Soejarto, D. D., & Guo, Z. (1985). Medicinal plants in therapy. *Bulletin of the World Health Organization, 63*(6), 965–981.

Feng, Y., Liu, J. K., Lin, C. G., Chen, Y. Y., Xiang, M. M., & Liu, Z. Y. (2021). Additions to the genus *Arthrinium* (*Apiosporaceae*) from bamboos in China. *Frontiers in Microbiology, 12*, 661281. https://doi.org/10.3389/fmicb.2021.661281

Finley, D. E. (1967). *Virgatospora*: A new genus of *Stilbellaceae*. *Mycologia, 59*, 538–541. https://doi.org/10.2307/3756777

Freitas, E. F., Silva, M. d., Barros, M. V., & Kasuya, M. C. (2019). *Neopestalotiopsis hadrolaeliae* sp. nov., a new endophytic species from the roots of the endangered orchid *Hadrolaelia jongheana* in Brazil. *Phytotaxa, 416*(3), 211-220. https://doi.org/10.11646/phytotaxa.416.3.2

Gao, Y. H., Liu, F., Duan, W. J., Crous, P. W., & Cai, L. (2017). *Diaporthe* is paraphyletic. *IMA Fungus, 8*, 153–187. https://doi.org/10.5598/imafungus.2017.08.01.11

Gao, Y. H., Su, Y., Sun, W., & Cai, L. (2015). *Diaporthe* species occurring on *Lithocarpus glabra* in China, with descriptions of five new species. *Fungal Biology, 119*(5), 295–309. https://doi.org/10.1016/j.funbio.2014.06.006

Gawas, P., & Bhat, D. J. (2005). *Vamsapriya indica* gen. et sp. nov., a bambusicolous, synnematous fungus from India. *Mycotaxon, 94*, 149–154.

Goh, T.K., Hsieh, S. Y., & Kuo, C. H. (2023). Synonymy of *Parafuscosporella* with *Vanakripa* and descriptions of two new species from Taiwan. *Mycological Progress, 22*(8), 61. https://doi.org/10.1007/s11557-023-01907-3

Goh, T.K., Hyde, K. D., & Ho, W. H. (1999). A revision of the genus *Dictyosporium*, with descriptions of three new species. *Fungal Diversity, 2*, 65–100.

Gong, M. Q., Wang, F. Z., & Chen, Y. (2002). Application of arbuscular mycorrhiza in Aloe seedling raising. *Journal of Chinese Medicinal Materials, 25*, 1–3.

Gualberto, G. F., Catarino, A., Sousa, T. F., da Cruz, J., Hanada, R. E., Caniato, F. F., . . . da Silva, G. (2021). *Pseudopestalotiopsis gilvanii* sp. nov. and *Neopestalotiopsis formicarum* leaves spot pathogens from guarana plant: A new threat to global tropical hosts. *Phytotaxa, 489*, 121–139. https://doi.org/10.11646/phytotaxa.489.2.2

Hall, T. A. (1999). BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series, 41*, 95–98.

Hao, Y. Y., Aluthmuhandiram, J. V. S., Chethana, K. W. T., Manawasinghe, I. S., Li, X. H., Liu, M., . . . Zhang, W. (2020). *Nigrospora* species associated with various hosts from Shandong Peninsula, China. *Mycobiology, 48*(3), 169–183. https://doi.org/10.1080/12298093.2020.1761747

Harkness, H. W. (1884). New species of Californian fungi. *Bulletin of the Southern California Academy of Sciences, 1*, 29–47.

Hashimoto, A., Sato, G., Matsuda, T., Matsumura, M., Hatakeyama, S., Harada, Y., Ikeda, H., & Tanaka, K. (2015). Taxonomic revision of *Pseudolachnea* and *Pseudolachnella* and establishment of *Neopseudolachnella* and *Pseudodinemasporium* gen. nov. *Mycologia, 107*(2), 383–408. https://doi.org/10.3852/14-171

Hattori, Y., Ando, Y., Sasaki, A., Uechi, N., & Nakashima, C. (2021). Taxonomical study of noteworthy species of *Botryosphaeria* in Japan. *Mycobiology, 49*(2), 122–132. https://doi.org/10.1080/12298093.2021.1895486

Hawksworth, D. L. (1985). *Kirschsteiniothelia*, a new genus for the *Microthelia incrustans*-group (*Dothideales*). *Botanical Journal of the Linnean Society, 91*, 181–202. https://doi.org/10.1111/j.1095-8339.1985.tb01144.x

He, Y. K., Yang, Q., Sun, Y. R., Zeng, X. Y., Jayawardena, R. S., Hyde, K. D., . . . Wang, Y. (2022). Additions to *Neopestalotiopsis* (*Amphisphaeriales, Sporocadaceae*) fungi: Two new species and one new host record from China. *Biodiversity Data Journal, 10*, e90709. https://doi.org/10.3897/BDJ.10.e90709

Hirayama, K., & Tanaka, K. (2011). Taxonomic revision of *Lophiostoma* and *Lophiotrema* based on reevaluation of morphological characters and molecular analyses. *Mycoscience, 52*(6), 401–412. https://doi.org/10.1007/S10267-011-0126-3

Höhnel, F. V. (1904). Mycologische Fragmente. *Annales Mycologici, 2*, 38–60.

Höhnel, F. V. (1914). Fragmente zur Mykologie XVI (XVI. Mitteilung, Nr. 813 bis 875). *Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften Mathematisch-Naturwissenschaftliche Klasse Abteilung I, 123*, 49–155.

Höhnel, V. (1919). Fragmente zur Mykologie. XXIII Mitteilung, Nr. 1154 bis 1188. *Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften Mathematisch-Naturwissenschaftliche Klasse Abteilung I, 128*, 535–625.

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C., Sarma, V. V., . . . Xie, N. (2020a). Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. *Mycosphere, 11*(1), 1553–2107. https://doi.org/10.5943/mycosphere/11/1/13

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C., Sarma, V. V., . . . Xie, N. (2020b). Refined families of Dothideomycetes: Orders and families incertae sedis in Dothideomycetes. *Fungal Diversity, 105*, 17-318. https://doi.org/10.1007/s13225-020-00462-6

Hongsanan, S., Li, Y. M., Liu, J. K., Hofmann, T., Piepenbring, M., Bhat, J. D., . . . Hyde, K. D. (2014). Revision of genera in Asterinales. *Fungal Diversity, 68*, 1–68. https://doi.org/10.1007/s13225-014-0307-4

Hongsanan, S., Maharachchikumbura, S. S. N., Hyde, K. D., Samarakoon, M. C., Jeewon, R., Zhao, Q., . . . Bahkali, A. H. (2017). An updated phylogeny of *Sordariomycetes* based on phylogenetic and molecular clock evidence. *Fungal Diversity*, *84*, 25-41. https://doi.org/10.1007/s13225-017-0384-2

Hongsanan, S., Norphanphoun, C., Senanayake, I. C., Jayawardena, R. S., Manawasinghe, I. S., Abeywickrama, P. D., . . . Bhunjun, C. S. (2023). Annotated notes on *Diaporthe* species. *Mycosphere, 14*, 918–1189. https://doi.org/10.5943/mycosphere/14/1/12

Htet, Z. H., Prematunga, C., Mapook, A., Jones, E. B. G., & Chethana, K. W. T. (2023). Taxonomy and phylogeny of *Paradictyoarthrinium salsipaludicola* sp. nov. (*Paradictyoarthriniaceae*, *Pleosporales*) from mangroves. *Phytotaxa, 620*(4), 283–292. https://doi.org/10.11646/phytotaxa.620.4.4

Htet, Z. H., Tibpromma, S., Mapook, A., Chethana, K. W. T., & Hyde, K. D. (2023). *Murichromolaenicola thailandensis* sp. nov. (Phaeosphaeriaceae, Dothideomycetes) from *Chromolaena odorata* (Asteraceae) in northern Thailand. *Phytotaxa, 618*(2), 120–132. https://doi.org/10.11646/phytotaxa.618.2.2

Huanaluek, N., Jayawardena, R. S., Maharachchikumbura, S. S., & Harishchandra, D. L. (2021). Additions to pestalotioid fungi in Thailand: *Neopestalotiopsis hydeana* sp. nov. and *Pestalotiopsis hydei* sp. nov. *Phytotaxa, 479*, 23–43. https://doi.org/10.11646/phytotaxa.479.1.2

Hu, H., He, M., Wu, Y., Long, S., Zhang, X., Liu, L., . . . Li, Q. (2023). Taxonomic and phylogenetic characterisations of six species of *Pleosporales* (in Didymosphaeriaceae, Roussoellaceae and Nigrogranaceae) from China. *MycoKeys, 100*, 123–151. https://doi.org/10.3897/mycokeys.100.109423

Hu, S. Y. (1979). A contribution to our knowledge of Tu-chung — *Eucommia ulmoides*. *The American Journal of Chinese Medicine, 7*(1), 5–37. https://doi.org/10.1142/S0192415X79000039

Hu, Y. F., Liu, J. W., Luo, X. X., Xu, Z. H., Xia, J. W., Zhang, X. G., . . . Ma, J. (2023). Multi-locus phylogenetic analyses reveal eight novel species of *Distoseptispora* from southern China. *Microbiology Spectrum, 11*(6), e02468-02423. https://doi.org/10.1128/spectrum.02468-23

Hu, Y. F., Liu, J. W., Xu, Z. H., Castañeda-Ruíz, R. F., Zhang, K., & Ma, J. (2023). Morphology and multigene phylogeny revealed three new species of *Helminthosporium* (Massarinaceae, Pleosporales) from China. *Journal of Fungi, 9*(2). https://doi.org/10.3390/jof9020280

Huang, F., Hou, X., Dewdney, M. M., Fu, Y. S., Chen, G. Q., Hyde, K. D., & Li, H. Y. (2013). *Diaporthe* species occurring on citrus in China. *Fungal Diversity, 61*, 237–250. https://doi.org/10.1007/s13225-013-0245-6

Huang, F., Udayanga, D., Wang, X. H., Hou, X., Mei, X. F., Fu, Y. S., . . . Li, H. Y. (2015). Endophytic *Diaporthe* associated with citrus: A phylogenetic reassessment with seven new species from China. *Fungal Biology, 119*(5), 331–347. https://doi.org/10.1016/j.funbio.2015.02.006

Huang, S. K., Tangthirasunun, N., Phillips, A. J. L., Dai, D. Q., Wanasinghe, D. N., Wen, T. C., . . . Kang, J. C. (2016). Morphology and phylogeny of *Neoscytalidium orchidacearum* sp. nov. (*Botryosphaeriaceae*). *Mycobiology, 44*(2), 79-84. https://doi.org/10.5941/MYCO.2016.44.2.79

Huanraluek, N., Thambugala, K. M., Wang, Y., & Hyde, K. D. (2018). Introducing *Massarioramusculicola*, a novel genus in *Massariaceae*. *Phytotaxa, 371*(1), 17–24. https://doi.org/10.11646/phytotaxa.371.1.2

Hyde, K. D., Suwannarach, N., Jayawardena, R. S., Manawasinghe, I. S., Liao, C. F., Doilom, M., . . . Bao, D. F. (2021). Mycosphere notes 325-344-Novel species and records of fungal taxa from around the world. *Mycosphere, 12*(1), 1101-1156. https://doi.org/10.5943/mycosphere/12/1/14

Hyde, K. D. (1996). Fungi from palms. XXIX. *Arecophila* gen. nov. (Amphisphaeriaceae, Ascomycota), with five new species and two new combinations. *Nova Hedwigia, 63*(1/2), 81–100.

Hyde, K. D., de Silva, N. I., Jeewon, R., Bhat, D. J., Phookamsak, R., Doilom, M., . . . Bulgakov, T. S. (2020). AJOM new records and collections of fungi: 1–100. *Asian Journal of Mycology, 3*(1), 22–294. https://doi.org/10.5943/ajom/3/1/3

Hyde, K. D., Dong, Y., Phookamsak, R., Jeewon, R., Bhat, D. J., Jones, E. B. G., . . . Sheng, J. (2020). Fungal diversity notes 1151–1276: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 100*, 5–277. https://doi.org/10.1007/s13225-020-00439-5

Hyde, K. D., Hongsanan, S., Jeewon, R., Bhat, D. J., McKenzie, E. H. C., Jones, E. B. G., . . . Tanaka, K. (2016). Fungal diversity notes 367–490: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity, 80*, 1–270. https://doi.org/10.1007/s13225-016-0373-x

Hyde, K. D., Maharachchikumbura, S. S. N., Hongsanan, S., Samarakoon, M. C., Lücking, R., Pem, D., . . . Bahkali, A. H. (2017). The ranking of fungi: A tribute to David L. Hawksworth on his 70th birthday. *Fungal Diversity, 84*, 1-23. https://doi.org/10.1007/s13225-017-0383-3

Hyde, K. D., Nilsson, R. H., Alias, S. A., Ariyawansa, H. A., Blair, J. E., Cai, L., . . . Zhou, N. (2014). One stop shop: Backbone trees for important phytopathogenic genera: I (2014). *Fungal Diversity, 67*(1), 21–125. https://doi.org/10.1007/s13225-014-0298-1

Hyde, K. D., Norphanphoun, C., Abreu, V. P., Bazzicalupo, A., Thilini Chethana, K. W., Clericuzio, M., . . . Mortimer, P. E. (2017). Fungal diversity notes 603–708: Taxonomic and phylogenetic notes on genera and species. *Fungal Diversity, 87*, 1–235. https://doi.org/10.1007/s13225-017-0391-3

Hyde, K. D., Norphanphoun, C., Ma, J., Yang, H. D., Zhang, J. Y., Du, T. Y., . . . Zhao, Q. (2023). Mycosphere notes 387–412 – novel species of fungal taxa from around the world. *Mycosphere, 16*, 663–744. https://doi.org/10.5943/mycosphere/14/1/8

Hyde, K. D., Norphanphoun, C., Maharachchikumbura, S. S. N., Bhat, D. J., Jones, E. B. G., Bundhun, D., . . . Xiang, M. M. (2020). Refined families of *Sordariomycetes*. *Mycosphere, 11*(1), 305-1059. https://doi.org/10.5943/mycosphere/11/1/7

Hyde, K. D., Tennakoon, D. S., Jeewon, R., Bhat, D. J., Maharachchikumbura, S. S. N., Rossi, W., . . . Doilom, M. (2019). Fungal diversity notes 1036–1150: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 96*, 1-242.

Hyde, K. D., Xu, J. C., Rapior, S., Jeewon, R., Lumyong, S., Niego, A. G. T., . . . Stadler, M. (2019). The amazing potential of fungi: 50 ways we can exploit fungi industrially. *Fungal Diversity*, *97*(1), 1–136. https://doi.org/10.1007/s13225-019-00430-9

Index Fungorum. (2024). http://www.indexfungorum.org/Names/IndexFungorum Partnership.htm

Jaklitsch, W. M., & Voglmayr, H. (2016). Hidden diversity in *Thyridaria* and a new circumscription of the *Thyridariaceae*. *Studies in Mycology*, *85*(1), 35–64. https://doi.org/10.1016/j.simyco.2016.09.002

Jayasiri, S. C., Hyde, K. D., Ariyawansa, H. A., Bhat, J., Buyck, B., Cai, L., . . . Promputtha, I. (2015). The Faces of Fungi database: Fungal names linked with morphology, phylogeny and human impacts. *Fungal Diversity, 74*, 3–18. https://doi.org/10.1007/s13225-015-0351-8

Jayasiri, S. C., Hyde, K. D., Jones, E. B. G., McKenzie, E. H. C., Jeewon, R., Phillips, A. J. L., . . . Karunarathna, S. C. (2019). Diversity, morphology and molecular phylogeny of *Dothideomycetes* on decaying wild seed pods and fruits. *Mycosphere, 10*(1), 1−186. https://doi.org/10.5943/mycosphere/10/1/1

Jayawardena, R. S., Bhunjun, C. S., Hyde, K. D., Gentekaki, E., & Itthayakorn, P. (2021). *Colletotrichum*: Lifestyles, biology, morpho-species, species complexes and accepted species. *Mycosphere, 12*(1), 519-669. https://doi.org/10.5943/mycosphere/12/1/7

Jayawardena, R. S., Hyde, K. D., Chen, Y. J., Papp, V., Palla, B., Papp, D., . . . Wang, Y. (2020). One stop shop IV: Taxonomic update with molecular phylogeny for important phytopathogenic genera: 76–100 (2020). *Fungal Diversity, 103*(1), 87-218. https://doi.org/10.1007/s13225-020-00460-8

Jayawardena, R. S., Hyde, K. D., de Farias, A. R. G., Bhunjun, C. S., Ferdinandez, H. S., Manamgoda, D. S., . . . Promputtha, I. (2021). What is a species in fungal plant pathogens? *Fungal Diversity, 109*(1), 239-266. https://doi.org/10.1007/s13225-021-00484-8

Jayawardena, R. S., Hyde, K. D., Wang, S., Sun, Y.R., Suwannarach, N., Sysouphanthong, P., . . . Wang, Y. (2022). Fungal diversity notes 1512–1610: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 117*, 1–272. https://doi.org/10.1007/s13225-022-00513-0

Jeewon, R., Edward, C. Y., & Hyde, K. D. (2003). Molecular systematics of the *Amphisphaeriaceae* based on cladistic analyses of partial LSU rDNA gene sequences. *Mycological Research, 107*(12), 1392–1402. https://doi.org/10.1017/S095375620300875X

Jeewon, R., & Hyde, K. D. (2016). Establishing species boundaries and new taxa among fungi: Recommendations to resolve taxonomic ambiguities. *Mycosphere, 7*(11), 1669–1677. https://doi.org/10.5943/mycosphere/7/11/4

Jia, M., Chen, L., Xin, H. L., Zheng, C. J., Rahman, K., Han, T., . . . Qin, L. P. (2016). A friendly relationship between endophytic fungi and medicinal plants: A systematic review. *Frontiers in Microbiology, 7*, 906. https://doi.org/10.3389/fmicb.2016.00906

Jiang, H. B., Hyde, K. D., Doilom, M., Karunarathna, S. C., Xu, J. C., & Phookamsak, R. (2019). *Arthrinium setostromum* (Apiosporaceae, Xylariales), a novel species associated with dead bamboo from Yunnan, China. *AJOM, 2*, 254–268. https://doi.org/10.5943/ajom/2/1/16

Jiang, H. B., Phookamsak, R., Bhat, D. J., Khan, S., Bahkali, A., Elgorban, A. M., . . . Hyde, K. D. (2018). *Vamsapriya yunnana*, a new species of *Vamsapriya* (Xylariaceae, Xylariales) associated with bamboo from Yunnan, China. *Phytotaxa, 356*(1), 61–70. https://doi.org/10.11646/phytotaxa.356.1.5

Jiang, H. B., Phookamsak, R., Doilom, M., Mortimer, P. E., Xu, J. C., Lumyong, S., . . . Karunarathna, S. C. (2019). Taxonomic and phylogenetic characterizations of *Keissleriella bambusicola* sp. nov. (Lentitheciaceae, Pleosporales) from Yunnan, China. *Phytotaxa, 423*(3), 129–144. https://doi.org/10.11646/phytotaxa.423.3.2

Jiang, H. B., Phookamsak, R., Hyde, K. D., Mortimer, P. E., Xu, J. C., Kakumyan, P., . . . Kumla, J. (2021). A taxonomic appraisal of bambusicolous fungi in Occultibambusaceae (Pleosporales, Dothideomycetes) with new collections from Yunnan Province, China. *Life, 11*, 932. https://doi.org/10.3390/life11090932

Jiang, N., Fan, X. L., & Tian, C. M. (2021). Identification and characterization of leaf-inhabiting fungi from *Castanea* plantations in China. *Journal of Fungi, 7*, 64. https://doi.org/10.3390/jof7010064

Jiang, N., Liang, Y. M., & Tian, C. M. (2019). Morphological and phylogenic evidences reveal a new *Seiridium* species in China. *Phytotaxa, 418*(3), 287–293. https://doi.org/10.11646/phytotaxa.418.3.4

Jiang, N., Voglmayr, H., Xue, H., Piao, C. G., & Li, Y. (2022). Morphology and phylogeny of *Pestalotiopsis* (Sporocadaceae, Amphisphaeriales) from *Fagaceae* leaves in China. *Microbiology Spectrum, 10*(6), e03272-03222. https://doi.org/10.1128/spectrum.03272-22

Jones, E. B. G., Pang, K. L., Abdel-Wahab, M. A., Scholz, B., Hyde, K. D., Boekhout, T., . . . Sakayaroj, J. (2019). An online resource for marine fungi. *Fungal Diversity, 96*, 347-433. https://doi.org/10.1007/s13225-019-00426-5

Karunarathna, A., Działak, P., Jayawardena, R. S., Karunarathna, S. C., Kuo, C. H., Suwannarach, N., . . . Lumyong, S. (2021). A novel addition to the *Pezizellaceae* (Rhytismatales, Ascomycota). *Phytotaxa, 480*(3), 251–261. https://doi.org/10.11646/phytotaxa.480.3.4

Kirschner, R., & Chen, C. J. (2004). Two new species of the staurosporous hyphomycetous genera *Ceratosporium* and *Diplocladiella* from Taiwan. *Mycologia, 96*, 917–924. https://doi.org/10.1080/15572536.2005.11832938

Kjer, J., Debbab, A., Aly, A. H., & Proksch, P. (2010). Methods for isolation of marine-derived endophytic fungi and their bioactive secondary products. *Nature Protocols, 5*(3), 479-490. https://doi.org/10.1038/nprot.2009.233

Köberl, M., Schmidt, R., Ramadan, E. M., Bauer, R., & Berg, G. (2013). The microbiome of medicinal plants: Diversity and importance for plant growth, quality and health. *Frontiers in Microbiology, 4*, 70293. https://doi.org/10.3389/fmicb.2013.00400

Koide, K., Osono, T., & Takeda, H. (2005). Fungal succession and decomposition of *Camellia japonica* leaf litter. *Ecological Research, 20*(5), 599–609. https://doi.org/10.1007/s11284-005-0077-2

Kolařík, M. (2018). New taxonomic combinations in endophytic representatives of the genus *Nigrograna*. *Czech Mycology, 70*, 123–126. https://doi.org/10.33585/cmy.70202

Konta, S., Hyde, K. D., Karunarathna, S. C., Mapook, A., Senwanna, C., Dauner, L. A. P., . . . Lumyong, S. (2021). Multi-gene phylogeny and morphology reveal *Haplohelminthosporium* gen. nov. and *Helminthosporiella* gen. nov. associated with palms in Thailand and a checklist for *Helminthosporium* reported worldwide. *Life, 11*(5). https://doi.org/10.3390/life11050454

Konta, S., Phillips, A. J. L., Bahkali, A. H., Jones, E. B. G., Eungwanichayapant, D. P., Hyde, K. D., . . . Boonmee, S. (2016). Botryosphaeriaceae from palms in Thailand-*Barriopsis archontophoenicis* sp. nov, from *Archontophoenix alexandrae*. *Mycosphere, 7,* 921-932. https://doi.org/10.5943/mycosphere/si/1b/1

Konta, S., Tibpromma, S., Karunarathna, S. C., Samarakoon, M. C., Steven, L. S., Mapook, A., . . . Eungwanichayapant, P. D. (2023). Morphology and multigene phylogeny reveal ten novel taxa in *Ascomycota* from terrestrial palm substrates (Arecaceae) in Thailand. *Mycosphere, 14*, 107–152. https://doi.org/10.5943/mycosphere/14/1/2

Koukol, O., & Delgado, G. (2021). Why morphology matters: The negative consequences of hasty descriptions of putative novelties in asexual ascomycetes. *IMA Fungus, 12*(1), 26. https://doi.org/10.1186/s43008-021-00073-z

Kovač, M., Diminić, D., Orlović, S., & Zlatković, M. (2021). *Botryosphaeria dothidea* and *Neofusicoccum yunnanense* causing canker and die-back of *Sequoiadendron giganteum* in Croatia. *Forests, 12*(6). https://doi.org/10.3390/f12060695

Kumar, S., Dobos, G. J., & Rampp, T. (2017). The significance of ayurvedic medicinal plants. *Journal of Evidence-Based Complementary & Alternative Medicine, 22*(3), 494-501. https://doi.org/10.1177/2156587216671392

Kurbetli, İ., & Demirci, F. (2014). Outbreak of stem canker and dieback of pear trees caused by *Botryosphaeria obtusa* (anamorph *Diplodia seriata*) in Turkey. *New Disease Reports, 30*, 6–6. https://doi.org/10.5197/j.2044-0588.2014.030.006

Larsson, A. (2014). AliView: A fast and lightweight alignment viewer and editor for large datasets. *Bioinformatics, 30*(22), 3276–3278. https://doi.org/10.1093/bioinformatics/btu531

Lechat, C., Fournier, J., & Priou, J. P. (2021). *Striatibotrys alpina* (*Hypocreales*), a new species from the French Alps. *Ascomycete.org, 13*(1), 1–4.

Li, G., Kusari, S., Kusari, P., Kayser, O., & Spiteller, M. (2015). Endophytic *Diaporthe* sp. LG23 produces a potent antibacterial tetracyclic triterpenoid. *Journal of Natural Products, 78*(8), 2128–2132. https://doi.org/10.1021/acs.jnatprod.5b00170

Li, G. J., Hyde, K. D., Zhao, R. L., Hongsanan, S., Abdel-Aziz, F. A., Abdel-Wahab, M. A., . . . Góes-Neto, A. (2016). Fungal diversity notes 253–366: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity, 78*, 1-237. https://doi.org/10.1007/s13225-016-0366-9

Li, J. F., Jeewon, R., Luo, Z. L., Phookamsak, R., Bhat, D. J., Mapook, A., . . . Hyde, K. D. (2017). Morphological characterization and DNA based taxonomy of *Fusiconidium* gen. nov. with two novel taxa within Melanommataceae (Pleosporales). *Phytotaxa, 308*(2), 206–218. https://doi.org/10.11646/phytotaxa.308.2.2

Li, L., Du, H. Z., Thiyagaraja, V., Bhat, D. J., Phookamsak, R., & Cheewangkoon, R. (2024). Two novel freshwater hyphomycetes, in *Acrogenospora* (Minutisphaerales, Dothideomycetes) and *Conioscypha* (Conioscyphales, Sordariomycetes) from Southwestern China. *MycoKeys, 101*, 249–273. https://doi.org/10.3897/mycokeys.101.115209

Li, Q. R., Zhang, X., Lin, Y., Samarakoon, M. C., Hyde, K. D., Shen, X. C., . . . Kang, Y. Q. (2022). Morpho-molecular characterisation of *Arecophila*, with *A. australis* and *A. clypeata* sp. nov. and *A. miscanthi* comb. nov. *MycoKeys, 88*, 123. https://doi.org/10.3897/mycokeys.88.79475

Li, W. J., McKenzie, E. H. C., Liu, J. K., Bhat, D. J., Dai, D. Q., Camporesi, E., . . . Hyde, K. D. (2020). Taxonomy and phylogeny of hyaline-spored coelomycetes. *Fungal Diversity, 100*(1), 279-801. https://doi.org/10.1007/s13225-020-00440-y

Li, W. L., Dissanayake, A. J., Zhang, T., Maharachchikumbura, S. S. N., & Liu, J. K. (2022). Identification and pathogenicity of pestalotioid fungi associated with woody oil plants in Sichuan Province, China. *Journal of Fungi, 8*, 1175. https://doi.org/10.3390/jof8111175

Li, W. L., Liang, R. R., Dissanayake, A. J., & Liu, J. K. (2023). Mycosphere notes 413–448: Dothideomycetes associated with woody oil plants in China. *Mycosphere, 14*, 1436–1529. https://doi.org/10.5943/mycosphere/14/1/16

Li, W. L., Liang, R. R., Yang, J., & Liu, J. K. (2024). Morpho-molecular characterization reveals a new genus, three novel species and two new host records in Xylariomycetidae. *Journal of Fungi, 10*(3), 189. https://doi.org/10.3390/jof10030189

Li, W. L., Luo, Z. L., Liu, J. K., Bhat, D. J., Bao, D. F., Su, H. Y., . . . Hyde, K. D. (2017). Lignicolous freshwater fungi from China I: *Aquadictyospora lignicola* gen. et sp. nov. and new record of *Pseudodictyosporium wauense* from northwestern Yunnan Province. *Mycosphere, 8*(10), 1587–1597. https://doi.org/10.5943/mycosphere/8/10/1

Lim, T. K. (2012). *Edible medicinal and non-medicinal plants* (Vol. 1). Springer.

Lin, C. G., McKenzie, E. H. C., Bhat, D. J., Ran, S. F., Chen, Y., Hyde, K. D., . . . Wang, Y. (2016). *Stachybotrys*-like taxa from karst areas and a checklist of *Stachybotrys*-like species from Thailand. *Mycosphere, 7*, 1273–1291. https://doi.org/10.5943/mycosphere/7/9/3

Lin, Y. Z., Chang, T. D., Wen, C. J., Tsai, S. H., & Lin, Y. H. (2022). First report of leaf brown blight caused by *Neopestalotiopsis formicarum* on jabuticaba in Taiwan. *Plant Disease, 106*, 2527. https://doi.org/10.1094/PDIS-07-21-1414-PDN.

Link, H. F. (1809a). Observationes in ordines plantarum naturales. Dissertatio I. *Magazin der Gesellschaft Naturforschender Freunde zu Berlin, 1*, 3–42.

Link, H. F. (1809b). Observationes in ordines plantarum naturales. Dissertatio I. *Magazin der Gesellschaft Naturforschenden Freunde Berlin, 3*, 3–42.

Liu, F., Bonthond, G., Groenewald, J. Z., Cai, L., & Crous, P. W. (2019). *Sporocadaceae*, a family of coelomycetous fungi with appendage-bearing conidia. *Studies in Mycology, 92*, 287–415. https://doi.org/10.1016/j.simyco.2018.11.001

Liu, F., Ma, Z. Y., Hou, L. W., Diao, Y. Z., Wu, W. P., Damm, U., . . . Cai, L. (2022). Updating species diversity of *Colletotrichum*, with a phylogenomic overview. *Studies in Mycology, 101*, 1-86. https://doi.org/10.3114/sim.2022.101.01

Liu, H. X., Chen, Y. C., Li, S. N., Zhang, W. G., Liu, Z. M., Tan, H. B., . . . Zhang, W. M. (2020). Trichothecene macrolides from the endophytic fungus *Paramyrothecium roridum* and their cytotoxic activity. *Fitoterapia, 147*, 104768. https://doi.org/10.1016/j.fitote.2020.104768

Liu, J. K., Hyde, K. D., Jones, E. B. G., Ariyawansa, H. A., Bhat, D. J., Boonmee, S., . . . Camporesi, E. (2015). Fungal diversity notes 1–110: Taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity*, *72*, 1–197. https://doi.org/10.1007/s13225-015-0324-y

Liu, J. K., Luo, Z. L., Liu, N. G., Cheewangkoon, R., & To-Anun, C. (2018). Two novel species of *Paradictyoarthrinium* from decaying wood. *Phytotaxa, 338*(3), 285–293. https://doi.org/10.11646/phytotaxa.338.3.6

Liu, J. K., Phookamsak, R., Dai, D. Q., Tanaka, K., Jones, E. B. G., Xu, J. C., . . . Hyde, K. D. (2014). *Roussoellaceae*, a new pleosporalean family to accommodate the genera *Neoroussoella* gen. nov., *Roussoella* and *Roussoellopsis*. *Phytotaxa, 181*, 1–33. https://doi.org/10.11646/phytotaxa.181.1.1

Liu, J. K., Phookamsak, R., Doilom, M., Wikee, S., Li, Y. M., Ariyawansha, H., . . . Hyde, K. D. (2012). Towards a natural classification of Botryosphaeriales. *Fungal Diversity*, *57*, 149-210. https://doi.org/10.1007/s13225-012-0207-4

Liu, J. W., Hu, Y. F., Luo, X. X., Castañeda-Ruíz, R. F., & Ma, J. (2022). Three novel species of *Helminthosporium* (Massarinaceae, Pleosporales) from China. *MycoKeys, 94*, 73–89. https://doi.org/10.3897/mycokeys.94.95888

Liu, J., Hu, Y., Luo, X., Xu, Z., Castañeda-Ruíz, R. F., Xia, J., . . . Ma, J. (2023). Morphological and phylogenetic analyses reveal three new species of *Distoseptispora* (Distoseptisporaceae, Distoseptisporales) from Yunnan, China. *Journal of Fungi, 9*(4), 470. https://doi.org/10.3390/jof9040470

Liu, N. G., Bhat, D. J., Hyde, K. D., & Liu, J. K. (2019). *Conioscypha tenebrosa* sp. nov. (*Conioscyphaceae*) from China and notes on *Conioscypha* species. *Phytotaxa, 413*(2), 159-171. https://doi.org/10.11646/phytotaxa.413.2.5

Liu, N. G., Hyde, K. D., Bhat, D. J., Jumpathong, J., & Liu, J. K. (2019). Morphological and phylogenetic studies of *Pleopunctum* gen. nov. (*Phaeoseptaceae*, *Pleosporales*) from China. *Mycosphere*, *10*(1), 757-775. https://doi.org/10.5943/mycosphere/10/1/17

Liu, N. G., Hyde, K. D., Sun, Y. R., Bhat, D. J., Jones, E. B. G., Jumpathong, J., . . . Liu, J. K. (2024). Notes, outline, taxonomy and phylogeny of brown-spored hyphomycetes [Manuscript preparation]. *Fungal Diversity.*

Liu, S. L., Wang, X. W., Li, G. J., Deng, C. Y., Rossi, W., Leonardi, M., . . . Zhou, L. W. (2024). Fungal diversity notes 1717–1817: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity*, *124*, 1–216. https://doi.org/10.1007/s13225-023-00529-0

Liu, Y. W., & Zeng, X. Y. (2022). *Acrocalymma chuxiongense* sp. nov., a new species of Acrocalymmaceae (Pleosporales) on leaves of *Quercus*. *Biodiversity Data Journal*, *10*, e89635. https://doi.org/10.3897/BDJ.10.e89635

Lombard, L., Houbraken, J., Decock, C., Samson, R., Meijer, M., Réblová, M., . . . Crous, P. W. (2016). Generic hyper-diversity in Stachybotriaceae. *Persoonia-Molecular Phylogeny and Evolution of Fungi*, *36*(1), 156–246. https://doi.org/10.3767/003158516X691582

Lu, L., Karunarathna, S. C., Dai, D. Q., Jayawardena, R. S., Suwannarach, N., & Tibpromma, S. (2022). Three new species of *Nigrograna* (Dothideomycetes, Pleosporales) associated with Arabica coffee from Yunnan Province, China. *MycoKeys*, *94*, 51–71. https://doi.org/10.3897/mycokeys.94.95751

Lu, Y. Z., Liu, J. K., Hyde, K. D., Jeewon, R., Kang, J. C., Fan, C., . . . Eungwanichayapant, P. D. (2018). A taxonomic reassessment of Tubeufiales

based on multi-locus phylogeny and morphology. *Fungal Diversity, 92*(1), 131–344. https://doi.org/10.1007/s13225-018-0411-y

Lu, Y. Z., Ma, J., Xiao, X. J., Zhang, L. J., Xiao, Y. P., & Kang, J. C. (2022). Four new species and three new records of helicosporous hyphomycetes from China and their multi-gene phylogenies. *Frontiers in Microbiology, 13*, 1053849. https://doi.org/10.3389/fmicb.2022.1053849

Luo, H. Y., Zhou, Q. Y., Deng, Y. C., Deng, Z. Y., Qing, Z., & Sun, W. B. (2017). Antifungal activity of the extract and the active substances of endophytic *Nigrospora* sp. from the traditional Chinese medicinal plant *Stephania kwangsiensis*. *Natural Product Communications, 12*(12), 1934578X1701201219. https://doi.org/10.1177/1934578X1701201219

Luo, M., Guo, W., Zhao, M. P., Manawasinghe, I. S., Guarnaccia, V., Liu, J. W., . . . You, C. P. (2022). Endophytic *Diaporthe* associated with *Morinda officinalis* in China. *Journal of Fungi, 8*(8), 806. https://doi.org/10.3390/jof8080806

Luo, X. Y., Tang, G. D., Xu, H., Huang, Y. F., Zhuang, X. Y., & Zhang, K. H. (2004). Effect of VAM fungi on the growth of *Cinnamomum cassia* Presl. under non-sterilized soil condition. *Forestry and Environmental Science, 3*, 16–18.

Luo, Z. L., Bhat, D. J., Jeewon, R., Boonmee, S., Bao, D. F., Zhao, Y. C., . . . Hyde, K. D. (2017). Molecular phylogeny and morphological characterization of asexual fungi (Tubeufiaceae) from freshwater habitats in Yunnan, China. *Cryptogamie, Mycologie, 38*(1), 27–53. https://doi.org/10.7872/crym/v38.iss1.2017.27

Luo, Z. L., Hyde, K. D., Liu, J. K., Bhat, D. J., Bao, D. F., Li, W. L., . . . Su, H. Y. (2018). Lignicolous freshwater fungi from China II: Novel *Distoseptispora*

(Distoseptisporaceae) species from northwestern Yunnan Province and a suggested unified method for studying lignicolous freshwater fungi. *Mycosphere, 9*(3), 444-461. https://doi.org/10.5943/mycosphere/9/3/2

Luo, Z. L., Hyde, K. D., Liu, J. K., Maharachchikumbura, S. S. N., Jeewon, R., Bao, D. F., . . . Su, H. Y. (2019). Freshwater *Sordariomycetes*. *Fungal Diversity, 99*, 451–660. https://doi.org/10.1007/s13225-019-00438-1

Luo, Z. L., Yang, J., Liu, J. K., Su, H. Y., Bahkali, A. H., & Hyde, K. D. (2016). Two new species of *Helicascus* (Morosphaeriaceae) from submerged wood in northern Thailand. *Phytotaxa, 270*(3), 182–190. https://doi.org/10.11646/phytotaxa.270.3.2

Ma, L. J., Geiser, D. M., Proctor, R. H., Rooney, A. P., O'Donnell, K., Trail, F., . . . Kazan, K. (2013). *Fusarium* pathogenomics. *Annual Review of Microbiology, 67*, 399-416. https://doi.org/10.1146/annurev-micro-092412-155650

Magaña-Dueñas, V., Cano-Lira, J. F., & Stchigel, A. M. (2021). New Dothideomycetes from freshwater habitats in Spain. *Journal of Fungi, 7*, 1102. https://doi.org/10.3390/jof7121102

Maharachchikumbura, S. S. N., Chen, Y., Ariyawansa, H. A., Hyde, K. D., Haelewaters, D., Perera, R. H., . . . Stadler, M. (2021). Integrative approaches for species delimitation in *Ascomycota*. *Fungal Diversity, 109*(1), 155–179. https://doi.org/10.1007/s13225-021-00486-6

Maharachchikumbura, S. S. N., Hyde, K. D., Groenewald, J. Z., Xu, J., & Crous, P. W. (2014). *Pestalotiopsis* revisited. *Studies in Mycology, 79*, 121–186. https://doi.org/10.1016/j.simyco.2014.09.005

Manawasinghe, I. S., Calabon, M. S., Jones, E. B. G., Zhang, Y. X., Liao, C. F., Xiong, Y. R., . . . Hyde, K. D. (2022). Mycosphere notes 345–386. *Mycosphere, 13*, 454–557. https://doi.org/10.5943/mycosphere/13/1/3

Manawasinghe, I. S., Dissanayake, A. J., Li, X. H., Liu, M., Wanasinghe, D. N., Xu, J. P., . . . Hyde, K. D. (2019). High genetic diversity and species complexity of *Diaporthe* associated with grapevine dieback in China. *Frontiers in Microbiology, 10*, 473533. https://doi.org/10.3389/fmicb.2019.01936

Mapook, A., Hyde, K. D., McKenzie, E. H. C., Jones, E. B. G., Bhat, D. J., Jeewon, R., . . . Purahong, W. (2020). Taxonomic and phylogenetic contributions to fungi associated with the invasive weed *Chromolaena odorata* (Siam weed). *Fungal Diversity*, *101*, 1–175. https://doi.org/10.1007/s13225-020-00444-8

Marin-Felix, Y., Hernández-Restrepo, M., Iturrieta-González, I., García, D., Gené, J., Groenewald, J. Z., . . . Crous, P. W. (2019). Genera of phytopathogenic fungi: GOPHY 3. *Studies in Mycology*, *94*, 1–124. https://doi.org/10.1016/j.simyco.2019.05.001

Mason, E. W. (1927). On species of the genus *Nigro-spora* Zimmermann recorded on monocotyledons. *Transactions of the British Mycological Society, 12*, 152–165. https://doi.org/10.1016/S0007-1536(27)80011-2

Mathiassen, G., Granmo, A., & Stensrud, Ø. (2017a). *Lophiotrema borealiforme*, a new species close to *L. boreale*. *Karstenia*, *57*, 11–15. https://doi.org/10.29203/ka.2017.479

Mathiassen, G., Granmo, A., & Stensrud, Ø. (2017b). *Lophiotrema lennartii* and *Lophiotrema kerstiniae*–two new species from Norway and Sweden. *Sydowia, 69*, 199–203.

Matić, S., Gilardi, G., Gullino, M. L., & Garibaldi, A. (2019). Emergence of leaf spot disease on leafy vegetable and ornamental crops caused by *Paramyrothecium* and *Albifimbria* species. *Phytopathology, 109*(6), 1053–1061. https://doi.org/10.1094/PHYTO-10-18-0396-R

Matsushima, T. (1996). *Matsushima Mycological Memoirs 9*. *Matsushima Mycological Memoirs, 9*, 1–30.

Meng, C.R., Zhang, Q., Yang, Z.-F., Geng, K., Zeng, X.-Y., Chethana, K. T., . . . Wang, Y. (2021). *Lasiodiplodia syzygii* sp. nov. (Botryosphaeriaceae) causing post-harvest water-soaked brown lesions on *Syzygium samarangense* in Chiang Rai, Thailand. *Biodiversity Data Journal, 9*. https://doi.org/10.3897/BDJ.9.e60604

Miller, M. A., Pfeiffer, W., & Schwartz, T. (2010). Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In *Proceeding of the 2010 gateway computing environments workshop (GCE)* (pp. 1–8). New Orleans, Louisiana. https://doi.org/10.1109/GCE.2010.5676129

Mofokeng, M. M., Du Plooy, C. P., Araya, H. T., Amoo, S. O., Mokgehle, S. N., Pofu, K. M., . . . Mashela, P. W. (2022). Medicinal plant cultivation for sustainable use and commercialization of high-value crops. *South African Journal of Science, 118*(7-8), 1-7. https://doi.org/10.17159/sajs.2022/12190

Monkai, J., Hongsanan, S., Bhat, D. J., Dawoud, T. M., & Lumyong, S. (2023). Integrative taxonomy of novel *Diaporthe* species associated with medicinal plants in Thailand. *Journal of Fungi, 9*(6), 603. https://doi.org/10.3390/jof9060603

Monteiro, P., Gonçalves, M. F. M., Pinto, G., Silva, B., Martín-García, J., Diez, J. J., . . . Alves, A. (2021). Three novel species of fungi associated with pine species showing needle blight-like disease symptoms. *European Journal of Plant Pathology*, 1-20. https://doi.org/10.1007/s10658-021-02395-5

Mortimer, P. E., Jeewon, R., Xu, J.C., Lumyong, S., & Wanasinghe, D. N. (2021). Morpho-phylo taxonomy of novel dothideomycetous fungi associated with dead woody twigs in Yunnan Province, China. *Frontiers in Microbiology, 12*, 654683. https://doi.org/10.3389/fmicb.2021.654683

Moslemi, A., & Taylor, P. W. J. (2015). *Pestalotiopsis chamaeropis* causing leaf spot disease of round leaf mint-bush (*Prostanthera rotundifolia*) in Australia. *Australasian Plant Disease Notes, 10*(1), 29. https://doi.org/10.1007/s13314-015-0179-9

Nag Raj, T. R. (1993). *Coelomycetous anamorphs with appendage-bearing conidia*. Mycologue Publications.

Namdeo, A. G. (2018). Chapter 20 - Cultivation of medicinal and aromatic plants. In S. C. Mandal, V. Mandal & T. Konishi (Eds.), *Natural products and drug discovery* (pp. 525–553). Elsevier. https://doi.org/10.1016/B978-0-08-102081-4.00020-4

Netto, M. S. B., Assunção, I. P., Lima, G. S. A., Marques, M. W., Lima, W. G., Monteiro, J. H. A., . . . Câmara, M. P. S. (2014). Species of *Lasiodiplodia* associated with papaya stem-end rot in Brazil. *Fungal Diversity, 67*, 127–141. https://doi.org/10.1007/s13225-014-0279-4

Nguyen, L.T., Schmidt, H. A., Von Haeseler, A., & Minh, B. Q. (2015). IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution, 32*(1), 268–274. https://doi.org/10.1093/molbev/msu300

Nguyen, T. T. T., Hee Lee, S., Jeong Jeon, S., & Burm Lee, H. (2019). First records of rare Ascomycete fungi, *Acrostalagmus luteoalbus*, *Bartalinia robillardoides*, and *Collariella carteri* from freshwater samples in Korea. *Mycobiology, 47*(1), 1–11. https://doi.org/10.1080/12298093.2018.1550894

Niu, X. P., Gao, H., Qi, J. M., Chen, M. C., Tao, A., Xu, J. T., . . . Su, J. G. (2016). *Colletotrichum* species associated with jute (*Corchorus capsularis* L.) anthracnose in southeastern China. *Scientific Reports, 6*(1), 1–9. https://doi.org/10.1038/srep25179

Norphanphoun, C., Gentekaki, E., Hongsanan, S., Jayawardena, R., Senanayake, I., Manawasinghe, I. S., . . . Hyde, K. D. (2022). *Diaporthe*: Formalizing the species-group concept. *Mycosphere, 13*(1), 752–819. https://doi.org/10.5943/mycosphere/13/1/9

Norphanphoun, C., Jayawardena, R. S., Chen, Y., Wen, T. C., Meepol, W., & Hyde, K. D. (2019). Morphological and phylogenetic characterization of novel pestalotioid species associated with mangroves in Thailand. *Mycosphere, 10,* 531–578. https://doi.org/10.5943/mycosphere/10/1/9

Nouri, M. T., Lawrence, D. P., Yaghmour, M. A., Michailides, T. J., & Trouillas, F. P. (2018). *Neoscytalidium dimidiatum* causing canker, shoot blight and fruit rot of almond in California. *Plant Disease, 102*(8), 1638–1647. https://doi.org/10.1094/PDIS-12-17-1967-RE

Ntemafack, A., Kapoor, N., Ali, S., Jamwal, V. L., Hassan, Q. P., & Gandhi, S. G. (2021). Comprehensive review of endophytic flora from African medicinal plants. *Current Microbiology*, *78*(8), 2860–2898. https://doi.org/10.1007/s00284-021-02566-x

Nylander, J. A. A. (2004). *MrModeltest v2.2. Program distributed by the author: 2*. Evolutionary Biology Centre, Uppsala University.

Obregón, V. G., Meneguzzi, N. G., Ibañez, J. M., Lattar, T. E., & Kirschbaum, D. S. (2018). First report of *Neopestalotiopsis clavispora* causing root and crown rot on strawberry plants in Argentina. *Plant Disease, 102*(9), 1856-1856. https://doi.org/10.1094/PDIS-02-18-0330-PDN

Park, H., Shim, J. S., Kim, J. S., & Choi, H. S. (2017). Five previously unreported endophytic fungi isolated from the leaves of woody plants in Korea. *Korean Journal of Mycology*, *45*, 345–354.

Pereira, D. S., Hilário, S., Gonçalves, M. F. M., & Phillips, A. J. L. (2023). *Diaporthe* species on palms: Molecular re-assessment and species boundaries delimitation in the *D. arecae* species complex. *Microorganisms, 11*(11), 2717. https://doi.org/10.3390/microorganisms11112717

Petrak, F. (1921). Mykologische Notizen. III. *Annalen des Mykologischen Instituts, 19*(3–4), 176–223.

Phillips, A. J. L., Alves, A., Abdollahzadeh, J., Slippers, B., Wingfield, M. J., Groenewald, J. Z., . . . Crous, P. W. (2013). The Botryosphaeriaceae: Genera and species known from culture. *Studies in Mycology, 76*, 51–167. https://doi.org/10.3114/sim0021

Phillips, A. J. L., Alves, A., Pennycook, S. R., Johnston, P. R., Ramaley, A., Akulov, A., . . . Crous, P. W. (2008). Resolving the phylogenetic and taxonomic status of dark-spored teleomorph genera in the Botryosphaeriaceae. *Persoonia, 21*(1), 29–55. https://doi.org/10.3767/003158508X340742

Phillips, A. J. L., Hyde, K. D., Alves, A., & Liu, J. K. (2019). Families in Botryosphaeriales: A phylogenetic, morphological and evolutionary perspective. *Fungal Diversity, 94*, 1-22. https://doi.org/10.1007/s13225-018-0416-6

Pitt, W., Úrbez-Torres, J. R., & Trouillas, F. P. (2014). *Munkovalsaria donacina* from grapevines and Desert Ash in Australia. *Mycosphere, 5*, 656–661. https://doi.org/10.5943/mycosphere/5/5/6

Phookamsak, R., Hyde, K. D., Jeewon, R., Bhat, D. J., Gareth Jones, E. B., Maharachchikumbura, S. S. N., . . . Xu, J. C. (2019). Fungal diversity notes 929–1035: Taxonomic and phylogenetic contributions on genera and species of fungi. *Fungal Diversity, 95*, 1–273. https://doi.org/10.1007/s13225-019-00421-w

Phookamsak, R., Liu, J. K., McKenzie, E. H. C., Manamgoda, D. S., Ariyawansa, H., Thambugala, K. M., . . . Hyde, K. D. (2014). Revision of Phaeosphaeriaceae. *Fungal Diversity, 68,* 159–238. https://doi.org/10.1007/s13225-014-0308-3

Phukhamsakda, C., McKenzie, E. H. C., Phillips, A. J. L., Gareth Jones, E. B., Jayarama Bhat, D., Stadler, M., . . . Hyde, K. D. (2020). Microfungi associated with *Clematis* (Ranunculaceae) with an integrated approach to delimiting species boundaries. *Fungal Diversity, 102*(1), 1–203. https://doi.org/10.1007/s13225-020-00448-4

Phukhamsakda, C., Nilsson, R. H., Bhunjun, C. S., de Farias, A. R. G., Sun, Y. R., Wijesinghe, S. N., . . . Hyde, K. D. (2022). The numbers of fungi: Contributions from traditional taxonomic studies and challenges of metabarcoding. *Fungal Diversity, 114*, 327–386. https://doi.org/10.1007/s13225-022-00502-3

Phumthum, M., Balslev, H., & Barfod, A. S. (2019). Important medicinal plant families in Thailand. *Frontiers in Pharmacology, 10*, 1125–1125. https://doi.org/10.3389/fphar.2019.01125

Pinruan, U., Unartngam, J., Unartngam, A., Piyaboon, O., Sommai, S., & Khamsuntorn, P. (2022). *Paramyrothecium eichhorniae* sp. nov., causing leaf blight disease of water hyacinth from Thailand. *Mycobiology, 50*(1), 12–19. https://doi.org/10.1080/12298093.2022.2027683

Poli, A., Bovio, E., Ranieri, L., Varese, G. C., & Prigione, V. (2020). News from the sea: A new genus and seven new species in the Pleosporalean families Roussoellaceae and Thyridariaceae. *Diversity, 12*, 144. https://doi.org/10.3390/d12040144

Prabhugaonkar, A., & Bhat, D. J. (2011). New record of *Megacapitula villosa* and *Paradictyoarthrinium diffractum* from India. *Mycosphere, 2*, 463–467.

Pornsuriya, C., Chairin, T., Thaochan, N., & Sunpapao, A. (2020). Identification and characterization of *Neopestalotiopsis* fungi associated with a novel leaf fall disease of rubber trees (*Hevea brasiliensis*) in Thailand. *Journal of Phytopathology, 168*, 416–427. https://doi.org/10.1111/jph.12906

Prasher, I. B., & Verma, R. K. (2015). Two new species of *Dictyosporium* from India. *Phytotaxa, 204*(3), 193–202. https://doi.org/10.11646/phytotaxa.204.3.2

Prasannath, K., Shivas, R. G., Galea, V. J., & Akinsanmi, O. A. (2021). *Neopestalotiopsis* species associated with flower diseases of *Macadamia integrifolia* in Australia. *Journal of Fungi, 7*, 771. https://doi.org/10.3390/jof7090771

Quaedvlieg, W., Verkley, G. J. M., Shin, H. D., Barreto, R. W., Alfenas, A. C., Swart, W. J., . . . Crous, P. W. (2013). Sizing up *Septoria*. *Studies in Mycology*, *75*(1), 307–390. https://doi.org/10.3114/sim0017

Rabenhorst, (1857). Ein Notizblatt für kryptogamische Studien. *Hedwigia, 1*, 116.

Rai, M., Gade, A., Rathod, D., Dar, M., & Varma, A. (2012). Mycoendophytes in medicinal plants: Diversity and bioactivities. *Nusantara Bioscience, 4*(2), 86–96. https://doi.org/10.13057/nusbiosci/n040207

Rajeshkumar, K. C., Bhat, D. J., Lad, S. S., Wijayawardene, N. W., Singh, S. K., Pandkar, M. R., . . . Hyde, K. D. (2018). Morphology and phylogeny of *Tamhinispora srinivasanii* sp. nov. (Tubeufiaceae) from northern Western Ghats, India. *Phytotaxa*, *346*(1), 113–120. https://doi.org/10.11646/phytotaxa.346.1.7

Rajeshkumar, K. C., & Sharma, R. (2013). *Tamhinispora* a new genus belongs to family Tubeufiaceae from the Western Ghats, India based on morphology and phylogenetic analysis. *Mycosphere, 4*, 165–174. https://doi.org/10.5943/mycosphere/4/2/2

Rampersad, S. N. (2020). Pathogenomics and management of *Fusarium* diseases in plants. *Pathogens, 9*(5), 340. https://doi.org/10.3390/pathogens9050340

Rana, K. L., Kour, D., Kaur, T., Devi, R., Negi, C., Yadav, A. N., . . . Saxena, A. K. (2020). Endophytic fungi from medicinal plants: Biodiversity and biotechnological applications. In *Microbial endophytes* (pp. 273–305). Elsevier.

Rannala, B., & Yang, Z. H. (1996). Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference. *Journal of Molecular Evolution, 43*, 304–311. https://doi.org/10.1007/BF02338839

Rasool-Hassan, B. A. (2012). Medicinal plants (importance and uses). *Pharmaceutical Analytical Acta*, *3*(10), 2153–2435. https://doi.org/10.4172/2153-2435.1000e139

Rasool, A., Bhat, K. M., Sheikh, A. A., Jan, A., & Hassan, S. (2020). Medicinal plants: Role, distribution and future. *Journal of Pharmacognosy and Phytochemistry*, *9*(2), 2111–2114.

Rathnayaka, A. R., Dayarathne, M. C., Maharachchikumbura, S. S. N., Liu, J. K., Tennakoon, D. S., & Hyde, K. D. (2019). Introducing *Seriascoma yunnanense* sp. nov. (Occultibambusaceae, Pleosporales) based on evidence from morphology and phylogeny. *Asian Journal of Mycology, 2*, 245–253. https://doi.org/10.5943/ajom/2/1/15

Rathnayaka, A. R., Wedaralalage, T. C. K., Phillips, A. J. L., Liu, J. K., & Hyde, K. D. (2021). First report of Botryosphaeriaceae species on *Camellia sinensis* from Taiwan with a global checklist of Botryosphaeriaceae species on this host. *Chiang Mai Journal of Science, 48*, 1199–1223.

Réblová, M., Gams, W., & Seifert, K. A. (2011). *Monilochaetes* and allied genera of the Glomerellales, and a reconsideration of families in the Microascales. *Studies in Mycology, 68*(1), 163–191. https://doi.org/10.3114/sim.2011.68.07

Réblová, M., & Seifert, K. A. (2004). *Conioscyphascus*, a new ascomycetous genus for holomorphs with *Conioscypha* anamorphs. *Studies in Mycology, 50*(1), 95–108.

Réblová, M., Seifert, K. A., Fournier, J., & Štěpánek, V. (2016). Newly recognised lineages of perithecial ascomycetes: The new orders Conioscyphales and Pleurotheciales. *Persoonia, 37*(1), 57–81. https://doi.org/10.3767/003158516X689819

Ren, G. C., Wanasinghe, D. N., Jeewon, R., Monkai, J., Mortimer, P. E., Hyde, K. D., . . . Gui, H. (2022). Taxonomy and phylogeny of the novel *Rhytidhysteron*-like collections in the Greater Mekong Subregion. *MycoKeys, 86*, 65–85. https://doi.org/10.3897/mycokeys.86.70668

Revay, A. (1995). Two new species of *Oncopodiella* from Hungary. *Mycotaxon, 56*, 479–482.

Rifai, M. A. (1965). On *Sporidesmium trigonellum* Sacc. *Persoonia, 3*(4), 407–411.

Rogers, J. D., & Ju, Y. M. (2003). *Occultitheca costaricensis* gen. et sp. nov. and *Apiocamarops pulvinata* sp. nov. from Costa Rica. *Sydowia, 55*, 359–364.

Ronquist, F., Teslenko, M., Van Der Mark, P., Ayres, D. L., Darling, A., Höhna, S., . . . Huelsenbeck, J. P. (2012). MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology, 61*(3), 539–542. https://doi.org/10.1093/sysbio/sys029

Rossman, A. Y., Allen, W. C., & Castlebury, L. A. (2016). New combinations of plant-associated fungi resulting from the change to one name for fungi. *IMA Fungus, 7*(1), 1–7. https://doi.org/10.5598/imafungus.2016.07.01.01

Saccardo, P. A. (1880). Fungi Gallici lecti a cl. viris P. Brunaud, Abb Letendre, A Malbranche, J Therry, vel editi in Mycotheca Gallica C Roumeguèri Series II. *Michelia, 2*(6), 39–135.

Saccardo, P. A. (1883). Sylloge pyrenomycetum. Vol II. *Sylloge Fungorum, 2*, 1–813.

Saccardo, P. A., & Paoletti, G. (1885). Mycetes Malacenses. Funghi della penisola di Malacca raccolti nel 1885 dell'Ab. Benedetto Scortechini. *Atti Accad. Sci. Veneto-Trentino-Istriana In, 6*, 387–428.

Samarakoon, B. C., Wanasinghe, D. N., Phookamsak, R., Bhat, J., Chomnunti, P., Karunarathna, S. C., . . . Lumyong, S. (2021). *Stachybotrys musae* sp. nov., *S. microsporus*, and *Memnoniella levispora* (Stachybotryaceae, Hypocreales) Found on Bananas in China and Thailand. *Life, 11*, 323. https://doi.org/10.3390/life11040323

Samarakoon, M. C. (2023). Additions to the Xylariomycetidae (Sordariomycetes) Fungal Flora from Northern Thailand: *Amphisphaeria chiangmaiensis* sp. nov. and *A. hydei* sp. nov. *New Zealand Journal of Botany*, 1–17.

Samarakoon, M. C., Hyde, K. D., Maharachchikumbura, S. S. N., Stadler, M., Gareth Jones, E. B., Promputtha, I., . . . Liu, J. K. (2022). Taxonomy, phylogeny, molecular dating and ancestral state reconstruction of Xylariomycetidae (Sordariomycetes). *Fungal Diversity*, *112*(1), 1-88. https://doi.org/10.1007/s13225-021-00495-5

Samarakoon, M. C., Maharachchikumbura, S. S. N., Liu, J. K. J., Hyde, K. D., & Promputtha, I., Stadler, M. (2020). Molecular phylogeny and morphology of *Amphisphaeria* (= *Lepteutypa*) (Amphisphaeriaceae). *Journal of Fungi, 6*, 174. https://doi.org/10.3390/jof6030174

Schippmann, U., Leaman, D. J., & Cunningham, A. B. (2002). Impact of cultivation and gathering of medicinal plants on biodiversity: Global trends and issues. In *FAO. 2002. Biodiversity and the ecosystem approach in agriculture, forestry and fisheries. Satellite event on the occasion of the Ninth Regular Session of the Commission on Genetic Resources for Food and Agriculture. Rome, 12-13 October 2002.* Inter-Departmental Working Group on Biological Diversity for Food and Agriculture.

Seifert, K. (1990). Contributions toward a mycobiota of Indonesia: Synnematous hyphomycetes. *Memoirs of the New York Botanical Garden, 59,* 109–154.

Seifert, K., Morgan-Jones, G., Gams, W., & Kendrick, B. (2011). *The genera of hyphomycetes*. CBS-KNAW Fungal Biodiversity Centre.

Seifert, K. A., Louis-Seize, G., & Sampson, G. (2003). *Myrothecium acadiense*, a new hyphomycete isolated from the weed *Tussilago farfara*. *Mycotaxon, 87*, 317–327.

Senanayake, I. C., Maharachchikumbura, S. S. N., Hyde, K. D., Bhat, J. D., Jones, E. B. G., McKenzie, E. H. C., . . . Camporesi, E. (2015). Towards unraveling relationships in Xylariomycetidae (Sordariomycetes). *Fungal Diversity, 73*(1), 73-144. https://doi.org/10.1007/s13225-015-0340-y

Senanayake, I. C., Rathnayake, A. R., Marasinghe, D. S., Calabon, M. S., Gentekaki, E., Lee, H. B., . . . Xiang, M. M. (2020). Morphological approaches in studying fungi: Collection, examination, isolation, sporulation and preservation. *Mycosphere, 11*(1), 2678–2754. https://doi.org/10.5943/mycosphere/11/1/20

Senanayake, I. C., Rossi, W., Leonardi, M., Weir, A., McHugh, M., Rajeshkumar, K. C., . . . Song, J. (2023). Fungal diversity notes 1611–1716: Taxonomic and phylogenetic contributions on fungal genera and species emphasis in South China. *Fungal Diversity, 122*(1), 161–403. https://doi.org/10.1007/s13225-023-00523-6

Shanthi, S., & Vittal, B. (2010). Fungi associated with decomposing leaf litter of cashew (*Anacardium occidentale*). *Mycology*, *1*(2), 121–129. https://doi.org/10.1080/21501201003743154

Shen, H. W., Bao, D. F., Boonmee, S., Lu, Y. Z., Su, X. J., Li, Y. X., . . . Luo, Z. L. (2024). Diversity of *Distoseptispora* (Distoseptisporaceae) taxa on submerged decaying wood from the Red River in Yunnan, China. *MycoKeys, 102*, 1. https://doi.org/10.3897/mycokeys.102.116096

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. W., Bao, D. F., Wanasinghe, D. N., Boonmee, S., Liu, J. K., & Luo, Z. L. (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

Sher, H., Aldosari, A., Ali, A., & de Boer, H. J. (2014). Economic benefits of high value medicinal plants to Pakistani communities: An analysis of current practice and potential. *Journal of Ethnobiology and Ethnomedicine, 10*(1), 71. https://doi.org/10.1186/1746-4269-10-71

Shu, Y. X., Cheng, R. L., Huang, J. L., Li, K. L., Zhao, S. Z., Zhao, H. J., . . . Xu, B. (2023). Introducing *Nigrograna wuhanensis* sp. nov. (Nigrograna ceae, Pleosporales) from *Camellia japonica* in China. *Chiang Mai Journal of Science, 50*(3), 1–11.

Silva, C. R., Gusmão, L. F. P., & Castañeda-Ruiz, R. F. (2015). *Dictyosporium amoenum* sp. nov. from Chapada Diamantina, Bahia, Brazil. *Mycotaxon, 130*(4), 1125–1133. https://doi.org/10.5248/130.1125

Sivanesan, A. (1996). *Corynesporasca caryotae* gen. et sp. nov. with a *Corynespora* anamorph, and the family Corynesporascaceae. *Mycological Research, 7*(100), 783–788. https://doi.org/10.1016/S0953-7562(96)80022-0

Slippers, B., Crous, P. W., Denman, S., Coutinho, T. A., Wingfield, B. D., & Wingfield, M. J. (2004). Combined multiple gene genealogies and phenotypic characters differentiate several species previously identified as *Botryosphaeria dothidea*. *Mycologia, 96*(1), 83–101. https://doi.org/10.1080/15572536.2005.11833000

Smith, G. J. D., Liew, E. C. Y., & Hyde, K. D. (2003). The Xylariales: A monophyletic order containing 7 families. *Fungal Diversity, 13*, 185–218.

Sofowora, A. (1996). Research on medicinal plants and traditional medicine in Africa. *The Journal of Alternative and Complementary Medicine, 2*(3), 365-372. https://doi.org/10.1089/acm.1996.2.365

Sofowora, A., Ogunbodede, E., & Onayade, A. (2013). The role and place of medicinal plants in the strategies for disease prevention. *African Journal of Traditional, Complementary and Alternative Medicines, 10*(5), 210-229. https://doi.org/10.4314/ajtcam.v10i5.2

Sommai, S., Nuankaew, S., Khamsuntorn, P., Suetrong, S., & Pinruan, U. (2019). *Tamhinispora saraburiensis* sp. nov. (Tubeufiaceae, Dothideomycetes) on bamboo in Thailand based on morphology & phylogenetic analysis. *Phytotaxa, 402*(1), 1–12. https://doi.org/10.11646/phytotaxa.402.1.1

Soto-Medina, E., & Lücking, R. (2017). A new species of *Rhytidhysteron* (Ascomycota: Patellariaceae) from Colombia, with a provisional working key to known species in the world. *Revista de la Academia Colombiana de Ciencias Exactas, Físicas Naturales, 41*(158), 59–63. https://doi.org/10.18257/raccefyn.423

Species Fungorum. (2024). http://www.speciesfungorum.org/Names/Names.asp

Spegazzini, C. (1910). Ramillete de hongos chilenos. *Revista de la Facultad de Agronomía, La Plata, 6*, 1–205.

Strobel, G., Stierle, A., Stierle, D., & Hess, W. M. (1993). *Taxomyces andreanae*, a proposed new taxon for a bulbilliferous hyphomycete associated with Pacific yew (*Taxus brevifolia*). *Mycotaxon, 47*, 71-80.

Stukenbrock, E. H., Banke, S., & McDonald, B. A. (2006). Global migration patterns in the fungal wheat pathogen *Phaeosphaeria nodorum*. *Molecular Ecology, 15*(10), 2895–2904. https://doi.org/10.1111/j.1365-294X.2006.02986.x

Su, H. Y., Hyde, K. D., Maharachchikumbura, S. S. N., Ariyawansa, H. A., Luo, Z. L., Promputtha, I., . . . Zhou, D. Q. (2016). The families Distoseptisporaceae fam. nov., Kirschsteiniotheliaceae, Sporormiaceae and Torulaceae, with new species from freshwater in Yunnan Province, China. *Fungal Diversity, 80*, 375-409. https://doi.org/10.1007/s13225-016-0362-0

Subramanian, C. V. (1958). Hyphomycetes v. *Journal of the Indian Botanical Society, 37*, 47–64.

Subramanian, C. V. (1954). Fungi Imperfecti from Madras–VI. *Journal of the Indian Botanical Society, 33*, 36–42. https://doi.org/10.1007/BF03050206

Sun, R. T., Zhang, Z., Zhou, N., Srivastava, A. K., Kamil, K., Abd-Allah, E. F., . . . Wu, Q. S. (2021). A review of the interaction of medicinal plants and arbuscular mycorrhizal fungi in the rhizosphere. *Notulae Botanicae Horti Agrobotanici Cluj-Napoca*, *49*(3), 12454. https://doi.org/10.15835/nbha49312454

Sun, W. X., Huang, S. T., Xia, J. W., Zhang, X. G., & Li, Z. (2021). Morphological and molecular identification of *Diaporthe* species in southwestern China, with description of eight new species. *MycoKeys, 77*, 65–95. https://doi.org/10.3897/mycokeys.77.59852

Sun, Y. R., Goonasekara, I., Thambugala, K. M., Jayawardena, R. S., Wang, Y., & Hyde, K. D. (2020). *Distoseptispora bambusae* sp. nov. (Distoseptisporaceae) on bamboo from China and Thailand. *Biodiversity Data Journal, 8*, e53678. https://doi.org/10.3897/BDJ.8.e53678

Sun, Y. R., Jayawardena, R. S., Sun, J. E., & Wang, Y. (2023). Pestalotioid species associated with medicinal plants in Southwest China and Thailand. *Microbiology Spectrum, 11*(1), e03987-03922. https://doi.org/10.1128/spectrum.03987-22

Sun, Y. R., Liu, N. G., Samarakoon, M. C., Jayawardena, R. S., Hyde, K. D., & Wang, Y. (2021). Morphology and phylogeny reveal Vamsapriyaceae fam. nov. (Xylariales, Sordariomycetes) with two novel *Vamsapriya* species. *Journal of Fungi, 7*, 891. https://doi.org/10.3390/jof7110891

Sun, Y. R., Liu, N. G., Hyde, K. D., Jayawardena, R. S., & Wang, Y. (2022). *Pleocatenata chiangraiensis* gen. et. sp. nov. (Pleosporales, Dothideomycetes) from medicinal plants in northern Thailand. *MycoKeys, 87*, 77–98. https://doi.org/10.3897/mycokeys.87.79433

Sun, Y. R., Jayawardena, R. S., Hyde, K. D., & Wang, Y. (2021). *Kirschsteiniothelia thailandica* sp. nov. (Kirschsteiniotheliaceae) from Thailand. *Phytotaxa, 490*(2), 172–182. https://doi.org/10.11646/phytotaxa.490.2.3

Sun, Y. R., Zhang, J. Y., Hyde, K. D., Wang, Y., & Jayawardena, R. S. (2023). Morphology and phylogeny reveal three *Montagnula* species from China and Thailand. *Plants, 12*(4), 738. https://doi.org/10.3390/plants12040738

Tanaka, K., & Harada, Y. (2003). Pleosporales in Japan (2): The genus *Lophiotrema*. *Mycoscience, 44*(2), 115-121. https://doi.org/10.1007/S10267-003-0092-5

Tanaka, K., Hashimoto, A., Matsumura, M., & Sato, T. (2017). *Brevicollum*, a new genus in Neohendersoniaceae, Pleosporales. *Mycologia, 109*(4), 608–619. https://doi.org/10.1080/00275514.2017.1387432

Tanaka, K., Hirayama, K., Yonezawa, H., Sato, G., Toriyabe, A., Kudo, H., . . . Hosoya, T. (2015). Revision of the Massarineae (Pleosporales, Dothideomycetes). *Studies in Mycology, 82*, 75–136. https://doi.org/10.1016/j.simyco.2015.10.002

Teng, S. C. (1936). Additional fungi from China IV. *Sinensia, 7*, 752–823.

Tennakoon, D. S., de Silva, N. I., Maharachchikumbura, S. S. N., Bhat, D. J., Kumla, J., Suwannarach, N., & Lumyong, S. (2023). Exploring more on Dictyosporiaceae: The species geographical distribution and intriguing novel additions from plant litter. *Diversity, 15*(3), 410. https://doi.org/10.3390/d15030410

Tennakoon, D. S., Kuo, C.-H., Maharachchikumbura, S. S. N., Thambugala, K. M., Gentekaki, E., Phillips, A. J. L., . . . Hyde, K. D. (2021). Taxonomic and phylogenetic contributions to *Celtis formosana*, *Ficus ampelas*, *F. septica*, *Macaranga tanarius* and *Morus australis* leaf litter inhabiting microfungi. *Fungal Diversity, 108*(1), 1–215. https://doi.org/10.1007/s13225-021-00474-w

Tennakoon, D. S., Thambugala, K. M., de Silva, N. I., Suwannarach, N., & Lumyong, S. (2022). A taxonomic assessment of novel and remarkable fungal species in Didymosphaeriaceae (Pleosporales, Dothideomycetes) from plant litter. *Frontiers in Microbiology, 13*, 1016285. https://doi.org/10.3389/fmicb.2022.1016285

Thambugala, K. M., Daranagama, D. A., Phillips, A. J. L., Bulgakov, T. S., Bhat, D. J., Camporesi, E., . . . Hyde, K. D. (2017). Microfungi on *Tamarix*. *Fungal Diversity, 82*(1), 239–306. https://doi.org/10.1007/s13225-016-0371-z

Thambugala, K. M., Hyde, K. D., Eungwanichayapant, P. D., Romero, A. I., & Liu, Z. Y. (2016). Additions to the genus *Rhytidhysteron* in Hysteriaceae. *Cryptogamie, Mycologie, 37*(1), 99–116. https://doi.org/10.7872/crym/v37.iss1.2016.99

Thompson, S. M., Tan, Y. P., Shivas, R. G., Neate, S. M., Morin, L., Bissett, A., . . . Aitken, E. A. B. (2015). Green and brown bridges between weeds and crops reveal novel *Diaporthe* species in Australia. *Persoonia, 35*(1), 39–49. https://doi.org/10.3767/003158515X687506

Tian, X. G., Bao, D. F., Karunarathna, S. C., Jayawardena, R. S., Hyde, K. D., Bhat, D. J., . . . Tibpromma, S. (2024). Taxonomy and phylogeny of ascomycetes associated with selected economically important monocotyledons in China and Thailand. *Mycosphere, 15*(1), 1–274.

Tibpromma, S., Hyde, K. D., Bhat, J. D., Mortimer, P. E., Xu, J. C., Promputtha, I., . . . Karunarathna, S. C. (2018). Identification of endophytic fungi from leaves of Pandanaceae based on their morphotypes and DNA sequence data from southern Thailand. *MycoKeys, 33*, 25–67. https://doi.org/10.3897/mycokeys.32.23670.figure7

Tibpromma, S., Hyde, K. D., Jeewon, R., Maharachchikumbura, S. S. N., Liu, J. K., Bhat, D. J., . . . Karunarathna, S. C. (2017). Fungal diversity notes 491–602: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity, 83*, 1-261. https://doi.org/10.1007/s13225-017-0378-0

Tibpromma, S., Hyde, K. D., McKenzie, E. H. C., Bhat, D. J., Phillips, A. J. L., Wanasinghe, D. N., . . . Karunarathna, S. C. (2018). Fungal diversity notes 840–928: Micro-fungi associated with *Pandanaceae*. *Fungal Diversity, 93*, 1–160. https://doi.org/10.1007/s13225-018-0408-6

Tibpromma, S., Karunarathna, S. C., Mortimer, P. E., Xu, J. C., Doilom, M., & Lumyong, S. (2020). *Bartalinia kevinhydei* (Ascomycota), a new leaf-spot causing fungus on teak (*Tectona grandis*) from Northern Thailand. *Phytotaxa, 474*(1), 27–39. https://doi.org/10.11646/phytotaxa.474.1.3

Toghueo, R. M. K., de Aldana, B. R. V., & Zabalgogeazcoa, I. (2023). *Diaporthe* species associated with the maritime grass *Festuca rubra* subsp. *pruinosa*. *Frontiers in Microbiology, 14*. https://doi.org/10.3389/fmicb.2023.1105299

Trifinopoulos, J., Nguyen, L.-T., von Haeseler, A., & Minh, B. Q. (2016). W-IQ-TREE: A fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research, 44*(W1), W232-W235. https://doi.org/10.1093/nar/gkw256

Tsui, C. K. M., Hyde, K. D., & Hodgkiss, I. J. (2001). *Paraniesslia tuberculata* gen. et sp. nov., and new records or species of *Clypeosphaeria*, *Leptosphaeria*, and *Astrosphaeriella* in Hong Kong freshwater habitats. *Mycologia, 93*(5), 1002–1009. https://doi.org/10.1080/00275514.2001.12063232

Udayanga, D., Castlebury, L. A., Rossman, A. Y., Chukeatirote, E., & Hyde, K. D. (2015). The *Diaporthe sojae* species complex: Phylogenetic re-assessment of pathogens associated with soybean, cucurbits and other field crops. *Fungal Biology, 119*(5), 383–407. https://doi.org/10.1016/j.funbio.2014.10.009

Udayanga, D., Liua, X. Z., McKenzie, E. H. C., Chukeatirote, E., & Hyde, K. D. (2012). Multi-locus phylogeny reveals three new species of *Diaporthe* from Thailand. *Cryptogamie, Mycologie, 33*(3), 295–309. https://doi.org/10.7872/crym.v33.iss3.2012.295

Umali, T. E., Hyde, K. D., & Quimio, T. H. (1999). *Arecophila bambusae* sp. nov. and *A. coronata* comb. nov., from dead culms of bamboo. *Mycoscience, 40,* 185–188. https://doi.org/10.1007/BF02464296

Vajna, L., & Bagyinka, T. (2002). Occurrence of privet anthracnose in Hungary caused by *Glomerella cingulata*. *Plant Pathology, 51*(3), 403. https://doi.org/10.1046/j.1365-3059.2002.00719.x

Valenzuela-Lopez, N., Sutton, D. A., Cano-Lira, J. F., Paredes, K., Wiederhold, N., Guarro, J., . . . Stchigel, A. M. (2017). Coelomycetous fungi in the clinical setting: Morphological convergence and cryptic diversity. *Journal of Clinical Microbiology*, *55*(2), 552–567. https://doi.org/10.1128/JCM.02221-16

Van Emden, J. H. (1975). Three new fungi from Surinam soil. *Acta Botanica Neerlandica*, *24*(2), 193–197. https://doi.org/10.1111/j.1438-8677.1975.tb01006.x

Varjani, S. J., & Patel, R. K. (2017). Fungi: A remedy to eliminate environmental pollutants. In R. Prasad (Ed.), *Mycoremediation and environmental sustainability: volume 1* (pp. 53-67). Springer International Publishing. https://doi.org/10.1007/978-3-319-68957-9_4

Verkley, G. J. M., Dukik, K., Renfurm, R., Göker, M., & Stielow, J. (2014). Novel genera and species of coniothyrium-like fungi in Montagnulaceae (Ascomycota). *Persoonia, 32*(1), 25–51. https://doi.org/10.3767/003158514X679191

Vieto, S., Escudero-Leyva, E., Avendaño, R., Rechnitzer, N., Barrantes-Madrigal, M. D., Conejo-Barboza, G., . . . Chavarría, M. (2022). Biodeterioration and cellulolytic activity by fungi isolated from a nineteenth-century painting at the National Theatre of Costa Rica. *Fungal Biology, 126*(2), 101–112. https://doi.org/10.1016/j.funbio.2021.11.001

Voglmayr, H., & Jaklitsch, W. M. (2017). *Corynespora*, *Exosporium*, and *Helminthosporium* revisited: New species and generic reclassification. *Studies in Mycology, 87*(1), 43–76. https://doi.org/10.1016/j.simyco.2017.05.001

Wanasinghe, D. N., & Maharachchikumbura, S. S. N. (2023). Exploring the diversity and systematics of Phaeosphaeriaceae: Taxonomic novelties from ecologically diverse habitats and their phylogenetic resolution. *Journal of Fungi, 9*(8), 853. https://doi.org/10.3390/jof9080853

Wanasinghe, D. N., Mortimer, P. E., & Xu, J. C. (2021). Insight into the systematics of microfungi colonizing dead woody twigs of *Dodonaea viscosa* in Honghe (China). *Journal of Fungi, 7*(3), 180. https://doi.org/10.3390/jof7030180

Wanasinghe, D. N., Phukhamsakda, C., Hyde, K. D., Jeewon, R., Lee, H. B., Gareth Jones, E. B., . . . Karunarathna, S. C. (2018). Fungal diversity notes 709–839: Taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on Rosaceae. *Fungal Diversity, 89*, 1–236. https://doi.org/10.1007/s13225-018-0395-7

Wanasinghe, D. N., Ren, G. C., Xu, J. C., Cheewangkoon, R., & Mortimer, P. E. (2022). Insight into the taxonomic resolution of the pleosporalean species associated with dead woody litter in natural forests from Yunnan, China. *Journal of Fungi*, *8*(4), 375. https://doi.org/10.3390/jof8040375

Wanasinghe, D. N., Wijayawardene, N. N., Xu, J. C., Cheewangkoon, R., & Mortimer, P. E. (2020). Taxonomic novelties in *Magnolia*-associated pleosporalean fungi in the Kunming Botanical Gardens (Yunnan, China). *PLOS ONE*, *15*(7), e0235855. https://doi.org/10.1371/journal.pone.0235855

Wang, F., Wang, K., Cai, L., Zhao, M. J., Kirk, P. M., Fan, G. M., . . . Yu, Z. F. (2022). Fungal names: A comprehensive nomenclatural repository and knowledge base for fungal taxonomy. *Nucleic Acids Research*. https://doi.org/10.1093/nar/gkac926

Wang, J. Y., Zhang, K., Yang, C. L., Xia, J. W., Ma, Y. R., Gao, J. M., . . . Cai, Y. M. (2016). *Podosporium bacilliforme* sp. nov. and a first record of *Phaeoblastophora peckii* from southern China. *Mycotaxon, 131*, 841–846. https://doi.org/10.5248/131.841

Wang, R. X., Luo, Z. L., Hyde, K. D., Bhat, D. J., Su, X. J., & Su, H. Y. (2016). New species and records of *Dictyocheirospora* from submerged wood in north-western Yunnan, China. *Mycosphere*, *7*(9), 1357–1367. https://doi.org/10.5943/mycosphere/7/9/9

Wang, S. Y., McKenzie, E. H. C., Phillips, A. J. L., Li, Y., & Wang, Y. (2022). Taxonomy and multigene phylogeny of *Diaporthales* in Guizhou Province, China. *Journal of Fungi, 8*, 1301. https://doi.org/10.3390/jof8121301

Wang, X., Wanasinghe, D. N., Zhang, J., Ma, J., Zhou, P., Zhang, L., . . . Zhang, Z. (2023). Insights from the endophytic fungi in *Amphisphaeria* (Sordariomycetes): *A. orixae* sp. nov. from *Orixa japonica* and its secondary metabolites. *Microorganisms, 11*(5). https://doi.org/10.3390/microorganisms11051268

Wang, Y., Hyde, K. D., McKenzie, E. H. C., Jiang, Y. L., Li, D. W., & Zhao, D. G. (2015). Overview of *Stachybotrys* (*Memnoniella*) and current species status. *Fungal Diversity, 71*, 17–83. https://doi.org/10.1007/s13225-014-0319-0

Wang, Y. C., Xiong, F., Lu, Q. H., Hao, X. Y., Zheng, M. X., Wang, L., . . . Yang, Y. J. (2019). Diversity of *Pestalotiopsis*-like species causing gray blight disease of tea plants (*Camellia sinensis*) in China, including two novel *Pestalotiopsis* species, and analysis of their pathogenicity. *Plant Disease, 103*(10), 2548–2558. https://doi.org/10.1094/PDIS-02-19-0264-RE

Wanasinghe, D. N., Jones, E. B. G., Camporesi, E., Dissanayake, A. J., Kamolhan, S., Mortimer, P. E., . . . Hyde, K. D. (2016). Taxonomy and phylogeny of *Laburnicola* gen. nov. and *Paramassariosphaeria* gen. nov. (*Didymosphaeriaceae, Massarineae, Pleosporales*). *Fungal Biology, 120*, 1354–1373. https://doi.org/10.1016/j.funbio.2016.06.006

Weber, D., Sterner, O., Anke, T., Gorzalczancy, S., Martino, V., & Acevedo, C. (2004). Phomol, a new anti-inflammatory metabolite from an endophyte of the medicinal plant *Erythrina crista-galli*. *The Journal of Antibiotics, 57*(9), 559−563. https://doi.org/10.7164/antibiotics.57.559

Wijayawardene, N. N., Hyde, K. D., Al-Ani, L. K. T., Tedersoo, L., Haelewaters, D., Rajeshkumar, K. C., . . . Mortimer, P. E. (2020). Outline of fungi and fungus-like taxa. *Mycosphere, 11*(1), 1060–1456. https://doi.org/10.5943/mycosphere/11/1/8

Wijayawardene, N. N., Hyde, K. D., Dai, D. Q., Sánchez-García, M., Goto, B., Saxena, R., . . . Thines, M. (2022). Outline of Fungi and fungus-like taxa-2021. *Mycosphere, 13*(1), 53–453. https://doi.org/10.5943/mycosphere/13/1/2

Wijayawardene, N. N., Hyde, K. D., Wanasinghe, D. N., Papizadeh, M., Goonasekara, I. D., Camporesi, E., . . . Wang, Y. (2016). Taxonomy and phylogeny of dematiaceous coelomycetes. *Fungal Diversity, 77*(1), 1–316. https://doi.org/10.1007/s13225-016-0360-2

Wonglom, P., Pornsuriya, C., & Sunpapao, A. (2023). A New Species of *Neoscytalidium hylocereum* sp. nov. Causing Canker on Red-Fleshed Dragon Fruit (*Hylocereus polyrhizus*) in Southern Thailand. *Journal of Fungi, 9*(2), 197. https://doi.org/10.3390/jof9020197

Wongsawas, M., Wang, H. K., Hyde, K. D., & Lin, F. C. (2009). *Dictyosporium zhejiangense* sp. nov., a new freshwater anamorphic fungus from China. *Cryptogamie, Mycologie, 30*(4), 355–362.

Wu, B., Hussain, M., Zhang, W., Stadler, M., Liu, X., & Xiang, M. (2019). Current insights into fungal species diversity and perspective on naming the environmental DNA sequences of fungi. *Mycology, 10*(3), 127-140. https://doi.org/10.1080/21501203.2019.1614106

Wu, N., Chethana, K. W. T., & Liu, J.-K. (2024). *Velutinus*, a novel genus in Patellariopsidaceae from medicinal plants in Sichuan Province, China. *Phytotaxa, 638*(2), 165-174. https://doi.org/10.11646/phytotaxa.638.2.5

Wu, N., Dissanayake, A. J., Chethana, K. W. T., Hyde, K. D., & Liu, J.-K. (2021). Morpho-phylogenetic evidence reveals *Lasiodiplodia chiangraiensis* sp. nov. (Botryosphaeriaceae) associated with woody hosts in northern Thailand. *Phytotaxa, 508*(2), 142–154. https://doi.org/10.11646/phytotaxa.508.2.3

Wu, N., Dissanayake, A. J., Manawasinghe, I. S., Rathnayaka, A. R., Liu, J.-K., Phillips, A. J. L., . . . Hyde, K. D. (2021). https://botryosphaeriales.org/, an online platform for up-to-date classification and account of taxa of Botryosphaeriales. *Database, 2021*: baab061. https://doi.org/10.1093/database/baab061

Wu, W., & Diao, Y. (2022). Anamorphic chaetosphaeriaceous fungi from China. *Fungal Diversity, 116*, 1-546. https://doi.org/10.1007/s13225-022-00509-w

Xia, G. Y., Manawasinghe, I. S., Phillips, A. J. L., You, C., Jayawardena, R. S., Luo, M., . . . Hyde, K. D. (2022). *Lasiodiplodia fici* sp. nov., Causing Leaf Spot on *Ficus altissima* in China. *Pathogens, 11*(8), 840. https://doi.org/10.3390/pathogens11080840

Xiao, X. E., Wang, W., Crous, P. W., Wang, H. K., Jiao, C., Huang, F., . . . Li, H. Y. (2021). Species of Botryosphaeriaceae associated with citrus branch diseases in China. *Persoonia-Molecular Phylogeny and Evolution of Fungi, 47*(1), 106–135. https://doi.org/10.3767/persoonia.2021.47.03

Xiao, X. J., Ma, J., Zhang, L. J., Liu, N. G., Xiao, Y. P., Tian, X. G., . . . Lu, Y. Z. (2023). Additions to the genus *Helicosporium* (Tubeufiaceae, Tubeufiales) from China with an identification key for *Helicosporium* taxa. *Journal of Fungi, 9*(7), 775. https://doi.org/10.3390/jof9070775

Xiao, Y. S., Zou, M. Y., Zhou, X., Yang, C. X., & Cui, C. Y. (2023). First report of postharvest fruit brown rot disease on navel orange caused by *Diaporthe sojae* in China. *Plant Disease, 107*(3), 948. https://doi.org/10.1094/PDIS-04-22-0922-PDN

Xie, J., Chen, Y., Cai, G., Cai, R., Hu, Z., & Wang, H. (2023). Tree Visualization by One Table (tvBOT): A web application for visualizing, modifying and annotating phylogenetic trees. *Nucleic Acids Research, 51*(W1), W587-W592. https://doi.org/10.1093/nar/gkad359

Xu, H. Y., Zhang, Y. Q., Liu, Z. M., Chen, T., Lv, C. Y., Tang, S. H., . . . Zhou, R. R. (2019). ETCM: An encyclopaedia of traditional Chinese medicine. *Nucleic Acids Research, 47*(D1), D976-D982. https://doi.org/10.1093/nar/gky987

Xu, R. F., Karunarathna, S. C., Phukhamsakda, C., Dai, D. Q., Elgorban, A. M., Suwannarach, N., . . . Tibpromma, S. (2024). Four new species of Dothideomycetes (Ascomycota) from Pará Rubber (*Hevea brasiliensis*) in Yunnan Province, China. *MycoKeys, 103*, 71. https://doi.org/10.3897/mycokeys.103.117580

Xu, R. J., Thiyagaraja, V., Li, Y., Zhou, D. Q., Boonmee, S., & Zhao, Q. (2024). Two novel lignicolous freshwater fungi, *Conioscypha xizangensis* and *Cordana linzhiensis*, from the Tibetan Plateau, China. *New Zealand Journal of Botany*, 1–17.

Xu, R. J., Zhu, Y. A., Liu, N. G., Boonmee, S., Zhou, D. Q., & Zhao, Q. (2023). Taxonomy and phylogeny of hyphomycetous muriform conidial taxa from the Tibetan Plateau, China. *Journal of Fungi, 9*(5), 560. https://doi.org/10.3390/jof9050560.

Yang, C. L., Xu, X. L., & Liu, Y. G. (2019). Two new species of *Bambusicola* (*Bambusicolaceae*, *Pleosporales*) on *Phyllostachys heteroclada* from Sichuan, China. *Nova Hedwigia, 108*, 527–545. https://doi.org/10.1127/nova_hedwigia/2019/0526

Yang, E. F., Tibpromma, S., Karunarathna, S. C., Phookamsak, R., Xu, J. C., Zhao, Z. X., . . . Promputtha, I. (2022). Taxonomy and phylogeny of novel and extant taxa in *Pleosporales* associated with *Mangifera indica* from Yunnan, China (Series I). *Journal of Fungi, 8*(2). https://doi.org/10.3390/jof8020152

Yang, E. F., Tibpromma, S., Karunarathna, S. C., Phookamsak, R., Xu, J. C., Zhao, Z. X., Karunanayake, C., & Promputtha, I. (2022). Taxonomy and phylogeny of novel and extant taxa in *Pleosporales* associated with *Mangifera indica* from Yunnan, China (Series I). *Journal of Fungi*, *8*(2), 152. https://doi.org/10.3390/jof8020152.

Yang, H., Dong, W., Yu, X. D., Bhat, D. J., Boonmee, S., & Zhang, H. (2020). Four freshwater dematiaceous hyphomycetes in *Sordariomycetes* with two new species of *Parafuscosporella*. *Phytotaxa, 441*(1), 19-34. https://doi.org/10.11646/phytotaxa.441.1.2

Yang, J., Liu, J. K., Hyde, K. D., Jones, E. B. G., & Liu, Z. Y. (2018). New species in *Dictyosporium*, new combinations in *Dictyocheirospora* and an updated backbone tree for Dictyosporiaceae. *MycoKeys, 36*, 83–105. https://doi.org/10.3897/mycokeys.36.27051

Yang, J., Maharachchikumbura, S. S. N., Liu, J. K., Hyde, K. D., Jones, E. B. G., Al-Sadi, A. M., . . . Liu, Z. Y. (2018). *Pseudostanjehughesia aquitropica* gen. et sp. nov. and *Sporidesmium* sensu lato species from freshwater habitats. *Mycological Progress, 17*, 591-616. https://doi.org/10.1007/s11557-017-1339-4

Yang, J., Liu, L. L., Jones, E., Li, W. L., Hyde, K. D., & Liu, Z. Y. (2021). Morphological variety in *Distoseptispora* and introduction of six novel species. *Journal of Fungi, 7*(11), 945. https://doi.org/10.3390/jof7110945

Yang, J., Liu, L. L., Jones, E. B. G., Hyde, K. D., Liu, Z. Y., Bao, D. F., . . . Liu, J. K. (2023). Freshwater fungi from karst landscapes in China and Thailand. *Fungal Diversity, 119*, 1–212. https://doi.org/10.1007/s13225-023-00514-7

Yang, Q., Fan, X. L., Guarnaccia, V., & Tian, C. M. (2018). High diversity of *Diaporthe* species associated with dieback diseases in China, with twelve new species described. *MycoKeys, 39*, 97–149. https://doi.org/10.3897/mycokeys.39.26914

Yang, Q., Zeng, X. Y., Yuan, J., Zhang, Q., He, Y. K., & Wang, Y. (2021). Two new species of *Neopestalotiopsis* from southern China. *Biodivers Data J, 9*, e70446. https://doi.org/10.3897/BDJ.9.e70446

Yang, S., Berry, R. W., Luttrell, E. S., & Vongkaysone, T. (1984). A new sunflower disease in Texas caused by *Diaporthe helianthi*. *Plant Disease, 68*(3), 254–255. https://doi.org/10.1094/PD-69-254

Yang, Y. H., Liao, C. F., Manawasinghe, I. S., de Farias, A. R. G., & Dong, Z. Y. (2023). *Neomassaria khayae* sp. nov., a novel pleosporalean species on *Khaya senegalensis* from Guangdong Province, China. *Phytotaxa, 599*(1), 65-77. https://doi.org/10.11646/phytotaxa.599.1.4

Yeh, Y. W., Hsieh, C. M., Yeh, Y. H., Huang, Y. M., & Kirschner, R. (2023). A new species of *Memnoniella* (Hypocreales, Stachybotryaceae), *Memnoniella pseudodichroa*, from the ancient subtropical giant fern *Angiopteris lygodiifolia* (Marattiaceae) in Taiwan. *Plant Systematics and Evolution, 309*(3), 19. https://doi.org/10.1007/s00606-023-01855-1

Yu, X. D., Zhang, S. N., & Liu, J. K. (2022). Morpho-phylogenetic evidence reveals novel pleosporalean taxa from Sichuan Province, China. *Journal of Fungi, 8,* 720. https://doi.org/10.3390/jof8070720.

Yuan, H. S., Lu, X., Dai, Y. C., Hyde, K. D., Kan, Y. H., Kušan, I., . . . Zhou, L. W. (2020). Fungal diversity notes 1277–1386: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity, 104*, 1-266. https://doi.org/10.1007/s13225-020-00461-7

Zahra, W., Rai, S. N., Birla, H., Singh, S. S., Rathore, A. S., Dilnashin, H., . . . Singh, S. P. (2020). Economic importance of medicinal plants in Asian countries. In C. Keswani (Ed.), *Bioeconomy for sustainable development* (pp. 359–377). Springer Singapore.

Zare, R., Gams, W., & Schroers, H. J. (2004). The type species of *Verticillium* is not congeneric with the plant-pathogenic species placed in *Verticillium* and it is not the anamorph of '*Nectria*' inventa. *Mycological Research, 108*, 576–582. https://doi.org/10.1017/S0953756204009839

Zeilinger, S., Gupta, V. K., Dahms, T. E. S., Silva, R. N., Singh, H. B., Upadhyay, R. S., . . . Nayak, S. C. (2015). Friends or foes? Emerging insights from fungal interactions with plants. *FEMS Microbiology Reviews, 40*(2), 182–207. https://doi.org/10.1093/femsre/fuv045

Zelski, S. E., Raja, H. A., Miller, A. N., & Shearer, C. A. (2015). *Conioscypha peruviana* sp. nov., its phylogenetic placement based on 28S rRNA gene, and a report of *Conioscypha gracilis* comb. nov. from Peru. *Mycoscience, 56*(3), 319-325. https://doi.org/10.1016/j.myc.2014.09.002

Zhai, Z. J., Yan, J. Q., Li, W. W., Gao, Y., Hu, H. J., Zhou, J. P., . . . Hu, D. M. (2022). Three novel species of *Distoseptispora* (Distoseptisporaceae) isolated from bamboo in Jiangxi Province, China. *MycoKeys*, *88*, 35. https://doi.org/10.3897/mycokeys.88.79346

Zhang, J. F., Liu, J. K., Hyde, K. D., Chen, Y. Y., Ran, H. Y., & Liu, Z. Y. (2023). Ascomycetes from karst landscapes of Guizhou Province, China. *Fungal Diversity*, *122*(1), 1–160. https://doi.org/10.1007/s13225-023-00524-5

Zhang, J. F., Liu, J. K., Hyde, K. D., Yang, W., & Liu, Z. Y. (2017). Fungi from Asian Karst formations II. Two new species of *Occultibambusa* (*Occultibambusaceae, Dothideomycetes*) from karst landforms of China. *Mycosphere, 8*(4), 550–559. https://doi.org/10.5943/mycosphere/8/4/4

Zhang, J. F., Liu, J. K., Jeewon, R., Wanasinghe, D. N., & Liu, Z. Y. (2019). Fungi from Asian Karst formations III. Molecular and morphological characterization reveal new taxa in *Phaeosphaeriaceae*. *Mycosphere, 10*, 202–220. https://doi.org/10.5943/mycosphere/10/1/3

Zhang, J. F., Liu, J. K., Ran, H. Y., Khongphinitbunjong, K., & Liu, Z. Y. (2018). A new species and new record of *Lophiotrema* (Lophiotremataceae, Dothideomycetes) from karst landforms in southwest China. *Phytotaxa, 379*(2), 169–179. https://doi.org/10.11646/phytotaxa.379.2.5

Zhang, J. F., Liu, J. K., Thambugala, K. M., Yang, J., Meng, Z. H., & Liu, Z. Y. (2020). Two new species and a new record of *Nigrograna* (Nigrograna ceae, Pleosporales) from China and Thailand. *Mycological Progress, 19*, 1365–1375. https://doi.org/10.1007/s11557-020-01633-0

Zhang, Q., Wijayawardene, N. N., Hyde, K. D., Wang, Y., & Pan, X. J. (2020). *Xepicula yifeii* sp. nov. caused a leaf blight of *Lasia spinosa* (Araceae) in South China karst. *European Journal of Plant Pathology, 158*(1), 121−134. https://doi.org/10.1007/s10658-020-02060-3

Zhang, Y., Liu, Y. J., Zhou, Y. P., Zhang, X. D., Cui, B. K., He, S. H., . . . Fournier, J. (2014). *Helicascus gallicus* sp. nov., a new freshwater pleosporalean ascomycete from France. *Phytotaxa, 183*(3), 183–192. https://doi.org/10.11646/phytotaxa.183.3.5

Zhang, Y., Schoch, C. L., Fournier, J., Crous, P. W., De Gruyter, J., Woudenberg, J. H. C., . . . Hyde, K. D. (2009). Multi-locus phylogeny of Pleosporales: A taxonomic, ecological and evolutionary re-evaluation. *Studies in Mycology, 64*(1), 85–102. https://doi.org/10.3114/sim.2009.64.04

Zhang, Y. Y., Zhang, T., Li, H. Y., Zheng, R., Ren, J., Yang, Q., . . . Jiang, N. (2024). *Nigrospora humicola* (Apiosporaceae, Amphisphaeriales), a new fungus from soil in China. *Diversity*, *16*(2), 118. https://doi.org/10.3390/d16020118

Zhang, Y. Z., Chen, Q. L., Ma, J., Lu, Y. Z., Chen, H. B., & Liu, N. G. (2023). Morphological and multi-gene phylogenetic analyses reveal five new hyphomycetes from freshwater habitats. *Frontiers in Microbiology, 14*, 1253239. https://doi.org/10.3389/fmicb.2023.1253239

Zhao, J. H., Zhang, Y. L., Wang, L. W., Wang, J. Y., & Zhang, C. L. (2012). Bioactive secondary metabolites from *Nigrospora* sp. LLGLM003, an endophytic fungus of the medicinal plant *Moringa oleifera* Lam. *World Journal of Microbiology and Biotechnology, 28*, 2107–2112. https://doi.org/10.1007/s11274-012-1015-4

Zhao, R. L., Yang, Y. M., & Zhao, G. C. (2004). *Pseudolachnella vermospora* sp. nov. from *Yushania vigens* in China. *Fungal Diversity, 15*, 255–260.

Zhao, X. L., Li, K. N., Zheng, S. J., Yang, J., Chen, C. J., Zheng, X. B., . . . Ye, W. W. (2022). *Diaporthe* diversity and pathogenicity revealed from a broad survey of soybean stem blight in China. *Plant Disease*, *106*(11), 2892–2903. https://doi.org/10.1094/PDIS-12-21-2785-RE

Zheng, H., Zhang, Z., Liu, D. Z., & Yu, Z. F. (2019). *Memnoniella sinensis* sp. nov., a new species from China and a key to species of the genus. *International Journal of Systematic and Evolutionary Microbiology*, *69*(10), 3161–3169. https://doi.org/10.1099/ijsem.0.003605

Zheng, X. R., Zhang, M. J., Shang, X. L., Fang, S. Z., & Chen, F. M. (2020). Stem canker on *Cyclocarya paliurus* is caused by *Botryosphaeria dothidea*. *Plant Disease, 104*(4), 1032−1040. https://doi.org/10.1094/PDIS-11-18-1990-RE

Zhu, D., Luo, Z. L., Baht, D. J., McKenzie, E. H. C., Bahkali, A. H., Zhou, D. Q., . . . Hyde, K. D. (2016). *Helminthosporium velutinum* and *H. aquaticum* sp. nov. from aquatic habitats in Yunnan Province, China. *Phytotaxa, 253*(3), 179–190. https://doi.org/10.11646/phytotaxa.253.3.1

Zimmerman, A. (1902). Ueber einige an tropischen Kulturpflanzen beobachtete Pilze III. *Zentralblatt für Bakteriologie, Parasitenkunde, 8*, 216–221.

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 121ºC 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 121ºC for 20 minutes.

3. Water Agar (WA) Used for Fungal Isolation

Agar 15 g

Suspend 15 g of 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°C for 20 minutes.

4. Indian ink used for observing gelatinous appendages of ascospores in some species

APPENDIX B

ABSTRACT OF PUBLICATIONS

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open access

Taxonomic Paper

Distoseptispora bambusae sp. nov. (*Distoseptisporaceae*) on bamboo from China and Thailand

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Abstract

Background

Bamboo is a widespread plant with medicinal value. During our taxonomic study on medicinal plants, three collections of *Distoseptispora* were made from China and Thailand. Phylogenetic analyses of combined LSU, ITS and *RPB2* sequence data showed that two collections represented a new species, phylogenetically distinct from other described species in *Distoseptispora*.

New information

This new species has macronematous, mononematous conidiophores, polyblastic or monoblastic conidiogenous cells and acrogenous, solitary, straight, obclavate, multi-septate, thick-walled conidia. *Distoseptispora bambusae* sp. nov. is introduced with

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Kirschsteiniothelia thailandica sp. nov. (Kirschsteiniotheliaceae) from Thailand

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Abstract

A *Kirschsteiniothelia* species was found on decayed twigs of *Ficus microcarpa* collected at the Garden of Medicinal Plants in Chiang Rai, Thailand. Phylogenetic analyses of combined ITS, LSU and SSU sequence data showed the new isolate was phylogenetically distinct from other known species of *Kirschsteiniothelia*. Accordingly, *Kirschsteiniothelia thailandica sp. nov.* is described and illustrated and compared with other species in the genus.

Keywords: 1 new taxon, hyphomycetes, Kirschsteiniotheliales, multi-gene phylogeny, taxonomy

Introduction

Kirschsteiniothelia was introduced by Hawksworth (1985) based on the type species *Kirschsleiniothelia aethiops*. It has both asexual and sexual morphs. The sexual morph of *Kirschsleiniothelia* has brown or black, hemisphaerical or subglobose ascomata, cylindrical-clavate, bitunicate, 8-spored asci and ellipsoidal, brown to dark brown, smooth-walled, 1–2-septate ascospores (Hawksworth 1985, Boonmee *et al*. 2012, Hyde *et al*. 2013, Mehrabi *et al*. 2017). There are two types of asexual morphs in *Kirschsteiniothelia*, *viz*. dendryphiopsis-like and sporidesmium-like. *Dendryphiopsis* was linked with *Kirschsteiniothelia,* which was confirmed by Hawksworth (1985) and Boonmee *et al*. (2012). Subsequently, Su *et al*. (2016) reported a sporidesmium-like asexual morph (*Kirchsteiniothelia submerse*) in *Kirschsteiniothelia*. Wijayawardene *et al*. (2014) recommended using *Kirschsteiniothelia* over *Dendryphiopsis* considering fewer names changes.

Kirschsteiniothelia was assigned to Pleosporaceae by Hawksworth (1985) and Barr (1987). Barr (1993) suggested that *Kirschsteiniothelia* should be transferred to the Pleomassariaceae considering its asexual morph, host and morphology. Schoch *et al*. (2006) proposed that *Kirschsteiniothelia* should has its own family as the type species *K. aethiops* did not group with Pleosporaceae in their phylogenetic analyses. In a further study, Schoch *et al*. (2009) showed that *K. maritima* clustered within *Mytilinidion* (Mytilinidiaceae), while *K. elaterascus* grouped within *Morosphaeria* (Morosphaeriaceae) (Suetrong *et al*. 2009). Kirschsteiniotheliaceae was established to accommodate *Kirschsteiniothelia* based on morphology and phylogenetic analyses (Boonmee *et al*. 2012). In this study, *Halokirschsteiniothelia* was introduced to accommodate formerly species *K. maritima*, and *K. elaterascus* was transferred to *Morosphaeria* (Boonmee *et al*. 2012). Kirschsteiniotheliaceae was distantly related to other orders in Dothideomycetes in the study performed by Hernandez-Restrepo *et al*. (2017). Therefore, a new order Kirschsteiniotheliales was established. Hongsanan *et al*. (2020) provided a refined, updated document on families of Dothideomycetes. Kirschsteiniotheliales is a monotypic order grouped with Asterinales in Dothideomycetidae, but the monophyly of these two orders is not well-supported. Moreover, Kirschsteiniotheliales and Asterinales diverged approximately 221 MYA in divergence time estimates (Hongsanan *et al*. 2020).

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Article

Morphology and Phylogeny Reveal *Vamsapriyaceae* fam. nov. (*Xylariales*, *Sordariomycetes*) with Two Novel *Vamsapriya* Species

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Abstract: Phylogenetic analyses of combined *LSU*, rpb2, tub2 and *ITS* sequence data of representative *Xylariales* taxa indicated that *Diabolocovidia*, *Didymobotryum* and *Vamsapriya* cluster together and form a distinct clade in *Xylariales*. Morphological comparison also shows their distinctiveness from other families of *Xylariales*. Therefore, we introduce it as a novel family, *Vamsapriyaceae*. Based on morphological characteristics, *Podosporium* and *Tretophragmia*, which were previously classified in *Ascomycota* genera *incertae sedis*, are now included in the *Vamsapriyaceae*. In addition, three *Vamsapriya* species, *V. chiangmaiensis* sp. nov, *V. uniseptata* sp. nov, and *V. indica* are described and illustrated in this paper.

Keywords: three new taxa; *Ascomycota* genera *incertae sedis*; multi-gene phylogeny; new family; taxonomy

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1. Introduction

Xylariales is a large order with both conspicuous and inconspicuous fruiting bodies, and unitunicate, perithecial ascomycetes [1,2]. Many species of *Xylariales* are saprobes and endophytes [3,4]. Some *Xylariales* species can produce secondary metabolites which are especially important for the pharmaceutical chemical industry [3,5,6].

Xylariales was established by Nannfeldt [7] to accommodate the type family *Xylariaceae*, along with *Diatrypaceae*, *Hypocreaceae*, *Hyponectriaceae*, *Lasiosphaeriaceae* and *Polystigmataceae*. The previous classification of *Xylariales* was mainly based on morphology [8–13]. With the development of molecular technology, the classification basis of *Xylariales* was gradually diversified [2,14–16]. Smith et al. [2] performed the first multigene analysis to find the familial relationships within *Xylariales and* treated the order with seven families. Lumbsch and Huhndorf [17] listed six families in *Xylariales*, while Senanayake et al. [18] revised *Xylariales* and accepted 11 families. Hyde et al. [19] redefined the families of *Sordariomycetes* and accepted 15 families in *Xylariales* based on morphology and multigene analysis, viz. *Barrmaeliaceae*, *Cainiaceae*, *Clypeosphaeriaceae*, *Coniocessiaceae*, *Diatrypaceae*, *Graphostromataceae*, *Hansfordiaceae*, *Hypoxylaceae*, *Induratiaceae*, *Lopadostomataceae*, *Microdochiaceae*, *Polystigmataceae*, *Requienellaceae*, *Xylariaceae* and *Zygosporiaceae*. Hyde et al. [20]

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Pleocatenata chiangraiensis gen. et. sp. nov. (Pleosporales, Dothideomycetes) from medicinal plants in northern Thailand

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Abstract

Pleocatenata, a new genus, is introduced with its type species, *Pleocatenata chiangraiensis*, which was isolated from withered twigs of two medicinal plants, *Clerodendrum quadriloculare* (Blanco) Merr (Verbenaceae) and *Tarenna stellulata* (Hook.f.) Ridl (Rubiaceae) in northern Thailand. The genus is characterized by mononematous, septate, brown or dark brown conidiophores, monotretic conidiogenous cells and catenate, obclavate, olivaceous to blackish brown conidia. Phylogenetic analysis of combined LSU, SSU, *tef1-α*, *rpb2* and ITS sequence data showed *Pleocatenata* forms a distinct phylogenetic lineage in Pleosporales, Dothideomycetes. Therefore, we treat *Pleocatenata* as Pleosporales genera *incertae sedis* based on morphology and phylogenetic analyses. Descriptions and illustrations of the new taxa are provided, and it is compared with morphologically similar genera.

Keywords

Genera *incertae sedis*, hyphomycetes, multi-gene phylogeny, taxonomy

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RESEARCH ARTICLE

Pestalotioid Species Associated with Medicinal Plants in Southwest China and Thailand

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ABSTRACT In this paper, a total of 26 pestalotioid isolates associated with different medicinal plants from southwest China and Thailand were studied. Based on morphological examinations and multigene analyses of three gene loci (*ITS*, *tef1-α*, and *tub2*), these 26 isolates represent 17 species distributed in three genera, including seven new species and eight new records. The concatenated three loci tree was used to infer the occurrence of sexual recombination within each pestalotioid genus through the pairwise homoplasy index (PHI) test implemented in SplitsTree. Further, simplifying the description of pestalotioid species is discussed, and a checklist for pestalotioid species associated with medicinal plants worldwide is provided.

IMPORTANCE Pestalotioid species are an important fungal group, occurring commonly as plant pathogens, endophytes, and saprophytes. The study of pestalotioid species associated with medicinal plants is significant for agriculture, industry, and pharmaceutical industry but remains poorly studied. In this study, we report 17 pestalotioid species related to medicinal plants based on morphology and molecular analyses. Our study significantly enriches the species richness of pestalotioids and provides a basis for follow-up studies.

KEYWORDS 7 new species, 8 new records, diversity, endophytes, plant pathogens, phylogeny, saprophytes, taxonomy

Medicinal plants play a crucial role in the development of human cultures and are a rich source of natural products with both biological and chemical properties. Medicinal plants are used in health care, serve as treatments for various diseases, and have been used since prehistoric times across the world (1, 2). It is estimated that more than 70% of the world's population relies on medicinal plants (3). Microfungi can affect the growth and quality of medicinal plants. Some endophytes isolated from medicinal plants have broad developmental prospects (4, 5). Microfungi associated with medicinal plants are research hot spots (6–9).

Pestalotioid species are a very common group of fungi that form important associations with different plants as pathogens, endophytes, or saprophytes and are widely distributed in tropical and temperate regions (10–17). Traditional taxonomy of pestalotioid species mainly depend on their hosts and color intensities of the median conidial cell (10, 18–21). With the development of DNA-based phylogenetic analysis, the traditional classification system based on hosts and conidial colors is controversial. The use of molecular data in resolving pestalotioid species was revisited by Maharachchikumbura et al. (13), who separated this group into three genera, *viz. Neopestalotiopsis*, *Pestalotiopsis*, and *Pseudopestalotiopsis*. *Neopestalotiopsis* differs from *Pseudopestalotiopsis* and *Pestalotiopsis* by its versicolorous (two upper median cells darker than the lowest median cell) median cells and indistinct conidiophores, while *Pseudopestalotiopsis* can be easily distinguished

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Article

Morphology and Phylogeny Reveal Three *Montagnula* Species from China and Thailand

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Abstract: Four stains were isolated from two fresh twigs of *Helwingia himalaica* and two dead woods during investigations of micro-fungi in China and Thailand. Phylogenetic analyses of four gene regions LSU, ITS, SSU and tef1-α revealed the placement of these species in *Montagnula*. Based on the morphological examination and molecular data, two new species, *M. aquatica* and *M. guiyangensis*, and a known species *M. donacina* are described. Descriptions and illustrations of the new collections and a key to the *Montagnula* species are provided. *Montagnula chromolaenicola*, *M. puerensis*, *M. saikhuensis*, and *M. thailandica* are discussed and synonymized under *M. donacina*.

Keywords: two new species; multi-gene phylogeny; Pleosporales; sexual morph; taxonomy

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1. Introduction

Didymosphaeriaceae (Pleosporales) was established by Munk [1] and with Didymosphaeria as the type genus. There are 33 genera accepted in this family based on morphology and phylogenetic analyses [2,3]. Species belonging to Didymosphaeriaceae have a wide geographical and host distribution and have different modes of nutrition, such as saprobic on plant litter, herbaceous stems, or in soil; endophytic on healthy leaves or twigs; and pathogenic on plants, animals, or humans [2,4–9].

Berlese [10] introduced *Montagnula*, typified by *M. infernalis*, which has bitunicate asci and dictyosporous ascospores. Around a century later, Crivelli [11] refined *Pleospora* and transferred eight *Pleospora* species and one *Teichospora* species to *Montagnula* based on morphology. Leuchtmann [12] included phragmosporous and didymosporous species in this genus, making species identification heterogeneous. Aptroot [13] established *Munkovalsaria* to accommodate *Mu. donacina* based on valsoid ascomata, bitunicate, fissitunicate asci, and 1-septate ascospores, however, Wanasinghe et al. [14] synonymized *Munkovalsaria* under *Montagnula* based on analyses of combined LSU, SSU, and ITS sequence data. Crous et al. [7] reported the first coelomycetous asexual morph species *M. cylindrospora* in this genus. So far, there are 39 validly published *Montagnula* species in Species Fungorum (accessed on 28 January 2023) [15]. However, only 18 species have molecular data. Morphologically, sexual morphs of *Montagnula* have three different types of ascospores (didymospore, phragmospore, and dictyospore) [8,16]. Phylogenetically, species with the same type of ascospore tend to cluster together [9,17]. In recent years, there have been many reports on *Montagnula* species [8,9,18–20], but there are very few comprehensive and systematic papers.

Montagnula species occur on terrestrial habitats with a wide geographic and host distribution [8,21]. Most *Montagnula* species have been found on dead leaves and twigs by their sexual morph [8,10,17,18,21–23]. The sexual morph is characterized by globose to pyriform, immersed to erumpent or superficial, brown to dark brown ascomata with or

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First Author Publications

Sun, Y. R., Goonasekara, I., Thambugala, K. M., Jayawardena, R. S., Wang, Y., & Hyde, K. D. (2020). *Distoseptispora bambusae* sp. nov. (Distoseptisporaceae) on bamboo from China and Thailand. *Biodiversity Data Journal, 8*, e53678. https://doi.org/10.3897/BDJ.8.e53678

Sun, Y. R., Jayawardena, R. S., Hyde, K. D., & Wang, Y. (2021). *Kirschsteiniothelia thailandica* sp. nov. (Kirschsteiniotheliaceae) from Thailand. *Phytotaxa*, *490*, 172–182. https://doi.org/10.11646/PHYTOTAXA.490.2.3

Sun, Y. R., Liu, N. G., Samarakoon, M. C., Jayawardena, R. S., Hyde, K. D., & Wang, Y. (2021). Morphology and phylogeny reveal Vamsapriyaceae fam. nov. (Xylariales, Sordariomycetes) with two novel *Vamsapriya* species. *Journal of Fungi, 7*, 891. https://doi.org/10.3390/jof7110891

Sun, Y. R., Liu, N. G., Hyde, K. D., Jayawardena, R. S., & Wang, Y. (2022). *Pleocatenata chiangraiensis* gen. et. sp. nov. (Pleosporales, Dothideomycetes) from medicinal plants in northern Thailand. *MycoKeys*, *87*, 77–98. https://doi.org/10.3897/mycokeys.87.79433

Sun, Y. R., Zhang, J. Y., Hyde, K. D., Wang, Y., & Jayawardena, R. S. (2023). Morphology and phylogeny reveal three *Montagnula* species from China and Thailand. *Plants, 12*(4), 738. https://doi.org/10.3390/plants12040738

Sun, Y. R., Jayawardena, R. S., Sun, J. E., & Wang, Y. (2023). Pestalotioid species associated with medicinal plants in Southwest China and Thailand. *Microbiology Spectrum, 11*(1), e03987-03922. https://doi.org/10.1128/spectrum.03987-22

Sun, Y. R., Hyde, K. D., Liu, N. G., Al-Otibi, F., Wang, Y., & Jayawardena, R. S. (2024). Four fungal species associated with *Mahonia* in Guizhou Province, China [Manuscript preparation]. *Mycological progress*.

Sun, Y. R., Liu, N. G., Al-Otibi, F., Wang, Y., Hyde, K. D., & Jayawardena, R. S. (2024). A new endophytic species, *Diaporthe litseae*, from medicinal plants in Guizhou Province, China [Manuscript preparation]. *Phytotaxa.*

Sun, Y. R., Hyde, K. D., Liu, N. G., Al-Otibi, F., Wijayawardene, N. N., Jayawardena, R. S., . . . Wang, Y. (2024). Microfungi on medicinal plants in southern China and northern Thailand [Manuscript preparation]. *Fungal Diversity*.

Co-author

Chethana, K. W. T., Niranjan, M., Dong, W., Samarakoon, M. C., Bao, D. F., Calabon, M. S., . . . Hyde, K. D. (2021). AJOM new records and collections of fungi: 101–150. *Asian Journal of Mycology*, *4*, 113-260. https://doi.org/10.5943/ajom/4/1/8

He, Y. K., Yang, Q., Sun, Y. R., Zeng, X. Y., Jayawardena, R., Hyde, K., . . . Wang, Y. (2022). Additions to *Neopestalotiopsis* (Amphisphaeriales, Sporocadaceae) fungi: Two new species and one new host record from China. *Biodiversity Data Journal*, *10*, e90709. https://doi.org/10.3897/BDJ.10.e90709

Jayawardena, R. S., Hyde, K. D., de Farias, A. R. G., Bhunjun, C. S., Ferdinandez, H. S., Manamgoda, D. S., . . . Thines, M. (2021). What is a species in fungal plant pathogens? *Fungal Diversity*, *109*, 239-266. https://doi.org/10.1007/s13225-021-00484-8

Jayawardena, R. S., Hyde, K. D., Wang, S., Sun, Y. R., Suwannarach, N., Sysouphanthong, P., . . . Wang, Y. (2022). Fungal diversity notes 1512–1610: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 117*, 1–272. https://doi.org/10.1007/s13225-022-00513-0

Liu, N. G., Hyde, K. D., Sun, Y. R., Bhat, D. J., Jones, E. B. G., Jumpathong, J., . . . Liu, J. K. (2024). Notes, outline, taxonomy and phylogeny of brown-spored hyphomycetes [Manuscript preparation]. *Fungal Diversity*.

Liu, N. G., Liu, J. K., & Sun, Y. R. (2023). Phylogenetic placement of *Tretospeira cheirospora* in Phaeosphaeriaceae. *Phytotaxa, 579*(3), 175–186. https://doi.org/10.11646/PHYTOTAXA.579.3.3

Lu, Q. T., Zhang, J. Y., Sun, Y. R., Tang, X., Lu, Y. Z., & Zhang, Z. (2022). *Diaporthe orixae* sp. nov., an endophytic species isolated from Orixa japonica in southern China. *Phytotaxa, 544*, 37–51. https://doi.org/10.11646/PHYTOTAXA.544.1.3