

ARTICLE

Saprobic ascomycetes associated with woody litter from the Greater Mekong Subregion (Southwestern China and Northern Thailand)

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Abstract

The Greater Mekong Subregion (GMS) is a global biodiversity hotspot. Over the last decade, the number of studies on microfungal diversity in the GMS has increased greatly. However, in the GMS, the fungi of terrestrial habitats, such as woody litter, are still poorly studied. This research provided morphological descriptions, illustrations, and phylogenetic analyses of saprobic microfungi associated with woody litter collected from Southwestern China and Northern Thailand of GMS areas. Here, we revealed 41 fungal species, including 15 new species and 26 new host records. The newly described species are *Anastomitrabeculia xishuangbannaensis*, *Camarosporidiella xianggelilaensis*, *Crassimassarina baoshanensis*, *Cucurbitaria lijiangensis*, *Homortomyces xianggelilaensis*, *Melomastia diqingensis*, *Neoaquastroma ehretiae*, *Nigrograna lancangensis*, *N. schimae*, *Nigropunctata yunnanensis*, *Pararoussoella lincangensis*, *Pseudolachnella lancangensis*, *Scolecohyalosporium baoshanense*, *Setoarthopyrenia jinghongensis* and *Stagonosporopsis lijiangensis*. The new host records are *Angustimassarina kunmingense*, *Acrocalymma magnoliae*, *A. pterocarpi*, *Aplosporella artocarpi*, *A. prunicola*, *Aurantiascoma minimum*, *Boeremia linicola*, *Clonostachys capitata*, *Corylicola italica*, *Crassiparies quadrisporus*, *Creosphaeria sassafras*, *Fuscostagonospora banksiae*, *Hongkongmyces thailandica*, *Lentithecium yunnanense*, *Magnibotryascoma mali*, *Melomastia sichuanensis*, *Melomastia thamplaensis*, *Nigrograna kunmingensis*, *N. magnoliae*, *N. thymi*, *Palmiascoma gregariascomum*, *P. qujingense*,

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Plenodomus artemisiae, *P. sinensis*, *Ramusculicola thailandica* and *Stylodothis puccinioides*. In addition, the sexual morph of *Fuscostagonospora banksiae* is reported from *Rhododendron rubiginosum* in China.

Keywords – 15 new species – 26 new host records – *Dothideomycetes* – Microfungi – *Sordariomycetes* – Taxonomy

INTRODUCTION

Fungi are decomposers, mutualists, and pathogens, and play an essential role in ecosystem functions (Carris et al. 2012, Sun et al. 2019, Hyde et al. 2020a, Niego et al. 2023a). Woody litter fungi are directly involved in nutrient cycling in terrestrial ecosystems (Lonsdale et al. 2008, Niego et al. 2023b). They are the decomposers of tree trunks, branches, twigs, and leaves in forests and other terrestrial environments (Juutilainen et al. 2011). They are important in nutrition recycling which enhances plant growth (Bucher et al. 2004, Bebbler et al. 2006) and associated with other microorganisms, enabling forest regeneration (Lonsdale et al. 2008). In addition, fungi have a great potential for their application in biotechnology and industry, including their uses in agriculture as bio-control agents, bio-fertilizers, and growth-promoting hormones, and they provide resources for biofuels, beverages, cosmeceuticals, food, mycoremediation, and pharmaceutical industries (Hyde et al. 2019a, b).

The kingdom of fungi is estimated to comprise between 2.2 to 3.8 million species based on host association (Hawksworth & Lücking 2017) and 11.7 to 13.2 million species based on high-throughput sequencing (Wu et al. 2019). However, only about 155,000 species have been named and classified (Chethana et al. 2020, Phukhamsakda et al. 2022), and many more species are yet to be discovered (Hyde et al. 2020c). With the advent of modern molecular techniques, studies on fungal classification have increased rapidly in recent years, and numerous taxonomic novelties have been introduced from various substrates, including woody litters (Boonmee et al. 2021, Maharachchikumbura et al. 2021). Among these in Asia, mycology and related publications have been significantly increased (Hyde et al. 2020b).

Wood-associated microfungi including the different associations and lifestyles, such as arenicolous, nematode-trapping, and Ingoldian have been studied worldwide (Maria & Sridhar 2003, Prasannarai 2003, Ananda & Sridhar 2004, Fryar et al. 2004, Lee et al. 2004, Swe et al. 2009, Seephueak et al. 2010, Sudheep 2011, Sridhar et al. 2011, Senn-Irlet et al. 2012). The early studies on woody litter fungi were mainly from aquatic habitats, such as mangrove and brackish water environments (Fryar et al. 2004, Sridhar & Maria 2006, Swe et al. 2009) whereas few studies were published on woody litter fungi in terrestrial habitats before 2010 (Hyde et al. 1998a, b, Kodsueb et al. 2008a, b). However, in the last decade, studies on woody litter fungi were rapidly increased in terrestrial habitats (Thambugala et al. 2014, Ariyawansa et al. 2015a, Tian et al. 2015, Maharachchikumbura et al. 2016, Wanasinghe et al. 2017, 2018, 2020a, 2023, Huang et al. 2021, Mortimer et al. 2021, Ren et al. 2022, Samarakoon et al. 2022) and freshwater habitats (Luo et al. 2018, Dong et al. 2020, Calabon et al. 2022, 2023a, Bao et al. 2023, Yang et al. 2023).

The Greater Mekong Subregion (GMS) is a transboundary river basin distributed across East and Southeast Asia. The Mekong River flows 4,909 kilometers from its source across the Tibetan Plateau (Xizang) in China through Myanmar, Laos, Thailand, and Cambodia and flows into the sea at the Mekong Delta in Vietnam (Asian Development Bank 2012). The Phi Pan Nam mountains and the Mekong River form a natural boundary along the frontier with Laos (Kunstadter et al. 1978). The GMS has a diverse geographic landscape, including mountains, plateaus, limestone karsts, fast-flowing rocky mountain streams, lowlands, fertile floodplains, and deltas (Asian Development Bank 2012). These varied environmental conditions create a rich habitat for a multitude of flora, fauna, and microorganisms, resulting in exceptionally high diversity levels of those organisms (Costenbader et al. 2015, Phookamsak et al. 2019). The GMS is recognized as one of the world's richest biodiversity hotspots and harbors several irreplaceable biomes, including fungi (Li et al. 2018). The two research areas (Southwestern China and Northern Thailand) are

amongst the world's wealthiest forests in terms of biodiversity (Asian Development Bank 2012). The monsoonal climate of Northern Thailand is characterized by a distinct rainy season, reaching its peak in July, August, and September, followed by a cool-dry and then a hot-dry seasons, ending with the return of the southwest monsoon rains in May or June (Kunstadter et al. 1978). Northern Thailand is composed of hills and mountains with relatively narrow valleys with evergreen and deciduous forests. The evergreen forests in Northern Thailand include lower montane, coniferous, and dry evergreen forests, while deciduous forests include moist mixed deciduous, dry mixed deciduous, and dry deciduous *Dipterocarpus* (Kunstadter et al. 1978). Yunnan Province, located in southwestern China, covers a total area of 394,000 square kilometers with high biological diversity, of which about 94% is mountainous (Asian Development Bank 2012). The climate of GMS is characterized as the subtropical monsoon (East Asia monsoon) in southeast Yunnan and the South Asia monsoon in southwest Yunnan. The complex topography, geography, highly variable climates, and rich vegetation (Liu et al. 2009, Sun et al. 2019) lead to high fungal diversity in Yunnan Province (Feng & Yang 2018).

Microfungi studies in the GMS have increased rapidly over the past few years. Most of these studies were based on morphology and molecular-based approaches, especially on freshwater and woody litter fungi in Yunnan and Thailand (Luo et al. 2018, Bao et al. 2019, Hapuarachchi et al. 2019, Dissanayake et al. 2020, Dong et al. 2020, Monkai et al. 2020, Yasanthika et al. 2020, Mortimer et al. 2021, Wanasinghe et al. 2020a, 2021). Thailand is home to a high diversity of woody litter fungi due to its diverse forest types with ideal tropical monsoon climates, which assist rapid fungal speciation (Promputtha et al. 2002, Hyde et al. 2018). Hyde et al. (2018) stated that 96% of fungi from Northern Thailand are new to science. According to Feng & Yang (2018), approximately 104,000 fungal species should be present in Yunnan, China. However, only about 6,000 have been reported and classified to date, and no comprehensive studies have been carried out to investigate and compare the diversity of microfungi associated with woody litter in this region. In general, terrestrial woody litter-associated microfungi have been mostly ignored in fungal studies in the GMS, and many new species are believed to be discovered (Ren et al. 2022). Thus, obtaining more collections and sequence data of microfungi associated with woody litter is essential to expand the knowledge of woody litter fungal diversity.

This study aimed to investigate saprobic ascomycetes associated with woody litter from Southwestern China and Northern Thailand, focusing on *Dothideomycetes* and *Sordariomycetes* based on morphological characteristics and molecular data. This research is the first effort to fill the knowledge gap in the diversity, taxonomy, and phylogeny of woody litter microfungi in the GMS.

MATERIALS AND METHODS

Sample collection and Morphological observation

Samples were randomly collected from 2019 to 2021 from seven sites of native pristine forests in temperate and tropical climate zones of the GMS region. Among these sites, six sites were in Yunnan Province, Southwestern China from which Baoshan, Diqing, Lincang, Lijiang, and Puer (Lancang) with temperate climates and Xishuangbanna with a tropical climate and one site was located in Tak Province, Northern Thailand, with a tropical climate (Fig. 1). At each site, 20 woody litter pieces were collected from an area of 100 m × 100 m. After collection, each litter piece was cut into no more than 20 cm in length, placed in plastic bags, and taken to the mycology laboratory at the Kunming Institute of Botany, Chinese Academy of Sciences and Mae Fah Luang University, Thailand. After taking to the laboratory, all the samples were stored inside paper envelopes for further check.

Specimens were first examined with a stereomicroscope (Olympus SZ61, Tokyo, Japan). Micro-morphological characteristics were photographed using a Canon EOS 600D (Tokyo, Japan) digital camera mounted on a Nikon ECLIPSE 80i (Tokyo, Japan) compound microscope. All microscopic measurements were taken using the Tarosoft^(R) Image Frame Work v.09 program and

reported as minimum–maximum and average values. Images used for the morphological figures were processed with Adobe Photoshop CS6 software v.13 (Adobe Systems, San Jose, CA, USA).

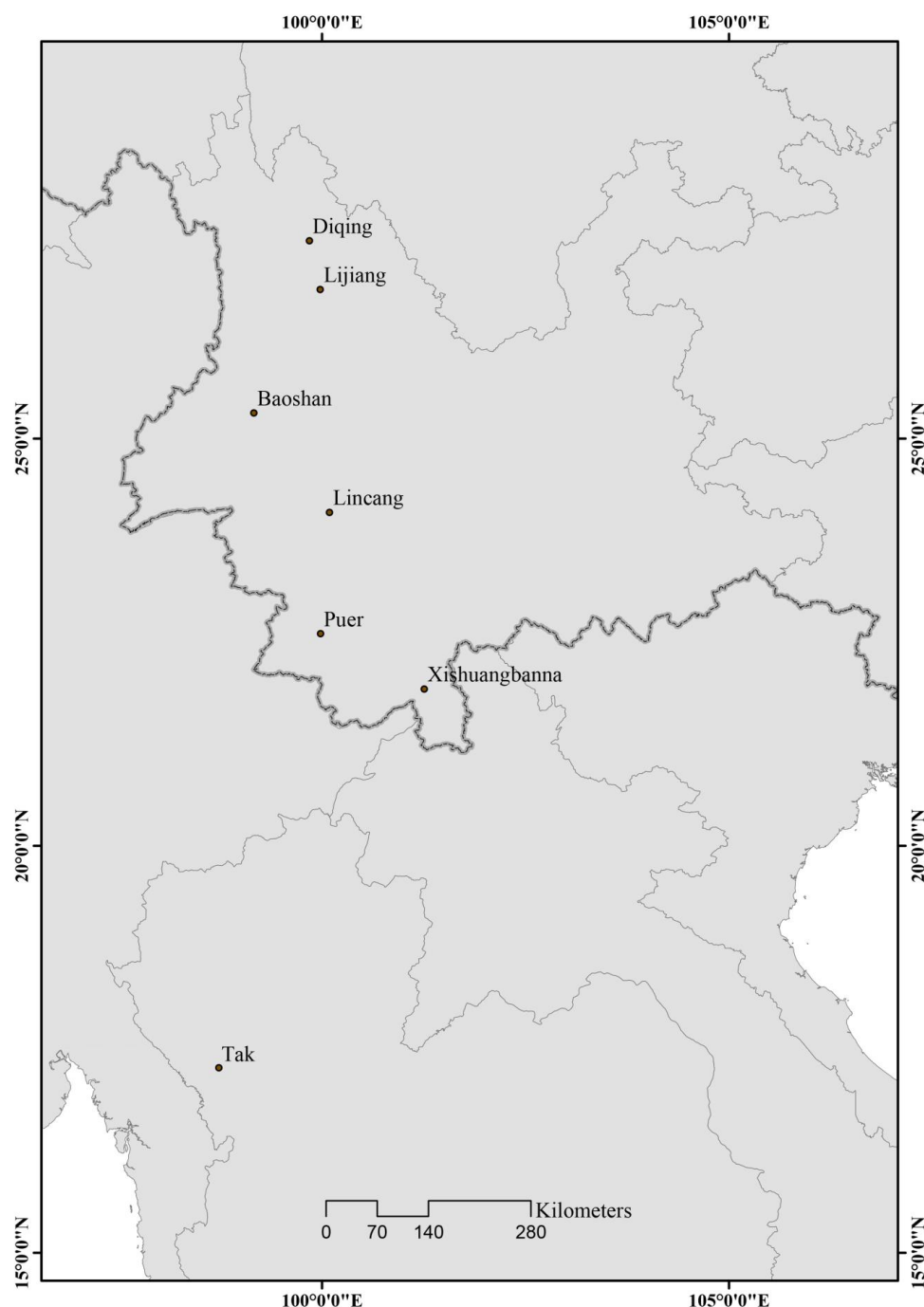


Figure 1 – Distribution of collecting sites in the GMS region (Southwestern China and Northern Thailand).

Isolation of fungi and Observation of cultures

Single-spore isolation was used to obtain pure cultures following Senanayake et al. (2020). Germinating spores were photographed, transferred to potato dextrose agar (PDA) media, and then incubated at room temperature (25 °C) for seven days. After incubation, cultures were photographed, and their characteristics, such as size, growth rate, mycelium color, shape, and texture, were recorded. Herbarium materials were deposited in the Cryptogams Kunming Institute of Botany, Academia Sinica (HKAS), Kunming Institute of Botany, Chinese Academy of Sciences, China, and Mae Fah Luang University (MFLU) fungarium, Chiang Rai, Thailand, and living

cultures were deposited at the Culture Collection of Kunming Institute of Botany Culture Collection (KUMCC), Kunming Institute of Botany, Chinese Academy of Sciences, China. Faces of fungi (Jayasiri et al. 2015) and Index Fungorum (Index Fungorum 2023) numbers were obtained for all the new taxa, while the information on the GMS fungal taxa was added to the GMS webpage (Chaiwan et al. 2021).

DNA extraction, PCR amplification, and Sequencing

Fungal mycelia were scraped from the 14-day-old colonies grown on PDA at 25–30 °C, and the DNA was extracted using the Biospin Fungus Genomic DNA Extraction Kit (BioFlux® Hangzhou, China). Polymerase chain reactions (PCRs) were conducted to amplify parts of the small nuclear ribosomal subunit rDNA (SSU), internal transcribed spacer region (ITS), large nuclear ribosomal subunit rDNA (LSU), translation elongation factor 1- α gene (*tef1- α*), RNA polymerase II second largest subunit (*rpb2*), and β -tubulin (*tub2*) using primer pairs NS1/NS4 (White et al. 1990), ITS5/ITS4 (White et al. 1990), LR0R/LR5 (Vilgalys & Hester 1990), EF1-983F/EF1-2218R (Rehner & Buckley 2005), fRPB2-5F/fRPB2-7cR (Liu et al. 1999) and T1/T22 (O'Donnell & Cigelnik 1997), respectively. PCR was carried out in a 25 μ L reaction volume containing 12.5 μ L 2X PCR MasterMix (TIANGEN Co., Beijing, China), 8.5 μ L double distilled water, 2 μ L genomic DNA, and 1 μ L of each primer. PCR thermal cycles for SSU, LSU, ITS, *tef1- α* , *tub2*, and *rpb2* gene regions followed Ren et al. (2021). PCR products were sequenced at the Qingke Company, Yunnan Province, China.

Phylogenetic analyses

Phylogenetic analyses were performed as described in Dissanayake et al. (2020). Each newly generated sequence was assembled using BioEdit 7.0.9.0 (Hall 1999) and subjected to BLAST searches against the NCBI nucleotide non-redundant database (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) for selection of the closest matching taxa. Based on BLAST search results and recently published data, sequences of representative taxa were downloaded and used for phylogenetic analysis. Individual gene regions were aligned using MAFFT v.7 (<http://mafft.cbrc.jp/alignment/server/>, Katoh et al. 2019), the uninformative gaps and ambiguous regions were manually removed, and different gene regions were concatenated using BioEdit 7.0.9.0. The maximum likelihood (ML) analysis was performed on the CIPRES Science Gateway v.3.3 (<http://www.phylo.org/portal2/>, Miller et al. 2010) using RAxML-HPC2 on XSEDE v.8.2.12 (Stamatakis 2014) with parameters adjusted for 1000 bootstrap iterations and the GTRGAMMA substitution model. Gaps were treated as missing data, and zero-length branches collapsed (Hillis & Bull 1993). Bayesian inference was performed in MrBayes v.3.2.2 using Markov chain Monte-Carlo sampling (BMCMC) (Ronquist et al. 2012, Zeng et al. 2023) to determine posterior probabilities (PPs) (Rannala & Yang 1996, Zhaxybayeva et al. 2002). The evolution model was estimated using MrModeltest v.2.3 (Nylander et al. 2008) via PAUP v.4.0b10 (Ronquist et al. 2003). Six simultaneous Markov chains were run for 2,000,000 generations, with trees sampled every 200 generations, until it was stopped when the standard deviation of split frequencies between the two simultaneous runs dropped below 0.01. Phylogenetic trees were visualized with FigTree v.1.4.0 (Rambaut 2012) and edited using Microsoft PowerPoint (Microsoft, 2010) and Adobe Illustrator® CS6 v.26.0 (Adobe Systems, San Jose, CA, USA).

RESULTS

Phylogenetic analyses and Taxonomy

Based on polyphasic approaches, a total of 41 species were identified, including 15 new species and 26 new host records (Table 1). Updated phylogenetic trees and descriptions for all these taxa are given below. The taxa are in order according to the classification proposed by Wijayawardene et al. (2022).

Table 1 Saprobic ascomycetes associated with woody litter were isolated and identified in this study.

Class	Order	Family	Species	Collecting sites	Host plant species
<i>Dothideomycetes</i>	<i>Botryosphaerales</i>	<i>Aplosporellaceae</i>	<i>Aplosporella artocarpi</i>	Thailand (Tak)	<i>Hevea brasiliensis</i> (Euphorbiaceae)
			<i>Aplosporella prunicola</i>	China (Baoshan)	<i>Terminalia chebula</i> (Combretaceae)
	<i>Dothideales</i>	<i>Dothideaceae</i>	<i>Stylodothis puccinioides</i>	China (Lancang)	<i>Cinnamomum glanuliferum</i> (Lauraceae)
	<i>Dyfrulomycetales</i>	<i>Pleurotremataceae</i>	<i>Melomastia diqingensis</i>	China (Diqing)	<i>Rhododendron rubiginosum</i> (Ericaceae)
			<i>Melomastia sichuanensis</i>	China (Xishuangbanna)	<i>Millettia leptobotrya</i> (Fabaceae)
			<i>Melomastia thamplaensis</i>	China (Xishuangbanna)	<i>Millettia leptobotrya</i> (Fabaceae)
	<i>Homortomycetales</i>	<i>Homortomycetaceae</i>	<i>Homortomyces xianggelilaensis</i>	China (Diqing)	<i>Quercus serrata</i> (Fagaceae)
	<i>Pleosporales</i>	<i>Acrocalymmaeae</i>	<i>Acrocalymma magnoliae</i>	China (Xishuangbanna)	<i>Parashorea chinensis</i> (Dipterocarpaceae)
			<i>Acrocalymma pterocarpi</i>	China (Xishuangbanna)	<i>Parashorea chinensis</i> (Dipterocarpaceae)
		<i>Amorosiaceae</i>	<i>Angustimassarina kunmingense</i>	China (Lancang, Diqing)	<i>Quercus kingiana</i> (Fagaceae), <i>Rhododendron rubiginosum</i> (Ericaceae)
		<i>Anastomitrabeculiaceae</i>	<i>Anastomitrabeculia xishuangbannaensis</i>	China (Xishuangbanna)	<i>Knema furfuracea</i> (Myristicaceae)
		<i>Bambusicolaceae</i>	<i>Corylicola italica</i>	China (Lancang, Lincang)	<i>Quercus kingiana</i> (Fagaceae), <i>Cryptocarya hainanensis</i> (Lauraceae)
			<i>Palmiascoma gregariascomum</i>	China (Lincang)	<i>Cryptocarya hainanensis</i> (Lauraceae)
			<i>Palmiascoma qujingense</i>	China (Xishuangbanna)	<i>Myristica yunnanensis</i> (Myristicaceae)
		<i>Camarosporidiellaceae</i>	<i>Camarosporidiella xianggelilaensis</i>	China (Diqing)	<i>Rhododendron rubiginosum</i> (Ericaceae)
		<i>Cucurbitariaceae</i>	<i>Cucurbitaria lijiangensis</i>	China (Lijiang)	<i>Rhododendron rubiginosum</i> (Ericaceae)
		<i>Didymellaceae</i>	<i>Boeremia linicola</i>	China (Lancang)	<i>Castanopsis mekongensis</i> (Fagaceae)
			<i>Stagonosporopsis lijiangensis</i>	China (Lijiang)	<i>Quercus serrata</i> (Fagaceae)
		<i>Fuscostagonosporaceae</i>	<i>Fuscostagonospora banksiae</i>	China (Diqing)	<i>Rhododendron rubiginosum</i> (Ericaceae)
		<i>Lentitheciaceae</i>	<i>Lentithecium yunnanense</i>	China (Baoshan)	<i>Castanopsis orthacantha</i> (Fagaceae)

Table 1 Continued.

Class	Order	Family	Species	Collecting sites	Host plant species
		<i>Leptosphaeriaceae</i>	<i>Plenodomus artemisiae</i>	China (Diqing)	<i>Quercus serrata</i> (Fagaceae)
			<i>Plenodomus sinensis</i>	China (Baoshan, Diqing)	<i>Lyonia ovalifolia</i> (Ericaceae), <i>Castanopsis orthacantha</i> (Fagaceae)
		<i>Lindgomycetaceae</i>	<i>Hongkongmyces thailandica</i>	China (Baoshan)	<i>Dipterocarpus gracilis</i> (Dipterocarpaceae)
		<i>Lophiotremataceae</i>	<i>Crassimassarina baoshanensis</i>	China (Baoshan)	<i>Castanopsis orthacantha</i> (Fagaceae)
		<i>Neohendersoniaceae</i>	<i>Crassiparies quadrisporus</i>	China (Baoshan)	<i>Shorea assamica</i> (Dipterocarpaceae)
		<i>Nigrogranaaceae</i>	<i>Nigrograna kunmingensis</i>	China (Lancang)	<i>Castanopsis mekongensis</i> (Fagaceae)
			<i>Nigrograna lancangensis</i>	China (Lancang)	<i>Castanopsis mekongensis</i> (Fagaceae)
			<i>Nigrograna magnoliae</i>	China (Lancang)	<i>Castanopsis indica</i> (Fagaceae)
			<i>Nigrograna schimae</i>	China (Baoshan)	<i>Schima khasiana</i> (Theaceae)
			<i>Nigrograna thymi</i>	China (Lancang)	<i>Castanopsis mekongensis</i> (Fagaceae)
		<i>Parabambusicolaceae</i>	<i>Neoaquastroma ehretiae</i>	China (Xishuangbanna)	<i>Ehretia acuminata</i> (Boraginaceae)
			<i>Scolecohyalosporium baoshanense</i>	China (Baoshan)	<i>Dipterocarpus gracilis</i> (Dipterocarpaceae)
		<i>Roussoellaceae</i>	<i>Pararoussoella lincangensis</i>	China (Lincang)	<i>Heliciopsis terminalis</i> (Proteaceae)
			<i>Setoarthopyrenia jinghongensis</i>	China (Xishuangbanna)	<i>Ehretia acuminata</i> (Boraginaceae)
		<i>Teichosporaceae</i>	<i>Aurantiascoma minimum</i>	China (Baoshan)	<i>Shorea assamica</i> (Dipterocarpaceae)
			<i>Magnibotryascoma mali</i>	China (Baoshan)	<i>Shorea assamica</i> (Dipterocarpaceae)
			<i>Ramusculicola thailandica</i>	China (Lijiang)	<i>Rhododendron rubiginosum</i> (Ericaceae)
Sordariomycetes	<i>Chaetosphaeriales</i>	<i>Chaetosphaeriaceae</i>	<i>Pseudolachnella lancangensis</i>	China (Lancang)	<i>Castanopsis mekongensis</i> (Fagaceae)
	<i>Hypocreales</i>	<i>Bionectriaceae</i>	<i>Clonostachys capitata</i>	China (Lijiang)	<i>Magnolia henryi</i> (Magnoliaceae)
	<i>Xylariales</i>	<i>Lopadostomataceae</i>	<i>Creosphaeria sassafras</i>	China (Lancang)	<i>Myrsine sequinii</i> (Myrsinaceae)
	<i>Xylariales</i> genera <i>incertae sedis</i>		<i>Nigropunctata yunnanensis</i>	China (Lijiang)	<i>Magnolia henryi</i> (Magnoliaceae)

Dothideomycetes O.E. Erikss. & Winka

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Aplosporellaceae Slippers, Boissin & Crous, Stud. Mycol. 76(1): 41 (2013)

Aplosporellaceae was introduced by Slippers et al. (2013) to accommodate *Aplosporella* and *Bagnisiella*. *Aplosporella*, originally introduced by Spegazzini (1880), was previously classified in *Botryosphaeriaceae*. Slippers et al. (2013) re-described this genus and placed it in the newly proposed family, *Aplosporellaceae*. *Bagnisiella* is a sexual genus in *Aplosporellaceae*, and recent literature suggests that *Aplosporella* might be the asexual morph of *Bagnisiella* (Hyde et al. 2012, Slippers et al. 2013, Wijayawardene et al. 2014a). However, this connection has never been proven in culture (Damm et al. 2007, Slippers et al. 2013). Based on our multi-gene phylogenetic analysis (LSU, ITS and *tef1-α* genes), *Bagnisiella examinans* clustered with other *Aplosporella* spp. with 92% ML, 1.00 Bayesian posterior probabilities (BYPP) bootstrap support. Based on molecular data, we consider *Bagnisiella* to be the sexual morph of *Aplosporella*. The sexual morphs of this family are characterized by pseudothecial, mostly multilocular ascomata mostly multilocular; bitunicate, clavate, stalked or sessile, with a well-developed apical chamber; hyaline to pigmented, septate or not, ellipsoid to ovoid ascospores (Slippers et al. 2013). The asexual morphs of *Aplosporellaceae* are coelomycetous, which are characterized by uni- to multilocular pycnidial conidiomata embedded in stromatic tissue; hyaline, phialidic conidiogenous cell, proliferating percurrently or with periclinal thickening at apex; ellipsoid to subcylindrical, initially hyaline becoming pigmented, aseptate conidia (Slippers et al. 2013). In this study, we report on a new host record of *Aplosporella artocarpi* in Thailand and *Aplosporella prunicola* in China.

Aplosporella artocarpi Trakun., L. Lombard & Crous, Persoonia 34: 91 (2014)

Fig. 3

Index Fungorum number: IF810167; Facesofungi number: FoF10747

Saprobic on dead woody twigs of *Hevea brasiliensis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 270–330 µm high × 320–450 µm diam., ($\bar{x}$ = 300 × 370 µm, n = 5), scattered, semi-immersed, loculate, coriaceous, globose to subglobose, brown to dark-brown with central ostioles. *Conidiomatal wall* 22–90 µm wide, composed of several layers of thick-walled, dark brown cells of *textura angularis*. *Paraphyses* 1.5–2 µm wide, cylindrical to filiform, septate, branching. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.8–8.3 × 2.2–3.7 µm ($\bar{x}$ = 5.7 × 3.1 µm, n = 10), holoblastic, phialidic, determinate, discrete, oblong to ampulliform, hyaline, smooth-walled, arising from stratum. *Conidia* 15.5–19 × 8.5–10.5 µm ($\bar{x}$ = 18 × 10 µm, n = 30), straight, initially hyaline, becoming brown to dark at maturity, ellipsoid or oval, one-celled, ends rounded, thick and smooth-walled.

Culture Characters – Conidia germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apex. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, velvety, fluffy, dense, granular, white on the surface, reverse white with grey spots.

Material examined – Thailand, Tak Province, on dead woody twigs of *Hevea brasiliensis* (Euphorbiaceae), 21 April 2019, G.C. Ren, T701 (MFLU 23-0387, HKAS 122767), living culture KUMCC 21-0654; *ibid.*, DC07 (MFLU 23-0386, HKAS 122768), living culture KUMCC 21-0527.

Known distribution – On twigs of *Artocarpus heterophyllus* (Moraceae) and dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Trakunyingcharoen et al. 2015, Jayawardena et al. 2022); on asymptomatic leaves of *Stoechospermum marginatum* (Dictyotaceae) and *Caulerpa taxifolia* (Caulerpaceae) in India (Sahoo et al. 2021); on a dead branch of *Mangifera indica* (Anacardiaceae) in China (Yang et al. 2022); on dead woody twigs of *Hevea brasiliensis* (Euphorbiaceae) in Thailand (this study).

GenBank numbers – KUMCC 21-0654: LSU: OQ170836, ITS: OQ158916, *tef1-α*: OR613411; KUMCC 21-0527: LSU: OQ170837, ITS: OQ158917.

Notes – Multi-gene phylogenetic analyses (Fig. 2) show that our strains (KUMCC 21-0654, KUMCC 21-0527) clustered with *Aplosporella artocarpi* (CPC 22791 and KUMCC 21-0460), *A. abexaminans* (NFCCI:5010), *A. chromolaenae* (MFLUCC 17-1517), and *Bagnisiella examinans*

(CBS 551.66), with 92% ML bootstrap support and 1.00 BYPP value. Comparison of LSU and ITS sequence data reveals there is no significant difference between our new isolates (KUMCC 21-

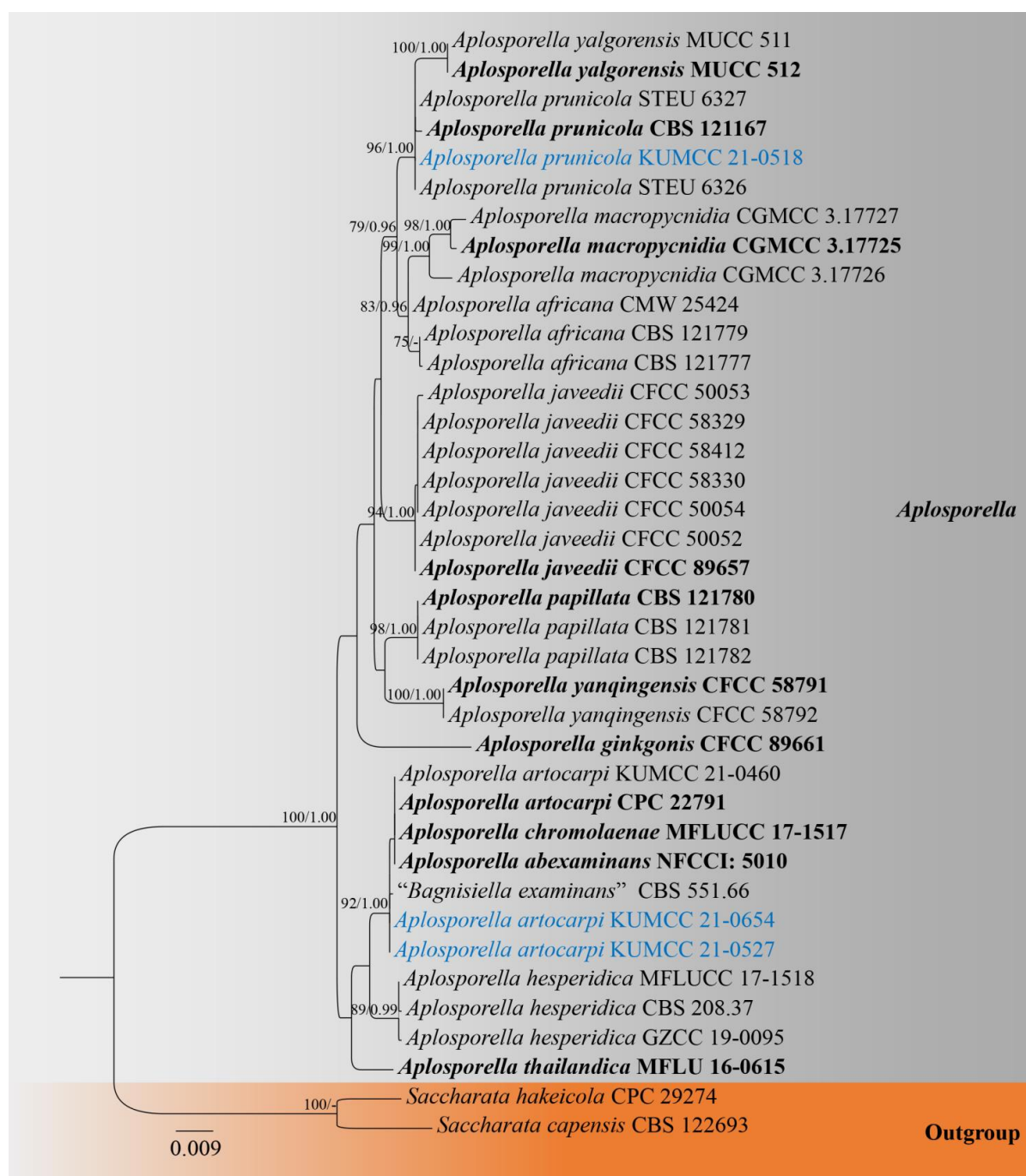


Figure 2 – Phylogram generated from ML analysis based on LSU, ITS and *tef1-α* sequence data representing *Aplosporellaceae*. Related sequences are obtained following Mapook et al. (2020). Thirty-eight strains are included in the combined analyses, which comprise 1744 characters for LSU, ITS, and *tef1-α* alignment. *Saccharata capensis* (CBS 122693) and *S. hakeicola* (CPC 29274) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -4298.071324 is presented. The matrix had 291 distinct alignment patterns, with 31.42% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.230309, C = 0.247107, G = 0.280459, T = 0.242124; substitution rates AC = 3.196527, AG = 3.478657, AT = 2.442084, CG = 2.519431, CT = 7.947277, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP

values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

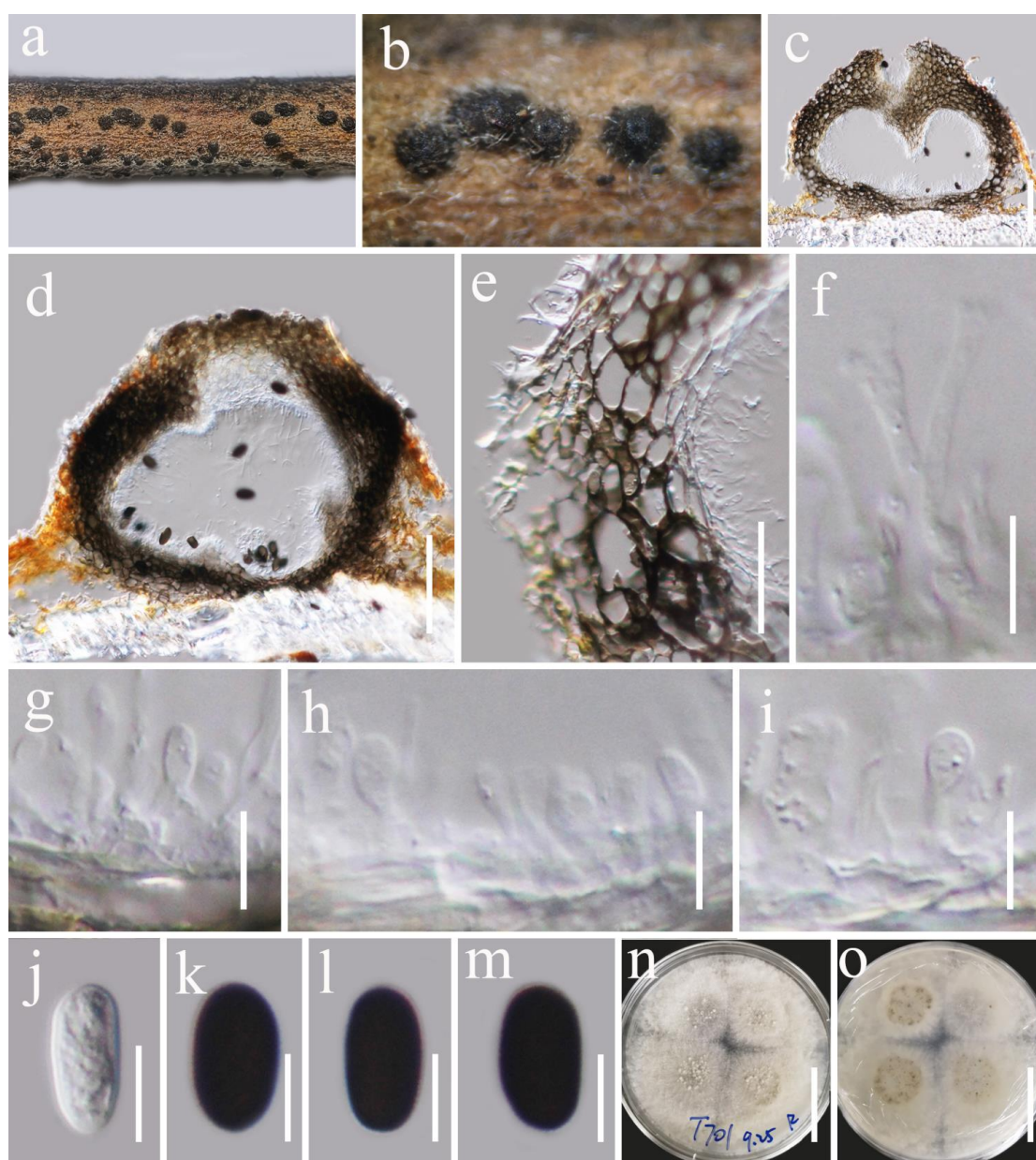


Figure 3 – *Aplosporella artocarpi* (HKAS 122767). a Material examined. b Conidiomata on the natural wood surface. c, d Sections through a conidioma. e Conidioma wall. f Paraphyses. g–i Conidiogenous cells and developing conidia. j–m Conidia. n, o Culture characters on PDA (n = from above, o = from below). Scale bars: c, d = 100 µm, e = 20 µm, f–m = 10 µm, n, o = 30 mm.

0654, KUMCC 21-0527) and *Aplosporella artocarpi* (CPC 22791 and KUMCC 21-0460), *A. abexaminans* (NFCCI:5010), *A. chromolaenae* (MFLUCC 17-1517), and *Bagnisiella examians* (CBS 551.66) isolates. A comparison of *tef1-α* nucleotide shows 0.38% (1/266) differences between our new isolates (KUMCC 21-0527) and *Aplosporella artocarpi* (CPC 22791). Sequences for *tef1-α* are lacking for *A. abexaminans*, *A. chromolaenae* and *Bagnisiella examians*. *Bagnisiella examians* was introduced as a sexual morph and clustered within *Aplosporella* in this study and Wijayawardene et al. (2014a). The morphological characters of the examined collections of our study largely overlap with *Aplosporella artocarpi* (Trakunyingcharoen et al. 2015). Therefore, we identify our collection as the first record of *A. artocarpi* on *Hevea brasiliensis* (Euphorbiaceae) from Thailand.

Aplosporella prunicola Damm & Crous, Fungal Diversity 27(1): 39 (2007)

Fig. 4

Index Fungorum number: IF504373; Facesofungi number: FoF04955

Saprobic on dead woody twigs of *Terminalia chebula*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 320–470 µm high × 500–700 µm diam., ($\bar{x}$ = 380 × 580 µm, n = 5), scattered, immersed, visible as dome-shaped areas on the host surface, multiloculate, coriaceous, globose to subglobose, brown to dark brown with central ostioles. *Conidiomata wall* 45–90 µm thick, composed of outer layers of dark brown cells and inner layers of hyaline, thick-walled cells of *textura angularis*. *Paraphyses* 1.4–2 µm wide, cylindrical to filiform, septate, unbranching. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–8 × 2.5–4.4 µm ($\bar{x}$ = 6.3 × 3 µm, n = 10), holoblastic, phialidic, determinate, discrete, oblong to ampulliform, hyaline, smooth-walled, arising from stratum. *Conidia* 19–23 × 10–12 µm ($\bar{x}$ = 21 × 11 µm, n = 30), straight, initially hyaline, becoming brown to dark brown at maturity, ellipsoid or oval, one-celled, aseptate, ends rounded, thick and smooth-walled.

Culture Characters – Conidia germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the side of conidia. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, fluffy, pale gray, reverse grayish with dark brown spots.

Material examined – China, Yunnan Province, Baoshan, on dead woody twigs of *Terminalia chebula* (Combretaceae), 13 July 2020, G.C. Ren, BS33 (HKAS 122712), living culture KUMCC 21-0518.

Known distribution – On dead branch of *Prunus persica* var. *nucipersica* (Rosaceae) from South Africa (Damm et al. 2007), *Ficus septica* (Moraceae) and *Zanthoxylum bungeanum* (Rutaceae) in China (Yuan et al. 2020, Li et al. 2023), on dead woody twigs of *Terminalia chebula* (Combretaceae) in China (This study).

GenBank numbers – LSU: OQ170838, ITS: OQ158918, *tef1-α*: OR613410.

Notes – In our phylogenetic analysis, our new collection KUMCC 21-0518 clustered with *Aplosporella prunicola* (CBS 121167, STEU 6326, STEU 6327) and *Aplosporella yalgorensis* (MUCC 511, MUCC 512) with 96% ML bootstrap support and 1.00 BYPP value (Fig. 2). Our isolate shares similar characteristics with *A. prunicola* in having globose to subglobose, coriaceous conidiomata, holoblastic, hyaline conidiogenous cell and initially hyaline, becoming brown to dark brown, ellipsoid, one-celled, aseptate conidia (Damm et al. 2007, Yuan et al. 2020). A comparison of LSU and ITS sequence data reveals no significant difference between our new isolate and *A. prunicola*. Therefore, we identify our collection as the first record of *A. prunicola* on *Terminalia chebula* (Combretaceae) from Yunnan Province, China.

Dothideales Lindau

Dothideaceae Chevall. [as ‘Dothideae’], Fl. Gén. Env. Paris (Paris) 1: 446 (1826)

Dothideaceae was introduced by Chevallier (1826), and 13 genera are accepted in *Dothideaceae*, viz., *Delphinella*, *Dictyodothis*, *Dothidea*, *Dothiora*, *Endoconidioma*, *Endodothora*, *Kabatina*, *Neocylindroseptoria*, *Phaeocryptopus*, *Plowrightia*, *Stylodothis*, *Sydowia* and *Uleodothis* (Hongnan et al. 2020). Members of this family are mostly saprobes and pathogens (Thambugala et al. 2014). The sexual morphs of this family are characterised by immersed to erumpent or superficial, uniloculate to multiloculate ascostromata lacking ostioles; 8- or poly-spored, bitunicate asci and hyaline or brown, transversely septate, or muriform and often guttulate ascospores (Hongnan et al. 2020). The asexual morph of *Dothideaceae* is either Coelomycetous or hyphomycetous (Hongnan et al. 2020). In this study, we report on a new host record of *Stylodothis puccinioides* from *Cinnamomum glanuliferum* in China.

Stylodothis puccinioides (DC.) Arx & E. Müll., Stud. Mycol. 9: 11 (1975)

Fig. 6

≡ *Sphaeria puccinioides* DC., in de Candolle & Lamarck, Fl. franç., Edn 3 (Paris) 5/6: 118 (1815)

Index Fungorum number: IF324309; Facesofungi number: FoF00092

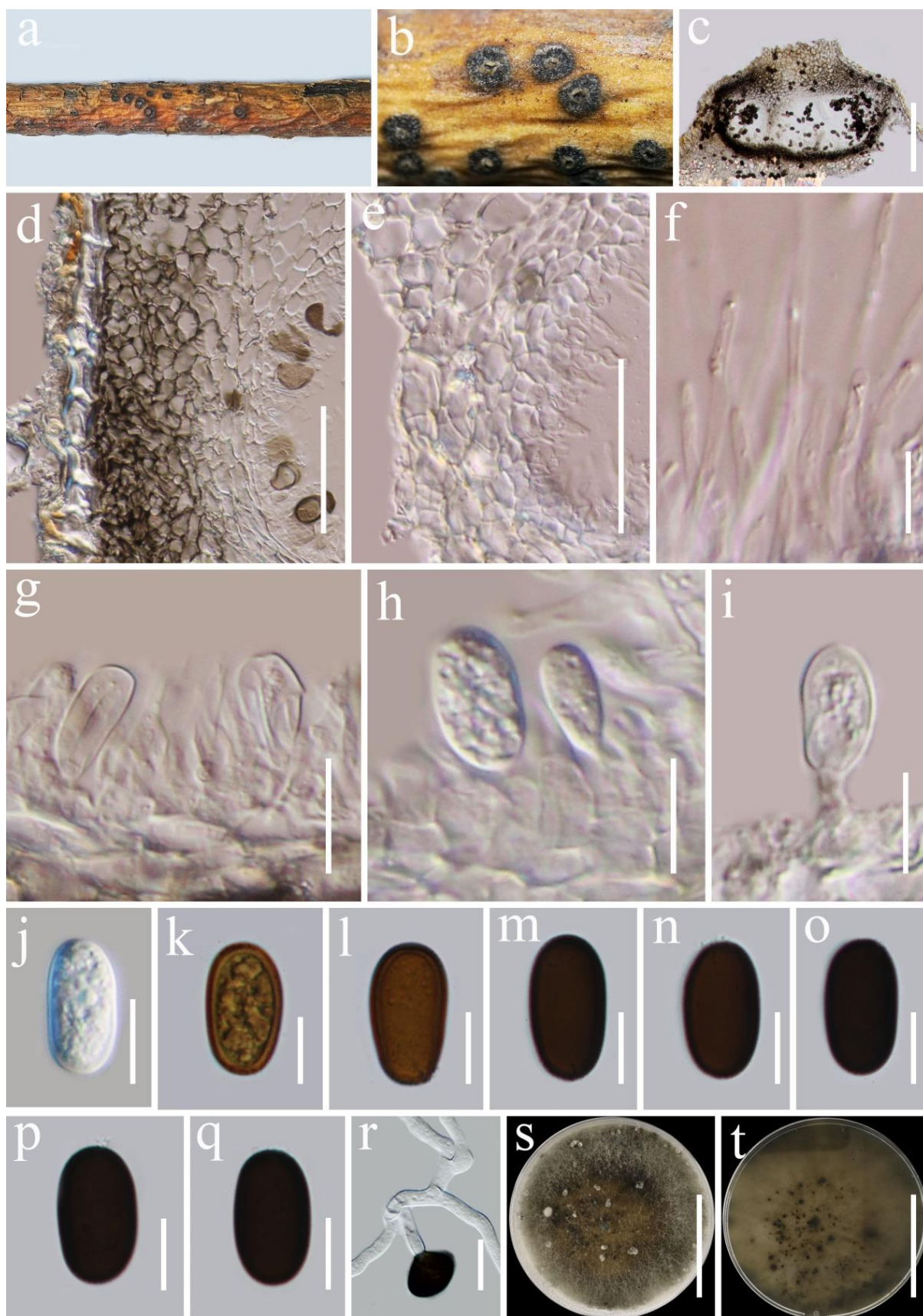


Figure 4 – *Aplosporella prunicola* (HKAS 122712). a Material examined. b Conidiomata on the natural wood surface. c Sections through conidioma. d, e Conidioma wall. f Paraphyses. g–i Conidiogenous cells and developing conidia. j–q Conidia. r Germinated conidium. s, t Culture characters on PDA (s = from above, t = from below). Scale bars: c = 200 μ m, d, e = 50 μ m, f–q = 10 μ m, r = 20 μ m, s, t = 30 mm.

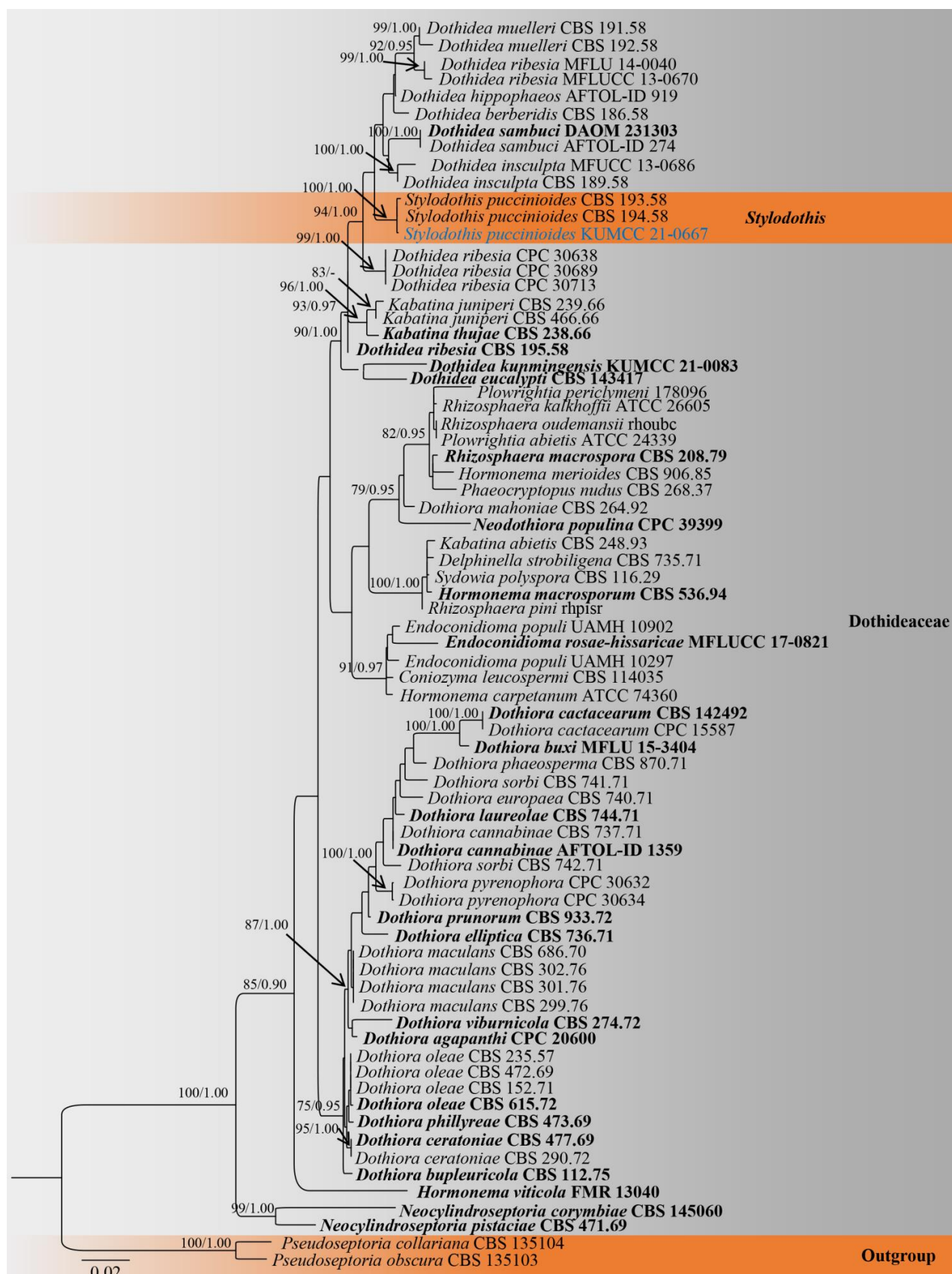


Figure 5 – Phylogram generated from ML analysis based on SSU, LSU, ITS, and *tef1-α* sequence data representing the family *Dothideaceae*. Related sequences are obtained following Gao et al. (2021). Seventy-three strains are included in the combined analyses, which comprise 3,269 characters for SSU, LSU, ITS, and *tef1-α* alignment. *Pseudoseptoria collariana* (CBS 135104) and *P. obscura* (CBS 135103) were used as the outgroup taxa. The best-scoring RAxML tree with a

final likelihood value of -10479.098412 is presented. The matrix had 542 distinct alignment patterns, with 46.82% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.255562, C = 0.226743, G = 0.272307, T = 0.245389; substitution rates AC = 1.641499, AG = 2.398302, AT = 2.112839, CG = 0.924816, CT = 9.289773, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Saprobic on dead woody twigs of *Cinnamomum glanuliferum*. Sexual morph: *Ascostromata* 400–500 µm high × 600–1100 µm diam., ($\bar{x}$ = 445 × 890 µm, n = 5), black, formed on erumpent basal stroma, solitary, thick at the base of the ascostromata, coriaceous, multiloculate, with 3–8 locules, cells of ascostromata composed of several layers of dark brown cells of *textura angularis*. *Locules* 90–160 µm high × 70–190 µm diam., ($\bar{x}$ = 135 × 140 µm, n = 10), globose to subglobose, without an ostiole. *Peridium* 8–15 µm thick, one layered, comprising brown to dark brown cells of *textura angularis*. *Hamathecium* 1–2 µm wide, comprising cylindrical, septate pseudoparaphyses embedded in a hyaline, gelatinous matrix. *Asci* 70–90 × 10–13 µm ($\bar{x}$ = 75 × 12 µm, n = 20), bitunicate, 4-spored, cylindrical-clavate, apically rounded, with short and rounded pedicellate. *Ascospores* 18–23 × 6.5–9 µm ($\bar{x}$ = 20 × 7.7 µm, n = 30), uniseriate, slightly overlapping, ellipsoidal, brown, 1-septate, constricted at the central septum, upper cell wider than lower cell, thick and smooth-walled, without a gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA, reaching 45–50 mm diameter after two weeks at 20–25 °C, filamentous, filamentous margin, flat, mycelium embedded in the medium, sparse, white to gray.

Material examined – China, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Cinnamomum glanuliferum* (Lauraceae), 23 March 2020, G.C. Ren, W04 (HKAS 122772), living culture KUMCC 21-0667.

Known distribution – On bark and stem of *Buxus sempervirens* (Buxaceae) in Germany (Thambugala et al. 2014), dead woody twigs of *Cinnamomum glanuliferum* (Lauraceae) in China (This study).

GenBank numbers – LSU: OQ170850, ITS: OQ158930, SSU: OQ168206, *tef1-α*: OR613412.

Notes – Our new collection groups with two strains of *Stylodothis puccinioides* (CBS 193.58 and CBS 194.58), isolated from *Buxus sempervirens* in Germany (Lumbsch et al. 2005) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 5). The new collection shares similar morphology with the type material of *Stylodothis puccinioides* (PC 0084648) in having black, coriaceous, multiloculate ascostromata, bitunicate, 4-spored, cylindrical-clavate asci, uniseriate, ellipsoidal, brown, 1-septate ascospores with thick and smooth-walled (Thambugala et al. 2014). DNA sequences of *Stylodothis puccinioides* (CBS 193.58) differ in 4 nucleotides in the *tef1-α* region (0.4%, no gaps), while LSU and ITS sequences were identical. Hence, the new isolate is described as the first record of *S. puccinioides* from *Cinnamomum glanuliferum* (Lauraceae) in China.

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

Pleurotremataceae Walt. Watson, New Phytol. 28: 113 (1929)

Pleurotremataceae was introduced by Watson (1929) for the monotypic *Pleurotrema* with *P. polysemum* as the type species. Wijayawardene et al. (2022) accepted three genera, *Dyfrlomycetes*, *Melomastia*, and *Pleurotrema* in *Pleurotremataceae*. Subsequently, Li et al. (2022) synonymized *Dyfrlomycetes* under *Melomastia* based on detailed morphological characteristics and phylogenetic analyses. Kularathnage et al. (2023) conducted a re-evaluation of the classification of *Dyfrlomycetes* and *Melomastia*; *Dyfrlomycetes* was reinstated to accommodate *M. tiomanensis* and *M. chromolaenae*, primarily based on their ascospore morphology and septation. Currently, *Pleurotremataceae* comprises three saprobic genera found on decaying wood in terrestrial, mangrove, and freshwater habitats (Li et al. 2022, Kularathnage et al. 2023). The family is

characterized by a clypeus on the substrate, immersed ascromata, cylindrical asci and multi-septate ascospores with or without a sheath (Li et al. 2022, Kularathnage et al. 2023). In this study, we report one new species and two new host records of *Melomastia sichuanensis* and *Melomastia thamplaensis* from *Millettia leptobotrya* from China.

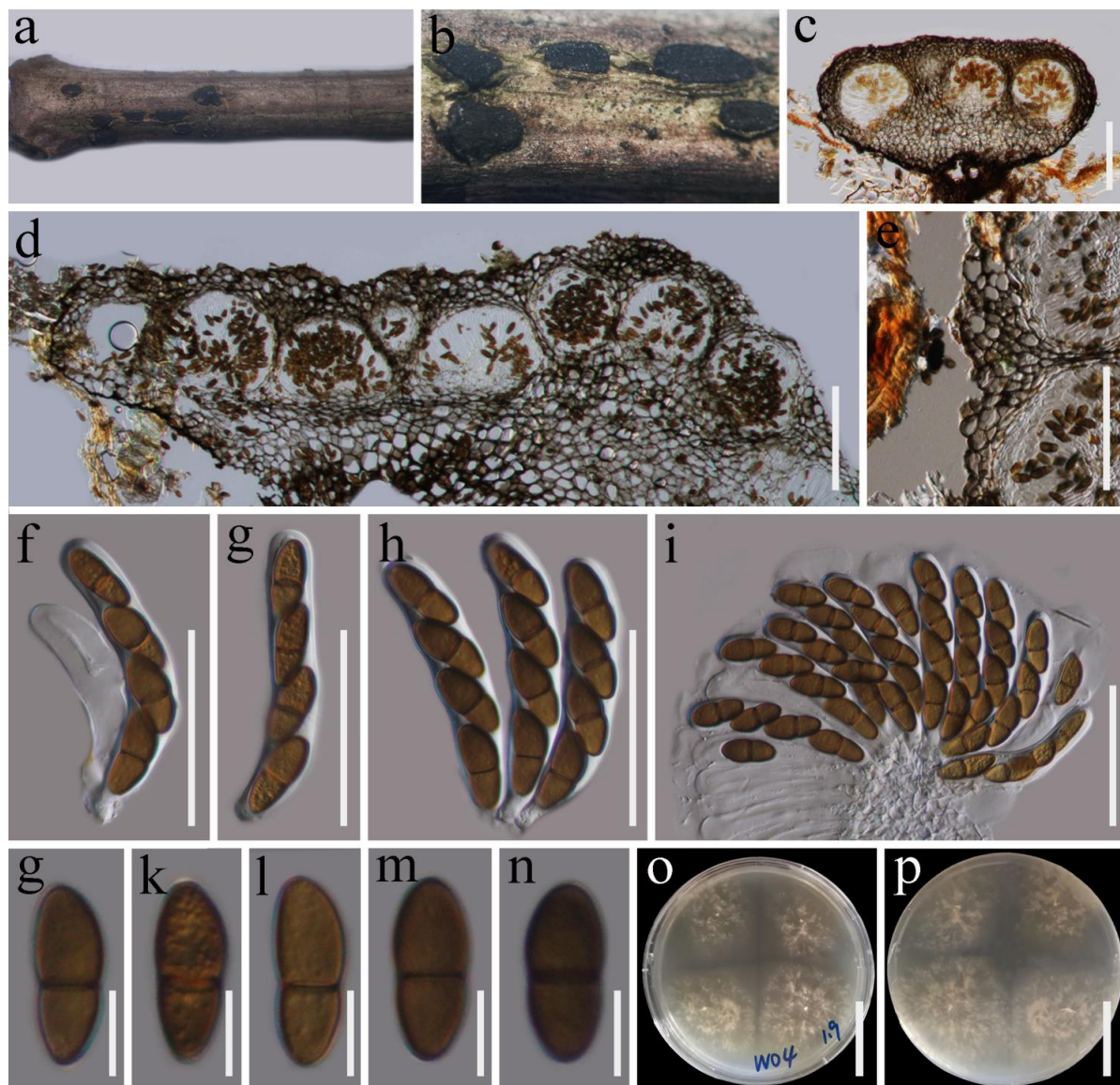


Figure 6 – *Stylodothis puccinioides* (HKAS 122772). a Material examined. b Appearance of ascostromata on the host substrate. c, d Sections of an ascostroma. e Peridium. f–i Asci. g–n Ascospores. o, p Culture characters on PDA (o = from above, p = from below). Scale bars: c, d = 150 μ m, e = 100 μ m, f–i = 50 μ m, g–n = 10 μ m, o, p = 30 mm.

Melomastia diqingensis G.C Ren & K.D. Hyde, sp. nov.

Fig. 8

Index Fungorum number: IF901346; Facesoffungi Number: FoF13890

Holotype – HKAS 122718

Etymology – The species epithet “diqing” refers to the location where the species was collected.

Saprobic on dead woody twigs of *Rhododendron rubiginosum*. Sexual morph: *Ascomata* 320–600 μ m high $\times$ 240–400 μ m diam., ($\bar{x}$ = 440 $\times$ 300 μ m, n = 5), semi-immersed to immersed in host tissue, solitary or scattered, subglobose to obpyriform, coriaceous, black, with an ostiolar neck. *Ostioles* 195–210 $\times$ 130–180 μ m ($\bar{x}$ = 200 $\times$ 150 μ m, n = 5), carbonaceous, black, papillate. *Peridium* 15–30 μ m wide, 3–4 layered, composed of hyaline to brown cells of *textura angularis*

and *textura prismatica*. Asci $100\text{--}127 \times 5.5\text{--}6.7 \mu\text{m}$ ($\bar{x} = 116 \times 6 \mu\text{m}$, $n = 20$), 8-spored, bitunicate, long cylindrical, straight or curved, apically rounded, short pedicellate, with a small ocular chamber. Ascospores $12.8\text{--}15 \times 4\text{--}5 \mu\text{m}$ ($\bar{x} = 14 \times 4.5 \mu\text{m}$, $n = 30$), uniseriate, oval to oblong, hyaline, 2-septate, slightly constricted at the septum, with guttules in each cell, with gelatinous sheath, thick and smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of ascospore. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, undulate, umbonate, surface rough, yellowish at edge and white at center; reverse, yellowish.

Material examined – China, Yunnan Province, Diqing, on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae), 20 August 2020, G.C. Ren, DQ19 (HKAS 122718, holotype), ex-type living culture KUMCC 21-0536.

GenBank numbers – SSU: OQ168224, LSU: OQ170873, ITS: OQ158951, *tef1-α*: OR613413.

Notes – *Melomastia diqingensis* is introduced as a new species based on its distinct morphology and the phylogeny of the combined SSU, LSU, ITS, and *tef1-α* dataset. In our phylogenetic study, the new strain (KUMCC 21-0536) formed a sister clade to *Melomastia italica* (MFLUCC 15-0160) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 7). Our species (KUMCC 21-0536) is similar to *Melomastia italica* in having subglobose to obpyriform, black ascomata, 8-spored, bitunicate, cylindrical asci and hyaline, 2-septate ascospores with a gelatinous sheath (Norphanphoun et al. 2017). However, *Melomastia diqingensis* differs from *M. italica* in having oval to oblong ascospores ($12.8\text{--}15 \times 4\text{--}5 \mu\text{m}$), while *M. italica* has ellipsoid ascospores ($8.8\text{--}10.5 \times 2.8\text{--}4.1 \mu\text{m}$) and asci with prominent apical ring (Norphanphoun et al. 2017). A pairwise nucleotide comparison showed that *Melomastia diqingensis* differs from *M. italica* in 5/860 bp of LSU (0.58%, without gaps) and 3/990 bp of SSU (0.3% without gaps) because *Melomastia italica* only has the sequence of LSU and SSU, therefore, we did not comparison base pair for *tef1-α* and ITS. Naziazeno & Aptroot (2023) described *Melomastia septemseptata* as a new species, based only on morphology, which was found on the living bark of a Cerrado tree in a dry, terrestrial environment from Brazil. However, *M. septemseptata* differs from *M. diqingensis* in having 7–9-septate ascospores.

Melomastia sichuanensis W.L. Li, Maharachch. & Jian K. Liu, Journal of Fungi 8 (1, no. 76): 12 (2022) Fig. 9

Index Fungorum number: IF841501; Facesoffungi number: FoF10535

Saprobic on dead woody twigs of *Millettia leptobotrya*. Sexual morph: Ascomata 260–500 μm high $\times$ 200–400 μm diam., ($\bar{x} = 390 \times 300 \mu\text{m}$, $n = 5$), immersed to semi-immersed, solitary or scattered, subglobose to obpyriform, coriaceous, black, with a central ostiole. Ostioles $110\text{--}170 \times 100\text{--}160 \mu\text{m}$ ($\bar{x} = 140 \times 120 \mu\text{m}$, $n = 5$), carbonaceous, black, papillate. Peridium 12–20 μm wide, 3–4 layered, composed of light brown to brown cells of *textura angularis*. Hamathecium 1.5–3 μm wide, comprising numerous filiform, unbranched, septate, hyaline, cellular pseudoparaphyses. Asci $125\text{--}145 \times 6.3\text{--}7.2 \mu\text{m}$ ($\bar{x} = 135 \times 7 \mu\text{m}$, $n = 20$), 8-spored, bitunicate, long cylindrical, straight or curved, short pedicellate, apically round with a small ocular chamber. Ascospores $15.5\text{--}18.4 \times 4.7\text{--}5.7 \mu\text{m}$ ($\bar{x} = 17 \times 5 \mu\text{m}$, $n = 30$), uniseriate, broad fusiform with rounded ends, hyaline, 2–3-septate (mostly 3-septate), constricted at the septa, guttules, thick and smooth-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of an ascospore. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, embedded in the medium, circular, fimbriate, umbonate, surface rough, granular, yellowish-brown at the edge and white at the center, reverse white at edge, dark brown at center, pale yellow between the edge and center.

Material examined – China, Yunnan Province, Xishuangbanna, on dead woody twigs of *Millettia leptobotrya* (Fabaceae), 23 September 2019, G.C. Ren, MY10 (HKAS 122762), living culture KUMCC 21-0628.

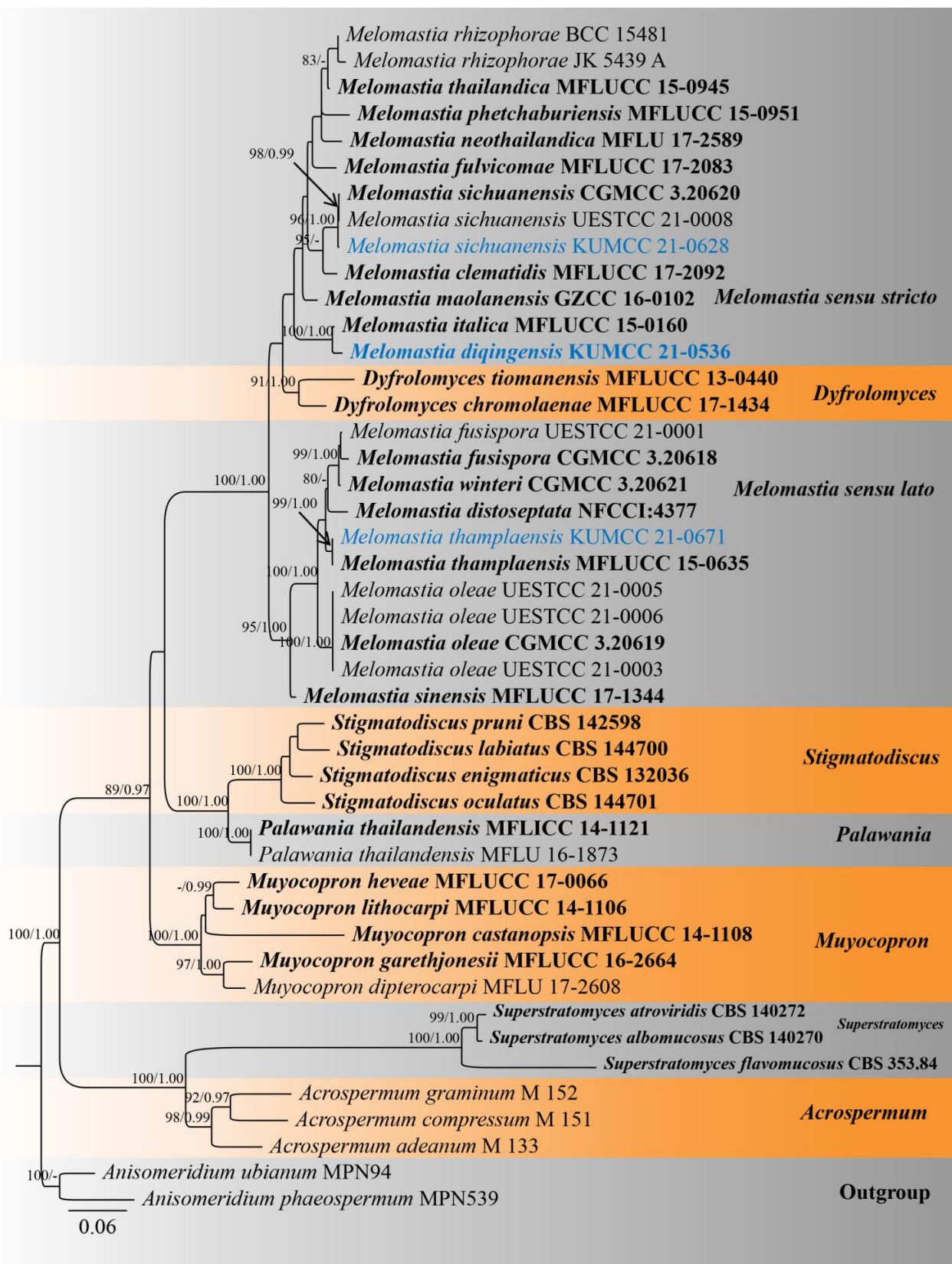


Figure 7 – Phylogram generated from ML analysis based on SSU, LSU, ITS, *tef1-α*, and *rpb2* sequence data representing *Pleurotremataceae*. Related sequences are obtained following Li et al. (2022). Forty-six strains are included in the combined analyses, which comprise 3948 characters for SSU, LSU, ITS, *tef1-α*, and *rpb2* alignment. *Anisomeridium phaeospermum* (MPN539) and *A. ubianum* (MPN94) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -28755.342067 is presented. The matrix had 2026 distinct alignment patterns,

with 32.59% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238390, C = 0.263023, G = 0.288210, T = 0.210377; substitution rates AC = 1.022596, AG = 2.177198, AT = 1.179336, CG = 1.031321, CT = 5.495584, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Known distribution – On dead branches of *Olea europaea* (Oleaceae) and *Millettia leptobotrya* (Fabaceae) in China (Li et al. 2022, this study).

GenBank numbers – SSU: OQ168225, LSU: OQ170874, ITS: OQ158952, *tef1-α*: OR613414.

Notes – *Melomastia sichuanensis* was introduced by Li et al. (2022), collected from dead branches of *Olea europaea* in China, based on the combined phylogeny of LSU, SSU, and *tef1-α* sequence data. In the present study, a multi-gene phylogenetic analyses indicated our strain (KUMCC 21-0628) clustered together with *Melomastia sichuanensis* (CGMCC 3.20620, HUEST 21.0008) with 96% ML bootstrap support and 1.00 BYPP value (Fig. 7). Our collection (KUMCC 21-0628) is similar to *Melomastia sichuanensis* in having globose, coriaceous to carbonaceous ascomata with papillate ostioles, long cylindrical, short-pedicellate asci with a small ocular chamber, and hyaline, broad-fusiform ascospores with 3-septa, and constricted at the septa (Li et al. 2022). Based on the genetic similarity and phylogenetic results, we report our saprobic collection (KUMCC 21-0628) as the first record of *M. sichuanensis* on woody litter of *Millettia leptobotrya* (Fabaceae) in China.

Melomastia thamplaensis (J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu) W.L. Li, Maharachch. & J.K. Liu, Journal of Fungi 8(1, no. 76): 16 (2022) Fig 10

Index Fungorum number: IF552496; Facesoffungi number: FoF02612

Saprobic on dead woody twigs of *Millettia leptobotrya*. Sexual morph: *Ascomata* 240–420 µm high × 140–440 µm diam., ($\bar{x}$ = 320 × 330 µm, n = 5), immersed under the bark of the host, solitary or scattered, globose to subglobose, coriaceous to carbonaceous, black, with a central ostiole. *Ostioles* 175–230 × 80–130 µm ($\bar{x}$ = 200 × 110 µm, n = 5), papillate, black. *Peridium* 30–50 µm wide, composed of dark brown outer layers and inner layers of hyaline, thick-walled cells of *textura prismatica*. *Hamathecium* 1.5–2.5 µm wide, comprising numerous, unbranching, septate, hyaline pseudoparaphyses embedded in a gelatinous matrix. *Asci* 140–170 × 5.8–6.4 µm ($\bar{x}$ = 162 × 6 µm, n = 20), 8-spored, bitunicate, long cylindrical, straight or curved, apically rounded with an obvious apical ring, short pedicellate. *Ascospores* 23–27 × 4.4–5.3 µm ($\bar{x}$ = 25 × 4.9 µm, n = 30), uniseriate, hyaline, fusiform with acute angular ends, 3-septate, slightly constricted at the septa, with guttules in each cell, thick and smooth-walled, without a gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of the ascospore. Colonies on PDA, reaching 20 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, flat, lobate edge, pale yellow reverse, pale yellow at the edge, dark brown at center.

Material examined – China, Yunnan Province, Xishuangbanna, on dead woody twigs of *Millettia leptobotrya* (Fabaceae), 15 December 2019, G.C. Ren, XS18 (HKAS 122773), living culture KUMCC 21-0671.

Known distribution – On dead branch of an unidentified plant in Thailand (Zhang et al. 2017), on dead woody twigs of *Millettia leptobotrya* (Fabaceae) in China (This study).

GenBank numbers – SSU: OQ168226, LSU: OQ170875, ITS: OQ158953, *tef1-α*: OR613415.

Notes – *Dyfrulomyces thamplaensis* was introduced by Zhang et al. (2017) based on the combined phylogeny of LSU, SSU, and *tef1-α* sequence data and has been found from dead branches in karst landforms of China and Thailand. Li et al. (2022) synonymized *Dyfrulomyces*

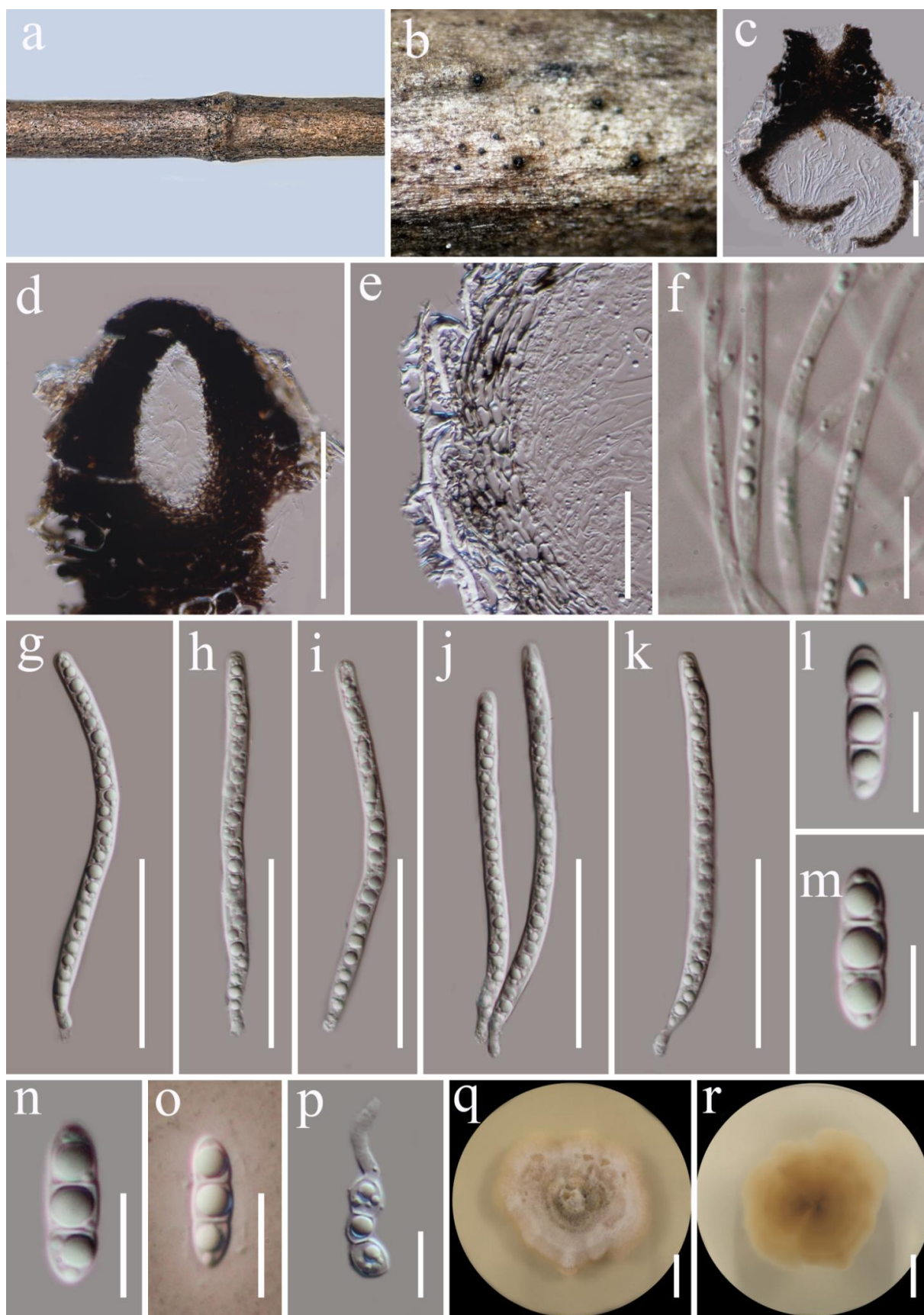


Figure 8 – *Melomastia diqingensis* (HKAS 122718, holotype). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Vertical section through the ostiole. e Peridium. f Pseudoparaphyses. g–k Asci. l–n Ascospores. o Ascospore in Indian ink showing sheath. p Germinated ascospore. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: c, d = 100 μ m, e = 30 μ m, f = 10 μ m, g–k = 50 μ m, l–p = 10 μ m, q, r = 10 mm.

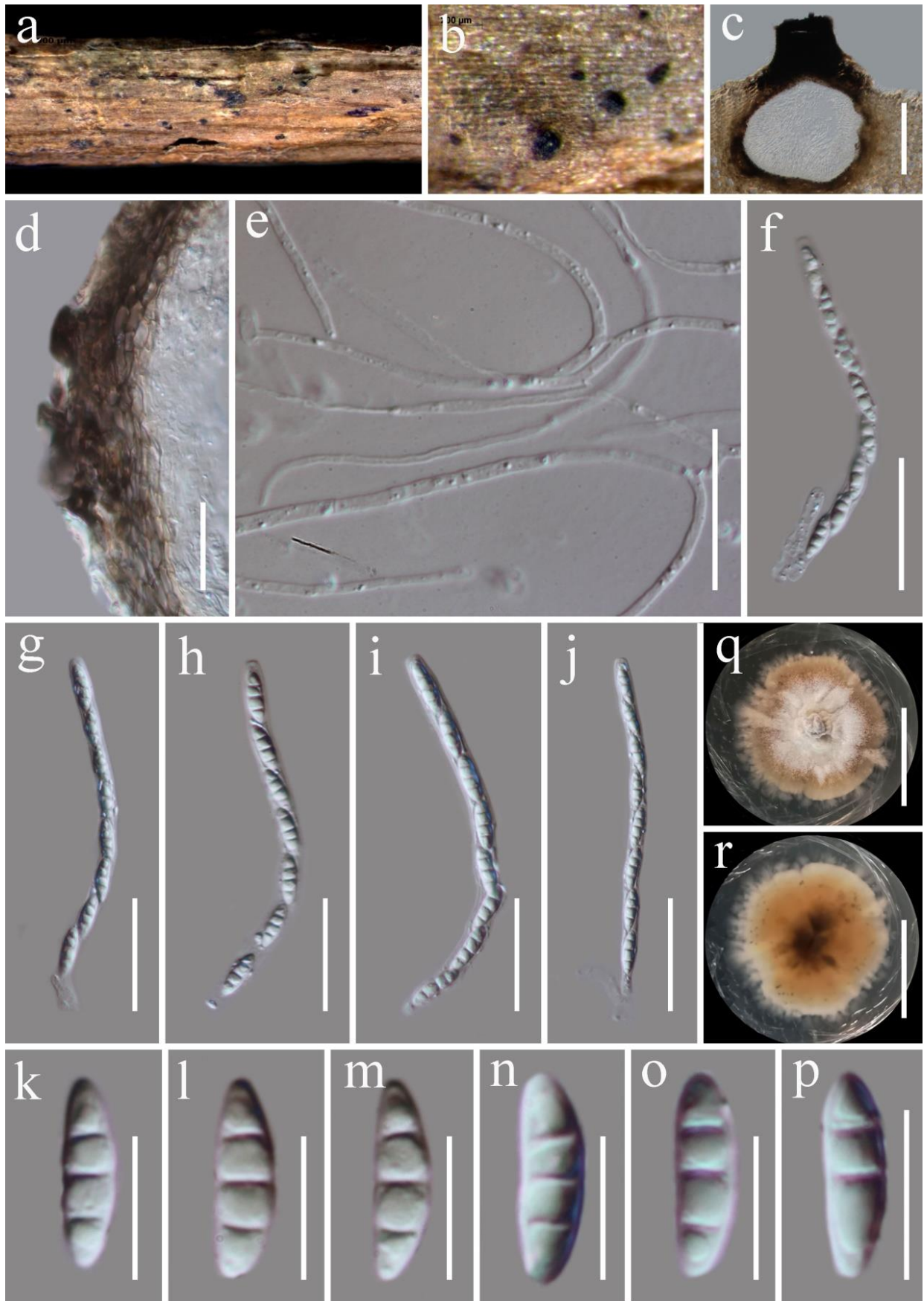


Figure 9 – *Melomastia sichuanensis* (HKAS 122762). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–j Asci. k–p Ascospores. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: c = 200 µm, d, e = 20 µm, f–j = 30 µm, k–p = 10 µm, q, r = 20 mm.

thamplaensis under *Melomastia thamplaensis* based on morphological characterization and phylogenetic analyses. In the present study, a multi-gene phylogeny indicates that our strain (KUMCC 21-0671) clustered together with *Melomastia thamplaensis* (MFLUCC 15-0635) with 99% ML bootstrap support and 1.00 BYPP value (Fig. 7). Our collection (KUMCC 21-0671) is similar to *M. thamplaensis* in having globose to subglobose, coriaceous to carbonaceous ascomata with papillate ostioles, long cylindrical, short-pedicellate asci with a prominent apical ring, and hyaline, fusiform, 3-septate ascospores (Zhang et al. 2017). Taking into consideration the genetic similarity and phylogenetic results, we report our saprobic fungal collection (KUMCC 21-0671) as the first record of *M. thamplaensis* on the woody litter of *Millettia leptobotrya* (Fabaceae) in China.

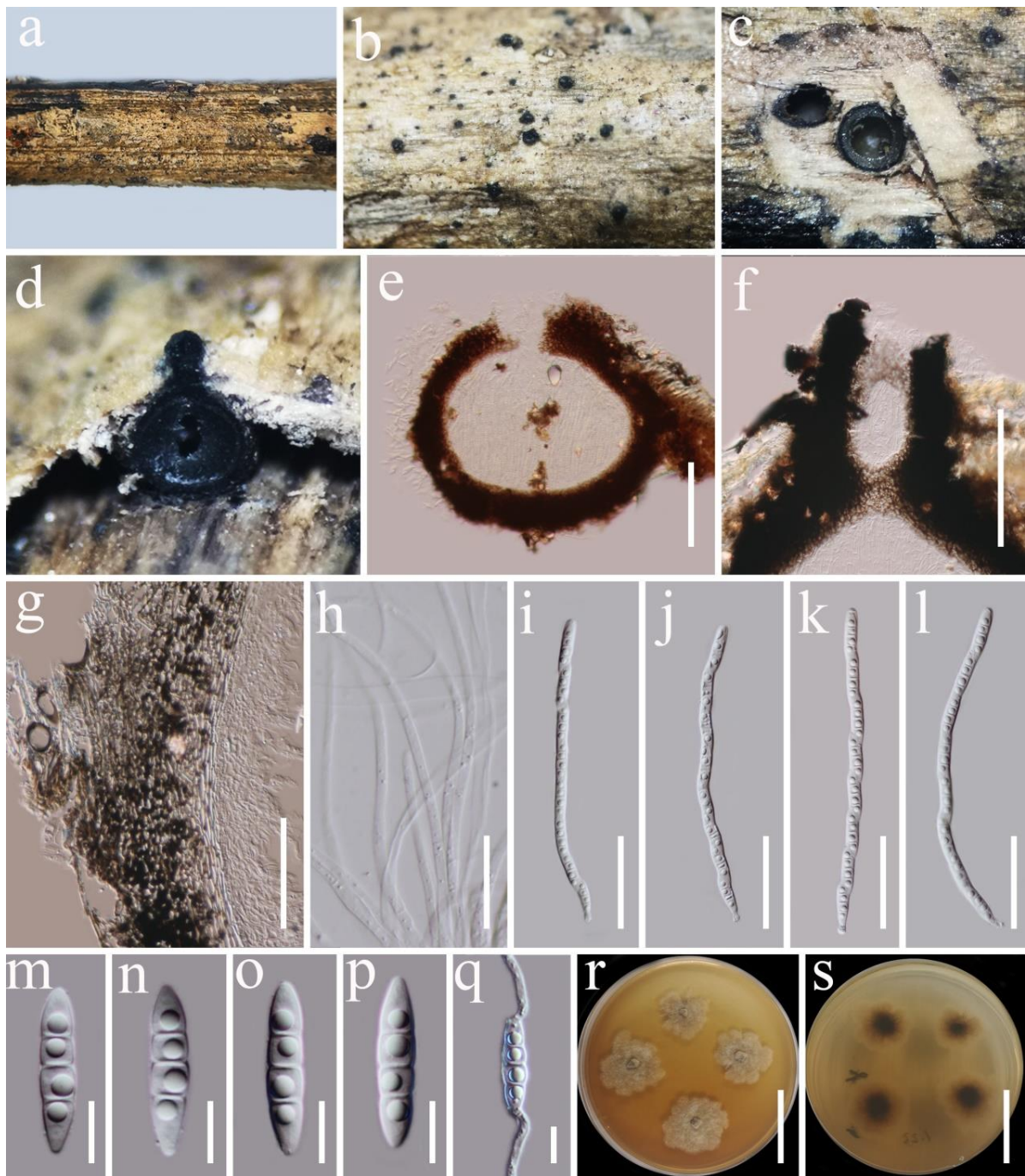


Figure 10 – *Melomastia thamplaensis* (HKAS 122773). a Material examined. b Appearance of ascomata on the host substrate. c horizontal section of ascomata. d vertical sections of ascomata. e Section of an ascus. f Vertical section of an ostiole. g Peridium. h Pseudoparaphyses. i–l Asci. m–p Ascospores. q Germinated ascospore. r, s Culture characters on PDA (r = from above, s =

from below). Scale bars: e–f = 150 μ m, g = 50 μ m, h = 20 μ m, i–l = 50 μ m, m–q = 10 mm, r, s = 30 mm.

Homortomycetales Maharachch. & Wanas.

Homortomycetaceae Thambug., A.J.L. Phillips & K.D. Hyde, in Thambugala et al., Fungal Diversity 82: 45 (2016)

Maharachchikumbura et al. (2021) introduced *Homortomycetales* to accommodate *Homortomycetaceae*. *Homortomycetaceae* was introduced by Thambugala et al. (2017) to accommodate *Homortomyces* and it comprises a single genus (Wijayawardene et al. 2022). The sexual morphs of this family are characterized by immersed to partially erumpent, globose to subglobose ascomata; peridium containing cell layers of textura angularis; cylindrical, 2–6-spored asci with uni to bi-seriate, fusiform, yellowish brown to brown, 3-septate ascospores (Thambugala et al. 2017). The asexual morphs of *Homortomycetaceae* are coelomycetous, which are characterized by pycnidial, uniloculate or multi-loculate, globose to subglobose conidiomata; conidiomatal wall containing cell layers of textura angularis; hyaline conidiogenous cell with supporting cell; ellipsoid to subcylindrical, golden brown to dark brown conidia with 3(–4)-euseptate (Thambugala et al. 2017). Herein, we introduced a novel sexual morph of *Homortomyces* based on morphology and molecular data.

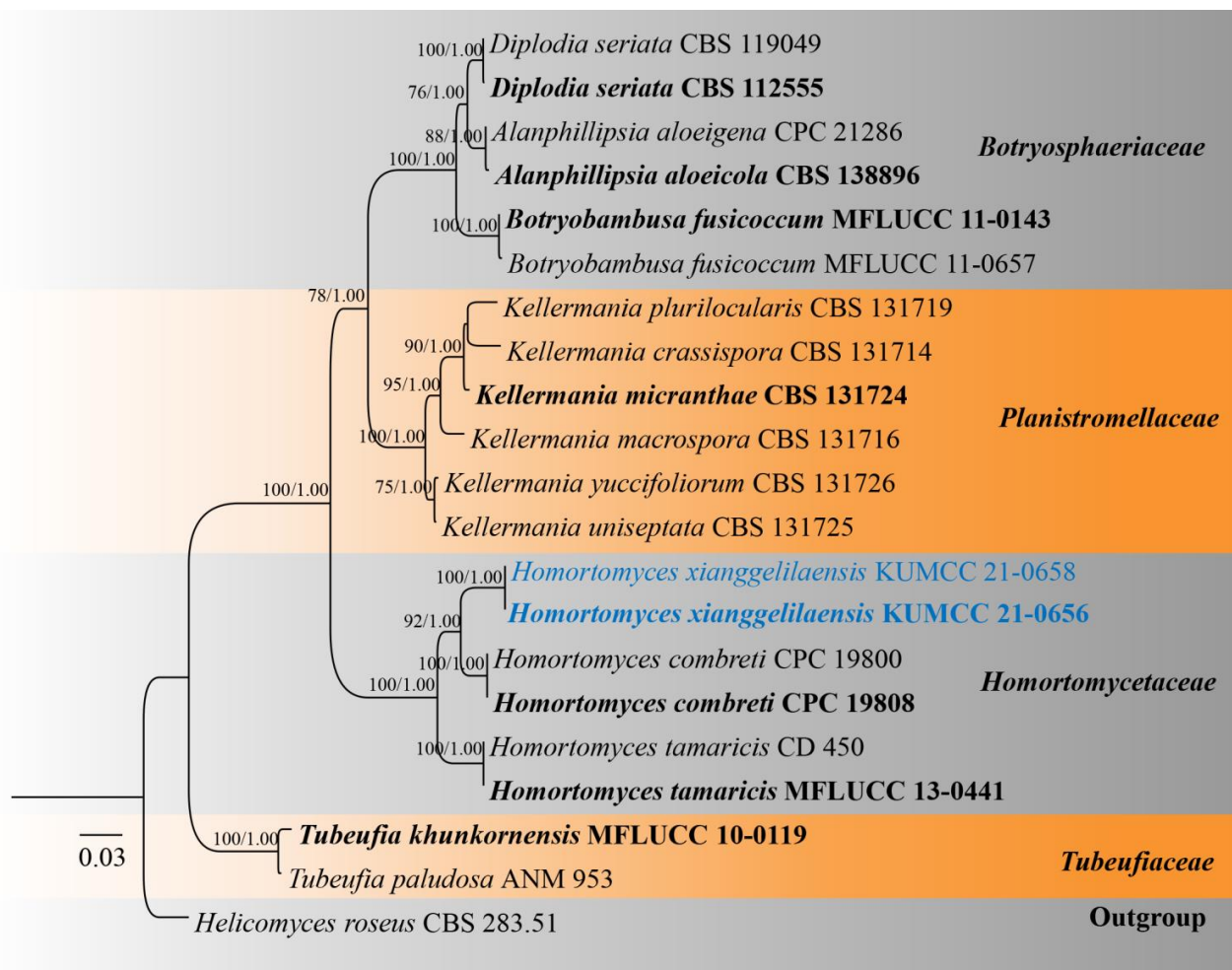


Figure 11 – Phylogram generated from ML analysis based on LSU and ITS sequence data. Related sequences are obtained following Wijayawardene et al. (2014b) and BLAST search results in GenBank. Twenty-one strains are included in the combined analyses which comprise 1375 characters for LSU and ITS alignment. *Helicomyces roseus* (CBS 28351) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -5336.843287 is presented.

The matrix had 381 distinct alignment patterns, with 14.32% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237833, C = 0.239976, G = 0.293129, T = 0.229062; substitution rates AC = 1.383847, AG = 2.064248, AT = 1.659808, CG = 0.843518, CT = 5.572533, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Homortomyces xianggelilaensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 12

Index Fungorum number: IF901347; Facesoffungi Number: FoF13883

Holotype – MFLU 122769

Etymology – The species epithet “xianggelila” refers to the location where the specimen was collected.

Saprobic on dead woody twigs of *Quercus serrata*. Sexual morph: *Ascomata* 230–350 µm high × 300–320 µm diam., ($\bar{x}$ = 315 × 310 µm, n = 6), scattered, solitary, immersed to partially erumpent through the host tissues, black, globose to subglobose, unilocular, ostiolate. *Peridium* 15–30 µm wide, comprising 2–3 layers of brown, thick-walled cells of *textura angularis*. *Hamathecium* comprising 2–3.5 µm wide, scarce, filiform, hyaline, septate, pseudoparaphyses embedded in a gelatinous matrix. *Asci* 85–110 × 27–35 µm ($\bar{x}$ = 97 × 30 µm, n = 25), mostly 6–8-spored, bitunicate, cylindric-clavate to broadly clavate, straight or slightly curved, with short truncate pedicel, apically rounded. *Ascospores* 20–26 × 10–13 µm ($\bar{x}$ = 22.9 × 11.8 µm, n = 30), biserial, oblong or fabiform, pale brown to light brown when immature, becoming brown to dark brown when mature, 1-septate, smooth-walled, with rounded ends. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cells of ascospore. Colonies on PDA, slow growing, reaching 15 mm diameter after two weeks at 20–25 °C, mycelia medium dense, superficial, raised, circular, surface rough with crenate edge, pale yellow, reverse dark grey, pale yellow at margin.

Material examined – China, Yunnan Province, Diqing, Xianggelila, on dead woody twigs of *Quercus serrate* (Fagaceae), 21 August 2019, G.C. Ren, T904 (HKAS 122769, holotype), ex-type living culture KUMCC 21-0656. *ibid.*, T910 (HKAS 122770, isotype), ex-isotype KUMCC 21-0658.

GenBank numbers – KUMCC 21-0656: LSU: OQ170852, ITS: PP408196; KUMCC 21-0658: LSU: OQ170853, ITS: PP408197.

Notes – *Homortomyces xianggelilaensis* is introduced as a new species based on its distinct morphology and phylogenetic analyses of the combined LSU and ITS dataset. Two of our strains (KUMCC 21-0656 and KUMCC 21-0658) clustered sister to *H. combreti* with 92% ML bootstrap support and 1.00 BYPP value (Fig. 11). Our species can be distinguished from *H. tamaricis* in having cylindric-clavate to broadly clavate, 6–8-spored asci with oblong or fabiform, 1-septate ascospores, while *H. tamaricis* has cylindrical, 2–6-spored asci with fusiform, 3-septate ascospores (Thambugala et al. 2017). *Homortomyces combreti* is only known from their asexual morphs and was associated with leaf spots on *Combretum erythrophyllum* (Crous et al. 2012). As we did not obtain the asexual morph from *Homortomyces xianggelilaensis*, the morphological comparison between our new species and *Homortomyces combreti* is not possible. A nucleotide pairwise comparison showed that *Homortomyces xianggelilaensis* differs from *H. combreti* in 24/832 bp of LSU (2.59%, without gaps). However, based on the phylogenetic distinctiveness, *Homortomyces xianggelilaensis* is introduced as a new species.

Pleosporales Luttr. Ex M.E. Barr

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

Acrocalymmaceae was introduced by Trakunyingcharoen et al. (2014) to accommodate *Acrocalymma* as the type genus. This family comprises a single genus (Hongsanan et al. 2020).

The sexual morph of this family is characterized by globose ascomata with central beak ostioles; cylindrical, bitunicate, 8-spored asci with 2–3-seriate, narrowly fusoid, pale brown, 1–3-septate ascospores (Trakunyingcharoen et al. 2014, Hongsanan et al. 2020). The asexual morph of

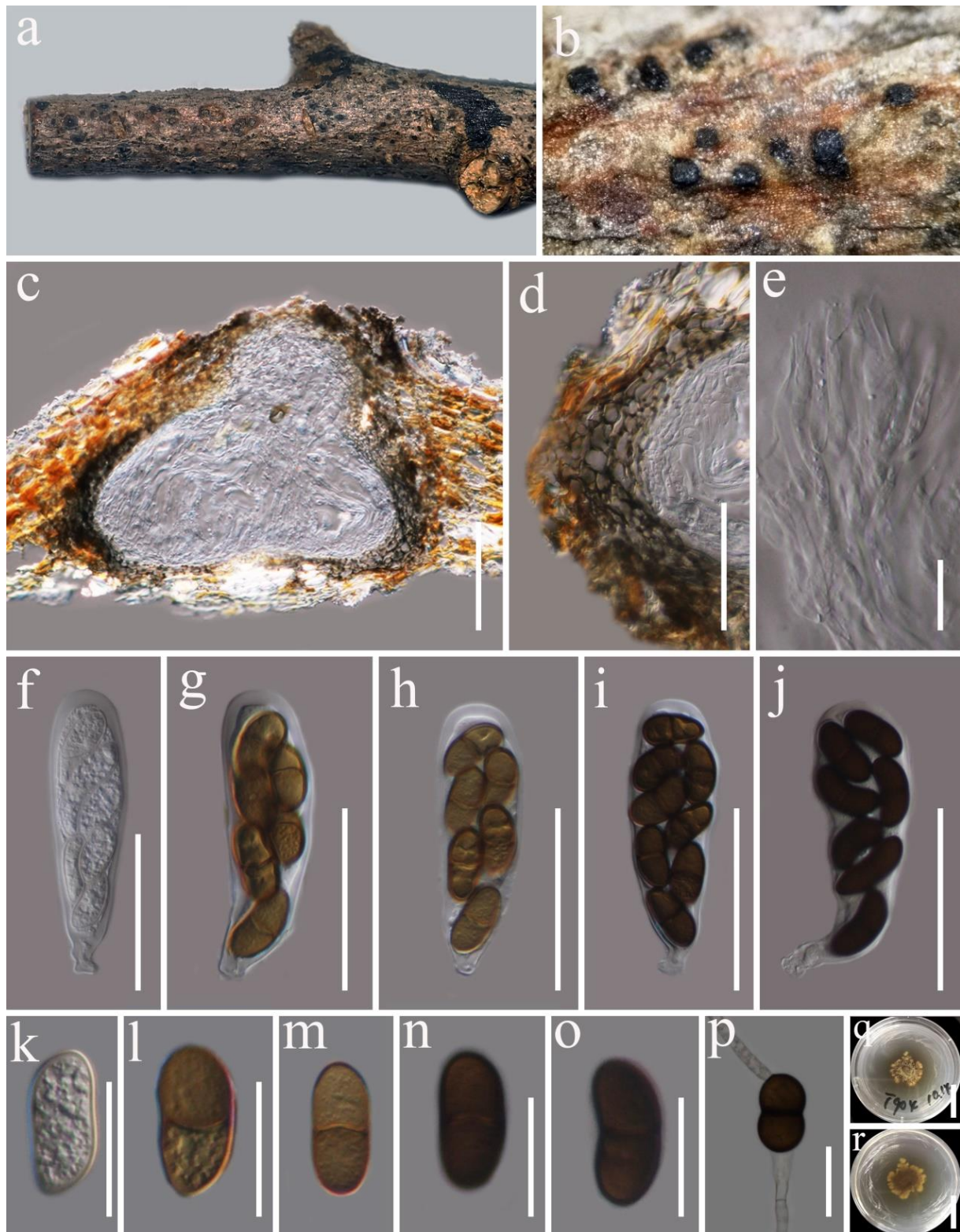


Figure 12 – *Homortomyces xianggelilaensis* (HKAS 122769, holotype). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–j Asci. k–o Ascospores. p Germinated ascospore. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: c = 100 μ m, d, f–j = 50 μ m, e = 30 μ m, k–p = 20 μ m, q, r = 30 mm.

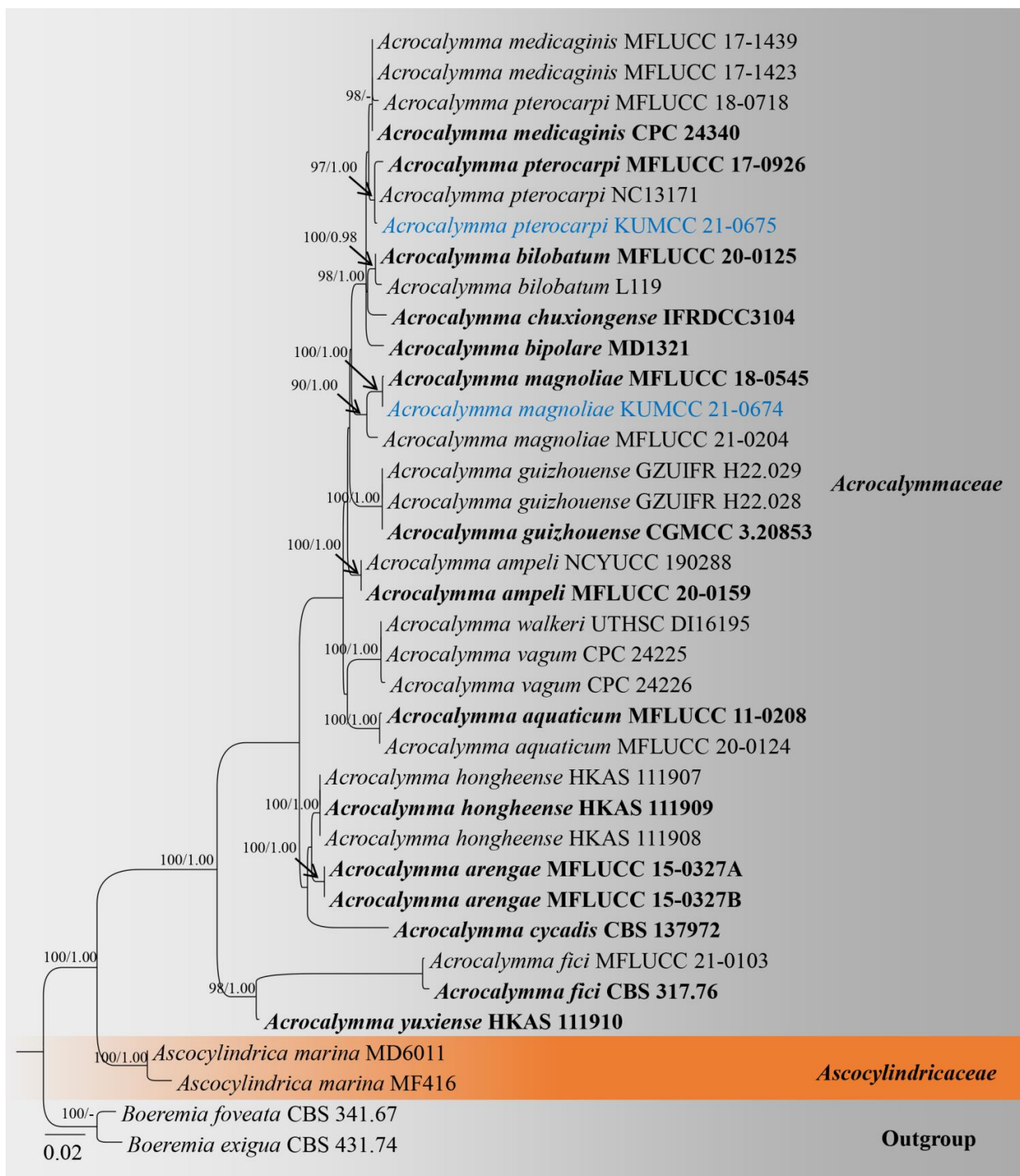


Figure 13 – Phylogram generated from ML analysis based on SSU, LSU, ITS and *tef1- α* sequence data, representing *Acrocalymma* family. Related sequences are obtained following Jayasiri et al. (2019), Mortimer et al. (2021) and Calabon et al. (2023b). Thirty-seven strains are included in the combined analyses, which comprise 3301 characters for SSU, LSU, ITS and *tef1- α* alignment. *Boeremia exigua* (CBS 431.74) and *B. foveata* (CBS 341.67) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -9402.946202 is presented. The matrix had 563 distinct alignment patterns with 39.03% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245541, C = 0.224280, G = 0.269962, T = 0.260217; substitution rates AC = 1.707655, AG = 3.127362, AT = 2.668674, CG = 1.135340, CT = 8.212547, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the

rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Acrocalymmaceae is coelomycetous, which are characterized by pycnidial, dark brown or black, globose conidiomata; ampulliform to doliiform or cylindrical, hyaline conidiogenous cell; hyaline, but becoming pigmented with age, 0–3-septate conidia (Trakunyingcharoen et al. 2014, Hongsanan et al. 2020). In this study, we report two new host records of *Acrocalymma magnolia* and *A. pterocarpi* from *Parashorea chinensis* in China.

Acrocalymma magnoliae N.I. de Silva, S. Lumyong & K.D. Hyde, Mycosphere 13(1): 967 (2022)
Fig. 14

Index Fungorum number: IF559515; Facesofungi number: FoF10713

Saprobic on dead twigs of *Parashorea chinensis*. Sexual morph: *Ascomata* 190–230 µm high, 140–200 µm diam., ($\bar{x}$ = 210 × 170 µm, n = 5), immersed under host tissue, solitary or scattered, subglobose to elliptical, uni-loculate, coriaceous, black. *Ostioles* central. *Peridium* 8–13 µm wide, 3–4-layered, composed of dark brown outer layers and hyaline inner layers, thick-walled cells of *textura angularis* to *textura prismatica*. *Hamathecium* 2.5–4 µm wide, comprising numerous branching, septate, hyaline pseudoparaphyses. *Asci* 100–140 × 15–18 µm ($\bar{x}$ = 117 × 16 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, slightly curved, with a furcate to truncate pedicel, apically rounded. *Ascospores* 25–30 × 6–7 µm ($\bar{x}$ = 27.1 × 6.3 µm, n = 30), overlapping 1–2-seriate, hyaline, fusiform with acute ends, slightly curved, 3-septate, slightly constricted at the septum, the second cell of the ascospore from the apex wider than other cells, smooth-walled, large guttules in each cell, without mucilaginous sheath. Asexual morph: Coelomycetous. *Conidiomata* 135–160 × 200–230 µm ($\bar{x}$ = 145 × 215 µm, n = 10), subglobose, dark brown or black, semi-immersed to erumpent, solitary, scattered without ostioles. *Conidiomatal wall* 20–35 µm wide, composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, cells in the inner layer lightly pigmented, arranged in a *textura angularis*, in the outer layer, darker, fusing cells and indistinguishable from the host tissues. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–12 × 3–7 µm ($\bar{x}$ = 10 × 5 µm, n = 10), phialidic, hyaline, smooth, ampulliform to doliiform, proliferating with visible periclinal thickening at apex. *Conidia* 22–30 × 5–7 µm ($\bar{x}$ = 26 × 6 µm, n = 40), hyaline, cylindrical to fusoid, smooth, guttulate, thin-walled, straight, apex obtuse, unicellular, 2–3 pseudosepta present with flaring mucoid. Apical appendage visible in water mounts (de Silva et al. 2022).

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cells of the ascospore. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, fimbriate, marginal hyphae emission, dense, flat, gray with white spots; reverse, black.

Material examined – China, Yunnan Province, Xishuangbanna, on dead woody twigs of *Parashorea chinensis* (Dipterocarpaceae), 15 December 2019, G.C. Ren, XS23 (HKAS 122776), living culture KUMCC 21-0674.

Known distribution – On dead twigs attached to *Magnolia* sp. (Magnoliaceae) and *Anomianthus dulcis* (Annonaceae) in Thailand (de Silva et al. 2022), on dead woody twigs of *Parashorea chinensis* (Dipterocarpaceae) in China (This study).

GenBank numbers – LSU: OQ170830, ITS: OQ158910, SSU: OQ168190, *tef1-α*: OR613416.

Notes – *Acrocalymma magnoliae* was introduced by de Silva et al. (2022) based on its distinct morphology and analysis of a combined SSU, LSU, and ITS dataset. In the phylogenetic analysis, our isolate (KUMCC 21-0674) clustered with the ex-type strain of *A. magnoliae* (MFLUCC 18-0545) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 13). Sequence comparison for the ITS region between our isolate (KUMCC 21-0674) and *A. magnoliae* (MFLUCC 18-0545) showed no significant base pair differences. We did not obtain the asexual morph from our isolate (KUMCC 21-0674). Therefore, the morphological comparison between our isolate and *Acrocalymma magnoliae* is not possible. However, sexual morphs of *Acrocalymma*

chuxiongense, *A. hongheense*, *A. medicaginis*, *A. pterocarpi* and *A. walker* have been described by Shoemaker et al. (1991), Jayasiri et al. (2019), Mapook et al. (2020), Mortimer et al. (2021), and Liu & Zeng (2022). The morphology of our isolate (KUMCC 21-0674) aligns with the sexual morph criteria given for *Acrocalymma* species but differs from known species (see Table 2). Based on the phylogenetic analyses, our saprobic isolate (KUMCC 21-0674) is introduced as the first record of *Acrocalymma magnoliae* on the woody litter of *Parashorea chinensis* (Dipterocarpaceae) in China. Moreover, our collection is the first sexual morph recording in *A. magnolia*.

Table 2 Synopsis of characters of the sexual morph for *Acrocalymma* species.

Species	Ascospores				Reference
	Shape	Colour	Septa	Sheath	
<i>A. magnoliae</i>	Fusiform	Hyaline	3-septate	Without	This study
<i>A. chuxiongense</i>	Obovoid to ellipsoid	Hyaline	1-septate	Without	Liu & Zeng (2022)
<i>A. hongheense</i>	Fusiform	Hyaline	1-septate	With a sheath	Mortimer et al. (2021)
<i>A. medicaginis</i>	Oblong to fusiform	Hyaline	1-septate	With a sheath	Mapook et al. (2020)
<i>A. pterocarpi</i>	Fusiform	Hyaline	1–3-septate	With a sheath	Jayasiri et al. (2019)
<i>A. walker</i>	Fusiform	Pale reddish-brown	3-septate	With a sheath	Shoemaker et al. (1991)

Acrocalymma pterocarpi Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 20 (2019)

Fig. 15

Index Fungorum number: IF555528; Facesofungi number: FoF0522

Saprobic on dead woody twigs of *Parashorea chinensis*. Sexual morph: *Ascomata* 110–240 µm high, 35–120 µm diam., ($\bar{x}$ = 195 × 70 µm, n = 5), semi-immersed, clustered, sometimes solitary, scattered, globose to subglobose, elliptical or obpyriform, uni-loculate, coriaceous, black. *Ostioles* central, 65–95 µm long, 35–63 µm diam., ($\bar{x}$ = 74 × 49 µm, n = 5). *Peridium* 7–11 µm wide, 2–3-layered, composed of dark brown outer layers and hyaline inner layers, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, comprising numerous, branching, septate, hyaline pseudoparaphyses, embedded in a gel matrix. *Asci* 53–76 × 9–11 µm ($\bar{x}$ = 65.5 × 9.7 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, slightly curved, with a truncated pedicel, apically rounded. *Ascospores* 16–19 × 3.7–4.3 µm ($\bar{x}$ = 18.1 × 4 µm, n = 30), overlapping 1–2-seriate, hyaline, fusiform with acute ends, slightly curved, 1–3-septate, slightly constricted at the septum, smooth-walled, large guttules in each cell. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of an ascospore. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, marginal hyphae emission, flat, gray with white spots, producing pigmentation on PDA; reverse, black.

Material examined – China, Yunnan Province, Xishuangbanna, on dead woody twigs of *Parashorea chinensis* (Dipterocarpaceae), 15 December 2019, G.C. Ren, XS24 (HKAS 122777), living culture KUMCC 21-0675.

Known distribution – On a fallen pod of *Pterocarpus indicus* (Fabaceae) in Thailand (Jayasiri et al. 2019), dead twigs attached to the *Magnolia* sp. in China (de Silva et al. 2022), dead twigs of *Bidens* sp. (Chethana et al. 2023) on dead woody twigs of *Parashorea chinensis* (Dipterocarpaceae) in China (This study).

GenBank numbers – LSU: OQ170831, ITS: OQ158911, SSU: OQ168191, *tef1-α*: OR613417.

Notes – *Acrocalymma pterocarpi* was introduced by Jayasiri et al. (2019) from a fallen pod of *Pterocarpus indicus* in Thailand. In the phylogenetic analysis, our isolate (KUMCC 21-0675) clustered with *A. pterocarpi* with 97% ML bootstrap support and 1.00 BYPP value (Fig. 13).

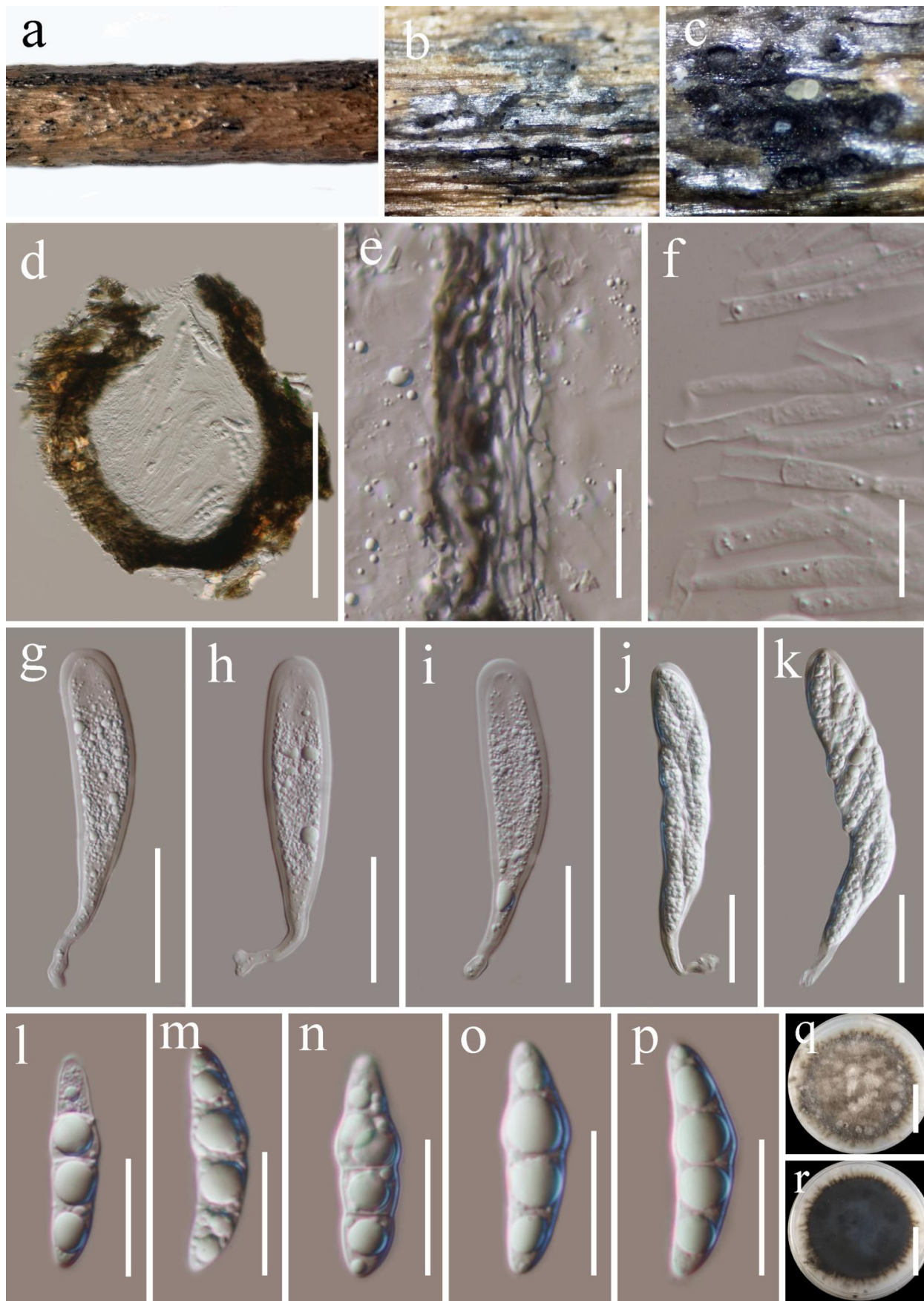


Figure 14 – *Acrocalymma magnoliae* (HKAS 122776). a Material examined. b, c Appearance of ascomata on the host substrate. d Section of an ascoma. e Peridium. f Pseudoparaphyses. g–k Asci. l–p Ascospores. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: d = 150 μ m, e = 20 μ m, f = 10 μ m, g–k = 30 μ m, l–o = 15 μ m, q, r = 30 mm.

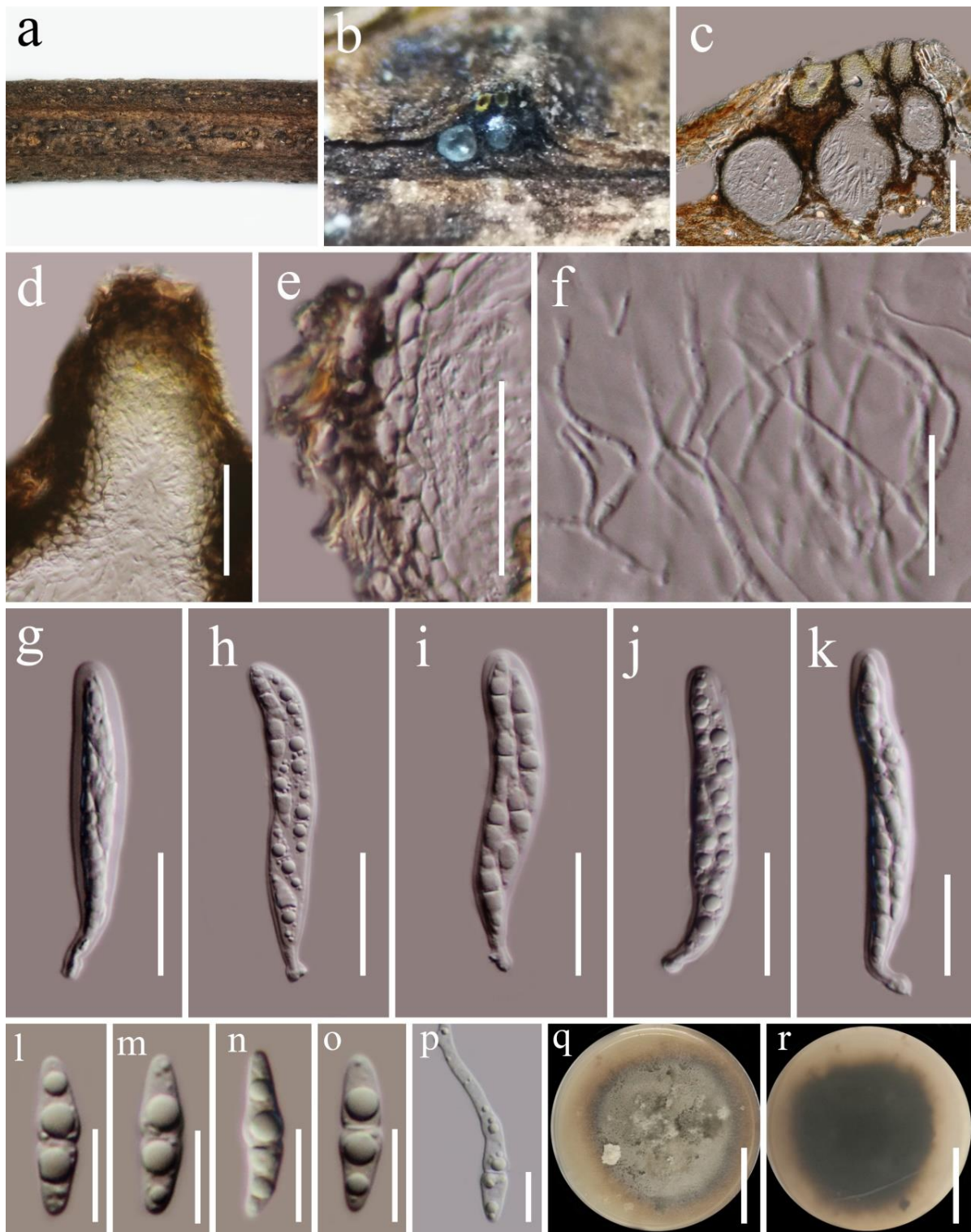


Figure 15 – *Acrocalymma pterocarpi* (HKAS 122777). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d. Ostioles. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p Germinated ascospore. q, r. Culture characters on PDA (q = from above, r = from below). Scale bars: c = 100 μ m, d, e = 30 μ m, f–k = 20 μ m, l–p = 10 μ m, q, r = 30 mm.

A pairwise nucleotide comparison showed that our isolate (KUMCC 21-0675) differs from *A. pterocarpi* (MFLUCC 17-0926) in 4/901 bp of *tef1- α* (0.44%, without gaps) and 5/464 bp of ITS (1.08% without gaps). Our collection (KUMCC 21-0675) resembles *A. pterocarpi* (MFLUCC 17-0926) in having globose to subglobose, dark brown to black ascomata, cylindrical, hyaline asci

(65.5 × 9.7 μm vs 70 × 10 μm), fusiform, 1–3-septate ascospores (18.1 × 4 μm vs 19.5 × 4 μm) (Jayasiri et al. 2019). Therefore, we introduce our collection as the first record of *A. pterocarpi* from *Parashorea chinensis* (Dipterocarpaceae) in China.

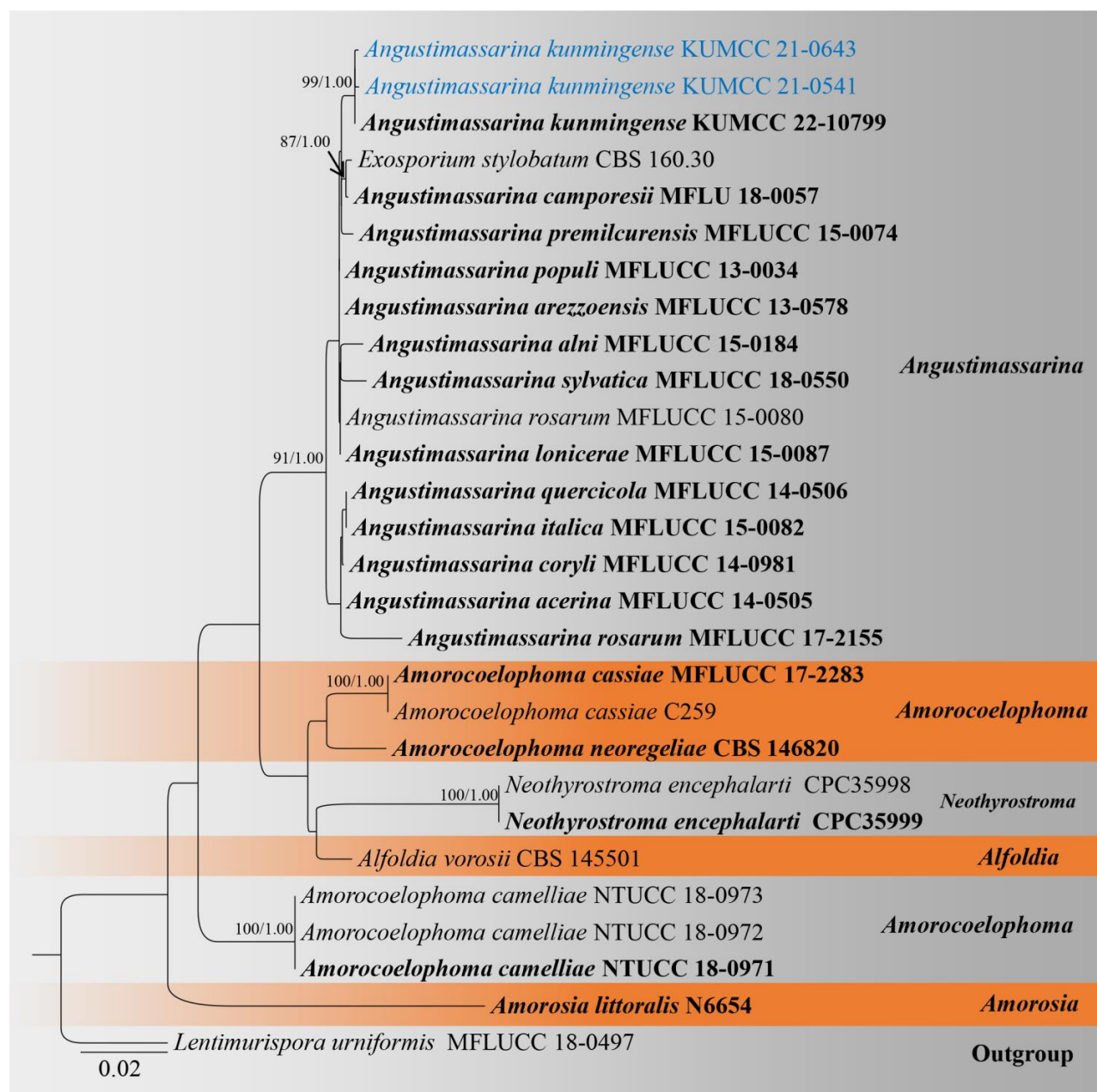


Figure 16 – Phylogram generated from ML analysis based on SSU, LSU, ITS, and *tef1-α* sequence data, representing *Amorosiaceae*. Related sequences are obtained following Jayasiri et al. (2019), Hyde et al. (2020b) and Jayawardena et al. (2022). Twenty-eight strains are included in the combined analyses, which comprise 3226 characters for SSU, LSU, ITS and *tef1-α* alignment. *Lentimurispora urniformis* (MFLUCC 18-0497) was used as the outgroup taxon. The best-scoring RAXML tree with a final likelihood value of -7833.074271 is presented. The matrix had 495 distinct alignment patterns with 31.58% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240851, C = 0.246837, G = 0.270734, T = 0.241579; substitution rates AC = 0.915906, AG = 1.756917, AT = 1.538751, CG = 0.835070, CT = 8.179217, GT = 1.0000. The tree topology of ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Amorosiaceae Thambug. & K.D. Hyde, Fungal Diversity 74: 252 (2015)

Amorosiaceae was introduced by Thambugala et al. (2015) to include *Amorosia* as the type genus. Four genera are accepted in this family, viz., *Alfoldia*, *Amorosia*, *Amorocoelophoma* and *Angustimassarina* (Hongsan et al. 2020). The sexual morphs of this family are characterized by solitary or gregarious, coriaceous, globose to subglobose or conical ascomata; crest-like ostioles; peridium containing cell layers of *textura angularis*; cylindrical to cylindric-clavate, 8-spored asci with 1–3-seriate, fusiform, to cylindrical, or ellipsoidal-fusiform, hyaline or light brown, 1-septate ascospores with a mucilaginous sheath (Thambugala et al. 2015, Hongsan et al. 2020). The asexual morphs of this family are either coelomycetous or hyphomycetous (Hongsan et al. 2020). In this study, we report new host records of *A. kunmingense* from *Quercus kingiana* and *Rhododendron rubiginosum* in China.

Angustimassarina kunmingense H.D. Yang & K.D. Hyde, Fungal Diversity 117: 18 (2023) [2022] Fig. 17

Index Fungorum number: IF559764; Facesofungi number: FoF11804

Saprobic on dead woody twigs of *Quercus kingiana* and *Rhododendron rubiginosum*. Sexual morph: *Ascomata* 180–300 μm high, 160–290 μm diam., ($\bar{x}$ = 225 $\times$ 211 μm , n = 5), immersed under the host tissue, solitary or scattered, globose to subglobose, uni-loculate, coriaceous, dark brown, without papilla, and with a short central ostiole. *Peridium* 25–38 μm wide, 4–5-layered, composed dark brown cells of *textura angularis* to *textura globulosa*. *Hamathecium* comprising 1.7–2.9 μm wide, unbranched, septate, hyaline, cellular pseudoparaphyses, constricted at the septa, embedded in a gelatinous matrix. *Asci* 67–85 $\times$ 10–12 μm ($\bar{x}$ = 74.6 $\times$ 10.6 μm , n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, slightly curved, with a truncated pedicel, apically rounded with a minute ocular chamber. *Ascospores* 19–23 $\times$ 4–5 μm ($\bar{x}$ = 19.4 $\times$ 4.1 μm , n = 30), overlapping 1–2-seriate, hyaline, fusiform with tapering towards rounded ends, straight to slightly curved, 1(–3)-septate, constricted at the primary septum with asymmetric two cells, smooth-walled, large guttules in each cell, and surrounded by a large spreading sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cell of ascospore. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, fimbriate, dense, flat, entire edge, grayish white; reverse, atrovirens, white at the edge.

Material examined – China, Yunnan Province, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Quercus kingiana* (Fagaceae), 19 July 2020, G.C. Ren, LGY01 (HKAS 122719), living culture KUMCC 21-0541; *ibid.*, Diqing, Xianggelila, Nixi, on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae), 1 September 2020, G.C. Ren, NX18 (HKAS 122763), living culture KUMCC 21-0643.

Known distribution – On dead aerial stem of *Camellia semiserrata* (Jayawardena et al. 2022), on dead woody twigs of *Quercus kingiana* (Fagaceae) and *Rhododendron rubiginosum* (Ericaceae) in China (This study).

GenBank numbers – KUMCC 21-0541: LSU: OQ170832, ITS: OQ158912, SSU: OQ168192, *tef1- α* : OR613418; KUMCC 21-0643: ITS: OQ158913, LSU: OQ170833, SSU: OQ168193, *tef1- α* : OR613419.

Notes – *Angustimassarina kunmingense* was introduced by Jayawardena et al. (2022) from a dead aerial stem of *Camellia semiserrata* in China. Our collection (KUMCC 21-0541, KUMCC 21-0643) resemble *A. kunmingense* (KUMCC22-10799) in having globose to subglobose ascomata, cylindrical to cylindric-clavate asci (74.6 $\times$ 10.6 μm vs 68 $\times$ 8.1 μm) with a minute ocular chamber, and hyaline, fusiform ascospores (19.4 $\times$ 4.1 μm vs 20 $\times$ 3.5 μm) with 1(–3) septa (Jayawardena et al. 2022). In the phylogenetic analysis, our isolate (KUMCC 21-0541, KUMCC 21-0643) clustered with the ex-type strain of *A. kunmingense* (KUMCC 22-10799) with 99% ML bootstrap support and 1.00 BYPP value (Fig. 16). Sequence comparison for the ITS and *tef1- α* region between our isolates (KUMCC 21-0541, KUMCC 21-0643) and *A. kunmingense* (KUMCC22-10799) showed

no significant base pair differences. Therefore, we introduce our collection as the first record of *A. kunmingense* from *Quercus kingiana* (Fagaceae) and *Rhododendron rubiginosum* (Ericaceae) in China.

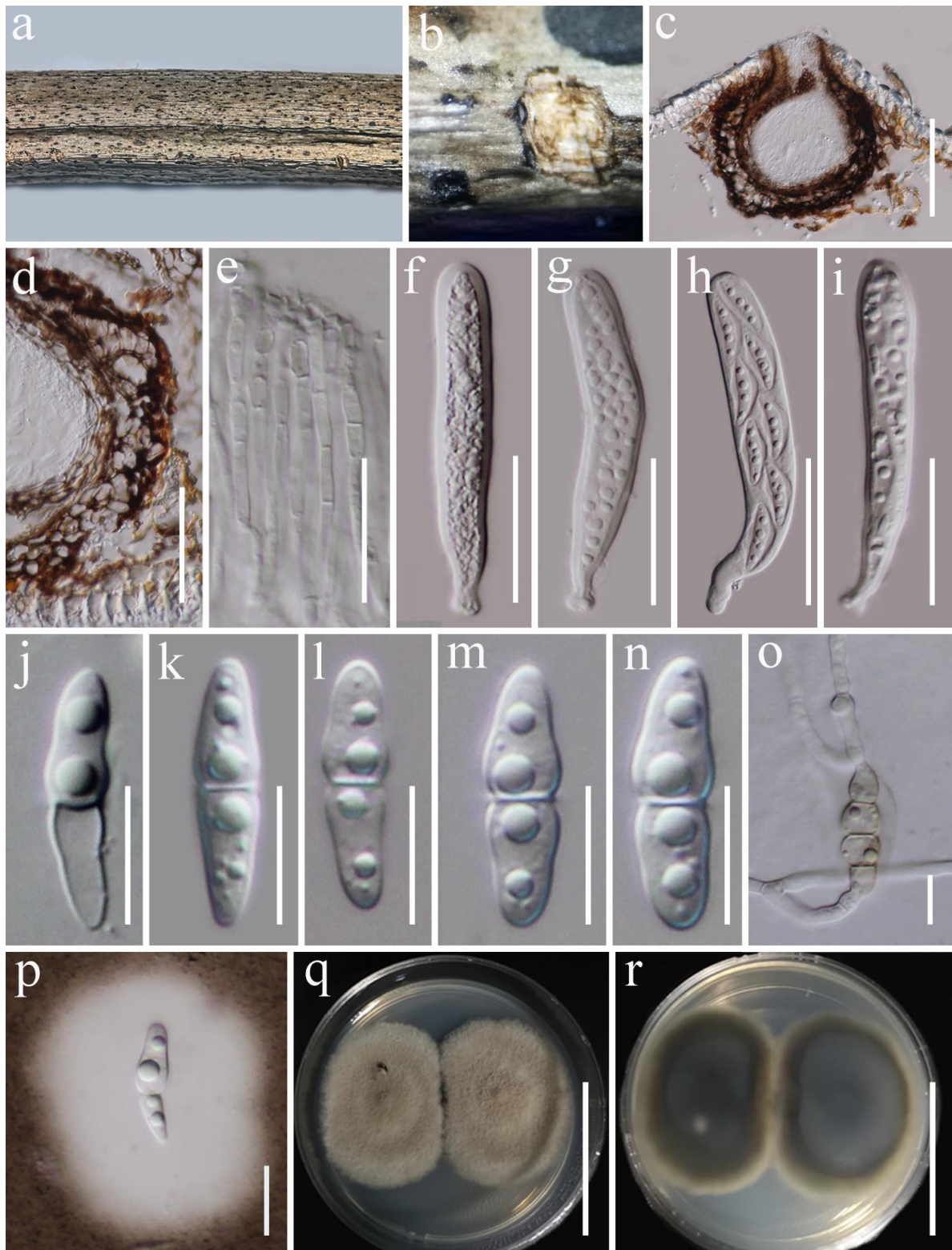


Figure 17 – *Angustimassarina kunmingense* (HKAS 122719). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–n Ascospores. o Germinated ascospore. p Ascospore in Indian ink showing sheath. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: c = 250 μ m, d = 50 μ m, e = 20 μ m, f–i = 30 μ m, j–p = 10 μ m, q, r = 30 mm.

Anastomitrabeculiaceae Bhunjun, Phukhams. & K.D. Hyde, in Journal of Fungi 7: 12 (2021)

Anastomitrabeculiaceae was introduced by Bhunjun et al. (2021) to accommodate *Anastomitrabeculia* and comprises a single genus with a single species (Wijayawardene et al. 2022). The family is characterized by semi-immersed, coriaceous or carbonaceous ascomata with septate, trabeculate pseudoparaphyses (Liew et al. 2000) and hyaline ascospores with longitudinally striate wall ornamentation, surrounded by a mucilaginous sheath (Bhunjun et al. 2021). In this study, we report on a new species of *Anastomitrabeculia* from *Knema furfuracea* in China.

Anastomitrabeculia xishuangbannaensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 19

Index Fungorum number: IF901348; Facesoffungi Number: FoF13875

Holotype – HKAS 122741

Etymology – The species epithet “xishuangbannaensis” refers to the city where the species was collected.

Saprobic on dead woody twigs of *Knema furfuracea*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 500–570 μm high $\times$ 450–650 μm diam., ($\bar{x}$ = 550 $\times$ 570 μm , n = 5), solitary, scattered, immersed beneath the host epidermis, coriaceous, globose to subglobose, brown to dark-brown, ostiolate. *Ostiole* 230–540 μm long, 110–160 μm diam. ($\bar{x}$ = 400 $\times$ 130 μm , n = 5), centrally located, filled with hyaline cells. *Conidiomata wall* 21–30 μm wide, composed several layers of thick-walled, dark brown to brown outer layer and inner layer comprising hyaline cells of *textura angularis*. *Paraphyses* 2.5–3.8 μm wide, cylindrical to fusiform, septate, branched. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 10–32 $\times$ 4–11 μm ($\bar{x}$ = 23 $\times$ 7 μm , n = 10), enteroblastic, phialidic, determinate, discrete, cylindrical or ampulliform, hyaline, smooth-walled, arising from stratum. *Conidia* 42–50 $\times$ 21–30 μm ($\bar{x}$ = 45 $\times$ 26 μm , n = 30), oval to obovoid, dictyosporous, muriform, initially hyaline, becoming brown to dark brown at maturity, multi-septate, sectoried.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25°C). Germ tubes produced from around the conidia. Colonies on PDA, reaching 55 mm diameter after two weeks at 20–25 °C, mycelia superficial, surface smooth, circular, velvety, fluffy, dense, white at margin, grey at centre; reverse, white at margin, dark grey at the centre.

Material examined – China, Yunnan Province, Xishuangbanna, on dead woody twigs of *Knema furfuracea* (Myristicaceae), 4 March 2020, G.C. Ren, JH42 (HKAS 122741, holotype), ex-type living culture KUMCC 21-0585. *ibid.*, JH43, KUMCC 21-0586.

GenBank numbers – KUMCC 21-0585: LSU: OQ170834, ITS: OQ158914, SSU: OQ168194, *tef1- α* : OR613420; KUMCC 21-0586: LSU: OQ170835, ITS: OQ158915, SSU: OQ168195.

Notes – In our phylogenetic analysis, *Anastomitrabeculia xishuangbannaensis* clustered as a sister clade to type strain of *A. didymospora* with 100% ML bootstrap support and 1.00 BYPP value (Fig. 18). Sequence comparison between *A. didymospora* (MFLUCC 16-0412) and *A. xishuangbannaensis* (KUMCC 21-0585) showed a 17.58% (80/455 bp, without gaps) base pair difference in the ITS region, 4.87% (40/821 bp, without gaps) base pair difference in the LSU region, 17.06% (138/809 bp, without gaps) base pair difference in *tef1- α* region. *Anastomitrabeculia didymospora* was introduced from its sexual morph (Bhunjun et al. 2021), while we introduced *A. xishuangbannaensis* from its asexual morph. Therefore, we were unable to compare our new species and *A. didymospora*. However, based on the phylogenetic distinctiveness, *Anastomitrabeculia xishuangbannaensis* is introduced as a new species, and our species is the first asexual morph recorded in this genus.

Bambusicolaceae D.Q. Dai & K.D. Hyde, Fungal Diversity 63 (1): 49 (2013)

Bambusicolaceae was introduced by Hyde et al. (2013) to accommodate *Bambusicola*. Currently, *Bambusicolaceae* comprises four genera, viz., *Bambusicola*, *Corylicola*, *Leucaenicola*, and *Palmiascoma* (Monkai et al. 2021). The morphological characters of the family are immersed to superficial, globose to subglobose ascomata; cylindrical to clavate asci and hyaline, fusiform ascospores surrounded by a gelatinous sheath (Hyde et al. 2013, Hongsan et al. 2020).

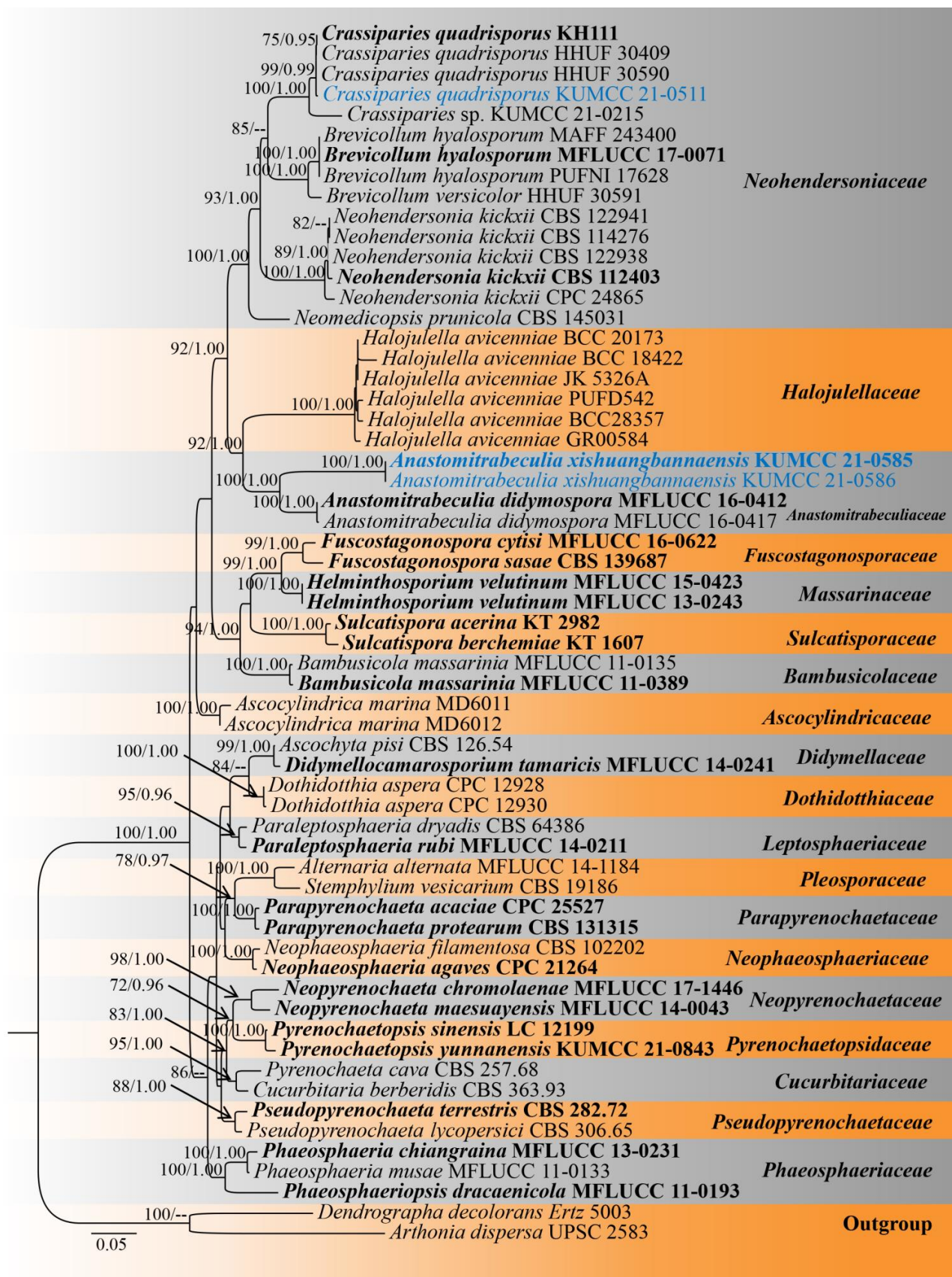


Figure 18 – Phylogram generated from ML analysis based on SSU, LSU, ITS and *tef1-α* sequence data. Related sequences are obtained following Bhunjun et al. (2021) and BLAST search results in GenBank. Sixty strains are included in the combined analyses, which comprise 3210 characters for SSU, LSU, ITS and *tef1-α* alignment. *Arthonia dispersa* (UPSC 2583) and *Dendrographa decolorans* (Ertz 5003) were used as the outgroup taxa. The best-scoring RAXML tree with a final

likelihood value of -19749.079335 is presented. The matrix had 1152 distinct alignment patterns with 30.83% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244104, C = 0.237282, G = 0.273441, T = 0.245174; substitution rates AC = 1.279169, AG = 2.990662, AT = 1.843852, CG = 0.776990, CT = 7.343522, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

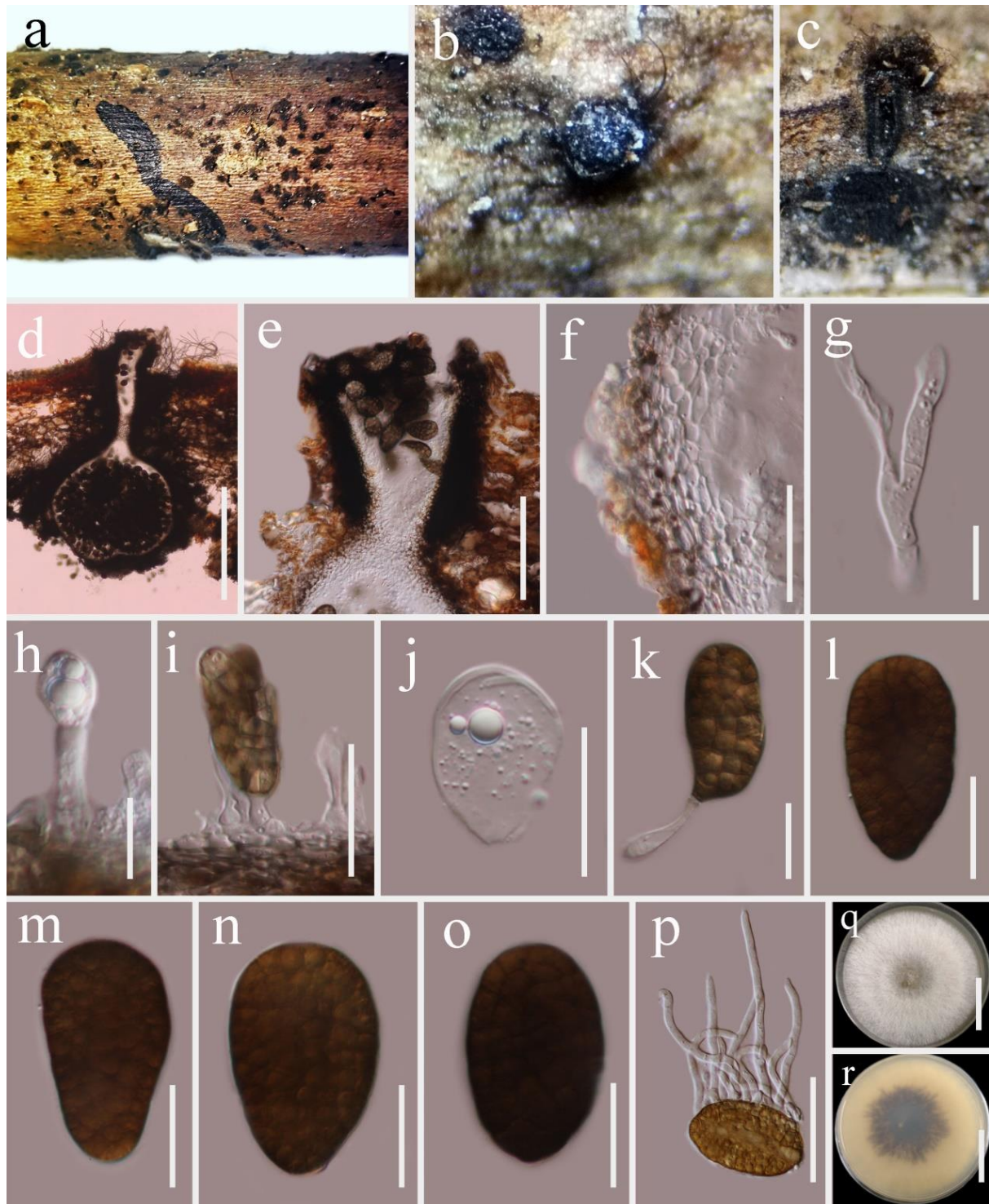


Figure 19 – *Anastomitrabeculia xishuangbannaensis* (HKAS 122741, holotype). a Material examined. b Conidiomata on the natural wood surface. c, d Section through conidioma. e Ostiolar

neck. f Conidioma wall. g Paraphyses. h, i Conidiogenous cells and developing conidia. j–o Conidia. p Germinated conidium. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: d = 500 μ m, e = 100 μ m, f, h, i = 30 μ m, g = 10 μ m, j–o = 20 μ m, p = 50 μ m, q, r = 30 mm.

The asexual morphs are characterized by pycnothyrial, acerous or subglobose conidiomata; enteroblastic, annelidic, or phialidic, cylindrical conidiogenous cells; cylindrical and oblong to ellipsoidal, pale brown to dark brown, aseptate to 1–3-septate conidia (Hyde et al. 2013, Hongsanan et al. 2020). In this study, we report on new host records in China, viz., *Corylicola italica* from *Quercus kingiana* and *Cryptocarya hainanensis*, *Palmiascoma gregariascomum* from *Cryptocarya hainanensis*, and *Palmiascoma qujingense* from *Myristica yunnanensis*.

Corylicola italica Wijesinghe, Camporesi, Yong Wang bis & K.D. Hyde, Biodiversity Data Journal 8 (e55957): 8 (2020) Fig. 21

Index Fungorum number: IF557768; Facesofungi number: FoF08685

Saprobic on dead woody twigs of *Quercus kingiana*. Sexual morph: *Ascomata* 95–170 μ m high $\times$ 150–180 μ m diam., ($\bar{x}$ = 127 $\times$ 164 μ m, n = 5), immersed to erumpent, solitary or scattered, coriaceous, globose to subglobose, uni-loculate, black. *Ostioles* central, minute papilla. *Peridium* 7–16 μ m wide, 3–4-layered, comprising brown cells of *textura angularis*. *Hamathecium* 1.5–2.7 μ m wide, comprising cylindrical, branched, septate, cellular pseudoparaphyses embedded in a hyaline gelatinous matrix. *Asci* 53–65 $\times$ 5.6–6.8 μ m ($\bar{x}$ = 56 $\times$ 6.1 μ m, n = 20), 8-spored, bitunicate, cylindrical-clavate, straight or curved, apically rounded, short pedicellate, furcate pedicels, with a minute ocular chamber. *Ascospores* 8.5–11 $\times$ 2.7–3.4 μ m ($\bar{x}$ = 10 $\times$ 3 μ m, n = 30), uniseriate, ellipsoidal, initially hyaline to pale brown, 1-septate, becoming brown at maturity, constricted at the septum, the cells above central septum often broader than the lower ones, guttulate, thick and smooth-walled, without a gelatinous sheath. Asexual morph: Coelomycetous. *Conidiomata* 175–200 high 150–170 μ m diam., ($\bar{x}$ = 183 $\times$ 161 μ m) pycnidial, solitary to gregarious, scattered, semi-immersed to superficial, visible as black spore mass surrounded by cellular vegetative hyphae (1–2 μ m width), globose to subglobose, glabrous, uniloculate to multi-loculate, ostiolate. *Ostioles* 45–50 μ m long, 50–60 μ m wide, central and circular. *Conidiomata wall* 7–20 μ m wide, composed of several layers of pale to dark brown, pseudoparenchymatous cells, outermost layers comprising 3–5 layers of dark brown cells of *textura prismatica* to *textura angularis*, inner layers comprising 2–3 layers of pale brown to hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells, originated from the basal cavity of conidiomata. *Conidiogenous cells* 3–4.5 $\times$ 2–4 μ m ($\bar{x}$ = 3.6 $\times$ 3 μ m, n = 30), holoblastic, phialidic, ampulliform, yellowish to pale brown, aseptate, smooth-walled. *Conidia* 3–5 $\times$ 2–3 μ m ($\bar{x}$ = 4 $\times$ 2.5 μ m, n = 30), solitary, globose or oblong to ellipsoid, rounded or obtuse ends, yellowish to pale brown, aseptate, rarely guttulated, one-celled, smooth-walled (Wijesinghe et al. 2020).

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of the ascospore. Colonies on PDA, reaching 15 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, flat, lobate edge, raised at the center, white, granular and circular crack on the surface; reverse, white at edge, grayish white at center.

Material examined – China, Yunnan Province, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Quercus kingiana* (Fagaceae), 20 July 2020, G.C. Ren, LGY31 (HKAS 122733), living culture KUMCC 21-0563; *ibid.*, LGY16 (HKAS 122731), living culture KUMCC 21-0553; *ibid.*, LGY22 (HKAS 122732), living culture KUMCC 21-0559; China, Yunnan Province, Lincang, on dead woody twigs of *Cryptocarya hainanensis* (Lauraceae) LC22 (HKAS 122734) living culture KUMCC 21-0605.

Known distribution – On dead hanging branch of *Corylus avellana* (Betulaceae) in Italy (Wijesinghe et al. 2020), dead woody twigs of *Quercus kingiana* (Fagaceae) and *Cryptocarya hainanensis* (Lauraceae) in China (This study).

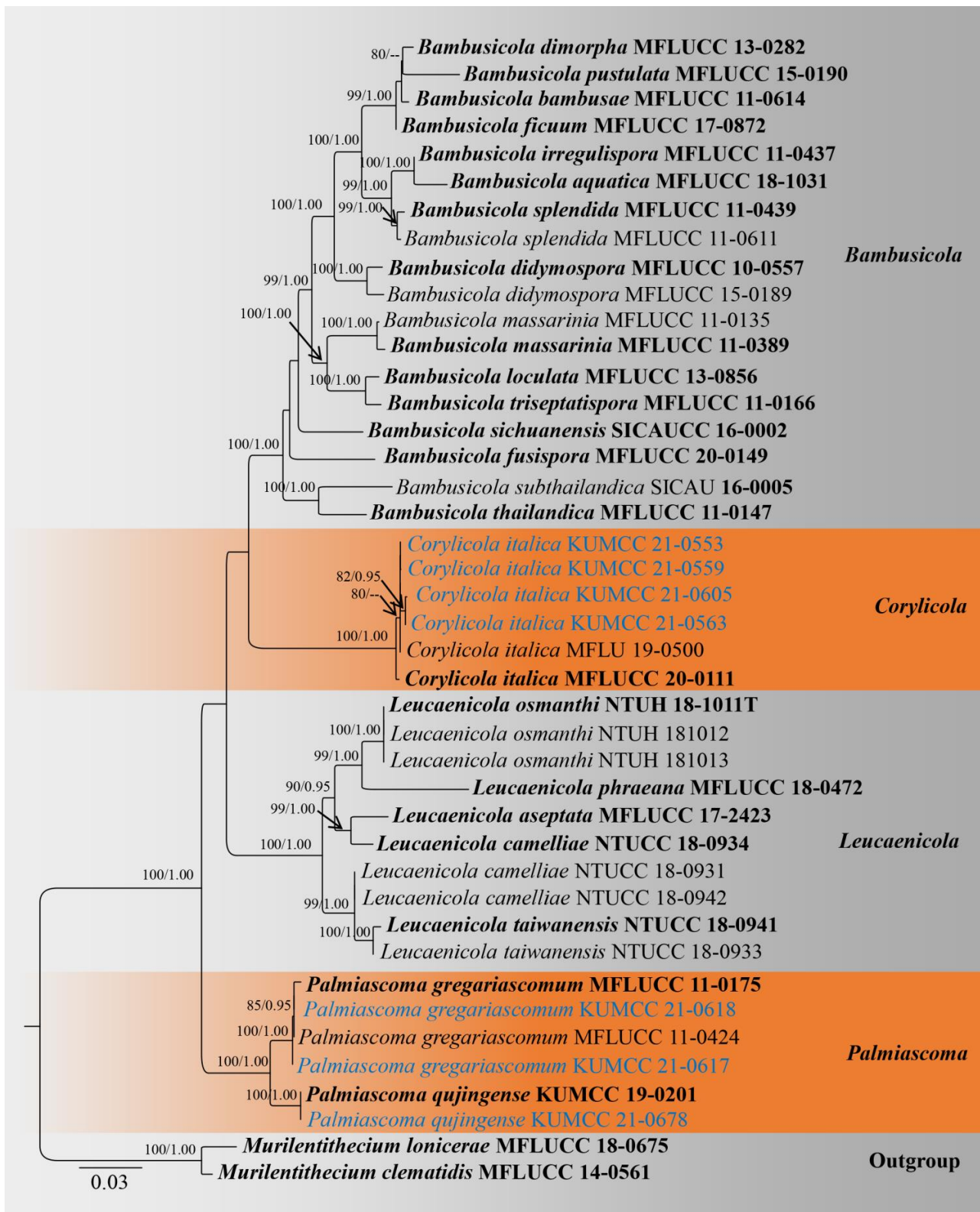


Figure 20 – Phylogram generated from ML analysis based on SSU, LSU, ITS, *tef1- α* , and *rpb2* sequence data, representing *Bambusicolaceae*. Related sequences are obtained following Phukhamsakda et al. (2022). Forty-two strains are included in the combined analyses, which comprise 4040 characters for SSU, LSU, ITS, *tef1- α* , and *rpb2* alignment. *Murilentithecium clematidis* (MFLUCC 14-0561) and *M. lonicerae* (MFLUCC 18-0675) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -17373.628804 is presented. The matrix had 939 distinct alignment patterns, with 17.41% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242291, C = 0.257231, G = 0.271517, T =

0.228961; substitution rates AC = 1.354747, AG = 2.926058, AT = 1.006416, CG = 0.994544, CT = 6.807971, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

GenBank numbers – KUMCC 21-0563: LSU: OQ170841, ITS: OQ158921, SSU: OQ168198, *tef1- α* : OR613421, *rpb2*: OR578553; KUMCC 21-0553: LSU: OQ170839, ITS: OQ158919, SSU: OQ168196; KUMCC 21-0559: LSU: OQ170840, ITS: OQ158920, SSU: OQ168197, *tef1- α* : OR613422, *rpb2*: OR578554; KUMCC 21-0605: LSU: OQ170842, ITS: OQ158922, SSU: OQ168199, *tef1- α* : OR613423, *rpb2*: OR578555.

Notes – Multi-gene phylogenetic analyses show that four strains of *Corylicola italica* (KUMCC 21-0563, KUMCC 21-0553, KUMCC 21-0559 and KUMCC 21-0605) grouped with type strains of *Corylicola italica* (MFLU 19-0500 and MFLUCC 20-0111) (Fig. 20). In a BLASTn search of NCBI GenBank, the closest match of the ITS sequences showed that the strains (KUMCC 21-0563, KUMCC 21-0553 and KUMCC 21-0559) are identical to *Corylicola italica* with 100% similarity (except KUMCC 21-0605). The holotype of *C. italica* and the new collections both have uni-loculate ascomata, central ostioles with minute papilla, cellular pseudoparaphyses, and cylindrical asci with short, furcate pedicels with single-septate, brown ascospores. Therefore, we identified our four collections as *Corylicola italica*. The collections are introduced here as the first records from *Quercus kingiana* (Fagaceae) and *Cryptocarya hainanensis* (Lauraceae) from China.

Palmiascoma gregariascomum Phookamsak & K.D. Hyde, Fungal Divers 72: 65 (2015)
Figs 22, 23

Index Fungorum number: IF550927; Facesofungi number: FoF00429

Saprobic on dead woody twigs of *Cryptocarya hainanensis*. Sexual morph: *Ascomata* 150–210 μm high $\times$ 130–200 μm diam., ($\bar{x}$ = 180 $\times$ 170 μm , n = 5), immersed to erumpent, solitary or scattered, coriaceous, globose to subglobose, black. *Ostioles* central. *Peridium* 16–26 μm wide, 3–4-layered, comprising brown cells of *textura angularis*. *Hamathecium* 1.2–1.8 μm wide, comprising cylindrical, branched, septate, cellular pseudoparaphyses embedded in a hyaline gelatinous matrix. *Asci* 45–57 $\times$ 6–8 μm ($\bar{x}$ = 52 $\times$ 7 μm , n = 20), 8-spored, bitunicate, cylindrical-clavate, straight or curved, apically rounded, short pedicellate. *Ascospores* 10.5–12.5 $\times$ 3–4 μm ($\bar{x}$ = 11.5 $\times$ 3.4 μm , n = 30), uniseriate, didymosporous, ellipsoidal, pale-brown to brown, 1-septate, constricted at the septum, guttulate, conical at both ends, thick-walled. Asexual morph: Coelomycetous. *Conidiomata* 110–220 μm high $\times$ 140–270 μm diam., ($\bar{x}$ = 150 $\times$ 190 μm , n = 5), scattered, immersed, coriaceous, globose to subglobose, brown to dark-brown, ostioles central, with minute papilla. *Conidiomata wall* 10–17 μm wide, 3–4-layered, composed of brown outer layers and hyaline inner layers of thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4.5–7.5 $\times$ 2.1–3.3 μm ($\bar{x}$ = 5.6 $\times$ 2.5 μm , n = 10), enteroblastic, phialidic, determinate, discrete, oblong to ampulliform, hyaline, smooth-walled, arising from stratum. *Conidia* 4–5 $\times$ 2–2.5 μm ($\bar{x}$ = 4.4 $\times$ 2.2 μm , n = 30), subglobose to oval, one-celled, aseptate, rounded ends, initially hyaline, becoming brown at maturity, thick-walled, guttulate.

Culture characters – Conidia germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apex. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, sparse mycelia, zonate, white at the margin, atrovirens at the center. Ascospores germinated on PDA within 24 h at room temperature (25 °C), Germ tubes produced from the apical cell of ascospore. Colonies on PDA, reaching 15 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, flat, gray at the margin, greyish white at the center, white between the margin and zonate; reverse, zonate, atrovirens at the margin, black at the center, yellow at the center and zonate.

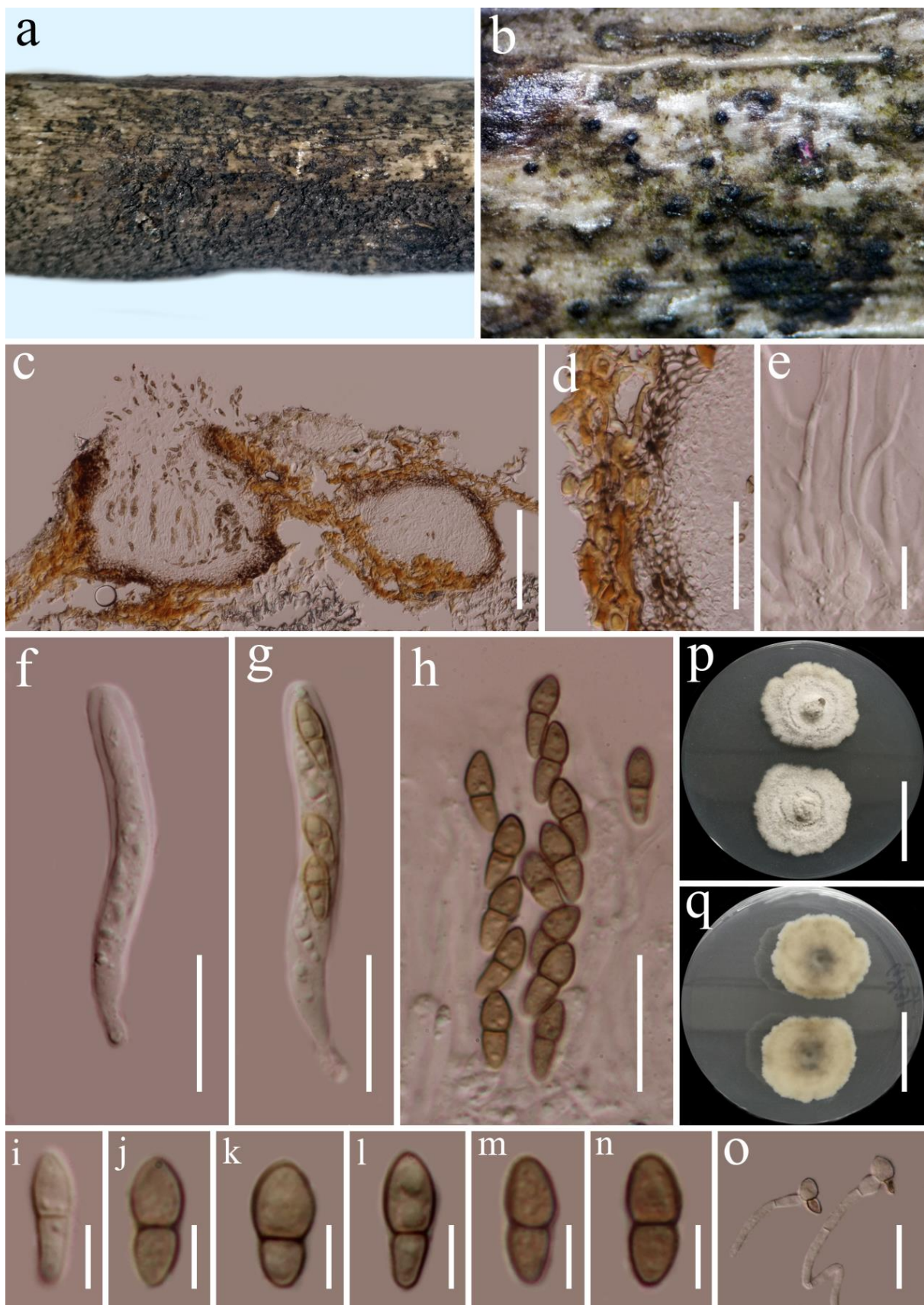


Figure 21 – *Corylicola italica* (HKAS 122733). a Material examined. b Appearance of ascomata on the host substrate. c Section of ascoma. d Peridium. e Pseudoparaphyses. f–h Asci. i–n Ascospores. o Germinated ascospores. p, q Culture characters on PDA (p = from above, q = from below). Scale bars: c = 100 μm, d = 30 μm, e, o = 10 μm, f–h = 20 μm, i–n = 5 μm, p, q = 30 mm.

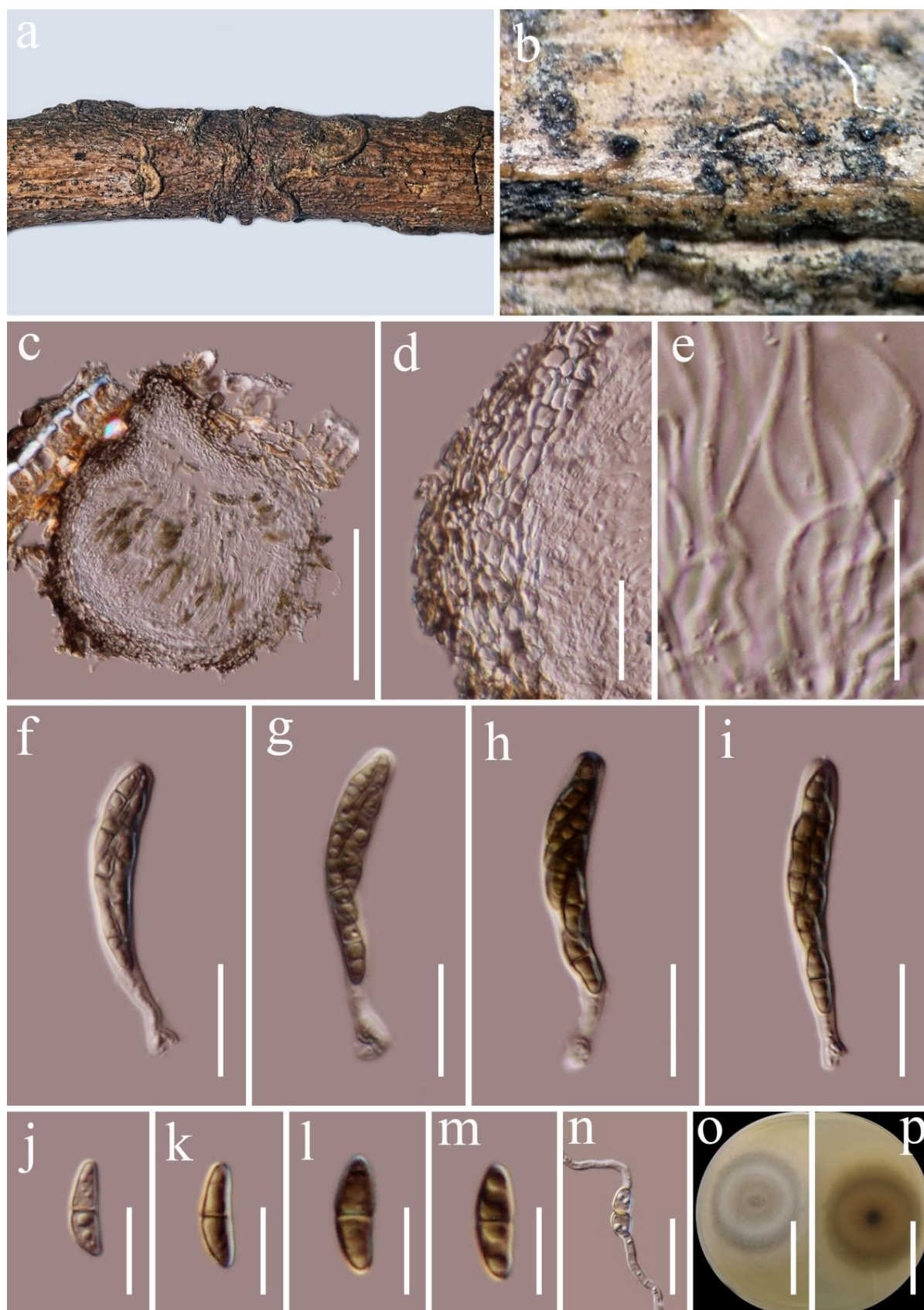


Figure 22 – *Palmiascoma gregariascomum* (HKAS 122755 sexual morph) a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–m Ascospores. n Germinated ascospore. o, p Culture characters on PDA (o = from above, p = from below). Scale bars: c = 100 μ m, d–i, n = 20 μ m, j–m = 10 μ m, o, p = 20 mm.

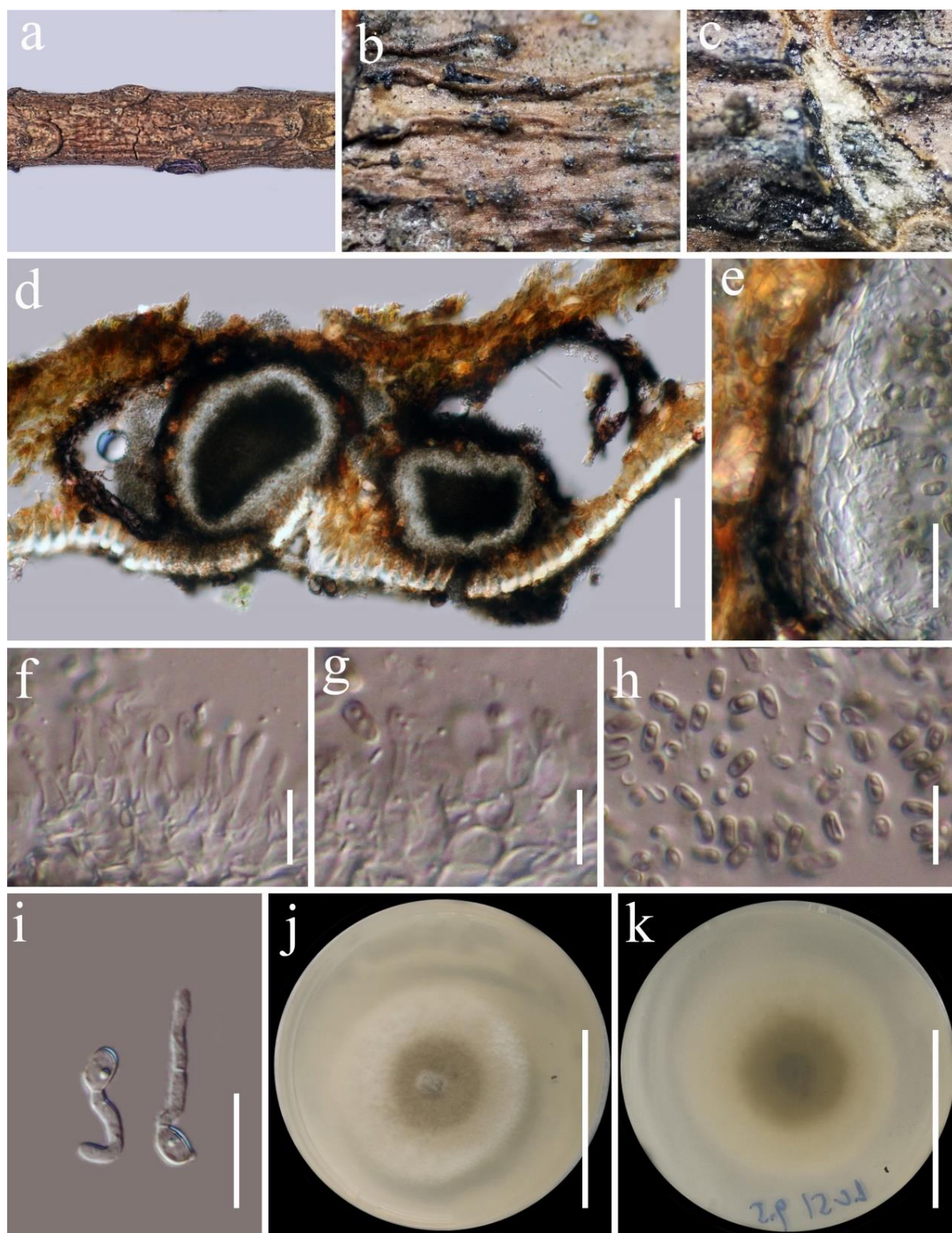


Figure 23 – *Palmiascoma gregariascomum* (HKAS 122754 asexual morph). a Material examined. b, c Conidiomata on the natural wood surface. d Sections through conidiomata. e Conidioma wall. f, g Conidiogenous cells and developing conidia. h Conidia. i Germinated conidia. j, k Culture characters on PDA. Scale bars: d = 100 μ m, e = 30 μ m, f–i = 20 μ m, j, k = 30 mm.

Material examined – China, Yunnan Province, Lincang, on dead woody twigs of *Cryptocarya hainanensis* (Lauraceae), 11 August 2020, G.C. Ren, LC51 (HKAS 122754), living culture KUMCC 21-0617; LC52 (HKAS 122755), living culture KUMCC 21-0618.

Known distribution – Dead fronds of palm, dead twigs of *Rosa* sp. (Rosaceae) and dead branches of *Eucalyptus* sp. (Myrtaceae) in Thailand (Liu et al. 2015, Hongsanan et al. 2020), dead woody twigs of *Cryptocarya hainanensis* (Lauraceae) in China (This study).

GenBank numbers – KUMCC 21-0617: LSU: OQ170843, ITS: OQ158923, SSU: OQ168200, *tef1-α*: OR613424, *rpb2*: OR578556; KUMCC 21-0618: LSU: OQ170844, ITS: OQ158924, SSU: OQ168201, *tef1-α*: OR613425, *rpb2*: OR578557.

Notes – *Palmiascoma gregariascomum* was introduced from Thailand with both asexual and sexual morphs (Liu et al. 2015). The sexual morph occurred on a dead frond of a palm, and the asexual morph was found on dead twigs of *Rosa* sp. (Rosaceae) and dead branches of *Eucalyptus* sp. (Myrtaceae) (Hongsanan et al. 2020, Jayawardena et al. 2022). The new collections (HKAS 122754 and HKAS 122755) and the type material (MFLU 11-0211 and asexual morph in culture MFLUCC 11-0175, Liu et al. 2015) have similar morphological characters. In addition, there are also no phylogenetic divergences among the strains KUMCC 21-0617 and KUMCC 21-0618, compared to the ex-type strain of *P. gregariascomum* (Fig. 20). Therefore, our new collections are introduced here as the first record of *P. gregariascomum* from *Cryptocarya hainanensis* (Lauraceae) in China.

Palmiascoma qujingense Monkai & Phookamsak, in Monkai, Wanasinghe, Jeewon, Promputtha & Phookamsak, Mycol. Progr. 20: 727 (2021) Fig. 24

Index Fungorum number: IF556132; Facesofungi number: FoF09505

Saprobic on dead woody twigs of *Myristica yunnanensis*. Sexual morph: *Ascomata* 280–400 µm high, 200–300 µm wide ($\bar{x} = 322.1 \times 258.4$ µm, $n = 10$), clustered or scattered, immersed to semi-immersed, slightly erumpent, conical to subglobose or irregular in shape, glabrous, black, short-papillate, ostiolate. *Peridium* 15–40 µm wide, thin to thick-walled, of unequal thickness, slightly thick at sides, comprising dark brown cells of *textura angularis*. *Hamathecium* of dense, 1.5–3 µm wide, hyaline, septate, branched, cellular pseudoparaphyses, anastomosing above the asci, embedded in a mucilaginous matrix. *Asci* 60–80 × 9–10 µm ($\bar{x} = 69.6 \pm 6 \times 9.6 \pm 0.8$ µm, $n = 20$), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short pedicellate, apically rounded, with a minute ocular chamber. *Ascospores* 12–16 × 4.5–5.5 µm ($\bar{x} = 14.1 \pm 1.1 \times 4.6 \pm 0.5$ µm, $n = 25$), overlapping 1–2-seriate, clavate to ellipsoidal, slightly curved, pale yellowish when young, becoming brown to dark brown at maturity, 1-septate, slightly constricted at the septum, upper part slightly wider, rough-walled, echinulate, lacking a mucilaginous sheath (Monkai et al. 2021). Asexual morph: Coelomycetous. *Conidiomata* 90–250 µm high × 80–150 µm diam., ($\bar{x} = 170 \times 130$ µm, $n = 5$), scattered, immersed, coriaceous, globose to subglobose, brown to dark-brown. *Conidiomatal wall* 15–45 µm thick, 3–4 layered, composed of brown outer layers and hyaline inner layers of thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–6 × 3–4 µm ($\bar{x} = 4.8 \times 3.1$ µm, $n = 10$), enteroblastic, phialidic, determinate, discrete, oblong to ampulliform, hyaline, smooth-walled, arising from the stratum. *Conidia* 4–6 × 2–3 µm ($\bar{x} = 4.6 \times 2.4$ µm, $n = 30$), straight, initially hyaline, becoming brown at maturity, subglobose to oval, one-celled, rounded ends, thick-walled, guttulate.

Culture Characters – Conidia germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apex. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, sparse mycelia, zonate, white at the margin, atrovirens at the center.

Material examined – China, Yunnan Province, Xishuangbanna, on dead woody twigs of *Myristica yunnanensis* (Myristicaceae), 15 December 2019, G.C. Ren, XS36 (HKAS 122889), living culture KUMCC 21-0678.

Known distribution – On dead twigs of *Fagaceae* sp. in China (Monkai et al. 2021), branch blight pathogen of *Juglans regia* (Juglandaceae) in China (Wang et al. 2022), on dead woody twigs of *Myristica yunnanensis* (Myristicaceae) in China (This study).

GenBank numbers – LSU: OQ170845, ITS: OQ158925, *tef1-α*: OR613426.

Notes – Phylogenetic analyses show that our strain KUMCC 21-0678 grouped within *Palmiascoma qujingense* with 100% ML bootstrap support and 1.00 BYPP value (Fig. 20). The

type strain of *P. qujingense* (KUMCC 19-0201) was only described from the sexual morph (Monkai et al. 2021), and later Wang et al. (2022) introduced both sexual and asexual morphs of *P. qujingense*. A BLASTn search of the ITS sequence, our strain showed 100% similarity to *P. qujingense* and the closest match of the *tef1-α* sequence with 98.5% similarity was *P. qujingense* (CAUCC 21-0013). *Palmiascoma qujingense* (CAUCC 21-0013) was identified as a disease of *Juglans regia* (walnut species) (Wang et al. 2022). The morphology of the new isolate is similar to the description of *P. qujingense* (CAUCC 21-0013) provided by Wang et al. (2022). Therefore, we identified our collections as asexual morphs of *P. qujingense* based on morphological characterization and phylogenetic analyses and introduced *P. qujingense* as a saprobic fungi from China.

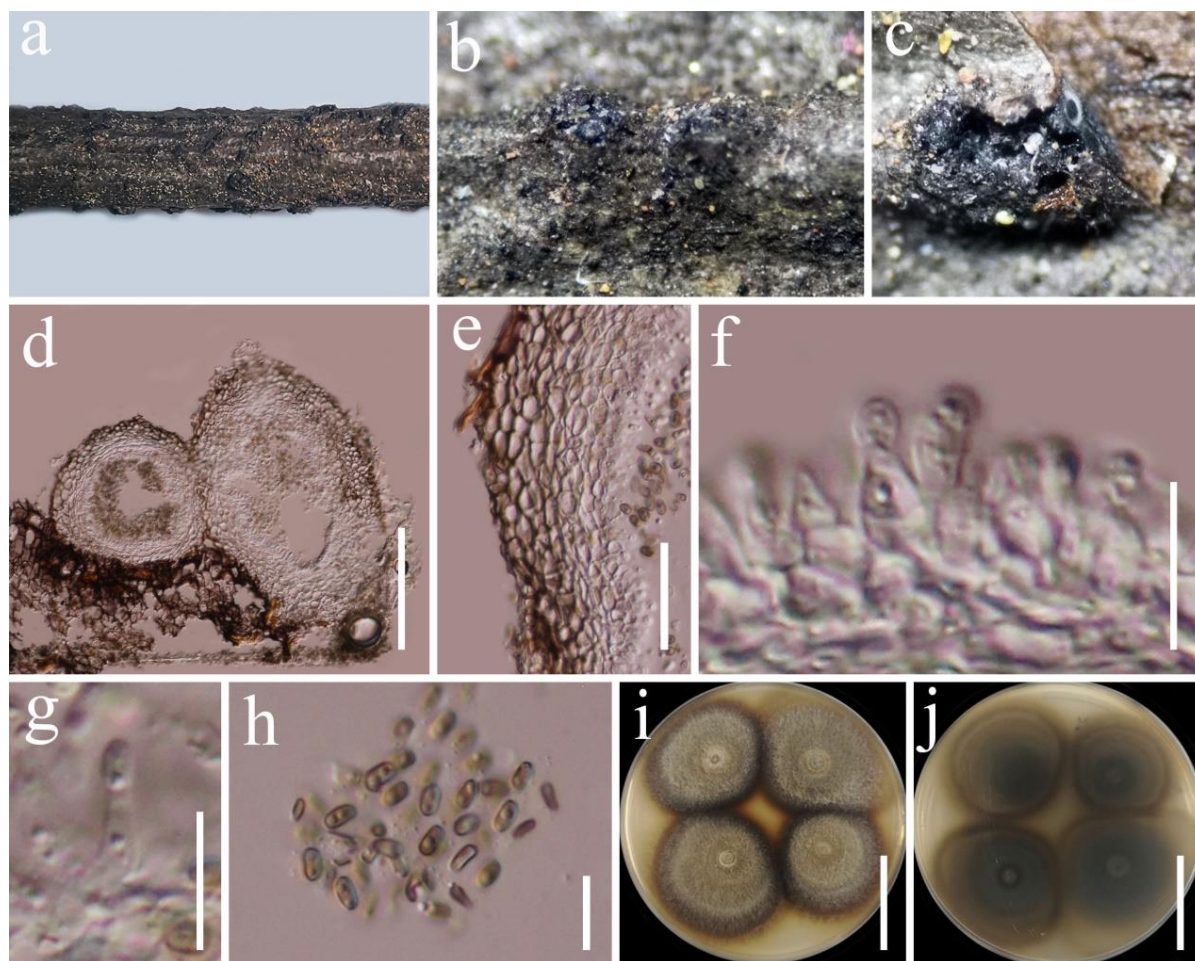


Figure 24 – *Palmiascoma qujingense* (HKAS 122889). a Material examined. b, c Conidiomata on the natural wood surface. d Sections through conidiomata. e Conidiomata wall. f, g Conidiogenous cells and developing conidia. h Conidia. i, j Culture characters on PDA. Scale bars: d = 100 μ m, e = 30 μ m, f–h = 10 μ m, i, j = 30 mm.

Camarosporidiellaceae Wanas., Wijayaw., Crous & K.D. Hyde, Stud. Mycol. 87: 216 (2017)

Camarosporidiellaceae was introduced by Wanasinghe et al. (2017) to accommodate *Camarosporidiella* and comprises a single genus. This family is mainly characterized by its coelomycetous asexual morph, which comprises pycnidial conidiomata, with papillate single ostiole; enteroblastic, annellidic, integrated to discrete, doliiform, lageniform or cylindrical, hyaline conidiogenous cells; pale to dark brown conidia that are phragmosporous to muriform and mostly ellipsoidal (Hongsanant et al. 2020). The sexual morphs of this family are characterized by gregarious to solitary, globose to subglobose ascomata that have a papillate, central ostiole; peridium containing cell layers of textura angularis; cylindrical, (2–)4–8-spored asci with 1-seriate,

ellipsoidal, brown, muriform ascospores (Wanasinghe et al. 2017, Hongsanan et al. 2020). In this study, we report a new species of *Camarosporidiella* from *Rhododendron rubiginosum* in China.

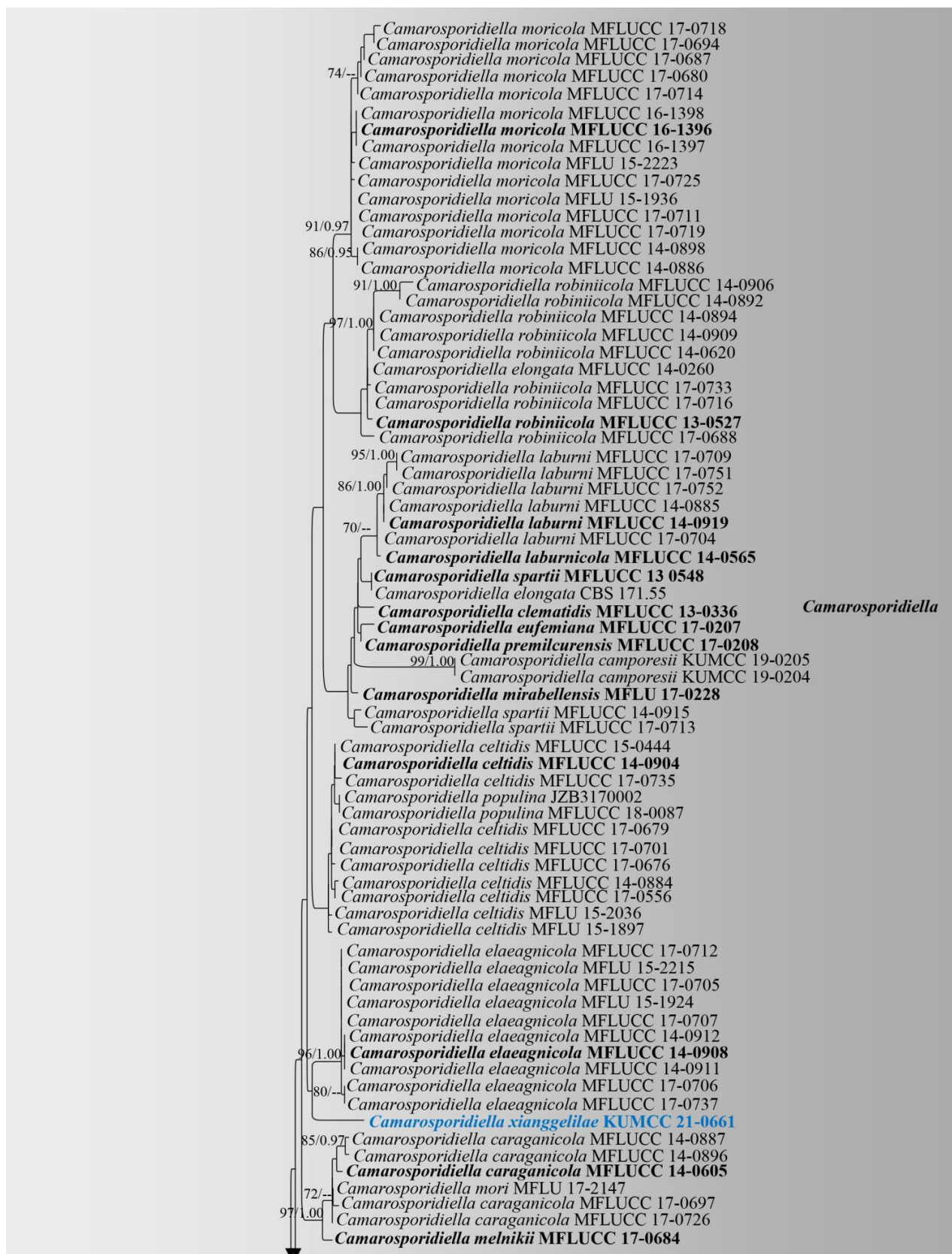


Figure 25 – Phylogram generated from ML analysis based on SSU, LSU, ITS, and *tef1-α* sequence data, representing *Camarosporidiellaceae*. Related sequences are obtained following Hyde et al. (2020b). Ninety-nine strains are included in the combined analyses, which comprise 3310

characters for SSU, LSU, ITS, and *tef1-α* alignment. Two strains of *Staurosphaeria lycii* (MFLUCC 17-0210 and MFLUCC 17-0211) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -7756.134870 is presented. The matrix had 353 distinct alignment patterns with 7.05% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242018, C = 0.243119, G = 0.267054, T = 0.247809; substitution rates AC = 1.456305, AG = 3.573390, AT = 2.277000, CG = 0.814859, CT = 7.520960, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

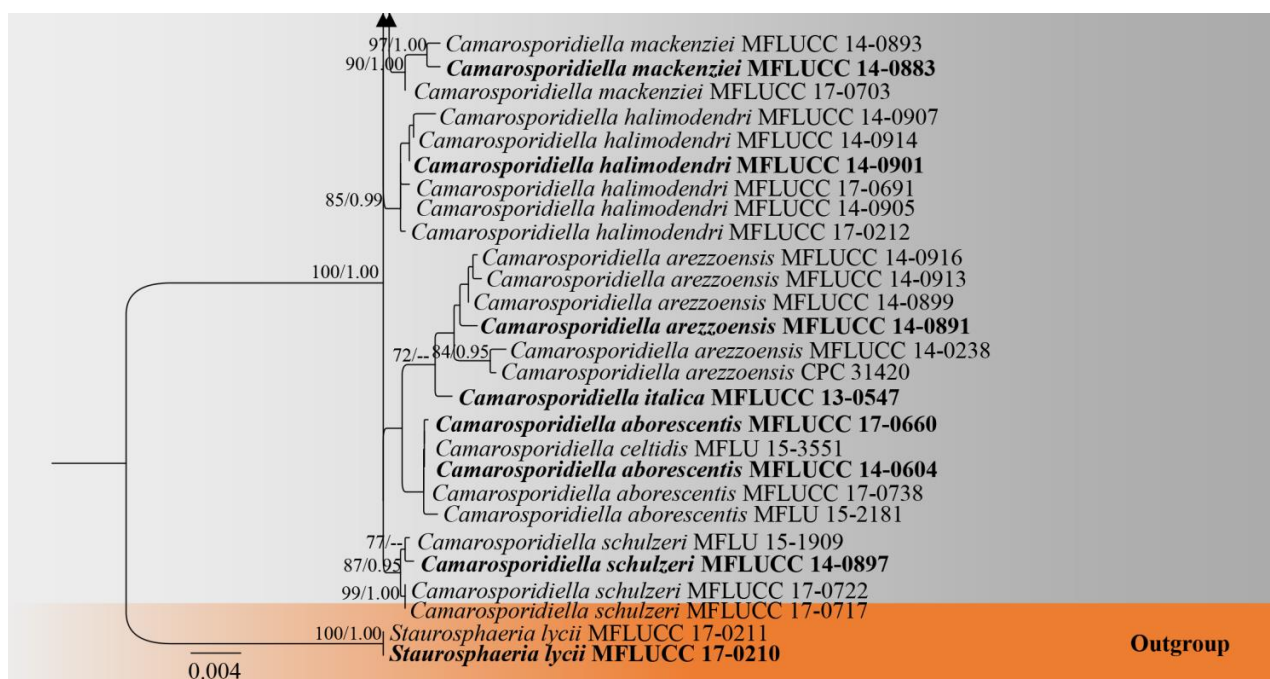


Figure 25 – Continued.

Camarosporidiella xianggelilaensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 26

Index Fungorum number: IF901349; Facesofungi number: FoF13878

Holotype – HKAS 122771

Etymology – The specific epithet reflects Xianggelila, from where the holotype was collected.

Saprobic on dead twigs of *Rhododendron rubiginosum*. Sexual morph: *Ascomata* 480–620 µm high, 560–690 µm diam., ($\bar{x}$ = 530 × 610 µm, n = 5), black, superficial to semi-immersed, gregarious, subglobose to globose, coriaceous, clustered beneath the host periderm, unilocular, with a central ostiole. *Peridium* 50–160 µm wide, thin at the base, thick at the sides, composed of dark brown outer layers and inner layers comprising hyaline cells of *textura angularis*, thick-walled. *Hamathecium* 2.5–3.3 µm wide, comprising filamentous, branched, septate pseudoparaphyses embedded in a gelatinous matrix. *Asci* 200–290 × 15–17.5 µm ($\bar{x}$ = 241 × 16 µm, n = 20), 4–8-spored, bitunicate, fissitunicate, cylindrical, slightly curved, with a short furcate to truncate pedicel, apically rounded. *Ascospores* 37–50 × 9.6–12.6 µm ($\bar{x}$ = 42 × 11 µm, n = 30), uniseriate, muriform, fusiform, conical and pointed at the ends, 6–9-transversely septate, with 1–2 vertical septa, slightly constricted at the middle septum, slightly curved or straight, initially hyaline, becoming brown when mature, thick-walled, guttulate, not surrounded by a mucilaginous sheath. Asexual morph: Undetermined.

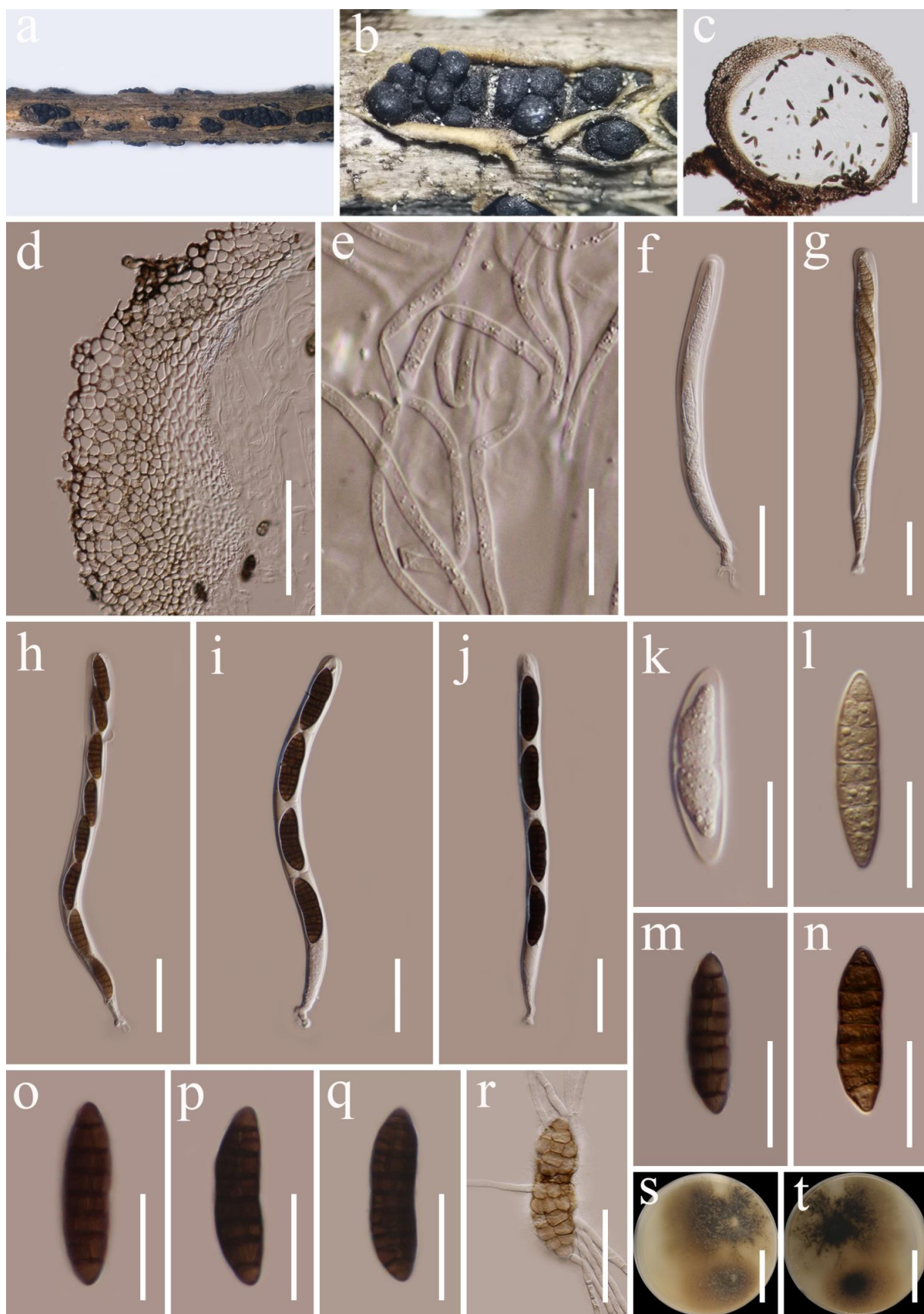


Figure 26 – *Camarosporidiella xianggelilaensis* (HKAS 122771, holotype). a, b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–j Asci. k–q Ascospores. r Germinated ascospore. s, t Culture characters on PDA (s = from above, t = from below). Scale bars: c = 200 μ m, d = 100 μ m, e = 20 μ m, f–j = 50 μ m, k–r = 30 μ m, s, t = 20 μ m.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from ascospores. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, irregular or rhizoid colonies, filamentous, flat, surface rough with rhizoid edge, grey with greyish white spots; reverse, black.

Material examined – China, Yunnan Province, Diqing, Xianggelila, on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae), 1 September 2020, G.C. Ren, TM13 (HKAS 122771, holotype), ex-type living culture KUMCC 21-0661.

GenBank numbers – SSU: OQ168202, LSU: OQ170846, ITS: OQ158926, *tef1-α*: OR613427.

Notes – Our phylogenetic analyses show that *Camarosporidiella xianggelilaensis* (KUMCC 21-0661) clustered sister to ten strains of *C. elaeagnicola* with 55% ML bootstrap support and 0.75 BYPP value (Fig. 25). *Camarosporidiella xianggelilaensis* was recorded from its sexual morph, while *C. elaeagnicola* has only been reported from its asexual morph from *Elaeagnus angustifolia* in Russia (Wanasinghe et al. 2017). Therefore, we are unable to compare the morphologies between these two species. *Camarosporidiella xianggelilaensis* shared similar morphology with other sexual morphs of *Camarosporidiella* in having superficial to semi-immersed, gregarious, globose, black, unilocular conidiomata; thick-walled peridium; branched, septate hamathecium; bitunicate, fissitunicate, cylindrical asci, uniseriate, muriform, fusiform ascospores (Wanasinghe et al. 2017) however it differed in having 4–8-spored asci. In the sequence comparison for the ITS region between *Camarosporidiella xianggelilaensis* (KUMCC 21-0661) and *C. elaeagnicola* (MFLUCC 14-0908) showed a 2.1% (11/523 bp, without gaps) base pair difference in ITS region, 1.3% (12/923 bp, without gaps) base pair difference in the *tef1-α* region. Therefore, based on morphological characterization and phylogenetic analyses, *Camarosporidiella xianggelilaensis* is introduced as a new species.

Cucurbitariaceae G. Winter, Rabenhorst's Kryptogamen-Flora, Pilze – Ascomyceten 1(2): 308 (1885)

Cucurbitariaceae was introduced by Winter (1885) and typified by *Cucurbitaria*. Currently, 13 genera are accepted in this family (Wijayawardene et al. 2022). This family is mainly characterized by its sexual morph, which has globose to subglobose, uni-loculate ascomata; black ostiole with inconspicuous or papillate to cylindrical; multi-layered peridium with light brown to reddish-brown; septate hamathecium, cellular pseudoparaphyses; bitunicate, fissitunicate, cylindrical to clavate asci with furcate pedicel and minute ocular chamber; 1-seriate, or partially overlapping, ellipsoidal, golden brown to dark brown, multi-septate, muriform ascospores (Hongnan et al. 2020). The asexual morphs of this family are coelomycetous, phoma- or pyrenochaeta-like (Doilom et al. 2013, Jaklitsch et al. 2018). In this study, we report on a new species of *Cucurbitaria* from *Rhododendron rubiginosum* in China.

Cucurbitaria lijiangensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 28

Index Fungorum number: IF901350; Facesofungi number: FoF13879

Holotype – HKAS 122716

Etymology – The specific epithet reflects Lijiang, from where the holotype was collected.

Saprobic on dead twigs of *Rhododendron rubiginosum*. Sexual morph: *Ascomata* 420–510 µm high, 400–450 µm diam., ($\bar{x}$ = 470 × 430 µm, n = 5), clustered, immersed to erumpent through the host periderm, visible as raised, globose to subglobose, uni-loculate, coriaceous, black, ostiolate. *Ostioles* central, 150–200 µm high, 140–170 µm diam., ($\bar{x}$ = 171 × 161 µm, n = 5). *Peridium* 25–85 µm wide, sometime thick at the base, comprising 4–9 layers, composed of dark outer layers, inner layers comprising hyaline to reddish-brown, flattened, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, comprising numerous, branched, filamentous, septate, hyaline pseudoparaphyses. *Asci* 170–225 × 24–31 µm ($\bar{x}$ = 200 × 27.3 µm, n = 30), 6–8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short-pedicellate, apically rounded, with a minute ocular chamber. *Ascospores* 33–43 × 14–19 µm ($\bar{x}$ = 39 × 17 µm, n = 40), uniseriate, muriform, ellipsoidal to broadly fusiform, hyaline to pale brown when young, becoming dark

brown at maturity, paler at the extreme ends, with 6–15 transverse septa and 2–6 longitudinal septa, slightly constricted at the central septum, lower part larger than the upper part, guttulate in each cell, ends remaining cone-shaped, with acute ends. Asexual morph: Undetermined.

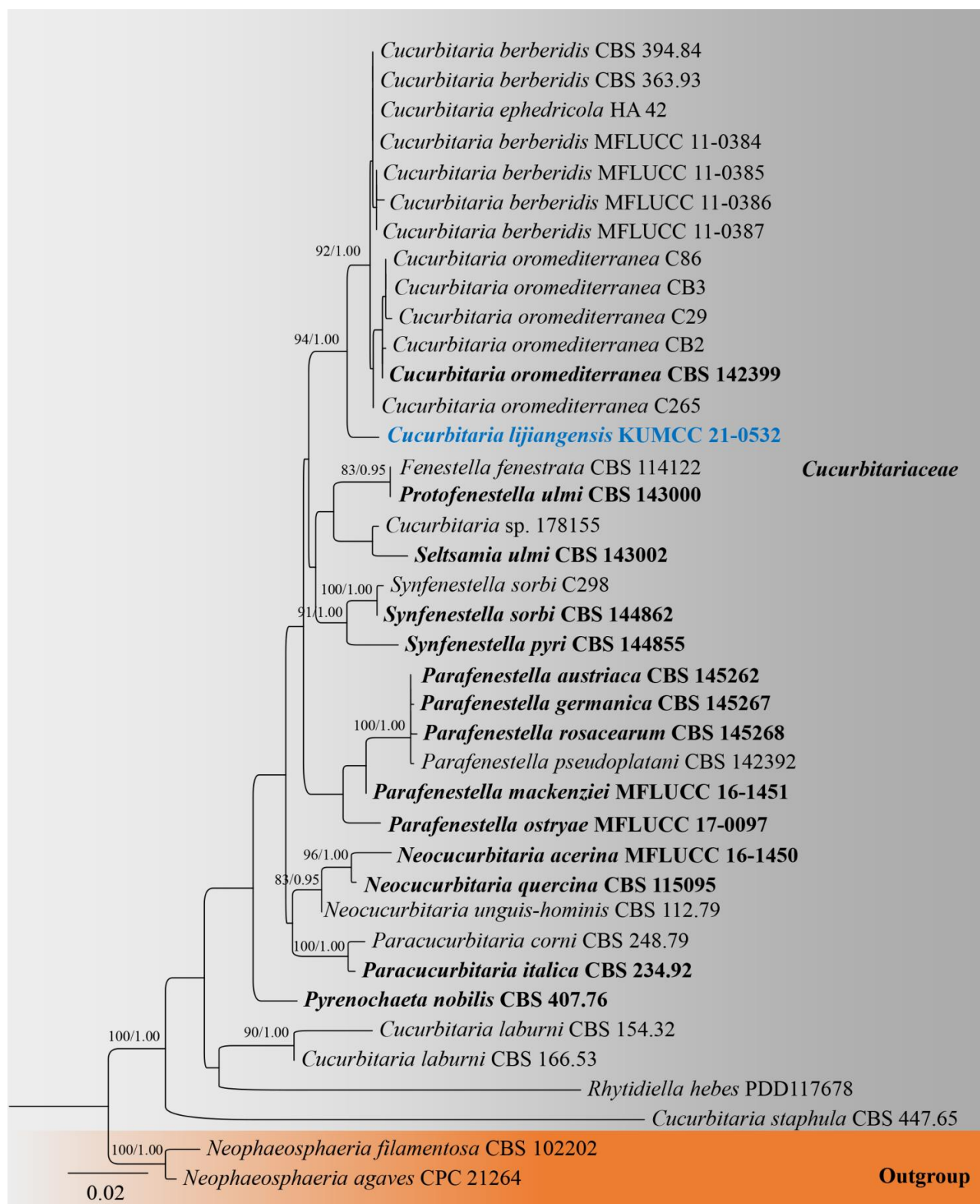


Figure 27 – Phylogram generated from ML analysis based on SSU, LSU, and ITS sequence data representing *Cucurbitariaceae*. Related sequences obtained following Jayawardena et al. (2019) and Dayarathne et al. (2020). Thirty-nine strains are included in the combined analyses, which comprise 1645 characters for SSU, LSU, and ITS alignment. *Neophaeosphaeria agaves* (CPC 21264) and *N. filamentosa* (CBS 102202) were used as the outgroup taxa. The best-scoring

RAxML tree with a final likelihood value of -5781.224323 is presented. The matrix had 285 distinct alignment patterns with 25.91% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245250, C = 0.217613, G = 0.282353, T = 0.254784; substitution rates AC = 2.091807, AG = 3.145516, AT = 3.237090, CG = 0.505851, CT = 9.326419, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from every cell of the spore. Colonies on PDA, reaching 10–20 mm diameter after two weeks at 20–25 °C, mycelia superficial, irregular, grey to greenish brown, floccose, umbonate, flat, lobate edge; reverse, white, light yellow at center.

Material examined – China Yunnan Province, Lijiang, on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae), 30 August 2020, G.C. Ren, DQ11 (HKAS 122716, holotype), ex-type living culture KUMCC 21-0532.

GenBank numbers – SSU: OQ168203, LSU: OQ170847, ITS: OQ158927, *tef1-α*: OR613428.

Notes – In our phylogenetic analysis, *Cucurbitaria lijiangensis* clustered basal to the strains of *C. oromediterranea* and *C. berberidis* with 94% ML bootstrap support and 1.00 BYPP value (Fig. 27). The BLASTn search of the ITS sequence showed that close match of the ITS sequence with 97.25% and 96.89% similarities with *C. oromediterranea* (CB2) and *C. berberidis* (CB, CB 39 and CBS 394.84), respectively. *Cucurbitaria berberidis* is the type species of *Cucurbitaria*, and many generic synonyms are listed under *Cucurbitaria* (Doilom et al. 2013, Species Fungorum 2024). *Cucurbitaria lijiangensis* differs from *C. oromediterranea* and *C. berberidis* in having large ascospores (Table 3) and clearly shows changing the transverse septa with maturity. Furthermore, ascomata of *C. oromediterranea* and *C. berberidis* are seated on a thick-walled basal pseudostroma; however, in *C. Lijiangensis*, a basal pseudostroma is absent (Doilom et al. 2013, Jaklitsch et al. 2018).

Table 3 Synopsis of *Cucurbitaria berberidis*, *C. lijiangae* and *C. oromediterranea* species with morphological features discussed in this study.

Species	Ascomata (µm)	Asci (µm)	Ascospores			Reference
			Size (µm)	Transverse septa	Longitudinal septa	
<i>Cucurbitaria berberidis</i>	500–650 high, 380–595 diam.	180–200 × 15–20	23–32 × 9–14	7–9	3–4	Doilom et al. (2013)
<i>C. lijiangensis</i>	420–510 high, 400–450 diam.	170–225 × 24–31	33–43 × 14–19	6–15	2–6	This study
<i>C. oromediterranea</i>	500–630 high, 430–620 diam.	165–225 × 16–20	25–33 × 11.3–14.5	7–8	2–4	Jaklitsch et al. (2018)

Didymellaceae Gruyter, Aveskamp & Verkley, Mycol. Res. 113 (4): 516 (2009)

Didymellaceae was introduced by de Gruyter et al. (2009) and this is the largest family in *Pleosporales* and includes species that inhabit a wide range of ecosystems (Chen et al. 2017). *Didymellaceae* is mainly characterized by its sexual morph, which has immersed, separate or gregarious, globose to flattened, ostiolate pseudothecia with 2–5(–8) layers of pseudoparenchymatal cells; bitunicate, cylindrical to clavate or saccate; hyaline, or brownish, 1-septate spores (didymospores) or multi-septate dictyospores (Hongsanan et al. 2020). The asexual morphs of this family are coelomycetous, which are characterized by immersed, or semi immersed, uni-locular, globose conidiomata; enteroblastic, phialidic, doliiform to lageniform, ampulliform or cylindrical, hyaline conidiogenous cells; ellipsoid, cylindrical, fusiform, pyriform or globose, hyaline or pigmented, septate or aseptate conidia (Chen et al. 2015, 2017, Hongsanan et al. 2020).

Currently, 44 genera are accepted in this family (Wijayawardene et al. 2022). In this study, we report on a new species of *Stagonosporopsis* and a new host record of *Boeremia linicola* from *Castanopsis mekongensis*.

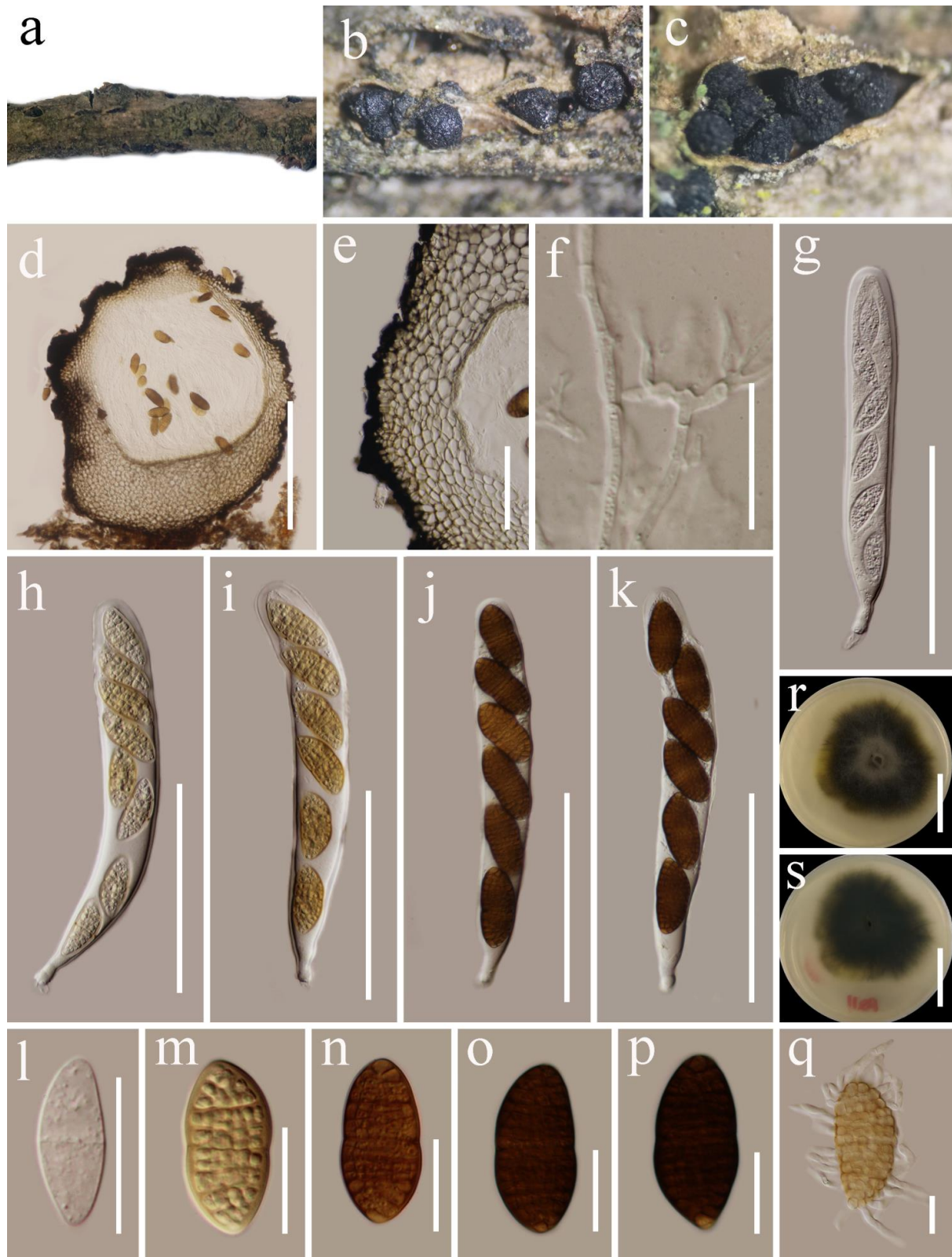


Figure 28 – *Cucurbitaria lijiangensis* (HKAS 122716, holotype). a The host twig. b, c Appearance of ascomata on host substrate. d Section of ascoma. e Peridium. f Pseudoparaphyses. g–k Asci. l–p Ascospores. q Germinated ascospore. r, s Culture characters on PDA (r = from above, s = from below). Scale bars: d = 250 μ m, e = 50 μ m, f = 20 μ m, g–k = 100 μ m, l–q = 20 μ m, r, s = 30 mm.

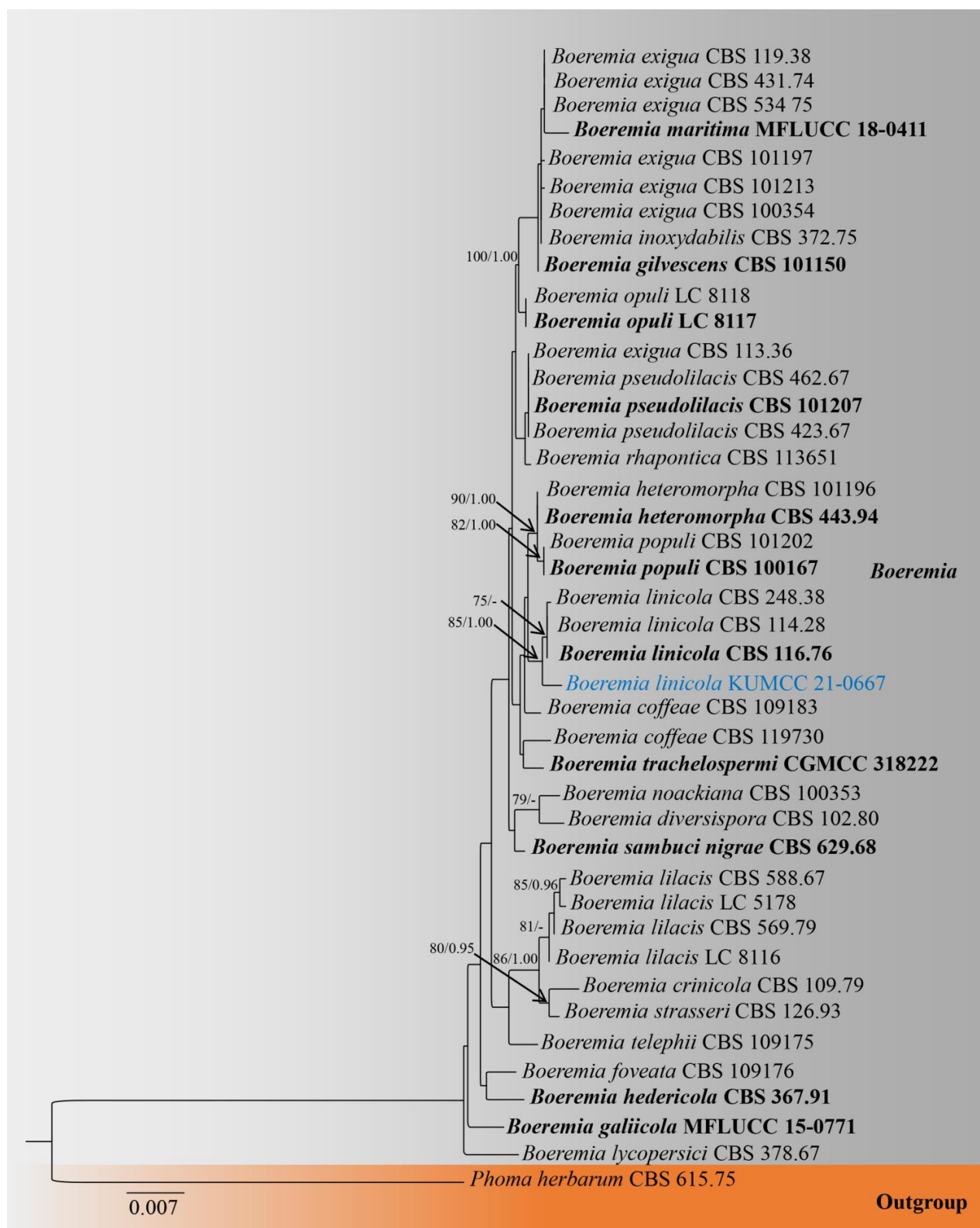


Figure 29 – Phylogram generated from ML analysis based on LSU, ITS, *rpb2* and *tub2* sequence data representing *Boeremia*. Related sequences are obtained following Jayawardena et al. (2019) and Dayaratne et al. (2020). Forty-two strains are included in the combined analyses, which comprise 2746 characters for LSU, ITS, *rpb2*, and *tub2* alignment. *Phoma herbarum* (CBS 615.75) was used as the outgroup taxon. The best-scoring RAXML tree with a final likelihood value of -5948.314119 is presented. The matrix had 234 distinct alignment patterns with 15.71% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242542, C = 0.237458, G = 0.272062, T = 0.247938; substitution rates AC = 1.303992, AG = 3.475548, AT =

1.174892, CG = 0.799946, CT = 10.609598, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

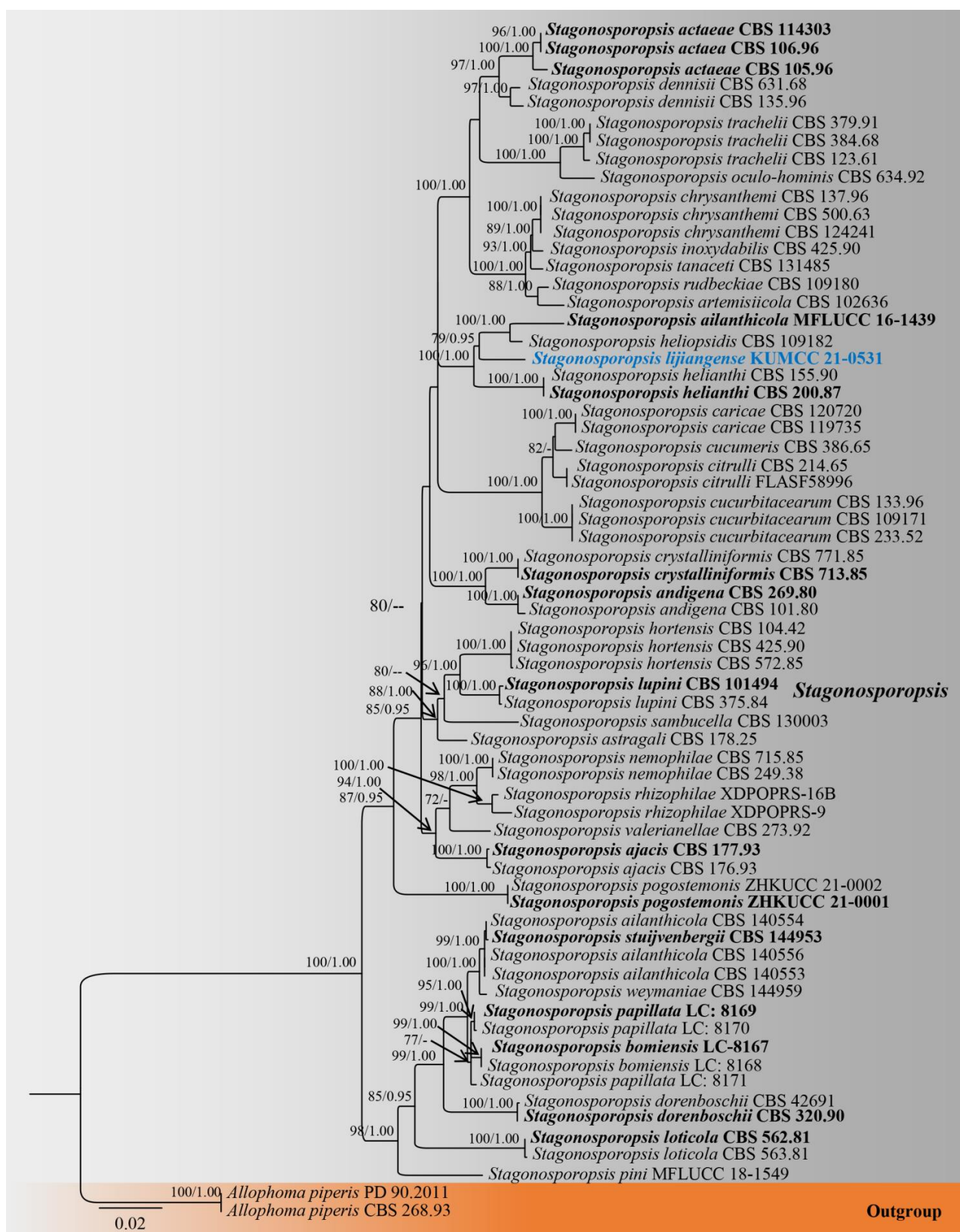


Figure 30 – Phylogram generated from ML analysis based on LSU, ITS, *rpb2*, and *tub2* sequence data representing *Stagonosporopsis*. Related sequences are obtained following Dong et al. (2021).

Sixty-six strains are included in the combined analyses, which comprise 2388 characters for LSU, ITS, *rpb2*, and *tub2* alignment. Two *Allophoma piperis* strains (PD 90.2011 and CBS 268.93) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -9973.267368 is presented. The matrix had 530 distinct alignment patterns, with 4.37% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244019, C = 0.238910, G = 0.272866, T = 0.244205; substitution rates AC = 2.397927, AG = 5.305500, AT = 1.951399, CG = 0.899750, CT = 14.000885, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Boeremia linicola (Naumov & Vassiljevsky) Jayaward., Jayasiri & K.D. Hyde, in Jayawardena et al., Fungal Diversity 94 :51 (2019) Fig. 31

Index Fungorum number: IF555807; Facesofungi number: FoF13880

Saprobic on dead woody twigs of *Castanopsis mekongensis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 110–130 µm high × 140–160 µm diam., ($\bar{x}$ = 120 × 150 µm, n = 5), scattered, immersed, coriaceous, globose to subglobose, brown to dark-brown. *Conidiomatal wall* 10–18 µm wide, 2–3-layered, composed of brown outer layers and hyaline inner layers comprising thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.7–5 × 2.9–4.1 µm ($\bar{x}$ = 4.2 × 3.6 µm, n = 10), enteroblastic, phialidic, determinate, discrete, ampulliform, hyaline, smooth-walled, arising from stratum. *Conidia* 5.3–7 × 2.4–3.4 µm ($\bar{x}$ = 6.3 × 2.9 µm, n = 30), straight, hyaline, oval, one-celled, aseptate, rounded ends, thick-walled, guttulate.

Culture Characters – Conidia germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the ends of conidia. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, surface rough with sparse mycelium, cultures atrovirens with white; reverse, atrovirens.

Material examined – China, Yunnan Province, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Castanopsis mekongensis* (Fagaceae), 23 March 2020, G.C. Ren, LGY07 (HKAS 122772), living culture KUMCC 21-0667.

Known distribution – see Table 4.

GenBank numbers – LSU: OQ170848, ITS: OQ158928, SSU: OQ168204, *rpb2*: OR578558, *tub2*: OR578551.

Notes – The type strain of *Boeremia linicola* (CBS 116.76) was identified from living stems of *Linum usitatissimum* from Russia and introduced without morphological descriptions. Qian et al. (2023) described *Boeremia linicola* as hyphomycetous oatmeal agar (OA) medium. The asexual morphs of *B. linicola* are characterized by hyaline, ampulliform to doliiiform conidiogenous cells and ellipsoidal to cylindrical, piriform, columnar, drop-shaped, dumbbell-shaped or oval, hyaline, thin-walled, smooth, aseptate conidia with guttules (Guan et al. 2021, Qian et al. 2023). Our isolate shares similar characteristics to *B. linicola* in having ampulliform, hyaline conidiogenous cells and hyaline, oval, one-celled, aseptate conidia with guttules. Furthermore, the morphology of our collection is compared to the generic description and our isolate shares similar characteristics to *Boeremia* (Aveskamp et al. 2010). In the phylogenetic analysis, our new isolate clustered with *Boeremia linicola* strains (CBS 116.76, CBS 114.28 and CBS 248.38 with 85% ML bootstrap support and 1.00 BYPP value (Fig. 29). Based on morphological characteristics and phylogenetic results, our isolates were identified as *B. linicola*. *Boeremia linicola* was reported as a pathogen from many important plant species (Irinyi et al. 2009, Aveskamp et al. 2010, Chen et al. 2015, Guan et al. 2021, Lee et al. 2022); however, in our study, it was isolated from *Castanopsis mekongensis* as a saprobe. This is the first report of *Boeremia linicola* from *Castanopsis mekongensis*. Based on its distribution, *Boeremia linicola* shows a very broad host range (Table 4).

Stagonosporopsis lijiangensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 32

Index Fungorum number: IF901351; Facesofungi number: FoF13881

Holotype – HKAS 122715

Etymology – The specific epithet reflects Lijiang, from where the holotype was collected.

Saprobic on dead twigs of *Quercus serrata*. Sexual morph: *Ascomata* 120–140 µm high, 110–160 µm diam., ($\bar{x}$ = 130 × 140 µm, n = 5), immersed to erumpent, solitary or scattered, globose to subglobose, uni-loculate, coriaceous, black, with short papilla. *Ostioles* central, short, slightly raised, 32–42 × 36–41 µm ($\bar{x}$ = 36 × 38 µm, n = 5). *Peridium* 8–12 µm wide, 2–3 layered, composed dark brown cells of *textura angularis*. *Hamathecium* 2.2–4.4 µm wide, comprising branched, septate, hyaline, cellular pseudoparaphyses, constricted at the septa, embedded in a gelatinous matrix. *Asci* 46–59 × 8–10 µm ($\bar{x}$ = 53 × 9 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric, slightly curved, with a broadest truncate pedicel, apically rounded. *Ascospores* 14–14.7 × 3.8–4.6 µm ($\bar{x}$ = 14.3 × 4.2 µm, n = 30), overlapping, 1–2-seriate, hyaline, fusiform, tapering towards rounded ends, straight to slightly curved, 1-septate, constricted at the septum, smooth-walled, guttules. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cell of ascospore. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, fimbriate, dense, flat, entire edge, surface rough, raised, grayish white; reverse, light brown.

Material examined – China, Yunnan Province, Lijiang, on dead woody twigs of *Quercus serrata* (Fagaceae), 30 August 2020, G.C. Ren, DQ10 (HKAS 122715, holotype), ex-type living culture KUMCC 21-0531.

GenBank numbers – LSU: OQ170849, ITS: OQ158929, SSU: OQ168205, *rpb2*: OR578559.

Notes – In our phylogenetic analysis, *Stagonosporopsis lijiangensis* clustered with *Stagonosporopsis ailanthicola* (MFLUCC 16-1439) and *S. heliopsidis* (CBS 109182), with 79% ML bootstrap support and 0.95 BYPP value (Fig. 30). However, these two species are only reported from their asexual morph (Aveskamp et al. 2010, Tibpromma et al. 2017, Boggess et al. 2022), and our isolation is recorded with its sexual morph. Therefore, we could not conduct a morphological comparison among these three collections. However, *S. lijiangensis* shares similar morphology with

Table 4 Known distribution of *Boeremia linicola* (Source: GenBank).

Isolate/Strain number	Country	Host
CBS 109.49	–	<i>Linum usitatissimum</i>
CBS 100.15	–	<i>Clematis paniculata</i>
CBS 112.28	Russia	<i>Linum usitatissimum</i>
CBS 113.28	The Netherlands	<i>Linum usitatissimum</i>
CBS 114.28	The Netherlands	<i>Linum usitatissimum</i>
CBS 116.76	The Netherlands	<i>Linum usitatissimum</i>
CBS 248.38	The Netherlands	<i>Nemophila insignis</i>
CBS 289.29	Japan	–
CBS 729.68	Brazil	<i>Solanum melongena</i>
CBS 113651	Turkey	<i>Rhaponticum repens</i>
CWJ7	China	On the leaf of <i>Eleutherococcus sessiliflorus</i>
D/071	Hungary	<i>Linum usita-tissimum</i>
KUMCC 21-0667	China	<i>Castanopsis mekongensis</i>
MF-010-051(17.29)	Russia	<i>Arctium</i> sp.
PAPE-1, PAPE-2	China	<i>Atractylodes macrocephala</i>
TOPH-2001, TOPH-2008, TOPH-2014, TOPH-2015, TOPH-2018, TOPH-2019, TOPH-2020	South Korea	Stem and leaf rot of <i>Solanum lycopersicum</i>
Y3-1, Y3-2, Y3-3, Y3-4	China	On the leaf of <i>Trifolium repens</i> as pathogen
LYB-2, LYB-3	China	On the leaf of <i>Panax notoginseng</i>
CBS 100.15	–	<i>Clematis paniculata</i>

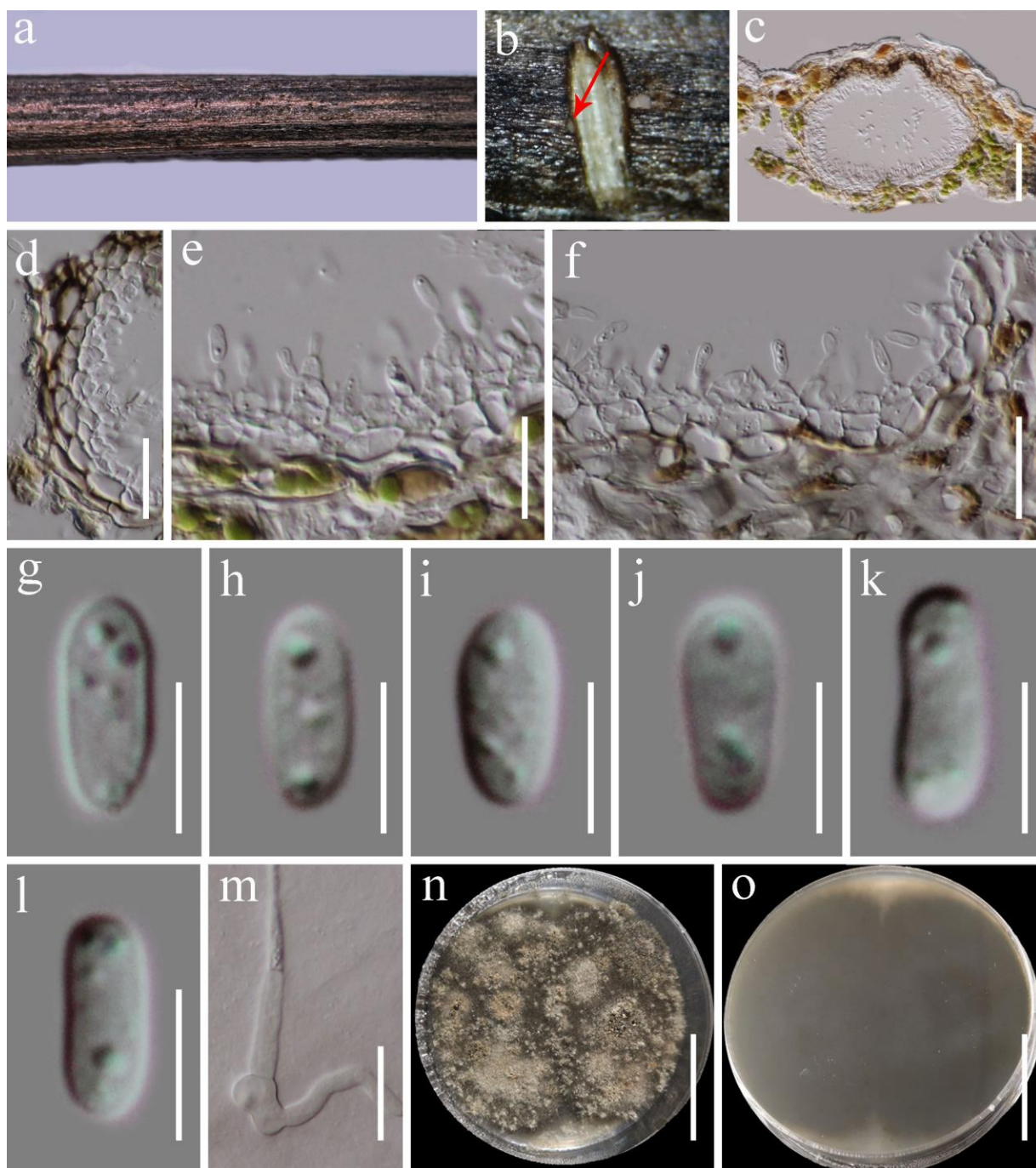


Figure 31 – *Boeremia linicola* (HKAS 122726). a Material examined. b Conidiomata on the natural wood surface. c Sections through conidioma. d Conidioma wall. e, f Conidiogenous cells and developing conidia. g–l Conidia. m Germinated conidium. n, o Culture characters on PDA (n = from above, o = from below). Scale bars: c = 50 μ m, d–f, m = 20 μ m, g–l = 5 μ m, n, o = 20 mm.

Stagonosporopsis in having globose to subglobose ascomata, cylindrical to subclavate, 8-spored, biseriate asci and fusiform or obovoid, 1-septate, guttulate ascospores (Aveskamp et al. 2010). Sequence comparison for the ITS region between *Stagonosporopsis lijiangensis* (KUMCC 21-0531) and *S. ailanthalicola* (MFLUCC 16-1439) showed a 2.9% (13/455 bp, without gaps) base pair difference in ITS region, 3.4% (20/595 bp, without gaps) base pair difference in *rpb2* region, 0.7% (6/873 bp, without gaps) base pair difference in LSU region. Additionally, comparison for the ITS region between *Stagonosporopsis lijiangensis* (KUMCC 21-0531) and *S. heliopsidis* (CBS 109182) showed a 1.2% (6/488 bp, without gaps) base pair difference in ITS region, 3.2% (19/595 bp, without gaps) base pair difference in *rpb2* region, 0.6% (5/876 bp, without gaps) base pair

difference in LSU region. Based on the evidence from morphology and phylogeny, we introduced *S. lijiangensis* as a new species in *Stagonosporopsis*. *Stagonosporopsis* species are recorded from different host plant families (Amaranthaceae, Asteraceae, Campanulaceae, Caryophyllaceae, Cucurbitaceae, Fabaceae, Lamiaceae, Pinaceae, Ranunculaceae, Solanaceae and Valerianaceae) and represents serious plant pathogens, such as ray blight disease of pyrethrum, leaf spot and stem blight on *Pogostemon cablin* and leaf spot on whorled sunflower (Fox 1998, Vaghefi et al. 2012, Jayawardena et al. 2019, Boggess et al. 2022). Our novel species was isolated from the dead woody twigs of *Quercus serrata* (Fagaceae).

Fuscostagonosporaceae Jayasiri, Camporesi & K.D. Hyde, in Hyde et al., Fungal Diversity 87: 34 (2017)

Fuscostagonosporaceae was introduced by Hyde et al. (2017) to accommodate *Fuscostagonospora* as the type genus and comprises a single genus (Wijayawardene et al. 2022). This family is characterised by having immersed, globose to subglobose ascomata; branched, cellular or trabeculate pseudoparaphyses, and narrowly fusiform, hyaline ascospores with a sheath (Hyde et al. 2017). The asexual morphs of this family are characterized by immersed, scattered, depressed globose, ostiolate conidiomata; thin-walled cells of conidiomatal wall; doliiform, annellidic conidiogenous cells; globose, yellow to pale brown conidia with septate (Hongsanan et al. 2020). In this study, we report on a new host record of *F. banksiae* from *Rhododendron rubiginosum* in China.

Fuscostagonospora banksiae Crous & Carnegie, Fungal Systematics and Evolution 3: 82 (2019)

Fig. 34

Index Fungorum number: IF829304; Facesofungi number: FoF13882

Saprobic on dead woody twigs of *Rhododendron rubiginosum*. Sexual morph: *Ascomata* 400–530 µm high × 600–650 µm diam., ($\bar{x}$ = 460 × 640 µm, n = 5), immersed to erumpent, solitary or scattered, coriaceous, ampulliform, dark brown, multiloculate, with 2–3 locules, cells of ascostromata composed of several layers of dark brown cells of *textura angularis*. *Locules* 160–300 µm high × 200–320 µm diam., ($\bar{x}$ = 260 × 250 µm, n = 10), globose to subglobose. *Ostiolar* neck clypeate, central, short papillate, 60–80 × 70–90 µm ($\bar{x}$ = 70 × 80 µm, n = 5). *Peridium* of locules 12–17 µm wide, 3–4-layered, comprising pale brown cells of *textura angularis*. *Hamathecium* 1.5–2 µm wide, comprising cylindrical, septate, branched and anastomosed pseudoparaphyses, embedded in a hyaline, gelatinous matrix. *Asci* 64–78 × 7.6–9.8 µm ($\bar{x}$ = 72 × 8.6 µm, n = 15), bitunicate, 8-spored, cylindrical-clavate, straight, slightly curved at the end, apically rounded, pedicellate. *Ascospores* 11–14 × 3–4 µm ($\bar{x}$ = 12.7 × 3.5 µm, n = 30), uniseriate, ellipsoidal, hyaline, 1-septate, constricted at the septum, guttulate, thick and smooth-walled, upper cell wider than lower cell, without a gelatinous sheath. Asexual morph: *Conidiomata* solitary, pycnidial, globose, brown, 180–200 µm diam, exuding a milky white conidial mass. *Conidiophores* lining the inner cavity, reduced to conidiogenous cells or with a supporting cell, branched at base or not, 5–12 × 3–4 µm. *Conidiogenous cells* ampulliform to doliiform, hyaline, smooth, 5–7 × 3–4 µm, proliferating indistinctly percurrently at apex. *Conidia* solitary, aseptate, hyaline, smooth, guttulate, ellipsoid, apex obtuse, base bluntly rounded, (3–)4(–5) × (2–)2.5(–3) µm (Crous et al. 2019).

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cells of ascospore. Colonies on PDA, reaching 20–30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, grey, smooth, downy, fimbriate; reverse dark grey.

Material examined – China, Yunnan Province, Diqing, Xianggelila, Nixi, on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae), 31 August 2020, G.C. Ren, NX10 (HKAS 122762), living culture KUMCC 21-0640.

Known distribution – *Banksia* sp. (Proteaceae) in Australia (Crous et al. 2019), on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae) in China (This study).

GenBank numbers – LSU: OQ170851, ITS: OQ158931, SSU: OQ168207, *tef1-α*: OR613429.

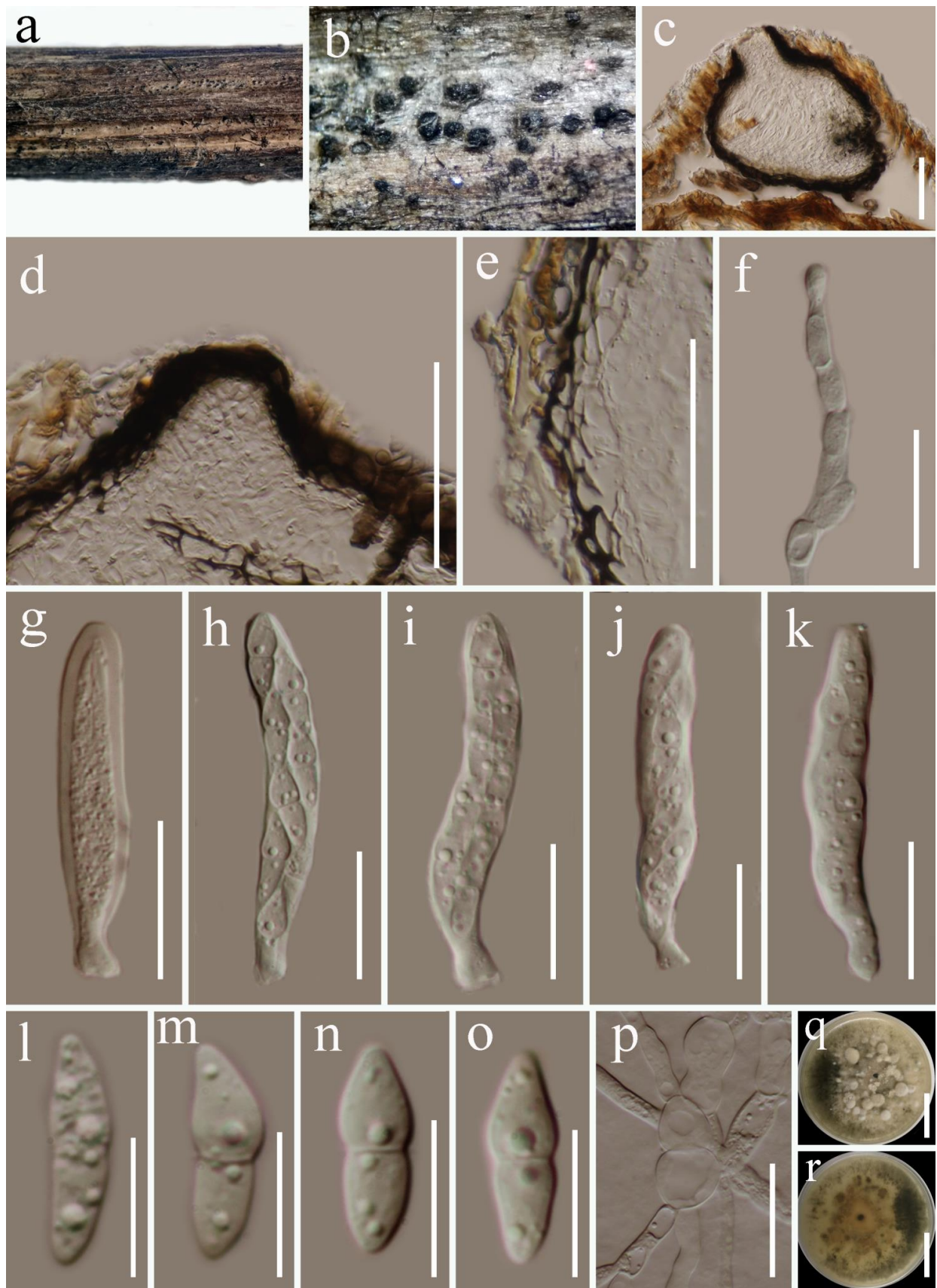


Figure 32 – *Stagonosporopsis lijiangensis* (HKAS 122715, holotype). a Material examined. b Appearance of ascomata on host substrate. c Section of ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g–k Asci. l–o Ascospores. p Germinated ascospore. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: c, d, e = 50 μm , f–k = 20 μm , l–o = 10 μm , p = 30 μm , q, r = 30 mm.

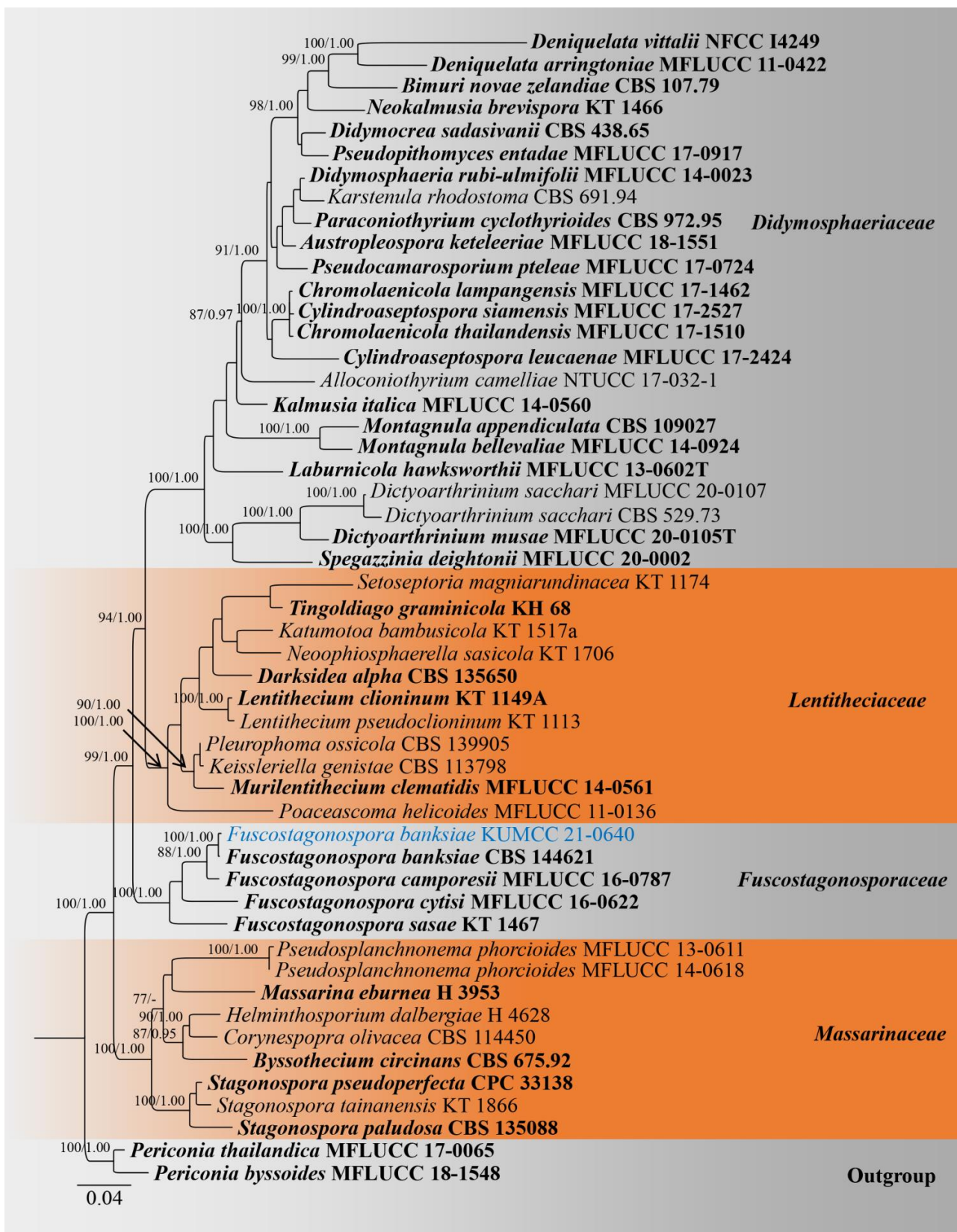


Figure 33 – Phylogram generated from ML analysis based on SSU, LSU, ITS, and *tef1-α* sequence data representing *Fusicostagonosporaceae*. Related sequences are obtained following Hyde et al. (2020b). Fifty-one strains are included in the combined analyses, which comprise 3368 characters for SSU, LSU, ITS, and *tef1-α* alignment. *Periconia byssoides* (MFLUCC 18-1548) and *P. thailandica* (MFLUCC 17-0065) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -21124.171380 is presented. The matrix had 1176 distinct alignment

patterns, with 24.30% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.238450, C = 0.247333, G = 0.272652, T = 0.241565; substitution rates AC = 1.491762, AG = 2.507287, AT = 1.659077, CG = 1.294230, CT = 7.094483, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Notes – According to the multi-gene phylogenetic analyses of a combined SSU, LSU, ITS and *tef1-α* sequence dataset, the new isolate (KUMCC 21-0640) nested together with *Fuscostagonospora banksiae* (CBS 144621), which was isolated from *Banksia* sp. (Proteaceae) in Australia (Crous et al. 2019) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 33). However, there were no sexual morphs reported for *F. banksiae* (Crous et al. 2019). The characteristics of the new strain (KUMCC 21-0640) fit with the generic description of *Fuscostagonospora* by having immersed, scattered ascomata, pale brown peridium, branched and anastomosed pseudoparaphyses embedded in a hyaline, gelatinous matrix, cylindrical asci with pedicellate, hyaline, septate ascospores (Tanaka et al. 2015). The new isolate and *F. banksiae* (CBS 144621) clustered closer to *F. camporesii* with 88% ML bootstrap support and 1.00 BYPP value (Fig. 33). The characteristics of the new strain (KUMCC 21-0640) resemble *F. camporesii* in having semi-immersed to erumpent, subglobose to globose ascomata, cylindric-clavate, short pedicellate asci and 1-septate, ellipsoid to obovoid ascospores (Hyde et al. 2020b). However, the new isolate can be distinguished from *F. camporesii* in having multiloculate ascomata and hyaline ascospores, whereas *F. camporesii* has uni-loculate ascomata and light brown ascospores (Hyde et al. 2020b).

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

Lentitheciaceae was introduced by Zhang et al. (2009) to accommodate *Lentithecium*, *Katumotoa* and *Keissleriella*. Currently, 14 genera are accepted in this family (Wijayawardene et al. 2022). This family is characterised by having immersed to superficial, globose to lenticular ascomata; peridium composed of hyaline to brown, polygonal to angular, thin-walled cells; cellular, septate and branched pseudoparaphyses; bitunicate, fissitunicate, cylindrical to broadly clavate asci; narrowly fusiform to broadly cylindrical, hyaline, septate ascospores with an entire mucilaginous sheath or elongated appendage-like sheath (Zhang et al. 2009, Hongnan et al. 2020). The asexual morphs of this family are characterized by pycnidial, globose, ostiolate conidiomata; blastic or phialidic conidiogenous cells; blastic or phialidic conidiogenous cells; cylindrical to oblong, hyaline to pigmented, one celled to muriform conidia (Hongnan et al. 2020). In this study, we report on a new host record of *L. yunnanense* from *Castanopsis orthacantha* in China.

Lentithecium yunnanense W.H. Lu, Karun. & Tibpromma [as ‘*yunnanensis*’], in Lu, Dai, Lu, Liu, Wei, Karunaratna & Tibpromma, Phytotaxa 554 (2): 108 (2022) Fig. 36

Index Fungorum number: IF559622; Facesoffungi Number: FoF10778

Saprobic on dead woody twigs of *Castanopsis orthacantha*. Sexual morph: *Ascomata* 140 – 210 µm diam., 150 – 200 µm high ($\bar{x}$ = 180 × 160 µm, n = 5), scattered to gregarious, semi-immersed to immersed beneath the host epidermis, sometimes sparse erumpent, subglobose to globose in section, with a short papillate, ostiolar neck. *Ostioles* 58–93 µm long, 83–120 µm diam., ($\bar{x}$ = 76 × 98 µm, n = 5), central, black. *Peridium* 17–25 µm wide, multi-layered, consists of dark-brown, thick-walled cells of *textura angularis* in the outermost layers of unequal thickness. *Hamathecium* comprising 1.5–2 µm wide, hyaline, slenderly cylindrical, septate, unbranched, rarely anastomosing, tubular pseudoparaphyses. *Asci* 73–90 × 12.7–16 µm ($\bar{x}$ = 80 × 14.4 µm, n = 20), 8-spored, fissitunicate, bitunicate, oblong to cylindrical, broadly rounded apex, with visible apical chambers, short, club-shaped pedicel. *Ascospores* 24–29 × 6–7.7 µm ($\bar{x}$ = 26.6 × 7 µm, n =

20), overlapping biserial, hyaline, clavate to broadly fusiform, slightly curved, 1–3-septate, slightly constricted at the middle septum, widest at the centre, tapering towards the broadly rounded ends, smooth-walled, with large guttules, surrounded by a hyaline, mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cell of ascospore. Colonies on PDA, reaching 45 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, atrovirens, smooth, downy, fimbriate; reverse atrovirens, crack.

Material examined – China, Yunnan Province, Baoshan, on dead woody twigs of *Castanopsis orthacantha* (Fagaceae), 23 July 2020, G.C. Ren, BS47 (HKAS 122714), living culture KUMCC 21-0525.

Known distribution – On dead culms of *Artemisia* sp. (Proteaceae) and dead woody twigs of *Castanopsis orthacantha* (Fagaceae) in China (Lu et al. 2022a, this study).

GenBank numbers – SSU: OQ168208, LSU: OQ170854, ITS: OQ158932, *tef1-α*: OR613430.

Notes – According to the multi-gene phylogenetic analyses of combined SSU, LSU, ITS and *tef1-α* sequence dataset, our new isolate (KUMCC 21-0525) nested with *Lentithecium yunnanense* (KUNCC 22-10776 and KUNCC 22-10777), which was isolated from *Artemisia* sp. (Proteaceae) in China (Lu et al. 2022a) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 35). Our new isolate fits well with the characters of the holotype of *L. yunnanense* in having semi-immersed to erumpent, subglobose to globose ascomata with short papillate, ostiolar neck, oblong to cylindrical, short, club-shaped, pedicellate asci and 1–3-septate, hyaline, clavate to broadly fusiform ascospores with a mucilaginous sheath (Lu et al. 2022a). Therefore, we identified our taxon as a new host record of *L. yunnanense* from *Castanopsis orthacantha* (Fagaceae) in China.

Leptosphaeriaceae M.E. Barr, Mycotaxon 29: 503 (1987)

Leptosphaeriaceae was introduced by Barr (1987) and has been reviewed by Ariyawansa et al. (2015b). Currently, 14 genera are accepted in this family (Wijayawardene et al. 2022). *Leptosphaeriaceae* is characterised by having globose, subglobose or obpyriform ascomata; peridium composed of large, pigmented, thin-walled, scleroplectenchymatous or plectenchymatous cells; cellular pseudoparaphyses; bitunicate, fissitunicate, cylindrical to oblong asci with a pedicel and ocular chamber; fusoid, obovoid, oblong or filiform, brown, reddish brown or yellowish brown, septate ascospores with or without guttules (Hongsan et al. 2020). The asexual morphs of this family are either coelomycetous or hyphomycetous. Coelomycetous members are characterized by immersed to nearly superficial, globose conidiomata; scleroplectenchymatous conidiomata wall; oblong, ellipsoidal to subcylindrical conidia (Ariyawansa et al. 2015b). Hyphomycetous members are characterized by solitary or in small groups, 3–6-septate, pale to chestnut brown conidiophores; integrated, terminal to intercalary, sympodial, cylindrical, yellowish to pale brown conidiogenous cells; solitary, cylindrical to subcylindrical, subhyaline to pale brown, aseptate or presenting of transversely septate conidia (Zhang et al. 2012). In this study, we report two new host records of *Plenodomus*, viz., *P. artemisiae* from *Quercus serrate* and *P. sinensis* from *Lyonia ovalifolia* in China.

Plenodomus artemisiae A. Karunarathna, Phookamsak & K.D. Hyde, Fungal Diversity 95: 1–273 (2019) Fig. 38

Index Fungorum number: IF556118; Facesoffungi Number: FoF05696

Saprobic on dead branch of *Quercus serrate*. Sexual morph: *Ascomata* 160–200 µm high, 200–320 µm diam., solitary to aggregate, immersed, uniloculate, subglobose black, shiny on the host surface, with truncated base, glabrous, ostiolate central. *Peridium* 10–50 µm wide, thick-walled of unequal thickness, thickened at the sides, thin at the base and apex, composed of several cell layers of light brown cells, arranged in a *textura angularis* to *textura globulosa*. *Hamathecium* 2.5–4.7 µm wide, composed of hyaline, filamentous, septate, pseudoparaphyses.

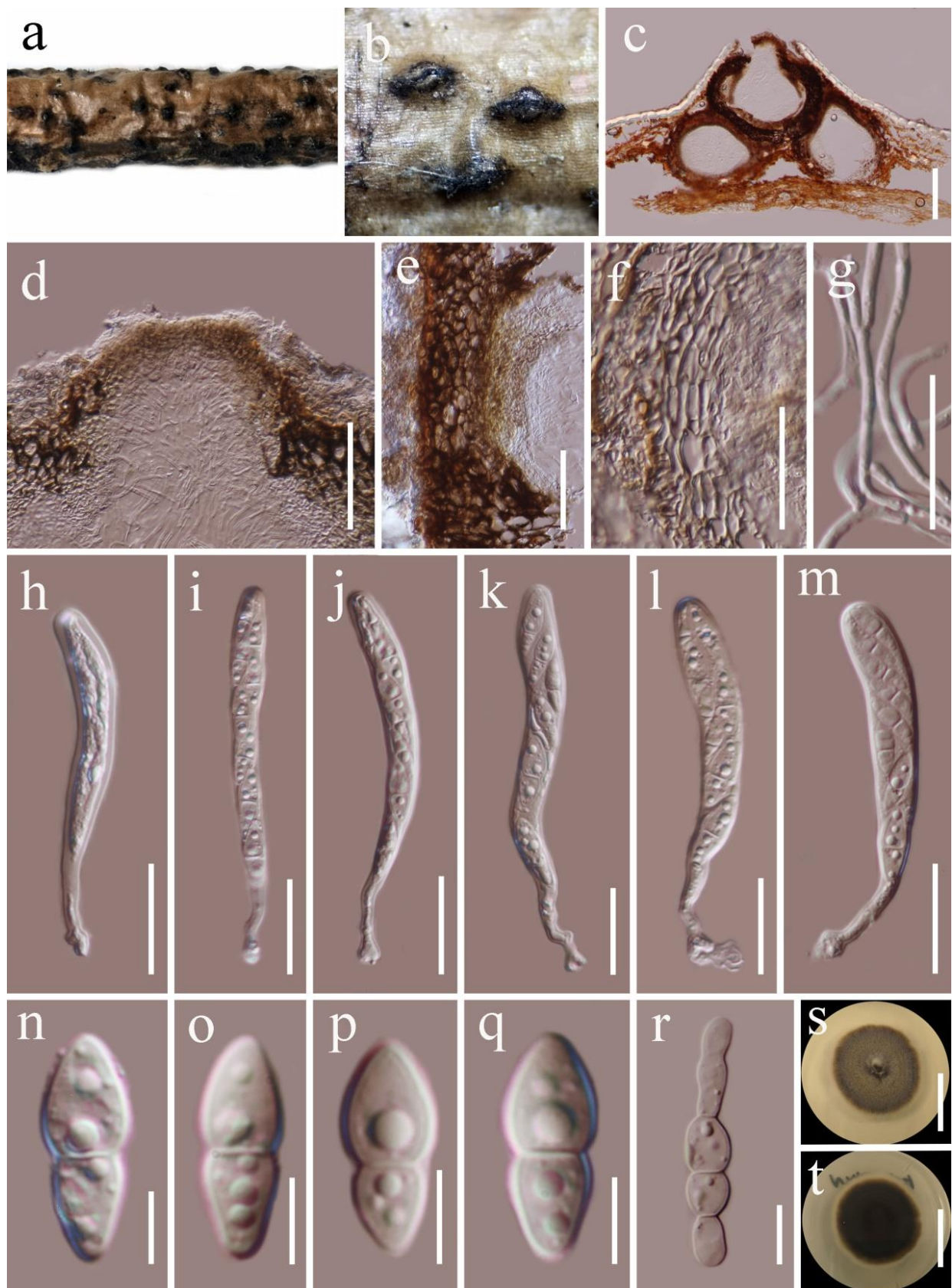


Figure 34 – *Fuscostagonospora banksiae* (HKAS 122762). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Ostiole. e, f Peridium. g Pseudoparaphyses. h–m Asci. n–q Ascospores. r Germinated ascospore. s, t Culture characters on PDA (p = from above, q = from below). Scale bars: c = 150 μ m, d, e = 50 μ m, f = 30 μ m, g–m = 20 μ m, n–q = 5 μ m, r = 10 μ m, s, t = 20 mm.

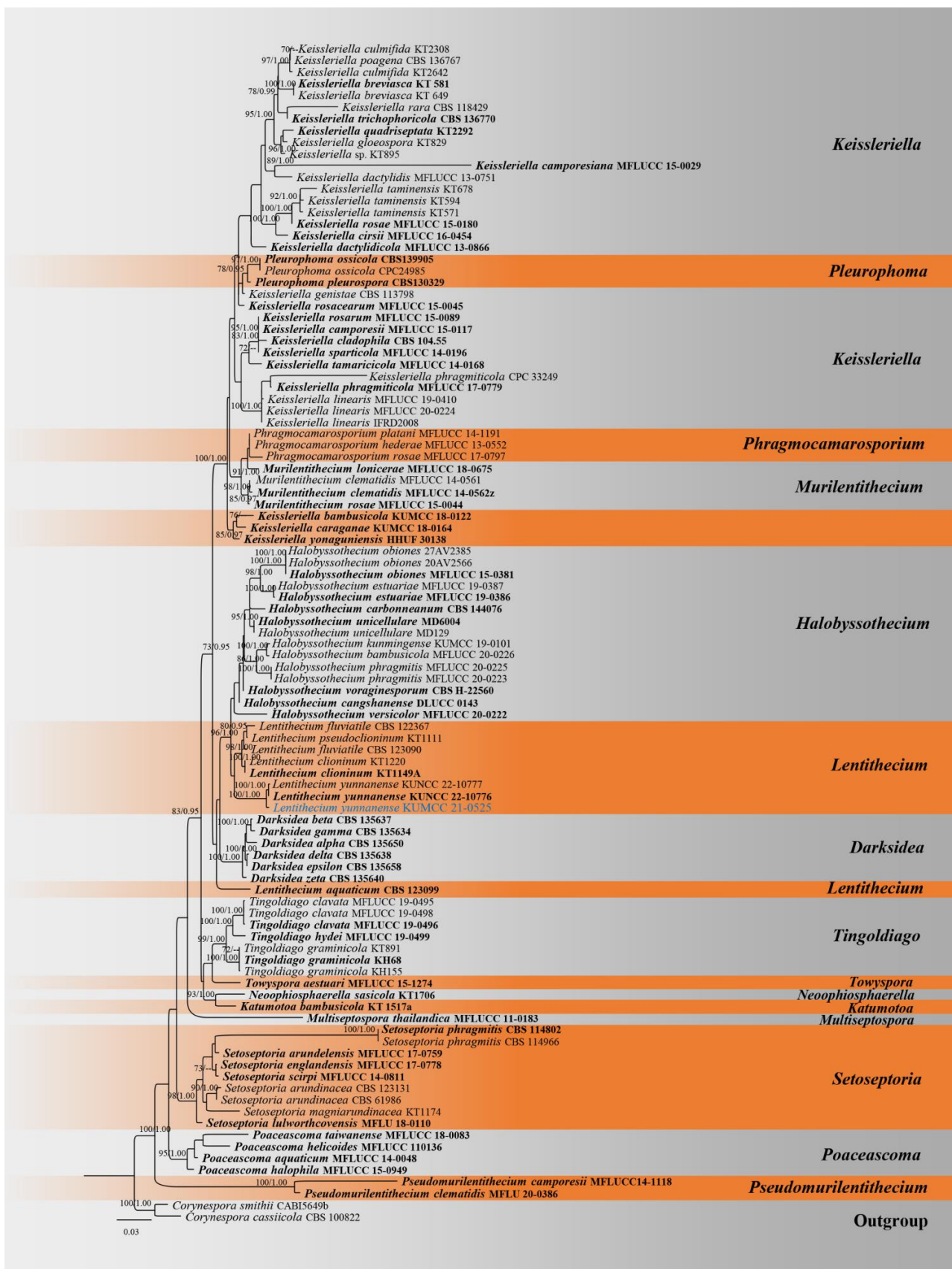


Figure 35 – Phylogram generated from ML analysis based on SSU, LSU, ITS, and *tef1-α* sequence data, representing *Lentitheciaceae*. Related sequences are obtained following Calabon et al. (2021) and Lu et al. (2022a). One hundred and one strains are included in the combined analyses, which comprise 3231 characters for SSU, LSU, ITS, and *tef1-α* alignment. *Corynespora cassicola* (CBS 100822) and *C. smithii* (CABI5649b) were used as the outgroup taxa. The best-scoring RAXML

tree with a final likelihood value of -21283.940390 is presented. The matrix had 1239 distinct alignment patterns, with 25.09% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240228, C = 0.247293, G = 0.273128, T = 0.239351; substitution rates AC = 1.200390, AG = 2.125722, AT = 1.347877, CG = 1.314457, CT = 8.272345, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Asci 80–100 × 11–13.8 µm ($\bar{x}$ = 92 × 12.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate, apically rounded with a distinct ocular chamber. **Ascospores** 32–37 × 5–7 µm ($\bar{x}$ = 35 × 5.8 µm, n = 20), overlapping biseriate, pale brown, fusiform, slightly curve, 5-septate, slightly constricted at the septa, enlarge at the third cell from above, gettules, lacking a mucilaginous sheath and appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cell of ascospore. Colonies on PDA, reaching 55 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, white-grey, smooth, downy, fimbriate; reverse atrovirens.

Material examined – China, Yunnan Province, Lijiang, on dead woody twigs of *Quercus serrate* (Fagaceae), 30 August 2020, G.C. Ren, DQ17 (HKAS 122717), living culture KUMCC 21-0534.

Known distribution – *Artemisia* sp. (Anthemideae) in China (Phookamsak et al. 2019), dead stems of *Artemisia argyi* (Anthemideae) in China (Doilom et al. 2021) and *Quercus serrate* (Fagaceae) in China (This study).

GenBank numbers – SSU: OQ168211, LSU: OQ170857, ITS: OQ158935.

Notes – In phylogenetic analyses, our new collection (KUMCC 21-0534) clustered with other *Plenodomus artemisiae* strains (KUMCC 18-0151, KUMCC 20-0200A and KUMCC 20-0200B) with 98% ML bootstrap support and 1.00 BYPP value (Fig. 37). The new collection shares similar morphology with the type of *P. artemisiae* in having immersed, uniloculate, subglobose black ascomata with truncated base, thick-walled of unequal thickness, thickened at the sides, thin at the base and apex peridium, bitunicate, fissitunicate, cylindrical asci with a distinct ocular chamber, overlapping biseriate, pale brown, fusiform, slightly curve, 5-septate ascospores (KUMCC 18-0151) (Phookamsak et al. 2019). Our collection has 99.60%, 99.64%, and 99.9% similarities with the ex-type strain (KUMCC 18-0151) of *P. artemisiae* in ITS, LSU and SSU sequence data, respectively, which indicate them to be conspecific. Therefore, we identified our collection as *P. artemisiae* based on morphological and molecular evidence. Our new collection was collected from the same region as the previous records (Phookamsak et al. 2019, Doilom et al. 2021) but from a different host (*Quercus serrata*).

Plenodomus sinensis Tennakoon, Phook. & K.D. Hyde, in Tennakoon, Phookamsak, Wanasinghe, Yang, Lumyong & Hyde, Phytotaxa 324 (1): 76 (2017) Fig. 39

Index Fungorum number: IF553195; Facesoffungi Number: FoF03235

Saprobic on dead branch of *Castanopsis orthacantha* and *Lyonia ovalifolia*. Sexual morph: **Ascomata** 160–400 µm high, 200–460 µm diam., ($\bar{x}$ = 300 × 350 µm, n = 5), solitary, scattered, appearing as small, immersed black dots on the host, globose to subglobose, smooth, with truncate base, black, ostiolate central. **Peridium** 13–20 µm ($\bar{x}$ = 17 µm, n = 10) at sides and base, 18–27 µm ($\bar{x}$ = 24 µm, n = 10) at apex, slightly thick at the apex, composed of three layers of scleroplectenchymatous cells, inner layer comprising 2–3 cell layers of flattened, light brown cells, arranged in a *textura angularis*, middle layer comprising several layers of sub-hyaline cells arranged in a *textura globulosa*, outer layer composed of heavily pigmented, thick-walled, dark brown cells, *textura angularis*. **Hamathecium** 2.2–3.3 µm wide ($\bar{x}$ = 2.9 µm, n = 10) wide, septate,

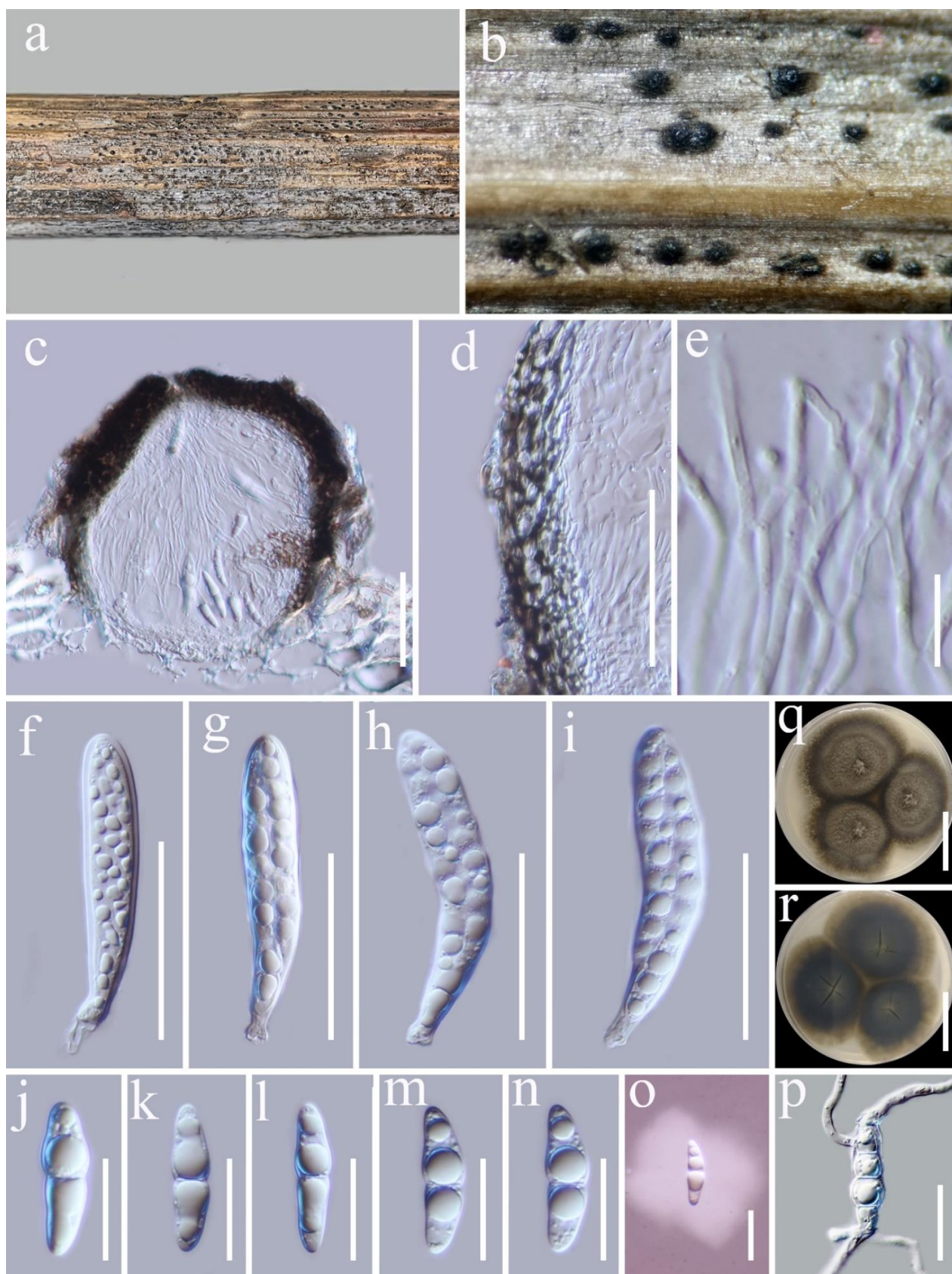


Figure 36 – *Lentithecium yunnanense* (HKAS 122714). a Material examined. b Appearance of ascomata on the host substrate. c Section of ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–o Ascospores. p Germinated ascospore. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: c, d = 50 µm, e = 10 µm, f–i = 50 µm, j–p = 20 µm, q, r = 30 mm.

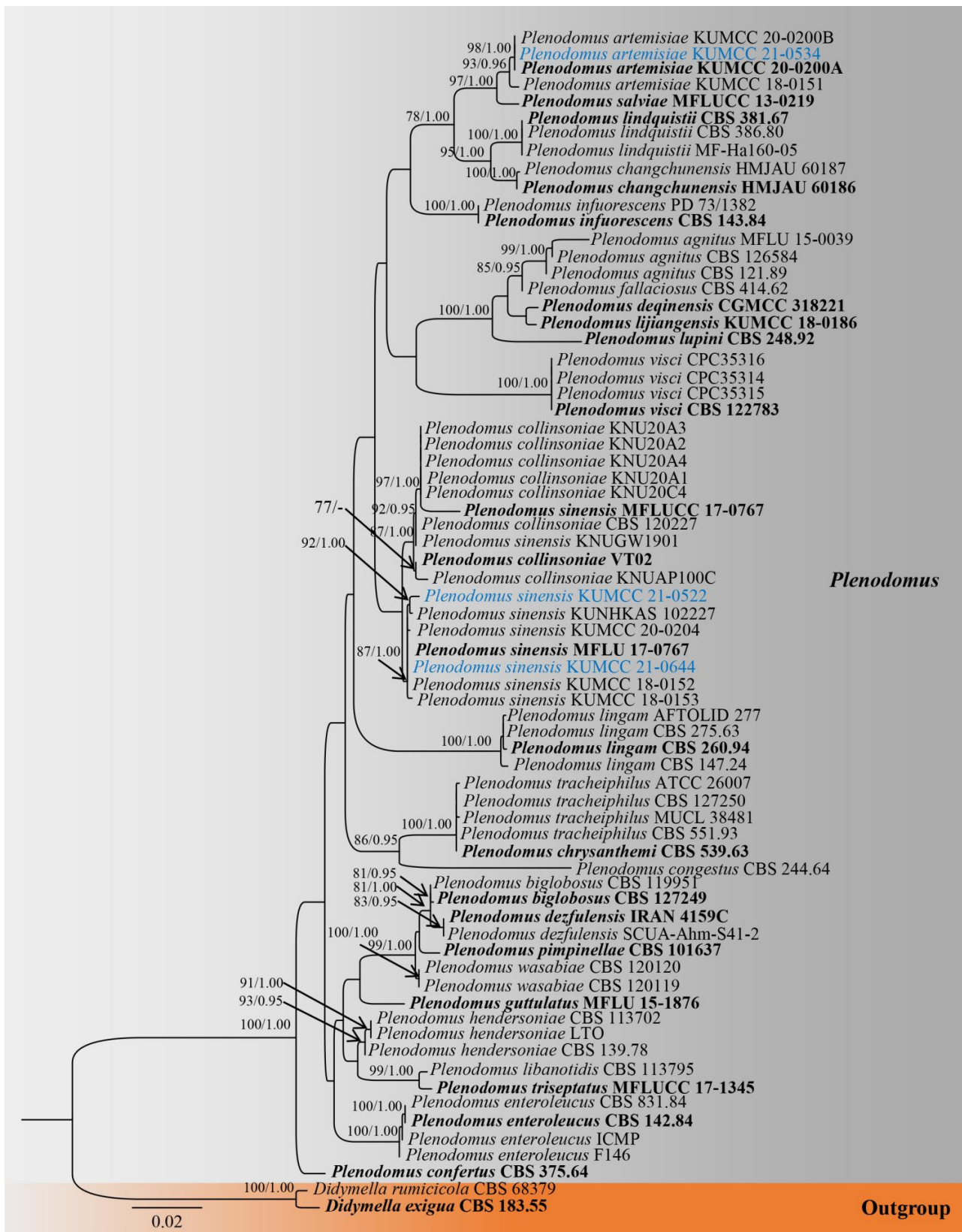


Figure 37 – Phylogram generated from ML analysis based on SSU, LSU and ITS sequence data representing *Plenodomus* (*Leptosphaeriaceae*). Related sequences are obtained following Xu et al. (2022). Seventy strains are included in the combined analyses, which comprise 2333 characters for SSU, LSU, and ITS alignment. *Didymella exigua* (CBS 18.355) and *D. rumicicola* (CBS 68.379) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -7397.120776 is presented. The matrix had 356 distinct alignment patterns, with 32.14% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242656, C =

0.221744, G = 0.273758, T = 0.261843; substitution rates AC = 1.594965, AG = 3.148804, AT = 1.629126, CG = 0.839376, CT = 8.693924, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

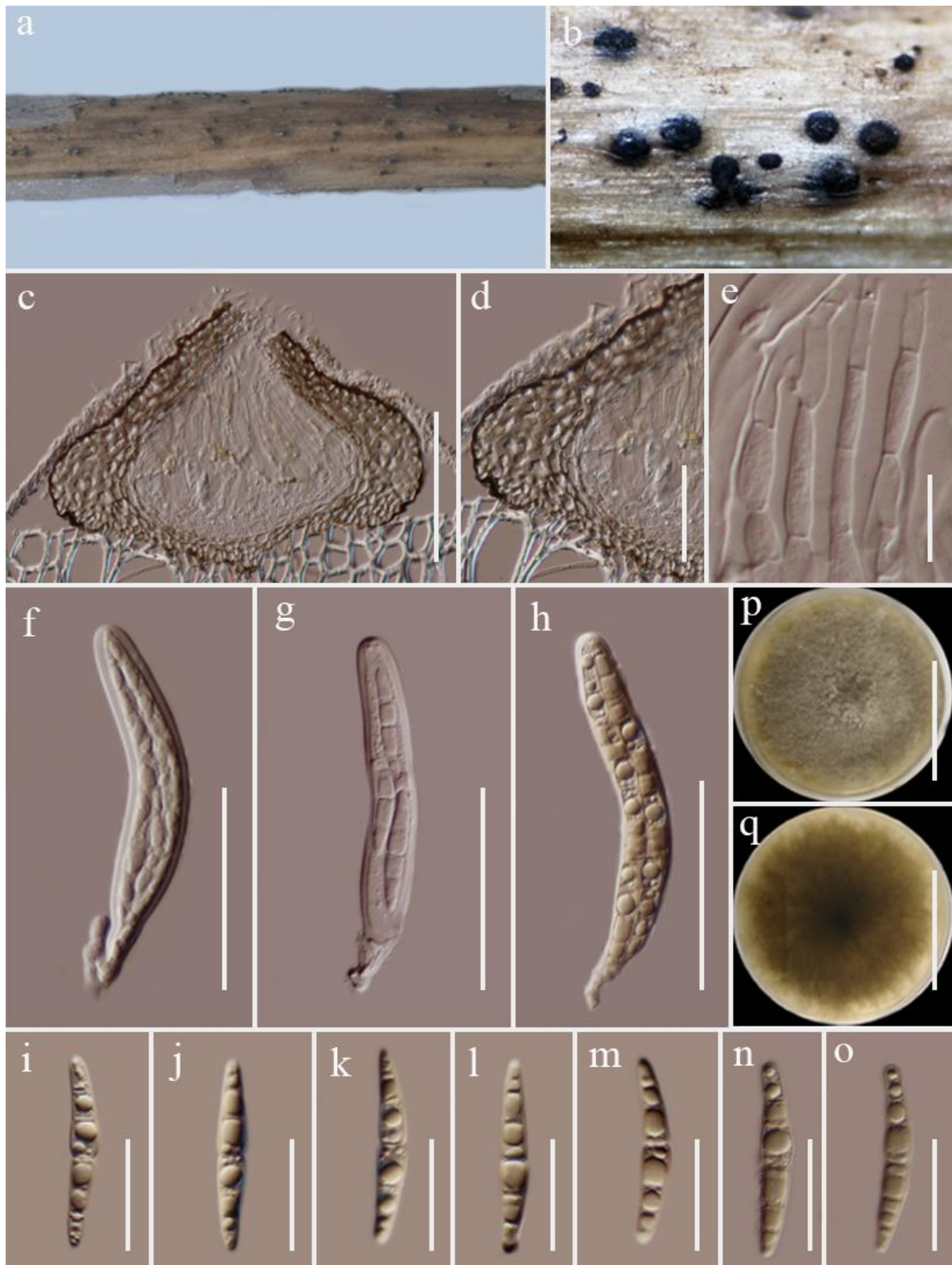


Figure 38 – *Plenodomus artemisiae* (HKAS 122717). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–h Asci. i–o Ascospores. p, q Petri dishes showing growth on agar.

i–o Ascospores. p, q Culture characters on PDA (p = from above, q = from below). Scale bar: c = 100 μ m, d = 50 μ m, e = 10 μ m, f–h = 50 μ m, i–o = 20 μ m, p, q = 30 mm.

cellular pseudoparaphyses, branching between the asci, embedded in a gelatinous matrix. Asci 65–85 $\times$ 11.8–13.5 μ m ($\bar{x}$ = 77.5 $\times$ 12.5 μ m, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, apically rounded, with a distinct ocular chamber and a short pedicel. Ascospores 33–38 $\times$ 5–6.3 μ m ($\bar{x}$ = 35.6 $\times$ 5.6 μ m, n = 20), overlapping 1–2-seriate, olivaceous to yellowish, cylindrical to subfusoid, with obtuse ends, 6–7 septa, not or slightly constricted at each septum, cell above central septum slightly wider, guttulate, thick and smooth-walled, with mucilaginous, globoid-shaped, apical and basal appendages. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 $^{\circ}$ C). Germ tubes produced from the basal and apical cell of ascospore. Colonies on PDA, reaching 25 mm diameter after two weeks at 20–25 $^{\circ}$ C, mycelia superficial, circular, grey at the centre, atrovirens at the margin, smooth, downy, fimbriate; reverse atrovirens.

Material examined – China, Yunnan Province, Diqing, Xianggelila, Nixi, on dead woody twigs of *Lyonia ovalifolia* (Ericaceae), 31 August 2020, G.C. Ren, NX22 (HKAS 122764), living culture KUMCC 21-0644; China, Yunnan Province, Baoshan, on dead woody twigs of *Castanopsis orthacantha* (Fagaceae), 30 August 2020, G.C. Ren, BS39 (HKAS 122765), living culture KUMCC 21-0522.

Known distribution – *Tamarindus indica* (Fabaceae) and *Plukenetia volubilis* (Euphorbiaceae) in China (Tennakoon et al. 2017), *Cirsium* sp. (Asteraceae) and ferns in China (Phookamsak et al. 2019), *Ageratina adenophora* (Asteraceae) in China (Doilom et al. 2021), from soil in Korea (Moe et al. 2020), *Castanopsis orthacantha* (Fagaceae) and *Lyonia ovalifolia* (Ericaceae) in China (This study).

GenBank numbers – KUMCC 21-0644: SSU: OQ168209, LSU: OQ170855, ITS: OQ158933; KUMCC 21-0522: SSU: OQ168210, LSU: OQ170856, ITS: OQ158934, *tef1- α* : OR613431.

Notes – Our isolate (HKAS 122764) and the holotype of *Plenodomus sinensis* (MFLU 17-0767) have globose to subglobose ascomata, cylindrical to subfusoid asci, 6–7-septate ascospores with mucilaginous globoid-shaped appendages at both ends, but they are slightly different; holotype differs in having flattened ascomatal base (Tennakoon et al. 2017) in addition to the prominent ostiole canal observed in the holotype. Multi-locus phylogeny shows that our collections (KUMCC 21-0644 and KUMCC 21-0522) clustered with five collections of *P. sinensis*. Although *Plenodomus sinensis* (MFLU 17-0767) clustered with *P. collinsoniae* (Fig. 37), *P. sinensis* differs in having larger asci (80–100 $\times$ 10–12 μ m vs. 70 $\times$ 10 μ m), longer ascospores (27–40 $\times$ 3.8–4.4 μ m vs. 30–32 $\times$ 4 μ m) with olivaceous to yellowish pigmentation as discussed in Tennakoon et al. (2017). Thus we confirm our collection as *Plenodomus sinensis*, as its characteristics are more similar to *P. sinensis* (MFLU 17-0767). *Plenodomus sinensis* appears to have a wider host range, occurring on *Ageratina adenophora*, *Cirsium* sp., *Plukenetia volubilis*, *Tamarindus indica* and ferns in China (Tennakoon et al. 2017, Phookamsak et al. 2019, Doilom et al. 2021). Our collections are the first reports of *P. sinensis* on *Castanopsis orthacantha* and *Lyonia ovalifolia* in China.

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

Lindgomycetaceae was introduced by Hirayama et al. (2010) with *Lindgomyces* (*L. ingoldianus*) as the type genus. The family comprises eight genera, *Arundellina*, *Aquimassariosphaeria*, *Clohesyomyces*, *Hongkongmyces*, *Lindgomyces*, *Lolia*, *Neolindgomyces* and *Xenovaginatispota* (Wijayawardene et al. 2022). Members of *Lindgomycetaceae* are generally found in aquatic and terrestrial habitats (Hongsanan et al. 2020). *Lindgomycetaceae* is characterised by having subglobose to globose ascomata; hyaline to pale brown, small, thin-walled cells; septate, branched, anastomosing, usually cellular, or trabeculate pseudoparaphyses; fissitunicate, cylindrical to clavate asci with an ocular chamber; fusiform to cylindrical, hyaline to brown, uni- to multi-

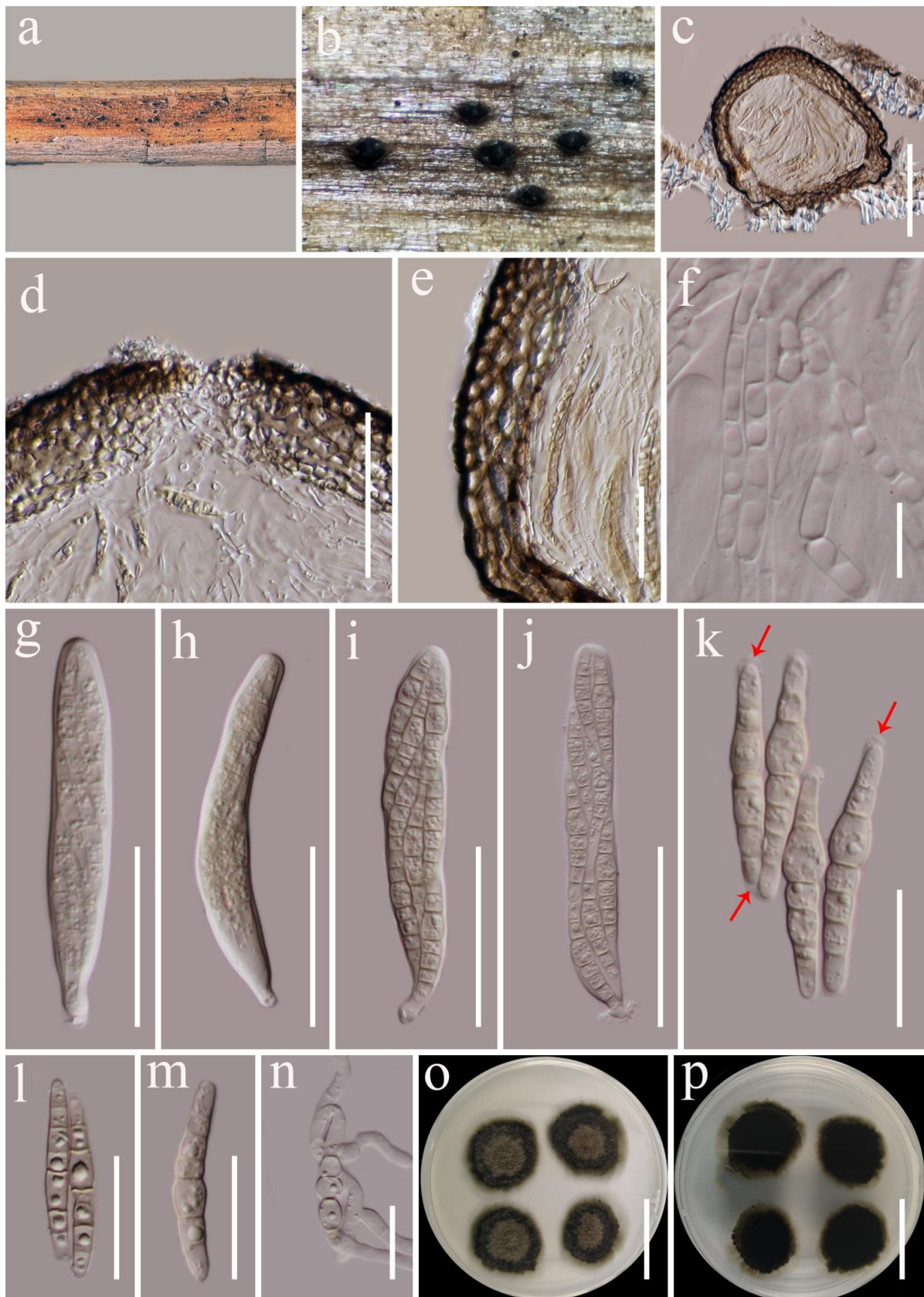


Figure 39 – *Plenodomus sinensis* (HKAS 122764). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g–j Asci. k–m Ascospores (red arrows indicate mucilaginous globoid-shaped apical and basal appendages). n Germinated ascospore. o, p Culture characters on PDA (o = from above, p = from below). Scale bar: c = 100 μ m, d = 50 μ m, e = 30 μ m, f = 10 μ m, g–j = 30 μ m, k–n = 20 μ m, o, p = 30 mm.

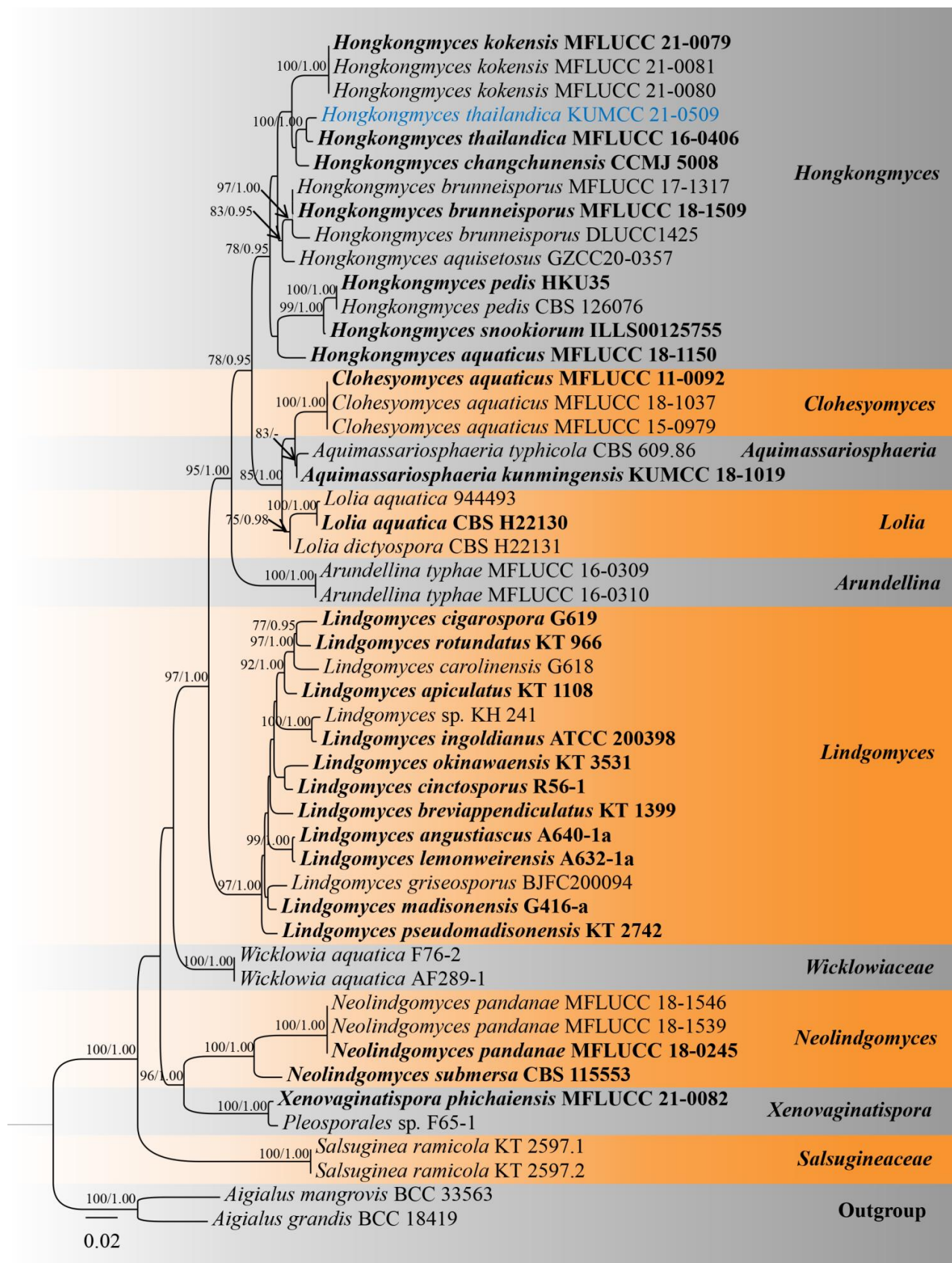


Figure 40 – Phylogram generated from ML analysis based on LSU, SSU, ITS, and *tef1-α* sequence data, representing *Lindgomycetaceae*. Related sequences are obtained following previous publications (Bao et al. 2021, Boonmee et al. 2021, Jayawardena et al. 2022, Yang et al. 2023). Fifty strains are included in the combined analyses, which comprise 3163 characters for LSU, SSU, ITS, and *tef1-α* alignment. *Aigialus grandis* (BCC 18419) and *A. mangroveis* (BCC 33563) were

used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -13379.802355 is presented. The matrix had 857 distinct alignment patterns, with 30.81% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245565, C = 0.237980, G = 0.275632, T = 0.240823; substitution rates AC = 0.981732, AG = 3.119278, AT = 1.607343, CG = 1.127231, CT = 9.059792, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

septate ascospores with an entire sheath and/or bipolar mucilaginous appendages (Hirayama et al. 2010, Hongsanan et al. 2020). The asexual morphs of this family are coelomycetous. Coelomycetous members are characterized by semi-immersed to superficial, subglobose to ellipsoidal conidiomata; branched, septate, smooth conidiophores; hyaline, smooth, cylindrical to sub-cylindrical conidiogenous cells; unicellular, ellipsoidal aseptate or septate conidia with or without appendages, with without an irregular mucilaginous sheath (Hongsanan et al. 2020). In this study, we report a new record of *Hongkongmyces thailandica* from *Dipterocarpus gracilis* in China.

Hongkongmyces thailandica Phukhams. & K.D. Hyde Fungal Diversity 87: 54 (2017)
Fig. 41

Index Fungorum number: IF552955; Facesoffungi Number: FoF03116

Saprobic on dead woody twigs of *Dipterocarpus gracilis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 130–150 µm high × 80–110 µm diam., ($\bar{x}$ = 140 × 100 µm, n = 5), pycnidial, semi-immersed or erumpent, solitary or scattered, unilocular, coriaceous, elliptical, dark-brown to black. *Ostioles* central. *Conidiomata* wall 14–22 µm thick, 3–4-layered, composed of brown outer layers and inner layers comprising hyaline, thick-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–9 × 1.5–2.5 ($\bar{x}$ = 7 × 1.8, n = 10) µm, enteroblastic, phialidic, determinate, discrete, cylindrical, hyaline, smooth-walled, arising from the stratum. *Conidia* 3.1–4.3 × 2.4–3 µm ($\bar{x}$ = 3.8 × 2.6 µm, n = 30), hyaline, subglobose to obovoid, one-celled, aseptate, smooth-walled, verruculose, lacking a mucilaginous sheath.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of conidia. Colonies on PDA, reaching 50 mm diameter after two weeks at 20–25 °C, mycelia superficial, velvety, circular, flat, umbonate, entire edge, gray; reverse, atrovirens.

Material examined – China, Yunnan Province, Baoshan, on dead woody twigs of *Dipterocarpus gracilis* (Dipterocarpaceae), 12 July 2020, G.C. Ren, BS20 (HKAS 122708), living culture KUMCC 21-0509.

Known distribution – On decay bark in Thailand (Hyde et al. 2017).

GenBank numbers – SSU: OQ168214, LSU: OQ170860, ITS: OQ158938, *tef1-α*: OR613432.

Notes – *Hongkongmyces thailandica* was introduced as a wood-decaying saprobe based on the combined phylogeny of LSU, SSU and ITS sequence data from Thailand, and it was known only from its sexual morph. In the multi-gene phylogenetic analyses, the isolates of the asexual species (KUMCC 21-0509) formed a sister clade to the type strain of *Hongkongmyces thailandica* (MFLUCC 16-0406) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 40). A comparison of ITS, LSU, and *tef1-α* sequence data reveals no significant difference between our new isolate and *H. thailandica* (MFLUCC 16-0406). Our strain of *Hongkongmyces thailandica* and *H. changchunensis* share characteristics, such as phialidic, cylindrical, hyaline conidiogenous cells and obovoid, aseptate conidia; however, *H. thailandica* has shorter conidiogenous cells and smaller conidia than *H. changchunensis* (conidiogenous cells 2.6–23.5 × 1.6–4.9 µm ($\bar{x}$ = 10 × 3 µm, n = 20), conidia 10–18 × 7–13 µm ($\bar{x}$ = 13 × 10 µm, n = 43)) (Jayawardena et al. 2022). Sequence comparison for the ITS region between *Hongkongmyces thailandica* (KUMCC 21-0509) and *H. changchunensis* (CCMJ 5008) showed a 2.5% (13/526 bp, without gaps) base pair difference in

the ITS region, 4.2% (35/834 bp, without gaps) base pair difference in the *tef1- α* region. Moreover, *H. changchunensis* and *H. thailandica* were collected from freshwater habitats, and our species, our strain of *H. thailandica* was collected from a terrestrial habitat on woody litter. Therefore, we report our saprobic collection KUMCC 21-0511 as the first record of the asexual species *Hongkongmyces thailandica* on the woody litter of *Dipterocarpus gracilis* in China.

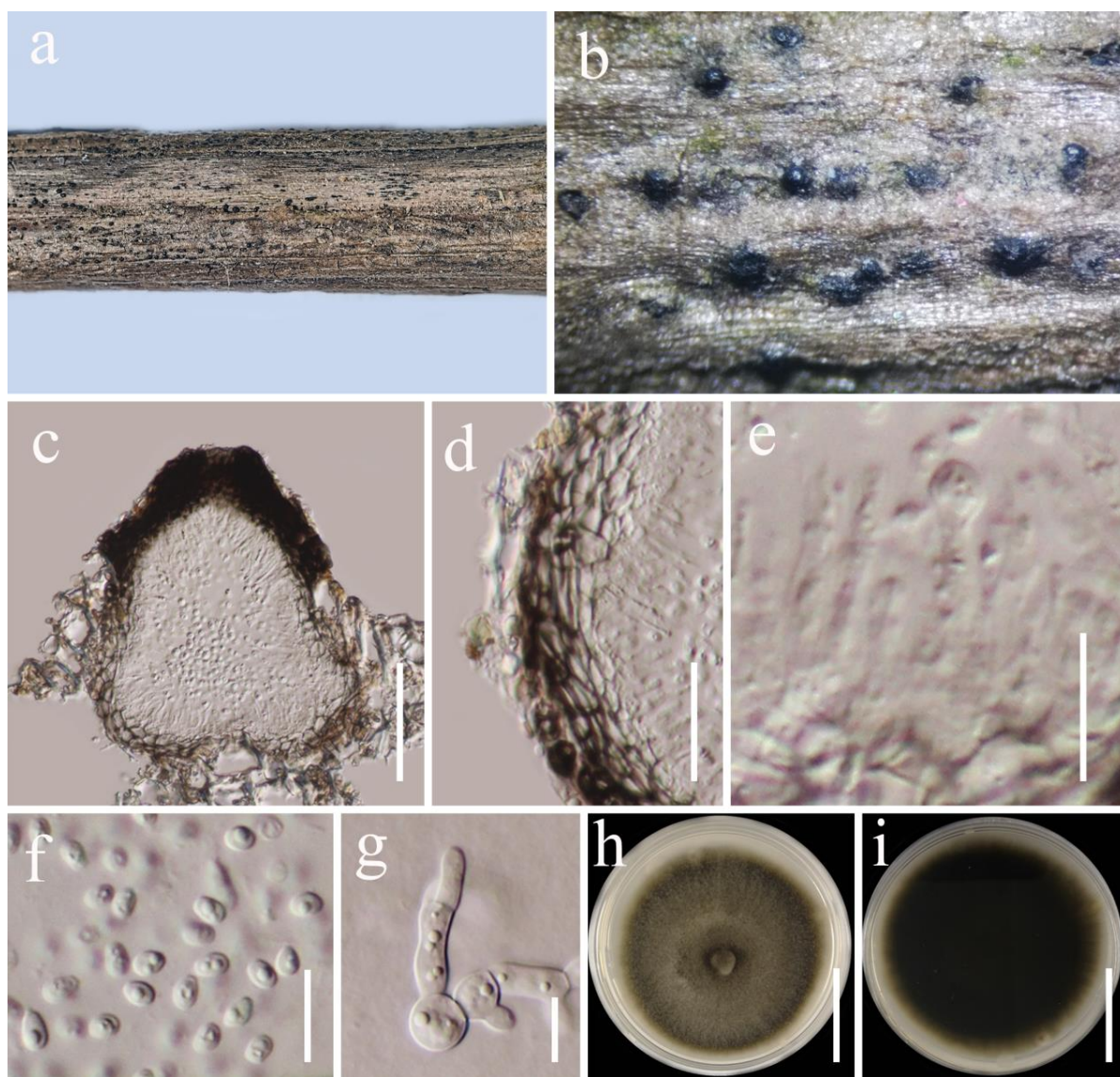


Figure 41 – *Hongkongmyces thailandica* (HKAS 122708). a Material examined. b Appearance of conidiomata on the host substrate. c Section of a conidioma. d Conidioma wall. e Conidiogenous cells and developing conidia. f Conidia. g Germinated conidium. h, i Culture characters on PDA (h = from above, i = from below). Scale bars: c = 50 μ m, d = 20 μ m, e, f = 10 μ m, g = 5 μ m, h, i = 20 mm.

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

Lophiotremataceae was introduced by Hirayama & Tanaka (2011) based on morphological characters and molecular phylogenetic data using LSU and SSU sequence data. This family is characterised by having immersed, subglobose to globose ascomata with a crest-like ostiolar neck; pale brown peridium, composed of rectangular to globose cells; septate, branched and anastomosed, trabeculate pseudoparaphyses; bitunicate, fissitunicate, cylindrical asci with an ocular chamber; fusiform to broadly fusiform or cylindrical, hyaline to brown, 1- to multi-septate ascospores (Hashimoto et al. 2017, Hongsanan et al. 2020). The asexual morphs of this family are

coelomycetous. Coelomycetous members are characterized by pycnidial, globose to subglobose conidiomata; holoblastic or phialidic, ampulliform to cylindrical, hyaline conidiogenous cells; ellipsoidal to cylindrical with rounded ends or slightly angular ends, hyaline, aseptate or 1-septate or multi-septate conidia (Hashimoto et al. 2017, Hongsanan et al. 2020). Currently, eight genera are accepted in this family (Wijayawardene et al. 2022). In this study, we report a new species of *Crassimassarina* from *Castanopsis orthacantha* in China.

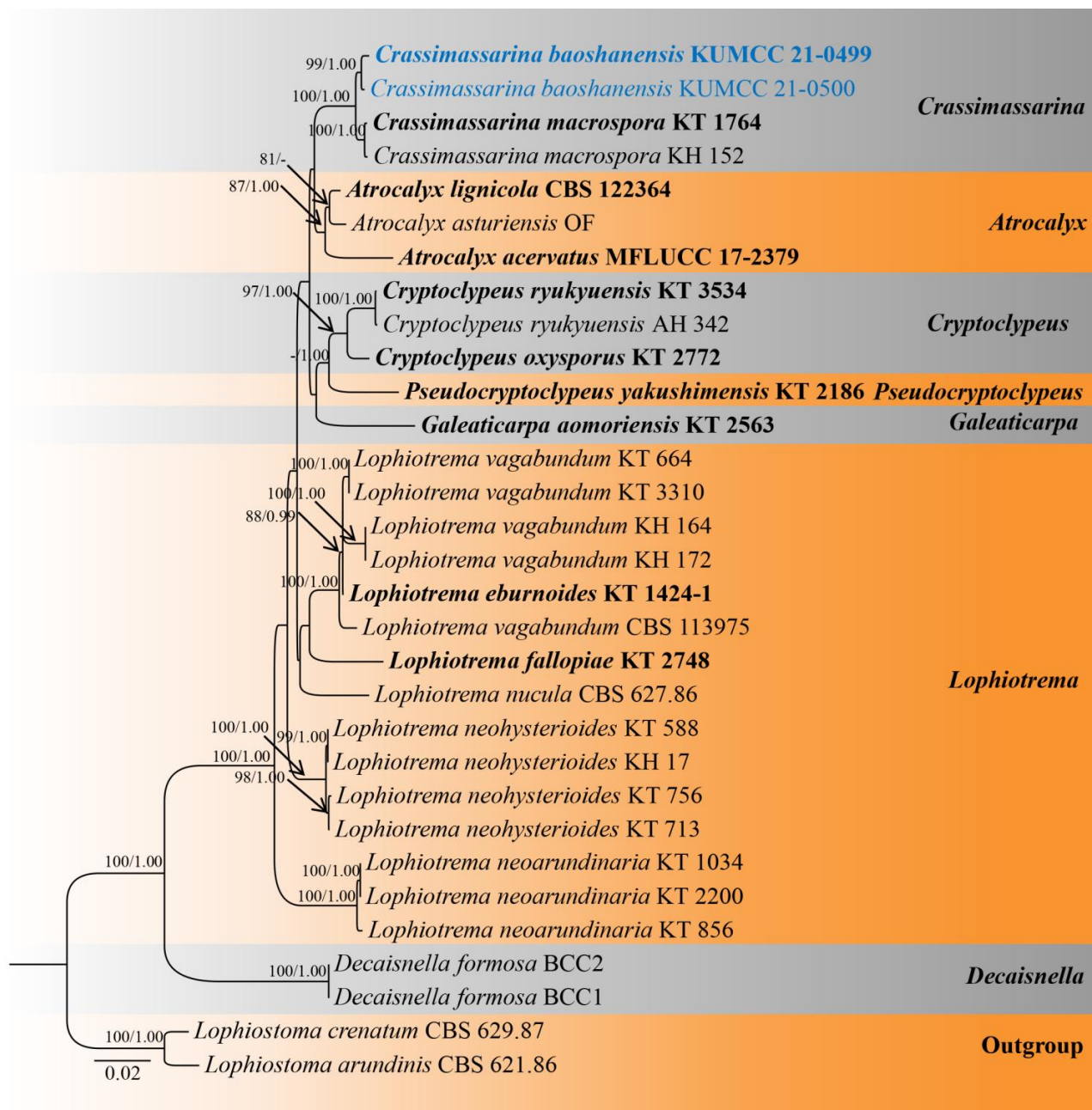


Figure 42 – Phylogram generated from ML analysis based on SSU, LSU, ITS, and *tef1-α* sequence data, representing *Lophiotremataceae*. Related sequences are obtained following de Silva et al. (2018) and Phookamsak et al. (2019). Thirty-one strains are included in the combined analyses, which comprise 3639 characters for SSU, LSU, ITS, and *tef1-α* alignment. *Lophiostoma arundinis* (CBS 621.86) and *L. crenatum* (CBS 629.87) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -11856.946004 is presented. The matrix had 630 distinct alignment patterns, with 9.85% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244862, C = 0.255944, G = 0.269198, T = 0.229995; substitution rates AC = 1.462154, AG = 2.709696, AT = 1.642078, CG = 1.234650, CT =

9.229432, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Crassimassarina baoshanensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 43

Index Fungorum number: IF901353; Facesoffungi Number: FoF13884

Holotype – HKAS 122702

Etymology – The species epithet “baoshan” refers to the country where the specimen was collected.

Saprobic on dead woody twigs of *Castanopsis orthacantha*. Sexual morph: *Ascomata* 270–400 µm high × 250–300 µm diam., ($\bar{x}$ = 350 × 285 µm, n = 5), immersed, solitary or scattered, coriaceous, globose to subglobose, black. *Ostioles* central, 120–140 µm high × 110–160 µm diam., ($\bar{x}$ = 135 × 136 µm, n = 5), globose in section. *Peridium* 12–22 µm wide, 2–4-layered, comprising brown cells of *textura angularis*. *Hamathecium* 1–2 µm wide, comprising cylindrical, branched, septate, anastomosed pseudoparaphyses embedded in a hyaline gelatinous matrix. *Asci* 130–180 × 24–29 µm ($\bar{x}$ = 155 × 27 µm, n = 20), 8-spored, bitunicate, clavate, straight or curved, apically rounded, short pedicellate, with a minute ocular chamber. *Ascospores* 37–45 × 10–13 µm ($\bar{x}$ = 40 × 11.5 µm, n = 30), overlapping biserial, broadly fusiform with rounded ends, straight, initially hyaline, becoming brown at maturity, 1(–3)-septate, strongly constricted at the septum, guttulate in each cell, thick and smooth-walled, with a gelatinous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of ascospore. Colonies on PDA, reaching 40–50 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, flat, entire edge, gray white at the center, atrovirens at the margin; reverse, atrovirens.

Material examined – China, Yunnan Province, Baoshan, on dead woody twigs of *Castanopsis orthacantha* (Fagaceae), 12 July 2020, G.C. Ren, BS07 (HKAS 122702, holotype), ex-type living culture KUMCC 21-0499; *ibid.*, BS08 (HKAS 122703, isotype), ex-isotype living culture KUMCC 21-0500.

GenBank numbers – KUMCC 21-0499: SSU: OQ168212, LSU: OQ170858, ITS: OQ158936, *tef1-α*: OR613433; KUMCC 21-0500: SSU: OQ168213, LSU: OQ170859, ITS: OQ158937, *tef1-α*: OR613434.

Notes – *Crassimassarina baoshanensis* is introduced as a new species based on its distinct morphology and the phylogeny of the combined SSU, LSU, ITS, and *tef1-α* dataset. Our species formed a sister clade to *C. macrospora* with 100% ML bootstrap support and 1.00 BYPP value (Fig. 42). Our species is similar to *C. macrospora* in having globose to subglobose ascomata, papillate ostiolar, cylindrical asci and broadly fusiform ascospores with a gelatinous sheath. However, *C. baoshanensis* differs from *C. macrospora* in having coriaceous, globose ostioles, 12–22 µm wide, a 2–4-layered peridium, clavate asci and brown ascospores, while *C. macrospora* has carbonaceous ostioles, 25–60 µm wide, composed of 6–8 layers of peridium, cylindrical asci and hyaline ascospores (Hashimoto et al. 2017). Sequence comparison for the ITS region between *Crassimassarina baoshanensis* (KUMCC 21-0499) and *C. macrospora* (KT 1764) showed a 1.5% (7/484 bp, without gaps) base pair difference in ITS region, 1% (9/981 bp, without gaps) base pair difference in *tef1-α* region, 0.6% (5/850 bp, without gaps) base pair difference in LSU region.

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

Neohendersoniaceae was introduced by Giraldo et al. (2017), with *Neohendersonia* as the type genus. Wijayawardene et al. (2022) accepted five genera in *Neohendersoniaceae*, *Brevicollum*, *Crassiparies*, *Medicopsis*, *Neohendersonia* and *Neomedicopsis*. This family is characterised by having immersed, globose to depressed globose ascomata with short cylindrical or erumpent at ostiolar neck; peridium composed of polygonal to rectangular, thin-walled cells; septate, branched

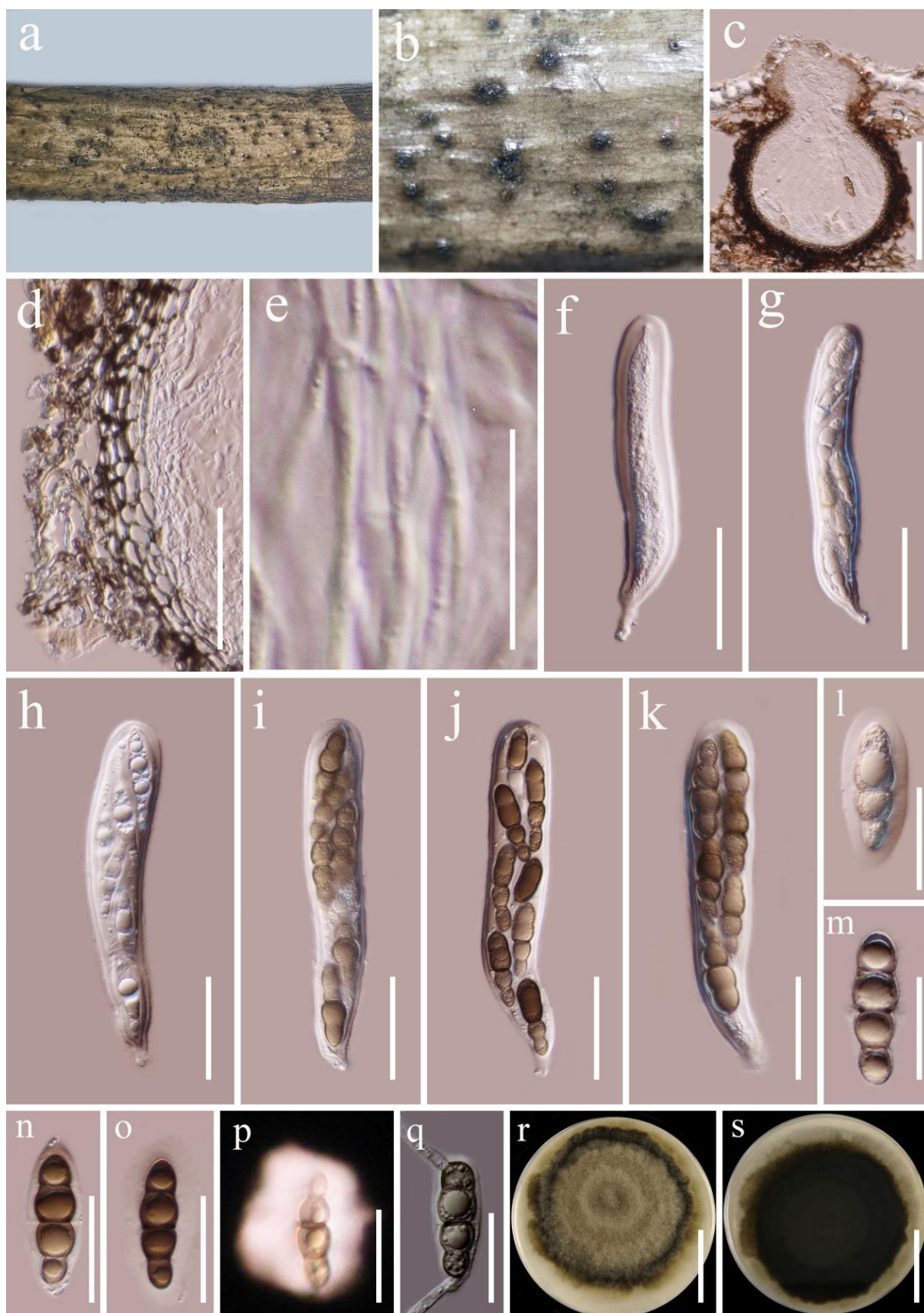


Figure 43 – *Crassimassarina baoshanensis* (HKAS 122702, holotype). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–k Asci. l–o Ascospores. p Ascospore stained in Indian ink to show the mucilaginous sheath. q Germinated ascospore. r, s Culture characters on PDA (r = from above, s = from below). Scale bars: c = 200 μ m, d, f–k = 50 μ m, e = 20 μ m, l–q = 30 μ m, r, s = 20 mm.

and anastomosed, cellular pseudoparaphyses; cylindrical to clavate, bitunicate, fissitunicate asci; cylindrical to clavate, bitunicate, fissitunicate ascospores (Tanaka et al. 2017, Hongsanan et al. 2020). The asexual morphs of this family are coelomycetous. Coelomycetous members are characterized by pycnidial, globose to subglobose conidiomata; holoblastic or phialidic, ampulliform to cylindrical, hyaline conidiogenous cells; ellipsoidal to cylindrical with rounded ends or slightly angular ends, hyaline, aseptate or 1-septate or multi-septate conidia (Hongsanan et al. 2020). In this study, we report a new host record of *Crassiparies quadrisporus* from *Shorea assamica* in China.

Crassiparies quadrisporus M. Matsum., K. Hiray. & Kaz. Tanaka, in Li et al., Fungal Diversity 78: 63 (2016) Fig. 44

Index Fungorum number: IF815295; Facesoffungi number: FoF02025

Saprobic on dead woody twigs of *Shorea assamica*. Sexual morph: *Ascomata* 160–360 µm high × 270–420 µm diam., ($\bar{x}$ = 240 × 340 µm, n = 6), scattered, solitary, sometimes in groups of 2–3, globose to subglobose, immersed to partially erumpent through the host tissues, black, with a central ostiole. *Peridium* 19–26 µm wide, comprising two types of cell layers, outer layer brown, inner layer comprising hyaline, thick-walled cells of *textura angularis*. *Hamathecium* comprising 1.5–2.5 µm wide, filiform, hyaline, septate, branched pseudoparaphyses embedded in a gelatinous matrix. *Asci* 80–120 × 18–23 µm ($\bar{x}$ = 99 × 20 µm, n = 25), 4-spored, bitunicate, cylindric to broadly clavate, straight or slightly curved, apically rounded, with short truncated pedicel. *Ascospores* 30–33 × 9–13 µm ($\bar{x}$ = 31.3 × 11.4 µm, n = 30), 1–2-seriate, hyaline, broadly fusiform, straight or slightly curved with rounded ends, 1-septate, constricted at the septum, smooth-walled, large guttules in each cell. Asexual morph: *Conidiomata* pycnidial, scattered, globose to depressed globose, 170–530 µm high, 130–300 µm diam., ostiolate. *Ostiolar* neck 60–230 µm high, 60–130 µm diam., central, cylindrical to papillate, composed of rectangular to subglobose, thick-walled, 3–10 µm, dark brown cells. *Conidiomatal* wall 5–10 µm thick at the side, composed of rectangular to polygonal, thin-walled, 3.5–10 × 2–5 µm, pale brown cells. *Paraphyses* and *conidiophores* absent. *Conidiogenous cells* cylindrical to lageniform, 5.5–10 × 2–3.5 µm, phialidic. *Conidia* cylindrical, 6.5–14.5(–17) × 2.5–4 µm (mean ± SD = 10.2 ± 2.2 × 3.1 ± 0.3 µm, n = 50), l/w (2.2–)2.5–4.0(–4.5) (mean ± SD = 3.3 ± 0.6, n = 50), hyaline, aseptate, without sheath (Tanaka et al. 2017).

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cell of ascospore. Colonies on PDA, reaching 40 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, fimbriate, atrovirens, dense, flat; reverse, atrovirens.

Material examined – China, Yunnan Province, Baoshan, on dead woody twigs of *Shorea assamica* (Dipterocarpaceae), 13 July 2020, G.C. Ren, BS22 (HKAS 122709), living culture KUMCC 21-0511.

Known distribution – On dead twigs of *Acer* sp. in Japan (Li et al. 2016), on dead woody twigs of *Shorea assamica* in China (This study).

GenBank numbers – LSU: OQ170861, ITS: OQ158939, *tef1-α*: OR613435.

Notes – *Crassiparies quadrisporus* was introduced by Li et al. (2016) based on the combined phylogeny of LSU and SSU sequence data. In the present study, a multi-gene phylogeny indicates that our strain of *C. quadrisporus* (KUMCC 21-0511) formed a sister clade with other strains of *C. quadrisporus* (HHUF 30409, KH111, HHUF 30590) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 18). Our collection (KUMCC 21-0511) is similar to *C. quadrisporus* (HHUF 30409, HHUF 30590) in having 4-spored, bitunicate, cylindric to broadly clavate asci and hyaline, broadly fusiform, 1-septate ascospores (Li et al. 2016, Tanaka et al. 2017). *Crassiparies quadrisporus* is a saprobic on dead twigs of *Acer* sp. (Sapindaceae) and *Machilus japonica* (Lauraceae) in Japan (Li et al. 2016, Tanaka et al. 2017). Therefore, we report our saprobic collection KUMCC 21-0511 as the first record of *Crassiparies quadrisporus* on the woody litter of *Shorea assamica* in China.

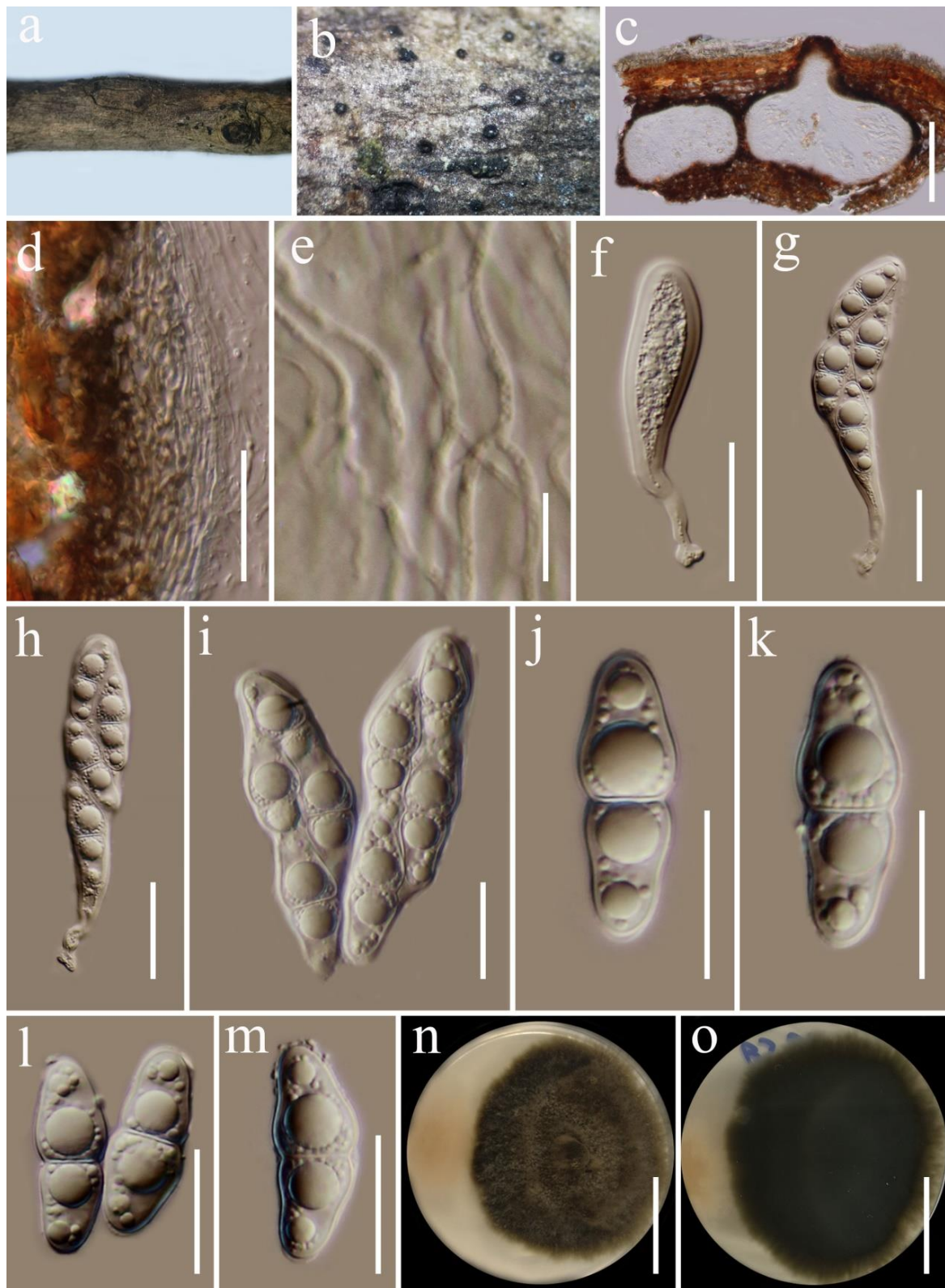


Figure 44 – *Crassiparies quadrisporus* (HKAS 122709). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–m Ascospores. n, o Culture characters on PDA (n = from above, o = from below). Scale bars: c = 200 μ m, d, f–i = 30 μ m, e = 10 μ m, j–m = 20 μ m, n, o = 20 mm.

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

Nigrogranaceae was introduced by Jaklitsch & Voglmayr (2016) to accommodate *Nigrograna* and comprises a single genus (Wijayawardene et al. 2022). This family is characterised

by having immersed-erumpent, globose to sub-globose, black ascomata with papillate to cylindrical ostiole; cellular, septate and branched pseudoparaphyses; bitunicate, fissitunicate, cylindric clavate to broadly clavate asci with a knob-like pedicel; fusoid to narrowly ellipsoid, pale to chocolate brown, mostly 1–3-septate ascospores (Jaklitsch & Voglmayr 2016, Hongsan et al. 2020). The asexual morphs of this family are characterized by pycnidial, globose conidiomata; peridium brown, pseudoparenchymatous; ampulliform, lageniform, or subcylindrical phialides; rod-like to ellipsoid, hyaline or subhyaline, aseptate conidia (Jaklitsch & Voglmayr 2016). In this study, we report on two new species and three new host records of *Nigrograna* in China.

Nigrograna kunmingensis T.Y. Du & Tibpromma Fungal Diversity (2023)

Fig. 46

Index Fungorum number: IF559865; Facesoffungi Number: FoF12956

Saprobic on dead twigs of *Castanopsis mekongensis*. Sexual morph: *Ascomata* 97–160 µm high, 150–320 µm diam., ($\bar{x}$ = 133 × 213 µm, n = 6), immersed under a small blackened pseudoclypeus, appearing as black, circle regions on the host surface, solitary or gregarious, subglobose or elliptical to ampulliform, dark brown, with an ostiole. *Peridium* 8–16 µm wide, 2–5-layered, composed of dark brown cells of *textura angularis*. *Hamathecium* 1.3–2.5 µm wide, comprising numerous, filamentous, branching, septate, hyaline pseudoparaphyses. *Asci* 70–97 × 9.5–14 µm ($\bar{x}$ = 84 × 12 µm, n = 20), 3–8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, slightly curved, short pedicellate, apically rounded, with a minute ocular chamber when immature. *Ascospores* 14–17 × 5.5–7.5 µm ($\bar{x}$ = 15.6 × 6.3 µm, n = 30), overlapping 1–2-seriate, broadly fusiform to ellipsoid, straight, initially yellowish brown with 1-septate, becoming to brown with 3-septate when mature, the upper cell is slightly wider than the lower cell, slightly constricted at the primary median septum, guttulate. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, flat, umbonate, surface rough with undulate edge, white, velvety; reverse, dark brown at the center, white at the margin.

Material examined – China, Yunnan Province, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Castanopsis mekongensis* (Fagaceae), 20 July 2020, G.C. Ren, LGY13 (HKAS 122729), living culture KUMCC 21-0551.

Known distribution – On dead stems of *Gleditsia sinensis* (Fabaceae) and dead twigs of *Castanopsis mekongensis* in China (Liu et al. 2024, this study).

GenBank numbers – SSU: OQ168219, LSU: OQ170866, ITS: OQ158944, *tef1-α*: OR613436.

Notes – *Nigrograna kunmingensis* was introduced by Liu et al. (2024) based on the combined phylogenetic analyses of SSU, LSU, ITS, *rpb2*, and *tef1-α* sequence data. In the present study, the multi-gene phylogeny indicates that our strain (KUMCC 21-0551) and other existing strains of *N. kunmingensis* (ZHKUCC 22-0242, ZHKUCC 22-0243) group together and formed a monophyletic clade with 100% ML bootstrap support and 1.00 BYPP value (Fig. 45). Our collection (KUMCC 21-0551) have no significant differences with the type species of *N. kunmingensis* (ZHKUCC 22-0242) (Liu et al. 2024). Based on morphological characteristics and phylogenetic analyses, we report our isolation as the first record of *N. kunmingensis* from decaying wood of *Castanopsis mekongensis* in China.

Nigrograna lancangensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 47

Index Fungorum number: IF901354; Facesoffungi number: FoF13886

Holotype – HKAS 122735

Etymology – The epithet “lancang” refers to Lancang, where the specimen was collected.

Saprobic on dead twigs of *Castanopsis mekongensis*. Sexual morph: *Ascomata* 140–306 µm high, 189–509 µm diam., ($\bar{x}$ = 196 × 323 µm, n = 5), immersed to erumpent, solitary or scattered, elliptical to ampulliform, dark brown, 1–2-loculate. *Ostioles* 110–170 × 62–103 ($\bar{x}$ = 141 × 81, n = 5) µm, black, papillate, central. *Peridium* 12–20 µm wide, 3–4-layered, composed of dark brown cells of *textura angularis*. *Hamathecium* 1.4–2.5 µm wide, comprising numerous, filamentous,

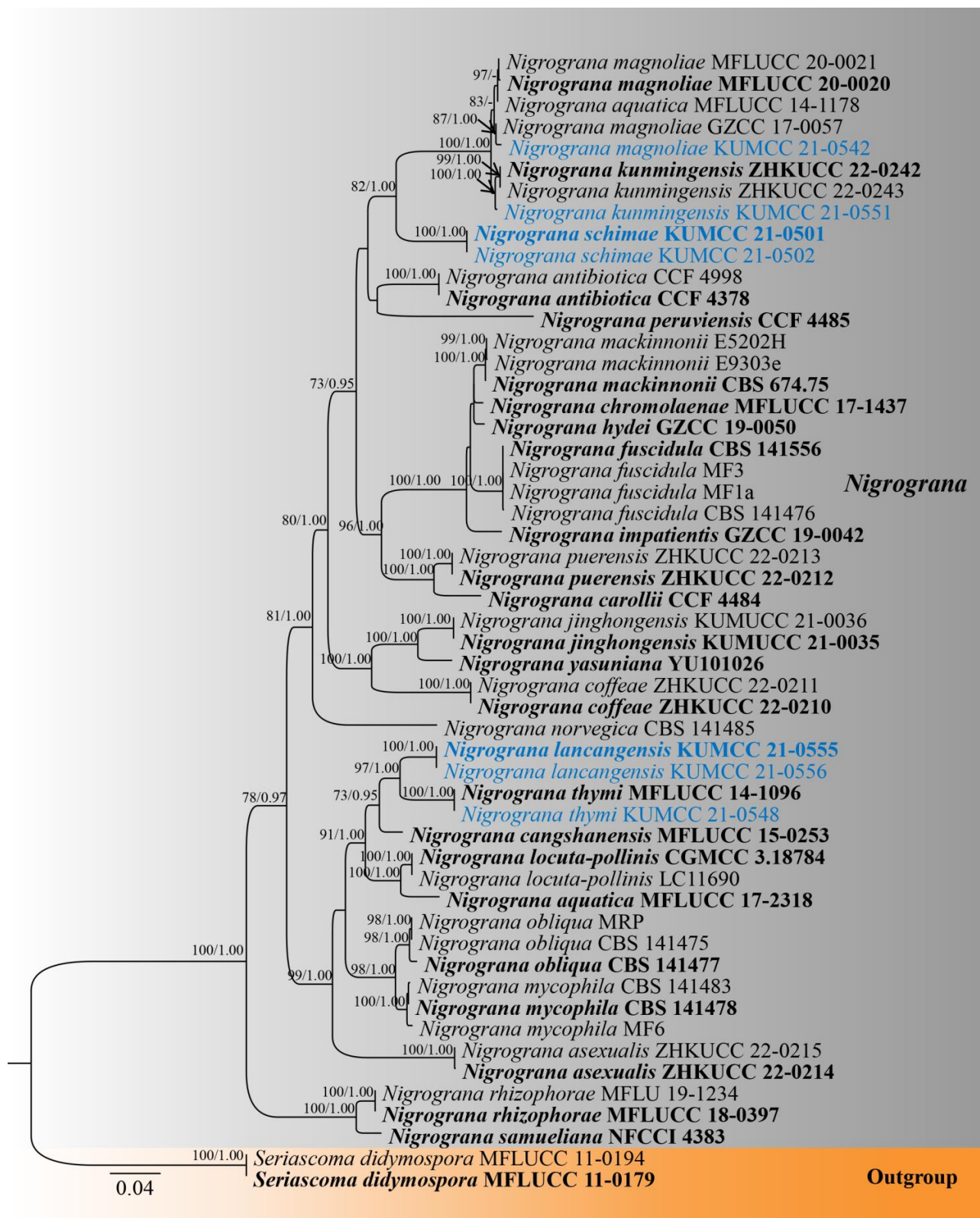


Figure 45 – Phylogram generated from ML analysis based on SSU, LSU, ITS, *tef1-α*, and *rpb2* sequence data, representing *Nigrograna* (*Nigrogranaceae*). Related sequences are obtained following de Lu et al. (2022b) and Boonmee et al. (2021). Forty-six strains are included in the combined analyses, which comprise 4194 characters for SSU, LSU, ITS, *tef1-α*, and *rpb2* alignment. *Seriascoma didymospora* (MFLUCC 11-0194, MFLUCC 11-0179) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -17623.075885 is presented. The matrix had 1076 distinct alignment patterns, with 31.53% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.248028, C = 0.248350, G =

0.266441, T = 0.237180; substitution rates AC = 1.506227, AG = 4.589175, AT = 1.553542, CG = 1.033267, CT = 10.958332, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

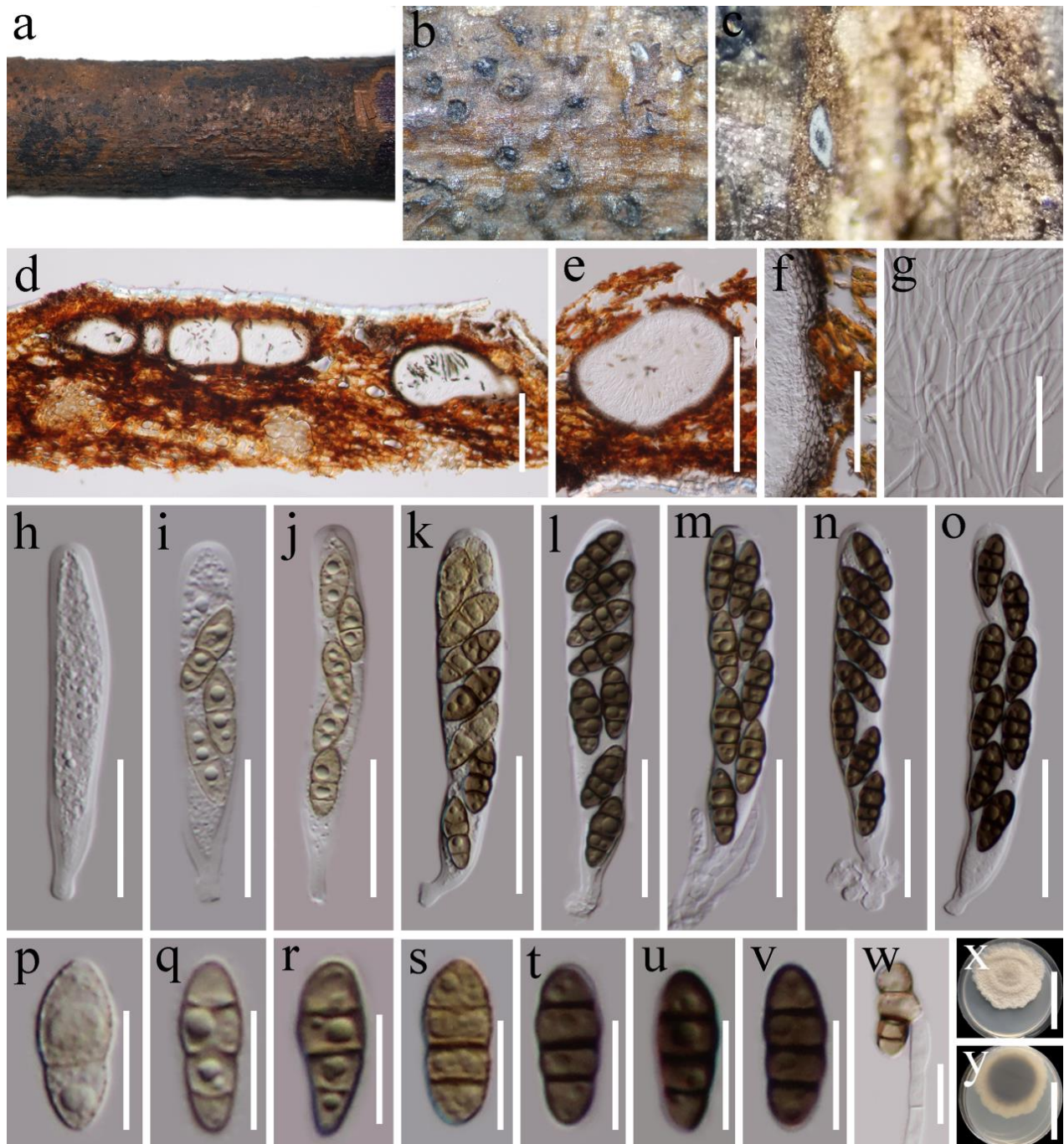


Figure 46 – *Nigrograna kunmingensis* (HKAS 122729). a Material examined. b, c Appearance of ascomata on the host substrate. d, e Section of an ascoma. f Peridium. g Pseudoparaphyses. h–o Asci. p–v Ascospores. w Germinated ascospore. x, y Culture characters on PDA (x = from above, y = from below). Scale bars: d, e = 200 µm, f = 50 µm, g = 25 µm, h–o = 30 µm, p–w = 10 µm, x, y = 30 mm.

branching, septate, cellular pseudoparaphyses. Asci 75–95 × 13–15 µm ($\bar{x}$ = 79 × 14 µm, n = 20), 4–8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, slightly curved, short pedicellate,

apically rounded. Ascospores $16\text{--}21 \times 5.5\text{--}7.5 \mu\text{m}$ ($\bar{x} = 17.4 \times 6.5 \mu\text{m}$, $n = 40$), overlapping 1–2-seriate, ellipsoid, straight, initially hyaline to yellowish brown, 0–1-septate, becoming dark brown, 3-septate when mature, smooth-walled, with large guttules when mature, in most cases, the upper cell is slightly wider than the lower cell, rounded at both ends, slightly constricted at the primary median septum. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the first and second cell of ascospore from the apex. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, dense, filamentous, flat, slightly raised at the center, surface smooth with fimbriate edge, velvety, dark gray; reverse gray at margin, dark brown at center.

Material examined – China, Yunnan Province, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Castanopsis mekongensis* (Fagaceae), 20 July 2020, G.C. Ren, LGY18 (HKAS 122735, holotype), ex-type living culture KUMCC 21-0555, KUMCC 21-0556.

GenBank numbers – KUMCC 21-0555: SSU: OQ168220, LSU: OQ170867, ITS: OQ158945, *tef1-α*: OR613437, *rpb2*: OR578560; KUMCC 21-0556: SSU: OQ168221, LSU: OQ170868, ITS: OQ158946.

Notes – In the phylogenetic analyses, *Nigrograna lancangensis* formed a clade sister to *N. thymi* (MFLUCC 14-1096, KUMCC 21-0548) with 91% ML bootstrap support and 1.00 BYPP value (Fig. 45). *Nigrograna lancangensis* fits well with the generic concept of *Nigrograna* in having immersed to erumpent ascomata with ostiolar, clavate and fissitunicate asci, ellipsoid, straight, septate, and smooth or verruculose ascospores, but distinct from *N. thymi* in having bilocular ascomata, ellipsoid, 3-septate ascospores, while *N. thymi* is characterised by broadly fusiform to inequilateral, 4–5-septate ascospores (Hyde et al. 2017). Sequence comparison for the ITS region between *Nigrograna lancangensis* (KUMCC 21-0555) and *N. thymi* (MFLUCC 14-1096) showed a 1.5% (7/484 bp, without gaps) base pair difference in ITS region, 3.7% (34/929 bp, without gaps) base pair difference in the *tef1-α* region, 0.8% (7/881 bp, without gaps) base pair difference in LSU region. Therefore, *Nigrograna lancangensis* is introduced as a new species based on its distinct morphology and phylogenetic position.

Nigrograna magnoliae Wanas., PLoS One 15 (7, e0235855): 10 (2020)

Fig. 48

Index Fungorum number: IF557331; Facesoffungi Number: FoF06278

Saprobic on dead twigs of *Castanopsis indica*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 140–250 μm high $\times$ 110–140 μm diam., ($\bar{x} = 200 \times 120 \mu\text{m}$, $n = 5$), scattered, immersed to erumpent, formed a dome-shaped areas on the host surface, black, unilocular, coriaceous, subglobose or obpyriform, with central ostioles. *Conidiomata* wall 15–30 μm thick, of unequal thickness, composed of dark brown outer layers and inner layers comprising brown, thick-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4.7–6.3 $\times$ 1.5–2.6 μm ($\bar{x} = 5.6 \times 2.1 \mu\text{m}$, $n = 10$), enteroblastic, phialidic, determinate, discrete, cylindrical, hyaline, smooth-walled, arising from the stratum. *Conidia* 3–4 $\times$ 1.4–1.8 ($\bar{x} = 3.5 \times 1.8$, $n = 30$) μm , straight, hyaline, oblong, one-celled, aseptate, ends rounded, smooth-walled, guttulates.

Culture characteristics – Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, flat, umbonate, surface rough with undulate edge, white, velvety; reverse, dark brown at the center, white at the margin.

Material examined – China, Yunnan Province, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Castanopsis indica* (Fagaceae), 19 July 2020, G.C. Ren, LGY01-1 (HKAS 122720), living culture KUMCC 21-0542.

Known distribution – Saprobic on dead twigs of *Magnolia denudate* (Magnoliaceae) in China (Wanasinghe et al. 2020b), on submerged wood in Thailand (Zhang et al. 2020a), dead twigs of *Magnolia grandiflora* (Magnoliaceae) in Thailand (<https://www.ncbi.nlm.nih.gov/nuccore/MN081891.1>), on dead twigs of *Castanopsis indica* (Fagaceae) in China (This study).

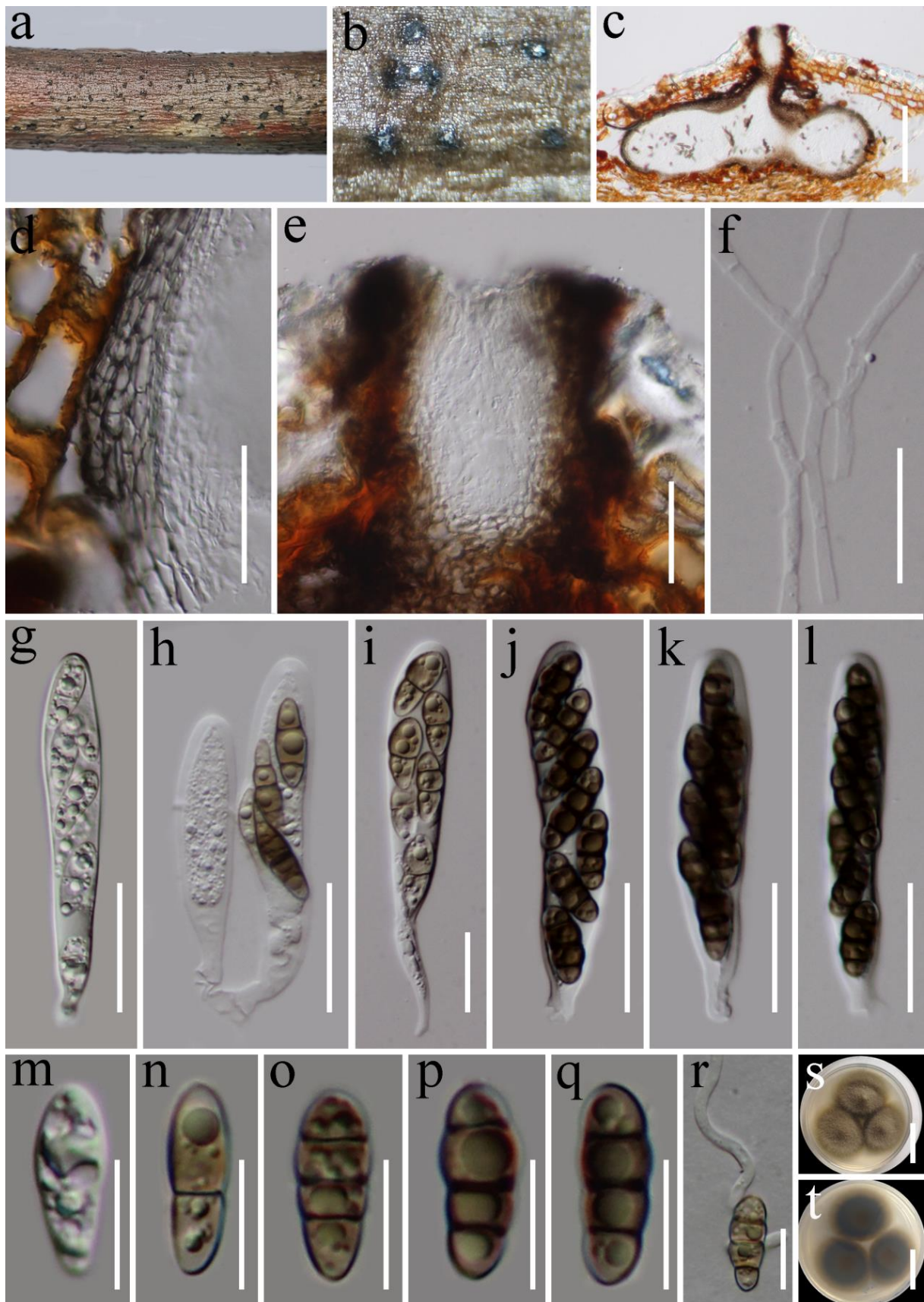


Figure 47 – *Nigrograna lancangensis* (HKAS 122735, holotype). a, b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Ostiolar neck. f Pseudoparaphyses. g–l Asci. m–q Ascospores. r Germinated ascospore. s, t Culture characters on PDA (s = from above, t = from below). Scale bars: c = 150 μ m, d, e = 30 μ m, f, g–l = 20 μ m, m–r = 10 μ m, s, t = 30 mm.

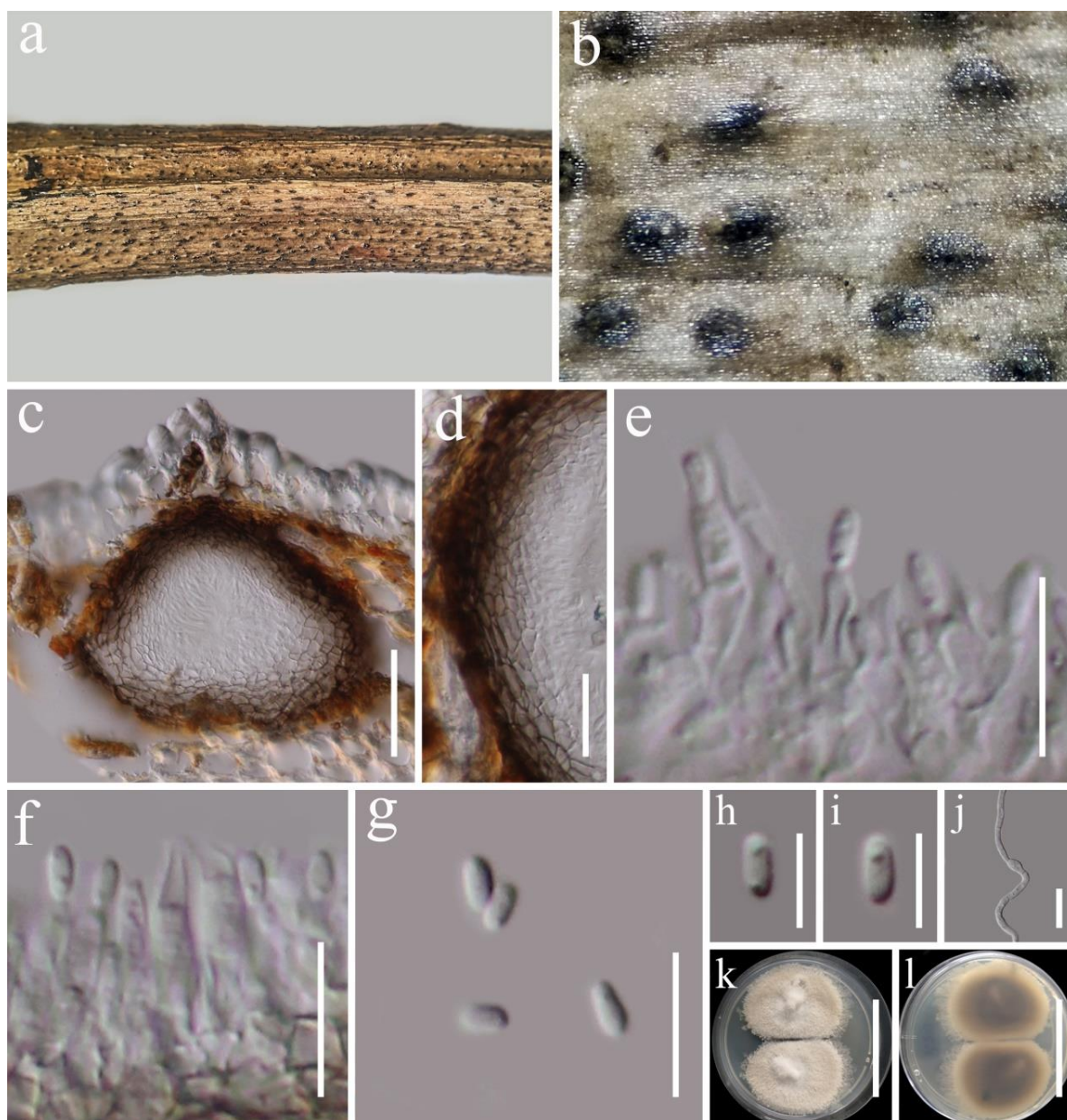


Figure 48 – *Nigrograna magnolia* (HKAS 122720) a Material examined. b Appearance of conidiomata on host substrate. c Sections through conidiomata. d Conidiomatal wall. e, f Conidiogenous cells and developing conidia. g–i Conidia. j Germinated conidium. k, l Culture characters on PDA (k = from above, l = from below). Scale bars: c = 50 μ m, d, j = 20 μ m, e–g = 10 μ m, h, i = 5 μ m, k, l = 30 mm.

GenBank numbers – SSU: OQ168217, LSU: OQ170864, ITS: OQ158942, *tef1- α* : OR613438, *rpb2*: OR578561.

Notes – In the phylogenetic analysis of present study, our strain KUMCC 21-0542 clustered with *N. magnoliae* (GZCC 17-0057) with 87% ML bootstrap support and 1.00 BYPP value (Fig. 45). *Nigrograna magnoliae* was introduced by Wanasinghe et al. (2020b) based on the combined phylogeny of SSU, LSU, *rpb2*, and *tef1- α* sequence data. Our asexual collection (KUMCC 21-0542) has no significant differences with the type species of *N. magnoliae* (MFLUCC 20-0020) (Wanasinghe et al. 2020b). Based on morphological characteristics and phylogenetic analysis, we report our isolation as a new host record of *N. magnoliae* from decaying wood of *Castanopsis indica* in China and provide the asexual morph for *N. magnoliae*. Furthermore, the sequence data of *N. aquatica* (MFLUCC 14-1178) was a direct submission without any publication, and we found that this species clustered with *N. magnolia* in our multi-gene phylogeny, while the type of

N. aquatica (MFLUCC 17-2318) clustered with *N. locuta-pollinis*. However, the comparison of SSU, LSU, ITS, *rpb2* and *tef1-α* sequence data reveals there is no significant difference between *N. aquatica* (MFLUCC 14-1178) and *N. magnoliae* (MFLUCC 20-0020). Therefore, we suspect that the author may have misidentified the *N. aquatica* when submitting the strain MFLUCC 14-1178 sequence.

Nigrograna schimae G.C. Ren & K.D. Hyde, sp. nov.

Fig. 49

Index Fungorum number: IF901356; Facesoffungi number: FoF13887

Holotype – HKAS 122704.

Etymology – The epithet refers to the host genus “*Schima*”.

Saprobic on dead twigs of *Schima khasiana*. Sexual morph: Ascomata 100–300 µm high, 65–200 µm diam., ($\bar{x}$ = 215 × 140 µm, n = 5), immersed beneath the host epidermis, solitary or gregarious, subglobose or obpyriform, dark brown, coriaceous, ostiolate, 1–2-loculate, with few brown, septate tomentum on the outer surface. Ostioles central. Peridium 15–23 µm wide, 3–5 layered, composed of hyaline to brown cells of *textura angularis*. Hamathecium 2–4.5 µm wide, comprising numerous, branching, septate, cellular pseudoparaphyses constricted at the septum. Asci 58–77 × 10.5–11 µm ($\bar{x}$ = 65 × 10.8 µm, n = 20), 4–8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, slightly curved, short pedicellate, apically rounded. Ascospores 13.5–16.5 × 4.5–5.5 µm ($\bar{x}$ = 15 × 5.2 µm, n = 30), overlapping 1–2-seriate, broadly fusiform to ellipsoid, straight, initially hyaline to yellowish brown, aseptate to one-septate, becoming dark brown, 3-septate when mature, smooth-walled, with guttules when mature, the upper cell is slightly wider than the lower cell, rounded at both ends, slightly constricted at the primary median septum. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cell of ascospore. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, umbonate, filamentous, surface smooth with fimbriate edge, velvety, grayish white, gray at margin; reverse, dark brown, white at margin.

Material examined – China, Yunnan Province, Baoshan, on dead woody twigs of *Schima khasiana* (Theaceae), 11 July 2020, G.C. Ren, BS09 (HKAS 122704, holotype), ex-type culture KUMCC 21-0501. *ibid.*, living culture KUMCC 21-0502.

GenBank numbers – KUMCC 21-0501: SSU: OQ168215, LSU: OQ170862, ITS: OQ158940, *tef1-α*: OR613439, *rpb2*: OR578562; KUMCC 21-0502: SSU: OQ168216, LSU: OQ170863, ITS: OQ158941.

Notes – In the phylogenetic analyses, *N. schimae* formed a sister clade to *N. magnoliae* and *N. kunmingensis* with 82% ML bootstrap support 1.00 BYPP value (Fig. 45). This species shares similar morphology with *N. magnoliae* in having solitary or gregarious, brown ascomata, fissitunicate, clavate to cylindric-clavate, short pedicellate, apically rounded, with minute ocular chamber asci, and ellipsoid, brown, 3-septate, guttulate ascospores. However, *N. schimae* is distinct from *N. magnoliae* in having bilocular ascomata with brown, septate tomentum, tapering pseudoparaphyses, constricted at the septum, while *N. magnoliae* has unilocular ascomata brown to dark brown, septate pseudoparaphyses without constricted at the septum (Wanasinghe et al. 2020b, Zhang et al. 2020a). *Nigrograna schimae* shares similar morphology with *N. kunmingensis* in having immersed, subglobose to globose ascomata with septate tomentum on the outer surface, septate, branched pseudoparaphyses, cylindrical to clavate asci, and dark brown, 3-septate ascospores when mature. However, *N. schimae* is distinct from *N. kunmingensis* in having bilocular ascomata and thinner peridium (15–23 µm vs. 20–60 µm). Sequence comparison for the ITS region between *Nigrograna schima* (KUMCC 21-0501) and *N. magnoliae* (MFLUCC 20-0020) showed a 7.1% (33/466 bp, without gaps) base pair difference in ITS region, 3.9% (36/912 bp, without gaps) base pair difference in *tef1-α* region, 1.8% (15/831 bp, without gaps) base pair difference in LSU region, 11% (110/999 bp, without gaps) base pair difference in *rpb2* region. Sequence comparison for the ITS region between *Nigrograna schima* (KUMCC 21-0501) and *N. kunmingensis*

(ZHKUCC 22-0242) showed a 6.4% (30/466 bp, without gaps) base pair difference in ITS region, 3.8% (35/911 bp, without gaps) base pair difference in *tef1- α* region, 1.9% (16/831 bp, without gaps) base pair difference in LSU region. Herein, *Nigrograna schima* is introduced as a new species based on its distinct morphology and phylogenetic position.

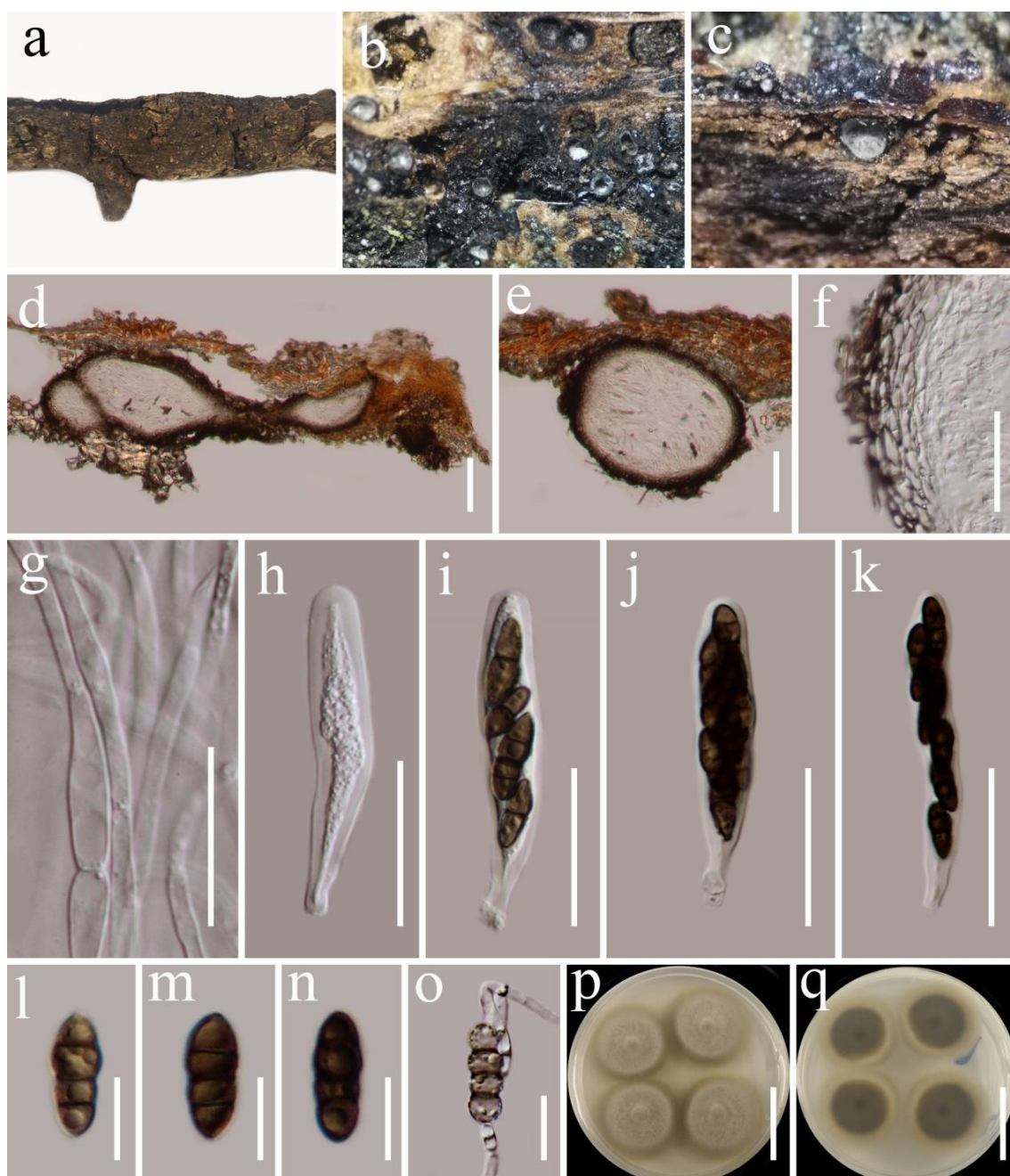


Figure 49 – *Nigrograna schimae* (HKAS 122704, holotype). a Material examined. b Horizontal sections of ascomata. c–e Vertical section through an ascoma. f Peridium. g Pseudoparaphyses. h–k Asci. l–n Ascospores. o Germinated ascospore. p, q Culture characters on PDA (p = from above, q = from below). Scale bars: d, e = 100 μ m, f, h–k = 30 μ m, g = 20 μ m, l–o = 10 μ m, p, q = 30 mm.

Nigrograna thymi Mapook, Camporesi & K.D. Hyde Fungal Diversity 87: 68 (2017) Fig. 50
Index Fungorum number: IF552958; Facesoffungi Number: FoF03119
Saprobic on dead twigs of *Castanopsis mekongensis*. Sexual morph: *Ascomata* 140–250 μ m high, 110–140 μ m diam., ($\bar{x}$ = 210 $\times$ 120 μ m, n = 5), immersed to erumpent, solitary or scattered,

subglobose or obpyriform, dark brown. *Ostioles* central, 125–145 × 50–80 ($\bar{x}$ = 135 × 60, n = 5) μm , immersed, long papillate, long, hyaline hyphae with periphyses. *Peridium* 11–30 μm wide, 3–7-layered, slightly thin at the base, composed of dark brown outer layers and light brown inner layers of thick-walled cells of *textura angularis*. *Hamathecium* 1–2.5 μm wide, comprising filamentous, branched, septate pseudoparaphyses, constricted at septa, embedded in a gelatinous matrix. *Asci* 50–75 × 8–11 μm ($\bar{x}$ = 64 × 9.5 μm , n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, slightly curved, short pedicellate, apically rounded. *Ascospores* 12–15 × 3.4–4.5 μm ($\bar{x}$ = 13.8 × 4 μm , n = 30), overlapping 1–2-seriate, ellipsoid to fusiform, straight, initially yellowish brown, 1-septate, becoming brown, 3-septate when mature, slightly constricted at the primary median septum, guttules. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cell of ascospores. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, filamentous, flat, slightly raised at the center, surface smooth with fimbriate edge, velvety, light brown at the margin, white at the center; reverse, grayish brown.

Material examined – China, Yunnan Province, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Castanopsis mekongensis* (Fagaceae), 20 July 2020, G.C. Ren, LGY08 (HKAS 122727), living culture KUMCC 21-0548.

Known distribution – Saprobiic on dead aerial stem of *Thymus oenipontanus* (Lamiaceae) in Italy (Hyde et al. 2017), dead twigs attached to *Magnolia grandiflora* (Magnoliaceae) in China (de Silva et al. 2022), dead woody twigs of *Castanopsis mekongensis* (Fagaceae) in China (This study).

GenBank numbers – SSU: OQ168218, LSU: OQ170865, ITS: OQ158943, *tef1- α* : OR613440, *rpb2*: OR578563.

Notes – In the present study, the multi-gene phylogeny indicates that our strain (KUMCC 21-0548) clustered with *Nigrograna thymi* (MFLUCC 14-1096) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 45). However, our strain (KUMCC 21-0548) differs from MFLUCC 14-1096 in having shorter asci (50–75 × 8–11 μm vs. 90–94(–98) × 8–11 μm), ellipsoid to fusiform, 3-septate ascospores, while MFLUCC 14-1096 has fusiform to inequilateral, 4–5-septate ascospores. Hence, the sexual characteristics of *N. thymi* should be studied and compared with further fresh collections. *Nigrograna thymi*, collected from a dead aerial stem of *Thymus oenipontanus* in Italy, was introduced by Hyde et al. (2017) based on the combined phylogeny of LSU, ITS, SSU, and *rpb2* sequence data. Taking into consideration the phylogenetic analyses, we report our saprobic strain (KUMCC 21-0548) as a new record of *N. thymi* on the woody litter of *Castanopsis mekongensis* in China.

Parabambusicolaceae Kaz. Tanaka and K. Hiray., Studies in Mycology 82: 115 (2015)

Parabambusicolaceae was introduced by Tanaka et al. (2015) to accommodate *Parabambusicola* as the type genus. Wijayawardene et al. (2022) accepted nine genera in *Parabambusicolaceae*. Subsequently, Xie et al. (2022) introduced two novel genera, *Scolecohyalosporium* and *Neomultiseptospora*, in *Parabambusicolaceae* based on multi-gene phylogeny coupled with morphological differences. Therefore, twelve genera are currently accepted in *Parabambusicolaceae*, *Aquastroma*, *Lonicericola*, *Multilocularia*, *Multiseptospora*, *Neoaquastroma*, *Neomultiseptospora*, *Parabambusicola*, *Paramonodictys*, *Paratrimmatostroma*, *Pseudomonodictys*, and *Scolecohyalosporium*. The sexual morphs of this family are characterized by immersed to erumpent, globose, subglobose to hemisphaerical ascomata; peridium containing cell layers of *textura angularis*; 8-spored, bitunicate, clavate to broadly cylindrical asci with an ocular chamber; 2–3-seriate, clavate, ellipsoidal to subfusiform, hyaline, reddish-brown or pale, 1- to multi-septate ascospores, generally surrounded by an irregular, hyaline, gelatinous sheath. The asexual morphs of *Parabambusicolaceae* is coelomycetous, phoma-like, or sporodochial, monodictys-like hyphomycetous (Tanaka et al. 2015, Hongsan et al. 2020). In this study, we report two new species, *Neoaquastroma ehretia* and *Scolecohyalosporium baoshanense*.

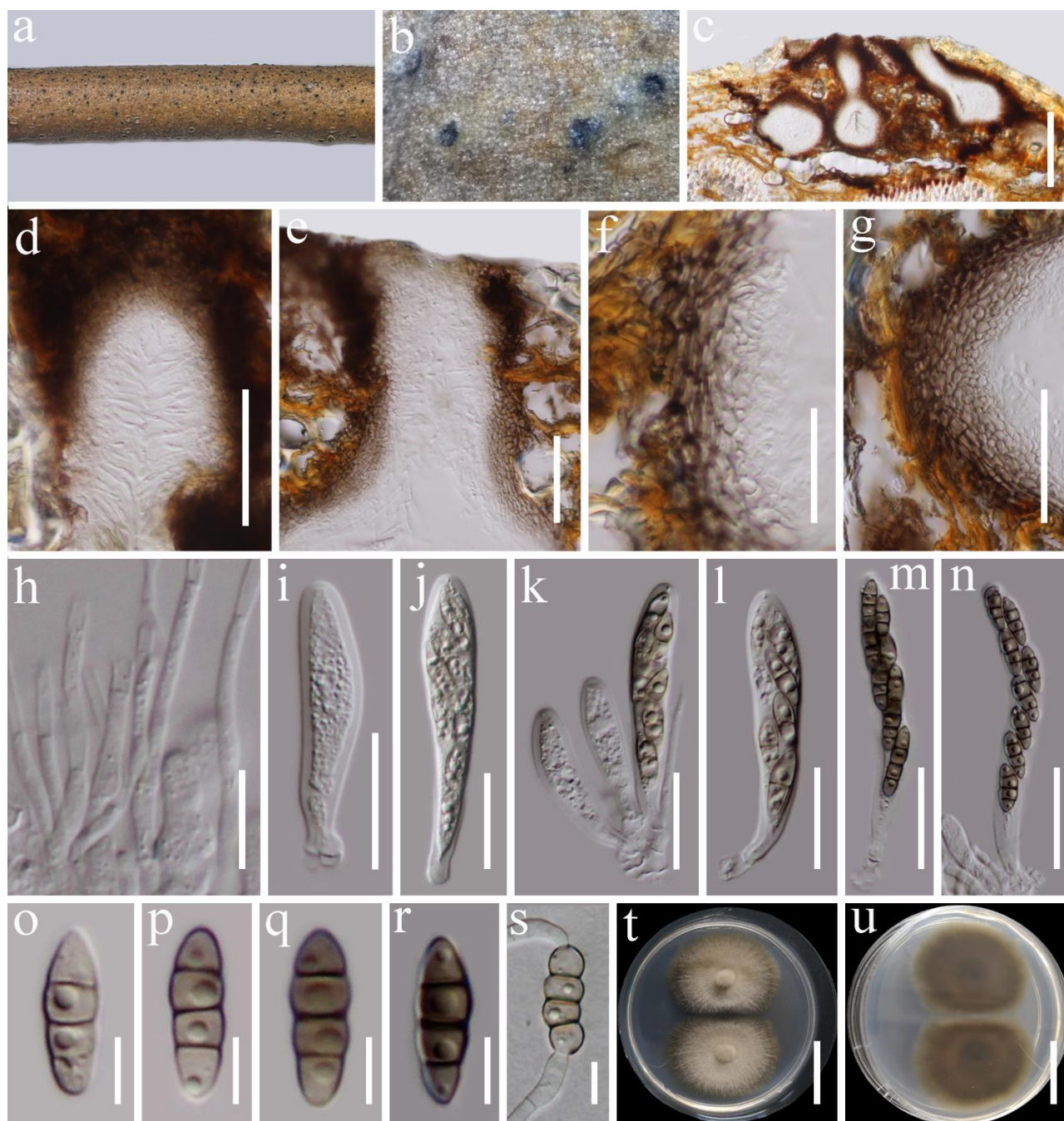


Figure 50 – *Nigrograna thymi* (HKAS 122727). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d, e Ostiolar neck. f, g Peridium. h Pseudoparaphyses. i–n Asci. o–r Ascospores. s Germinated ascospore. t, u Culture characters on PDA (t = from above, u = from below). Scale bars: c = 150 μ m, d, e, g = 50 μ m, f = 25 μ m, h = 10 μ m, i–n = 20 μ m, o–s = 5 μ m, t, u = 30 mm.

Neoaquastroma ehretiae G.C. Ren & K.D. Hyde, sp. nov.

Fig. 52

Index Fungorum number: IF901357; Facesoffungi Number: FoF13888

Holotype – HKAS 122743

Etymology – The epithet refers to the host genus “ehretia”.

Saprobic on dead woody twigs of *Ehretia acuminata*. Sexual morph: *Ascomata* 360–420 μ m high, 380–430 μ m diam., ($\bar{x}$ = 390 $\times$ 410 μ m, n = 5), solitary, scattered, immersed under small, blackened pseudoclypeus, uni-loculate, obpyriform or globose to subglobose, brown to dark brown, glabrous, ostioles central. *Peridium* 24–33 μ m wide, comprising two layers, outer layers composed

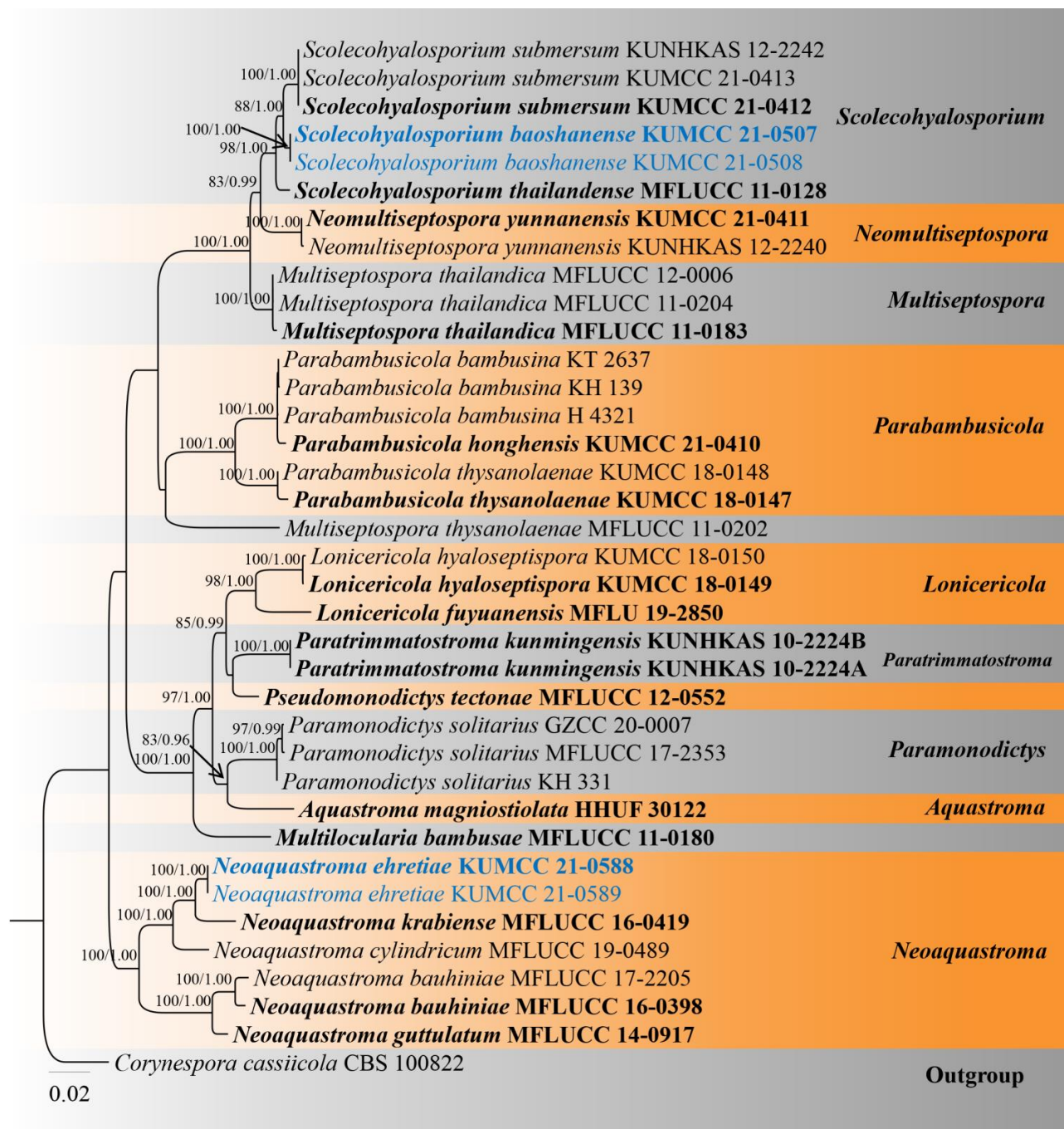


Figure 51 –Phylogram generated from ML analysis based on SSU, LSU, ITS, and *tef1-α* sequence data, representing *Nigrogranaceae*. Related sequences are obtained following Xie et al. (2022) and Phookamsak et al. (2023). Thirty-five strains are included in the combined analyses, which comprise 3311 characters for SSU, LSU, ITS, and *tef1-α* alignment. *Corynespora cassiicola* (CBS 100822) was used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -13584.772234 is presented. The matrix had 871 distinct alignment patterns, with 10.96% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.235255, C = 0.258240, G = 0.273696, T = 0.232809; substitution rates AC = 1.077058, AG = 2.178658, AT = 1.107003, CG = 1.470438, CT = 6.032092, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

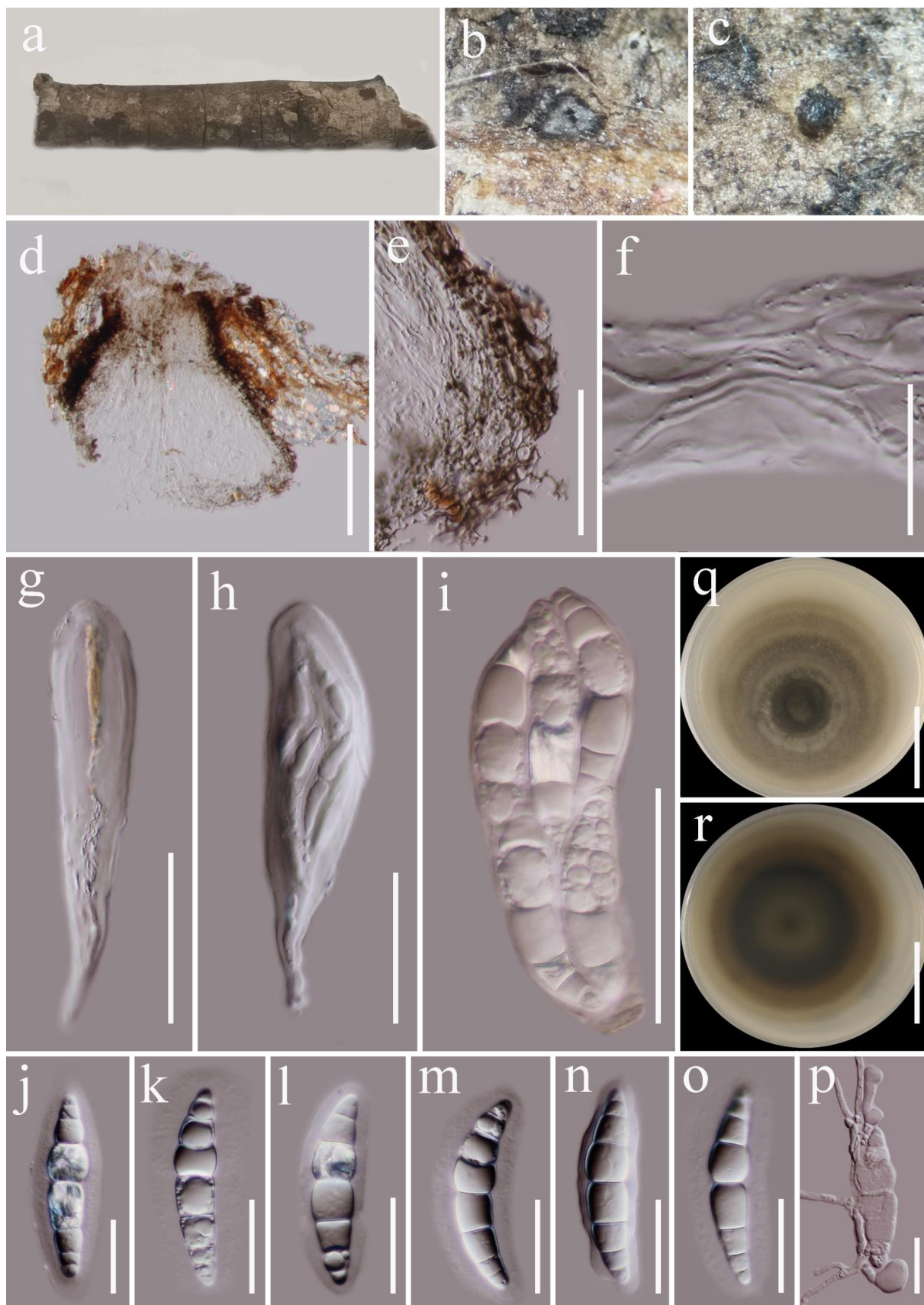


Figure 52 – *Neoaquastroma ehretiae* (HKAS 122743, holotype). a Material examined. b, c Appearance of ascomata on the host substrate. d Section of an ascoma. e Peridium. f Pseudoparaphyses. g–i Asci. j–o Ascospores. p Germinated ascospore. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: d = 200 μm , e, g–i = 100 μm , f, j–p = 50 μm , q, r = 30 mm.

of reddish to dark brown, thick-walled cell of *textura angularis* fused with host tissues, inner layer composed of hyaline cells of *textura angularis*. *Hamathecium* composed of dense, 1.2–2.4 µm wide, filamentous, branched, septate cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 115–135 × 30–36 µm ($\bar{x}$ = 126 × 33 µm, n = 20), 4–8-spored, bitunicate, fissitunicate, clavate, apically rounded with an ocular chamber and a short pedicel. *Ascospores* 50–60 × 10–13 µm ($\bar{x}$ = 56 × 11 µm, n = 20), overlapping biserial, hyaline, fusiform, straight to curved, narrow towards the apex, 5–7-transversely septate, deeply constricted at the middle, smooth-walled with small to large guttules, surrounded by a distinct mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the around cell of ascospore. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, flat, entire edge, band, dark grey at the center with greyish white margin, white grey; reverse, greenish grey at center, pale yellow at margin.

Material examined – China, Yunnan Province, Xishuangbanna, on dead woody twigs of *Ehretia acuminata* (Boraginaceae), 4 March 2020, G.C. Ren, JH48 (HKAS 122743, holotype), ex-type living culture KUMCC 21-0588, KUMCC 21-0589.

GenBank numbers – KUMCC 21-0588: LSU: OQ170869, ITS: OQ158947, *tef1-α*: OR613441; KUMCC 21-0589: LSU: OQ170870, ITS: OQ158948.

Notes – In the phylogenetic analyses of the present study, our strains (KUMCC 21-0588, KUMCC 21-0589) formed a sister clade to *N. krabiense* (MFLUCC 16-0419, type species) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 51). Our species differs from *N. krabiense* in having immersed, small, blackened pseudoclypeus, apicillate ascomata, and a peridium of 24–33 µm wide, while *N. krabiense* has semi-immersed to immersed ascomata with short hyphae projecting from peridium, which is 8–25 µm wide (Phukhamsakda et al. 2018). Sequence comparison for the ITS region between *Neoaquastroma ehretiae* (KUMCC 21-0588) and *N. krabiense* (MFLUCC 16-0419) showed a 5.4% (25/462 bp, without gaps) base pair difference in ITS region, 1.6% (14/903 bp, without gaps) base pair difference in the *tef1-α* region, 1% (7/689 bp, without gaps) base pair difference in LSU region. Here in, *Neoaquastroma ehretiae* is introduced as a new species based on its distinct morphology and the phylogeny of the combined SSU, LSU, ITS, and *tef1-α* dataset.

***Scolecophyalosporium baoshanense* G.C. Ren & K.D. Hyde, sp. nov.**

Fig. 53

Index Fungorum number: IF901358; Facesoffungi Number: FoF13889

Holotype – HKAS 122707

Etymology – The species epithet “baoshanense” refers to the location where the holotype was collected.

Saprobic on dead woody twigs of *Dipterocarpus gracilis*. Sexual morph: *Ascomata* 400–470 µm high, 390–460 µm diam., solitary, scattered, soft at the base and carbonaceous towards narrow apices, erumpent through the host surface, superficial, uni-loculate, conical to ovoid, black, glabrous, central ostiole. *Peridium* 40–55 µm wide, thick-walled, the outer layers composed of small, dark brown cells of *textura angularis* and the outer layers composed of swollen, brown cells of *textura angularis*. *Hamathecium* composed of dense, 1.7–2.5 µm wide, filamentous, branched, septate, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 170–270 × 8.7–9.7 µm ($\bar{x}$ = 221 × 9.3 µm, n = 20), 8-spored, bitunicate, fissitunicate, long cylindrical, slightly curved, apically rounded with an ocular chamber and a short pedicel. *Ascospores* 190–230 × 1.4–1.8 µm ($\bar{x}$ = 213 × 1.6 µm, n = 20), overlapping 1–2-seriate, hyaline, filiform, spirally arranged within the ascus, narrower towards the end cell, multi-septate, smooth-walled, guttulate. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the around cell of ascospore. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, flat, entire edge,

gray white with granular droplets of oil, black, glistening; reverse, light brown at center, pale yellow at margin.

Material examined – China, Yunnan Province, Baoshan, on dead woody twigs of *Dipterocarpus gracilis* (Dipterocarpaceae), 12 July 2020, G.C. Ren, BS17-1 (HKAS 122707, holotype), ex-type living culture KUMCC 21-0507, KUMCC 21-0508.

GenBank numbers – KUMCC 21-0507: SSU: OQ168222, LSU: OQ170871, ITS: OQ158949, *tef1-α*: OR613442; KUMCC 21-0508: SSU: OQ168222, LSU: OQ170872, ITS: OQ158950.

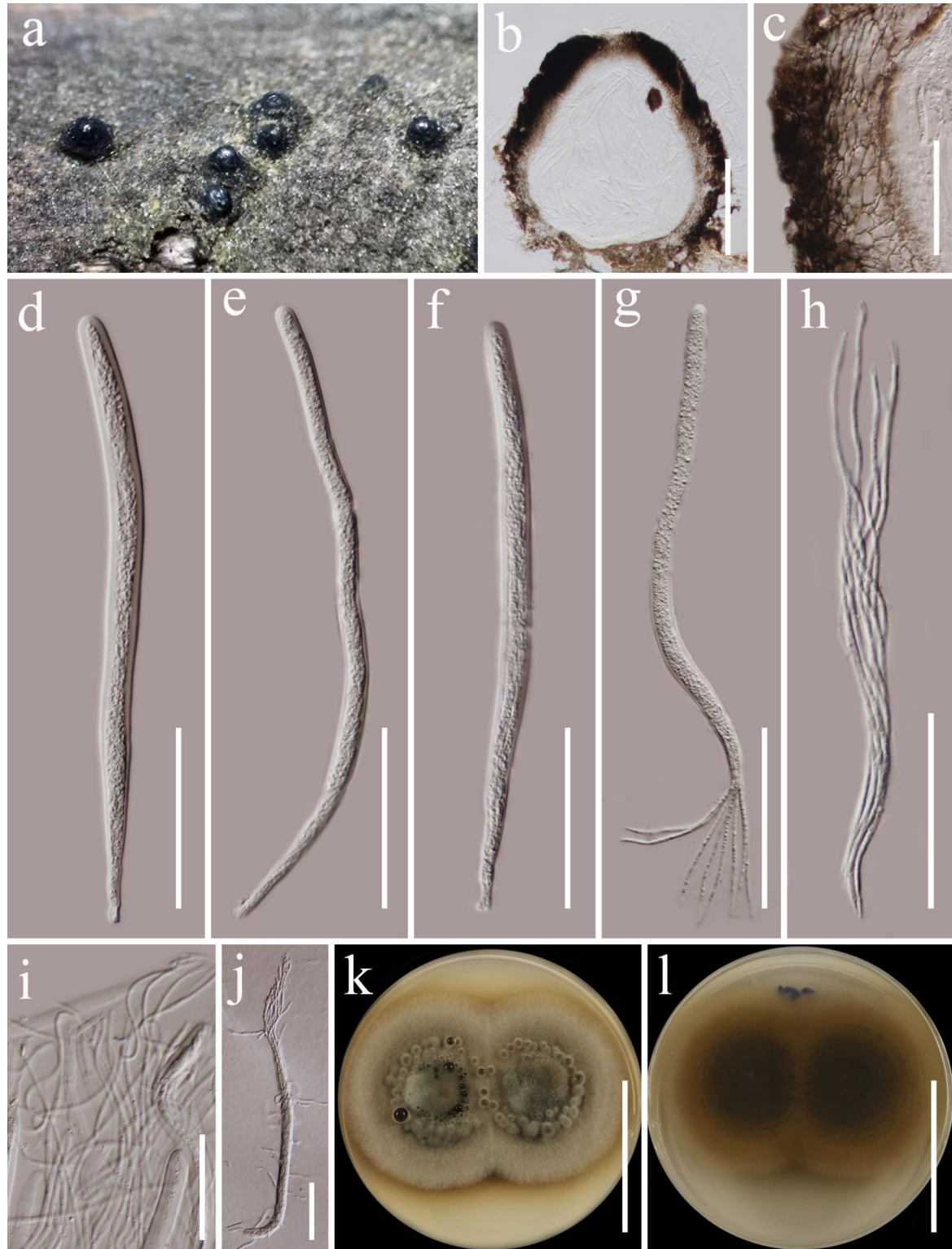


Figure 53 – *Scolecohyalosporium baoshanense* (HKAS 122707, holotype). a Appearance of ascomata on the host substrate. b Section of an ascoma. c Peridium. d–g Asci. h Ascospores.

i Pseudoparaphyses. j Ascospores germinated within the ascus. k, l Culture characters on PDA (k = from above, l = from below). Scale bars: b = 200 μ m, c–j = 50 μ m, k, l = 30 mm.

Notes – In our phylogenetic analysis, new strains (KUMCC 21-0507 and KUMCC 21-0508) formed a clade sister to *S. submersum* (KUMCC 21-0412, KUMCC 21-0413, KUN-HKAS 122242) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 51). Our isolations are similar to *S. submersum* in having conical to ovoid, black, glabrous ascomata, 8-spored, bitunicate, fissitunicate, long cylindrical asci and hyaline, filiform, multi-septate ascospores. However, *S. baoshanense* differs from *S. submersum* in having smaller asci (170–270 $\times$ 8.7–9.7 μ m vs. (200–)250–300(–370) $\times$ 7–9(–11) μ m) and ascospores (190–230 $\times$ 1.4–1.8 μ m vs. (230–)260–285(–315) $\times$ 1.5–2.2 μ m) (Xie et al. 2022). Moreover, the culture of *S. baoshanense* is greyish white with black, glistening granular droplets of oil, while the culture of *S. submersum* is pale grey at the margin, grey to dark grey at the center. In pairwise nucleotide comparison for the ITS region between *Scolecohyalosporium baoshanense* (KUMCC 21-0507) and *S. submersum* (KUMCC 21-0412) showed a 1.6% (10/611 bp, without gaps) base pair difference in ITS region, 2.7% (25/914 bp, without gaps) base pair difference in *tef1- α* region. Based on its distinct morphology and the phylogeny of the combined SSU, LSU, ITS, and *tef1- α* dataset *Scolecohyalosporium baoshanense* is introduced as a new species.

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

Roussoellaceae was introduced by Liu et al. (2014) to accommodate three genera, *Neoroussoella*, *Roussoella* and *Roussoellopsis*. This family has been relatively well-studied in recent years, and the number of species has increased (Tibpromma et al. 2017, 2018, Wanasinghe et al. 2018, Jiang et al. 2019, Karunarathna et al. 2019, Phookamsak et al. 2019, Dong et al. 2020, Mapook et al. 2020, Zhang et al. 2020b). Wijayawardene et al. (2022) listed 12 genera in *Roussoellaceae*. *Roussoellaceae* species are characterised by having solitary or gregarious, black, immersed to semi-immersed, uni- to multi-loculate ascostromata; immersed to semi-immersed, solitary to gregarious, globose to subglobose, or ampulliform ascomata; peridium composed of brown to dark brown pseudoparenchymatous cells, arranged in *textura angularis* to *textura prismatica*; septate, branched, anastomosed cellular pseudoparaphyses; bitunicate, cylindrical to cylindric-clavate, or clavate asci with the well-developed ocular chamber; ellipsoidal to fusiform, septate, hyaline or brown to dark brown ascospores with constricted at the septum (Liu et al. 2014, Hongsanan et al. 2020). The asexual morphs of this family are characterized by pycnidial, stromatic, immersed, globose to subglobose, or dome-shaped, uni- to multi-loculate conidiomata; pycnidial walls comprising several layers of brown to dark brown pseudoparenchymatous cells, arranged *textura angularis*; holoblastic, annellidic, discrete, hyaline, cylindrical to ampulliform, or doliform, unbranched, aseptate or septate conidiogenous cells; globose, oblong or ellipsoidal, hyaline to brown or dark brown, aseptate or septate conidia with minutely warty, or verrucose (Liu et al. 2014). In this study, we report two new species, *Pararoussoella lincangensis* and *Setoarthopyrenia jinghongense*.

Pararoussoella lincangensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 55

Index Fungorum number: IF901359; Facesoffungi Number: FoF13893

Holotype – HKAS 122756

Etymology – The species epithet “lincangensis” refers to the location where the specimen was first collected.

Saprobic on dead woody twigs of *Heliciopsis terminalis*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 75–140 μ m high $\times$ 140–160 μ m diam., ($\bar{x}$ = 110 $\times$ 150 μ m, n = 5), immersed under a blackened pseudoclypeus, appearing as black, solitary or scattered, unilocular, coriaceous, elliptical to ampulliform, brown to dark-brown. *Ostioles* central. *Conidiomata wall* 10–14 μ m wide, 3–4-layered, intermixed with the host tissue, composed of brown outer layers and inner layers comprising hyaline, thick-walled cells of *textura angularis*.

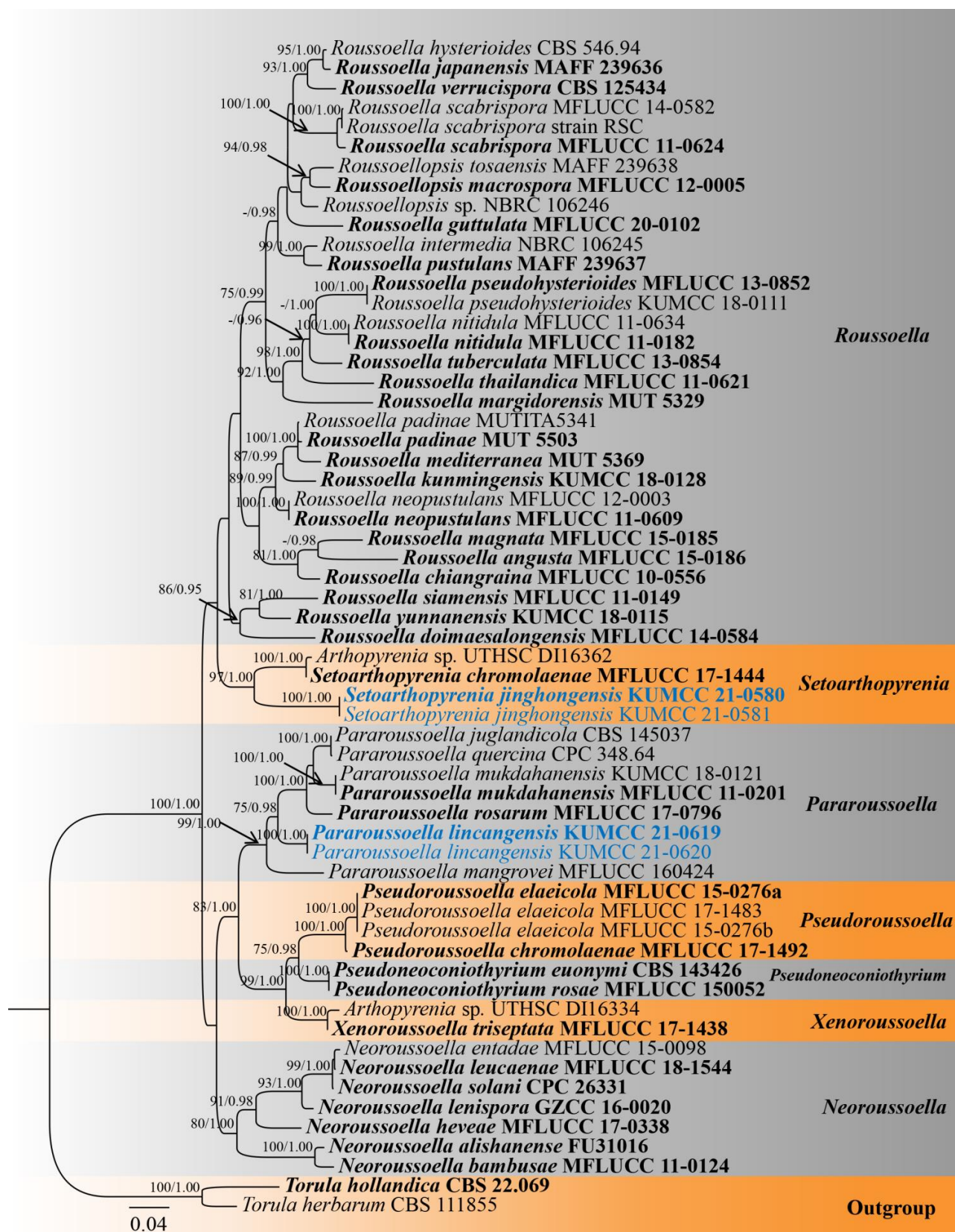


Figure 54 – Phylogram generated from ML analysis based on LSU, ITS, *tef1-α*, and *rpb2* sequence data, representing *Roussoellaceae*. Related sequences are obtained following Zhang et al. (2020b). Sixty strains are included in the combined analyses, which comprise 3136 characters for LSU, ITS, *tef1-α*, and *rpb2* alignment. *Torula herbarum* (CBS 111855) and *T. hollandica* (CBS 22.069) were used as the outgroup taxa. The best-scoring RAXML tree with a final likelihood value of -22805.534061 is presented. The matrix had 1172 distinct alignment patterns, with 25.96% of

undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240512, C = 0.264779, G = 0.272734, T = 0.221974; substitution rates AC = 1.942253, AG = 5.228557, AT = 2.132197, CG = 1.362679, CT = 10.344711, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* $4.4\text{--}5.4 \times 2.6\text{--}3.6 \mu\text{m}$ ($\bar{x} = 5 \times 3.1 \mu\text{m}$, $n = 10$), enteroblastic, phialidic, determinate, discrete, doliiiform to ampulliform, hyaline, smooth-walled, arising from the stratum. *Conidia* $3.1\text{--}3.8 \times 2\text{--}2.2 \mu\text{m}$ ($\bar{x} = 3.4 \times 2.1 \mu\text{m}$, $n = 30$), straight, initially hyaline, becoming yellowish at maturity, ovate, one-celled, aseptate, rounded ends, thick and smooth-walled.

Culture characteristics – *Conidia* germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and apical cell of conidia. Colonies on PDA, reaching 45 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, flat, umbonate, entire edge, white at the margin, grey at the center; reverse white at the margin, atrovirens at the center.

Material examined – China, Yunnan Province, Lincang, on dead woody twigs of *Heliciopsis terminalis* (Proteaceae), 12 August 2020, G.C. Ren, LC55 (HKAS 122756, holotype), ex-type culture KUMCC 21-0619, KUMCC 21-0620.

GenBank numbers – KUMCC 21-0619: SSU: OQ168233, LSU: OQ170882, ITS: OQ158960, *tef1-α*: OR613443; KUMCC 21-0620: SSU: OQ168234, LSU: OQ170883, ITS: OQ158961.

Notes – Our strains (KUMCC 21-0619 and KUMCC 21-0620) clustered with other *Pararoussoella* species with 75% ML bootstrap support and 0.98 BYPP value (Fig. 54). Our collections can be distinguished from *P. juglandicola* and *P. quercina* based on its ovate yellowish conidia. In contrast, *P. juglandicola* has subcylindrical, brown conidia, and *P. quercina* has broadly ellipsoid, brown conidia (Crous et al. 2019, 2020). In addition, *P. juglandicola* and *P. quercina* were found as asexual morphs in sporulated cultures, whereas we obtained our strains asexual morph in nature. We did not find the sexual morph of *P. lincangensis* in nature. Therefore, a comparison between our new collections and other sexual morphs of *Pararoussoella* species (*Roussoella mangrovei*, *P. mukdahanensis*, *P. rosarum*) was not possible. However, based on the phylogenetic distinctiveness, *P. lincangensis* can be distinguished from *Roussoella mangrovei*, *P. Mukdahanensis* and *P. rosarum*. Herein, we introduce *Pararoussoella lincangensis* as a new species based on its distinct morphology and analysis of the combined LSU, ITS, *tef1-α*, and *rpb2* dataset.

Setoarthopyrenia jinghongensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 56

Index Fungorum number: IF901360; FacesofFungi number: FoF13892

Holotype – HKAS 122740

Etymology – The epithet reflects Jinghong, where the species was collected.

Saprobic on dead twigs of *Ehretia acuminata*. Sexual morph: *Ascomata* 120–345 μm high, 87–197 μm diam., ($\bar{x} = 200 \times 129 \mu\text{m}$, $n = 5$), immersed to erumpent, solitary or scattered, coriaceous, uni- to bi-loculate, oval or obpyriform, black. *Ostioles* central. *Peridium* 15–25 μm wide, 2–4-layered, composed of hyaline or light brown cells of *textura angularis*. *Hamathecium* 1.6–2.3 μm wide, hyaline, comprising numerous, filamentous, branched, septate, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 90–120 $\times$ 10–11 μm ($\bar{x} = 107.4 \times 10.6 \mu\text{m}$, $n = 10$), 8-spored, bitunicate, fissitunicate, clavate or cylindrical, slightly curved, short pedicellate, apically rounded. *Ascospores* 14.5–18.5 $\times$ 5.5–6.7 μm ($\bar{x} = 16.5 \times 6 \mu\text{m}$, $n = 30$), overlapping uniseriate, ellipsoid, straight, initially hyaline, becoming yellowish brown to dark brown when mature, 1-septate, 2-celled, slightly constricted at the septum, guttulate. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from one cell of the ascospore. Colonies on PDA, reaching 50 mm

diameter after two weeks at 20–25 °C, mycelia superficial, circular, dense, filamentous, flat, slightly raised at the center, circular zonate on the surface, white at the margin, light brown at the center; reverse, pale yellow at the margin, dark brown at the center.

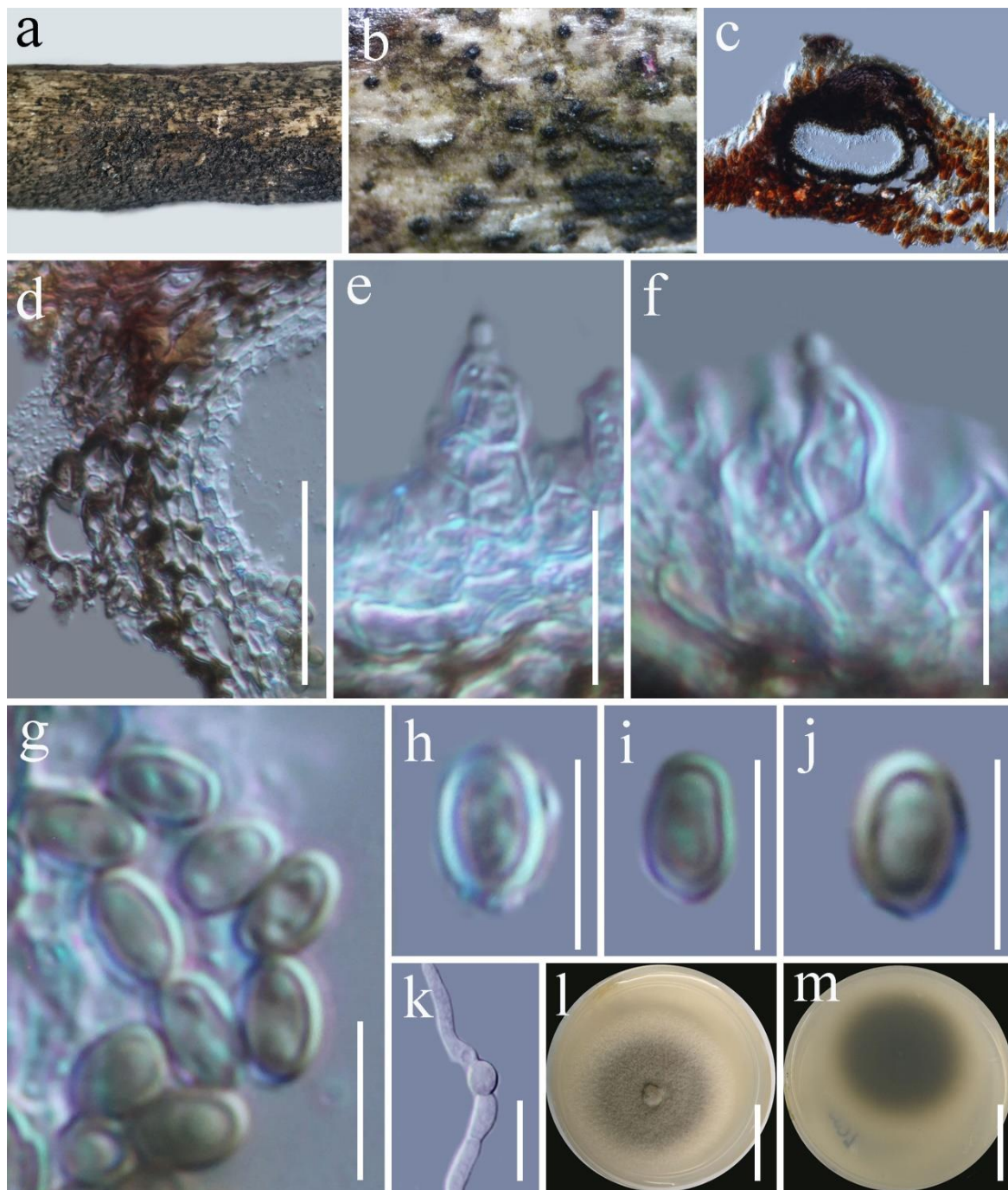


Figure 55 – *Pararousoella lincangensis* (HKAS 122756, holotype). a Material examined. b Appearance of conidiomata on the host substrate. c Section of conidioma. d Conidioma wall. e, f Conidiogenous cells and developing conidia. g–j Conidia. k Germinated conidium. l, m Culture characters on PDA (l = from above, m = from below). Scale bars: c = 150 μ m, d = 30 μ m, e, f = 10 μ m, g–j = 5 μ m, k = 15 μ m, l, m = 30 mm.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong, Xishuangbanna Tropical Botanical Garden (21°55.19'N, 101°15.24'E), on dead woody twigs of *Ehretia acuminata* (Boraginaceae), 4 March 2020, G.C. Ren, JH31 (HKAS 122740, holotype), ex-type culture KUMCC 21-0580. *ibid.*, living culture KUMCC 21-0581.

GenBank numbers – KUMCC 21-0580: SSU: OQ168231, LSU: OQ170880, ITS: OQ158958, *tef1-α*: OR613444; KUMCC 21-0581: SSU: OQ168232, LSU: OQ170881, ITS: OQ158959.

Notes – In the phylogenetic analyses, our isolates formed a sister clade to *S. chromolaenae* with 100% ML bootstrap support and 1.00 BYPP value (Fig. 54). *Setoarthopyrenia jinghongensis* fits well with the generic concept of *Setoarthopyrenia* in having immersed, coriaceous, black ascomata, clavate or cylindrical, slightly curved, short pedicellate asci, ellipsoid, 1-septate ascospores with guttulate (Mapook et al. 2020), but distinct from *S. chromolaenae* in having oval or obpyriform ascomata, clavate or cylindrical asci, uniseriate, ellipsoid, brown to dark brown ascospores, while *S. chromolaenae* has globose ascomata with brown to dark brown setae, cylindric-clavate asci, biseriate, hyaline, ellipsoid to obovoid ascospores (Mapook et al. 2020). Sequence comparison for the ITS region between *Setoarthopyrenia jinghongensis* (KUMCC 21-0580) and *S. chromolaenae* (MFLUCC 17-1444) showed 8.2% (39/475 bp, without gaps) base pair difference in ITS region, and 3.9% (35/890 bp, without gaps) base pair difference in the *tef1-α* region. Based on distinct morphology and phylogenetic position, *Setoarthopyrenia jinghongensis* is introduced as a new species.

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

Teichosporaceae was established by Barr (2002) to accommodate eight genera, with *Teichospora* as the type genus. This family is characterised by having pyriform or globose to subglobose, dark brown to black ascomata with papillate to elongate ostiolate; peridium composed of several layers of lightly pigmented to dark brown to black, textura angularis cells; septate, branching, anastomosing, cellular or trabeculate pseudoparaphyses; bitunicate, fissitunicate, cylindrical to subclavate, pedicellate asci with a small ocular chamber; fusoid or clavate, oblong, septate, hyaline or brown, 1–3-septate or muriform ascospores (Barr 2002, Hongsanan et al. 2020). The asexual morphs of this family are characterized by pycnidial, brown septate or brown, rarely hyaline, aseptate conidia (Hongsanan et al. 2020). Currently, 17 genera are accepted in this family (Wijayawardene et al. 2022). In this study, we report three new host records, *Aurantiascoma minimum* and *Magnibotryascoma mali* from *Shorea assamica* and *Ramusculicola thailandica* from *Rhododendron rubiginosum*.

Aurantiascoma minimum (Mugambi, A.N. Mill. & Huhndorf) Thambug. & K.D. Hyde, in Thambugala et al., Fungal Diversity, [51] (2015) Fig. 58

≡ *Misturatosphaeria minima* Mugambi, A.N. Mill. & Huhndorf, in Mugambi & Huhndorf, Stud. Mycol. 64: 114 (2009)

Index Fungorum number: IF551263; Facesoffungi Number: FoF551263

Saprobic on dead woody twigs of *Shorea assamica*. Sexual morph: *Ascomata* 250–280 µm high × 250–300 µm diam., ($\bar{x}$ = 260 × 280 µm, n = 5), immersed under the bark of the host, solitary or clustered, subglobose to globose, coriaceous, black, with an ostiole in the central. *Peridium* 20–30 µm thick, 3–4-layered, composed of dark brown outer layers and inner layers comprising hyaline, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2 µm wide, comprising numerous, branched, septate, hyaline pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 125–147 × 14–17.5 µm ($\bar{x}$ = 137 × 16 µm, n = 20), 8-spored, unitunicate, long cylindrical, straight or curved, apically rounded with an obvious apical ring and a short pedicel. *Ascospores* 34–40 × 6.9–8 µm ($\bar{x}$ = 37.5 × 7.5 µm, n = 30), uniseriate, hyaline, fusiform with acute angular ends, 1-septate, slightly constricted at the septum, with guttules in each cell, thick-walled, smooth, with a small mucilaginous sheath that extends at the tips of the spore. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical and the basal cell of ascospore. Colonies on PDA, reaching 40 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, flat, smooth surface with shiny liquid drop, entire edge, from above grey at the margin, grayish white at the center; reverse, dark brown at edge, grey white at center.

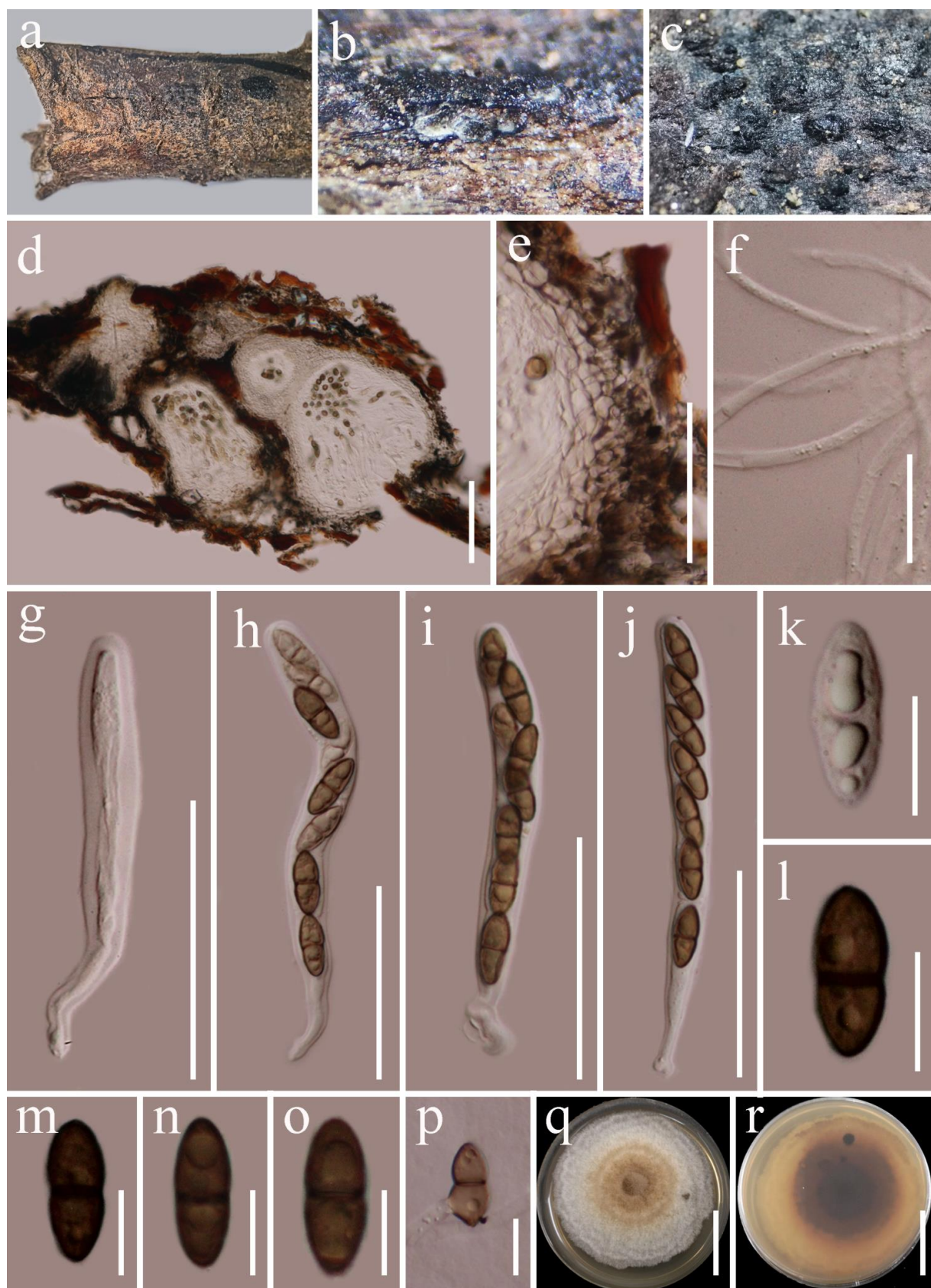


Figure 56 – *Setoarthopyrenia jinghongensis* (HKAS 122740, holotype). a Material examined. b, c Appearance of ascomata on the host substrate. d Section of an ascoma. e Peridium. f Pseudoparaphyses. g–j Asci. k–o Ascospores. p Germinated ascospore. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: d = 100 μm, e, f–j = 50 μm, f = 20 μm, k–o, p = 10 μm, q, r = 30 mm.

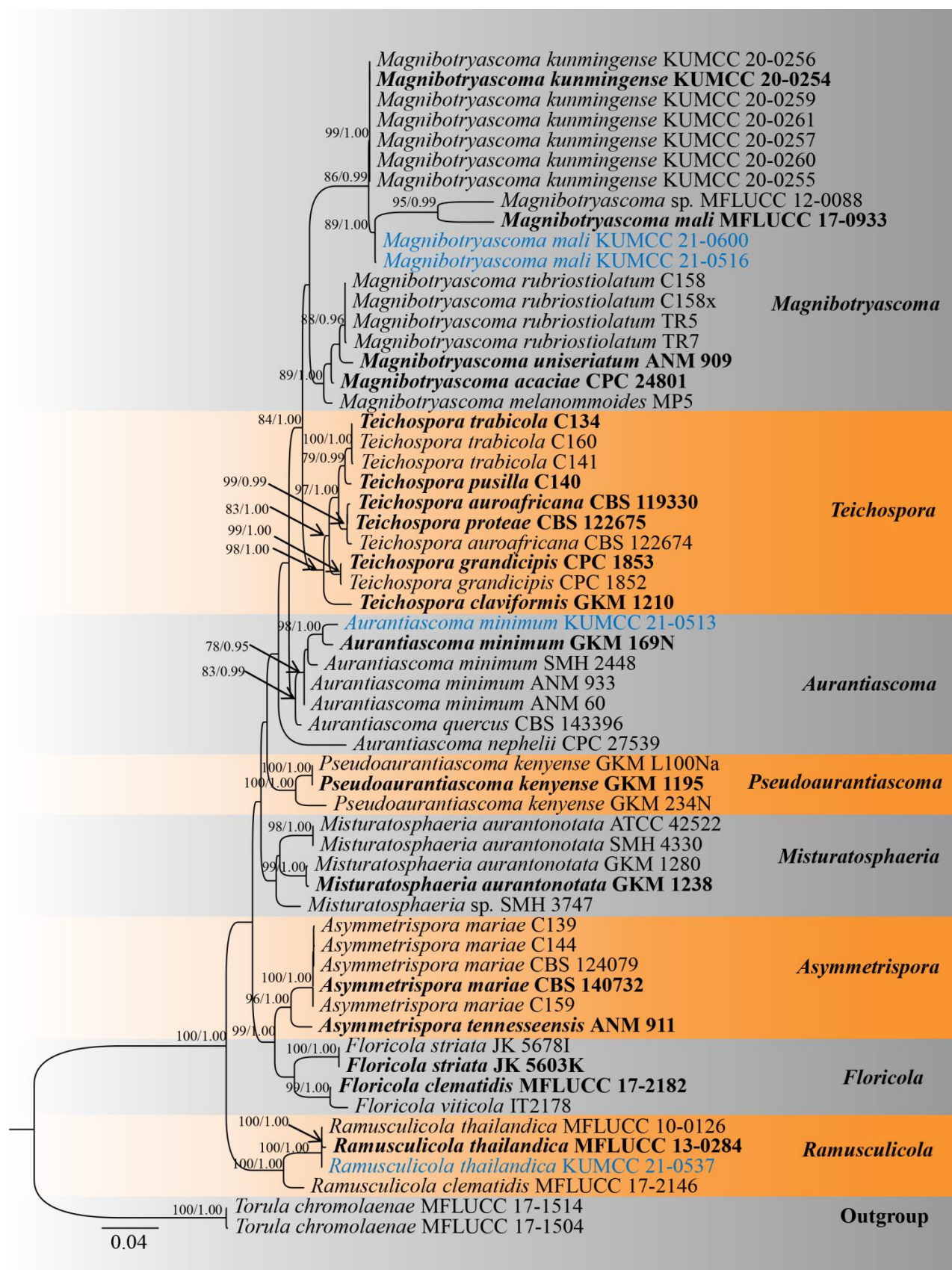


Figure 57 – Phylogram generated from ML analysis based on LSU, ITS and *tef1-α* sequence data, representing *Teichosporaceae*. Related sequences are obtained following Mortimer et al. (2021) and Tennakoon et al. (2021a). Fifty-nine strains are included in the combined analyses, which comprise 2318 characters for LSU, ITS and *tef1-α* alignment. Two strains of *Torula chromolaenae* (MFLUCC 17-1514 and MFLUCC 17-1504) were used as the outgroup taxa. The best-scoring

RAxML tree with a final likelihood value of -9734.934654 is presented. The matrix had 677 distinct alignment patterns, with 24.3% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.234134, C = 0.266021, G = 0.286439, T = 0.213407; substitution rates AC = 1.098317, AG = 2.075137, AT = 1.878071, CG = 1.064618, CT = 9.116965, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

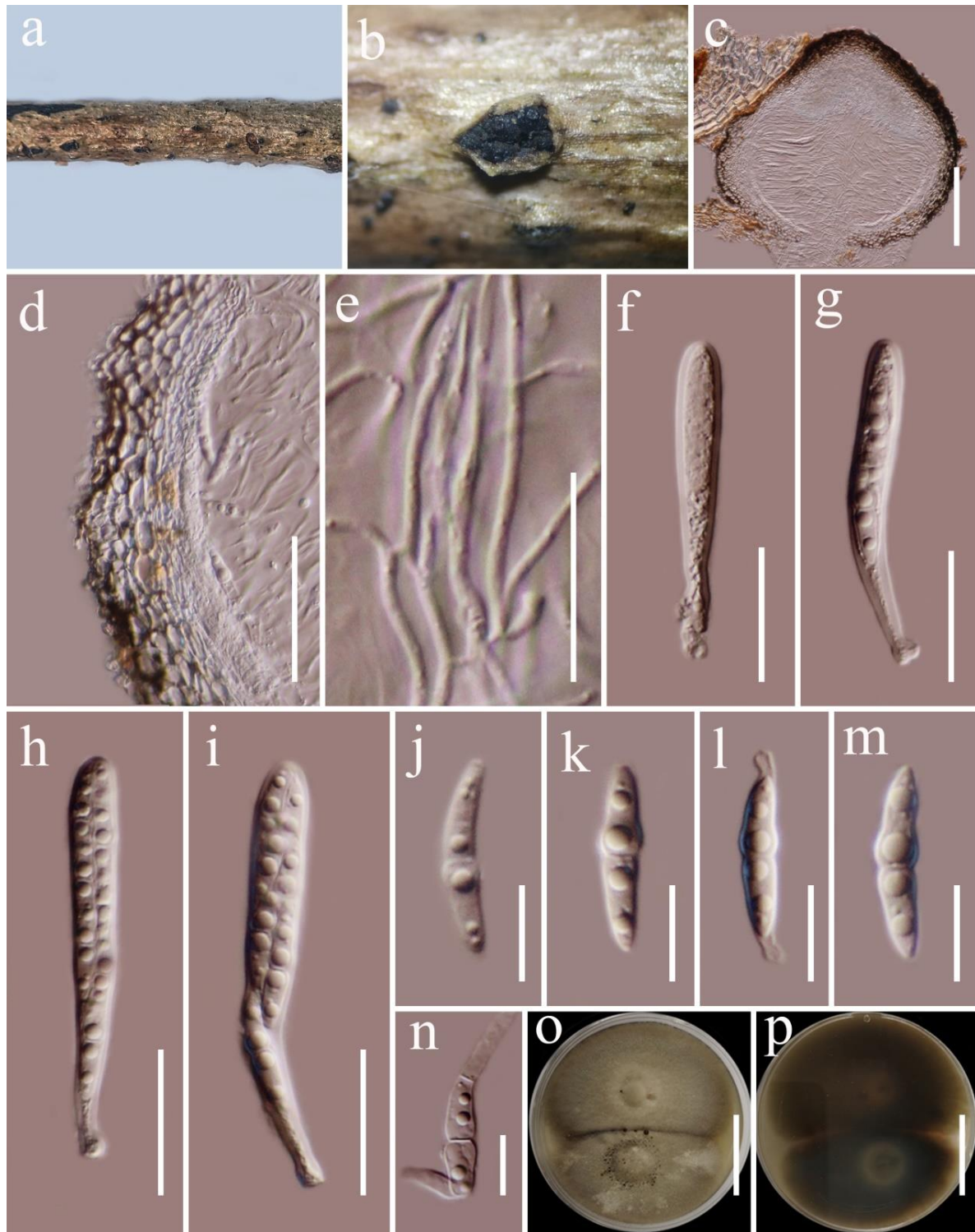


Figure 58 – *Aurantiascoma minimum* (HKAS 122710). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci.

j–m Ascospores. n Germinated ascospore. o, p Culture characters on PDA (o = from above, p = from below). Scale bars: c = 100 μ m, d = 50 μ m, e = 20 μ m, f–i = 50 μ m, j–n = 10 mm, o, p = 20 mm.

Material examined – China, Yunnan Province, Baoshan, on dead woody twigs of *Shorea assamica* (Dipterocarpaceae), 10 August 2020, G.C. Ren, BS25 (HKAS 122710), living culture KUMCC 21-0513.

Known distribution – On decorticated woody branches of unidentified plant in Costa Rica, Kenya and the USA (Mugambi & Huhndorf 2009), on dead woody twigs of *Shorea assamica* in China (This study).

GenBank numbers – SSU: OQ168227, LSU: OQ170876, ITS: OQ158954, *tef1- α* : OR613445.

Notes – Thambugala et al. (2015) synonymized *Misturatosphaeria minima* under *Aurantiascoma* based on the phylogenetic analyses of the combined LSU, SSU, ITS, and *tef1- α* sequence data. *Aurantiascoma minimum* was introduced by its sexual morph, which is characterized by pyriform to subglobose ascomata, cylindrical-clavate asci with an ocular chamber, and fusiform, 1-(–3)-septate ascospores with a small mucilaginous sheath that extends at the tips of the spore (Mugambi & Huhndorf 2009, Thambugala et al. 2015). *Aurantiascoma minimum* was found on decorticated woody branches from Costa Rica, Kenya and the USA (Mugambi & Huhndorf 2009). The ascomata, asci and ascospores of this new collection (KUMCC 21-0513) is similar to *A. minimum*. The multi-gene phylogenetic analysis based on the combined LSU, ITS, and *tef1- α* sequences showed that our collection (KUMCC 21-0513) forms a monophyletic group with the type of *A. minimum* (GKM 1690) with 98% ML bootstrap support and 1.00 BYPP value (Fig. 57). Based on morphological characteristics and phylogenetic analysis, we report our collection as the first record of *A. minimum* from decaying wood of *Shorea assamica* in China.

Magnibotryascoma mali Phukhams., Wanas. & K.D. Hyde, in Hyde et al., Fungal Diversity 87: 105 (2017) Fig. 59

Index Fungorum number: IF553255; Facesoffungi Number: FoF03387

Saprobic on dead twigs of *Shorea assamica*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 160–180 μ m high, 190–210 μ m diam., ($\bar{x}$ = 170 $\times$ 200 μ m, n = 5), pycnidial, solitary or scattered, globose to subglobose, coriaceous, uniloculate, immersed, dark brown to brown, papillate, with a central ostiole. *Pycnidia wall* 10–20 μ m wide, thick, 2–4-layered, with outer layer composed of light brown to brown cells of *textura angularis*, with a hyaline innermost layer. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–7 $\times$ 2–3.5 μ m ($\bar{x}$ = 5.6 $\times$ 2.9 μ m, n = 20), enteroblastic, phialidic, discrete, cylindrical to ampulliform, hyaline, arising from the inner layer of pycnidium wall. *Conidia* 3.6–4.5 $\times$ 2.8–3.6 μ m ($\bar{x}$ = 4 $\times$ 3.2 μ m, n = 30), subglobose, oval, guttulate, initially hyaline, pale brown at maturity, one-celled, smooth-walled.

Culture characteristics – Conidia germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the basal and the apical cell of conidia. Colonies on PDA, reaching 20 mm diameter after two weeks at 20–25 °C, mycelia superficial, velvety, circular, convex, rough surface with shiny liquid drop, entire edge, from above grayish white at the margin, sandybrown at the center, yellowish circular zonate; reverse, dark brown at the margin, pale yellowish at the center.

Material examined – China, Yunnan Province, Baoshan, on woody litter of *Shorea assamica* (Dipterocarpaceae), 12 July 2020, G.C. Ren, BS30 (HKAS 122711), living culture KUMCC 21-0516, KUMCC 21-0600.

Known distribution – On decaying twigs of *Malus halliana* (Rosaceae) (Hyde et al. 2017), on dead woody twigs of *Shorea assamica* (Dipterocarpaceae) in China (This study).

GenBank numbers – KUMCC 21-0516: SSU: OQ168228, LSU: OQ170877, ITS: OQ158955, *tef1- α* : OR613446; KUMCC 21-0600: SSU: OQ168229, LSU: OQ170878, ITS: OQ158956.

Notes – Hyde et al. (2017) introduced *Magnibotryascoma mali* based on the phylogenetic analyses of the combined *tef1- α* and *rpb2* sequence data. The sexual morph is characterized by globose to subglobose conidiomata with a central ostiole, phialidic, hyaline, cylindrical conidiogenous cells, and aseptate conidia with guttules (Hyde et al. 2017). The collections were similar to *M. mali* (MFLUCC 17-0933) in terms of their conidial and conidiomatal characteristics (Hyde et al. 2017). Our isolates (KUMCC 21-0516 and KUMCC 21-0600) were obtained from *Shorea assamica* (Dipterocarpaceae) from China, respectively. Both species were collected from terrestrial habitats in Yunnan Province (China) but from different hosts. In our phylogenetic analyses of combined LSU, ITS, and *tef1- α* sequence data, our isolates (KUMCC 21-0516 and KUMCC 21-0600) are related to *M. mali* (MFLUCC 17-0933) with 89% ML bootstrap support and 1.00 BYPP value (Fig. 57). Comparisons of the LSU and *tef1- α* sequence of our new isolates (KUMCC 21-0516 and KUMCC 21-0600) and *M. mali* (MFLUCC 17-0933) showed 100% (793/793 bp) and 100% (870/870 bp) similarity, respectively; however, ITS region shows 9.9% (29/292 bp) base pair difference. Therefore, further taxonomic work is needed to resolve identification, phylogenetic position and relationships between *M. mali* and other *Magnibotryascoma* species. Based on morphological characteristics and phylogenetic analyses, we report our collections as the first record of *M. mali* from decaying wood of *Shorea assamica* in China.

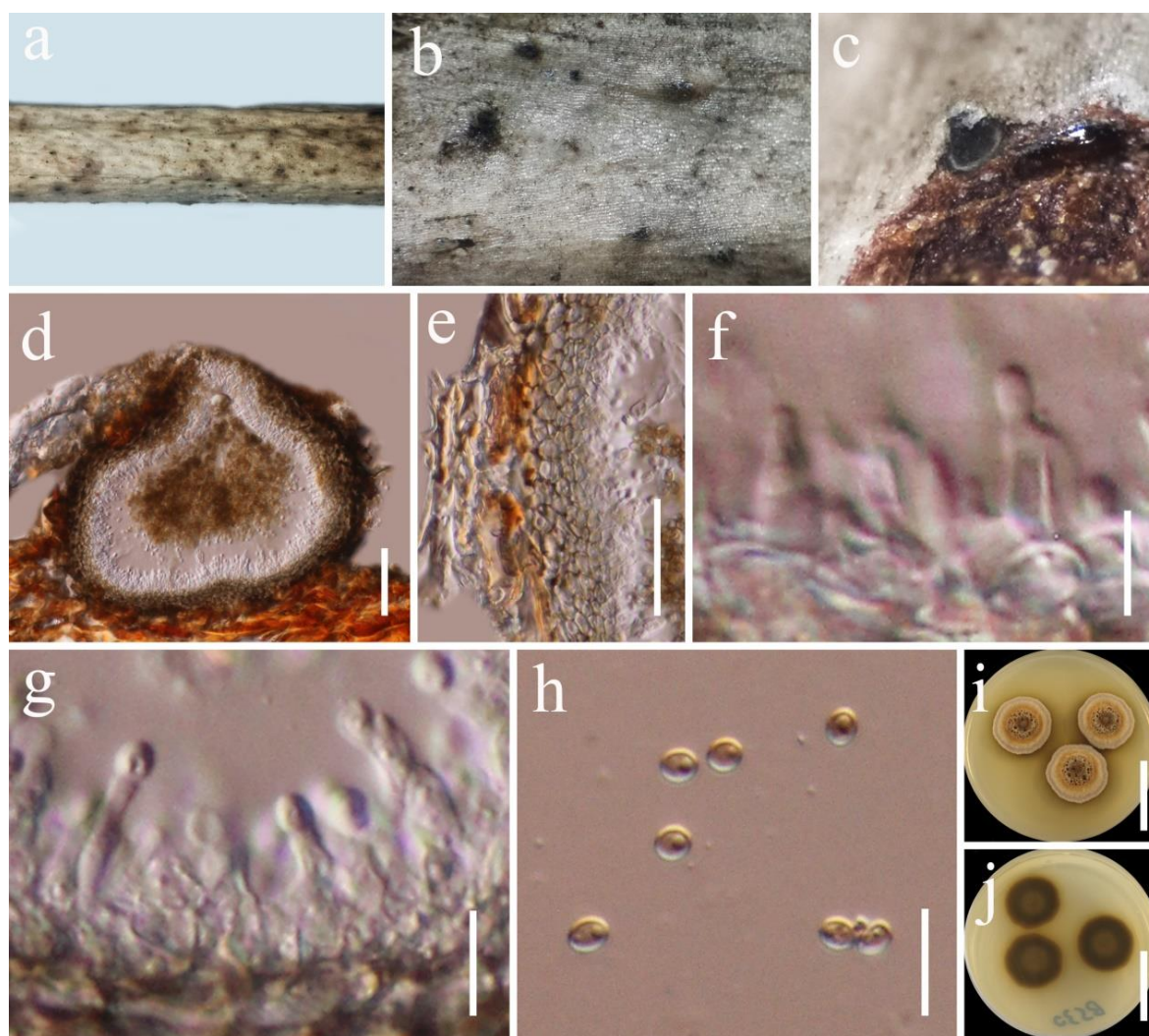


Figure 59 – *Magnibotryascoma mali* (HKAS 122711) a Material examined. b Conidiomata on the natural wood surface. c, d Sections through conidiomata. e Conidiomata wall. f, g Conidiogenous cells and developing conidia. h Conidia. i, j Culture characters on PDA (i = from above, j = from below). Scale bars: d = 50 μ m, e = 30 μ m, f, g = 5 μ m, h = 10 μ m, i, j = 30 mm.

Ramusculicola thailandica Thambug. & K.D. Hyde, Fungal Diversity, [53] (2015)

Fig. 60

Index Fungorum number: IF551265; Facesoffungi Number: FoF01092

Saprobic on dead woody twigs of *Rhododendron rubiginosum*. Sexual morph: *Ascomata* 115–150 µm high × 145–200 µm diam., ($\bar{x}$ = 135 × 175 µm, n = 5), unilocular, immersed under the bark of the host, solitary or scattered, globose to subglobose, coriaceous, black, with an ostiole in the central. *Peridium* 5–16 µm thick, composed of dark brown outer layers and inner layers comprising hyaline, thick-walled cells of *textura angularis*. *Hamathecium* 1.5–2.2 µm wide, comprising numerous, unbranched, septate, hyaline pseudoparaphyses embedded in a gelatinous matrix. *Asci* 64–88 × 8.3–9.9 µm ($\bar{x}$ = 75.8 × 9.2 µm, n = 20), 8-spored, unitunicate, long cylindrical, straight or curved, apically rounded with an ocular chamber and a short pedicel. *Ascospores* 25–31.5 × 4–5.2 µm ($\bar{x}$ = 28.5 × 4.5 µm, n = 30), uniseriate, hyaline, fusiform with acute angular ends, 1–3-septate, slightly constricted at the septum, thick-walled, smooth, with guttules in each immature cell, and surrounded by a thin mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical and the basal cell of ascospores. Colonies on PDA, reaching 30 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, flat, smooth surface with shiny liquid drop, entire edge, from above light pink at the margin, grey white at the center, reverse brown.

Material examined – Chian, Yunnan Province, Lijiang, on dead woody twigs of *Rhododendron rubiginosum* (Ericaceae), 30 August 2020, G.C. Ren, DQ23 (HKAS 122758), living culture KUMCC 21-0537.

Known distribution – On dead stems of *Clematis sikkimensis* (Ranunculaceae), *Ficus septica* (Moraceae), *Leucaena* sp. (Fabaceae) in Thailand (Jayasiri et al. 2019, Phukhamsakda et al. 2020, Tennakoon et al. 2021a), on dead woody twigs of *Rhododendron rubiginosum* in China (This study).

GenBank numbers – SSU: OQ168230, LSU: OQ170879, ITS: OQ158957, *tef1-α*: OR613447.

Notes – *Ramusculicola thailandica* was introduced by Thambugala et al. (2015) based on morphological and phylogenetic evidence. Our new isolate (KUMCC 21-0537) shares similar characters with *R. thailandica* by having unilocular, immersed, globose to subglobose ascomata with an ostiole, cylindrical asci with an ocular chamber and a short pedicel, and fusiform, 1–3-septate ascospores with guttules (Jayasiri et al. 2019, Phukhamsakda et al. 2020, Tennakoon et al. 2021a). The multi-gene phylogenetic analyses based on the combined LSU, ITS, and *tef1-α* sequences showed that our collection (KUMCC 21-0537) clustered with the type of *R. thailandica* (MFLUCC 13-0284) with 100% ML bootstrap support and 1.00 BYPP value (Fig. 57). Based on characteristics and phylogenetic analyses, we report our collection as the first record of *R. thailandica* from decaying wood of *Rhododendron rubiginosum* in China.

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

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández, Mycologia 96 (2): 378 (2004)

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels, Sydowia 51 (1): 56 (1999)

Chaetosphaeriaceae was introduced by Réblová et al. (1999) based on *Chaetosphaeria* to accommodate additional six genera: *Ascocodinaea*, *Melanochaeta*, *Melanopsammella*, *Porosphaerella*, *Porosphaerellopsis*, and *Striatosphaeria*. Currently, 52 genera are accepted in this family (Wijayawardene et al. 2022). *Chaetosphaeriaceae* family is characterised by having immersed, ovoid, globose to subglobose, carbonaceous, coriaceous or membranaceous, dark brown to black ascomata with papillate; unitunicate, clavate to cylindrical, long or short pedicellate asci with J-, apical ring; fusiform, cylindrical to ellipsoid, 0–3-septate, hyaline or brown or dark ascospores with guttules, sheath or appendages. The asexual morphs of this family are either coelomycetous or hyphomycetous. Coelomycetous members are characterized by superficial, cupuliform or globose, unilocular conidiomata with setose; black to brown, septate, ovoid to cylindrical multi-septate setae; brown, 4–6-septate, unbranched, cylindrical conidiophores;

holoblastic or enteroblastic, phialidic, brown, subcylindrical to lageniform conidiogenous cells; aseptate, globose to subglobose or ellipsoid, fusiform to allantoid, hyaline to brown conidia. Hyphomycetous members are characterized by dark brown or hyaline, septate conidiophores with short encircling collar hyphae; hyaline conidiogenous cells with a distinct funnel-shaped collarette; continuous or mucilaginous, aseptate to multi-septate, fusiform, allantoid, cylindrical or doliiform, hyaline to dark brown conidia (Hyde et al. 2020d). In this study, we report a new species, *Pseudolachnella lancangense*.

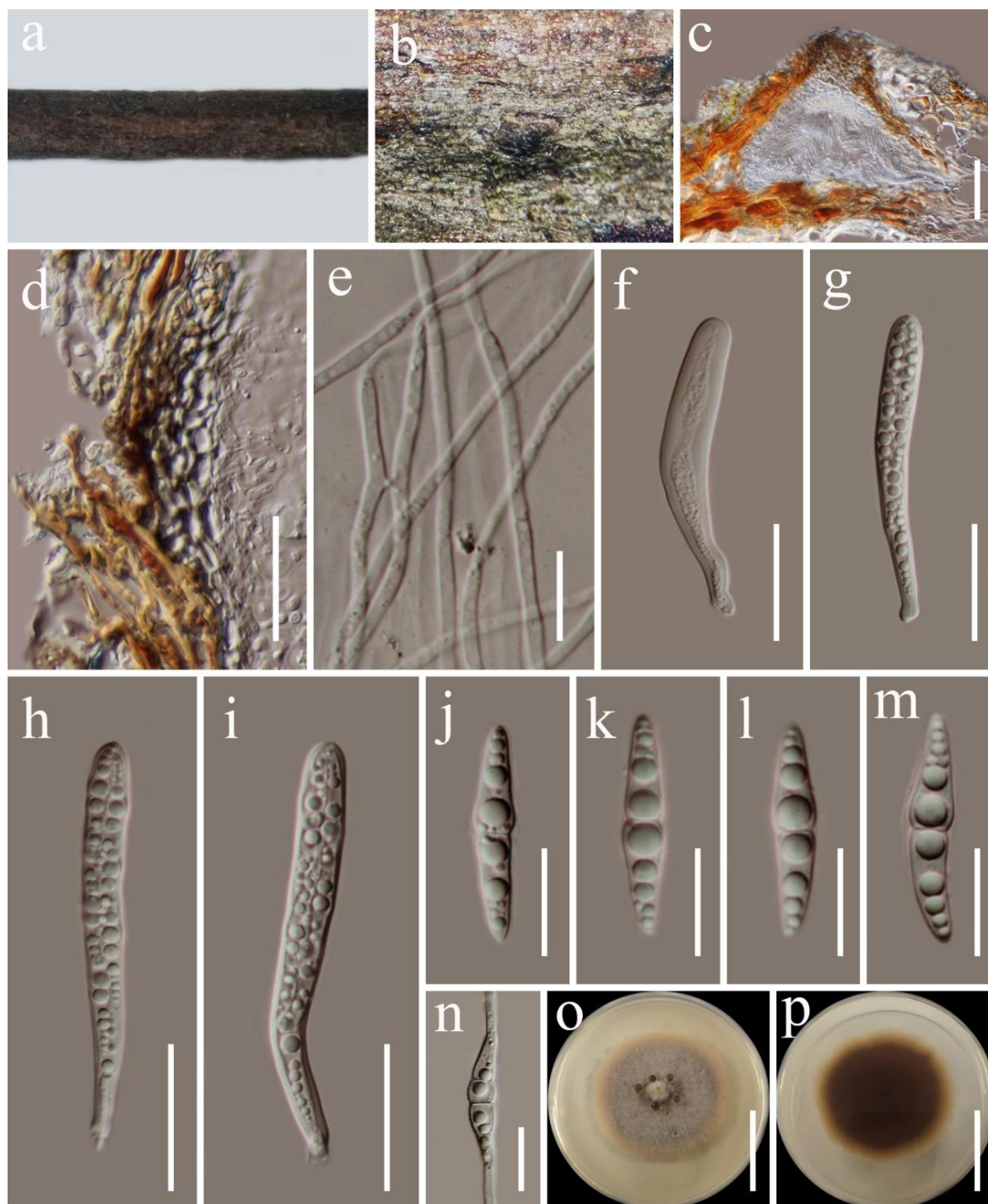


Figure 60 – *Ramusculicola thailandica* (HKAS 122758). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–m Ascospores. n Germinated ascospore. o, p Culture characters on PDA (o = from above, p = from below). Scale bars: c = 50 μ m, d = 25 μ m, e = 10 μ m, f–i = 25 μ m, j–n = 15 μ m, o, p = 20 mm.

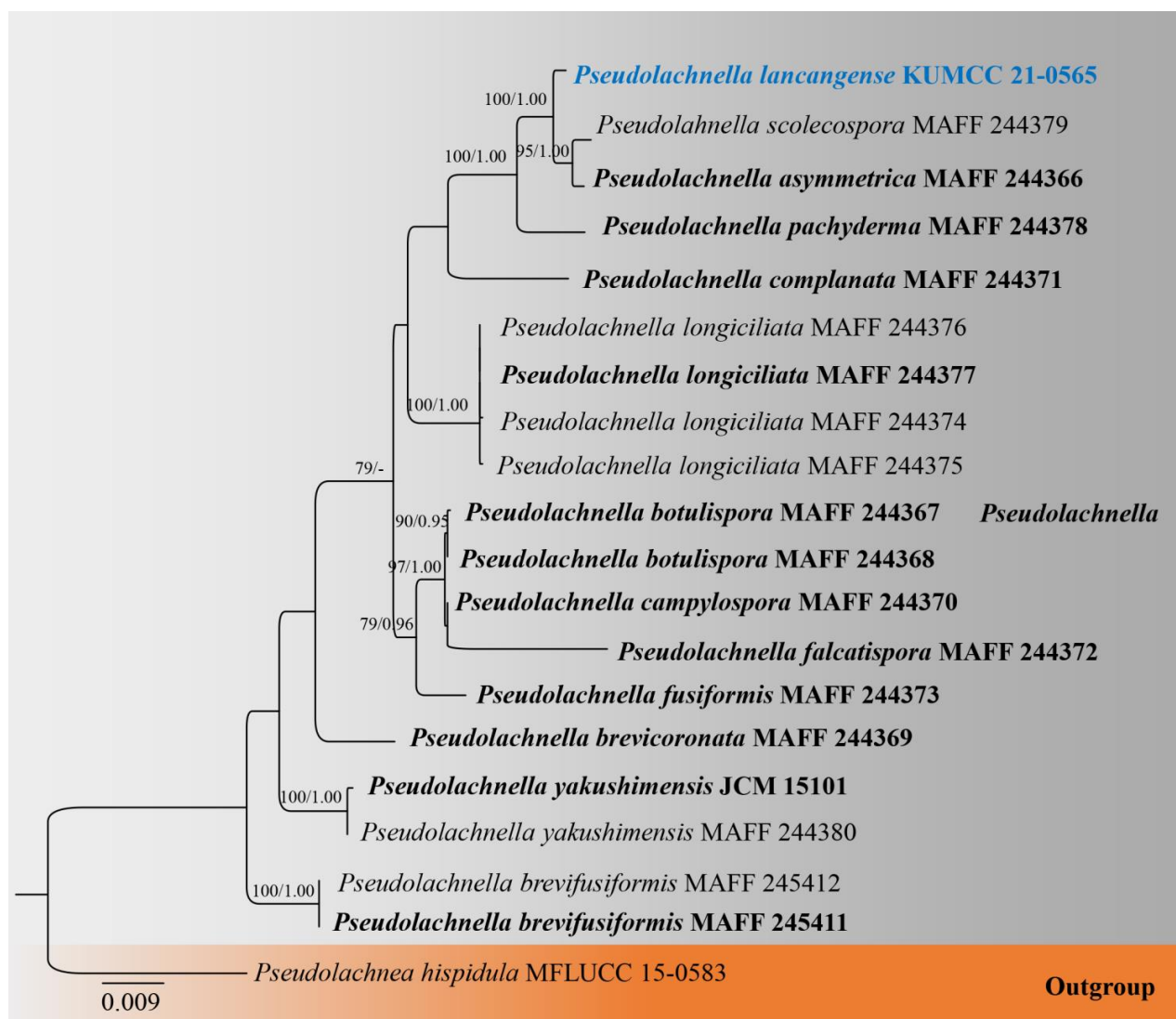


Figure 61 – Phylogram generated from ML analysis based on LSU, ITS, and *tef1-α* sequence data, representing *Chaetosphaeriaceae*. Related sequences are obtained following Hashimoto et al. (2015) and Li et al. (2016). Twenty-one strains are included in the combined analyses, which comprise 1292 characters for LSU, ITS, and *tef1-α* alignment. *Pseudolachnea hispidula* (MFLUCC 15-0583) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -6450.343293 is presented. The matrix had 287 distinct alignment patterns, with 6.83% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.227964, C = 0.290149, G = 0.282030, T = 0.199857; substitution rates AC = 1.213122, AG = 1.620223, AT = 0.842547, CG = 0.887486, CT = 9.028758, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Pseudolachnella lancangensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 62

Index Fungorum number: IF901361; Facesofungi number: FoF13895

Holotype – HKAS 122737

Etymology – The specific epithet reflects Lancang, from where the holotype was collected.

Saprobic on dead woody twigs of *Castanopsis mekongensis*. Sexual morph: *Ascomata* 215–320 µm high × 225–310 µm diam., ($\bar{x}$ = 270 × 260 µm, n = 5), perithecial, immersed, solitary or scattered, globose to subglobose, yellowish orange. *Ostioles* central. *Peridium* 14–25 µm wide, composed of hyaline cells of *textura angularis* with guttules. *Paraphyses* 2–3 µm wide, comprising cylindrical, unbranched, aseptate, embedded in a hyaline gelatinous matrix. *Asci* 95–124 × 7.3–9.4

μm ($\bar{x} = 106 \times 8.3 \mu\text{m}$, $n = 20$), 8-spored, unitunicata, cylindrical, straight or curved, rounded at the apex, short pedicellate. *Ascospores* $18.4\text{--}22.5 \times 4.9\text{--}5.3 \mu\text{m}$ ($\bar{x} = 20 \times 5.1 \mu\text{m}$, $n = 30$), overlapping uniseriate, fusiform, hyaline, 3-septate, constricted at the septum, tapering towards the ends, guttulate, thin and smooth-walled, with a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – *Ascospores* germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from both ends. Colonies on PDA, reaching 10–20 mm diameter after two weeks at 20–25 °C, mycelia superficial, irregular, white, floccose, umbonate, flat, lobate edge, reverse white, light yellow at center.

Material examined – China, Yunnan Province, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Castanopsis mekongensis* (Fagaceae), 20 July 2020, G.C. Ren, LGY34 (HKAS 122737, holotype), ex-type living culture KUMCC 21-0565.

GenBank numbers – LSU: OQ170885, ITS: OQ158963, *tef1- α* : OR613448.

Notes – *Pseudolachnella lancangensis* (KUMCC 21-0565) forms a separate clade sister to *P. scolecospora* (MAFF 244379) and *P. asymmetrica* (MAFF 244366) with 100% ML bootstrap support and 1.00 BYPP value (Fig 61). *Pseudolachnella lancangensis* represents the first record of a sexual morph for this genus and we were unable to isolate the asexual morph in culture. Therefore, we compared the morphology of *P. lancangensis* with *Chaetosphaeriaceae* family descriptions for characters, including astromatic perithecia, cylindrical asci, and transversely septate ascospores (Réblová et al. 1999, Li et al. 2016). Sequence comparison for the ITS region between *Pseudolachnella lancangensis* (KUMCC 21-0565) and *P. scolecospora* (MAFF 244379) showed a 1.6% (8/490 bp, without gaps) base pair difference in ITS region, 1.4% (13/903 bp, without gaps) base pair difference in the *tef1- α* region. Sequence comparison for the ITS region between *Pseudolachnella lancangensis* (KUMCC 21-0565) and *P. asymmetrica* (MAFF 244366) showed a 1.6% (8/490 bp, without gaps) base pair difference in ITS region, 0.7% (6/903 bp, without gaps) base pair difference in *tef1- α* region. Therefore, based on morphological characteristics and phylogenetic analysis, we report our collection as a new species from the decaying wood of *Castanopsis mekongensis* in China.

Hypocreales Lindau, in Engler & Prantl, Nat. Pflanzenfam., Teil. I (Leipzig) 1 (1): 343 (1897)

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

Bionectriaceae was introduced by Rossman et al. (1999), and currently, 47 genera are accepted in this family (Wijayawardene et al. 2022). This family is characterised by having superficial, solitary or densely aggregated, crowded, perithecial ascomata; unitunicate, clavate, saccate, cylindrical, sessile or short pedicellate asci with J-, apical ring; uniseriate, biseriate, multiseriate or irregular, hyaline, aseptate to multi-septate, sometimes muriform, globose, fusiform, ellipsoid or broadly ellipsoid, smooth-walled, spinulose to tuberculate or striate ascospores. The asexual morphs are characterized by dimorphic or monomorphic, mostly sporodochial or synnematosus, hyaline, subhyaline to brown or blackish brown conidiophores; phialidic conidiogenous cells; cylindrical to flask-shaped phialides; unicellular to multi-septate, ellipsoidal, fusiform to subfusiform, hyaline to greenish hyaline or olivaceous grey conidia (Hyde et al. 2020d). In this study, we report a new host record of *Clonostachys capitata* from *Magnolia henryi* in China.

Clonostachys capitata Schroers, Stud. Mycol. 46: 87 (2001)

Fig. 64

Index Fungorum number: IF485122; Facesoffungi Number: FoF13894

Saprobic on dead woody twigs of *Magnolia henryi*. Sexual morph: *Ascomata* 107–187 μm high $\times$ 88–166 μm diam., ($\bar{x} = 144 \times 124 \mu\text{m}$, $n = 5$), perithecial, superficial, solitary or scattered, globose to subglobose, yellowish orange. *Ostiole* periphysate. *Peridium* 26–40 μm thick, composed of outer layers of hyaline to brownish yellow cells of *textura angularis*, and inner layers comprising hyaline cells of *textura angularis*. *Paraphyses* absent. *Asci* 68–89 $\times$ 8.4–11.8 μm ($\bar{x} = 75.9 \times 10.4 \mu\text{m}$, $n = 20$), 8-spored, unitunicate, cylindrical, straight or curved, apically truncate, short pedicellate, with apical ring J-. *Ascospores* 13–17 $\times$ 5–6.5 μm ($\bar{x} = 14.9 \times 5.6 \mu\text{m}$, $n = 30$), overlapping uniseriate, ellipsoidal, hyaline, 1-septate, constricted at the septum, the cells above

central septum often broader than the lower ones, guttulate, spinulose, thick-walled, smooth, without a gelatinous sheath. Asexual morph: Undetermined.

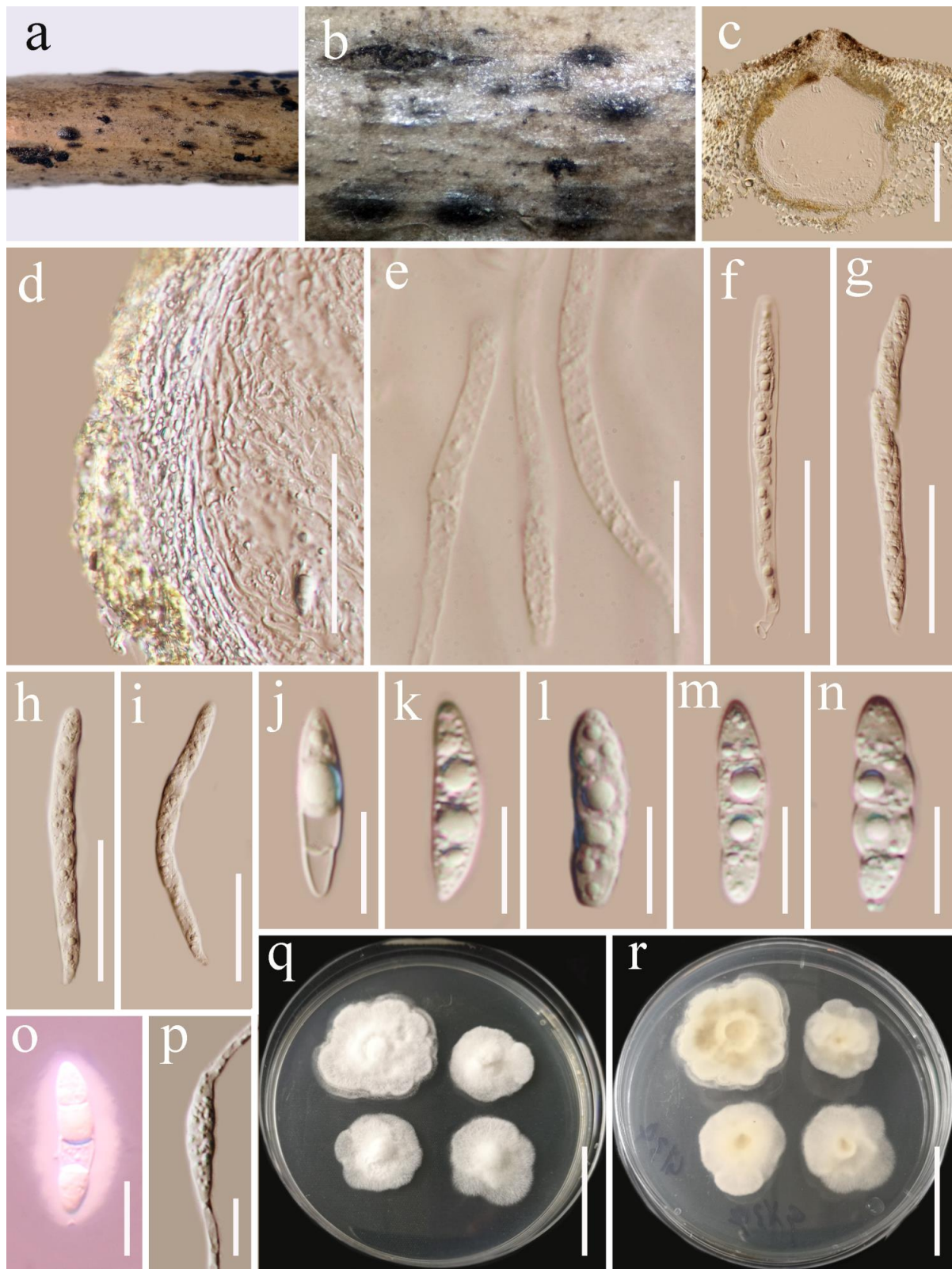


Figure 62 – *Pseudolachnella lancangensis* (HKAS 122737, holotype). a Material examined. b Appearance of ascomata on the host substrate. c Section of an ascoma. d Peridium. e Paraphyses. f–i Asci. j–n Ascospores. o Ascospore with mucilaginous sheath in Indian ink. p Germinated ascospore. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: c = 150 μ m, d, f–i = 50 μ m, e = 15 μ m, j–p = 10 μ m, q, r = 30 mm.

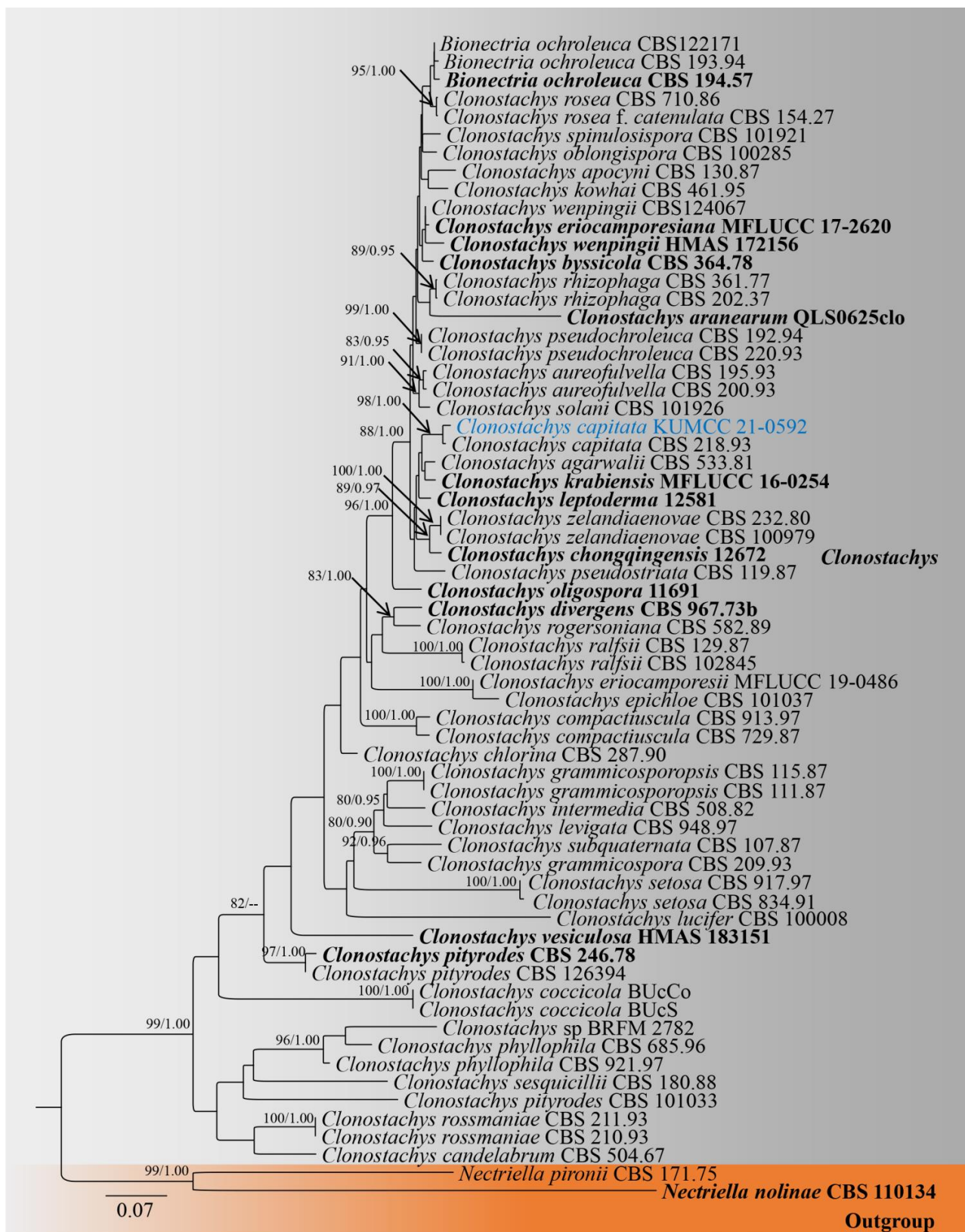


Figure 63 – Phylogram generated from ML analysis based on LSU, ITS, and *tub2* sequence data, representing *Bionectriaceae*. Related sequences are obtained following Hyde et al. (2020b). Sixty-two strains are included in the combined analyses, which comprise 1922 characters for LSU, ITS, and *tub 2* alignment. *Nectriella nolinae* (CBS 110134) and *N. pironii* (CBS 171.75) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -12223.574719 is presented. The matrix had 614 distinct alignment patterns, with 46.89% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.220809, C = 0.269031, G = 0.262409, T

= 0.247751; substitution rates AC = 1.147279, AG = 2.699630, AT = 1.218618, CG = 0.695890, CT = 4.229125, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of ascospore. Colonies on PDA, reaching 15 mm diameter after two weeks at 20–25 °C, mycelia superficial, irregular, white, yellowish at the center, flat, undulate edge, white and yellowish granular on the surface, reverse light yellow.

Material examined – China, Yunnan Province, Lijiang, on dead woody twigs of *Magnolia henryi* (Magnoliaceae), 21 December 2019, G.C. Ren, KM08 (HKAS 122744), living culture KUMCC 21-0592.

Known distribution – On bark of an unidentified tree in Japan (Schroers 2001), on dead woody twigs of *Magnolia henryi* in China (This study).

GenBank numbers – SSU: OQ168235, LSU: OQ170884, ITS: OQ158962, *tub2*: OR578552.

Notes – The isolation obtained from dead woody twigs of *Magnolia henryi* is identified as *Clonostachys capitata* with support from both morphology and phylogeny (Fig. 63). The new collection most resembles *Clonostachys capitata* (CBS 218.93) in having superficial, solitary to gregarious ascomata and clavate to subcylindrical asci with eight, ellipsoidal, single-septate, spinulose ascospores (Schroers 2001). They are conspecific. Based on the known distribution and host of *C. capitata*, the new collection is reported as a saprobe on *Magnolia henryi* in Yunnan, China, for the first time.

Xylariales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 66 (1932)

Lopadostomataceae Daranag. & K.D. Hyde [as ‘Lopadostomaceae’], in Senanayake et al., Fungal Diversity 73: 129 (2015)

Lopadostomataceae was introduced by Senanayake et al. (2015) to accommodate *Creosphaeria* and *Lopadostoma*. This family is characterised by having cylindrical-subglobose or flask-shaped, multi-peritheciate, single to multi-layered, clustered into valsoid groups ascomata; umbilicate ostioles; amorphous peridium; long, rarely branched, apically free paraphyses; unitunicate, cylindrical, pedicellate, discoid to wedged-shaped asci with J+, apical ring; uniseriate, biseriate, multiseriate or irregular, hyaline, aseptate to multi-septate, sometimes muriform, uniseriate or partially biseriate, initially hyaline, turning light brown to nearly black, unicellular, oblong, narrowly ellipsoidal, smooth-walled, germ slit full-length ascospores. The asexual morphs of this family are either coelomycetous or hyphomycetous, libertella-like or sometimes nodulisporium or geniculosporium-like synanamorph (Hyde et al. 2020d). Currently, the family consists of four genera, including *Creosphaeria*, *Jumillera*, *Lopadostoma* and *Whalleya* (Wijayawardene et al. 2022). In this study, we report a new host record of *Creosphaeria sassafras* from *Myrsine sequinii* in China.

Creosphaeria sassafras (Schwein.) Y.M. Ju, F. San Martín & J.D. Rogers, Mycotaxon 47: 223 (1993) Fig. 66

Index Fungorum number: IF360144; Facesofungi number: FoF03011

Saprobic on dead woody twigs of *Myrsine sequinii*. Sexual morph: *Ascomata* 750–900 µm high × 570–730 µm diam., ($\bar{x}$ = 840 × 670 µm, n = 5), erumpent to superficial, cover the wood surface, solitary or scattered, globose to subglobose, dull black, roughened, carbonaceous, brittle, with an ostiolar canal. *Ostioles* 160–170 × 136–150 µm ($\bar{x}$ = 170 × 144 µm, n = 5), at the centre. *Peridium* 32–50 µm wide, composed of several layers of dark brown cells of *textura intricata*. *Paraphyses* 2–4.5 µm ($\bar{x}$ = 3 µm, n = 20), abundant, filamentous, cylindrical, septate, unbranched. *Asci* 156–195 × 5.4–8.2 µm ($\bar{x}$ = 169 × 6.5 µm, n = 20), 8-spored, unitunicate, cylindrical, straight or curved, long pedicellate, apically rounded, with a J+, apical ring. *Ascospores* 8.5–10.5 × 3.4–4.3

μm ($\bar{x} = 9.4 \times 3.9 \mu\text{m}$, $n = 30$), uniseriate, unicellular, ellipsoidal to oblong or cylindrical, straight, initially hyaline, becoming light brown to brown at maturity, small guttules, smooth-walled, without a gelatinous sheath. Asexual morph: *Conidiophores* dichotomously branched, with pale brown to brown stipes that become paler upwards, smooth, loosely arranged when arising from aerial hyphae. *Conidiogenous cells* 12–32 $\times$ 1.2–2.4 μm , terminal, cylindrical, smooth, often bearing denticulate conidial secession scars, infrequently with several annellations. *Conidia* 23–34 $\times$ 1.4–2 μm , hyaline, smooth, strongly curved with flattened bases (Daranagama et al. 2018).

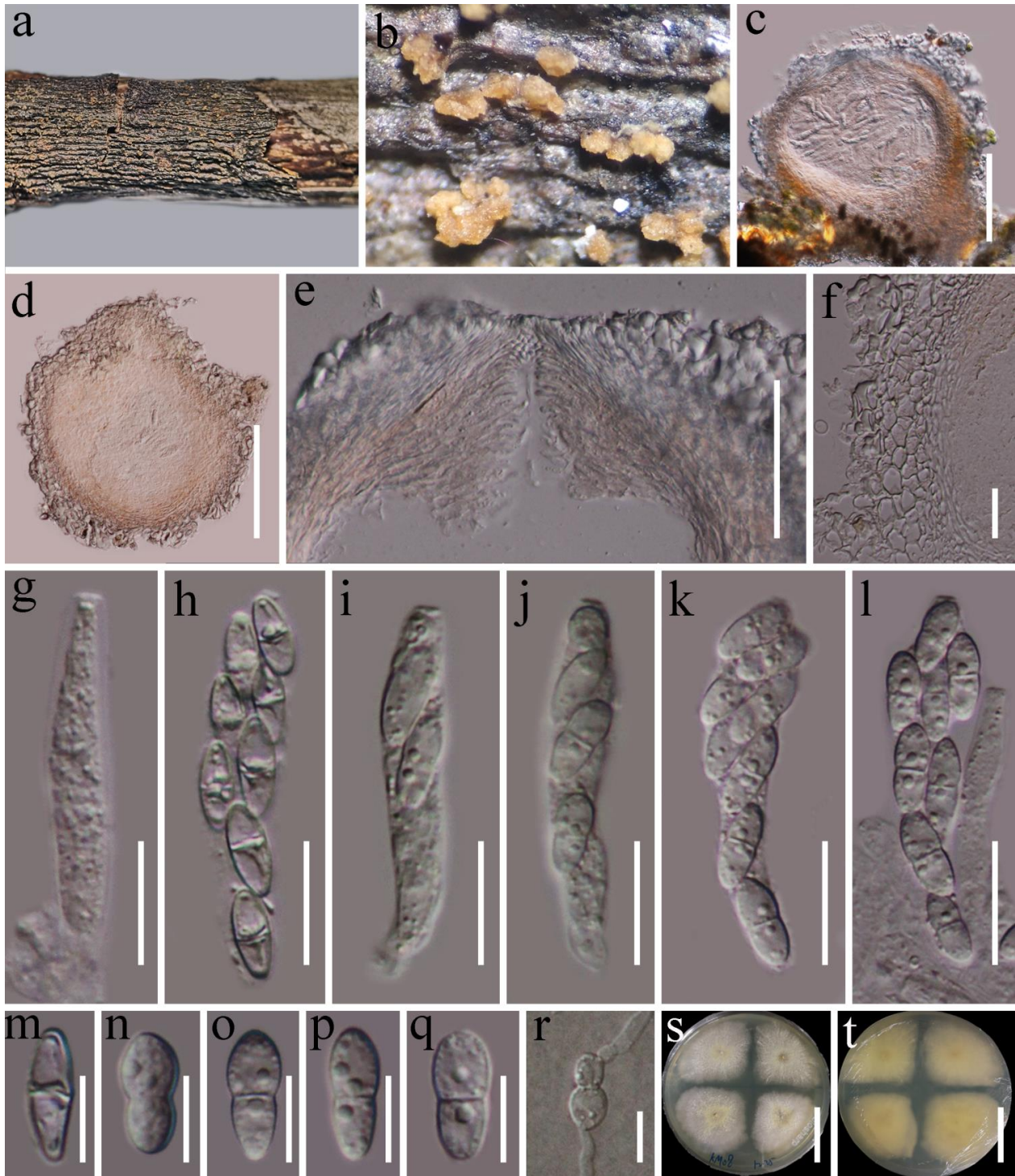


Figure 64 – *Clonostachys capitata* (HKAS 122744). a Material examined. b Appearance of ascomata on the host substrate. c, d Section of an ascoma. e Paraphyses. f Peridium. g–l Asci. m–q Ascospores. r Germinated ascospore. s, t Culture characters on PDA (s = from above, t = from below). Scale bars: c = 100 μm , d, e = 50 μm , f, g–l = 20 μm , m–r = 10 μm , s, t = 30 mm.

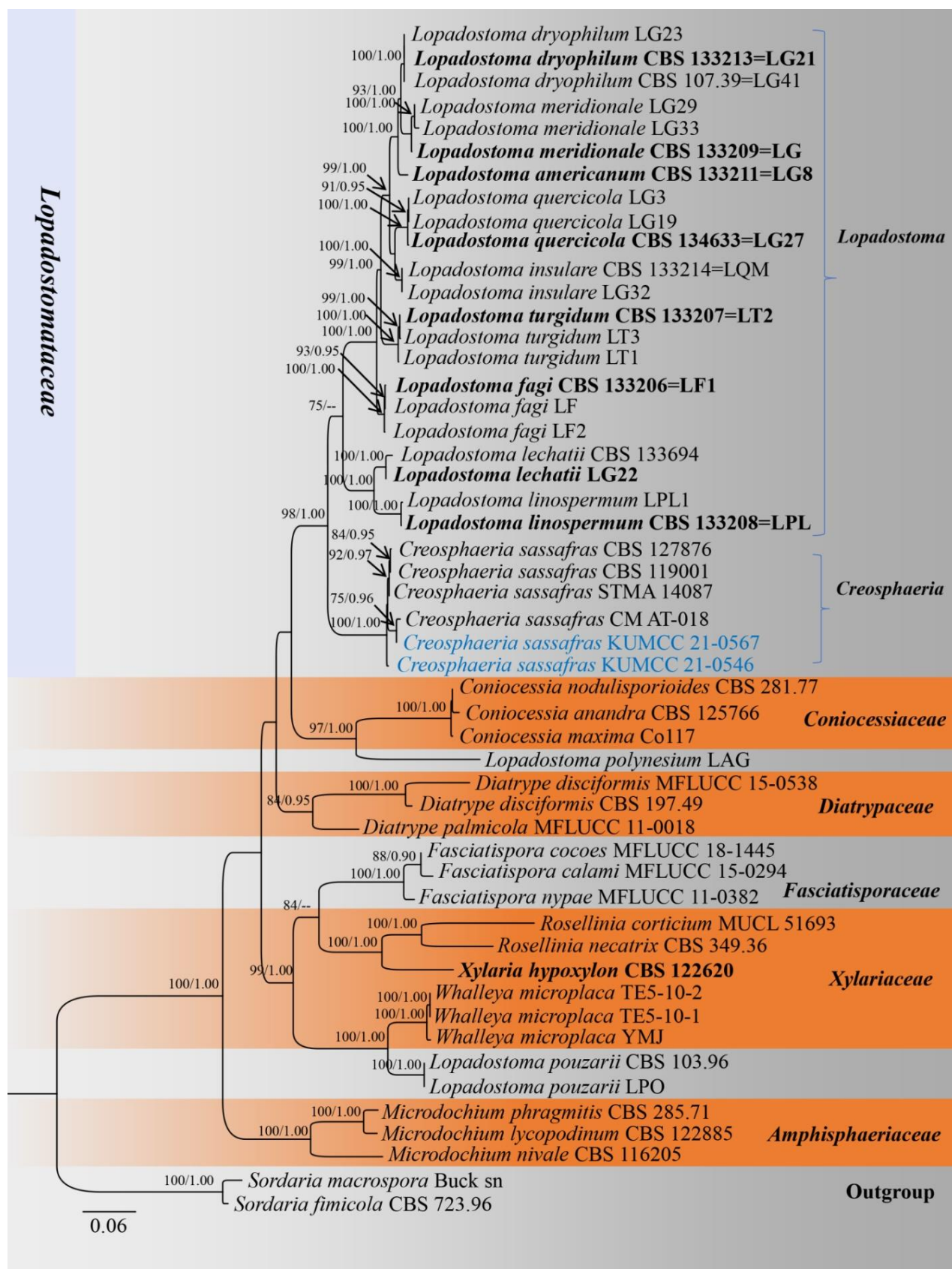


Figure 65 – Phylogram generated from ML analysis based on LSU, ITS and *rpb2* sequence data, representing *Creosphaeria* (*Lopadostomataceae*). Related sequences are obtained following Jaklitsch et al. (2014). Fifty-one strains are included in the combined analyses, which comprise 2734 characters for LSU, ITS and *rpb2* alignment. *Sordaria macrospora* (Buck s.n.) and *S. fimicola* (CBS 723.96) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood

value of -19422.149203 is presented. The matrix had 1308 distinct alignment patterns, with 25.06% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.257735, C = 0.240155, G = 0.266558, T = 0.235552; substitution rates AC = 1.278993, AG = 2.823294, AT = 1.374073, CG = 0.941424, CT = 5.402412, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of an ascospore. Colonies on PDA, reaching 20 mm diameter after two weeks at 20–25 °C, mycelia superficial, flat, medium dense, slightly raised, surface smooth, white, reverse white.

Material examined – China, Lancang, Lahu Autonomous Prefecture, Hani, on dead woody twigs of *Myrsine sequinii* (Myrsinaceae), 19 July 2020, G.C. Ren, LGY06 (HKAS 122724), living culture KUMCC 21-0546; *ibid.*, LGY39 (HKAS 122725), living culture KUMCC 21-0567.

Known distribution – Corticated wood in Brazil, Chile, Italy, Switzerland, and Taiwan Province, China (Miller 1961, Petrini & Müller 1986, Ju et al. 1993), *Fargesia denudate*, *Lindera glauca*, *Yushania dafengdingensis*, *Yushania*, *Mabianensis* in China (Helander et al. 2013), *Lauraceae* sp. in Spain (U'Ren et al. 2016), *Juniperus rigida* in Korea (Eo et al. 2018), *Fraxinus ornus* in Italy (Schlegel et al. 2018), *Panicum virgatum* in USA (Whitaker et al. 2018), *Laurus nobilis* (Lauraceae) in Spain Crous et al. (2019), *Myrsine sequinii* (Myrsinaceae) in China (This study).

GenBank numbers – KUMCC 21-0546: SSU: OQ168236, LSU: OQ170886, ITS: OQ158964, *rpb2*: OR578564; KUMCC 21-0567: SSU: OQ168237, LSU: OQ170887, ITS: OQ158965.

Notes – Our two new collections clustered with *Creosphaeria sassafras* with 100% ML bootstrap support and 1.0 BYPP value in the multi-gene phylogeny (Fig. 65). Our new collections share similar morphological characters with *C. sassafras*, such as erumpent, small stromata with orange granules, stromata arranged in linear rows with a flattened apex, a greyish ostiole and frequently oblong ascospores (Miller 1961, Petrini & Müller 1986). A comparison of nucleotide between our two new strains and *Creosphaeria sassafras* strains (CM AT 018, CBS 119001, CBS 127876 and STMA 14087) identified base pair differences of less than 1.5% for LSU, ITS and *rpb2* genes 0.36%, 0.62% and 0.5% respectively. Therefore, our new collections are identified as new host records of *C. sassafras*. *Creosphaeria sassafras* is widespread and reported as a saprobe and an endophyte (Miller 1961, Ju et al. 1993, Bills & Peláez 1996, Wendt et al. 2018, Crous et al. 2019).

Xylariales, genera incertae sedis

Nigropunctata Samarak. & K. D. Hyde, Fungal Diversity 112: 68

Nigropunctata was introduced by Samarakoon et al. (2022) based on the morphology and multi-gene phylogeny analyses of taxa in *Xylariales*. Several morpho-molecular studies have introduced anthostomella-like taxa as new genera in an attempt to resolve the polyphyletic nature of *Anthostomella* (Daranagama et al. 2015, 2016, Konta et al. 2021). However, the type species has not yet been designated formally and sequenced to provide a phylogenetic affinity (Voglmayr et al. 2018). *Nigropunctata* does not fit with either *Anthostomella limitata* or *A. tomicoides*; therefore, Samarakoon et al. (2022) introduced *Nigropunctata*. Our isolate also clustered within *Nigropunctata* with few distinct morphological characters. In our study, we introduced new species in *Nigropunctata*.

Nigropunctata yunnanensis G.C. Ren & K.D. Hyde, sp. nov.

Fig. 69

Index Fungorum number: IF901362; Facesofungi number: FoF13896

Holotype – HKAS 122747

Etymology – The specific epithet reflects Yunnan Province, from where the holotype was collected.

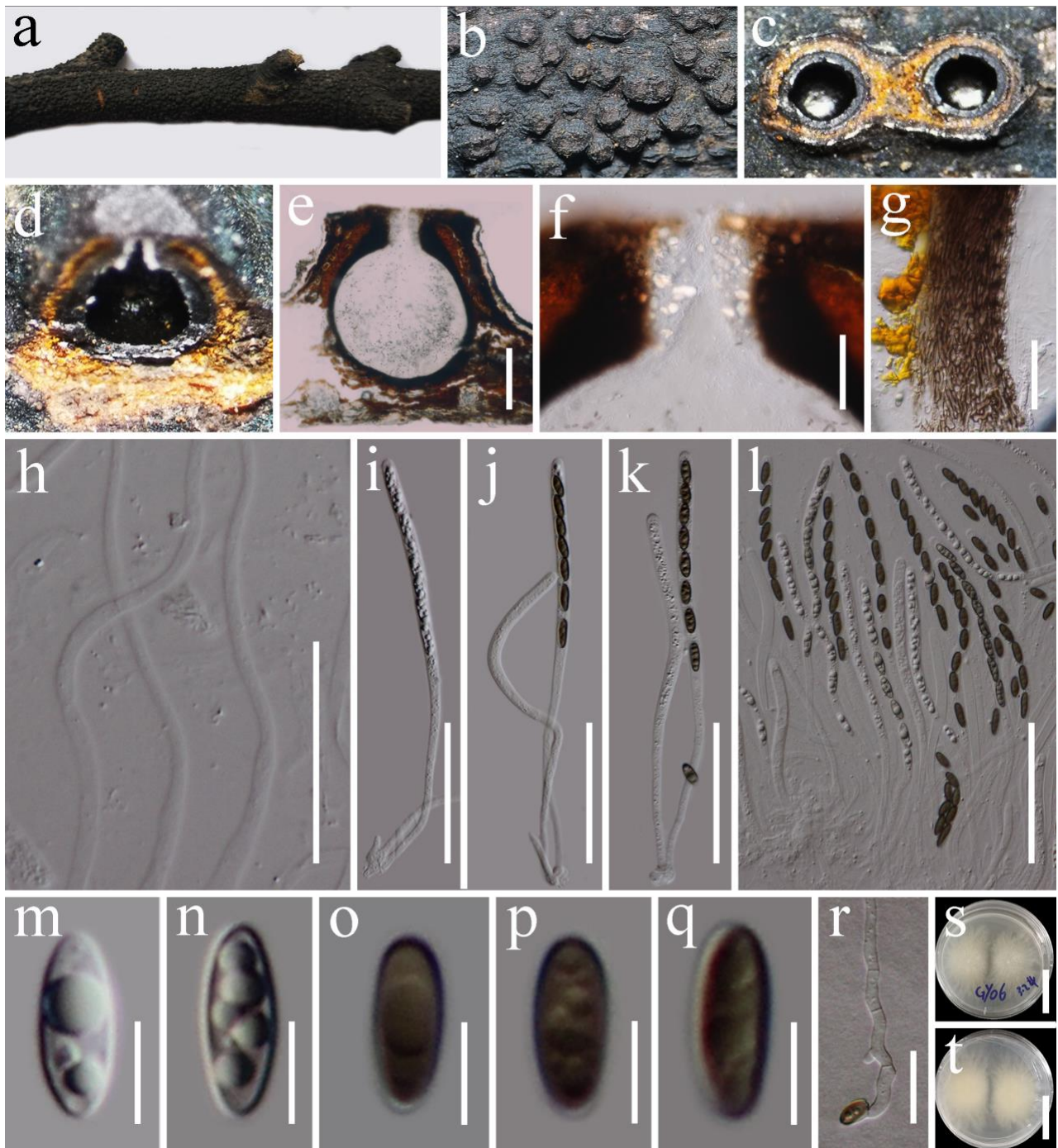


Figure 66 – *Creosphaeria sassafras* (HKAS 122724). a Material examined. b Appearance of ascostromata on the host substrate. c Transverse section of an ascostroma. d, e Vertical section of an ascostroma. f Ostiole. g Peridium. h Paraphyses. i–l Asci. m–q Ascospores. r Germinated ascospore. s, t Culture characters on PDA (s = from above, t = from below). Scale bars: e = 300 μ m, f = 100 μ m, g, h = 30 μ m, i–l = 50 μ m, m–q = 5 μ m, r = 20 mm, s, t = 20 mm.

Saprobic on dead woody twigs of *Magnolia henryi*. Sexual morph: *Ascomata* 227–288 μ m high $\times$ 244–283 μ m diam., ($\bar{x}$ = 264 $\times$ 263 μ m, n = 5), immersed to semi-immersed, papillate on the host surface, solitary or scattered, coriaceous, globose to subglobose, dark brown to dull black. *Ostiole* central, 70–80 μ m high $\times$ 51–65 μ m diam., ($\bar{x}$ = 76 $\times$ 59 μ m, n = 5). *Peridium* 8–12 μ m wide, 2–3-layered, comprising light brown cells of *textura angularis*. *Paraphyses* 2–3 μ m wide,

hyaline, filamentous, comprising cylindrical, unbranched, septate, embedded in a hyaline gelatinous matrix. Asci 120–147 × 27–37 µm ($\bar{x}$ = 133 × 32 µm, n = 20), 8-spored, unitunicate, clavate, straight or curved, apically rounded, short pedicellate. Ascospores 40–51 × 20–22.6 µm ($\bar{x}$ = 44.5 × 21 µm, n = 30), overlapping unicellular, fusiform with rounded ends, straight, initially hyaline, becoming brown to dark brown at maturity, rough-walled with small guttules. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at room temperature (25 °C). Germ tubes produced from the apical cell of an ascospore. Colonies on PDA, reaching 40 mm diameter after two weeks at 20–25 °C, mycelia superficial, circular, fimbriate, flat, entire edge, grayish white, reverse reddish brown.

Material examined – China, Yunnan Province, Lijiang, on dead woody twigs of *Magnolia henryi* (Magnoliaceae) 21 December 2019, G.C. Ren, KM16 (HKAS 122747, holotype), ex-type living culture KUMCC 21-0597.

GenBank numbers – SSU: OQ168238, LSU: OQ170888, ITS: OQ158966.

Notes – Our new isolate clustered within the *Nigropunctata* clade and separated from *Melanographium phoenicis* (MFLUCC 18-1481) (Figs 67, 68). Samarakoon et al. (2022) introduced *Nigropunctata* based on its distinct morphology and its formed independent lineage in *Xylariales*. The hyphomycetous *Melanographium* was erected based on *M. Spleniosporum* (Saccardo 1913). The taxonomic placement of *Melanographium* is unresolved, while Hyde et al. (2020b) provided sequence data for *Melanographium* and carried out multi-gene phylogeny, which showed *Melanographium* nested in *Xylariales*. *Nigropunctata* species have immersed

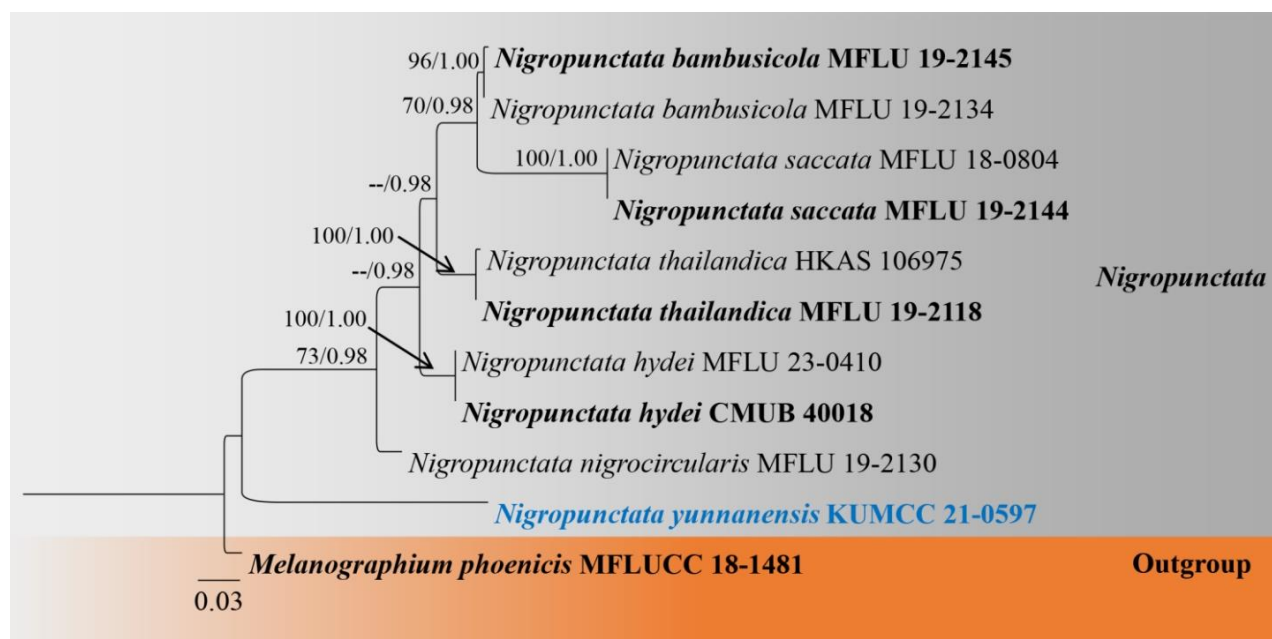


Figure 67 – Phylogram generated from ML analysis based on LSU, ITS, and *rpb2* sequence data, representing *Nigropunctata*. Related sequences are obtained following Samarakoon et al. (2023). Eleven strains are included in the combined analyses, which comprise 2474 characters for LSU, ITS and *rpb2* alignment. *Melanographium phoenicis* (MFLUCC 18-1481) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -7311.307258 is presented. The matrix had 342 distinct alignment patterns, with 18.48% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.256017, C = 0.238844, G = 0.264852, T = 0.240287; substitution rates AC = 1.458036, AG = 2.752551, AT = 1.461815, CG = 1.185047, CT = 5.554355, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

The matrix had 1883 distinct alignment patterns, with 32.94% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.254460, C = 0.236490, G = 0.266123, T = 0.242927; substitution rates AC = 1.523402, AG = 4.360938, AT = 1.479081, CG = 1.095252, CT = 6.614189, GT = 1.0000. The tree topology of the ML analysis is similar to the Bayesian analysis. Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.95 (the rounding of values to 2 decimal proportions) are labelled on the nodes. Strains of the newly described species are in blue, while type strains are in bold.

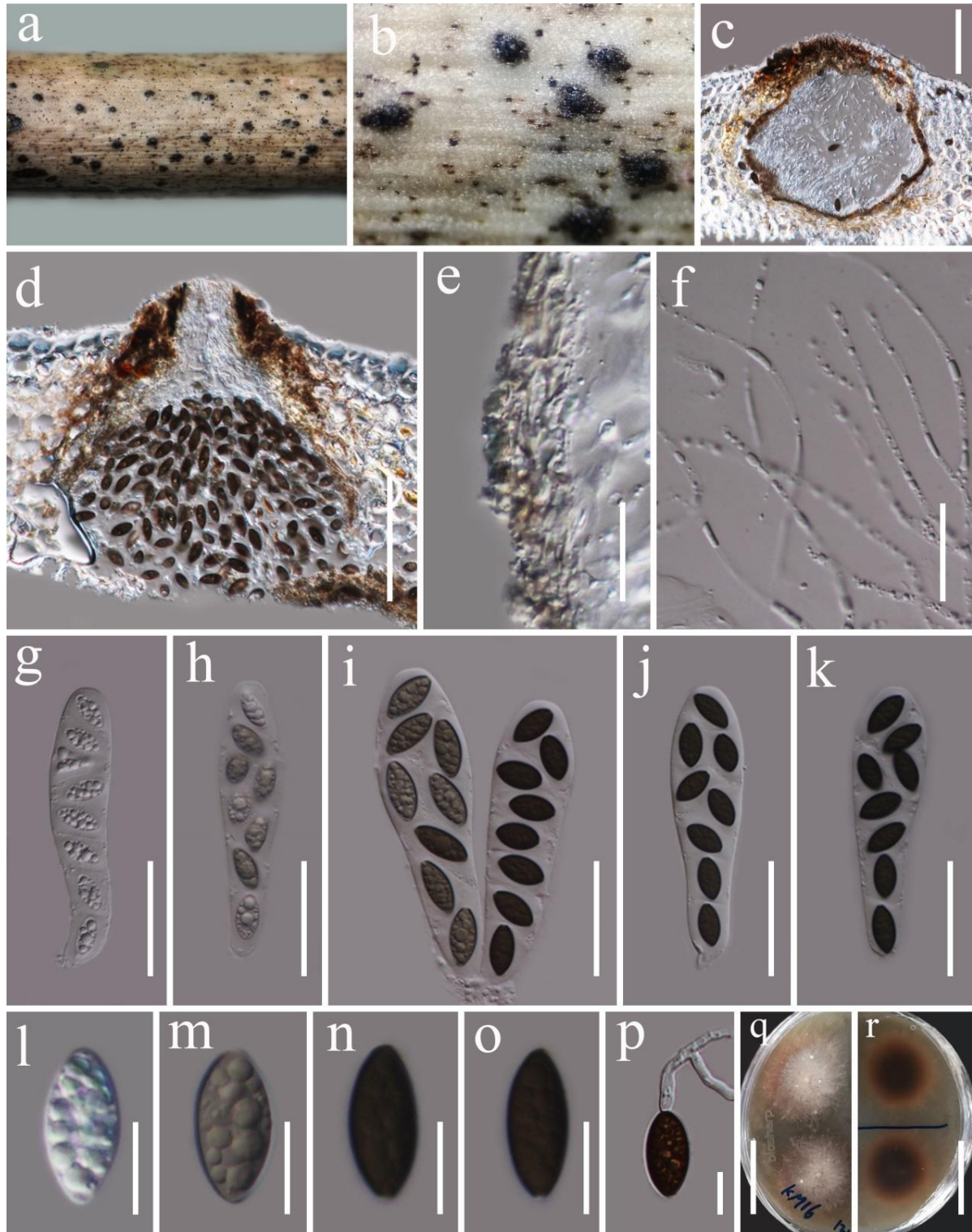


Figure 69 – *Nigropunctata yunnanensis* (HKAS 122747, holotype). a Material examined. b Appearance of ascomata on the host substrate. c, d Section of through ascoma. e Peridium.

f Paraphyses. g–k Asci. l–o Ascospores. p Germinated ascospore. q, r Culture characters on PDA (q = from above, r = from below). Scale bars: c, d = 100 μ m, e = 20 μ m, f = 30 μ m, g–k = 50 μ m, l–p = 10 μ m, q, r = 30 mm.

ascomata with a thick clypeus, white or yellow ectostroma, cylindrical, short pedicel, apically rounded asci with J+, discoid or inverted, hat-shaped, apical ring and uniseriate, cylindrical to broadly ellipsoidal, aseptate, ascospores with a germ slit, while our species *N. yunnanensis* have clavate, apically rounded asci and overlapping, fusiform ascospores with rounded ends and small guttules. In a comparison of nucleotide between our new strains (KUMCC 21-0597) and *Nigropunctata bambusicola* (MFLU 19-2145), *N. hydei* (CMUB 40018), *N. nigrocircularis* (MFLU 19-2130), *N. saccata* (MFLU 19-2144) and *N. thailandica* (MFLU 19-2118) identified base pair differences for LSU gene 3.2% (23/710), 3.3% (25/747), 3.5% (26/747), 8.8% (66/747) and 3.6% (27/747) respectively, ITS gene 10.8 % (57/526), 11.1% (59/529), 8.9% (44/493), 20.5% (101/493), 12.3% (66/535). Therefore, *N. yunnanensis* is introduced as a new species based on its distinct morphology and phylogenetic analyses of a combined LSU, ITS, and *rpb2* dataset.

DISCUSSION

This study describes saprobic ascomycetes on woody litter, mainly collected in Southern China, which belongs to the GMS region. Based on morphological comparisons and multi-gene phylogenetic analyses, herein we introduce 15 new species, 26 new records belonging to 24 families and 31 genera. Furthermore, the sexual morph of *Fuscostagonospora banksiae* from *Rhododendron rubiginosum* (Ericaceae) and *Acrocallymma magnolia* from *Parashorea chinensis* (Dipterocarpaceae) are reported for the first time.

The GMS is one of the world's richest biodiversity hotspots, and the forests in the GMS are simultaneously among the richest forests in the world in terms of biodiversity (Asian Development Bank 2012). Therefore, studying fungal diversity in this area is worthwhile since it can contribute to discovering more about its intricate ecological variety. In the present study, samples were collected from 22 plant species belonging to 12 plant families, which are dominant in this area (<https://powo.science.kew.org/>). The 12 plant families comprised Boraginaceae, Combretaceae, Dipterocarpaceae, Ericaceae, Euphorbiaceae, Fagaceae, Lauraceae, Magnoliaceae, Myristicaceae, Myrsinaceae, Proteaceae and Theaceae. The distribution of the fungal diversity was not uniform among these hosts. Dipterocarpaceae, Ericaceae, and Fagaceae harboured more fungal species (7, 7 and 14, respectively). *Castanopsis* is the most speciose host genus, with nine species identified in this study. From the current study, *Angustimassarina kunmingense* was recorded from the two host plants, *Quercus kingiana* (Fagaceae) and *Rhododendron rubiginosum* (Ericaceae), *Corylicola italic* from *Quercus kingiana* (Fagaceae) and *Cryptocarya hainanensis* (Ericaceae), *Plenodomus sinensis* from *Lyonia ovalifolia* (Ericaceae) and *Castanopsis orthacantha* (Fagaceae), and *Palmiascoma gregariascomum* is introduced with both asexual and sexual morphs from *Cryptocarya hainanensis* (Lauraceae). Our study shows that the fungal distribution in this area is diverse. In addition, this study is important to identify host-fungal relationships.

Many studies indicated that the selected GMS regions like Southwestern China and Northern Thailand have a high fungal diversity, especially *Dothideomycetes* (Schoch et al. 2009, Hyde et al. 2013). Numerous studies have reported the capability of *Dothideomycetes* to survive in extreme environments, such as high temperatures, severe droughts, and high levels of solar radiation (Pem et al. 2021). Murgia et al. (2019) reported Ascomycota was the most abundant phylum identified in all the samples from hot desert sands, with *Dothideomycetes* as its dominant group. Therefore, this group of fungi played an essential role in the desert ecosystem and extreme conditions on rock surfaces (Ruibal et al. 2009). In this study, even in the forest, *Dothideomycetes* were the dominant group of saprobic fungi on woody litter in Southwestern China.

Woody litter fungi have been commonly found in aquatic and terrestrial habitats worldwide, and fungi are the major woody litter decomposers (Bucher et al. 2004). Therefore, woody litter inhabiting fungi gathered more attention. The early studies have primarily focused on aquatic

environments, including freshwater and marine habitats (Kohlmeyer 1984, Hyde et al. 2000, Fryar et al. 2004, Sridhar & Maria 2006, Jones & Pang et al. 2012, Hyde et al. 2016, Devadatha et al. 2017, 2021, Bao et al. 2018, Jones et al. 2019, Luo et al. 2019, Dong et al. 2020, Calabon et al. 2022, 2023a, Shen et al. 2022, Yang et al. 2023). Several studies have revealed a significantly higher conidial release in submerged leaf litter in streams compared to terrestrial leaf and woody litter (Sharathchandra et al. 2020), and rivers as potentially overlooked avenues of dispersal for terrestrial fungi (LeBrun et al. 2018). This suggests that woody litter fungi in aquatic and terrestrial ecosystems may have great overlap in fungal diversity. However, Kodsueb et al. (2016) investigated the fungal communities on *Magnolia liliifera* wood in terrestrial and freshwater habitats in Northern Thailand and found that the fungal communities on wood in freshwater were distinct from those in the terrestrial habitat. In our study, only one species, *Nigrograna magnolia*, was found on both submerged wood and terrestrial woody litter, while the remaining 40 species were exclusively found on terrestrial woody litter. The disparity in overlap rates may be attributed to the relatively fewer studies on terrestrial saprophytic fungi.

Host-exclusivity and host-recurrence described saprobe-plant interactions instead of host-specificity (Zhou & Hyde 2001, de Silva et al. 2022). However, woody litter fungi were generally not studied enough to be able to provide a conclusion regarding the host-exclusivity, and most woody litter fungi have broad host ranges in tropical and subtropical areas (Lindblad 2000, Tennakoon et al. 2021b, de Silva et al. 2022). Therefore, host-exclusivity interactions might not be observed among woody litter fungi. For example, *Plenodomus sinensis* was found in woody litter (Tennakoon et al. 2017, Phookamsak et al. 2019, Doilom et al. 2021 and this study) and soil (Moe et al. 2020). *Boeremia linicola* was found in woody litter and on leaves as a pathogen (Guan et al. 2021, Lee et al. 2022). *Palmiascoma qujingense* was found in woody litter and on *Juglans regia* as a pathogen (Wang et al. 2022). We recorded 41 woody litter fungi from 22 tree species, of which 17 species showed signs of host specialization in the current study. However, these species were new, and we believe that the host range will continue to increase with the number of studies and new collections. Among the other 24 fungal taxa recorded as new host records, more than one host is recorded elsewhere. Overall, the host-exclusivity of woody litter fungi found in our study can help us to better understand the ecology and functioning of forest ecosystems.

The woody litter fungi have an incubation period in plant tissues as endophytes, of which some fungi become saprobes after the plant dies, and some could also become pathogens (de Silva et al. 2022). In this study, most of the woody litter fungi found were saprobes on various plants, however, some species displayed different lifestyles. For example, *Boeremia lignicola*, previously reported as a pathogen in numerous significant plant species, was identified as a saprobe from *Cinnamomum glanuliferum* in our study. This is the first report of *Boeremia linicola* from *Cinnamomum glanuliferum*. *Stagonosporopsis* species have been recorded as significant plant pathogens (Vaghefi et al. 2012, Jayawardena et al. 2019). However, our study revealed the isolation of a novel species, *Stagonosporopsis lijiangensis*, from dead woody twigs of *Quercus serrata* (Fagaceae). *Palmiascoma qujingense* has previously been reported as a pathogen and saprobe in China (Wang et al. 2022, this study). *Plenodomus sinensis* has been reported from soil and woody litter (Tennakoon et al. 2017, Phookamsak et al. 2019, Doilom et al. 2021, this study). *Creosphaeria sassafras* is widespread and reported as a saprobe and an endophyte (Wendt et al. 2018, Crous et al. 2019, this study). Therefore, saprophytic, endophytic and pathogenic fungi have distinct lifestyles and ecological roles but can exhibit some overlap in their interactions with plants and other organisms. Understanding the relationship between these three functional groups of fungi can provide valuable insights into ecosystem processes and plant-fungal interactions.

Over the past few years, many studies found new species from woody litter in tropical and temperate regions of the GMS (Southern China and Northern Thailand), especially the freshwater fungi growing on woody litter have increased rapidly (Luo et al. 2018, Bao et al. 2019, Hapuarachchi et al. 2019, Dissanayake et al. 2020, Dong et al. 2020, Monkai et al. 2020, Yasanthika et al. 2020, Mortimer et al. 2021, Wanasinghe et al. 2020a, 2021, Ren et al. 2022, Hyde et al. 2023, Konta et al. 2023). Only a few investigations of saprobic fungi on terrestrial wood have

been reported (Fryar et al. 2004, Kodsueb et al. 2008a, 2019, Ren et al. 2022). Our study collected samples from both the tropical region, represented by Xishuangbanna, China and Tak, Thailand and the temperate regions, which include Baoshan, Lancang, Lincang, Lijiang and Diqing (China, Yunnan Province). Our results show that only three species overlapped between temperate and tropical regions, viz., *Palmiascoma gregariascomum*, *Nigrograna magnolia*, and *Ramusculicola thailandica*. Despite the differences between tropical and temperate regions, some woody litter fungi are found in both environments. These fungi may have broader ecological tolerance and adaptability, allowing them to thrive in diverse conditions. It is important to note that while some overlapping species exist, the overall composition and diversity of woody litter fungi communities can still differ significantly between tropical and temperate regions. Further research is needed to understand the factors shaping these communities and their ecological roles in different environments.

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